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Abstract: The aspergilli comprise a diverse group of filamentous fungi spanning over 200 million years of evolution. Here we report the genome sequence of the model organism *Aspergillus nidulans*, and a comparative study with *Aspergillus fumigatus*, a serious human pathogen, and *Aspergillus oryzae*, used in the production of sake, miso, and soy sauce. Our analysis of genome structure provided a quantitative evaluation of forces driving long-term eukaryotic genome evolution. It also led to an experimentally validated model of mating-type locus evolution, suggesting the potential for sexual reproduction in *A. fumigatus* and *A. oryzae*. Our analysis of sequence conservation revealed over 5,000 non-coding regions actively conserved across all three species. Within these regions, we identified potential functional elements including a previously uncharacterized TPP riboswitch and motifs suggesting regulation in filamentous fungi by Puf family genes. We further obtained comparative and experimental evidence indicating widespread translational regulation by upstream open reading frames. These results enhance our understanding of these widely studied fungi as well as provide new insight into eukaryotic genome evolution and gene regulation.

The aspergilli are a ubiquitous group of filamentous fungi spanning over 200 million years of evolution. Among the over 185 aspergilli are several that have an impact on human health and society, including 20 human pathogens as well as beneficial species used to produce foodstuffs and industrial enzymes.[1] Within this genus, *A. nidulans* has a central role as a model organism. In contrast to most aspergilli, *A. nidulans* possesses a well-characterized sexual cycle and thus a well-developed genetics system. Half a century of *A. nidulans* research has advanced the study of eukaryotic cellular physiology, contributing to our understanding of metabolic regulation, development, cell cycle control, chromatin structure, cytoskeletal function, DNA repair, pH control, morphogenesis, mitochondrial DNA structure and human genetic diseases.

We present here the genome sequence for *A. nidulans*, and a comparative genomics study with two related aspergilli: *A. fumigatus*[2] and *A. oryzae*.[3] *A. fumigatus* is a life-threatening human pathogen, and *A. oryzae* is used in the production of sake, miso, and soy sauce. *A. oryzae* and *A. fumigatus* lack known sexual cycles, and their study relies on *A. nidulans* as a genetic model. Our analysis of these organisms focused on the genomic bases of their differing physiologies, while investigating their common eukaryotic biology. Our results yield new insights into eukaryotic genome evolution, the evolution of mating-type loci, the potential for sexual reproduction in the two asexual species, and the role of conserved sequence elements in gene regulation.

Genome assembly and annotation

The genome sequence of *A. nidulans* was assembled from deep whole-genome shotgun (WGS) coverage obtained by paired-end sequencing from a variety of clone types (see Methods). An average of 13× sequence coverage was generated including ×3 coverage produced and provided by Monsanto. The Arachne package (http://0-www.broad.mit.edu/wga/) was used to assemble the sequence, and the resulting assembly consists of 248 sequence contigs with an N50 length of 282 kilobases (kb) (that is, 50% of all bases are contained in contigs of at least 282 kb). Contigs were assembled into 89 scaffolds with a total length of 30.06 megabases (Mb) (including gaps between contigs) and an N50 length of 2.44 Mb. A total of 28.5 Mb (95%) of the assembly was anchored to the *A. nidulans* genetic map[4, 5] through meiotically mapped markers with sequence and markers located by haploidization or hybridization to electrophoretically separated chromosomes (see Supplementary Information). By comparison with previously published pulse-field gel electrophoresis data, we estimate that the assembly comprises 96.3% of the complete genome. The assembly was annotated using the Calhoun system, as described in the Methods and Supplementary Information.

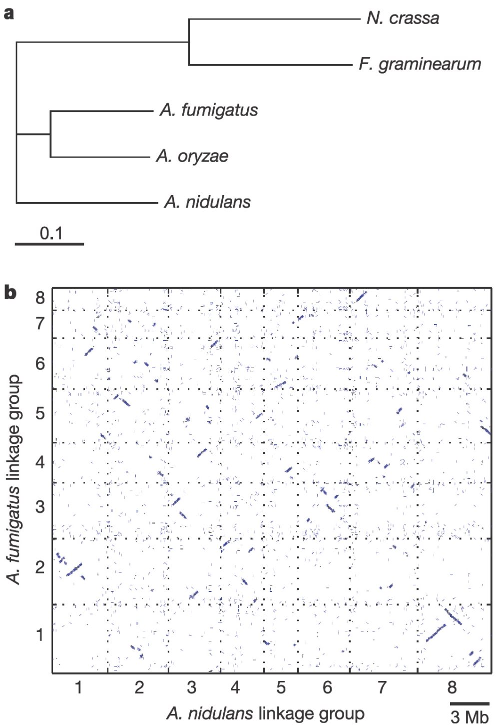


Figure 1. Phylogenetic tree and representative dot plot. **(a)** Phylogenetic tree showing the relationship between three *Aspergillus* species compared using *N. crassa* and *F. graminearum* as an outgroup. Branch lengths correspond to substitutions per site calculated using a maximum likelihood approach. An identical topology was predicted using *C. immitis* as an outgroup. **(b)** Dot plot of *A. nidulans* (horizontal) and *A. fumigatus* (vertical) genomes. Axes represent the concatenation of all chromosomes for the corresponding genome. Gridlines indicate the boundaries between chromosomes and axis labels indicate chromosome number. Elements in the dot plot represent protein homology translated to genomic coordinates.

Phylogenetic relationship

Previous work based on large subunit rDNA data has led to a widely accepted phylogeny of the aspergilli in which *A. nidulans* and *A. oryzae* are more related to one another than *A. fumigatus*.[6] However, single gene phylogenies can contradict organismal phylogenies.[7] In principle, whole-genome data provide greater resolving power by allowing trees to be constructed based on concatenated sets of genes.[7] Using this approach to study the relationship of the three aspergilli, we find support for an alternative phylogeny.[8] (Figure 1a)

We established this relationship using a set of 3,034 predicted orthologues across the three aspergilli, *Neurospora crassa* and *Fusarium graminearum*. We constructed trees for 75 randomly selected sets of 20 concatenated genes,[7] using the *N. crassa* and *F. graminearum* genes to root the trees (see Methods). All 75 cases produced the phylogeny shown in Figure 1a in which *A. fumigatus* and *A. oryzae* are sister taxa and *A. nidulans* branches earlier. This phylogeny is further supported by 86% of trees built for each of the 3,034 orthologues individually. Consistent with this phylogeny, *A. fumigatus* has over twice as many genes with top Blast hits to *A. oryzae* than to *A. nidulans*, and *A. oryzae* has almost twice as many genes closer to *A. fumigatus* than *A. nidulans*. *A. nidulans* has roughly a similar number of top hits to *A. fumigatus* and *A. oryzae*. To confirm further the rooting of the tree, we repeated the analysis using predicted gene fragments (see Methods) from the genome sequence of *Coccidioides immitis* as an outgroup (which is closer to the aspergilli than *N. crassa* and *F. graminearum*). Ninety-four per cent (34 out of 36) of 50-gene phylogenies with *C. immitis* as the outgroup support the relationship of Figure 1a, as do 60.8% (93 out of 153) of single gene phylogenies (only 21% support the rDNA phylogeny).

Overall genome and proteome comparison

Although in the same genus, the three aspergilli differ considerably in their genome sequences. Predicted orthologues shared by all three species (three-way orthologues) display an average of only 68% amino acid identity. *A. fumigatus* and *A. oryzae* share 70% identity, and each has 66–67% identity with *A. nidulans*. This protein identity is comparable to that between mammals and fish,[9] which diverged ~450 million years ago. The three species also differ considerably in genome size (Table 1). The largest, *A. oryzae* (36 Mb), is 31% bigger than the smallest, *A. fumigatus* (28 Mb), and 24% bigger than *A. nidulans* (30 Mb). This difference seems to be due to an acquisition of sequence in *A. oryzae*[3] rather than loss in both *A. nidulans* and *A. fumigatus*. Finally, the genomes show extensive structural reorganization (Figure 1b).

Conserved synteny and genome evolution

These three aspergilli provide an opportunity to study eukaryotic genome evolution over a divergence approaching the limit of conserved long-range synteny. To characterize pairwise conserved synteny, we used an algorithm based on hierarchical clustering that delineates regions of conserved synteny while also retaining information about internal micro-rearrangements (see Methods). Using this method, the majority (77–79%) of each genome assembly could be mapped to conserved syntenic blocks with at least one other genome (Table 2). Figure 2 shows a projection of the homologous blocks onto the chromosomes of *A. nidulans* and, contrasted with Figure 1b, illustrates the considerable extent of conserved synteny despite extensive rearrangement.

The results of this analysis reveal two notable trends. First, large regions lacking detectable long-range synteny are readily apparent. As has been observed for mammals, nematodes and yeasts,[10] repeats and subtelomeric sequences are associated with these heavily rearranged regions. This may have specific implications for fungi, as subtelomeric regions in the aspergilli are enriched for secondary metabolite genes thought to have a role in

Table 1. Comparison of genome characteristics

Genome characteristic	*A. nidulans*	*A. fumigatus*	*A. oryzae*
General			
Assembly size (bp)	30,068,514	27,980,910	37,047,050
G+C (%)	50	49	48
Protein coding genes	9,541	9,926	14,063
Protein coding genes >100 amino acids	9,396	9,009	12,074
Predicted protein coding sequences >100 amino acids			
Coding (%)	50	49	45
Gene density (1 gene every *n* bp)	3,151	2,938	2,613
Median gene length (mean)	1,547 (1,868)	1,389 (1,644)	1,152 (1,414)
Average number of exons per gene	3.6	2.8	2.9

niche adaptation and virulence. The rapid rearrangement of subtelomeric regions may facilitate the species-specific evolution of these genes (Supplementary Information).

The second notable trend is the distribution of lengths of unbroken regions between micro-rearrangements within pairwise syntenic blocks. The random breakage model of genome evolution predicts that such lengths should be exponentially distributed. Although the mean breakpoint lengths differ, in all three pairwise comparisons the distribution of lengths shows close agreement with the model prediction (Supplementary Information). It thus seems that syntenic blocks, comprising the majority of the *Aspergillus* chromosomes, are evolving in a manner consistent with random breakage.

For each pairwise comparison, the third *Aspergillus* genome allows the determination of rearrangements specific to each branch of the unrooted tree (see Methods). The results of this analysis provide a quantitative estimate of the different rearrangements contributing to long-term eukaryotic genome evolution (Figure 3).

Structural evolution not correlated with molecular evolution

In vertebrates, nematodes and arthropods, it has been reported that the rates of structural evolution and nucleotide evolution are correlated.[11, 12, 13] However, our analysis of the *Aspergillus* genomes suggests that this expected correlation does not always hold for eukaryotes.

The data in Figure 3 reveal a considerably higher overall rate of genome reorganization in the lineage of *A. oryzae* compared to *A. fumigatus*. Nearly all categories of disruption are at least twofold greater in *A. oryzae* relative to *A. fumigatus*. For example, *A. oryzae* displays a more than twofold greater rate of insertion than *A. fumigatus*. This is consistent with the larger genome size of *A. oryzae*.[3] Surprisingly, our analysis also indicates that chromosomal breaks are more common in *A. oryzae* than *A. fumigatus*. Although apparent intrachromosomal rearrangements could arise from successive inversion events, this cannot explain interchromosomal rearrangements. These interchromosomal breaks are also not the result of assembly error, as confirmed by optical mapping[3] and polymerase chain reaction (PCR) validation of eight predicted interchromosomal breaks.

In contrast, several measures indicate that the rates of amino acid evolution in predicted orthologues are similar between these two species. An examination of predicted three-way orthologues shows that the distribution of amino acid identity is roughly similar for both *A. oryzae* and *A. fumigatus* compared to *A. nidulans*, as are non-synonymous divergences (Supplementary Information). In addition, branch lengths predicted from phylogenetic trees (see above) indicate a comparable rate of substitution for both *A. oryzae* and *A. fumigatus*. Taken together, these data lead to the conclusion that structural and molecular evolution in the aspergilli is not correlated. A similar conclusion has been reached in the analysis of two microsporidian genomes, although in this case gene evolution seems to be accelerated relative to genome rearrangement.[14] Thus, large-scale and small-scale evolutionary processes in eukaryotes can operate at different relative rates in a species-specific manner.

Sex and the evolution of the mating-type loci

Unlike *A. nidulans*, which has a known sexual cycle, *A. fumigatus* and *A. oryzae* are only known to reproduce through asexual mitotic spores. We sought insight into the evolution of this apparent difference by comparing the three genomes. Our results, in conjunction with an accompanying paper and another study,[2, 15] suggest that both *A. fumigatus* and *A. oryzae* may be capable of sexual reproduction.

Sexual reproduction in ascomycete filamentous fungi is governed, in part, by two different mating-type genes that establish sexual compatibility: one gene encodes a protein with a high mobility group (HMG) domain, whereas the other encodes a protein with an alpha box domain. We refer to these genes here as the HMG and alpha mating-type genes, and to their chromosomal locations as MAT loci. Homothallic fungi typically possess both mating-type genes and are self-fertile. Heterothallic fungi possess only one mating-type gene and require a partner with a different mating-type gene. In heterothallics, the two mating-type genes typically occupy the same chromosomal location in different haploid genomes but lack sequence similarity, and are thus termed idiomorphs rather than alleles.[16]

A. nidulans is known to be homothallic, and both HMG and alpha mating-type genes have been identified.[17, 18] Our analysis confirmed that the HMG and alpha loci are unlinked, which is unusual although not unprecedented in homothallic fungi.[19] We identified a single HMG mating-type gene in *A. fumigatus*, as previously reported,[20] and a single alpha mating-type gene in *A. oryzae*.

A comparison of all four MAT loci revealed extensive conserved synteny (Figure 4a). The *A. oryzae* alpha locus and the *A.*

Table 2. Characteristics of pairwise conserved synteny

Reference	Coverage (Mb) (percentage of reference)*				Maximum/mean block length (kb)‡		
	A. nidulans	*A. fumigatus*	*A. oryzae*	Either †	*A. nidulans*	*A. fumigatus*	*A. oryzae*
A. nidulans	–	20.5 (68)	20.4 (68)	21.6 (72)	–	175	114
A. fumigatus	20.4 (73)	–	20.7 (74)	21.5 (77)	2,429	–	168
A. oryzae	23.3 (63)	24.3 (66)	–	25.4 (69)	943	1,159	–

* Coverage of reference organism assembly by pairwise conserved syntenic blocks (>10 kb in length) to each target genome.

† Coverage of reference organism assembly by pairwise conserved syntenic blocks (>10 kb in length) in either other genome.

‡ Upper right half shows mean blocks sizes and lower left half shows maximum sizes across all blocks using either organism as reference.

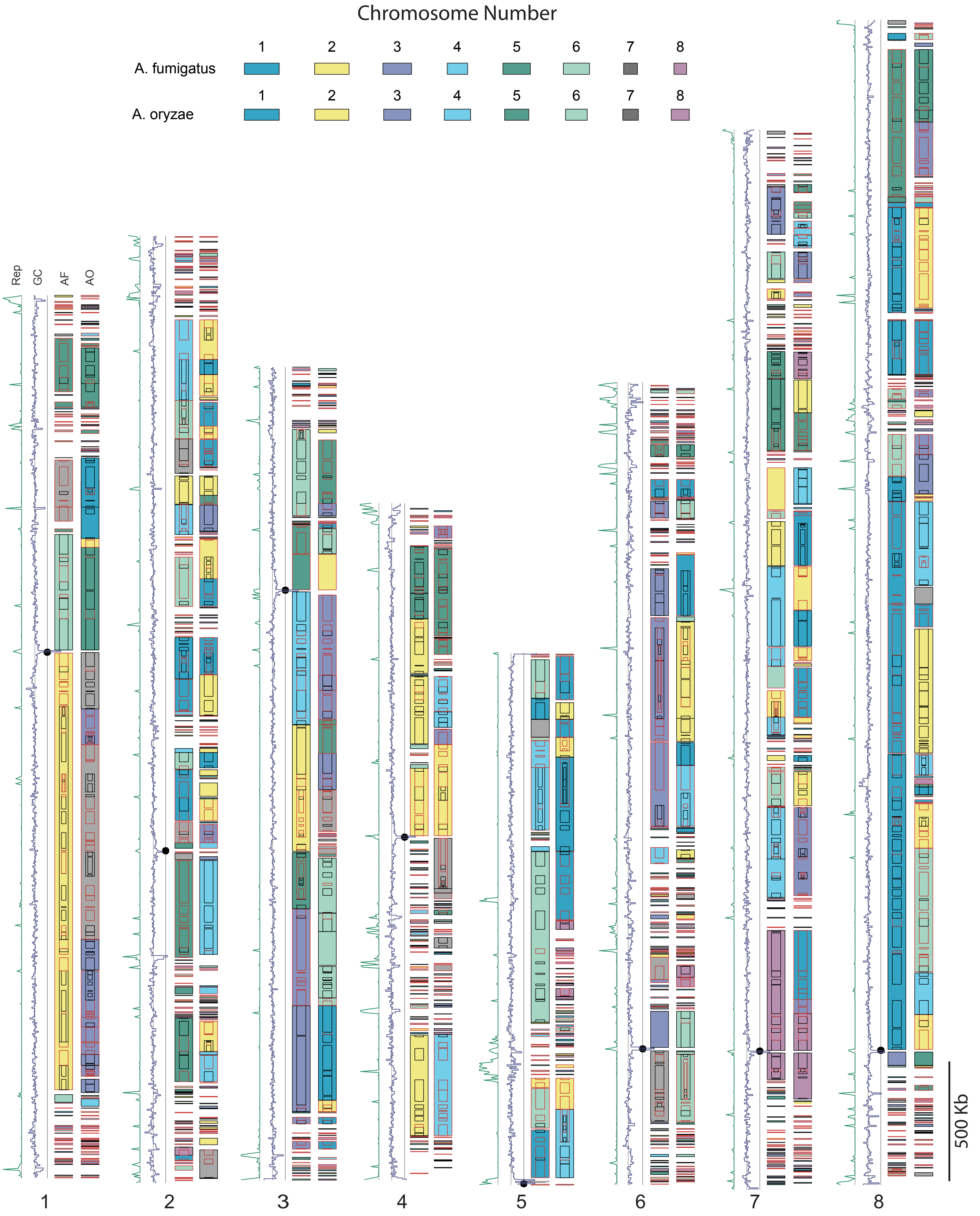


Figure 2. *Aspergillus* comparative map. Conserved synteny between *A. nidulans* and *A. oryzae* and *A. fumigatus*. Syntenic regions are represented by two vertical columns of colored blocks. The left and right columns represent syntenic blocks to *A. fumigatus* and *A. oryzae*, respectively, colored by chromosome as indicated by the key. Nested blocks show synteny at finer resolutions. Blocks outlined in black are in opposite orientations in *A. nidulans* relative to those in red. Red blocks in black blocks (and vice versa) represent inversions. The green and purple lines display repeat density (Rep) and G + C content (G + C) in *A. nidulans*, both in 5-kb windows with increasing values to the left. Black circles represent centromeres.

fumigatus HMG locus display conserved synteny over 1.7 Mb on either side of the mating-type genes. Within this region of conserved synteny, the two mating-type genes occupy nearly identical positions, although offset with different orientations. Furthermore, one flank of both the *A. fumigatus* and *A. oryzae* loci is syntenic with 409 kb of the *A. nidulans* HMG locus downstream region, whereas the other flank is syntenic with 34 kb of the *A. nidulans* alpha locus downstream region (Figure 4a). The four loci also show conservation of a number of genes associated with MAT loci in other species including *N. crassa* or one of nine yeast species previously analyzed.[21]

Extending the analysis to 215 genes implicated in the fungal mating process, pheromone response, meiosis and fruiting body development revealed that every gene (except for the mating-type genes) that can be identified in *A. nidulans* is also present in both *A. fumigatus* and *A. oryzae* (Supplementary Information), including several genes for which the only known function is related to sexual reproduction.

Although sexual reproduction may have been lost very recently in both *A. fumigatus* and *A. oryzae*, providing one explanation for the residual presence of mating process genes, these data suggested the possibility that both *A. fumigatus* and *A. oryzae* may be capable of sexual reproduction. Moreover, the pattern of synteny among the four MAT loci leads to an evolutionary scenario for this hypothesis, as shown in Figure 4b. According to this model, it is predicted that *A. oryzae* and *A. fumigatus* isolates exist with the opposite mating-type genes to those present in the strains that were sequenced. In addition, these opposite mating-type genes should be present at the identical locus, consistent with a heterothallic idiomorphic configuration.

As reported in detail in another study,[15] these predictions have been experimentally verified. Using a PCR-based multiplex mating-type assay, isolates of both mating types of *A. fumigatus* and *A. oryzae* were identified. For both species, the opposite MAT locus from the complete genome was sequenced and demonstrated to have the idiomorphic organization predicted. Within the idiomorphic region the opposite mating-type genes appear to be offset with respect to one another, as predicted by our model. In addition, the *A. fumigatus* alpha MAT locus was found to contain a 360-base pair (bp) fragment of an HMG gene[15] neighboring the idiomorphic region, suggesting that the transition from homothallism to heterothallism in the *A. oryzae* and *A. fumigatus* ancestor occurred by gene loss (Figure 4b).

Although the model of Figure 4b predicts a homothallic ancestor for all three species, it is possible that heterothallism was ancestral and a transition to homothallism occurred in the *A. nidulans* lineage. This would be consistent with data from *Cochliobolus* species for which heterothallism appears to be ancestral, and conversions to homothallism have been described.[19] However, two factors conflict with this scenario for the aspergilli. First, the offset positions of the mating-type genes within the idiomorphic regions of the *A. fumigatus* and *A. oryzae* MAT loci, and the apparent fragment of the HMG gene neighboring the *A. fumigatus* alpha locus, are consistent with gene loss from a homothallic ancestor. Second, heterothallism in the aspergilli is rare.[22, 23] Only three heterothallic aspergilli have been previously characterized, of which one, *A. heterothallicus*, groups in phylogenies with known homothallic species, suggesting a conversion to heterothallism in this case as well.[22] Mitotic, homothallic and heterothallic species are observed intermixed in several fungal lineages, leading to debates about the fungal ancestral state.[19, 24, 25, 26] Taken together, our results provide evidence that conversion from homothallism to heterothallism is possible, and suggest that the predominance of a particular sexual strategy may vary within different clades.

Although the finding of MAT genes in supposedly asexual fungi has been previously reported[15, 27, 28, 29, 30, 31, 32] and genes related to sexual reproduction have been found in the "asexual" yeast *Candida albicans*, this report is the first comprehensive survey of sexual reproduction genes in two different filamentous fungi thought to be asexual. In addition, our results provide an experimentally supported evolutionary model associating large-scale synteny and genome rearrangement with a specific and significant difference in biology between these aspergilli. These results for *A. fumigatus* and *A. oryzae* have important and specific potential implications for health and industry. The lack of a sexual cycle in *A. fumigatus* and *A. oryzae* has precluded classical genetic analysis, impeding efforts to study these organisms and necessitating the use of the relatively distant *A. nidulans* as a genetic model. The possibility for mating—still speculative at this stage—raises the medically and industrially important potential for developing genetic tools for these fungi.

Conserved non-coding sequences

Detecting and characterizing conservation of sequences outside of protein coding regions is a promising method for identifying potential functional elements. Regulation in yeast has been extensively studied; however, in the aspergilli few transcription factor binding sites have been experimentally verified. Comparing the three aspergilli provides an opportunity to identify the most constrained functional elements.

To do so we aligned three-way orthologous genes including 1 kb of sequence upstream and downstream using Mlagan.[33] Strict filters were then applied to delineate unambiguous orthologous intergenic regions (see Methods). Given the divergence of the aspergilli, it is expected that intergenic regions would not show significant conservation, and frequently this was found to be the case. However, in many instances, blocks of nearly perfect

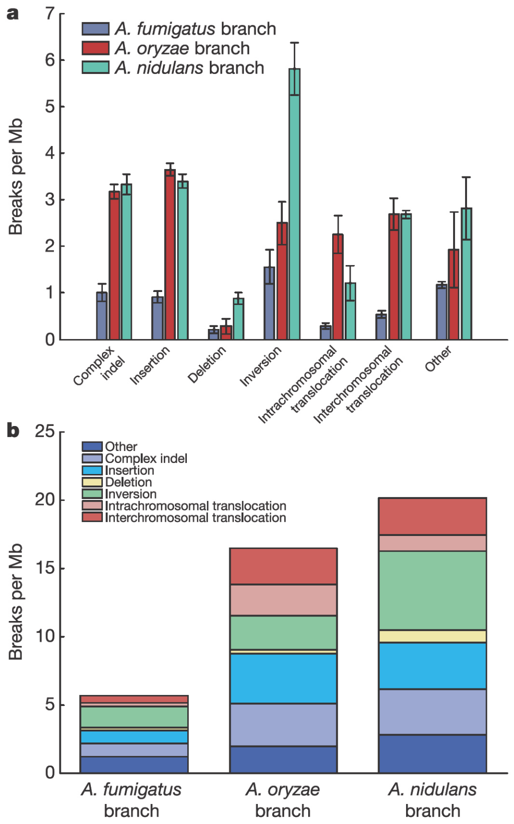


Figure 3: Rates of branch-specific rearrangements. **(a)** The rates of different breaks broken down by break type for each branch. Bars represent minimum and maximum values obtained using either of the two non-target genomes as reference (see Methods). **(b)** A stacked plot of the same data showing the relative contribution of break types within each branch for all three branches. See text and Methods for more details.

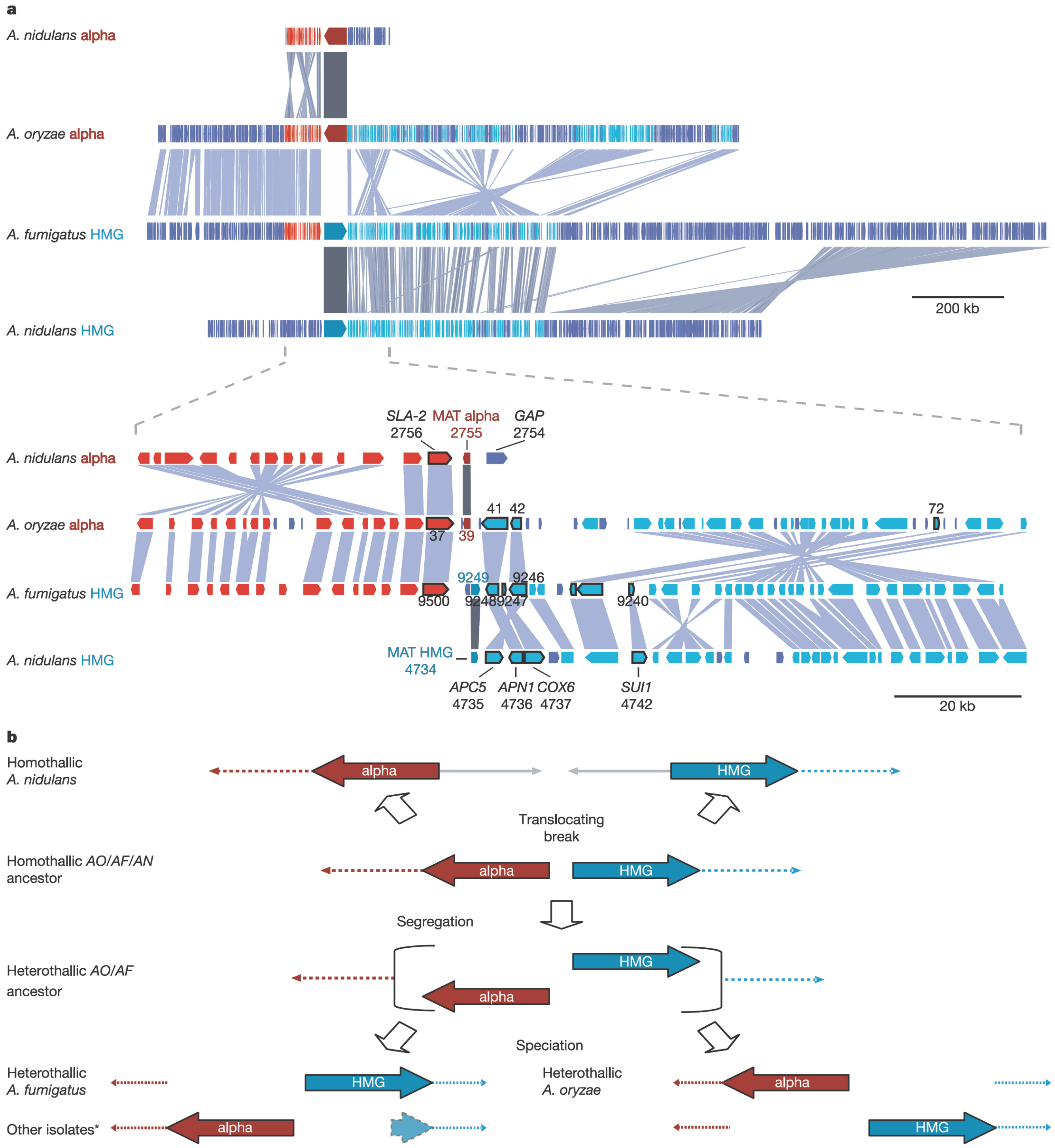


Figure 4. Comparison and evolutionary model of *Aspergillus* MAT loci. (**a**) Conserved synteny between loci. Grey lines indicate predicted orthologues. Red genes indicate orthologues from the left flank (as drawn) of the *A. nidulans* alpha locus with the left flanks of the *A. fumigatus* and *A. oryzae* loci. Cyan genes indicate orthologues with the right flank of the *A. nidulans* HMG locus. The bottom panel shows the region near mating-type genes. Genes labeled and outlined in black are associated with MAT loci in other fungi. Only partial accession numbers (suffixes) are shown in the figure. For full accession numbers, the numbers shown in the panel should replace the asterisks in the following examples: *A. nidulans* (AN****.1); *A. fumigatus* (59.m0****); *A. oryzae* (AO0703270000**). (**b**) Model of structural evolution of the MAT loci. Braces represent multiple haplotypes at the same genomic locus. The experimental identification of other isolates (indicated by an asterisk) was reported in another study[15]. The light blue arrow indicates a 360-bp HMG gene fragment. *AF*, *A. fumigatus*; *AN*, *A. nidulans*; *AO*, *A. oryzae*.

three-way conservation are observed. An example for one intergenic region is shown in Figure 5a.

To assess which regions were conserved owing to purifying selection rather than neutral mutation or chance, we developed models for alignments of neutral and random sequence. Unlike mammals, where ancient conserved repeats provide a natural model for neutral evolution, few such repeats exist in the aspergilli (see below). Instead, we synthesized alignments of neutral sequence by concatenating randomly selected aligned columns of fourfold degenerate sites. We also controlled for chance alignment introduced by potential aligner bias by aligning randomly selected intergenic regions. Using a simple conservation scoring function we calculated maximal scoring subsequences and compared results between orthologous regions and the control models (Figure 5b). A noteworthy aspect of the data in Figure 5b is the similarity between the neutral and random models. According to our models, neutral sequence is effectively saturated for mutation, confirmed by an independent analysis of synonymous sites in protein coding sequences.

Comparing results between real and control alignments, we selected a minimum score of 22 for regions unlikely ($P < 0.015$) to be conserved by neutral evolution or chance. We denote a subsequence scoring above this threshold as a high-scoring conserved sequence (HCS). On the basis of this analysis, we predict 5,801 HCSs corresponding to ~2% of alignable orthologous intergenic regions.

Prediction of functional motifs

We expect HCSs to be enriched for functional elements. The challenge is to discover these functional elements and make testable predictions about their biological functions. In preliminary analyses, several conserved regions could be identified as known functional elements. For example, we observed conservation delimiting a known 3′ untranslated region (UTR) element of the *A. nidulans areA* gene that regulates messenger RNA stability in response to cellular nitrogen levels.[34] We also identified three TPP binding riboswitches, one of which has not been described in *Aspergillus* (Supplementary Information).

To enrich computationally HCSs for sequences corresponding to functional elements, and to derive clues about their biological functions, we modified the approach used by Reference 35 (see Methods). Briefly, we identified common subsequences (or ‘patterns’) that appeared in at least four HCSs across all three *Aspergillus* genomes. These patterns were searched in three-way conserved orthologues to identify genes in which the subsequence occurred in the 500-bp upstream or downstream regions (a “co-occurrence”). A number of conservation criteria were then applied (see Methods). We identified a total of 69 conserved patterns (“conpats”), occurring in at least four HCSs, that showed enrichment for co-occurrences and exhibited a bias for occurring 500 bp upstream or downstream of genes.

The results of this analysis for the 35 most common patterns are shown in Figure 6 (all 69 patterns available in Supplementary Information). These include motifs that match known or predicted *Aspergillus* or other fungal functional sequences. For example, CPCA/GCN4, the master regulator of the cross pathway control system in fungi, is known to bind to the palindromic site TGASTCA.[36] In yeast, microarray studies have identified 539 genes probably regulated by GCN4 that show a preference for amino acid biosynthetic genes and several ribosomal proteins and translation factors.[37] One of the patterns identified by our analysis (ID 2483) matched the CPCA binding site, co-occurred preferentially upstream of genes, and was enriched in genes associated with amino acid transport and metabolism (COG category E), and translation, ribosomal structure and biogenesis (category J). Furthermore, the 19 genes with co-occurrences of this pattern include 7 (37%) predicted orthologues to the 539 known yeast regulated

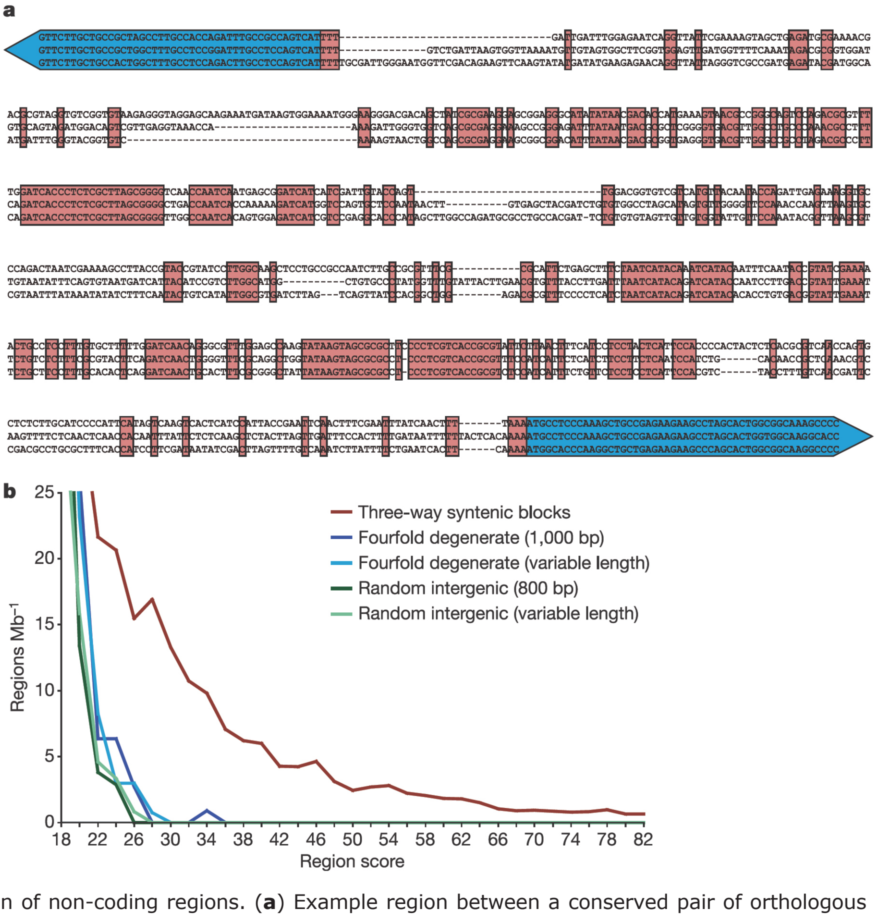


Figure 5. Active conservation of non-coding regions. (**a**) Example region between a conserved pair of orthologous histone H2A and H2B genes (left and right blue arrows). The three lines from top to bottom correspond to the sequences of *A. nidulans*, *A. fumigatus* and *A. oryzae* aligned using Mlagan. Letters on the red background indicate 100% conserved bases. (**b**) Conservation scores of maximal subsequences for observed intergenic alignments (red), and models of neutral and random sequence alignment (both fixed and variable length).

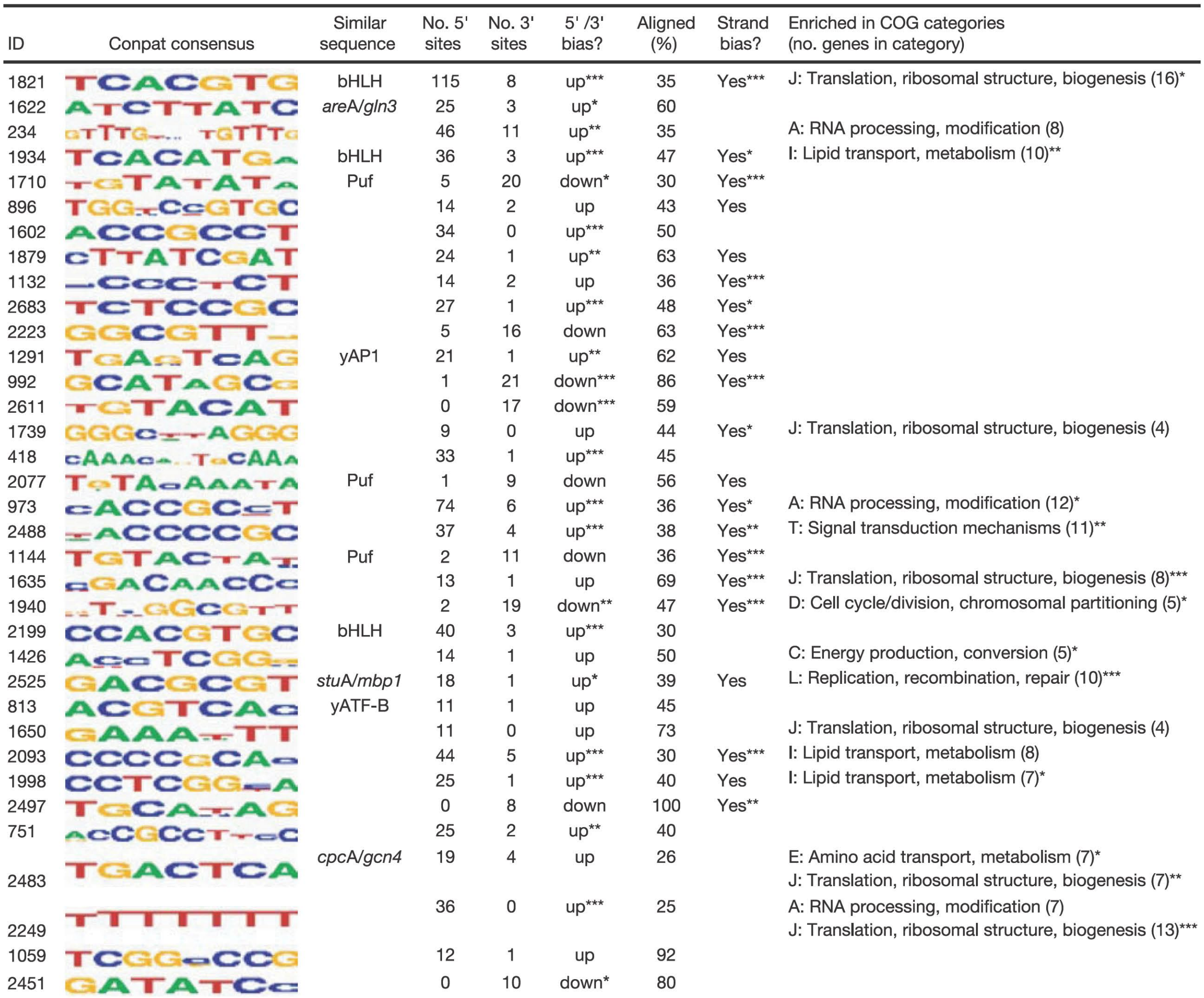
genes, representing a sixfold enrichment (*P*-value $< 1 \times 10^{-5}$). This includes two known *A. nidulans* CPCA regulated genes (*trpB*[38] and *hisHF*[39]). This pattern probably corresponds to the known *Aspergillus* CPCA binding site.

A second pattern shows strong correspondence with the binding site for Puf family genes.[40] Puf proteins regulate mRNA translation and mRNA decay through interactions with 3′ UTR sequences. In *Saccharomyces cerevisiae*, which has five Puf genes, Puf3p has been shown to bind specifically mRNAs encoding mitochondrial proteins[40] and requires a 3′ UTR motif with consensus UGUANAUA.[40] Four different patterns identified by our analysis (ID 1710, 2077, 1144 and 2378; see the full table in Supplementary Information) match or include the Puf binding motif and display a strong downstream bias. Three also show enrichment for predicted orthologues in *S. cerevisiae* that localize to mitochondria. Taking all four patterns together, we find a 6.8-fold enrichment ($P < 4.3 \times 10^{-11}$) for genes with orthologues to yeast mitochondrial genes. In addition, we find a threefold enrichment ($P < 0.0003$) for genes with yeast orthologues predicted to be bound by Puf genes in a genome-wide affinity tag analysis.[40] Although a functional role for the Puf family has not been experimentally demonstrated in *Aspergillus*, all three genomes possess five loci with 5–8 Puf domains, as predicted by HMMER and PFAM (including one with a predicted RNA binding domain, as with Puf1p and Puf2p in yeast). Together these data suggest that, as in yeast, Puf genes may bind to and regulate mitochondrial mRNAs in the aspergilli.

Only a small number of transcription factor binding sites and control elements are known for filamentous fungi in general, including *Aspergillus*. These predicted patterns are thus promising targets for future experimental validation.

Regulatory upstream open reading frames

A significant proportion (32%) of HCSs are conservatively predicted to lie within transcribed but untranslated regions of genes (UTRs), consistent with the known role of UTRs in regulating gene expression, particularly mRNA translation (for example, Puf binding domains). One important class of translational control elements is short upstream open reading frames (uORFs) in 5′ UTRs,[41] which can regulate the expression of downstream protein-coding genes in several ways. First, they can modulate the efficiency of ribosome re-initiation at downstream start codons in



ID	Conpat consensus	Similar sequence	No. 5' sites	No. 3' sites	5' /3' bias?	Aligned (%)	Strand bias?	Enriched in COG categories (no. genes in category)
1821	TCACGTG	bHLH	115	8	up***	35	Yes***	J: Translation, ribosomal structure, biogenesis (16)*
1622	ATCTTATC	*areA/gln3*	25	3	up*	60		
234	gTTTG... TGTTTg		46	11	up**	35		A: RNA processing, modification (8)
1934	TCACATGa	bHLH	36	3	up***	47	Yes*	I: Lipid transport, metabolism (10)**
1710	tgTATATa	Puf	5	20	down*	30	Yes***	
896	TGGtCcGTGC		14	2	up	43	Yes	
1602	ACCGCCT		34	0	up***	50		
1879	cTTATCGAT		24	1	up**	63	Yes	
1132	CccCtCT		14	2	up	36	Yes***	
2683	TcTCCGC		27	1	up***	48	Yes*	
2223	GGCGTT		5	16	down	63	Yes***	
1291	TgAgTcAG	yAP1	21	1	up**	62	Yes	
992	GCATaGCg		1	21	down***	86	Yes***	
2611	tgTACAT		0	17	down***	59		
1739	GGGctAGGG		9	0	up	44	Yes*	J: Translation, ribosomal structure, biogenesis (4)
418	cAAAc..TaCAAa		33	1	up***	45		
2077	TgTAgAAATA	Puf	1	9	down	56	Yes	
973	cACCGCcT		74	6	up***	36	Yes*	A: RNA processing, modification (12)*
2488	tACCCCCGC		37	4	up***	38	Yes**	T: Signal transduction mechanisms (11)**
1144	TGTACtAt	Puf	2	11	down	36	Yes***	
1635	gGACAACCc		13	1	up	69	Yes***	J: Translation, ribosomal structure, biogenesis (8)***
1940	T.GGcGTT		2	19	down**	47	Yes***	D: Cell cycle/division, chromosomal partitioning (5)*
2199	CCACGTGC	bHLH	40	3	up***	30		
1426	AcgTCGG		14	1	up	50		C: Energy production, conversion (5)*
2525	GACGCGT	*stuA/mbp1*	18	1	up*	39	Yes	L: Replication, recombination, repair (10)***
813	ACGTCAc	yATF-B	11	1	up	45		
1650	GAAAtTT		11	0	up	73		J: Translation, ribosomal structure, biogenesis (4)
2093	CCCCgCAg		44	5	up***	30	Yes***	I: Lipid transport, metabolism (8)
1998	CCTCGGgA		25	1	up***	40	Yes	I: Lipid transport, metabolism (7)*
2497	TGCAtAG		0	8	down	100	Yes**	
751	aCCGCCTtgC		25	2	up**	40		
2483	TGACTCA	*cpcA/gcn4*	19	4	up	26		E: Amino acid transport, metabolism (7)* J: Translation, ribosomal structure, biogenesis (7)**
2249	TTTTTTTT		36	0	up***	25		A: RNA processing, modification (7) J: Translation, ribosomal structure, biogenesis (13)***
1059	TCGGgCCG		12	1	up	92		
2451	GATATCc		0	10	down*	80		

Figure 6. Selected conserved patterns. Column one shows the conpat unique ID. Column two shows the sequence logo representation of conpat weight matrix. Column three shows fungal binding factors with sequence similarity to the conpat. Columns four and five show the number of genes with a co-occurrence of conpat upstream and downstream. Column six shows the preference for co-occurring preferentially 5′ or 3′ of the gene. Column seven shows the fraction of co-occurrences overlapping three-way conserved regions. Column eight shows the preference for co-occurring on a particular strand relative to the gene. Column nine shows COG categories showing significant enrichment (the number of genes with co-occurring conpats in the category is indicated in parentheses). Enrichment results for yeast orthologue cellular location are available in the Supplementary Information. * $P < 1 \times 10^{-3}$; ** $P < 1 \times 10^{-4}$; *** $P < 1 \times 10^{-5}$. bHLH, basic helix-loop-helix.

a manner dependent on cellular state. Second, uORFs can produce *cis*-acting peptides that stall ribosomes. Finally, the presence of uORFs can affect mRNA stability. Functional uORFs can be as short as three amino acids and occur at varying distances and multiplicity upstream of the protein-coding gene, occasionally overlapping the downstream start codon. Functional uORFs have been reported in a range of species including plants, animals and fungi.[41] In *Aspergillus*, a small number of genes with validated uORFs have been reported (Supplementary Information). To determine the full extent with which they may regulate gene expression, we analyzed the three *Aspergillus* genomes for uORFs.

We identified UTR sequences using expressed sequence tag (EST) alignments for *A. nidulans* genes, and examined them for open reading frames (see Methods). Of 1,606 genes with identified UTRs, 21% (358) have upstream ORFs. A similar proportion was found (18% or 82 out of 463) when we restricted our analysis to three-way orthologues for which the start codons align exactly within multiple alignments, suggesting that these uORFs are not due to misannotation. A corresponding analysis of genes with ESTs in the *N. crassa*, *F. graminearum* and *Magnaporthe grisea* genomes found uORFs associated with 22%, 10% and 16% of genes, respectively. We further extended the analysis in *A. nidulans* using a conservative estimate of 5′ UTR length (see Methods), and identified an additional 958 genes with potential uORFs of which 165 genes have three-way orthologues. In total, 1,316 genes in *A. nidulans* are predicted to possess uORFs.

Not all identified uORFs have a detectable impact on gene expression.[41] To enrich the set of predicted uORFs for those likely to be functional, we looked for those conserved in all three aspergilli. On the basis of a strict criterion requiring alignment of the uORF start and stop codons, we find 38 conserved uORFs (13% of 331 genes with uORFs and predicted orthologues) (Supplementary Information). Of these corresponding *Aspergillus* genes, 14 have predicted uORFs upstream of orthologues in *N. crassa*, *F. graminearum* or *M. grisea*. Additionally, three also have predicted orthologues in *S. cerevisiae* with uORFs conserved across four related yeast species.

These 38 conserved uORFs represent strong candidates for experimental investigation. As a preliminary validation, we tested two novel conserved uORFs for their ability to modulate protein synthesis *in vitro* (Figure 7). Briefly, oligonucleotides containing each uORF were fused to a luciferase reporter gene, and controls were constructed with disabled uORF and/or reporter gene start codons. Differential expression in a cell-free translation system between intact and control constructs measures the impact of the uORF on translation. This system can detect small (twofold) changes in translation, and can discriminate uORFs that do not reduce translation *in vivo* from those that do (see Methods). As can be seen in Figure 7, both uORFs tested display a 5–10-fold repressive effect on the translation of the downstream reporter gene.

These results provide the first genome-wide list of predicted conserved uORFs for any organism, and suggest that uORFs could have a substantial role in regulating gene expression in *Aspergillus*. Previous reports estimate that 2–4% of genes in *S. cerevisiae* contain uORFs,[42] whereas a review of sequences in UTRdb predicted that 5–10% of eukaryotic UTRs contain ORFs.[43] Our results predict that in filamentous fungi the proportion may be twice as high.

Aspergillus physiology

Peroxisomes are organelles containing enzymes for the breakdown of fatty acids (β-oxidation), removal of hydrogen peroxide and synthesis of cholesterol and bile acids. Peroxisomes have critical roles in fungi where they are involved in growth, secondary metabolism and pathogenesis. In mammals, defects can lead to developmental and neurological disorders. Proteins are targeted to the peroxisome either by a carboxy-terminal tripeptide sequence or an amino-terminal nine-amino-acid sequence. Using these signals we predicted peroxisomal proteins in *Aspergillus* (Supplementary Information). Our analysis reveals peroxisomes in *Aspergillus* to be more similar to mammals than yeasts in two respects. First, our data suggest that the aspergilli, like mammalian cells, perform β-oxidation in both peroxisomes and mitochondria and possess two sets of genes for all β-oxidation enzymes targeted to both the mitochondria and the peroxisome, as supported by recent experimental results.[44] In contrast, *S. cerevisiae* metabolizes fatty acids fully to acetyl-CoA only in peroxisomes.[45] Second, *Aspergillus* peroxisomes are more similar to those of mammals than those of yeasts in that they possess putative peroxisomal acyl-CoA dehydrogenases. In addition, all three aspergilli appear to encode both mitochondrial and peroxisome forms of an ATP-dependent protease of the LON (La domain) family associated with peroxisomes in mammals.[46] *S. cerevisiae* has a single copy of this protease (*Pim1*/*Lon1*) targeted to mitochondria.[47]

One of the hallmarks of the filamentous fungi is their ability to undergo polarized hyphal growth. This requires positional cues that mark polarized growth sites, locally activating Rho-related GTPase signaling modules that promote cytoskeletal reorganization.[48] The three aspergilli possess the expected genes involved in signaling and cytoskeletal organization for polarized growth, but there is a marked lack of known positional markers (such as the yeast bud site markers Bud3p, Bud8p and Bud9p; see Supplementary Information). Proteins implicated in the transport or modification of bud markers, including Axl1p, Rax1p, and Bud7p, were predicted, however. This suggests that filamentous fungi mark polarized growth sites with positional cues, but that the markers themselves may consist of novel cell wall proteins.

Most of the interspersed repeats in all three genome sequences correspond to relics of transposable elements (see Supplementary Information). Surprisingly, only 1.3% of the largest genome

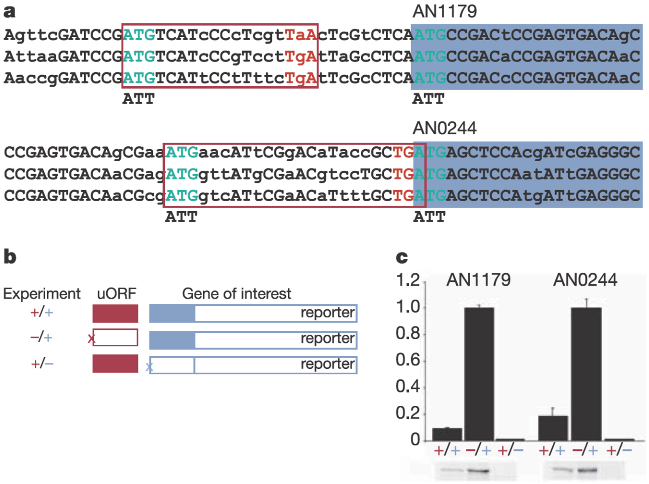


Figure 7. Prediction and validation of conserved uORFs. Conserved uORFs show a 5–10 times repressive effect on reporter gene translation. (**a**) Alignments of two tested uORFs. uORFs are shown in purple boxes, and protein-coding genes in a blue background. Conserved bases are in upper case and start/stop codons are highlighted. (**b**) Experimental design. The *A. nidulans* sequence from 26 nucleotides upstream of each uORF to four codons in the protein-coding gene was fused with a firefly luciferase gene. Controls were generated with start codons for both the uORF and the luciferase gene (+/+), the luciferase gene only (-/+), and the uORF only (+/-). Starts were deleted by alteration to ATT. mRNA from each construct was used to program a cell-free translation system. **c**, Results of translation assays. The luciferase activity of all constructs (normalized to the -/+ construct) is shown on the *y* axis. Error bars show the average of the absolute deviation from the mean. The autoradiogram shows ^{35}S-Met-labeled firefly luciferase obtained by *in vitro* translation of the same mRNAs.

assembly of *A. oryzae* consists of transposable elements, compared to 3% of *A. nidulans* and *A. fumigatus*. All three genomes contain essentially all major classes of eukaryotic transposable elements, although the overall variety is relatively low. A number of unusual features were also observed in *Aspergillus* transposable elements (Supplementary Information). Copy numbers per family range from 1 to ~100; there are also many fragments and "footprints" (evidence of recombinational excision). In addition, some members of all transposable element families longer than ~400 nucleotides are characterized by numerous C to T transitions. In *A. nidulans* and *A. fumigatus*, these predominantly affect cytosines in CpG and CpA doublets (no preference is apparent in *A. oryzae*). Moreover, repeat density is correlated with A + T richness in all three species (Figure 2). The predominance of transition mutations is consistent with the operation of RIP (repeat-induced point mutation),[49] and all three aspergilli have a single predicted homologue (called DmtA) to the DNA methyltransferase *rid* that is essential for RIP in *N. crassa*.[49] Apart from the putative *rid* homologue, no additional DNA methyltransferase genes were identified, consistent with failures to demonstrate methylation in these fungi. Although RIP has not been demonstrated in any *Aspergillus* species, if active it may be more similar to the mild form in *M. grisea*,[49] as many transposable elements in these species are mutation-free.

Conclusion and perspective

The *A. nidulans* genome sequence and our comparative analysis with the genome sequences of *A. fumigatus* and *A. oryzae* have shed new light on the physiology of these fungi, as well as insight into aspects of genome evolution and gene regulation likely to be common to all eukaryotes. These results represent the initial step in realizing the full potential of these genomes. As a result of the genome analysis, efforts are underway to cross different isolates of *A. fumigatus* and *A. oryzae*. The identified conserved sequences also represent a rich set of targets for further experimental investigation. These efforts and ongoing sequencing projects for additional aspergilli promise to change fundamentally our understanding of this important group of medically, industrially and scientifically relevant fungi.

Methods

Complete details of the methods used are available in the Supplementary Information section.

A. nidulans sequencing, assembly and analysis

The *A. nidulans* genome strain FGSC A4 was sequenced by the WGS method to a depth of 10 ×. An additional 3 × sequence coverage was provided by Monsanto (http://www.monsanto.com/). All sequence was assembled using Arachne. The *A. nidulans* genome was annotated as described in Supplementary Information. *A. fumigatus* and *A. oryzae* were assembled and annotated as described separately.[2, 3]

Phylogenetic analysis

A total of 3,034 predicted orthologues among *A. nidulans*, *A. oryzae*, *A. fumigatus*, *N. crassa* and *F. graminearum* were aligned at the protein level, back translated to DNA codons, and large gaps (> 9 bp) were removed. Random sets of 20 DNA alignments were concatenated and passed to Phylip to generate 100 bootstrap replicates and a consensus maximum parsimony tree. Maximum likelihood trees were calculated on each replicate and a consensus tree was produced. Repeating with 1,000 bootstrap samples led to essentially identical results. For rooting with *C. immitis*, *C. immitis* orthologous CDS regions based on TBlastN were retrieved, translated and aligned at the protein level with the aligned portions of the *Aspergillus* genes. Maximum parsimony trees were then generated and filtered for those with 100% bootstrap values at all nodes. The *C. immitis* sequence is available at http://www.broad.mit.edu/annotation/genome/coccidioides_immitis/MultiHome.html

Hierarchical synteny mapping and branch-specific rearrangements

Protein homology anchors were detected using BlastP and filtered to retain only hits scoring >80% of the score of the best hit to each query protein. Contiguous sets of homologous proteins with conserved order and orientation were grouped into clusters. Pairs of clusters were then merged into successively larger clusters by tolerating successively larger breaks between clusters. Branch-specific breaks were determined by identifying regions without breaks between a reference species and query species, and then identifying breaks in that region between the reference and the third (target) species. Such breaks were considered specific to the third species. Breaks were classified according to the pattern of apparent rearrangement.

Identification of non-coding conserved sequences

Genomic sequence for predicted three-way orthologues, including 1 kb upstream and downstream, were multiply aligned using Mlagan.[33] An additive scoring function was used to identify maximal scoring subsequences. A cutoff of 22 was used to define HCSs unlikely to occur by chance ($P < 0.015$) according to models of neutral sequence and random sequence alignment. To model alignments of neutrally evolving sequence, aligned columns of fourfold degenerate sites were selected randomly and concatenated. To model alignments of random sequence, randomly selected intergenic regions from each genome were aligned. Fixed and variable length alignments were generated for both models. For each model, 1,000 simulated alignments were generated and maximal scoring subsequences were identified. The number of subsequences for each score was normalized by the number of aligned nucleotides. These rates were used to determine the score cutoff above.

Prediction of functional motifs

Each HCS was represented as a position-specific probability matrix (PSPM) derived from the three-way alignment. Each PSPM was compared to each other PSPM and matching PSPMs were clustered. Local multiple alignments for each cluster were generated and the resulting multiple alignments and corresponding weight matrices were termed conpats. For each conpat, we used the corresponding weight matrix with MAST to identify instances where the conpat co-occurred upstream or downstream of orthologous genes in all three of the aspergilli. A series of conservation tests was then applied to the set of predicted co-occurrences for each conpat as described in Supplementary Information.

Prediction and validation of upstream open reading frames

Genome sequences for three-way orthologues, including 1,000 bp upstream and downstream, were multiply aligned using Mlagan. For 25% of *A. nidulans* genes 5′ UTR sequences were predicted from EST alignments. On the basis of the length distribution of these EST-predicted UTRs, we used 60 bp upstream of predicted AUG codons as a conservative estimate of 5′ UTRs for genes lacking ESTs. When no ESTs were available, UTRs for orthologues where considered when all three annotated start codons aligned within 40 bp. We identified uORFs ≥ 12 bp, with a maximum 1-bp overlap with the protein-coding gene's ATG. Conserved uORFs were identified as those for which the start and stop codons were exactly aligned within the multiple alignments. To experimentally validate uORFs, synthetic oligonucleotides containing each uORF, 26 nucleotides upstream of the uORF, the region between the uORF and the protein coding AUG, and the first four codons of the protein coding gene were fused in frame with a firefly luciferase gene. Three different control constructs were also generated. Capped and polyadenylated synthetic mRNA were prepared from each construct and equal amounts were used to program cell-free extracts from *N. crassa*. Differential translation between the intact construct and the controls was measured using a luciferase activity assay as well as through the production of ^{35}S-Met-labeled firefly luciferase obtained by *in vitro* translation of the same mRNAs.

The *A. nidulans* genome sequence is available at http://www.broad.mit.edu/annotation/genome/aspergillus_nidulans/MultiHome.html and has been deposited at DDBJ/EMBL/GenBank under the project accession AACD00000000.

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Author Contributions

B.W.B. developed and led the *A. nidulans* sequencing project. J.B. performed the assembly of *A. nidulans*. C.C. and J.E.G. analyzed the phylogenic relationship of the three organisms. J.E.G. performed the analysis of conserved synteny and genome evolution. R.F., B.M., and P.D. performed the comparative analysis of sexual reproduction genes. J.E.G., M.P., P.D., and B.M. analyzed the mating-type loci. S.E.C. and J.E.G. analyzed conserved non-coding sequences and computationally analyzed uORFs. S. Batzoglou and S.-I.L. assisted with the use of Mlagan. M.B., C.C.S., and M.S.S. performed the experimental uORF validation. M.C., M.H., G.H.B., O.D., and C.D. analyzed transcription, known transcription factors, and binding sites. A.P. and S.G.J. predicted non-coding RNAs using PFAM and RFAM. J.C., V.K., J.J., S.P., and J.E.G. analyzed repeat sequences and RIP. M. Farman analyzed telomeres and subtelomeric gene content. M.H. analyzed the *Aspergillus* peroxisomes. S.H. and M. Momany analyzed hyphal growth and RhoGTPases. J.R.W. and W.C.N. provided the sequence and annotation for *A. fumigatus*. T.T., T.K., K.A., and M. Machida provided the sequence and annotation for *A. oryzae*. D.W.D. co-ordinated interactions between the different sequencing centers and scientific communities. J.E.G. and S.A.O. coordinated the comparative analyses. J.E.G. wrote and edited the paper, and produced the figures.

Supplementary Information can be found on the following pages.

Supplementary Information — Contents

Contents listings are actively linked to the first page of the supplementary sections.

§S0. Detailed Methods

***A. nidulans* Sequencing and Assembly.** The *A. nidulans* genome strain FGSC A4 was sequenced by the whole-genome shotgun method. A total of 10x coverage was produced at the Broad Institute from Plasmid (4kb and 10kb inserts), Fosmids (40kb inserts), and BACs (110kb inserts) (http://www.broad.mit.edu/annotation/fungi/aspergillus/background.html). The BAC library for strain FGSC A4 was provided by Ralph Dean at North Carolina State University and is available at Clemson University Genomics Institute (https://www.genome.clemson.edu/orders/). All inserts were sequenced from both ends to generate paired-reads. An additional 3x sequence coverage was provided by Monsanto (http://www.monsanto.com/). All sequence was assembled using Arachne[1]. The assembly was anchored to a genetic map based on 260 markers (201 with unambiguous sequences in Genbank). Six discrepancies in the genome assembly were detected by comparison with the genetic map and corrected (see http://www.broad.mit.edu/annotation/fungi/aspergillus/markers.html for more details). *A. fumigatus* and *A. oryzae* genomes were assembled as described in separate reports[2,3].

***A. nidulans* Annotation and Analysis.** The *A. nidulans* genome was annotated using the Calhoun annotation system. The genome sequence was searched against the public protein databases using BLASTX with threshold $E \leq 1e\text{-}5$. Genes were predicted using a combination of FGENESH, FGENESH+, and GENEWISE. Predicted genes were validated against ESTs aligned to the genome using Blat[4]. All predicted proteins were searched against the PFAM set of hidden Markov models[5] using the HMMER program and the public protein databases using BLASTP. Transfer RNAs were identified using the tRNAScan-SE program[6]. Repeat sequences were detected by searching the genome sequence against itself using CrossMatch, filtering for alignments longer than 200bp in length, and clustering pairs based on region overlap. Repeats were characterized using RepeatMasker (http://ftp.genome.washington.edu/RM/RepeatMasker.html) and RepBase[7] followed by manual inspection. The *A. fumigatus* and *A. oryzae* genomes were annotated as described in separated reports[2,3].

Phylogenetic Analysis. A total of 3034 orthologs among *A. nidulans, A. oryzae, A. fumigatus, N. crassa,* and *F. graminearum* were predicted using the COG definition[8] using BlastP ($e<10^{-5}$ and alignment length at least 60% of both genes) and aligned at the protein level using ClustalW[9]. Alignments were then back translated to DNA codons and large gaps (>9b) were removed. Random sets of 20 DNA alignments were concatenated and passed to Phylip to generate 100 bootstrap replicates of alignments using seqboot and a consensus maximum parsimony tree using protpars and consense. Maximum likelihood trees were calculated on each replicate and a consensus tree produced. Repeating the analysis with 1000 bootstrap samples led to essentially identical results. For rooting with *C. immitis*, orthologs from each Aspergillus species were compared to the *C. immitis* genome sequence with TBlastN (e<1e-10). Results were filtered such that: (1) only genes in the Aspergilli that hit to a single locus in *C. immitis* were considered, (2) the best HSP for each gene must not contain a stop codon in *C. immitis* not aligned with a gap position, and (3) all three Aspergillus orthologs must hit the same locus in *C. immitis*. Regions of the *C. immitis* genome corresponding to the intersection of the Aspergillus hits were retrieved, translated, and aligned at the protein level with the aligned portions of the Aspergillus genes. Alignment regions with large gaps (>9bp) were removed. Maximum parsimony trees were then generated using the protpars program of Phylip and trees filtered for those with 100% bootstrap values at all nodes. Raw data are available in Supplementary Material. The C. immitis genome sequence is available at http://www.broad.mit.edu/annotation/fungi/coccidioides_immitis/.

Hierarchical Synteny Mapping. Protein homology anchors were detected using BlastP (e<1e-5 and length >60% of longest protein) and then filtering to retain only those hits scoring >80% of the score of the best hit to each query protein. The clustering algorithm was initiated by finding contiguous sets of homologous proteins with conserved order and orientation and grouping each into a cluster. Then during each iteration of the algorithm, pairs of clusters were merged into successively larger clusters by tolerating successively larger breaks between clusters. The distance between cluster X and Y was the Euclidean distance between the two nearest points of the rectangle bounding the clusters in a dot plot if (1) the cluster X is orientated toward cluster Y and (2) both are on the same supercontig. Otherwise the distance was infinite. After merging two clusters, the slope of the resulting merged cluster was determined as the slope of a line through the merged clusters. During each merge, the characteristics of the break (microrearrangement) between the merged clusters were tracked. The algorithm was terminated when no clusters within 100Kb of one another were available to be merged.

Branch-Specific Rearrangements. Branch-specific breaks were determined by identifying regions without breaks between a reference species, R, and query species, Q, and then identifying breaks in that region between R and a target species, T. Such breaks are considered specific to T. For example, if region 1-10Kb in *A. nidulans* (R) is conserved without microrearrangements when compared to *A. fumigatus* (Q), but the same region shows an inversion when compared to *A. oryzae* (T), this inversion would be considered an *A. oryzae*-specific rearrangement. For a given R, Q, and T, only pairwise blocks longer than 20kb, breaks between R and T larger than 10 kb on either genome, and breaks between R and Q larger than 5kb on either genome were considered. Also, breaks between R and T within 5 kb of contig ends were not considered. Breaks in T that are wholly contained within an inversion between R and Q were considered T specific breaks. The number of breaks specific to T was converted to a rate by dividing by the total number of nucleotides in R used in the analysis. For each target genome, two different R versus Q comparisons were possible. The error bars in **Error! Reference source not found.**A correspond to the minimum and maximum values for the two comparisons. Breaks were characterized as follows:

- Insertion – at least 10Kb is present in T that does not map to R,Q
- Deletion – at least 10Kb is present in R,Q but does not map to T
- Complex Indel – a combination of Insertion and Deletion
- Inversion – a block of at least 10kb is inverted in T relative to R,Q
- Intrachromosomal Translocation – a break between two syntenic blocks between R,T that are adjacent in R and where the blocks between R,T are on the same chromosome.
- Interchromosomal Translocation – a break between two syntenic blocks between R,T that are adjacent in R and where the blocks between R,T are on different chromosome.

Identification of Non-coding Conserved Sequences. Pairwise orthologs were identified as best bidirectional hits (BBHs) within all-vs-all comparison of two genome protein sets using Blastp (e<1e-5) and requiring > 60% coverage of each gene. Threeway orthologs were identified as sets of three genes from each genome in which each gene is a BBH of each of the other two genes. A total of 4936 threeway orthologs were thus predicted.

Genomic sequence for threeway orthologs including 1kb upstream and downstream were multiply aligned using the Mlagan program[10] with the phylogenetic tree (AN, (AF, AO)). Within the multiple alignments, unambiguous non-coding regions were defined as regions not annotated as a coding sequence in any of the three genomes. Duplicate regions in alignments of neighboring genes were removed. An additive scoring function (match=3, mismatch=-2, and gap=-20) was used with a linear time algorithm[11] to identify maximal scoring subsequences. A score cutoff of 22 was used to define High-scoring Conserved Sequences (HCSs) unlikely to occur by chance ($p<0.015$) according to models of neutral sequence and random sequence alignment as described next.

Models of Neutral and Random Alignments. To model alignments of neutrally evolving sequence, ortholog protein sequences were aligned using ClustalW and subsequently back-translated to DNA codons. Aligned columns of 4-fold degenerate sites from these alignments were placed into a pool, and columns from this pool were then selected randomly with replacement and concatenated to generate synthetic aligned sequences. Both 1000bp fixed length synthetic alignments were generated as well as variable length alignments drawn from a normal distribution approximating observed intergenic lengths in *A. nidulans* ($\mu=1110$, $\sigma=140$). To model alignments of random sequence, randomly selected intergenic regions were aligned from unrelated loci from each of the three genomes. Both fixed length alignments (800bp clipped from selected intergenic regions) and variable length alignments (full length of each intergenic region aligned) were generated.

A total of 1000 simulated alignments from both the fixed and variable length neutral and random models were generated. For each set of alignments from each model, maximal scoring subsequences were identified as described above. The number of subsequences for each score was normalized by the number of aligned nucleotides in the set of the alignments to produce a spatial rate of the number of subsequences of score X per Mb. These distributions were used to determine a threshold for identifying HCSs as described in the text.

Prediction of Functional Motifs. Each HCS was represented as a position specific probability matrix (PSPM) derived from the threeway alignment. The probability assigned to each base at each position of the matrix was (Cn+B/4)/(N+B) where Cn is the number of occurrences of the letter at that position, N is the number of sequences, and B is the total number of pseudocounts added at each position (0.001). Pseudocounts adjust for the small number of observed sequences by preventing entries of zero in the PSPM as required for log-odds scoring[12]. Each PSPM was then compared to each other PSPM to find the best scoring pairwise local alignment. Local alignments were scored by summing a log-odds function, F, across each aligned column where F=log2(q/p) and q=dot-product of the columns from the two PSPMs and p=0.25. A minimum length of 8bp and score of 12 was required for local alignments. PSPMs were then clustered according to an iterative greedy clustering algorithm. Specifically, at each iteration if PSPMs X and Y share a local alignment and are part of cluster C, and PSPMs X and Z share a local alignment, and if the local alignments overlap on X within 3bp at each boundary, Z would be added to cluster C. The region of X and Z covered by the corresponding local alignment was then masked, and the algorithm re-iterated. Given clusters of PSPMs, local multiple alignments for each cluster were generated from the genomic sequences corresponding to each PSPM. Specifically, the sequences from all three species corresponding to each PSPM, as well as 6bp of padding on each side, were aligned using the program MEME[13] (with the “oops” model). The resulting multiple alignments and corresponding weight matrices were termed CONserved PATterns (conpats). Raw conpats from MEME were trimmed to require 2 consecutive bases with information content exceeding 0.75 bits/position at each end. Additionally, low quality patterns (MEME expect >1e-5 or conpats with <1.2 bits/base information content) were removed.

For each conpat, we used the corresponding weight matrix with the MAST[14] program to identify instances where the conpat co-occurred upstream or co-occurred downstream of orthologous genes in each of the three Aspergillus species. Matches on either strand were permitted. To associate matches with upstream/downstream regions, we identified a unique non-coding “upstream-half region” and “downstream-half region” for each ortholog triplet: for orthologs with no neighboring gene within 1000bp, 500bp of aligned sequence upstream/downstream was used; for orthologs with a neighboring gene, the unambiguous intergenic region was split in half. The MAST expect threshold was determined in order to generate <1 false positive co-occurrence in the 4936 orthologous genes, based on a null model assuming randomly occurring motifs will occur independently in each of 3 orthologous regions according to background base frequency. A series of conservation tests were then applied to the set of predicted co-occurrences for each conpat:

- ◊ *Co-occurrence enrichment*: used to identify conpats that co-occur more often than random patterns of the same length and degeneracy. For each conpat, we generated 1000 different patterns by randomly assigning the weights at each position of the conpat to letters (A,C,G,T). Co-occurrences of randomized patterns were then identified as described above. The co-occurrence p-value was defined based on the number of random patterns with co-occurrence counts at least as great as the actual conpat. Conpats with p-values <0.01 were considered enriched by this test.

- ◊ *Upstream/Downstream Bias*: used to identify conpats with a preference for co-occurring in upstream or downstream regions. We assigned p-values based on binomial distribution with Prob(upstream co-occurrence)=p=0.56 (calculated from upstream/downstream distribution of all HCSs). Conpats with p-values <0.01 were considered biased by this test.

- ◊ *Functional Category Enrichment*: used to identify conpats that were enriched in co-occurrences neighboring genes of particular COG categories. COG categories were assigned using the NCBI COG database followed by manual inspection. For each conpat and each category C, we calculated the enrichment p-value according to a hypergeometric distribution and corrected for multiple testing using the Bonferroni correction (multiplying by the number of categories associated with the particular conpat). If a conpat exhibits upstream/downstream preference, only the corresponding upstream/downstream co-occurrences were used for category enrichment testing. Categories with corrected p-values<0.01 were considered enriched.

- ◊ *Cellular Location Enrichment*: used to identify conpats that are enriched in co-occurrences associated with genes whose predicted yeast BBHs have a particular cellular localization. Cellular localization for S. cerevisiae genes from http://yeastgfp.ucsf.edu/[15]. Categories "ambiguous" and "punctuate" were not considered. The enrichment p-value was calculated using a hypergeometric distribution with Bonferroni corrections in the same manner as with the functional category enrichment test.

Conpats with similar weight matrices (CompareACE[16] score>0.85 and manual inspection) and identical statistical signatures were collapsed. A total of 69 conserved patterns ("conpats") that occurred in at least 4 HCSs, showed enrichment in co-occurrences, and a bias for occurring upstream or downstream of genes were identified and considered in this analysis. The full set of conpats are provided in Supplementary Material.

Prediction of Upstream Open Reading Frames. Genome sequences for the set of 4936 ortholog triplets, including 1000bp upstream and downstream, were multiply aligned using Mlagan. For 25% of *A. nidulans* genes with overlapping EST alignments, the entire length of the EST alignment upstream of the predicted AUG was taken as the 5' UTR. Using the length distribution of these EST-predicted UTRs, we found that 60% of all predicted 5' UTR first exons were longer than 60bp. Thus for genes lacking EST alignments, we used 60bp upstream of predicted AUGs as a conservative estimate of 5' UTRs. To correct for annotation ambiguities when no ESTs were available, UTRs for orthologs where considered when all three annotated start codons aligned within 40bp. For each species, we identified all upstream open reading frames >= 12bp, with a maximum 1bp overlap with the protein-coding gene's ATG. Conserved uORFs were identified as those whose start and stop codons were aligned within the multiple species alignment, with no minimum uORF protein identity.

Experimental Validation of Upstream Open Reading Frames. The impact of predicted uORFs on downstream gene translation was assessed by adapting a protocol previously described[17-20]. Synthetic oligonucleotides were designed to obtain 5'-leader sequences containing each uORF including 26nt upstream of the uORF, the region between the uORF and the protein coding AUG, and the first four codons of the protein coding gene. Oligonucleotides were obtained from Sigma-Genosys. These leader sequences were fused in frame with a firefly luciferase gene. Three different control constructs were also generated: one eliminated the initiation codon for the uORF, one eliminated the initiation codon for the predicted gene luciferase fusion, and the third eliminated both. Thus four constructs were made for each uORF: +/+ (both uORF and downstream product AUG codons), -/+ (no uORF AUG), +/- (no downstream AUG) and -/- (neither AUG). The first two constructs evaluate uORF function; the latter two establish that reporter activity is arising from initiation at the correct downstream start codon. Capped and polyadenylated synthetic mRNA were prepared from each construct and equal amounts were used to program cell-free extracts from *N. crassa*. Each set of transcripts was produced by two independent transcription reactions and analyzed in the linear activity range using two independently prepared extracts from each organism. All reactions contained Renilla luciferase mRNA as an internal control for normalization. Differential expression of the reporter gene between the intact construct and the controls was measured using a luciferase activity assay[21] as well as through the production of ^{35}S-Met labeled firefly luciferase obtained by in vitro translation of the same mRNAs.

Only a small number of genes in Aspergillus with validated uORFs have been previously reported[22-27].

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§S1 Aspergillus Phylogenetic Analysis - Raw Data

Methods

A total of 3034 orthologs between *A. nidulans, A. oryzae, A. fumigatus, N. crassa,* and *F. graminearum* were predicted using the COG definition[89] using BlastP ($e<10^{-5}$ and alignment length at least 60% of both genes) and aligned at the protein level using ClustalW[90]. Alignments were then back translated to DNA codons and large gaps (>9b) were removed. Random sets of 20 DNA alignments were concatenated and passed to Phylip to generate 100 bootstrap replicates of alignments and a consensus maximum parsimony tree. Maximum likelihood trees were calculated on each replicate and a consensus tree produced. For rooting with *C. immitis*, orthologs from each Aspergillus species were compared to the *C. immitis* genome sequence with TBlastN (e<1e-10). Results were filtered such that: (1) only genes in the Aspergilli that hit to a single locus in *C. immitis* were considered, (2) the best HSP for each gene must not contain a stop codon in *C. immitis* not aligned with a gap position, and (3) all three Aspergillus orthologs must hit the same locus in *C. immitis*. Regions of the *C. immitis* genome corresponding to the intersection of the Aspergillus hits were retrieved, translated, and aligned at the protein level with the aligned portions of the Aspergillus genes. Alignment regions with large gaps (>9bp) were removed. Maximum parsimony trees were then generated using the protpars program of Phylip and trees filtered for those with 100% bootstrap values at all nodes.

Tabs

Orthologs: Five way orthologs (*A. nidulans, A. oryzae, A. fumigatus, F. graminearum*, and *N. crassa*) used in analysis

Concatenated Genes: The random sets of concatenated genes. Each set is identified by an "ID" (i.e. concat1), and for each ID there are 20 groups of five way orthologs

Concatenated Tree Topologies: Summary of tree topologies for all concatenated gene sets

Single Gene Topologies: Summary of topologies for all single fiveway ortholog trees

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1099.1	70.m15774	AO070285000041	FG04118.1	NCU00006.1
AN6886.1	71.m16031	AO070314000039	FG05524.1	NCU00007.1
AN2464.1	69.m15203	AO070264000006	FG05525.1	NCU00008.1
AN4517.1	57.m05611	AO070321000123	FG05527.1	NCU00010.1
AN7254.1	72.m19795	AO070297000010	FG05530.1	NCU00018.1
AN2854.1	59.m08698	AO070338000167	FG05388.1	NCU00019.1
AN4908.1	59.m08812	AO070338000038	FG05387.1	NCU00021.1
AN4906.1	59.m08810	AO070338000039	FG05385.1	NCU00023.1
AN4209.1	54.m07042	AO070231000015	FG05384.1	NCU00025.1
AN8406.1	52.m04077	AO070302000057	FG04703.1	NCU00028.1
AN6122.1	72.m19037	AO070340000075	FG06685.1	NCU00029.1
AN2185.1	72.m19038	AO070340000081	FG06686.1	NCU00030.1
AN6162.1	72.m19009	AO070340000046	FG06689.1	NCU00034.1
AN6159.1	72.m19006	AO070340000043	FG06688.1	NCU00035.1
AN6160.1	72.m19007	AO070340000044	FG06687.1	NCU00037.1
AN2748.1	54.m06683	AO070338000223	FG06684.1	NCU00038.1
AN2743.1	54.m06688	AO070338000228	FG07237.1	NCU00040.1
AN2741.1	54.m06957	AO070338000230	FG07234.1	NCU00042.1
AN0410.1	54.m06664	AO070294000082	FG07233.1	NCU00043.1
AN6675.1	65.m07305	AO070289000014	FG07232.1	NCU00045.1
AN0409.1	54.m07007	AO070338000252	FG07231.1	NCU00046.1
AN3895.1	54.m06704	AO070342000047	FG03666.1	NCU00052.1
AN7489.1	57.m05949	AO070287000051	FG07226.1	NCU00056.1
AN2259.1	71.m15900	AO070326000104	FG06660.1	NCU00058.1
AN2258.1	71.m15899	AO070326000105	FG06661.1	NCU00059.1
AN0956.1	70.m15605	AO070320000158	FG07217.1	NCU00065.1
AN9448.1	54.m06486	AO070334000061	FG07212.1	NCU00068.1
AN4559.1	57.m05571	AO070321000169	FG06723.1	NCU00075.1
AN4553.1	57.m05564	AO070321000177	FG06720.1	NCU00078.1
AN4556.1	57.m05568	AO070321000172	FG06717.1	NCU00080.1
AN4062.1	54.m06705	AO070342000050	FG06715.1	NCU00083.1
AN2970.1	59.m09047	AO070337000156	FG06718.1	NCU00088.1
AN4534.1	57.m05587	AO070321000148	FG06972.1	NCU00092.1
AN8838.1	71.m15970	AO070271000039	FG06948.1	NCU00095.1
AN2240.1	71.m16107	AO070326000134	FG05478.1	NCU00101.1
AN0860.1	70.m15469	AO070320000008	FG05481.1	NCU00102.1
AN8491.1	72.m19790	AO070297000017	FG06962.1	NCU00105.1
AN5817.1	72.m18945	AO070260000030	FG06961.1	NCU00106.1
AN5815.1	72.m18944	AO070260000032	FG06959.1	NCU00108.1
AN5814.1	72.m18943	AO070260000033	FG06963.1	NCU00109.1
AN7731.1	71.m15755	AO070325000145	FG02604.1	NCU00113.1
AN6492.1	62.m03078	AO070222000005	FG02608.1	NCU00116.1
AN6493.1	62.m03441	AO070222000006	FG02609.1	NCU00117.1
AN6494.1	62.m03081	AO070222000007	FG02610.1	NCU00118.1
AN5456.1	69.m15476	AO070341000410	FG06694.1	NCU00120.1
AN6107.1	72.m19051	AO070340000100	FG05555.1	NCU00121.1
AN2966.1	59.m09423	AO070337000161	FG06655.1	NCU00122.1
AN4201.1	54.m07043	AO070231000023	FG07277.1	NCU00129.1
AN9183.1	55.m03198	AO070315000076	FG01685.1	NCU00130.1
AN0812.1	70.m15412	AO070288000092	FG07274.1	NCU00130.1
AN6687.1	65.m07501	AO070339000094	FG02518.1	NCU00133.1
AN8787.1	71.m15583	AO070276000074	FG06659.1	NCU00134.1
AN6577.1	62.m03163	AO070326000023	FG02594.1	NCU00136.1
AN7742.1	71.m15770	AO070325000166	FG07269.1	NCU00137.1
AN9527.1	62.m03164	AO070326000022	FG02600.1	NCU00147.1
AN6532.1	62.m03120	AO070270000032	FG02599.1	NCU00148.1
AN2293.1	71.m15941	AO070295000072	FG07313.1	NCU00150.1
AN5307.1	70.m15393	AO070316000053	FG07263.1	NCU00153.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1491.1	55.m02999	AO070334000203	FG02532.1	NCU00157.1
AN0632.1	70.m15650	AO070318000122	FG02533.1	NCU00158.1
AN0631.1	70.m15651	AO070318000121	FG02534.1	NCU00159.1
AN3751.1	65.m07382	AO070309000071	FG05442.1	NCU00161.1
AN7302.1	72.m19765	AO070297000048	FG02529.1	NCU00162.1
AN7301.1	72.m19764	AO070297000049	FG02528.1	NCU00163.1
AN7303.1	72.m20021	AO070297000050	FG02527.1	NCU00164.1
AN6139.1	72.m19025	AO070340000063	FG06642.1	NCU00168.1
AN0834.1	70.m15804	AO070255000011	FG06644.1	NCU00169.1
AN4192.1	54.m06754	AO070342000112	FG06678.1	NCU00170.1
AN0268.1	54.m06475	AO070334000074	FG06680.1	NCU00172.1
AN8782.1	71.m15582	AO070289000007	FG06681.1	NCU00173.1
AN6541.1	62.m03133	AO070270000044	FG02506.1	NCU00177.1
AN2499.1	59.m09383	AO070312000049	FG05531.1	NCU00178.1
AN6894.1	71.m16019	AO070314000028	FG05403.1	NCU00181.1
AN6041.1	72.m19117	AO070340000241	FG05405.1	NCU00183.1
AN3805.1	57.m05678	AO070337000222	FG11137.1	NCU00187.1
AN1632.1	58.m07722	AO070299000042	FG05547.1	NCU00188.1
AN1811.1	58.m07714	AO070299000060	FG05545.1	NCU00193.1
AN1810.1	58.m07713	AO070299000061	FG05546.1	NCU00194.1
AN2282.1	71.m16112	AO070295000059	FG04217.1	NCU00195.1
AN7649.1	57.m05407	AO070268000005	FG05543.1	NCU00198.1
AN6341.1	72.m19517	AO070298000009	FG07311.1	NCU00202.1
AN8783.1	71.m15597	AO070289000008	FG05504.1	NCU00205.1
AN7230.1	72.m20024	AO070290000040	FG09085.1	NCU00206.1
AN6143.1	72.m19021	AO070340000060	FG05487.1	NCU00209.1
AN6138.1	72.m19026	AO070340000064	FG05492.1	NCU00213.1
AN6365.1	72.m19495	AO070340000205	FG05495.1	NCU00215.1
AN6366.1	72.m19494	AO070279000052	FG06947.1	NCU00216.1
AN0837.1	70.m15437	AO070255000006	FG06641.1	NCU00219.1
AN4112.1	54.m07047	AO070342000107	FG06666.1	NCU00222.1
AN4900.1	59.m08799	AO070338000044	FG06664.1	NCU00223.1
AN1489.1	55.m02996	AO070334000202	FG06669.1	NCU00226.1
AN0988.1	70.m15629	AO070318000150	FG06637.1	NCU00230.1
AN0951.1	70.m15597	AO070320000152	FG06635.1	NCU00232.1
AN0876.1	70.m15479	AO070320000035	FG06634.1	NCU00236.1
AN0842.1	70.m15442	AO070216000002	FG06631.1	NCU00239.1
AN2862.1	59.m08708	AO070338000160	FG06627.1	NCU00243.1
AN1257.1	56.m02387	AO070327000016	FG10282.1	NCU00244.1
AN4917.1	59.m08820	AO070338000026	FG06588.1	NCU00257.1
AN4916.1	59.m08819	AO070338000027	FG06587.1	NCU00258.1
AN2860.1	59.m08704	AO070338000162	FG06619.1	NCU00260.1
AN8825.1	71.m15957	AO070271000056	FG05558.1	NCU00269.1
AN0038.1	71.m15313	AO070314000116	FG05519.1	NCU00274.1
AN0040.1	71.m15315	AO070314000119	FG05516.1	NCU00276.1
AN1934.1	58.m08870	AO070342000199	FG07035.1	NCU00279.1
AN6596.1	62.m03202	AO070326000045	FG05557.1	NCU00280.1
AN0568.1	69.m15274	AO070272000047	FG04683.1	NCU00289.1
AN6369.1	72.m19491	AO070279000072	FG05589.1	NCU00290.1
AN8204.1	53.m03770	AO070310000113	FG05580.1	NCU00293.1
AN1122.1	70.m15112	AO070331000114	FG06924.1	NCU00294.1
AN7335.1	72.m19736	AO070297000108	FG05515.1	NCU00295.1
AN2591.1	58.m08876	AO070245000015	FG04215.1	NCU00298.1
AN0653.1	70.m15257	AO070343000573	FG05533.1	NCU00303.1
AN0732.1	70.m15321	AO070343000493	FG03725.1	NCU00306.1
AN0625.1	70.m15660	AO070280000077	FG06776.1	NCU00308.1
AN0407.1	54.m06667	AO070338000247	FG05376.1	NCU00310.1
AN0406.1	54.m06668	AO070338000246	FG05377.1	NCU00311.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN0256.1	54.m06525	AO070334000101	FG05380.1	NCU00317.1
AN6304.1	72.m19330	AO070308000059	FG05459.1	NCU00324.1
AN6309.1	72.m19325	AO070308000064	FG05460.1	NCU00325.1
AN1688.1	58.m07763	AO070305000008	FG06649.1	NCU00326.1
AN0634.1	70.m15648	AO070318000124	FG05510.1	NCU00333.1
AN6111.1	72.m19047	AO070340000094	FG05509.1	NCU00334.1
AN5455.1	69.m15477	AO070341000411	FG07262.1	NCU00336.1
AN7260.1	72.m19789	AO070297000018	FG05465.1	NCU00337.1
AN6487.1	62.m03075	AO070222000002	FG05471.1	NCU00338.1
AN2290.1	71.m15938	AO070295000069	FG07310.1	NCU00340.1
AN6068.1	72.m19057	AO070340000109	FG05573.1	NCU00345.1
AN7291.1	72.m20019	AO070297000031	FG06745.1	NCU00349.1
AN6112.1	72.m19046	AO070340000093	FG06743.1	NCU00352.1
AN9339.1	52.m03838	AO070315000069	FG06733.1	NCU00355.1
AN2055.1	58.m07643	AO070292000025	FG06736.1	NCU00357.1
AN1854.1	58.m08938	AO070292000029	FG06735.1	NCU00358.1
AN1859.1	58.m07653	AO070292000036	FG06737.1	NCU00359.1
AN1860.1	58.m08924	AO070292000037	FG06738.1	NCU00360.1
AN6067.1	72.m19056	AO070340000108	FG05425.1	NCU00366.1
AN6348.1	72.m19507	AO070275000017	FG05578.1	NCU00371.1
AN6349.1	72.m19506	AO070275000018	FG06925.1	NCU00372.1
AN4088.1	54.m06733	AO070342000091	FG06917.1	NCU00373.1
AN0953.1	70.m15600	AO070320000154	FG05438.1	NCU00376.1
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AN4080.1	54.m06721	AO070342000072	FG07241.1	NCU00389.1
AN4077.1	54.m06720	AO070342000069	FG07243.1	NCU00392.1
AN5452.1	69.m15743	AO070239000031	FG07245.1	NCU00396.1
AN6064.1	72.m19053	AO070340000104	FG04677.1	NCU00397.1
AN8333.1	52.m03916	AO070330000167	FG07988.1	NCU00399.1
AN8834.1	71.m15964	AO070271000043	FG05466.1	NCU00404.1
AN8835.1	71.m15965	AO070271000044	FG06958.1	NCU00405.1
AN8836.1	71.m15967	AO070271000042	FG06957.1	NCU00406.1
AN8853.1	71.m15988	AO070271000021	FG06927.1	NCU00410.1
AN2272.1	71.m15917	AO070295000048	FG06932.1	NCU00414.1
AN8857.1	71.m15995	AO070271000016	FG06935.1	NCU00417.1
AN6558.1	62.m03146	AO070270000062	FG06937.1	NCU00419.1
AN6560.1	62.m03147	AO070326000001	FG06938.1	NCU00420.1
AN7299.1	72.m19767	AO070297000045	FG06955.1	NCU00422.1
AN7296.1	72.m19770	AO070297000039	FG06953.1	NCU00424.1
AN6893.1	71.m16018	AO070314000027	FG05523.1	NCU00427.1
AN6895.1	71.m15245	AO070314000026	FG05522.1	NCU00428.1
AN7250.1	72.m19799	AO070297000005	FG04095.1	NCU00430.1
AN1105.1	70.m15127	AO070285000033	FG04115.1	NCU00431.1
AN0071.1	71.m15347	AO070314000160	FG04110.1	NCU00432.1
AN6892.1	71.m15247	AO070314000029	FG04111.1	NCU00434.1
AN6898.1	71.m16034	AO070314000023	FG04112.1	NCU00435.1
AN0662.1	70.m15265	AO070343000558	FG04114.1	NCU00438.1
AN0081.1	71.m15359	AO070311000136	FG04104.1	NCU00440.1
AN0082.1	71.m15360	AO070311000135	FG04105.1	NCU00441.1
AN0083.1	71.m16062	AO070311000134	FG04108.1	NCU00444.1
AN6889.1	71.m15250	AO070314000032	FG04109.1	NCU00445.1
AN1103.1	70.m15129	AO070285000035	FG04103.1	NCU00446.1
AN1102.1	70.m15130	AO070285000036	FG04102.1	NCU00447.1
AN2289.1	71.m15936	AO070295000068	FG06890.1	NCU00450.1
AN7252.1	72.m19797	AO070297000007	FG04101.1	NCU00455.1
AN7350.1	72.m19727	AO070278000050	FG02575.1	NCU00457.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN7348.1	72.m19729	AO070278000051	FG02577.1	NCU00459.1
AN7451.1	57.m05891	AO070229000024	FG04117.1	NCU00461.1
AN7354.1	72.m19725	AO070278000046	FG04137.1	NCU00464.1
AN7360.1	72.m19716	AO070278000039	FG04121.1	NCU00465.1
AN2129.1	72.m19712	AO070278000034	FG02584.1	NCU00467.1
AN5959.1	72.m19175	AO070340000312	FG04139.1	NCU00468.1
AN5934.1	72.m19195	AO070340000336	FG04140.1	NCU00469.1
AN1855.1	58.m07647	AO070292000031	FG06730.1	NCU00473.1
AN5441.1	69.m15493	AO070333000104	FG06893.1	NCU00475.1
AN5443.1	69.m15491	AO070333000106	FG06894.1	NCU00476.1
AN5442.1	69.m15492	AO070333000105	FG06895.1	NCU00477.1
AN2740.1	54.m06691	AO070338000231	FG06914.1	NCU00478.1
AN6354.1	72.m19501	AO070275000057	FG06912.1	NCU00480.1
AN8044.1	53.m03900	AO070292000105	FG06911.1	NCU00481.1
AN4543.1	57.m05576	AO070321000163	FG05429.1	NCU00487.1
AN4087.1	54.m06728	AO070342000080	FG05433.1	NCU00489.1
AN0924.1	70.m15807	AO070320000103	FG05434.1	NCU00490.1
AN0922.1	70.m15529	AO070320000101	FG05436.1	NCU00493.1
AN4066.1	54.m06710	AO070342000056	FG06926.1	NCU00495.1
AN0955.1	70.m15604	AO070320000157	FG06901.1	NCU00497.1
AN0947.1	70.m15586	AO070320000146	FG06900.1	NCU00498.1
AN1536.1	55.m03054	AO070334000256	FG00515.1	NCU00499.1
AN1533.1	55.m03051	AO070334000253	FG00372.1	NCU00501.1
AN1534.1	55.m03052	AO070334000254	FG00373.1	NCU00502.1
AN2104.1	57.m05805	AO070341000262	FG00357.1	NCU00504.1
AN2105.1	57.m05806	AO070341000263	FG00358.1	NCU00505.1
AN7588.1	72.m19610	AO070343000302	FG00589.1	NCU00519.1
AN7554.1	72.m19572	AO070277000055	FG00590.1	NCU00520.1
AN0681.1	71.m15200	AO070303000069	FG00454.1	NCU00522.1
AN4633.1	57.m05544	AO070340000373	FG09220.1	NCU00527.1
AN4632.1	57.m05543	AO070340000375	FG09221.1	NCU00528.1
AN8565.1	71.m15702	AO070311000007	FG00186.1	NCU00536.1
AN1451.1	55.m02953	AO070302000016	FG00185.1	NCU00537.1
AN7749.1	71.m15779	AO070325000178	FG00243.1	NCU00541.1
AN5236.1	71.m15778	AO070325000177	FG00257.1	NCU00542.1
AN4706.1	71.m15694	AO070329000170	FG08719.1	NCU00551.1
AN4793.1	59.m09188	AO070329000053	FG08498.1	NCU00554.1
AN4771.1	59.m09211	AO070329000081	FG00265.1	NCU00560.1
AN4768.1	59.m09217	AO070329000089	FG09414.1	NCU00562.1
AN4611.1	57.m05983	AO070267000026	FG00168.1	NCU00564.1
AN9486.1	59.m09213	AO070329000083	FG09444.1	NCU00565.1
AN8769.1	62.m03316	AO070343000429	FG08537.1	NCU00566.1
AN4219.1	54.m06799	AO070315000080	FG08551.1	NCU00570.1
AN4220.1	54.m06798	AO070315000079	FG08550.1	NCU00571.1
AN0866.1	70.m15462	AO070320000017	FG08548.1	NCU00573.1
AN8686.1	62.m03486	AO070315000105	FG08776.1	NCU00577.1
AN8680.1	62.m03391	AO070315000100	FG08777.1	NCU00578.1
AN9063.1	66.m04527	AO070332000210	FG08586.1	NCU00579.1
AN0868.1	70.m15459	AO070320000019	FG08585.1	NCU00580.1
AN6140.1	72.m19024	AO070340000062	FG08779.1	NCU00581.1
AN4615.1	57.m05532	AO070267000032	FG08692.1	NCU00586.1
AN0931.1	70.m15539	AO070320000122	FG08691.1	NCU00587.1
AN0930.1	70.m15538	AO070320000120	FG08690.1	NCU00589.1
AN4690.1	71.m15673	AO070284000045	FG08688.1	NCU00591.1
AN4783.1	59.m09200	AO070329000067	FG00182.1	NCU00593.1
AN4613.1	57.m05530	AO070267000029	FG09447.1	NCU00599.1
AN4782.1	59.m09201	AO070329000068	FG00170.1	NCU00600.1
AN4774.1	59.m09209	AO070329000078	FG09448.1	NCU00602.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN4714.1	71.m16089	AO070337000217	FG09413.1	NCU00605.1
AN4659.1	71.m15715	AO070316000143	FG09424.1	NCU00608.1
AN4716.1	71.m15704	AO070311000005	FG09425.1	NCU00609.1
AN4728.1	71.m15638	AO070284000080	FG00261.1	NCU00614.1
AN4635.1	57.m05546	AO070248000030	FG06405.1	NCU00615.1
AN4561.1	57.m05556	AO070321000186	FG06406.1	NCU00617.1
AN4777.1	59.m09469	AO070329000074	FG06407.1	NCU00618.1
AN0846.1	70.m15445	AO070216000005	FG06408.1	NCU00619.1
AN4639.1	57.m05552	AO070321000194	FG08704.1	NCU00621.1
AN4564.1	57.m05553	AO070321000192	FG08703.1	NCU00622.1
AN6626.1	62.m03217	AO070315000108	FG05676.1	NCU00623.1
AN6628.1	62.m03224	AO070326000079	FG08784.1	NCU00624.1
AN3224.1	67.m02932	AO070330000074	FG08541.1	NCU00628.1
AN3223.1	67.m02931	AO070330000073	FG09456.1	NCU00629.1
AN5483.1	69.m15470	AO070341000402	FG08540.1	NCU00631.1
AN7550.1	72.m19567	AO070277000047	FG08539.1	NCU00632.1
AN6629.1	62.m03225	AO070326000081	FG08561.1	NCU00634.1
AN6630.1	62.m03226	AO070326000082	FG08560.1	NCU00635.1
AN0756.1	70.m15358	AO070343000444	FG03904.1	NCU00642.1
AN0942.1	70.m15574	AO070320000137	FG00655.1	NCU00643.1
AN0943.1	70.m15575	AO070320000138	FG00656.1	NCU00644.1
AN9116.1	66.m04582	AO070332000151	FG00269.1	NCU00649.1
AN3794.1	57.m05968	AO070337000233	FG00270.1	NCU00650.1
AN3787.1	57.m05696	AO070337000242	FG00271.1	NCU00651.1
AN9401.1	52.m04028	AO070274000016	FG08521.1	NCU00655.1
AN4709.1	71.m15697	AO070329000166	FG08522.1	NCU00656.1
AN4711.1	71.m15699	AO070329000164	FG11353.1	NCU00659.1
AN4672.1	71.m15660	AO070284000034	FG06411.1	NCU00662.1
AN4707.1	71.m15695	AO070329000169	FG00188.1	NCU00664.1
AN9402.1	52.m04029	AO070274000015	FG00259.1	NCU00665.1
AN4719.1	71.m15707	AO070311000002	FG08572.1	NCU00668.1
AN4683.1	71.m15667	AO070284000018	FG00189.1	NCU00669.1
AN0239.1	71.m15643	AO070284000068	FG00191.1	NCU00671.1
AN0238.1	71.m15644	AO070284000067	FG00192.1	NCU00673.1
AN2496.1	59.m08494	AO070312000124	FG08819.1	NCU00675.1
AN9062.1	66.m04526	AO070332000211	FG08841.1	NCU00676.1
AN6639.1	62.m03234	AO070326000091	FG08851.1	NCU00680.1
AN7784.1	71.m15815	AO070286000028	FG08728.1	NCU00681.1
AN4717.1	71.m15705	AO070311000004	FG08729.1	NCU00682.1
AN4563.1	57.m05554	AO070321000191	FG08731.1	NCU00685.1
AN8691.1	62.m03474	AO070315000112	FG08642.1	NCU00690.1
AN4616.1	57.m05533	AO070267000033	FG08644.1	NCU00692.1
AN4617.1	57.m05535	AO070267000034	FG08645.1	NCU00693.1
AN0768.1	70.m15371	AO070316000076	FG02859.1	NCU00695.1
AN2985.1	59.m09028	AO070337000137	FG03726.1	NCU00711.1
AN3817.1	57.m05666	AO070311000014	FG09197.1	NCU00712.1
AN3809.1	57.m05673	AO070337000220	FG09196.1	NCU00713.1
AN6226.1	72.m19427	AO070304000076	FG01713.1	NCU00722.1
AN6721.1	53.m03953	AO070335000072	FG05798.1	NCU00722.1
AN3814.1	57.m05668	AO070311000012	FG00777.1	NCU00726.1
AN9125.1	66.m04585	AO070332000149	FG00778.1	NCU00727.1
AN2327.1	71.m15526	AO070323000030	FG05028.1	NCU00736.1
AN0356.1	54.m06398	AO070318000032	FG05024.1	NCU00741.1
AN0351.1	54.m06404	AO070318000028	FG05023.1	NCU00742.1
AN0352.1	54.m06403	AO070318000029	FG09704.1	NCU00743.1
AN8122.1	53.m03834	AO070322000030	FG09697.1	NCU00754.1
AN0581.1	69.m15267	AO070280000003	FG03080.1	NCU00755.1
AN1433.1	55.m02939	AO070232000013	FG03601.1	NCU00761.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN9090.1	66.m04770	AO070332000188	FG05737.1	NCU00768.1
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AN5675.1	65.m07401	AO070309000090	FG05735.1	NCU00771.1
AN5790.1	69.m14806	AO070249000036	FG05733.1	NCU00775.1
AN7060.1	70.m15693	AO070336000179	FG05628.1	NCU00776.1
AN5789.1	69.m14807	AO070249000035	FG05728.1	NCU00777.1
AN0628.1	70.m15655	AO070299000112	FG09696.1	NCU00780.1
AN0375.1	54.m06372	AO070228000007	FG05238.1	NCU00782.1
AN1111.1	70.m15122	AO070285000025	FG09695.1	NCU00784.1
AN0385.1	54.m06359	AO070318000082	FG05696.1	NCU00792.1
AN4262.1	65.m07437	AO070277000028	FG05697.1	NCU00793.1
AN0361.1	54.m06388	AO070318000041	FG05698.1	NCU00794.1
AN3378.1	53.m03951	AO070317000065	FG09214.1	NCU00799.1
AN9377.1	52.m03906	AO070315000006	FG04176.1	NCU00811.1
AN3812.1	57.m05670	AO070311000009	FG09363.1	NCU00812.1
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AN4492.1	57.m05639	AO070311000044	FG00781.1	NCU00823.1
AN4493.1	57.m05638	AO070343000131	FG00780.1	NCU00824.1
AN1483.1	55.m03255	AO070334000189	FG00622.1	NCU00828.1
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AN3813.1	57.m05669	AO070311000011	FG00773.1	NCU00830.1
AN7231.1	72.m19815	AO070290000019	FG02204.1	NCU00831.1
AN3772.1	63.m00625	AO070330000061	FG09303.1	NCU00860.1
AN8099.1	72.m19551	AO070309000130	FG06612.1	NCU00865.1
AN9483.1	56.m02448	AO070313000069	FG11114.1	NCU00866.1
AN7705.1	71.m15730	AO070325000111	FG02812.1	NCU00879.1
AN7704.1	71.m15725	AO070325000110	FG02811.1	NCU00880.1
AN4702.1	71.m15684	AO070329000178	FG02810.1	NCU00881.1
AN4701.1	71.m15685	AO070329000177	FG02809.1	NCU00882.1
AN4177.1	56.m02500	AO070319000001	FG02822.1	NCU00884.1
AN9072.1	66.m04522	AO070332000216	FG00808.1	NCU00889.1
AN3368.1	66.m04636	AO070281000024	FG04679.1	NCU00890.1
AN9064.1	66.m04521	AO070332000217	FG04922.1	NCU00891.1
AN3840.1	58.m07816	AO070305000075	FG00684.1	NCU00892.1
AN3843.1	58.m07819	AO070305000078	FG00686.1	NCU00894.1
AN3841.1	58.m07817	AO070305000076	FG00688.1	NCU00896.1
AN0430.1	54.m06619	AO070338000280	FG00716.1	NCU00897.1
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AN3619.1	58.m07406	AO070342000161	FG00711.1	NCU00901.1
AN3607.1	58.m07405	AO070342000160	FG00710.1	NCU00902.1
AN9066.1	66.m04520	AO070332000218	FG00706.1	NCU00904.1
AN0827.1	70.m15428	AO070255000018	FG00700.1	NCU00913.1
AN4550.1	57.m05560	AO070321000181	FG04554.1	NCU00915.1
AN9070.1	66.m04524	AO070332000215	FG00698.1	NCU00918.1
AN0944.1	70.m15576	AO070320000139	FG00877.1	NCU00919.1
AN3362.1	66.m04778	AO070281000034	FG00690.1	NCU00920.1
AN3802.1	57.m05972	AO070337000226	FG00691.1	NCU00921.1
AN3803.1	57.m05973	AO070337000224	FG00693.1	NCU00923.1
AN3826.1	58.m07802	AO070305000062	FG00694.1	NCU00924.1
AN3827.1	58.m07803	AO070305000064	FG00695.1	NCU00925.1
AN3363.1	66.m04629	AO070281000032	FG00697.1	NCU00927.1
AN0428.1	54.m06617	AO070338000279	FG00875.1	NCU00931.1
AN3829.1	58.m07805	AO070305000066	FG06752.1	NCU00936.1
AN3620.1	58.m07407	AO070342000132	FG00281.1	NCU00942.1
AN7564.1	72.m19997	AO070343000407	FG05623.1	NCU00944.1
AN2967.1	59.m09040	AO070337000149	FG06863.1	NCU00950.1
AN2968.1	59.m09041	AO070337000151	FG00496.1	NCU00951.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN0293.1	54.m06491	AO070334000049	FG00587.1	NCU00954.1
AN5400.1	69.m15773	AO070333000134	FG03163.1	NCU00955.1
AN1445.1	55.m02948	AO070302000002	FG01355.1	NCU00956.1
AN1467.1	55.m02969	AO070306000090	FG05611.1	NCU00958.1
AN2332.1	71.m15534	AO070323000014	FG05610.1	NCU00959.1
AN1524.1	55.m03268	AO070334000242	FG00417.1	NCU00963.1
AN1525.1	55.m03280	AO070334000243	FG05600.1	NCU00965.1
AN1526.1	55.m03269	AO070334000244	FG05601.1	NCU00966.1
AN1444.1	55.m02947	AO070302000001	FG00393.1	NCU00969.1
AN5997.1	72.m19143	AO070340000279	FG00395.1	NCU00971.1
AN5727.1	54.m06847	AO070324000124	FG11048.1	NCU00972.1
AN2927.1	59.m09068	AO070337000182	FG01137.1	NCU00978.1
AN5996.1	72.m19144	AO070340000281	FG05605.1	NCU00979.1
AN2926.1	59.m09069	AO070337000185	FG01135.1	NCU00981.1
AN2395.1	72.m19542	AO070298000064	FG03320.1	NCU00985.1
AN5734.1	69.m14862	AO070341000025	FG06235.1	NCU00988.1
AN4377.1	58.m07955	AO070261000012	FG07387.1	NCU00998.1
AN4375.1	58.m07954	AO070261000014	FG07446.1	NCU00999.1
AN6743.1	66.m04708	AO070313000143	FG04970.1	NCU01000.1
AN0665.1	70.m15268	AO070343000555	FG10180.1	NCU01002.1
AN3188.1	59.m08502	AO070312000135	FG10007.1	NCU01004.1
AN7450.1	57.m05893	AO070229000023	FG10217.1	NCU01006.1
AN6171.1	72.m19002	AO070340000034	FG10219.1	NCU01008.1
AN1403.1	70.m14821	AO070233000018	FG10080.1	NCU01013.1
AN1350.1	70.m14882	AO070237000010	FG10072.1	NCU01016.1
AN1354.1	70.m14876	AO070237000006	FG10076.1	NCU01022.1
AN1348.1	70.m14885	AO070247000017	FG10077.1	NCU01023.1
AN1950.1	58.m07346	AO070342000218	FG10167.1	NCU01036.1
AN8361.1	57.m05343	AO070286000054	FG02643.1	NCU01039.1
AN7745.1	71.m15773	AO070325000172	FG02090.1	NCU01047.1
AN2110.1	57.m05816	AO070341000275	FG02691.1	NCU01057.1
AN2045.1	58.m07633	AO070292000012	FG01892.1	NCU01059.1
AN1181.1	70.m15760	AO070331000179	FG00620.1	NCU01065.1
AN1808.1	65.m07153	AO070319000057	FG04716.1	NCU01066.1
AN2211.1	71.m15854	AO070294000011	FG02126.1	NCU01067.1
AN8831.1	71.m15962	AO070271000048	FG02092.1	NCU01069.1
AN8832.1	71.m15963	AO070271000047	FG02093.1	NCU01070.1
AN7663.1	57.m05430	AO070268000034	FG02407.1	NCU01078.1
AN8231.1	53.m03738	AO070310000077	FG09035.1	NCU01083.1
AN4099.1	69.m15711	AO070343000059	FG09059.1	NCU01089.1
AN3888.1	72.m19605	AO070343000294	FG08575.1	NCU01095.1
AN8796.1	71.m15603	AO070276000064	FG05865.1	NCU01099.1
AN8228.1	53.m03745	AO070310000083	FG05864.1	NCU01100.1
AN3305.1	71.m15151	AO070329000026	FG07570.1	NCU01107.1
AN4105.1	54.m07046	AO070342000105	FG06995.1	NCU01111.1
AN8404.1	52.m03910	AO070276000017	FG02975.1	NCU01112.1
AN8806.1	71.m16076	AO070276000052	FG05955.1	NCU01116.1
AN8805.1	71.m15612	AO070276000053	FG05948.1	NCU01121.1
AN3083.1	52.m03887	AO070339000016	FG07661.1	NCU01123.1
AN4148.1	58.m07369	AO070342000182	FG01484.1	NCU01132.1
AN2037.1	55.m03233	AO070281000048	FG02886.1	NCU01138.1
AN8060.1	54.m06354	AO070323000153	FG08346.1	NCU01138.1
AN2261.1	71.m15902	AO070326000103	FG09004.1	NCU01141.1
AN2140.1	72.m20004	AO070343000185	FG07412.1	NCU01146.1
AN8145.1	71.m15392	AO070311000100	FG03521.1	NCU01149.1
AN3150.1	59.m08509	AO070191000004	FG09991.1	NCU01157.1
AN7659.1	57.m05423	AO070268000028	FG10087.1	NCU01160.1
AN7658.1	57.m05422	AO070268000027	FG10361.1	NCU01161.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN7657.1	57.m05419	AO070268000020	FG09980.1	NCU01162.1
AN5102.1	54.m06919	AO070291000077	FG10040.1	NCU01164.1
AN5100.1	54.m06960	AO070291000079	FG10041.1	NCU01165.1
AN4987.1	59.m08890	AO070288000055	FG09908.1	NCU01166.1
AN4244.1	54.m06806	AO070324000168	FG09907.1	NCU01167.1
AN8810.1	71.m15616	AO070276000047	FG06805.1	NCU01170.1
AN7994.1	53.m03853	AO070322000052	FG06777.1	NCU01171.1
AN7993.1	53.m03854	AO070322000053	FG06778.1	NCU01172.1
AN8013.1	53.m03861	AO070322000061	FG06781.1	NCU01174.1
AN8012.1	53.m03860	AO070322000060	FG06784.1	NCU01175.1
AN8032.1	53.m03880	AO070322000129	FG06786.1	NCU01177.1
AN6510.1	62.m03096	AO070270000003	FG07331.1	NCU01179.1
AN2267.1	71.m16116	AO070295000039	FG07332.1	NCU01180.1
AN2244.1	71.m15878	AO070326000129	FG05139.1	NCU01183.1
AN2245.1	71.m15879	AO070326000128	FG05138.1	NCU01184.1
AN2247.1	71.m15881	AO070326000126	FG05136.1	NCU01186.1
AN2246.1	71.m15880	AO070326000127	FG05135.1	NCU01187.1
AN0226.1	71.m16095	AO070284000066	FG05134.1	NCU01188.1
AN6515.1	62.m03102	AO070270000010	FG07320.1	NCU01190.1
AN7325.1	72.m19745	AO070297000077	FG07175.1	NCU01192.1
AN4376.1	58.m07953	AO070261000018	FG07174.1	NCU01195.1
AN1158.1	70.m15083	AO070331000148	FG07009.1	NCU01197.1
AN4467.1	58.m07853	AO070305000123	FG07439.1	NCU01200.1
AN5685.1	65.m07411	AO070309000100	FG07442.1	NCU01203.1
AN5686.1	65.m07412	AO070309000101	FG07443.1	NCU01204.1
AN5687.1	65.m07413	AO070309000102	FG07444.1	NCU01205.1
AN6550.1	62.m03123	AO070270000035	FG05195.1	NCU01210.1
AN7732.1	71.m15754	AO070325000143	FG02049.1	NCU01211.1
AN4216.1	54.m06773	AO070231000008	FG02096.1	NCU01218.1
AN4215.1	54.m06772	AO070231000009	FG02097.1	NCU01219.1
AN4202.1	54.m06762	AO070231000022	FG02099.1	NCU01221.1
AN2295.1	71.m15944	AO070295000075	FG02030.1	NCU01227.1
AN2294.1	71.m15943	AO070295000074	FG02040.1	NCU01229.1
AN6095.1	72.m19092	AO070340000163	FG05882.1	NCU01231.1
AN8016.1	53.m03863	AO070322000065	FG05858.1	NCU01234.1
AN8015.1	53.m04142	AO070322000064	FG05857.1	NCU01235.1
AN8211.1	53.m03763	AO070310000102	FG05855.1	NCU01238.1
AN8797.1	71.m15604	AO070276000063	FG05861.1	NCU01240.1
AN8785.1	65.m07308	AO070289000010	FG07131.1	NCU01241.1
AN2136.1	72.m19704	AO070343000181	FG07133.1	NCU01243.1
AN2144.1	72.m19697	AO070343000192	FG07138.1	NCU01246.1
AN2143.1	72.m19698	AO070343000190	FG07139.1	NCU01247.1
AN2141.1	72.m19700	AO070343000187	FG07140.1	NCU01248.1
AN2142.1	72.m19699	AO070343000188	FG07141.1	NCU01249.1
AN0275.1	54.m06468	AO070334000082	FG07129.1	NCU01250.1
AN0078.1	71.m15357	AO070311000137	FG07456.1	NCU01252.1
AN1076.1	70.m15150	AO070285000076	FG07454.1	NCU01254.1
AN1093.1	70.m15138	AO070285000054	FG07453.1	NCU01255.1
AN1092.1	70.m15139	AO070285000055	FG06147.1	NCU01256.1
AN7331.1	72.m19738	AO070297000093	FG07458.1	NCU01258.1
AN2146.1	72.m19695	AO070343000195	FG07460.1	NCU01259.1
AN0664.1	70.m15267	AO070343000556	FG05898.1	NCU01266.1
AN2965.1	59.m09050	AO070337000162	FG01908.1	NCU01269.1
AN3846.1	58.m07821	AO070305000083	FG05903.1	NCU01271.1
AN3853.1	58.m07830	AO070305000093	FG05902.1	NCU01272.1
AN3852.1	58.m07832	AO070305000091	FG05918.1	NCU01274.1
AN3855.1	58.m07827	AO070305000095	FG05919.1	NCU01275.1
AN2745.1	54.m06686	AO070338000226	FG01906.1	NCU01276.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN1382.1	70.m14839	AO070243000014	FG10376.1	NCU01279.1
AN4240.1	54.m06803	AO070324000174	FG10092.1	NCU01282.1
AN9101.1	66.m04562	AO070332000172	FG10185.1	NCU01284.1
AN4482.1	57.m05649	AO070311000031	FG07881.1	NCU01285.1
AN8851.1	71.m15986	AO070271000025	FG07206.1	NCU01290.1
AN6536.1	62.m03136	AO070270000048	FG06093.1	NCU01300.1
AN0266.1	54.m06496	AO070334000087	FG01895.1	NCU01310.1
AN0265.1	54.m06967	AO070334000094	FG01916.1	NCU01315.1
AN0261.1	54.m06965	AO070334000097	FG01917.1	NCU01318.1
AN6114.1	72.m19045	AO070340000090	FG01896.1	NCU01321.1
AN6166.1	72.m19013	AO070340000049	FG01903.1	NCU01322.1
AN2963.1	59.m09052	AO070337000166	FG01910.1	NCU01323.1
AN2940.1	59.m09054	AO070337000170	FG01909.1	NCU01324.1
AN7680.1	57.m05457	AO070325000070	FG10348.1	NCU01327.1
AN0688.1	70.m15291	AO070343000525	FG09998.1	NCU01328.1
AN0925.1	70.m15533	AO070320000104	FG10000.1	NCU01330.1
AN1319.1	57.m05886	AO070287000068	FG10001.1	NCU01331.1
AN3088.1	59.m09372	AO070266000041	FG10002.1	NCU01332.1
AN5184.1	54.m07057	AO070291000019	FG10003.1	NCU01333.1
AN4385.1	58.m08969	AO070261000030	FG10381.1	NCU01335.1
AN4384.1	58.m07940	AO070261000029	FG10379.1	NCU01337.1
AN2510.1	59.m09341	AO070263000047	FG10378.1	NCU01338.1
AN2911.1	59.m09396	AO070338000094	FG10142.1	NCU01345.1
AN6869.1	71.m15260	AO070314000053	FG02206.1	NCU01348.1
AN4645.1	57.m05476	AO070316000119	FG10018.1	NCU01356.1
AN4188.1	54.m06746	AO070342000109	FG01911.1	NCU01361.1
AN0077.1	71.m16046	AO070311000138	FG07012.1	NCU01364.1
AN4456.1	58.m07868	AO070173000001	FG06802.1	NCU01367.1
AN4457.1	58.m07867	AO070305000136	FG06803.1	NCU01368.1
AN5931.1	72.m19952	AO070340000344	FG04132.1	NCU01369.1
AN7723.1	71.m15750	AO070325000138	FG06122.1	NCU01370.1
AN2493.1	59.m08496	AO070312000127	FG07375.1	NCU01376.1
AN8002.1	53.m03844	AO070322000044	FG06092.1	NCU01377.1
AN1482.1	55.m02988	AO070334000186	FG06090.1	NCU01378.1
AN8000.1	53.m04194	AO070322000046	FG06089.1	NCU01379.1
AN8120.1	53.m03831	AO070322000028	FG07371.1	NCU01387.1
AN8119.1	53.m03830	AO070322000027	FG07370.1	NCU01388.1
AN8167.1	53.m03810	AO070266000001	FG05979.1	NCU01395.1
AN5638.1	58.m07325	AO070342000239	FG10110.1	NCU01397.1
AN0657.1	70.m15789	AO070343000569	FG10106.1	NCU01401.1
AN9108.1	66.m04760	AO070332000164	FG09040.1	NCU01402.1
AN9099.1	66.m04767	AO070332000175	FG10105.1	NCU01409.1
AN5656.1	58.m08892	AO070342000244	FG10120.1	NCU01411.1
AN5799.1	72.m18927	AO070260000050	FG10121.1	NCU01412.1
AN5833.1	72.m18961	AO070260000012	FG10126.1	NCU01417.1
AN7194.1	54.m06399	AO070197000003	FG10124.1	NCU01419.1
AN5005.1	59.m08905	AO070255000035	FG09912.1	NCU01421.1
AN2996.1	59.m09439	AO070337000121	FG10179.1	NCU01422.1
AN7594.1	72.m19619	AO070343000316	FG10177.1	NCU01424.1
AN0654.1	70.m15258	AO070343000572	FG10097.1	NCU01427.1
AN2409.1	62.m03436	AO070298000018	FG05221.1	NCU01429.1
AN5733.1	69.m14863	AO070341000027	FG06234.1	NCU01430.1
AN8863.1	71.m16001	AO070271000008	FG07467.1	NCU01438.1
AN8866.1	71.m16005	AO070271000005	FG07468.1	NCU01439.1
AN8862.1	71.m16000	AO070271000009	FG07469.1	NCU01440.1
AN8868.1	71.m16007	AO070271000003	FG07473.1	NCU01444.1
AN8869.1	71.m16009	AO070271000002	FG07475.1	NCU01446.1
AN7660.1	57.m05936	AO070268000029	FG07477.1	NCU01449.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN8870.1	71.m16010	AO070271000001	FG07480.1	NCU01452.1
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AN6913.1	71.m15219	AO070219000018	FG06107.1	NCU01457.1
AN6119.1	72.m19041	AO070340000085	FG01898.1	NCU01464.1
AN6851.1	71.m16037	AO070314000088	FG08998.1	NCU01471.1
AN6842.1	71.m15299	AO070314000097	FG09002.1	NCU01473.1
AN6843.1	71.m15300	AO070314000096	FG09003.1	NCU01474.1
AN4558.1	57.m05570	AO070321000170	FG06810.1	NCU01478.1
AN4557.1	57.m05569	AO070321000171	FG06816.1	NCU01479.1
AN4428.1	58.m09004	AO070273000065	FG04398.1	NCU01481.1
AN5741.1	69.m14856	AO070341000018	FG04401.1	NCU01485.1
AN4413.1	58.m08967	AO070273000034	FG04361.1	NCU01486.1
AN4410.1	58.m07898	AO070273000030	FG04362.1	NCU01487.1
AN2005.1	58.m07613	AO070301000107	FG04363.1	NCU01489.1
AN6243.1	72.m19414	AO070304000097	FG04418.1	NCU01498.1
AN6265.1	72.m19392	AO070304000023	FG04404.1	NCU01502.1
AN6266.1	72.m19391	AO070304000022	FG04403.1	NCU01503.1
AN6249.1	72.m19407	AO070304000039	FG01450.1	NCU01504.1
AN5624.1	58.m07546	AO070301000021	FG04378.1	NCU01510.1
AN0232.1	72.m19983	AO070304000024	FG04402.1	NCU01511.1
AN6253.1	72.m19404	AO070304000103	FG01449.1	NCU01512.1
AN6254.1	72.m19981	AO070304000034	FG01448.1	NCU01514.1
AN6252.1	72.m19410	AO070304000035	FG01447.1	NCU01515.1
AN6248.1	72.m19405	AO070304000104	FG00305.1	NCU01516.1
AN7402.1	57.m05372	AO070293000033	FG06278.1	NCU01517.1
AN0347.1	54.m06410	AO070318000025	FG04327.1	NCU01523.1
AN8042.1	53.m04190	AO070330000004	FG04324.1	NCU01525.1
AN8041.1	53.m03905	AO070330000005	FG06257.1	NCU01528.1
AN6258.1	72.m19398	AO070304000030	FG04329.1	NCU01535.1
AN5121.1	54.m06903	AO070291000058	FG10738.1	NCU01547.1
AN5126.1	54.m06899	AO070291000052	FG10736.1	NCU01549.1
AN5122.1	54.m06902	AO070291000057	FG10737.1	NCU01550.1
AN2172.1	72.m19668	AO070343000243	FG04355.1	NCU01563.1
AN0115.1	71.m15391	AO070311000099	FG04351.1	NCU01569.1
AN0114.1	71.m15390	AO070311000098	FG04358.1	NCU01570.1
AN1981.1	58.m08945	AO070301000066	FG10730.1	NCU01571.1
AN2169.1	72.m19671	AO070343000239	FG10727.1	NCU01575.1
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AN6089.1	72.m19080	AO070340000143	FG06246.1	NCU01589.1
AN4226.1	54.m06790	AO070234000023	FG01446.1	NCU01595.1
AN9303.1	59.m08580	AO070275000031	FG00828.1	NCU01598.1
AN3178.1	59.m08579	AO070256000001	FG00827.1	NCU01599.1
AN6288.1	72.m19347	AO070308000004	FG00301.1	NCU01605.1
AN6287.1	72.m19348	AO070308000005	FG00300.1	NCU01606.1
AN0145.1	71.m15429	AO070321000098	FG01557.1	NCU01608.1
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AN0134.1	71.m15418	AO070321000119	FG10756.1	NCU01613.1
AN2456.1	69.m15673	AO070264000017	FG10760.1	NCU01615.1
AN9436.1	70.m15786	AO070343000484	FG04295.1	NCU01625.1
AN0734.1	70.m15319	AO070343000495	FG05491.1	NCU01634.1
AN0733.1	70.m15320	AO070343000494	FG04290.1	NCU01635.1
AN3849.1	58.m07833	AO070332000050	FG07224.1	NCU01636.1
AN0727.1	70.m15330	AO070343000486	FG04292.1	NCU01637.1
AN0707.1	70.m15314	AO070343000502	FG10716.1	NCU01643.1
AN0706.1	70.m15313	AO070343000503	FG10717.1	NCU01644.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN5107.1	54.m06915	AO070291000072	FG01533.1	NCU01646.1
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AN5105.1	54.m06917	AO070291000074	FG01535.1	NCU01648.1
AN8277.1	53.m04091	AO070310000023	FG01417.1	NCU01652.1
AN8280.1	53.m03681	AO070310000020	FG01419.1	NCU01654.1
AN4349.1	58.m07968	AO070240000029	FG06284.1	NCU01659.1
AN4430.1	58.m07895	AO070273000027	FG06282.1	NCU01666.1
AN4409.1	58.m07897	AO070273000029	FG06281.1	NCU01667.1
AN4408.1	58.m07896	AO070273000028	FG06280.1	NCU01668.1
AN3096.1	59.m08647	AO070334000138	FG10718.1	NCU01669.1
AN6267.1	72.m19390	AO070304000021	FG06277.1	NCU01674.1
AN6200.1	72.m19298	AO070308000096	FG01553.1	NCU01675.1
AN0318.1	54.m06983	AO070334000014	FG01425.1	NCU01680.1
AN8274.1	53.m03686	AO070310000027	FG01421.1	NCU01689.1
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AN5116.1	54.m06907	AO070291000063	FG00317.1	NCU01713.1
AN6049.1	72.m19110	AO070340000217	FG00316.1	NCU01715.1
AN3925.1	69.m15003	AO070324000121	FG00314.1	NCU01720.1
AN5155.1	54.m06863	AO070291000012	FG01444.1	NCU01725.1
AN5144.1	54.m06876	AO070291000029	FG01445.1	NCU01728.1
AN5157.1	54.m07060	AO070291000010	FG01439.1	NCU01737.1
AN5127.1	54.m06892	AO070291000046	FG01435.1	NCU01741.1
AN5134.1	54.m06889	AO070291000041	FG01433.1	NCU01744.1
AN5143.1	54.m06878	AO070291000032	FG01432.1	NCU01745.1
AN0137.1	71.m15420	AO070321000115	FG01473.1	NCU01747.1
AN0315.1	54.m06443	AO070334000017	FG00640.1	NCU01750.1
AN1014.1	70.m15232	AO070312000004	FG06012.1	NCU01751.1
AN3767.1	65.m07499	AO070309000038	FG09141.1	NCU01753.1
AN8979.1	66.m04668	AO070295000065	FG10855.1	NCU01754.1
AN0140.1	71.m15423	AO070321000112	FG10856.1	NCU01756.1
AN0139.1	71.m15422	AO070321000113	FG10857.1	NCU01757.1
AN5110.1	54.m07050	AO070291000069	FG05197.1	NCU01758.1
AN5109.1	54.m06913	AO070296000005	FG06240.1	NCU01759.1
AN9411.1	53.m04180	AO070310000008	FG05198.1	NCU01765.1
AN5722.1	54.m06842	AO070324000128	FG05205.1	NCU01767.1
AN6286.1	72.m19991	AO070308000006	FG00299.1	NCU01768.1
AN1051.1	70.m15778	AO070336000071	FG00844.1	NCU01771.1
AN0321.1	54.m06984	AO070334000005	FG00843.1	NCU01772.1
AN0445.1	54.m06637	AO070338000307	FG00845.1	NCU01776.1
AN0446.1	54.m06638	AO070338000308	FG00846.1	NCU01777.1
AN3169.1	59.m09379	AO070256000021	FG10840.1	NCU01786.1
AN2701.1	71.m15184	AO070313000083	FG10835.1	NCU01789.1
AN6920.1	71.m15192	AO070313000059	FG10832.1	NCU01791.1
AN6922.1	71.m15188	AO070313000063	FG10829.1	NCU01795.1
AN0144.1	71.m15427	AO070321000101	FG04382.1	NCU01797.1
AN6250.1	72.m19408	AO070304000038	FG10878.1	NCU01803.1
AN6251.1	72.m19409	AO070304000036	FG10876.1	NCU01804.1
AN6244.1	72.m19413	AO070304000098	FG10879.1	NCU01806.1
AN6245.1	72.m19412	AO070304000099	FG10880.1	NCU01807.1
AN1366.1	70.m14863	AO070215000015	FG10882.1	NCU01809.1
AN5152.1	54.m07059	AO070291000016	FG06003.1	NCU01814.1
AN3093.1	59.m08651	AO070334000133	FG05993.1	NCU01817.1
AN1342.1	70.m14891	AO070247000022	FG10893.1	NCU01821.1
AN1341.1	70.m15733	AO070247000023	FG01552.1	NCU01822.1
AN3102.1	59.m08641	AO070334000143	FG05996.1	NCU01823.1
AN3112.1	59.m08626	AO070303000038	FG05997.1	NCU01824.1
AN3113.1	59.m09373	AO070303000036	FG05998.1	NCU01826.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN4222.1	54.m06795	AO070234000028	FG05999.1	NCU01827.1
AN3101.1	59.m08643	AO070334000142	FG05990.1	NCU01833.1
AN8900.1	66.m04787	AO070317000064	FG02944.1	NCU01839.1
AN3134.1	59.m08591	AO070303000010	FG05985.1	NCU01843.1
AN4983.1	59.m08885	AO070288000051	FG05987.1	NCU01845.1
AN4310.1	58.m09009	AO070207000015	FG01544.1	NCU01847.1
AN5113.1	54.m07051	AO070291000066	FG02804.1	NCU01850.1
AN6274.1	65.m07379	AO070309000069	FG02792.1	NCU01861.1
AN5099.1	54.m06962	AO070291000080	FG02791.1	NCU01862.1
AN8534.1	71.m15593	AO070323000188	FG11617.1	NCU01882.1
AN7699.1	71.m15724	AO070325000105	FG08949.1	NCU01894.1
AN1477.1	55.m02982	AO070334000159	FG08946.1	NCU01900.1
AN8743.1	62.m03337	AO070250000032	FG08945.1	NCU01901.1
AN8706.1	62.m03363	AO070315000133	FG08944.1	NCU01902.1
AN3889.1	70.m15376	AO070316000069	FG08943.1	NCU01904.1
AN5986.1	72.m19155	AO070340000293	FG08941.1	NCU01906.1
AN9526.1	59.m09117	AO070327000084	FG08940.1	NCU01907.1
AN4759.1	59.m09224	AO070327000057	FG08936.1	NCU01911.1
AN4761.1	59.m09222	AO070327000055	FG08935.1	NCU01912.1
AN4798.1	59.m09183	AO070329000048	FG08932.1	NCU01914.1
AN8698.1	62.m03470	AO070315000125	FG08919.1	NCU01918.1
AN8699.1	62.m03370	AO070315000126	FG08920.1	NCU01919.1
AN3717.1	69.m15422	AO070341000346	FG08923.1	NCU01922.1
AN0770.1	70.m15373	AO070316000074	FG08927.1	NCU01928.1
AN4678.1	71.m15665	AO070284000022	FG08914.1	NCU01936.1
AN6006.1	72.m19136	AO070340000272	FG08910.1	NCU01939.1
AN3222.1	67.m02930	AO070330000072	FG11629.1	NCU01945.1
AN2757.1	59.m09254	AO070327000036	FG08905.1	NCU01947.1
AN4802.1	59.m09174	AO070329000037	FG08895.1	NCU01948.1
AN4803.1	59.m09173	AO070329000036	FG08896.1	NCU01949.1
AN4788.1	59.m09460	AO070329000059	FG08897.1	NCU01950.1
AN7755.1	71.m15787	AO070325000188	FG08901.1	NCU01954.1
AN7718.1	71.m15744	AO070325000132	FG08900.1	NCU01955.1
AN4736.1	59.m09248	AO070327000041	FG08889.1	NCU01961.1
AN4735.1	59.m09246	AO070327000042	FG08887.1	NCU01963.1
AN1484.1	55.m02990	AO070334000191	FG06850.1	NCU01965.1
AN4787.1	59.m09462	AO070329000060	FG08670.1	NCU01966.1
AN4817.1	59.m09158	AO070327000170	FG08672.1	NCU01968.1
AN1009.1	70.m15227	AO070312000024	FG08507.1	NCU01970.1
AN4804.1	59.m09172	AO070329000035	FG08501.1	NCU01971.1
AN4740.1	59.m09244	AO070329000136	FG08886.1	NCU01975.1
AN0764.1	70.m15368	AO070316000081	FG11347.1	NCU01979.1
AN8721.1	62.m03352	AO070315000143	FG08879.1	NCU01980.1
AN4769.1	59.m09216	AO070329000088	FG08875.1	NCU01985.1
AN4636.1	57.m05549	AO070248000018	FG08504.1	NCU01989.1
AN4814.1	59.m09162	AO070329000018	FG08873.1	NCU01990.1
AN4547.1	57.m05557	AO070321000185	FG08840.1	NCU01992.1
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AN4857.1	59.m09114	AO070327000081	FG08709.1	NCU01997.1
AN4221.1	54.m06797	AO070234000030	FG08813.1	NCU02001.1
AN4218.1	54.m06800	AO070315000081	FG08811.1	NCU02003.1
AN4770.1	59.m09215	AO070329000086	FG08528.1	NCU02005.1
AN0906.1	70.m15515	AO070320000082	FG09454.1	NCU02011.1
AN8696.1	62.m03488	AO070315000121	FG08527.1	NCU02014.1
AN4763.1	59.m09489	AO070327000053	FG08531.1	NCU02015.1
AN4762.1	59.m09221	AO070327000054	FG08530.1	NCU02016.1
AN9357.1	52.m04075	AO070315000043	FG09216.1	NCU02018.1
AN8683.1	62.m03388	AO070315000103	FG08579.1	NCU02020.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN8700.1	62.m03368	AO070315000128	FG02343.1	NCU02023.1
AN8748.1	62.m03453	AO070250000024	FG06404.1	NCU02027.1
AN8764.1	62.m03313	AO070277000062	FG06401.1	NCU02028.1
AN9384.1	54.m06360	AO070253000015	FG08320.1	NCU02031.1
AN6638.1	62.m03233	AO070326000090	FG08648.1	NCU02034.1
AN8671.1	62.m03399	AO070315000088	FG08650.1	NCU02036.1
AN1284.1	70.m14923	AO070332000035	FG02764.1	NCU02044.1
AN1280.1	70.m14929	AO070332000040	FG02766.1	NCU02048.1
AN1494.1	55.m03004	AO070334000211	FG09406.1	NCU02052.1
AN3909.1	69.m15021	AO070324000094	FG01035.1	NCU02053.1
AN3924.1	69.m15005	AO070324000120	FG01036.1	NCU02054.1
AN4050.1	54.m06541	AO070328000106	FG00718.1	NCU02056.1
AN0304.1	54.m06978	AO070334000034	FG00736.1	NCU02060.1
AN9512.1	69.m15026	AO070324000088	FG06864.1	NCU02064.1
AN6268.1	72.m19984	AO070304000019	FG00912.1	NCU02065.1
AN0946.1	70.m15580	AO070320000143	FG00292.1	NCU02066.1
AN4053.1	54.m06538	AO070342000038	FG00748.1	NCU02069.1
AN4056.1	54.m07014	AO070342000042	FG00724.1	NCU02070.1
AN1510.1	55.m03022	AO070334000228	FG04911.1	NCU02074.1
AN3411.1	66.m04621	AO070281000041	FG00286.1	NCU02076.1
AN1413.1	55.m03241	AO070242000017	FG04907.1	NCU02082.1
AN9083.1	66.m04541	AO070332000196	FG00722.1	NCU02090.1
AN4486.1	57.m05645	AO070311000037	FG00719.1	NCU02094.1
AN0809.1	70.m15793	AO070239000006	FG00916.1	NCU02103.1
AN0808.1	70.m15409	AO070239000007	FG00915.1	NCU02104.1
AN0804.1	70.m15405	AO070239000013	FG00914.1	NCU02105.1
AN3417.1	66.m04616	AO070203000003	FG00287.1	NCU02107.1
AN9094.1	66.m04552	AO070332000181	FG00872.1	NCU02109.1
AN5457.1	69.m15475	AO070341000409	FG00739.1	NCU02110.1
AN1558.1	55.m03276	AO070339000295	FG01410.1	NCU02111.1
AN8701.1	62.m03367	AO070315000129	FG08557.1	NCU02112.1
AN8702.1	62.m03366	AO070315000130	FG08558.1	NCU02113.1
AN3795.1	57.m05687	AO070337000232	FG00941.1	NCU02114.1
AN1947.1	71.m15303	AO070342000209	FG10497.1	NCU02116.1
AN1565.1	55.m03091	AO070339000287	FG01411.1	NCU02118.1
AN4708.1	71.m15696	AO070329000168	FG08517.1	NCU02123.1
AN8664.1	62.m03479	AO070205000007	FG08780.1	NCU02124.1
AN4688.1	71.m15671	AO070284000043	FG08510.1	NCU02126.1
AN4687.1	71.m15670	AO070284000042	FG08509.1	NCU02127.1
AN4691.1	71.m15674	AO070284000047	FG08511.1	NCU02128.1
AN7783.1	71.m15816	AO070286000029	FG08568.1	NCU02131.1
AN0241.1	71.m15641	AO070284000071	FG08721.1	NCU02133.1
AN0242.1	71.m15640	AO070284000072	FG08722.1	NCU02134.1
AN0240.1	71.m15642	AO070284000070	FG08723.1	NCU02136.1
AN7736.1	71.m15766	AO070325000157	FG08845.1	NCU02147.1
AN4684.1	71.m15668	AO070284000040	FG08571.1	NCU02148.1
AN4800.1	59.m09180	AO070329000041	FG08872.1	NCU02151.1
AN4743.1	59.m09236	AO070327000077	FG08857.1	NCU02160.1
AN4753.1	59.m09232	AO070327000066	FG08860.1	NCU02162.1
AN4751.1	59.m09234	AO070327000068	FG08849.1	NCU02169.1
AN4986.1	59.m08889	AO070288000054	FG08717.1	NCU02176.1
AN4792.1	59.m09189	AO070329000054	FG08715.1	NCU02179.1
AN7535.1	72.m19814	AO070299000067	FG10918.1	NCU02191.1
AN9490.1	66.m04696	AO070214000003	FG00161.1	NCU02195.1
AN8233.1	53.m03736	AO070310000075	FG08917.1	NCU02200.1
AN7786.1	63.m00612	AO070167000003	FG02964.1	NCU02206.1
AN0381.1	54.m06365	AO070318000065	FG05778.1	NCU02207.1
AN0359.1	54.m06392	AO070318000037	FG05777.1	NCU02208.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1037.1	70.m15195	AO070336000072	FG05784.1	NCU02209.1
AN3752.1	65.m07375	AO070309000065	FG05780.1	NCU02211.1
AN4453.1	58.m07872	AO070273000002	FG05769.1	NCU02218.1
AN3036.1	59.m08981	AO070337000078	FG06302.1	NCU02219.1
AN2767.1	59.m09256	AO070327000034	FG06045.1	NCU02224.1
AN1038.1	70.m15196	AO070336000073	FG05054.1	NCU02225.1
AN4290.1	58.m08029	AO070158000001	FG05053.1	NCU02226.1
AN5749.1	69.m14847	AO070341000006	FG03481.1	NCU02227.1
AN5760.1	69.m14838	AO070193000006	FG05766.1	NCU02228.1
AN5006.1	59.m08904	AO070255000034	FG06330.1	NCU02230.1
AN3010.1	59.m09008	AO070337000106	FG06338.1	NCU02231.1
AN3033.1	59.m08985	AO070337000074	FG06339.1	NCU02232.1
AN3013.1	59.m09003	AO070337000103	FG06325.1	NCU02233.1
AN4273.1	65.m07451	AO070277000013	FG09691.1	NCU02244.1
AN5759.1	69.m14839	AO070193000004	FG05764.1	NCU02245.1
AN1624.1	58.m07694	AO070299000090	FG06048.1	NCU02250.1
AN3059.1	59.m08959	AO070337000014	FG06055.1	NCU02252.1
AN5001.1	59.m08901	AO070255000031	FG06049.1	NCU02256.1
AN4598.1	57.m05520	AO070267000015	FG10768.1	NCU02259.1
AN2904.1	59.m08755	AO070338000101	FG10769.1	NCU02260.1
AN4997.1	59.m09454	AO070288000080	FG10779.1	NCU02263.1
AN4602.1	57.m05525	AO070267000019	FG06294.1	NCU02264.1
AN4250.1	54.m06812	AO070324000162	FG06300.1	NCU02269.1
AN4884.1	59.m08778	AO070338000076	FG06301.1	NCU02270.1
AN4875.1	59.m09495	AO070338000085	FG10780.1	NCU02271.1
AN2898.1	59.m08748	AO070338000110	FG10781.1	NCU02272.1
AN2903.1	59.m08754	AO070338000102	FG10782.1	NCU02273.1
AN3058.1	59.m08957	AO070337000016	FG06290.1	NCU02274.1
AN4894.1	59.m08792	AO070338000062	FG06291.1	NCU02276.1
AN4895.1	59.m08794	AO070338000061	FG06292.1	NCU02277.1
AN4991.1	59.m08894	AO070288000071	FG00338.1	NCU02282.1
AN3065.1	59.m08933	AO070337000007	FG00337.1	NCU02283.1
AN0247.1	54.m06700	AO070338000240	FG00732.1	NCU02284.1
AN1699.1	58.m07775	AO070305000023	FG10790.1	NCU02287.1
AN2761.1	59.m09263	AO070327000023	FG10805.1	NCU02289.1
AN2762.1	59.m09262	AO070327000024	FG10804.1	NCU02291.1
AN5008.1	59.m08910	AO070255000045	FG10793.1	NCU02293.1
AN2766.1	59.m09488	AO070327000031	FG10792.1	NCU02295.1
AN4603.1	57.m05527	AO070267000024	FG10934.1	NCU02296.1
AN6817.1	65.m07380	AO070309000070	FG10920.1	NCU02299.1
AN9039.1	66.m04597	AO070332000128	FG02001.1	NCU02302.1
AN4282.1	53.m03675	AO070310000014	FG01604.1	NCU02319.1
AN1715.1	58.m08959	AO070305000031	FG05330.1	NCU02322.1
AN5566.1	52.m03724	AO070279000055	FG10358.1	NCU02325.1
AN6423.1	52.m03708	AO070342000207	FG10974.1	NCU02329.1
AN2901.1	59.m08751	AO070338000106	FG10967.1	NCU02333.1
AN1548.1	55.m03068	AO070339000306	FG11409.1	NCU02335.1
AN5103.1	54.m06964	AO070291000076	FG02041.1	NCU02337.1
AN3438.1	59.m09298	AO070265000012	FG06992.1	NCU02347.1
AN5527.1	69.m15430	AO070341000362	FG07962.1	NCU02348.1
AN4623.1	57.m05537	AO070267000035	FG07940.1	NCU02349.1
AN3445.1	59.m09479	AO070265000021	FG07937.1	NCU02351.1
AN3449.1	59.m09312	AO070265000024	FG07965.1	NCU02353.1
AN4578.1	57.m05942	AO070316000167	FG07966.1	NCU02360.1
AN4577.1	57.m05504	AO070316000168	FG09042.1	NCU02361.1
AN3125.1	59.m09374	AO070303000022	FG07968.1	NCU02363.1
AN5525.1	69.m15433	AO070341000364	FG07953.1	NCU02366.1
AN4372.1	56.m03102	AO070275000045	FG11011.1	NCU02369.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN3716.1	69.m15421	AO070341000345	FG07956.1	NCU02374.1
AN3711.1	69.m15416	AO070341000337	FG07958.1	NCU02375.1
AN5524.1	69.m15434	AO070341000365	FG07959.1	NCU02376.1
AN3714.1	69.m15418	AO070341000340	FG07960.1	NCU02378.1
AN5662.1	58.m07312	AO070342000256	FG01248.1	NCU02380.1
AN5661.1	58.m08891	AO070342000254	FG06370.1	NCU02381.1
AN3453.1	59.m09483	AO070265000029	FG06362.1	NCU02382.1
AN3018.1	59.m08991	AO070337000096	FG06378.1	NCU02388.1
AN3720.1	69.m15726	AO070341000352	FG06384.1	NCU02391.1
AN3719.1	69.m15727	AO070341000350	FG06385.1	NCU02393.1
AN3004.1	59.m09010	AO070337000108	FG06386.1	NCU02394.1
AN4888.1	59.m08784	AO070338000070	FG09834.1	NCU02397.1
AN5848.1	72.m18979	AO070340000006	FG06366.1	NCU02399.1
AN3063.1	59.m08951	AO070337000010	FG09837.1	NCU02401.1
AN3460.1	59.m09482	AO070265000037	FG09838.1	NCU02402.1
AN3738.1	69.m15377	AO070342000269	FG09839.1	NCU02403.1
AN4581.1	57.m05499	AO070316000164	FG09843.1	NCU02406.1
AN4592.1	57.m05515	AO070267000008	FG09845.1	NCU02408.1
AN3062.1	59.m08952	AO070337000011	FG06364.1	NCU02411.1
AN4881.1	59.m08776	AO070338000078	FG06368.1	NCU02412.1
AN3688.1	69.m15397	AO070341000311	FG06359.1	NCU02413.1
AN4880.1	59.m09409	AO070338000081	FG06369.1	NCU02415.1
AN4992.1	59.m08895	AO070288000075	FG06375.1	NCU02416.1
AN4993.1	59.m08896	AO070288000076	FG06376.1	NCU02417.1
AN3691.1	69.m15402	AO070341000316	FG09851.1	NCU02420.1
AN3723.1	69.m15392	AO070342000294	FG09850.1	NCU02421.1
AN3690.1	69.m15716	AO070341000315	FG09849.1	NCU02423.1
AN3463.1	59.m09324	AO070265000041	FG09848.1	NCU02424.1
AN5671.1	69.m15375	AO070342000266	FG06373.1	NCU02425.1
AN2759.1	59.m09265	AO070327000021	FG09853.1	NCU02428.1
AN3456.1	59.m09318	AO070265000032	FG09855.1	NCU02430.1
AN9060.1	59.m09514	AO070265000048	FG09857.1	NCU02432.1
AN3469.1	59.m09329	AO070265000045	FG11626.1	NCU02435.1
AN3466.1	59.m09327	AO070265000043	FG07970.1	NCU02438.1
AN3830.1	58.m07808	AO070305000068	FG00296.1	NCU02450.1
AN3838.1	58.m07814	AO070305000073	FG09393.1	NCU02452.1
AN3373.1	66.m04641	AO070281000015	FG01406.1	NCU02457.1
AN3789.1	57.m05693	AO070337000239	FG00949.1	NCU02459.1
AN3416.1	66.m04618	AO070203000005	FG00950.1	NCU02460.1
AN1133.1	71.m15635	AO070276000007	FG09422.1	NCU02463.1
AN4667.1	71.m15708	AO070311000001	FG09421.1	NCU02464.1
AN4332.1	58.m07986	AO070240000011	FG09423.1	NCU02468.1
AN1063.1	70.m15759	AO070218000007	FG09547.1	NCU02472.1
AN7630.1	71.m15820	AO070294000040	FG09544.1	NCU02477.1
AN6654.1	62.m03256	AO070269000012	FG00178.1	NCU02479.1
AN6655.1	62.m03451	AO070269000011	FG00177.1	NCU02480.1
AN8755.1	62.m03322	AO070250000017	FG00176.1	NCU02481.1
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AN5770.1	69.m14828	AO070249000008	FG07359.1	NCU02490.1
AN3938.1	69.m14987	AO070341000049	FG00567.1	NCU02494.1
AN3937.1	69.m14989	AO070341000048	FG00566.1	NCU02495.1
AN3941.1	69.m14983	AO070341000053	FG00565.1	NCU02496.1
AN3939.1	69.m14985	AO070341000051	FG00359.1	NCU02498.1
AN4475.1	58.m07845	AO070305000110	FG01081.1	NCU02509.1
AN4463.1	58.m07848	AO070305000114	FG05619.1	NCU02510.1
AN8073.1	53.m03926	AO070330000031	FG06243.1	NCU02511.1
AN5994.1	72.m19938	AO070340000283	FG01069.1	NCU02513.1
AN2946.1	59.m09093	AO070337000196	FG05621.1	NCU02515.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1639.1	58.m07718	AO070299000037	FG01085.1	NCU02520.1
AN4276.1	65.m07454	AO070277000008	FG01068.1	NCU02526.1
AN2417.1	72.m19468	AO070228000027	FG00363.1	NCU02531.1
AN2416.1	72.m19467	AO070228000028	FG00364.1	NCU02532.1
AN2415.1	72.m19466	AO070228000029	FG00365.1	NCU02533.1
AN2414.1	72.m19465	AO070228000030	FG00376.1	NCU02534.1
AN3586.1	58.m07385	AO070342000163	FG00375.1	NCU02536.1
AN6080.1	72.m19927	AO070340000130	FG00505.1	NCU02538.1
AN6070.1	72.m19062	AO070340000114	FG00504.1	NCU02539.1
AN7472.1	57.m05872	AO070287000054	FG00499.1	NCU02541.1
AN7459.1	57.m05882	AO070287000066	FG00500.1	NCU02542.1
AN5194.1	69.m14893	AO070237000024	FG01388.1	NCU02544.1
AN1666.1	58.m07732	AO070299000048	FG01386.1	NCU02546.1
AN3089.1	59.m08658	AO070334000128	FG00731.1	NCU02548.1
AN0747.1	70.m15361	AO070343000435	FG00863.1	NCU02549.1
AN3874.1	58.m08993	AO070305000055	FG00862.1	NCU02550.1
AN9421.1	55.m02908	AO070242000003	FG00883.1	NCU02552.1
AN0244.1	54.m06697	AO070338000236	FG00881.1	NCU02554.1
AN3907.1	69.m15658	AO070324000091	FG09338.1	NCU02556.1
AN0442.1	54.m06632	AO070338000299	FG09305.1	NCU02559.1
AN4861.1	59.m09110	AO070329000146	FG00902.1	NCU02563.1
AN1513.1	55.m03253	AO070334000232	FG00903.1	NCU02564.1
AN1512.1	55.m03031	AO070334000233	FG00905.1	NCU02565.1
AN9419.1	55.m02906	AO070242000001	FG00906.1	NCU02566.1
AN0810.1	70.m15803	AO070239000005	FG00909.1	NCU02569.1
AN0806.1	70.m15407	AO070239000011	FG09322.1	NCU02570.1
AN1409.1	55.m02916	AO070242000012	FG09321.1	NCU02571.1
AN1408.1	55.m02915	AO070242000011	FG09320.1	NCU02572.1
AN1407.1	55.m02914	AO070242000010	FG09319.1	NCU02573.1
AN1546.1	55.m03274	AO070339000308	FG09306.1	NCU02578.1
AN1543.1	55.m03061	AO070339000311	FG09341.1	NCU02580.1
AN1710.1	58.m07790	AO070305000038	FG04934.1	NCU02585.1
AN5224.1	57.m05709	AO070337000254	FG09167.1	NCU02586.1
AN1668.1	58.m07735	AO070299000050	FG09166.1	NCU02587.1
AN5181.1	69.m14878	AO070247000011	FG09165.1	NCU02588.1
AN1669.1	58.m07734	AO070299000051	FG00682.1	NCU02589.1
AN2096.1	57.m05799	AO070341000255	FG09327.1	NCU02591.1
AN8750.1	62.m03325	AO070250000010	FG08564.1	NCU02595.1
AN6856.1	71.m15269	AO070314000073	FG08562.1	NCU02596.1
AN0819.1	70.m15802	AO070288000083	FG00898.1	NCU02599.1
AN4729.1	71.m15637	AO070276000001	FG10971.1	NCU02600.1
AN2536.1	59.m08417	AO070300000039	FG00048.1	NCU02603.1
AN1995.1	58.m07604	AO070301000090	FG00887.1	NCU02609.1
AN0814.1	70.m15414	AO070288000089	FG00660.1	NCU02616.1
AN0813.1	70.m15413	AO070288000091	FG00661.1	NCU02617.1
AN1511.1	55.m03024	AO070334000229	FG00666.1	NCU02618.1
AN0818.1	70.m15418	AO070288000084	FG00665.1	NCU02619.1
AN0817.1	70.m15416	AO070288000087	FG00662.1	NCU02621.1
AN1066.1	70.m15166	AO070218000011	FG00663.1	NCU02623.1
AN8283.1	65.m07459	AO070277000005	FG01000.1	NCU02624.1
AN8286.1	65.m07462	AO070277000002	FG01004.1	NCU02626.1
AN4464.1	58.m07849	AO070305000118	FG00969.1	NCU02629.1
AN1163.1	70.m15058	AO070331000153	FG01015.1	NCU02630.1
AN3666.1	58.m07426	AO070342000003	FG01007.1	NCU02631.1
AN3665.1	58.m07425	AO070342000001	FG01006.1	NCU02632.1
AN1188.1	70.m15761	AO070331000183	FG01010.1	NCU02633.1
AN1167.1	70.m15053	AO070331000161	FG01009.1	NCU02634.1
AN7672.1	57.m05448	AO070325000052	FG06856.1	NCU02635.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1883.1	57.m05730	AO070306000016	FG06098.1	NCU02639.1
AN4699.1	71.m15687	AO070329000175	FG08733.1	NCU02644.1
AN4775.1	59.m09208	AO070329000077	FG09432.1	NCU02650.1
AN1222.1	70.m15003	AO070331000222	FG00421.1	NCU02657.1
AN1522.1	55.m03041	AO070334000240	FG01219.1	NCU02660.1
AN1521.1	55.m03040	AO070334000239	FG01220.1	NCU02661.1
AN6697.1	65.m07286	AO070339000128	FG01351.1	NCU02668.1
AN8880.1	56.m02291	AO070293000010	FG00615.1	NCU02669.1
AN1652.1	58.m07719	AO070299000039	FG06871.1	NCU02671.1
AN1436.1	55.m02941	AO070232000009	FG01101.1	NCU02674.1
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AN5999.1	72.m19141	AO070340000277	FG01217.1	NCU02677.1
AN1432.1	55.m02938	AO070232000014	FG06985.1	NCU02678.1
AN0295.1	54.m06466	AO070334000046	FG01216.1	NCU02680.1
AN1442.1	55.m02942	AO070232000005	FG01215.1	NCU02681.1
AN1478.1	55.m02985	AO070334000161	FG01210.1	NCU02685.1
AN2969.1	59.m09048	AO070337000155	FG01208.1	NCU02687.1
AN7577.1	72.m19594	AO070343000422	FG01207.1	NCU02688.1
AN7576.1	72.m19595	AO070343000423	FG01204.1	NCU02689.1
AN1266.1	70.m14945	AO070332000014	FG01024.1	NCU02696.1
AN4321.1	58.m08002	AO070230000012	FG11021.1	NCU02701.1
AN1230.1	70.m14989	AO070331000242	FG01019.1	NCU02705.1
AN1229.1	70.m14990	AO070331000241	FG01020.1	NCU02706.1
AN1166.1	70.m15054	AO070331000160	FG01016.1	NCU02707.1
AN1455.1	55.m02957	AO070302000021	FG00430.1	NCU02708.1
AN4914.1	59.m09399	AO070338000033	FG01297.1	NCU02712.1
AN1260.1	70.m14959	AO070214000005	FG01299.1	NCU02716.1
AN1259.1	70.m14960	AO070214000006	FG01300.1	NCU02717.1
AN1288.1	70.m14920	AO070303000049	FG01304.1	NCU02720.1
AN1198.1	70.m15021	AO070331000203	FG01151.1	NCU02727.1
AN4032.1	54.m06561	AO070328000123	FG00448.1	NCU02728.1
AN0310.1	54.m06449	AO070334000023	FG00449.1	NCU02729.1
AN3576.1	58.m07374	AO070342000173	FG00439.1	NCU02733.1
AN3577.1	58.m07375	AO070342000172	FG00440.1	NCU02734.1
AN2988.1	59.m09025	AO070337000134	FG00443.1	NCU02737.1
AN1237.1	70.m14981	AO070331000251	FG01157.1	NCU02741.1
AN3642.1	58.m07459	AO070328000088	FG01155.1	NCU02743.1
AN9465.1	70.m14852	AO070215000004	FG01154.1	NCU02744.1
AN1211.1	70.m15009	AO070331000217	FG01152.1	NCU02746.1
AN4028.1	54.m06555	AO070328000115	FG00437.1	NCU02747.1
AN0308.1	54.m06450	AO070334000026	FG00435.1	NCU02749.1
AN7563.1	72.m19998	AO070343000404	FG00433.1	NCU02751.1
AN3651.1	58.m07448	AO070342000036	FG01292.1	NCU02753.1
AN3649.1	58.m07450	AO070328000097	FG01290.1	NCU02757.1
AN3648.1	58.m07451	AO070328000096	FG01291.1	NCU02758.1
AN1168.1	70.m15052	AO070331000162	FG01364.1	NCU02762.1
AN5480.1	69.m15473	AO070341000406	FG01267.1	NCU02765.1
AN2733.1	54.m07005	AO070338000215	FG01361.1	NCU02771.1
AN0363.1	54.m06386	AO070318000043	FG01362.1	NCU02775.1
AN5676.1	65.m07402	AO070309000091	FG01030.1	NCU02776.1
AN1637.1	58.m07727	AO070299000056	FG01107.1	NCU02777.1
AN5748.1	69.m14846	AO070341000005	FG00612.1	NCU02778.1
AN5778.1	69.m14819	AO070249000023	FG00610.1	NCU02781.1
AN1673.1	58.m09023	AO070299000007	FG01486.1	NCU02785.1
AN1661.1	58.m07742	AO070299000021	FG01511.1	NCU02788.1
AN3753.1	65.m07374	AO070309000064	FG01042.1	NCU02791.1
AN9148.1	66.m04587	AO070332000144	FG00524.1	NCU02797.1
AN7544.1	72.m19561	AO070277000041	FG01106.1	NCU02800.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN8959.1	52.m03755	AO070336000205	FG01031.1	NCU02801.1
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AN1634.1	58.m09021	AO070299000045	FG06849.1	NCU02803.1
AN1636.1	58.m07726	AO070299000057	FG06848.1	NCU02804.1
AN4501.1	57.m05629	AO070311000054	FG06847.1	NCU02806.1
AN4470.1	58.m07860	AO070305000129	FG06843.1	NCU02810.1
AN4264.1	65.m07441	AO070277000021	FG06842.1	NCU02811.1
AN4259.1	65.m07433	AO070277000032	FG07122.1	NCU02813.1
AN4265.1	65.m07442	AO070277000020	FG07115.1	NCU02828.1
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AN9079.1	66.m04537	AO070332000200	FG07119.1	NCU02833.1
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AN6890.1	71.m15249	AO070314000031	FG09180.1	NCU02846.1
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AN4487.1	57.m05644	AO070311000038	FG03825.1	NCU02877.1
AN1833.1	58.m07676	AO070318000086	FG06331.1	NCU02879.1
AN8597.1	70.m15665	AO070319000106	FG03466.1	NCU02887.1
AN2948.1	59.m09085	AO070337000205	FG00762.1	NCU02888.1
AN8898.1	56.m02311	AO070293000031	FG11298.1	NCU02894.1
AN1202.1	71.m15197	AO070328000070	FG09179.1	NCU02895.1
AN4030.1	54.m06559	AO070328000122	FG00800.1	NCU02896.1
AN4024.1	54.m06547	AO070328000111	FG00804.1	NCU02899.1
AN6933.1	66.m04776	AO070332000207	FG00805.1	NCU02906.1
AN8482.1	52.m03715	AO070342000378	FG04160.1	NCU02917.1
AN7292.1	72.m20020	AO070297000033	FG06744.1	NCU02924.1
AN1731.1	69.m15037	AO070324000062	FG04886.1	NCU02936.1
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AN4495.1	57.m05636	AO070311000047	FG04883.1	NCU02940.1
AN4491.1	57.m05640	AO070311000043	FG09360.1	NCU02942.1
AN4490.1	57.m05641	AO070311000042	FG09359.1	NCU02943.1
AN0297.1	54.m06465	AO070334000045	FG01403.1	NCU02948.1
AN5203.1	69.m15625	AO070199000002	FG01394.1	NCU02951.1
AN5206.1	69.m14903	AO070199000006	FG01392.1	NCU02954.1
AN3832.1	58.m07811	AO070305000070	FG01391.1	NCU02955.1
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AN1516.1	55.m03035	AO070334000235	FG01174.1	NCU02960.1
AN7566.1	72.m19585	AO070343000409	FG01167.1	NCU02961.1
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AN1207.1	70.m15767	AO070331000213	FG01336.1	NCU02965.1
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AN1209.1	70.m15768	AO070331000215	FG01338.1	NCU02967.1
AN1210.1	70.m15011	AO070331000216	FG01339.1	NCU02968.1
AN3673.1	58.m07433	AO070342000015	FG01377.1	NCU02970.1
AN3663.1	58.m07435	AO070342000021	FG01375.1	NCU02973.1
AN4224.1	54.m06793	AO070234000026	FG01373.1	NCU02977.1
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AN8875.1	56.m03110	AO070293000004	FG01370.1	NCU02980.1
AN7579.1	72.m19597	AO070343000426	FG01123.1	NCU02982.1
AN7578.1	72.m19596	AO070343000425	FG01122.1	NCU02983.1
AN7589.1	72.m19611	AO070343000303	FG01120.1	NCU02988.1
AN1148.1	70.m15090	AO070331000139	FG01150.1	NCU02996.1
AN0160.1	71.m16052	AO070321000087	FG00452.1	NCU02997.1
AN3431.1	59.m09294	AO070265000010	FG09549.1	NCU02998.1
AN9403.1	52.m04030	AO070274000014	FG02782.1	NCU03004.1
AN5610.1	58.m07534	AO070301000010	FG06041.1	NCU03010.1
AN1131.1	70.m15105	AO070331000123	FG00576.1	NCU03013.1
AN7458.1	57.m05884	AO070287000067	FG00485.1	NCU03018.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN7471.1	57.m05873	AO070287000055	FG00486.1	NCU03020.1
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AN0299.1	54.m06976	AO070334000042	FG00952.1	NCU03026.1
AN1709.1	58.m08968	AO070305000039	FG00744.1	NCU03030.1
AN0896.1	70.m15502	AO070320000070	FG00743.1	NCU03031.1
AN5914.1	72.m19959	AO070248000032	FG00742.1	NCU03032.1
AN7545.1	72.m19562	AO070277000042	FG00352.1	NCU03033.1
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AN6681.1	65.m07299	AO070289000025	FG07049.1	NCU03039.1
AN6682.1	65.m07298	AO070289000024	FG07050.1	NCU03040.1
AN2420.1	72.m19472	AO070228000003	FG07051.1	NCU03042.1
AN6685.1	65.m07296	AO070339000093	FG07053.1	NCU03045.1
AN1538.1	55.m03057	AO070334000262	FG01116.1	NCU03047.1
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AN8757.1	62.m03452	AO070321000005	FG11270.1	NCU03049.1
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AN0305.1	54.m06453	AO070334000033	FG07055.1	NCU03051.1
AN1535.1	55.m03053	AO070334000255	FG00514.1	NCU03054.1
AN4184.1	57.m05471	AO070325000093	FG03942.1	NCU03057.1
AN1226.1	70.m14994	AO070331000235	FG00460.1	NCU03059.1
AN1255.1	70.m14969	AO070223000014	FG07102.1	NCU03060.1
AN1256.1	70.m14971	AO070223000013	FG07101.1	NCU03061.1
AN1249.1	70.m14972	AO070223000012	FG07100.1	NCU03062.1
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AN3657.1	58.m07443	AO070342000031	FG01184.1	NCU03065.1
AN1215.1	70.m14996	AO070331000233	FG01185.1	NCU03066.1
AN1216.1	70.m14997	AO070331000232	FG07096.1	NCU03068.1
AN1180.1	70.m15037	AO070331000178	FG00408.1	NCU03071.1
AN1221.1	70.m15002	AO070331000223	FG07098.1	NCU03072.1
AN1733.1	69.m15036	AO070324000063	FG01141.1	NCU03076.1
AN9466.1	70.m15753	AO070215000006	FG01142.1	NCU03079.1
AN1372.1	70.m14857	AO070215000009	FG00461.1	NCU03080.1
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AN3954.1	69.m14968	AO070341000069	FG01111.1	NCU03100.1
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AN4019.1	54.m06552	AO070328000118	FG00924.1	NCU03107.1
AN4018.1	54.m06553	AO070328000117	FG00925.1	NCU03108.1
AN0432.1	54.m06625	AO070338000285	FG00926.1	NCU03112.1
AN3819.1	57.m05664	AO070311000016	FG00929.1	NCU03113.1
AN3810.1	57.m05672	AO070337000218	FG00930.1	NCU03114.1
AN3815.1	57.m05667	AO070311000013	FG00932.1	NCU03115.1
AN9463.1	57.m05660	AO070311000018	FG01497.1	NCU03116.1
AN1485.1	55.m02991	AO070334000192	FG00677.1	NCU03124.1
AN9067.1	66.m04519	AO070332000219	FG00728.1	NCU03125.1
AN0431.1	54.m06627	AO070338000291	FG00740.1	NCU03127.1
AN0936.1	70.m15567	AO070320000127	FG00749.1	NCU03129.1
AN0897.1	70.m15501	AO070320000071	FG00751.1	NCU03130.1
AN6939.1	71.m15187	AO070313000064	FG10537.1	NCU03131.1
AN0803.1	70.m15404	AO070239000014	FG00869.1	NCU03136.1
AN0802.1	70.m15403	AO070239000016	FG00866.1	NCU03137.1
AN0797.1	70.m15398	AO070239000020	FG00865.1	NCU03139.1
AN1675.1	58.m07753	AO070299000004	FG02073.1	NCU03141.1
AN1795.1	72.m19547	AO070309000136	FG00947.1	NCU03145.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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AN8704.1	62.m03491	AO070315000132	FG08676.1	NCU03150.1
AN8692.1	62.m03473	AO070315000113	FG08677.1	NCU03151.1
AN9446.1	59.m09152	AO070327000156	FG08680.1	NCU03154.1
AN8763.1	62.m03312	AO070277000063	FG08566.1	NCU03156.1
AN5175.1	69.m14872	AO070247000006	FG03947.1	NCU03158.1
AN8682.1	62.m03389	AO070315000102	FG08578.1	NCU03159.1
AN4841.1	59.m09136	AO070327000129	FG08581.1	NCU03170.1
AN7597.1	72.m19615	AO070343000314	FG08669.1	NCU03171.1
AN4549.1	57.m05559	AO070321000182	FG09541.1	NCU03173.1
AN4851.1	59.m09124	AO070327000095	FG08589.1	NCU03175.1
AN0929.1	70.m15537	AO070320000117	FG09539.1	NCU03176.1
AN4842.1	59.m09137	AO070327000130	FG09542.1	NCU03177.1
AN8723.1	62.m03343	AO070315000151	FG09409.1	NCU03179.1
AN8741.1	62.m03339	AO070250000041	FG09410.1	NCU03184.1
AN9504.1	62.m03341	AO070315000153	FG09408.1	NCU03187.1
AN0836.1	70.m15436	AO070255000007	FG08694.1	NCU03188.1
AN8679.1	62.m03392	AO070315000099	FG08577.1	NCU03191.1
AN3626.1	58.m07413	AO070342000124	FG10669.1	NCU03194.1
AN4980.1	59.m08882	AO070288000047	FG00469.1	NCU03197.1
AN4238.1	54.m07034	AO070234000002	FG00472.1	NCU03200.1
AN3632.1	58.m07469	AO070328000069	FG00475.1	NCU03204.1
AN1254.1	70.m14968	AO070223000015	FG00477.1	NCU03206.1
AN4862.1	59.m09109	AO070329000148	FG00562.1	NCU03207.1
AN5230.1	57.m05701	AO070337000247	FG00670.1	NCU03211.1
AN4528.1	57.m05598	AO070321000138	FG09163.1	NCU03214.1
AN4504.1	57.m05627	AO070311000057	FG00294.1	NCU03215.1
AN0259.1	54.m06522	AO070334000099	FG09162.1	NCU03216.1
AN2939.1	59.m09055	AO070337000169	FG09158.1	NCU03217.1
AN3584.1	58.m07383	AO070342000165	FG09157.1	NCU03218.1
AN3583.1	58.m07381	AO070342000166	FG09156.1	NCU03219.1
AN1493.1	55.m03317	AO070334000206	FG09403.1	NCU03222.1
AN4505.1	57.m05626	AO070311000058	FG04914.1	NCU03226.1
AN1281.1	70.m14927	AO070332000039	FG02761.1	NCU03229.1
AN3131.1	59.m08594	AO070303000013	FG02769.1	NCU03231.1
AN3921.1	69.m15007	AO070324000117	FG01197.1	NCU03232.1
AN3923.1	69.m15006	AO070324000119	FG01194.1	NCU03234.1
AN2730.1	54.m06671	AO070338000210	FG02163.1	NCU03235.1
AN0281.1	54.m06477	AO070334000072	FG01065.1	NCU03237.1
AN5151.1	69.m14882	AO070237000013	FG01064.1	NCU03238.1
AN3908.1	69.m15023	AO070324000092	FG01058.1	NCU03242.1
AN3927.1	69.m15001	AO070341000039	FG01057.1	NCU03243.1
AN3926.1	69.m15002	AO070341000040	FG00414.1	NCU03244.1
AN5057.1	59.m08669	AO070338000201	FG00543.1	NCU03246.1
AN8363.1	52.m04104	AO070274000030	FG00530.1	NCU03255.1
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AN5048.1	59.m08678	AO070338000188	FG01100.1	NCU03266.1
AN7666.1	57.m05437	AO070268000051	FG07150.1	NCU03267.1
AN0679.1	70.m15283	AO070343000536	FG01092.1	NCU03269.1
AN3905.1	69.m15030	AO070324000083	FG09229.1	NCU03269.1
AN3757.1	65.m07367	AO070309000049	FG07077.1	NCU03276.1
AN5681.1	65.m07407	AO070309000096	FG07078.1	NCU03277.1
AN5682.1	65.m07408	AO070309000097	FG07062.1	NCU03278.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN2938.1	59.m09056	AO070337000168	FG07060.1	NCU03280.1
AN2930.1	59.m09064	AO070337000178	FG07057.1	NCU03283.1
AN2572.1	72.m19060	AO070340000111	FG01095.1	NCU03290.1
AN7465.1	57.m05876	AO070287000061	FG00509.1	NCU03291.1
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AN3758.1	65.m07366	AO070309000048	FG05598.1	NCU03296.1
AN1630.1	58.m07716	AO070299000035	FG01245.1	NCU03297.1
AN8288.1	65.m07464	AO070190000002	FG01243.1	NCU03298.1
AN5744.1	69.m15615	AO070341000001	FG01241.1	NCU03300.1
AN5777.1	69.m14820	AO070249000022	FG01240.1	NCU03301.1
AN4449.1	58.m07876	AO070273000004	FG01236.1	NCU03304.1
AN5743.1	69.m14841	AO070193000002	FG01265.1	NCU03305.1
AN6073.1	72.m19947	AO070340000117	FG01119.1	NCU03310.1
AN5856.1	72.m18985	AO070340000012	FG00371.1	NCU03312.1
AN7560.1	72.m19581	AO070343000400	FG05608.1	NCU03316.1
AN4864.1	59.m09108	AO070329000150	FG05607.1	NCU03317.1
AN1117.1	70.m15118	AO070331000109	FG00538.1	NCU03319.1
AN1367.1	70.m14862	AO070215000014	FG11603.1	NCU03321.1
AN9287.1	57.m05386	AO070294000075	FG02360.1	NCU03322.1
AN0573.1	69.m15273	AO070272000052	FG01644.1	NCU03330.1
AN0574.1	69.m15771	AO070272000053	FG01469.1	NCU03332.1
AN4440.1	58.m07885	AO070273000014	FG01670.1	NCU03334.1
AN4441.1	58.m09014	AO070273000013	FG01620.1	NCU03335.1
AN0932.1	70.m15540	AO070320000123	FG05183.1	NCU03339.1
AN1988.1	58.m07595	AO070301000075	FG05181.1	NCU03341.1
AN4434.1	58.m08979	AO070273000023	FG01653.1	NCU03343.1
AN5616.1	58.m08957	AO070301000016	FG01560.1	NCU03347.1
AN5613.1	58.m07536	AO070301000012	FG01561.1	NCU03350.1
AN6293.1	72.m19341	AO070308000051	FG01562.1	NCU03352.1
AN4442.1	58.m09016	AO070273000012	FG01568.1	NCU03357.1
AN5977.1	72.m19939	AO070281000046	FG01476.1	NCU03358.1
AN5588.1	58.m07509	AO070328000021	FG01475.1	NCU03359.1
AN4435.1	58.m08980	AO070273000022	FG00627.1	NCU03360.1
AN1968.1	58.m08921	AO070301000052	FG00629.1	NCU03362.1
AN4412.1	58.m08981	AO070273000032	FG01656.1	NCU03363.1
AN0575.1	69.m15270	AO070272000054	FG05179.1	NCU03364.1
AN1390.1	70.m14831	AO070342000349	FG10854.1	NCU03368.1
AN1460.1	55.m03259	AO070306000076	FG05168.1	NCU03369.1
AN4353.1	58.m07978	AO070240000022	FG10853.1	NCU03372.1
AN3176.1	59.m08566	AO070256000014	FG10896.1	NCU03380.1
AN3177.1	59.m08567	AO070256000013	FG10897.1	NCU03381.1
AN3098.1	59.m08645	AO070334000139	FG10903.1	NCU03387.1
AN3163.1	59.m08551	AO070256000032	FG10909.1	NCU03388.1
AN3172.1	59.m08562	AO070256000018	FG10905.1	NCU03393.1
AN3173.1	59.m08563	AO070256000017	FG10906.1	NCU03394.1
AN3168.1	59.m08557	AO070256000022	FG10907.1	NCU03395.1
AN3167.1	59.m09511	AO070256000023	FG10908.1	NCU03396.1
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AN0862.1	70.m15466	AO070320000011	FG10822.1	NCU03401.1
AN4055.1	54.m06944	AO070342000041	FG07678.1	NCU03404.1
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AN0554.1	69.m15293	AO070272000027	FG00979.1	NCU03415.1
AN0131.1	71.m15415	AO070321000122	FG01466.1	NCU03423.1
AN3031.1	59.m08989	AO070331000089	FG05713.1	NCU03425.1
AN0129.1	71.m15409	AO070311000084	FG04296.1	NCU03426.1
AN0504.1	69.m15297	AO070226000008	FG01464.1	NCU03436.1
AN4919.1	59.m08822	AO070338000024	FG00822.1	NCU03438.1
AN4918.1	59.m08821	AO070338000025	FG00823.1	NCU03439.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN0127.1	71.m15413	AO070311000081	FG04297.1	NCU03441.1
AN5595.1	58.m07519	AO070328000009	FG05208.1	NCU03458.1
AN5600.1	58.m07524	AO070328000004	FG00298.1	NCU03460.1
AN5568.1	58.m07492	AO070328000040	FG00817.1	NCU03462.1
AN5606.1	58.m07529	AO070301000003	FG00818.1	NCU03463.1
AN1355.1	70.m14875	AO070237000005	FG05212.1	NCU03471.1
AN0990.1	70.m15631	AO070318000147	FG00819.1	NCU03479.1
AN1971.1	58.m07576	AO070301000055	FG05150.1	NCU03482.1
AN6323.1	72.m19441	AO070304000044	FG05152.1	NCU03483.1
AN0919.1	70.m15526	AO070320000099	FG05156.1	NCU03488.1
AN0917.1	70.m15524	AO070320000097	FG05165.1	NCU03491.1
AN0918.1	70.m15525	AO070320000098	FG05164.1	NCU03492.1
AN2167.1	72.m19673	AO070343000229	FG05163.1	NCU03493.1
AN0914.1	70.m15523	AO070320000095	FG05162.1	NCU03495.1
AN5591.1	58.m07515	AO070328000012	FG05169.1	NCU03500.1
AN0903.1	70.m15512	AO070320000077	FG05167.1	NCU03501.1
AN6874.1	71.m16021	AO070314000047	FG01640.1	NCU03503.1
AN2688.1	71.m15176	AO070313000100	FG06028.1	NCU03504.1
AN1394.1	70.m14828	AO070233000008	FG06035.1	NCU03515.1
AN1387.1	70.m14829	AO070233000007	FG06033.1	NCU03517.1
AN2450.1	69.m15208	AO070264000026	FG06030.1	NCU03526.1
AN4360.1	58.m07961	AO070261000003	FG05172.1	NCU03537.1
AN4425.1	58.m09002	AO070273000062	FG05173.1	NCU03538.1
AN4380.1	58.m07945	AO070261000025	FG05174.1	NCU03539.1
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AN0978.1	70.m15616	AO070341000131	FG01575.1	NCU03548.1
AN5612.1	58.m08906	AO070301000011	FG10842.1	NCU03554.1
AN4280.1	53.m03677	AO070310000016	FG00308.1	NCU03556.1
AN8273.1	53.m03687	AO070310000028	FG00644.1	NCU03559.1
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AN3185.1	59.m08569	AO070256000011	FG04385.1	NCU03563.1
AN5557.1	57.m05387	AO070294000076	FG03375.1	NCU03566.1
AN3107.1	59.m08630	AO070334000152	FG04359.1	NCU03567.1
AN3110.1	59.m08628	AO070303000041	FG10725.1	NCU03571.1
AN4225.1	54.m06792	AO070234000025	FG10724.1	NCU03572.1
AN0705.1	70.m15312	AO070343000504	FG10722.1	NCU03575.1
AN3095.1	59.m08648	AO070334000137	FG10723.1	NCU03576.1
AN4223.1	54.m06794	AO070234000027	FG00647.1	NCU03578.1
AN9481.1	71.m15629	AO070276000025	FG05981.1	NCU03588.1
AN9482.1	71.m15630	AO070276000024	FG05982.1	NCU03589.1
AN2011.1	58.m08942	AO070202000001	FG09020.1	NCU03592.1
AN2009.1	58.m07618	AO070179000005	FG09019.1	NCU03593.1
AN6853.1	71.m15279	AO070314000087	FG05890.1	NCU03596.1
AN6855.1	71.m15277	AO070314000086	FG07021.1	NCU03597.1
AN9121.1	66.m04577	AO070332000155	FG10132.1	NCU03600.1
AN1331.1	70.m14901	AO070303000094	FG10170.1	NCU03601.1
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AN5828.1	72.m18955	AO070260000018	FG10193.1	NCU03603.1
AN7423.1	57.m05922	AO070197000002	FG10122.1	NCU03606.1
AN2525.1	59.m08455	AO070286000098	FG10119.1	NCU03607.1
AN2526.1	59.m08453	AO070220000001	FG10118.1	NCU03608.1
AN2523.1	59.m08459	AO070286000091	FG10116.1	NCU03611.1
AN2522.1	59.m08460	AO070286000088	FG10115.1	NCU03613.1
AN5832.1	72.m18960	AO070260000013	FG10114.1	NCU03616.1
AN5830.1	72.m18958	AO070260000016	FG10113.1	NCU03617.1
AN8798.1	71.m15605	AO070276000062	FG05978.1	NCU03622.1
AN8258.1	53.m03703	AO070310000045	FG05977.1	NCU03623.1
AN8821.1	71.m15632	AO070276000021	FG05966.1	NCU03624.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN4460.1	58.m07864	AO070305000133	FG06788.1	NCU03628.1
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AN8046.1	53.m04164	AO070336000153	FG05906.1	NCU03639.1
AN3904.1	69.m15656	AO070324000068	FG03570.1	NCU03641.1
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AN0076.1	71.m15354	AO070311000140	FG07011.1	NCU03662.1
AN4214.1	54.m06959	AO070231000010	FG02002.1	NCU03667.1
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AN0910.1	70.m15519	AO070320000091	FG01865.1	NCU03695.1
AN2343.1	71.m15577	AO070319000157	FG01866.1	NCU03696.1
AN2042.1	58.m07630	AO070292000002	FG01867.1	NCU03697.1
AN1500.1	55.m03010	AO070334000217	FG01877.1	NCU03699.1
AN0776.1	70.m15382	AO070316000062	FG01871.1	NCU03703.1
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AN0089.1	71.m16059	AO070311000126	FG05141.1	NCU03711.1
AN1082.1	70.m15156	AO070285000082	FG05143.1	NCU03713.1
AN6915.1	71.m16035	AO070219000020	FG05144.1	NCU03714.1
AN6863.1	71.m15274	AO070314000083	FG07143.1	NCU03715.1
AN1080.1	70.m15154	AO070285000079	FG07146.1	NCU03717.1
AN6609.1	62.m03184	AO070326000058	FG07155.1	NCU03719.1
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AN7710.1	71.m15734	AO070325000117	FG05132.1	NCU03731.1
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AN0600.1	69.m15248	AO070280000025	FG07160.1	NCU03735.1
AN1084.1	70.m15158	AO070285000084	FG07182.1	NCU03737.1
AN0075.1	71.m15353	AO070311000141	FG07180.1	NCU03739.1
AN6824.1	71.m15292	AO070314000104	FG07150.1	NCU03741.1
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AN9496.1	72.m19484	AO070241000013	FG07151.1	NCU03752.1
AN8206.1	53.m03768	AO070310000111	FG00712.1	NCU03755.1
AN8172.1	53.m03806	AO070209000006	FG07188.1	NCU03756.1
AN8176.1	53.m03803	AO070209000002	FG07186.1	NCU03757.1
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AN4217.1	54.m06777	AO070342000115	FG07162.1	NCU03761.1
AN4469.1	58.m07855	AO070305000124	FG06821.1	NCU03764.1
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AN8169.1	53.m03812	AO070266000003	FG07410.1	NCU03768.1
AN8170.1	53.m03814	AO070266000007	FG07377.1	NCU03769.1
AN6844.1	71.m15301	AO070314000095	FG07019.1	NCU03777.1
AN0034.1	71.m16043	AO070314000113	FG07017.1	NCU03779.1
AN3847.1	58.m08991	AO070305000084	FG05145.1	NCU03781.1
AN9467.1	53.m03848	AO070322000047	FG05894.1	NCU03786.1
AN8200.1	53.m03775	AO070310000119	FG05892.1	NCU03791.1
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AN7517.1	53.m03773	AO070310000116	FG07378.1	NCU03793.1
AN8183.1	53.m03796	AO070310000142	FG07379.1	NCU03794.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN8182.1	53.m03797	AO070310000143	FG07380.1	NCU03795.1
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AN8180.1	53.m03800	AO070310000147	FG06116.1	NCU03799.1
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AN7568.1	72.m19587	AO070343000414	FG05953.1	NCU03802.1
AN8819.1	71.m15627	AO070276000028	FG10025.1	NCU03803.1
AN8820.1	71.m15631	AO070276000022	FG06103.1	NCU03804.1
AN6549.1	62.m03124	AO070270000036	FG06100.1	NCU03809.1
AN6551.1	62.m03122	AO070270000034	FG06097.1	NCU03811.1
AN6525.1	62.m03114	AO070270000024	FG06127.1	NCU03813.1
AN6526.1	62.m03435	AO070270000025	FG07128.1	NCU03814.1
AN6614.1	62.m03213	AO070326000063	FG05149.1	NCU03818.1
AN6615.1	62.m03212	AO070326000064	FG05213.1	NCU03819.1
AN8841.1	71.m15972	AO070271000036	FG07396.1	NCU03822.1
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AN6561.1	62.m03148	AO070326000002	FG07399.1	NCU03824.1
AN6563.1	62.m03150	AO070326000004	FG07401.1	NCU03826.1
AN6564.1	62.m03151	AO070326000005	FG07402.1	NCU03827.1
AN6566.1	62.m03153	AO070326000009	FG07404.1	NCU03833.1
AN6567.1	62.m03154	AO070326000010	FG07405.1	NCU03834.1
AN6569.1	62.m03156	AO070326000012	FG07406.1	NCU03836.1
AN6570.1	62.m03157	AO070326000013	FG07407.1	NCU03837.1
AN7355.1	72.m19724	AO070278000045	FG02630.1	NCU03846.1
AN3735.1	69.m15380	AO070342000272	FG10353.1	NCU03852.1
AN4583.1	57.m05507	AO070316000171	FG10352.1	NCU03853.1
AN4584.1	57.m05945	AO070316000173	FG10351.1	NCU03854.1
AN2999.1	59.m09440	AO070337000118	FG10347.1	NCU03857.1
AN4178.1	70.m14840	AO070243000013	FG09989.1	NCU03859.1
AN1383.1	70.m14838	AO070243000016	FG09990.1	NCU03860.1
AN5642.1	58.m07334	AO070342000232	FG10270.1	NCU03874.1
AN5643.1	58.m07335	AO070342000231	FG10269.1	NCU03875.1
AN2997.1	59.m09019	AO070337000120	FG10268.1	NCU03876.1
AN2998.1	59.m09018	AO070337000119	FG10267.1	NCU03877.1
AN1357.1	70.m14873	AO070237000003	FG10005.1	NCU03880.1
AN1333.1	70.m14898	AO070303000098	FG09951.1	NCU03882.1
AN1334.1	70.m14897	AO070303000099	FG09952.1	NCU03883.1
AN1337.1	70.m14896	AO070303000102	FG09954.1	NCU03885.1
AN4171.1	69.m14953	AO070341000090	FG08449.1	NCU03886.1
AN4170.1	69.m15618	AO070341000092	FG08448.1	NCU03887.1
AN4168.1	69.m14950	AO070341000095	FG09497.1	NCU03888.1
AN2068.1	57.m05768	AO070341000217	FG09491.1	NCU03897.1
AN4969.1	59.m08873	AO070288000035	FG09262.1	NCU03899.1
AN2890.1	59.m08737	AO070338000122	FG09264.1	NCU03903.1
AN7513.1	69.m15155	AO070258000018	FG08800.1	NCU03905.1
AN2082.1	57.m05781	AO070341000235	FG08744.1	NCU03906.1
AN1753.1	69.m15054	AO070324000040	FG08628.1	NCU03908.1
AN5498.1	69.m15455	AO070341000387	FG08619.1	NCU03909.1
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AN2126.1	69.m15671	AO070306000108	FG08621.1	NCU03911.1
AN8559.1	52.m03757	AO070306000062	FG08622.1	NCU03913.1
AN7533.1	69.m15085	AO070324000008	FG08623.1	NCU03914.1
AN7549.1	72.m19566	AO070277000046	FG09267.1	NCU03921.1
AN4923.1	59.m08826	AO070338000020	FG09266.1	NCU03922.1
AN3660.1	58.m07438	AO070342000025	FG08400.1	NCU03924.1
AN3661.1	58.m07437	AO070342000024	FG08751.1	NCU03925.1
AN2883.1	59.m08730	AO070338000131	FG09285.1	NCU03932.1
AN2882.1	59.m08729	AO070338000132	FG09284.1	NCU03935.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN7468.1	57.m05952	AO070287000059	FG08626.1	NCU03938.1
AN7466.1	57.m05951	AO070287000060	FG00226.1	NCU03942.1
AN1339.1	70.m14893	AO070247000025	FG10272.1	NCU03947.1
AN4268.1	65.m07446	AO070343000043	FG10065.1	NCU03949.1
AN4298.1	58.m08025	AO070189000008	FG10033.1	NCU03952.1
AN4297.1	58.m08027	AO070189000005	FG10276.1	NCU03953.1
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AN4570.1	57.m05491	AO070316000153	FG09919.1	NCU03956.1
AN4569.1	57.m05490	AO070316000152	FG09918.1	NCU03957.1
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AN4166.1	69.m15622	AO070341000097	FG08447.1	NCU03965.1
AN4167.1	69.m15621	AO070341000096	FG08446.1	NCU03966.1
AN7469.1	57.m05953	AO070287000057	FG08627.1	NCU03970.1
AN1922.1	69.m14940	AO070341000114	FG08444.1	NCU03972.1
AN1997.1	58.m07606	AO070301000092	FG08617.1	NCU03975.1
AN1904.1	69.m14918	AO070341000146	FG09465.1	NCU03980.1
AN2062.1	57.m05760	AO070341000205	FG09471.1	NCU03982.1
AN5800.1	72.m19917	AO070260000049	FG09866.1	NCU03988.1
AN5801.1	72.m19905	AO070260000048	FG09865.1	NCU03989.1
AN5803.1	72.m18931	AO070260000046	FG09862.1	NCU03992.1
AN1402.1	70.m14822	AO070233000017	FG10069.1	NCU04001.1
AN4446.1	58.m09017	AO070273000007	FG10067.1	NCU04003.1
AN5757.1	69.m14854	AO070341000016	FG10066.1	NCU04005.1
AN4293.1	58.m08028	AO070189000002	FG09965.1	NCU04007.1
AN3426.1	59.m09280	AO070327000005	FG09961.1	NCU04009.1
AN5644.1	58.m07332	AO070342000235	FG09960.1	NCU04013.1
AN2072.1	57.m05770	AO070341000219	FG08544.1	NCU04014.1
AN1873.1	57.m05745	AO070341000189	FG03103.1	NCU04016.1
AN1745.1	69.m15048	AO070324000051	FG09476.1	NCU04019.1
AN1913.1	69.m14928	AO070341000134	FG08761.1	NCU04020.1
AN8812.1	71.m15619	AO070276000042	FG08373.1	NCU04021.1
AN1286.1	70.m14922	AO070303000047	FG05344.1	NCU04035.1
AN5330.1	62.m03273	AO070333000250	FG08082.1	NCU04039.1
AN1751.1	69.m15052	AO070324000042	FG09300.1	NCU04040.1
AN1750.1	69.m15051	AO070324000043	FG05336.1	NCU04041.1
AN1767.1	69.m15070	AO070324000025	FG09298.1	NCU04042.1
AN5629.1	58.m07554	AO070301000028	FG09250.1	NCU04044.1
AN4315.1	58.m08009	AO070230000003	FG09528.1	NCU04051.1
AN1182.1	70.m15763	AO070331000182	FG09530.1	NCU04054.1
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AN4317.1	58.m08007	AO070230000006	FG09271.1	NCU04063.1
AN1769.1	69.m15067	AO070324000028	FG09532.1	NCU04069.1
AN1151.1	69.m15307	AO070226000022	FG09485.1	NCU04071.1
AN8566.1	52.m03913	AO070307000099	FG03349.1	NCU04072.1
AN1728.1	69.m15042	AO070324000059	FG09234.1	NCU04074.1
AN3117.1	59.m08620	AO070303000031	FG08466.1	NCU04076.1
AN1752.1	69.m15053	AO070324000041	FG08463.1	NCU04077.1
AN8024.1	53.m03869	AO070322000071	FG01991.1	NCU04086.1
AN5602.1	58.m07526	AO070328000002	FG09535.1	NCU04087.1
AN5603.1	58.m08909	AO070328000001	FG09534.1	NCU04088.1
AN7359.1	52.m03956	AO070302000084	FG01745.1	NCU04089.1
AN2119.1	69.m15159	AO070332000052	FG09254.1	NCU04090.1
AN0828.1	70.m15429	AO070255000017	FG03177.1	NCU04092.1
AN6512.1	62.m03099	AO070270000007	FG07165.1	NCU04097.1
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AN9522.1	53.m04094	AO070310000070	FG07173.1	NCU04099.1
AN8023.1	53.m03868	AO070322000070	FG07172.1	NCU04100.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN6591.1	62.m03207	AO070326000039	FG07169.1	NCU04104.1
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AN4905.1	59.m08809	AO070338000040	FG02000.1	NCU04109.1
AN3604.1	58.m07402	AO070342000157	FG01846.1	NCU04111.1
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AN8859.1	71.m15997	AO070271000014	FG07421.1	NCU04118.1
AN2048.1	58.m07636	AO070292000015	FG01890.1	NCU04119.1
AN2047.1	58.m07635	AO070292000014	FG01891.1	NCU04120.1
AN4207.1	54.m06766	AO070231000017	FG01893.1	NCU04121.1
AN0762.1	70.m15365	AO070316000082	FG01873.1	NCU04124.1
AN5658.1	58.m07323	AO070342000246	FG04564.1	NCU04130.1
AN6600.1	62.m03197	AO070326000049	FG07166.1	NCU04131.1
AN0292.1	54.m06490	AO070334000050	FG02010.1	NCU04136.1
AN3594.1	58.m08904	AO070342000146	FG02011.1	NCU04137.1
AN6347.1	72.m19508	AO070275000012	FG01842.1	NCU04143.1
AN4208.1	54.m06767	AO070231000016	FG02016.1	NCU04144.1
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AN6522.1	62.m03111	AO070270000021	FG05220.1	NCU04149.1
AN0072.1	71.m15348	AO070314000161	FG07326.1	NCU04153.1
AN0451.1	54.m06643	AO070328000185	FG07315.1	NCU04156.1
AN8168.1	53.m03813	AO070266000006	FG07197.1	NCU04158.1
AN6443.1	58.m08930	AO070238000002	FG11028.1	NCU04161.1
AN2262.1	71.m15903	AO070295000025	FG07195.1	NCU04165.1
AN2263.1	71.m15904	AO070295000026	FG07194.1	NCU04166.1
AN2268.1	71.m15913	AO070295000040	FG07333.1	NCU04171.1
AN6543.1	62.m03131	AO070270000041	FG07334.1	NCU04172.1
AN6542.1	62.m03132	AO070253000011	FG07335.1	NCU04173.1
AN6511.1	62.m03098	AO070270000006	FG07338.1	NCU04176.1
AN6502.1	62.m03090	AO070222000018	FG07341.1	NCU04180.1
AN6508.1	62.m03095	AO070270000001	FG07329.1	NCU04185.1
AN6507.1	62.m03094	AO070222000023	FG07328.1	NCU04187.1
AN6544.1	62.m03493	AO070270000040	FG07322.1	NCU04188.1
AN7730.1	71.m16098	AO070325000147	FG06999.1	NCU04190.1
AN6514.1	62.m03101	AO070270000009	FG07345.1	NCU04191.1
AN8252.1	53.m03709	AO070310000055	FG06133.1	NCU04192.1
AN4854.1	59.m09119	AO070327000089	FG04161.1	NCU04193.1
AN8799.1	71.m15606	AO070276000061	FG05964.1	NCU04196.1
AN8237.1	53.m03732	AO070310000071	FG06138.1	NCU04199.1
AN4733.1	71.m16082	AO070276000009	FG06139.1	NCU04201.1
AN8216.1	53.m03757	AO070310000096	FG05972.1	NCU04202.1
AN3504.1	54.m06814	AO070306000123	FG02920.1	NCU04203.1
AN8217.1	53.m03756	AO070310000095	FG05973.1	NCU04203.1
AN7571.1	72.m19590	AO070343000417	FG05974.1	NCU04207.1
AN4162.1	58.m07363	AO070342000192	FG10159.1	NCU04212.1
AN4329.1	58.m07991	AO070240000007	FG10160.1	NCU04213.1
AN6637.1	62.m03232	AO070326000089	FG05278.1	NCU04216.1
AN4912.1	59.m08815	AO070338000036	FG02119.1	NCU04218.1
AN5635.1	58.m07328	AO070342000242	FG09895.1	NCU04221.1
AN5657.1	58.m07322	AO070342000247	FG10356.1	NCU04224.1
AN3458.1	59.m09319	AO070265000035	FG10355.1	NCU04225.1
AN4647.1	57.m05486	AO070316000121	FG10257.1	NCU04228.1
AN3811.1	57.m05671	AO070311000008	FG10221.1	NCU04229.1
AN5634.1	58.m07331	AO070342000238	FG09896.1	NCU04230.1
AN9489.1	65.m07290	AO070339000098	FG09915.1	NCU04232.1
AN1748.1	66.m04624	AO070320000028	FG02113.1	NCU04234.1
AN4305.1	58.m08019	AO070330000015	FG04568.1	NCU04237.1
AN7440.1	57.m05911	AO070229000004	FG10032.1	NCU04238.1
AN0646.1	70.m15248	AO070343000583	FG09930.1	NCU04242.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN0647.1	70.m15249	AO070343000582	FG09929.1	NCU04243.1
AN7687.1	57.m05468	AO070325000085	FG09927.1	NCU04245.1
AN1953.1	58.m07342	AO070342000222	FG10385.1	NCU04247.1
AN1952.1	58.m07343	AO070342000221	FG10386.1	NCU04249.1
AN4566.1	57.m05488	AO070316000145	FG10327.1	NCU04251.1
AN2518.1	59.m08469	AO070286000074	FG10345.1	NCU04252.1
AN3425.1	59.m09279	AO070327000006	FG10259.1	NCU04256.1
AN1948.1	58.m07348	AO070342000213	FG09976.1	NCU04258.1
AN4386.1	58.m08970	AO070261000031	FG09938.1	NCU04259.1
AN2825.1	67.m02963	AO070330000091	FG07016.1	NCU04262.1
AN8421.1	52.m03816	AO070302000061	FG07016.1	NCU04262.1
AN4819.1	59.m09156	AO070327000168	FG10043.1	NCU04264.1
AN3428.1	59.m09284	AO070265000001	FG09995.1	NCU04272.1
AN3427.1	59.m09282	AO070327000003	FG10156.1	NCU04273.1
AN4411.1	58.m08982	AO070273000031	FG10157.1	NCU04274.1
AN4407.1	58.m08972	AO070273000067	FG10158.1	NCU04275.1
AN8843.1	71.m15975	AO070271000034	FG10211.1	NCU04277.1
AN1326.1	70.m14905	AO070303000090	FG10196.1	NCU04279.1
AN3894.1	54.m07025	AO070324000132	FG10198.1	NCU04280.1
AN1335.1	70.m14899	AO070303000097	FG10251.1	NCU04281.1
AN1379.1	70.m14844	AO070243000010	FG10280.1	NCU04288.1
AN4303.1	58.m08021	AO070207000007	FG04571.1	NCU04289.1
AN5957.1	72.m19941	AO070340000309	FG04570.1	NCU04292.1
AN7679.1	57.m05456	AO070325000069	FG10388.1	NCU04293.1
AN4350.1	58.m07970	AO070240000028	FG10031.1	NCU04298.1
AN4399.1	58.m07932	AO070261000044	FG09935.1	NCU04302.1
AN4401.1	58.m07925	AO070261000045	FG09934.1	NCU04303.1
AN4402.1	58.m07924	AO070261000046	FG09933.1	NCU04304.1
AN4295.1	58.m09012	AO070207000004	FG10319.1	NCU04307.1
AN4382.1	58.m07943	AO070261000027	FG10322.1	NCU04309.1
AN4378.1	58.m08998	AO070261000021	FG10028.1	NCU04310.1
AN1384.1	70.m14837	AO070243000018	FG10145.1	NCU04316.1
AN4867.1	59.m08762	AO070338000092	FG09910.1	NCU04319.1
AN2531.1	59.m08446	AO070300000119	FG10029.1	NCU04322.1
AN4160.1	58.m07365	AO070342000189	FG10148.1	NCU04325.1
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AN2491.1	59.m08498	AO070312000129	FG02622.1	NCU04327.1
AN1013.1	70.m15230	AO070312000015	FG10010.1	NCU04331.1
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AN7995.1	53.m03852	AO070322000050	FG05114.1	NCU04339.1
AN7620.1	72.m19654	AO070343000264	FG05647.1	NCU04343.1
AN0167.1	71.m15442	AO070321000079	FG05648.1	NCU04344.1
AN2174.1	72.m19665	AO070343000247	FG09689.1	NCU04370.1
AN2178.1	72.m19662	AO070343000251	FG09568.1	NCU04374.1
AN6014.1	72.m19129	AO070340000265	FG08543.1	NCU04380.1
AN5886.1	72.m19244	AO070245000021	FG09589.1	NCU04385.1
AN5880.1	72.m19251	AO070245000028	FG09587.1	NCU04387.1
AN5879.1	72.m19252	AO070245000029	FG09586.1	NCU04388.1
AN5891.1	72.m19239	AO070245000016	FG09585.1	NCU04389.1
AN2334.1	71.m16080	AO070323000005	FG08044.1	NCU04401.1
AN1170.1	70.m15051	AO070331000165	FG02778.1	NCU04402.1
AN1177.1	70.m15040	AO070331000173	FG02780.1	NCU04404.1
AN1179.1	70.m15038	AO070331000176	FG11637.1	NCU04406.1
AN1296.1	70.m14912	AO070303000056	FG11594.1	NCU04410.1
AN3634.1	58.m07467	AO070328000078	FG00598.1	NCU04411.1
AN3635.1	58.m07466	AO070328000079	FG11596.1	NCU04412.1
AN4236.1	54.m06779	AO070234000007	FG11597.1	NCU04414.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN4940.1	59.m08844	AO070338000003	FG11602.1	NCU04415.1
AN2427.1	72.m19482	AO070241000010	FG00986.1	NCU04421.1
AN0697.1	70.m15300	AO070343000515	FG04946.1	NCU04427.1
AN0696.1	70.m15299	AO070343000516	FG04944.1	NCU04428.1
AN0716.1	70.m15351	AO070343000451	FG04945.1	NCU04429.1
AN8445.1	52.m03678	AO070341000302	FG04936.1	NCU04430.1
AN0589.1	69.m15260	AO070280000011	FG05687.1	NCU04439.1
AN4727.1	71.m15496	AO070323000057	FG05689.1	NCU04442.1
AN0158.1	71.m15435	AO070321000089	FG05690.1	NCU04443.1
AN2149.1	72.m19692	AO070343000198	FG05250.1	NCU04448.1
AN2150.1	72.m19691	AO070343000199	FG05249.1	NCU04449.1
AN0730.1	70.m15326	AO070343000491	FG09683.1	NCU04450.1
AN5228.1	57.m05703	AO070337000249	FG03262.1	NCU04452.1
AN0729.1	70.m15328	AO070343000488	FG05243.1	NCU04454.1
AN6299.1	72.m18968	AO070260000007	FG09673.1	NCU04457.1
AN6182.1	72.m19274	AO070308000124	FG05668.1	NCU04460.1
AN5861.1	72.m19272	AO070308000126	FG05670.1	NCU04462.1
AN6738.1	65.m07229	AO070339000184	FG05671.1	NCU04463.1
AN6188.1	72.m19286	AO070308000113	FG08678.1	NCU04470.1
AN8058.1	53.m03885	AO070322000142	FG07500.1	NCU04474.1
AN7503.1	57.m05836	AO070287000009	FG05686.1	NCU04485.1
AN5158.1	54.m06858	AO070291000007	FG04981.1	NCU04495.1
AN4232.1	54.m06784	AO070234000014	FG04027.1	NCU04503.1
AN4233.1	54.m06783	AO070234000013	FG04028.1	NCU04504.1
AN5535.1	58.m07481	AO070328000056	FG03976.1	NCU04505.1
AN5536.1	58.m07482	AO070328000055	FG04038.1	NCU04507.1
AN3122.1	59.m08614	AO070303000025	FG04031.1	NCU04511.1
AN3123.1	59.m08613	AO070303000024	FG04030.1	NCU04512.1
AN3126.1	59.m09375	AO070303000021	FG03999.1	NCU04519.1
AN7484.1	57.m05866	AO070287000045	FG04003.1	NCU04522.1
AN6197.1	69.m15437	AO070305000025	FG05038.1	NCU04534.1
AN5632.1	58.m07556	AO070301000031	FG10503.1	NCU04541.1
AN3067.1	59.m08932	AO070337000006	FG06065.1	NCU04548.1
AN4871.1	59.m08766	AO070338000089	FG10939.1	NCU04554.1
AN3972.1	69.m15765	AO070333000216	FG10203.1	NCU04569.1
AN2505.1	59.m08485	AO070312000059	FG10047.1	NCU04576.1
AN6346.1	72.m19509	AO070275000011	FG02056.1	NCU04579.1
AN6345.1	72.m19510	AO070275000008	FG02055.1	NCU04580.1
AN6340.1	72.m19518	AO070298000007	FG02054.1	NCU04581.1
AN5806.1	72.m18936	AO070260000042	FG10186.1	NCU04584.1
AN2393.1	54.m06368	AO070296000121	FG04251.1	NCU04592.1
AN5232.1	69.m15308	AO070343000101	FG10039.1	NCU04594.1
AN2513.1	59.m08471	AO070263000053	FG10037.1	NCU04595.1
AN2514.1	59.m08472	AO070263000052	FG10036.1	NCU04596.1
AN7681.1	57.m05947	AO070325000071	FG10035.1	NCU04597.1
AN1358.1	70.m15731	AO070237000002	FG10239.1	NCU04600.1
AN7447.1	57.m05898	AO070229000019	FG10242.1	NCU04606.1
AN3424.1	59.m09278	AO070327000007	FG09981.1	NCU04610.1
AN3423.1	59.m09501	AO070327000008	FG09904.1	NCU04611.1
AN3422.1	59.m09275	AO070327000010	FG09903.1	NCU04612.1
AN1945.1	58.m07351	AO070342000203	FG09902.1	NCU04613.1
AN7448.1	57.m05896	AO070229000021	FG09900.1	NCU04614.1
AN1800.1	57.m05369	AO070335000095	FG10042.1	NCU04615.1
AN0980.1	70.m15621	AO070250000038	FG03343.1	NCU04623.1
AN8262.1	53.m04209	AO070310000038	FG07716.1	NCU04626.1
AN2508.1	59.m08476	AO070263000056	FG10049.1	NCU04636.1
AN7683.1	57.m05461	AO070325000076	FG09968.1	NCU04639.1
AN5492.1	69.m15459	AO070341000393	FG10205.1	NCU04642.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN0260.1	54.m06521	AO070334000098	FG01839.1	NCU04646.1
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AN8291.1	65.m07469	AO070190000007	FG07432.1	NCU04652.1
AN4712.1	71.m16086	AO070329000163	FG07373.1	NCU04653.1
AN8214.1	53.m03759	AO070310000098	FG07374.1	NCU04654.1
AN8822.1	71.m15633	AO070276000020	FG07372.1	NCU04655.1
AN8899.1	57.m05984	AO070294000091	FG02678.1	NCU04657.1
AN1940.1	58.m07359	AO070342000196	FG10046.1	NCU04661.1
AN5849.1	72.m19897	AO070281000056	FG10057.1	NCU04663.1
AN5324.1	69.m15364	AO070323000167	FG10051.1	NCU04667.1
AN6169.1	72.m19000	AO070340000031	FG02709.1	NCU04669.1
AN6870.1	71.m15261	AO070314000052	FG02207.1	NCU04672.1
AN7175.1	65.m07223	AO070335000146	FG04216.1	NCU04695.1
AN4663.1	71.m15712	AO070250000002	FG09525.1	NCU04698.1
AN1376.1	70.m14847	AO070243000006	FG08613.1	NCU04699.1
AN1900.1	57.m05718	AO070341000154	FG09462.1	NCU04713.1
AN1902.1	57.m05716	AO070341000151	FG09457.1	NCU04718.1
AN1007.1	70.m15225	AO070312000026	FG08402.1	NCU04720.1
AN4245.1	54.m06807	AO070324000167	FG04738.1	NCU04721.1
AN1768.1	69.m15068	AO070324000027	FG08615.1	NCU04724.1
AN1428.1	55.m02927	AO070242000023	FG08396.1	NCU04725.1
AN1416.1	55.m02923	AO070242000019	FG08395.1	NCU04726.1
AN1418.1	55.m02924	AO070242000020	FG08398.1	NCU04727.1
AN4255.1	65.m07427	AO070309000125	FG08399.1	NCU04728.1
AN1519.1	55.m03038	AO070334000237	FG08752.1	NCU04730.1
AN7661.1	57.m05428	AO070268000032	FG08403.1	NCU04731.1
AN3797.1	57.m05686	AO070337000231	FG08405.1	NCU04733.1
AN1189.1	70.m15033	AO070331000187	FG09515.1	NCU04736.1
AN4959.1	59.m08864	AO070288000021	FG09520.1	NCU04738.1
AN4958.1	59.m08863	AO070288000020	FG09519.1	NCU04740.1
AN4960.1	59.m08865	AO070288000022	FG09517.1	NCU04742.1
AN4967.1	59.m08870	AO070288000032	FG09516.1	NCU04743.1
AN1171.1	70.m15050	AO070331000166	FG09274.1	NCU04747.1
AN3653.1	58.m07446	AO070342000034	FG09509.1	NCU04749.1
AN1374.1	70.m14849	AO070215000001	FG08748.1	NCU04750.1
AN3655.1	58.m07445	AO070342000033	FG09511.1	NCU04753.1
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AN4322.1	58.m08001	AO070230000013	FG09513.1	NCU04755.1
AN4929.1	59.m08831	AO070338000014	FG09507.1	NCU04757.1
AN2868.1	59.m08713	AO070338000154	FG08476.1	NCU04761.1
AN4973.1	59.m08876	AO070288000039	FG08471.1	NCU04765.1
AN4965.1	59.m08868	AO070288000030	FG08474.1	NCU04766.1
AN4977.1	59.m09403	AO070288000044	FG08425.1	NCU04768.1
AN4976.1	59.m08879	AO070288000043	FG08427.1	NCU04770.1
AN4975.1	59.m08878	AO070288000042	FG08428.1	NCU04771.1
AN4943.1	59.m08847	AO070338000001	FG08430.1	NCU04772.1
AN5520.1	69.m15439	AO070341000371	FG08478.1	NCU04779.1
AN0450.1	54.m06642	AO070165000001	FG08479.1	NCU04780.1
AN5640.1	58.m07562	AO070301000036	FG08481.1	NCU04782.1
AN3696.1	69.m15403	AO070341000317	FG08485.1	NCU04783.1
AN5627.1	58.m08920	AO070301000027	FG08487.1	NCU04784.1
AN7525.1	69.m15143	AO070258000031	FG08382.1	NCU04788.1
AN2081.1	57.m05780	AO070341000234	FG08604.1	NCU04789.1
AN2080.1	57.m05779	AO070341000233	FG08603.1	NCU04790.1
AN5646.1	58.m07559	AO070301000034	FG09503.1	NCU04796.1
AN5604.1	58.m07528	AO070301000002	FG09280.1	NCU04797.1
AN3999.1	54.m06592	AO070328000163	FG08422.1	NCU04800.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1921.1	69.m14938	AO070341000116	FG09281.1	NCU04802.1
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AN1915.1	69.m14931	AO070341000128	FG08760.1	NCU04817.1
AN1924.1	69.m14942	AO070341000109	FG08393.1	NCU04830.1
AN9008.1	69.m15086	AO070336000118	FG08608.1	NCU04834.1
AN1299.1	70.m14909	AO070303000060	FG08489.1	NCU04837.1
AN2073.1	57.m05774	AO070341000227	FG08490.1	NCU04838.1
AN2076.1	57.m05775	AO070341000228	FG08491.1	NCU04840.1
AN8687.1	62.m03487	AO070315000106	FG02462.1	NCU04855.1
AN1563.1	55.m03084	AO070339000290	FG02203.1	NCU04857.1
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AN8019.1	54.m06297	AO070236000022	FG03980.1	NCU04881.1
AN3146.1	59.m08519	AO070256000046	FG02460.1	NCU04898.1
AN6717.1	65.m07257	AO070339000157	FG02461.1	NCU04899.1
AN8100.1	69.m14871	AO070281000022	FG01995.1	NCU04902.1
AN3511.1	69.m15741	AO070263000017	FG07314.1	NCU04908.1
AN2404.1	55.m03089	AO070339000289	FG04609.1	NCU04921.1
AN5563.1	58.m07489	AO070328000044	FG07908.1	NCU04923.1
AN5564.1	58.m07490	AO070328000043	FG07907.1	NCU04924.1
AN3421.1	67.m02958	AO070323000200	FG08465.1	NCU04933.1
AN5552.1	69.m15337	AO070335000011	FG00202.1	NCU04935.1
AN7527.1	69.m15119	AO070343000364	FG08125.1	NCU04940.1
AN1797.1	72.m19549	AO070309000134	FG02641.1	NCU04963.1
AN4949.1	59.m08854	AO070288000001	FG04050.1	NCU04986.1
AN4932.1	59.m08836	AO070338000011	FG04051.1	NCU04987.1
AN6452.1	66.m04679	AO070337000057	FG03427.1	NCU04991.1
AN7401.1	69.m15499	AO070333000099	FG06445.1	NCU04997.1
AN2064.1	52.m03876	AO070323000172	FG10617.1	NCU05000.1
AN3447.1	59.m09478	AO070265000023	FG07864.1	NCU05007.1
AN0172.1	71.m15445	AO070321000073	FG04299.1	NCU05013.1
AN5528.1	69.m15427	AO070341000360	FG10911.1	NCU05029.1
AN3440.1	59.m09302	AO070265000015	FG08084.1	NCU05045.1
AN1628.1	58.m07687	AO070299000099	FG04919.1	NCU05046.1
AN4248.1	54.m07032	AO070324000164	FG07933.1	NCU05053.1
AN3418.1	66.m04615	AO070203000002	FG08253.1	NCU05057.1
AN9383.1	72.m19553	AO070336000233	FG02866.1	NCU05063.1
AN5003.1	59.m08907	AO070255000039	FG07928.1	NCU05064.1
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AN3461.1	59.m09322	AO070265000039	FG07875.1	NCU05075.1
AN3464.1	59.m09325	AO070265000042	FG07872.1	NCU05078.1
AN2746.1	54.m06685	AO070338000225	FG08229.1	NCU05089.1
AN0052.1	71.m15330	AO070314000137	FG03318.1	NCU05094.1
AN3824.1	57.m05656	AO070311000023	FG01104.1	NCU05095.1
AN9119.1	66.m04780	AO070332000153	FG02662.1	NCU05117.1
AN2953.1	59.m09089	AO070337000200	FG09885.1	NCU05136.1
AN4913.1	59.m08816	AO070338000034	FG06553.1	NCU05151.1
AN5918.1	72.m19885	AO070340000367	FG05695.1	NCU05169.1
AN7418.1	57.m05460	AO070323000154	FG09110.1	NCU05188.1
AN0228.1	71.m15484	AO070323000081	FG02470.1	NCU05194.1
AN7310.1	72.m19754	AO070297000058	FG04259.1	NCU05195.1
AN4328.1	58.m09008	AO070240000006	FG03985.1	NCU05198.1
AN5436.1	69.m15503	AO070333000093	FG05095.1	NCU05200.1
AN1022.1	70.m15780	AO070343000592	FG05070.1	NCU05202.1
AN1019.1	70.m15237	AO070343000596	FG09616.1	NCU05204.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1016.1	70.m15234	AO070312000002	FG09614.1	NCU05206.1
AN2341.1	71.m15579	AO070319000152	FG04851.1	NCU05208.1
AN7311.1	72.m19752	AO070297000059	FG04266.1	NCU05213.1
AN7493.1	57.m05851	AO070287000024	FG04252.1	NCU05214.1
AN7497.1	57.m05844	AO070287000017	FG02474.1	NCU05221.1
AN7501.1	57.m05838	AO070287000012	FG02475.1	NCU05222.1
AN7502.1	57.m05837	AO070287000010	FG02476.1	NCU05224.1
AN7500.1	57.m05839	AO070287000013	FG02477.1	NCU05225.1
AN0561.1	69.m15286	AO070272000038	FG09732.1	NCU05226.1
AN4731.1	71.m15500	AO070323000053	FG09733.1	NCU05227.1
AN4732.1	71.m15501	AO070323000052	FG09734.1	NCU05228.1
AN5950.1	72.m19166	AO070340000303	FG09735.1	NCU05232.1
AN7494.1	57.m05849	AO070287000022	FG02478.1	NCU05233.1
AN4560.1	57.m05572	AO070321000168	FG06724.1	NCU05235.1
AN7601.1	72.m19646	AO070343000271	FG02481.1	NCU05237.1
AN7600.1	72.m19648	AO070343000270	FG02482.1	NCU05238.1
AN6733.1	65.m07235	AO070339000179	FG09770.1	NCU05242.1
AN7306.1	72.m19759	AO070297000054	FG09756.1	NCU05245.1
AN6222.1	72.m19976	AO070304000059	FG06157.1	NCU05246.1
AN7498.1	57.m05843	AO070287000016	FG09773.1	NCU05252.1
AN6711.1	65.m07264	AO070339000151	FG04261.1	NCU05254.1
AN6731.1	65.m07239	AO070339000175	FG06184.1	NCU05259.1
AN6193.1	72.m19291	AO070308000106	FG06183.1	NCU05261.1
AN6325.1	72.m19443	AO070304000043	FG06179.1	NCU05264.1
AN6326.1	72.m19445	AO070304000041	FG06181.1	NCU05266.1
AN6695.1	65.m07491	AO070339000125	FG01948.1	NCU05267.1
AN1047.1	70.m15203	AO070313000109	FG01950.1	NCU05269.1
AN4036.1	54.m06576	AO070328000140	FG01953.1	NCU05272.1
AN4014.1	54.m06948	AO070328000150	FG01954.1	NCU05273.1
AN4016.1	54.m06578	AO070328000142	FG01956.1	NCU05275.1
AN4017.1	54.m06577	AO070328000141	FG01957.1	NCU05276.1
AN4042.1	54.m06570	AO070328000135	FG01959.1	NCU05278.1
AN1026.1	70.m15209	AO070312000119	FG09794.1	NCU05280.1
AN1005.1	70.m15223	AO070312000029	FG09793.1	NCU05282.1
AN5895.1	72.m19235	AO070245000008	FG06166.1	NCU05288.1
AN5865.1	72.m19269	AO070308000129	FG06165.1	NCU05289.1
AN5884.1	72.m19247	AO070245000024	FG06164.1	NCU05290.1
AN6741.1	65.m07476	AO070339000188	FG06162.1	NCU05292.1
AN5871.1	72.m19263	AO070308000137	FG06161.1	NCU05293.1
AN5872.1	72.m19262	AO070308000138	FG06159.1	NCU05295.1
AN5873.1	72.m19261	AO070308000139	FG06158.1	NCU05296.1
AN1006.1	70.m15224	AO070312000028	FG01947.1	NCU05298.1
AN5971.1	72.m19187	AO070340000329	FG01941.1	NCU05299.1
AN0889.1	70.m15493	AO070320000058	FG09745.1	NCU05302.1
AN0212.1	71.m15475	AO070321000032	FG05308.1	NCU05306.1
AN0751.1	70.m15349	AO070343000448	FG09749.1	NCU05307.1
AN4048.1	54.m07017	AO070328000128	FG05311.1	NCU05309.1
AN6224.1	72.m19430	AO070304000073	FG05313.1	NCU05312.1
AN8038.1	53.m03908	AO070330000008	FG01629.1	NCU05343.1
AN8039.1	53.m03907	AO070330000007	FG01627.1	NCU05347.1
AN5154.1	54.m06864	AO070291000014	FG01632.1	NCU05375.1
AN2219.1	71.m15846	AO070326000185	FG10532.1	NCU05377.1
AN4365.1	58.m09005	AO070261000008	FG01614.1	NCU05385.1
AN4364.1	58.m07963	AO070261000007	FG01613.1	NCU05386.1
AN7367.1	69.m15484	AO070239000027	FG01698.1	NCU05387.1
AN0870.1	70.m15456	AO070320000023	FG01591.1	NCU05390.1
AN0128.1	71.m16053	AO070311000082	FG04298.1	NCU05392.1
AN1325.1	70.m14906	AO070303000088	FG00643.1	NCU05400.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1150.1	72.m19355	AO070308000028	FG01573.1	NCU05410.1
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AN8075.1	53.m03928	AO070330000033	FG00323.1	NCU05418.1
AN5731.1	54.m06850	AO070341000029	FG01643.1	NCU05420.1
AN5732.1	54.m06851	AO070341000028	FG01642.1	NCU05421.1
AN2461.1	69.m15676	AO070264000008	FG01612.1	NCU05422.1
AN5569.1	58.m07493	AO070328000037	FG04308.1	NCU05423.1
AN5571.1	58.m07497	AO070328000034	FG04309.1	NCU05425.1
AN1385.1	70.m14836	AO070243000019	FG04304.1	NCU05426.1
AN0349.1	54.m06406	AO070318000027	FG04314.1	NCU05427.1
AN2314.1	71.m15520	AO070323000036	FG04313.1	NCU05429.1
AN2315.1	71.m15519	AO070323000037	FG04312.1	NCU05430.1
AN5098.1	53.m04123	AO070310000002	FG04320.1	NCU05452.1
AN4287.1	53.m03672	AO070310000009	FG04319.1	NCU05453.1
AN1396.1	70.m14826	AO070233000012	FG03249.1	NCU05454.1
AN2316.1	71.m15518	AO070323000038	FG04315.1	NCU05457.1
AN6004.1	72.m19138	AO070340000274	FG08365.1	NCU05488.1
AN9370.1	71.m15574	AO070333000225	FG03772.1	NCU05492.1
AN1378.1	70.m14845	AO070243000008	FG08359.1	NCU05498.1
AN1897.1	57.m05721	AO070341000158	FG06450.1	NCU05499.1
AN2230.1	55.m03093	AO070330000121	FG10229.1	NCU05500.1
AN5693.1	65.m07417	AO070309000108	FG08333.1	NCU05515.1
AN6055.1	72.m19102	AO070340000199	FG08329.1	NCU05516.1
AN7641.1	71.m15823	AO070294000037	FG02271.1	NCU05518.1
AN3221.1	67.m02927	AO070330000069	FG11084.1	NCU05519.1
AN6059.1	72.m19094	AO070340000190	FG08327.1	NCU05521.1
AN1896.1	57.m05722	AO070341000159	FG06449.1	NCU05537.1
AN5701.1	65.m07424	AO070309000122	FG08338.1	NCU05548.1
AN5988.1	72.m19152	AO070340000290	FG08325.1	NCU05575.1
AN7396.1	70.m15691	AO070343000134	FG03387.1	NCU05577.1
AN5983.1	72.m19943	AO070340000297	FG08316.1	NCU05578.1
AN3220.1	67.m02928	AO070330000070	FG10483.1	NCU05585.1
AN7633.1	72.m19474	AO070181000001	FG06515.1	NCU05586.1
AN5694.1	65.m07419	AO070309000110	FG08158.1	NCU05588.1
AN1420.1	55.m02936	AO070232000016	FG08128.1	NCU05589.1
AN0771.1	70.m15374	AO070316000073	FG08312.1	NCU05591.1
AN7621.1	65.m07418	AO070309000109	FG08131.1	NCU05594.1
AN1421.1	55.m02935	AO070232000017	FG08388.1	NCU05602.1
AN5697.1	65.m07421	AO070309000115	FG08126.1	NCU05606.1
AN5982.1	72.m19942	AO070340000299	FG08133.1	NCU05608.1
AN5607.1	58.m08908	AO070301000004	FG06417.1	NCU05620.1
AN1892.1	57.m05726	AO070341000163	FG06415.1	NCU05623.1
AN1287.1	70.m14921	AO070303000048	FG09294.1	NCU05633.1
AN1775.1	69.m15062	AO070324000034	FG02191.1	NCU05644.1
AN1776.1	69.m15061	AO070324000035	FG02192.1	NCU05645.1
AN3295.1	56.m02513	AO070319000059	FG07015.1	NCU05647.1
AN3508.1	53.m03968	AO070296000076	FG02084.1	NCU05649.1
AN2120.1	69.m15160	AO070332000051	FG02233.1	NCU05650.1
AN0086.1	71.m15362	AO070311000130	FG02714.1	NCU05680.1
AN4058.1	54.m07016	AO070342000043	FG02717.1	NCU05683.1
AN4515.1	57.m05614	AO070311000076	FG02720.1	NCU05686.1
AN0629.1	70.m15652	AO070318000119	FG05830.1	NCU05706.1
AN7249.1	72.m20026	AO070297000004	FG02732.1	NCU05715.1
AN1069.1	70.m15145	AO070285000067	FG02729.1	NCU05720.1
AN1089.1	70.m15143	AO070285000061	FG02738.1	NCU05721.1
AN1096.1	70.m15136	AO070285000048	FG02730.1	NCU05726.1
AN3108.1	59.m08629	AO070303000042	FG05279.1	NCU05733.1
AN3301.1	58.m07301	AO070299000104	FG04426.1	NCU05735.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN2509.1	59.m08475	AO070263000057	FG02657.1	NCU05752.1
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AN7388.1	56.m02393	AO070293000057	FG02974.1	NCU05770.1
AN7777.1	57.m05337	AO070286000057	FG01382.1	NCU05775.1
AN8990.1	56.m02476	AO070272000025	FG06473.1	NCU05776.1
AN7422.1	57.m05923	AO070197000001	FG02640.1	NCU05777.1
AN7424.1	57.m05921	AO070197000004	FG02637.1	NCU05782.1
AN9087.1	66.m04545	AO070332000190	FG02650.1	NCU05791.1
AN9086.1	66.m04759	AO070332000191	FG02649.1	NCU05796.1
AN9085.1	66.m04772	AO070332000192	FG02648.1	NCU05797.1
AN5839.1	72.m18975	AO070340000003	FG09875.1	NCU05802.1
AN5840.1	72.m18976	AO070340000004	FG09874.1	NCU05803.1
AN5835.1	72.m18963	AO070260000010	FG08350.1	NCU05805.1
AN4163.1	58.m07362	AO070342000193	FG09870.1	NCU05810.1
AN3085.1	59.m08662	AO070334000123	FG09881.1	NCU05818.1
AN5678.1	65.m07404	AO070309000093	FG00613.1	NCU05830.1
AN5579.1	58.m07506	AO070328000025	FG10530.1	NCU05837.1
AN9103.1	66.m04564	AO070332000170	FG02433.1	NCU05850.1
AN0012.1	71.m15481	AO070300000077	FG11360.1	NCU05852.1
AN0233.1	69.m15589	AO070283000035	FG05720.1	NCU05853.1
AN1967.1	58.m07572	AO070301000051	FG10960.1	NCU05858.1
AN4351.1	58.m07976	AO070240000023	FG01703.1	NCU05876.1
AN2015.1	58.m07623	AO070202000008	FG05770.1	NCU05878.1
AN9166.1	71.m15125	AO070343000045	FG11184.1	NCU05882.1
AN2320.1	62.m03412	AO070269000057	FG03637.1	NCU05883.1
AN2321.1	62.m03411	AO070283000059	FG03636.1	NCU05884.1
AN2558.1	59.m08403	AO070268000059	FG11568.1	NCU05885.1
AN2562.1	59.m08408	AO070343000339	FG11567.1	NCU05886.1
AN2559.1	59.m08405	AO070268000057	FG11566.1	NCU05887.1
AN9004.1	70.m15707	AO070330000107	FG11565.1	NCU05888.1
AN2907.1	59.m08758	AO070338000098	FG06073.1	NCU05889.1
AN5010.1	59.m08913	AO070224000002	FG06070.1	NCU05894.1
AN5011.1	59.m08914	AO070224000003	FG06069.1	NCU05895.1
AN5742.1	69.m14840	AO070193000003	FG01593.1	NCU05897.1
AN6177.1	72.m19918	AO070340000022	FG01705.1	NCU05899.1
AN2772.1	59.m09271	AO070327000014	FG06074.1	NCU05901.1
AN4876.1	59.m08772	AO070338000084	FG06075.1	NCU05902.1
AN1818.1	58.m07683	AO070333000196	FG11304.1	NCU05924.1
AN1912.1	69.m14927	AO070341000136	FG05351.1	NCU05936.1
AN5517.1	69.m15442	AO070341000376	FG02237.1	NCU05939.1
AN2124.1	69.m15163	AO070306000103	FG05366.1	NCU05941.1
AN1757.1	69.m15056	AO070324000038	FG05365.1	NCU05942.1
AN1777.1	69.m15060	AO070324000036	FG05364.1	NCU05943.1
AN0323.1	54.m06433	AO070334000004	FG04347.1	NCU05953.1
AN7781.1	57.m05368	AO070343000355	FG03905.1	NCU05965.1
AN1780.1	69.m15651	AO070324000015	FG09309.1	NCU05971.1
AN1779.1	69.m15647	AO070324000017	FG09310.1	NCU05972.1
AN1782.1	69.m15081	AO070324000013	FG09514.1	NCU05973.1
AN1503.1	55.m03013	AO070334000220	FG09521.1	NCU05977.1
AN1375.1	70.m15754	AO070243000005	FG08612.1	NCU05979.1
AN2237.1	71.m15826	AO070326000136	FG08454.1	NCU05980.1
AN1999.1	58.m07607	AO070301000093	FG08453.1	NCU05982.1
AN5497.1	69.m15456	AO070341000388	FG08452.1	NCU05983.1
AN3629.1	58.m07472	AO070328000067	FG08451.1	NCU05984.1
AN5599.1	58.m07523	AO070328000005	FG08766.1	NCU05985.1
AN5596.1	58.m07520	AO070328000008	FG09490.1	NCU05990.1
AN2944.1	59.m09073	AO070337000189	FG09524.1	NCU05994.1
AN2000.1	58.m08944	AO070301000095	FG08768.1	NCU05995.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN2002.1	58.m07610	AO070301000101	FG08771.1	NCU05999.1
AN5586.1	58.m07511	AO070328000020	FG08773.1	NCU06003.1
AN3916.1	69.m15661	AO070324000103	FG03247.1	NCU06005.1
AN9474.1	58.m07532	AO070301000008	FG01809.1	NCU06009.1
AN3365.1	66.m04631	AO070281000028	FG01508.1	NCU06017.1
AN5177.1	69.m14874	AO070247000008	FG07494.1	NCU06021.1
AN1136.1	70.m15101	AO070331000127	FG05701.1	NCU06022.1
AN1135.1	70.m15102	AO070331000126	FG05702.1	NCU06023.1
AN1140.1	70.m15097	AO070331000131	FG03879.1	NCU06024.1
AN1137.1	70.m15100	AO070331000128	FG05704.1	NCU06025.1
AN1138.1	70.m15099	AO070331000129	FG00107.1	NCU06026.1
AN1132.1	70.m15104	AO070331000124	FG05709.1	NCU06027.1
AN1694.1	58.m07769	AO070305000018	FG07479.1	NCU06029.1
AN3973.1	55.m03215	AO070263000041	FG07536.1	NCU06031.1
AN5192.1	69.m14892	AO070237000022	FG07539.1	NCU06032.1
AN5150.1	69.m14884	AO070237000015	FG07540.1	NCU06033.1
AN1162.1	70.m15059	AO070331000152	FG01008.1	NCU06035.1
AN1695.1	58.m07771	AO070305000019	FG07525.1	NCU06039.1
AN5226.1	57.m05706	AO070337000252	FG09374.1	NCU06043.1
AN3413.1	66.m04623	AO070281000039	FG01509.1	NCU06047.1
AN3376.1	66.m04646	AO070281000020	FG09381.1	NCU06054.1
AN3371.1	66.m04639	AO070281000010	FG09384.1	NCU06056.1
AN3370.1	66.m04638	AO070281000023	FG09385.1	NCU06057.1
AN6723.1	65.m07247	AO070339000166	FG09061.1	NCU06058.1
AN3367.1	66.m04635	AO070281000025	FG09386.1	NCU06059.1
AN0403.1	70.m15669	AO070280000032	FG04335.1	NCU06061.1
AN6234.1	52.m04099	AO070302000121	FG04334.1	NCU06062.1
AN0609.1	70.m15670	AO070280000031	FG04333.1	NCU06063.1
AN5592.1	58.m07516	AO070328000011	FG10511.1	NCU06067.1
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AN3035.1	59.m08982	AO070337000077	FG07043.1	NCU06089.1
AN5705.1	54.m06820	AO070324000154	FG06346.1	NCU06091.1
AN4878.1	59.m09408	AO070338000082	FG06356.1	NCU06095.1
AN2775.1	59.m09269	AO070327000017	FG06353.1	NCU06099.1
AN2888.1	59.m08735	AO070338000126	FG06347.1	NCU06102.1
AN5711.1	54.m06826	AO070324000151	FG06349.1	NCU06104.1
AN3928.1	69.m15000	AO070341000038	FG02469.1	NCU06110.1
AN3434.1	59.m09474	AO070265000007	FG07024.1	NCU06111.1
AN4998.1	59.m09453	AO070255000029	FG00355.1	NCU06122.1
AN8430.1	71.m15302	AO070317000096	FG05828.1	NCU06131.1
AN4481.1	57.m05651	AO070311000027	FG08802.1	NCU06167.1
AN5179.1	69.m14876	AO070247000010	FG07484.1	NCU06168.1
AN4270.1	65.m07444	AO070277000018	FG06945.1	NCU06171.1
AN8858.1	71.m15996	AO070271000015	FG06944.1	NCU06173.1
AN2280.1	71.m15925	AO070295000057	FG06943.1	NCU06174.1
AN2281.1	71.m15926	AO070295000058	FG06942.1	NCU06175.1
AN8828.1	71.m15960	AO070271000052	FG06941.1	NCU06176.1
AN2269.1	71.m15914	AO070295000041	FG05484.1	NCU06182.1
AN2266.1	71.m15910	AO070295000038	FG05469.1	NCU06183.1
AN2284.1	71.m15930	AO070295000061	FG07266.1	NCU06189.1
AN6531.1	62.m03119	AO070270000031	FG02595.1	NCU06192.1
AN9528.1	62.m03165	AO070326000021	FG02596.1	NCU06193.1
AN8848.1	71.m15983	AO070271000028	FG02699.1	NCU06198.1
AN2056.1	58.m07644	AO070292000026	FG06749.1	NCU06200.1
AN4194.1	54.m06757	AO070315000084	FG05586.1	NCU06202.1
AN6505.1	62.m03092	AO070222000021	FG02501.1	NCU06205.1
AN6506.1	62.m03093	AO070222000022	FG02502.1	NCU06207.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN6500.1	62.m03439	AO070222000014	FG02503.1	NCU06210.1
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AN8056.1	53.m03887	AO070322000144	FG02510.1	NCU06216.1
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AN4535.1	57.m05586	AO070321000149	FG06969.1	NCU06250.1
AN4546.1	57.m05579	AO070321000159	FG06979.1	NCU06251.1
AN4544.1	57.m05577	AO070321000162	FG06977.1	NCU06252.1
AN6351.1	72.m19504	AO070275000048	FG06950.1	NCU06259.1
AN7473.1	57.m05871	AO070287000053	FG06951.1	NCU06260.1
AN2133.1	72.m19708	AO070278000026	FG04155.1	NCU06261.1
AN3627.1	58.m07414	AO070342000123	FG02585.1	NCU06265.1
AN0091.1	71.m15366	AO070311000124	FG02567.1	NCU06266.1
AN0090.1	71.m15365	AO070311000125	FG02566.1	NCU06267.1
AN6911.1	71.m15221	AO070219000015	FG02565.1	NCU06268.1
AN1104.1	70.m15128	AO070285000034	FG02563.1	NCU06270.1
AN0093.1	71.m15368	AO070311000122	FG02562.1	NCU06271.1
AN2147.1	72.m19694	AO070343000196	FG02561.1	NCU06272.1
AN9523.1	71.m15373	AO070311000118	FG02581.1	NCU06273.1
AN7256.1	72.m19794	AO070297000012	FG03351.1	NCU06275.1
AN6907.1	71.m15230	AO070314000006	FG02570.1	NCU06278.1
AN5954.1	72.m19170	AO070340000308	FG02571.1	NCU06279.1
AN8523.1	71.m15587	AO070323000193	FG11302.1	NCU06282.1
AN4951.1	59.m08856	AO070288000003	FG02756.1	NCU06284.1
AN4925.1	59.m08827	AO070338000018	FG02757.1	NCU06285.1
AN9200.1	67.m02973	AO070289000054	FG00055.1	NCU06294.1
AN8660.1	62.m03415	AO070269000054	FG07636.1	NCU06296.1
AN7636.1	57.m05400	AO070294000081	FG01630.1	NCU06303.1
AN7609.1	72.m19650	AO070343000267	FG05016.1	NCU06308.1
AN3779.1	53.m03765	AO070310000104	FG05014.1	NCU06310.1
AN0161.1	71.m16051	AO070321000086	FG04996.1	NCU06314.1
AN0156.1	71.m15433	AO070321000094	FG04998.1	NCU06315.1
AN2312.1	71.m15515	AO070323000042	FG05001.1	NCU06317.1
AN4721.1	71.m15491	AO070323000062	FG05002.1	NCU06318.1
AN5901.1	72.m19229	AO070248000039	FG05247.1	NCU06322.1
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AN4046.1	54.m06564	AO070328000129	FG05008.1	NCU06332.1
AN6269.1	72.m19366	AO070304000007	FG06177.1	NCU06333.1
AN9406.1	52.m04033	AO070274000011	FG09705.1	NCU06336.1
AN5406.1	69.m15507	AO070333000120	FG09801.1	NCU06338.1
AN1423.1	55.m02933	AO070232000019	FG09804.1	NCU06341.1
AN1023.1	70.m15244	AO070343000591	FG09721.1	NCU06347.1
AN7188.1	69.m15181	AO070252000016	FG09782.1	NCU06352.1
AN6735.1	65.m07233	AO070339000181	FG02746.1	NCU06354.1
AN0717.1	70.m15350	AO070343000449	FG09647.1	NCU06360.1
AN5404.1	69.m15505	AO070333000090	FG09796.1	NCU06361.1
AN5407.1	69.m15524	AO070333000121	FG09797.1	NCU06362.1
AN5925.1	72.m19206	AO070340000359	FG01945.1	NCU06365.1
AN5821.1	72.m18948	AO070260000024	FG01802.1	NCU06366.1
AN4725.1	71.m15494	AO070323000059	FG09685.1	NCU06368.1
AN4726.1	71.m15495	AO070323000058	FG05870.1	NCU06369.1
AN4723.1	71.m15492	AO070323000061	FG09022.1	NCU06371.1
AN7491.1	57.m05853	AO070287000026	FG08668.1	NCU06372.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN5450.1	69.m15482	AO070239000029	FG09665.1	NCU06374.1
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AN7673.1	57.m05449	AO070325000053	FG05293.1	NCU06380.1
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AN7715.1	71.m15740	AO070325000127	FG06214.1	NCU06386.1
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AN8907.1	56.m02323	AO070319000030	FG09830.1	NCU06402.1
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AN0050.1	71.m15332	AO070314000139	FG07302.1	NCU06417.1
AN4903.1	59.m08803	AO070338000043	FG07296.1	NCU06418.1
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AN8201.1	53.m03774	AO070310000118	FG07280.1	NCU06438.1
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AN6311.1	72.m19323	AO070308000066	FG05451.1	NCU06444.1
AN5910.1	72.m19955	AO070248000036	FG07289.1	NCU06446.1
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AN8029.1	53.m03875	AO070322000075	FG07279.1	NCU06449.1
AN8057.1	53.m03886	AO070322000143	FG07287.1	NCU06452.1
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AN7479.1	57.m05859	AO070287000036	FG08865.1	NCU06457.1
AN7480.1	57.m05861	AO070287000037	FG05444.1	NCU06459.1
AN0641.1	70.m15635	AO070318000142	FG02523.1	NCU06464.1
AN0640.1	70.m15636	AO070318000141	FG02522.1	NCU06465.1
AN6310.1	72.m19324	AO070308000065	FG07258.1	NCU06468.1
AN2057.1	58.m07659	AO070292000042	FG07257.1	NCU06469.1
AN4355.1	52.m03842	AO070315000047	FG07255.1	NCU06471.1
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AN6217.1	72.m19316	AO070308000074	FG05455.1	NCU06483.1
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AN0651.1	70.m15256	AO070343000576	FG05535.1	NCU06493.1
AN6594.1	62.m03203	AO070326000044	FG05537.1	NCU06497.1
AN2130.1	72.m19711	AO070278000033	FG05398.1	NCU06500.1
AN9538.1	72.m19710	AO070278000028	FG05399.1	NCU06503.1
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AN0204.1	71.m15469	AO070321000040	FG09740.1	NCU06520.1
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AN3516.1	55.m03299	AO070302000081	FG10662.1	NCU06523.1
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AN5909.1	72.m19222	AO070245000003	FG09678.1	NCU06532.1
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AN9437.1	70.m15333	AO070343000483	FG04948.1	NCU06534.1
AN2751.1	71.m15497	AO070323000056	FG09663.1	NCU06540.1
AN0824.1	70.m15426	AO070255000021	FG09661.1	NCU06543.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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AN0593.1	69.m15255	AO070280000019	FG05284.1	NCU06559.1
AN0162.1	71.m16050	AO070321000085	FG05283.1	NCU06560.1
AN0163.1	71.m15438	AO070321000084	FG05282.1	NCU06561.1
AN0164.1	71.m15439	AO070321000083	FG05281.1	NCU06563.1
AN0166.1	71.m15441	AO070321000080	FG05288.1	NCU06568.1
AN0165.1	71.m15440	AO070321000081	FG05286.1	NCU06569.1
AN2139.1	72.m20010	AO070343000184	FG07145.1	NCU06572.1
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AN3868.1	58.m07840	AO070305000104	FG01992.1	NCU06614.1
AN6732.1	65.m07236	AO070339000178	FG05235.1	NCU06617.1
AN6442.1	55.m03221	AO070325000114	FG09039.1	NCU06619.1
AN0211.1	71.m15474	AO070321000033	FG05305.1	NCU06622.1
AN2308.1	71.m15511	AO070323000046	FG05303.1	NCU06624.1
AN0576.1	69.m15269	AO070272000056	FG05306.1	NCU06626.1
AN2318.1	71.m15516	AO070323000040	FG09811.1	NCU06628.1
AN6391.1	69.m15695	AO070343000154	FG09815.1	NCU06630.1
AN0560.1	69.m15287	AO070272000037	FG09816.1	NCU06631.1
AN0559.1	69.m15288	AO070272000036	FG09817.1	NCU06632.1
AN0502.1	69.m15301	AO070226000015	FG09818.1	NCU06633.1
AN0655.1	70.m15259	AO070343000571	FG10100.1	NCU06636.1
AN7677.1	57.m05454	AO070325000067	FG10096.1	NCU06637.1
AN7678.1	57.m05455	AO070325000068	FG10095.1	NCU06638.1
AN5484.1	69.m15469	AO070341000401	FG10064.1	NCU06643.1
AN2529.1	59.m08450	AO070300000122	FG09979.1	NCU06647.1
AN4496.1	57.m05635	AO070311000048	FG10016.1	NCU06648.1
AN9109.1	66.m04576	AO070332000159	FG10199.1	NCU06649.1
AN7632.1	57.m05406	AO070268000004	FG10200.1	NCU06652.1
AN3084.1	59.m08663	AO070334000122	FG10308.1	NCU06655.1
AN0689.1	70.m15292	AO070343000524	FG09921.1	NCU06656.1
AN0690.1	70.m15293	AO070343000523	FG09923.1	NCU06658.1
AN5014.1	59.m08665	AO070334000120	FG09974.1	NCU06661.1
AN7671.1	57.m05939	AO070325000051	FG09975.1	NCU06662.1
AN7625.1	57.m05404	AO070294000090	FG09940.1	NCU06666.1
AN7428.1	57.m05916	AO070197000009	FG10226.1	NCU06672.1
AN9460.1	53.m03783	AO070310000131	FG06800.1	NCU06677.1
AN8185.1	53.m03793	AO070310000139	FG06799.1	NCU06678.1
AN8187.1	53.m03792	AO070310000138	FG06798.1	NCU06679.1
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AN1146.1	70.m15385	AO070316000058	FG01883.1	NCU06699.1
AN2296.1	71.m15945	AO070295000077	FG07420.1	NCU06701.1
AN2279.1	71.m15924	AO070295000056	FG07419.1	NCU06702.1
AN6604.1	62.m03192	AO070326000055	FG05227.1	NCU06706.1
AN8488.1	58.m08926	AO070299000105	FG06394.1	NCU06708.1
AN6601.1	62.m03196	AO070326000052	FG05224.1	NCU06710.1
AN6548.1	62.m03125	AO070270000037	FG05223.1	NCU06711.1
AN6547.1	62.m03126	AO070270000038	FG05222.1	NCU06712.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN6546.1	62.m03127	AO070270000039	FG05194.1	NCU06713.1
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AN7688.1	57.m05465	AO070325000082	FG10309.1	NCU06719.1
AN2555.1	57.m05650	AO070319000164	FG05797.1	NCU06720.1
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AN4159.1	58.m08894	AO070342000188	FG10264.1	NCU06724.1
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AN0687.1	70.m15290	AO070343000527	FG10249.1	NCU06727.1
AN5812.1	72.m18942	AO070260000035	FG10188.1	NCU06732.1
AN1363.1	70.m14866	AO070243000001	FG01545.1	NCU06735.1
AN6257.1	72.m19399	AO070304000031	FG06265.1	NCU06738.1
AN6256.1	72.m19400	AO070304000032	FG06266.1	NCU06739.1
AN4307.1	58.m09013	AO070207000012	FG01542.1	NCU06748.1
AN3771.1	70.m15746	AO070233000011	FG06571.1	NCU06750.1
AN1364.1	70.m14865	AO070215000017	FG01540.1	NCU06751.1
AN0444.1	54.m06635	AO070338000306	FG06272.1	NCU06756.1
AN6291.1	72.m19344	AO070308000001	FG00958.1	NCU06758.1
AN6207.1	72.m19305	AO070308000086	FG04416.1	NCU06760.1
AN1989.1	58.m07597	AO070301000077	FG04413.1	NCU06761.1
AN1969.1	58.m07574	AO070301000053	FG04412.1	NCU06762.1
AN6725.1	65.m07245	AO070339000169	FG04411.1	NCU06763.1
AN6726.1	65.m07244	AO070339000170	FG04410.1	NCU06764.1
AN6303.1	72.m19331	AO070308000058	FG00327.1	NCU06767.1
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AN6300.1	72.m19334	AO070308000056	FG00329.1	NCU06769.1
AN6289.1	72.m19346	AO070308000003	FG00957.1	NCU06774.1
AN4417.1	58.m07906	AO070273000038	FG10865.1	NCU06776.1
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AN5724.1	54.m06844	AO070324000127	FG10863.1	NCU06778.1
AN5725.1	54.m06845	AO070324000126	FG10858.1	NCU06779.1
AN0141.1	71.m15424	AO070321000108	FG10860.1	NCU06780.1
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AN2435.1	69.m15223	AO070264000043	FG06039.1	NCU06783.1
AN1991.1	58.m07600	AO070301000081	FG06043.1	NCU06790.1
AN1048.1	70.m15205	AO070313000110	FG01615.1	NCU06792.1
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AN7606.1	72.m19640	AO070343000278	FG04302.1	NCU06804.1
AN6282.1	72.m19357	AO070308000029	FG01571.1	NCU06809.1
AN7604.1	72.m19642	AO070343000276	FG04294.1	NCU06812.1
AN0135.1	71.m15419	AO070321000117	FG10861.1	NCU06821.1
AN6875.1	71.m15259	AO070314000048	FG01690.1	NCU06832.1
AN5619.1	58.m08956	AO070301000020	FG11224.1	NCU06834.1
AN5626.1	58.m07549	AO070301000025	FG00330.1	NCU06836.1
AN3693.1	69.m15405	AO070341000321	FG00332.1	NCU06838.1
AN3692.1	69.m15406	AO070341000323	FG00333.1	NCU06839.1
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AN4316.1	58.m08008	AO070230000004	FG04369.1	NCU06846.1
AN0328.1	54.m06431	AO070334000002	FG06256.1	NCU06855.1
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AN4241.1	54.m06804	AO070324000173	FG06354.1	NCU06860.1
AN7313.1	56.m03103	AO070319000136	FG11366.1	NCU06861.1
AN3073.1	59.m08925	AO070224000013	FG10797.1	NCU06866.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN3080.1	59.m08918	AO070224000006	FG10799.1	NCU06868.1
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AN3708.1	69.m15413	AO070341000333	FG07949.1	NCU06876.1
AN3687.1	69.m15395	AO070342000308	FG00353.1	NCU06880.1
AN5669.1	69.m15371	AO070342000262	FG06342.1	NCU06881.1
AN3689.1	69.m15400	AO070341000313	FG07044.1	NCU06882.1
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AN6730.1	65.m07240	AO070339000174	FG07495.1	NCU06918.1
AN5196.1	69.m14895	AO070237000026	FG01399.1	NCU06921.1
AN5195.1	69.m14894	AO070237000025	FG01398.1	NCU06922.1
AN5199.1	69.m14898	AO070237000029	FG01397.1	NCU06923.1
AN5200.1	69.m14899	AO070237000030	FG01395.1	NCU06924.1
AN3833.1	58.m07812	AO070305000071	FG09396.1	NCU06927.1
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AN3061.1	59.m08953	AO070337000012	FG10964.1	NCU06942.1
AN3069.1	59.m08928	AO070337000005	FG10940.1	NCU06943.1
AN8354.1	63.m00662	AO070342000083	FG03042.1	NCU06945.1
AN5558.1	58.m07484	AO070328000053	FG03315.1	NCU06949.1
AN5578.1	58.m07505	AO070328000026	FG10526.1	NCU06950.1
AN6036.1	72.m19121	AO070340000252	FG05873.1	NCU06959.1
AN8891.1	56.m02304	AO070293000026	FG07551.1	NCU06961.1
AN8761.1	62.m03458	AO070277000065	FG10708.1	NCU06961.1
AN1965.1	58.m07570	AO070301000046	FG09299.1	NCU06970.1
AN0118.1	71.m15397	AO070311000095	FG09607.1	NCU06976.1
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AN0229.1	71.m15482	AO070323000079	FG05653.1	NCU06986.1
AN0823.1	70.m15424	AO070255000022	FG05645.1	NCU06989.1
AN9399.1	52.m04025	AO070274000017	FG09564.1	NCU06993.1
AN7495.1	57.m05848	AO070287000021	FG09807.1	NCU06994.1
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AN2229.1	71.m15836	AO070326000151	FG05658.1	NCU07001.1
AN6472.1	57.m05371	AO070290000063	FG09751.1	NCU07005.1
AN8293.1	52.m04044	AO070274000002	FG05081.1	NCU07011.1
AN5979.1	72.m19162	AO070307000027	FG05640.1	NCU07014.1
AN2233.1	71.m15832	AO070326000146	FG09598.1	NCU07019.1
AN2224.1	71.m15842	AO070326000179	FG09600.1	NCU07020.1
AN2223.1	71.m15843	AO070326000180	FG05083.1	NCU07021.1
AN0774.1	70.m15380	AO070316000064	FG08942.1	NCU07022.1
AN1018.1	70.m15236	AO070343000597	FG09615.1	NCU07023.1
AN1017.1	70.m15235	AO070343000598	FG09612.1	NCU07024.1
AN1015.1	70.m15233	AO070312000003	FG09613.1	NCU07027.1
AN6221.1	72.m19434	AO070304000053	FG05073.1	NCU07039.1
AN5875.1	72.m19257	AO070308000144	FG06203.1	NCU07041.1
AN6229.1	72.m19424	AO070304000080	FG06202.1	NCU07042.1
AN0476.1	54.m06594	AO070328000164	FG08747.1	NCU07057.1
AN7524.1	69.m15112	AO070258000032	FG08746.1	NCU07059.1
AN1909.1	69.m14923	AO070341000140	FG08629.1	NCU07060.1
AN7537.1	69.m15084	AO070324000009	FG08631.1	NCU07062.1
AN0787.1	70.m15397	AO070239000021	FG03922.1	NCU07067.1
AN1290.1	55.m03194	AO070339000255	FG02820.1	NCU07068.1
AN6374.1	72.m19487	AO070241000031	FG02752.1	NCU07070.1
AN3669.1	58.m07430	AO070342000010	FG09275.1	NCU07071.1
AN0471.1	54.m06598	AO070328000167	FG08758.1	NCU07075.1
AN0472.1	54.m07063	AO070328000166	FG08757.1	NCU07076.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN6240.1	72.m19417	AO070304000091	FG08756.1	NCU07078.1
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AN0314.1	54.m06444	AO070334000018	FG01976.1	NCU07082.1
AN1826.1	66.m04793	AO070275000025	FG11291.1	NCU07111.1
AN8346.1	66.m04732	AO070275000024	FG03259.1	NCU07112.1
AN5823.1	72.m18952	AO070260000021	FG05371.1	NCU07117.1
AN7959.1	71.m15297	AO070314000099	FG10480.1	NCU07120.1
AN1878.1	57.m05738	AO070341000173	FG02232.1	NCU07125.1
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AN7430.1	57.m05914	AO070229000001	FG09984.1	NCU07156.1
AN7454.1	57.m05889	AO070287000072	FG09986.1	NCU07158.1
AN0667.1	70.m15270	AO070343000553	FG04481.1	NCU07165.1
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AN0673.1	70.m15275	AO070343000547	FG04485.1	NCU07171.1
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AN5020.1	59.m09512	AO070338000180	FG04483.1	NCU07173.1
AN0670.1	70.m15272	AO070343000550	FG04473.1	NCU07188.1
AN8583.1	70.m15077	AO070339000078	FG11217.1	NCU07195.1
AN5022.1	59.m09494	AO070338000182	FG10315.1	NCU07196.1
AN6362.1	69.m15744	AO070337000045	FG00756.1	NCU07197.1
AN5101.1	54.m06961	AO070291000078	FG00028.1	NCU07200.1
AN0055.1	71.m15326	AO070314000132	FG07700.1	NCU07231.1
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AN0675.1	70.m15787	AO070343000544	FG10216.1	NCU07240.1
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AN5346.1	69.m15558	AO070333000176	FG09631.1	NCU07261.1
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AN5351.1	69.m15553	AO070333000172	FG09630.1	NCU07264.1
AN0714.1	70.m15347	AO070343000454	FG09629.1	NCU07265.1
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AN5529.1	58.m07475	AO070328000064	FG01188.1	NCU07296.1
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AN9407.1	52.m04034	AO070274000010	FG05321.1	NCU07308.1
AN5972.1	72.m19188	AO070340000330	FG05844.1	NCU07319.1
AN0243.1	71.m15639	AO070284000073	FG04985.1	NCU07320.1
AN5512.1	69.m15451	AO070341000384	FG04986.1	NCU07321.1
AN5338.1	69.m15570	AO070333000229	FG06539.1	NCU07332.1
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AN7534.1	69.m15544	AO070330000186	FG08902.1	NCU07338.1
AN0494.1	69.m15310	AO070285000063	FG00571.1	NCU07340.1
AN0635.1	70.m15647	AO070318000125	FG02806.1	NCU07345.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN3024.1	59.m08997	AO070337000065	FG10915.1	NCU07349.1
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AN1469.1	55.m02972	AO070306000092	FG01028.1	NCU07360.1
AN1539.1	55.m03058	AO070334000263	FG00623.1	NCU07361.1
AN5146.1	54.m07055	AO070291000027	FG01027.1	NCU07362.1
AN0301.1	54.m06460	AO070334000040	FG01026.1	NCU07363.1
AN5783.1	69.m14814	AO070249000028	FG01200.1	NCU07365.1
AN5747.1	69.m14845	AO070341000004	FG01198.1	NCU07367.1
AN5935.1	72.m19194	AO070340000335	FG01311.1	NCU07375.1
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AN1458.1	55.m02962	AO070306000074	FG01039.1	NCU07385.1
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AN5169.1	69.m14867	AO070247000004	FG07068.1	NCU07389.1
AN1848.1	58.m07662	AO070292000046	FG07067.1	NCU07392.1
AN7652.1	57.m05411	AO070268000009	FG06867.1	NCU07395.1
AN1476.1	55.m02978	AO070306000099	FG02675.1	NCU07399.1
AN1475.1	55.m02977	AO070306000098	FG06823.1	NCU07400.1
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AN2936.1	59.m09058	AO070337000172	FG06831.1	NCU07404.1
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AN2735.1	54.m07004	AO070338000216	FG06826.1	NCU07409.1
AN2739.1	54.m06953	AO070338000234	FG06834.1	NCU07411.1
AN2731.1	54.m06673	AO070338000213	FG06825.1	NCU07414.1
AN2092.1	57.m05795	AO070341000250	FG06836.1	NCU07415.1
AN3578.1	58.m07376	AO070342000171	FG06839.1	NCU07418.1
AN2933.1	59.m09061	AO070337000174	FG06840.1	NCU07419.1
AN8676.1	62.m03394	AO070315000096	FG08696.1	NCU07430.1
AN8712.1	62.m03357	AO070315000138	FG08655.1	NCU07437.1
AN8713.1	62.m03468	AO070315000139	FG08658.1	NCU07440.1
AN6636.1	62.m03467	AO070326000087	FG08596.1	NCU07442.1
AN8672.1	62.m03398	AO070315000089	FG08595.1	NCU07443.1
AN8674.1	62.m03396	AO070315000092	FG08593.1	NCU07446.1
AN1380.1	70.m14843	AO070343000393	FG08614.1	NCU07451.1
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AN3118.1	59.m08619	AO070303000030	FG01132.1	NCU07457.1
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AN1370.1	70.m14859	AO070215000011	FG00518.1	NCU07460.1
AN1231.1	70.m14988	AO070331000243	FG00621.1	NCU07461.1
AN2977.1	59.m09424	AO070337000144	FG01230.1	NCU07465.1
AN2976.1	59.m09037	AO070337000145	FG01229.1	NCU07466.1
AN3590.1	58.m07390	AO070342000142	FG01228.1	NCU07467.1
AN0254.1	54.m06529	AO070334000106	FG01227.1	NCU07468.1
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AN3588.1	58.m07388	AO070342000139	FG01233.1	NCU07472.1
AN1607.1	55.m03177	AO070309000147	FG01530.1	NCU07473.1
AN6087.1	72.m19077	AO070340000139	FG09323.1	NCU07478.1
AN2983.1	59.m09031	AO070337000139	FG00910.1	NCU07481.1
AN7435.1	57.m05905	AO070229000009	FG00911.1	NCU07482.1
AN1796.1	72.m19548	AO070309000135	FG00283.1	NCU07483.1
AN2227.1	71.m15838	AO070326000160	FG00088.1	NCU07487.1
AN3793.1	57.m05691	AO070337000236	FG00852.1	NCU07489.1
AN5213.1	69.m14911	AO070337000268	FG00849.1	NCU07491.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN5215.1	69.m14913	AO070337000264	FG00848.1	NCU07492.1
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AN3747.1	65.m07387	AO070309000075	FG07110.1	NCU07509.1
AN6132.1	72.m19030	AO070340000067	FG06568.1	NCU07513.1
AN1472.1	55.m02974	AO070306000093	FG03643.1	NCU07517.1
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AN2304.1	71.m15953	AO070271000061	FG06767.1	NCU07542.1
AN6574.1	62.m03168	AO070326000017	FG06769.1	NCU07544.1
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AN6904.1	71.m15232	AO070314000010	FG06703.1	NCU07549.1
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AN6364.1	72.m19496	AO070279000050	FG06754.1	NCU07554.1
AN6313.1	72.m19320	AO070308000069	FG06759.1	NCU07558.1
AN7284.1	72.m19781	AO070297000024	FG06755.1	NCU07560.1
AN7294.1	72.m19772	AO070297000036	FG06756.1	NCU07561.1
AN7293.1	72.m19774	AO070297000034	FG06758.1	NCU07563.1
AN5167.1	69.m14865	AO070247000001	FG06762.1	NCU07565.1
AN1851.1	58.m07660	AO070292000043	FG06761.1	NCU07567.1
AN0902.1	70.m15511	AO070320000074	FG06382.1	NCU07575.1
AN2184.1	72.m19039	AO070340000082	FG05395.1	NCU07577.1
AN8261.1	53.m03696	AO070310000040	FG05393.1	NCU07580.1
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AN6715.1	65.m07269	AO070339000143	FG04220.1	NCU07587.1
AN5336.1	69.m15573	AO070333000217	FG04235.1	NCU07590.1
AN2434.1	69.m15225	AO070264000045	FG04211.1	NCU07604.1
AN6703.1	65.m07276	AO070339000139	FG04204.1	NCU07607.1
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AN6230.1	72.m19977	AO070304000083	FG02471.1	NCU07617.1
AN3799.1	57.m05681	AO070337000228	FG02589.1	NCU07621.1
AN8943.1	69.m15305	AO070226000019	FG09370.1	NCU07649.1
AN6709.1	65.m07261	AO070339000154	FG04168.1	NCU07658.1
AN6708.1	65.m07259	AO070339000155	FG04171.1	NCU07659.1
AN0880.1	70.m15483	AO070320000040	FG05109.1	NCU07662.1
AN0881.1	70.m15484	AO070320000049	FG05110.1	NCU07663.1
AN0891.1	70.m15490	AO070320000062	FG05120.1	NCU07669.1
AN0894.1	70.m15505	AO070320000067	FG05108.1	NCU07670.1
AN5900.1	72.m19230	AO070248000034	FG05099.1	NCU07672.1
AN6190.1	72.m19288	AO070308000111	FG05101.1	NCU07674.1
AN5899.1	72.m19231	AO070248000035	FG05105.1	NCU07679.1
AN5867.1	72.m19267	AO070308000132	FG01939.1	NCU07682.1
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AN5883.1	72.m19248	AO070245000025	FG09572.1	NCU07690.1
AN1003.1	70.m15221	AO070312000031	FG09580.1	NCU07697.1
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AN5808.1	72.m18938	AO070260000039	FG05068.1	NCU07705.1
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AN0583.1	69.m15265	AO070280000005	FG09766.1	NCU07712.1
AN0590.1	69.m15259	AO070280000012	FG09767.1	NCU07713.1
AN0582.1	69.m15266	AO070280000004	FG09724.1	NCU07717.1
AN0579.1	69.m15690	AO070280000001	FG09722.1	NCU07719.1
AN0125.1	71.m15406	AO070311000087	FG09783.1	NCU07721.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN0124.1	71.m15405	AO070311000088	FG09784.1	NCU07722.1
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AN3600.1	58.m07398	AO070342000153	FG02044.1	NCU07784.1
AN6273.1	72.m19370	AO070304000011	FG11205.1	NCU07787.1
AN8248.1	53.m03717	AO070310000058	FG06111.1	NCU07793.1
AN2875.1	59.m08724	AO070338000136	FG02770.1	NCU07807.1
AN8945.1	56.m03091	AO070319000047	FG04837.1	NCU07815.1
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AN4109.1	52.m04073	AO070342000385	FG11475.1	NCU07820.1
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AN7258.1	72.m19792	AO070297000014	FG04119.1	NCU07842.1
AN6046.1	72.m19945	AO070340000236	FG04123.1	NCU07850.1
AN6045.1	72.m19114	AO070340000237	FG04124.1	NCU07851.1
AN9469.1	72.m19180	AO070340000318	FG04125.1	NCU07852.1
AN9470.1	72.m19181	AO070340000319	FG04126.1	NCU07853.1
AN5958.1	72.m19176	AO070340000315	FG04127.1	NCU07854.1
AN5688.1	65.m07414	AO070309000104	FG05593.1	NCU07859.1
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AN4471.1	58.m07861	AO070305000130	FG05585.1	NCU07864.1
AN5932.1	72.m19197	AO070340000348	FG05421.1	NCU07870.1
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AN8791.1	71.m15585	AO070276000072	FG05506.1	NCU07879.1
AN0066.1	71.m15343	AO070314000155	FG05414.1	NCU07884.1
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AN0067.1	71.m15344	AO070314000157	FG05409.1	NCU07887.1
AN0061.1	71.m15337	AO070314000148	FG05410.1	NCU07888.1
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AN1247.1	70.m15739	AO070223000010	FG03994.1	NCU07915.1
AN6700.1	65.m07265	AO070339000147	FG04181.1	NCU07922.1
AN9157.1	57.m05493	AO070286000083	FG02555.1	NCU07926.1
AN1261.1	70.m14958	AO070214000004	FG05613.1	NCU07928.1
AN1270.1	70.m14937	AO070332000019	FG05614.1	NCU07929.1
AN1263.1	70.m14953	AO070332000001	FG05615.1	NCU07930.1
AN5534.1	58.m07480	AO070328000057	FG04024.1	NCU07931.1
AN8767.1	52.m03894	AO070299000022	FG02772.1	NCU07934.1
AN3628.1	58.m07473	AO070328000066	FG02774.1	NCU07936.1
AN6047.1	72.m19946	AO070340000229	FG09738.1	NCU07939.1
AN6048.1	72.m19935	AO070340000228	FG09739.1	NCU07941.1
AN1239.1	66.m04595	AO070315000009	FG01385.1	NCU07943.1
AN3147.1	59.m08516	AO070256000043	FG01974.1	NCU07947.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN5353.1	69.m15760	AO070302000060	FG03674.1	NCU07948.1
AN5726.1	54.m06846	AO070324000125	FG01341.1	NCU07952.1
AN2099.1	57.m05801	AO070341000258	FG01342.1	NCU07953.1
AN5786.1	69.m14811	AO070249000032	FG01344.1	NCU07955.1
AN5785.1	69.m14812	AO070249000030	FG01345.1	NCU07956.1
AN7770.1	71.m15812	AO070286000023	FG00407.1	NCU07958.1
AN8063.1	53.m03914	AO070330000019	FG00406.1	NCU07959.1
AN5763.1	69.m15632	AO070193000009	FG00405.1	NCU07960.1
AN4947.1	59.m08852	AO070166000003	FG04044.1	NCU07965.1
AN2880.1	59.m08727	AO070338000135	FG04042.1	NCU07971.1
AN2256.1	71.m15896	AO070326000107	FG09828.1	NCU07975.1
AN4956.1	59.m08861	AO070288000018	FG01086.1	NCU07982.1
AN9491.1	72.m19436	AO070304000051	FG01931.1	NCU07986.1
AN4035.1	54.m07018	AO070328000127	FG06915.1	NCU08000.1
AN6194.1	72.m19293	AO070308000104	FG05329.1	NCU08001.1
AN6279.1	72.m19361	AO070308000038	FG01924.1	NCU08002.1
AN6705.1	65.m07280	AO070339000135	FG01925.1	NCU08003.1
AN6272.1	72.m19369	AO070304000012	FG01927.1	NCU08005.1
AN0991.1	70.m15632	AO070318000146	FG02168.1	NCU08011.1
AN0331.1	54.m06427	AO070318000004	FG03940.1	NCU08017.1
AN7312.1	72.m19751	AO070297000060	FG04282.1	NCU08022.1
AN0112.1	71.m15387	AO070311000096	FG04279.1	NCU08023.1
AN2153.1	72.m19688	AO070343000202	FG04277.1	NCU08026.1
AN0210.1	71.m15473	AO070321000034	FG04270.1	NCU08027.1
AN0193.1	71.m15463	AO070321000051	FG04272.1	NCU08029.1
AN0191.1	71.m15461	AO070321000052	FG04274.1	NCU08031.1
AN0190.1	71.m15460	AO070321000053	FG04275.1	NCU08032.1
AN2442.1	69.m15216	AO070264000033	FG04276.1	NCU08033.1
AN0109.1	71.m16048	AO070311000111	FG04286.1	NCU08034.1
AN0111.1	71.m15386	AO070311000109	FG04284.1	NCU08036.1
AN2441.1	69.m15217	AO070264000038	FG04268.1	NCU08040.1
AN0179.1	71.m16064	AO070321000059	FG04260.1	NCU08044.1
AN2154.1	72.m20002	AO070343000203	FG05066.1	NCU08045.1
AN6652.1	62.m03252	AO070269000016	FG00166.1	NCU08054.1
AN6581.1	62.m03171	AO070326000030	FG07383.1	NCU08056.1
AN3862.1	71.m15562	AO070308000044	FG02137.1	NCU08060.1
AN2754.1	71.m16097	AO070276000006	FG09437.1	NCU08066.1
AN7698.1	71.m15720	AO070325000103	FG09435.1	NCU08067.1
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AN7701.1	71.m15727	AO070325000108	FG09438.1	NCU08071.1
AN4779.1	59.m09204	AO070329000071	FG09429.1	NCU08092.1
AN4776.1	59.m09207	AO070329000076	FG09431.1	NCU08094.1
AN6072.1	72.m19948	AO070340000116	FG00501.1	NCU08111.1
AN0013.1	69.m15595	AO070333000040	FG11495.1	NCU08114.1
AN3749.1	65.m07385	AO070309000073	FG07112.1	NCU08115.1
AN5991.1	72.m19149	AO070340000286	FG07104.1	NCU08118.1
AN5992.1	72.m19148	AO070340000285	FG07105.1	NCU08119.1
AN3744.1	65.m07391	AO070309000079	FG07106.1	NCU08120.1
AN3745.1	65.m07390	AO070309000078	FG07107.1	NCU08121.1
AN8317.1	70.m15829	AO070323000152	FG08715.1	NCU08126.1
AN1708.1	58.m07794	AO070305000041	FG07549.1	NCU08135.1
AN5753.1	69.m14851	AO070329000011	FG10755.1	NCU08137.1
AN4415.1	58.m07904	AO070273000036	FG10422.1	NCU08138.1
AN9394.1	52.m04017	AO070274000022	FG02146.1	NCU08145.1
AN7664.1	57.m05434	AO070268000037	FG04995.1	NCU08147.1
AN5493.1	69.m15460	AO070341000392	FG10531.1	NCU08148.1
AN5751.1	69.m14849	AO070341000008	FG10482.1	NCU08151.1
AN6923.1	59.m08483	AO070318000108	FG01734.1	NCU08152.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN8622.1	69.m15032	AO070289000005	FG06610.1	NCU08153.1
AN4419.1	58.m07908	AO070273000041	FG10516.1	NCU08158.1
AN5758.1	69.m14855	AO070341000017	FG10514.1	NCU08161.1
AN2914.1	59.m09099	AO070329000158	FG03694.1	NCU08162.1
AN1783.1	56.m02532	AO070329000184	FG01586.1	NCU08164.1
AN2003.1	58.m07611	AO070301000104	FG10425.1	NCU08166.1
AN0455.1	54.m06616	AO070328000183	FG10426.1	NCU08167.1
AN1633.1	58.m07728	AO070299000055	FG07485.1	NCU08169.1
AN3337.1	55.m03098	AO070293000073	FG02386.1	NCU08176.1
AN1665.1	58.m07733	AO070299000047	FG07520.1	NCU08177.1
AN5537.1	57.m05385	AO070294000074	FG07519.1	NCU08178.1
AN6368.1	72.m19492	AO070279000054	FG06576.1	NCU08195.1
AN3268.1	69.m15764	AO070304000069	FG06556.1	NCU08199.1
AN5820.1	72.m18947	AO070260000026	FG06544.1	NCU08216.1
AN5819.1	72.m18946	AO070260000028	FG06543.1	NCU08217.1
AN5824.1	72.m18951	AO070260000022	FG06542.1	NCU08218.1
AN6115.1	72.m19044	AO070340000089	FG06513.1	NCU08225.1
AN9172.1	56.m02468	AO070317000027	FG04232.1	NCU08228.1
AN9159.1	56.m02469	AO070317000031	FG01701.1	NCU08233.1
AN0120.1	71.m15400	AO070311000093	FG09800.1	NCU08268.1
AN2357.1	52.m03833	AO070307000082	FG05295.1	NCU08275.1
AN3156.1	59.m08547	AO070256000036	FG06220.1	NCU08277.1
AN6690.1	65.m07291	AO070339000097	FG06222.1	NCU08278.1
AN0565.1	69.m15281	AO070272000043	FG09638.1	NCU08287.1
AN7752.1	71.m15784	AO070325000184	FG05316.1	NCU08291.1
AN1045.1	70.m15201	AO070336000078	FG01968.1	NCU08295.1
AN5164.1	54.m06854	AO070291000003	FG05327.1	NCU08296.1
AN6688.1	65.m07502	AO070339000095	FG05315.1	NCU08297.1
AN6211.1	72.m19309	AO070308000082	FG01969.1	NCU08298.1
AN0997.1	70.m15214	AO070312000043	FG01970.1	NCU08299.1
AN0122.1	71.m15403	AO070311000090	FG09725.1	NCU08303.1
AN0126.1	71.m15408	AO070311000085	FG09728.1	NCU08309.1
AN4724.1	71.m15493	AO070323000060	FG09686.1	NCU08312.1
AN4576.1	57.m05496	AO070316000158	FG05063.1	NCU08315.1
AN5893.1	72.m19237	AO070245000013	FG06228.1	NCU08319.1
AN9398.1	52.m04024	AO070274000018	FG05229.1	NCU08323.1
AN9409.1	52.m04039	AO070274000006	FG05230.1	NCU08324.1
AN7304.1	72.m20022	AO070297000051	FG06226.1	NCU08326.1
AN0123.1	71.m15404	AO070311000089	FG06224.1	NCU08329.1
AN4015.1	54.m06579	AO070328000151	FG01955.1	NCU08332.1
AN1128.1	70.m15107	AO070331000120	FG09914.1	NCU08338.1
AN1126.1	70.m15114	AO070331000119	FG01014.1	NCU08340.1
AN3624.1	58.m07411	AO070342000127	FG01501.1	NCU08341.1
AN3622.1	58.m07409	AO070342000129	FG01503.1	NCU08343.1
AN5495.1	69.m15458	AO070341000391	FG01505.1	NCU08345.1
AN5494.1	69.m15722	AO070341000390	FG01506.1	NCU08346.1
AN5496.1	69.m15723	AO070341000389	FG00923.1	NCU08348.1
AN3581.1	58.m07379	AO070342000168	FG00871.1	NCU08352.1
AN0303.1	54.m06455	AO070334000035	FG00955.1	NCU08354.1
AN3785.1	57.m05971	AO070337000246	FG00667.1	NCU08357.1
AN8957.1	71.m15746	AO070319000071	FG00669.1	NCU08358.1
AN2721.1	70.m15715	AO070309000062	FG02280.1	NCU08361.1
AN1721.1	58.m07788	AO070305000036	FG00276.1	NCU08363.1
AN5449.1	69.m15483	AO070239000028	FG01496.1	NCU08364.1
AN1720.1	58.m08961	AO070305000035	FG01495.1	NCU08365.1
AN1696.1	58.m07772	AO070305000020	FG10081.1	NCU08366.1
AN1486.1	55.m02992	AO070334000193	FG01490.1	NCU08368.1
AN1996.1	58.m07605	AO070301000091	FG01498.1	NCU08370.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN1798.1	72.m19550	AO070309000133	FG05597.1	NCU08372.1
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AN3589.1	58.m07389	AO070342000140	FG01263.1	NCU08375.1
AN3913.1	69.m15016	AO070324000100	FG01234.1	NCU08377.1
AN0426.1	54.m06650	AO070338000276	FG01526.1	NCU08382.1
AN0433.1	54.m06624	AO070338000284	FG01516.1	NCU08389.1
AN0987.1	70.m15627	AO070317000115	FG01514.1	NCU08390.1
AN8412.1	56.m02506	AO070336000018	FG10464.1	NCU08399.1
AN8731.1	52.m03823	AO070327000127	FG04229.1	NCU08406.1
AN5653.1	52.m03867	AO070335000212	FG10989.1	NCU08406.1
AN6231.1	72.m19978	AO070304000084	FG10743.1	NCU08409.1
AN1993.1	58.m07603	AO070301000084	FG10746.1	NCU08411.1
AN9393.1	52.m04014	AO070274000027	FG03330.1	NCU08425.1
AN8064.1	53.m03915	AO070330000020	FG06027.1	NCU08427.1
AN5019.1	59.m08688	AO070338000179	FG07880.1	NCU08434.1
AN4179.1	69.m15306	AO070226000020	FG01581.1	NCU08436.1
AN6237.1	52.m03954	AO070302000118	FG04336.1	NCU08439.1
AN6236.1	52.m03953	AO070302000119	FG03747.1	NCU08441.1
AN1324.1	70.m14907	AO070303000087	FG04366.1	NCU08468.1
AN4281.1	53.m03676	AO070310000015	FG10873.1	NCU08477.1
AN5139.1	54.m07054	AO070291000038	FG10869.1	NCU08484.1
AN1056.1	70.m15179	AO070336000055	FG10870.1	NCU08485.1
AN1980.1	58.m08946	AO070301000065	FG00632.1	NCU08499.1
AN0465.1	54.m06603	AO070328000172	FG00631.1	NCU08500.1
AN1964.1	58.m07569	AO070301000045	FG00634.1	NCU08502.1
AN2455.1	69.m15204	AO070264000021	FG01470.1	NCU08507.1
AN2449.1	69.m15211	AO070264000029	FG01480.1	NCU08510.1
AN2447.1	69.m15212	AO070264000030	FG01481.1	NCU08511.1
AN8035.1	53.m03912	AO070330000012	FG00946.1	NCU08512.1
AN8061.1	53.m03913	AO070330000013	FG00945.1	NCU08514.1
AN6232.1	72.m19422	AO070304000085	FG00637.1	NCU08515.1
AN3184.1	59.m08570	AO070256000010	FG01829.1	NCU08516.1
AN6126.1	72.m19031	AO070340000068	FG06580.1	NCU08535.1
AN5811.1	72.m18941	AO070260000036	FG06524.1	NCU08550.1
AN7287.1	72.m19777	AO070297000028	FG06566.1	NCU08561.1
AN6359.1	72.m19499	AO070279000047	FG05455.1	NCU08563.1
AN2877.1	59.m08718	AO070338000146	FG02771.1	NCU08578.1
AN2873.1	59.m08723	AO070338000139	FG00380.1	NCU08579.1
AN2101.1	57.m05803	AO070341000259	FG00552.1	NCU08600.1
AN8562.1	67.m02865	AO070332000127	FG00550.1	NCU08603.1
AN2085.1	57.m05786	AO070341000243	FG00367.1	NCU08605.1
AN0302.1	54.m06459	AO070334000037	FG00368.1	NCU08606.1
AN2738.1	54.m06679	AO070338000220	FG00369.1	NCU08607.1
AN3933.1	69.m14994	AO070341000044	FG05627.1	NCU08616.1
AN9468.1	72.m19967	AO070340000317	FG04136.1	NCU08620.1
AN0387.1	54.m06351	AO070290000083	FG00797.1	NCU08626.1
AN4519.1	57.m05609	AO070321000125	FG00796.1	NCU08637.1
AN4510.1	57.m05618	AO070311000065	FG00816.1	NCU08642.1
AN2360.1	66.m04689	AO070298000079	FG04504.1	NCU08643.1
AN0189.1	71.m15459	AO070321000054	FG04185.1	NCU08660.1
AN0205.1	71.m15470	AO070321000039	FG04187.1	NCU08661.1
AN1711.1	72.m19761	AO070297000053	FG09760.1	NCU08663.1
AN9498.1	69.m15234	AO070188000007	FG04190.1	NCU08664.1
AN9497.1	69.m15233	AO070188000006	FG04189.1	NCU08666.1
AN7305.1	72.m19762	AO070297000052	FG09761.1	NCU08668.1
AN2311.1	71.m15506	AO070323000049	FG09764.1	NCU08671.1
AN7771.1	71.m15811	AO070286000022	FG00549.1	NCU08676.1
AN4953.1	59.m08858	AO070288000006	FG04068.1	NCU08683.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN8121.1	53.m03832	AO070322000029	FG09440.1	NCU08685.1
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AN7314.1	72.m19749	AO070297000067	FG04280.1	NCU08689.1
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AN1975.1	58.m07580	AO070301000060	FG10890.1	NCU08708.1
AN0458.1	54.m06612	AO070328000180	FG10749.1	NCU08712.1
AN0154.1	71.m15432	AO070321000096	FG01623.1	NCU08729.1
AN4439.1	58.m07886	AO070273000015	FG01611.1	NCU08736.1
AN6888.1	71.m15251	AO070314000034	FG07775.1	NCU08739.1
AN8071.1	53.m03924	AO070330000029	FG01665.1	NCU08741.1
AN3784.1	53.m03922	AO070330000028	FG01666.1	NCU08742.1
AN4102.1	54.m06742	AO070342000101	FG06605.1	NCU08755.1
AN1602.1	55.m03185	AO070339000250	FG06397.1	NCU08760.1
AN4095.1	54.m06738	AO070342000096	FG06607.1	NCU08761.1
AN4094.1	54.m06498	AO070342000095	FG06606.1	NCU08762.1
AN6360.1	72.m19498	AO070279000048	FG06510.1	NCU08766.1
AN6363.1	72.m19497	AO070279000049	FG06502.1	NCU08767.1
AN8829.1	72.m19523	AO070271000051	FG06585.1	NCU08770.1
AN6336.1	72.m19456	AO070236000020	FG06557.1	NCU08771.1
AN2425.1	72.m19478	AO070241000006	FG06493.1	NCU08779.1
AN3017.1	59.m09446	AO070337000098	FG01765.1	NCU08783.1
AN8637.1	62.m03219	AO070326000073	FG06554.1	NCU08791.1
AN0464.1	54.m06604	AO070328000173	FG08553.1	NCU08795.1
AN3957.1	69.m14963	AO070341000077	FG03963.1	NCU08803.1
AN6845.1	71.m16044	AO070314000094	FG05096.1	NCU08804.1
AN6195.1	72.m19295	AO070308000098	FG09715.1	NCU08807.1
AN6034.1	72.m19950	AO070340000254	FG09713.1	NCU08810.1
AN6033.1	72.m19123	AO070340000255	FG09712.1	NCU08811.1
AN0183.1	71.m15454	AO070321000057	FG09776.1	NCU08824.1
AN2155.1	72.m19686	AO070343000207	FG09774.1	NCU08825.1
AN3129.1	71.m15827	AO070341000298	FG05924.1	NCU08852.1
AN5985.1	72.m19156	AO070340000294	FG02751.1	NCU08856.1
AN2957.1	58.m07219	AO070307000048	FG11338.1	NCU08857.1
AN5917.1	72.m19214	AO070340000369	FG10747.1	NCU08858.1
AN8234.1	53.m03735	AO070310000074	FG08986.1	NCU08859.1
AN6343.1	72.m19512	AO070298000012	FG02048.1	NCU08869.1
AN6825.1	71.m15291	AO070314000105	FG05888.1	NCU08874.1
AN2458.1	69.m15196	AO070264000020	FG05884.1	NCU08875.1
AN1074.1	70.m15148	AO070285000074	FG08351.1	NCU08877.1
AN1199.1	70.m15020	AO070331000204	FG10375.1	NCU08880.1
AN2208.1	71.m15856	AO070294000014	FG02075.1	NCU08882.1
AN6640.1	62.m03237	AO070295000024	FG02121.1	NCU08886.1
AN4086.1	54.m06727	AO070342000079	FG05431.1	NCU08888.1
AN8225.1	53.m03749	AO070310000087	FG05932.1	NCU08893.1
AN8224.1	53.m03750	AO070310000088	FG04582.1	NCU08894.1
AN3128.1	59.m08597	AO070303000018	FG06509.1	NCU08895.1
AN7721.1	71.m15748	AO070325000136	FG09016.1	NCU08897.1
AN6521.1	71.m15675	AO070270000019	FG10949.1	NCU08898.1
AN6167.1	72.m19901	AO070343000365	FG04755.1	NCU08900.1
AN8043.1	53.m03902	AO070330000003	FG04735.1	NCU08907.1
AN3730.1	69.m15387	AO070342000284	FG02022.1	NCU08909.1
AN2210.1	71.m15855	AO070294000012	FG02025.1	NCU08920.1
AN5111.1	54.m06911	AO070291000068	FG10286.1	NCU08923.1
AN6394.1	69.m15243	AO070343000149	FG10285.1	NCU08924.1
AN5025.1	59.m08679	AO070338000186	FG10284.1	NCU08925.1
AN5491.1	69.m15461	AO070341000394	FG10283.1	NCU08926.1
AN4405.1	58.m07921	AO070261000048	FG10374.1	NCU08927.1
AN5827.1	72.m18954	AO070260000019	FG10391.1	NCU08928.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN4397.1	58.m07930	AO070261000042	FG10362.1	NCU08935.1
AN4390.1	58.m07933	AO070261000036	FG10089.1	NCU08936.1
AN4389.1	58.m07935	AO070261000034	FG10090.1	NCU08938.1
AN4395.1	58.m07928	AO070261000040	FG10091.1	NCU08939.1
AN4387.1	58.m07937	AO070261000033	FG10295.1	NCU08941.1
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AN5013.1	59.m08664	AO070334000121	FG10307.1	NCU08945.1
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AN1344.1	70.m14889	AO070247000020	FG10301.1	NCU08952.1
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AN6081.1	72.m19926	AO070340000131	FG10244.1	NCU08962.1
AN6082.1	72.m19923	AO070340000132	FG10245.1	NCU08963.1
AN6083.1	72.m19924	AO070340000133	FG10246.1	NCU08964.1
AN6084.1	72.m19074	AO070340000134	FG10247.1	NCU08965.1
AN3313.1	65.m07345	AO070339000070	FG05049.1	NCU08968.1
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AN0627.1	70.m15658	AO070280000079	FG06897.1	NCU08974.1
AN0981.1	70.m15622	AO070318000167	FG06896.1	NCU08976.1
AN0623.1	70.m15662	AO070280000074	FG06918.1	NCU08977.1
AN1094.1	70.m15137	AO070285000053	FG04130.1	NCU08980.1
AN0848.1	70.m15448	AO070216000007	FG05390.1	NCU08981.1
AN0874.1	70.m15477	AO070320000033	FG05389.1	NCU08983.1
AN1068.1	70.m15144	AO070285000068	FG07305.1	NCU08984.1
AN5912.1	72.m19957	AO070248000038	FG06920.1	NCU08989.1
AN2302.1	71.m15951	AO070271000063	FG06922.1	NCU08991.1
AN6598.1	62.m03431	AO070326000047	FG06903.1	NCU08993.1
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AN2248.1	71.m15887	AO070326000122	FG05554.1	NCU08998.1
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AN7628.1	71.m15822	AO070294000038	FG05565.1	NCU09001.1
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AN7720.1	71.m15747	AO070325000135	FG05563.1	NCU09003.1
AN8824.1	71.m15956	AO070271000057	FG05428.1	NCU09004.1
AN2298.1	71.m15947	AO070295000079	FG05561.1	NCU09006.1
AN7729.1	71.m15765	AO070325000156	FG05571.1	NCU09012.1
AN8050.1	53.m03894	AO070292000100	FG06908.1	NCU09013.1
AN8045.1	53.m03898	AO070292000104	FG06907.1	NCU09014.1
AN1706.1	58.m07796	AO070305000044	FG09401.1	NCU09018.1
AN2900.1	59.m08750	AO070338000107	FG06078.1	NCU09025.1
AN1772.1	69.m15064	AO070324000030	FG02133.1	NCU09026.1
AN5673.1	65.m07399	AO070309000086	FG09884.1	NCU09033.1
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AN4186.1	65.m07397	AO070309000084	FG09882.1	NCU09035.1
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AN2824.1	67.m02987	AO070330000093	FG02314.1	NCU09042.1
AN2773.1	59.m09486	AO070327000015	FG10788.1	NCU09056.1
AN2896.1	59.m08746	AO070338000112	FG06084.1	NCU09058.1
AN4597.1	57.m05519	AO070267000013	FG10944.1	NCU09063.1
AN8742.1	62.m03338	AO070250000039	FG08702.1	NCU09065.1
AN8667.1	62.m03407	AO070269000068	FG08634.1	NCU09068.1
AN8751.1	62.m03324	AO070250000011	FG08635.1	NCU09071.1
AN4830.1	59.m09147	AO070327000152	FG08803.1	NCU09090.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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AN2973.1	59.m09039	AO070337000148	FG01275.1	NCU09106.1
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AN2980.1	59.m09034	AO070337000142	FG01278.1	NCU09109.1
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AN4608.1	65.m07143	AO070337000243	FG09372.1	NCU09169.1
AN2533.1	52.m03778	AO070325000028	FG03049.1	NCU09170.1
AN4673.1	71.m15661	AO070284000033	FG05679.1	NCU09173.1
AN1857.1	58.m07651	AO070292000034	FG04829.1	NCU09183.1
AN6718.1	65.m07256	AO070339000158	FG04177.1	NCU09187.1
AN6079.1	72.m19071	AO070340000129	FG08738.1	NCU09191.1
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AN5311.1	52.m03720	AO070285000028	FG11450.1	NCU09199.1
AN1065.1	70.m15167	AO070218000010	FG02797.1	NCU09203.1
AN4483.1	57.m05648	AO070311000032	FG00786.1	NCU09212.1
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AN2094.1	57.m05797	AO070341000252	FG07084.1	NCU09219.1
AN2090.1	57.m05792	AO070341000248	FG07094.1	NCU09227.1
AN1638.1	58.m07724	AO070299000044	FG08340.1	NCU09228.1
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AN1437.1	55.m03263	AO070232000002	FG00584.1	NCU09252.1
AN7443.1	57.m05901	AO070229000015	FG00583.1	NCU09253.1
AN6085.1	72.m19075	AO070340000136	FG01357.1	NCU09254.1
AN1520.1	55.m03039	AO070334000238	FG00614.1	NCU09259.1
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AN2369.1	59.m08374	AO070289000068	FG07869.1	NCU09262.1
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AN8184.1	53.m03795	AO070310000141	FG11536.1	NCU09274.1
AN6881.1	55.m03218	AO070342000371	FG07895.1	NCU09277.1
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AN2869.1	59.m08714	AO070338000153	FG00830.1	NCU09287.1
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AN3451.1	59.m09314	AO070265000026	FG07854.1	NCU09297.1
AN3444.1	59.m09309	AO070265000020	FG07857.1	NCU09298.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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AN8884.1	56.m02296	AO070293000016	FG01252.1	NCU09310.1
AN8878.1	56.m02289	AO070293000007	FG01256.1	NCU09312.1
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AN8271.1	53.m03690	AO070310000030	FG00545.1	NCU09315.1
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AN1554.1	55.m03071	AO070339000300	FG01273.1	NCU09322.1
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AN8102.1	52.m03735	AO070319000053	FG04345.1	NCU09350.1
AN5784.1	69.m14813	AO070249000029	FG01160.1	NCU09366.1
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AN5049.1	63.m00628	AO070338000189	FG01162.1	NCU09368.1
AN9146.1	66.m04608	AO070332000116	FG01166.1	NCU09374.1
AN1545.1	55.m03064	AO070339000309	FG01369.1	NCU09377.1
AN1235.1	70.m14984	AO070331000248	FG01128.1	NCU09380.1
AN3646.1	58.m07456	AO070328000091	FG01129.1	NCU09381.1
AN3668.1	58.m07429	AO070342000007	FG01365.1	NCU09388.1
AN6075.1	72.m19066	AO070340000119	FG09311.1	NCU09391.1
AN8144.1	69.m15536	AO070340000167	FG04461.1	NCU09400.1
AN1713.1	58.m07780	AO070305000029	FG07555.1	NCU09407.1
AN6422.1	57.m05357	AO070337000266	FG03612.1	NCU09416.1
AN1884.1	57.m05728	AO070341000165	FG01048.1	NCU09419.1
AN4890.1	59.m08787	AO070338000068	FG00343.1	NCU09432.1
AN4892.1	59.m08790	AO070338000064	FG00349.1	NCU09435.1
AN3455.1	59.m09317	AO070265000031	FG06340.1	NCU09437.1
AN3014.1	59.m09004	AO070337000102	FG06322.1	NCU09438.1
AN1662.1	58.m07743	AO070299000024	FG07515.1	NCU09442.1
AN9315.1	52.m03741	AO070315000078	FG07389.1	NCU09447.1
AN1700.1	58.m07776	AO070305000026	FG07499.1	NCU09450.1
AN5519.1	69.m15725	AO070341000374	FG06007.1	NCU09461.1
AN3702.1	69.m15408	AO070341000324	FG06009.1	NCU09463.1
AN0624.1	70.m15661	AO070280000076	FG06026.1	NCU09466.1
AN0316.1	54.m06442	AO070334000016	FG00639.1	NCU09468.1
AN0317.1	54.m06441	AO070334000015	FG05182.1	NCU09469.1
AN0843.1	70.m15443	AO070216000003	FG06019.1	NCU09475.1
AN4064.1	54.m06707	AO070342000052	FG06021.1	NCU09477.1
AN0954.1	70.m15601	AO070320000155	FG06024.1	NCU09480.1
AN0847.1	70.m15446	AO070216000006	FG10819.1	NCU09485.1
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AN7248.1	72.m19802	AO070297000002	FG02733.1	NCU09499.1
AN0048.1	71.m15322	AO070314000127	FG02735.1	NCU09511.1
AN0047.1	71.m16041	AO070314000125	FG02736.1	NCU09513.1
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AN0043.1	71.m15318	AO070314000122	FG02725.1	NCU09517.1
AN2515.1	59.m08473	AO070263000051	FG02703.1	NCU09519.1
AN2859.1	59.m08702	AO070338000163	FG05128.1	NCU09532.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN2858.1	59.m08701	AO070338000164	FG05130.1	NCU09533.1
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AN8181.1	53.m03799	AO070310000145	FG07005.1	NCU09541.1
AN8215.1	53.m03758	AO070310000097	FG07127.1	NCU09545.1
AN4458.1	58.m07866	AO070305000135	FG06789.1	NCU09547.1
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AN5574.1	58.m07500	AO070328000032	FG04453.1	NCU09561.1
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AN5321.1	59.m08511	AO070191000002	FG03687.1	NCU09575.1
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AN1243.1	70.m14976	AO070223000005	FG03033.1	NCU09580.1
AN6053.1	72.m19105	AO070340000201	FG00831.1	NCU09595.1
AN5137.1	54.m06886	AO070291000040	FG00836.1	NCU09598.1
AN5129.1	54.m06894	AO070291000048	FG00838.1	NCU09602.1
AN5114.1	54.m06909	AO070291000065	FG00834.1	NCU09608.1
AN1085.1	70.m15159	AO070285000085	FG00833.1	NCU09610.1
AN6815.1	69.m15180	AO070252000017	FG02941.1	NCU09621.1
AN8095.1	70.m15204	AO070298000078	FG08749.1	NCU09640.1
AN3157.1	59.m08548	AO070256000037	FG04242.1	NCU09642.1
AN5166.1	54.m06857	AO070291000006	FG04237.1	NCU09643.1
AN1050.1	70.m15207	AO070312000117	FG04243.1	NCU09646.1
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AN3776.1	52.m03795	AO070302000047	FG03956.1	NCU09654.1
AN5376.1	69.m15731	AO070333000163	FG02819.1	NCU09656.1
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AN7741.1	71.m16099	AO070325000162	FG02105.1	NCU09673.1
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AN0993.1	69.m15282	AO070272000042	FG04668.1	NCU09678.1
AN4572.1	57.m05494	AO070316000155	FG04016.1	NCU09683.1
AN8795.1	71.m15602	AO070276000071	FG08982.1	NCU09688.1
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AN5713.1	54.m06828	AO070324000145	FG06306.1	NCU09700.1
AN3432.1	59.m09292	AO070265000009	FG06059.1	NCU09705.1
AN4883.1	59.m08777	AO070338000077	FG06316.1	NCU09706.1
AN3055.1	59.m08960	AO070337000019	FG06315.1	NCU09707.1
AN3056.1	59.m08955	AO070337000018	FG06314.1	NCU09708.1
AN3070.1	59.m08929	AO070337000004	FG06313.1	NCU09709.1
AN3005.1	59.m09009	AO070337000107	FG06052.1	NCU09711.1
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AN5343.1	69.m15563	AO070333000181	FG05088.1	NCU09730.1
AN7307.1	72.m19758	AO070297000055	FG04255.1	NCU09737.1
AN0594.1	69.m15254	AO070280000020	FG09787.1	NCU09740.1
AN0595.1	69.m15252	AO070280000021	FG09786.1	NCU09741.1
AN2439.1	69.m15219	AO070264000040	FG06219.1	NCU09744.1
AN2438.1	69.m15220	AO070264000041	FG05298.1	NCU09745.1
AN3778.1	72.m19643	AO070343000274	FG05299.1	NCU09746.1
AN7603.1	72.m19644	AO070343000273	FG05300.1	NCU09747.1

A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
AN2181.1	72.m19657	AO070343000260	FG05301.1	NCU09748.1
AN1986.1	58.m07593	AO070301000073	FG06006.1	NCU09754.1
AN0636.1	70.m15646	AO070318000126	FG00960.1	NCU09757.1
AN4369.1	58.m07958	AO070261000009	FG10889.1	NCU09758.1
AN0392.1	54.m06345	AO070278000009	FG03365.1	NCU09759.1
AN1547.1	55.m03067	AO070339000307	FG08266.1	NCU09770.1
AN1427.1	55.m02928	AO070242000025	FG07917.1	NCU09771.1
AN5267.1	72.m19543	AO070275000042	FG11036.1	NCU09774.1
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AN4182.1	69.m14961	AO070341000081	FG08468.1	NCU09778.1
AN0893.1	70.m15488	AO070320000065	FG05187.1	NCU09789.1
AN5515.1	69.m15446	AO070341000381	FG05346.1	NCU09792.1
AN7353.1	72.m20007	AO070278000047	FG02628.1	NCU09794.1
AN8329.1	67.m02964	AO070330000092	FG03475.1	NCU09798.1
AN8018.1	53.m04191	AO070322000067	FG03429.1	NCU09799.1
AN8594.1	70.m15668	AO070280000033	FG07590.1	NCU09800.1
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AN8874.1	56.m02287	AO070293000003	FG01320.1	NCU09808.1
AN3658.1	58.m07442	AO070342000030	FG09376.1	NCU09811.1
AN1191.1	70.m15030	AO070331000192	FG01322.1	NCU09813.1
AN1190.1	70.m15031	AO070331000190	FG01323.1	NCU09814.1
AN0357.1	54.m06397	AO070318000033	FG00561.1	NCU09816.1
AN0354.1	54.m06940	AO070318000031	FG00478.1	NCU09817.1
AN0380.1	54.m06366	AO070318000064	FG00480.1	NCU09819.1
AN3679.1	58.m08026	AO070189000006	FG00578.1	NCU09821.1
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AN8489.1	52.m03751	AO070342000405	FG08830.1	NCU09830.1
AN7747.1	71.m15775	AO070325000174	FG02078.1	NCU09838.1
AN4648.1	57.m05479	AO070316000120	FG10060.1	NCU09843.1
AN5085.1	52.m03801	AO070246000035	FG03582.1	NCU09858.1
AN1743.1	69.m15046	AO070324000053	FG09239.1	NCU09862.1
AN1726.1	69.m15044	AO070324000057	FG09240.1	NCU09864.1
AN0462.1	54.m06607	AO070328000176	FG09244.1	NCU09869.1
AN1918.1	69.m14936	AO070341000122	FG08601.1	NCU09873.1
AN0700.1	70.m15303	AO070343000510	FG10719.1	NCU09874.1
AN6761.1	65.m07180	AO070339000213	FG10950.1	NCU09885.1
AN5191.1	69.m15628	AO070237000021	FG10948.1	NCU09886.1
AN1201.1	70.m15018	AO070331000207	FG01333.1	NCU09892.1
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AN1747.1	69.m15050	AO070324000049	FG01330.1	NCU09895.1
AN1196.1	70.m15024	AO070331000200	FG01330.1	NCU09895.1
AN1194.1	70.m15765	AO070331000198	FG01329.1	NCU09896.1
AN1195.1	70.m15025	AO070331000199	FG01328.1	NCU09897.1
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AN6651.1	62.m03251	AO070269000002	FG08532.1	NCU09903.1
AN0418.1	54.m06657	AO070338000266	FG03111.1	NCU09909.1
AN0495.1	69.m15311	AO070226000029	FG08971.1	NCU09911.1
AN6623.1	62.m03222	AO070326000077	FG00152.1	NCU09912.1
AN8401.1	52.m03820	AO070302000072	FG07993.1	NCU09923.1
AN2060.1	57.m05964	AO070328000072	FG03054.1	NCU09924.1
AN6032.1	72.m19949	AO070340000256	FG09710.1	NCU09930.1
AN9405.1	52.m04032	AO070274000012	FG02789.1	NCU09972.1
AN8164.1	53.m03817	AO070266000011	FG02787.1	NCU09974.1
AN2528.1	59.m08451	AO070300000123	FG04848.1	NCU09976.1
AN1057.1	70.m15178	AO070336000001	FG09417.1	NCU09980.1
AN2886.1	59.m08733	AO070338000128	FG00383.1	NCU09996.1
AN2887.1	59.m08734	AO070338000127	FG00382.1	NCU09998.1
AN6653.1	62.m03255	AO070269000013	FG08700.1	NCU10007.1

A. nidulans	**A. fumigatus**	**A. oryzae**	**F. graminearum**	**N. crassa**
AN8707.1	62.m03362	AO070315000134	FG08712.1	NCU10008.1
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AN4514.1	57.m05978	AO070311000070	FG00815.1	NCU10029.1
AN4342.1	58.m07982	AO070240000017	FG04395.1	NCU10034.1
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AN5746.1	69.m14844	AO070341000003	FG01346.1	NCU10042.1
AN3946.1	69.m14975	AO070341000066	FG01347.1	NCU10043.1
AN3390.1	55.m03190	AO070290000088	FG03406.1	NCU10045.1
AN1761.1	69.m15654	AO070324000020	FG09313.1	NCU10046.1
AN1778.1	69.m15077	AO070324000018	FG09312.1	NCU10048.1
AN3361.1	66.m04779	AO070281000037	FG07554.1	NCU10055.1
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AN3026.1	59.m09001	AO070337000068	FG07939.1	NCU10066.1
AN3019.1	59.m09445	AO070337000095	FG07938.1	NCU10067.1
AN8873.1	56.m02286	AO070293000002	FG01316.1	NCU10073.1
AN4247.1	54.m07033	AO070324000165	FG07924.1	NCU10080.1

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concat1	AN3577.1	58.m07375	AO070342000172	FG00440.1	NCU02734.1
concat1	AN9357.1	52.m04075	AO070315000043	FG09216.1	NCU02018.1
concat1	AN1343.1	70.m14890	AO070247000021	FG10302.1	NCU08948.1
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concat1	AN7628.1	71.m15822	AO070294000038	FG05565.1	NCU09001.1
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concat1	AN0866.1	70.m15462	AO070320000017	FG08548.1	NCU00573.1
concat1	AN8050.1	53.m03894	AO070292000100	FG06908.1	NCU09013.1
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concat1	AN2918.1	59.m09095	AO070329000153	FG00558.1	NCU02839.1
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concat3	AN6923.1	59.m08483	AO070318000108	FG01734.1	NCU08152.1
concat3	AN3128.1	59.m08597	AO070303000018	FG06509.1	NCU08895.1
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concat3	AN7254.1	72.m19795	AO070297000010	FG05530.1	NCU00018.1
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concat4	AN3849.1	58.m07833	AO070332000050	FG07224.1	NCU01636.1
concat4	AN1339.1	70.m14893	AO070247000025	FG10272.1	NCU03947.1
concat4	AN4817.1	59.m09158	AO070327000170	FG08672.1	NCU01968.1
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concat4	AN1524.1	55.m03268	AO070334000242	FG00417.1	NCU00963.1
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concat4	AN1913.1	69.m14928	AO070341000134	FG08761.1	NCU04020.1
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concat5	AN1668.1	58.m07735	AO070299000050	FG09166.1	NCU02587.1
concat5	AN7683.1	57.m05461	AO070325000076	FG09968.1	NCU04639.1
concat5	AN5693.1	65.m07417	AO070309000108	FG08333.1	NCU05515.1
concat5	AN7680.1	57.m05457	AO070325000070	FG10348.1	NCU01327.1
concat5	AN8216.1	53.m03757	AO070310000096	FG05972.1	NCU04202.1
concat5	AN6870.1	71.m15261	AO070314000052	FG02207.1	NCU04672.1
concat5	AN1380.1	70.m14843	AO070343000393	FG08614.1	NCU07451.1
concat5	AN4792.1	59.m09189	AO070329000054	FG08715.1	NCU02179.1
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concat5	AN8824.1	71.m15956	AO070271000057	FG05428.1	NCU09004.1
concat5	AN9483.1	56.m02448	AO070313000069	FG11114.1	NCU00866.1
concat5	AN1706.1	58.m07796	AO070305000044	FG09401.1	NCU09018.1
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concat5	AN6351.1	72.m19504	AO070275000048	FG06950.1	NCU06259.1
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concat6	AN1699.1	58.m07775	AO070305000023	FG10790.1	NCU02287.1
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concat6	AN8430.1	71.m15302	AO070317000096	FG05828.1	NCU06131.1
concat6	AN1986.1	58.m07593	AO070301000073	FG06006.1	NCU09754.1
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concat6	AN5515.1	69.m15446	AO070341000381	FG05346.1	NCU09792.1
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concat7	AN1768.1	69.m15068	AO070324000027	FG08615.1	NCU04724.1
concat7	AN1065.1	70.m15167	AO070218000010	FG02797.1	NCU09203.1
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concat7	AN1022.1	70.m15780	AO070343000592	FG05070.1	NCU05202.1
concat7	AN4458.1	58.m07866	AO070305000135	FG06789.1	NCU09547.1
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concat7	AN6888.1	71.m15251	AO070314000034	FG07775.1	NCU08739.1
concat7	AN0233.1	69.m15589	AO070283000035	FG05720.1	NCU05853.1
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concat7	AN7709.1	71.m15733	AO070325000116	FG05131.1	NCU03730.1
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concat8	AN2456.1	69.m15673	AO070264000017	FG10760.1	NCU01615.1
concat8	AN0314.1	54.m06444	AO070334000018	FG01976.1	NCU07082.1
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concat8	AN5768.1	69.m14831	AO070249000004	FG07425.1	NCU03660.1
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concat12	AN7175.1	65.m07223	AO070335000146	FG04216.1	NCU04695.1
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ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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concat14	AN2141.1	72.m19700	AO070343000187	FG07140.1	NCU01248.1
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concat14	AN5848.1	72.m18979	AO070340000006	FG06366.1	NCU02399.1
concat14	AN6055.1	72.m19102	AO070340000199	FG08329.1	NCU05516.1
concat14	AN0876.1	70.m15479	AO070320000035	FG06634.1	NCU00236.1
concat14	AN0732.1	70.m15321	AO070343000493	FG03725.1	NCU00306.1
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concat14	AN8099.1	72.m19551	AO070309000130	FG06612.1	NCU00865.1
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concat14	AN0655.1	70.m15259	AO070343000571	FG10100.1	NCU06636.1
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concat15	AN0240.1	71.m15642	AO070284000070	FG08723.1	NCU02136.1
concat15	AN0134.1	71.m15418	AO070321000119	FG10756.1	NCU01613.1
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concat15	AN3146.1	59.m08519	AO070256000046	FG02460.1	NCU04898.1
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concat16	AN3840.1	58.m07816	AO070305000075	FG00684.1	NCU00892.1
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concat16	AN1076.1	70.m15150	AO070285000076	FG07454.1	NCU01254.1
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concat18	AN5757.1	69.m14854	AO070341000016	FG10066.1	NCU04005.1
concat19	AN4441.1	58.m09014	AO070273000013	FG01620.1	NCU03335.1
concat19	AN6705.1	65.m07280	AO070339000135	FG01925.1	NCU08003.1
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concat19	AN1201.1	70.m15018	AO070331000207	FG01333.1	NCU09892.1
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concat22	AN6226.1	72.m19427	AO070304000076	FG01713.1	NCU00722.1
concat22	AN4053.1	54.m06538	AO070342000038	FG00748.1	NCU02069.1
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concat23	AN6240.1	72.m19417	AO070304000091	FG08756.1	NCU07078.1
concat23	AN4412.1	58.m08981	AO070273000032	FG01656.1	NCU03363.1
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concat24	AN0472.1	54.m07063	AO070328000166	FG08757.1	NCU07076.1
concat24	AN9303.1	59.m08580	AO070275000031	FG00828.1	NCU01598.1
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concat24	AN1179.1	70.m15038	AO070331000176	FG11637.1	NCU04406.1
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concat31	AN2862.1	59.m08708	AO070338000160	FG06627.1	NCU00243.1
concat31	AN7498.1	57.m05843	AO070287000016	FG09773.1	NCU05252.1
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concat31	AN9467.1	53.m03848	AO070322000047	FG05894.1	NCU03786.1
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concat31	AN8010.1	53.m03857	AO070322000057	FG06822.1	NCU06687.1
concat31	AN1662.1	58.m07743	AO070299000024	FG07515.1	NCU09442.1
concat31	AN8041.1	53.m03905	AO070330000005	FG06257.1	NCU01528.1
concat31	AN2523.1	59.m08459	AO070286000091	FG10116.1	NCU03611.1
concat31	AN4303.1	58.m08021	AO070207000007	FG04571.1	NCU04289.1
concat32	AN4553.1	57.m05564	AO070321000177	FG06720.1	NCU00078.1
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concat32	AN7303.1	72.m20021	AO070297000050	FG02527.1	NCU00164.1
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concat32	AN3888.1	72.m19605	AO070343000294	FG08575.1	NCU01095.1
concat32	AN3738.1	69.m15377	AO070342000269	FG09839.1	NCU02403.1
concat32	AN4993.1	59.m08896	AO070288000076	FG06376.1	NCU02417.1
concat32	AN3010.1	59.m09008	AO070337000106	FG06338.1	NCU02231.1
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concat32	AN4515.1	57.m05614	AO070311000076	FG02720.1	NCU05686.1
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concat33	AN9007.1	62.m03484	AO070315000107	FG06068.1	NCU06895.1
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concat34	AN4684.1	71.m15668	AO070284000040	FG08571.1	NCU02148.1
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concat34	AN5217.1	69.m14916	AO070337000262	FG00900.1	NCU07495.1
concat34	AN3888.1	72.m19605	AO070343000294	FG08575.1	NCU01095.1
concat34	AN1007.1	70.m15225	AO070312000026	FG08402.1	NCU04720.1
concat34	AN5749.1	69.m14847	AO070341000006	FG03481.1	NCU02227.1
concat34	AN4992.1	59.m08895	AO070288000075	FG06375.1	NCU02416.1
concat34	AN1486.1	55.m02992	AO070334000193	FG01490.1	NCU08368.1
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concat34	AN1138.1	70.m15099	AO070331000129	FG00107.1	NCU06026.1
concat34	AN4390.1	58.m07933	AO070261000036	FG10089.1	NCU08936.1
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concat34	AN4470.1	58.m07860	AO070305000129	FG06843.1	NCU02810.1
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concat35	AN4399.1	58.m07932	AO070261000044	FG09935.1	NCU04302.1
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concat35	AN2953.1	59.m09089	AO070337000200	FG09885.1	NCU05136.1
concat35	AN4276.1	65.m07454	AO070277000008	FG01068.1	NCU02526.1
concat35	AN2090.1	57.m05792	AO070341000248	FG07094.1	NCU09227.1
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concat35	AN6505.1	62.m03092	AO070222000021	FG02501.1	NCU06205.1
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concat35	AN6678.1	65.m07302	AO070289000018	FG07046.1	NCU03036.1
concat35	AN4550.1	57.m05560	AO070321000181	FG04554.1	NCU00915.1
concat35	AN6638.1	62.m03233	AO070326000090	FG08648.1	NCU02034.1
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concat36	AN6525.1	62.m03114	AO070270000024	FG06127.1	NCU03813.1
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concat36	AN4957.1	59.m08862	AO070288000019	FG04085.1	NCU08687.1
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concat37	AN5569.1	58.m07493	AO070328000037	FG04308.1	NCU05423.1
concat37	AN2047.1	58.m07635	AO070292000014	FG01891.1	NCU04120.1
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concat37	AN7175.1	65.m07223	AO070335000146	FG04216.1	NCU04695.1
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concat37	AN3313.1	65.m07345	AO070339000070	FG05049.1	NCU08968.1
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concat37	AN1427.1	55.m02928	AO070242000025	FG07917.1	NCU09771.1
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concat39	AN8837.1	71.m15968	AO070271000041	FG02072.1	NCU07742.1
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concat39	AN5640.1	58.m07562	AO070301000036	FG08481.1	NCU04782.1
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concat39	AN8863.1	71.m16001	AO070271000008	FG07467.1	NCU01438.1
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concat39	AN1092.1	70.m15139	AO070285000055	FG06147.1	NCU01256.1
concat39	AN3758.1	65.m07366	AO070309000048	FG05598.1	NCU03296.1
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concat40	AN2190.1	69.m14881	AO070247000014	FG07428.1	NCU04647.1
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concat40	AN0865.1	70.m15463	AO070320000016	FG01856.1	NCU03692.1
concat40	AN0141.1	71.m15424	AO070321000108	FG10860.1	NCU06780.1
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concat40	AN1652.1	58.m07719	AO070299000039	FG06871.1	NCU02671.1
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concat41	AN7388.1	56.m02393	AO070293000057	FG02974.1	NCU05770.1
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concat43	AN7494.1	57.m05849	AO070287000022	FG02478.1	NCU05233.1
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concat43	AN8824.1	71.m15956	AO070271000057	FG05428.1	NCU09004.1
concat43	AN8810.1	71.m15616	AO070276000047	FG06805.1	NCU01170.1
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concat43	AN3946.1	69.m14975	AO070341000066	FG01347.1	NCU10043.1
concat43	AN1158.1	70.m15083	AO070331000148	FG07009.1	NCU01197.1
concat43	AN0808.1	70.m15409	AO070239000007	FG00915.1	NCU02104.1
concat44	AN5486.1	69.m15721	AO070341000397	FG10250.1	NCU06726.1
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concat44	AN2442.1	69.m15216	AO070264000033	FG04276.1	NCU08033.1
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concat44	AN6274.1	65.m07379	AO070309000069	FG02792.1	NCU01861.1
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concat44	AN1775.1	69.m15062	AO070324000034	FG02191.1	NCU05644.1
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concat44	AN6234.1	52.m04099	AO070302000121	FG04334.1	NCU06062.1
concat44	AN2873.1	59.m08723	AO070338000139	FG00380.1	NCU08579.1
concat44	AN7741.1	71.m16099	AO070325000162	FG02105.1	NCU09673.1
concat44	AN7388.1	56.m02393	AO070293000057	FG02974.1	NCU05770.1
concat44	AN6628.1	62.m03224	AO070326000079	FG08784.1	NCU00624.1
concat44	AN8959.1	52.m03755	AO070336000205	FG01031.1	NCU02801.1
concat44	AN5746.1	69.m14844	AO070341000003	FG01346.1	NCU10042.1
concat44	AN4469.1	58.m07855	AO070305000124	FG06821.1	NCU03764.1
concat44	AN6221.1	72.m19434	AO070304000053	FG05073.1	NCU07039.1
concat44	AN8117.1	53.m03827	AO070322000025	FG07347.1	NCU06694.1
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concat45	AN6217.1	72.m19316	AO070308000074	FG05455.1	NCU06483.1
concat45	AN5828.1	72.m18955	AO070260000018	FG10193.1	NCU03603.1
concat45	AN4932.1	59.m08836	AO070338000011	FG04051.1	NCU04987.1
concat45	AN4867.1	59.m08762	AO070338000092	FG09910.1	NCU04319.1
concat45	AN4417.1	58.m07906	AO070273000038	FG10865.1	NCU06776.1
concat45	AN4888.1	59.m08784	AO070338000070	FG09834.1	NCU02397.1
concat45	AN5169.1	69.m14867	AO070247000004	FG07068.1	NCU07389.1
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concat45	AN1037.1	70.m15195	AO070336000072	FG05784.1	NCU02209.1
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concat45	AN1135.1	70.m15102	AO070331000126	FG05702.1	NCU06023.1
concat45	AN5932.1	72.m19197	AO070340000348	FG05421.1	NCU07870.1
concat45	AN1247.1	70.m15739	AO070223000010	FG03994.1	NCU07915.1
concat45	AN4603.1	57.m05527	AO070267000024	FG10934.1	NCU02296.1
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concat45	AN7332.1	63.m00650	AO070342000220	FG00625.1	NCU09549.1
concat45	AN2281.1	71.m15926	AO070295000058	FG06942.1	NCU06175.1
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concat45	AN4919.1	59.m08822	AO070338000024	FG00822.1	NCU03438.1
concat46	AN6594.1	62.m03203	AO070326000044	FG05537.1	NCU06497.1
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concat46	AN1721.1	58.m07788	AO070305000036	FG00276.1	NCU08363.1
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concat46	AN1379.1	70.m14844	AO070243000010	FG10280.1	NCU04288.1
concat46	AN0124.1	71.m15405	AO070311000088	FG09784.1	NCU07722.1
concat46	AN3665.1	58.m07425	AO070342000001	FG01006.1	NCU02632.1
concat46	AN7335.1	72.m19736	AO070297000108	FG05515.1	NCU00295.1
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concat46	AN4940.1	59.m08844	AO070338000003	FG11602.1	NCU04415.1
concat46	AN9339.1	52.m03838	AO070315000069	FG06733.1	NCU00355.1
concat46	AN0913.1	70.m15522	AO070320000094	FG05154.1	NCU09192.1
concat46	AN0554.1	69.m15293	AO070272000027	FG00979.1	NCU03415.1
concat46	AN6651.1	62.m03251	AO070269000002	FG08532.1	NCU09903.1
concat46	AN8488.1	58.m08926	AO070299000105	FG06394.1	NCU06708.1
concat46	AN7479.1	57.m05859	AO070287000036	FG08865.1	NCU06457.1
concat46	AN8787.1	71.m15583	AO070276000074	FG06659.1	NCU00134.1
concat47	AN6564.1	62.m03151	AO070326000005	FG07402.1	NCU03827.1
concat47	AN8180.1	53.m03800	AO070310000147	FG06116.1	NCU03799.1
concat47	AN7537.1	69.m15084	AO070324000009	FG08631.1	NCU07062.1
concat47	AN1163.1	70.m15058	AO070331000153	FG01015.1	NCU02630.1
concat47	AN4612.1	57.m05529	AO070267000028	FG09434.1	NCU08068.1
concat47	AN2154.1	72.m20002	AO070343000203	FG05066.1	NCU08045.1
concat47	AN8945.1	56.m03091	AO070319000047	FG04837.1	NCU07815.1
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ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat47	AN7535.1	72.m19814	AO070299000067	FG10918.1	NCU02191.1
concat47	AN5861.1	72.m19272	AO070308000126	FG05670.1	NCU04462.1
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concat47	AN8683.1	62.m03388	AO070315000103	FG08579.1	NCU02020.1
concat47	AN2877.1	59.m08718	AO070338000146	FG02771.1	NCU08578.1
concat47	AN0561.1	69.m15286	AO070272000038	FG09732.1	NCU05226.1
concat47	AN7194.1	54.m06399	AO070197000003	FG10124.1	NCU01419.1
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concat47	AN8363.1	52.m04104	AO070274000030	FG00530.1	NCU03255.1
concat49	AN2223.1	71.m15843	AO070326000180	FG05083.1	NCU07021.1
concat49	AN7524.1	69.m15112	AO070258000032	FG08746.1	NCU07059.1
concat49	AN6244.1	72.m19413	AO070304000098	FG10879.1	NCU01806.1
concat49	AN4743.1	59.m09236	AO070327000077	FG08857.1	NCU02160.1
concat49	AN6055.1	72.m19102	AO070340000199	FG08329.1	NCU05516.1
concat49	AN6347.1	72.m19508	AO070275000012	FG01842.1	NCU04143.1
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concat49	AN1132.1	70.m15104	AO070331000124	FG05709.1	NCU06027.1
concat49	AN7422.1	57.m05923	AO070197000001	FG02640.1	NCU05777.1
concat49	AN3371.1	66.m04639	AO070281000010	FG09384.1	NCU06056.1
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concat49	AN7732.1	71.m15754	AO070325000143	FG02049.1	NCU01211.1
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concat49	AN1452.1	55.m02954	AO070302000017	FG00398.1	NCU09131.1
concat49	AN8794.1	71.m15601	AO070276000069	FG09009.1	NCU09826.1
concat49	AN3905.1	69.m15030	AO070324000083	FG09229.1	NCU03269.1
concat50	AN2146.1	72.m19695	AO070343000195	FG07460.1	NCU01259.1
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concat50	AN6169.1	72.m19000	AO070340000031	FG02709.1	NCU04669.1
concat50	AN6890.1	71.m15249	AO070314000031	FG09180.1	NCU02846.1
concat50	AN4236.1	54.m06779	AO070234000007	FG11597.1	NCU04414.1
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concat50	AN1257.1	56.m02387	AO070327000016	FG10282.1	NCU00244.1
concat50	AN8799.1	71.m15606	AO070276000061	FG05964.1	NCU04196.1
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concat50	AN2167.1	72.m19673	AO070343000229	FG05163.1	NCU03493.1
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concat50	AN3169.1	59.m09379	AO070256000021	FG10840.1	NCU01786.1
concat50	AN1394.1	70.m14828	AO070233000008	FG06035.1	NCU03515.1
concat51	AN4223.1	54.m06794	AO070234000027	FG00647.1	NCU03578.1
concat51	AN6541.1	62.m03133	AO070270000044	FG02506.1	NCU00177.1
concat51	AN0583.1	69.m15265	AO070280000005	FG09766.1	NCU07712.1
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concat51	AN0141.1	71.m15424	AO070321000108	FG10860.1	NCU06780.1

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concat51	AN6059.1	72.m19094	AO070340000190	FG08327.1	NCU05521.1
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concat51	AN3132.1	59.m08593	AO070303000012	FG09261.1	NCU07271.1
concat51	AN5114.1	54.m06909	AO070291000065	FG00834.1	NCU09608.1
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concat51	AN7484.1	57.m05866	AO070287000045	FG04003.1	NCU04522.1
concat51	AN1949.1	58.m07347	AO070342000215	FG04350.1	NCU09349.1
concat51	AN4615.1	57.m05532	AO070267000032	FG08692.1	NCU00586.1
concat51	AN0896.1	70.m15502	AO070320000070	FG00743.1	NCU03031.1
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concat51	AN7463.1	57.m05879	AO070287000063	FG00529.1	NCU03257.1
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concat52	AN8262.1	53.m04209	AO070310000038	FG07716.1	NCU04626.1
concat52	AN3305.1	71.m15151	AO070329000026	FG07570.1	NCU01107.1
concat52	AN5806.1	72.m18936	AO070260000042	FG10186.1	NCU04584.1
concat52	AN2456.1	69.m15673	AO070264000017	FG10760.1	NCU01615.1
concat52	AN4691.1	71.m15674	AO070284000047	FG08511.1	NCU02128.1
concat52	AN6194.1	72.m19293	AO070308000104	FG05329.1	NCU08001.1
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concat52	AN0072.1	71.m15348	AO070314000161	FG07326.1	NCU04153.1
concat52	AN4255.1	65.m07427	AO070309000125	FG08399.1	NCU04728.1
concat52	AN8850.1	71.m15985	AO070271000026	FG05566.1	NCU09000.1
concat52	AN0126.1	71.m15408	AO070311000085	FG09728.1	NCU08309.1
concat52	AN5549.1	69.m14939	AO070341000115	FG04957.1	NCU04809.1
concat52	AN0627.1	70.m15658	AO070280000079	FG06897.1	NCU08974.1
concat52	AN4244.1	54.m06806	AO070324000168	FG09907.1	NCU01167.1
concat52	AN3737.1	69.m15379	AO070342000271	FG07849.1	NCU09302.1
concat52	AN6558.1	62.m03146	AO070270000062	FG06937.1	NCU00419.1
concat52	AN4241.1	54.m06804	AO070324000173	FG06354.1	NCU06860.1
concat52	AN2918.1	59.m09095	AO070329000153	FG00558.1	NCU02839.1
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concat52	AN0243.1	71.m15639	AO070284000073	FG04985.1	NCU07320.1
concat54	AN3134.1	59.m08591	AO070303000010	FG05985.1	NCU01843.1
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concat54	AN2515.1	59.m08473	AO070263000051	FG02703.1	NCU09519.1
concat54	AN2909.1	59.m08759	AO070338000097	FG09891.1	NCU06717.1
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concat54	AN0260.1	54.m06521	AO070334000098	FG01839.1	NCU04646.1
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concat54	AN8329.1	67.m02964	AO070330000092	FG03475.1	NCU09798.1
concat54	AN1215.1	70.m14996	AO070331000233	FG01185.1	NCU03066.1
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concat57	AN5986.1	72.m19155	AO070340000293	FG08941.1	NCU01906.1
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concat57	AN2210.1	71.m15855	AO070294000012	FG02025.1	NCU08920.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat57	AN7493.1	57.m05851	AO070287000024	FG04252.1	NCU05214.1
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concat57	AN1128.1	70.m15107	AO070331000120	FG09914.1	NCU08338.1
concat57	AN0577.1	69.m15692	AO070272000057	FG05259.1	NCU06601.1
concat57	AN6391.1	69.m15695	AO070343000154	FG09815.1	NCU06630.1
concat57	AN4594.1	57.m05517	AO070267000010	FG05493.1	NCU06892.1
concat57	AN0306.1	54.m06979	AO070334000032	FG07054.1	NCU03050.1
concat57	AN0139.1	71.m15422	AO070321000113	FG10857.1	NCU01757.1
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concat58	AN1200.1	70.m15019	AO070331000206	FG01332.1	NCU09894.1
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concat58	AN4329.1	58.m07991	AO070240000007	FG10160.1	NCU04213.1
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concat58	AN1485.1	55.m02991	AO070334000192	FG00677.1	NCU03124.1
concat60	AN0431.1	54.m06627	AO070338000291	FG00740.1	NCU03127.1
concat60	AN7302.1	72.m19765	AO070297000048	FG02529.1	NCU00162.1
concat60	AN8699.1	62.m03370	AO070315000126	FG08920.1	NCU01919.1
concat60	AN8234.1	53.m03735	AO070310000074	FG08986.1	NCU08859.1
concat60	AN2510.1	59.m09341	AO070263000047	FG10378.1	NCU01338.1
concat60	AN5139.1	54.m07054	AO070291000038	FG10869.1	NCU08484.1
concat60	AN1779.1	69.m15647	AO070324000017	FG09310.1	NCU05972.1
concat60	AN2977.1	59.m09424	AO070337000144	FG01230.1	NCU07465.1
concat60	AN0733.1	70.m15320	AO070343000494	FG04290.1	NCU01635.1
concat60	AN7314.1	72.m19749	AO070297000067	FG04280.1	NCU08689.1
concat60	AN1437.1	55.m03263	AO070232000002	FG00584.1	NCU09252.1
concat60	AN6626.1	62.m03217	AO070315000108	FG05676.1	NCU00623.1
concat60	AN0392.1	54.m06345	AO070278000009	FG03365.1	NCU09759.1
concat60	AN8401.1	52.m03820	AO070302000072	FG07993.1	NCU09923.1
concat60	AN0445.1	54.m06637	AO070338000307	FG00845.1	NCU01776.1
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concat60	AN4514.1	57.m05978	AO070311000070	FG00815.1	NCU10029.1
concat60	AN0229.1	71.m15482	AO070323000079	FG05653.1	NCU06986.1
concat60	AN0860.1	70.m15469	AO070320000008	FG05481.1	NCU00102.1
concat60	AN0293.1	54.m06491	AO070334000049	FG00587.1	NCU00954.1
concat61	AN1358.1	70.m15731	AO070237000002	FG10239.1	NCU04600.1
concat63	AN6569.1	62.m03156	AO070326000012	FG07406.1	NCU03836.1
concat63	AN4880.1	59.m09409	AO070338000081	FG06369.1	NCU02415.1
concat63	AN5768.1	69.m14831	AO070249000004	FG07425.1	NCU03660.1
concat63	AN0988.1	70.m15629	AO070318000150	FG06637.1	NCU00230.1
concat63	AN3222.1	67.m02930	AO070330000072	FG11629.1	NCU01945.1

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concat63	AN0818.1	70.m15418	AO070288000084	FG00665.1	NCU02619.1
concat63	AN1521.1	55.m03040	AO070334000239	FG01220.1	NCU02661.1
concat63	AN1688.1	58.m07763	AO070305000008	FG06649.1	NCU00326.1
concat63	AN1652.1	58.m07719	AO070299000039	FG06871.1	NCU02671.1
concat63	AN0247.1	54.m06700	AO070338000240	FG00732.1	NCU02284.1
concat63	AN7705.1	71.m15730	AO070325000111	FG02812.1	NCU00879.1
concat63	AN2896.1	59.m08746	AO070338000112	FG06084.1	NCU09058.1
concat63	AN5656.1	58.m08892	AO070342000244	FG10120.1	NCU01411.1
concat63	AN7603.1	72.m19644	AO070343000273	FG05300.1	NCU09747.1
concat63	AN6874.1	71.m16021	AO070314000047	FG01640.1	NCU03503.1
concat63	AN3107.1	59.m08630	AO070334000152	FG04359.1	NCU03567.1
concat63	AN8488.1	58.m08926	AO070299000105	FG06394.1	NCU06708.1
concat63	AN1778.1	69.m15077	AO070324000018	FG09312.1	NCU10048.1
concat63	AN3462.1	59.m09323	AO070265000040	FG04578.1	NCU06721.1
concat63	AN7681.1	57.m05947	AO070325000071	FG10035.1	NCU04597.1
concat64	AN5602.1	58.m07526	AO070328000002	FG09535.1	NCU04087.1
concat64	AN6705.1	65.m07280	AO070339000135	FG01925.1	NCU08003.1
concat64	AN0431.1	54.m06627	AO070338000291	FG00740.1	NCU03127.1
concat64	AN7302.1	72.m19765	AO070297000048	FG02529.1	NCU00162.1
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concat64	AN3693.1	69.m15405	AO070341000321	FG00332.1	NCU06838.1
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concat64	AN5528.1	69.m15427	AO070341000360	FG10911.1	NCU05029.1
concat64	AN3440.1	59.m09302	AO070265000015	FG08084.1	NCU05045.1
concat64	AN4227.1	54.m06789	AO070234000022	FG01453.1	NCU06845.1
concat64	AN6900.1	71.m15236	AO070314000015	FG06702.1	NCU07550.1
concat64	AN8683.1	62.m03388	AO070315000103	FG08579.1	NCU02020.1
concat64	AN7576.1	72.m19595	AO070343000423	FG01204.1	NCU02689.1
concat64	AN7250.1	72.m19799	AO070297000005	FG04095.1	NCU00430.1
concat64	AN6064.1	72.m19053	AO070340000104	FG04677.1	NCU00397.1
concat64	AN0081.1	71.m15359	AO070311000136	FG04104.1	NCU00440.1
concat64	AN1023.1	70.m15244	AO070343000591	FG09721.1	NCU06347.1
concat64	AN7431.1	57.m05913	AO070229000002	FG09892.1	NCU06718.1
concat64	AN7360.1	72.m19716	AO070278000039	FG04121.1	NCU00465.1
concat65	AN2092.1	57.m05795	AO070341000250	FG06836.1	NCU07415.1
concat65	AN6567.1	62.m03154	AO070326000010	FG07405.1	NCU03834.1
concat65	AN4401.1	58.m07925	AO070261000045	FG09934.1	NCU04303.1
concat65	AN8702.1	62.m03366	AO070315000130	FG08558.1	NCU02113.1
concat65	AN6618.1	62.m03214	AO070326000068	FG05191.1	NCU03661.1
concat65	AN5351.1	69.m15553	AO070333000172	FG09630.1	NCU07264.1
concat65	AN0158.1	71.m15435	AO070321000089	FG05690.1	NCU04443.1
concat65	AN6313.1	72.m19320	AO070308000069	FG06759.1	NCU07558.1
concat65	AN4458.1	58.m07866	AO070305000135	FG06789.1	NCU09547.1
concat65	AN3367.1	66.m04635	AO070281000025	FG09386.1	NCU06059.1
concat65	AN3827.1	58.m07803	AO070305000064	FG00695.1	NCU00925.1
concat65	AN4270.1	65.m07444	AO070277000018	FG06945.1	NCU06171.1
concat65	AN3833.1	58.m07812	AO070305000071	FG09396.1	NCU06927.1
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concat65	AN8797.1	71.m15604	AO070276000063	FG05861.1	NCU01240.1
concat65	AN6119.1	72.m19041	AO070340000085	FG01898.1	NCU01464.1
concat65	AN4053.1	54.m06538	AO070342000038	FG00748.1	NCU02069.1
concat65	AN3905.1	69.m15030	AO070324000083	FG09229.1	NCU03269.1
concat65	AN6726.1	65.m07244	AO070339000170	FG04410.1	NCU06764.1
concat65	AN6907.1	71.m15230	AO070314000006	FG02570.1	NCU06278.1
concat66	AN8841.1	71.m15972	AO070271000036	FG07396.1	NCU03822.1
concat66	AN9303.1	59.m08580	AO070275000031	FG00828.1	NCU01598.1
concat66	AN1290.1	55.m03194	AO070339000255	FG02820.1	NCU07068.1
concat66	AN8851.1	71.m15986	AO070271000025	FG07206.1	NCU01290.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat66	AN1607.1	55.m03177	AO070309000147	FG01530.1	NCU07473.1
concat66	AN0988.1	70.m15629	AO070318000150	FG06637.1	NCU00230.1
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concat66	AN1380.1	70.m14843	AO070343000393	FG08614.1	NCU07451.1
concat66	AN5150.1	69.m14884	AO070237000015	FG07540.1	NCU06033.1
concat66	AN6900.1	71.m15236	AO070314000015	FG06702.1	NCU07550.1
concat66	AN7601.1	72.m19646	AO070343000271	FG02481.1	NCU05237.1
concat66	AN0442.1	54.m06632	AO070338000299	FG09305.1	NCU02559.1
concat66	AN2902.1	59.m08753	AO070338000104	FG07853.1	NCU09300.1
concat66	AN1451.1	55.m02953	AO070302000016	FG00185.1	NCU00537.1
concat66	AN5678.1	65.m07404	AO070309000093	FG00613.1	NCU05830.1
concat66	AN1715.1	58.m08959	AO070305000031	FG05330.1	NCU02322.1
concat66	AN8824.1	71.m15956	AO070271000057	FG05428.1	NCU09004.1
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concat66	AN5833.1	72.m18961	AO070260000012	FG10126.1	NCU01417.1
concat66	AN1777.1	69.m15060	AO070324000036	FG05364.1	NCU05943.1
concat67	AN3692.1	69.m15406	AO070341000323	FG00333.1	NCU06839.1
concat67	AN4384.1	58.m07940	AO070261000029	FG10379.1	NCU01337.1
concat67	AN4208.1	54.m06767	AO070231000016	FG02016.1	NCU04144.1
concat67	AN7435.1	57.m05905	AO070229000009	FG00911.1	NCU07482.1
concat67	AN6236.1	52.m03953	AO070302000119	FG03747.1	NCU08441.1
concat67	AN2107.1	57.m05807	AO070341000264	FG01359.1	NCU09241.1
concat67	AN7672.1	57.m05448	AO070325000052	FG06856.1	NCU02635.1
concat67	AN4297.1	58.m08027	AO070189000005	FG10276.1	NCU03953.1
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concat67	AN4194.1	54.m06757	AO070315000084	FG05586.1	NCU06202.1
concat67	AN8872.1	56.m03128	AO070293000001	FG01371.1	NCU02979.1
concat67	AN5893.1	72.m19237	AO070245000013	FG06228.1	NCU08319.1
concat67	AN4259.1	65.m07433	AO070277000032	FG07122.1	NCU02813.1
concat67	AN2824.1	67.m02987	AO070330000093	FG02314.1	NCU09042.1
concat67	AN5143.1	54.m06878	AO070291000032	FG01432.1	NCU01745.1
concat67	AN8820.1	71.m15631	AO070276000022	FG06103.1	NCU03804.1
concat67	AN0690.1	70.m15293	AO070343000523	FG09923.1	NCU06658.1
concat67	AN8117.1	53.m03827	AO070322000025	FG07347.1	NCU06694.1
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concat69	AN5528.1	69.m15427	AO070341000360	FG10911.1	NCU05029.1
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concat69	AN3940.1	69.m14984	AO070341000052	FG00482.1	NCU09261.1
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concat69	AN6064.1	72.m19053	AO070340000104	FG04677.1	NCU00397.1
concat69	AN2246.1	71.m15880	AO070326000127	FG05135.1	NCU01187.1
concat69	AN1547.1	55.m03067	AO070339000307	FG08266.1	NCU09770.1
concat69	AN6911.1	71.m15221	AO070219000015	FG02565.1	NCU06268.1
concat69	AN6226.1	72.m19427	AO070304000076	FG01713.1	NCU00722.1
concat69	AN5529.1	58.m07475	AO070328000064	FG01188.1	NCU07296.1
concat69	AN3758.1	65.m07366	AO070309000048	FG05598.1	NCU03296.1
concat70	AN1051.1	70.m15778	AO070336000071	FG00844.1	NCU01771.1
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concat70	AN5113.1	54.m07051	AO070291000066	FG02804.1	NCU01850.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat70	AN8676.1	62.m03394	AO070315000096	FG08696.1	NCU07430.1
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concat70	AN0065.1	71.m15342	AO070314000154	FG05413.1	NCU07885.1
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concat70	AN2311.1	71.m15506	AO070323000049	FG09764.1	NCU08671.1
concat70	AN8764.1	62.m03313	AO070277000062	FG06401.1	NCU02028.1
concat70	AN2761.1	59.m09263	AO070327000023	FG10805.1	NCU02289.1
concat70	AN4639.1	57.m05552	AO070321000194	FG08704.1	NCU00621.1
concat70	AN3607.1	58.m07405	AO070342000160	FG00710.1	NCU00902.1
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concat70	AN6093.1	55.m03163	AO070340000162	FG11049.1	NCU04870.1
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concat70	AN9149.1	66.m04586	AO070332000147	FG06885.1	NCU03263.1
concat70	AN6893.1	71.m16018	AO070314000027	FG05523.1	NCU00427.1
concat70	AN0229.1	71.m15482	AO070323000079	FG05653.1	NCU06986.1
concat70	AN1366.1	70.m14863	AO070215000015	FG10882.1	NCU01809.1
concat71	AN1190.1	70.m15031	AO070331000190	FG01323.1	NCU09814.1
concat71	AN7679.1	57.m05456	AO070325000069	FG10388.1	NCU04293.1
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concat71	AN0731.1	70.m15325	AO070343000492	FG10979.1	NCU06533.1
concat71	AN0347.1	54.m06410	AO070318000025	FG04327.1	NCU01523.1
concat71	AN5564.1	58.m07490	AO070328000043	FG07907.1	NCU04924.1
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concat71	AN8346.1	66.m04732	AO070275000024	FG03259.1	NCU07112.1
concat71	AN6869.1	71.m15260	AO070314000053	FG02206.1	NCU01348.1
concat71	AN6543.1	62.m03131	AO070270000041	FG07334.1	NCU04172.1
concat71	AN4332.1	58.m07986	AO070240000011	FG09423.1	NCU02468.1
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concat71	AN6070.1	72.m19062	AO070340000114	FG00504.1	NCU02539.1
concat71	AN9066.1	66.m04520	AO070332000218	FG00706.1	NCU00904.1
concat71	AN4569.1	57.m05490	AO070316000152	FG09918.1	NCU03957.1
concat71	AN0075.1	71.m15353	AO070311000141	FG07180.1	NCU03739.1
concat71	AN6653.1	62.m03255	AO070269000013	FG08700.1	NCU10007.1
concat71	AN6160.1	72.m19007	AO070340000044	FG06687.1	NCU00037.1
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concat73	AN5524.1	69.m15434	AO070341000365	FG07959.1	NCU02376.1
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concat73	AN8489.1	52.m03751	AO070342000405	FG08830.1	NCU09830.1
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concat74	AN0593.1	69.m15255	AO070280000019	FG05284.1	NCU06559.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
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concat74	AN5528.1	69.m15427	AO070341000360	FG10911.1	NCU05029.1
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concat74	AN1964.1	58.m07569	AO070301000045	FG00634.1	NCU08502.1
concat74	AN4778.1	59.m09470	AO070329000073	FG08706.1	NCU01993.1
concat74	AN2357.1	52.m03833	AO070307000082	FG05295.1	NCU08275.1
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concat74	AN3458.1	59.m09319	AO070265000035	FG10355.1	NCU04225.1
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concat75	AN7995.1	53.m03852	AO070322000050	FG05114.1	NCU04339.1
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concat75	AN5158.1	54.m06858	AO070291000007	FG04981.1	NCU04495.1
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concat75	AN6162.1	72.m19009	AO070340000046	FG06689.1	NCU00034.1
concat75	AN5821.1	72.m18948	AO070260000024	FG01802.1	NCU06366.1
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concat75	AN5634.1	58.m07331	AO070342000238	FG09896.1	NCU04230.1
concat75	AN2523.1	59.m08459	AO070286000091	FG10116.1	NCU03611.1
concat75	AN5499.1	69.m15454	AO070341000386	FG05337.1	NCU04059.1
concat76	AN1710.1	58.m07790	AO070305000038	FG04934.1	NCU02585.1
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concat76	AN6143.1	72.m19021	AO070340000060	FG05487.1	NCU00209.1
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concat76	AN6047.1	72.m19946	AO070340000229	FG09738.1	NCU07939.1
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concat76	AN1921.1	69.m14938	AO070341000116	FG09281.1	NCU04802.1
concat76	AN8766.1	62.m03315	AO070277000060	FG08674.1	NCU03147.1
concat76	AN3177.1	59.m08567	AO070256000013	FG10897.1	NCU03381.1
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concat76	AN3390.1	55.m03190	AO070290000088	FG03406.1	NCU10045.1
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concat77	AN0163.1	71.m15438	AO070321000084	FG05282.1	NCU06561.1
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concat77	AN6825.1	71.m15291	AO070314000105	FG05888.1	NCU08874.1
concat77	AN1432.1	55.m02938	AO070232000014	FG06985.1	NCU02678.1
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concat77	AN5811.1	72.m18941	AO070260000036	FG06524.1	NCU08550.1
concat77	AN4917.1	59.m08820	AO070338000026	FG06588.1	NCU00257.1
concat77	AN0730.1	70.m15326	AO070343000491	FG09683.1	NCU04450.1
concat77	AN3649.1	58.m07450	AO070328000097	FG01290.1	NCU02757.1
concat77	AN2280.1	71.m15925	AO070295000057	FG06943.1	NCU06174.1
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concat77	AN1045.1	70.m15201	AO070336000078	FG01968.1	NCU08295.1
concat77	AN0981.1	70.m15622	AO070318000167	FG06896.1	NCU08976.1
concat77	AN0600.1	69.m15248	AO070280000025	FG07160.1	NCU03735.1
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concat77	AN0139.1	71.m15422	AO070321000113	FG10857.1	NCU01757.1
concat77	AN0902.1	70.m15511	AO070320000074	FG06382.1	NCU07575.1
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concat78	AN0579.1	69.m15690	AO070280000001	FG09722.1	NCU07719.1
concat78	AN0124.1	71.m15405	AO070311000088	FG09784.1	NCU07722.1
concat78	AN6534.1	62.m03432	AO070270000051	FG03803.1	NCU07761.1
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concat78	AN6080.1	72.m19927	AO070340000130	FG00505.1	NCU02538.1
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concat78	AN4517.1	57.m05611	AO070321000123	FG05527.1	NCU00010.1
concat78	AN5785.1	69.m14812	AO070249000030	FG01345.1	NCU07956.1
concat78	AN4241.1	54.m06804	AO070324000173	FG06354.1	NCU06860.1
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concat78	AN0462.1	54.m06607	AO070328000176	FG09244.1	NCU09869.1
concat78	AN1748.1	66.m04624	AO070320000028	FG02113.1	NCU04234.1
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concat78	AN4442.1	58.m09016	AO070273000012	FG01568.1	NCU03357.1
concat78	AN4019.1	54.m06552	AO070328000118	FG00924.1	NCU03107.1
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concat80	AN0732.1	70.m15321	AO070343000493	FG03725.1	NCU00306.1
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concat80	AN5914.1	72.m19959	AO070248000032	FG00742.1	NCU03032.1
concat80	AN5005.1	59.m08905	AO070255000035	FG09912.1	NCU01421.1
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concat80	AN4719.1	71.m15707	AO070311000002	FG08572.1	NCU00668.1
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concat80	AN2555.1	57.m05650	AO070319000164	FG05797.1	NCU06720.1
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concat81	AN6240.1	72.m19417	AO070304000091	FG08756.1	NCU07078.1
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concat81	AN5661.1	58.m08891	AO070342000254	FG06370.1	NCU02381.1
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concat81	AN5753.1	69.m14851	AO070329000011	FG10755.1	NCU08137.1
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concat81	AN1924.1	69.m14942	AO070341000109	FG08393.1	NCU04830.1
concat81	AN8850.1	71.m15985	AO070271000026	FG05566.1	NCU09000.1
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concat81	AN7350.1	72.m19727	AO070278000050	FG02575.1	NCU00457.1
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concat81	AN2741.1	54.m06957	AO070338000230	FG07234.1	NCU00042.1
concat81	AN0315.1	54.m06443	AO070334000017	FG00640.1	NCU01750.1
concat81	AN1256.1	70.m14971	AO070223000013	FG07101.1	NCU03061.1
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concat83	AN1115.1	70.m15120	AO070331000106	FG00465.1	NCU03084.1
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concat83	AN2963.1	59.m09052	AO070337000166	FG01910.1	NCU01323.1
concat83	AN0164.1	71.m15439	AO070321000083	FG05281.1	NCU06563.1
concat83	AN6328.1	72.m19447	AO070304000106	FG09576.1	NCU07701.1
concat83	AN2096.1	57.m05799	AO070341000255	FG09327.1	NCU02591.1
concat83	AN8945.1	56.m03091	AO070319000047	FG04837.1	NCU07815.1
concat83	AN4875.1	59.m09495	AO070338000085	FG10780.1	NCU02271.1
concat83	AN0458.1	54.m06612	AO070328000180	FG10749.1	NCU08712.1
concat83	AN2771.1	59.m09272	AO070327000013	FG06352.1	NCU06859.1
concat83	AN6506.1	62.m03093	AO070222000022	FG02502.1	NCU06207.1
concat83	AN0654.1	70.m15258	AO070343000572	FG10097.1	NCU01427.1
concat83	AN9401.1	52.m04028	AO070274000016	FG08521.1	NCU00655.1
concat83	AN7451.1	57.m05891	AO070229000024	FG04117.1	NCU00461.1
concat83	AN2572.1	72.m19060	AO070340000111	FG01095.1	NCU03290.1
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concat84	AN9172.1	56.m02468	AO070317000027	FG04232.1	NCU08228.1
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concat84	AN8406.1	52.m04077	AO070302000057	FG04703.1	NCU00028.1
concat84	AN7307.1	72.m19758	AO070297000055	FG04255.1	NCU09737.1
concat84	AN8032.1	53.m03880	AO070322000129	FG06786.1	NCU01177.1
concat84	AN6638.1	62.m03233	AO070326000090	FG08648.1	NCU02034.1
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concat84	AN6853.1	71.m15279	AO070314000087	FG05890.1	NCU03596.1
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concat84	AN2450.1	69.m15208	AO070264000026	FG06030.1	NCU03526.1
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concat85	AN4867.1	59.m08762	AO070338000092	FG09910.1	NCU04319.1
concat85	AN1796.1	72.m19548	AO070309000135	FG00283.1	NCU07483.1
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concat85	AN2085.1	57.m05786	AO070341000243	FG00367.1	NCU08605.1
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concat85	AN1999.1	58.m07607	AO070301000093	FG08453.1	NCU05982.1
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concat85	AN2259.1	71.m15900	AO070326000104	FG06660.1	NCU00058.1
concat85	AN7603.1	72.m19644	AO070343000273	FG05300.1	NCU09747.1
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concat86	AN3669.1	58.m07430	AO070342000010	FG09275.1	NCU07071.1
concat86	AN4407.1	58.m08972	AO070273000067	FG10158.1	NCU04275.1
concat86	AN5085.1	52.m03801	AO070246000035	FG03582.1	NCU09858.1
concat86	AN8283.1	65.m07459	AO070277000005	FG01000.1	NCU02624.1
concat86	AN0347.1	54.m06410	AO070318000025	FG04327.1	NCU01523.1
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concat86	AN1902.1	57.m05716	AO070341000151	FG09457.1	NCU04718.1
concat86	AN7494.1	57.m05849	AO070287000022	FG02478.1	NCU05233.1
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concat86	AN1783.1	56.m02532	AO070329000184	FG01586.1	NCU08164.1
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concat86	AN5895.1	72.m19235	AO070245000008	FG06166.1	NCU05288.1
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concat86	AN3361.1	66.m04779	AO070281000037	FG07554.1	NCU10055.1
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ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat87	AN3110.1	59.m08628	AO070303000041	FG10725.1	NCU03571.1
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concat91	AN3797.1	57.m05686	AO070337000231	FG08405.1	NCU04733.1
concat91	AN3849.1	58.m07833	AO070332000050	FG07224.1	NCU01636.1
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concat91	AN5568.1	58.m07492	AO070328000040	FG00817.1	NCU03462.1
concat91	AN8045.1	53.m03898	AO070292000104	FG06907.1	NCU09014.1
concat91	AN5141.1	54.m06880	AO070291000035	FG10820.1	NCU03399.1
concat91	AN1971.1	58.m07576	AO070301000055	FG05150.1	NCU03482.1
concat91	AN4557.1	57.m05569	AO070321000171	FG06816.1	NCU01479.1
concat91	AN0246.1	54.m06699	AO070338000238	FG07290.1	NCU06430.1
concat91	AN2184.1	72.m19039	AO070340000082	FG05395.1	NCU07577.1
concat91	AN9062.1	66.m04526	AO070332000211	FG08841.1	NCU00676.1
concat92	AN6243.1	72.m19414	AO070304000097	FG04418.1	NCU01498.1
concat92	AN8262.1	53.m04209	AO070310000038	FG07716.1	NCU04626.1
concat92	AN3712.1	69.m15419	AO070341000341	FG02231.1	NCU07127.1
concat92	AN4456.1	58.m07868	AO070173000001	FG06802.1	NCU01367.1
concat92	AN8859.1	71.m15997	AO070271000014	FG07421.1	NCU04118.1
concat92	AN6200.1	72.m19298	AO070308000096	FG01553.1	NCU01675.1
concat92	AN4975.1	59.m08878	AO070288000042	FG08428.1	NCU04771.1
concat92	AN6596.1	62.m03202	AO070326000045	FG05557.1	NCU00280.1
concat92	AN6079.1	72.m19071	AO070340000129	FG08738.1	NCU09191.1
concat92	AN9470.1	72.m19181	AO070340000319	FG04126.1	NCU07853.1
concat92	AN3832.1	58.m07811	AO070305000070	FG01391.1	NCU02955.1
concat92	AN4177.1	56.m02500	AO070319000001	FG02822.1	NCU00884.1
concat92	AN9486.1	59.m09213	AO070329000083	FG09444.1	NCU00565.1
concat92	AN0339.1	54.m06418	AO070318000017	FG04322.1	NCU06857.1
concat92	AN9398.1	52.m04024	AO070274000018	FG05229.1	NCU08323.1
concat92	AN1084.1	70.m15158	AO070285000084	FG07182.1	NCU03737.1
concat92	AN7350.1	72.m19727	AO070278000050	FG02575.1	NCU00457.1
concat92	AN4725.1	71.m15494	AO070323000059	FG09685.1	NCU06368.1
concat92	AN1284.1	70.m14923	AO070332000035	FG02764.1	NCU02044.1
concat92	AN1092.1	70.m15139	AO070285000055	FG06147.1	NCU01256.1
concat93	AN0581.1	69.m15267	AO070280000003	FG03080.1	NCU00755.1
concat93	AN6277.1	72.m19363	AO070304000003	FG07564.1	NCU06519.1
concat93	AN2963.1	59.m09052	AO070337000166	FG01910.1	NCU01323.1
concat93	AN2126.1	69.m15671	AO070306000108	FG08621.1	NCU03911.1
concat93	AN3635.1	58.m07466	AO070328000079	FG11596.1	NCU04412.1
concat93	AN9172.1	56.m02468	AO070317000027	FG04232.1	NCU08228.1
concat93	AN4405.1	58.m07921	AO070261000048	FG10374.1	NCU08927.1
concat93	AN5353.1	69.m15760	AO070302000060	FG03674.1	NCU07948.1
concat93	AN5713.1	54.m06828	AO070324000145	FG06306.1	NCU09700.1
concat93	AN2244.1	71.m15878	AO070326000129	FG05139.1	NCU01183.1
concat93	AN2298.1	71.m15947	AO070295000079	FG05561.1	NCU09006.1
concat93	AN2247.1	71.m15881	AO070326000126	FG05136.1	NCU01186.1
concat93	AN5144.1	54.m06876	AO070291000029	FG01445.1	NCU01728.1
concat93	AN0128.1	71.m16053	AO070311000082	FG04298.1	NCU05392.1
concat93	AN1535.1	55.m03053	AO070334000255	FG00514.1	NCU03054.1
concat93	AN0416.1	54.m06658	AO070338000264	FG00714.1	NCU00899.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat93	AN8169.1	53.m03812	AO070266000003	FG07410.1	NCU03768.1
concat93	AN4819.1	59.m09156	AO070327000168	FG10043.1	NCU04264.1
concat93	AN1093.1	70.m15138	AO070285000054	FG07453.1	NCU01255.1
concat93	AN1444.1	55.m02947	AO070302000001	FG00393.1	NCU00969.1
concat94	AN6577.1	62.m03163	AO070326000023	FG02594.1	NCU00136.1
concat94	AN4386.1	58.m08970	AO070261000031	FG09938.1	NCU04259.1
concat94	AN3719.1	69.m15727	AO070341000350	FG06385.1	NCU02393.1
concat94	AN5107.1	54.m06915	AO070291000072	FG01533.1	NCU01646.1
concat94	AN4486.1	57.m05645	AO070311000037	FG00719.1	NCU02094.1
concat94	AN7230.1	72.m20024	AO070290000040	FG09085.1	NCU00206.1
concat94	AN3795.1	57.m05687	AO070337000232	FG00941.1	NCU02114.1
concat94	AN5599.1	58.m07523	AO070328000005	FG08766.1	NCU05985.1
concat94	AN2154.1	72.m20002	AO070343000203	FG05066.1	NCU08045.1
concat94	AN7418.1	57.m05460	AO070323000154	FG09110.1	NCU05188.1
concat94	AN1229.1	70.m14990	AO070331000241	FG01020.1	NCU02706.1
concat94	AN1066.1	70.m15166	AO070218000011	FG00663.1	NCU02623.1
concat94	AN7287.1	72.m19777	AO070297000028	FG06566.1	NCU08561.1
concat94	AN0067.1	71.m15344	AO070314000157	FG05409.1	NCU07887.1
concat94	AN9004.1	70.m15707	AO070330000107	FG11565.1	NCU05888.1
concat94	AN2056.1	58.m07644	AO070292000026	FG06749.1	NCU06200.1
concat94	AN2332.1	71.m15534	AO070323000014	FG05610.1	NCU00959.1
concat94	AN0446.1	54.m06638	AO070338000308	FG00846.1	NCU01777.1
concat94	AN0034.1	71.m16043	AO070314000113	FG07017.1	NCU03779.1
concat94	AN6494.1	62.m03081	AO070222000007	FG02610.1	NCU00118.1
concat95	AN5997.1	72.m19143	AO070340000279	FG00395.1	NCU00971.1
concat95	AN1025.1	70.m15210	AO070312000120	FG06193.1	NCU07688.1
concat95	AN0814.1	70.m15414	AO070288000089	FG00660.1	NCU02616.1
concat95	AN0381.1	54.m06365	AO070318000065	FG05778.1	NCU02207.1
concat95	AN5569.1	58.m07493	AO070328000037	FG04308.1	NCU05423.1
concat95	AN4751.1	59.m09234	AO070327000068	FG08849.1	NCU02169.1
concat95	AN3824.1	57.m05656	AO070311000023	FG01104.1	NCU05095.1
concat95	AN6313.1	72.m19320	AO070308000069	FG06759.1	NCU07558.1
concat95	AN7443.1	57.m05901	AO070229000015	FG00583.1	NCU09253.1
concat95	AN1068.1	70.m15144	AO070285000068	FG07305.1	NCU08984.1
concat95	AN4861.1	59.m09110	AO070329000146	FG00902.1	NCU02563.1
concat95	AN2737.1	54.m06678	AO070338000219	FG00547.1	NCU09317.1
concat95	AN0929.1	70.m15537	AO070320000117	FG09539.1	NCU03176.1
concat95	AN7729.1	71.m15765	AO070325000156	FG05571.1	NCU09012.1
concat95	AN1409.1	55.m02916	AO070242000012	FG09321.1	NCU02571.1
concat95	AN2247.1	71.m15881	AO070326000126	FG05136.1	NCU01186.1
concat95	AN2896.1	59.m08746	AO070338000112	FG06084.1	NCU09058.1
concat95	AN7750.1	71.m15776	AO070325000175	FG06212.1	NCU06389.1
concat95	AN2743.1	54.m06688	AO070338000228	FG07237.1	NCU00040.1
concat95	AN0574.1	69.m15771	AO070272000053	FG01469.1	NCU03332.1
concat96	AN4983.1	59.m08885	AO070288000051	FG05987.1	NCU01845.1
concat96	AN2064.1	52.m03876	AO070323000172	FG10617.1	NCU05000.1
concat96	AN4775.1	59.m09208	AO070329000077	FG09432.1	NCU02650.1
concat96	AN0426.1	54.m06650	AO070338000276	FG01526.1	NCU08382.1
concat96	AN0141.1	71.m15424	AO070321000108	FG10860.1	NCU06780.1
concat96	AN1230.1	70.m14989	AO070331000242	FG01019.1	NCU02705.1
concat96	AN6870.1	71.m15261	AO070314000052	FG02207.1	NCU04672.1
concat96	AN7498.1	57.m05843	AO070287000016	FG09773.1	NCU05252.1
concat96	AN3690.1	69.m15716	AO070341000315	FG09849.1	NCU02423.1
concat96	AN3033.1	59.m08985	AO070337000074	FG06339.1	NCU02232.1
concat96	AN3628.1	58.m07473	AO070328000066	FG02774.1	NCU07936.1
concat96	AN1602.1	55.m03185	AO070339000250	FG06397.1	NCU08760.1
concat96	AN4998.1	59.m09453	AO070255000029	FG00355.1	NCU06122.1
concat96	AN4174.1	69.m14956	AO070341000088	FG09482.1	NCU04815.1
concat96	AN0504.1	69.m15297	AO070226000008	FG01464.1	NCU03436.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat96	AN8979.1	66.m04668	AO070295000065	FG10855.1	NCU01754.1
concat96	AN8054.1	53.m03889	AO070322000146	FG07282.1	NCU06440.1
concat96	AN0914.1	70.m15523	AO070320000095	FG05162.1	NCU03495.1
concat96	AN1182.1	70.m15763	AO070331000182	FG09530.1	NCU04054.1
concat96	AN4440.1	58.m07885	AO070273000014	FG01670.1	NCU03334.1
concat97	AN1751.1	69.m15052	AO070324000042	FG09300.1	NCU04040.1
concat97	AN0880.1	70.m15483	AO070320000040	FG05109.1	NCU07662.1
concat97	AN6244.1	72.m19413	AO070304000098	FG10879.1	NCU01806.1
concat97	AN4168.1	69.m14950	AO070341000095	FG09497.1	NCU03888.1
concat97	AN1797.1	72.m19549	AO070309000134	FG02641.1	NCU04963.1
concat97	AN3634.1	58.m07467	AO070328000078	FG00598.1	NCU04411.1
concat97	AN4732.1	71.m15501	AO070323000052	FG09734.1	NCU05228.1
concat97	AN3033.1	59.m08985	AO070337000074	FG06339.1	NCU02232.1
concat97	AN1857.1	58.m07651	AO070292000034	FG04829.1	NCU09183.1
concat97	AN1478.1	55.m02985	AO070334000161	FG01210.1	NCU02685.1
concat97	AN4762.1	59.m09221	AO070327000054	FG08530.1	NCU02016.1
concat97	AN4016.1	54.m06578	AO070328000142	FG01956.1	NCU05275.1
concat97	AN4034.1	54.m06562	AO070328000126	FG07087.1	NCU09248.1
concat97	AN8990.1	56.m02476	AO070272000025	FG06473.1	NCU05776.1
concat97	AN5154.1	54.m06864	AO070291000014	FG01632.1	NCU05375.1
concat97	AN7431.1	57.m05913	AO070229000002	FG09892.1	NCU06718.1
concat97	AN4616.1	57.m05533	AO070267000033	FG08644.1	NCU00692.1
concat97	AN8010.1	53.m03857	AO070322000057	FG06822.1	NCU06687.1
concat97	AN6687.1	65.m07501	AO070339000094	FG02518.1	NCU00133.1
concat97	AN5338.1	69.m15570	AO070333000229	FG06539.1	NCU07332.1
concat98	AN1146.1	70.m15385	AO070316000058	FG01883.1	NCU06699.1
concat98	AN6265.1	72.m19392	AO070304000023	FG04404.1	NCU01502.1
concat98	AN5773.1	69.m15638	AO070249000017	FG07413.1	NCU03652.1
concat98	AN1968.1	58.m08921	AO070301000052	FG00629.1	NCU03362.1
concat98	AN8089.1	66.m04728	AO070332000054	FG10823.1	NCU07740.1
concat98	AN3083.1	52.m03887	AO070339000016	FG07661.1	NCU01123.1
concat98	AN1720.1	58.m08961	AO070305000035	FG01495.1	NCU08365.1
concat98	AN2946.1	59.m09093	AO070337000196	FG05621.1	NCU02515.1
concat98	AN9157.1	57.m05493	AO070286000083	FG02555.1	NCU07926.1
concat98	AN1022.1	70.m15780	AO070343000592	FG05070.1	NCU05202.1
concat98	AN0067.1	71.m15344	AO070314000157	FG05409.1	NCU07887.1
concat98	AN4177.1	56.m02500	AO070319000001	FG02822.1	NCU00884.1
concat98	AN5376.1	69.m15731	AO070333000163	FG02819.1	NCU09656.1
concat98	AN9403.1	52.m04030	AO070274000014	FG02782.1	NCU03004.1
concat98	AN4504.1	57.m05627	AO070311000057	FG00294.1	NCU03215.1
concat98	AN4541.1	70.m15825	AO070321000164	FG01875.1	NCU03708.1
concat98	AN5496.1	69.m15723	AO070341000389	FG00923.1	NCU08348.1
concat98	AN6653.1	62.m03255	AO070269000013	FG08700.1	NCU10007.1
concat98	AN5972.1	72.m19188	AO070340000330	FG05844.1	NCU07319.1
concat98	AN6726.1	65.m07244	AO070339000170	FG04410.1	NCU06764.1
concat99	AN3785.1	57.m05971	AO070337000246	FG00667.1	NCU08357.1
concat99	AN8214.1	53.m03759	AO070310000098	FG07374.1	NCU04654.1
concat99	AN1720.1	58.m08961	AO070305000035	FG01495.1	NCU08365.1
concat99	AN5596.1	58.m07520	AO070328000008	FG09490.1	NCU05990.1
concat99	AN2976.1	59.m09037	AO070337000145	FG01229.1	NCU07466.1
concat99	AN3613.1	52.m03647	AO070315000027	FG10999.1	NCU02855.1
concat99	AN5646.1	58.m07559	AO070301000034	FG09503.1	NCU04796.1
concat99	AN1421.1	55.m02935	AO070232000017	FG08388.1	NCU05602.1
concat99	AN4633.1	57.m05544	AO070340000373	FG09220.1	NCU00527.1
concat99	AN5114.1	54.m06909	AO070291000065	FG00834.1	NCU09608.1
concat99	AN0126.1	71.m15408	AO070311000085	FG09728.1	NCU08309.1
concat99	AN0868.1	70.m15459	AO070320000019	FG08585.1	NCU00580.1
concat99	AN1512.1	55.m03031	AO070334000233	FG00905.1	NCU02565.1
concat99	AN4501.1	57.m05629	AO070311000054	FG06847.1	NCU02806.1

ID	A. nidulans	A. fumigatus	A. oryzae	F. graminearum	N. crassa
concat99	AN3624.1	58.m07411	AO070342000127	FG01501.1	NCU08341.1
concat99	AN1915.1	69.m14931	AO070341000128	FG08760.1	NCU04817.1
concat99	AN3827.1	58.m07803	AO070305000064	FG00695.1	NCU00925.1
concat99	AN4369.1	58.m07958	AO070261000009	FG10889.1	NCU09758.1
concat99	AN8691.1	62.m03474	AO070315000112	FG08642.1	NCU00690.1
concat99	AN6214.1	72.m19992	AO070308000078	FG07254.1	NCU06472.1
concat100	AN6345.1	72.m19510	AO070275000008	FG02055.1	NCU04580.1
concat100	AN5336.1	69.m15573	AO070333000217	FG04235.1	NCU07590.1
concat100	AN1364.1	70.m14865	AO070215000017	FG01540.1	NCU06751.1
concat100	AN1151.1	69.m15307	AO070226000022	FG09485.1	NCU04071.1
concat100	AN0664.1	70.m15267	AO070343000556	FG05898.1	NCU01266.1
concat100	AN8421.1	52.m03816	AO070302000061	FG07016.1	NCU04262.1
concat100	AN3661.1	58.m07437	AO070342000024	FG08751.1	NCU03925.1
concat100	AN1768.1	69.m15068	AO070324000027	FG08615.1	NCU04724.1
concat100	AN5101.1	54.m06961	AO070291000078	FG00028.1	NCU07200.1
concat100	AN2089.1	57.m05789	AO070341000245	FG01055.1	NCU09237.1
concat100	AN3613.1	52.m03647	AO070315000027	FG10999.1	NCU02855.1
concat100	AN4030.1	54.m06559	AO070328000122	FG00800.1	NCU02896.1
concat100	AN4491.1	57.m05640	AO070311000043	FG09360.1	NCU02942.1
concat100	AN9465.1	70.m14852	AO070215000004	FG01154.1	NCU02744.1
concat100	AN3432.1	59.m09292	AO070265000009	FG06059.1	NCU09705.1
concat100	AN3583.1	58.m07381	AO070342000166	FG09156.1	NCU03219.1
concat100	AN5517.1	69.m15442	AO070341000376	FG02237.1	NCU05939.1
concat100	AN4216.1	54.m06773	AO070231000008	FG02096.1	NCU01218.1
concat100	AN0048.1	71.m15322	AO070314000127	FG02735.1	NCU09511.1
concat100	AN1526.1	55.m03269	AO070334000244	FG05601.1	NCU00966.1

num	treenum	MPtree	MP bootstrap	MLtree	ML bootstrap
1	concat1	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):98.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	98	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):96.0):100.0,NCUcat:100.0);	96
3	concat3	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
4	concat4	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
5	concat5	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):97.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	97	(FGcat:100.0,(ANcat:100.0,(AOcat:100.0,AFcat:100.0):91.0):100.0,NCUcat:100.0);	91
6	concat6	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):99.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	99	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
7	concat7	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
8	concat8	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
12	concat12	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):97.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	97	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):92.0):100.0,NCUcat:100.0);	92
13	concat13	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
14	concat14	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
15	concat15	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
16	concat16	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
18	concat18	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
19	concat19	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
22	concat22	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
23	concat23	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):93.0):100.0,NCUcat:100.0);	93
24	concat24	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
25	concat25	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
27	concat27	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
30	concat30	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):99.0):100.0,NCUcat:100.0);	99
31	concat31	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
32	concat32	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
33	concat33	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
34	concat34	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
35	concat35	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
36	concat36	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
37	concat37	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):98.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	98	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
39	concat39	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):99.5,ANcat:100.0):100.0):100.0,NCUcat:100.0);	99.5	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
40	concat40	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
41	concat41	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):91.0):100.0,NCUcat:100.0);	91
42	concat42	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
43	concat43	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
44	concat44	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):99.0):100.0,NCUcat:100.0);	99
45	concat45	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):97.0,ANcat:100.0):100.0,NCUcat:100.0);	97
46	concat46	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
47	concat47	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
49	concat49	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):99.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	99	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):92.0):100.0,NCUcat:100.0);	92
50	concat50	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
51	concat51	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):98.0):100.0,NCUcat:100.0);	98
52	concat52	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
54	concat54	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
57	concat57	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
58	concat58	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
60	concat60	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
63	concat63	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
64	concat64	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
65	concat65	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
66	concat66	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AOcat:100.0,AFcat:100.0):97.0):100.0,NCUcat:100.0);	97

num	treenum	MPtree	MP bootstrap	MLtree	ML bootstrap
67	concat67	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):95.0):100.0,NCUcat:100.0);	95
69	concat69	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
70	concat70	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
71	concat71	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):85.0):100.0,NCUcat:100.0);	85
73	concat73	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):98.0):100.0,NCUcat:100.0);	98
74	concat74	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
75	concat75	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
76	concat76	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):62.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	62	(FGcat:100.0,((ANcat:100.0,AOcat:100.0):82.0,AFcat:100.0):100.0,NCUcat:100.0);	82
77	concat77	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):95.0):100.0,NCUcat:100.0);	95
78	concat78	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
80	concat80	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
81	concat81	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
83	concat83	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):84.0):100.0,NCUcat:100.0);	84
84	concat84	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
85	concat85	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
86	concat86	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):61.0,ANcat:100.0):100.0,NCUcat:100.0);	61
87	concat87	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):97.0,ANcat:100.0):100.0,NCUcat:100.0);	97
91	concat91	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
92	concat92	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
93	concat93	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
94	concat94	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):95.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	95	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):80.0):100.0,NCUcat:100.0);	80
95	concat95	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
96	concat96	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
97	concat97	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
98	concat98	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
99	concat99	((FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):100.0):100.0):100.0,NCUcat:100.0);	100	(FGcat:100.0,((AFcat:100.0,AOcat:100.0):100.0,ANcat:100.0):100.0,NCUcat:100.0);	100
100	concat100	((FGcat:100.0,((AOcat:100.0,AFcat:100.0):97.0,ANcat:100.0):100.0):100.0,NCUcat:100.0);	97	(FGcat:100.0,(ANcat:100.0,(AFcat:100.0,AOcat:100.0):86.0):100.0,NCUcat:100.0);	86
					97.44
					6.23
					0.16

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1	70.m15774	AN1099.1	AO070285000041	FG04118.1	ANAO	yes	yes	((FG04118.1:100.0,(70.m15774:100.0,(AN1099.1:100.0,AO07028500:100.0):97.0):100.0):100.0,
2	71.m16031	AN6886.1	AO070314000039	FG05524.1	AFAO		yes	((FG05524.1:100.0,((AO07031400:100.0,71.m16031:100.0):77.5,AN6886.1:100.0):100.0):100.0,
3	69.m15203	AN2464.1	AO070264000006	FG05525.1	AFAN		yes	((FG05525.1:100.0,(AO07026400:100.0,(AN2464.1:100.0,69.m15203:100.0):76.0):100.0):100.0,
4	57.m05611	AN4517.1	AO070321000123	FG05527.1	AFAO			((FG05527.1:100.0,((AO07032100:100.0,57.m05611:100.0):55.5,AN4517.1:100.0):100.0):100.0,
5	72.m19795	AN7254.1	AO070297000010	FG05530.1	AFAO			((FG05530.1:100.0,((72.m19795:100.0,AO07029700:100.0):62.5,AN7254.1:100.0):100.0):100.0,
6	59.m08698	AN2854.1	AO070338000167	FG05388.1	AFAN		yes	((FG05388.1:100.0,(AO07033800:100.0,(AN2854.1:100.0,59.m08698:100.0):84.0):100.0):100.0,
7	59.m08812	AN4908.1	AO070338000038	FG05387.1	AFAO	yes	yes	((FG05387.1:100.0,((59.m08812:100.0,AO07033800:100.0):91.5,AN4908.1:100.0):100.0):100.0,
8	59.m08810	AN4906.1	AO070338000039	FG05385.1	AFAO		yes	((FG05385.1:100.0,((AO07033800:100.0,59.m08810:100.0):76.5,AN4906.1:100.0):100.0):100.0,
9	54.m07042	AN4209.1	AO070231000015	FG05384.1	ANAO			((FG05384.1:100.0,(54.m07042:100.0,(AN4209.1:100.0,AO07023100:100.0):68.5):100.0):100.0,
10	52.m04077	AN8406.1	AO070302000057	FG04703.1	ANAO		yes	(((52.m04077:100.0,(AN8406.1:100.0,AO07030200:100.0):75.0):96.0,FG04703.1:100.0):100.0,
11	72.m19037	AN6122.1	AO070340000075	FG06685.1	AFAO			((FG06685.1:100.0,((72.m19037:100.0,AO07034000:100.0):55.5,AN6122.1:100.0):100.0):100.0,
12	72.m19038	AN2185.1	AO070340000081	FG06686.1	AFAO	yes	yes	((FG06686.1:100.0,((AO07034000:100.0,72.m19038:100.0):98.0,AN2185.1:100.0):100.0):100.0,
13	72.m19009	AN6162.1	AO070340000046	FG06689.1	AFAN			((FG06689.1:100.0,(AO07034000:100.0,(AN6162.1:100.0,72.m19009:100.0):65.5):100.0):100.0,
14	72.m19006	AN6159.1	AO070340000043	FG06688.1	AFAO	yes	yes	((FG06688.1:100.0,((AO07034000:100.0,72.m19006:100.0):98.5,AN6159.1:100.0):100.0):100.0,
15	72.m19007	AN6160.1	AO070340000044	FG06687.1	ANAO		yes	((FG06687.1:100.0,(72.m19007:100.0,(AN6160.1:100.0,AO07034000:100.0):78.5):100.0):100.0,
16	54.m06683	AN2748.1	AO070338000223	FG06684.1	ANAO			((FG06684.1:100.0,((AO07033800:100.0,AN2748.1:100.0):73.0,54.m06683:100.0):100.0):100.0,
17	54.m06688	AN2743.1	AO070338000228	FG07237.1	ANAO			((FG07237.1:100.0,(54.m06688:100.0,(AN2743.1:100.0,AO07033800:100.0):66.5):100.0):100.0,
18	54.m06957	AN2741.1	AO070338000230	FG07234.1	ANAO		yes	((((AN2741.1:100.0,AO07033800:100.0):78.0,54.m06957:100.0):89.5,FG07234.1:100.0):100.0,
19	54.m06664	AN0410.1	AO070294000082	FG07233.1	AFAO			(((AN0410.1:100.0,(AO07029400:100.0,54.m06664:100.0):46.5):72.0,FG07233.1:100.0):100.0,
20	65.m07305	AN6675.1	AO070289000014	FG07232.1	AFAN			((FG07232.1:100.0,((65.m07305:100.0,AN6675.1:100.0):41.0,AO07028900:100.0):100.0):100.0,
21	54.m07007	AN0409.1	AO070338000252	FG07231.1	ANAO			((FG07231.1:100.0,(54.m07007:100.0,(AN0409.1:100.0,AO07033800:100.0):63.2):100.0):100.0,
22	54.m06704	AN3895.1	AO070342000047	FG03666.1	AFAO	yes	yes	((FG03666.1:100.0,((AO07034200:100.0,54.m06704:100.0):98.5,AN3895.1:100.0):100.0):100.0,
23	57.m05949	AN7489.1	AO070287000051	FG07226.1	AFAO			((FG07226.1:100.0,((AO07028700:100.0,57.m05949:100.0):48.0,AN7489.1:100.0):100.0):100.0,
24	71.m15900	AN2259.1	AO070326000104	FG06660.1	AFAO	yes	yes	((FG06660.1:100.0,((AO07032600:100.0,71.m15900:100.0):98.0,AN2259.1:100.0):100.0):100.0,
25	71.m15899	AN2258.1	AO070326000105	FG06661.1	AFAO		yes	((FG06661.1:100.0,((AO07032600:100.0,71.m15899:100.0):86.5,AN2258.1:100.0):100.0):100.0,
26	70.m15605	AN0956.1	AO070320000158	FG07217.1	AFAO		yes	((FG07217.1:100.0,((AO07032000:100.0,70.m15605:100.0):86.0,AN0956.1:100.0):100.0):100.0,
27	54.m06486	AN9448.1	AO070334000061	FG07212.1	AFAO	yes	yes	((FG07212.1:100.0,((54.m06486:100.0,AO07033400:100.0):91.5,AN9448.1:100.0):100.0):100.0,
28	57.m05571	AN4559.1	AO070321000169	FG06723.1	AFAO			((FG06723.1:100.0,((AO07032100:100.0,57.m05571:100.0):51.3,AN4559.1:100.0):100.0):100.0,
29	57.m05564	AN4553.1	AO070321000177	FG06720.1	AFAO			(((AN4553.1:100.0,(57.m05564:100.0,AO07032100:100.0):73.3):93.8,FG06720.1:100.0):100.0,
30	57.m05568	AN4556.1	AO070321000172	FG06717.1	AFAN			((FG06717.1:100.0,(AO07032100:100.0,(AN4556.1:100.0,57.m05568:100.0):46.8):100.0):100.0,
31	54.m06705	AN4062.1	AO070342000050	FG06715.1	AFAO			((FG06715.1:100.0,((54.m06705:100.0,AO07034200:100.0):73.0,AN4062.1:100.0):100.0):100.0,
32	59.m09047	AN2970.1	AO070337000156	FG06718.1	AFAN			((FG06718.1:100.0,(AO07033700:100.0,(AN2970.1:100.0,59.m09047:100.0):57.8):100.0):100.0,
33	57.m05587	AN4534.1	AO070321000148	FG06972.1	AFAO	yes	yes	((FG06972.1:100.0,((AO07032100:100.0,57.m05587:100.0):98.0,AN4534.1:100.0):100.0):100.0,
34	71.m15970	AN8838.1	AO070271000039	FG06948.1	ANAO			((FG06948.1:100.0,((AO07027100:100.0,AN8838.1:100.0):53.5,71.m15970:100.0):100.0):100.0,
35	71.m16107	AN2240.1	AO070326000134	FG05478.1	AFAO			((FG05478.1:100.0,((AO07032600:100.0,71.m16107:100.0):61.5,AN2240.1:100.0):100.0):100.0,
36	70.m15469	AN0860.1	AO070320000008	FG05481.1	AFAO		yes	((FG05481.1:100.0,((70.m15469:100.0,AO07032000:100.0):79.0,AN0860.1:100.0):100.0):100.0,
37	72.m19790	AN8491.1	AO070297000017	FG06962.1			yes	((((72.m19790:100.0,AO07029700:100.0):100.0,FG06962.1:100.0):85.8,AN8491.1:100.0):100.0,
38	72.m18945	AN5817.1	AO070260000030	FG06961.1	AFAO			((FG06961.1:100.0,((72.m18945:100.0,AO07026000:100.0):73.5,AN5817.1:100.0):100.0):100.0,
39	72.m18944	AN5815.1	AO070260000032	FG06959.1	ANAO			((FG06959.1:100.0,(72.m18944:100.0,(AN5815.1:100.0,AO07026000:100.0):50.5):100.0):100.0,
40	72.m18943	AN5814.1	AO070260000033	FG06963.1	AFAO		yes	((FG06963.1:100.0,((AO07026000:100.0,72.m18943:100.0):83.5,AN5814.1:100.0):100.0):100.0,
41	71.m15755	AN7731.1	AO070325000145	FG02604.1	AFAO			((FG02604.1:100.0,((AO07032500:100.0,71.m15755:100.0):63.0,AN7731.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
42	62.m03078	AN6492.1	AO070222000005	FG02608.1	AFAO			((FG02608.1:100.0,((62.m03078:100.0,AO07022200:100.0):65.0,AN6492.1:100.0):100.0):100.0,
43	62.m03441	AN6493.1	AO070222000006	FG02609.1	AFAN			((FG02609.1:100.0,(AO07022200:100.0,(AN6493.1:100.0,62.m03441:100.0):67.0):100.0):100.0,
44	62.m03081	AN6494.1	AO070222000007	FG02610.1	ANAO			((FG02610.1:100.0,(62.m03081:100.0,(AN6494.1:100.0,AO07022200:100.0):43.5):100.0):100.0,
45	69.m15476	AN5456.1	AO070341000410	FG06694.1	AFAO		yes	((FG06694.1:100.0,((AO07034100:100.0,69.m15476:100.0):81.5,AN5456.1:100.0):100.0):100.0,
46	72.m19051	AN6107.1	AO070340000100	FG05555.1	AFAO		yes	((FG05555.1:100.0,((AO07034000:100.0,72.m19051:100.0):78.5,AN6107.1:100.0):100.0):100.0,
47	59.m09423	AN2966.1	AO070337000161	FG06655.1	AFAO		yes	((FG06655.1:100.0,((AO07033700:100.0,59.m09423:100.0):84.0,AN2966.1:100.0):100.0):100.0,
48	54.m07043	AN4201.1	AO070231000023	FG07277.1	ANAO			((FG07277.1:100.0,((AO07023100:100.0,AN4201.1:100.0):69.0,54.m07043:100.0):100.0):100.0,
49	55.m03198	AN9183.1	AO070315000076	FG01685.1				((AO07031500:100.0,((55.m03198:100.0,AN9183.1:100.0):69.5,FG01685.1:100.0):91.0):100.0,
50	70.m15412	AN0812.1	AO070288000092	FG07274.1	ANAO			((FG07274.1:100.0,((AO07028800:100.0,AN0812.1:100.0):49.0,70.m15412:100.0):100.0):100.0,
51	65.m07501	AN6687.1	AO070339000094	FG02518.1	AFAN			((FG02518.1:100.0,(AO07033900:100.0,(AN6687.1:100.0,65.m07501:100.0):64.5):100.0):100.0,
52	71.m15583	AN8787.1	AO070276000074	FG06659.1	AFAO	yes	yes	((FG06659.1:100.0,((AO07027600:100.0,71.m15583:100.0):97.5,AN8787.1:100.0):100.0):100.0,
53	62.m03163	AN6577.1	AO070326000023	FG02594.1	AFAO	yes	yes	((FG02594.1:100.0,((AO07032600:100.0,62.m03163:100.0):98.0,AN6577.1:100.0):100.0):100.0,
54	71.m15770	AN7742.1	AO070325000166	FG07269.1	AFAO	yes	yes	((((AO07032500:100.0,71.m15770:100.0):100.0,AN7742.1:100.0):99.5,FG07269.1:100.0):100.0,
55	62.m03164	AN9527.1	AO070326000022	FG02600.1	AFAO			((FG02600.1:100.0,(AN9527.1:100.0,(62.m03164:100.0,AO07032600:100.0):62.2):93.7):100.0,
56	62.m03120	AN6532.1	AO070270000032	FG02599.1	AFAO			((FG02599.1:100.0,((AO07027000:100.0,62.m03120:100.0):65.0,AN6532.1:100.0):100.0):100.0,
57	71.m15941	AN2293.1	AO070295000072	FG07313.1	AFAO		yes	((FG07313.1:100.0,((AO07029500:100.0,71.m15941:100.0):86.0,AN2293.1:100.0):100.0):100.0,
58	70.m15393	AN5307.1	AO070316000053	FG07263.1	AFAO		yes	((FG07263.1:100.0,((AO07031600:100.0,70.m15393:100.0):79.0,AN5307.1:100.0):100.0):100.0,
59	55.m02999	AN1491.1	AO070334000203	FG02532.1	AFAO		yes	((FG02532.1:100.0,((55.m02999:100.0,AO07033400:100.0):86.8,AN1491.1:100.0):100.0):100.0,
60	70.m15650	AN0632.1	AO070318000122	FG02533.1	ANAO			((FG02533.1:100.0,((AO07031800:100.0,AN0632.1:100.0):40.0,70.m15650:100.0):100.0):100.0,
61	70.m15651	AN0631.1	AO070318000121	FG02534.1	AFAO		yes	((FG02534.1:100.0,((AO07031800:100.0,70.m15651:100.0):88.0,AN0631.1:100.0):100.0):100.0,
62	65.m07382	AN3751.1	AO070309000071	FG05442.1	AFAO	yes	yes	((FG05442.1:100.0,(AN3751.1:100.0,(65.m07382:100.0,AO07030900:100.0):100.0):100.0):100.0,
63	72.m19765	AN7302.1	AO070297000048	FG02529.1	AFAO			((FG02529.1:100.0,((AO07029700:100.0,72.m19765:100.0):56.0,AN7302.1:100.0):100.0):100.0,
64	72.m19764	AN7301.1	AO070297000049	FG02528.1	AFAO	yes	yes	((FG02528.1:100.0,(AN7301.1:100.0,(72.m19764:100.0,AO07029700:100.0):100.0):100.0):100.0,
65	72.m20021	AN7303.1	AO070297000050	FG02527.1	AFAO	yes	yes	((FG02527.1:100.0,((AO07029700:100.0,72.m20021:100.0):97.5,AN7303.1:100.0):100.0):100.0,
66	72.m19025	AN6139.1	AO070340000063	FG06642.1	AFAO			((FG06642.1:100.0,((AO07034000:100.0,72.m19025:100.0):56.3,AN6139.1:100.0):100.0):100.0,
67	70.m15804	AN0834.1	AO070255000011	FG06644.1	AFAO			((FG06644.1:100.0,((70.m15804:100.0,AO07025500:100.0):57.5,AN0834.1:100.0):100.0):100.0,
68	54.m06754	AN4192.1	AO070342000112	FG06678.1	AFAN			((FG06678.1:100.0,(AO07034200:100.0,(AN4192.1:100.0,54.m06754:100.0):58.8):100.0):100.0,
69	54.m06475	AN0268.1	AO070334000074	FG06680.1	ANAO		yes	((FG06680.1:100.0,(54.m06475:100.0,(AN0268.1:100.0,AO07033400:100.0):86.5):100.0):100.0,
70	71.m15582	AN8782.1	AO070289000007	FG06681.1	AFAO			((FG06681.1:100.0,((AO07028900:100.0,71.m15582:100.0):49.0,AN8782.1:100.0):100.0):100.0,
71	62.m03133	AN6541.1	AO070270000044	FG02506.1	AFAO			((FG02506.1:100.0,((AO07027000:100.0,62.m03133:100.0):71.0,AN6541.1:100.0):100.0):100.0,
72	59.m09383	AN2499.1	AO070312000049	FG05531.1	AFAN			((FG05531.1:100.0,(AO07031200:100.0,(AN2499.1:100.0,59.m09383:100.0):52.0):100.0):100.0,
73	71.m16019	AN6894.1	AO070314000028	FG05403.1	AFAN			((FG05403.1:100.0,(AO07031400:100.0,(AN6894.1:100.0,71.m16019:100.0):58.5):100.0):100.0,
74	72.m19117	AN6041.1	AO070340000241	FG05405.1	AFAN	yes	yes	((FG05405.1:100.0,((AN6041.1:100.0,72.m19117:100.0):100.0,AO07034000:100.0):100.0):100.0,
75	57.m05678	AN3805.1	AO070337000222	FG11137.1	AFAO			(((AN3805.1:100.0,(AO07033700:100.0,57.m05678:100.0):69.5):99.0,FG11137.1:100.0):100.0,
76	58.m07722	AN1632.1	AO070299000042	FG05547.1	AFAO	yes	yes	((FG05547.1:100.0,(AN1632.1:100.0,(58.m07722:100.0,AO07029900:100.0):100.0):100.0):100.0,
77	58.m07714	AN1811.1	AO070299000060	FG05545.1	AFAN		yes	((FG05545.1:100.0,(AO07029900:100.0,(AN1811.1:100.0,58.m07714:100.0):88.5):100.0):100.0,
78	58.m07713	AN1810.1	AO070299000061	FG05546.1	AFAO	yes	yes	((FG05546.1:100.0,((AO07029900:100.0,58.m07713:100.0):95.0,AN1810.1:100.0):100.0):100.0,
79	71.m16112	AN2282.1	AO070295000059	FG04217.1	AFAO			((FG04217.1:100.0,((AO07029500:100.0,71.m16112:100.0):66.0,AN2282.1:100.0):100.0):100.0,
80	57.m05407	AN7649.1	AO070268000005	FG05543.1	AFAN			((FG05543.1:100.0,(AO07026800:100.0,(AN7649.1:100.0,57.m05407:100.0):74.3):100.0):100.0,
81	72.m19517	AN6341.1	AO070298000009	FG07311.1	AFAN		yes	((FG07311.1:100.0,(AO07029800:100.0,(AN6341.1:100.0,72.m19517:100.0):89.0):100.0):100.0,
82	71.m15597	AN8783.1	AO070289000008	FG05504.1	ANAO			((FG05504.1:100.0,(71.m15597:100.0,(AN8783.1:100.0,AO07028900:100.0):60.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
83	72.m20024	AN7230.1	AO070290000040	FG09085.1	AFAO		yes	((FG09085.1:100.0,((AO07029000:100.0,72.m20024:100.0):75.5,AN7230.1:100.0):100.0):100.0,
84	72.m19021	AN6143.1	AO070340000060	FG05487.1	AFAO			((FG05487.1:100.0,((72.m19021:100.0,AO07034000:100.0):49.5,AN6143.1:100.0):100.0):100.0,
85	72.m19026	AN6138.1	AO070340000064	FG05492.1	AFAO	yes	yes	((FG05492.1:100.0,((AO07034000:100.0,72.m19026:100.0):94.5,AN6138.1:100.0):100.0):100.0,
86	72.m19495	AN6365.1	AO070340000205	FG05495.1	AFAN	yes	yes	((FG05495.1:100.0,(AO07034000:100.0,(72.m19495:100.0,AN6365.1:100.0):99.0):100.0):100.0,
87	72.m19494	AN6366.1	AO070279000052	FG06947.1	ANAO			((FG06947.1:100.0,(72.m19494:100.0,(AN6366.1:100.0,AO07027900:100.0):70.5):100.0):100.0,
88	70.m15437	AN0837.1	AO070255000006	FG06641.1	AFAO	yes	yes	((FG06641.1:100.0,((AO07025500:100.0,70.m15437:100.0):95.5,AN0837.1:100.0):100.0):100.0,
89	54.m07047	AN4112.1	AO070342000107	FG06666.1	AFAO			((FG06666.1:100.0,((AO07034200:100.0,54.m07047:100.0):42.8,AN4112.1:100.0):100.0):100.0,
90	59.m08799	AN4900.1	AO070338000044	FG06664.1	ANAO			((FG06664.1:100.0,(59.m08799:100.0,(AN4900.1:100.0,AO07033800:100.0):66.0):100.0):100.0,
91	55.m02996	AN1489.1	AO070334000202	FG06669.1	AFAN			((FG06669.1:100.0,(AO07033400:100.0,(AN1489.1:100.0,55.m02996:100.0):56.0):100.0):100.0,
92	70.m15629	AN0988.1	AO070318000150	FG06637.1	AFAN			((FG06637.1:100.0,(AO07031800:100.0,(AN0988.1:100.0,70.m15629:100.0):59.5):100.0):100.0,
93	70.m15597	AN0951.1	AO070320000152	FG06635.1	AFAO	yes	yes	((FG06635.1:100.0,((AO07032000:100.0,70.m15597:100.0):99.0,AN0951.1:100.0):100.0):100.0,
94	70.m15479	AN0876.1	AO070320000035	FG06634.1	AFAO			((FG06634.1:100.0,((70.m15479:100.0,AO07032000:100.0):54.3,AN0876.1:100.0):100.0):100.0,
95	70.m15442	AN0842.1	AO070216000002	FG06631.1	AFAO		yes	((FG06631.1:100.0,((AO07021600:100.0,70.m15442:100.0):83.5,AN0842.1:100.0):100.0):100.0,
96	59.m08708	AN2862.1	AO070338000160	FG06627.1	AFAN			((FG06627.1:100.0,(AO07033800:100.0,(AN2862.1:100.0,59.m08708:100.0):43.3):100.0):100.0,
97	56.m02387	AN1257.1	AO070327000016	FG10282.1				((((FG10282.1:100.0,AN1257.1:100.0):41.0,AO07032700:100.0):36.0,56.m02387:100.0):100.0,
98	59.m08820	AN4917.1	AO070338000026	FG06588.1	AFAO		yes	((FG06588.1:100.0,((AO07033800:100.0,59.m08820:100.0):83.5,AN4917.1:100.0):100.0):100.0,
99	59.m08819	AN4916.1	AO070338000027	FG06587.1	AFAO			((FG06587.1:100.0,((59.m08819:100.0,AO07033800:100.0):70.3,AN4916.1:100.0):100.0):100.0,
100	59.m08704	AN2860.1	AO070338000162	FG06619.1	ANAO			((FG06619.1:100.0,((AO07033800:100.0,AN2860.1:100.0):70.8,59.m08704:100.0):100.0):100.0,
101	71.m15957	AN8825.1	AO070271000056	FG05558.1	AFAO			((FG05558.1:100.0,((AO07027100:100.0,71.m15957:100.0):55.0,AN8825.1:100.0):100.0):100.0,
102	71.m15313	AN0038.1	AO070314000116	FG05519.1	AFAO	yes	yes	((FG05519.1:100.0,((AO07031400:100.0,71.m15313:100.0):95.5,AN0038.1:100.0):100.0):100.0,
103	71.m15315	AN0040.1	AO070314000119	FG05516.1	AFAO	yes	yes	((FG05516.1:100.0,((AO07031400:100.0,71.m15315:100.0):96.0,AN0040.1:100.0):100.0):100.0,
104	58.m08870	AN1934.1	AO070342000199	FG07035.1	AFAO	yes	yes	((FG07035.1:100.0,(AN1934.1:100.0,(58.m08870:100.0,AO07034200:100.0):100.0):100.0):100.0,
105	62.m03202	AN6596.1	AO070326000045	FG05557.1	AFAO	yes	yes	((FG05557.1:100.0,((AO07032600:100.0,62.m03202:100.0):91.0,AN6596.1:100.0):100.0):100.0,
106	69.m15274	AN0568.1	AO070272000047	FG04683.1	AFAO			((FG04683.1:100.0,((AO07027200:100.0,69.m15274:100.0):55.0,AN0568.1:100.0):100.0):100.0,
107	72.m19491	AN6369.1	AO070279000072	FG05589.1	AFAO			((FG05589.1:100.0,((72.m19491:100.0,AO07027900:100.0):68.0,AN6369.1:100.0):100.0):100.0,
108	53.m03770	AN8204.1	AO070310000113	FG05580.1	AFAN			((FG05580.1:100.0,(AO07031000:100.0,(AN8204.1:100.0,53.m03770:100.0):40.5):100.0):100.0,
109	70.m15112	AN1122.1	AO070331000114	FG06924.1	ANAO			((FG06924.1:100.0,((AO07033100:100.0,AN1122.1:100.0):47.5,70.m15112:100.0):100.0):100.0,
110	72.m19736	AN7335.1	AO070297000108	FG05515.1	AFAO	yes	yes	((FG05515.1:100.0,((AO07029700:100.0,72.m19736:100.0):97.0,AN7335.1:100.0):100.0):100.0,
111	58.m08876	AN2591.1	AO070245000015	FG04215.1				((((58.m08876:100.0,AO07024500:100.0):100.0,FG04215.1:100.0):60.5,AN2591.1:100.0):100.0,
112	70.m15257	AN0653.1	AO070343000573	FG05533.1	AFAN	yes	yes	((FG05533.1:100.0,(AO07034300:100.0,(AN0653.1:100.0,70.m15257:100.0):99.0):100.0):100.0,
113	70.m15321	AN0732.1	AO070343000493	FG03725.1	AFAO			((FG03725.1:100.0,((70.m15321:100.0,AO07034300:100.0):58.5,AN0732.1:100.0):100.0):100.0,
114	70.m15660	AN0625.1	AO070280000077	FG06776.1	AFAO			((FG06776.1:100.0,((AO07028000:100.0,70.m15660:100.0):59.0,AN0625.1:100.0):100.0):100.0,
115	54.m06667	AN0407.1	AO070338000247	FG05376.1	AFAO	yes	yes	((FG05376.1:100.0,((AO07033800:100.0,54.m06667:100.0):95.0,AN0407.1:100.0):100.0):100.0,
116	54.m06668	AN0406.1	AO070338000246	FG05377.1	AFAO	yes	yes	((FG05377.1:100.0,((AO07033800:100.0,54.m06668:100.0):92.5,AN0406.1:100.0):100.0):100.0,
117	54.m06525	AN0256.1	AO070334000101	FG05380.1	AFAO			((FG05380.1:100.0,((AO07033400:100.0,54.m06525:100.0):44.0,AN0256.1:100.0):100.0):100.0,
118	72.m19330	AN6304.1	AO070308000059	FG05459.1	ANAO		yes	((FG05459.1:100.0,(72.m19330:100.0,(AN6304.1:100.0,AO07030800:100.0):79.0):100.0):100.0,
119	72.m19325	AN6309.1	AO070308000064	FG05460.1	ANAO			((FG05460.1:100.0,((AO07030800:100.0,AN6309.1:100.0):67.0,72.m19325:100.0):100.0):100.0,
120	58.m07763	AN1688.1	AO070305000008	FG06649.1	ANAO			((FG06649.1:100.0,(58.m07763:100.0,(AN1688.1:100.0,AO07030500:100.0):61.0):100.0):100.0,
121	70.m15648	AN0634.1	AO070318000124	FG05510.1	AFAO		yes	((FG05510.1:100.0,((AO07031800:100.0,70.m15648:100.0):86.3,AN0634.1:100.0):100.0):100.0,
122	72.m19047	AN6111.1	AO070340000094	FG05509.1	AFAO			((FG05509.1:100.0,((AO07034000:100.0,72.m19047:100.0):73.5,AN6111.1:100.0):100.0):100.0,
123	69.m15477	AN5455.1	AO070341000411	FG07262.1	AFAO	yes	yes	((FG07262.1:100.0,(AN5455.1:100.0,(69.m15477:100.0,AO07034100:100.0):100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
124	72.m19789	AN7260.1	AO070297000018	FG05465.1	AFAO	yes	yes	((FG05465.1:100.0,((AO07029700:100.0,72.m19789:100.0):96.5,AN7260.1:100.0):100.0):100.0,
125	62.m03075	AN6487.1	AO070222000002	FG05471.1	ANAO			((FG05471.1:100.0,((AO07022200:100.0,AN6487.1:100.0):59.0,62.m03075:100.0):100.0):100.0,
126	71.m15938	AN2290.1	AO070295000069	FG07310.1	ANAO		yes	((FG07310.1:100.0,(71.m15938:100.0,(AN2290.1:100.0,AO07029500:100.0):85.0):100.0):100.0,
127	72.m19057	AN6068.1	AO070340000109	FG05573.1	AFAO			((FG05573.1:100.0,((AO07034000:100.0,72.m19057:100.0):70.5,AN6068.1:100.0):100.0):100.0,
128	72.m20019	AN7291.1	AO070297000031	FG06745.1	AFAO		yes	((FG06745.1:100.0,((AO07029700:100.0,72.m20019:100.0):85.0,AN7291.1:100.0):100.0):100.0,
129	72.m19046	AN6112.1	AO070340000093	FG06743.1	AFAO		yes	((FG06743.1:100.0,((72.m19046:100.0,AO07034000:100.0):86.0,AN6112.1:100.0):100.0):100.0,
130	52.m03838	AN9339.1	AO070315000069	FG06733.1	AFAO	yes	yes	((FG06733.1:100.0,((AO07031500:100.0,52.m03838:100.0):98.0,AN9339.1:100.0):100.0):100.0,
131	58.m07643	AN2055.1	AO070292000025	FG06736.1	ANAO			((FG06736.1:100.0,(58.m07643:100.0,(AN2055.1:100.0,AO07029200:100.0):52.5):100.0):100.0,
132	58.m08938	AN1854.1	AO070292000029	FG06735.1	AFAN			((FG06735.1:100.0,((58.m08938:100.0,AN1854.1:100.0):44.5,AO07029200:100.0):100.0):100.0,
133	58.m07653	AN1859.1	AO070292000036	FG06737.1	ANAO			((FG06737.1:100.0,((AO07029200:100.0,AN1859.1:100.0):62.5,58.m07653:100.0):100.0):100.0,
134	58.m08924	AN1860.1	AO070292000037	FG06738.1	ANAO		yes	((FG06738.1:100.0,(58.m08924:100.0,(AN1860.1:100.0,AO07029200:100.0):83.5):100.0):100.0,
135	72.m19056	AN6067.1	AO070340000108	FG05425.1	AFAN			((FG05425.1:100.0,(AO07034000:100.0,(AN6067.1:100.0,72.m19056:100.0):63.0):100.0):100.0,
136	72.m19507	AN6348.1	AO070275000017	FG05578.1	AFAO			((FG05578.1:100.0,((AO07027500:100.0,72.m19507:100.0):65.5,AN6348.1:100.0):100.0):100.0,
137	72.m19506	AN6349.1	AO070275000018	FG06925.1	AFAO	yes	yes	((FG06925.1:100.0,(AN6349.1:100.0,(72.m19506:100.0,AO07027500:100.0):100.0):100.0):100.0,
138	54.m06733	AN4088.1	AO070342000091	FG06917.1	ANAO		yes	((FG06917.1:100.0,((AO07034200:100.0,AN4088.1:100.0):77.0,54.m06733:100.0):100.0):100.0,
139	70.m15600	AN0953.1	AO070320000154	FG05438.1	ANAO		yes	((FG05438.1:100.0,(70.m15600:100.0,(AN0953.1:100.0,AO07032000:100.0):84.5):100.0):100.0,
140	54.m06770	AN4211.1	AO070231000013	FG07253.1	ANAO			((FG07253.1:100.0,((AO07023100:100.0,AN4211.1:100.0):55.5,54.m06770:100.0):100.0):100.0,
141	58.m07764	AN1689.1	AO070305000009	FG02273.1	AFAO		yes	((FG02273.1:100.0,((AO07030500:100.0,58.m07764:100.0):88.8,AN1689.1:100.0):100.0):100.0,
142	54.m06996	AN4071.1	AO070342000060	FG07239.1	ANAO		yes	((FG07239.1:100.0,((AO07034200:100.0,AN4071.1:100.0):75.8,54.m06996:100.0):100.0):100.0,
143	54.m06721	AN4080.1	AO070342000072	FG07241.1	ANAO			((FG07241.1:100.0,(54.m06721:100.0,(AN4080.1:100.0,AO07034200:100.0):64.0):100.0):100.0,
144	54.m06720	AN4077.1	AO070342000069	FG07243.1	AFAO			((FG07243.1:100.0,((AO07034200:100.0,54.m06720:100.0):56.5,AN4077.1:100.0):100.0):100.0,
145	69.m15743	AN5452.1	AO070239000031	FG07245.1	AFAO		yes	((FG07245.1:100.0,((AO07023900:100.0,69.m15743:100.0):86.5,AN5452.1:100.0):100.0):100.0,
146	72.m19053	AN6064.1	AO070340000104	FG04677.1	AFAN			((FG04677.1:100.0,(AO07034000:100.0,(72.m19053:100.0,AN6064.1:100.0):51.8):99.0):100.0,
147	52.m03916	AN8333.1	AO070330000167	FG07988.1	ANAO			((((AN8333.1:100.0,AO07033000:100.0):39.0,52.m03916:100.0):69.0,FG07988.1:100.0):100.0,
148	71.m15964	AN8834.1	AO070271000043	FG05466.1	AFAO			((FG05466.1:100.0,((AO07027100:100.0,71.m15964:100.0):69.0,AN8834.1:100.0):100.0):100.0,
149	71.m15965	AN8835.1	AO070271000044	FG06958.1	AFAO	yes	yes	((FG06958.1:100.0,((AO07027100:100.0,71.m15965:100.0):94.0,AN8835.1:100.0):100.0):100.0,
150	71.m15967	AN8836.1	AO070271000042	FG06957.1	AFAO			((FG06957.1:100.0,((71.m15967:100.0,AO07027100:100.0):68.5,AN8836.1:100.0):100.0):100.0,
151	71.m15988	AN8853.1	AO070271000021	FG06927.1	AFAO		yes	((FG06927.1:100.0,((AO07027100:100.0,71.m15988:100.0):81.5,AN8853.1:100.0):100.0):100.0,
152	71.m15917	AN2272.1	AO070295000048	FG06932.1	AFAO			((FG06932.1:100.0,((AO07029500:100.0,71.m15917:100.0):69.0,AN2272.1:100.0):100.0):100.0,
153	71.m15995	AN8857.1	AO070271000016	FG06935.1	AFAO	yes	yes	((FG06935.1:100.0,((AO07027100:100.0,71.m15995:100.0):92.3,AN8857.1:100.0):100.0):100.0,
154	62.m03146	AN6558.1	AO070270000062	FG06937.1	ANAO		yes	((FG06937.1:100.0,((AO07027000:100.0,AN6558.1:100.0):80.5,62.m03146:100.0):100.0):100.0,
155	62.m03147	AN6560.1	AO070326000001	FG06938.1	ANAO			((FG06938.1:100.0,(62.m03147:100.0,(AN6560.1:100.0,AO07032600:100.0):63.0):100.0):100.0,
156	72.m19767	AN7299.1	AO070297000045	FG06955.1	ANAO	yes	yes	((FG06955.1:100.0,(72.m19767:100.0,(AN7299.1:100.0,AO07029700:100.0):95.5):100.0):100.0,
157	72.m19770	AN7296.1	AO070297000039	FG06953.1	AFAO	yes	yes	((FG06953.1:100.0,((AO07029700:100.0,72.m19770:100.0):96.5,AN7296.1:100.0):100.0):100.0,
158	71.m16018	AN6893.1	AO070314000027	FG05523.1	AFAO	yes	yes	((FG05523.1:100.0,((AO07031400:100.0,71.m16018:100.0):99.0,AN6893.1:100.0):100.0):100.0,
159	71.m15245	AN6895.1	AO070314000026	FG05522.1	AFAO		yes	((FG05522.1:100.0,((AO07031400:100.0,71.m15245:100.0):79.0,AN6895.1:100.0):100.0):100.0,
160	72.m19799	AN7250.1	AO070297000005	FG04095.1	AFAO		yes	((FG04095.1:100.0,((AO07029700:100.0,72.m19799:100.0):85.5,AN7250.1:100.0):100.0):100.0,
161	70.m15127	AN1105.1	AO070285000033	FG04115.1	AFAN		yes	((FG04115.1:100.0,(AO07028500:100.0,(AN1105.1:100.0,70.m15127:100.0):76.0):100.0):100.0,
162	71.m15347	AN0071.1	AO070314000160	FG04110.1	AFAO		yes	((FG04110.1:100.0,((AO07031400:100.0,71.m15347:100.0):88.5,AN0071.1:100.0):100.0):100.0,
163	71.m15247	AN6892.1	AO070314000029	FG04111.1	AFAO		yes	((FG04111.1:100.0,((AO07031400:100.0,71.m15247:100.0):82.0,AN6892.1:100.0):100.0):100.0,
164	71.m16034	AN6898.1	AO070314000023	FG04112.1	AFAO	yes	yes	((FG04112.1:100.0,((AO07031400:100.0,71.m16034:100.0):95.5,AN6898.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
165	70.m15265	AN0662.1	AO070343000558	FG04114.1	AFAN		yes	((FG04114.1:100.0,((70.m15265:100.0,AN0662.1:100.0):93.0,AO07034300:100.0):83.5):100.0,
166	71.m15359	AN0081.1	AO070311000136	FG04104.1	AFAN			((FG04104.1:100.0,(AO07031100:100.0,(AN0081.1:100.0,71.m15359:100.0):73.0):100.0):100.0,
167	71.m15360	AN0082.1	AO070311000135	FG04105.1	AFAO			((FG04105.1:100.0,((AO07031100:100.0,71.m15360:100.0):67.2,AN0082.1:100.0):100.0):100.0,
168	71.m16062	AN0083.1	AO070311000134	FG04108.1	ANAO	yes	yes	((FG04108.1:100.0,(71.m16062:100.0,(AN0083.1:100.0,AO07031100:100.0):90.0):100.0):100.0,
169	71.m15250	AN6889.1	AO070314000032	FG04109.1	AFAO	yes	yes	((FG04109.1:100.0,((AO07031400:100.0,71.m15250:100.0):91.0,AN6889.1:100.0):100.0):100.0,
170	70.m15129	AN1103.1	AO070285000035	FG04103.1	ANAO			((FG04103.1:100.0,((AO07028500:100.0,AN1103.1:100.0):52.0,70.m15129:100.0):100.0):100.0,
171	70.m15130	AN1102.1	AO070285000036	FG04102.1	AFAO	yes	yes	((FG04102.1:100.0,((AO07028500:100.0,70.m15130:100.0):93.5,AN1102.1:100.0):100.0):100.0,
172	71.m15936	AN2289.1	AO070295000068	FG06890.1	AFAO			((FG06890.1:100.0,((AO07029500:100.0,71.m15936:100.0):47.0,AN2289.1:100.0):100.0):100.0,
173	72.m19797	AN7252.1	AO070297000007	FG04101.1	AFAO			((FG04101.1:100.0,((72.m19797:100.0,AO07029700:100.0):53.5,AN7252.1:100.0):100.0):100.0,
174	72.m19727	AN7350.1	AO070278000050	FG02575.1	AFAO	yes	yes	((FG02575.1:100.0,(AN7350.1:100.0,(72.m19727:100.0,AO07027800:100.0):100.0):100.0):100.0,
175	72.m19729	AN7348.1	AO070278000051	FG02577.1	AFAO	yes	yes	((FG02577.1:100.0,((AO07027800:100.0,72.m19729:100.0):95.0,AN7348.1:100.0):100.0):100.0,
176	57.m05891	AN7451.1	AO070229000024	FG04117.1	ANAO	yes	yes	((FG04117.1:100.0,(57.m05891:100.0,(AN7451.1:100.0,AO07022900:100.0):96.0):100.0):100.0,
177	72.m19725	AN7354.1	AO070278000046	FG04137.1	AFAN			((FG04137.1:100.0,(AO07027800:100.0,(AN7354.1:100.0,72.m19725:100.0):65.0):100.0):100.0,
178	72.m19716	AN7360.1	AO070278000039	FG04121.1	AFAO		yes	((FG04121.1:100.0,((AO07027800:100.0,72.m19716:100.0):79.5,AN7360.1:100.0):100.0):100.0,
179	72.m19712	AN2129.1	AO070278000034	FG02584.1	ANAO		yes	((FG02584.1:100.0,((AO07027800:100.0,AN2129.1:100.0):81.0,72.m19712:100.0):100.0):100.0,
180	72.m19175	AN5959.1	AO070340000312	FG04139.1	AFAO			((FG04139.1:100.0,((AO07034000:100.0,72.m19175:100.0):42.0,AN5959.1:100.0):100.0):100.0,
181	72.m19195	AN5934.1	AO070340000336	FG04140.1	AFAO		yes	((FG04140.1:100.0,((AO07034000:100.0,72.m19195:100.0):79.5,AN5934.1:100.0):100.0):100.0,
182	58.m07647	AN1855.1	AO070292000031	FG06730.1	AFAO	yes	yes	((FG06730.1:100.0,((AO07029200:100.0,58.m07647:100.0):99.0,AN1855.1:100.0):100.0):100.0,
183	69.m15493	AN5441.1	AO070333000104	FG06893.1	ANAO			((FG06893.1:100.0,(69.m15493:100.0,(AO07033300:100.0,AN5441.1:100.0):37.5):98.2):100.0,
184	69.m15491	AN5443.1	AO070333000106	FG06894.1	ANAO			((FG06894.1:100.0,(69.m15491:100.0,(AN5443.1:100.0,AO07033300:100.0):66.0):100.0):100.0,
185	69.m15492	AN5442.1	AO070333000105	FG06895.1	AFAO		yes	((FG06895.1:100.0,((AO07033300:100.0,69.m15492:100.0):79.5,AN5442.1:100.0):100.0):100.0,
186	54.m06691	AN2740.1	AO070338000231	FG06914.1	AFAO		yes	((FG06914.1:100.0,((AO07033800:100.0,54.m06691:100.0):88.0,AN2740.1:100.0):100.0):100.0,
187	72.m19501	AN6354.1	AO070275000057	FG06912.1	AFAO			((FG06912.1:100.0,((AO07027500:100.0,72.m19501:100.0):73.5,AN6354.1:100.0):100.0):100.0,
188	53.m03900	AN8044.1	AO070292000105	FG06911.1	ANAO		yes	((FG06911.1:100.0,((AO07029200:100.0,AN8044.1:100.0):76.0,53.m03900:100.0):100.0):100.0,
189	57.m05576	AN4543.1	AO070321000163	FG05429.1	AFAO	yes	yes	((FG05429.1:100.0,((AO07032100:100.0,57.m05576:100.0):99.5,AN4543.1:100.0):100.0):100.0,
190	54.m06728	AN4087.1	AO070342000080	FG05433.1	AFAO		yes	((FG05433.1:100.0,((AO07034200:100.0,54.m06728:100.0):88.0,AN4087.1:100.0):100.0):100.0,
191	70.m15807	AN0924.1	AO070320000103	FG05434.1	AFAO			((FG05434.1:100.0,((AO07032000:100.0,70.m15807:100.0):52.5,AN0924.1:100.0):100.0):100.0,
192	70.m15529	AN0922.1	AO070320000101	FG05436.1	ANAO			((FG05436.1:100.0,(70.m15529:100.0,(AN0922.1:100.0,AO07032000:100.0):55.0):100.0):100.0,
193	54.m06710	AN4066.1	AO070342000056	FG06926.1	AFAO		yes	((FG06926.1:100.0,((AO07034200:100.0,54.m06710:100.0):86.5,AN4066.1:100.0):100.0):100.0,
194	70.m15604	AN0955.1	AO070320000157	FG06901.1	ANAO			((FG06901.1:100.0,(70.m15604:100.0,(AN0955.1:100.0,AO07032000:100.0):67.0):100.0):100.0,
195	70.m15586	AN0947.1	AO070320000146	FG06900.1	AFAO			((FG06900.1:100.0,((AO07032000:100.0,70.m15586:100.0):67.8,AN0947.1:100.0):100.0):100.0,
196	55.m03054	AN1536.1	AO070334000256	FG00515.1	ANAO			((FG00515.1:100.0,(55.m03054:100.0,(AN1536.1:100.0,AO07033400:100.0):70.5):100.0):100.0,
197	55.m03051	AN1533.1	AO070334000253	FG00372.1	AFAO			((FG00372.1:100.0,((55.m03051:100.0,AO07033400:100.0):54.0,AN1533.1:100.0):100.0):100.0,
198	55.m03052	AN1534.1	AO070334000254	FG00373.1	ANAO			((FG00373.1:100.0,(55.m03052:100.0,(AN1534.1:100.0,AO07033400:100.0):58.5):100.0):100.0,
199	57.m05805	AN2104.1	AO070341000262	FG00357.1	AFAO	yes	yes	((FG00357.1:100.0,((AO07034100:100.0,57.m05805:100.0):98.0,AN2104.1:100.0):100.0):100.0,
200	57.m05806	AN2105.1	AO070341000263	FG00358.1	AFAN		yes	((((AN2105.1:100.0,57.m05806:100.0):80.3,AO07034100:100.0):97.2,FG00358.1:100.0):100.0,
201	72.m19610	AN7588.1	AO070343000302	FG00589.1	AFAN			((FG00589.1:100.0,(AO07034300:100.0,(AN7588.1:100.0,72.m19610:100.0):44.8):100.0):100.0,
202	72.m19572	AN7554.1	AO070277000055	FG00590.1	AFAO	yes	yes	((FG00590.1:100.0,((AO07027700:100.0,72.m19572:100.0):94.0,AN7554.1:100.0):100.0):100.0,
203	71.m15200	AN0681.1	AO070303000069	FG00454.1	ANAO	yes	yes	((FG00454.1:100.0,(71.m15200:100.0,(AN0681.1:100.0,AO07030300:100.0):95.5):100.0):100.0,
204	57.m05544	AN4633.1	AO070340000373	FG09220.1	ANAO		yes	((((AN4633.1:100.0,AO07034000:100.0):82.3,57.m05544:100.0):99.0,FG09220.1:100.0):100.0,
205	57.m05543	AN4632.1	AO070340000375	FG09221.1	AFAO		yes	((FG09221.1:100.0,((AO07034000:100.0,57.m05543:100.0):83.5,AN4632.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
206	71.m15702	AN8565.1	AO070311000007	FG00186.1	AFAO	yes	yes	((FG00186.1:100.0,((AO07031100:100.0,71.m15702:100.0):97.5,AN8565.1:100.0):100.0):100.0,
207	55.m02953	AN1451.1	AO070302000016	FG00185.1	AFAO	yes	yes	((FG00185.1:100.0,((AO07030200:100.0,55.m02953:100.0):99.0,AN1451.1:100.0):100.0):100.0,
208	71.m15779	AN7749.1	AO070325000178	FG00243.1	AFAO			((FG00243.1:100.0,((AO07032500:100.0,71.m15779:100.0):62.0,AN7749.1:100.0):100.0):100.0,
209	71.m15778	AN5236.1	AO070325000177	FG00257.1	AFAO	yes	yes	((FG00257.1:100.0,(AN5236.1:100.0,(71.m15778:100.0,AO07032500:100.0):100.0):100.0):100.0,
210	71.m15694	AN4706.1	AO070329000170	FG08719.1	AFAO	yes	yes	((FG08719.1:100.0,((AO07032900:100.0,71.m15694:100.0):96.0,AN4706.1:100.0):100.0):100.0,
211	59.m09188	AN4793.1	AO070329000053	FG08498.1	ANAO			((FG08498.1:100.0,(59.m09188:100.0,(AN4793.1:100.0,AO07032900:100.0):55.0):100.0):100.0,
212	59.m09211	AN4771.1	AO070329000081	FG00265.1	AFAO			((FG00265.1:100.0,((AO07032900:100.0,59.m09211:100.0):68.5,AN4771.1:100.0):100.0):100.0,
213	59.m09217	AN4768.1	AO070329000089	FG09414.1	AFAO	yes	yes	((FG09414.1:100.0,((AO07032900:100.0,59.m09217:100.0):99.5,AN4768.1:100.0):100.0):100.0,
214	57.m05983	AN4611.1	AO070267000026	FG00168.1	AFAO		yes	((FG00168.1:100.0,((AO07026700:100.0,57.m05983:100.0):76.5,AN4611.1:100.0):100.0):100.0,
215	59.m09213	AN9486.1	AO070329000083	FG09444.1	AFAN		yes	((FG09444.1:100.0,(AO07032900:100.0,(AN9486.1:100.0,59.m09213:100.0):78.5):100.0):100.0,
216	62.m03316	AN8769.1	AO070343000429	FG08537.1	AFAO			((FG08537.1:100.0,((AO07034300:100.0,62.m03316:100.0):57.7,AN8769.1:100.0):100.0):100.0,
217	54.m06799	AN4219.1	AO070315000080	FG08551.1	AFAO			((FG08551.1:100.0,((AO07031500:100.0,54.m06799:100.0):68.0,AN4219.1:100.0):100.0):100.0,
218	54.m06798	AN4220.1	AO070315000079	FG08550.1	AFAO			((FG08550.1:100.0,((AO07031500:100.0,54.m06798:100.0):68.5,AN4220.1:100.0):100.0):100.0,
219	70.m15462	AN0866.1	AO070320000017	FG08548.1	ANAO			((FG08548.1:100.0,(70.m15462:100.0,(AN0866.1:100.0,AO07032000:100.0):69.5):100.0):100.0,
220	62.m03486	AN8686.1	AO070315000105	FG08776.1	ANAO			((FG08776.1:100.0,((AO07031500:100.0,AN8686.1:100.0):68.5,62.m03486:100.0):100.0):100.0,
221	62.m03391	AN8680.1	AO070315000100	FG08777.1	ANAO			((((AN8680.1:100.0,AO07031500:100.0):71.7,62.m03391:100.0):99.7,FG08777.1:100.0):100.0,
222	66.m04527	AN9063.1	AO070332000210	FG08586.1	AFAN			((FG08586.1:100.0,(AO07033200:100.0,(AN9063.1:100.0,66.m04527:100.0):54.5):100.0):100.0,
223	70.m15459	AN0868.1	AO070320000019	FG08585.1	ANAO			((FG08585.1:100.0,(70.m15459:100.0,(AN0868.1:100.0,AO07032000:100.0):54.5):100.0):100.0,
224	72.m19024	AN6140.1	AO070340000062	FG08779.1	AFAO	yes	yes	((FG08779.1:100.0,((AO07034000:100.0,72.m19024:100.0):99.5,AN6140.1:100.0):100.0):100.0,
225	57.m05532	AN4615.1	AO070267000032	FG08692.1	AFAO		yes	((FG08692.1:100.0,((AO07026700:100.0,57.m05532:100.0):85.0,AN4615.1:100.0):100.0):100.0,
226	70.m15539	AN0931.1	AO070320000122	FG08691.1	AFAO	yes	yes	((FG08691.1:100.0,((AO07032000:100.0,70.m15539:100.0):98.0,AN0931.1:100.0):100.0):100.0,
227	70.m15538	AN0930.1	AO070320000120	FG08690.1	AFAN			((FG08690.1:100.0,(AO07032000:100.0,(AN0930.1:100.0,70.m15538:100.0):74.0):100.0):100.0,
228	71.m15673	AN4690.1	AO070284000045	FG08688.1	AFAO	yes	yes	((FG08688.1:100.0,((AO07028400:100.0,71.m15673:100.0):97.5,AN4690.1:100.0):100.0):100.0,
229	59.m09200	AN4783.1	AO070329000067	FG00182.1	ANAO		yes	((FG00182.1:100.0,((AO07032900:100.0,AN4783.1:100.0):84.5,59.m09200:100.0):100.0):100.0,
230	57.m05530	AN4613.1	AO070267000029	FG09447.1	AFAO	yes	yes	((FG09447.1:100.0,((AO07026700:100.0,57.m05530:100.0):98.0,AN4613.1:100.0):100.0):100.0,
231	59.m09201	AN4782.1	AO070329000068	FG00170.1	ANAO			((FG00170.1:100.0,(59.m09201:100.0,(AN4782.1:100.0,AO07032900:100.0):65.5):100.0):100.0,
232	59.m09209	AN4774.1	AO070329000078	FG09448.1	AFAO			((FG09448.1:100.0,((59.m09209:100.0,AO07032900:100.0):62.0,AN4774.1:100.0):100.0):100.0,
233	71.m16089	AN4714.1	AO070337000217	FG09413.1	AFAO		yes	((FG09413.1:100.0,((AO07033700:100.0,71.m16089:100.0):86.0,AN4714.1:100.0):100.0):100.0,
234	71.m15715	AN4659.1	AO070316000143	FG09424.1	AFAO		yes	((FG09424.1:100.0,((AO07031600:100.0,71.m15715:100.0):79.0,AN4659.1:100.0):100.0):100.0,
235	71.m15704	AN4716.1	AO070311000005	FG09425.1	ANAO			((FG09425.1:100.0,(71.m15704:100.0,(AN4716.1:100.0,AO07031100:100.0):56.8):100.0):100.0,
236	71.m15638	AN4728.1	AO070284000080	FG00261.1	AFAO		yes	((FG00261.1:100.0,((AO07028400:100.0,71.m15638:100.0):84.0,AN4728.1:100.0):100.0):100.0,
237	57.m05546	AN4635.1	AO070248000030	FG06405.1	AFAO		yes	((FG06405.1:100.0,((57.m05546:100.0,AO07024800:100.0):80.5,AN4635.1:100.0):100.0):100.0,
238	57.m05556	AN4561.1	AO070321000186	FG06406.1	AFAO		yes	((FG06406.1:100.0,((AO07032100:100.0,57.m05556:100.0):88.0,AN4561.1:100.0):100.0):100.0,
239	59.m09469	AN4777.1	AO070329000074	FG06407.1	ANAO		yes	((FG06407.1:100.0,(59.m09469:100.0,(AN4777.1:100.0,AO07032900:100.0):83.3):100.0):100.0,
240	70.m15445	AN0846.1	AO070216000005	FG06408.1	AFAN			((FG06408.1:100.0,(AO07021600:100.0,(AN0846.1:100.0,70.m15445:100.0):63.5):100.0):100.0,
241	57.m05552	AN4639.1	AO070321000194	FG08704.1	AFAO		yes	((FG08704.1:100.0,((AO07032100:100.0,57.m05552:100.0):87.5,AN4639.1:100.0):100.0):100.0,
242	57.m05553	AN4564.1	AO070321000192	FG08703.1	AFAN			((FG08703.1:100.0,((57.m05553:100.0,AN4564.1:100.0):63.5,AO07032100:100.0):100.0):100.0,
243	62.m03217	AN6626.1	AO070315000108	FG05676.1			yes	(((62.m03217:100.0,AN6626.1:100.0):100.0,(FG05676.1:100.0,AO07031500:100.0):78.0):100.0,
244	62.m03224	AN6628.1	AO070326000079	FG08784.1	AFAO			((FG08784.1:100.0,((AO07032600:100.0,62.m03224:100.0):73.0,AN6628.1:100.0):100.0):100.0,
245	67.m02932	AN3224.1	AO070330000074	FG08541.1	AFAO	yes	yes	((FG08541.1:100.0,((AO07033000:100.0,67.m02932:100.0):99.0,AN3224.1:100.0):100.0):100.0,
246	67.m02931	AN3223.1	AO070330000073	FG09456.1	AFAN			((FG09456.1:100.0,(AO07033000:100.0,(AN3223.1:100.0,67.m02931:100.0):55.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
247	69.m15470	AN5483.1	AO070341000402	FG08540.1	AFAO		yes	((FG08540.1:100.0,((AO07034100:100.0,69.m15470:100.0):84.5,AN5483.1:100.0):100.0):100.0,
248	72.m19567	AN7550.1	AO070277000047	FG08539.1	AFAO		yes	((FG08539.1:100.0,((AO07027700:100.0,72.m19567:100.0):89.0,AN7550.1:100.0):100.0):100.0,
249	62.m03225	AN6629.1	AO070326000081	FG08561.1	AFAN			((FG08561.1:100.0,(AO07032600:100.0,(62.m03225:100.0,AN6629.1:100.0):68.5):100.0):100.0,
250	62.m03226	AN6630.1	AO070326000082	FG08560.1	AFAO	yes	yes	((FG08560.1:100.0,((AO07032600:100.0,62.m03226:100.0):92.0,AN6630.1:100.0):100.0):100.0,
251	70.m15358	AN0756.1	AO070343000444	FG03904.1	AFAO	yes	yes	((FG03904.1:100.0,(AN0756.1:100.0,(70.m15358:100.0,AO07034300:100.0):100.0):100.0):100.0,
252	70.m15574	AN0942.1	AO070320000137	FG00655.1	AFAO			((FG00655.1:100.0,((AO07032000:100.0,70.m15574:100.0):38.5,AN0942.1:100.0):100.0):100.0,
253	70.m15575	AN0943.1	AO070320000138	FG00656.1	ANAO			((FG00656.1:100.0,(70.m15575:100.0,(AN0943.1:100.0,AO07032000:100.0):46.0):100.0):100.0,
254	66.m04582	AN9116.1	AO070332000151	FG00269.1	ANAO			((FG00269.1:100.0,(66.m04582:100.0,(AN9116.1:100.0,AO07033200:100.0):48.5):100.0):100.0,
255	57.m05968	AN3794.1	AO070337000233	FG00270.1	AFAO	yes	yes	((FG00270.1:100.0,(AN3794.1:100.0,(57.m05968:100.0,AO07033700:100.0):100.0):100.0):100.0,
256	57.m05696	AN3787.1	AO070337000242	FG00271.1	AFAO	yes	yes	((FG00271.1:100.0,((AO07033700:100.0,57.m05696:100.0):93.5,AN3787.1:100.0):100.0):100.0,
257	52.m04028	AN9401.1	AO070274000016	FG08521.1	AFAO	yes	yes	((FG08521.1:100.0,(AN9401.1:100.0,(52.m04028:100.0,AO07027400:100.0):100.0):100.0):100.0,
258	71.m15697	AN4709.1	AO070329000166	FG08522.1	ANAO			((FG08522.1:100.0,((AO07032900:100.0,AN4709.1:100.0):66.0,71.m15697:100.0):100.0):100.0,
259	71.m15699	AN4711.1	AO070329000164	FG11353.1	AFAO	yes	yes	((FG11353.1:100.0,((AO07032900:100.0,71.m15699:100.0):97.0,AN4711.1:100.0):100.0):100.0,
260	71.m15660	AN4672.1	AO070284000034	FG06411.1	AFAO			((FG06411.1:100.0,((AO07028400:100.0,71.m15660:100.0):66.2,AN4672.1:100.0):100.0):100.0,
261	71.m15695	AN4707.1	AO070329000169	FG00188.1	AFAN			((FG00188.1:100.0,(AO07032900:100.0,(AN4707.1:100.0,71.m15695:100.0):65.0):100.0):100.0,
262	52.m04029	AN9402.1	AO070274000015	FG00259.1	AFAO	yes	yes	((FG00259.1:100.0,((AO07027400:100.0,52.m04029:100.0):95.0,AN9402.1:100.0):100.0):100.0,
263	71.m15707	AN4719.1	AO070311000002	FG08572.1	AFAO		yes	((FG08572.1:100.0,((AO07031100:100.0,71.m15707:100.0):78.5,AN4719.1:100.0):100.0):100.0,
264	71.m15667	AN4683.1	AO070284000018	FG00189.1	AFAO		yes	((FG00189.1:100.0,((AO07028400:100.0,71.m15667:100.0):83.0,AN4683.1:100.0):100.0):100.0,
265	71.m15643	AN0239.1	AO070284000068	FG00191.1	AFAO	yes	yes	((FG00191.1:100.0,((AO07028400:100.0,71.m15643:100.0):94.5,AN0239.1:100.0):100.0):100.0,
266	71.m15644	AN0238.1	AO070284000067	FG00192.1	AFAO	yes	yes	((FG00192.1:100.0,((71.m15644:100.0,AO07028400:100.0):99.5,AN0238.1:100.0):100.0):100.0,
267	59.m08494	AN2496.1	AO070312000124	FG08819.1	ANAO			((FG08819.1:100.0,(59.m08494:100.0,(AN2496.1:100.0,AO07031200:100.0):53.0):100.0):100.0,
268	66.m04526	AN9062.1	AO070332000211	FG08841.1	AFAO		yes	((FG08841.1:100.0,((AO07033200:100.0,66.m04526:100.0):88.0,AN9062.1:100.0):100.0):100.0,
269	62.m03234	AN6639.1	AO070326000091	FG08851.1	AFAO			((FG08851.1:100.0,((62.m03234:100.0,AO07032600:100.0):58.0,AN6639.1:100.0):100.0):100.0,
270	71.m15815	AN7784.1	AO070286000028	FG08728.1	AFAO	yes	yes	((FG08728.1:100.0,(AN7784.1:100.0,(71.m15815:100.0,AO07028600:100.0):100.0):100.0):100.0,
271	71.m15705	AN4717.1	AO070311000004	FG08729.1	AFAO		yes	((FG08729.1:100.0,((AO07031100:100.0,71.m15705:100.0):83.5,AN4717.1:100.0):100.0):100.0,
272	57.m05554	AN4563.1	AO070321000191	FG08731.1	AFAN		yes	((FG08731.1:100.0,(AO07032100:100.0,(AN4563.1:100.0,57.m05554:100.0):78.0):100.0):100.0,
273	62.m03474	AN8691.1	AO070315000112	FG08642.1	AFAO	yes	yes	((FG08642.1:100.0,((AO07031500:100.0,62.m03474:100.0):97.5,AN8691.1:100.0):100.0):100.0,
274	57.m05533	AN4616.1	AO070267000033	FG08644.1	AFAO	yes	yes	((FG08644.1:100.0,((AO07026700:100.0,57.m05533:100.0):91.0,AN4616.1:100.0):100.0):100.0,
275	57.m05535	AN4617.1	AO070267000034	FG08645.1	AFAN		yes	((FG08645.1:100.0,(AO07026700:100.0,(AN4617.1:100.0,57.m05535:100.0):78.0):100.0):100.0,
276	70.m15371	AN0768.1	AO070316000076	FG02859.1	AFAO		yes	((FG02859.1:100.0,((AO07031600:100.0,70.m15371:100.0):85.5,AN0768.1:100.0):100.0):100.0,
277	59.m09028	AN2985.1	AO070337000137	FG03726.1	ANAO		yes	((FG03726.1:100.0,(59.m09028:100.0,(AN2985.1:100.0,AO07033700:100.0):77.5):100.0):100.0,
278	57.m05666	AN3817.1	AO070311000014	FG09197.1	ANAO	yes	yes	((FG09197.1:100.0,(57.m05666:100.0,(AN3817.1:100.0,AO07031100:100.0):93.5):100.0):100.0,
279	57.m05673	AN3809.1	AO070337000220	FG09196.1	AFAN			((FG09196.1:100.0,(AO07033700:100.0,(AN3809.1:100.0,57.m05673:100.0):51.0):100.0):100.0,
280	72.m19427	AN6226.1	AO070304000076	FG01713.1	AFAO			((FG01713.1:100.0,((AO07030400:100.0,72.m19427:100.0):63.5,AN6226.1:100.0):100.0):100.0,
281	53.m03953	AN6721.1	AO070335000072	FG05798.1				((((AN6721.1:100.0,53.m03953:100.0):77.0,FG05798.1:100.0):72.3,AO07033500:100.0):100.0,
282	57.m05668	AN3814.1	AO070311000012	FG00777.1	AFAN	yes	yes	((FG00777.1:100.0,((57.m05668:100.0,AN3814.1:100.0):94.5,AO07031100:100.0):100.0):100.0,
283	66.m04585	AN9125.1	AO070332000149	FG00778.1	AFAO		yes	((FG00778.1:100.0,((AO07033200:100.0,66.m04585:100.0):83.0,AN9125.1:100.0):100.0):100.0,
284	71.m15526	AN2327.1	AO070323000030	FG05028.1	AFAN			((FG05028.1:100.0,(AO07032300:100.0,(AN2327.1:100.0,71.m15526:100.0):39.0):100.0):100.0,
285	54.m06398	AN0356.1	AO070318000032	FG05024.1	AFAO	yes	yes	((FG05024.1:100.0,(AN0356.1:100.0,(54.m06398:100.0,AO07031800:100.0):100.0):100.0):100.0,
286	54.m06404	AN0351.1	AO070318000028	FG05023.1	AFAO			((FG05023.1:100.0,((AO07031800:100.0,54.m06404:100.0):58.5,AN0351.1:100.0):100.0):100.0,
287	54.m06403	AN0352.1	AO070318000029	FG09704.1	AFAO			((FG09704.1:100.0,((AO07031800:100.0,54.m06403:100.0):62.0,AN0352.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
288	53.m03834	AN8122.1	AO070322000030	FG09697.1	AFAO		yes	((FG09697.1:100.0,((AO07032200:100.0,53.m03834:100.0):88.5,AN8122.1:100.0):100.0):100.0,
289	69.m15267	AN0581.1	AO070280000003	FG03080.1	AFAO	yes	yes	((FG03080.1:100.0,((AO07028000:100.0,69.m15267:100.0):95.0,AN0581.1:100.0):100.0):100.0,
290	55.m02939	AN1433.1	AO070232000013	FG03601.1	AFAO		yes	((FG03601.1:100.0,((55.m02939:100.0,AO07023200:100.0):86.5,AN1433.1:100.0):100.0):100.0,
291	66.m04770	AN9090.1	AO070332000188	FG05737.1	AFAO		yes	((FG05737.1:100.0,((AO07033200:100.0,66.m04770:100.0):82.0,AN9090.1:100.0):100.0):100.0,
292	69.m14823	AN5774.1	AO070249000018	FG05736.1	AFAO	yes	yes	((FG05736.1:100.0,((AO07024900:100.0,69.m14823:100.0):96.0,AN5774.1:100.0):100.0):100.0,
293	65.m07401	AN5675.1	AO070309000090	FG05735.1	AFAO	yes	yes	((FG05735.1:100.0,((AO07030900:100.0,65.m07401:100.0):94.5,AN5675.1:100.0):100.0):100.0,
294	69.m14806	AN5790.1	AO070249000036	FG05733.1	AFAO			((FG05733.1:100.0,((69.m14806:100.0,AO07024900:100.0):60.2,AN5790.1:100.0):100.0):100.0,
295	70.m15693	AN7060.1	AO070336000179	FG05628.1	ANAO	yes	yes	((FG05628.1:100.0,((AN7060.1:100.0,AO07033600:100.0):100.0,70.m15693:100.0):100.0):100.0,
296	69.m14807	AN5789.1	AO070249000035	FG05728.1	AFAO			((FG05728.1:100.0,((69.m14807:100.0,AO07024900:100.0):53.5,AN5789.1:100.0):100.0):100.0,
297	70.m15655	AN0628.1	AO070299000112	FG09696.1	AFAO			(((AN0628.1:100.0,(70.m15655:100.0,AO07029900:100.0):70.0):99.0,FG09696.1:100.0):100.0,
298	54.m06372	AN0375.1	AO070228000007	FG05238.1	AFAO			((FG05238.1:100.0,((AO07022800:100.0,54.m06372:100.0):64.0,AN0375.1:100.0):100.0):100.0,
299	70.m15122	AN1111.1	AO070285000025	FG09695.1	AFAO	yes	yes	((FG09695.1:100.0,(AN1111.1:100.0,(70.m15122:100.0,AO07028500:100.0):100.0):100.0):100.0,
300	54.m06359	AN0385.1	AO070318000082	FG05696.1	AFAO	yes	yes	((FG05696.1:100.0,(AN0385.1:100.0,(54.m06359:100.0,AO07031800:100.0):100.0):100.0):100.0,
301	65.m07437	AN4262.1	AO070277000028	FG05697.1	AFAO	yes	yes	((FG05697.1:100.0,((AO07027700:100.0,65.m07437:100.0):99.0,AN4262.1:100.0):100.0):100.0,
302	54.m06388	AN0361.1	AO070318000041	FG05698.1	AFAO			((FG05698.1:100.0,((AO07031800:100.0,54.m06388:100.0):46.3,AN0361.1:100.0):100.0):100.0,
303	53.m03951	AN3378.1	AO070317000065	FG09214.1		yes	yes	(((AN3378.1:100.0,AO07031700:100.0):100.0,(FG09214.1:100.0,53.m03951:100.0):96.5):100.0,
304	52.m03906	AN9377.1	AO070315000006	FG04176.1	AFAO			((FG04176.1:100.0,((AO07031500:100.0,52.m03906:100.0):57.3,AN9377.1:100.0):100.0):100.0,
305	57.m05670	AN3812.1	AO070311000009	FG09363.1	AFAO			((FG09363.1:100.0,((AO07031100:100.0,57.m05670:100.0):50.0,AN3812.1:100.0):100.0):100.0,
306	54.m06701	AN0248.1	AO070338000241	FG09362.1	AFAO			((FG09362.1:100.0,((54.m06701:100.0,AO07033800:100.0):64.0,AN0248.1:100.0):100.0):100.0,
307	57.m05639	AN4492.1	AO070311000044	FG00781.1	AFAO		yes	((FG00781.1:100.0,((AO07031100:100.0,57.m05639:100.0):83.5,AN4492.1:100.0):100.0):100.0,
308	57.m05638	AN4493.1	AO070343000131	FG00780.1	AFAN	yes	yes	((((57.m05638:100.0,AN4493.1:100.0):100.0,AO07034300:100.0):96.0,FG00780.1:100.0):100.0,
309	55.m03255	AN1483.1	AO070334000189	FG00622.1	AFAO	yes	yes	((FG00622.1:100.0,((AO07033400:100.0,55.m03255:100.0):98.5,AN1483.1:100.0):100.0):100.0,
310	69.m15514	AN3208.1	AO070333000140	FG06060.1	AFAO	yes	yes	((FG06060.1:100.0,(AN3208.1:100.0,(69.m15514:100.0,AO07033300:100.0):100.0):100.0):100.0,
311	57.m05669	AN3813.1	AO070311000011	FG00773.1	AFAO			((((57.m05669:100.0,AO07031100:100.0):41.0,AN3813.1:100.0):67.5,FG00773.1:100.0):100.0,
312	72.m19815	AN7231.1	AO070290000019	FG02204.1	AFAO		yes	((FG02204.1:100.0,((AO07029000:100.0,72.m19815:100.0):89.0,AN7231.1:100.0):100.0):100.0,
313	63.m00625	AN3772.1	AO070330000061	FG09303.1	AFAO			((FG09303.1:100.0,((AO07033000:100.0,63.m00625:100.0):65.0,AN3772.1:100.0):100.0):100.0,
314	72.m19551	AN8099.1	AO070309000130	FG06612.1	AFAO	yes	yes	((FG06612.1:100.0,((AO07030900:100.0,72.m19551:100.0):96.5,AN8099.1:100.0):100.0):100.0,
315	56.m02448	AN9483.1	AO070313000069	FG11114.1	AFAO			((FG11114.1:100.0,((AO07031300:100.0,56.m02448:100.0):65.0,AN9483.1:100.0):100.0):100.0,
316	71.m15730	AN7705.1	AO070325000111	FG02812.1	AFAN			((FG02812.1:100.0,(AO07032500:100.0,(AN7705.1:100.0,71.m15730:100.0):36.5):100.0):100.0,
317	71.m15725	AN7704.1	AO070325000110	FG02811.1	AFAO	yes	yes	((FG02811.1:100.0,((AO07032500:100.0,71.m15725:100.0):99.0,AN7704.1:100.0):100.0):100.0,
318	71.m15684	AN4702.1	AO070329000178	FG02810.1	AFAO	yes	yes	((FG02810.1:100.0,((AO07032900:100.0,71.m15684:100.0):94.0,AN4702.1:100.0):100.0):100.0,
319	71.m15685	AN4701.1	AO070329000177	FG02809.1	AFAO			((FG02809.1:100.0,((71.m15685:100.0,AO07032900:100.0):73.0,AN4701.1:100.0):100.0):100.0,
320	56.m02500	AN4177.1	AO070319000001	FG02822.1	AFAO			((FG02822.1:100.0,((AO07031900:100.0,56.m02500:100.0):71.0,AN4177.1:100.0):100.0):100.0,
321	66.m04522	AN9072.1	AO070332000216	FG00808.1	AFAN			((FG00808.1:100.0,(AO07033200:100.0,(AN9072.1:100.0,66.m04522:100.0):72.3):100.0):100.0,
322	66.m04636	AN3368.1	AO070281000024	FG04679.1	AFAO			((FG04679.1:100.0,((AO07028100:100.0,66.m04636:100.0):74.0,AN3368.1:100.0):100.0):100.0,
323	66.m04521	AN9064.1	AO070332000217	FG04922.1	AFAO			((FG04922.1:100.0,((AO07033200:100.0,66.m04521:100.0):38.5,AN9064.1:100.0):100.0):100.0,
324	58.m07816	AN3840.1	AO070305000075	FG00684.1	AFAO	yes	yes	((FG00684.1:100.0,((AO07030500:100.0,58.m07816:100.0):93.0,AN3840.1:100.0):100.0):100.0,
325	58.m07819	AN3843.1	AO070305000078	FG00686.1	AFAO	yes	yes	((FG00686.1:100.0,((AO07030500:100.0,58.m07819:100.0):99.0,AN3843.1:100.0):100.0):100.0,
326	58.m07817	AN3841.1	AO070305000076	FG00688.1	AFAO		yes	((FG00688.1:100.0,((AO07030500:100.0,58.m07817:100.0):78.0,AN3841.1:100.0):100.0):100.0,
327	54.m06619	AN0430.1	AO070338000280	FG00716.1	AFAO		yes	((FG00716.1:100.0,((AO07033800:100.0,54.m06619:100.0):76.5,AN0430.1:100.0):100.0):100.0,
328	54.m06621	AN0436.1	AO070338000281	FG00715.1	ANAO			((FG00715.1:100.0,(54.m06621:100.0,(AN0436.1:100.0,AO07033800:100.0):57.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
329	54.m06658	AN0416.1	AO070338000264	FG00714.1	AFAN			((FG00714.1:100.0,(AO07033800:100.0,(AN0416.1:100.0,54.m06658:100.0):49.0):100.0):100.0,
330	58.m07406	AN3619.1	AO070342000161	FG00711.1	AFAO			((FG00711.1:100.0,((AO07034200:100.0,58.m07406:100.0):59.0,AN3619.1:100.0):100.0):100.0,
331	58.m07405	AN3607.1	AO070342000160	FG00710.1	AFAO	yes	yes	((FG00710.1:100.0,(AN3607.1:100.0,(58.m07405:100.0,AO07034200:100.0):100.0):100.0):100.0,
332	66.m04520	AN9066.1	AO070332000218	FG00706.1	AFAO			((FG00706.1:100.0,((AO07033200:100.0,66.m04520:100.0):61.5,AN9066.1:100.0):100.0):100.0,
333	70.m15428	AN0827.1	AO070255000018	FG00700.1	AFAO		yes	((FG00700.1:100.0,((AO07025500:100.0,70.m15428:100.0):75.0,AN0827.1:100.0):100.0):100.0,
334	57.m05560	AN4550.1	AO070321000181	FG04554.1	AFAO		yes	((FG04554.1:100.0,((AO07032100:100.0,57.m05560:100.0):79.0,AN4550.1:100.0):100.0):100.0,
335	66.m04524	AN9070.1	AO070332000215	FG00698.1	AFAO			((FG00698.1:100.0,((AO07033200:100.0,66.m04524:100.0):46.0,AN9070.1:100.0):100.0):100.0,
336	70.m15576	AN0944.1	AO070320000139	FG00877.1	AFAO			((FG00877.1:100.0,((AO07032000:100.0,70.m15576:100.0):50.0,AN0944.1:100.0):100.0):100.0,
337	66.m04778	AN3362.1	AO070281000034	FG00690.1	AFAO			((FG00690.1:100.0,((AO07028100:100.0,66.m04778:100.0):73.5,AN3362.1:100.0):100.0):100.0,
338	57.m05972	AN3802.1	AO070337000226	FG00691.1	AFAO			((FG00691.1:100.0,((AO07033700:100.0,57.m05972:100.0):52.5,AN3802.1:100.0):100.0):100.0,
339	57.m05973	AN3803.1	AO070337000224	FG00693.1	AFAO			((FG00693.1:100.0,((AO07033700:100.0,57.m05973:100.0):71.5,AN3803.1:100.0):100.0):100.0,
340	58.m07802	AN3826.1	AO070305000062	FG00694.1	AFAO			((FG00694.1:100.0,((AO07030500:100.0,58.m07802:100.0):58.0,AN3826.1:100.0):100.0):100.0,
341	58.m07803	AN3827.1	AO070305000064	FG00695.1	AFAO	yes	yes	((FG00695.1:100.0,(AN3827.1:100.0,(58.m07803:100.0,AO07030500:100.0):100.0):100.0):100.0,
342	66.m04629	AN3363.1	AO070281000032	FG00697.1	AFAO			((FG00697.1:100.0,((AO07028100:100.0,66.m04629:100.0):69.5,AN3363.1:100.0):100.0):100.0,
343	54.m06617	AN0428.1	AO070338000279	FG00875.1	AFAO	yes	yes	((FG00875.1:100.0,(AN0428.1:100.0,(54.m06617:100.0,AO07033800:100.0):100.0):100.0):100.0,
344	58.m07805	AN3829.1	AO070305000066	FG06752.1	AFAO	yes	yes	((FG06752.1:100.0,((AO07030500:100.0,58.m07805:100.0):93.0,AN3829.1:100.0):100.0):100.0,
345	58.m07407	AN3620.1	AO070342000132	FG00281.1	AFAO	yes	yes	((FG00281.1:100.0,((AO07034200:100.0,58.m07407:100.0):94.0,AN3620.1:100.0):100.0):100.0,
346	72.m19997	AN7564.1	AO070343000407	FG05623.1	AFAO			((FG05623.1:100.0,((AO07034300:100.0,72.m19997:100.0):57.5,AN7564.1:100.0):100.0):100.0,
347	59.m09040	AN2967.1	AO070337000149	FG06863.1	AFAO	yes	yes	((FG06863.1:100.0,((AO07033700:100.0,59.m09040:100.0):95.5,AN2967.1:100.0):100.0):100.0,
348	59.m09041	AN2968.1	AO070337000151	FG00496.1	AFAO			((FG00496.1:100.0,((AO07033700:100.0,59.m09041:100.0):54.8,AN2968.1:100.0):100.0):100.0,
349	54.m06491	AN0293.1	AO070334000049	FG00587.1	AFAN			((FG00587.1:100.0,(AO07033400:100.0,(AN0293.1:100.0,54.m06491:100.0):66.5):100.0):100.0,
350	69.m15773	AN5400.1	AO070333000134	FG03163.1	ANAO			((FG03163.1:100.0,(69.m15773:100.0,(AN5400.1:100.0,AO07033300:100.0):45.0):100.0):100.0,
351	55.m02948	AN1445.1	AO070302000002	FG01355.1	AFAO			((FG01355.1:100.0,((AO07030200:100.0,55.m02948:100.0):48.8,AN1445.1:100.0):100.0):100.0,
352	55.m02969	AN1467.1	AO070306000090	FG05611.1	AFAO			((FG05611.1:100.0,((AO07030600:100.0,55.m02969:100.0):73.5,AN1467.1:100.0):100.0):100.0,
353	71.m15534	AN2332.1	AO070323000014	FG05610.1	AFAO		yes	((FG05610.1:100.0,((AO07032300:100.0,71.m15534:100.0):78.0,AN2332.1:100.0):100.0):100.0,
354	55.m03268	AN1524.1	AO070334000242	FG00417.1	AFAO			((FG00417.1:100.0,((AO07033400:100.0,55.m03268:100.0):65.3,AN1524.1:100.0):100.0):100.0,
355	55.m03280	AN1525.1	AO070334000243	FG05600.1	AFAO			((FG05600.1:100.0,((AO07033400:100.0,55.m03280:100.0):58.0,AN1525.1:100.0):100.0):100.0,
356	55.m03269	AN1526.1	AO070334000244	FG05601.1	AFAO			((FG05601.1:100.0,((AO07033400:100.0,55.m03269:100.0):73.3,AN1526.1:100.0):100.0):100.0,
357	55.m02947	AN1444.1	AO070302000001	FG00393.1	AFAO		yes	((FG00393.1:100.0,((AO07030200:100.0,55.m02947:100.0):84.0,AN1444.1:100.0):100.0):100.0,
358	72.m19143	AN5997.1	AO070340000279	FG00395.1	AFAO			((((72.m19143:100.0,AO07034000:100.0):71.5,AN5997.1:100.0):98.5,FG00395.1:100.0):100.0,
359	54.m06847	AN5727.1	AO070324000124	FG11048.1	ANAO	yes	yes	((FG11048.1:100.0,(54.m06847:100.0,(AN5727.1:100.0,AO07032400:100.0):99.0):100.0):100.0,
360	59.m09068	AN2927.1	AO070337000182	FG01137.1	ANAO		yes	((FG01137.1:100.0,((AO07033700:100.0,AN2927.1:100.0):75.5,59.m09068:100.0):100.0):100.0,
361	72.m19144	AN5996.1	AO070340000281	FG05605.1	ANAO			((((AN5996.1:100.0,AO07034000:100.0):51.0,72.m19144:100.0):93.5,FG05605.1:100.0):100.0,
362	59.m09069	AN2926.1	AO070337000185	FG01135.1	ANAO		yes	((FG01135.1:100.0,(59.m09069:100.0,(AN2926.1:100.0,AO07033700:100.0):85.0):100.0):100.0,
363	72.m19542	AN2395.1	AO070298000064	FG03320.1	AFAO	yes	yes	((FG03320.1:100.0,((AO07029800:100.0,72.m19542:100.0):96.5,AN2395.1:100.0):100.0):100.0,
364	69.m14862	AN5734.1	AO070341000025	FG06235.1	AFAO			((FG06235.1:100.0,((AO07034100:100.0,69.m14862:100.0):52.3,AN5734.1:100.0):100.0):100.0,
365	58.m07955	AN4377.1	AO070261000012	FG07387.1	AFAO	yes	yes	((FG07387.1:100.0,((AO07026100:100.0,58.m07955:100.0):95.0,AN4377.1:100.0):100.0):100.0,
366	58.m07954	AN4375.1	AO070261000014	FG07446.1	AFAO	yes	yes	((FG07446.1:100.0,(AN4375.1:100.0,(58.m07954:100.0,AO07026100:100.0):100.0):100.0):100.0,
367	66.m04708	AN6743.1	AO070313000143	FG04970.1	ANAO			((((AO07031300:100.0,AN6743.1:100.0):44.0,66.m04708:100.0):51.5,FG04970.1:100.0):100.0,
368	70.m15268	AN0665.1	AO070343000555	FG10180.1	AFAO	yes	yes	((FG10180.1:100.0,((AO07034300:100.0,70.m15268:100.0):97.0,AN0665.1:100.0):100.0):100.0,
369	59.m08502	AN3188.1	AO070312000135	FG10007.1	ANAO		yes	((FG10007.1:100.0,(59.m08502:100.0,(AN3188.1:100.0,AO07031200:100.0):80.3):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
370	57.m05893	AN7450.1	AO070229000023	FG10217.1	AFAO			((FG10217.1:100.0,((AO07022900:100.0,57.m05893:100.0):72.0,AN7450.1:100.0):100.0):100.0,
371	72.m19002	AN6171.1	AO070340000034	FG10219.1	AFAN			((FG10219.1:100.0,(AO07034000:100.0,(AN6171.1:100.0,72.m19002:100.0):57.5):100.0):100.0,
372	70.m14821	AN1403.1	AO070233000018	FG10080.1	ANAO			((FG10080.1:100.0,(70.m14821:100.0,(AN1403.1:100.0,AO07023300:100.0):48.0):100.0):100.0,
373	70.m14882	AN1350.1	AO070237000010	FG10072.1	AFAO	yes	yes	((FG10072.1:100.0,((AO07023700:100.0,70.m14882:100.0):98.5,AN1350.1:100.0):100.0):100.0,
374	70.m14876	AN1354.1	AO070237000006	FG10076.1	ANAO		yes	((FG10076.1:100.0,(70.m14876:100.0,(AN1354.1:100.0,AO07023700:100.0):86.5):100.0):100.0,
375	70.m14885	AN1348.1	AO070247000017	FG10077.1	ANAO			((FG10077.1:100.0,(70.m14885:100.0,(AN1348.1:100.0,AO07024700:100.0):74.0):100.0):100.0,
376	58.m07346	AN1950.1	AO070342000218	FG10167.1	AFAO	yes	yes	((FG10167.1:100.0,((AO07034200:100.0,58.m07346:100.0):97.5,AN1950.1:100.0):100.0):100.0,
377	57.m05343	AN8361.1	AO070286000054	FG02643.1	AFAO			((FG02643.1:100.0,((AO07028600:100.0,57.m05343:100.0):74.0,AN8361.1:100.0):100.0):100.0,
378	71.m15773	AN7745.1	AO070325000172	FG02090.1	AFAO	yes	yes	((FG02090.1:100.0,((71.m15773:100.0,AO07032500:100.0):93.0,AN7745.1:100.0):100.0):100.0,
379	57.m05816	AN2110.1	AO070341000275	FG02691.1	AFAO			((FG02691.1:100.0,((AO07034100:100.0,57.m05816:100.0):50.0,AN2110.1:100.0):100.0):100.0,
380	58.m07633	AN2045.1	AO070292000012	FG01892.1	AFAN			((FG01892.1:100.0,(AO07029200:100.0,(AN2045.1:100.0,58.m07633:100.0):36.8):100.0):100.0,
381	70.m15760	AN1181.1	AO070331000179	FG00620.1	AFAO			((FG00620.1:100.0,((AO07033100:100.0,70.m15760:100.0):53.0,AN1181.1:100.0):100.0):100.0,
382	65.m07153	AN1808.1	AO070319000057	FG04716.1	AFAN	yes	yes	((FG04716.1:100.0,((AN1808.1:100.0,65.m07153:100.0):100.0,AO07031900:100.0):100.0):100.0,
383	71.m15854	AN2211.1	AO070294000011	FG02126.1	AFAN			((FG02126.1:100.0,((71.m15854:100.0,AN2211.1:100.0):72.5,AO07029400:100.0):100.0):100.0,
384	71.m15962	AN8831.1	AO070271000048	FG02092.1	AFAO			((FG02092.1:100.0,((AO07027100:100.0,71.m15962:100.0):64.0,AN8831.1:100.0):100.0):100.0,
385	71.m15963	AN8832.1	AO070271000047	FG02093.1	AFAO		yes	((FG02093.1:100.0,((71.m15963:100.0,AO07027100:100.0):87.0,AN8832.1:100.0):100.0):100.0,
386	57.m05430	AN7663.1	AO070268000034	FG02407.1	AFAO	yes	yes	((((AO07026800:100.0,57.m05430:100.0):100.0,AN7663.1:100.0):99.5,FG02407.1:100.0):100.0,
387	53.m03738	AN8231.1	AO070310000077	FG09035.1	ANAO			((FG09035.1:100.0,(53.m03738:100.0,(AN8231.1:100.0,AO07031000:100.0):67.5):100.0):100.0,
388	69.m15711	AN4099.1	AO070343000059	FG09059.1	AFAO			((FG09059.1:100.0,((AO07034300:100.0,69.m15711:100.0):42.0,AN4099.1:100.0):100.0):100.0,
389	72.m19605	AN3888.1	AO070343000294	FG08575.1	AFAO	yes	yes	((FG08575.1:100.0,((AO07034300:100.0,72.m19605:100.0):99.0,AN3888.1:100.0):100.0):100.0,
390	71.m15603	AN8796.1	AO070276000064	FG05865.1	AFAN			((FG05865.1:100.0,((71.m15603:100.0,AN8796.1:100.0):60.5,AO07027600:100.0):100.0):100.0,
391	53.m03745	AN8228.1	AO070310000083	FG05864.1	AFAO	yes	yes	((FG05864.1:100.0,((AO07031000:100.0,53.m03745:100.0):97.5,AN8228.1:100.0):100.0):100.0,
392	71.m15151	AN3305.1	AO070329000026	FG07570.1	AFAO			((FG07570.1:100.0,((AO07032900:100.0,71.m15151:100.0):62.8,AN3305.1:100.0):100.0):100.0,
393	54.m07046	AN4105.1	AO070342000105	FG06995.1	AFAO	yes	yes	((FG06995.1:100.0,(AN4105.1:100.0,(54.m07046:100.0,AO07034200:100.0):100.0):100.0):100.0,
394	52.m03910	AN8404.1	AO070276000017	FG02975.1	AFAO			((((AO07027600:100.0,52.m03910:100.0):43.0,AN8404.1:100.0):47.5,FG02975.1:100.0):100.0,
395	71.m16076	AN8806.1	AO070276000052	FG05955.1	AFAO		yes	((FG05955.1:100.0,((71.m16076:100.0,AO07027600:100.0):85.0,AN8806.1:100.0):100.0):100.0,
396	71.m15612	AN8805.1	AO070276000053	FG05948.1	AFAO	yes	yes	((FG05948.1:100.0,(AN8805.1:100.0,(71.m15612:100.0,AO07027600:100.0):100.0):100.0):100.0,
397	52.m03887	AN3083.1	AO070339000016	FG07661.1	AFAN			((FG07661.1:100.0,(AO07033900:100.0,(AN3083.1:100.0,52.m03887:100.0):42.0):100.0):100.0,
398	58.m07369	AN4148.1	AO070342000182	FG01484.1	AFAO			((FG01484.1:100.0,((AO07034200:100.0,58.m07369:100.0):58.0,AN4148.1:100.0):100.0):100.0,
399	55.m03233	AN2037.1	AO070281000048	FG02886.1	AFAO			(((AN2037.1:100.0,(55.m03233:100.0,AO07028100:100.0):97.0):68.0,FG02886.1:100.0):100.0,
400	54.m06354	AN8060.1	AO070323000153	FG08346.1	AFAO	yes	yes	((FG08346.1:100.0,((AO07032300:100.0,54.m06354:100.0):99.0,AN8060.1:100.0):100.0):100.0,
401	71.m15902	AN2261.1	AO070326000103	FG09004.1	AFAO	yes	yes	((FG09004.1:100.0,((AO07032600:100.0,71.m15902:100.0):96.5,AN2261.1:100.0):100.0):100.0,
402	72.m20004	AN2140.1	AO070343000185	FG07412.1	ANAO			((FG07412.1:100.0,(72.m20004:100.0,(AN2140.1:100.0,AO07034300:100.0):48.8):100.0):100.0,
403	71.m15392	AN8145.1	AO070311000100	FG03521.1				(((FG03521.1:100.0,AN8145.1:100.0):100.0,(AO07031100:100.0,71.m15392:100.0):69.5):100.0,
404	59.m08509	AN3150.1	AO070191000004	FG09991.1	AFAO			((FG09991.1:100.0,((AO07019100:100.0,59.m08509:100.0):61.5,AN3150.1:100.0):100.0):100.0,
405	57.m05423	AN7659.1	AO070268000028	FG10087.1	AFAO			((FG10087.1:100.0,((57.m05423:100.0,AO07026800:100.0):58.0,AN7659.1:100.0):100.0):100.0,
406	57.m05422	AN7658.1	AO070268000027	FG10361.1	AFAO			((FG10361.1:100.0,((AO07026800:100.0,57.m05422:100.0):49.0,AN7658.1:100.0):100.0):100.0,
407	57.m05419	AN7657.1	AO070268000020	FG09980.1	AFAO	yes	yes	((FG09980.1:100.0,((AO07026800:100.0,57.m05419:100.0):97.5,AN7657.1:100.0):100.0):100.0,
408	54.m06919	AN5102.1	AO070291000077	FG10040.1	AFAO		yes	((FG10040.1:100.0,((54.m06919:100.0,AO07029100:100.0):75.5,AN5102.1:100.0):100.0):100.0,
409	54.m06960	AN5100.1	AO070291000079	FG10041.1	ANAO			((FG10041.1:100.0,((AO07029100:100.0,AN5100.1:100.0):51.0,54.m06960:100.0):98.5):100.0,
410	59.m08890	AN4987.1	AO070288000055	FG09908.1	AFAO	yes	yes	((FG09908.1:100.0,((AO07028800:100.0,59.m08890:100.0):92.0,AN4987.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
411	54.m06806	AN4244.1	AO070324000168	FG09907.1	ANAO	yes	yes	((FG09907.1:100.0,((AO07032400:100.0,AN4244.1:100.0):95.5,54.m06806:100.0):100.0):100.0,
412	71.m15616	AN8810.1	AO070276000047	FG06805.1	AFAO		yes	((FG06805.1:100.0,((AO07027600:100.0,71.m15616:100.0):85.3,AN8810.1:100.0):100.0):100.0,
413	53.m03853	AN7994.1	AO070322000052	FG06777.1	AFAO		yes	((FG06777.1:100.0,((AO07032200:100.0,53.m03853:100.0):88.0,AN7994.1:100.0):100.0):100.0,
414	53.m03854	AN7993.1	AO070322000053	FG06778.1	AFAO	yes	yes	((FG06778.1:100.0,((AO07032200:100.0,53.m03854:100.0):99.5,AN7993.1:100.0):100.0):100.0,
415	53.m03861	AN8013.1	AO070322000061	FG06781.1	ANAO			((FG06781.1:100.0,(53.m03861:100.0,(AN8013.1:100.0,AO07032200:100.0):46.5):100.0):100.0,
416	53.m03860	AN8012.1	AO070322000060	FG06784.1	ANAO		yes	((FG06784.1:100.0,(53.m03860:100.0,(AN8012.1:100.0,AO07032200:100.0):79.0):100.0):100.0,
417	53.m03880	AN8032.1	AO070322000129	FG06786.1	AFAN			((FG06786.1:100.0,(AO07032200:100.0,(AN8032.1:100.0,53.m03880:100.0):59.0):100.0):100.0,
418	62.m03096	AN6510.1	AO070270000003	FG07331.1	AFAO	yes	yes	((FG07331.1:100.0,((AO07027000:100.0,62.m03096:100.0):97.0,AN6510.1:100.0):100.0):100.0,
419	71.m16116	AN2267.1	AO070295000039	FG07332.1	AFAO	yes	yes	((FG07332.1:100.0,((AO07029500:100.0,71.m16116:100.0):99.5,AN2267.1:100.0):100.0):100.0,
420	71.m15878	AN2244.1	AO070326000129	FG05139.1	ANAO			((FG05139.1:100.0,(71.m15878:100.0,(AN2244.1:100.0,AO07032600:100.0):66.0):100.0):100.0,
421	71.m15879	AN2245.1	AO070326000128	FG05138.1	AFAN	yes	yes	((FG05138.1:100.0,(AO07032600:100.0,(AN2245.1:100.0,71.m15879:100.0):95.5):100.0):100.0,
422	71.m15881	AN2247.1	AO070326000126	FG05136.1	AFAO	yes	yes	((FG05136.1:100.0,((AO07032600:100.0,71.m15881:100.0):94.5,AN2247.1:100.0):100.0):100.0,
423	71.m15880	AN2246.1	AO070326000127	FG05135.1	AFAO	yes	yes	((FG05135.1:100.0,((AO07032600:100.0,71.m15880:100.0):99.0,AN2246.1:100.0):100.0):100.0,
424	71.m16095	AN0226.1	AO070284000066	FG05134.1	AFAO			((FG05134.1:100.0,((AO07028400:100.0,71.m16095:100.0):58.5,AN0226.1:100.0):100.0):100.0,
425	62.m03102	AN6515.1	AO070270000010	FG07320.1	AFAO	yes	yes	((FG07320.1:100.0,((AO07027000:100.0,62.m03102:100.0):97.0,AN6515.1:100.0):100.0):100.0,
426	72.m19745	AN7325.1	AO070297000077	FG07175.1	AFAO			((FG07175.1:100.0,((AO07029700:100.0,72.m19745:100.0):59.5,AN7325.1:100.0):100.0):100.0,
427	58.m07953	AN4376.1	AO070261000018	FG07174.1	ANAO			((FG07174.1:100.0,((AO07026100:100.0,AN4376.1:100.0):51.0,58.m07953:100.0):100.0):100.0,
428	70.m15083	AN1158.1	AO070331000148	FG07009.1	AFAO			((FG07009.1:100.0,((AO07033100:100.0,70.m15083:100.0):61.5,AN1158.1:100.0):100.0):100.0,
429	58.m07853	AN4467.1	AO070305000123	FG07439.1	AFAO	yes	yes	((FG07439.1:100.0,((AO07030500:100.0,58.m07853:100.0):93.0,AN4467.1:100.0):100.0):100.0,
430	65.m07411	AN5685.1	AO070309000100	FG07442.1	ANAO			((FG07442.1:100.0,((AO07030900:100.0,AN5685.1:100.0):50.8,65.m07411:100.0):100.0):100.0,
431	65.m07412	AN5686.1	AO070309000101	FG07443.1	AFAO			((FG07443.1:100.0,((AO07030900:100.0,65.m07412:100.0):71.3,AN5686.1:100.0):100.0):100.0,
432	65.m07413	AN5687.1	AO070309000102	FG07444.1	AFAO			((FG07444.1:100.0,((AO07030900:100.0,65.m07413:100.0):62.5,AN5687.1:100.0):100.0):100.0,
433	62.m03123	AN6550.1	AO070270000035	FG05195.1	AFAO			((FG05195.1:100.0,((AO07027000:100.0,62.m03123:100.0):71.5,AN6550.1:100.0):100.0):100.0,
434	71.m15754	AN7732.1	AO070325000143	FG02049.1	AFAN			((FG02049.1:100.0,(AO07032500:100.0,(AN7732.1:100.0,71.m15754:100.0):74.5):100.0):100.0,
435	54.m06773	AN4216.1	AO070231000008	FG02096.1	AFAO	yes	yes	((FG02096.1:100.0,((AO07023100:100.0,54.m06773:100.0):99.0,AN4216.1:100.0):100.0):100.0,
436	54.m06772	AN4215.1	AO070231000009	FG02097.1	ANAO			((FG02097.1:100.0,((AO07023100:100.0,AN4215.1:100.0):51.8,54.m06772:100.0):99.7):100.0,
437	54.m06762	AN4202.1	AO070231000022	FG02099.1	AFAN			((FG02099.1:100.0,(AO07023100:100.0,(AN4202.1:100.0,54.m06762:100.0):65.5):100.0):100.0,
438	71.m15944	AN2295.1	AO070295000075	FG02030.1	ANAO			((FG02030.1:100.0,((AO07029500:100.0,AN2295.1:100.0):62.5,71.m15944:100.0):100.0):100.0,
439	71.m15943	AN2294.1	AO070295000074	FG02040.1	AFAN		yes	((FG02040.1:100.0,(AO07029500:100.0,(AN2294.1:100.0,71.m15943:100.0):82.5):100.0):100.0,
440	72.m19092	AN6095.1	AO070340000163	FG05882.1	AFAO	yes	yes	((FG05882.1:100.0,((AO07034000:100.0,72.m19092:100.0):95.0,AN6095.1:100.0):100.0):100.0,
441	53.m03863	AN8016.1	AO070322000065	FG05858.1	AFAO	yes	yes	((FG05858.1:100.0,(AN8016.1:100.0,(53.m03863:100.0,AO07032200:100.0):100.0):100.0):100.0,
442	53.m04142	AN8015.1	AO070322000064	FG05857.1	AFAN			((FG05857.1:100.0,(AO07032200:100.0,(AN8015.1:100.0,53.m04142:100.0):49.0):100.0):100.0,
443	53.m03763	AN8211.1	AO070310000102	FG05855.1	AFAO	yes	yes	((FG05855.1:100.0,(AN8211.1:100.0,(53.m03763:100.0,AO07031000:100.0):100.0):100.0):100.0,
444	71.m15604	AN8797.1	AO070276000063	FG05861.1	AFAO			((FG05861.1:100.0,((71.m15604:100.0,AO07027600:100.0):52.3,AN8797.1:100.0):100.0):100.0,
445	65.m07308	AN8785.1	AO070289000010	FG07131.1	AFAO	yes	yes	((FG07131.1:100.0,((AO07028900:100.0,65.m07308:100.0):97.5,AN8785.1:100.0):100.0):100.0,
446	72.m19704	AN2136.1	AO070343000181	FG07133.1	AFAN			((FG07133.1:100.0,((72.m19704:100.0,AN2136.1:100.0):56.0,AO07034300:100.0):100.0):100.0,
447	72.m19697	AN2144.1	AO070343000192	FG07138.1	AFAO	yes	yes	((FG07138.1:100.0,((AO07034300:100.0,72.m19697:100.0):98.0,AN2144.1:100.0):100.0):100.0,
448	72.m19698	AN2143.1	AO070343000190	FG07139.1	AFAO			((FG07139.1:100.0,((AO07034300:100.0,72.m19698:100.0):57.5,AN2143.1:100.0):100.0):100.0,
449	72.m19700	AN2141.1	AO070343000187	FG07140.1	AFAO			((FG07140.1:100.0,((AO07034300:100.0,72.m19700:100.0):62.5,AN2141.1:100.0):100.0):100.0,
450	72.m19699	AN2142.1	AO070343000188	FG07141.1	ANAO			((FG07141.1:100.0,((AO07034300:100.0,AN2142.1:100.0):54.0,72.m19699:100.0):100.0):100.0,
451	54.m06468	AN0275.1	AO070334000082	FG07129.1	AFAN		yes	((FG07129.1:100.0,(AO07033400:100.0,(AN0275.1:100.0,54.m06468:100.0):76.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
452	71.m15357	AN0078.1	AO070311000137	FG07456.1	AFAO	yes	yes	((FG07456.1:100.0,((AO07031100:100.0,71.m15357:100.0):92.0,AN0078.1:100.0):100.0):100.0,
453	70.m15150	AN1076.1	AO070285000076	FG07454.1	AFAO	yes	yes	((FG07454.1:100.0,((AO07028500:100.0,70.m15150:100.0):90.5,AN1076.1:100.0):100.0):100.0,
454	70.m15138	AN1093.1	AO070285000054	FG07453.1	AFAO			((FG07453.1:100.0,((AO07028500:100.0,70.m15138:100.0):42.5,AN1093.1:100.0):100.0):100.0,
455	70.m15139	AN1092.1	AO070285000055	FG06147.1	AFAO			((FG06147.1:100.0,((70.m15139:100.0,AO07028500:100.0):65.0,AN1092.1:100.0):100.0):100.0,
456	72.m19738	AN7331.1	AO070297000093	FG07458.1	AFAO		yes	((FG07458.1:100.0,((72.m19738:100.0,AO07029700:100.0):81.7,AN7331.1:100.0):100.0):100.0,
457	72.m19695	AN2146.1	AO070343000195	FG07460.1	AFAO	yes	yes	((FG07460.1:100.0,((AO07034300:100.0,72.m19695:100.0):90.0,AN2146.1:100.0):100.0):100.0,
458	70.m15267	AN0664.1	AO070343000556	FG05898.1	AFAO	yes	yes	((FG05898.1:100.0,((AO07034300:100.0,70.m15267:100.0):99.0,AN0664.1:100.0):100.0):100.0,
459	59.m09050	AN2965.1	AO070337000162	FG01908.1	AFAO			((FG01908.1:100.0,((AO07033700:100.0,59.m09050:100.0):49.3,AN2965.1:100.0):100.0):100.0,
460	58.m07821	AN3846.1	AO070305000083	FG05903.1	AFAO	yes	yes	((FG05903.1:100.0,((AO07030500:100.0,58.m07821:100.0):98.0,AN3846.1:100.0):100.0):100.0,
461	58.m07830	AN3853.1	AO070305000093	FG05902.1	AFAO	yes	yes	((FG05902.1:100.0,(AN3853.1:100.0,(58.m07830:100.0,AO07030500:100.0):100.0):100.0):100.0,
462	58.m07832	AN3852.1	AO070305000091	FG05918.1	ANAO	yes	yes	((FG05918.1:100.0,(58.m07832:100.0,(AN3852.1:100.0,AO07030500:100.0):97.5):100.0):100.0,
463	58.m07827	AN3855.1	AO070305000095	FG05919.1	AFAO		yes	((FG05919.1:100.0,((AO07030500:100.0,58.m07827:100.0):79.5,AN3855.1:100.0):100.0):100.0,
464	54.m06686	AN2745.1	AO070338000226	FG01906.1	AFAO			((FG01906.1:100.0,((AO07033800:100.0,54.m06686:100.0):61.0,AN2745.1:100.0):100.0):100.0,
465	70.m14839	AN1382.1	AO070243000014	FG10376.1	AFAN			((FG10376.1:100.0,((70.m14839:100.0,AN1382.1:100.0):49.0,AO07024300:100.0):100.0):100.0,
466	54.m06803	AN4240.1	AO070324000174	FG10092.1	AFAO	yes	yes	((FG10092.1:100.0,((AO07032400:100.0,54.m06803:100.0):99.5,AN4240.1:100.0):100.0):100.0,
467	66.m04562	AN9101.1	AO070332000172	FG10185.1	AFAO	yes	yes	((FG10185.1:100.0,(AN9101.1:100.0,(66.m04562:100.0,AO07033200:100.0):100.0):100.0):100.0,
468	57.m05649	AN4482.1	AO070311000031	FG07881.1	AFAO	yes	yes	((FG07881.1:100.0,(AN4482.1:100.0,(57.m05649:100.0,AO07031100:100.0):100.0):100.0):100.0,
469	71.m15986	AN8851.1	AO070271000025	FG07206.1	AFAO		yes	((FG07206.1:100.0,((AO07027100:100.0,71.m15986:100.0):86.5,AN8851.1:100.0):100.0):100.0,
470	62.m03136	AN6536.1	AO070270000048	FG06093.1	ANAO			((FG06093.1:100.0,(62.m03136:100.0,(AN6536.1:100.0,AO07027000:100.0):71.5):100.0):100.0,
471	54.m06496	AN0266.1	AO070334000087	FG01895.1	AFAO	yes	yes	((FG01895.1:100.0,((AO07033400:100.0,54.m06496:100.0):92.5,AN0266.1:100.0):100.0):100.0,
472	54.m06967	AN0265.1	AO070334000094	FG01916.1	AFAO			((FG01916.1:100.0,((AO07033400:100.0,54.m06967:100.0):53.0,AN0265.1:100.0):100.0):100.0,
473	54.m06965	AN0261.1	AO070334000097	FG01917.1	AFAO		yes	((FG01917.1:100.0,((AO07033400:100.0,54.m06965:100.0):84.0,AN0261.1:100.0):100.0):100.0,
474	72.m19045	AN6114.1	AO070340000090	FG01896.1	AFAO			((FG01896.1:100.0,((AO07034000:100.0,72.m19045:100.0):49.3,AN6114.1:100.0):100.0):100.0,
475	72.m19013	AN6166.1	AO070340000049	FG01903.1	ANAO			((FG01903.1:100.0,(72.m19013:100.0,(AN6166.1:100.0,AO07034000:100.0):59.5):100.0):100.0,
476	59.m09052	AN2963.1	AO070337000166	FG01910.1	AFAO			((FG01910.1:100.0,((AO07033700:100.0,59.m09052:100.0):70.5,AN2963.1:100.0):100.0):100.0,
477	59.m09054	AN2940.1	AO070337000170	FG01909.1	AFAO			((FG01909.1:100.0,((AO07033700:100.0,59.m09054:100.0):67.5,AN2940.1:100.0):100.0):100.0,
478	57.m05457	AN7680.1	AO070325000070	FG10348.1	AFAO		yes	((FG10348.1:100.0,((AO07032500:100.0,57.m05457:100.0):76.5,AN7680.1:100.0):100.0):100.0,
479	70.m15291	AN0688.1	AO070343000525	FG09998.1	AFAO	yes	yes	((FG09998.1:100.0,((AO07034300:100.0,70.m15291:100.0):90.5,AN0688.1:100.0):100.0):100.0,
480	70.m15533	AN0925.1	AO070320000104	FG10000.1	ANAO		yes	((FG10000.1:100.0,(70.m15533:100.0,(AN0925.1:100.0,AO07032000:100.0):76.5):100.0):100.0,
481	57.m05886	AN1319.1	AO070287000068	FG10001.1	AFAO		yes	((FG10001.1:100.0,((57.m05886:100.0,AO07028700:100.0):90.5,AN1319.1:100.0):89.0):100.0,
482	59.m09372	AN3088.1	AO070266000041	FG10002.1	AFAN			((((AN3088.1:100.0,59.m09372:100.0):60.2,AO07026600:100.0):93.1,FG10002.1:100.0):100.0,
483	54.m07057	AN5184.1	AO070291000019	FG10003.1	AFAO		yes	((FG10003.1:100.0,((AO07029100:100.0,54.m07057:100.0):85.5,AN5184.1:100.0):100.0):100.0,
484	58.m08969	AN4385.1	AO070261000030	FG10381.1	AFAO			((FG10381.1:100.0,((58.m08969:100.0,AO07026100:100.0):68.0,AN4385.1:100.0):100.0):100.0,
485	58.m07940	AN4384.1	AO070261000029	FG10379.1	ANAO			((FG10379.1:100.0,(58.m07940:100.0,(AN4384.1:100.0,AO07026100:100.0):54.0):100.0):100.0,
486	59.m09341	AN2510.1	AO070263000047	FG10378.1	AFAO	yes	yes	((FG10378.1:100.0,((AO07026300:100.0,59.m09341:100.0):95.5,AN2510.1:100.0):100.0):100.0,
487	59.m09396	AN2911.1	AO070338000094	FG10142.1	AFAO		yes	((FG10142.1:100.0,((AO07033800:100.0,59.m09396:100.0):76.0,AN2911.1:100.0):100.0):100.0,
488	71.m15260	AN6869.1	AO070314000053	FG02206.1	AFAO			((FG02206.1:100.0,((71.m15260:100.0,AO07031400:100.0):60.5,AN6869.1:100.0):100.0):100.0,
489	57.m05476	AN4645.1	AO070316000119	FG10018.1	AFAO	yes	yes	((((AO07031600:100.0,57.m05476:100.0):100.0,AN4645.1:100.0):99.0,FG10018.1:100.0):100.0,
490	54.m06746	AN4188.1	AO070342000109	FG01911.1	AFAO	yes	yes	((FG01911.1:100.0,((AO07034200:100.0,54.m06746:100.0):93.0,AN4188.1:100.0):100.0):100.0,
491	71.m16046	AN0077.1	AO070311000138	FG07012.1	AFAO		yes	((FG07012.1:100.0,((71.m16046:100.0,AO07031100:100.0):81.0,AN0077.1:100.0):100.0):100.0,
492	58.m07868	AN4456.1	AO070173000001	FG06802.1	AFAO			((FG06802.1:100.0,((AO07017300:100.0,58.m07868:100.0):63.5,AN4456.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
493	58.m07867	AN4457.1	AO070305000136	FG06803.1	AFAO			((FG06803.1:100.0,((AO07030500:100.0,58.m07867:100.0):74.5,AN4457.1:100.0):100.0):100.0,
494	72.m19952	AN5931.1	AO070340000344	FG04132.1	AFAO			((FG04132.1:100.0,((72.m19952:100.0,AO07034000:100.0):67.5,AN5931.1:100.0):100.0):100.0,
495	71.m15750	AN7723.1	AO070325000138	FG06122.1	AFAO		yes	((FG06122.1:100.0,((AO07032500:100.0,71.m15750:100.0):82.5,AN7723.1:100.0):100.0):100.0,
496	59.m08496	AN2493.1	AO070312000127	FG07375.1	AFAO	yes	yes	((FG07375.1:100.0,((AO07031200:100.0,59.m08496:100.0):95.0,AN2493.1:100.0):100.0):100.0,
497	53.m03844	AN8002.1	AO070322000044	FG06092.1	AFAO	yes	yes	((FG06092.1:100.0,((AO07032200:100.0,53.m03844:100.0):98.0,AN8002.1:100.0):100.0):100.0,
498	55.m02988	AN1482.1	AO070334000186	FG06090.1	AFAO	yes	yes	((FG06090.1:100.0,(AN1482.1:100.0,(55.m02988:100.0,AO07033400:100.0):100.0):100.0):100.0,
499	53.m04194	AN8000.1	AO070322000046	FG06089.1	AFAO	yes	yes	((FG06089.1:100.0,(AN8000.1:100.0,(53.m04194:100.0,AO07032200:100.0):100.0):100.0):100.0,
500	53.m03831	AN8120.1	AO070322000028	FG07371.1	AFAO		yes	((FG07371.1:100.0,((AO07032200:100.0,53.m03831:100.0):86.0,AN8120.1:100.0):100.0):100.0,
501	53.m03830	AN8119.1	AO070322000027	FG07370.1	AFAO	yes	yes	((FG07370.1:100.0,((AO07032200:100.0,53.m03830:100.0):92.5,AN8119.1:100.0):100.0):100.0,
502	53.m03810	AN8167.1	AO070266000001	FG05979.1	AFAO		yes	((FG05979.1:100.0,((AO07026600:100.0,53.m03810:100.0):87.0,AN8167.1:100.0):100.0):100.0,
503	58.m07325	AN5638.1	AO070342000239	FG10110.1	AFAO	yes	yes	((FG10110.1:100.0,((AO07034200:100.0,58.m07325:100.0):91.0,AN5638.1:100.0):100.0):100.0,
504	70.m15789	AN0657.1	AO070343000569	FG10106.1	AFAN	yes	yes	((FG10106.1:100.0,(AO07034300:100.0,(AN0657.1:100.0,70.m15789:100.0):93.5):100.0):100.0,
505	66.m04760	AN9108.1	AO070332000164	FG09040.1	AFAN			((FG09040.1:100.0,(AO07033200:100.0,(AN9108.1:100.0,66.m04760:100.0):64.0):100.0):100.0,
506	66.m04767	AN9099.1	AO070332000175	FG10105.1	AFAO	yes	yes	((FG10105.1:100.0,(AN9099.1:100.0,(66.m04767:100.0,AO07033200:100.0):100.0):100.0):100.0,
507	58.m08892	AN5656.1	AO070342000244	FG10120.1	AFAO	yes	yes	((FG10120.1:100.0,((AO07034200:100.0,58.m08892:100.0):98.0,AN5656.1:100.0):100.0):100.0,
508	72.m18927	AN5799.1	AO070260000050	FG10121.1	AFAO			((FG10121.1:100.0,((AO07026000:100.0,72.m18927:100.0):53.5,AN5799.1:100.0):100.0):100.0,
509	72.m18961	AN5833.1	AO070260000012	FG10126.1	AFAO		yes	((FG10126.1:100.0,((AO07026000:100.0,72.m18961:100.0):79.0,AN5833.1:100.0):100.0):100.0,
510	54.m06399	AN7194.1	AO070197000003	FG10124.1	ANAO			((FG10124.1:100.0,(54.m06399:100.0,(AN7194.1:100.0,AO07019700:100.0):47.0):100.0):100.0,
511	59.m08905	AN5005.1	AO070255000035	FG09912.1	AFAO		yes	((FG09912.1:100.0,((AO07025500:100.0,59.m08905:100.0):89.5,AN5005.1:100.0):100.0):100.0,
512	59.m09439	AN2996.1	AO070337000121	FG10179.1	ANAO			((FG10179.1:100.0,(59.m09439:100.0,(AN2996.1:100.0,AO07033700:100.0):54.3):100.0):100.0,
513	72.m19619	AN7594.1	AO070343000316	FG10177.1	AFAO			(((AN7594.1:100.0,(72.m19619:100.0,AO07034300:100.0):48.2):65.8,FG10177.1:100.0):100.0,
514	70.m15258	AN0654.1	AO070343000572	FG10097.1	AFAO			((FG10097.1:100.0,((70.m15258:100.0,AO07034300:100.0):56.3,AN0654.1:100.0):100.0):100.0,
515	62.m03436	AN2409.1	AO070298000018	FG05221.1	ANAO		yes	((((AN2409.1:100.0,AO07029800:100.0):100.0,62.m03436:100.0):85.0,FG05221.1:100.0):100.0,
516	69.m14863	AN5733.1	AO070341000027	FG06234.1	ANAO			((FG06234.1:100.0,(69.m14863:100.0,(AN5733.1:100.0,AO07034100:100.0):73.0):100.0):100.0,
517	71.m16001	AN8863.1	AO070271000008	FG07467.1	ANAO		yes	((FG07467.1:100.0,(71.m16001:100.0,(AN8863.1:100.0,AO07027100:100.0):77.5):100.0):100.0,
518	71.m16005	AN8866.1	AO070271000005	FG07468.1	AFAO		yes	((FG07468.1:100.0,((AO07027100:100.0,71.m16005:100.0):76.5,AN8866.1:100.0):100.0):100.0,
519	71.m16000	AN8862.1	AO070271000009	FG07469.1	AFAO			((FG07469.1:100.0,((71.m16000:100.0,AO07027100:100.0):63.0,AN8862.1:100.0):100.0):100.0,
520	71.m16007	AN8868.1	AO070271000003	FG07473.1	ANAO			((FG07473.1:100.0,(71.m16007:100.0,(AN8868.1:100.0,AO07027100:100.0):60.5):100.0):100.0,
521	71.m16009	AN8869.1	AO070271000002	FG07475.1	AFAO		yes	((FG07475.1:100.0,((71.m16009:100.0,AO07027100:100.0):87.5,AN8869.1:100.0):100.0):100.0,
522	57.m05936	AN7660.1	AO070268000029	FG07477.1	AFAO	yes	yes	((FG07477.1:100.0,((AO07026800:100.0,57.m05936:100.0):96.0,AN7660.1:100.0):100.0):100.0,
523	71.m16010	AN8870.1	AO070271000001	FG07480.1	AFAO		yes	((FG07480.1:100.0,((AO07027100:100.0,71.m16010:100.0):85.5,AN8870.1:100.0):100.0):100.0,
524	58.m07622	AN2014.1	AO070202000006	FG01900.1	ANAO			((FG01900.1:100.0,((AO07020200:100.0,AN2014.1:100.0):38.0,58.m07622:100.0):100.0):100.0,
525	71.m15219	AN6913.1	AO070219000018	FG06107.1	AFAN			((FG06107.1:100.0,((71.m15219:100.0,AN6913.1:100.0):70.5,AO07021900:100.0):100.0):100.0,
526	72.m19041	AN6119.1	AO070340000085	FG01898.1	AFAO	yes	yes	((FG01898.1:100.0,(AN6119.1:100.0,(72.m19041:100.0,AO07034000:100.0):100.0):100.0):100.0,
527	71.m16037	AN6851.1	AO070314000088	FG08998.1	AFAN			((FG08998.1:100.0,(AO07031400:100.0,(AN6851.1:100.0,71.m16037:100.0):39.8):100.0):100.0,
528	71.m15299	AN6842.1	AO070314000097	FG09002.1	AFAO			((FG09002.1:100.0,((AO07031400:100.0,71.m15299:100.0):43.0,AN6842.1:100.0):100.0):100.0,
529	71.m15300	AN6843.1	AO070314000096	FG09003.1	AFAO		yes	((FG09003.1:100.0,((71.m15300:100.0,AO07031400:100.0):83.3,AN6843.1:100.0):100.0):100.0,
530	57.m05570	AN4558.1	AO070321000170	FG06810.1	AFAN			((FG06810.1:100.0,(AO07032100:100.0,(AN4558.1:100.0,57.m05570:100.0):38.5):100.0):100.0,
531	57.m05569	AN4557.1	AO070321000171	FG06816.1	AFAO	yes	yes	((FG06816.1:100.0,((AO07032100:100.0,57.m05569:100.0):99.5,AN4557.1:100.0):100.0):100.0,
532	58.m09004	AN4428.1	AO070273000065	FG04398.1	AFAN			((FG04398.1:100.0,(AO07027300:100.0,(AN4428.1:100.0,58.m09004:100.0):48.0):100.0):100.0,
533	69.m14856	AN5741.1	AO070341000018	FG04401.1	ANAO			((FG04401.1:100.0,((AO07034100:100.0,AN5741.1:100.0):57.5,69.m14856:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
534	58.m08967	AN4413.1	AO070273000034	FG04361.1	AFAO	yes	yes	((FG04361.1:100.0,(AN4413.1:100.0,(58.m08967:100.0,AO07027300:100.0):100.0):100.0):100.0,
535	58.m07898	AN4410.1	AO070273000030	FG04362.1	AFAO	yes	yes	((FG04362.1:100.0,((AO07027300:100.0,58.m07898:100.0):99.0,AN4410.1:100.0):100.0):100.0,
536	58.m07613	AN2005.1	AO070301000107	FG04363.1	ANAO			((((AN2005.1:100.0,AO07030100:100.0):60.0,58.m07613:100.0):99.0,FG04363.1:100.0):100.0,
537	72.m19414	AN6243.1	AO070304000097	FG04418.1	ANAO			((FG04418.1:100.0,(72.m19414:100.0,(AN6243.1:100.0,AO07030400:100.0):68.0):100.0):100.0,
538	72.m19392	AN6265.1	AO070304000023	FG04404.1	AFAO	yes	yes	((FG04404.1:100.0,(AN6265.1:100.0,(72.m19392:100.0,AO07030400:100.0):100.0):100.0):100.0,
539	72.m19391	AN6266.1	AO070304000022	FG04403.1	AFAO	yes	yes	((FG04403.1:100.0,((AO07030400:100.0,72.m19391:100.0):90.0,AN6266.1:100.0):100.0):100.0,
540	72.m19407	AN6249.1	AO070304000039	FG01450.1	AFAO		yes	((FG01450.1:100.0,((AO07030400:100.0,72.m19407:100.0):87.0,AN6249.1:100.0):100.0):100.0,
541	58.m07546	AN5624.1	AO070301000021	FG04378.1	AFAO		yes	((FG04378.1:100.0,((AO07030100:100.0,58.m07546:100.0):85.5,AN5624.1:100.0):100.0):100.0,
542	72.m19983	AN0232.1	AO070304000024	FG04402.1	AFAO			((FG04402.1:100.0,((AO07030400:100.0,72.m19983:100.0):71.5,AN0232.1:100.0):100.0):100.0,
543	72.m19404	AN6253.1	AO070304000103	FG01449.1	AFAO			((FG01449.1:100.0,((72.m19404:100.0,AO07030400:100.0):49.5,AN6253.1:100.0):100.0):100.0,
544	72.m19981	AN6254.1	AO070304000034	FG01448.1	AFAO			((FG01448.1:100.0,((AO07030400:100.0,72.m19981:100.0):69.0,AN6254.1:100.0):100.0):100.0,
545	72.m19410	AN6252.1	AO070304000035	FG01447.1	AFAN			((FG01447.1:100.0,(AO07030400:100.0,(AN6252.1:100.0,72.m19410:100.0):68.0):100.0):100.0,
546	72.m19405	AN6248.1	AO070304000104	FG00305.1	ANAO			((FG00305.1:100.0,(72.m19405:100.0,(AN6248.1:100.0,AO07030400:100.0):50.8):100.0):100.0,
547	57.m05372	AN7402.1	AO070293000033	FG06278.1	AFAN	yes	yes	((FG06278.1:100.0,((AN7402.1:100.0,57.m05372:100.0):100.0,AO07029300:100.0):100.0):100.0,
548	54.m06410	AN0347.1	AO070318000025	FG04327.1				((AN0347.1:100.0,((AO07031800:100.0,54.m06410:100.0):98.2,FG04327.1:100.0):58.8):100.0,
549	53.m04190	AN8042.1	AO070330000004	FG04324.1	AFAO		yes	((FG04324.1:100.0,((AO07033000:100.0,53.m04190:100.0):81.0,AN8042.1:100.0):100.0):100.0,
550	53.m03905	AN8041.1	AO070330000005	FG06257.1	AFAO			((FG06257.1:100.0,((AO07033000:100.0,53.m03905:100.0):61.5,AN8041.1:100.0):100.0):100.0,
551	72.m19398	AN6258.1	AO070304000030	FG04329.1	AFAO	yes	yes	((FG04329.1:100.0,((AO07030400:100.0,72.m19398:100.0):98.5,AN6258.1:100.0):100.0):100.0,
552	54.m06903	AN5121.1	AO070291000058	FG10738.1	ANAO			((FG10738.1:100.0,(54.m06903:100.0,(AN5121.1:100.0,AO07029100:100.0):53.5):100.0):100.0,
553	54.m06899	AN5126.1	AO070291000052	FG10736.1	AFAO	yes	yes	((FG10736.1:100.0,(AN5126.1:100.0,(54.m06899:100.0,AO07029100:100.0):100.0):100.0):100.0,
554	54.m06902	AN5122.1	AO070291000057	FG10737.1	AFAO	yes	yes	((FG10737.1:100.0,(AN5122.1:100.0,(54.m06902:100.0,AO07029100:100.0):100.0):100.0):100.0,
555	72.m19668	AN2172.1	AO070343000243	FG04355.1	AFAO	yes	yes	((FG04355.1:100.0,((AO07034300:100.0,72.m19668:100.0):90.0,AN2172.1:100.0):100.0):100.0,
556	71.m15391	AN0115.1	AO070311000099	FG04351.1	AFAO	yes	yes	((FG04351.1:100.0,((AO07031100:100.0,71.m15391:100.0):98.0,AN0115.1:100.0):100.0):100.0,
557	71.m15390	AN0114.1	AO070311000098	FG04358.1	AFAO		yes	((FG04358.1:100.0,((AO07031100:100.0,71.m15390:100.0):83.0,AN0114.1:100.0):100.0):100.0,
558	58.m08945	AN1981.1	AO070301000066	FG10730.1	AFAO		yes	((FG10730.1:100.0,((AO07030100:100.0,58.m08945:100.0):86.0,AN1981.1:100.0):100.0):100.0,
559	72.m19671	AN2169.1	AO070343000239	FG10727.1	AFAO			((FG10727.1:100.0,((AO07034300:100.0,72.m19671:100.0):63.0,AN2169.1:100.0):100.0):100.0,
560	71.m15421	AN0138.1	AO070321000114	FG10862.1	AFAO	yes	yes	((FG10862.1:100.0,((AO07032100:100.0,71.m15421:100.0):91.0,AN0138.1:100.0):100.0):100.0,
561	53.m03669	AN9413.1	AO070310000006	FG06242.1	ANAO	yes	yes	((FG06242.1:100.0,(53.m03669:100.0,(AN9413.1:100.0,AO07031000:100.0):94.0):100.0):100.0,
562	71.m16072	AN2317.1	AO070323000039	FG06245.1	AFAO		yes	((FG06245.1:100.0,((AO07032300:100.0,71.m16072:100.0):75.5,AN2317.1:100.0):100.0):100.0,
563	72.m19080	AN6089.1	AO070340000143	FG06246.1	ANAO		yes	((FG06246.1:100.0,(72.m19080:100.0,(AN6089.1:100.0,AO07034000:100.0):86.0):100.0):100.0,
564	54.m06790	AN4226.1	AO070234000023	FG01446.1	AFAO	yes	yes	((FG01446.1:100.0,((AO07023400:100.0,54.m06790:100.0):94.0,AN4226.1:100.0):100.0):100.0,
565	59.m08580	AN9303.1	AO070275000031	FG00828.1	AFAN			((((AN9303.1:100.0,59.m08580:100.0):56.0,AO07027500:100.0):93.5,FG00828.1:100.0):100.0,
566	59.m08579	AN3178.1	AO070256000001	FG00827.1	ANAO			((FG00827.1:100.0,(59.m08579:100.0,(AN3178.1:100.0,AO07025600:100.0):69.2):100.0):100.0,
567	72.m19347	AN6288.1	AO070308000004	FG00301.1	AFAO		yes	((FG00301.1:100.0,((AO07030800:100.0,72.m19347:100.0):87.3,AN6288.1:100.0):100.0):100.0,
568	72.m19348	AN6287.1	AO070308000005	FG00300.1	AFAO	yes	yes	((FG00300.1:100.0,((AO07030800:100.0,72.m19348:100.0):94.5,AN6287.1:100.0):100.0):100.0,
569	71.m15429	AN0145.1	AO070321000098	FG01557.1	AFAO			((FG01557.1:100.0,((AO07032100:100.0,71.m15429:100.0):74.0,AN0145.1:100.0):100.0):100.0,
570	70.m15175	AN1059.1	AO070218000002	FG00840.1	AFAO	yes	yes	((FG00840.1:100.0,((AO07021800:100.0,70.m15175:100.0):98.0,AN1059.1:100.0):100.0):100.0,
571	71.m15417	AN0133.1	AO070321000120	FG10757.1	AFAO			((FG10757.1:100.0,((AO07032100:100.0,71.m15417:100.0):60.5,AN0133.1:100.0):100.0):100.0,
572	71.m15418	AN0134.1	AO070321000119	FG10756.1	AFAO	yes	yes	((FG10756.1:100.0,((AO07032100:100.0,71.m15418:100.0):92.5,AN0134.1:100.0):100.0):100.0,
573	69.m15673	AN2456.1	AO070264000017	FG10760.1	AFAO	yes	yes	((FG10760.1:100.0,(AN2456.1:100.0,(69.m15673:100.0,AO07026400:100.0):100.0):100.0):100.0,
574	70.m15786	AN9436.1	AO070343000484	FG04295.1	AFAO	yes	yes	((FG04295.1:100.0,((AO07034300:100.0,70.m15786:100.0):94.0,AN9436.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
575	70.m15319	AN0734.1	AO070343000495	FG05491.1	AFAO			(((AN0734.1:100.0,(AO07034300:100.0,70.m15319:100.0):54.4):40.0,FG05491.1:100.0):100.0,
576	70.m15320	AN0733.1	AO070343000494	FG04290.1	AFAO	yes	yes	(((AN0733.1:100.0,(70.m15320:100.0,AO07034300:100.0):91.0):99.5,FG04290.1:100.0):100.0,
577	58.m07833	AN3849.1	AO070332000050	FG07224.1	AFAN			((((58.m07833:100.0,AN3849.1:100.0):59.8,AO07033200:100.0):54.7,FG07224.1:100.0):100.0,
578	70.m15330	AN0727.1	AO070343000486	FG04292.1	ANAO		yes	((FG04292.1:100.0,(70.m15330:100.0,(AN0727.1:100.0,AO07034300:100.0):86.0):100.0):100.0,
579	70.m15314	AN0707.1	AO070343000502	FG10716.1	AFAO		yes	((FG10716.1:100.0,((AO07034300:100.0,70.m15314:100.0):86.0,AN0707.1:100.0):100.0):100.0,
580	70.m15313	AN0706.1	AO070343000503	FG10717.1	AFAO		yes	((FG10717.1:100.0,((AO07034300:100.0,70.m15313:100.0):81.0,AN0706.1:100.0):100.0):100.0,
581	54.m06915	AN5107.1	AO070291000072	FG01533.1	ANAO		yes	((FG01533.1:100.0,(54.m06915:100.0,(AN5107.1:100.0,AO07029100:100.0):77.0):100.0):100.0,
582	54.m06916	AN5106.1	AO070291000073	FG01534.1	AFAO			((FG01534.1:100.0,((AO07029100:100.0,54.m06916:100.0):67.0,AN5106.1:100.0):100.0):100.0,
583	54.m06917	AN5105.1	AO070291000074	FG01535.1	AFAO			((FG01535.1:100.0,((AO07029100:100.0,54.m06917:100.0):60.5,AN5105.1:100.0):100.0):100.0,
584	53.m04091	AN8277.1	AO070310000023	FG01417.1	AFAO		yes	((FG01417.1:100.0,((53.m04091:100.0,AO07031000:100.0):79.5,AN8277.1:100.0):100.0):100.0,
585	53.m03681	AN8280.1	AO070310000020	FG01419.1	AFAO		yes	((FG01419.1:100.0,((AO07031000:100.0,53.m03681:100.0):89.0,AN8280.1:100.0):100.0):100.0,
586	58.m07968	AN4349.1	AO070240000029	FG06284.1	AFAO	yes	yes	((FG06284.1:100.0,((AO07024000:100.0,58.m07968:100.0):92.0,AN4349.1:100.0):100.0):100.0,
587	58.m07895	AN4430.1	AO070273000027	FG06282.1	AFAO	yes	yes	((FG06282.1:100.0,((AO07027300:100.0,58.m07895:100.0):92.0,AN4430.1:100.0):100.0):100.0,
588	58.m07897	AN4409.1	AO070273000029	FG06281.1	AFAO		yes	((FG06281.1:100.0,((AO07027300:100.0,58.m07897:100.0):89.5,AN4409.1:100.0):100.0):100.0,
589	58.m07896	AN4408.1	AO070273000028	FG06280.1	AFAO			((FG06280.1:100.0,((AO07027300:100.0,58.m07896:100.0):62.5,AN4408.1:100.0):100.0):100.0,
590	59.m08647	AN3096.1	AO070334000138	FG10718.1	ANAO			((FG10718.1:100.0,((AO07033400:100.0,AN3096.1:100.0):51.0,59.m08647:100.0):100.0):100.0,
591	72.m19390	AN6267.1	AO070304000021	FG06277.1	ANAO		yes	((FG06277.1:100.0,(72.m19390:100.0,(AN6267.1:100.0,AO07030400:100.0):84.5):100.0):100.0,
592	72.m19298	AN6200.1	AO070308000096	FG01553.1	AFAO	yes	yes	((FG01553.1:100.0,((AO07030800:100.0,72.m19298:100.0):96.0,AN6200.1:100.0):100.0):100.0,
593	54.m06983	AN0318.1	AO070334000014	FG01425.1	AFAO			((FG01425.1:100.0,((AO07033400:100.0,54.m06983:100.0):62.5,AN0318.1:100.0):100.0):100.0,
594	53.m03686	AN8274.1	AO070310000027	FG01421.1	AFAO			((FG01421.1:100.0,((AO07031000:100.0,53.m03686:100.0):58.8,AN8274.1:100.0):100.0):100.0,
595	53.m03685	AN8275.1	AO070310000026	FG01422.1	ANAO			((FG01422.1:100.0,(53.m03685:100.0,(AN8275.1:100.0,AO07031000:100.0):56.5):100.0):100.0,
596	54.m06901	AN5123.1	AO070291000056	FG00320.1	AFAO	yes	yes	((FG00320.1:100.0,((AO07029100:100.0,54.m06901:100.0):97.0,AN5123.1:100.0):100.0):100.0,
597	54.m06907	AN5116.1	AO070291000063	FG00317.1	AFAO	yes	yes	((FG00317.1:100.0,((AO07029100:100.0,54.m06907:100.0):99.0,AN5116.1:100.0):100.0):100.0,
598	72.m19110	AN6049.1	AO070340000217	FG00316.1	AFAN			((FG00316.1:100.0,((72.m19110:100.0,AN6049.1:100.0):49.0,AO07034000:100.0):100.0):100.0,
599	69.m15003	AN3925.1	AO070324000121	FG00314.1	AFAO			((FG00314.1:100.0,((AO07032400:100.0,69.m15003:100.0):65.5,AN3925.1:100.0):100.0):100.0,
600	54.m06863	AN5155.1	AO070291000012	FG01444.1	ANAO			((FG01444.1:100.0,((AO07029100:100.0,AN5155.1:100.0):50.0,54.m06863:100.0):100.0):100.0,
601	54.m06876	AN5144.1	AO070291000029	FG01445.1	AFAO			((FG01445.1:100.0,((AO07029100:100.0,54.m06876:100.0):69.0,AN5144.1:100.0):100.0):100.0,
602	54.m07060	AN5157.1	AO070291000010	FG01439.1	AFAO		yes	((FG01439.1:100.0,((AO07029100:100.0,54.m07060:100.0):78.0,AN5157.1:100.0):100.0):100.0,
603	54.m06892	AN5127.1	AO070291000046	FG01435.1	AFAO	yes	yes	((FG01435.1:100.0,((AO07029100:100.0,54.m06892:100.0):92.5,AN5127.1:100.0):100.0):100.0,
604	54.m06889	AN5134.1	AO070291000041	FG01433.1	AFAO	yes	yes	((FG01433.1:100.0,(AN5134.1:100.0,(54.m06889:100.0,AO07029100:100.0):100.0):100.0):100.0,
605	54.m06878	AN5143.1	AO070291000032	FG01432.1	AFAO			((FG01432.1:100.0,((AO07029100:100.0,54.m06878:100.0):60.0,AN5143.1:100.0):100.0):100.0,
606	71.m15420	AN0137.1	AO070321000115	FG01473.1	AFAO		yes	((FG01473.1:100.0,((71.m15420:100.0,AO07032100:100.0):87.5,AN0137.1:100.0):100.0):100.0,
607	54.m06443	AN0315.1	AO070334000017	FG00640.1	AFAN		yes	((FG00640.1:100.0,(AO07033400:100.0,(AN0315.1:100.0,54.m06443:100.0):88.0):100.0):100.0,
608	70.m15232	AN1014.1	AO070312000004	FG06012.1	AFAO			((FG06012.1:100.0,((AO07031200:100.0,70.m15232:100.0):60.5,AN1014.1:100.0):100.0):100.0,
609	65.m07499	AN3767.1	AO070309000038	FG09141.1	ANAO		yes	((FG09141.1:100.0,(65.m07499:100.0,(AN3767.1:100.0,AO07030900:100.0):87.0):100.0):100.0,
610	66.m04668	AN8979.1	AO070295000065	FG10855.1	AFAN	yes	yes	((FG10855.1:100.0,((AN8979.1:100.0,66.m04668:100.0):100.0,AO07029500:100.0):100.0):100.0,
611	71.m15423	AN0140.1	AO070321000112	FG10856.1	ANAO			((FG10856.1:100.0,(71.m15423:100.0,(AN0140.1:100.0,AO07032100:100.0):70.5):100.0):100.0,
612	71.m15422	AN0139.1	AO070321000113	FG10857.1	ANAO	yes	yes	((FG10857.1:100.0,(71.m15422:100.0,(AN0139.1:100.0,AO07032100:100.0):90.5):100.0):100.0,
613	54.m07050	AN5110.1	AO070291000069	FG05197.1	AFAO	yes	yes	((FG05197.1:100.0,(AN5110.1:100.0,(54.m07050:100.0,AO07029100:100.0):100.0):100.0):100.0,
614	54.m06913	AN5109.1	AO070296000005	FG06240.1	AFAN	yes	yes	((FG06240.1:100.0,(AO07029600:100.0,(AN5109.1:100.0,54.m06913:100.0):97.0):100.0):100.0,
615	53.m04180	AN9411.1	AO070310000008	FG05198.1	AFAO	yes	yes	((FG05198.1:100.0,((AO07031000:100.0,53.m04180:100.0):96.5,AN9411.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
616	54.m06842	AN5722.1	AO070324000128	FG05205.1	AFAO		yes	((FG05205.1:100.0,((AO07032400:100.0,54.m06842:100.0):83.0,AN5722.1:100.0):100.0):100.0,
617	72.m19991	AN6286.1	AO070308000006	FG00299.1	AFAO			((FG00299.1:100.0,((72.m19991:100.0,AO07030800:100.0):49.5,AN6286.1:100.0):100.0):100.0,
618	70.m15778	AN1051.1	AO070336000071	FG00844.1	AFAO			((FG00844.1:100.0,((AO07033600:100.0,70.m15778:100.0):66.0,AN1051.1:100.0):100.0):100.0,
619	54.m06984	AN0321.1	AO070334000005	FG00843.1	ANAO		yes	((FG00843.1:100.0,(54.m06984:100.0,(AN0321.1:100.0,AO07033400:100.0):80.0):100.0):100.0,
620	54.m06637	AN0445.1	AO070338000307	FG00845.1	AFAN			((FG00845.1:100.0,(AO07033800:100.0,(AN0445.1:100.0,54.m06637:100.0):61.5):100.0):100.0,
621	54.m06638	AN0446.1	AO070338000308	FG00846.1	AFAO		yes	((FG00846.1:100.0,((AO07033800:100.0,54.m06638:100.0):85.0,AN0446.1:100.0):100.0):100.0,
622	59.m09379	AN3169.1	AO070256000021	FG10840.1	AFAN			((FG10840.1:100.0,(AO07025600:100.0,(AN3169.1:100.0,59.m09379:100.0):51.8):100.0):100.0,
623	71.m15184	AN2701.1	AO070313000083	FG10835.1	AFAO	yes	yes	((FG10835.1:100.0,((AO07031300:100.0,71.m15184:100.0):91.5,AN2701.1:100.0):100.0):100.0,
624	71.m15192	AN6920.1	AO070313000059	FG10832.1	AFAO		yes	((FG10832.1:100.0,((AO07031300:100.0,71.m15192:100.0):77.5,AN6920.1:100.0):100.0):100.0,
625	71.m15188	AN6922.1	AO070313000063	FG10829.1	ANAO			((FG10829.1:100.0,(71.m15188:100.0,(AN6922.1:100.0,AO07031300:100.0):69.5):100.0):100.0,
626	71.m15427	AN0144.1	AO070321000101	FG04382.1	AFAO	yes	yes	((FG04382.1:100.0,((AO07032100:100.0,71.m15427:100.0):98.0,AN0144.1:100.0):100.0):100.0,
627	72.m19408	AN6250.1	AO070304000038	FG10878.1	AFAO	yes	yes	((FG10878.1:100.0,((AO07030400:100.0,72.m19408:100.0):90.5,AN6250.1:100.0):100.0):100.0,
628	72.m19409	AN6251.1	AO070304000036	FG10876.1	AFAO			((FG10876.1:100.0,((AO07030400:100.0,72.m19409:100.0):45.8,AN6251.1:100.0):100.0):100.0,
629	72.m19413	AN6244.1	AO070304000098	FG10879.1	AFAO	yes	yes	((FG10879.1:100.0,((AO07030400:100.0,72.m19413:100.0):98.0,AN6244.1:100.0):100.0):100.0,
630	72.m19412	AN6245.1	AO070304000099	FG10880.1	AFAO			((FG10880.1:100.0,((AO07030400:100.0,72.m19412:100.0):64.8,AN6245.1:100.0):100.0):100.0,
631	70.m14863	AN1366.1	AO070215000015	FG10882.1	ANAO			((FG10882.1:100.0,(70.m14863:100.0,(AN1366.1:100.0,AO07021500:100.0):48.5):100.0):100.0,
632	54.m07059	AN5152.1	AO070291000016	FG06003.1	AFAO			((FG06003.1:100.0,((AO07029100:100.0,54.m07059:100.0):70.8,AN5152.1:100.0):100.0):100.0,
633	59.m08651	AN3093.1	AO070334000133	FG05993.1	ANAO			((FG05993.1:100.0,(59.m08651:100.0,(AN3093.1:100.0,AO07033400:100.0):70.0):100.0):100.0,
634	70.m14891	AN1342.1	AO070247000022	FG10893.1	AFAO			((FG10893.1:100.0,((AO07024700:100.0,70.m14891:100.0):62.8,AN1342.1:100.0):100.0):100.0,
635	70.m15733	AN1341.1	AO070247000023	FG01552.1	ANAO			((FG01552.1:100.0,(70.m15733:100.0,(AN1341.1:100.0,AO07024700:100.0):48.3):100.0):100.0,
636	59.m08641	AN3102.1	AO070334000143	FG05996.1	AFAO	yes	yes	((FG05996.1:100.0,((AO07033400:100.0,59.m08641:100.0):98.0,AN3102.1:100.0):100.0):100.0,
637	59.m08626	AN3112.1	AO070303000038	FG05997.1	AFAO	yes	yes	((FG05997.1:100.0,((AO07030300:100.0,59.m08626:100.0):93.0,AN3112.1:100.0):100.0):100.0,
638	59.m09373	AN3113.1	AO070303000036	FG05998.1	AFAN	yes	yes	((FG05998.1:100.0,(AO07030300:100.0,(AN3113.1:100.0,59.m09373:100.0):94.0):100.0):100.0,
639	54.m06795	AN4222.1	AO070234000028	FG05999.1	AFAO		yes	((FG05999.1:100.0,((AO07023400:100.0,54.m06795:100.0):80.8,AN4222.1:100.0):100.0):100.0,
640	59.m08643	AN3101.1	AO070334000142	FG05990.1	ANAO		yes	((FG05990.1:100.0,(59.m08643:100.0,(AN3101.1:100.0,AO07033400:100.0):80.5):100.0):100.0,
641	66.m04787	AN8900.1	AO070317000064	FG02944.1		yes	yes	(((AO07031700:100.0,66.m04787:100.0):100.0,(FG02944.1:100.0,AN8900.1:100.0):90.0):100.0,
642	59.m08591	AN3134.1	AO070303000010	FG05985.1	AFAO			((FG05985.1:100.0,((59.m08591:100.0,AO07030300:100.0):50.0,AN3134.1:100.0):100.0):100.0,
643	59.m08885	AN4983.1	AO070288000051	FG05987.1	AFAO		yes	((FG05987.1:100.0,((AO07028800:100.0,59.m08885:100.0):78.0,AN4983.1:100.0):100.0):100.0,
644	58.m09009	AN4310.1	AO070207000015	FG01544.1	AFAO			((FG01544.1:100.0,((AO07020700:100.0,58.m09009:100.0):49.0,AN4310.1:100.0):100.0):100.0,
645	54.m07051	AN5113.1	AO070291000066	FG02804.1	AFAO			((FG02804.1:100.0,((AO07029100:100.0,54.m07051:100.0):67.5,AN5113.1:100.0):100.0):100.0,
646	65.m07379	AN6274.1	AO070309000069	FG02792.1	AFAO	yes	yes	((FG02792.1:100.0,((AO07030900:100.0,65.m07379:100.0):98.0,AN6274.1:100.0):100.0):100.0,
647	54.m06962	AN5099.1	AO070291000080	FG02791.1	AFAO		yes	((FG02791.1:100.0,((AO07029100:100.0,54.m06962:100.0):87.0,AN5099.1:100.0):100.0):100.0,
648	71.m15593	AN8534.1	AO070323000188	FG11617.1	AFAO	yes	yes	((FG11617.1:100.0,((AO07032300:100.0,71.m15593:100.0):90.8,AN8534.1:100.0):100.0):100.0,
649	71.m15724	AN7699.1	AO070325000105	FG08949.1	AFAO			((FG08949.1:100.0,((AO07032500:100.0,71.m15724:100.0):46.3,AN7699.1:100.0):100.0):100.0,
650	55.m02982	AN1477.1	AO070334000159	FG08946.1	ANAO	yes	yes	((FG08946.1:100.0,(55.m02982:100.0,(AN1477.1:100.0,AO07033400:100.0):90.5):100.0):100.0,
651	62.m03337	AN8743.1	AO070250000032	FG08945.1	ANAO			((FG08945.1:100.0,((AO07025000:100.0,AN8743.1:100.0):68.5,62.m03337:100.0):100.0):100.0,
652	62.m03363	AN8706.1	AO070315000133	FG08944.1	ANAO			((FG08944.1:100.0,(62.m03363:100.0,(AN8706.1:100.0,AO07031500:100.0):39.8):100.0):100.0,
653	70.m15376	AN3889.1	AO070316000069	FG08943.1	AFAO	yes	yes	((((AO07031600:100.0,70.m15376:100.0):100.0,AN3889.1:100.0):95.0,FG08943.1:100.0):100.0,
654	72.m19155	AN5986.1	AO070340000293	FG08941.1	AFAO	yes	yes	((((AO07034000:100.0,72.m19155:100.0):100.0,AN5986.1:100.0):99.5,FG08941.1:100.0):100.0,
655	59.m09117	AN9526.1	AO070327000084	FG08940.1	AFAO		yes	((FG08940.1:100.0,((AO07032700:100.0,59.m09117:100.0):89.5,AN9526.1:100.0):100.0):100.0,
656	59.m09224	AN4759.1	AO070327000057	FG08936.1	AFAO		yes	((FG08936.1:100.0,((AO07032700:100.0,59.m09224:100.0):86.5,AN4759.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
657	59.m09222	AN4761.1	AO070327000055	FG08935.1	AFAO		yes	((FG08935.1:100.0,((AO07032700:100.0,59.m09222:100.0):86.5,AN4761.1:100.0):100.0):100.0,
658	59.m09183	AN4798.1	AO070329000048	FG08932.1	AFAO			((FG08932.1:100.0,((AO07032900:100.0,59.m09183:100.0):72.2,AN4798.1:100.0):100.0):100.0,
659	62.m03470	AN8698.1	AO070315000125	FG08919.1	ANAO			((FG08919.1:100.0,((AO07031500:100.0,AN8698.1:100.0):64.5,62.m03470:100.0):99.0):100.0,
660	62.m03370	AN8699.1	AO070315000126	FG08920.1	AFAO			((FG08920.1:100.0,((62.m03370:100.0,AO07031500:100.0):59.0,AN8699.1:100.0):100.0):100.0,
661	69.m15422	AN3717.1	AO070341000346	FG08923.1	ANAO			((FG08923.1:100.0,((AO07034100:100.0,AN3717.1:100.0):54.0,69.m15422:100.0):100.0):100.0,
662	70.m15373	AN0770.1	AO070316000074	FG08927.1	AFAO			((FG08927.1:100.0,((70.m15373:100.0,AO07031600:100.0):72.5,AN0770.1:100.0):100.0):100.0,
663	71.m15665	AN4678.1	AO070284000022	FG08914.1	AFAO	yes	yes	((FG08914.1:100.0,((AO07028400:100.0,71.m15665:100.0):93.5,AN4678.1:100.0):100.0):100.0,
664	72.m19136	AN6006.1	AO070340000272	FG08910.1	AFAO		yes	((FG08910.1:100.0,((AO07034000:100.0,72.m19136:100.0):89.5,AN6006.1:100.0):100.0):100.0,
665	67.m02930	AN3222.1	AO070330000072	FG11629.1	AFAO	yes	yes	((FG11629.1:100.0,(AN3222.1:100.0,(67.m02930:100.0,AO07033000:100.0):100.0):100.0):100.0,
666	59.m09254	AN2757.1	AO070327000036	FG08905.1	AFAO			((FG08905.1:100.0,((AO07032700:100.0,59.m09254:100.0):59.5,AN2757.1:100.0):100.0):100.0,
667	59.m09174	AN4802.1	AO070329000037	FG08895.1	AFAO			((FG08895.1:100.0,((59.m09174:100.0,AO07032900:100.0):52.5,AN4802.1:100.0):100.0):100.0,
668	59.m09173	AN4803.1	AO070329000036	FG08896.1	AFAN			((FG08896.1:100.0,(AO07032900:100.0,(AN4803.1:100.0,59.m09173:100.0):56.3):100.0):100.0,
669	59.m09460	AN4788.1	AO070329000059	FG08897.1	AFAN		yes	((FG08897.1:100.0,(AO07032900:100.0,(AN4788.1:100.0,59.m09460:100.0):80.5):100.0):100.0,
670	71.m15787	AN7755.1	AO070325000188	FG08901.1	ANAO			((FG08901.1:100.0,(71.m15787:100.0,(AN7755.1:100.0,AO07032500:100.0):52.0):100.0):100.0,
671	71.m15744	AN7718.1	AO070325000132	FG08900.1	AFAO			((FG08900.1:100.0,((AO07032500:100.0,71.m15744:100.0):56.0,AN7718.1:100.0):100.0):100.0,
672	59.m09248	AN4736.1	AO070327000041	FG08889.1	AFAO			((FG08889.1:100.0,((AO07032700:100.0,59.m09248:100.0):45.8,AN4736.1:100.0):100.0):100.0,
673	59.m09246	AN4735.1	AO070327000042	FG08887.1	AFAN			((FG08887.1:100.0,((59.m09246:100.0,AN4735.1:100.0):64.5,AO07032700:100.0):100.0):100.0,
674	55.m02990	AN1484.1	AO070334000191	FG06850.1	AFAO	yes	yes	((FG06850.1:100.0,((AO07033400:100.0,55.m02990:100.0):91.5,AN1484.1:100.0):100.0):100.0,
675	59.m09462	AN4787.1	AO070329000060	FG08670.1	AFAN			(((AO07032900:100.0,(AN4787.1:100.0,59.m09462:100.0):59.7):83.0,FG08670.1:100.0):100.0,
676	59.m09158	AN4817.1	AO070327000170	FG08672.1	AFAO			((FG08672.1:100.0,((AO07032700:100.0,59.m09158:100.0):69.5,AN4817.1:100.0):100.0):100.0,
677	70.m15227	AN1009.1	AO070312000024	FG08507.1	AFAO			((FG08507.1:100.0,((AO07031200:100.0,70.m15227:100.0):62.2,AN1009.1:100.0):100.0):100.0,
678	59.m09172	AN4804.1	AO070329000035	FG08501.1	AFAO			((FG08501.1:100.0,((AO07032900:100.0,59.m09172:100.0):55.5,AN4804.1:100.0):100.0):100.0,
679	59.m09244	AN4740.1	AO070329000136	FG08886.1	AFAO			((FG08886.1:100.0,((AO07032900:100.0,59.m09244:100.0):56.7,AN4740.1:100.0):100.0):100.0,
680	70.m15368	AN0764.1	AO070316000081	FG11347.1	AFAO	yes	yes	(((AN0764.1:100.0,(AO07031600:100.0,70.m15368:100.0):95.5):95.8,FG11347.1:100.0):100.0,
681	62.m03352	AN8721.1	AO070315000143	FG08879.1	AFAO	yes	yes	((FG08879.1:100.0,(AN8721.1:100.0,(62.m03352:100.0,AO07031500:100.0):100.0):100.0):100.0,
682	59.m09216	AN4769.1	AO070329000088	FG08875.1	AFAO	yes	yes	((FG08875.1:100.0,((AO07032900:100.0,59.m09216:100.0):93.0,AN4769.1:100.0):100.0):100.0,
683	57.m05549	AN4636.1	AO070248000018	FG08504.1	AFAO		yes	((FG08504.1:100.0,((AO07024800:100.0,57.m05549:100.0):78.0,AN4636.1:100.0):100.0):100.0,
684	59.m09162	AN4814.1	AO070329000018	FG08873.1	AFAO		yes	((FG08873.1:100.0,((AO07032900:100.0,59.m09162:100.0):86.5,AN4814.1:100.0):100.0):100.0,
685	57.m05557	AN4547.1	AO070321000185	FG08840.1	AFAO			((FG08840.1:100.0,((AO07032100:100.0,57.m05557:100.0):53.5,AN4547.1:100.0):100.0):100.0,
686	59.m09470	AN4778.1	AO070329000073	FG08706.1	AFAO			((FG08706.1:100.0,((AO07032900:100.0,59.m09470:100.0):58.5,AN4778.1:100.0):100.0):100.0,
687	59.m09114	AN4857.1	AO070327000081	FG08709.1	AFAO			((FG08709.1:100.0,((AO07032700:100.0,59.m09114:100.0):62.5,AN4857.1:100.0):100.0):100.0,
688	54.m06797	AN4221.1	AO070234000030	FG08813.1	AFAN			((FG08813.1:100.0,(AO07023400:100.0,(AN4221.1:100.0,54.m06797:100.0):57.0):100.0):100.0,
689	54.m06800	AN4218.1	AO070315000081	FG08811.1	AFAO			((FG08811.1:100.0,((AO07031500:100.0,54.m06800:100.0):63.5,AN4218.1:100.0):100.0):100.0,
690	59.m09215	AN4770.1	AO070329000086	FG08528.1	AFAO		yes	((FG08528.1:100.0,((AO07032900:100.0,59.m09215:100.0):86.0,AN4770.1:100.0):100.0):100.0,
691	70.m15515	AN0906.1	AO070320000082	FG09454.1	AFAO	yes	yes	((FG09454.1:100.0,((AO07032000:100.0,70.m15515:100.0):97.0,AN0906.1:100.0):100.0):100.0,
692	62.m03488	AN8696.1	AO070315000121	FG08527.1	AFAO		yes	((FG08527.1:100.0,((AO07031500:100.0,62.m03488:100.0):82.0,AN8696.1:100.0):100.0):100.0,
693	59.m09489	AN4763.1	AO070327000053	FG08531.1	ANAO			((FG08531.1:100.0,(59.m09489:100.0,(AN4763.1:100.0,AO07032700:100.0):59.5):100.0):100.0,
694	59.m09221	AN4762.1	AO070327000054	FG08530.1	AFAO	yes	yes	((FG08530.1:100.0,((AO07032700:100.0,59.m09221:100.0):90.8,AN4762.1:100.0):100.0):100.0,
695	52.m04075	AN9357.1	AO070315000043	FG09216.1	AFAO	yes	yes	((FG09216.1:100.0,((AO07031500:100.0,52.m04075:100.0):95.0,AN9357.1:100.0):100.0):100.0,
696	62.m03388	AN8683.1	AO070315000103	FG08579.1	AFAO	yes	yes	((FG08579.1:100.0,((AO07031500:100.0,62.m03388:100.0):91.0,AN8683.1:100.0):100.0):100.0,
697	62.m03368	AN8700.1	AO070315000128	FG02343.1	AFAO		yes	((FG02343.1:100.0,((AO07031500:100.0,62.m03368:100.0):84.8,AN8700.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
698	62.m03453	AN8748.1	AO070250000024	FG06404.1	AFAN			((FG06404.1:100.0,((62.m03453:100.0,AN8748.1:100.0):52.5,AO07025000:100.0):100.0):100.0,
699	62.m03313	AN8764.1	AO070277000062	FG06401.1	AFAO			((FG06401.1:100.0,((62.m03313:100.0,AO07027700:100.0):60.5,AN8764.1:100.0):100.0):100.0,
700	54.m06360	AN9384.1	AO070253000015	FG08320.1	AFAO	yes	yes	((FG08320.1:100.0,((AO07025300:100.0,54.m06360:100.0):99.0,AN9384.1:100.0):100.0):100.0,
701	62.m03233	AN6638.1	AO070326000090	FG08648.1	AFAO			((FG08648.1:100.0,((AO07032600:100.0,62.m03233:100.0):74.0,AN6638.1:100.0):100.0):100.0,
702	62.m03399	AN8671.1	AO070315000088	FG08650.1	AFAO		yes	((FG08650.1:100.0,((AO07031500:100.0,62.m03399:100.0):86.0,AN8671.1:100.0):100.0):100.0,
703	70.m14923	AN1284.1	AO070332000035	FG02764.1	AFAN			((FG02764.1:100.0,(AO07033200:100.0,(AN1284.1:100.0,70.m14923:100.0):72.0):100.0):100.0,
704	70.m14929	AN1280.1	AO070332000040	FG02766.1	AFAO	yes	yes	((FG02766.1:100.0,((AO07033200:100.0,70.m14929:100.0):97.0,AN1280.1:100.0):100.0):100.0,
705	55.m03004	AN1494.1	AO070334000211	FG09406.1	AFAO	yes	yes	((FG09406.1:100.0,(AN1494.1:100.0,(55.m03004:100.0,AO07033400:100.0):100.0):100.0):100.0,
706	69.m15021	AN3909.1	AO070324000094	FG01035.1	AFAO	yes	yes	((FG01035.1:100.0,(AN3909.1:100.0,(69.m15021:100.0,AO07032400:100.0):100.0):100.0):100.0,
707	69.m15005	AN3924.1	AO070324000120	FG01036.1	AFAO	yes	yes	((FG01036.1:100.0,((AO07032400:100.0,69.m15005:100.0):90.0,AN3924.1:100.0):100.0):100.0,
708	54.m06541	AN4050.1	AO070328000106	FG00718.1	AFAO	yes	yes	((FG00718.1:100.0,(AN4050.1:100.0,(54.m06541:100.0,AO07032800:100.0):100.0):100.0):100.0,
709	54.m06978	AN0304.1	AO070334000034	FG00736.1	AFAO	yes	yes	((FG00736.1:100.0,(AN0304.1:100.0,(54.m06978:100.0,AO07033400:100.0):100.0):100.0):100.0,
710	69.m15026	AN9512.1	AO070324000088	FG06864.1	AFAO	yes	yes	((FG06864.1:100.0,((AO07032400:100.0,69.m15026:100.0):92.5,AN9512.1:100.0):100.0):100.0,
711	72.m19984	AN6268.1	AO070304000019	FG00912.1	AFAO		yes	((FG00912.1:100.0,((AO07030400:100.0,72.m19984:100.0):80.5,AN6268.1:100.0):100.0):100.0,
712	70.m15580	AN0946.1	AO070320000143	FG00292.1	AFAO	yes	yes	((FG00292.1:100.0,((AO07032000:100.0,70.m15580:100.0):98.5,AN0946.1:100.0):100.0):100.0,
713	54.m06538	AN4053.1	AO070342000038	FG00748.1	AFAO	yes	yes	((FG00748.1:100.0,((AO07034200:100.0,54.m06538:100.0):92.0,AN4053.1:100.0):100.0):100.0,
714	54.m07014	AN4056.1	AO070342000042	FG00724.1	AFAO	yes	yes	((FG00724.1:100.0,((AO07034200:100.0,54.m07014:100.0):99.0,AN4056.1:100.0):100.0):100.0,
715	55.m03022	AN1510.1	AO070334000228	FG04911.1	AFAO			((FG04911.1:100.0,((AO07033400:100.0,55.m03022:100.0):74.5,AN1510.1:100.0):100.0):100.0,
716	66.m04621	AN3411.1	AO070281000041	FG00286.1	AFAO			((FG00286.1:100.0,((AO07028100:100.0,66.m04621:100.0):59.0,AN3411.1:100.0):100.0):100.0,
717	55.m03241	AN1413.1	AO070242000017	FG04907.1	AFAO	yes	yes	((FG04907.1:100.0,((AO07024200:100.0,55.m03241:100.0):94.0,AN1413.1:100.0):100.0):100.0,
718	66.m04541	AN9083.1	AO070332000196	FG00722.1	AFAO	yes	yes	((FG00722.1:100.0,((AO07033200:100.0,66.m04541:100.0):90.5,AN9083.1:100.0):100.0):100.0,
719	57.m05645	AN4486.1	AO070311000037	FG00719.1	ANAO		yes	((FG00719.1:100.0,(57.m05645:100.0,(AN4486.1:100.0,AO07031100:100.0):85.5):100.0):100.0,
720	70.m15793	AN0809.1	AO070239000006	FG00916.1	AFAO	yes	yes	((FG00916.1:100.0,((AO07023900:100.0,70.m15793:100.0):90.5,AN0809.1:100.0):100.0):100.0,
721	70.m15409	AN0808.1	AO070239000007	FG00915.1	AFAO		yes	((FG00915.1:100.0,((AO07023900:100.0,70.m15409:100.0):77.0,AN0808.1:100.0):100.0):100.0,
722	70.m15405	AN0804.1	AO070239000013	FG00914.1	AFAN			((FG00914.1:100.0,(AO07023900:100.0,(AN0804.1:100.0,70.m15405:100.0):58.5):100.0):100.0,
723	66.m04616	AN3417.1	AO070203000003	FG00287.1	AFAN			((FG00287.1:100.0,(AO07020300:100.0,(AN3417.1:100.0,66.m04616:100.0):56.0):100.0):100.0,
724	66.m04552	AN9094.1	AO070332000181	FG00872.1	AFAN			((FG00872.1:100.0,(AO07033200:100.0,(AN9094.1:100.0,66.m04552:100.0):48.5):100.0):100.0,
725	69.m15475	AN5457.1	AO070341000409	FG00739.1	AFAO		yes	((FG00739.1:100.0,((AO07034100:100.0,69.m15475:100.0):83.0,AN5457.1:100.0):100.0):100.0,
726	55.m03276	AN1558.1	AO070339000295	FG01410.1	AFAO	yes	yes	((FG01410.1:100.0,((AO07033900:100.0,55.m03276:100.0):91.0,AN1558.1:100.0):100.0):100.0,
727	62.m03367	AN8701.1	AO070315000129	FG08557.1	AFAO	yes	yes	((FG08557.1:100.0,((AO07031500:100.0,62.m03367:100.0):92.0,AN8701.1:100.0):100.0):100.0,
728	62.m03366	AN8702.1	AO070315000130	FG08558.1	AFAO			((FG08558.1:100.0,((62.m03366:100.0,AO07031500:100.0):53.0,AN8702.1:100.0):100.0):100.0,
729	57.m05687	AN3795.1	AO070337000232	FG00941.1	AFAO			((FG00941.1:100.0,((AO07033700:100.0,57.m05687:100.0):50.0,AN3795.1:100.0):100.0):100.0,
730	71.m15303	AN1947.1	AO070342000209	FG10497.1	ANAO			((FG10497.1:100.0,((AO07034200:100.0,AN1947.1:100.0):72.0,71.m15303:100.0):100.0):100.0,
731	55.m03091	AN1565.1	AO070339000287	FG01411.1	ANAO		yes	((FG01411.1:100.0,(55.m03091:100.0,(AN1565.1:100.0,AO07033900:100.0):75.5):100.0):100.0,
732	71.m15696	AN4708.1	AO070329000168	FG08517.1	AFAO		yes	((FG08517.1:100.0,((AO07032900:100.0,71.m15696:100.0):87.0,AN4708.1:100.0):100.0):100.0,
733	62.m03479	AN8664.1	AO070205000007	FG08780.1	AFAN			((FG08780.1:100.0,(AO07020500:100.0,(AN8664.1:100.0,62.m03479:100.0):51.0):100.0):100.0,
734	71.m15671	AN4688.1	AO070284000043	FG08510.1	ANAO			((FG08510.1:100.0,((AO07028400:100.0,AN4688.1:100.0):66.5,71.m15671:100.0):100.0):100.0,
735	71.m15670	AN4687.1	AO070284000042	FG08509.1	AFAO			((FG08509.1:100.0,((AO07028400:100.0,71.m15670:100.0):45.0,AN4687.1:100.0):100.0):100.0,
736	71.m15674	AN4691.1	AO070284000047	FG08511.1	AFAN			((FG08511.1:100.0,(AO07028400:100.0,(AN4691.1:100.0,71.m15674:100.0):48.8):100.0):100.0,
737	71.m15816	AN7783.1	AO070286000029	FG08568.1	AFAO		yes	((FG08568.1:100.0,((AO07028600:100.0,71.m15816:100.0):82.5,AN7783.1:100.0):100.0):100.0,
738	71.m15641	AN0241.1	AO070284000071	FG08721.1	AFAO	yes	yes	((FG08721.1:100.0,((AO07028400:100.0,71.m15641:100.0):92.5,AN0241.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
739	71.m15640	AN0242.1	AO070284000072	FG08722.1	AFAO			((FG08722.1:100.0,((71.m15640:100.0,AO07028400:100.0):63.5,AN0242.1:100.0):100.0):100.0,
740	71.m15642	AN0240.1	AO070284000070	FG08723.1	AFAN		yes	((((AN0240.1:100.0,71.m15642:100.0):82.5,AO07028400:100.0):99.0,FG08723.1:100.0):100.0,
741	71.m15766	AN7736.1	AO070325000157	FG08845.1	AFAO		yes	((FG08845.1:100.0,((71.m15766:100.0,AO07032500:100.0):77.5,AN7736.1:100.0):100.0):100.0,
742	71.m15668	AN4684.1	AO070284000040	FG08571.1	AFAN			((FG08571.1:100.0,(AO07028400:100.0,(AN4684.1:100.0,71.m15668:100.0):74.5):100.0):100.0,
743	59.m09180	AN4800.1	AO070329000041	FG08872.1	AFAO	yes	yes	((FG08872.1:100.0,((AO07032900:100.0,59.m09180:100.0):98.0,AN4800.1:100.0):100.0):100.0,
744	59.m09236	AN4743.1	AO070327000077	FG08857.1	AFAO			((FG08857.1:100.0,((AO07032700:100.0,59.m09236:100.0):73.0,AN4743.1:100.0):100.0):100.0,
745	59.m09232	AN4753.1	AO070327000066	FG08860.1	AFAN			((FG08860.1:100.0,((59.m09232:100.0,AN4753.1:100.0):56.8,AO07032700:100.0):100.0):100.0,
746	59.m09234	AN4751.1	AO070327000068	FG08849.1	ANAO			((FG08849.1:100.0,(59.m09234:100.0,(AN4751.1:100.0,AO07032700:100.0):63.0):100.0):100.0,
747	59.m08889	AN4986.1	AO070288000054	FG08717.1	AFAO			((FG08717.1:100.0,((AO07028800:100.0,59.m08889:100.0):53.5,AN4986.1:100.0):100.0):100.0,
748	59.m09189	AN4792.1	AO070329000054	FG08715.1	AFAO		yes	((FG08715.1:100.0,((AO07032900:100.0,59.m09189:100.0):75.5,AN4792.1:100.0):100.0):100.0,
749	72.m19814	AN7535.1	AO070299000067	FG10918.1				((((72.m19814:100.0,AN7535.1:100.0):100.0,FG10918.1:100.0):61.0,AO07029900:100.0):100.0,
750	66.m04696	AN9490.1	AO070214000003	FG00161.1				((((AN9490.1:100.0,66.m04696:100.0):68.0,FG00161.1:100.0):48.5,AO07021400:100.0):100.0,
751	53.m03736	AN8233.1	AO070310000075	FG08917.1	AFAO	yes	yes	((((AO07031000:100.0,53.m03736:100.0):97.5,AN8233.1:100.0):98.0,FG08917.1:100.0):100.0,
752	63.m00612	AN7786.1	AO070167000003	FG02964.1	AFAO	yes	yes	((((AO07016700:100.0,63.m00612:100.0):100.0,AN7786.1:100.0):95.5,FG02964.1:100.0):100.0,
753	54.m06365	AN0381.1	AO070318000065	FG05778.1	AFAO		yes	((FG05778.1:100.0,((AO07031800:100.0,54.m06365:100.0):89.5,AN0381.1:100.0):100.0):100.0,
754	54.m06392	AN0359.1	AO070318000037	FG05777.1	AFAO			((FG05777.1:100.0,((AO07031800:100.0,54.m06392:100.0):53.5,AN0359.1:100.0):100.0):100.0,
755	70.m15195	AN1037.1	AO070336000072	FG05784.1	AFAO	yes	yes	((FG05784.1:100.0,((AO07033600:100.0,70.m15195:100.0):94.0,AN1037.1:100.0):100.0):100.0,
756	65.m07375	AN3752.1	AO070309000065	FG05780.1	AFAO	yes	yes	((FG05780.1:100.0,((AO07030900:100.0,65.m07375:100.0):96.0,AN3752.1:100.0):100.0):100.0,
757	58.m07872	AN4453.1	AO070273000002	FG05769.1	AFAO	yes	yes	((FG05769.1:100.0,((AO07027300:100.0,58.m07872:100.0):93.5,AN4453.1:100.0):100.0):100.0,
758	59.m08981	AN3036.1	AO070337000078	FG06302.1	AFAO	yes	yes	((FG06302.1:100.0,((AO07033700:100.0,59.m08981:100.0):94.0,AN3036.1:100.0):100.0):100.0,
759	59.m09256	AN2767.1	AO070327000034	FG06045.1	ANAO			((FG06045.1:100.0,((AO07032700:100.0,AN2767.1:100.0):50.5,59.m09256:100.0):100.0):100.0,
760	70.m15196	AN1038.1	AO070336000073	FG05054.1	AFAO			((FG05054.1:100.0,((70.m15196:100.0,AO07033600:100.0):54.0,AN1038.1:100.0):100.0):100.0,
761	58.m08029	AN4290.1	AO070158000001	FG05053.1	AFAO		yes	((FG05053.1:100.0,((AO07015800:100.0,58.m08029:100.0):80.0,AN4290.1:100.0):100.0):100.0,
762	69.m14847	AN5749.1	AO070341000006	FG03481.1	AFAO	yes	yes	((FG03481.1:100.0,((AO07034100:100.0,69.m14847:100.0):93.0,AN5749.1:100.0):100.0):100.0,
763	69.m14838	AN5760.1	AO070193000006	FG05766.1	ANAO	yes	yes	((FG05766.1:100.0,(69.m14838:100.0,(AN5760.1:100.0,AO07019300:100.0):95.0):100.0):100.0,
764	59.m08904	AN5006.1	AO070255000034	FG06330.1	AFAO	yes	yes	((FG06330.1:100.0,((AO07025500:100.0,59.m08904:100.0):91.5,AN5006.1:100.0):100.0):100.0,
765	59.m09008	AN3010.1	AO070337000106	FG06338.1	AFAO	yes	yes	((FG06338.1:100.0,((AO07033700:100.0,59.m09008:100.0):99.0,AN3010.1:100.0):100.0):100.0,
766	59.m08985	AN3033.1	AO070337000074	FG06339.1	AFAO			((FG06339.1:100.0,((AO07033700:100.0,59.m08985:100.0):69.5,AN3033.1:100.0):100.0):100.0,
767	59.m09003	AN3013.1	AO070337000103	FG06325.1	AFAO		yes	((FG06325.1:100.0,((AO07033700:100.0,59.m09003:100.0):79.5,AN3013.1:100.0):100.0):100.0,
768	65.m07451	AN4273.1	AO070277000013	FG09691.1	AFAO	yes	yes	((FG09691.1:100.0,((AO07027700:100.0,65.m07451:100.0):97.5,AN4273.1:100.0):100.0):100.0,
769	69.m14839	AN5759.1	AO070193000004	FG05764.1	ANAO	yes	yes	((FG05764.1:100.0,(69.m14839:100.0,(AN5759.1:100.0,AO07019300:100.0):92.5):100.0):100.0,
770	58.m07694	AN1624.1	AO070299000090	FG06048.1	AFAO	yes	yes	((FG06048.1:100.0,((AO07029900:100.0,58.m07694:100.0):91.5,AN1624.1:100.0):100.0):100.0,
771	59.m08959	AN3059.1	AO070337000014	FG06055.1	AFAO			((FG06055.1:100.0,((AO07033700:100.0,59.m08959:100.0):52.0,AN3059.1:100.0):100.0):100.0,
772	59.m08901	AN5001.1	AO070255000031	FG06049.1	AFAO	yes	yes	((FG06049.1:100.0,(AN5001.1:100.0,(59.m08901:100.0,AO07025500:100.0):100.0):100.0):100.0,
773	57.m05520	AN4598.1	AO070267000015	FG10768.1	AFAO		yes	((FG10768.1:100.0,((AO07026700:100.0,57.m05520:100.0):79.3,AN4598.1:100.0):100.0):100.0,
774	59.m08755	AN2904.1	AO070338000101	FG10769.1	AFAO			((FG10769.1:100.0,((AO07033800:100.0,59.m08755:100.0):64.5,AN2904.1:100.0):100.0):100.0,
775	59.m09454	AN4997.1	AO070288000080	FG10779.1	AFAO	yes	yes	((FG10779.1:100.0,((AO07028800:100.0,59.m09454:100.0):90.0,AN4997.1:100.0):100.0):100.0,
776	57.m05525	AN4602.1	AO070267000019	FG06294.1	ANAO		yes	((FG06294.1:100.0,(57.m05525:100.0,(AN4602.1:100.0,AO07026700:100.0):76.0):100.0):100.0,
777	54.m06812	AN4250.1	AO070324000162	FG06300.1	AFAO			((FG06300.1:100.0,((AO07032400:100.0,54.m06812:100.0):61.5,AN4250.1:100.0):100.0):100.0,
778	59.m08778	AN4884.1	AO070338000076	FG06301.1	AFAO	yes	yes	((FG06301.1:100.0,((AO07033800:100.0,59.m08778:100.0):93.0,AN4884.1:100.0):100.0):100.0,
779	59.m09495	AN4875.1	AO070338000085	FG10780.1	ANAO		yes	((FG10780.1:100.0,(59.m09495:100.0,(AN4875.1:100.0,AO07033800:100.0):79.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
780	59.m08748	AN2898.1	AO070338000110	FG10781.1	AFAO	yes	yes	((FG10781.1:100.0,((AO07033800:100.0,59.m08748:100.0):96.5,AN2898.1:100.0):100.0):100.0,
781	59.m08754	AN2903.1	AO070338000102	FG10782.1	AFAO			((FG10782.1:100.0,((59.m08754:100.0,AO07033800:100.0):60.5,AN2903.1:100.0):100.0):100.0,
782	59.m08957	AN3058.1	AO070337000016	FG06290.1	AFAN		yes	((FG06290.1:100.0,(AO07033700:100.0,(AN3058.1:100.0,59.m08957:100.0):80.5):100.0):100.0,
783	59.m08792	AN4894.1	AO070338000062	FG06291.1	AFAO		yes	((FG06291.1:100.0,((AO07033800:100.0,59.m08792:100.0):84.0,AN4894.1:100.0):100.0):100.0,
784	59.m08794	AN4895.1	AO070338000061	FG06292.1	ANAO			((FG06292.1:100.0,((AO07033800:100.0,AN4895.1:100.0):64.5,59.m08794:100.0):100.0):100.0,
785	59.m08894	AN4991.1	AO070288000071	FG00338.1	ANAO			((FG00338.1:100.0,(59.m08894:100.0,(AN4991.1:100.0,AO07028800:100.0):48.0):100.0):100.0,
786	59.m08933	AN3065.1	AO070337000007	FG00337.1	AFAO			((FG00337.1:100.0,((AO07033700:100.0,59.m08933:100.0):65.8,AN3065.1:100.0):100.0):100.0,
787	54.m06700	AN0247.1	AO070338000240	FG00732.1	AFAO	yes	yes	((FG00732.1:100.0,((AO07033800:100.0,54.m06700:100.0):93.5,AN0247.1:100.0):100.0):100.0,
788	58.m07775	AN1699.1	AO070305000023	FG10790.1	AFAO	yes	yes	((FG10790.1:100.0,((AO07030500:100.0,58.m07775:100.0):91.3,AN1699.1:100.0):100.0):100.0,
789	59.m09263	AN2761.1	AO070327000023	FG10805.1	AFAN			((((59.m09263:100.0,AN2761.1:100.0):47.5,AO07032700:100.0):76.2,FG10805.1:100.0):100.0,
790	59.m09262	AN2762.1	AO070327000024	FG10804.1	ANAO		yes	((FG10804.1:100.0,(59.m09262:100.0,(AN2762.1:100.0,AO07032700:100.0):81.0):100.0):100.0,
791	59.m08910	AN5008.1	AO070255000045	FG10793.1	AFAO			((FG10793.1:100.0,((59.m08910:100.0,AO07025500:100.0):57.8,AN5008.1:100.0):100.0):100.0,
792	59.m09488	AN2766.1	AO070327000031	FG10792.1	AFAO	yes	yes	((FG10792.1:100.0,((AO07032700:100.0,59.m09488:100.0):98.0,AN2766.1:100.0):100.0):100.0,
793	57.m05527	AN4603.1	AO070267000024	FG10934.1	ANAO	yes	yes	((FG10934.1:100.0,(57.m05527:100.0,(AN4603.1:100.0,AO07026700:100.0):90.0):100.0):100.0,
794	65.m07380	AN6817.1	AO070309000070	FG10920.1	AFAO	yes	yes	((FG10920.1:100.0,(AN6817.1:100.0,(65.m07380:100.0,AO07030900:100.0):100.0):100.0):100.0,
795	66.m04597	AN9039.1	AO070332000128	FG02001.1	ANAO			((FG02001.1:100.0,(66.m04597:100.0,(AN9039.1:100.0,AO07033200:100.0):63.0):100.0):100.0,
796	53.m03675	AN4282.1	AO070310000014	FG01604.1	AFAO			((FG01604.1:100.0,((AO07031000:100.0,53.m03675:100.0):68.0,AN4282.1:100.0):100.0):100.0,
797	58.m08959	AN1715.1	AO070305000031	FG05330.1	AFAO	yes	yes	((FG05330.1:100.0,((AO07030500:100.0,58.m08959:100.0):99.0,AN1715.1:100.0):100.0):100.0,
798	52.m03724	AN5566.1	AO070279000055	FG10358.1	AFAO		yes	((((AO07027900:100.0,52.m03724:100.0):75.5,AN5566.1:100.0):81.5,FG10358.1:100.0):100.0,
799	52.m03708	AN6423.1	AO070342000207	FG10974.1				(((AN6423.1:100.0,52.m03708:100.0):59.0,(FG10974.1:100.0,AO07034200:100.0):76.5):100.0,
800	59.m08751	AN2901.1	AO070338000106	FG10967.1	ANAO			((FG10967.1:100.0,(59.m08751:100.0,(AN2901.1:100.0,AO07033800:100.0):66.5):100.0):100.0,
801	55.m03068	AN1548.1	AO070339000306	FG11409.1	ANAO		yes	((((AN1548.1:100.0,AO07033900:100.0):77.0,55.m03068:100.0):97.5,FG11409.1:100.0):100.0,
802	54.m06964	AN5103.1	AO070291000076	FG02041.1	AFAO		yes	((FG02041.1:100.0,((AO07029100:100.0,54.m06964:100.0):89.0,AN5103.1:100.0):100.0):100.0,
803	59.m09298	AN3438.1	AO070265000012	FG06992.1	AFAO			((FG06992.1:100.0,((59.m09298:100.0,AO07026500:100.0):71.5,AN3438.1:100.0):100.0):100.0,
804	69.m15430	AN5527.1	AO070341000362	FG07962.1	AFAO	yes	yes	((FG07962.1:100.0,((AO07034100:100.0,69.m15430:100.0):99.5,AN5527.1:100.0):100.0):100.0,
805	57.m05537	AN4623.1	AO070267000035	FG07940.1	AFAO	yes	yes	((FG07940.1:100.0,((AO07026700:100.0,57.m05537:100.0):90.0,AN4623.1:100.0):100.0):100.0,
806	59.m09479	AN3445.1	AO070265000021	FG07937.1	AFAO			((FG07937.1:100.0,((59.m09479:100.0,AO07026500:100.0):48.5,AN3445.1:100.0):100.0):100.0,
807	59.m09312	AN3449.1	AO070265000024	FG07965.1	AFAO	yes	yes	((FG07965.1:100.0,((AO07026500:100.0,59.m09312:100.0):99.0,AN3449.1:100.0):100.0):100.0,
808	57.m05942	AN4578.1	AO070316000167	FG07966.1	AFAO		yes	((FG07966.1:100.0,((AO07031600:100.0,57.m05942:100.0):84.0,AN4578.1:100.0):100.0):100.0,
809	57.m05504	AN4577.1	AO070316000168	FG09042.1	AFAN			((FG09042.1:100.0,(AO07031600:100.0,(AN4577.1:100.0,57.m05504:100.0):62.5):100.0):100.0,
810	59.m09374	AN3125.1	AO070303000022	FG07968.1	AFAO	yes	yes	((FG07968.1:100.0,((AO07030300:100.0,59.m09374:100.0):99.0,AN3125.1:100.0):100.0):100.0,
811	69.m15433	AN5525.1	AO070341000364	FG07953.1	AFAN			((FG07953.1:100.0,(AO07034100:100.0,(AN5525.1:100.0,69.m15433:100.0):61.0):100.0):100.0,
812	56.m03102	AN4372.1	AO070275000045	FG11011.1	AFAO			((FG11011.1:100.0,((AO07027500:100.0,56.m03102:100.0):65.5,AN4372.1:100.0):100.0):100.0,
813	69.m15421	AN3716.1	AO070341000345	FG07956.1	AFAO		yes	((FG07956.1:100.0,((AO07034100:100.0,69.m15421:100.0):75.0,AN3716.1:100.0):100.0):100.0,
814	69.m15416	AN3711.1	AO070341000337	FG07958.1	AFAN			((FG07958.1:100.0,((69.m15416:100.0,AN3711.1:100.0):73.0,AO07034100:100.0):100.0):100.0,
815	69.m15434	AN5524.1	AO070341000365	FG07959.1	AFAO	yes	yes	((FG07959.1:100.0,((AO07034100:100.0,69.m15434:100.0):96.0,AN5524.1:100.0):100.0):100.0,
816	69.m15418	AN3714.1	AO070341000340	FG07960.1	AFAO	yes	yes	((FG07960.1:100.0,((AO07034100:100.0,69.m15418:100.0):94.0,AN3714.1:100.0):100.0):100.0,
817	58.m07312	AN5662.1	AO070342000256	FG01248.1	AFAO	yes	yes	((FG01248.1:100.0,(AN5662.1:100.0,(58.m07312:100.0,AO07034200:100.0):100.0):100.0):100.0,
818	58.m08891	AN5661.1	AO070342000254	FG06370.1	AFAO		yes	((FG06370.1:100.0,((AO07034200:100.0,58.m08891:100.0):81.5,AN5661.1:100.0):100.0):100.0,
819	59.m09483	AN3453.1	AO070265000029	FG06362.1	AFAO		yes	((FG06362.1:100.0,((AO07026500:100.0,59.m09483:100.0):83.5,AN3453.1:100.0):100.0):100.0,
820	59.m08991	AN3018.1	AO070337000096	FG06378.1	AFAO			((FG06378.1:100.0,((AO07033700:100.0,59.m08991:100.0):45.0,AN3018.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
821	69.m15726	AN3720.1	AO070341000352	FG06384.1	AFAO	yes	yes	((FG06384.1:100.0,((AO07034100:100.0,69.m15726:100.0):97.5,AN3720.1:100.0):100.0):100.0,
822	69.m15727	AN3719.1	AO070341000350	FG06385.1	AFAN			((FG06385.1:100.0,(AO07034100:100.0,(AN3719.1:100.0,69.m15727:100.0):54.5):100.0):100.0,
823	59.m09010	AN3004.1	AO070337000108	FG06386.1	ANAO			((FG06386.1:100.0,((AO07033700:100.0,AN3004.1:100.0):48.5,59.m09010:100.0):100.0):100.0,
824	59.m08784	AN4888.1	AO070338000070	FG09834.1	ANAO			((FG09834.1:100.0,((AO07033800:100.0,AN4888.1:100.0):37.5,59.m08784:100.0):100.0):100.0,
825	72.m18979	AN5848.1	AO070340000006	FG06366.1	AFAO		yes	((FG06366.1:100.0,((AO07034000:100.0,72.m18979:100.0):83.0,AN5848.1:100.0):100.0):100.0,
826	59.m08951	AN3063.1	AO070337000010	FG09837.1	AFAN			((FG09837.1:100.0,(AO07033700:100.0,(AN3063.1:100.0,59.m08951:100.0):57.5):100.0):100.0,
827	59.m09482	AN3460.1	AO070265000037	FG09838.1	AFAO	yes	yes	((FG09838.1:100.0,((AO07026500:100.0,59.m09482:100.0):93.0,AN3460.1:100.0):100.0):100.0,
828	69.m15377	AN3738.1	AO070342000269	FG09839.1	AFAO			((FG09839.1:100.0,((69.m15377:100.0,AO07034200:100.0):50.5,AN3738.1:100.0):100.0):100.0,
829	57.m05499	AN4581.1	AO070316000164	FG09843.1	AFAO			((FG09843.1:100.0,((AO07031600:100.0,57.m05499:100.0):60.5,AN4581.1:100.0):100.0):100.0,
830	57.m05515	AN4592.1	AO070267000008	FG09845.1	AFAO	yes	yes	((FG09845.1:100.0,(AN4592.1:100.0,(57.m05515:100.0,AO07026700:100.0):100.0):100.0):100.0,
831	59.m08952	AN3062.1	AO070337000011	FG06364.1	AFAO	yes	yes	((FG06364.1:100.0,((AO07033700:100.0,59.m08952:100.0):91.5,AN3062.1:100.0):100.0):100.0,
832	59.m08776	AN4881.1	AO070338000078	FG06368.1	AFAO	yes	yes	((FG06368.1:100.0,((AO07033800:100.0,59.m08776:100.0):90.5,AN4881.1:100.0):100.0):100.0,
833	69.m15397	AN3688.1	AO070341000311	FG06359.1	AFAO	yes	yes	((FG06359.1:100.0,(AN3688.1:100.0,(69.m15397:100.0,AO07034100:100.0):100.0):100.0):100.0,
834	59.m09409	AN4880.1	AO070338000081	FG06369.1	AFAO			((FG06369.1:100.0,((AO07033800:100.0,59.m09409:100.0):53.8,AN4880.1:100.0):100.0):100.0,
835	59.m08895	AN4992.1	AO070288000075	FG06375.1	AFAO			((FG06375.1:100.0,((AO07028800:100.0,59.m08895:100.0):46.3,AN4992.1:100.0):100.0):100.0,
836	59.m08896	AN4993.1	AO070288000076	FG06376.1	AFAO	yes	yes	((FG06376.1:100.0,((AO07028800:100.0,59.m08896:100.0):93.5,AN4993.1:100.0):100.0):100.0,
837	69.m15402	AN3691.1	AO070341000316	FG09851.1	AFAO		yes	((FG09851.1:100.0,((AO07034100:100.0,69.m15402:100.0):81.5,AN3691.1:100.0):100.0):100.0,
838	69.m15392	AN3723.1	AO070342000294	FG09850.1	AFAO			((FG09850.1:100.0,((AO07034200:100.0,69.m15392:100.0):65.5,AN3723.1:100.0):100.0):100.0,
839	69.m15716	AN3690.1	AO070341000315	FG09849.1	AFAO			((FG09849.1:100.0,((AO07034100:100.0,69.m15716:100.0):40.2,AN3690.1:100.0):100.0):100.0,
840	59.m09324	AN3463.1	AO070265000041	FG09848.1	AFAO		yes	((FG09848.1:100.0,((59.m09324:100.0,AO07026500:100.0):89.0,AN3463.1:100.0):100.0):100.0,
841	69.m15375	AN5671.1	AO070342000266	FG06373.1	AFAO	yes	yes	((FG06373.1:100.0,((AO07034200:100.0,69.m15375:100.0):92.5,AN5671.1:100.0):100.0):100.0,
842	59.m09265	AN2759.1	AO070327000021	FG09853.1	AFAO		yes	((FG09853.1:100.0,((AO07032700:100.0,59.m09265:100.0):78.0,AN2759.1:100.0):100.0):100.0,
843	59.m09318	AN3456.1	AO070265000032	FG09855.1	AFAO	yes	yes	((FG09855.1:100.0,((AO07026500:100.0,59.m09318:100.0):99.0,AN3456.1:100.0):100.0):100.0,
844	59.m09514	AN9060.1	AO070265000048	FG09857.1	ANAO			((FG09857.1:100.0,((AO07026500:100.0,AN9060.1:100.0):44.5,59.m09514:100.0):100.0):100.0,
845	59.m09329	AN3469.1	AO070265000045	FG11626.1	ANAO			((FG11626.1:100.0,((AO07026500:100.0,AN3469.1:100.0):57.5,59.m09329:100.0):100.0):100.0,
846	59.m09327	AN3466.1	AO070265000043	FG07970.1	AFAO			((FG07970.1:100.0,((AO07026500:100.0,59.m09327:100.0):40.0,AN3466.1:100.0):100.0):100.0,
847	58.m07808	AN3830.1	AO070305000068	FG00296.1	AFAN			((FG00296.1:100.0,(AO07030500:100.0,(AN3830.1:100.0,58.m07808:100.0):60.0):100.0):100.0,
848	58.m07814	AN3838.1	AO070305000073	FG09393.1	AFAO		yes	((FG09393.1:100.0,((58.m07814:100.0,AO07030500:100.0):77.5,AN3838.1:100.0):100.0):100.0,
849	66.m04641	AN3373.1	AO070281000015	FG01406.1	AFAO		yes	((FG01406.1:100.0,((AO07028100:100.0,66.m04641:100.0):88.5,AN3373.1:100.0):100.0):100.0,
850	57.m05693	AN3789.1	AO070337000239	FG00949.1	AFAO		yes	((FG00949.1:100.0,((AO07033700:100.0,57.m05693:100.0):78.0,AN3789.1:100.0):100.0):100.0,
851	66.m04618	AN3416.1	AO070203000005	FG00950.1	AFAO	yes	yes	((FG00950.1:100.0,(AN3416.1:100.0,(66.m04618:100.0,AO07020300:100.0):100.0):100.0):100.0,
852	71.m15635	AN1133.1	AO070276000007	FG09422.1	ANAO		yes	((FG09422.1:100.0,(71.m15635:100.0,(AN1133.1:100.0,AO07027600:100.0):83.0):100.0):100.0,
853	71.m15708	AN4667.1	AO070311000001	FG09421.1	ANAO		yes	((FG09421.1:100.0,(71.m15708:100.0,(AN4667.1:100.0,AO07031100:100.0):76.0):100.0):100.0,
854	58.m07986	AN4332.1	AO070240000011	FG09423.1	AFAO			((FG09423.1:100.0,((AO07024000:100.0,58.m07986:100.0):61.5,AN4332.1:100.0):100.0):100.0,
855	70.m15759	AN1063.1	AO070218000007	FG09547.1	AFAO			((FG09547.1:100.0,((AO07021800:100.0,70.m15759:100.0):48.0,AN1063.1:100.0):100.0):100.0,
856	71.m15820	AN7630.1	AO070294000040	FG09544.1	AFAO			((FG09544.1:100.0,((AO07029400:100.0,71.m15820:100.0):55.5,AN7630.1:100.0):100.0):100.0,
857	62.m03256	AN6654.1	AO070269000012	FG00178.1	ANAO			((FG00178.1:100.0,(62.m03256:100.0,(AN6654.1:100.0,AO07026900:100.0):72.0):100.0):100.0,
858	62.m03451	AN6655.1	AO070269000011	FG00177.1	AFAO		yes	((FG00177.1:100.0,((AO07026900:100.0,62.m03451:100.0):86.0,AN6655.1:100.0):100.0):100.0,
859	62.m03322	AN8755.1	AO070250000017	FG00176.1	AFAO		yes	((FG00176.1:100.0,((AO07025000:100.0,62.m03322:100.0):87.5,AN8755.1:100.0):100.0):100.0,
860	62.m03250	AN6650.1	AO070269000001	FG00175.1	AFAO	yes	yes	((FG00175.1:100.0,((AO07026900:100.0,62.m03250:100.0):97.0,AN6650.1:100.0):100.0):100.0,
861	69.m14828	AN5770.1	AO070249000008	FG07359.1	ANAO			((FG07359.1:100.0,(69.m14828:100.0,(AN5770.1:100.0,AO07024900:100.0):62.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
862	69.m14987	AN3938.1	AO070341000049	FG00567.1	AFAO	yes	yes	((FG00567.1:100.0,((AO07034100:100.0,69.m14987:100.0):95.0,AN3938.1:100.0):100.0):100.0,
863	69.m14989	AN3937.1	AO070341000048	FG00566.1	AFAO		yes	((FG00566.1:100.0,((AO07034100:100.0,69.m14989:100.0):87.0,AN3937.1:100.0):100.0):100.0,
864	69.m14983	AN3941.1	AO070341000053	FG00565.1	AFAO			((FG00565.1:100.0,((AO07034100:100.0,69.m14983:100.0):51.5,AN3941.1:100.0):100.0):100.0,
865	69.m14985	AN3939.1	AO070341000051	FG00359.1	AFAO		yes	((FG00359.1:100.0,((AO07034100:100.0,69.m14985:100.0):89.0,AN3939.1:100.0):100.0):100.0,
866	58.m07845	AN4475.1	AO070305000110	FG01081.1	AFAO		yes	((FG01081.1:100.0,((AO07030500:100.0,58.m07845:100.0):79.5,AN4475.1:100.0):100.0):100.0,
867	58.m07848	AN4463.1	AO070305000114	FG05619.1	AFAO	yes	yes	((FG05619.1:100.0,((AO07030500:100.0,58.m07848:100.0):99.5,AN4463.1:100.0):100.0):100.0,
868	53.m03926	AN8073.1	AO070330000031	FG06243.1	AFAO		yes	((FG06243.1:100.0,((AO07033000:100.0,53.m03926:100.0):84.5,AN8073.1:100.0):100.0):100.0,
869	72.m19938	AN5994.1	AO070340000283	FG01069.1	ANAO		yes	((FG01069.1:100.0,(72.m19938:100.0,(AN5994.1:100.0,AO07034000:100.0):81.0):100.0):100.0,
870	59.m09093	AN2946.1	AO070337000196	FG05621.1	AFAO			((FG05621.1:100.0,((AO07033700:100.0,59.m09093:100.0):44.5,AN2946.1:100.0):100.0):100.0,
871	58.m07718	AN1639.1	AO070299000037	FG01085.1	AFAO		yes	((FG01085.1:100.0,((AO07029900:100.0,58.m07718:100.0):86.5,AN1639.1:100.0):100.0):100.0,
872	65.m07454	AN4276.1	AO070277000008	FG01068.1	AFAO	yes	yes	((FG01068.1:100.0,((AO07027700:100.0,65.m07454:100.0):91.5,AN4276.1:100.0):100.0):100.0,
873	72.m19468	AN2417.1	AO070228000027	FG00363.1	AFAO		yes	((FG00363.1:100.0,((AO07022800:100.0,72.m19468:100.0):83.0,AN2417.1:100.0):100.0):100.0,
874	72.m19467	AN2416.1	AO070228000028	FG00364.1	AFAO			((FG00364.1:100.0,((AO07022800:100.0,72.m19467:100.0):74.3,AN2416.1:100.0):100.0):100.0,
875	72.m19466	AN2415.1	AO070228000029	FG00365.1	AFAO			((FG00365.1:100.0,((AO07022800:100.0,72.m19466:100.0):49.8,AN2415.1:100.0):100.0):100.0,
876	72.m19465	AN2414.1	AO070228000030	FG00376.1	ANAO		yes	((FG00376.1:100.0,(72.m19465:100.0,(AN2414.1:100.0,AO07022800:100.0):85.5):100.0):100.0,
877	58.m07385	AN3586.1	AO070342000163	FG00375.1	ANAO			((FG00375.1:100.0,((AO07034200:100.0,AN3586.1:100.0):53.0,58.m07385:100.0):100.0):100.0,
878	72.m19927	AN6080.1	AO070340000130	FG00505.1	AFAN			((FG00505.1:100.0,(AO07034000:100.0,(AN6080.1:100.0,72.m19927:100.0):42.3):100.0):100.0,
879	72.m19062	AN6070.1	AO070340000114	FG00504.1	AFAO			((FG00504.1:100.0,((72.m19062:100.0,AO07034000:100.0):54.5,AN6070.1:100.0):100.0):100.0,
880	57.m05872	AN7472.1	AO070287000054	FG00499.1	AFAO		yes	((FG00499.1:100.0,((AO07028700:100.0,57.m05872:100.0):85.0,AN7472.1:100.0):100.0):100.0,
881	57.m05882	AN7459.1	AO070287000066	FG00500.1	AFAO		yes	((FG00500.1:100.0,((AO07028700:100.0,57.m05882:100.0):86.5,AN7459.1:100.0):100.0):100.0,
882	69.m14893	AN5194.1	AO070237000024	FG01388.1	AFAO	yes	yes	((FG01388.1:100.0,(AN5194.1:100.0,(69.m14893:100.0,AO07023700:100.0):100.0):100.0):100.0,
883	58.m07732	AN1666.1	AO070299000048	FG01386.1	ANAO			((FG01386.1:100.0,(58.m07732:100.0,(AN1666.1:100.0,AO07029900:100.0):66.5):100.0):100.0,
884	59.m08658	AN3089.1	AO070334000128	FG00731.1	AFAO		yes	((FG00731.1:100.0,((AO07033400:100.0,59.m08658:100.0):89.0,AN3089.1:100.0):100.0):100.0,
885	70.m15361	AN0747.1	AO070343000435	FG00863.1	AFAO	yes	yes	((FG00863.1:100.0,((AO07034300:100.0,70.m15361:100.0):93.5,AN0747.1:100.0):100.0):100.0,
886	58.m08993	AN3874.1	AO070305000055	FG00862.1	AFAO		yes	((FG00862.1:100.0,((AO07030500:100.0,58.m08993:100.0):87.5,AN3874.1:100.0):100.0):100.0,
887	55.m02908	AN9421.1	AO070242000003	FG00883.1	AFAO	yes	yes	((FG00883.1:100.0,((AO07024200:100.0,55.m02908:100.0):93.0,AN9421.1:100.0):100.0):100.0,
888	54.m06697	AN0244.1	AO070338000236	FG00881.1	AFAO	yes	yes	((FG00881.1:100.0,((AO07033800:100.0,54.m06697:100.0):98.5,AN0244.1:100.0):100.0):100.0,
889	69.m15658	AN3907.1	AO070324000091	FG09338.1	AFAO	yes	yes	((FG09338.1:100.0,((AO07032400:100.0,69.m15658:100.0):99.5,AN3907.1:100.0):100.0):100.0,
890	54.m06632	AN0442.1	AO070338000299	FG09305.1	AFAO		yes	((FG09305.1:100.0,((54.m06632:100.0,AO07033800:100.0):87.5,AN0442.1:100.0):100.0):100.0,
891	59.m09110	AN4861.1	AO070329000146	FG00902.1	AFAO			((FG00902.1:100.0,((59.m09110:100.0,AO07032900:100.0):56.5,AN4861.1:100.0):100.0):100.0,
892	55.m03253	AN1513.1	AO070334000232	FG00903.1	AFAO		yes	((FG00903.1:100.0,((AO07033400:100.0,55.m03253:100.0):79.0,AN1513.1:100.0):100.0):100.0,
893	55.m03031	AN1512.1	AO070334000233	FG00905.1	AFAO			((FG00905.1:100.0,((AO07033400:100.0,55.m03031:100.0):73.5,AN1512.1:100.0):100.0):100.0,
894	55.m02906	AN9419.1	AO070242000001	FG00906.1	AFAN			((FG00906.1:100.0,(AO07024200:100.0,(AN9419.1:100.0,55.m02906:100.0):57.0):100.0):100.0,
895	70.m15803	AN0810.1	AO070239000005	FG00909.1	AFAO			((FG00909.1:100.0,((AO07023900:100.0,70.m15803:100.0):51.8,AN0810.1:100.0):100.0):100.0,
896	70.m15407	AN0806.1	AO070239000011	FG09322.1	AFAO			((FG09322.1:100.0,((AO07023900:100.0,70.m15407:100.0):49.0,AN0806.1:100.0):100.0):100.0,
897	55.m02916	AN1409.1	AO070242000012	FG09321.1	AFAO		yes	((FG09321.1:100.0,((AO07024200:100.0,55.m02916:100.0):87.0,AN1409.1:100.0):100.0):100.0,
898	55.m02915	AN1408.1	AO070242000011	FG09320.1	AFAO			((FG09320.1:100.0,((55.m02915:100.0,AO07024200:100.0):61.0,AN1408.1:100.0):100.0):100.0,
899	55.m02914	AN1407.1	AO070242000010	FG09319.1	ANAO		yes	((FG09319.1:100.0,(55.m02914:100.0,(AN1407.1:100.0,AO07024200:100.0):89.5):100.0):100.0,
900	55.m03274	AN1546.1	AO070339000308	FG09306.1	ANAO			((FG09306.1:100.0,((AO07033900:100.0,AN1546.1:100.0):67.5,55.m03274:100.0):100.0):100.0,
901	55.m03061	AN1543.1	AO070339000311	FG09341.1	AFAO			((FG09341.1:100.0,((55.m03061:100.0,AO07033900:100.0):71.0,AN1543.1:100.0):100.0):100.0,
902	58.m07790	AN1710.1	AO070305000038	FG04934.1	AFAN			((FG04934.1:100.0,(AO07030500:100.0,(AN1710.1:100.0,58.m07790:100.0):68.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
903	57.m05709	AN5224.1	AO070337000254	FG09167.1	AFAO	yes	yes	((FG09167.1:100.0,((AO07033700:100.0,57.m05709:100.0):96.5,AN5224.1:100.0):100.0):100.0,
904	58.m07735	AN1668.1	AO070299000050	FG09166.1	AFAO		yes	((FG09166.1:100.0,((AO07029900:100.0,58.m07735:100.0):84.8,AN1668.1:100.0):100.0):100.0,
905	69.m14878	AN5181.1	AO070247000011	FG09165.1	AFAO		yes	((FG09165.1:100.0,((AO07024700:100.0,69.m14878:100.0):76.5,AN5181.1:100.0):100.0):100.0,
906	58.m07734	AN1669.1	AO070299000051	FG00682.1	AFAO		yes	((FG00682.1:100.0,((AO07029900:100.0,58.m07734:100.0):82.0,AN1669.1:100.0):100.0):100.0,
907	57.m05799	AN2096.1	AO070341000255	FG09327.1	AFAO			((FG09327.1:100.0,((57.m05799:100.0,AO07034100:100.0):55.0,AN2096.1:100.0):100.0):100.0,
908	62.m03325	AN8750.1	AO070250000010	FG08564.1	AFAO	yes	yes	((FG08564.1:100.0,((AO07025000:100.0,62.m03325:100.0):93.5,AN8750.1:100.0):100.0):100.0,
909	71.m15269	AN6856.1	AO070314000073	FG08562.1	AFAO	yes	yes	((((AO07031400:100.0,71.m15269:100.0):98.5,AN6856.1:100.0):98.5,FG08562.1:100.0):100.0,
910	70.m15802	AN0819.1	AO070288000083	FG00898.1	ANAO			((FG00898.1:100.0,(70.m15802:100.0,(AN0819.1:100.0,AO07028800:100.0):41.5):100.0):100.0,
911	71.m15637	AN4729.1	AO070276000001	FG10971.1	AFAO			((FG10971.1:100.0,((AO07027600:100.0,71.m15637:100.0):53.5,AN4729.1:100.0):100.0):100.0,
912	59.m08417	AN2536.1	AO070300000039	FG00048.1	ANAO			((FG00048.1:100.0,(59.m08417:100.0,(AN2536.1:100.0,AO07030000:100.0):73.0):100.0):100.0,
913	58.m07604	AN1995.1	AO070301000090	FG00887.1	AFAO		yes	((FG00887.1:100.0,((AO07030100:100.0,58.m07604:100.0):82.0,AN1995.1:100.0):100.0):100.0,
914	70.m15414	AN0814.1	AO070288000089	FG00660.1	AFAO	yes	yes	((FG00660.1:100.0,((AO07028800:100.0,70.m15414:100.0):91.0,AN0814.1:100.0):100.0):100.0,
915	70.m15413	AN0813.1	AO070288000091	FG00661.1	AFAO	yes	yes	((FG00661.1:100.0,(AN0813.1:100.0,(70.m15413:100.0,AO07028800:100.0):100.0):100.0):100.0,
916	55.m03024	AN1511.1	AO070334000229	FG00666.1	AFAO	yes	yes	((FG00666.1:100.0,((AO07033400:100.0,55.m03024:100.0):95.5,AN1511.1:100.0):100.0):100.0,
917	70.m15418	AN0818.1	AO070288000084	FG00665.1	ANAO			((FG00665.1:100.0,((AO07028800:100.0,AN0818.1:100.0):47.0,70.m15418:100.0):100.0):100.0,
918	70.m15416	AN0817.1	AO070288000087	FG00662.1	ANAO			((FG00662.1:100.0,(70.m15416:100.0,(AN0817.1:100.0,AO07028800:100.0):58.0):100.0):100.0,
919	70.m15166	AN1066.1	AO070218000011	FG00663.1	AFAO		yes	((FG00663.1:100.0,((AO07021800:100.0,70.m15166:100.0):87.0,AN1066.1:100.0):100.0):100.0,
920	65.m07459	AN8283.1	AO070277000005	FG01000.1	AFAO	yes	yes	((FG01000.1:100.0,((AO07027700:100.0,65.m07459:100.0):99.5,AN8283.1:100.0):100.0):100.0,
921	65.m07462	AN8286.1	AO070277000002	FG01004.1	AFAO	yes	yes	((FG01004.1:100.0,((AO07027700:100.0,65.m07462:100.0):98.0,AN8286.1:100.0):100.0):100.0,
922	58.m07849	AN4464.1	AO070305000118	FG00969.1	AFAO			((FG00969.1:100.0,((58.m07849:100.0,AO07030500:100.0):66.5,AN4464.1:100.0):100.0):100.0,
923	70.m15058	AN1163.1	AO070331000153	FG01015.1	ANAO			((FG01015.1:100.0,((AO07033100:100.0,AN1163.1:100.0):54.0,70.m15058:100.0):100.0):100.0,
924	58.m07426	AN3666.1	AO070342000003	FG01007.1	ANAO			((FG01007.1:100.0,(58.m07426:100.0,(AN3666.1:100.0,AO07034200:100.0):70.5):100.0):100.0,
925	58.m07425	AN3665.1	AO070342000001	FG01006.1	AFAO	yes	yes	((FG01006.1:100.0,(AN3665.1:100.0,(58.m07425:100.0,AO07034200:100.0):100.0):100.0):100.0,
926	70.m15761	AN1188.1	AO070331000183	FG01010.1	AFAO		yes	((FG01010.1:100.0,((AO07033100:100.0,70.m15761:100.0):87.8,AN1188.1:100.0):100.0):100.0,
927	70.m15053	AN1167.1	AO070331000161	FG01009.1	AFAO	yes	yes	((FG01009.1:100.0,((AO07033100:100.0,70.m15053:100.0):95.0,AN1167.1:100.0):100.0):100.0,
928	57.m05448	AN7672.1	AO070325000052	FG06856.1	AFAO		yes	((FG06856.1:100.0,((AO07032500:100.0,57.m05448:100.0):87.0,AN7672.1:100.0):100.0):100.0,
929	57.m05730	AN1883.1	AO070306000016	FG06098.1	AFAN	yes	yes	((FG06098.1:100.0,((AN1883.1:100.0,57.m05730:100.0):100.0,AO07030600:100.0):100.0):100.0,
930	71.m15687	AN4699.1	AO070329000175	FG08733.1	AFAO			((FG08733.1:100.0,((AO07032900:100.0,71.m15687:100.0):47.5,AN4699.1:100.0):100.0):100.0,
931	59.m09208	AN4775.1	AO070329000077	FG09432.1	ANAO			((FG09432.1:100.0,(59.m09208:100.0,(AN4775.1:100.0,AO07032900:100.0):45.8):100.0):100.0,
932	70.m15003	AN1222.1	AO070331000222	FG00421.1	AFAO	yes	yes	((FG00421.1:100.0,((AO07033100:100.0,70.m15003:100.0):92.0,AN1222.1:100.0):100.0):100.0,
933	55.m03041	AN1522.1	AO070334000240	FG01219.1	ANAO			((FG01219.1:100.0,(55.m03041:100.0,(AN1522.1:100.0,AO07033400:100.0):45.3):100.0):100.0,
934	55.m03040	AN1521.1	AO070334000239	FG01220.1	ANAO	yes	yes	((FG01220.1:100.0,(55.m03040:100.0,(AN1521.1:100.0,AO07033400:100.0):99.0):100.0):100.0,
935	65.m07286	AN6697.1	AO070339000128	FG01351.1	AFAN			((FG01351.1:100.0,((65.m07286:100.0,AN6697.1:100.0):52.5,AO07033900:100.0):100.0):100.0,
936	56.m02291	AN8880.1	AO070293000010	FG00615.1	AFAO	yes	yes	((FG00615.1:100.0,(AN8880.1:100.0,(56.m02291:100.0,AO07029300:100.0):100.0):100.0):100.0,
937	58.m07719	AN1652.1	AO070299000039	FG06871.1	AFAO	yes	yes	((FG06871.1:100.0,((AO07029900:100.0,58.m07719:100.0):93.5,AN1652.1:100.0):100.0):100.0,
938	55.m02941	AN1436.1	AO070232000009	FG01101.1	AFAO	yes	yes	((FG01101.1:100.0,(AN1436.1:100.0,(55.m02941:100.0,AO07023200:100.0):100.0):100.0):100.0,
939	55.m02975	AN1474.1	AO070306000096	FG01102.1	AFAN			((FG01102.1:100.0,((55.m02975:100.0,AN1474.1:100.0):45.0,AO07030600:100.0):100.0):100.0,
940	72.m19141	AN5999.1	AO070340000277	FG01217.1	AFAO			((FG01217.1:100.0,((72.m19141:100.0,AO07034000:100.0):55.8,AN5999.1:100.0):100.0):100.0,
941	55.m02938	AN1432.1	AO070232000014	FG06985.1	AFAO		yes	((FG06985.1:100.0,((AO07023200:100.0,55.m02938:100.0):85.5,AN1432.1:100.0):100.0):100.0,
942	54.m06466	AN0295.1	AO070334000046	FG01216.1	ANAO			((FG01216.1:100.0,(54.m06466:100.0,(AN0295.1:100.0,AO07033400:100.0):63.5):100.0):100.0,
943	55.m02942	AN1442.1	AO070232000005	FG01215.1	AFAN			((FG01215.1:100.0,(AO07023200:100.0,(AN1442.1:100.0,55.m02942:100.0):56.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
944	55.m02985	AN1478.1	AO070334000161	FG01210.1	AFAO	yes	yes	((FG01210.1:100.0,(AN1478.1:100.0,(55.m02985:100.0,AO07033400:100.0):100.0):100.0):100.0,
945	59.m09048	AN2969.1	AO070337000155	FG01208.1	AFAO			((FG01208.1:100.0,((AO07033700:100.0,59.m09048:100.0):73.0,AN2969.1:100.0):100.0):100.0,
946	72.m19594	AN7577.1	AO070343000422	FG01207.1	ANAO	yes	yes	((FG01207.1:100.0,(72.m19594:100.0,(AN7577.1:100.0,AO07034300:100.0):90.0):100.0):100.0,
947	72.m19595	AN7576.1	AO070343000423	FG01204.1	AFAO		yes	((FG01204.1:100.0,((AO07034300:100.0,72.m19595:100.0):79.5,AN7576.1:100.0):100.0):100.0,
948	70.m14945	AN1266.1	AO070332000014	FG01024.1	AFAO			((FG01024.1:100.0,((AO07033200:100.0,70.m14945:100.0):73.0,AN1266.1:100.0):100.0):100.0,
949	58.m08002	AN4321.1	AO070230000012	FG11021.1	ANAO			((FG11021.1:100.0,(58.m08002:100.0,(AN4321.1:100.0,AO07023000:100.0):43.5):100.0):100.0,
950	70.m14989	AN1230.1	AO070331000242	FG01019.1	AFAN			((FG01019.1:100.0,(AO07033100:100.0,(AN1230.1:100.0,70.m14989:100.0):59.5):100.0):100.0,
951	70.m14990	AN1229.1	AO070331000241	FG01020.1	AFAO	yes	yes	((FG01020.1:100.0,((AO07033100:100.0,70.m14990:100.0):91.0,AN1229.1:100.0):100.0):100.0,
952	70.m15054	AN1166.1	AO070331000160	FG01016.1	AFAN			((FG01016.1:100.0,(AO07033100:100.0,(AN1166.1:100.0,70.m15054:100.0):43.5):100.0):100.0,
953	55.m02957	AN1455.1	AO070302000021	FG00430.1	ANAO			((FG00430.1:100.0,(55.m02957:100.0,(AN1455.1:100.0,AO07030200:100.0):72.3):100.0):100.0,
954	59.m09399	AN4914.1	AO070338000033	FG01297.1	AFAO	yes	yes	((FG01297.1:100.0,((AO07033800:100.0,59.m09399:100.0):92.5,AN4914.1:100.0):100.0):100.0,
955	70.m14959	AN1260.1	AO070214000005	FG01299.1	ANAO	yes	yes	((FG01299.1:100.0,(70.m14959:100.0,(AN1260.1:100.0,AO07021400:100.0):95.0):100.0):100.0,
956	70.m14960	AN1259.1	AO070214000006	FG01300.1	ANAO	yes	yes	((FG01300.1:100.0,(70.m14960:100.0,(AN1259.1:100.0,AO07021400:100.0):90.5):100.0):100.0,
957	70.m14920	AN1288.1	AO070303000049	FG01304.1	AFAO		yes	((FG01304.1:100.0,((AO07030300:100.0,70.m14920:100.0):88.5,AN1288.1:100.0):100.0):100.0,
958	70.m15021	AN1198.1	AO070331000203	FG01151.1	AFAO	yes	yes	((FG01151.1:100.0,((AO07033100:100.0,70.m15021:100.0):95.0,AN1198.1:100.0):100.0):100.0,
959	54.m06561	AN4032.1	AO070328000123	FG00448.1	AFAO	yes	yes	((FG00448.1:100.0,((AO07032800:100.0,54.m06561:100.0):93.0,AN4032.1:100.0):100.0):100.0,
960	54.m06449	AN0310.1	AO070334000023	FG00449.1	AFAN			((FG00449.1:100.0,(AO07033400:100.0,(AN0310.1:100.0,54.m06449:100.0):62.5):100.0):100.0,
961	58.m07374	AN3576.1	AO070342000173	FG00439.1	AFAN			((FG00439.1:100.0,(AO07034200:100.0,(AN3576.1:100.0,58.m07374:100.0):55.5):100.0):100.0,
962	58.m07375	AN3577.1	AO070342000172	FG00440.1	AFAO		yes	((FG00440.1:100.0,((AO07034200:100.0,58.m07375:100.0):77.0,AN3577.1:100.0):100.0):100.0,
963	59.m09025	AN2988.1	AO070337000134	FG00443.1	AFAN	yes	yes	((FG00443.1:100.0,((AN2988.1:100.0,59.m09025:100.0):100.0,AO07033700:100.0):100.0):100.0,
964	70.m14981	AN1237.1	AO070331000251	FG01157.1	ANAO			((FG01157.1:100.0,(70.m14981:100.0,(AN1237.1:100.0,AO07033100:100.0):52.5):100.0):100.0,
965	58.m07459	AN3642.1	AO070328000088	FG01155.1	AFAO			((FG01155.1:100.0,((AO07032800:100.0,58.m07459:100.0):54.8,AN3642.1:100.0):100.0):100.0,
966	70.m14852	AN9465.1	AO070215000004	FG01154.1	AFAO		yes	((FG01154.1:100.0,((AO07021500:100.0,70.m14852:100.0):75.3,AN9465.1:100.0):100.0):100.0,
967	70.m15009	AN1211.1	AO070331000217	FG01152.1	ANAO			((FG01152.1:100.0,(70.m15009:100.0,(AN1211.1:100.0,AO07033100:100.0):60.0):100.0):100.0,
968	54.m06555	AN4028.1	AO070328000115	FG00437.1	AFAO			((FG00437.1:100.0,((54.m06555:100.0,AO07032800:100.0):69.0,AN4028.1:100.0):100.0):100.0,
969	54.m06450	AN0308.1	AO070334000026	FG00435.1	AFAO		yes	((FG00435.1:100.0,((54.m06450:100.0,AO07033400:100.0):81.0,AN0308.1:100.0):100.0):100.0,
970	72.m19998	AN7563.1	AO070343000404	FG00433.1	AFAO	yes	yes	((FG00433.1:100.0,((AO07034300:100.0,72.m19998:100.0):99.0,AN7563.1:100.0):100.0):100.0,
971	58.m07448	AN3651.1	AO070342000036	FG01292.1	AFAO		yes	((FG01292.1:100.0,((58.m07448:100.0,AO07034200:100.0):76.0,AN3651.1:100.0):100.0):100.0,
972	58.m07450	AN3649.1	AO070328000097	FG01290.1	AFAO	yes	yes	((FG01290.1:100.0,((AO07032800:100.0,58.m07450:100.0):96.5,AN3649.1:100.0):100.0):100.0,
973	58.m07451	AN3648.1	AO070328000096	FG01291.1	AFAN	yes	yes	((FG01291.1:100.0,(AO07032800:100.0,(58.m07451:100.0,AN3648.1:100.0):94.0):100.0):100.0,
974	70.m15052	AN1168.1	AO070331000162	FG01364.1	AFAO		yes	((FG01364.1:100.0,((AO07033100:100.0,70.m15052:100.0):78.5,AN1168.1:100.0):100.0):100.0,
975	69.m15473	AN5480.1	AO070341000406	FG01267.1	AFAN	yes	yes	((FG01267.1:100.0,(AO07034100:100.0,(AN5480.1:100.0,69.m15473:100.0):90.5):100.0):100.0,
976	54.m07005	AN2733.1	AO070338000215	FG01361.1	AFAO	yes	yes	((FG01361.1:100.0,(AN2733.1:100.0,(54.m07005:100.0,AO07033800:100.0):100.0):100.0):100.0,
977	54.m06386	AN0363.1	AO070318000043	FG01362.1	AFAO	yes	yes	((FG01362.1:100.0,((AO07031800:100.0,54.m06386:100.0):98.5,AN0363.1:100.0):100.0):100.0,
978	65.m07402	AN5676.1	AO070309000091	FG01030.1	AFAO			((FG01030.1:100.0,((AO07030900:100.0,65.m07402:100.0):56.0,AN5676.1:100.0):100.0):100.0,
979	58.m07727	AN1637.1	AO070299000056	FG01107.1	AFAO		yes	((FG01107.1:100.0,((AO07029900:100.0,58.m07727:100.0):81.0,AN1637.1:100.0):100.0):100.0,
980	69.m14846	AN5748.1	AO070341000005	FG00612.1	AFAO		yes	((FG00612.1:100.0,((AO07034100:100.0,69.m14846:100.0):80.5,AN5748.1:100.0):100.0):100.0,
981	69.m14819	AN5778.1	AO070249000023	FG00610.1	ANAO			((FG00610.1:100.0,(69.m14819:100.0,(AN5778.1:100.0,AO07024900:100.0):53.0):100.0):100.0,
982	58.m09023	AN1673.1	AO070299000007	FG01486.1	AFAO			((FG01486.1:100.0,((58.m09023:100.0,AO07029900:100.0):71.5,AN1673.1:100.0):100.0):100.0,
983	58.m07742	AN1661.1	AO070299000021	FG01511.1	ANAO			((FG01511.1:100.0,(58.m07742:100.0,(AN1661.1:100.0,AO07029900:100.0):57.5):100.0):100.0,
984	65.m07374	AN3753.1	AO070309000064	FG01042.1	AFAN			((FG01042.1:100.0,(AO07030900:100.0,(AN3753.1:100.0,65.m07374:100.0):50.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
985	66.m04587	AN9148.1	AO070332000144	FG00524.1	ANAO			((FG00524.1:100.0,(66.m04587:100.0,(AN9148.1:100.0,AO07033200:100.0):51.0):100.0):100.0,
986	72.m19561	AN7544.1	AO070277000041	FG01106.1	AFAO		yes	((FG01106.1:100.0,((AO07027700:100.0,72.m19561:100.0):76.0,AN7544.1:100.0):100.0):100.0,
987	52.m03755	AN8959.1	AO070336000205	FG01031.1	AFAO		yes	(((AN8959.1:100.0,(52.m03755:100.0,AO07033600:100.0):76.0):99.5,FG01031.1:100.0):100.0,
988	56.m02292	AN8881.1	AO070293000011	FG01032.1	AFAO			((FG01032.1:100.0,((AO07029300:100.0,56.m02292:100.0):43.8,AN8881.1:100.0):100.0):100.0,
989	58.m09021	AN1634.1	AO070299000045	FG06849.1	AFAO			((FG06849.1:100.0,((AO07029900:100.0,58.m09021:100.0):66.5,AN1634.1:100.0):100.0):100.0,
990	58.m07726	AN1636.1	AO070299000057	FG06848.1	ANAO			((FG06848.1:100.0,((AO07029900:100.0,AN1636.1:100.0):35.5,58.m07726:100.0):100.0):100.0,
991	57.m05629	AN4501.1	AO070311000054	FG06847.1	AFAN	yes	yes	((FG06847.1:100.0,(AO07031100:100.0,(57.m05629:100.0,AN4501.1:100.0):91.5):100.0):100.0,
992	58.m07860	AN4470.1	AO070305000129	FG06843.1	AFAO		yes	((FG06843.1:100.0,((AO07030500:100.0,58.m07860:100.0):81.0,AN4470.1:100.0):100.0):100.0,
993	65.m07441	AN4264.1	AO070277000021	FG06842.1	AFAO		yes	((FG06842.1:100.0,((AO07027700:100.0,65.m07441:100.0):76.0,AN4264.1:100.0):100.0):100.0,
994	65.m07433	AN4259.1	AO070277000032	FG07122.1	AFAO	yes	yes	((FG07122.1:100.0,((AO07027700:100.0,65.m07433:100.0):97.5,AN4259.1:100.0):100.0):100.0,
995	65.m07442	AN4265.1	AO070277000020	FG07115.1	AFAO	yes	yes	((FG07115.1:100.0,((AO07027700:100.0,65.m07442:100.0):97.0,AN4265.1:100.0):100.0):100.0,
996	69.m15634	AN5772.1	AO070249000014	FG07113.1	ANAO		yes	((FG07113.1:100.0,(69.m15634:100.0,(AN5772.1:100.0,AO07024900:100.0):82.5):100.0):100.0,
997	66.m04537	AN9079.1	AO070332000200	FG07119.1	AFAO		yes	((FG07119.1:100.0,((AO07033200:100.0,66.m04537:100.0):81.0,AN9079.1:100.0):100.0):100.0,
998	59.m09095	AN2918.1	AO070329000153	FG00558.1	AFAO		yes	((FG00558.1:100.0,((AO07032900:100.0,59.m09095:100.0):83.3,AN2918.1:100.0):100.0):100.0,
999	59.m09096	AN2917.1	AO070329000154	FG00559.1	AFAO			((FG00559.1:100.0,((59.m09096:100.0,AO07032900:100.0):73.8,AN2917.1:100.0):100.0):100.0,
1000	71.m15249	AN6890.1	AO070314000031	FG09180.1	ANAO			((FG09180.1:100.0,(71.m15249:100.0,(AN6890.1:100.0,AO07031400:100.0):67.3):100.0):100.0,
1001	52.m03647	AN3613.1	AO070315000027	FG10999.1	ANAO			((((AO07031500:100.0,AN3613.1:100.0):58.5,52.m03647:100.0):99.5,FG10999.1:100.0):100.0,
1002	57.m05644	AN4487.1	AO070311000038	FG03825.1	AFAO		yes	((FG03825.1:100.0,((AO07031100:100.0,57.m05644:100.0):86.0,AN4487.1:100.0):100.0):100.0,
1003	58.m07676	AN1833.1	AO070318000086	FG06331.1	AFAO			((FG06331.1:100.0,((58.m07676:100.0,AO07031800:100.0):43.5,AN1833.1:100.0):100.0):100.0,
1004	70.m15665	AN8597.1	AO070319000106	FG03466.1	ANAO			((FG03466.1:100.0,(70.m15665:100.0,(AN8597.1:100.0,AO07031900:100.0):65.5):100.0):100.0,
1005	59.m09085	AN2948.1	AO070337000205	FG00762.1	ANAO		yes	((FG00762.1:100.0,(59.m09085:100.0,(AN2948.1:100.0,AO07033700:100.0):77.5):100.0):100.0,
1006	56.m02311	AN8898.1	AO070293000031	FG11298.1	AFAO			((FG11298.1:100.0,((AO07029300:100.0,56.m02311:100.0):74.0,AN8898.1:100.0):100.0):100.0,
1007	71.m15197	AN1202.1	AO070328000070	FG09179.1	AFAN			((((AN1202.1:100.0,71.m15197:100.0):44.3,AO07032800:100.0):96.0,FG09179.1:100.0):100.0,
1008	54.m06559	AN4030.1	AO070328000122	FG00800.1	AFAO	yes	yes	((FG00800.1:100.0,((AO07032800:100.0,54.m06559:100.0):99.0,AN4030.1:100.0):100.0):100.0,
1009	54.m06547	AN4024.1	AO070328000111	FG00804.1	ANAO		yes	((FG00804.1:100.0,(54.m06547:100.0,(AN4024.1:100.0,AO07032800:100.0):77.5):100.0):100.0,
1010	66.m04776	AN6933.1	AO070332000207	FG00805.1	AFAO	yes	yes	((FG00805.1:100.0,((AO07033200:100.0,66.m04776:100.0):90.0,AN6933.1:100.0):100.0):100.0,
1011	52.m03715	AN8482.1	AO070342000378	FG04160.1	AFAO	yes	yes	((FG04160.1:100.0,((AO07034200:100.0,52.m03715:100.0):95.0,AN8482.1:100.0):100.0):100.0,
1012	72.m20020	AN7292.1	AO070297000033	FG06744.1	AFAO	yes	yes	((FG06744.1:100.0,((AO07029700:100.0,72.m20020:100.0):94.0,AN7292.1:100.0):100.0):100.0,
1013	69.m15037	AN1731.1	AO070324000062	FG04886.1	AFAO	yes	yes	((FG04886.1:100.0,((AO07032400:100.0,69.m15037:100.0):99.0,AN1731.1:100.0):100.0):100.0,
1014	57.m05617	AN4511.1	AO070311000067	FG04885.1	ANAO			((FG04885.1:100.0,(57.m05617:100.0,(AN4511.1:100.0,AO07031100:100.0):48.0):100.0):100.0,
1015	57.m05636	AN4495.1	AO070311000047	FG04883.1	AFAO			((FG04883.1:100.0,((AO07031100:100.0,57.m05636:100.0):67.5,AN4495.1:100.0):100.0):100.0,
1016	57.m05640	AN4491.1	AO070311000043	FG09360.1	ANAO		yes	((FG09360.1:100.0,((AO07031100:100.0,AN4491.1:100.0):82.0,57.m05640:100.0):100.0):100.0,
1017	57.m05641	AN4490.1	AO070311000042	FG09359.1	ANAO		yes	((FG09359.1:100.0,(57.m05641:100.0,(AN4490.1:100.0,AO07031100:100.0):86.5):100.0):100.0,
1018	54.m06465	AN0297.1	AO070334000045	FG01403.1	AFAO			((FG01403.1:100.0,((AO07033400:100.0,54.m06465:100.0):57.0,AN0297.1:100.0):100.0):100.0,
1019	69.m15625	AN5203.1	AO070199000002	FG01394.1	AFAO			((FG01394.1:100.0,((69.m15625:100.0,AO07019900:100.0):51.2,AN5203.1:100.0):100.0):100.0,
1020	69.m14903	AN5206.1	AO070199000006	FG01392.1	AFAO			((FG01392.1:100.0,((AO07019900:100.0,69.m14903:100.0):69.0,AN5206.1:100.0):100.0):100.0,
1021	58.m07811	AN3832.1	AO070305000070	FG01391.1	AFAO			((FG01391.1:100.0,((58.m07811:100.0,AO07030500:100.0):60.0,AN3832.1:100.0):100.0):100.0,
1022	72.m19570	AN7553.1	AO070277000052	FG01173.1	AFAO	yes	yes	((FG01173.1:100.0,((AO07027700:100.0,72.m19570:100.0):95.5,AN7553.1:100.0):100.0):100.0,
1023	55.m03035	AN1516.1	AO070334000235	FG01174.1	AFAO	yes	yes	((FG01174.1:100.0,(AN1516.1:100.0,(55.m03035:100.0,AO07033400:100.0):100.0):100.0):100.0,
1024	72.m19585	AN7566.1	AO070343000409	FG01167.1	AFAO		yes	((FG01167.1:100.0,((AO07034300:100.0,72.m19585:100.0):81.5,AN7566.1:100.0):100.0):100.0,
1025	70.m15017	AN1205.1	AO070331000209	FG01334.1	AFAN		yes	((FG01334.1:100.0,((70.m15017:100.0,AN1205.1:100.0):79.0,AO07033100:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1026	70.m15767	AN1207.1	AO070331000213	FG01336.1	AFAO			((FG01336.1:100.0,((AO07033100:100.0,70.m15767:100.0):69.3,AN1207.1:100.0):100.0):100.0,
1027	70.m15013	AN1208.1	AO070331000214	FG01337.1	ANAO			((FG01337.1:100.0,((AO07033100:100.0,AN1208.1:100.0):45.3,70.m15013:100.0):100.0):100.0,
1028	70.m15768	AN1209.1	AO070331000215	FG01338.1	AFAO		yes	((FG01338.1:100.0,((AO07033100:100.0,70.m15768:100.0):88.5,AN1209.1:100.0):100.0):100.0,
1029	70.m15011	AN1210.1	AO070331000216	FG01339.1	AFAO		yes	((FG01339.1:100.0,((AO07033100:100.0,70.m15011:100.0):89.0,AN1210.1:100.0):100.0):100.0,
1030	58.m07433	AN3673.1	AO070342000015	FG01377.1	AFAO		yes	(((AN3673.1:100.0,(AO07034200:100.0,58.m07433:100.0):79.8):97.0,FG01377.1:100.0):100.0,
1031	58.m07435	AN3663.1	AO070342000021	FG01375.1	AFAO	yes	yes	((FG01375.1:100.0,((AO07034200:100.0,58.m07435:100.0):90.5,AN3663.1:100.0):100.0):100.0,
1032	54.m06793	AN4224.1	AO070234000026	FG01373.1	AFAN			((FG01373.1:100.0,(AO07023400:100.0,(AN4224.1:100.0,54.m06793:100.0):58.0):100.0):100.0,
1033	56.m03128	AN8872.1	AO070293000001	FG01371.1	ANAO			((FG01371.1:100.0,(56.m03128:100.0,(AN8872.1:100.0,AO07029300:100.0):65.0):100.0):100.0,
1034	56.m03110	AN8875.1	AO070293000004	FG01370.1	AFAO	yes	yes	((FG01370.1:100.0,((AO07029300:100.0,56.m03110:100.0):98.0,AN8875.1:100.0):100.0):100.0,
1035	72.m19597	AN7579.1	AO070343000426	FG01123.1	AFAO		yes	((FG01123.1:100.0,((AO07034300:100.0,72.m19597:100.0):87.5,AN7579.1:100.0):100.0):100.0,
1036	72.m19596	AN7578.1	AO070343000425	FG01122.1	AFAO	yes	yes	((FG01122.1:100.0,((AO07034300:100.0,72.m19596:100.0):95.0,AN7578.1:100.0):100.0):100.0,
1037	72.m19611	AN7589.1	AO070343000303	FG01120.1	AFAO	yes	yes	((FG01120.1:100.0,(AN7589.1:100.0,(72.m19611:100.0,AO07034300:100.0):100.0):100.0):100.0,
1038	70.m15090	AN1148.1	AO070331000139	FG01150.1	ANAO			((FG01150.1:100.0,(70.m15090:100.0,(AN1148.1:100.0,AO07033100:100.0):64.3):100.0):100.0,
1039	71.m16052	AN0160.1	AO070321000087	FG00452.1			yes	(((AN0160.1:100.0,FG00452.1:100.0):86.5,(71.m16052:100.0,AO07032100:100.0):85.5):100.0,
1040	59.m09294	AN3431.1	AO070265000010	FG09549.1	AFAO	yes	yes	((FG09549.1:100.0,((AO07026500:100.0,59.m09294:100.0):99.0,AN3431.1:100.0):100.0):100.0,
1041	52.m04030	AN9403.1	AO070274000014	FG02782.1	AFAO			((FG02782.1:100.0,((52.m04030:100.0,AO07027400:100.0):74.3,AN9403.1:100.0):100.0):100.0,
1042	58.m07534	AN5610.1	AO070301000010	FG06041.1	AFAO	yes	yes	((FG06041.1:100.0,(AN5610.1:100.0,(58.m07534:100.0,AO07030100:100.0):100.0):100.0):100.0,
1043	70.m15105	AN1131.1	AO070331000123	FG00576.1	AFAN		yes	((FG00576.1:100.0,(AO07033100:100.0,(AN1131.1:100.0,70.m15105:100.0):88.5):100.0):100.0,
1044	57.m05884	AN7458.1	AO070287000067	FG00485.1	AFAO	yes	yes	((FG00485.1:100.0,(AN7458.1:100.0,(57.m05884:100.0,AO07028700:100.0):100.0):100.0):100.0,
1045	57.m05873	AN7471.1	AO070287000055	FG00486.1	AFAO	yes	yes	((FG00486.1:100.0,(AN7471.1:100.0,(57.m05873:100.0,AO07028700:100.0):100.0):100.0):100.0,
1046	58.m07667	AN1844.1	AO070292000063	FG01029.1	AFAO	yes	yes	((FG01029.1:100.0,((AO07029200:100.0,58.m07667:100.0):92.0,AN1844.1:100.0):100.0):100.0,
1047	54.m07003	AN2736.1	AO070338000218	FG00870.1	AFAO			((FG00870.1:100.0,((AO07033800:100.0,54.m07003:100.0):61.5,AN2736.1:100.0):100.0):100.0,
1048	54.m06976	AN0299.1	AO070334000042	FG00952.1	ANAO			((FG00952.1:100.0,(54.m06976:100.0,(AO07033400:100.0,AN0299.1:100.0):68.5):100.0):100.0,
1049	58.m08968	AN1709.1	AO070305000039	FG00744.1	AFAO		yes	((FG00744.1:100.0,((AO07030500:100.0,58.m08968:100.0):79.0,AN1709.1:100.0):100.0):100.0,
1050	70.m15502	AN0896.1	AO070320000070	FG00743.1	ANAO			((FG00743.1:100.0,((AO07032000:100.0,AN0896.1:100.0):55.7,70.m15502:100.0):100.0):100.0,
1051	72.m19959	AN5914.1	AO070248000032	FG00742.1	ANAO			((FG00742.1:100.0,((AO07024800:100.0,AN5914.1:100.0):73.0,72.m19959:100.0):100.0):100.0,
1052	72.m19562	AN7545.1	AO070277000042	FG00352.1	AFAO			((FG00352.1:100.0,((72.m19562:100.0,AO07027700:100.0):64.0,AN7545.1:100.0):100.0):100.0,
1053	65.m07302	AN6678.1	AO070289000018	FG07046.1	AFAO		yes	((FG07046.1:100.0,((AO07028900:100.0,65.m07302:100.0):79.0,AN6678.1:100.0):100.0):100.0,
1054	65.m07301	AN6679.1	AO070289000019	FG07048.1	AFAN			((((65.m07301:100.0,AN6679.1:100.0):51.7,AO07028900:100.0):53.4,FG07048.1:100.0):100.0,
1055	65.m07299	AN6681.1	AO070289000025	FG07049.1	AFAO			((FG07049.1:100.0,((AO07028900:100.0,65.m07299:100.0):72.5,AN6681.1:100.0):100.0):100.0,
1056	65.m07298	AN6682.1	AO070289000024	FG07050.1	AFAO	yes	yes	((FG07050.1:100.0,((AO07028900:100.0,65.m07298:100.0):95.5,AN6682.1:100.0):100.0):100.0,
1057	72.m19472	AN2420.1	AO070228000003	FG07051.1	AFAO	yes	yes	((FG07051.1:100.0,((AO07022800:100.0,72.m19472:100.0):91.5,AN2420.1:100.0):100.0):100.0,
1058	65.m07296	AN6685.1	AO070339000093	FG07053.1	AFAO			((FG07053.1:100.0,((AO07033900:100.0,65.m07296:100.0):64.5,AN6685.1:100.0):100.0):100.0,
1059	55.m03057	AN1538.1	AO070334000262	FG01116.1	AFAN	yes	yes	((FG01116.1:100.0,(AO07033400:100.0,(AN1538.1:100.0,55.m03057:100.0):96.5):100.0):100.0,
1060	55.m03277	AN1537.1	AO070334000260	FG00512.1	ANAO			((FG00512.1:100.0,((AO07033400:100.0,AN1537.1:100.0):62.8,55.m03277:100.0):100.0):100.0,
1061	62.m03452	AN8757.1	AO070321000005	FG11270.1	AFAO			((FG11270.1:100.0,((AO07032100:100.0,62.m03452:100.0):55.3,AN8757.1:100.0):100.0):100.0,
1062	54.m06979	AN0306.1	AO070334000032	FG07054.1	AFAO			((FG07054.1:100.0,((54.m06979:100.0,AO07033400:100.0):60.0,AN0306.1:100.0):100.0):100.0,
1063	54.m06453	AN0305.1	AO070334000033	FG07055.1	ANAO			((FG07055.1:100.0,(54.m06453:100.0,(AN0305.1:100.0,AO07033400:100.0):52.0):100.0):100.0,
1064	55.m03053	AN1535.1	AO070334000255	FG00514.1	AFAO			((((AO07033400:100.0,55.m03053:100.0):57.3,AN1535.1:100.0):69.8,FG00514.1:100.0):100.0,
1065	57.m05471	AN4184.1	AO070325000093	FG03942.1	AFAO	yes	yes	((FG03942.1:100.0,((AO07032500:100.0,57.m05471:100.0):97.5,AN4184.1:100.0):100.0):100.0,
1066	70.m14994	AN1226.1	AO070331000235	FG00460.1	AFAO	yes	yes	((FG00460.1:100.0,((AO07033100:100.0,70.m14994:100.0):95.0,AN1226.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1067	70.m14969	AN1255.1	AO070223000014	FG07102.1	ANAO	yes	yes	((FG07102.1:100.0,((AN1255.1:100.0,AO07022300:100.0):100.0,70.m14969:100.0):100.0):100.0,
1068	70.m14971	AN1256.1	AO070223000013	FG07101.1	AFAO	yes	yes	((FG07101.1:100.0,((AO07022300:100.0,70.m14971:100.0):90.0,AN1256.1:100.0):100.0):100.0,
1069	70.m14972	AN1249.1	AO070223000012	FG07100.1	AFAO	yes	yes	((FG07100.1:100.0,((70.m14972:100.0,AO07022300:100.0):91.0,AN1249.1:100.0):100.0):100.0,
1070	70.m15738	AN1248.1	AO070223000011	FG07099.1	AFAO	yes	yes	((FG07099.1:100.0,((AO07022300:100.0,70.m15738:100.0):99.0,AN1248.1:100.0):100.0):100.0,
1071	58.m07443	AN3657.1	AO070342000031	FG01184.1	AFAO		yes	((FG01184.1:100.0,((AO07034200:100.0,58.m07443:100.0):88.0,AN3657.1:100.0):100.0):100.0,
1072	70.m14996	AN1215.1	AO070331000233	FG01185.1	AFAO			((FG01185.1:100.0,((70.m14996:100.0,AO07033100:100.0):49.0,AN1215.1:100.0):100.0):100.0,
1073	70.m14997	AN1216.1	AO070331000232	FG07096.1	ANAO			((FG07096.1:100.0,((AO07033100:100.0,AN1216.1:100.0):64.5,70.m14997:100.0):100.0):100.0,
1074	70.m15037	AN1180.1	AO070331000178	FG00408.1	AFAO			((FG00408.1:100.0,((AO07033100:100.0,70.m15037:100.0):73.5,AN1180.1:100.0):100.0):100.0,
1075	70.m15002	AN1221.1	AO070331000223	FG07098.1	AFAO	yes	yes	((FG07098.1:100.0,((AO07033100:100.0,70.m15002:100.0):94.5,AN1221.1:100.0):100.0):100.0,
1076	69.m15036	AN1733.1	AO070324000063	FG01141.1	AFAO			((FG01141.1:100.0,((AO07032400:100.0,69.m15036:100.0):73.5,AN1733.1:100.0):100.0):100.0,
1077	70.m15753	AN9466.1	AO070215000006	FG01142.1	AFAO			((FG01142.1:100.0,((AO07021500:100.0,70.m15753:100.0):69.0,AN9466.1:100.0):100.0):100.0,
1078	70.m14857	AN1372.1	AO070215000009	FG00461.1	ANAO			((FG00461.1:100.0,((AO07021500:100.0,AN1372.1:100.0):55.0,70.m14857:100.0):100.0):100.0,
1079	70.m15120	AN1115.1	AO070331000106	FG00465.1	AFAO		yes	((FG00465.1:100.0,((70.m15120:100.0,AO07033100:100.0):87.0,AN1115.1:100.0):100.0):100.0,
1080	59.m09106	AN4866.1	AO070329000152	FG00999.1	AFAO			((FG00999.1:100.0,((AO07032900:100.0,59.m09106:100.0):70.5,AN4866.1:100.0):100.0):100.0,
1081	69.m14968	AN3954.1	AO070341000069	FG01111.1	AFAO	yes	yes	((FG01111.1:100.0,((AO07034100:100.0,69.m14968:100.0):98.0,AN3954.1:100.0):100.0):100.0,
1082	69.m14997	AN3930.1	AO070341000033	FG01112.1	AFAO			((FG01112.1:100.0,((69.m14997:100.0,AO07034100:100.0):71.5,AN3930.1:100.0):100.0):100.0,
1083	57.m05712	AN5222.1	AO070337000256	FG00671.1	AFAO			((FG00671.1:100.0,((AO07033700:100.0,57.m05712:100.0):47.3,AN5222.1:100.0):100.0):100.0,
1084	57.m05713	AN5221.1	AO070337000257	FG00672.1	AFAO	yes	yes	((FG00672.1:100.0,((AO07033700:100.0,57.m05713:100.0):91.5,AN5221.1:100.0):100.0):100.0,
1085	54.m06552	AN4019.1	AO070328000118	FG00924.1	AFAO	yes	yes	((FG00924.1:100.0,((AO07032800:100.0,54.m06552:100.0):96.5,AN4019.1:100.0):100.0):100.0,
1086	54.m06553	AN4018.1	AO070328000117	FG00925.1	AFAO		yes	((FG00925.1:100.0,((54.m06553:100.0,AO07032800:100.0):81.0,AN4018.1:100.0):100.0):100.0,
1087	54.m06625	AN0432.1	AO070338000285	FG00926.1	AFAN			((FG00926.1:100.0,(AO07033800:100.0,(AN0432.1:100.0,54.m06625:100.0):58.0):100.0):100.0,
1088	57.m05664	AN3819.1	AO070311000016	FG00929.1	AFAN			((FG00929.1:100.0,(AO07031100:100.0,(AN3819.1:100.0,57.m05664:100.0):68.5):100.0):100.0,
1089	57.m05672	AN3810.1	AO070337000218	FG00930.1	AFAN		yes	((FG00930.1:100.0,(AO07033700:100.0,(AN3810.1:100.0,57.m05672:100.0):79.0):100.0):100.0,
1090	57.m05667	AN3815.1	AO070311000013	FG00932.1	ANAO		yes	((FG00932.1:100.0,((AO07031100:100.0,AN3815.1:100.0):77.0,57.m05667:100.0):100.0):100.0,
1091	57.m05660	AN9463.1	AO070311000018	FG01497.1	ANAO		yes	((FG01497.1:100.0,(57.m05660:100.0,(AN9463.1:100.0,AO07031100:100.0):78.5):100.0):100.0,
1092	55.m02991	AN1485.1	AO070334000192	FG00677.1	ANAO		yes	((FG00677.1:100.0,(55.m02991:100.0,(AN1485.1:100.0,AO07033400:100.0):88.0):100.0):100.0,
1093	66.m04519	AN9067.1	AO070332000219	FG00728.1	AFAO			((FG00728.1:100.0,((AO07033200:100.0,66.m04519:100.0):67.0,AN9067.1:100.0):100.0):100.0,
1094	54.m06627	AN0431.1	AO070338000291	FG00740.1	ANAO			((FG00740.1:100.0,(54.m06627:100.0,(AN0431.1:100.0,AO07033800:100.0):69.5):100.0):100.0,
1095	70.m15567	AN0936.1	AO070320000127	FG00749.1	AFAO			((FG00749.1:100.0,((AO07032000:100.0,70.m15567:100.0):69.5,AN0936.1:100.0):100.0):100.0,
1096	70.m15501	AN0897.1	AO070320000071	FG00751.1	ANAO			((FG00751.1:100.0,(70.m15501:100.0,(AN0897.1:100.0,AO07032000:100.0):52.5):100.0):100.0,
1097	71.m15187	AN6939.1	AO070313000064	FG10537.1	AFAN			((FG10537.1:100.0,((71.m15187:100.0,AN6939.1:100.0):69.0,AO07031300:100.0):84.5):100.0,
1098	70.m15404	AN0803.1	AO070239000014	FG00869.1	ANAO			((FG00869.1:100.0,(70.m15404:100.0,(AN0803.1:100.0,AO07023900:100.0):56.0):100.0):100.0,
1099	70.m15403	AN0802.1	AO070239000016	FG00866.1	ANAO			((FG00866.1:100.0,(70.m15403:100.0,(AN0802.1:100.0,AO07023900:100.0):43.5):100.0):100.0,
1100	70.m15398	AN0797.1	AO070239000020	FG00865.1	ANAO		yes	((FG00865.1:100.0,(70.m15398:100.0,(AN0797.1:100.0,AO07023900:100.0):84.5):100.0):100.0,
1101	58.m07753	AN1675.1	AO070299000004	FG02073.1	AFAO	yes	yes	((FG02073.1:100.0,((AO07029900:100.0,58.m07753:100.0):95.5,AN1675.1:100.0):100.0):100.0,
1102	72.m19547	AN1795.1	AO070309000136	FG00947.1	AFAN			((FG00947.1:100.0,(AO07030900:100.0,(AN1795.1:100.0,72.m19547:100.0):61.5):100.0):100.0,
1103	72.m19076	AN6086.1	AO070340000137	FG09324.1	AFAN			((FG09324.1:100.0,(AO07034000:100.0,(AN6086.1:100.0,72.m19076:100.0):40.8):100.0):100.0,
1104	62.m03315	AN8766.1	AO070277000060	FG08674.1	AFAO		yes	((FG08674.1:100.0,((AO07027700:100.0,62.m03315:100.0):80.0,AN8766.1:100.0):100.0):100.0,
1105	62.m03333	AN8746.1	AO070250000027	FG08675.1	AFAN		yes	((FG08675.1:100.0,(AO07025000:100.0,(AN8746.1:100.0,62.m03333:100.0):76.0):100.0):100.0,
1106	62.m03491	AN8704.1	AO070315000132	FG08676.1	ANAO			((FG08676.1:100.0,(62.m03491:100.0,(AN8704.1:100.0,AO07031500:100.0):40.8):100.0):100.0,
1107	62.m03473	AN8692.1	AO070315000113	FG08677.1	AFAO			((FG08677.1:100.0,((62.m03473:100.0,AO07031500:100.0):74.3,AN8692.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1108	59.m09152	AN9446.1	AO070327000156	FG08680.1	AFAO			((FG08680.1:100.0,((AO07032700:100.0,59.m09152:100.0):65.8,AN9446.1:100.0):100.0):100.0,
1109	62.m03312	AN8763.1	AO070277000063	FG08566.1	ANAO			((((AN8763.1:100.0,AO07027700:100.0):29.8,62.m03312:100.0):55.2,FG08566.1:100.0):100.0,
1110	69.m14872	AN5175.1	AO070247000006	FG03947.1	ANAO			((FG03947.1:100.0,(69.m14872:100.0,(AN5175.1:100.0,AO07024700:100.0):50.0):100.0):100.0,
1111	62.m03389	AN8682.1	AO070315000102	FG08578.1	AFAO	yes	yes	((FG08578.1:100.0,(AN8682.1:100.0,(62.m03389:100.0,AO07031500:100.0):100.0):100.0):100.0,
1112	59.m09136	AN4841.1	AO070327000129	FG08581.1	AFAN		yes	((FG08581.1:100.0,(AO07032700:100.0,(AN4841.1:100.0,59.m09136:100.0):81.0):100.0):100.0,
1113	72.m19615	AN7597.1	AO070343000314	FG08669.1	AFAO		yes	((FG08669.1:100.0,((AO07034300:100.0,72.m19615:100.0):75.0,AN7597.1:100.0):100.0):100.0,
1114	57.m05559	AN4549.1	AO070321000182	FG09541.1	AFAN			((FG09541.1:100.0,(AO07032100:100.0,(AN4549.1:100.0,57.m05559:100.0):40.0):100.0):100.0,
1115	59.m09124	AN4851.1	AO070327000095	FG08589.1	AFAO	yes	yes	((FG08589.1:100.0,((AO07032700:100.0,59.m09124:100.0):92.0,AN4851.1:100.0):100.0):100.0,
1116	70.m15537	AN0929.1	AO070320000117	FG09539.1	AFAN			((FG09539.1:100.0,(AO07032000:100.0,(AN0929.1:100.0,70.m15537:100.0):71.0):100.0):100.0,
1117	59.m09137	AN4842.1	AO070327000130	FG09542.1	AFAN	yes	yes	((FG09542.1:100.0,(AO07032700:100.0,(AN4842.1:100.0,59.m09137:100.0):99.5):100.0):100.0,
1118	62.m03343	AN8723.1	AO070315000151	FG09409.1	AFAO		yes	((FG09409.1:100.0,((AO07031500:100.0,62.m03343:100.0):77.8,AN8723.1:100.0):100.0):100.0,
1119	62.m03339	AN8741.1	AO070250000041	FG09410.1	AFAO			((FG09410.1:100.0,((AO07025000:100.0,62.m03339:100.0):56.5,AN8741.1:100.0):100.0):100.0,
1120	62.m03341	AN9504.1	AO070315000153	FG09408.1	AFAO		yes	((FG09408.1:100.0,((AO07031500:100.0,62.m03341:100.0):85.0,AN9504.1:100.0):100.0):100.0,
1121	70.m15436	AN0836.1	AO070255000007	FG08694.1	AFAO			((FG08694.1:100.0,((AO07025500:100.0,70.m15436:100.0):55.0,AN0836.1:100.0):100.0):100.0,
1122	62.m03392	AN8679.1	AO070315000099	FG08577.1	AFAO			((FG08577.1:100.0,((AO07031500:100.0,62.m03392:100.0):52.8,AN8679.1:100.0):100.0):100.0,
1123	58.m07413	AN3626.1	AO070342000124	FG10669.1	AFAO	yes	yes	((FG10669.1:100.0,((AO07034200:100.0,58.m07413:100.0):96.0,AN3626.1:100.0):100.0):100.0,
1124	59.m08882	AN4980.1	AO070288000047	FG00469.1	AFAO			((FG00469.1:100.0,((AO07028800:100.0,59.m08882:100.0):73.0,AN4980.1:100.0):100.0):100.0,
1125	54.m07034	AN4238.1	AO070234000002	FG00472.1	AFAO			((FG00472.1:100.0,((54.m07034:100.0,AO07023400:100.0):48.3,AN4238.1:100.0):100.0):100.0,
1126	58.m07469	AN3632.1	AO070328000069	FG00475.1	ANAO			((FG00475.1:100.0,(58.m07469:100.0,(AN3632.1:100.0,AO07032800:100.0):52.0):100.0):100.0,
1127	70.m14968	AN1254.1	AO070223000015	FG00477.1	AFAO	yes	yes	((FG00477.1:100.0,((AO07022300:100.0,70.m14968:100.0):92.0,AN1254.1:100.0):100.0):100.0,
1128	59.m09109	AN4862.1	AO070329000148	FG00562.1	AFAN			((FG00562.1:100.0,(AO07032900:100.0,(AN4862.1:100.0,59.m09109:100.0):36.0):100.0):100.0,
1129	57.m05701	AN5230.1	AO070337000247	FG00670.1	AFAO	yes	yes	((FG00670.1:100.0,((AO07033700:100.0,57.m05701:100.0):98.0,AN5230.1:100.0):100.0):100.0,
1130	57.m05598	AN4528.1	AO070321000138	FG09163.1	AFAO			((FG09163.1:100.0,((AO07032100:100.0,57.m05598:100.0):47.8,AN4528.1:100.0):100.0):100.0,
1131	57.m05627	AN4504.1	AO070311000057	FG00294.1	AFAO		yes	((FG00294.1:100.0,((AO07031100:100.0,57.m05627:100.0):84.5,AN4504.1:100.0):100.0):100.0,
1132	54.m06522	AN0259.1	AO070334000099	FG09162.1	ANAO		yes	((FG09162.1:100.0,(54.m06522:100.0,(AN0259.1:100.0,AO07033400:100.0):77.0):100.0):100.0,
1133	59.m09055	AN2939.1	AO070337000169	FG09158.1	ANAO			((FG09158.1:100.0,(59.m09055:100.0,(AN2939.1:100.0,AO07033700:100.0):51.0):100.0):100.0,
1134	58.m07383	AN3584.1	AO070342000165	FG09157.1	AFAN			((FG09157.1:100.0,(AO07034200:100.0,(AN3584.1:100.0,58.m07383:100.0):50.0):100.0):100.0,
1135	58.m07381	AN3583.1	AO070342000166	FG09156.1	AFAO			((FG09156.1:100.0,((AO07034200:100.0,58.m07381:100.0):45.3,AN3583.1:100.0):100.0):100.0,
1136	55.m03317	AN1493.1	AO070334000206	FG09403.1	ANAO	yes	yes	((FG09403.1:100.0,(55.m03317:100.0,(AN1493.1:100.0,AO07033400:100.0):90.5):100.0):100.0,
1137	57.m05626	AN4505.1	AO070311000058	FG04914.1	AFAO			((FG04914.1:100.0,((AO07031100:100.0,57.m05626:100.0):48.5,AN4505.1:100.0):100.0):100.0,
1138	70.m14927	AN1281.1	AO070332000039	FG02761.1	AFAO			((FG02761.1:100.0,((AO07033200:100.0,70.m14927:100.0):40.8,AN1281.1:100.0):100.0):100.0,
1139	59.m08594	AN3131.1	AO070303000013	FG02769.1	AFAO	yes	yes	((FG02769.1:100.0,(AN3131.1:100.0,(59.m08594:100.0,AO07030300:100.0):100.0):100.0):100.0,
1140	69.m15007	AN3921.1	AO070324000117	FG01197.1	AFAO			((FG01197.1:100.0,((AO07032400:100.0,69.m15007:100.0):53.5,AN3921.1:100.0):100.0):100.0,
1141	69.m15006	AN3923.1	AO070324000119	FG01194.1	AFAO		yes	((FG01194.1:100.0,((AO07032400:100.0,69.m15006:100.0):78.5,AN3923.1:100.0):100.0):100.0,
1142	54.m06671	AN2730.1	AO070338000210	FG02163.1	AFAO	yes	yes	((FG02163.1:100.0,((AO07033800:100.0,54.m06671:100.0):92.0,AN2730.1:100.0):100.0):100.0,
1143	54.m06477	AN0281.1	AO070334000072	FG01065.1	ANAO			((FG01065.1:100.0,(54.m06477:100.0,(AN0281.1:100.0,AO07033400:100.0):69.0):100.0):100.0,
1144	69.m14882	AN5151.1	AO070237000013	FG01064.1	AFAO		yes	((FG01064.1:100.0,((69.m14882:100.0,AO07023700:100.0):79.5,AN5151.1:100.0):100.0):100.0,
1145	69.m15023	AN3908.1	AO070324000092	FG01058.1	AFAO	yes	yes	((FG01058.1:100.0,((AO07032400:100.0,69.m15023:100.0):95.0,AN3908.1:100.0):100.0):100.0,
1146	69.m15001	AN3927.1	AO070341000039	FG01057.1	ANAO	yes	yes	((FG01057.1:100.0,(69.m15001:100.0,(AN3927.1:100.0,AO07034100:100.0):99.0):100.0):100.0,
1147	69.m15002	AN3926.1	AO070341000040	FG00414.1	AFAO	yes	yes	((FG00414.1:100.0,((AO07034100:100.0,69.m15002:100.0):98.0,AN3926.1:100.0):100.0):100.0,
1148	59.m08669	AN5057.1	AO070338000201	FG00543.1	AFAO	yes	yes	((FG00543.1:100.0,((AO07033800:100.0,59.m08669:100.0):96.5,AN5057.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1149	52.m04104	AN8363.1	AO070274000030	FG00530.1	ANAO			((FG00530.1:100.0,(52.m04104:100.0,(AN8363.1:100.0,AO07027400:100.0):42.8):100.0):100.0,
1150	57.m05879	AN7463.1	AO070287000063	FG00529.1	AFAO			((FG00529.1:100.0,((57.m05879:100.0,AO07028700:100.0):62.0,AN7463.1:100.0):100.0):100.0,
1151	52.m03849	AN9362.1	AO070315000035	FG06860.1	AFAO			((FG06860.1:100.0,((AO07031500:100.0,52.m03849:100.0):68.3,AN9362.1:100.0):100.0):100.0,
1152	66.m04586	AN9149.1	AO070332000147	FG06885.1	AFAO	yes	yes	((FG06885.1:100.0,((AO07033200:100.0,66.m04586:100.0):93.0,AN9149.1:100.0):100.0):100.0,
1153	56.m03107	AN8877.1	AO070293000006	FG06859.1	ANAO			((FG06859.1:100.0,(56.m03107:100.0,(AN8877.1:100.0,AO07029300:100.0):69.5):100.0):100.0,
1154	59.m08678	AN5048.1	AO070338000188	FG01100.1	AFAO	yes	yes	((FG01100.1:100.0,((AO07033800:100.0,59.m08678:100.0):97.5,AN5048.1:100.0):100.0):100.0,
1155	57.m05437	AN7666.1	AO070268000051	FG07150.1	AFAN	yes	yes	((FG07150.1:100.0,(AO07026800:100.0,(AN7666.1:100.0,57.m05437:100.0):95.5):100.0):100.0,
1156	70.m15283	AN0679.1	AO070343000536	FG01092.1	AFAO	yes	yes	((FG01092.1:100.0,((AO07034300:100.0,70.m15283:100.0):93.5,AN0679.1:100.0):100.0):100.0,
1157	69.m15030	AN3905.1	AO070324000083	FG09229.1	AFAN	yes	yes	((FG09229.1:100.0,(AO07032400:100.0,(AN3905.1:100.0,69.m15030:100.0):96.0):100.0):100.0,
1158	65.m07367	AN3757.1	AO070309000049	FG07077.1	AFAO	yes	yes	((FG07077.1:100.0,((AO07030900:100.0,65.m07367:100.0):96.5,AN3757.1:100.0):100.0):100.0,
1159	65.m07407	AN5681.1	AO070309000096	FG07078.1	AFAO		yes	((FG07078.1:100.0,((AO07030900:100.0,65.m07407:100.0):80.0,AN5681.1:100.0):100.0):100.0,
1160	65.m07408	AN5682.1	AO070309000097	FG07062.1	ANAO	yes	yes	((FG07062.1:100.0,(65.m07408:100.0,(AO07030900:100.0,AN5682.1:100.0):99.0):100.0):100.0,
1161	59.m09056	AN2938.1	AO070337000168	FG07060.1	AFAO			((FG07060.1:100.0,((AO07033700:100.0,59.m09056:100.0):56.0,AN2938.1:100.0):100.0):100.0,
1162	59.m09064	AN2930.1	AO070337000178	FG07057.1	AFAN			((FG07057.1:100.0,(AO07033700:100.0,(59.m09064:100.0,AN2930.1:100.0):71.5):100.0):100.0,
1163	72.m19060	AN2572.1	AO070340000111	FG01095.1	AFAO		yes	((FG01095.1:100.0,((AO07034000:100.0,72.m19060:100.0):81.5,AN2572.1:100.0):100.0):100.0,
1164	57.m05876	AN7465.1	AO070287000061	FG00509.1	AFAO		yes	((FG00509.1:100.0,((AO07028700:100.0,57.m05876:100.0):87.5,AN7465.1:100.0):100.0):100.0,
1165	57.m05877	AN7464.1	AO070287000062	FG00508.1	ANAO			((FG00508.1:100.0,((AO07028700:100.0,AN7464.1:100.0):52.5,57.m05877:100.0):100.0):100.0,
1166	65.m07366	AN3758.1	AO070309000048	FG05598.1	AFAN			((FG05598.1:100.0,(AO07030900:100.0,(AN3758.1:100.0,65.m07366:100.0):55.5):100.0):100.0,
1167	58.m07716	AN1630.1	AO070299000035	FG01245.1	AFAO	yes	yes	((FG01245.1:100.0,((58.m07716:100.0,AO07029900:100.0):90.5,AN1630.1:100.0):100.0):100.0,
1168	65.m07464	AN8288.1	AO070190000002	FG01243.1	AFAO		yes	((FG01243.1:100.0,((65.m07464:100.0,AO07019000:100.0):80.5,AN8288.1:100.0):100.0):100.0,
1169	69.m15615	AN5744.1	AO070341000001	FG01241.1	AFAO	yes	yes	((FG01241.1:100.0,((AO07034100:100.0,69.m15615:100.0):95.5,AN5744.1:100.0):100.0):100.0,
1170	69.m14820	AN5777.1	AO070249000022	FG01240.1	AFAO		yes	((FG01240.1:100.0,((AO07024900:100.0,69.m14820:100.0):87.5,AN5777.1:100.0):100.0):100.0,
1171	58.m07876	AN4449.1	AO070273000004	FG01236.1	AFAO			((FG01236.1:100.0,((AO07027300:100.0,58.m07876:100.0):66.0,AN4449.1:100.0):100.0):100.0,
1172	69.m14841	AN5743.1	AO070193000002	FG01265.1	AFAO	yes	yes	((FG01265.1:100.0,((AO07019300:100.0,69.m14841:100.0):91.0,AN5743.1:100.0):100.0):100.0,
1173	72.m19947	AN6073.1	AO070340000117	FG01119.1	AFAO		yes	((FG01119.1:100.0,((72.m19947:100.0,AO07034000:100.0):82.5,AN6073.1:100.0):100.0):100.0,
1174	72.m18985	AN5856.1	AO070340000012	FG00371.1	ANAO			((FG00371.1:100.0,((AO07034000:100.0,AN5856.1:100.0):41.0,72.m18985:100.0):100.0):100.0,
1175	72.m19581	AN7560.1	AO070343000400	FG05608.1	AFAO			((FG05608.1:100.0,((AO07034300:100.0,72.m19581:100.0):56.5,AN7560.1:100.0):100.0):100.0,
1176	59.m09108	AN4864.1	AO070329000150	FG05607.1	ANAO			((FG05607.1:100.0,(59.m09108:100.0,(AN4864.1:100.0,AO07032900:100.0):71.5):100.0):100.0,
1177	70.m15118	AN1117.1	AO070331000109	FG00538.1	AFAN			((FG00538.1:100.0,(AO07033100:100.0,(AN1117.1:100.0,70.m15118:100.0):55.0):100.0):100.0,
1178	70.m14862	AN1367.1	AO070215000014	FG11603.1	AFAO			((FG11603.1:100.0,((AO07021500:100.0,70.m14862:100.0):69.0,AN1367.1:100.0):100.0):100.0,
1179	57.m05386	AN9287.1	AO070294000075	FG02360.1		yes	yes	(((FG02360.1:100.0,AN9287.1:100.0):100.0,(AO07029400:100.0,57.m05386:100.0):92.0):100.0,
1180	69.m15273	AN0573.1	AO070272000052	FG01644.1	AFAO	yes	yes	((FG01644.1:100.0,((AO07027200:100.0,69.m15273:100.0):99.0,AN0573.1:100.0):100.0):100.0,
1181	69.m15771	AN0574.1	AO070272000053	FG01469.1	AFAO		yes	(((AN0574.1:100.0,(69.m15771:100.0,AO07027200:100.0):79.0):92.5,FG01469.1:100.0):100.0,
1182	58.m07885	AN4440.1	AO070273000014	FG01670.1	AFAN			((FG01670.1:100.0,(AO07027300:100.0,(AN4440.1:100.0,58.m07885:100.0):53.8):100.0):100.0,
1183	58.m09014	AN4441.1	AO070273000013	FG01620.1	AFAO			((FG01620.1:100.0,((AO07027300:100.0,58.m09014:100.0):74.0,AN4441.1:100.0):100.0):100.0,
1184	70.m15540	AN0932.1	AO070320000123	FG05183.1	AFAN			((FG05183.1:100.0,(AO07032000:100.0,(AN0932.1:100.0,70.m15540:100.0):46.3):100.0):100.0,
1185	58.m07595	AN1988.1	AO070301000075	FG05181.1	ANAO			((FG05181.1:100.0,(58.m07595:100.0,(AN1988.1:100.0,AO07030100:100.0):65.5):100.0):100.0,
1186	58.m08979	AN4434.1	AO070273000023	FG01653.1	AFAO		yes	((FG01653.1:100.0,((AO07027300:100.0,58.m08979:100.0):79.0,AN4434.1:100.0):100.0):100.0,
1187	58.m08957	AN5616.1	AO070301000016	FG01560.1	AFAO			((FG01560.1:100.0,((AO07030100:100.0,58.m08957:100.0):69.0,AN5616.1:100.0):100.0):100.0,
1188	58.m07536	AN5613.1	AO070301000012	FG01561.1	AFAO			((FG01561.1:100.0,((AO07030100:100.0,58.m07536:100.0):72.0,AN5613.1:100.0):100.0):100.0,
1189	72.m19341	AN6293.1	AO070308000051	FG01562.1	AFAO			((FG01562.1:100.0,((AO07030800:100.0,72.m19341:100.0):57.0,AN6293.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1190	58.m09016	AN4442.1	AO070273000012	FG01568.1	AFAO		yes	((FG01568.1:100.0,((AO07027300:100.0,58.m09016:100.0):89.0,AN4442.1:100.0):100.0):100.0,
1191	72.m19939	AN5977.1	AO070281000046	FG01476.1	AFAN	yes	yes	((FG01476.1:100.0,(AO07028100:100.0,(AN5977.1:100.0,72.m19939:100.0):99.5):100.0):100.0,
1192	58.m07509	AN5588.1	AO070328000021	FG01475.1	ANAO			((FG01475.1:100.0,((AO07032800:100.0,AN5588.1:100.0):57.0,58.m07509:100.0):100.0):100.0,
1193	58.m08980	AN4435.1	AO070273000022	FG00627.1	AFAO	yes	yes	((FG00627.1:100.0,((AO07027300:100.0,58.m08980:100.0):90.0,AN4435.1:100.0):100.0):100.0,
1194	58.m08921	AN1968.1	AO070301000052	FG00629.1	AFAO			((FG00629.1:100.0,((58.m08921:100.0,AO07030100:100.0):54.0,AN1968.1:100.0):100.0):100.0,
1195	58.m08981	AN4412.1	AO070273000032	FG01656.1	ANAO			((FG01656.1:100.0,(58.m08981:100.0,(AN4412.1:100.0,AO07027300:100.0):64.5):100.0):100.0,
1196	69.m15270	AN0575.1	AO070272000054	FG05179.1	ANAO			((FG05179.1:100.0,(69.m15270:100.0,(AN0575.1:100.0,AO07027200:100.0):66.5):100.0):100.0,
1197	70.m14831	AN1390.1	AO070342000349	FG10854.1	AFAO			(((AN1390.1:100.0,(AO07034200:100.0,70.m14831:100.0):63.7):82.5,FG10854.1:100.0):100.0,
1198	55.m03259	AN1460.1	AO070306000076	FG05168.1	AFAO	yes	yes	((FG05168.1:100.0,((AO07030600:100.0,55.m03259:100.0):95.5,AN1460.1:100.0):100.0):100.0,
1199	58.m07978	AN4353.1	AO070240000022	FG10853.1	AFAO			((FG10853.1:100.0,((AO07024000:100.0,58.m07978:100.0):57.5,AN4353.1:100.0):100.0):100.0,
1200	59.m08566	AN3176.1	AO070256000014	FG10896.1	AFAO	yes	yes	((FG10896.1:100.0,(AN3176.1:100.0,(59.m08566:100.0,AO07025600:100.0):100.0):100.0):100.0,
1201	59.m08567	AN3177.1	AO070256000013	FG10897.1	AFAO			((FG10897.1:100.0,((AO07025600:100.0,59.m08567:100.0):57.0,AN3177.1:100.0):100.0):100.0,
1202	59.m08645	AN3098.1	AO070334000139	FG10903.1	AFAO	yes	yes	((FG10903.1:100.0,(AN3098.1:100.0,(59.m08645:100.0,AO07033400:100.0):100.0):100.0):100.0,
1203	59.m08551	AN3163.1	AO070256000032	FG10909.1	AFAO		yes	((FG10909.1:100.0,((AO07025600:100.0,59.m08551:100.0):89.5,AN3163.1:100.0):100.0):100.0,
1204	59.m08562	AN3172.1	AO070256000018	FG10905.1	AFAO			((FG10905.1:100.0,((AO07025600:100.0,59.m08562:100.0):44.8,AN3172.1:100.0):100.0):100.0,
1205	59.m08563	AN3173.1	AO070256000017	FG10906.1	AFAO	yes	yes	((FG10906.1:100.0,((AO07025600:100.0,59.m08563:100.0):96.5,AN3173.1:100.0):100.0):100.0,
1206	59.m08557	AN3168.1	AO070256000022	FG10907.1	AFAN			((FG10907.1:100.0,(AO07025600:100.0,(AN3168.1:100.0,59.m08557:100.0):63.5):100.0):100.0,
1207	59.m09511	AN3167.1	AO070256000023	FG10908.1	AFAO	yes	yes	((FG10908.1:100.0,((AO07025600:100.0,59.m09511:100.0):93.0,AN3167.1:100.0):100.0):100.0,
1208	54.m06880	AN5141.1	AO070291000035	FG10820.1	AFAO	yes	yes	((FG10820.1:100.0,((AO07029100:100.0,54.m06880:100.0):97.5,AN5141.1:100.0):100.0):100.0,
1209	70.m15466	AN0862.1	AO070320000011	FG10822.1	AFAN			((FG10822.1:100.0,((70.m15466:100.0,AN0862.1:100.0):43.0,AO07032000:100.0):100.0):100.0,
1210	54.m06944	AN4055.1	AO070342000041	FG07678.1	AFAO	yes	yes	((FG07678.1:100.0,((AO07034200:100.0,54.m06944:100.0):97.0,AN4055.1:100.0):100.0):100.0,
1211	71.m15175	AN2687.1	AO070313000101	FG00304.1	AFAO	yes	yes	((FG00304.1:100.0,((AO07031300:100.0,71.m15175:100.0):90.5,AN2687.1:100.0):100.0):100.0,
1212	69.m15293	AN0554.1	AO070272000027	FG00979.1	ANAO			((FG00979.1:100.0,(69.m15293:100.0,(AN0554.1:100.0,AO07027200:100.0):74.5):100.0):100.0,
1213	71.m15415	AN0131.1	AO070321000122	FG01466.1	AFAO		yes	((FG01466.1:100.0,((AO07032100:100.0,71.m15415:100.0):87.5,AN0131.1:100.0):100.0):100.0,
1214	59.m08989	AN3031.1	AO070331000089	FG05713.1		yes	yes	(((59.m08989:100.0,AN3031.1:100.0):100.0,(FG05713.1:100.0,AO07033100:100.0):97.5):100.0,
1215	71.m15409	AN0129.1	AO070311000084	FG04296.1	AFAO			((FG04296.1:100.0,((AO07031100:100.0,71.m15409:100.0):62.0,AN0129.1:100.0):100.0):100.0,
1216	69.m15297	AN0504.1	AO070226000008	FG01464.1	AFAO		yes	((FG01464.1:100.0,((AO07022600:100.0,69.m15297:100.0):81.0,AN0504.1:100.0):100.0):100.0,
1217	59.m08822	AN4919.1	AO070338000024	FG00822.1	AFAO		yes	((FG00822.1:100.0,((AO07033800:100.0,59.m08822:100.0):77.0,AN4919.1:100.0):100.0):100.0,
1218	59.m08821	AN4918.1	AO070338000025	FG00823.1	ANAO			((FG00823.1:100.0,(59.m08821:100.0,(AN4918.1:100.0,AO07033800:100.0):74.0):100.0):100.0,
1219	71.m15413	AN0127.1	AO070311000081	FG04297.1	AFAO		yes	((FG04297.1:100.0,((AO07031100:100.0,71.m15413:100.0):78.8,AN0127.1:100.0):100.0):100.0,
1220	58.m07519	AN5595.1	AO070328000009	FG05208.1	AFAO		yes	((FG05208.1:100.0,((AO07032800:100.0,58.m07519:100.0):84.0,AN5595.1:100.0):100.0):100.0,
1221	58.m07524	AN5600.1	AO070328000004	FG00298.1	AFAO			((FG00298.1:100.0,((58.m07524:100.0,AO07032800:100.0):59.5,AN5600.1:100.0):100.0):100.0,
1222	58.m07492	AN5568.1	AO070328000040	FG00817.1	ANAO			((FG00817.1:100.0,((AO07032800:100.0,AN5568.1:100.0):58.5,58.m07492:100.0):100.0):100.0,
1223	58.m07529	AN5606.1	AO070301000003	FG00818.1	AFAO		yes	((FG00818.1:100.0,((AO07030100:100.0,58.m07529:100.0):86.5,AN5606.1:100.0):100.0):100.0,
1224	70.m14875	AN1355.1	AO070237000005	FG05212.1	AFAO		yes	((FG05212.1:100.0,((AO07023700:100.0,70.m14875:100.0):87.5,AN1355.1:100.0):100.0):100.0,
1225	70.m15631	AN0990.1	AO070318000147	FG00819.1	AFAO		yes	((FG00819.1:100.0,((AO07031800:100.0,70.m15631:100.0):87.5,AN0990.1:100.0):100.0):100.0,
1226	58.m07576	AN1971.1	AO070301000055	FG05150.1	AFAO			((FG05150.1:100.0,((AO07030100:100.0,58.m07576:100.0):65.0,AN1971.1:100.0):100.0):100.0,
1227	72.m19441	AN6323.1	AO070304000044	FG05152.1	AFAO	yes	yes	((FG05152.1:100.0,(AN6323.1:100.0,(72.m19441:100.0,AO07030400:100.0):100.0):100.0):100.0,
1228	70.m15526	AN0919.1	AO070320000099	FG05156.1	AFAO			((FG05156.1:100.0,((AO07032000:100.0,70.m15526:100.0):49.8,AN0919.1:100.0):100.0):100.0,
1229	70.m15524	AN0917.1	AO070320000097	FG05165.1	AFAO		yes	((FG05165.1:100.0,((70.m15524:100.0,AO07032000:100.0):86.5,AN0917.1:100.0):100.0):100.0,
1230	70.m15525	AN0918.1	AO070320000098	FG05164.1	ANAO			((FG05164.1:100.0,(70.m15525:100.0,(AN0918.1:100.0,AO07032000:100.0):50.8):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1231	72.m19673	AN2167.1	AO070343000229	FG05163.1	AFAO			((FG05163.1:100.0,((AO07034300:100.0,72.m19673:100.0):68.5,AN2167.1:100.0):100.0):100.0,
1232	70.m15523	AN0914.1	AO070320000095	FG05162.1	AFAO	yes	yes	((FG05162.1:100.0,((AO07032000:100.0,70.m15523:100.0):99.5,AN0914.1:100.0):100.0):100.0,
1233	58.m07515	AN5591.1	AO070328000012	FG05169.1	AFAO	yes	yes	((FG05169.1:100.0,((AO07032800:100.0,58.m07515:100.0):99.0,AN5591.1:100.0):100.0):100.0,
1234	70.m15512	AN0903.1	AO070320000077	FG05167.1	AFAO		yes	(((AN0903.1:100.0,(70.m15512:100.0,AO07032000:100.0):77.0):93.5,FG05167.1:100.0):100.0,
1235	71.m16021	AN6874.1	AO070314000047	FG01640.1	AFAO	yes	yes	((FG01640.1:100.0,((AO07031400:100.0,71.m16021:100.0):99.0,AN6874.1:100.0):100.0):100.0,
1236	71.m15176	AN2688.1	AO070313000100	FG06028.1	ANAO			((FG06028.1:100.0,(71.m15176:100.0,(AN2688.1:100.0,AO07031300:100.0):73.0):100.0):100.0,
1237	70.m14828	AN1394.1	AO070233000008	FG06035.1	AFAO		yes	((FG06035.1:100.0,((AO07023300:100.0,70.m14828:100.0):82.0,AN1394.1:100.0):100.0):100.0,
1238	70.m14829	AN1387.1	AO070233000007	FG06033.1	AFAO		yes	((FG06033.1:100.0,((AO07023300:100.0,70.m14829:100.0):87.5,AN1387.1:100.0):100.0):100.0,
1239	69.m15208	AN2450.1	AO070264000026	FG06030.1	AFAO			((FG06030.1:100.0,((69.m15208:100.0,AO07026400:100.0):59.5,AN2450.1:100.0):100.0):100.0,
1240	58.m07961	AN4360.1	AO070261000003	FG05172.1	ANAO			((FG05172.1:100.0,(58.m07961:100.0,(AN4360.1:100.0,AO07026100:100.0):54.0):100.0):100.0,
1241	58.m09002	AN4425.1	AO070273000062	FG05173.1	AFAO	yes	yes	((FG05173.1:100.0,(AN4425.1:100.0,(58.m09002:100.0,AO07027300:100.0):100.0):100.0):100.0,
1242	58.m07945	AN4380.1	AO070261000025	FG05174.1	AFAO		yes	((FG05174.1:100.0,((AO07026100:100.0,58.m07945:100.0):86.5,AN4380.1:100.0):100.0):100.0,
1243	70.m15468	AN0861.1	AO070320000009	FG01574.1	AFAO			((FG01574.1:100.0,((AO07032000:100.0,70.m15468:100.0):58.5,AN0861.1:100.0):100.0):100.0,
1244	70.m15616	AN0978.1	AO070341000131	FG01575.1	AFAN	yes	yes	((FG01575.1:100.0,((AN0978.1:100.0,70.m15616:100.0):100.0,AO07034100:100.0):100.0):100.0,
1245	58.m08906	AN5612.1	AO070301000011	FG10842.1	AFAO	yes	yes	((FG10842.1:100.0,((AO07030100:100.0,58.m08906:100.0):99.0,AN5612.1:100.0):100.0):100.0,
1246	53.m03677	AN4280.1	AO070310000016	FG00308.1	AFAO		yes	((FG00308.1:100.0,((AO07031000:100.0,53.m03677:100.0):88.5,AN4280.1:100.0):100.0):100.0,
1247	53.m03687	AN8273.1	AO070310000028	FG00644.1	AFAO	yes	yes	((FG00644.1:100.0,((AO07031000:100.0,53.m03687:100.0):92.5,AN8273.1:100.0):100.0):100.0,
1248	53.m04172	AN8272.1	AO070310000029	FG00645.1	AFAO			((FG00645.1:100.0,((53.m04172:100.0,AO07031000:100.0):55.0,AN8272.1:100.0):100.0):100.0,
1249	59.m08569	AN3185.1	AO070256000011	FG04385.1	AFAO	yes	yes	((FG04385.1:100.0,(AN3185.1:100.0,(59.m08569:100.0,AO07025600:100.0):100.0):100.0):100.0,
1250	57.m05387	AN5557.1	AO070294000076	FG03375.1	AFAO			((FG03375.1:100.0,((AO07029400:100.0,57.m05387:100.0):67.8,AN5557.1:100.0):100.0):100.0,
1251	59.m08630	AN3107.1	AO070334000152	FG04359.1	ANAO			((FG04359.1:100.0,(59.m08630:100.0,(AN3107.1:100.0,AO07033400:100.0):70.5):100.0):100.0,
1252	59.m08628	AN3110.1	AO070303000041	FG10725.1	AFAO			((FG10725.1:100.0,((AO07030300:100.0,59.m08628:100.0):70.5,AN3110.1:100.0):100.0):100.0,
1253	54.m06792	AN4225.1	AO070234000025	FG10724.1	ANAO			((FG10724.1:100.0,(54.m06792:100.0,(AN4225.1:100.0,AO07023400:100.0):55.5):100.0):100.0,
1254	70.m15312	AN0705.1	AO070343000504	FG10722.1	AFAO	yes	yes	((FG10722.1:100.0,(AN0705.1:100.0,(70.m15312:100.0,AO07034300:100.0):100.0):100.0):100.0,
1255	59.m08648	AN3095.1	AO070334000137	FG10723.1	ANAO			((FG10723.1:100.0,(59.m08648:100.0,(AN3095.1:100.0,AO07033400:100.0):70.8):100.0):100.0,
1256	54.m06794	AN4223.1	AO070234000027	FG00647.1	AFAO			((FG00647.1:100.0,((AO07023400:100.0,54.m06794:100.0):49.5,AN4223.1:100.0):100.0):100.0,
1257	71.m15629	AN9481.1	AO070276000025	FG05981.1	AFAO		yes	((FG05981.1:100.0,((AO07027600:100.0,71.m15629:100.0):83.0,AN9481.1:100.0):100.0):100.0,
1258	71.m15630	AN9482.1	AO070276000024	FG05982.1	AFAO		yes	((FG05982.1:100.0,((AO07027600:100.0,71.m15630:100.0):87.0,AN9482.1:100.0):100.0):100.0,
1259	58.m08942	AN2011.1	AO070202000001	FG09020.1	AFAO			((FG09020.1:100.0,((AO07020200:100.0,58.m08942:100.0):65.0,AN2011.1:100.0):100.0):100.0,
1260	58.m07618	AN2009.1	AO070179000005	FG09019.1	ANAO			((FG09019.1:100.0,((AO07017900:100.0,AN2009.1:100.0):64.3,58.m07618:100.0):100.0):100.0,
1261	71.m15279	AN6853.1	AO070314000087	FG05890.1	AFAO	yes	yes	((FG05890.1:100.0,((AO07031400:100.0,71.m15279:100.0):90.5,AN6853.1:100.0):100.0):100.0,
1262	71.m15277	AN6855.1	AO070314000086	FG07021.1	ANAO			((FG07021.1:100.0,((AO07031400:100.0,AN6855.1:100.0):50.5,71.m15277:100.0):100.0):100.0,
1263	66.m04577	AN9121.1	AO070332000155	FG10132.1	AFAO	yes	yes	((FG10132.1:100.0,((AO07033200:100.0,66.m04577:100.0):95.5,AN9121.1:100.0):100.0):100.0,
1264	70.m14901	AN1331.1	AO070303000094	FG10170.1	AFAO		yes	((FG10170.1:100.0,((70.m14901:100.0,AO07030300:100.0):83.5,AN1331.1:100.0):100.0):100.0,
1265	70.m14902	AN1330.1	AO070303000093	FG10169.1	AFAO			((FG10169.1:100.0,((AO07030300:100.0,70.m14902:100.0):55.0,AN1330.1:100.0):100.0):100.0,
1266	72.m18955	AN5828.1	AO070260000018	FG10193.1	AFAO			(((AN5828.1:100.0,(AO07026000:100.0,72.m18955:100.0):50.3):66.5,FG10193.1:100.0):100.0,
1267	57.m05922	AN7423.1	AO070197000002	FG10122.1	AFAO		yes	((FG10122.1:100.0,((57.m05922:100.0,AO07019700:100.0):81.0,AN7423.1:100.0):100.0):100.0,
1268	59.m08455	AN2525.1	AO070286000098	FG10119.1	AFAN			((FG10119.1:100.0,(AO07028600:100.0,(AN2525.1:100.0,59.m08455:100.0):73.0):100.0):100.0,
1269	59.m08453	AN2526.1	AO070220000001	FG10118.1	AFAN			((FG10118.1:100.0,(AO07022000:100.0,(AN2526.1:100.0,59.m08453:100.0):57.0):100.0):100.0,
1270	59.m08459	AN2523.1	AO070286000091	FG10116.1	AFAO		yes	((FG10116.1:100.0,((AO07028600:100.0,59.m08459:100.0):88.5,AN2523.1:100.0):100.0):100.0,
1271	59.m08460	AN2522.1	AO070286000088	FG10115.1	AFAO	yes	yes	((FG10115.1:100.0,((AO07028600:100.0,59.m08460:100.0):90.0,AN2522.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1272	72.m18960	AN5832.1	AO070260000013	FG10114.1	AFAO			((FG10114.1:100.0,((AO07026000:100.0,72.m18960:100.0):55.5,AN5832.1:100.0):100.0):100.0,
1273	72.m18958	AN5830.1	AO070260000016	FG10113.1	AFAO		yes	((FG10113.1:100.0,((AO07026000:100.0,72.m18958:100.0):80.5,AN5830.1:100.0):100.0):100.0,
1274	71.m15605	AN8798.1	AO070276000062	FG05978.1	AFAO		yes	((FG05978.1:100.0,((AO07027600:100.0,71.m15605:100.0):85.5,AN8798.1:100.0):100.0):100.0,
1275	53.m03703	AN8258.1	AO070310000045	FG05977.1	AFAN			((FG05977.1:100.0,(AO07031000:100.0,(AN8258.1:100.0,53.m03703:100.0):52.8):100.0):100.0,
1276	71.m15632	AN8821.1	AO070276000021	FG05966.1	AFAO	yes	yes	((FG05966.1:100.0,(AN8821.1:100.0,(71.m15632:100.0,AO07027600:100.0):100.0):100.0):100.0,
1277	58.m07864	AN4460.1	AO070305000133	FG06788.1	AFAO		yes	((FG06788.1:100.0,((AO07030500:100.0,58.m07864:100.0):81.5,AN4460.1:100.0):100.0):100.0,
1278	58.m07839	AN3867.1	AO070305000103	FG05911.1	AFAN			((FG05911.1:100.0,(AO07030500:100.0,(AN3867.1:100.0,58.m07839:100.0):70.0):100.0):100.0,
1279	58.m07841	AN3869.1	AO070305000105	FG05912.1	AFAO			((FG05912.1:100.0,((AO07030500:100.0,58.m07841:100.0):64.5,AN3869.1:100.0):100.0):100.0,
1280	53.m04164	AN8046.1	AO070336000153	FG05906.1	AFAN	yes	yes	((FG05906.1:100.0,(AO07033600:100.0,(AN8046.1:100.0,53.m04164:100.0):93.5):100.0):100.0,
1281	69.m15656	AN3904.1	AO070324000068	FG03570.1	AFAO	yes	yes	((FG03570.1:100.0,((69.m15656:100.0,AO07032400:100.0):92.0,AN3904.1:100.0):100.0):100.0,
1282	65.m07448	AN4271.1	AO070277000015	FG05905.1	AFAO		yes	((FG05905.1:100.0,((65.m07448:100.0,AO07027700:100.0):77.0,AN4271.1:100.0):100.0):100.0,
1283	69.m15638	AN5773.1	AO070249000017	FG07413.1	AFAO	yes	yes	((FG07413.1:100.0,((AO07024900:100.0,69.m15638:100.0):92.5,AN5773.1:100.0):100.0):100.0,
1284	65.m07460	AN8284.1	AO070277000004	FG07414.1	AFAO	yes	yes	((FG07414.1:100.0,((AO07027700:100.0,65.m07460:100.0):96.5,AN8284.1:100.0):100.0):100.0,
1285	65.m07461	AN8285.1	AO070277000003	FG07423.1	AFAN		yes	((((AN8285.1:100.0,65.m07461:100.0):88.0,AO07027700:100.0):97.0,FG07423.1:100.0):100.0,
1286	69.m14831	AN5768.1	AO070249000004	FG07425.1	AFAN			((FG07425.1:100.0,(AO07024900:100.0,(AN5768.1:100.0,69.m14831:100.0):44.5):100.0):100.0,
1287	62.m03214	AN6618.1	AO070326000068	FG05191.1	AFAO		yes	((FG05191.1:100.0,((AO07032600:100.0,62.m03214:100.0):87.5,AN6618.1:100.0):100.0):100.0,
1288	71.m15354	AN0076.1	AO070311000140	FG07011.1	AFAO	yes	yes	((FG07011.1:100.0,(AN0076.1:100.0,(71.m15354:100.0,AO07031100:100.0):100.0):100.0):100.0,
1289	54.m06959	AN4214.1	AO070231000010	FG02002.1	AFAO		yes	((FG02002.1:100.0,((AO07023100:100.0,54.m06959:100.0):83.5,AN4214.1:100.0):100.0):100.0,
1290	70.m15432	AN0831.1	AO070255000014	FG01852.1	ANAO		yes	((FG01852.1:100.0,((AO07025500:100.0,AN0831.1:100.0):82.5,70.m15432:100.0):100.0):100.0,
1291	72.m19768	AN7298.1	AO070297000040	FG01849.1	ANAO	yes	yes	((FG01849.1:100.0,(72.m19768:100.0,(AO07029700:100.0,AN7298.1:100.0):96.5):100.0):100.0,
1292	70.m15535	AN0928.1	AO070320000113	FG01853.1	AFAO		yes	((FG01853.1:100.0,((AO07032000:100.0,70.m15535:100.0):87.5,AN0928.1:100.0):100.0):100.0,
1293	70.m15808	AN0926.1	AO070320000110	FG01854.1	AFAO	yes	yes	((FG01854.1:100.0,((AO07032000:100.0,70.m15808:100.0):96.0,AN0926.1:100.0):100.0):100.0,
1294	70.m15464	AN0864.1	AO070320000014	FG01855.1	AFAO		yes	((FG01855.1:100.0,((AO07032000:100.0,70.m15464:100.0):77.5,AN0864.1:100.0):100.0):100.0,
1295	70.m15463	AN0865.1	AO070320000016	FG01856.1	AFAO			((FG01856.1:100.0,((70.m15463:100.0,AO07032000:100.0):74.5,AN0865.1:100.0):100.0):100.0,
1296	70.m15519	AN0910.1	AO070320000091	FG01865.1	AFAO		yes	((FG01865.1:100.0,((AO07032000:100.0,70.m15519:100.0):83.5,AN0910.1:100.0):100.0):100.0,
1297	71.m15577	AN2343.1	AO070319000157	FG01866.1	AFAN			((FG01866.1:100.0,(AO07031900:100.0,(AN2343.1:100.0,71.m15577:100.0):51.8):100.0):100.0,
1298	58.m07630	AN2042.1	AO070292000002	FG01867.1	ANAO			((FG01867.1:100.0,(58.m07630:100.0,(AN2042.1:100.0,AO07029200:100.0):65.5):100.0):100.0,
1299	55.m03010	AN1500.1	AO070334000217	FG01877.1	AFAO			((FG01877.1:100.0,((AO07033400:100.0,55.m03010:100.0):64.5,AN1500.1:100.0):100.0):100.0,
1300	70.m15382	AN0776.1	AO070316000062	FG01871.1	AFAN		yes	((FG01871.1:100.0,((70.m15382:100.0,AN0776.1:100.0):86.0,AO07031600:100.0):100.0):100.0,
1301	70.m15536	AN0927.1	AO070320000116	FG01863.1	ANAO		yes	((FG01863.1:100.0,(70.m15536:100.0,(AN0927.1:100.0,AO07032000:100.0):82.0):100.0):100.0,
1302	70.m15825	AN4541.1	AO070321000164	FG01875.1	AFAO			((FG01875.1:100.0,((AO07032100:100.0,70.m15825:100.0):73.0,AN4541.1:100.0):100.0):100.0,
1303	71.m16059	AN0089.1	AO070311000126	FG05141.1	AFAN			((((AN0089.1:100.0,71.m16059:100.0):52.0,AO07031100:100.0):99.0,FG05141.1:100.0):100.0,
1304	70.m15156	AN1082.1	AO070285000082	FG05143.1	AFAO			((FG05143.1:100.0,((AO07028500:100.0,70.m15156:100.0):67.5,AN1082.1:100.0):100.0):100.0,
1305	71.m16035	AN6915.1	AO070219000020	FG05144.1	ANAO			((FG05144.1:100.0,((AO07021900:100.0,AN6915.1:100.0):49.7,71.m16035:100.0):93.9):100.0,
1306	71.m15274	AN6863.1	AO070314000083	FG07143.1	AFAN			((FG07143.1:100.0,(AO07031400:100.0,(AN6863.1:100.0,71.m15274:100.0):55.5):100.0):100.0,
1307	70.m15154	AN1080.1	AO070285000079	FG07146.1	ANAO			((FG07146.1:100.0,(70.m15154:100.0,(AN1080.1:100.0,AO07028500:100.0):63.3):100.0):100.0,
1308	62.m03184	AN6609.1	AO070326000058	FG07155.1	AFAO			((FG07155.1:100.0,((62.m03184:100.0,AO07032600:100.0):73.0,AN6609.1:100.0):100.0):100.0,
1309	71.m15733	AN7709.1	AO070325000116	FG05131.1	AFAO	yes	yes	((FG05131.1:100.0,((AO07032500:100.0,71.m15733:100.0):92.5,AN7709.1:100.0):100.0):100.0,
1310	71.m15734	AN7710.1	AO070325000117	FG05132.1	AFAO		yes	((FG05132.1:100.0,((AO07032500:100.0,71.m15734:100.0):88.0,AN7710.1:100.0):100.0):100.0,
1311	71.m15825	AN2238.1	AO070326000135	FG05133.1	AFAO			((FG05133.1:100.0,((AO07032600:100.0,71.m15825:100.0):64.0,AN2238.1:100.0):100.0):100.0,
1312	69.m15248	AN0600.1	AO070280000025	FG07160.1	AFAO		yes	((FG07160.1:100.0,((69.m15248:100.0,AO07028000:100.0):87.0,AN0600.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1313	70.m15158	AN1084.1	AO070285000084	FG07182.1	AFAO		yes	((FG07182.1:100.0,((AO07028500:100.0,70.m15158:100.0):84.5,AN1084.1:100.0):100.0):100.0,
1314	71.m15353	AN0075.1	AO070311000141	FG07180.1	AFAO			((FG07180.1:100.0,((AO07031100:100.0,71.m15353:100.0):61.8,AN0075.1:100.0):100.0):100.0,
1315	71.m15292	AN6824.1	AO070314000104	FG07150.1	AFAO		yes	((FG07150.1:100.0,((AO07031400:100.0,71.m15292:100.0):88.5,AN6824.1:100.0):100.0):100.0,
1316	58.m07525	AN5601.1	AO070328000003	FG00346.1	ANAO			((FG00346.1:100.0,(58.m07525:100.0,(AN5601.1:100.0,AO07032800:100.0):58.5):100.0):100.0,
1317	72.m19484	AN9496.1	AO070241000013	FG07151.1	AFAO			((FG07151.1:100.0,((AO07024100:100.0,72.m19484:100.0):68.5,AN9496.1:100.0):100.0):100.0,
1318	53.m03768	AN8206.1	AO070310000111	FG00712.1	AFAO	yes	yes	((FG00712.1:100.0,((AO07031000:100.0,53.m03768:100.0):99.0,AN8206.1:100.0):100.0):100.0,
1319	53.m03806	AN8172.1	AO070209000006	FG07188.1	AFAO			((FG07188.1:100.0,((AO07020900:100.0,53.m03806:100.0):72.5,AN8172.1:100.0):100.0):100.0,
1320	53.m03803	AN8176.1	AO070209000002	FG07186.1	AFAO	yes	yes	((FG07186.1:100.0,((AO07020900:100.0,53.m03803:100.0):94.5,AN8176.1:100.0):100.0):100.0,
1321	58.m07837	AN3865.1	AO070305000101	FG05909.1	AFAO		yes	((FG05909.1:100.0,((AO07030500:100.0,58.m07837:100.0):80.5,AN3865.1:100.0):100.0):100.0,
1322	54.m06777	AN4217.1	AO070342000115	FG07162.1	ANAO		yes	((FG07162.1:100.0,(54.m06777:100.0,(AN4217.1:100.0,AO07034200:100.0):75.5):100.0):100.0,
1323	58.m07855	AN4469.1	AO070305000124	FG06821.1	ANAO			((FG06821.1:100.0,(58.m07855:100.0,(AN4469.1:100.0,AO07030500:100.0):58.5):100.0):100.0,
1324	65.m07405	AN5679.1	AO070309000094	FG06819.1	AFAN			((((AN5679.1:100.0,65.m07405:100.0):66.5,AO07030900:100.0):74.7,FG06819.1:100.0):100.0,
1325	53.m03812	AN8169.1	AO070266000003	FG07410.1	AFAN			((FG07410.1:100.0,(AO07026600:100.0,(AN8169.1:100.0,53.m03812:100.0):61.0):100.0):100.0,
1326	53.m03814	AN8170.1	AO070266000007	FG07377.1	AFAN	yes	yes	((FG07377.1:100.0,(AO07026600:100.0,(AN8170.1:100.0,53.m03814:100.0):91.0):100.0):100.0,
1327	71.m15301	AN6844.1	AO070314000095	FG07019.1	AFAO	yes	yes	((FG07019.1:100.0,((AO07031400:100.0,71.m15301:100.0):98.5,AN6844.1:100.0):100.0):100.0,
1328	71.m16043	AN0034.1	AO070314000113	FG07017.1	AFAO	yes	yes	((FG07017.1:100.0,((AO07031400:100.0,71.m16043:100.0):95.0,AN0034.1:100.0):100.0):100.0,
1329	58.m08991	AN3847.1	AO070305000084	FG05145.1	AFAO	yes	yes	((FG05145.1:100.0,((AO07030500:100.0,58.m08991:100.0):98.5,AN3847.1:100.0):100.0):100.0,
1330	53.m03848	AN9467.1	AO070322000047	FG05894.1	AFAO		yes	((FG05894.1:100.0,((AO07032200:100.0,53.m03848:100.0):81.0,AN9467.1:100.0):100.0):100.0,
1331	53.m03775	AN8200.1	AO070310000119	FG05892.1	AFAN			((FG05892.1:100.0,(AO07031000:100.0,(AN8200.1:100.0,53.m03775:100.0):59.8):100.0):100.0,
1332	53.m04098	AN8053.1	AO070322000147	FG05891.1	AFAO		yes	((FG05891.1:100.0,((AO07032200:100.0,53.m04098:100.0):81.5,AN8053.1:100.0):100.0):100.0,
1333	53.m03773	AN7517.1	AO070310000116	FG07378.1	AFAO		yes	((FG07378.1:100.0,((53.m03773:100.0,AO07031000:100.0):82.0,AN7517.1:100.0):100.0):100.0,
1334	53.m03796	AN8183.1	AO070310000142	FG07379.1	AFAO		yes	((FG07379.1:100.0,((AO07031000:100.0,53.m03796:100.0):85.5,AN8183.1:100.0):100.0):100.0,
1335	53.m03797	AN8182.1	AO070310000143	FG07380.1	AFAO	yes	yes	((FG07380.1:100.0,((AO07031000:100.0,53.m03797:100.0):98.5,AN8182.1:100.0):100.0):100.0,
1336	53.m03781	AN9461.1	AO070310000129	FG07381.1	AFAO	yes	yes	((FG07381.1:100.0,((AO07031000:100.0,53.m03781:100.0):96.0,AN9461.1:100.0):100.0):100.0,
1337	53.m03884	AN8059.1	AO070322000124	FG06120.1	AFAO		yes	((FG06120.1:100.0,((AO07032200:100.0,53.m03884:100.0):82.5,AN8059.1:100.0):100.0):100.0,
1338	53.m03800	AN8180.1	AO070310000147	FG06116.1	AFAO	yes	yes	((FG06116.1:100.0,((AO07031000:100.0,53.m03800:100.0):94.5,AN8180.1:100.0):100.0):100.0,
1339	53.m03779	AN8194.1	AO070310000126	FG06115.1	AFAO	yes	yes	((FG06115.1:100.0,((AO07031000:100.0,53.m03779:100.0):97.0,AN8194.1:100.0):100.0):100.0,
1340	72.m19587	AN7568.1	AO070343000414	FG05953.1	AFAN	yes	yes	((FG05953.1:100.0,(AO07034300:100.0,(72.m19587:100.0,AN7568.1:100.0):91.5):99.5):100.0,
1341	71.m15627	AN8819.1	AO070276000028	FG10025.1	AFAO			((FG10025.1:100.0,((71.m15627:100.0,AO07027600:100.0):59.5,AN8819.1:100.0):96.5):100.0,
1342	71.m15631	AN8820.1	AO070276000022	FG06103.1	AFAO	yes	yes	((FG06103.1:100.0,((AO07027600:100.0,71.m15631:100.0):97.5,AN8820.1:100.0):100.0):100.0,
1343	62.m03124	AN6549.1	AO070270000036	FG06100.1	AFAO	yes	yes	((FG06100.1:100.0,((AO07027000:100.0,62.m03124:100.0):97.0,AN6549.1:100.0):100.0):100.0,
1344	62.m03122	AN6551.1	AO070270000034	FG06097.1	AFAO	yes	yes	((FG06097.1:100.0,(AN6551.1:100.0,(62.m03122:100.0,AO07027000:100.0):100.0):100.0):100.0,
1345	62.m03114	AN6525.1	AO070270000024	FG06127.1	AFAO	yes	yes	(((AN6525.1:100.0,(62.m03114:100.0,AO07027000:100.0):97.0):99.0,FG06127.1:100.0):100.0,
1346	62.m03435	AN6526.1	AO070270000025	FG07128.1	AFAO	yes	yes	((FG07128.1:100.0,(AN6526.1:100.0,(62.m03435:100.0,AO07027000:100.0):100.0):100.0):100.0,
1347	62.m03213	AN6614.1	AO070326000063	FG05149.1	ANAO			((FG05149.1:100.0,(62.m03213:100.0,(AN6614.1:100.0,AO07032600:100.0):55.5):100.0):100.0,
1348	62.m03212	AN6615.1	AO070326000064	FG05213.1	AFAO	yes	yes	((FG05213.1:100.0,((AO07032600:100.0,62.m03212:100.0):95.0,AN6615.1:100.0):100.0):100.0,
1349	71.m15972	AN8841.1	AO070271000036	FG07396.1	AFAO			((FG07396.1:100.0,((AO07027100:100.0,71.m15972:100.0):58.5,AN8841.1:100.0):100.0):100.0,
1350	62.m03169	AN6572.1	AO070326000015	FG07397.1	AFAO			((FG07397.1:100.0,((62.m03169:100.0,AO07032600:100.0):69.0,AN6572.1:100.0):100.0):100.0,
1351	62.m03148	AN6561.1	AO070326000002	FG07399.1	AFAO		yes	((FG07399.1:100.0,((AO07032600:100.0,62.m03148:100.0):84.5,AN6561.1:100.0):100.0):100.0,
1352	62.m03150	AN6563.1	AO070326000004	FG07401.1	AFAO			((FG07401.1:100.0,((62.m03150:100.0,AO07032600:100.0):59.0,AN6563.1:100.0):100.0):100.0,
1353	62.m03151	AN6564.1	AO070326000005	FG07402.1	AFAO	yes	yes	((FG07402.1:100.0,(AN6564.1:100.0,(62.m03151:100.0,AO07032600:100.0):100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1354	62.m03153	AN6566.1	AO070326000009	FG07404.1	ANAO			((((AN6566.1:100.0,AO07032600:100.0):36.5,62.m03153:100.0):92.0,FG07404.1:100.0):100.0,
1355	62.m03154	AN6567.1	AO070326000010	FG07405.1	AFAO	yes	yes	((FG07405.1:100.0,((AO07032600:100.0,62.m03154:100.0):99.5,AN6567.1:100.0):100.0):100.0,
1356	62.m03156	AN6569.1	AO070326000012	FG07406.1	AFAO			((FG07406.1:100.0,((AO07032600:100.0,62.m03156:100.0):51.8,AN6569.1:100.0):100.0):100.0,
1357	62.m03157	AN6570.1	AO070326000013	FG07407.1	AFAO		yes	((FG07407.1:100.0,((AO07032600:100.0,62.m03157:100.0):88.0,AN6570.1:100.0):100.0):100.0,
1358	72.m19724	AN7355.1	AO070278000045	FG02630.1	AFAO			((FG02630.1:100.0,((AO07027800:100.0,72.m19724:100.0):63.5,AN7355.1:100.0):100.0):100.0,
1359	69.m15380	AN3735.1	AO070342000272	FG10353.1	AFAO	yes	yes	((FG10353.1:100.0,((AO07034200:100.0,69.m15380:100.0):91.5,AN3735.1:100.0):100.0):100.0,
1360	57.m05507	AN4583.1	AO070316000171	FG10352.1	AFAO		yes	((FG10352.1:100.0,((AO07031600:100.0,57.m05507:100.0):80.5,AN4583.1:100.0):100.0):100.0,
1361	57.m05945	AN4584.1	AO070316000173	FG10351.1	AFAO	yes	yes	((FG10351.1:100.0,((AO07031600:100.0,57.m05945:100.0):92.0,AN4584.1:100.0):100.0):100.0,
1362	59.m09440	AN2999.1	AO070337000118	FG10347.1	AFAO	yes	yes	((FG10347.1:100.0,((AO07033700:100.0,59.m09440:100.0):92.0,AN2999.1:100.0):100.0):100.0,
1363	70.m14840	AN4178.1	AO070243000013	FG09989.1	AFAO	yes	yes	((FG09989.1:100.0,(AN4178.1:100.0,(70.m14840:100.0,AO07024300:100.0):100.0):100.0):100.0,
1364	70.m14838	AN1383.1	AO070243000016	FG09990.1	AFAO		yes	((FG09990.1:100.0,((AO07024300:100.0,70.m14838:100.0):76.5,AN1383.1:100.0):100.0):100.0,
1365	58.m07334	AN5642.1	AO070342000232	FG10270.1	AFAO		yes	((FG10270.1:100.0,((AO07034200:100.0,58.m07334:100.0):80.0,AN5642.1:100.0):100.0):100.0,
1366	58.m07335	AN5643.1	AO070342000231	FG10269.1	AFAO		yes	((FG10269.1:100.0,((AO07034200:100.0,58.m07335:100.0):88.5,AN5643.1:100.0):100.0):100.0,
1367	59.m09019	AN2997.1	AO070337000120	FG10268.1	ANAO	yes	yes	((FG10268.1:100.0,(59.m09019:100.0,(AN2997.1:100.0,AO07033700:100.0):97.5):100.0):100.0,
1368	59.m09018	AN2998.1	AO070337000119	FG10267.1	AFAO			((FG10267.1:100.0,((AO07033700:100.0,59.m09018:100.0):47.0,AN2998.1:100.0):100.0):100.0,
1369	70.m14873	AN1357.1	AO070237000003	FG10005.1	AFAO	yes	yes	((FG10005.1:100.0,(AN1357.1:100.0,(70.m14873:100.0,AO07023700:100.0):100.0):100.0):100.0,
1370	70.m14898	AN1333.1	AO070303000098	FG09951.1	ANAO			((FG09951.1:100.0,((AO07030300:100.0,AN1333.1:100.0):50.3,70.m14898:100.0):100.0):100.0,
1371	70.m14897	AN1334.1	AO070303000099	FG09952.1	AFAN			((FG09952.1:100.0,(AO07030300:100.0,(AN1334.1:100.0,70.m14897:100.0):52.5):100.0):100.0,
1372	70.m14896	AN1337.1	AO070303000102	FG09954.1	AFAO	yes	yes	((FG09954.1:100.0,((AO07030300:100.0,70.m14896:100.0):98.0,AN1337.1:100.0):100.0):100.0,
1373	69.m14953	AN4171.1	AO070341000090	FG08449.1	AFAO	yes	yes	((FG08449.1:100.0,((AO07034100:100.0,69.m14953:100.0):90.0,AN4171.1:100.0):100.0):100.0,
1374	69.m15618	AN4170.1	AO070341000092	FG08448.1	AFAN			((FG08448.1:100.0,(AO07034100:100.0,(AN4170.1:100.0,69.m15618:100.0):58.0):100.0):100.0,
1375	69.m14950	AN4168.1	AO070341000095	FG09497.1	ANAO			((FG09497.1:100.0,((AO07034100:100.0,AN4168.1:100.0):58.5,69.m14950:100.0):100.0):100.0,
1376	57.m05768	AN2068.1	AO070341000217	FG09491.1	AFAO			((FG09491.1:100.0,((AO07034100:100.0,57.m05768:100.0):70.0,AN2068.1:100.0):100.0):100.0,
1377	59.m08873	AN4969.1	AO070288000035	FG09262.1	ANAO			((FG09262.1:100.0,((AO07028800:100.0,AN4969.1:100.0):62.5,59.m08873:100.0):100.0):100.0,
1378	59.m08737	AN2890.1	AO070338000122	FG09264.1	AFAO	yes	yes	((FG09264.1:100.0,((AO07033800:100.0,59.m08737:100.0):98.0,AN2890.1:100.0):100.0):100.0,
1379	69.m15155	AN7513.1	AO070258000018	FG08800.1	ANAO			((FG08800.1:100.0,(69.m15155:100.0,(AN7513.1:100.0,AO07025800:100.0):73.5):100.0):100.0,
1380	57.m05781	AN2082.1	AO070341000235	FG08744.1	AFAO		yes	((FG08744.1:100.0,((AO07034100:100.0,57.m05781:100.0):87.0,AN2082.1:100.0):100.0):100.0,
1381	69.m15054	AN1753.1	AO070324000040	FG08628.1	AFAO	yes	yes	((FG08628.1:100.0,((AO07032400:100.0,69.m15054:100.0):98.0,AN1753.1:100.0):100.0):100.0,
1382	69.m15455	AN5498.1	AO070341000387	FG08619.1	ANAO		yes	((FG08619.1:100.0,(69.m15455:100.0,(AN5498.1:100.0,AO07034100:100.0):81.0):100.0):100.0,
1383	57.m05769	AN2069.1	AO070341000218	FG08620.1				(((57.m05769:100.0,FG08620.1:100.0):51.0,(AN2069.1:100.0,AO07034100:100.0):79.3):100.0,
1384	69.m15671	AN2126.1	AO070306000108	FG08621.1	AFAO	yes	yes	((FG08621.1:100.0,((AO07030600:100.0,69.m15671:100.0):95.0,AN2126.1:100.0):100.0):100.0,
1385	52.m03757	AN8559.1	AO070306000062	FG08622.1	AFAO	yes	yes	((FG08622.1:100.0,((AO07030600:100.0,52.m03757:100.0):94.0,AN8559.1:100.0):100.0):100.0,
1386	69.m15085	AN7533.1	AO070324000008	FG08623.1	AFAO	yes	yes	((FG08623.1:100.0,(AN7533.1:100.0,(69.m15085:100.0,AO07032400:100.0):100.0):100.0):100.0,
1387	72.m19566	AN7549.1	AO070277000046	FG09267.1	ANAO			((FG09267.1:100.0,((AO07027700:100.0,AN7549.1:100.0):42.0,72.m19566:100.0):100.0):100.0,
1388	59.m08826	AN4923.1	AO070338000020	FG09266.1	AFAO		yes	((FG09266.1:100.0,((AO07033800:100.0,59.m08826:100.0):83.0,AN4923.1:100.0):100.0):100.0,
1389	58.m07438	AN3660.1	AO070342000025	FG08400.1	AFAO	yes	yes	((FG08400.1:100.0,((AO07034200:100.0,58.m07438:100.0):97.0,AN3660.1:100.0):100.0):100.0,
1390	58.m07437	AN3661.1	AO070342000024	FG08751.1	ANAO			((FG08751.1:100.0,(58.m07437:100.0,(AO07034200:100.0,AN3661.1:100.0):52.0):99.0):100.0,
1391	59.m08730	AN2883.1	AO070338000131	FG09285.1	AFAO	yes	yes	((FG09285.1:100.0,((AO07033800:100.0,59.m08730:100.0):93.0,AN2883.1:100.0):100.0):100.0,
1392	59.m08729	AN2882.1	AO070338000132	FG09284.1	AFAN			((FG09284.1:100.0,(AO07033800:100.0,(AN2882.1:100.0,59.m08729:100.0):50.5):100.0):100.0,
1393	57.m05952	AN7468.1	AO070287000059	FG08626.1	AFAO			((FG08626.1:100.0,((AO07028700:100.0,57.m05952:100.0):57.5,AN7468.1:100.0):100.0):100.0,
1394	57.m05951	AN7466.1	AO070287000060	FG00226.1	AFAO			((FG00226.1:100.0,((57.m05951:100.0,AO07028700:100.0):48.5,AN7466.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1395	70.m14893	AN1339.1	AO070247000025	FG10272.1	AFAO			((FG10272.1:100.0,((AO07024700:100.0,70.m14893:100.0):63.5,AN1339.1:100.0):100.0):100.0,
1396	65.m07446	AN4268.1	AO070343000043	FG10065.1	AFAN	yes	yes	((FG10065.1:100.0,((AN4268.1:100.0,65.m07446:100.0):100.0,AO07034300:100.0):100.0):100.0,
1397	58.m08025	AN4298.1	AO070189000008	FG10033.1	AFAO			((FG10033.1:100.0,((AO07018900:100.0,58.m08025:100.0):71.5,AN4298.1:100.0):100.0):100.0,
1398	58.m08027	AN4297.1	AO070189000005	FG10276.1	AFAO			((FG10276.1:100.0,((AO07018900:100.0,58.m08027:100.0):47.3,AN4297.1:100.0):100.0):100.0,
1399	70.m15280	AN0676.1	AO070343000539	FG09993.1	AFAO			((FG09993.1:100.0,((AO07034300:100.0,70.m15280:100.0):66.5,AN0676.1:100.0):100.0):100.0,
1400	59.m09515	AN3443.1	AO070265000017	FG09917.1	AFAO	yes	yes	((FG09917.1:100.0,((AO07026500:100.0,59.m09515:100.0):99.0,AN3443.1:100.0):100.0):100.0,
1401	57.m05491	AN4570.1	AO070316000153	FG09919.1	AFAO			((FG09919.1:100.0,((AO07031600:100.0,57.m05491:100.0):54.5,AN4570.1:100.0):100.0):100.0,
1402	57.m05490	AN4569.1	AO070316000152	FG09918.1	AFAO			((FG09918.1:100.0,((57.m05490:100.0,AO07031600:100.0):62.3,AN4569.1:100.0):100.0):100.0,
1403	57.m05776	AN2077.1	AO070341000230	FG08439.1	AFAO		yes	((FG08439.1:100.0,((AO07034100:100.0,57.m05776:100.0):80.0,AN2077.1:100.0):100.0):100.0,
1404	69.m15622	AN4166.1	AO070341000097	FG08447.1	AFAO		yes	((FG08447.1:100.0,((AO07034100:100.0,69.m15622:100.0):87.5,AN4166.1:100.0):100.0):100.0,
1405	69.m15621	AN4167.1	AO070341000096	FG08446.1	AFAO			((FG08446.1:100.0,((AO07034100:100.0,69.m15621:100.0):55.5,AN4167.1:100.0):100.0):100.0,
1406	57.m05953	AN7469.1	AO070287000057	FG08627.1	AFAO	yes	yes	((FG08627.1:100.0,((AO07028700:100.0,57.m05953:100.0):90.0,AN7469.1:100.0):100.0):100.0,
1407	69.m14940	AN1922.1	AO070341000114	FG08444.1	ANAO			((FG08444.1:100.0,((AO07034100:100.0,AN1922.1:100.0):67.0,69.m14940:100.0):100.0):100.0,
1408	58.m07606	AN1997.1	AO070301000092	FG08617.1	ANAO			((FG08617.1:100.0,(58.m07606:100.0,(AN1997.1:100.0,AO07030100:100.0):45.0):100.0):100.0,
1409	69.m14918	AN1904.1	AO070341000146	FG09465.1	AFAO			((FG09465.1:100.0,((AO07034100:100.0,69.m14918:100.0):41.0,AN1904.1:100.0):100.0):100.0,
1410	57.m05760	AN2062.1	AO070341000205	FG09471.1	AFAO		yes	((FG09471.1:100.0,((AO07034100:100.0,57.m05760:100.0):86.5,AN2062.1:100.0):100.0):100.0,
1411	72.m19917	AN5800.1	AO070260000049	FG09866.1	AFAO		yes	((FG09866.1:100.0,((72.m19917:100.0,AO07026000:100.0):87.5,AN5800.1:100.0):100.0):100.0,
1412	72.m19905	AN5801.1	AO070260000048	FG09865.1	ANAO	yes	yes	((FG09865.1:100.0,(72.m19905:100.0,(AN5801.1:100.0,AO07026000:100.0):93.5):100.0):100.0,
1413	72.m18931	AN5803.1	AO070260000046	FG09862.1	AFAO			((FG09862.1:100.0,((AO07026000:100.0,72.m18931:100.0):69.5,AN5803.1:100.0):100.0):100.0,
1414	70.m14822	AN1402.1	AO070233000017	FG10069.1	ANAO	yes	yes	((FG10069.1:100.0,(70.m14822:100.0,(AN1402.1:100.0,AO07023300:100.0):92.0):100.0):100.0,
1415	58.m09017	AN4446.1	AO070273000007	FG10067.1	AFAO			((FG10067.1:100.0,((AO07027300:100.0,58.m09017:100.0):47.8,AN4446.1:100.0):100.0):100.0,
1416	69.m14854	AN5757.1	AO070341000016	FG10066.1	AFAO		yes	((FG10066.1:100.0,((AO07034100:100.0,69.m14854:100.0):88.5,AN5757.1:100.0):100.0):100.0,
1417	58.m08028	AN4293.1	AO070189000002	FG09965.1	AFAO		yes	((FG09965.1:100.0,((AO07018900:100.0,58.m08028:100.0):81.5,AN4293.1:100.0):100.0):100.0,
1418	59.m09280	AN3426.1	AO070327000005	FG09961.1	AFAO		yes	((FG09961.1:100.0,((AO07032700:100.0,59.m09280:100.0):81.5,AN3426.1:100.0):100.0):100.0,
1419	58.m07332	AN5644.1	AO070342000235	FG09960.1	ANAO			((FG09960.1:100.0,(58.m07332:100.0,(AN5644.1:100.0,AO07034200:100.0):40.5):100.0):100.0,
1420	57.m05770	AN2072.1	AO070341000219	FG08544.1	AFAN	yes	yes	((FG08544.1:100.0,(AO07034100:100.0,(AN2072.1:100.0,57.m05770:100.0):97.5):100.0):100.0,
1421	57.m05745	AN1873.1	AO070341000189	FG03103.1	ANAO			((FG03103.1:100.0,(57.m05745:100.0,(AN1873.1:100.0,AO07034100:100.0):51.0):100.0):100.0,
1422	69.m15048	AN1745.1	AO070324000051	FG09476.1	AFAO			((FG09476.1:100.0,((AO07032400:100.0,69.m15048:100.0):50.5,AN1745.1:100.0):100.0):100.0,
1423	69.m14928	AN1913.1	AO070341000134	FG08761.1	AFAO	yes	yes	((FG08761.1:100.0,((AO07034100:100.0,69.m14928:100.0):96.5,AN1913.1:100.0):100.0):100.0,
1424	71.m15619	AN8812.1	AO070276000042	FG08373.1	ANAO			((FG08373.1:100.0,(71.m15619:100.0,(AN8812.1:100.0,AO07027600:100.0):68.5):100.0):100.0,
1425	70.m14922	AN1286.1	AO070303000047	FG05344.1	AFAO	yes	yes	((FG05344.1:100.0,((AO07030300:100.0,70.m14922:100.0):94.5,AN1286.1:100.0):100.0):100.0,
1426	62.m03273	AN5330.1	AO070333000250	FG08082.1	ANAO		yes	(((62.m03273:100.0,(AN5330.1:100.0,AO07033300:100.0):96.0):88.8,FG08082.1:100.0):100.0,
1427	69.m15052	AN1751.1	AO070324000042	FG09300.1	AFAO			((FG09300.1:100.0,((69.m15052:100.0,AO07032400:100.0):46.5,AN1751.1:100.0):100.0):100.0,
1428	69.m15051	AN1750.1	AO070324000043	FG05336.1	AFAO			((FG05336.1:100.0,((69.m15051:100.0,AO07032400:100.0):61.5,AN1750.1:100.0):100.0):100.0,
1429	69.m15070	AN1767.1	AO070324000025	FG09298.1	ANAO			((FG09298.1:100.0,(69.m15070:100.0,(AN1767.1:100.0,AO07032400:100.0):50.5):100.0):100.0,
1430	58.m07554	AN5629.1	AO070301000028	FG09250.1	AFAO		yes	((FG09250.1:100.0,((AO07030100:100.0,58.m07554:100.0):81.5,AN5629.1:100.0):100.0):100.0,
1431	58.m08009	AN4315.1	AO070230000003	FG09528.1	AFAO			((FG09528.1:100.0,((58.m08009:100.0,AO07023000:100.0):70.0,AN4315.1:100.0):100.0):100.0,
1432	70.m15763	AN1182.1	AO070331000182	FG09530.1	AFAO			((((AO07033100:100.0,70.m15763:100.0):54.5,AN1182.1:100.0):99.0,FG09530.1:100.0):100.0,
1433	69.m15454	AN5499.1	AO070341000386	FG05337.1	AFAO	yes	yes	((FG05337.1:100.0,((AO07034100:100.0,69.m15454:100.0):99.0,AN5499.1:100.0):100.0):100.0,
1434	58.m08007	AN4317.1	AO070230000006	FG09271.1	AFAO	yes	yes	((FG09271.1:100.0,((AO07023000:100.0,58.m08007:100.0):95.8,AN4317.1:100.0):100.0):100.0,
1435	69.m15067	AN1769.1	AO070324000028	FG09532.1	AFAO			((FG09532.1:100.0,((AO07032400:100.0,69.m15067:100.0):59.5,AN1769.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1436	69.m15307	AN1151.1	AO070226000022	FG09485.1	ANAO	yes	yes	((FG09485.1:100.0,(69.m15307:100.0,(AN1151.1:100.0,AO07022600:100.0):96.0):100.0):100.0,
1437	52.m03913	AN8566.1	AO070307000099	FG03349.1	AFAN	yes	yes	((FG03349.1:100.0,(AO07030700:100.0,(AN8566.1:100.0,52.m03913:100.0):90.5):100.0):100.0,
1438	69.m15042	AN1728.1	AO070324000059	FG09234.1	AFAN			((FG09234.1:100.0,(AO07032400:100.0,(AN1728.1:100.0,69.m15042:100.0):53.0):100.0):100.0,
1439	59.m08620	AN3117.1	AO070303000031	FG08466.1	AFAO		yes	((FG08466.1:100.0,((AO07030300:100.0,59.m08620:100.0):77.5,AN3117.1:100.0):100.0):100.0,
1440	69.m15053	AN1752.1	AO070324000041	FG08463.1	AFAO	yes	yes	((FG08463.1:100.0,(AN1752.1:100.0,(69.m15053:100.0,AO07032400:100.0):100.0):100.0):100.0,
1441	53.m03869	AN8024.1	AO070322000071	FG01991.1	ANAO			((FG01991.1:100.0,(53.m03869:100.0,(AN8024.1:100.0,AO07032200:100.0):60.5):100.0):100.0,
1442	58.m07526	AN5602.1	AO070328000002	FG09535.1	AFAN			((FG09535.1:100.0,(AO07032800:100.0,(AN5602.1:100.0,58.m07526:100.0):62.5):100.0):100.0,
1443	58.m08909	AN5603.1	AO070328000001	FG09534.1	AFAO	yes	yes	((FG09534.1:100.0,((AO07032800:100.0,58.m08909:100.0):99.0,AN5603.1:100.0):100.0):100.0,
1444	52.m03956	AN7359.1	AO070302000084	FG01745.1	AFAN		yes	((FG01745.1:100.0,(AO07030200:100.0,(AN7359.1:100.0,52.m03956:100.0):87.0):100.0):100.0,
1445	69.m15159	AN2119.1	AO070332000052	FG09254.1	AFAO			((FG09254.1:100.0,((AO07033200:100.0,69.m15159:100.0):61.0,AN2119.1:100.0):100.0):100.0,
1446	70.m15429	AN0828.1	AO070255000017	FG03177.1	ANAO		yes	((FG03177.1:100.0,(70.m15429:100.0,(AN0828.1:100.0,AO07025500:100.0):85.5):100.0):100.0,
1447	62.m03099	AN6512.1	AO070270000007	FG07165.1	AFAO			((FG07165.1:100.0,((62.m03099:100.0,AO07027000:100.0):47.0,AN6512.1:100.0):100.0):100.0,
1448	58.m08020	AN4304.1	AO070207000008	FG04567.1	AFAN			((FG04567.1:100.0,(AO07020700:100.0,(AN4304.1:100.0,58.m08020:100.0):51.5):100.0):100.0,
1449	53.m04094	AN9522.1	AO070310000070	FG07173.1	AFAO	yes	yes	((FG07173.1:100.0,(AN9522.1:100.0,(53.m04094:100.0,AO07031000:100.0):100.0):100.0):100.0,
1450	53.m03868	AN8023.1	AO070322000070	FG07172.1	AFAO		yes	((FG07172.1:100.0,((AO07032200:100.0,53.m03868:100.0):86.0,AN8023.1:100.0):100.0):100.0,
1451	62.m03207	AN6591.1	AO070326000039	FG07169.1	AFAO		yes	((FG07169.1:100.0,((AO07032600:100.0,62.m03207:100.0):84.0,AN6591.1:100.0):100.0):100.0,
1452	54.m06312	AN2648.1	AO070263000025	FG07838.1	AFAO	yes	yes	((((AO07026300:100.0,54.m06312:100.0):100.0,AN2648.1:100.0):96.5,FG07838.1:100.0):100.0,
1453	59.m08809	AN4905.1	AO070338000040	FG02000.1	AFAN			((FG02000.1:100.0,(AO07033800:100.0,(AN4905.1:100.0,59.m08809:100.0):58.8):100.0):100.0,
1454	58.m07402	AN3604.1	AO070342000157	FG01846.1	ANAO		yes	((FG01846.1:100.0,(58.m07402:100.0,(AN3604.1:100.0,AO07034200:100.0):76.5):100.0):100.0,
1455	58.m07637	AN2049.1	AO070292000016	FG01886.1	AFAO	yes	yes	((FG01886.1:100.0,((AO07029200:100.0,58.m07637:100.0):95.5,AN2049.1:100.0):100.0):100.0,
1456	71.m15997	AN8859.1	AO070271000014	FG07421.1	AFAO			((FG07421.1:100.0,((AO07027100:100.0,71.m15997:100.0):63.0,AN8859.1:100.0):100.0):100.0,
1457	58.m07636	AN2048.1	AO070292000015	FG01890.1	AFAO			((FG01890.1:100.0,((58.m07636:100.0,AO07029200:100.0):55.5,AN2048.1:100.0):100.0):100.0,
1458	58.m07635	AN2047.1	AO070292000014	FG01891.1	AFAN			((((58.m07635:100.0,AN2047.1:100.0):58.7,AO07029200:100.0):82.0,FG01891.1:100.0):100.0,
1459	54.m06766	AN4207.1	AO070231000017	FG01893.1	AFAO			((FG01893.1:100.0,((AO07023100:100.0,54.m06766:100.0):65.0,AN4207.1:100.0):100.0):100.0,
1460	70.m15365	AN0762.1	AO070316000082	FG01873.1	ANAO			((FG01873.1:100.0,((AO07031600:100.0,AN0762.1:100.0):64.5,70.m15365:100.0):100.0):100.0,
1461	58.m07323	AN5658.1	AO070342000246	FG04564.1	AFAO	yes	yes	((FG04564.1:100.0,(AN5658.1:100.0,(58.m07323:100.0,AO07034200:100.0):100.0):100.0):100.0,
1462	62.m03197	AN6600.1	AO070326000049	FG07166.1	AFAO			((FG07166.1:100.0,((AO07032600:100.0,62.m03197:100.0):51.0,AN6600.1:100.0):100.0):100.0,
1463	54.m06490	AN0292.1	AO070334000050	FG02010.1	AFAO			((FG02010.1:100.0,((54.m06490:100.0,AO07033400:100.0):56.5,AN0292.1:100.0):100.0):100.0,
1464	58.m08904	AN3594.1	AO070342000146	FG02011.1	AFAO			((FG02011.1:100.0,((AO07034200:100.0,58.m08904:100.0):57.5,AN3594.1:100.0):100.0):100.0,
1465	72.m19508	AN6347.1	AO070275000012	FG01842.1	AFAO			((FG01842.1:100.0,((AO07027500:100.0,72.m19508:100.0):55.0,AN6347.1:100.0):100.0):100.0,
1466	54.m06767	AN4208.1	AO070231000016	FG02016.1	AFAO			((FG02016.1:100.0,((AO07023100:100.0,54.m06767:100.0):55.5,AN4208.1:100.0):100.0):100.0,
1467	54.m06763	AN4204.1	AO070231000020	FG02003.1	AFAO	yes	yes	((((AO07023100:100.0,54.m06763:100.0):100.0,AN4204.1:100.0):98.5,FG02003.1:100.0):100.0,
1468	62.m03111	AN6522.1	AO070270000021	FG05220.1	AFAN			((FG05220.1:100.0,(AO07027000:100.0,(AN6522.1:100.0,62.m03111:100.0):58.0):100.0):100.0,
1469	71.m15348	AN0072.1	AO070314000161	FG07326.1	AFAN	yes	yes	((FG07326.1:100.0,(AO07031400:100.0,(AN0072.1:100.0,71.m15348:100.0):98.0):100.0):100.0,
1470	54.m06643	AN0451.1	AO070328000185	FG07315.1	ANAO			((FG07315.1:100.0,(54.m06643:100.0,(AN0451.1:100.0,AO07032800:100.0):54.7):100.0):100.0,
1471	53.m03813	AN8168.1	AO070266000006	FG07197.1	AFAO	yes	yes	((FG07197.1:100.0,((AO07026600:100.0,53.m03813:100.0):96.5,AN8168.1:100.0):100.0):100.0,
1472	58.m08930	AN6443.1	AO070238000002	FG11028.1	AFAO	yes	yes	((FG11028.1:100.0,((58.m08930:100.0,AO07023800:100.0):99.0,AN6443.1:100.0):99.0):100.0,
1473	71.m15903	AN2262.1	AO070295000025	FG07195.1	AFAO	yes	yes	((FG07195.1:100.0,((AO07029500:100.0,71.m15903:100.0):99.0,AN2262.1:100.0):100.0):100.0,
1474	71.m15904	AN2263.1	AO070295000026	FG07194.1	AFAO	yes	yes	((FG07194.1:100.0,(AN2263.1:100.0,(71.m15904:100.0,AO07029500:100.0):100.0):100.0):100.0,
1475	71.m15913	AN2268.1	AO070295000040	FG07333.1	ANAO			((FG07333.1:100.0,(71.m15913:100.0,(AN2268.1:100.0,AO07029500:100.0):56.5):100.0):100.0,
1476	62.m03131	AN6543.1	AO070270000041	FG07334.1	AFAO			((FG07334.1:100.0,((AO07027000:100.0,62.m03131:100.0):54.0,AN6543.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1477	62.m03132	AN6542.1	AO070253000011	FG07335.1	AFAN		yes	((FG07335.1:100.0,((62.m03132:100.0,AN6542.1:100.0):87.5,AO07025300:100.0):77.0):100.0,
1478	62.m03098	AN6511.1	AO070270000006	FG07338.1	AFAO		yes	((FG07338.1:100.0,((AO07027000:100.0,62.m03098:100.0):83.5,AN6511.1:100.0):100.0):100.0,
1479	62.m03090	AN6502.1	AO070222000018	FG07341.1	AFAO	yes	yes	((FG07341.1:100.0,(AN6502.1:100.0,(62.m03090:100.0,AO07022200:100.0):100.0):100.0):100.0,
1480	62.m03095	AN6508.1	AO070270000001	FG07329.1	AFAO	yes	yes	((FG07329.1:100.0,((AO07027000:100.0,62.m03095:100.0):98.5,AN6508.1:100.0):100.0):100.0,
1481	62.m03094	AN6507.1	AO070222000023	FG07328.1	AFAO		yes	((FG07328.1:100.0,((AO07022200:100.0,62.m03094:100.0):82.0,AN6507.1:100.0):100.0):100.0,
1482	62.m03493	AN6544.1	AO070270000040	FG07322.1	AFAO			((FG07322.1:100.0,((62.m03493:100.0,AO07027000:100.0):61.7,AN6544.1:100.0):100.0):100.0,
1483	71.m16098	AN7730.1	AO070325000147	FG06999.1	AFAO		yes	((FG06999.1:100.0,((AO07032500:100.0,71.m16098:100.0):78.0,AN7730.1:100.0):100.0):100.0,
1484	62.m03101	AN6514.1	AO070270000009	FG07345.1	ANAO			((FG07345.1:100.0,((AO07027000:100.0,AN6514.1:100.0):71.5,62.m03101:100.0):100.0):100.0,
1485	53.m03709	AN8252.1	AO070310000055	FG06133.1	AFAO	yes	yes	((FG06133.1:100.0,((AO07031000:100.0,53.m03709:100.0):98.5,AN8252.1:100.0):100.0):100.0,
1486	59.m09119	AN4854.1	AO070327000089	FG04161.1	ANAO			((FG04161.1:100.0,(59.m09119:100.0,(AN4854.1:100.0,AO07032700:100.0):65.8):100.0):100.0,
1487	71.m15606	AN8799.1	AO070276000061	FG05964.1	AFAO	yes	yes	((FG05964.1:100.0,((AO07027600:100.0,71.m15606:100.0):99.0,AN8799.1:100.0):100.0):100.0,
1488	53.m03732	AN8237.1	AO070310000071	FG06138.1	AFAO			((FG06138.1:100.0,((AO07031000:100.0,53.m03732:100.0):58.0,AN8237.1:100.0):100.0):100.0,
1489	71.m16082	AN4733.1	AO070276000009	FG06139.1	AFAO		yes	((FG06139.1:100.0,((71.m16082:100.0,AO07027600:100.0):86.0,AN4733.1:100.0):100.0):100.0,
1490	53.m03757	AN8216.1	AO070310000096	FG05972.1	ANAO		yes	((((AO07031000:100.0,AN8216.1:100.0):75.6,53.m03757:100.0):75.7,FG05972.1:100.0):100.0,
1491	54.m06814	AN3504.1	AO070306000123	FG02920.1	AFAO	yes	yes	((FG02920.1:100.0,((AO07030600:100.0,54.m06814:100.0):96.0,AN3504.1:100.0):100.0):100.0,
1492	53.m03756	AN8217.1	AO070310000095	FG05973.1	ANAO		yes	((FG05973.1:100.0,(53.m03756:100.0,(AN8217.1:100.0,AO07031000:100.0):76.5):100.0):100.0,
1493	72.m19590	AN7571.1	AO070343000417	FG05974.1	AFAO	yes	yes	((FG05974.1:100.0,(AN7571.1:100.0,(72.m19590:100.0,AO07034300:100.0):100.0):100.0):100.0,
1494	58.m07363	AN4162.1	AO070342000192	FG10159.1	AFAO	yes	yes	((FG10159.1:100.0,((AO07034200:100.0,58.m07363:100.0):94.0,AN4162.1:100.0):100.0):100.0,
1495	58.m07991	AN4329.1	AO070240000007	FG10160.1	AFAO		yes	((FG10160.1:100.0,((AO07024000:100.0,58.m07991:100.0):78.3,AN4329.1:100.0):100.0):100.0,
1496	62.m03232	AN6637.1	AO070326000089	FG05278.1	AFAO			((FG05278.1:100.0,((AO07032600:100.0,62.m03232:100.0):69.0,AN6637.1:100.0):100.0):100.0,
1497	59.m08815	AN4912.1	AO070338000036	FG02119.1	AFAO		yes	((FG02119.1:100.0,((AO07033800:100.0,59.m08815:100.0):78.5,AN4912.1:100.0):100.0):100.0,
1498	58.m07328	AN5635.1	AO070342000242	FG09895.1	AFAO		yes	((FG09895.1:100.0,((AO07034200:100.0,58.m07328:100.0):75.0,AN5635.1:100.0):100.0):100.0,
1499	58.m07322	AN5657.1	AO070342000247	FG10356.1	ANAO			((FG10356.1:100.0,(58.m07322:100.0,(AN5657.1:100.0,AO07034200:100.0):57.0):100.0):100.0,
1500	59.m09319	AN3458.1	AO070265000035	FG10355.1	AFAO		yes	((FG10355.1:100.0,((AO07026500:100.0,59.m09319:100.0):88.5,AN3458.1:100.0):100.0):100.0,
1501	57.m05486	AN4647.1	AO070316000121	FG10257.1	AFAO			((FG10257.1:100.0,((AO07031600:100.0,57.m05486:100.0):66.0,AN4647.1:100.0):100.0):100.0,
1502	57.m05671	AN3811.1	AO070311000008	FG10221.1	AFAO	yes	yes	((FG10221.1:100.0,(AN3811.1:100.0,(57.m05671:100.0,AO07031100:100.0):100.0):100.0):100.0,
1503	58.m07331	AN5634.1	AO070342000238	FG09896.1	AFAO	yes	yes	((FG09896.1:100.0,((AO07034200:100.0,58.m07331:100.0):98.0,AN5634.1:100.0):100.0):100.0,
1504	65.m07290	AN9489.1	AO070339000098	FG09915.1	ANAO			((FG09915.1:100.0,(65.m07290:100.0,(AO07033900:100.0,AN9489.1:100.0):74.5):100.0):100.0,
1505	66.m04624	AN1748.1	AO070320000028	FG02113.1	ANAO			((FG02113.1:100.0,((AO07032000:100.0,AN1748.1:100.0):50.5,66.m04624:100.0):100.0):100.0,
1506	58.m08019	AN4305.1	AO070330000015	FG04568.1	AFAN	yes	yes	((((58.m08019:100.0,AN4305.1:100.0):100.0,AO07033000:100.0):92.0,FG04568.1:100.0):100.0,
1507	57.m05911	AN7440.1	AO070229000004	FG10032.1	AFAO		yes	((FG10032.1:100.0,((AO07022900:100.0,57.m05911:100.0):86.5,AN7440.1:100.0):100.0):100.0,
1508	70.m15248	AN0646.1	AO070343000583	FG09930.1	AFAO			((FG09930.1:100.0,((AO07034300:100.0,70.m15248:100.0):68.0,AN0646.1:100.0):100.0):100.0,
1509	70.m15249	AN0647.1	AO070343000582	FG09929.1	AFAN			((FG09929.1:100.0,(AO07034300:100.0,(AN0647.1:100.0,70.m15249:100.0):47.5):100.0):100.0,
1510	57.m05468	AN7687.1	AO070325000085	FG09927.1	AFAO	yes	yes	((FG09927.1:100.0,(AN7687.1:100.0,(57.m05468:100.0,AO07032500:100.0):100.0):100.0):100.0,
1511	58.m07342	AN1953.1	AO070342000222	FG10385.1	AFAO			((FG10385.1:100.0,((AO07034200:100.0,58.m07342:100.0):67.0,AN1953.1:100.0):100.0):100.0,
1512	58.m07343	AN1952.1	AO070342000221	FG10386.1	AFAN			((FG10386.1:100.0,(AO07034200:100.0,(AN1952.1:100.0,58.m07343:100.0):68.0):100.0):100.0,
1513	57.m05488	AN4566.1	AO070316000145	FG10327.1	ANAO			((FG10327.1:100.0,((AO07031600:100.0,AN4566.1:100.0):74.0,57.m05488:100.0):100.0):100.0,
1514	59.m08469	AN2518.1	AO070286000074	FG10345.1	AFAN			((FG10345.1:100.0,(AO07028600:100.0,(AN2518.1:100.0,59.m08469:100.0):74.5):100.0):100.0,
1515	59.m09279	AN3425.1	AO070327000006	FG10259.1	AFAO			((FG10259.1:100.0,((AO07032700:100.0,59.m09279:100.0):55.0,AN3425.1:100.0):100.0):100.0,
1516	58.m07348	AN1948.1	AO070342000213	FG09976.1	AFAO	yes	yes	((FG09976.1:100.0,((AO07034200:100.0,58.m07348:100.0):99.0,AN1948.1:100.0):100.0):100.0,
1517	58.m08970	AN4386.1	AO070261000031	FG09938.1	AFAN			((FG09938.1:100.0,(AO07026100:100.0,(AN4386.1:100.0,58.m08970:100.0):44.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1518	67.m02963	AN2825.1	AO070330000091	FG07016.1	AFAO	yes	yes	((FG07016.1:100.0,((AO07033000:100.0,67.m02963:100.0):92.5,AN2825.1:100.0):100.0):100.0,
1519	52.m03816	AN8421.1	AO070302000061	FG07016.1	ANAO			((FG07016.1:100.0,(52.m03816:100.0,(AN8421.1:100.0,AO07030200:100.0):74.0):100.0):100.0,
1520	59.m09156	AN4819.1	AO070327000168	FG10043.1	ANAO			((FG10043.1:100.0,((AO07032700:100.0,AN4819.1:100.0):68.5,59.m09156:100.0):100.0):100.0,
1521	59.m09284	AN3428.1	AO070265000001	FG09995.1	AFAO	yes	yes	((FG09995.1:100.0,((AO07026500:100.0,59.m09284:100.0):90.0,AN3428.1:100.0):100.0):100.0,
1522	59.m09282	AN3427.1	AO070327000003	FG10156.1	AFAO	yes	yes	((FG10156.1:100.0,((AO07032700:100.0,59.m09282:100.0):98.0,AN3427.1:100.0):100.0):100.0,
1523	58.m08982	AN4411.1	AO070273000031	FG10157.1	ANAO			((FG10157.1:100.0,(58.m08982:100.0,(AN4411.1:100.0,AO07027300:100.0):69.5):100.0):100.0,
1524	58.m08972	AN4407.1	AO070273000067	FG10158.1	AFAO	yes	yes	((FG10158.1:100.0,((AO07027300:100.0,58.m08972:100.0):97.5,AN4407.1:100.0):100.0):100.0,
1525	71.m15975	AN8843.1	AO070271000034	FG10211.1	AFAO	yes	yes	((FG10211.1:100.0,((AO07027100:100.0,71.m15975:100.0):94.0,AN8843.1:100.0):100.0):100.0,
1526	70.m14905	AN1326.1	AO070303000090	FG10196.1	AFAN	yes	yes	((FG10196.1:100.0,(AO07030300:100.0,(AN1326.1:100.0,70.m14905:100.0):95.5):100.0):100.0,
1527	54.m07025	AN3894.1	AO070324000132	FG10198.1	AFAO	yes	yes	((FG10198.1:100.0,((AO07032400:100.0,54.m07025:100.0):99.0,AN3894.1:100.0):100.0):100.0,
1528	70.m14899	AN1335.1	AO070303000097	FG10251.1	ANAO			((FG10251.1:100.0,((AO07030300:100.0,AN1335.1:100.0):43.5,70.m14899:100.0):100.0):100.0,
1529	70.m14844	AN1379.1	AO070243000010	FG10280.1	AFAO	yes	yes	((FG10280.1:100.0,((AO07024300:100.0,70.m14844:100.0):97.0,AN1379.1:100.0):100.0):100.0,
1530	58.m08021	AN4303.1	AO070207000007	FG04571.1	AFAO	yes	yes	((FG04571.1:100.0,((AO07020700:100.0,58.m08021:100.0):95.5,AN4303.1:100.0):100.0):100.0,
1531	72.m19941	AN5957.1	AO070340000309	FG04570.1	AFAO	yes	yes	((FG04570.1:100.0,((AO07034000:100.0,72.m19941:100.0):90.5,AN5957.1:100.0):100.0):100.0,
1532	57.m05456	AN7679.1	AO070325000069	FG10388.1	ANAO			((FG10388.1:100.0,((AO07032500:100.0,AN7679.1:100.0):67.0,57.m05456:100.0):100.0):100.0,
1533	58.m07970	AN4350.1	AO070240000028	FG10031.1	AFAO			((FG10031.1:100.0,((AO07024000:100.0,58.m07970:100.0):50.0,AN4350.1:100.0):100.0):100.0,
1534	58.m07932	AN4399.1	AO070261000044	FG09935.1	ANAO			((((AN4399.1:100.0,AO07026100:100.0):46.0,58.m07932:100.0):93.5,FG09935.1:100.0):100.0,
1535	58.m07925	AN4401.1	AO070261000045	FG09934.1	ANAO		yes	((FG09934.1:100.0,(58.m07925:100.0,(AN4401.1:100.0,AO07026100:100.0):81.0):100.0):100.0,
1536	58.m07924	AN4402.1	AO070261000046	FG09933.1	AFAO	yes	yes	((FG09933.1:100.0,((AO07026100:100.0,58.m07924:100.0):96.5,AN4402.1:100.0):100.0):100.0,
1537	58.m09012	AN4295.1	AO070207000004	FG10319.1	AFAN			((FG10319.1:100.0,(AO07020700:100.0,(AN4295.1:100.0,58.m09012:100.0):46.5):100.0):100.0,
1538	58.m07943	AN4382.1	AO070261000027	FG10322.1	AFAO			((FG10322.1:100.0,((AO07026100:100.0,58.m07943:100.0):69.5,AN4382.1:100.0):100.0):100.0,
1539	58.m08998	AN4378.1	AO070261000021	FG10028.1	AFAO	yes	yes	((FG10028.1:100.0,((AO07026100:100.0,58.m08998:100.0):92.0,AN4378.1:100.0):100.0):100.0,
1540	70.m14837	AN1384.1	AO070243000018	FG10145.1	AFAO		yes	((FG10145.1:100.0,((AO07024300:100.0,70.m14837:100.0):87.5,AN1384.1:100.0):100.0):100.0,
1541	59.m08762	AN4867.1	AO070338000092	FG09910.1	AFAO	yes	yes	((FG09910.1:100.0,((AO07033800:100.0,59.m08762:100.0):92.5,AN4867.1:100.0):100.0):100.0,
1542	59.m08446	AN2531.1	AO070300000119	FG10029.1	AFAO	yes	yes	((FG10029.1:100.0,((AO07030000:100.0,59.m08446:100.0):95.0,AN2531.1:100.0):100.0):100.0,
1543	58.m07365	AN4160.1	AO070342000189	FG10148.1	AFAO	yes	yes	((FG10148.1:100.0,((AO07034200:100.0,58.m07365:100.0):93.5,AN4160.1:100.0):100.0):100.0,
1544	72.m18953	AN5822.1	AO070260000020	FG10228.1	AFAO	yes	yes	((FG10228.1:100.0,((AO07026000:100.0,72.m18953:100.0):97.0,AN5822.1:100.0):100.0):100.0,
1545	59.m08498	AN2491.1	AO070312000129	FG02622.1	ANAO		yes	((FG02622.1:100.0,(59.m08498:100.0,(AN2491.1:100.0,AO07031200:100.0):89.5):100.0):100.0,
1546	70.m15230	AN1013.1	AO070312000015	FG10010.1	AFAN			((FG10010.1:100.0,(AO07031200:100.0,(AN1013.1:100.0,70.m15230:100.0):47.5):100.0):100.0,
1547	71.m15395	AN0116.1	AO070311000103	FG06204.1	AFAO	yes	yes	((FG06204.1:100.0,((AO07031100:100.0,71.m15395:100.0):96.0,AN0116.1:100.0):100.0):100.0,
1548	71.m15396	AN0117.1	AO070311000104	FG05072.1	ANAO			((FG05072.1:100.0,(71.m15396:100.0,(AN0117.1:100.0,AO07031100:100.0):71.0):100.0):100.0,
1549	53.m03852	AN7995.1	AO070322000050	FG05114.1	AFAO	yes	yes	((FG05114.1:100.0,((AO07032200:100.0,53.m03852:100.0):92.5,AN7995.1:100.0):100.0):100.0,
1550	72.m19654	AN7620.1	AO070343000264	FG05647.1	AFAO	yes	yes	((FG05647.1:100.0,((AO07034300:100.0,72.m19654:100.0):99.0,AN7620.1:100.0):100.0):100.0,
1551	71.m15442	AN0167.1	AO070321000079	FG05648.1	ANAO		yes	((FG05648.1:100.0,((AO07032100:100.0,AN0167.1:100.0):77.5,71.m15442:100.0):100.0):100.0,
1552	72.m19665	AN2174.1	AO070343000247	FG09689.1	AFAN		yes	((FG09689.1:100.0,(AO07034300:100.0,(AN2174.1:100.0,72.m19665:100.0):80.0):100.0):100.0,
1553	72.m19662	AN2178.1	AO070343000251	FG09568.1	AFAO	yes	yes	((FG09568.1:100.0,(AN2178.1:100.0,(72.m19662:100.0,AO07034300:100.0):100.0):100.0):100.0,
1554	72.m19129	AN6014.1	AO070340000265	FG08543.1	AFAO			((FG08543.1:100.0,((72.m19129:100.0,AO07034000:100.0):65.0,AN6014.1:100.0):100.0):100.0,
1555	72.m19244	AN5886.1	AO070245000021	FG09589.1	AFAO		yes	((FG09589.1:100.0,((72.m19244:100.0,AO07024500:100.0):80.5,AN5886.1:100.0):100.0):100.0,
1556	72.m19251	AN5880.1	AO070245000028	FG09587.1	ANAO			((((AN5880.1:100.0,AO07024500:100.0):39.3,72.m19251:100.0):98.5,FG09587.1:100.0):100.0,
1557	72.m19252	AN5879.1	AO070245000029	FG09586.1	AFAO			((FG09586.1:100.0,((AO07024500:100.0,72.m19252:100.0):58.0,AN5879.1:100.0):100.0):100.0,
1558	72.m19239	AN5891.1	AO070245000016	FG09585.1	ANAO			((FG09585.1:100.0,((AO07024500:100.0,AN5891.1:100.0):61.0,72.m19239:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1559	71.m16080	AN2334.1	AO070323000005	FG08044.1	AFAO			((((AO07032300:100.0,71.m16080:100.0):35.5,AN2334.1:100.0):47.8,FG08044.1:100.0):100.0,
1560	70.m15051	AN1170.1	AO070331000165	FG02778.1	AFAO	yes	yes	((FG02778.1:100.0,((AO07033100:100.0,70.m15051:100.0):90.5,AN1170.1:100.0):100.0):100.0,
1561	70.m15040	AN1177.1	AO070331000173	FG02780.1	AFAN			((FG02780.1:100.0,(AO07033100:100.0,(AN1177.1:100.0,70.m15040:100.0):54.5):100.0):100.0,
1562	70.m15038	AN1179.1	AO070331000176	FG11637.1	ANAO			((((AN1179.1:100.0,AO07033100:100.0):58.0,70.m15038:100.0):99.5,FG11637.1:100.0):100.0,
1563	70.m14912	AN1296.1	AO070303000056	FG11594.1	AFAO			((FG11594.1:100.0,((AO07030300:100.0,70.m14912:100.0):60.5,AN1296.1:100.0):100.0):100.0,
1564	58.m07467	AN3634.1	AO070328000078	FG00598.1	AFAO	yes	yes	((FG00598.1:100.0,((AO07032800:100.0,58.m07467:100.0):97.0,AN3634.1:100.0):100.0):100.0,
1565	58.m07466	AN3635.1	AO070328000079	FG11596.1	AFAN			((FG11596.1:100.0,(AO07032800:100.0,(AN3635.1:100.0,58.m07466:100.0):59.5):100.0):100.0,
1566	54.m06779	AN4236.1	AO070234000007	FG11597.1	AFAN			((FG11597.1:100.0,(AO07023400:100.0,(AN4236.1:100.0,54.m06779:100.0):51.5):100.0):100.0,
1567	59.m08844	AN4940.1	AO070338000003	FG11602.1	AFAO	yes	yes	((FG11602.1:100.0,((AO07033800:100.0,59.m08844:100.0):91.5,AN4940.1:100.0):100.0):100.0,
1568	72.m19482	AN2427.1	AO070241000010	FG00986.1	AFAO	yes	yes	((FG00986.1:100.0,((AO07024100:100.0,72.m19482:100.0):97.5,AN2427.1:100.0):100.0):100.0,
1569	70.m15300	AN0697.1	AO070343000515	FG04946.1	AFAN			((FG04946.1:100.0,(AO07034300:100.0,(AN0697.1:100.0,70.m15300:100.0):62.0):100.0):100.0,
1570	70.m15299	AN0696.1	AO070343000516	FG04944.1	AFAO	yes	yes	((FG04944.1:100.0,((AO07034300:100.0,70.m15299:100.0):94.3,AN0696.1:100.0):100.0):100.0,
1571	70.m15351	AN0716.1	AO070343000451	FG04945.1	AFAO			((FG04945.1:100.0,((AO07034300:100.0,70.m15351:100.0):65.5,AN0716.1:100.0):100.0):100.0,
1572	52.m03678	AN8445.1	AO070341000302	FG04936.1	AFAO		yes	((FG04936.1:100.0,((AO07034100:100.0,52.m03678:100.0):82.0,AN8445.1:100.0):100.0):100.0,
1573	69.m15260	AN0589.1	AO070280000011	FG05687.1	AFAO		yes	((FG05687.1:100.0,((AO07028000:100.0,69.m15260:100.0):84.5,AN0589.1:100.0):100.0):100.0,
1574	71.m15496	AN4727.1	AO070323000057	FG05689.1	AFAO	yes	yes	((FG05689.1:100.0,((AO07032300:100.0,71.m15496:100.0):97.5,AN4727.1:100.0):100.0):100.0,
1575	71.m15435	AN0158.1	AO070321000089	FG05690.1	AFAO			((FG05690.1:100.0,((AO07032100:100.0,71.m15435:100.0):73.0,AN0158.1:100.0):100.0):100.0,
1576	72.m19692	AN2149.1	AO070343000198	FG05250.1	AFAO			((FG05250.1:100.0,((AO07034300:100.0,72.m19692:100.0):60.5,AN2149.1:100.0):100.0):100.0,
1577	72.m19691	AN2150.1	AO070343000199	FG05249.1	AFAO		yes	((FG05249.1:100.0,((AO07034300:100.0,72.m19691:100.0):84.5,AN2150.1:100.0):100.0):100.0,
1578	70.m15326	AN0730.1	AO070343000491	FG09683.1	AFAO			((FG09683.1:100.0,((AO07034300:100.0,70.m15326:100.0):72.5,AN0730.1:100.0):100.0):100.0,
1579	57.m05703	AN5228.1	AO070337000249	FG03262.1	AFAO	yes	yes	((FG03262.1:100.0,((AO07033700:100.0,57.m05703:100.0):90.0,AN5228.1:100.0):100.0):100.0,
1580	70.m15328	AN0729.1	AO070343000488	FG05243.1	ANAO		yes	((FG05243.1:100.0,(70.m15328:100.0,(AN0729.1:100.0,AO07034300:100.0):78.5):100.0):100.0,
1581	72.m18968	AN6299.1	AO070260000007	FG09673.1	ANAO			((FG09673.1:100.0,(72.m18968:100.0,(AN6299.1:100.0,AO07026000:100.0):61.5):100.0):100.0,
1582	72.m19274	AN6182.1	AO070308000124	FG05668.1	AFAO	yes	yes	((FG05668.1:100.0,((AO07030800:100.0,72.m19274:100.0):97.5,AN6182.1:100.0):100.0):100.0,
1583	72.m19272	AN5861.1	AO070308000126	FG05670.1	AFAO		yes	((FG05670.1:100.0,((AO07030800:100.0,72.m19272:100.0):77.8,AN5861.1:100.0):100.0):100.0,
1584	65.m07229	AN6738.1	AO070339000184	FG05671.1	AFAO		yes	((FG05671.1:100.0,((AO07033900:100.0,65.m07229:100.0):88.0,AN6738.1:100.0):100.0):100.0,
1585	72.m19286	AN6188.1	AO070308000113	FG08678.1	AFAO		yes	((FG08678.1:100.0,((AO07030800:100.0,72.m19286:100.0):84.5,AN6188.1:100.0):100.0):100.0,
1586	53.m03885	AN8058.1	AO070322000142	FG07500.1	AFAO		yes	((FG07500.1:100.0,((AO07032200:100.0,53.m03885:100.0):79.0,AN8058.1:100.0):100.0):100.0,
1587	57.m05836	AN7503.1	AO070287000009	FG05686.1	ANAO			((FG05686.1:100.0,(57.m05836:100.0,(AN7503.1:100.0,AO07028700:100.0):41.5):100.0):100.0,
1588	54.m06858	AN5158.1	AO070291000007	FG04981.1	AFAO		yes	((FG04981.1:100.0,((AO07029100:100.0,54.m06858:100.0):86.0,AN5158.1:100.0):100.0):100.0,
1589	54.m06784	AN4232.1	AO070234000014	FG04027.1	AFAO		yes	((FG04027.1:100.0,((AO07023400:100.0,54.m06784:100.0):81.5,AN4232.1:100.0):100.0):100.0,
1590	54.m06783	AN4233.1	AO070234000013	FG04028.1	AFAN			((FG04028.1:100.0,(AO07023400:100.0,(AN4233.1:100.0,54.m06783:100.0):47.0):100.0):100.0,
1591	58.m07481	AN5535.1	AO070328000056	FG03976.1	AFAO	yes	yes	((FG03976.1:100.0,((AO07032800:100.0,58.m07481:100.0):96.0,AN5535.1:100.0):100.0):100.0,
1592	58.m07482	AN5536.1	AO070328000055	FG04038.1	AFAO			((FG04038.1:100.0,((AO07032800:100.0,58.m07482:100.0):46.7,AN5536.1:100.0):100.0):100.0,
1593	59.m08614	AN3122.1	AO070303000025	FG04031.1	AFAO			((FG04031.1:100.0,((AO07030300:100.0,59.m08614:100.0):66.0,AN3122.1:100.0):100.0):100.0,
1594	59.m08613	AN3123.1	AO070303000024	FG04030.1	AFAO		yes	((FG04030.1:100.0,((AO07030300:100.0,59.m08613:100.0):77.5,AN3123.1:100.0):100.0):100.0,
1595	59.m09375	AN3126.1	AO070303000021	FG03999.1	AFAO			((FG03999.1:100.0,((AO07030300:100.0,59.m09375:100.0):74.0,AN3126.1:100.0):100.0):100.0,
1596	57.m05866	AN7484.1	AO070287000045	FG04003.1	AFAO		yes	((FG04003.1:100.0,((AO07028700:100.0,57.m05866:100.0):77.0,AN7484.1:100.0):100.0):100.0,
1597	69.m15437	AN6197.1	AO070305000025	FG05038.1	AFAN			((((AN6197.1:100.0,69.m15437:100.0):69.0,AO07030500:100.0):50.5,FG05038.1:100.0):100.0,
1598	58.m07556	AN5632.1	AO070301000031	FG10503.1	ANAO			((FG10503.1:100.0,(58.m07556:100.0,(AN5632.1:100.0,AO07030100:100.0):59.8):100.0):100.0,
1599	59.m08932	AN3067.1	AO070337000006	FG06065.1	AFAO	yes	yes	((FG06065.1:100.0,((AO07033700:100.0,59.m08932:100.0):96.5,AN3067.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1600	59.m08766	AN4871.1	AO070338000089	FG10939.1	AFAO			((FG10939.1:100.0,((59.m08766:100.0,AO07033800:100.0):52.5,AN4871.1:100.0):100.0):100.0,
1601	69.m15765	AN3972.1	AO070333000216	FG10203.1	AFAO	yes	yes	((FG10203.1:100.0,((AO07033300:100.0,69.m15765:100.0):95.0,AN3972.1:100.0):100.0):100.0,
1602	59.m08485	AN2505.1	AO070312000059	FG10047.1	AFAO	yes	yes	((FG10047.1:100.0,(AN2505.1:100.0,(59.m08485:100.0,AO07031200:100.0):100.0):100.0):100.0,
1603	72.m19509	AN6346.1	AO070275000011	FG02056.1	AFAO		yes	((FG02056.1:100.0,((AO07027500:100.0,72.m19509:100.0):83.5,AN6346.1:100.0):100.0):100.0,
1604	72.m19510	AN6345.1	AO070275000008	FG02055.1	AFAO	yes	yes	((FG02055.1:100.0,((AO07027500:100.0,72.m19510:100.0):97.5,AN6345.1:100.0):100.0):100.0,
1605	72.m19518	AN6340.1	AO070298000007	FG02054.1	AFAO		yes	((FG02054.1:100.0,((AO07029800:100.0,72.m19518:100.0):85.5,AN6340.1:100.0):100.0):100.0,
1606	72.m18936	AN5806.1	AO070260000042	FG10186.1	ANAO			((FG10186.1:100.0,(72.m18936:100.0,(AN5806.1:100.0,AO07026000:100.0):63.5):100.0):100.0,
1607	54.m06368	AN2393.1	AO070296000121	FG04251.1				(((AO07029600:100.0,AN2393.1:100.0):80.2,(54.m06368:100.0,FG04251.1:100.0):45.7):100.0,
1608	69.m15308	AN5232.1	AO070343000101	FG10039.1	ANAO	yes	yes	((FG10039.1:100.0,(69.m15308:100.0,(AN5232.1:100.0,AO07034300:100.0):99.0):100.0):100.0,
1609	59.m08471	AN2513.1	AO070263000053	FG10037.1	AFAO	yes	yes	((FG10037.1:100.0,((AO07026300:100.0,59.m08471:100.0):91.5,AN2513.1:100.0):100.0):100.0,
1610	59.m08472	AN2514.1	AO070263000052	FG10036.1	AFAO	yes	yes	((FG10036.1:100.0,(AN2514.1:100.0,(59.m08472:100.0,AO07026300:100.0):100.0):100.0):100.0,
1611	57.m05947	AN7681.1	AO070325000071	FG10035.1	AFAN		yes	((FG10035.1:100.0,(AO07032500:100.0,(AN7681.1:100.0,57.m05947:100.0):80.5):100.0):100.0,
1612	70.m15731	AN1358.1	AO070237000002	FG10239.1	ANAO		yes	((FG10239.1:100.0,(70.m15731:100.0,(AN1358.1:100.0,AO07023700:100.0):75.0):100.0):100.0,
1613	57.m05898	AN7447.1	AO070229000019	FG10242.1	AFAO	yes	yes	((FG10242.1:100.0,((AO07022900:100.0,57.m05898:100.0):98.0,AN7447.1:100.0):100.0):100.0,
1614	59.m09278	AN3424.1	AO070327000007	FG09981.1	AFAO	yes	yes	((FG09981.1:100.0,((AO07032700:100.0,59.m09278:100.0):95.0,AN3424.1:100.0):100.0):100.0,
1615	59.m09501	AN3423.1	AO070327000008	FG09904.1	AFAO	yes	yes	((FG09904.1:100.0,(AN3423.1:100.0,(59.m09501:100.0,AO07032700:100.0):100.0):100.0):100.0,
1616	59.m09275	AN3422.1	AO070327000010	FG09903.1	ANAO			((FG09903.1:100.0,((AO07032700:100.0,AN3422.1:100.0):51.5,59.m09275:100.0):100.0):100.0,
1617	58.m07351	AN1945.1	AO070342000203	FG09902.1	ANAO	yes	yes	((FG09902.1:100.0,(58.m07351:100.0,(AO07034200:100.0,AN1945.1:100.0):93.0):100.0):100.0,
1618	57.m05896	AN7448.1	AO070229000021	FG09900.1	ANAO		yes	((FG09900.1:100.0,(57.m05896:100.0,(AN7448.1:100.0,AO07022900:100.0):83.0):100.0):100.0,
1619	57.m05369	AN1800.1	AO070335000095	FG10042.1	AFAO			((FG10042.1:100.0,((AO07033500:100.0,57.m05369:100.0):72.5,AN1800.1:100.0):100.0):100.0,
1620	70.m15621	AN0980.1	AO070250000038	FG03343.1		yes	yes	(((FG03343.1:100.0,AO07025000:100.0):100.0,(AN0980.1:100.0,70.m15621:100.0):100.0):100.0,
1621	53.m04209	AN8262.1	AO070310000038	FG07716.1	AFAO			((FG07716.1:100.0,((AO07031000:100.0,53.m04209:100.0):58.0,AN8262.1:100.0):100.0):100.0,
1622	59.m08476	AN2508.1	AO070263000056	FG10049.1	AFAO			((FG10049.1:100.0,((AO07026300:100.0,59.m08476:100.0):61.5,AN2508.1:100.0):100.0):100.0,
1623	57.m05461	AN7683.1	AO070325000076	FG09968.1	ANAO		yes	((FG09968.1:100.0,(57.m05461:100.0,(AN7683.1:100.0,AO07032500:100.0):84.0):100.0):100.0,
1624	69.m15459	AN5492.1	AO070341000393	FG10205.1	ANAO		yes	((FG10205.1:100.0,(69.m15459:100.0,(AN5492.1:100.0,AO07034100:100.0):78.5):100.0):100.0,
1625	54.m06521	AN0260.1	AO070334000098	FG01839.1	AFAO	yes	yes	((FG01839.1:100.0,(AN0260.1:100.0,(54.m06521:100.0,AO07033400:100.0):100.0):100.0):100.0,
1626	69.m14881	AN2190.1	AO070247000014	FG07428.1	AFAN			((FG07428.1:100.0,(AO07024700:100.0,(AN2190.1:100.0,69.m14881:100.0):63.0):100.0):100.0,
1627	53.m03771	AN8203.1	AO070310000114	FG07398.1	ANAO			((FG07398.1:100.0,(53.m03771:100.0,(AN8203.1:100.0,AO07031000:100.0):57.0):100.0):100.0,
1628	65.m07469	AN8291.1	AO070190000007	FG07432.1	AFAO			((FG07432.1:100.0,((65.m07469:100.0,AO07019000:100.0):42.5,AN8291.1:100.0):100.0):100.0,
1629	71.m16086	AN4712.1	AO070329000163	FG07373.1	AFAO	yes	yes	((FG07373.1:100.0,(AN4712.1:100.0,(71.m16086:100.0,AO07032900:100.0):100.0):100.0):100.0,
1630	53.m03759	AN8214.1	AO070310000098	FG07374.1	ANAO			((FG07374.1:100.0,((AO07031000:100.0,AN8214.1:100.0):53.5,53.m03759:100.0):100.0):100.0,
1631	71.m15633	AN8822.1	AO070276000020	FG07372.1	AFAO	yes	yes	((FG07372.1:100.0,((AO07027600:100.0,71.m15633:100.0):93.0,AN8822.1:100.0):100.0):100.0,
1632	57.m05984	AN8899.1	AO070294000091	FG02678.1			yes	(((FG02678.1:100.0,AN8899.1:100.0):89.3,(57.m05984:100.0,AO07029400:100.0):86.3):100.0,
1633	58.m07359	AN1940.1	AO070342000196	FG10046.1	AFAO	yes	yes	((FG10046.1:100.0,(AN1940.1:100.0,(58.m07359:100.0,AO07034200:100.0):100.0):100.0):100.0,
1634	72.m19897	AN5849.1	AO070281000056	FG10057.1	AFAN	yes	yes	((FG10057.1:100.0,(AO07028100:100.0,(AN5849.1:100.0,72.m19897:100.0):99.5):100.0):100.0,
1635	69.m15364	AN5324.1	AO070323000167	FG10051.1	AFAO	yes	yes	((FG10051.1:100.0,((AO07032300:100.0,69.m15364:100.0):93.0,AN5324.1:100.0):100.0):100.0,
1636	72.m19000	AN6169.1	AO070340000031	FG02709.1	AFAO	yes	yes	((FG02709.1:100.0,((AO07034000:100.0,72.m19000:100.0):91.0,AN6169.1:100.0):100.0):100.0,
1637	71.m15261	AN6870.1	AO070314000052	FG02207.1	AFAO	yes	yes	((FG02207.1:100.0,((AO07031400:100.0,71.m15261:100.0):96.0,AN6870.1:100.0):100.0):100.0,
1638	65.m07223	AN7175.1	AO070335000146	FG04216.1	ANAO		yes	((FG04216.1:100.0,(65.m07223:100.0,(AN7175.1:100.0,AO07033500:100.0):89.5):100.0):100.0,
1639	71.m15712	AN4663.1	AO070250000002	FG09525.1	AFAO	yes	yes	((FG09525.1:100.0,((AO07025000:100.0,71.m15712:100.0):98.0,AN4663.1:100.0):100.0):100.0,
1640	70.m14847	AN1376.1	AO070243000006	FG08613.1	AFAO			((FG08613.1:100.0,((70.m14847:100.0,AO07024300:100.0):69.5,AN1376.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1641	57.m05718	AN1900.1	AO070341000154	FG09462.1	ANAO			((FG09462.1:100.0,((AO07034100:100.0,AN1900.1:100.0):39.5,57.m05718:100.0):100.0):100.0,
1642	57.m05716	AN1902.1	AO070341000151	FG09457.1	AFAO			((FG09457.1:100.0,((57.m05716:100.0,AO07034100:100.0):59.0,AN1902.1:100.0):100.0):100.0,
1643	70.m15225	AN1007.1	AO070312000026	FG08402.1	AFAO			((FG08402.1:100.0,((70.m15225:100.0,AO07031200:100.0):49.3,AN1007.1:100.0):100.0):100.0,
1644	54.m06807	AN4245.1	AO070324000167	FG04738.1	AFAO		yes	((FG04738.1:100.0,((AO07032400:100.0,54.m06807:100.0):80.5,AN4245.1:100.0):100.0):100.0,
1645	69.m15068	AN1768.1	AO070324000027	FG08615.1	ANAO			((FG08615.1:100.0,(69.m15068:100.0,(AN1768.1:100.0,AO07032400:100.0):53.0):100.0):100.0,
1646	55.m02927	AN1428.1	AO070242000023	FG08396.1	AFAO			((FG08396.1:100.0,((AO07024200:100.0,55.m02927:100.0):70.8,AN1428.1:100.0):100.0):100.0,
1647	55.m02923	AN1416.1	AO070242000019	FG08395.1	AFAO			((FG08395.1:100.0,((AO07024200:100.0,55.m02923:100.0):70.5,AN1416.1:100.0):100.0):100.0,
1648	55.m02924	AN1418.1	AO070242000020	FG08398.1	ANAO		yes	((FG08398.1:100.0,(55.m02924:100.0,(AN1418.1:100.0,AO07024200:100.0):77.5):100.0):100.0,
1649	65.m07427	AN4255.1	AO070309000125	FG08399.1	AFAO	yes	yes	((FG08399.1:100.0,((AO07030900:100.0,65.m07427:100.0):95.5,AN4255.1:100.0):100.0):100.0,
1650	55.m03038	AN1519.1	AO070334000237	FG08752.1	AFAO	yes	yes	((FG08752.1:100.0,((AO07033400:100.0,55.m03038:100.0):96.5,AN1519.1:100.0):100.0):100.0,
1651	57.m05428	AN7661.1	AO070268000032	FG08403.1	AFAO		yes	((FG08403.1:100.0,((AO07026800:100.0,57.m05428:100.0):89.5,AN7661.1:100.0):100.0):100.0,
1652	57.m05686	AN3797.1	AO070337000231	FG08405.1	AFAO		yes	((FG08405.1:100.0,((AO07033700:100.0,57.m05686:100.0):89.5,AN3797.1:100.0):100.0):100.0,
1653	70.m15033	AN1189.1	AO070331000187	FG09515.1	AFAN	yes	yes	((FG09515.1:100.0,(AO07033100:100.0,(AN1189.1:100.0,70.m15033:100.0):90.0):100.0):100.0,
1654	59.m08864	AN4959.1	AO070288000021	FG09520.1	AFAO	yes	yes	((FG09520.1:100.0,((AO07028800:100.0,59.m08864:100.0):98.0,AN4959.1:100.0):100.0):100.0,
1655	59.m08863	AN4958.1	AO070288000020	FG09519.1	AFAO	yes	yes	((FG09519.1:100.0,(AN4958.1:100.0,(59.m08863:100.0,AO07028800:100.0):100.0):100.0):100.0,
1656	59.m08865	AN4960.1	AO070288000022	FG09517.1	AFAO		yes	((FG09517.1:100.0,((59.m08865:100.0,AO07028800:100.0):86.5,AN4960.1:100.0):100.0):100.0,
1657	59.m08870	AN4967.1	AO070288000032	FG09516.1	AFAO	yes	yes	((FG09516.1:100.0,((AO07028800:100.0,59.m08870:100.0):98.0,AN4967.1:100.0):100.0):100.0,
1658	70.m15050	AN1171.1	AO070331000166	FG09274.1	AFAO			((FG09274.1:100.0,((AO07033100:100.0,70.m15050:100.0):68.0,AN1171.1:100.0):100.0):100.0,
1659	58.m07446	AN3653.1	AO070342000034	FG09509.1	AFAO			((FG09509.1:100.0,((58.m07446:100.0,AO07034200:100.0):59.0,AN3653.1:100.0):100.0):100.0,
1660	70.m14849	AN1374.1	AO070215000001	FG08748.1	AFAO			((FG08748.1:100.0,((AO07021500:100.0,70.m14849:100.0):57.5,AN1374.1:100.0):100.0):100.0,
1661	58.m07445	AN3655.1	AO070342000033	FG09511.1	ANAO	yes	yes	((FG09511.1:100.0,(58.m07445:100.0,(AN3655.1:100.0,AO07034200:100.0):99.0):100.0):100.0,
1662	58.m08000	AN4323.1	AO070230000015	FG09512.1	ANAO			((FG09512.1:100.0,(58.m08000:100.0,(AN4323.1:100.0,AO07023000:100.0):64.5):100.0):100.0,
1663	58.m08001	AN4322.1	AO070230000013	FG09513.1	AFAO	yes	yes	((FG09513.1:100.0,((AO07023000:100.0,58.m08001:100.0):98.0,AN4322.1:100.0):100.0):100.0,
1664	59.m08831	AN4929.1	AO070338000014	FG09507.1	AFAN			((FG09507.1:100.0,(AO07033800:100.0,(AN4929.1:100.0,59.m08831:100.0):41.0):100.0):100.0,
1665	59.m08713	AN2868.1	AO070338000154	FG08476.1	AFAO	yes	yes	((FG08476.1:100.0,((AO07033800:100.0,59.m08713:100.0):99.0,AN2868.1:100.0):100.0):100.0,
1666	59.m08876	AN4973.1	AO070288000039	FG08471.1	AFAO	yes	yes	((FG08471.1:100.0,((AO07028800:100.0,59.m08876:100.0):96.0,AN4973.1:100.0):100.0):100.0,
1667	59.m08868	AN4965.1	AO070288000030	FG08474.1	AFAO			((FG08474.1:100.0,((AO07028800:100.0,59.m08868:100.0):72.0,AN4965.1:100.0):100.0):100.0,
1668	59.m09403	AN4977.1	AO070288000044	FG08425.1	AFAO			((FG08425.1:100.0,((59.m09403:100.0,AO07028800:100.0):63.5,AN4977.1:100.0):100.0):100.0,
1669	59.m08879	AN4976.1	AO070288000043	FG08427.1	AFAO			((FG08427.1:100.0,((AO07028800:100.0,59.m08879:100.0):46.0,AN4976.1:100.0):100.0):100.0,
1670	59.m08878	AN4975.1	AO070288000042	FG08428.1	AFAN			((FG08428.1:100.0,((59.m08878:100.0,AN4975.1:100.0):44.5,AO07028800:100.0):100.0):100.0,
1671	59.m08847	AN4943.1	AO070338000001	FG08430.1	AFAO		yes	((FG08430.1:100.0,((AO07033800:100.0,59.m08847:100.0):76.0,AN4943.1:100.0):100.0):100.0,
1672	69.m15439	AN5520.1	AO070341000371	FG08478.1	ANAO			((FG08478.1:100.0,(69.m15439:100.0,(AN5520.1:100.0,AO07034100:100.0):63.3):100.0):100.0,
1673	54.m06642	AN0450.1	AO070165000001	FG08479.1	AFAO		yes	((FG08479.1:100.0,((AO07016500:100.0,54.m06642:100.0):83.0,AN0450.1:100.0):100.0):100.0,
1674	58.m07562	AN5640.1	AO070301000036	FG08481.1	AFAO			((FG08481.1:100.0,((58.m07562:100.0,AO07030100:100.0):56.5,AN5640.1:100.0):100.0):100.0,
1675	69.m15403	AN3696.1	AO070341000317	FG08485.1	AFAO	yes	yes	((FG08485.1:100.0,((AO07034100:100.0,69.m15403:100.0):93.0,AN3696.1:100.0):100.0):100.0,
1676	58.m08920	AN5627.1	AO070301000027	FG08487.1	AFAO	yes	yes	((FG08487.1:100.0,((AO07030100:100.0,58.m08920:100.0):94.0,AN5627.1:100.0):100.0):100.0,
1677	69.m15143	AN7525.1	AO070258000031	FG08382.1	AFAO			((FG08382.1:100.0,((AO07025800:100.0,69.m15143:100.0):66.5,AN7525.1:100.0):100.0):100.0,
1678	57.m05780	AN2081.1	AO070341000234	FG08604.1	AFAO			((FG08604.1:100.0,((AO07034100:100.0,57.m05780:100.0):58.5,AN2081.1:100.0):100.0):100.0,
1679	57.m05779	AN2080.1	AO070341000233	FG08603.1	AFAO			((FG08603.1:100.0,((AO07034100:100.0,57.m05779:100.0):37.0,AN2080.1:100.0):100.0):100.0,
1680	58.m07559	AN5646.1	AO070301000034	FG09503.1	AFAO	yes	yes	((FG09503.1:100.0,((AO07030100:100.0,58.m07559:100.0):95.0,AN5646.1:100.0):100.0):100.0,
1681	58.m07528	AN5604.1	AO070301000002	FG09280.1	AFAN			((FG09280.1:100.0,(AO07030100:100.0,(AN5604.1:100.0,58.m07528:100.0):58.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1682	54.m06592	AN3999.1	AO070328000163	FG08422.1	ANAO		yes	((FG08422.1:100.0,(54.m06592:100.0,(AN3999.1:100.0,AO07032800:100.0):84.0):100.0):100.0,
1683	69.m14938	AN1921.1	AO070341000116	FG09281.1	ANAO			((FG09281.1:100.0,(69.m14938:100.0,(AN1921.1:100.0,AO07034100:100.0):61.0):100.0):100.0,
1684	71.m15608	AN8801.1	AO070276000060	FG08435.1	AFAN			((FG08435.1:100.0,(AO07027600:100.0,(AN8801.1:100.0,71.m15608:100.0):45.5):100.0):100.0,
1685	72.m19980	AN6247.1	AO070304000102	FG08420.1	AFAO			((FG08420.1:100.0,((AO07030400:100.0,72.m19980:100.0):69.0,AN6247.1:100.0):100.0):100.0,
1686	69.m14939	AN5549.1	AO070341000115	FG04957.1	AFAO	yes	yes	(((AN5549.1:100.0,(69.m14939:100.0,AO07034100:100.0):96.0):99.0,FG04957.1:100.0):100.0,
1687	57.m05742	AN1876.1	AO070341000183	FG09484.1	AFAN			((FG09484.1:100.0,(AO07034100:100.0,(AN1876.1:100.0,57.m05742:100.0):64.5):100.0):100.0,
1688	69.m14956	AN4174.1	AO070341000088	FG09482.1	AFAO		yes	((FG09482.1:100.0,((AO07034100:100.0,69.m14956:100.0):89.8,AN4174.1:100.0):100.0):100.0,
1689	69.m14931	AN1915.1	AO070341000128	FG08760.1	AFAO			((FG08760.1:100.0,((AO07034100:100.0,69.m14931:100.0):50.5,AN1915.1:100.0):100.0):100.0,
1690	69.m14942	AN1924.1	AO070341000109	FG08393.1	AFAO			((FG08393.1:100.0,((AO07034100:100.0,69.m14942:100.0):52.0,AN1924.1:100.0):100.0):100.0,
1691	69.m15086	AN9008.1	AO070336000118	FG08608.1	ANAO	yes	yes	((FG08608.1:100.0,((AN9008.1:100.0,AO07033600:100.0):100.0,69.m15086:100.0):100.0):100.0,
1692	70.m14909	AN1299.1	AO070303000060	FG08489.1	ANAO	yes	yes	((FG08489.1:100.0,((AN1299.1:100.0,AO07030300:100.0):100.0,70.m14909:100.0):100.0):100.0,
1693	57.m05774	AN2073.1	AO070341000227	FG08490.1	AFAO	yes	yes	((FG08490.1:100.0,(AN2073.1:100.0,(57.m05774:100.0,AO07034100:100.0):100.0):100.0):100.0,
1694	57.m05775	AN2076.1	AO070341000228	FG08491.1	AFAO			((FG08491.1:100.0,((AO07034100:100.0,57.m05775:100.0):60.5,AN2076.1:100.0):100.0):100.0,
1695	62.m03487	AN8687.1	AO070315000106	FG02462.1	AFAO			((FG02462.1:100.0,((AO07031500:100.0,62.m03487:100.0):70.5,AN8687.1:100.0):100.0):100.0,
1696	55.m03084	AN1563.1	AO070339000290	FG02203.1	AFAN			((FG02203.1:100.0,((55.m03084:100.0,AN1563.1:100.0):60.5,AO07033900:100.0):100.0):100.0,
1697	55.m03163	AN6093.1	AO070340000162	FG11049.1	ANAO		yes	(((55.m03163:100.0,(AN6093.1:100.0,AO07034000:100.0):86.5):78.0,FG11049.1:100.0):100.0,
1698	54.m06297	AN8019.1	AO070236000022	FG03980.1		yes	yes	((AO07023600:100.0,((AN8019.1:100.0,54.m06297:100.0):100.0,FG03980.1:100.0):100.0):100.0,
1699	59.m08519	AN3146.1	AO070256000046	FG02460.1	AFAO	yes	yes	((FG02460.1:100.0,((AO07025600:100.0,59.m08519:100.0):95.0,AN3146.1:100.0):100.0):100.0,
1700	65.m07257	AN6717.1	AO070339000157	FG02461.1	AFAO		yes	((FG02461.1:100.0,((AO07033900:100.0,65.m07257:100.0):79.8,AN6717.1:100.0):100.0):100.0,
1701	69.m14871	AN8100.1	AO070281000022	FG01995.1	ANAO			((((AO07028100:100.0,AN8100.1:100.0):99.0,69.m14871:100.0):69.0,FG01995.1:100.0):100.0,
1702	69.m15741	AN3511.1	AO070263000017	FG07314.1	ANAO			((FG07314.1:100.0,(69.m15741:100.0,(AN3511.1:100.0,AO07026300:100.0):74.0):100.0):100.0,
1703	55.m03089	AN2404.1	AO070339000289	FG04609.1		yes	yes	(((AO07033900:100.0,55.m03089:100.0):100.0,(FG04609.1:100.0,AN2404.1:100.0):99.0):100.0,
1704	58.m07489	AN5563.1	AO070328000044	FG07908.1	AFAN			((FG07908.1:100.0,(AO07032800:100.0,(AN5563.1:100.0,58.m07489:100.0):72.8):100.0):100.0,
1705	58.m07490	AN5564.1	AO070328000043	FG07907.1	AFAO	yes	yes	((FG07907.1:100.0,((AO07032800:100.0,58.m07490:100.0):94.0,AN5564.1:100.0):100.0):100.0,
1706	67.m02958	AN3421.1	AO070323000200	FG08465.1				((((AO07032300:100.0,AN3421.1:100.0):100.0,FG08465.1:100.0):64.0,67.m02958:100.0):100.0,
1707	69.m15337	AN5552.1	AO070335000011	FG00202.1	AFAN		yes	((FG00202.1:100.0,(AO07033500:100.0,(AN5552.1:100.0,69.m15337:100.0):86.5):100.0):100.0,
1708	69.m15119	AN7527.1	AO070343000364	FG08125.1	AFAO			((FG08125.1:100.0,((69.m15119:100.0,AO07034300:100.0):70.0,AN7527.1:100.0):99.0):100.0,
1709	72.m19549	AN1797.1	AO070309000134	FG02641.1	ANAO			((FG02641.1:100.0,(72.m19549:100.0,(AN1797.1:100.0,AO07030900:100.0):57.5):100.0):100.0,
1710	59.m08854	AN4949.1	AO070288000001	FG04050.1	AFAO		yes	((FG04050.1:100.0,((AO07028800:100.0,59.m08854:100.0):79.0,AN4949.1:100.0):100.0):100.0,
1711	59.m08836	AN4932.1	AO070338000011	FG04051.1	ANAO		yes	((FG04051.1:100.0,(59.m08836:100.0,(AN4932.1:100.0,AO07033800:100.0):84.0):100.0):100.0,
1712	66.m04679	AN6452.1	AO070337000057	FG03427.1	AFAO	yes	yes	((FG03427.1:100.0,((AO07033700:100.0,66.m04679:100.0):99.0,AN6452.1:100.0):100.0):100.0,
1713	69.m15499	AN7401.1	AO070333000099	FG06445.1	ANAO			((FG06445.1:100.0,(69.m15499:100.0,(AN7401.1:100.0,AO07033300:100.0):48.5):100.0):100.0,
1714	52.m03876	AN2064.1	AO070323000172	FG10617.1	AFAO		yes	((FG10617.1:100.0,((AO07032300:100.0,52.m03876:100.0):78.5,AN2064.1:100.0):100.0):100.0,
1715	59.m09478	AN3447.1	AO070265000023	FG07864.1	AFAO			((FG07864.1:100.0,((AO07026500:100.0,59.m09478:100.0):64.0,AN3447.1:100.0):100.0):100.0,
1716	71.m15445	AN0172.1	AO070321000073	FG04299.1	AFAO	yes	yes	((FG04299.1:100.0,((AO07032100:100.0,71.m15445:100.0):96.0,AN0172.1:100.0):100.0):100.0,
1717	69.m15427	AN5528.1	AO070341000360	FG10911.1	AFAO	yes	yes	((FG10911.1:100.0,((AO07034100:100.0,69.m15427:100.0):99.5,AN5528.1:100.0):100.0):100.0,
1718	59.m09302	AN3440.1	AO070265000015	FG08084.1	ANAO		yes	((FG08084.1:100.0,(59.m09302:100.0,(AN3440.1:100.0,AO07026500:100.0):84.5):100.0):100.0,
1719	58.m07687	AN1628.1	AO070299000099	FG04919.1	ANAO		yes	((FG04919.1:100.0,(58.m07687:100.0,(AN1628.1:100.0,AO07029900:100.0):75.0):100.0):100.0,
1720	54.m07032	AN4248.1	AO070324000164	FG07933.1	ANAO			((FG07933.1:100.0,(54.m07032:100.0,(AN4248.1:100.0,AO07032400:100.0):50.5):100.0):100.0,
1721	66.m04615	AN3418.1	AO070203000002	FG08253.1	AFAO		yes	(((AN3418.1:100.0,(66.m04615:100.0,AO07020300:100.0):92.0):76.5,FG08253.1:100.0):100.0,
1722	72.m19553	AN9383.1	AO070336000233	FG02866.1	AFAN			((((AN9383.1:100.0,72.m19553:100.0):48.3,AO07033600:100.0):95.5,FG02866.1:100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1723	59.m08907	AN5003.1	AO070255000039	FG07928.1	AFAO		yes	((FG07928.1:100.0,((AO07025500:100.0,59.m08907:100.0):86.0,AN5003.1:100.0):100.0):100.0,
1724	58.m07307	AN7962.1	AO070336000161	FG08289.1	AFAO	yes	yes	((FG08289.1:100.0,((AO07033600:100.0,58.m07307:100.0):98.0,AN7962.1:100.0):100.0):100.0,
1725	59.m09322	AN3461.1	AO070265000039	FG07875.1	AFAN			((FG07875.1:100.0,((59.m09322:100.0,AN3461.1:100.0):74.5,AO07026500:100.0):100.0):100.0,
1726	59.m09325	AN3464.1	AO070265000042	FG07872.1	AFAO			((FG07872.1:100.0,((59.m09325:100.0,AO07026500:100.0):60.0,AN3464.1:100.0):100.0):100.0,
1727	54.m06685	AN2746.1	AO070338000225	FG08229.1	AFAO		yes	((FG08229.1:100.0,((AO07033800:100.0,54.m06685:100.0):82.0,AN2746.1:100.0):100.0):100.0,
1728	71.m15330	AN0052.1	AO070314000137	FG03318.1	AFAO			((FG03318.1:100.0,((AO07031400:100.0,71.m15330:100.0):61.0,AN0052.1:100.0):100.0):100.0,
1729	57.m05656	AN3824.1	AO070311000023	FG01104.1	AFAO	yes	yes	((FG01104.1:100.0,(AN3824.1:100.0,(57.m05656:100.0,AO07031100:100.0):100.0):100.0):100.0,
1730	66.m04780	AN9119.1	AO070332000153	FG02662.1	ANAO		yes	((FG02662.1:100.0,(66.m04780:100.0,(AN9119.1:100.0,AO07033200:100.0):84.0):100.0):100.0,
1731	59.m09089	AN2953.1	AO070337000200	FG09885.1	AFAN			((FG09885.1:100.0,(AO07033700:100.0,(AN2953.1:100.0,59.m09089:100.0):71.0):100.0):100.0,
1732	59.m08816	AN4913.1	AO070338000034	FG06553.1	AFAO	yes	yes	((FG06553.1:100.0,((AO07033800:100.0,59.m08816:100.0):91.0,AN4913.1:100.0):100.0):100.0,
1733	72.m19885	AN5918.1	AO070340000367	FG05695.1				(((AO07034000:100.0,AN5918.1:100.0):100.0,(72.m19885:100.0,FG05695.1:100.0):65.0):100.0,
1734	57.m05460	AN7418.1	AO070323000154	FG09110.1	ANAO	yes	yes	((FG09110.1:100.0,(57.m05460:100.0,(AO07032300:100.0,AN7418.1:100.0):95.5):99.5):100.0,
1735	71.m15484	AN0228.1	AO070323000081	FG02470.1	AFAO			((FG02470.1:100.0,((71.m15484:100.0,AO07032300:100.0):70.0,AN0228.1:100.0):100.0):100.0,
1736	72.m19754	AN7310.1	AO070297000058	FG04259.1	AFAO			((FG04259.1:100.0,((AO07029700:100.0,72.m19754:100.0):48.5,AN7310.1:100.0):100.0):100.0,
1737	58.m09008	AN4328.1	AO070240000006	FG03985.1	AFAO			((FG03985.1:100.0,((AO07024000:100.0,58.m09008:100.0):71.0,AN4328.1:100.0):100.0):100.0,
1738	69.m15503	AN5436.1	AO070333000093	FG05095.1	ANAO		yes	((FG05095.1:100.0,(69.m15503:100.0,(AN5436.1:100.0,AO07033300:100.0):83.5):100.0):100.0,
1739	70.m15780	AN1022.1	AO070343000592	FG05070.1	AFAO	yes	yes	((FG05070.1:100.0,((AO07034300:100.0,70.m15780:100.0):92.0,AN1022.1:100.0):100.0):100.0,
1740	70.m15237	AN1019.1	AO070343000596	FG09616.1	AFAO	yes	yes	((FG09616.1:100.0,(AN1019.1:100.0,(70.m15237:100.0,AO07034300:100.0):100.0):100.0):100.0,
1741	70.m15234	AN1016.1	AO070312000002	FG09614.1	AFAN			((FG09614.1:100.0,(AO07031200:100.0,(AN1016.1:100.0,70.m15234:100.0):48.0):100.0):100.0,
1742	71.m15579	AN2341.1	AO070319000152	FG04851.1	AFAO			((FG04851.1:100.0,(AN2341.1:100.0,(71.m15579:100.0,AO07031900:100.0):58.5):95.5):100.0,
1743	72.m19752	AN7311.1	AO070297000059	FG04266.1	ANAO	yes	yes	((FG04266.1:100.0,(72.m19752:100.0,(AN7311.1:100.0,AO07029700:100.0):90.5):100.0):100.0,
1744	57.m05851	AN7493.1	AO070287000024	FG04252.1	ANAO			((FG04252.1:100.0,(57.m05851:100.0,(AN7493.1:100.0,AO07028700:100.0):58.3):100.0):100.0,
1745	57.m05844	AN7497.1	AO070287000017	FG02474.1	ANAO			((FG02474.1:100.0,(57.m05844:100.0,(AN7497.1:100.0,AO07028700:100.0):57.5):100.0):100.0,
1746	57.m05838	AN7501.1	AO070287000012	FG02475.1	ANAO			((FG02475.1:100.0,(57.m05838:100.0,(AN7501.1:100.0,AO07028700:100.0):72.5):100.0):100.0,
1747	57.m05837	AN7502.1	AO070287000010	FG02476.1	ANAO			((FG02476.1:100.0,((AO07028700:100.0,AN7502.1:100.0):55.8,57.m05837:100.0):100.0):100.0,
1748	57.m05839	AN7500.1	AO070287000013	FG02477.1	AFAO			((FG02477.1:100.0,((57.m05839:100.0,AO07028700:100.0):67.5,AN7500.1:100.0):100.0):100.0,
1749	69.m15286	AN0561.1	AO070272000038	FG09732.1	AFAO	yes	yes	((FG09732.1:100.0,((AO07027200:100.0,69.m15286:100.0):98.5,AN0561.1:100.0):100.0):100.0,
1750	71.m15500	AN4731.1	AO070323000053	FG09733.1	AFAN			((FG09733.1:100.0,(AO07032300:100.0,(AN4731.1:100.0,71.m15500:100.0):55.5):100.0):100.0,
1751	71.m15501	AN4732.1	AO070323000052	FG09734.1	AFAO	yes	yes	((FG09734.1:100.0,((AO07032300:100.0,71.m15501:100.0):93.5,AN4732.1:100.0):100.0):100.0,
1752	72.m19166	AN5950.1	AO070340000303	FG09735.1	AFAO	yes	yes	((FG09735.1:100.0,(AN5950.1:100.0,(72.m19166:100.0,AO07034000:100.0):100.0):100.0):100.0,
1753	57.m05849	AN7494.1	AO070287000022	FG02478.1	AFAN			((FG02478.1:100.0,(AO07028700:100.0,(AN7494.1:100.0,57.m05849:100.0):55.8):100.0):100.0,
1754	57.m05572	AN4560.1	AO070321000168	FG06724.1	ANAO			((FG06724.1:100.0,((AO07032100:100.0,AN4560.1:100.0):70.0,57.m05572:100.0):100.0):100.0,
1755	72.m19646	AN7601.1	AO070343000271	FG02481.1	AFAO	yes	yes	((FG02481.1:100.0,((AO07034300:100.0,72.m19646:100.0):94.0,AN7601.1:100.0):100.0):100.0,
1756	72.m19648	AN7600.1	AO070343000270	FG02482.1	AFAO		yes	((FG02482.1:100.0,((AO07034300:100.0,72.m19648:100.0):82.0,AN7600.1:100.0):100.0):100.0,
1757	65.m07235	AN6733.1	AO070339000179	FG09770.1	AFAO			((FG09770.1:100.0,((AO07033900:100.0,65.m07235:100.0):64.0,AN6733.1:100.0):100.0):100.0,
1758	72.m19759	AN7306.1	AO070297000054	FG09756.1	ANAO			((FG09756.1:100.0,(72.m19759:100.0,(AN7306.1:100.0,AO07029700:100.0):69.0):100.0):100.0,
1759	72.m19976	AN6222.1	AO070304000059	FG06157.1	AFAO	yes	yes	((FG06157.1:100.0,(AN6222.1:100.0,(72.m19976:100.0,AO07030400:100.0):100.0):100.0):100.0,
1760	57.m05843	AN7498.1	AO070287000016	FG09773.1	AFAO			((FG09773.1:100.0,((AO07028700:100.0,57.m05843:100.0):62.5,AN7498.1:100.0):100.0):100.0,
1761	65.m07264	AN6711.1	AO070339000151	FG04261.1	ANAO			((FG04261.1:100.0,((AO07033900:100.0,AN6711.1:100.0):64.5,65.m07264:100.0):100.0):100.0,
1762	65.m07239	AN6731.1	AO070339000175	FG06184.1	AFAO			((FG06184.1:100.0,((65.m07239:100.0,AO07033900:100.0):63.0,AN6731.1:100.0):100.0):100.0,
1763	72.m19291	AN6193.1	AO070308000106	FG06183.1	ANAO		yes	((FG06183.1:100.0,(72.m19291:100.0,(AN6193.1:100.0,AO07030800:100.0):79.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1764	72.m19443	AN6325.1	AO070304000043	FG06179.1	ANAO		yes	((FG06179.1:100.0,(72.m19443:100.0,(AN6325.1:100.0,AO07030400:100.0):85.0):100.0):100.0,
1765	72.m19445	AN6326.1	AO070304000041	FG06181.1	AFAO	yes	yes	((FG06181.1:100.0,((AO07030400:100.0,72.m19445:100.0):90.0,AN6326.1:100.0):100.0):100.0,
1766	65.m07491	AN6695.1	AO070339000125	FG01948.1	ANAO			((FG01948.1:100.0,((AO07033900:100.0,AN6695.1:100.0):46.5,65.m07491:100.0):100.0):100.0,
1767	70.m15203	AN1047.1	AO070313000109	FG01950.1	AFAN	yes	yes	((FG01950.1:100.0,(AO07031300:100.0,(AN1047.1:100.0,70.m15203:100.0):90.0):100.0):100.0,
1768	54.m06576	AN4036.1	AO070328000140	FG01953.1	AFAO			((FG01953.1:100.0,((AO07032800:100.0,54.m06576:100.0):54.0,AN4036.1:100.0):100.0):100.0,
1769	54.m06948	AN4014.1	AO070328000150	FG01954.1	AFAO		yes	((FG01954.1:100.0,((AO07032800:100.0,54.m06948:100.0):89.5,AN4014.1:100.0):100.0):100.0,
1770	54.m06578	AN4016.1	AO070328000142	FG01956.1	ANAO			((FG01956.1:100.0,(54.m06578:100.0,(AN4016.1:100.0,AO07032800:100.0):47.3):100.0):100.0,
1771	54.m06577	AN4017.1	AO070328000141	FG01957.1	AFAO	yes	yes	((FG01957.1:100.0,((AO07032800:100.0,54.m06577:100.0):92.0,AN4017.1:100.0):100.0):100.0,
1772	54.m06570	AN4042.1	AO070328000135	FG01959.1	AFAO			((FG01959.1:100.0,((54.m06570:100.0,AO07032800:100.0):48.5,AN4042.1:100.0):100.0):100.0,
1773	70.m15209	AN1026.1	AO070312000119	FG09794.1	AFAO		yes	((FG09794.1:100.0,((AO07031200:100.0,70.m15209:100.0):81.5,AN1026.1:100.0):100.0):100.0,
1774	70.m15223	AN1005.1	AO070312000029	FG09793.1	AFAO			((FG09793.1:100.0,((70.m15223:100.0,AO07031200:100.0):49.5,AN1005.1:100.0):100.0):100.0,
1775	72.m19235	AN5895.1	AO070245000008	FG06166.1	AFAO			((FG06166.1:100.0,((72.m19235:100.0,AO07024500:100.0):59.0,AN5895.1:100.0):100.0):100.0,
1776	72.m19269	AN5865.1	AO070308000129	FG06165.1	AFAO			((FG06165.1:100.0,((72.m19269:100.0,AO07030800:100.0):44.8,AN5865.1:100.0):100.0):100.0,
1777	72.m19247	AN5884.1	AO070245000024	FG06164.1	AFAO			((FG06164.1:100.0,((AO07024500:100.0,72.m19247:100.0):55.3,AN5884.1:100.0):100.0):100.0,
1778	65.m07476	AN6741.1	AO070339000188	FG06162.1	AFAO	yes	yes	((FG06162.1:100.0,((AO07033900:100.0,65.m07476:100.0):98.0,AN6741.1:100.0):100.0):100.0,
1779	72.m19263	AN5871.1	AO070308000137	FG06161.1	AFAO		yes	((FG06161.1:100.0,((AO07030800:100.0,72.m19263:100.0):89.5,AN5871.1:100.0):100.0):100.0,
1780	72.m19262	AN5872.1	AO070308000138	FG06159.1	ANAO			((FG06159.1:100.0,((AO07030800:100.0,AN5872.1:100.0):68.0,72.m19262:100.0):100.0):100.0,
1781	72.m19261	AN5873.1	AO070308000139	FG06158.1	ANAO			((FG06158.1:100.0,((AO07030800:100.0,AN5873.1:100.0):59.8,72.m19261:100.0):100.0):100.0,
1782	70.m15224	AN1006.1	AO070312000028	FG01947.1	AFAO	yes	yes	((((AO07031200:100.0,70.m15224:100.0):100.0,AN1006.1:100.0):98.0,FG01947.1:100.0):100.0,
1783	72.m19187	AN5971.1	AO070340000329	FG01941.1	AFAN			((FG01941.1:100.0,(AO07034000:100.0,(AN5971.1:100.0,72.m19187:100.0):50.0):100.0):100.0,
1784	70.m15493	AN0889.1	AO070320000058	FG09745.1	AFAO			((FG09745.1:100.0,((AO07032000:100.0,70.m15493:100.0):68.0,AN0889.1:100.0):100.0):100.0,
1785	71.m15475	AN0212.1	AO070321000032	FG05308.1	AFAO	yes	yes	((FG05308.1:100.0,((AO07032100:100.0,71.m15475:100.0):96.0,AN0212.1:100.0):100.0):100.0,
1786	70.m15349	AN0751.1	AO070343000448	FG09749.1	AFAO	yes	yes	((FG09749.1:100.0,((AO07034300:100.0,70.m15349:100.0):94.5,AN0751.1:100.0):100.0):100.0,
1787	54.m07017	AN4048.1	AO070328000128	FG05311.1	AFAO	yes	yes	((FG05311.1:100.0,(AN4048.1:100.0,(54.m07017:100.0,AO07032800:100.0):100.0):100.0):100.0,
1788	72.m19430	AN6224.1	AO070304000073	FG05313.1	AFAO			((FG05313.1:100.0,((AO07030400:100.0,72.m19430:100.0):44.8,AN6224.1:100.0):100.0):100.0,
1789	53.m03908	AN8038.1	AO070330000008	FG01629.1	AFAO			((FG01629.1:100.0,((53.m03908:100.0,AO07033000:100.0):47.0,AN8038.1:100.0):100.0):100.0,
1790	53.m03907	AN8039.1	AO070330000007	FG01627.1	ANAO			((FG01627.1:100.0,((AO07033000:100.0,AN8039.1:100.0):61.0,53.m03907:100.0):100.0):100.0,
1791	54.m06864	AN5154.1	AO070291000014	FG01632.1	AFAO	yes	yes	((FG01632.1:100.0,(AN5154.1:100.0,(54.m06864:100.0,AO07029100:100.0):100.0):100.0):100.0,
1792	71.m15846	AN2219.1	AO070326000185	FG10532.1	ANAO		yes	((FG10532.1:100.0,((AO07032600:100.0,AN2219.1:100.0):82.5,71.m15846:100.0):96.5):100.0,
1793	58.m09005	AN4365.1	AO070261000008	FG01614.1	AFAO	yes	yes	((FG01614.1:100.0,((AO07026100:100.0,58.m09005:100.0):93.5,AN4365.1:100.0):100.0):100.0,
1794	58.m07963	AN4364.1	AO070261000007	FG01613.1	AFAO	yes	yes	((FG01613.1:100.0,(AN4364.1:100.0,(58.m07963:100.0,AO07026100:100.0):100.0):100.0):100.0,
1795	69.m15484	AN7367.1	AO070239000027	FG01698.1	AFAO			((FG01698.1:100.0,((69.m15484:100.0,AO07023900:100.0):64.0,AN7367.1:100.0):100.0):100.0,
1796	70.m15456	AN0870.1	AO070320000023	FG01591.1	ANAO			((FG01591.1:100.0,(70.m15456:100.0,(AN0870.1:100.0,AO07032000:100.0):61.3):100.0):100.0,
1797	71.m16053	AN0128.1	AO070311000082	FG04298.1	AFAO	yes	yes	((FG04298.1:100.0,(AN0128.1:100.0,(71.m16053:100.0,AO07031100:100.0):100.0):100.0):100.0,
1798	70.m14906	AN1325.1	AO070303000088	FG00643.1	AFAO	yes	yes	((FG00643.1:100.0,((AO07030300:100.0,70.m14906:100.0):99.5,AN1325.1:100.0):100.0):100.0,
1799	72.m19355	AN1150.1	AO070308000028	FG01573.1	AFAO	yes	yes	((FG01573.1:100.0,((AO07030800:100.0,72.m19355:100.0):91.5,AN1150.1:100.0):100.0):100.0,
1800	59.m08921	AN3075.1	AO070224000009	FG10812.1	AFAO		yes	((FG10812.1:100.0,((AO07022400:100.0,59.m08921:100.0):78.0,AN3075.1:100.0):100.0):100.0,
1801	53.m03928	AN8075.1	AO070330000033	FG00323.1	AFAN			((FG00323.1:100.0,(AO07033000:100.0,(AN8075.1:100.0,53.m03928:100.0):52.5):100.0):100.0,
1802	54.m06850	AN5731.1	AO070341000029	FG01643.1	AFAO		yes	((FG01643.1:100.0,((AO07034100:100.0,54.m06850:100.0):82.5,AN5731.1:100.0):100.0):100.0,
1803	54.m06851	AN5732.1	AO070341000028	FG01642.1	AFAO			((FG01642.1:100.0,((AO07034100:100.0,54.m06851:100.0):57.0,AN5732.1:100.0):100.0):100.0,
1804	69.m15676	AN2461.1	AO070264000008	FG01612.1	AFAO			((FG01612.1:100.0,((69.m15676:100.0,AO07026400:100.0):62.0,AN2461.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1805	58.m07493	AN5569.1	AO070328000037	FG04308.1	ANAO			((FG04308.1:100.0,(58.m07493:100.0,(AN5569.1:100.0,AO07032800:100.0):50.5):100.0):100.0,
1806	58.m07497	AN5571.1	AO070328000034	FG04309.1	AFAO	yes	yes	((FG04309.1:100.0,((AO07032800:100.0,58.m07497:100.0):98.0,AN5571.1:100.0):100.0):100.0,
1807	70.m14836	AN1385.1	AO070243000019	FG04304.1	AFAO		yes	((FG04304.1:100.0,((AO07024300:100.0,70.m14836:100.0):75.0,AN1385.1:100.0):100.0):100.0,
1808	54.m06406	AN0349.1	AO070318000027	FG04314.1	AFAO		yes	((FG04314.1:100.0,((AO07031800:100.0,54.m06406:100.0):83.0,AN0349.1:100.0):100.0):100.0,
1809	71.m15520	AN2314.1	AO070323000036	FG04313.1	ANAO			((FG04313.1:100.0,((AO07032300:100.0,AN2314.1:100.0):54.0,71.m15520:100.0):100.0):100.0,
1810	71.m15519	AN2315.1	AO070323000037	FG04312.1	AFAN			((FG04312.1:100.0,(AO07032300:100.0,(AN2315.1:100.0,71.m15519:100.0):53.8):100.0):100.0,
1811	53.m04123	AN5098.1	AO070310000002	FG04320.1	AFAO			((FG04320.1:100.0,((53.m04123:100.0,AO07031000:100.0):58.5,AN5098.1:100.0):100.0):100.0,
1812	53.m03672	AN4287.1	AO070310000009	FG04319.1	AFAO	yes	yes	((FG04319.1:100.0,((AO07031000:100.0,53.m03672:100.0):99.0,AN4287.1:100.0):100.0):100.0,
1813	70.m14826	AN1396.1	AO070233000012	FG03249.1	AFAO	yes	yes	((FG03249.1:100.0,(AN1396.1:100.0,(70.m14826:100.0,AO07023300:100.0):100.0):100.0):100.0,
1814	71.m15518	AN2316.1	AO070323000038	FG04315.1	AFAO	yes	yes	((FG04315.1:100.0,((AO07032300:100.0,71.m15518:100.0):93.0,AN2316.1:100.0):100.0):100.0,
1815	72.m19138	AN6004.1	AO070340000274	FG08365.1	AFAO	yes	yes	((FG08365.1:100.0,((AO07034000:100.0,72.m19138:100.0):98.5,AN6004.1:100.0):100.0):100.0,
1816	71.m15574	AN9370.1	AO070333000225	FG03772.1	AFAO			((((71.m15574:100.0,AO07033300:100.0):36.5,AN9370.1:100.0):40.0,FG03772.1:100.0):100.0,
1817	70.m14845	AN1378.1	AO070243000008	FG08359.1	ANAO			((FG08359.1:100.0,((AO07024300:100.0,AN1378.1:100.0):58.5,70.m14845:100.0):100.0):100.0,
1818	57.m05721	AN1897.1	AO070341000158	FG06450.1	ANAO			((FG06450.1:100.0,(57.m05721:100.0,(AN1897.1:100.0,AO07034100:100.0):49.0):100.0):100.0,
1819	55.m03093	AN2230.1	AO070330000121	FG10229.1	AFAO	yes	yes	((FG10229.1:100.0,(AN2230.1:100.0,(55.m03093:100.0,AO07033000:100.0):100.0):100.0):100.0,
1820	65.m07417	AN5693.1	AO070309000108	FG08333.1	AFAO	yes	yes	((FG08333.1:100.0,(AN5693.1:100.0,(65.m07417:100.0,AO07030900:100.0):100.0):100.0):100.0,
1821	72.m19102	AN6055.1	AO070340000199	FG08329.1	AFAO	yes	yes	((FG08329.1:100.0,((AO07034000:100.0,72.m19102:100.0):95.0,AN6055.1:100.0):100.0):100.0,
1822	71.m15823	AN7641.1	AO070294000037	FG02271.1	AFAO			((FG02271.1:100.0,((71.m15823:100.0,AO07029400:100.0):44.0,AN7641.1:100.0):100.0):100.0,
1823	67.m02927	AN3221.1	AO070330000069	FG11084.1	AFAO			((FG11084.1:100.0,((AO07033000:100.0,67.m02927:100.0):72.5,AN3221.1:100.0):100.0):100.0,
1824	72.m19094	AN6059.1	AO070340000190	FG08327.1	AFAO	yes	yes	((FG08327.1:100.0,((AO07034000:100.0,72.m19094:100.0):98.5,AN6059.1:100.0):100.0):100.0,
1825	57.m05722	AN1896.1	AO070341000159	FG06449.1	AFAO		yes	((FG06449.1:100.0,((AO07034100:100.0,57.m05722:100.0):88.5,AN1896.1:100.0):100.0):100.0,
1826	65.m07424	AN5701.1	AO070309000122	FG08338.1	AFAO			((FG08338.1:100.0,((AO07030900:100.0,65.m07424:100.0):70.5,AN5701.1:100.0):100.0):100.0,
1827	72.m19152	AN5988.1	AO070340000290	FG08325.1	AFAO	yes	yes	((FG08325.1:100.0,(AN5988.1:100.0,(72.m19152:100.0,AO07034000:100.0):100.0):100.0):100.0,
1828	70.m15691	AN7396.1	AO070343000134	FG03387.1	AFAO	yes	yes	((((AO07034300:100.0,70.m15691:100.0):100.0,AN7396.1:100.0):99.0,FG03387.1:100.0):100.0,
1829	72.m19943	AN5983.1	AO070340000297	FG08316.1	AFAO	yes	yes	((FG08316.1:100.0,((AO07034000:100.0,72.m19943:100.0):95.0,AN5983.1:100.0):100.0):100.0,
1830	67.m02928	AN3220.1	AO070330000070	FG10483.1	AFAO			(((AN3220.1:100.0,(AO07033000:100.0,67.m02928:100.0):55.0):84.0,FG10483.1:100.0):100.0,
1831	72.m19474	AN7633.1	AO070181000001	FG06515.1				((((72.m19474:100.0,AO07018100:100.0):98.0,FG06515.1:100.0):54.0,AN7633.1:100.0):100.0,
1832	65.m07419	AN5694.1	AO070309000110	FG08158.1	AFAO		yes	((FG08158.1:100.0,((65.m07419:100.0,AO07030900:100.0):77.5,AN5694.1:100.0):100.0):100.0,
1833	55.m02936	AN1420.1	AO070232000016	FG08128.1	AFAO			((FG08128.1:100.0,((AO07023200:100.0,55.m02936:100.0):69.5,AN1420.1:100.0):100.0):100.0,
1834	70.m15374	AN0771.1	AO070316000073	FG08312.1	AFAO	yes	yes	((FG08312.1:100.0,((AO07031600:100.0,70.m15374:100.0):97.0,AN0771.1:100.0):100.0):100.0,
1835	65.m07418	AN7621.1	AO070309000109	FG08131.1	AFAO	yes	yes	((FG08131.1:100.0,((AO07030900:100.0,65.m07418:100.0):98.0,AN7621.1:100.0):100.0):100.0,
1836	55.m02935	AN1421.1	AO070232000017	FG08388.1	AFAO	yes	yes	((FG08388.1:100.0,((AO07023200:100.0,55.m02935:100.0):92.0,AN1421.1:100.0):100.0):100.0,
1837	65.m07421	AN5697.1	AO070309000115	FG08126.1	AFAO		yes	((FG08126.1:100.0,((AO07030900:100.0,65.m07421:100.0):89.5,AN5697.1:100.0):100.0):100.0,
1838	72.m19942	AN5982.1	AO070340000299	FG08133.1	AFAO			((FG08133.1:100.0,((AO07034000:100.0,72.m19942:100.0):69.0,AN5982.1:100.0):100.0):100.0,
1839	58.m08908	AN5607.1	AO070301000004	FG06417.1	AFAO			((FG06417.1:100.0,((AO07030100:100.0,58.m08908:100.0):58.5,AN5607.1:100.0):100.0):100.0,
1840	57.m05726	AN1892.1	AO070341000163	FG06415.1	AFAO	yes	yes	((((AO07034100:100.0,57.m05726:100.0):96.0,AN1892.1:100.0):96.5,FG06415.1:100.0):100.0,
1841	70.m14921	AN1287.1	AO070303000048	FG09294.1	AFAO	yes	yes	((FG09294.1:100.0,((AO07030300:100.0,70.m14921:100.0):98.0,AN1287.1:100.0):100.0):100.0,
1842	69.m15062	AN1775.1	AO070324000034	FG02191.1	AFAO	yes	yes	((FG02191.1:100.0,(AN1775.1:100.0,(69.m15062:100.0,AO07032400:100.0):100.0):100.0):100.0,
1843	69.m15061	AN1776.1	AO070324000035	FG02192.1	AFAO		yes	((FG02192.1:100.0,((AO07032400:100.0,69.m15061:100.0):85.0,AN1776.1:100.0):100.0):100.0,
1844	56.m02513	AN3295.1	AO070319000059	FG07015.1	ANAO			((((AO07031900:100.0,AN3295.1:100.0):100.0,56.m02513:100.0):60.5,FG07015.1:100.0):100.0,
1845	53.m03968	AN3508.1	AO070296000076	FG02084.1	AFAO			((FG02084.1:100.0,((AO07029600:100.0,53.m03968:100.0):64.0,AN3508.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1846	69.m15160	AN2120.1	AO070332000051	FG02233.1	AFAO	yes	yes	((FG02233.1:100.0,(AN2120.1:100.0,(69.m15160:100.0,AO07033200:100.0):100.0):100.0):100.0,
1847	71.m15362	AN0086.1	AO070311000130	FG02714.1	AFAO	yes	yes	((FG02714.1:100.0,((AO07031100:100.0,71.m15362:100.0):99.0,AN0086.1:100.0):100.0):100.0,
1848	54.m07016	AN4058.1	AO070342000043	FG02717.1	AFAO	yes	yes	((FG02717.1:100.0,((AO07034200:100.0,54.m07016:100.0):99.5,AN4058.1:100.0):100.0):100.0,
1849	57.m05614	AN4515.1	AO070311000076	FG02720.1	AFAO		yes	((FG02720.1:100.0,((57.m05614:100.0,AO07031100:100.0):78.0,AN4515.1:100.0):100.0):100.0,
1850	70.m15652	AN0629.1	AO070318000119	FG05830.1				((((FG05830.1:100.0,AO07031800:100.0):53.5,70.m15652:100.0):52.5,AN0629.1:100.0):100.0,
1851	72.m20026	AN7249.1	AO070297000004	FG02732.1	AFAO			((FG02732.1:100.0,((AO07029700:100.0,72.m20026:100.0):73.0,AN7249.1:100.0):100.0):100.0,
1852	70.m15145	AN1069.1	AO070285000067	FG02729.1	AFAO			((FG02729.1:100.0,((AO07028500:100.0,70.m15145:100.0):49.8,AN1069.1:100.0):100.0):100.0,
1853	70.m15143	AN1089.1	AO070285000061	FG02738.1	AFAO		yes	((FG02738.1:100.0,((AO07028500:100.0,70.m15143:100.0):78.5,AN1089.1:100.0):100.0):100.0,
1854	70.m15136	AN1096.1	AO070285000048	FG02730.1	AFAO	yes	yes	((FG02730.1:100.0,((AO07028500:100.0,70.m15136:100.0):93.5,AN1096.1:100.0):100.0):100.0,
1855	59.m08629	AN3108.1	AO070303000042	FG05279.1	AFAN			((FG05279.1:100.0,(AO07030300:100.0,(AN3108.1:100.0,59.m08629:100.0):65.8):100.0):100.0,
1856	58.m07301	AN3301.1	AO070299000104	FG04426.1	ANAO			((FG04426.1:100.0,(58.m07301:100.0,(AN3301.1:100.0,AO07029900:100.0):56.0):100.0):100.0,
1857	59.m08475	AN2509.1	AO070263000057	FG02657.1	AFAO	yes	yes	((FG02657.1:100.0,((AO07026300:100.0,59.m08475:100.0):95.0,AN2509.1:100.0):100.0):100.0,
1858	58.m07444	AN3656.1	AO070342000032	FG00821.1	AFAO			((FG00821.1:100.0,((58.m07444:100.0,AO07034200:100.0):70.0,AN3656.1:100.0):100.0):100.0,
1859	56.m02393	AN7388.1	AO070293000057	FG02974.1	ANAO			((((AO07029300:100.0,AN7388.1:100.0):63.0,56.m02393:100.0):50.5,FG02974.1:100.0):100.0,
1860	57.m05337	AN7777.1	AO070286000057	FG01382.1	ANAO	yes	yes	((FG01382.1:100.0,((AO07028600:100.0,AN7777.1:100.0):90.0,57.m05337:100.0):99.0):100.0,
1861	56.m02476	AN8990.1	AO070272000025	FG06473.1	ANAO			((FG06473.1:100.0,(56.m02476:100.0,(AN8990.1:100.0,AO07027200:100.0):63.0):100.0):100.0,
1862	57.m05923	AN7422.1	AO070197000001	FG02640.1	AFAO			((FG02640.1:100.0,((AO07019700:100.0,57.m05923:100.0):52.5,AN7422.1:100.0):100.0):100.0,
1863	57.m05921	AN7424.1	AO070197000004	FG02637.1	ANAO			((FG02637.1:100.0,(57.m05921:100.0,(AN7424.1:100.0,AO07019700:100.0):72.0):100.0):100.0,
1864	66.m04545	AN9087.1	AO070332000190	FG02650.1	AFAO	yes	yes	((FG02650.1:100.0,(AN9087.1:100.0,(66.m04545:100.0,AO07033200:100.0):100.0):100.0):100.0,
1865	66.m04759	AN9086.1	AO070332000191	FG02649.1	ANAO			((((AN9086.1:100.0,AO07033200:100.0):44.0,66.m04759:100.0):88.0,FG02649.1:100.0):100.0,
1866	66.m04772	AN9085.1	AO070332000192	FG02648.1	ANAO			((FG02648.1:100.0,((AO07033200:100.0,AN9085.1:100.0):69.5,66.m04772:100.0):100.0):100.0,
1867	72.m18975	AN5839.1	AO070340000003	FG09875.1	AFAO	yes	yes	((FG09875.1:100.0,((AO07034000:100.0,72.m18975:100.0):99.0,AN5839.1:100.0):100.0):100.0,
1868	72.m18976	AN5840.1	AO070340000004	FG09874.1	AFAO	yes	yes	((FG09874.1:100.0,((AO07034000:100.0,72.m18976:100.0):94.5,AN5840.1:100.0):100.0):100.0,
1869	72.m18963	AN5835.1	AO070260000010	FG08350.1	ANAO			((FG08350.1:100.0,(72.m18963:100.0,(AN5835.1:100.0,AO07026000:100.0):74.0):100.0):100.0,
1870	58.m07362	AN4163.1	AO070342000193	FG09870.1	AFAO		yes	((FG09870.1:100.0,((AO07034200:100.0,58.m07362:100.0):83.8,AN4163.1:100.0):100.0):100.0,
1871	59.m08662	AN3085.1	AO070334000123	FG09881.1	AFAO	yes	yes	((FG09881.1:100.0,((AO07033400:100.0,59.m08662:100.0):90.5,AN3085.1:100.0):100.0):100.0,
1872	65.m07404	AN5678.1	AO070309000093	FG00613.1	AFAO		yes	((FG00613.1:100.0,((AO07030900:100.0,65.m07404:100.0):89.5,AN5678.1:100.0):100.0):100.0,
1873	58.m07506	AN5579.1	AO070328000025	FG10530.1	ANAO			((FG10530.1:100.0,(58.m07506:100.0,(AN5579.1:100.0,AO07032800:100.0):71.5):100.0):100.0,
1874	66.m04564	AN9103.1	AO070332000170	FG02433.1	AFAO	yes	yes	((FG02433.1:100.0,((AO07033200:100.0,66.m04564:100.0):94.5,AN9103.1:100.0):100.0):100.0,
1875	71.m15481	AN0012.1	AO070300000077	FG11360.1	AFAO		yes	((FG11360.1:100.0,((AO07030000:100.0,71.m15481:100.0):87.0,AN0012.1:100.0):98.0):100.0,
1876	69.m15589	AN0233.1	AO070283000035	FG05720.1	AFAO	yes	yes	((FG05720.1:100.0,(AN0233.1:100.0,(69.m15589:100.0,AO07028300:100.0):100.0):100.0):100.0,
1877	58.m07572	AN1967.1	AO070301000051	FG10960.1	AFAO			((FG10960.1:100.0,((AO07030100:100.0,58.m07572:100.0):65.0,AN1967.1:100.0):100.0):100.0,
1878	58.m07976	AN4351.1	AO070240000023	FG01703.1	AFAO	yes	yes	((FG01703.1:100.0,(AN4351.1:100.0,(58.m07976:100.0,AO07024000:100.0):100.0):100.0):100.0,
1879	58.m07623	AN2015.1	AO070202000008	FG05770.1	AFAO		yes	((FG05770.1:100.0,((AO07020200:100.0,58.m07623:100.0):89.5,AN2015.1:100.0):100.0):100.0,
1880	71.m15125	AN9166.1	AO070343000045	FG11184.1	AFAN			((((AN9166.1:100.0,71.m15125:100.0):72.0,AO07034300:100.0):52.0,FG11184.1:100.0):100.0,
1881	62.m03412	AN2320.1	AO070269000057	FG03637.1				((((FG03637.1:100.0,AN2320.1:100.0):77.5,AO07026900:100.0):52.5,62.m03412:100.0):100.0,
1882	62.m03411	AN2321.1	AO070283000059	FG03636.1	AFAN			((((62.m03411:100.0,AN2321.1:100.0):47.5,AO07028300:100.0):72.5,FG03636.1:100.0):100.0,
1883	59.m08403	AN2558.1	AO070268000059	FG11568.1	AFAO			((FG11568.1:100.0,((AO07026800:100.0,59.m08403:100.0):62.0,AN2558.1:100.0):100.0):100.0,
1884	59.m08408	AN2562.1	AO070343000339	FG11567.1	AFAN	yes	yes	((((59.m08408:100.0,AN2562.1:100.0):100.0,AO07034300:100.0):97.5,FG11567.1:100.0):100.0,
1885	59.m08405	AN2559.1	AO070268000057	FG11566.1	AFAO	yes	yes	((FG11566.1:100.0,(AN2559.1:100.0,(59.m08405:100.0,AO07026800:100.0):100.0):100.0):100.0,
1886	70.m15707	AN9004.1	AO070330000107	FG11565.1	ANAO			((FG11565.1:100.0,(70.m15707:100.0,(AN9004.1:100.0,AO07033000:100.0):43.7):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1887	59.m08758	AN2907.1	AO070338000098	FG06073.1	ANAO			((FG06073.1:100.0,(59.m08758:100.0,(AN2907.1:100.0,AO07033800:100.0):46.5):100.0):100.0,
1888	59.m08913	AN5010.1	AO070224000002	FG06070.1	AFAO	yes	yes	((FG06070.1:100.0,((AO07022400:100.0,59.m08913:100.0):95.0,AN5010.1:100.0):100.0):100.0,
1889	59.m08914	AN5011.1	AO070224000003	FG06069.1	AFAN			((FG06069.1:100.0,((59.m08914:100.0,AN5011.1:100.0):36.5,AO07022400:100.0):100.0):100.0,
1890	69.m14840	AN5742.1	AO070193000003	FG01593.1	AFAO			((FG01593.1:100.0,((AO07019300:100.0,69.m14840:100.0):67.3,AN5742.1:100.0):100.0):100.0,
1891	72.m19918	AN6177.1	AO070340000022	FG01705.1	AFAO			((FG01705.1:100.0,((AO07034000:100.0,72.m19918:100.0):57.0,AN6177.1:100.0):100.0):100.0,
1892	59.m09271	AN2772.1	AO070327000014	FG06074.1	AFAO	yes	yes	((FG06074.1:100.0,((AO07032700:100.0,59.m09271:100.0):90.0,AN2772.1:100.0):100.0):100.0,
1893	59.m08772	AN4876.1	AO070338000084	FG06075.1	AFAO		yes	((FG06075.1:100.0,((AO07033800:100.0,59.m08772:100.0):89.5,AN4876.1:100.0):100.0):100.0,
1894	58.m07683	AN1818.1	AO070333000196	FG11304.1	AFAO		yes	((FG11304.1:100.0,((AO07033300:100.0,58.m07683:100.0):79.5,AN1818.1:100.0):100.0):100.0,
1895	69.m14927	AN1912.1	AO070341000136	FG05351.1	AFAO	yes	yes	((FG05351.1:100.0,(AN1912.1:100.0,(69.m14927:100.0,AO07034100:100.0):100.0):100.0):100.0,
1896	69.m15442	AN5517.1	AO070341000376	FG02237.1	AFAO		yes	((FG02237.1:100.0,((AO07034100:100.0,69.m15442:100.0):80.0,AN5517.1:100.0):100.0):100.0,
1897	69.m15163	AN2124.1	AO070306000103	FG05366.1	ANAO		yes	((FG05366.1:100.0,((AO07030600:100.0,AN2124.1:100.0):75.5,69.m15163:100.0):100.0):100.0,
1898	69.m15056	AN1757.1	AO070324000038	FG05365.1	AFAO			((FG05365.1:100.0,((AO07032400:100.0,69.m15056:100.0):49.0,AN1757.1:100.0):100.0):100.0,
1899	69.m15060	AN1777.1	AO070324000036	FG05364.1	AFAO	yes	yes	((FG05364.1:100.0,(AN1777.1:100.0,(69.m15060:100.0,AO07032400:100.0):100.0):100.0):100.0,
1900	54.m06433	AN0323.1	AO070334000004	FG04347.1	AFAN			((FG04347.1:100.0,(AO07033400:100.0,(AN0323.1:100.0,54.m06433:100.0):60.0):100.0):100.0,
1901	57.m05368	AN7781.1	AO070343000355	FG03905.1	ANAO		yes	((((AN7781.1:100.0,AO07034300:100.0):86.0,57.m05368:100.0):96.0,FG03905.1:100.0):100.0,
1902	69.m15651	AN1780.1	AO070324000015	FG09309.1	AFAO		yes	((FG09309.1:100.0,((69.m15651:100.0,AO07032400:100.0):88.5,AN1780.1:100.0):100.0):100.0,
1903	69.m15647	AN1779.1	AO070324000017	FG09310.1	AFAO	yes	yes	((FG09310.1:100.0,((AO07032400:100.0,69.m15647:100.0):92.5,AN1779.1:100.0):100.0):100.0,
1904	69.m15081	AN1782.1	AO070324000013	FG09514.1	AFAO	yes	yes	((FG09514.1:100.0,((AO07032400:100.0,69.m15081:100.0):96.5,AN1782.1:100.0):100.0):100.0,
1905	55.m03013	AN1503.1	AO070334000220	FG09521.1	AFAN			((FG09521.1:100.0,(AO07033400:100.0,(AN1503.1:100.0,55.m03013:100.0):54.0):100.0):100.0,
1906	70.m15754	AN1375.1	AO070243000005	FG08612.1	AFAN			((FG08612.1:100.0,(AO07024300:100.0,(AN1375.1:100.0,70.m15754:100.0):60.5):100.0):100.0,
1907	71.m15826	AN2237.1	AO070326000136	FG08454.1	ANAO			((FG08454.1:100.0,((AO07032600:100.0,AN2237.1:100.0):71.5,71.m15826:100.0):100.0):100.0,
1908	58.m07607	AN1999.1	AO070301000093	FG08453.1	AFAO		yes	((FG08453.1:100.0,((AO07030100:100.0,58.m07607:100.0):75.5,AN1999.1:100.0):100.0):100.0,
1909	69.m15456	AN5497.1	AO070341000388	FG08452.1	AFAO	yes	yes	((FG08452.1:100.0,((AO07034100:100.0,69.m15456:100.0):97.0,AN5497.1:100.0):100.0):100.0,
1910	58.m07472	AN3629.1	AO070328000067	FG08451.1	ANAO			((FG08451.1:100.0,(58.m07472:100.0,(AN3629.1:100.0,AO07032800:100.0):72.5):100.0):100.0,
1911	58.m07523	AN5599.1	AO070328000005	FG08766.1	AFAO			((FG08766.1:100.0,((58.m07523:100.0,AO07032800:100.0):61.0,AN5599.1:100.0):100.0):100.0,
1912	58.m07520	AN5596.1	AO070328000008	FG09490.1	ANAO			((FG09490.1:100.0,(58.m07520:100.0,(AN5596.1:100.0,AO07032800:100.0):52.0):100.0):100.0,
1913	59.m09073	AN2944.1	AO070337000189	FG09524.1	ANAO			((FG09524.1:100.0,(59.m09073:100.0,(AN2944.1:100.0,AO07033700:100.0):63.5):100.0):100.0,
1914	58.m08944	AN2000.1	AO070301000095	FG08768.1	ANAO			(((58.m08944:100.0,(AN2000.1:100.0,AO07030100:100.0):93.5):73.5,FG08768.1:100.0):100.0,
1915	58.m07610	AN2002.1	AO070301000101	FG08771.1	AFAN			((FG08771.1:100.0,((58.m07610:100.0,AN2002.1:100.0):64.0,AO07030100:100.0):100.0):100.0,
1916	58.m07511	AN5586.1	AO070328000020	FG08773.1	AFAO	yes	yes	((FG08773.1:100.0,((AO07032800:100.0,58.m07511:100.0):98.5,AN5586.1:100.0):100.0):100.0,
1917	69.m15661	AN3916.1	AO070324000103	FG03247.1	ANAO	yes	yes	((FG03247.1:100.0,(69.m15661:100.0,(AN3916.1:100.0,AO07032400:100.0):90.5):100.0):100.0,
1918	58.m07532	AN9474.1	AO070301000008	FG01809.1	AFAO			((FG01809.1:100.0,((AO07030100:100.0,58.m07532:100.0):61.5,AN9474.1:100.0):100.0):100.0,
1919	66.m04631	AN3365.1	AO070281000028	FG01508.1	ANAO			((FG01508.1:100.0,(66.m04631:100.0,(AN3365.1:100.0,AO07028100:100.0):71.0):100.0):100.0,
1920	69.m14874	AN5177.1	AO070247000008	FG07494.1	AFAO	yes	yes	((FG07494.1:100.0,((AO07024700:100.0,69.m14874:100.0):98.5,AN5177.1:100.0):100.0):100.0,
1921	70.m15101	AN1136.1	AO070331000127	FG05701.1	AFAN			((FG05701.1:100.0,(AO07033100:100.0,(AN1136.1:100.0,70.m15101:100.0):60.8):100.0):100.0,
1922	70.m15102	AN1135.1	AO070331000126	FG05702.1	AFAO			((((AO07033100:100.0,70.m15102:100.0):67.2,AN1135.1:100.0):96.8,FG05702.1:100.0):100.0,
1923	70.m15097	AN1140.1	AO070331000131	FG03879.1	AFAN			((((70.m15097:100.0,AN1140.1:100.0):61.0,AO07033100:100.0):90.0,FG03879.1:100.0):100.0,
1924	70.m15100	AN1137.1	AO070331000128	FG05704.1	AFAO		yes	((FG05704.1:100.0,((AO07033100:100.0,70.m15100:100.0):77.0,AN1137.1:100.0):100.0):100.0,
1925	70.m15099	AN1138.1	AO070331000129	FG00107.1	AFAO		yes	((FG00107.1:100.0,((AO07033100:100.0,70.m15099:100.0):88.0,AN1138.1:100.0):100.0):100.0,
1926	70.m15104	AN1132.1	AO070331000124	FG05709.1	AFAO	yes	yes	((FG05709.1:100.0,((AO07033100:100.0,70.m15104:100.0):92.0,AN1132.1:100.0):100.0):100.0,
1927	58.m07769	AN1694.1	AO070305000018	FG07479.1	AFAO			((FG07479.1:100.0,((AO07030500:100.0,58.m07769:100.0):56.5,AN1694.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1928	55.m03215	AN3973.1	AO070263000041	FG07536.1	AFAO	yes	yes	((FG07536.1:100.0,((AO07026300:100.0,55.m03215:100.0):97.5,AN3973.1:100.0):100.0):100.0,
1929	69.m14892	AN5192.1	AO070237000022	FG07539.1	AFAO	yes	yes	((FG07539.1:100.0,((AO07023700:100.0,69.m14892:100.0):95.0,AN5192.1:100.0):100.0):100.0,
1930	69.m14884	AN5150.1	AO070237000015	FG07540.1	AFAO	yes	yes	((FG07540.1:100.0,(AN5150.1:100.0,(69.m14884:100.0,AO07023700:100.0):100.0):100.0):100.0,
1931	70.m15059	AN1162.1	AO070331000152	FG01008.1	AFAO			((FG01008.1:100.0,((AO07033100:100.0,70.m15059:100.0):47.8,AN1162.1:100.0):100.0):100.0,
1932	58.m07771	AN1695.1	AO070305000019	FG07525.1	AFAO		yes	((FG07525.1:100.0,((AO07030500:100.0,58.m07771:100.0):82.5,AN1695.1:100.0):100.0):100.0,
1933	57.m05706	AN5226.1	AO070337000252	FG09374.1	AFAN			((FG09374.1:100.0,(AO07033700:100.0,(AN5226.1:100.0,57.m05706:100.0):48.5):100.0):100.0,
1934	66.m04623	AN3413.1	AO070281000039	FG01509.1	AFAO			((FG01509.1:100.0,((AO07028100:100.0,66.m04623:100.0):62.2,AN3413.1:100.0):100.0):100.0,
1935	66.m04646	AN3376.1	AO070281000020	FG09381.1	AFAO	yes	yes	((FG09381.1:100.0,((AO07028100:100.0,66.m04646:100.0):94.0,AN3376.1:100.0):100.0):100.0,
1936	66.m04639	AN3371.1	AO070281000010	FG09384.1	ANAO		yes	((FG09384.1:100.0,((AO07028100:100.0,AN3371.1:100.0):83.0,66.m04639:100.0):100.0):100.0,
1937	66.m04638	AN3370.1	AO070281000023	FG09385.1	AFAO		yes	((FG09385.1:100.0,((AO07028100:100.0,66.m04638:100.0):84.0,AN3370.1:100.0):100.0):100.0,
1938	65.m07247	AN6723.1	AO070339000166	FG09061.1	AFAO		yes	(((AN6723.1:100.0,(AO07033900:100.0,65.m07247:100.0):83.5):99.5,FG09061.1:100.0):100.0,
1939	66.m04635	AN3367.1	AO070281000025	FG09386.1	AFAO		yes	((FG09386.1:100.0,((AO07028100:100.0,66.m04635:100.0):76.3,AN3367.1:100.0):100.0):100.0,
1940	70.m15669	AN0403.1	AO070280000032	FG04335.1	AFAO	yes	yes	((((AO07028000:100.0,70.m15669:100.0):100.0,AN0403.1:100.0):99.0,FG04335.1:100.0):100.0,
1941	52.m04099	AN6234.1	AO070302000121	FG04334.1	AFAN			((FG04334.1:100.0,(AO07030200:100.0,(AN6234.1:100.0,52.m04099:100.0):39.0):100.0):100.0,
1942	70.m15670	AN0609.1	AO070280000031	FG04333.1	AFAO	yes	yes	((FG04333.1:100.0,((AO07028000:100.0,70.m15670:100.0):95.0,AN0609.1:100.0):100.0):100.0,
1943	58.m07516	AN5592.1	AO070328000011	FG10511.1	AFAO	yes	yes	((FG10511.1:100.0,(AN5592.1:100.0,(58.m07516:100.0,AO07032800:100.0):100.0):100.0):100.0,
1944	69.m14907	AN5210.1	AO070337000270	FG07528.1	AFAO			((FG07528.1:100.0,((AO07033700:100.0,69.m14907:100.0):74.0,AN5210.1:100.0):100.0):100.0,
1945	59.m08984	AN3034.1	AO070337000075	FG07041.1	AFAN			((FG07041.1:100.0,(AO07033700:100.0,(AN3034.1:100.0,59.m08984:100.0):66.0):100.0):100.0,
1946	59.m08982	AN3035.1	AO070337000077	FG07043.1	ANAO			((FG07043.1:100.0,(59.m08982:100.0,(AN3035.1:100.0,AO07033700:100.0):63.5):100.0):100.0,
1947	54.m06820	AN5705.1	AO070324000154	FG06346.1	AFAO			((FG06346.1:100.0,((AO07032400:100.0,54.m06820:100.0):70.5,AN5705.1:100.0):100.0):100.0,
1948	59.m09408	AN4878.1	AO070338000082	FG06356.1	AFAO			((FG06356.1:100.0,((AO07033800:100.0,59.m09408:100.0):56.0,AN4878.1:100.0):100.0):100.0,
1949	59.m09269	AN2775.1	AO070327000017	FG06353.1	AFAO		yes	((FG06353.1:100.0,((AO07032700:100.0,59.m09269:100.0):87.5,AN2775.1:100.0):100.0):100.0,
1950	59.m08735	AN2888.1	AO070338000126	FG06347.1	AFAN			((FG06347.1:100.0,(AO07033800:100.0,(AN2888.1:100.0,59.m08735:100.0):63.0):100.0):100.0,
1951	54.m06826	AN5711.1	AO070324000151	FG06349.1	ANAO			((FG06349.1:100.0,(54.m06826:100.0,(AN5711.1:100.0,AO07032400:100.0):46.5):100.0):100.0,
1952	69.m15000	AN3928.1	AO070341000038	FG02469.1	AFAN			((FG02469.1:100.0,(AO07034100:100.0,(AN3928.1:100.0,69.m15000:100.0):53.5):100.0):100.0,
1953	59.m09474	AN3434.1	AO070265000007	FG07024.1	AFAO		yes	((FG07024.1:100.0,((AO07026500:100.0,59.m09474:100.0):84.0,AN3434.1:100.0):100.0):100.0,
1954	59.m09453	AN4998.1	AO070255000029	FG00355.1	AFAO		yes	((FG00355.1:100.0,((AO07025500:100.0,59.m09453:100.0):77.5,AN4998.1:100.0):100.0):100.0,
1955	71.m15302	AN8430.1	AO070317000096	FG05828.1	ANAO	yes	yes	((((AN8430.1:100.0,AO07031700:100.0):98.0,71.m15302:100.0):90.0,FG05828.1:100.0):100.0,
1956	57.m05651	AN4481.1	AO070311000027	FG08802.1	AFAO	yes	yes	((FG08802.1:100.0,((AO07031100:100.0,57.m05651:100.0):95.5,AN4481.1:100.0):100.0):100.0,
1957	69.m14876	AN5179.1	AO070247000010	FG07484.1	AFAO	yes	yes	((FG07484.1:100.0,((AO07024700:100.0,69.m14876:100.0):93.5,AN5179.1:100.0):100.0):100.0,
1958	65.m07444	AN4270.1	AO070277000018	FG06945.1	AFAO	yes	yes	((FG06945.1:100.0,((AO07027700:100.0,65.m07444:100.0):98.0,AN4270.1:100.0):100.0):100.0,
1959	71.m15996	AN8858.1	AO070271000015	FG06944.1	AFAO		yes	((FG06944.1:100.0,((AO07027100:100.0,71.m15996:100.0):76.0,AN8858.1:100.0):100.0):100.0,
1960	71.m15925	AN2280.1	AO070295000057	FG06943.1	ANAO		yes	((FG06943.1:100.0,(71.m15925:100.0,(AN2280.1:100.0,AO07029500:100.0):75.0):100.0):100.0,
1961	71.m15926	AN2281.1	AO070295000058	FG06942.1	AFAO			((FG06942.1:100.0,((AO07029500:100.0,71.m15926:100.0):38.0,AN2281.1:100.0):100.0):100.0,
1962	71.m15960	AN8828.1	AO070271000052	FG06941.1	AFAO			((FG06941.1:100.0,((71.m15960:100.0,AO07027100:100.0):60.8,AN8828.1:100.0):100.0):100.0,
1963	71.m15914	AN2269.1	AO070295000041	FG05484.1	AFAO			((FG05484.1:100.0,((AO07029500:100.0,71.m15914:100.0):58.5,AN2269.1:100.0):100.0):100.0,
1964	71.m15910	AN2266.1	AO070295000038	FG05469.1	AFAO	yes	yes	((FG05469.1:100.0,((AO07029500:100.0,71.m15910:100.0):93.0,AN2266.1:100.0):100.0):100.0,
1965	71.m15930	AN2284.1	AO070295000061	FG07266.1	AFAO		yes	((FG07266.1:100.0,((AO07029500:100.0,71.m15930:100.0):79.5,AN2284.1:100.0):100.0):100.0,
1966	62.m03119	AN6531.1	AO070270000031	FG02595.1	ANAO		yes	((FG02595.1:100.0,((AO07027000:100.0,AN6531.1:100.0):89.5,62.m03119:100.0):100.0):100.0,
1967	62.m03165	AN9528.1	AO070326000021	FG02596.1	ANAO			((FG02596.1:100.0,(62.m03165:100.0,(AN9528.1:100.0,AO07032600:100.0):70.0):100.0):100.0,
1968	71.m15983	AN8848.1	AO070271000028	FG02699.1	AFAO	yes	yes	((FG02699.1:100.0,((AO07027100:100.0,71.m15983:100.0):94.5,AN8848.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
1969	58.m07644	AN2056.1	AO070292000026	FG06749.1	AFAO		yes	((FG06749.1:100.0,((AO07029200:100.0,58.m07644:100.0):79.0,AN2056.1:100.0):100.0):100.0,
1970	54.m06757	AN4194.1	AO070315000084	FG05586.1	AFAO		yes	((FG05586.1:100.0,((AO07031500:100.0,54.m06757:100.0):85.5,AN4194.1:100.0):100.0):100.0,
1971	62.m03092	AN6505.1	AO070222000021	FG02501.1	AFAO	yes	yes	((FG02501.1:100.0,((AO07022200:100.0,62.m03092:100.0):92.0,AN6505.1:100.0):100.0):100.0,
1972	62.m03093	AN6506.1	AO070222000022	FG02502.1	ANAO			((FG02502.1:100.0,(62.m03093:100.0,(AN6506.1:100.0,AO07022200:100.0):65.5):100.0):100.0,
1973	62.m03439	AN6500.1	AO070222000014	FG02503.1	ANAO			((FG02503.1:100.0,((AO07022200:100.0,AN6500.1:100.0):64.0,62.m03439:100.0):100.0):100.0,
1974	62.m03087	AN6499.1	AO070222000013	FG02504.1	AFAO			((FG02504.1:100.0,((62.m03087:100.0,AO07022200:100.0):61.5,AN6499.1:100.0):100.0):100.0,
1975	53.m03887	AN8056.1	AO070322000144	FG02510.1	AFAO	yes	yes	((FG02510.1:100.0,((AO07032200:100.0,53.m03887:100.0):94.5,AN8056.1:100.0):100.0):100.0,
1976	71.m15978	AN8844.1	AO070271000032	FG02497.1	ANAO			((FG02497.1:100.0,((AO07027100:100.0,AN8844.1:100.0):58.0,71.m15978:100.0):100.0):100.0,
1977	71.m15990	AN8855.1	AO070271000019	FG02492.1	AFAO		yes	((FG02492.1:100.0,((AO07027100:100.0,71.m15990:100.0):87.0,AN8855.1:100.0):100.0):100.0,
1978	70.m15521	AN0912.1	AO070320000093	FG06675.1	ANAO		yes	((FG06675.1:100.0,(70.m15521:100.0,(AN0912.1:100.0,AO07032000:100.0):79.0):100.0):100.0,
1979	72.m19954	AN5911.1	AO070248000037	FG06670.1	AFAO		yes	((FG06670.1:100.0,((AO07024800:100.0,72.m19954:100.0):86.5,AN5911.1:100.0):100.0):100.0,
1980	72.m19327	AN6307.1	AO070308000062	FG07250.1	AFAO		yes	((FG07250.1:100.0,((AO07030800:100.0,72.m19327:100.0):86.0,AN6307.1:100.0):100.0):100.0,
1981	59.m09084	AN2947.1	AO070337000207	FG06693.1	AFAN			((FG06693.1:100.0,(AO07033700:100.0,(AN2947.1:100.0,59.m09084:100.0):52.0):100.0):100.0,
1982	57.m05585	AN4536.1	AO070321000153	FG06970.1	AFAO			((FG06970.1:100.0,((AO07032100:100.0,57.m05585:100.0):57.5,AN4536.1:100.0):100.0):100.0,
1983	57.m05586	AN4535.1	AO070321000149	FG06969.1	AFAO	yes	yes	((FG06969.1:100.0,((AO07032100:100.0,57.m05586:100.0):98.5,AN4535.1:100.0):100.0):100.0,
1984	57.m05579	AN4546.1	AO070321000159	FG06979.1	AFAN			((FG06979.1:100.0,(AO07032100:100.0,(AN4546.1:100.0,57.m05579:100.0):72.5):100.0):100.0,
1985	57.m05577	AN4544.1	AO070321000162	FG06977.1	AFAO	yes	yes	((FG06977.1:100.0,((AO07032100:100.0,57.m05577:100.0):99.0,AN4544.1:100.0):100.0):100.0,
1986	72.m19504	AN6351.1	AO070275000048	FG06950.1	AFAO			((FG06950.1:100.0,((72.m19504:100.0,AO07027500:100.0):51.5,AN6351.1:100.0):100.0):100.0,
1987	57.m05871	AN7473.1	AO070287000053	FG06951.1	AFAO		yes	((FG06951.1:100.0,((AO07028700:100.0,57.m05871:100.0):87.0,AN7473.1:100.0):100.0):100.0,
1988	72.m19708	AN2133.1	AO070278000026	FG04155.1	ANAO			((FG04155.1:100.0,(72.m19708:100.0,(AN2133.1:100.0,AO07027800:100.0):50.0):100.0):100.0,
1989	58.m07414	AN3627.1	AO070342000123	FG02585.1	AFAO	yes	yes	((FG02585.1:100.0,((AO07034200:100.0,58.m07414:100.0):93.0,AN3627.1:100.0):100.0):100.0,
1990	71.m15366	AN0091.1	AO070311000124	FG02567.1	AFAN			((FG02567.1:100.0,(AO07031100:100.0,(AN0091.1:100.0,71.m15366:100.0):45.0):100.0):100.0,
1991	71.m15365	AN0090.1	AO070311000125	FG02566.1	AFAO			((FG02566.1:100.0,((AO07031100:100.0,71.m15365:100.0):50.5,AN0090.1:100.0):100.0):100.0,
1992	71.m15221	AN6911.1	AO070219000015	FG02565.1	AFAO			((FG02565.1:100.0,((AO07021900:100.0,71.m15221:100.0):67.5,AN6911.1:100.0):100.0):100.0,
1993	70.m15128	AN1104.1	AO070285000034	FG02563.1	AFAO	yes	yes	((FG02563.1:100.0,((AO07028500:100.0,70.m15128:100.0):95.0,AN1104.1:100.0):100.0):100.0,
1994	71.m15368	AN0093.1	AO070311000122	FG02562.1	AFAO			((FG02562.1:100.0,((71.m15368:100.0,AO07031100:100.0):67.0,AN0093.1:100.0):100.0):100.0,
1995	72.m19694	AN2147.1	AO070343000196	FG02561.1	AFAO	yes	yes	((FG02561.1:100.0,((AO07034300:100.0,72.m19694:100.0):98.5,AN2147.1:100.0):100.0):100.0,
1996	71.m15373	AN9523.1	AO070311000118	FG02581.1	AFAO		yes	((FG02581.1:100.0,((AO07031100:100.0,71.m15373:100.0):76.5,AN9523.1:100.0):100.0):100.0,
1997	72.m19794	AN7256.1	AO070297000012	FG03351.1	AFAO	yes	yes	((FG03351.1:100.0,(AN7256.1:100.0,(72.m19794:100.0,AO07029700:100.0):100.0):100.0):100.0,
1998	71.m15230	AN6907.1	AO070314000006	FG02570.1	ANAO		yes	((FG02570.1:100.0,(71.m15230:100.0,(AN6907.1:100.0,AO07031400:100.0):89.5):100.0):100.0,
1999	72.m19170	AN5954.1	AO070340000308	FG02571.1	AFAO			((FG02571.1:100.0,((AO07034000:100.0,72.m19170:100.0):67.0,AN5954.1:100.0):100.0):100.0,
2000	71.m15587	AN8523.1	AO070323000193	FG11302.1	AFAN			((FG11302.1:100.0,((71.m15587:100.0,AN8523.1:100.0):64.5,AO07032300:100.0):100.0):100.0,
2001	59.m08856	AN4951.1	AO070288000003	FG02756.1	ANAO	yes	yes	((FG02756.1:100.0,(59.m08856:100.0,(AN4951.1:100.0,AO07028800:100.0):94.0):100.0):100.0,
2002	59.m08827	AN4925.1	AO070338000018	FG02757.1	AFAO			((FG02757.1:100.0,((AO07033800:100.0,59.m08827:100.0):57.5,AN4925.1:100.0):100.0):100.0,
2003	67.m02973	AN9200.1	AO070289000054	FG00055.1				((AO07028900:100.0,((67.m02973:100.0,AN9200.1:100.0):64.3,FG00055.1:100.0):48.3):100.0,
2004	62.m03415	AN8660.1	AO070269000054	FG07636.1	AFAO		yes	((FG07636.1:100.0,((AO07026900:100.0,62.m03415:100.0):75.0,AN8660.1:100.0):100.0):100.0,
2005	57.m05400	AN7636.1	AO070294000081	FG01630.1	ANAO			((FG01630.1:100.0,((AO07029400:100.0,AN7636.1:100.0):59.5,57.m05400:100.0):100.0):100.0,
2006	72.m19650	AN7609.1	AO070343000267	FG05016.1	AFAO	yes	yes	((FG05016.1:100.0,(AN7609.1:100.0,(72.m19650:100.0,AO07034300:100.0):100.0):100.0):100.0,
2007	53.m03765	AN3779.1	AO070310000104	FG05014.1	AFAO			((FG05014.1:100.0,((AO07031000:100.0,53.m03765:100.0):71.0,AN3779.1:100.0):100.0):100.0,
2008	71.m16051	AN0161.1	AO070321000086	FG04996.1	AFAO			((FG04996.1:100.0,((AO07032100:100.0,71.m16051:100.0):58.5,AN0161.1:100.0):100.0):100.0,
2009	71.m15433	AN0156.1	AO070321000094	FG04998.1	ANAO			((FG04998.1:100.0,((AO07032100:100.0,AN0156.1:100.0):68.0,71.m15433:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2010	71.m15515	AN2312.1	AO070323000042	FG05001.1	AFAO	yes	yes	((FG05001.1:100.0,((AO07032300:100.0,71.m15515:100.0):99.0,AN2312.1:100.0):100.0):100.0,
2011	71.m15491	AN4721.1	AO070323000062	FG05002.1	AFAO	yes	yes	((FG05002.1:100.0,((AO07032300:100.0,71.m15491:100.0):98.0,AN4721.1:100.0):100.0):100.0,
2012	72.m19229	AN5901.1	AO070248000039	FG05247.1	AFAO			((FG05247.1:100.0,((AO07024800:100.0,72.m19229:100.0):55.0,AN5901.1:100.0):100.0):100.0,
2013	57.m05380	AN7646.1	AO070294000051	FG09291.1	ANAO	yes	yes	((FG09291.1:100.0,(57.m05380:100.0,(AN7646.1:100.0,AO07029400:100.0):93.0):100.0):100.0,
2014	54.m06564	AN4046.1	AO070328000129	FG05008.1	AFAO			((FG05008.1:100.0,((54.m06564:100.0,AO07032800:100.0):68.5,AN4046.1:100.0):100.0):100.0,
2015	72.m19366	AN6269.1	AO070304000007	FG06177.1	ANAO			((FG06177.1:100.0,(72.m19366:100.0,(AN6269.1:100.0,AO07030400:100.0):62.0):100.0):100.0,
2016	52.m04033	AN9406.1	AO070274000011	FG09705.1	AFAO	yes	yes	((FG09705.1:100.0,((AO07027400:100.0,52.m04033:100.0):92.0,AN9406.1:100.0):100.0):100.0,
2017	69.m15507	AN5406.1	AO070333000120	FG09801.1	AFAO	yes	yes	((FG09801.1:100.0,(AN5406.1:100.0,(69.m15507:100.0,AO07033300:100.0):100.0):100.0):100.0,
2018	55.m02933	AN1423.1	AO070232000019	FG09804.1	ANAO			((FG09804.1:100.0,((AO07023200:100.0,AN1423.1:100.0):46.0,55.m02933:100.0):100.0):100.0,
2019	70.m15244	AN1023.1	AO070343000591	FG09721.1	ANAO			((FG09721.1:100.0,(70.m15244:100.0,(AN1023.1:100.0,AO07034300:100.0):59.0):100.0):100.0,
2020	69.m15181	AN7188.1	AO070252000016	FG09782.1	AFAO		yes	((FG09782.1:100.0,((AO07025200:100.0,69.m15181:100.0):88.0,AN7188.1:100.0):100.0):100.0,
2021	65.m07233	AN6735.1	AO070339000181	FG02746.1	AFAO		yes	((FG02746.1:100.0,((AO07033900:100.0,65.m07233:100.0):76.3,AN6735.1:100.0):100.0):100.0,
2022	70.m15350	AN0717.1	AO070343000449	FG09647.1	AFAO	yes	yes	((FG09647.1:100.0,((AO07034300:100.0,70.m15350:100.0):97.0,AN0717.1:100.0):100.0):100.0,
2023	69.m15505	AN5404.1	AO070333000090	FG09796.1	AFAO	yes	yes	((FG09796.1:100.0,((AO07033300:100.0,69.m15505:100.0):91.5,AN5404.1:100.0):100.0):100.0,
2024	69.m15524	AN5407.1	AO070333000121	FG09797.1	AFAO	yes	yes	((FG09797.1:100.0,((AO07033300:100.0,69.m15524:100.0):92.0,AN5407.1:100.0):100.0):100.0,
2025	72.m19206	AN5925.1	AO070340000359	FG01945.1	AFAO			((FG01945.1:100.0,((72.m19206:100.0,AO07034000:100.0):51.5,AN5925.1:100.0):100.0):100.0,
2026	72.m18948	AN5821.1	AO070260000024	FG01802.1	AFAO			(((AN5821.1:100.0,(AO07026000:100.0,72.m18948:100.0):71.0):99.0,FG01802.1:100.0):100.0,
2027	71.m15494	AN4725.1	AO070323000059	FG09685.1	AFAO		yes	((FG09685.1:100.0,((71.m15494:100.0,AO07032300:100.0):87.0,AN4725.1:100.0):100.0):100.0,
2028	71.m15495	AN4726.1	AO070323000058	FG05870.1	AFAO	yes	yes	((FG05870.1:100.0,((AO07032300:100.0,71.m15495:100.0):94.0,AN4726.1:100.0):100.0):100.0,
2029	71.m15492	AN4723.1	AO070323000061	FG09022.1	AFAO	yes	yes	((FG09022.1:100.0,(AN4723.1:100.0,(71.m15492:100.0,AO07032300:100.0):100.0):100.0):100.0,
2030	57.m05853	AN7491.1	AO070287000026	FG08668.1	AFAO			((FG08668.1:100.0,((57.m05853:100.0,AO07028700:100.0):44.5,AN7491.1:100.0):100.0):100.0,
2031	69.m15482	AN5450.1	AO070239000029	FG09665.1	AFAO		yes	((FG09665.1:100.0,((AO07023900:100.0,69.m15482:100.0):88.0,AN5450.1:100.0):100.0):100.0,
2032	69.m15478	AN5453.1	AO070341000414	FG09038.1	AFAO	yes	yes	((FG09038.1:100.0,((AO07034100:100.0,69.m15478:100.0):99.0,AN5453.1:100.0):100.0):100.0,
2033	57.m05449	AN7673.1	AO070325000053	FG05293.1	AFAO			((FG05293.1:100.0,((AO07032500:100.0,57.m05449:100.0):65.0,AN7673.1:100.0):100.0):100.0,
2034	52.m03642	AN7950.1	AO070342000340	FG05292.1	AFAO			((FG05292.1:100.0,((AO07034200:100.0,52.m03642:100.0):45.5,AN7950.1:100.0):100.0):100.0,
2035	71.m15740	AN7715.1	AO070325000127	FG06214.1	AFAO	yes	yes	((FG06214.1:100.0,(AN7715.1:100.0,(71.m15740:100.0,AO07032500:100.0):100.0):100.0):100.0,
2036	71.m15776	AN7750.1	AO070325000175	FG06212.1	AFAO			((FG06212.1:100.0,((71.m15776:100.0,AO07032500:100.0):44.0,AN7750.1:100.0):100.0):100.0,
2037	56.m02323	AN8907.1	AO070319000030	FG09830.1	AFAO			((FG09830.1:100.0,((AO07031900:100.0,56.m02323:100.0):68.0,AN8907.1:100.0):100.0):100.0,
2038	54.m06739	AN4096.1	AO070342000097	FG05503.1	AFAO		yes	((FG05503.1:100.0,((AO07034200:100.0,54.m06739:100.0):89.0,AN4096.1:100.0):100.0):100.0,
2039	59.m09401	AN4915.1	AO070338000028	FG05501.1	AFAO			((FG05501.1:100.0,((59.m09401:100.0,AO07033800:100.0):46.0,AN4915.1:100.0):100.0):100.0,
2040	71.m15331	AN0051.1	AO070314000138	FG07303.1	AFAO	yes	yes	((FG07303.1:100.0,((AO07031400:100.0,71.m15331:100.0):97.0,AN0051.1:100.0):100.0):100.0,
2041	71.m15332	AN0050.1	AO070314000139	FG07302.1	AFAO		yes	((FG07302.1:100.0,((AO07031400:100.0,71.m15332:100.0):86.5,AN0050.1:100.0):100.0):100.0,
2042	59.m08803	AN4903.1	AO070338000043	FG07296.1	AFAO	yes	yes	((FG07296.1:100.0,((AO07033800:100.0,59.m08803:100.0):99.0,AN4903.1:100.0):100.0):100.0,
2043	54.m06745	AN4189.1	AO070342000110	FG07295.1	AFAO			((FG07295.1:100.0,((54.m06745:100.0,AO07034200:100.0):71.5,AN4189.1:100.0):100.0):100.0,
2044	70.m15624	AN0984.1	AO070318000164	FG07294.1	AFAO	yes	yes	((FG07294.1:100.0,((AO07031800:100.0,70.m15624:100.0):94.5,AN0984.1:100.0):100.0):100.0,
2045	71.m16102	AN7707.1	AO070325000113	FG07284.1	AFAN			((FG07284.1:100.0,(AO07032500:100.0,(AN7707.1:100.0,71.m16102:100.0):50.0):100.0):100.0,
2046	54.m06699	AN0246.1	AO070338000238	FG07290.1	ANAO			((FG07290.1:100.0,(54.m06699:100.0,(AN0246.1:100.0,AO07033800:100.0):69.5):100.0):100.0,
2047	70.m15516	AN0907.1	AO070320000083	FG07291.1	ANAO			((FG07291.1:100.0,((AO07032000:100.0,AN0907.1:100.0):54.3,70.m15516:100.0):100.0):100.0,
2048	54.m06715	AN4073.1	AO070342000062	FG07292.1	AFAN		yes	((((AN4073.1:100.0,54.m06715:100.0):84.0,AO07034200:100.0):97.0,FG07292.1:100.0):100.0,
2049	53.m03774	AN8201.1	AO070310000118	FG07280.1	AFAO			((FG07280.1:100.0,((53.m03774:100.0,AO07031000:100.0):65.5,AN8201.1:100.0):100.0):100.0,
2050	53.m03889	AN8054.1	AO070322000146	FG07282.1	AFAO			((FG07282.1:100.0,((AO07032200:100.0,53.m03889:100.0):56.2,AN8054.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2051	72.m19323	AN6311.1	AO070308000066	FG05451.1	ANAO			((FG05451.1:100.0,((AO07030800:100.0,AN6311.1:100.0):53.0,72.m19323:100.0):100.0):100.0,
2052	72.m19955	AN5910.1	AO070248000036	FG07289.1	AFAO			((FG07289.1:100.0,((AO07024800:100.0,72.m19955:100.0):44.3,AN5910.1:100.0):100.0):100.0,
2053	72.m19953	AN5915.1	AO070340000372	FG07288.1	AFAN	yes	yes	((FG07288.1:100.0,(AO07034000:100.0,(AN5915.1:100.0,72.m19953:100.0):92.5):100.0):100.0,
2054	53.m03875	AN8029.1	AO070322000075	FG07279.1	ANAO			((FG07279.1:100.0,(53.m03875:100.0,(AN8029.1:100.0,AO07032200:100.0):56.5):100.0):100.0,
2055	53.m03886	AN8057.1	AO070322000143	FG07287.1	AFAO	yes	yes	((FG07287.1:100.0,((AO07032200:100.0,53.m03886:100.0):98.5,AN8057.1:100.0):100.0):100.0,
2056	57.m05868	AN7487.1	AO070287000049	FG05447.1	ANAO			((((AN7487.1:100.0,AO07028700:100.0):49.2,57.m05868:100.0):55.6,FG05447.1:100.0):100.0,
2057	57.m05859	AN7479.1	AO070287000036	FG08865.1	ANAO		yes	((FG08865.1:100.0,(57.m05859:100.0,(AN7479.1:100.0,AO07028700:100.0):75.0):100.0):100.0,
2058	57.m05861	AN7480.1	AO070287000037	FG05444.1	AFAO			((FG05444.1:100.0,((57.m05861:100.0,AO07028700:100.0):47.5,AN7480.1:100.0):100.0):100.0,
2059	70.m15635	AN0641.1	AO070318000142	FG02523.1	AFAN	yes	yes	((FG02523.1:100.0,((AN0641.1:100.0,70.m15635:100.0):100.0,AO07031800:100.0):100.0):100.0,
2060	70.m15636	AN0640.1	AO070318000141	FG02522.1	AFAO	yes	yes	((FG02522.1:100.0,((AO07031800:100.0,70.m15636:100.0):99.0,AN0640.1:100.0):100.0):100.0,
2061	72.m19324	AN6310.1	AO070308000065	FG07258.1	AFAO	yes	yes	((FG07258.1:100.0,((AO07030800:100.0,72.m19324:100.0):99.0,AN6310.1:100.0):100.0):100.0,
2062	58.m07659	AN2057.1	AO070292000042	FG07257.1	AFAN		yes	((FG07257.1:100.0,(AO07029200:100.0,(AN2057.1:100.0,58.m07659:100.0):81.5):100.0):100.0,
2063	52.m03842	AN4355.1	AO070315000047	FG07255.1	AFAO			((FG07255.1:100.0,((AO07031500:100.0,52.m03842:100.0):56.0,AN4355.1:100.0):100.0):100.0,
2064	72.m19992	AN6214.1	AO070308000078	FG07254.1	AFAO		yes	((FG07254.1:100.0,((AO07030800:100.0,72.m19992:100.0):89.0,AN6214.1:100.0):100.0):100.0,
2065	72.m19058	AN6069.1	AO070340000110	FG05453.1	AFAO	yes	yes	((FG05453.1:100.0,((AO07034000:100.0,72.m19058:100.0):93.0,AN6069.1:100.0):100.0):100.0,
2066	54.m06852	AN5162.1	AO070291000001	FG05454.1	ANAO		yes	((FG05454.1:100.0,(54.m06852:100.0,(AN5162.1:100.0,AO07029100:100.0):80.0):100.0):100.0,
2067	72.m19316	AN6217.1	AO070308000074	FG05455.1	AFAO	yes	yes	((FG05455.1:100.0,((AO07030800:100.0,72.m19316:100.0):98.5,AN6217.1:100.0):100.0):100.0,
2068	71.m15929	AN2283.1	AO070295000060	FG05550.1	AFAO			((FG05550.1:100.0,((AO07029500:100.0,71.m15929:100.0):64.5,AN2283.1:100.0):100.0):100.0,
2069	71.m15767	AN7737.1	AO070325000160	FG05549.1	AFAN	yes	yes	((FG05549.1:100.0,(AO07032500:100.0,(71.m15767:100.0,AN7737.1:100.0):99.5):100.0):100.0,
2070	71.m15923	AN2278.1	AO070295000054	FG07306.1	AFAO		yes	((FG07306.1:100.0,((AO07029500:100.0,71.m15923:100.0):84.5,AN2278.1:100.0):100.0):100.0,
2071	71.m15852	AN2214.1	AO070294000008	FG07307.1	ANAO			((FG07307.1:100.0,(71.m15852:100.0,(AN2214.1:100.0,AO07029400:100.0):64.5):100.0):100.0,
2072	70.m15611	AN0966.1	AO070320000170	FG07308.1	AFAO			((FG07308.1:100.0,((AO07032000:100.0,70.m15611:100.0):60.5,AN0966.1:100.0):100.0):100.0,
2073	70.m15256	AN0651.1	AO070343000576	FG05535.1	AFAN			((FG05535.1:100.0,((70.m15256:100.0,AN0651.1:100.0):72.2,AO07034300:100.0):100.0):100.0,
2074	62.m03203	AN6594.1	AO070326000044	FG05537.1	AFAO		yes	((FG05537.1:100.0,((AO07032600:100.0,62.m03203:100.0):75.0,AN6594.1:100.0):100.0):100.0,
2075	72.m19711	AN2130.1	AO070278000033	FG05398.1	AFAO	yes	yes	((FG05398.1:100.0,(AN2130.1:100.0,(72.m19711:100.0,AO07027800:100.0):100.0):100.0):100.0,
2076	72.m19710	AN9538.1	AO070278000028	FG05399.1	AFAO			((FG05399.1:100.0,((72.m19710:100.0,AO07027800:100.0):68.5,AN9538.1:100.0):100.0):100.0,
2077	62.m03178	AN6589.1	AO070326000037	FG05591.1	AFAN			((FG05591.1:100.0,(AO07032600:100.0,(AN6589.1:100.0,62.m03178:100.0):50.0):100.0):100.0,
2078	58.m07882	AN4443.1	AO070273000010	FG10825.1	AFAO			((FG10825.1:100.0,((AO07027300:100.0,58.m07882:100.0):73.5,AN4443.1:100.0):100.0):100.0,
2079	72.m19363	AN6277.1	AO070304000003	FG07564.1	ANAO	yes	yes	((FG07564.1:100.0,(72.m19363:100.0,(AN6277.1:100.0,AO07030400:100.0):91.0):100.0):100.0,
2080	71.m15469	AN0204.1	AO070321000040	FG09740.1	AFAO			((FG09740.1:100.0,((AO07032100:100.0,71.m15469:100.0):68.0,AN0204.1:100.0):100.0):100.0,
2081	55.m03225	AN3515.1	AO070302000082	FG10661.1	AFAO		yes	((FG10661.1:100.0,((AO07030200:100.0,55.m03225:100.0):89.5,AN3515.1:100.0):100.0):100.0,
2082	55.m03299	AN3516.1	AO070302000081	FG10662.1	ANAO			((FG10662.1:100.0,(55.m03299:100.0,(AN3516.1:100.0,AO07030200:100.0):49.5):100.0):100.0,
2083	59.m08493	AN2497.1	AO070312000123	FG04980.1	AFAO		yes	((FG04980.1:100.0,((AO07031200:100.0,59.m08493:100.0):81.5,AN2497.1:100.0):100.0):100.0,
2084	72.m19222	AN5909.1	AO070245000003	FG09678.1	AFAO		yes	((FG09678.1:100.0,((AO07024500:100.0,72.m19222:100.0):79.5,AN5909.1:100.0):100.0):100.0,
2085	70.m15325	AN0731.1	AO070343000492	FG10979.1	ANAO		yes	((FG10979.1:100.0,(70.m15325:100.0,(AN0731.1:100.0,AO07034300:100.0):80.5):100.0):100.0,
2086	70.m15333	AN9437.1	AO070343000483	FG04948.1	AFAO	yes	yes	((FG04948.1:100.0,((AO07034300:100.0,70.m15333:100.0):99.0,AN9437.1:100.0):100.0):100.0,
2087	71.m15497	AN2751.1	AO070323000056	FG09663.1	ANAO			((FG09663.1:100.0,(71.m15497:100.0,(AN2751.1:100.0,AO07032300:100.0):68.5):100.0):100.0,
2088	70.m15426	AN0824.1	AO070255000021	FG09661.1	AFAO			((FG09661.1:100.0,((AO07025500:100.0,70.m15426:100.0):56.5,AN0824.1:100.0):100.0):100.0,
2089	72.m19023	AN6141.1	AO070340000061	FG05036.1	AFAO			(((AN6141.1:100.0,(72.m19023:100.0,AO07034000:100.0):60.0):99.0,FG05036.1:100.0):100.0,
2090	71.m15752	AN7725.1	AO070325000141	FG05035.1	AFAO	yes	yes	((FG05035.1:100.0,((AO07032500:100.0,71.m15752:100.0):93.5,AN7725.1:100.0):100.0):100.0,
2091	71.m15444	AN0170.1	AO070321000076	FG02403.1	AFAO			(((AN0170.1:100.0,(AO07032100:100.0,71.m15444:100.0):79.8):71.7,FG02403.1:100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2092	71.m15447	AN0174.1	AO070321000070	FG01730.1	AFAO			((FG01730.1:100.0,((AO07032100:100.0,71.m15447:100.0):60.0,AN0174.1:100.0):100.0):100.0,
2093	69.m15255	AN0593.1	AO070280000019	FG05284.1	ANAO			((FG05284.1:100.0,(69.m15255:100.0,(AN0593.1:100.0,AO07028000:100.0):65.0):100.0):100.0,
2094	71.m16050	AN0162.1	AO070321000085	FG05283.1	ANAO			((FG05283.1:100.0,((AO07032100:100.0,AN0162.1:100.0):41.3,71.m16050:100.0):100.0):100.0,
2095	71.m15438	AN0163.1	AO070321000084	FG05282.1	AFAO	yes	yes	((FG05282.1:100.0,((AO07032100:100.0,71.m15438:100.0):95.5,AN0163.1:100.0):100.0):100.0,
2096	71.m15439	AN0164.1	AO070321000083	FG05281.1	AFAO			((FG05281.1:100.0,((AO07032100:100.0,71.m15439:100.0):71.0,AN0164.1:100.0):100.0):100.0,
2097	71.m15441	AN0166.1	AO070321000080	FG05288.1	AFAO		yes	((FG05288.1:100.0,((AO07032100:100.0,71.m15441:100.0):85.5,AN0166.1:100.0):100.0):100.0,
2098	71.m15440	AN0165.1	AO070321000081	FG05286.1	AFAO		yes	((FG05286.1:100.0,((AO07032100:100.0,71.m15440:100.0):75.0,AN0165.1:100.0):100.0):100.0,
2099	72.m20010	AN2139.1	AO070343000184	FG07145.1	AFAO	yes	yes	(((AN2139.1:100.0,(AO07034300:100.0,72.m20010:100.0):93.5):99.0,FG07145.1:100.0):100.0,
2100	72.m20017	AN2164.1	AO070343000224	FG05276.1	ANAO			((FG05276.1:100.0,(72.m20017:100.0,(AN2164.1:100.0,AO07034300:100.0):70.5):100.0):100.0,
2101	72.m19284	AN6186.1	AO070308000114	FG05269.1	AFAO	yes	yes	((FG05269.1:100.0,(AN6186.1:100.0,(72.m19284:100.0,AO07030800:100.0):100.0):100.0):100.0,
2102	69.m15692	AN0577.1	AO070272000057	FG05259.1	AFAO	yes	yes	((FG05259.1:100.0,((AO07027200:100.0,69.m15692:100.0):99.0,AN0577.1:100.0):100.0):100.0,
2103	69.m15251	AN0596.1	AO070280000022	FG05252.1	AFAO	yes	yes	((FG05252.1:100.0,(AN0596.1:100.0,(69.m15251:100.0,AO07028000:100.0):100.0):100.0):100.0,
2104	71.m15513	AN2306.1	AO070323000044	FG05251.1	AFAO			((FG05251.1:100.0,((AO07032300:100.0,71.m15513:100.0):59.0,AN2306.1:100.0):100.0):100.0,
2105	59.m08845	AN4941.1	AO070338000002	FG05255.1	AFAO		yes	((FG05255.1:100.0,((AO07033800:100.0,59.m08845:100.0):86.5,AN4941.1:100.0):100.0):100.0,
2106	69.m15231	AN2430.1	AO070188000004	FG05256.1	AFAO		yes	((FG05256.1:100.0,((AO07018800:100.0,69.m15231:100.0):87.5,AN2430.1:100.0):100.0):100.0,
2107	58.m07840	AN3868.1	AO070305000104	FG01992.1	AFAO		yes	((FG01992.1:100.0,((AO07030500:100.0,58.m07840:100.0):86.5,AN3868.1:100.0):100.0):100.0,
2108	65.m07236	AN6732.1	AO070339000178	FG05235.1	AFAO		yes	((FG05235.1:100.0,((AO07033900:100.0,65.m07236:100.0):83.0,AN6732.1:100.0):100.0):100.0,
2109	55.m03221	AN6442.1	AO070325000114	FG09039.1	AFAO	yes	yes	((FG09039.1:100.0,((AO07032500:100.0,55.m03221:100.0):95.5,AN6442.1:100.0):100.0):100.0,
2110	71.m15474	AN0211.1	AO070321000033	FG05305.1	AFAN		yes	((FG05305.1:100.0,(AO07032100:100.0,(AN0211.1:100.0,71.m15474:100.0):77.5):100.0):100.0,
2111	71.m15511	AN2308.1	AO070323000046	FG05303.1	ANAO		yes	((FG05303.1:100.0,(71.m15511:100.0,(AN2308.1:100.0,AO07032300:100.0):75.5):100.0):100.0,
2112	69.m15269	AN0576.1	AO070272000056	FG05306.1	AFAO	yes	yes	((FG05306.1:100.0,((AO07027200:100.0,69.m15269:100.0):98.0,AN0576.1:100.0):100.0):100.0,
2113	71.m15516	AN2318.1	AO070323000040	FG09811.1	AFAO			((FG09811.1:100.0,((AO07032300:100.0,71.m15516:100.0):46.5,AN2318.1:100.0):100.0):100.0,
2114	69.m15695	AN6391.1	AO070343000154	FG09815.1	AFAN			((FG09815.1:100.0,(AO07034300:100.0,(69.m15695:100.0,AN6391.1:100.0):72.0):99.5):100.0,
2115	69.m15287	AN0560.1	AO070272000037	FG09816.1	AFAO			((FG09816.1:100.0,((AO07027200:100.0,69.m15287:100.0):55.5,AN0560.1:100.0):100.0):100.0,
2116	69.m15288	AN0559.1	AO070272000036	FG09817.1	AFAO		yes	((FG09817.1:100.0,((AO07027200:100.0,69.m15288:100.0):87.0,AN0559.1:100.0):100.0):100.0,
2117	69.m15301	AN0502.1	AO070226000015	FG09818.1	AFAO			((FG09818.1:100.0,((AO07022600:100.0,69.m15301:100.0):71.5,AN0502.1:100.0):100.0):100.0,
2118	70.m15259	AN0655.1	AO070343000571	FG10100.1	AFAN			((FG10100.1:100.0,(AO07034300:100.0,(70.m15259:100.0,AN0655.1:100.0):69.5):100.0):100.0,
2119	57.m05454	AN7677.1	AO070325000067	FG10096.1	ANAO	yes	yes	((FG10096.1:100.0,(57.m05454:100.0,(AN7677.1:100.0,AO07032500:100.0):96.0):100.0):100.0,
2120	57.m05455	AN7678.1	AO070325000068	FG10095.1	AFAO			((FG10095.1:100.0,((57.m05455:100.0,AO07032500:100.0):46.5,AN7678.1:100.0):100.0):100.0,
2121	69.m15469	AN5484.1	AO070341000401	FG10064.1	ANAO		yes	((FG10064.1:100.0,((AO07034100:100.0,AN5484.1:100.0):86.0,69.m15469:100.0):100.0):100.0,
2122	59.m08450	AN2529.1	AO070300000122	FG09979.1	AFAN			((FG09979.1:100.0,(AO07030000:100.0,(AN2529.1:100.0,59.m08450:100.0):64.0):100.0):100.0,
2123	57.m05635	AN4496.1	AO070311000048	FG10016.1	AFAO	yes	yes	((FG10016.1:100.0,((AO07031100:100.0,57.m05635:100.0):96.0,AN4496.1:100.0):100.0):100.0,
2124	66.m04576	AN9109.1	AO070332000159	FG10199.1	AFAO		yes	((FG10199.1:100.0,((AO07033200:100.0,66.m04576:100.0):88.5,AN9109.1:100.0):100.0):100.0,
2125	57.m05406	AN7632.1	AO070268000004	FG10200.1	ANAO			((FG10200.1:100.0,(57.m05406:100.0,(AN7632.1:100.0,AO07026800:100.0):63.0):100.0):100.0,
2126	59.m08663	AN3084.1	AO070334000122	FG10308.1	AFAO			((FG10308.1:100.0,((59.m08663:100.0,AO07033400:100.0):58.3,AN3084.1:100.0):100.0):100.0,
2127	70.m15292	AN0689.1	AO070343000524	FG09921.1	ANAO		yes	((FG09921.1:100.0,(70.m15292:100.0,(AN0689.1:100.0,AO07034300:100.0):82.0):100.0):100.0,
2128	70.m15293	AN0690.1	AO070343000523	FG09923.1	AFAN			((FG09923.1:100.0,(AO07034300:100.0,(AN0690.1:100.0,70.m15293:100.0):39.0):100.0):100.0,
2129	59.m08665	AN5014.1	AO070334000120	FG09974.1	AFAO		yes	((FG09974.1:100.0,((AO07033400:100.0,59.m08665:100.0):89.5,AN5014.1:100.0):100.0):100.0,
2130	57.m05939	AN7671.1	AO070325000051	FG09975.1	AFAN			((FG09975.1:100.0,(AO07032500:100.0,(AN7671.1:100.0,57.m05939:100.0):46.0):100.0):100.0,
2131	57.m05404	AN7625.1	AO070294000090	FG09940.1	AFAO	yes	yes	((FG09940.1:100.0,((AO07029400:100.0,57.m05404:100.0):91.0,AN7625.1:100.0):100.0):100.0,
2132	57.m05916	AN7428.1	AO070197000009	FG10226.1	AFAN		yes	((FG10226.1:100.0,(AO07019700:100.0,(AN7428.1:100.0,57.m05916:100.0):76.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2133	53.m03783	AN9460.1	AO070310000131	FG06800.1	AFAO	yes	yes	((FG06800.1:100.0,((AO07031000:100.0,53.m03783:100.0):92.5,AN9460.1:100.0):100.0):100.0,
2134	53.m03793	AN8185.1	AO070310000139	FG06799.1	AFAO			((FG06799.1:100.0,((53.m03793:100.0,AO07031000:100.0):66.0,AN8185.1:100.0):100.0):100.0,
2135	53.m03792	AN8187.1	AO070310000138	FG06798.1	ANAO			((FG06798.1:100.0,(53.m03792:100.0,(AN8187.1:100.0,AO07031000:100.0):58.0):100.0):100.0,
2136	53.m03857	AN8010.1	AO070322000057	FG06822.1	AFAO		yes	((FG06822.1:100.0,((53.m03857:100.0,AO07032200:100.0):81.8,AN8010.1:100.0):100.0):100.0,
2137	53.m03891	AN8051.1	AO070292000094	FG07349.1	AFAO	yes	yes	((FG07349.1:100.0,((AO07029200:100.0,53.m03891:100.0):97.0,AN8051.1:100.0):100.0):100.0,
2138	53.m03827	AN8117.1	AO070322000025	FG07347.1	ANAO		yes	((FG07347.1:100.0,(53.m03827:100.0,(AN8117.1:100.0,AO07032200:100.0):76.5):100.0):100.0,
2139	70.m15385	AN1146.1	AO070316000058	FG01883.1	AFAO			((FG01883.1:100.0,((70.m15385:100.0,AO07031600:100.0):51.5,AN1146.1:100.0):100.0):100.0,
2140	71.m15945	AN2296.1	AO070295000077	FG07420.1	AFAO		yes	((FG07420.1:100.0,((AO07029500:100.0,71.m15945:100.0):85.5,AN2296.1:100.0):100.0):100.0,
2141	71.m15924	AN2279.1	AO070295000056	FG07419.1	AFAO			((FG07419.1:100.0,((AO07029500:100.0,71.m15924:100.0):64.5,AN2279.1:100.0):100.0):100.0,
2142	62.m03192	AN6604.1	AO070326000055	FG05227.1	AFAO			((FG05227.1:100.0,((AO07032600:100.0,62.m03192:100.0):70.0,AN6604.1:100.0):100.0):100.0,
2143	58.m08926	AN8488.1	AO070299000105	FG06394.1	AFAO			(((AN8488.1:100.0,(AO07029900:100.0,58.m08926:100.0):89.2):50.8,FG06394.1:100.0):100.0,
2144	62.m03196	AN6601.1	AO070326000052	FG05224.1	AFAO		yes	((FG05224.1:100.0,((AO07032600:100.0,62.m03196:100.0):78.0,AN6601.1:100.0):100.0):100.0,
2145	62.m03125	AN6548.1	AO070270000037	FG05223.1	ANAO		yes	((FG05223.1:100.0,((AO07027000:100.0,AN6548.1:100.0):87.0,62.m03125:100.0):100.0):100.0,
2146	62.m03126	AN6547.1	AO070270000038	FG05222.1	ANAO		yes	((FG05222.1:100.0,(62.m03126:100.0,(AN6547.1:100.0,AO07027000:100.0):86.0):100.0):100.0,
2147	62.m03127	AN6546.1	AO070270000039	FG05194.1	AFAO			((FG05194.1:100.0,((AO07027000:100.0,62.m03127:100.0):69.5,AN6546.1:100.0):100.0):100.0,
2148	62.m03121	AN6533.1	AO070270000033	FG06239.1	AFAO	yes	yes	((FG06239.1:100.0,((AO07027000:100.0,62.m03121:100.0):99.0,AN6533.1:100.0):100.0):100.0,
2149	59.m08759	AN2909.1	AO070338000097	FG09891.1	ANAO	yes	yes	((FG09891.1:100.0,(59.m08759:100.0,(AN2909.1:100.0,AO07033800:100.0):98.0):100.0):100.0,
2150	57.m05913	AN7431.1	AO070229000002	FG09892.1	AFAO		yes	((FG09892.1:100.0,((AO07022900:100.0,57.m05913:100.0):77.0,AN7431.1:100.0):100.0):100.0,
2151	57.m05465	AN7688.1	AO070325000082	FG10309.1	AFAO			((FG10309.1:100.0,((AO07032500:100.0,57.m05465:100.0):71.5,AN7688.1:100.0):100.0):100.0,
2152	57.m05650	AN2555.1	AO070319000164	FG05797.1	AFAO			((FG05797.1:100.0,((57.m05650:100.0,AO07031900:100.0):62.0,AN2555.1:100.0):100.0):100.0,
2153	59.m09323	AN3462.1	AO070265000040	FG04578.1	AFAO	yes	yes	((FG04578.1:100.0,(AN3462.1:100.0,(59.m09323:100.0,AO07026500:100.0):100.0):100.0):100.0,
2154	58.m08894	AN4159.1	AO070342000188	FG10264.1	AFAO	yes	yes	((FG10264.1:100.0,(AN4159.1:100.0,(58.m08894:100.0,AO07034200:100.0):100.0):100.0):100.0,
2155	69.m15721	AN5486.1	AO070341000397	FG10250.1	ANAO			((FG10250.1:100.0,((AO07034100:100.0,AN5486.1:100.0):39.5,69.m15721:100.0):100.0):100.0,
2156	70.m15290	AN0687.1	AO070343000527	FG10249.1	AFAN		yes	((FG10249.1:100.0,(AO07034300:100.0,(AN0687.1:100.0,70.m15290:100.0):87.0):100.0):100.0,
2157	72.m18942	AN5812.1	AO070260000035	FG10188.1	AFAO	yes	yes	((FG10188.1:100.0,((72.m18942:100.0,AO07026000:100.0):93.0,AN5812.1:100.0):100.0):100.0,
2158	70.m14866	AN1363.1	AO070243000001	FG01545.1	AFAN			((FG01545.1:100.0,(AO07024300:100.0,(AN1363.1:100.0,70.m14866:100.0):59.0):100.0):100.0,
2159	72.m19399	AN6257.1	AO070304000031	FG06265.1	AFAO	yes	yes	((FG06265.1:100.0,((AO07030400:100.0,72.m19399:100.0):98.0,AN6257.1:100.0):100.0):100.0,
2160	72.m19400	AN6256.1	AO070304000032	FG06266.1	AFAO			((FG06266.1:100.0,((72.m19400:100.0,AO07030400:100.0):65.5,AN6256.1:100.0):100.0):100.0,
2161	58.m09013	AN4307.1	AO070207000012	FG01542.1	AFAO	yes	yes	((FG01542.1:100.0,((AO07020700:100.0,58.m09013:100.0):96.5,AN4307.1:100.0):100.0):100.0,
2162	70.m15746	AN3771.1	AO070233000011	FG06571.1	AFAO	yes	yes	((FG06571.1:100.0,(AN3771.1:100.0,(70.m15746:100.0,AO07023300:100.0):100.0):100.0):100.0,
2163	70.m14865	AN1364.1	AO070215000017	FG01540.1	ANAO	yes	yes	((FG01540.1:100.0,((AN1364.1:100.0,AO07021500:100.0):100.0,70.m14865:100.0):100.0):100.0,
2164	54.m06635	AN0444.1	AO070338000306	FG06272.1	AFAO	yes	yes	((FG06272.1:100.0,((AO07033800:100.0,54.m06635:100.0):96.5,AN0444.1:100.0):100.0):100.0,
2165	72.m19344	AN6291.1	AO070308000001	FG00958.1	ANAO		yes	((FG00958.1:100.0,(72.m19344:100.0,(AN6291.1:100.0,AO07030800:100.0):86.5):100.0):100.0,
2166	72.m19305	AN6207.1	AO070308000086	FG04416.1	ANAO		yes	((FG04416.1:100.0,(72.m19305:100.0,(AN6207.1:100.0,AO07030800:100.0):84.0):100.0):100.0,
2167	58.m07597	AN1989.1	AO070301000077	FG04413.1	AFAO			((FG04413.1:100.0,((AO07030100:100.0,58.m07597:100.0):66.0,AN1989.1:100.0):100.0):100.0,
2168	58.m07574	AN1969.1	AO070301000053	FG04412.1	AFAN			((FG04412.1:100.0,(AO07030100:100.0,(AN1969.1:100.0,58.m07574:100.0):58.5):100.0):100.0,
2169	65.m07245	AN6725.1	AO070339000169	FG04411.1	AFAO			((FG04411.1:100.0,((AO07033900:100.0,65.m07245:100.0):55.0,AN6725.1:100.0):100.0):100.0,
2170	65.m07244	AN6726.1	AO070339000170	FG04410.1	AFAO			((FG04410.1:100.0,((AO07033900:100.0,65.m07244:100.0):52.5,AN6726.1:100.0):100.0):100.0,
2171	72.m19331	AN6303.1	AO070308000058	FG00327.1	AFAO			((FG00327.1:100.0,((AO07030800:100.0,72.m19331:100.0):61.5,AN6303.1:100.0):100.0):100.0,
2172	72.m19332	AN6302.1	AO070308000057	FG00328.1	AFAO		yes	((FG00328.1:100.0,((AO07030800:100.0,72.m19332:100.0):82.5,AN6302.1:100.0):100.0):100.0,
2173	72.m19334	AN6300.1	AO070308000056	FG00329.1	AFAO			((FG00329.1:100.0,((AO07030800:100.0,72.m19334:100.0):61.5,AN6300.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2174	72.m19346	AN6289.1	AO070308000003	FG00957.1	ANAO			((FG00957.1:100.0,(72.m19346:100.0,(AN6289.1:100.0,AO07030800:100.0):69.5):100.0):100.0,
2175	58.m07906	AN4417.1	AO070273000038	FG10865.1	AFAO	yes	yes	((FG10865.1:100.0,((AO07027300:100.0,58.m07906:100.0):98.0,AN4417.1:100.0):100.0):100.0,
2176	58.m07905	AN4416.1	AO070273000037	FG10864.1	AFAO	yes	yes	((FG10864.1:100.0,((AO07027300:100.0,58.m07905:100.0):96.5,AN4416.1:100.0):100.0):100.0,
2177	54.m06844	AN5724.1	AO070324000127	FG10863.1	AFAO		yes	((FG10863.1:100.0,((AO07032400:100.0,54.m06844:100.0):77.5,AN5724.1:100.0):100.0):100.0,
2178	54.m06845	AN5725.1	AO070324000126	FG10858.1	AFAO	yes	yes	((FG10858.1:100.0,((AO07032400:100.0,54.m06845:100.0):94.5,AN5725.1:100.0):100.0):100.0,
2179	71.m15424	AN0141.1	AO070321000108	FG10860.1	AFAO		yes	((FG10860.1:100.0,((AO07032100:100.0,71.m15424:100.0):82.5,AN0141.1:100.0):100.0):100.0,
2180	69.m15289	AN0558.1	AO070272000034	FG06037.1	AFAO	yes	yes	((FG06037.1:100.0,((AO07027200:100.0,69.m15289:100.0):98.5,AN0558.1:100.0):100.0):100.0,
2181	69.m15223	AN2435.1	AO070264000043	FG06039.1	AFAO			((FG06039.1:100.0,((AO07026400:100.0,69.m15223:100.0):63.5,AN2435.1:100.0):100.0):100.0,
2182	58.m07600	AN1991.1	AO070301000081	FG06043.1	AFAO	yes	yes	((FG06043.1:100.0,((AO07030100:100.0,58.m07600:100.0):98.0,AN1991.1:100.0):100.0):100.0,
2183	70.m15205	AN1048.1	AO070313000110	FG01615.1	AFAO		yes	((FG01615.1:100.0,((AO07031300:100.0,70.m15205:100.0):76.5,AN1048.1:100.0):100.0):100.0,
2184	69.m15487	AN5447.1	AO070333000115	FG01572.1	AFAO			((FG01572.1:100.0,((AO07033300:100.0,69.m15487:100.0):61.5,AN5447.1:100.0):100.0):100.0,
2185	72.m19640	AN7606.1	AO070343000278	FG04302.1	AFAO		yes	((FG04302.1:100.0,((AO07034300:100.0,72.m19640:100.0):86.5,AN7606.1:100.0):100.0):100.0,
2186	72.m19357	AN6282.1	AO070308000029	FG01571.1	AFAO	yes	yes	((FG01571.1:100.0,(AN6282.1:100.0,(72.m19357:100.0,AO07030800:100.0):100.0):100.0):100.0,
2187	72.m19642	AN7604.1	AO070343000276	FG04294.1	AFAO	yes	yes	((FG04294.1:100.0,((AO07034300:100.0,72.m19642:100.0):97.0,AN7604.1:100.0):100.0):100.0,
2188	71.m15419	AN0135.1	AO070321000117	FG10861.1	AFAO			((FG10861.1:100.0,((AO07032100:100.0,71.m15419:100.0):64.5,AN0135.1:100.0):100.0):100.0,
2189	71.m15259	AN6875.1	AO070314000048	FG01690.1	AFAO	yes	yes	((FG01690.1:100.0,((AO07031400:100.0,71.m15259:100.0):92.5,AN6875.1:100.0):100.0):100.0,
2190	58.m08956	AN5619.1	AO070301000020	FG11224.1	AFAO	yes	yes	((FG11224.1:100.0,(AN5619.1:100.0,(58.m08956:100.0,AO07030100:100.0):100.0):100.0):100.0,
2191	58.m07549	AN5626.1	AO070301000025	FG00330.1	ANAO			((FG00330.1:100.0,((AO07030100:100.0,AN5626.1:100.0):73.0,58.m07549:100.0):100.0):100.0,
2192	69.m15405	AN3693.1	AO070341000321	FG00332.1	AFAO			((FG00332.1:100.0,((69.m15405:100.0,AO07034100:100.0):61.0,AN3693.1:100.0):100.0):100.0,
2193	69.m15406	AN3692.1	AO070341000323	FG00333.1	AFAO			((FG00333.1:100.0,((AO07034100:100.0,69.m15406:100.0):58.5,AN3692.1:100.0):100.0):100.0,
2194	72.m19301	AN6202.1	AO070308000092	FG06289.1	AFAO	yes	yes	((FG06289.1:100.0,((AO07030800:100.0,72.m19301:100.0):92.0,AN6202.1:100.0):100.0):100.0,
2195	72.m19302	AN6203.1	AO070308000091	FG06288.1	ANAO		yes	((FG06288.1:100.0,(72.m19302:100.0,(AN6203.1:100.0,AO07030800:100.0):81.5):100.0):100.0,
2196	54.m06789	AN4227.1	AO070234000022	FG01453.1	AFAN			((FG01453.1:100.0,(AO07023400:100.0,(AN4227.1:100.0,54.m06789:100.0):48.5):100.0):100.0,
2197	58.m08008	AN4316.1	AO070230000004	FG04369.1	AFAO			((FG04369.1:100.0,((AO07023000:100.0,58.m08008:100.0):70.5,AN4316.1:100.0):100.0):100.0,
2198	54.m06431	AN0328.1	AO070334000002	FG06256.1	ANAO			((FG06256.1:100.0,(54.m06431:100.0,(AN0328.1:100.0,AO07033400:100.0):60.0):100.0):100.0,
2199	54.m06432	AN0329.1	AO070334000003	FG06255.1	AFAO			((FG06255.1:100.0,((54.m06432:100.0,AO07033400:100.0):54.0,AN0329.1:100.0):100.0):100.0,
2200	54.m06418	AN0339.1	AO070318000017	FG04322.1	AFAO	yes	yes	((FG04322.1:100.0,(AN0339.1:100.0,(54.m06418:100.0,AO07031800:100.0):100.0):100.0):100.0,
2201	59.m09272	AN2771.1	AO070327000013	FG06352.1	AFAO		yes	((FG06352.1:100.0,((AO07032700:100.0,59.m09272:100.0):89.5,AN2771.1:100.0):100.0):100.0,
2202	54.m06804	AN4241.1	AO070324000173	FG06354.1	ANAO			((FG06354.1:100.0,(54.m06804:100.0,(AN4241.1:100.0,AO07032400:100.0):54.0):100.0):100.0,
2203	56.m03103	AN7313.1	AO070319000136	FG11366.1		yes	yes	(((AO07031900:100.0,56.m03103:100.0):100.0,(AN7313.1:100.0,FG11366.1:100.0):100.0):100.0,
2204	59.m08925	AN3073.1	AO070224000013	FG10797.1	AFAO		yes	((FG10797.1:100.0,((AO07022400:100.0,59.m08925:100.0):89.5,AN3073.1:100.0):100.0):100.0,
2205	59.m08918	AN3080.1	AO070224000006	FG10799.1	AFAO			((FG10799.1:100.0,((AO07022400:100.0,59.m08918:100.0):70.5,AN3080.1:100.0):100.0):100.0,
2206	59.m08916	AN3082.1	AO070224000004	FG10795.1	AFAO	yes	yes	((FG10795.1:100.0,((AO07022400:100.0,59.m08916:100.0):94.0,AN3082.1:100.0):100.0):100.0,
2207	69.m15413	AN3708.1	AO070341000333	FG07949.1	ANAO			((((AN3708.1:100.0,AO07034100:100.0):53.2,69.m15413:100.0):87.0,FG07949.1:100.0):100.0,
2208	69.m15395	AN3687.1	AO070342000308	FG00353.1	ANAO			((((AN3687.1:100.0,AO07034200:100.0):51.0,69.m15395:100.0):96.0,FG00353.1:100.0):100.0,
2209	69.m15371	AN5669.1	AO070342000262	FG06342.1	AFAO			((FG06342.1:100.0,((69.m15371:100.0,AO07034200:100.0):42.5,AN5669.1:100.0):100.0):100.0,
2210	69.m15400	AN3689.1	AO070341000313	FG07044.1	AFAO			((FG07044.1:100.0,((AO07034100:100.0,69.m15400:100.0):57.3,AN3689.1:100.0):100.0):100.0,
2211	57.m05517	AN4594.1	AO070267000010	FG05493.1	ANAO			((FG05493.1:100.0,(57.m05517:100.0,(AN4594.1:100.0,AO07026700:100.0):45.7):100.0):100.0,
2212	62.m03484	AN9007.1	AO070315000107	FG06068.1	AFAO	yes	yes	((FG06068.1:100.0,((AO07031500:100.0,62.m03484:100.0):99.0,AN9007.1:100.0):100.0):100.0,
2213	58.m07314	AN5660.1	AO070342000252	FG10787.1	AFAO			((FG10787.1:100.0,((AO07034200:100.0,58.m07314:100.0):55.5,AN5660.1:100.0):100.0):100.0,
2214	58.m07386	AN0046.1	AO070342000162	FG06880.1			yes	((((AO07034200:100.0,58.m07386:100.0):100.0,FG06880.1:100.0):88.0,AN0046.1:100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2215	65.m07240	AN6730.1	AO070339000174	FG07495.1	AFAO	yes	yes	((FG07495.1:100.0,((AO07033900:100.0,65.m07240:100.0):96.5,AN6730.1:100.0):100.0):100.0,
2216	69.m14895	AN5196.1	AO070237000026	FG01399.1	AFAO			((FG01399.1:100.0,((AO07023700:100.0,69.m14895:100.0):63.0,AN5196.1:100.0):100.0):100.0,
2217	69.m14894	AN5195.1	AO070237000025	FG01398.1	ANAO		yes	((((AN5195.1:100.0,AO07023700:100.0):75.0,69.m14894:100.0):94.7,FG01398.1:100.0):100.0,
2218	69.m14898	AN5199.1	AO070237000029	FG01397.1	AFAO			((FG01397.1:100.0,((AO07023700:100.0,69.m14898:100.0):60.0,AN5199.1:100.0):100.0):100.0,
2219	69.m14899	AN5200.1	AO070237000030	FG01395.1	AFAO	yes	yes	((FG01395.1:100.0,((AO07023700:100.0,69.m14899:100.0):94.5,AN5200.1:100.0):100.0):100.0,
2220	58.m07812	AN3833.1	AO070305000071	FG09396.1	AFAO		yes	((FG09396.1:100.0,((AO07030500:100.0,58.m07812:100.0):76.0,AN3833.1:100.0):100.0):100.0,
2221	58.m07774	AN1698.1	AO070305000022	FG07524.1	AFAO		yes	((FG07524.1:100.0,((AO07030500:100.0,58.m07774:100.0):79.5,AN1698.1:100.0):100.0):100.0,
2222	59.m08953	AN3061.1	AO070337000012	FG10964.1	AFAO			((FG10964.1:100.0,((AO07033700:100.0,59.m08953:100.0):56.0,AN3061.1:100.0):100.0):100.0,
2223	59.m08928	AN3069.1	AO070337000005	FG10940.1	AFAO	yes	yes	((FG10940.1:100.0,((AO07033700:100.0,59.m08928:100.0):99.0,AN3069.1:100.0):100.0):100.0,
2224	63.m00662	AN8354.1	AO070342000083	FG03042.1	AFAO	yes	yes	((FG03042.1:100.0,(AN8354.1:100.0,(63.m00662:100.0,AO07034200:100.0):100.0):100.0):100.0,
2225	58.m07484	AN5558.1	AO070328000053	FG03315.1	ANAO			((FG03315.1:100.0,(58.m07484:100.0,(AN5558.1:100.0,AO07032800:100.0):45.5):100.0):100.0,
2226	58.m07505	AN5578.1	AO070328000026	FG10526.1	AFAO	yes	yes	((FG10526.1:100.0,(AN5578.1:100.0,(58.m07505:100.0,AO07032800:100.0):100.0):100.0):100.0,
2227	72.m19121	AN6036.1	AO070340000252	FG05873.1	AFAO			((FG05873.1:100.0,((AO07034000:100.0,72.m19121:100.0):58.0,AN6036.1:100.0):100.0):100.0,
2228	56.m02304	AN8891.1	AO070293000026	FG07551.1	ANAO			((FG07551.1:100.0,(56.m02304:100.0,(AN8891.1:100.0,AO07029300:100.0):67.5):100.0):100.0,
2229	62.m03458	AN8761.1	AO070277000065	FG10708.1	AFAN			((FG10708.1:100.0,((62.m03458:100.0,AN8761.1:100.0):47.5,AO07027700:100.0):100.0):100.0,
2230	58.m07570	AN1965.1	AO070301000046	FG09299.1	AFAN		yes	((FG09299.1:100.0,(AO07030100:100.0,(AN1965.1:100.0,58.m07570:100.0):82.0):100.0):100.0,
2231	71.m15397	AN0118.1	AO070311000095	FG09607.1	AFAO	yes	yes	((FG09607.1:100.0,(AN0118.1:100.0,(71.m15397:100.0,AO07031100:100.0):100.0):100.0):100.0,
2232	71.m15745	AN7719.1	AO070325000133	FG06186.1	AFAO			((FG06186.1:100.0,((71.m15745:100.0,AO07032500:100.0):55.0,AN7719.1:100.0):100.0):100.0,
2233	71.m15482	AN0229.1	AO070323000079	FG05653.1	AFAO			((FG05653.1:100.0,((71.m15482:100.0,AO07032300:100.0):66.0,AN0229.1:100.0):100.0):100.0,
2234	70.m15424	AN0823.1	AO070255000022	FG05645.1	ANAO		yes	((FG05645.1:100.0,(70.m15424:100.0,(AN0823.1:100.0,AO07025500:100.0):80.5):100.0):100.0,
2235	52.m04025	AN9399.1	AO070274000017	FG09564.1	AFAO		yes	((FG09564.1:100.0,((AO07027400:100.0,52.m04025:100.0):80.0,AN9399.1:100.0):100.0):100.0,
2236	57.m05848	AN7495.1	AO070287000021	FG09807.1	ANAO			((FG09807.1:100.0,((AO07028700:100.0,AN7495.1:100.0):53.0,57.m05848:100.0):100.0):100.0,
2237	57.m05852	AN7492.1	AO070287000025	FG09810.1	AFAN			((FG09810.1:100.0,((57.m05852:100.0,AN7492.1:100.0):52.5,AO07028700:100.0):100.0):100.0,
2238	71.m15848	AN2216.1	AO070294000003	FG09604.1	ANAO	yes	yes	((FG09604.1:100.0,(71.m15848:100.0,(AN2216.1:100.0,AO07029400:100.0):99.0):100.0):100.0,
2239	71.m15836	AN2229.1	AO070326000151	FG05658.1	AFAO			((FG05658.1:100.0,((AO07032600:100.0,71.m15836:100.0):49.8,AN2229.1:100.0):100.0):100.0,
2240	57.m05371	AN6472.1	AO070290000063	FG09751.1	AFAO			((FG09751.1:100.0,((AO07029000:100.0,57.m05371:100.0):49.5,AN6472.1:100.0):100.0):100.0,
2241	52.m04044	AN8293.1	AO070274000002	FG05081.1	ANAO			((FG05081.1:100.0,((AO07027400:100.0,AN8293.1:100.0):54.5,52.m04044:100.0):100.0):100.0,
2242	72.m19162	AN5979.1	AO070307000027	FG05640.1	AFAN	yes	yes	((((72.m19162:100.0,AN5979.1:100.0):99.0,AO07030700:100.0):91.3,FG05640.1:100.0):100.0,
2243	71.m15832	AN2233.1	AO070326000146	FG09598.1	AFAO		yes	((FG09598.1:100.0,((71.m15832:100.0,AO07032600:100.0):77.5,AN2233.1:100.0):100.0):100.0,
2244	71.m15842	AN2224.1	AO070326000179	FG09600.1	AFAN	yes	yes	((FG09600.1:100.0,(AO07032600:100.0,(71.m15842:100.0,AN2224.1:100.0):99.5):100.0):100.0,
2245	71.m15843	AN2223.1	AO070326000180	FG05083.1	AFAO			((FG05083.1:100.0,((71.m15843:100.0,AO07032600:100.0):62.0,AN2223.1:100.0):100.0):100.0,
2246	70.m15380	AN0774.1	AO070316000064	FG08942.1	AFAO	yes	yes	((FG08942.1:100.0,((AO07031600:100.0,70.m15380:100.0):97.0,AN0774.1:100.0):100.0):100.0,
2247	70.m15236	AN1018.1	AO070343000597	FG09615.1	ANAO			((FG09615.1:100.0,(70.m15236:100.0,(AN1018.1:100.0,AO07034300:100.0):68.0):100.0):100.0,
2248	70.m15235	AN1017.1	AO070343000598	FG09612.1	AFAO			((FG09612.1:100.0,((70.m15235:100.0,AO07034300:100.0):59.5,AN1017.1:100.0):100.0):100.0,
2249	70.m15233	AN1015.1	AO070312000003	FG09613.1	AFAO		yes	((FG09613.1:100.0,((AO07031200:100.0,70.m15233:100.0):88.0,AN1015.1:100.0):100.0):100.0,
2250	72.m19434	AN6221.1	AO070304000053	FG05073.1	ANAO			((FG05073.1:100.0,(72.m19434:100.0,(AN6221.1:100.0,AO07030400:100.0):50.5):100.0):100.0,
2251	72.m19257	AN5875.1	AO070308000144	FG06203.1	ANAO			((FG06203.1:100.0,((AO07030800:100.0,AN5875.1:100.0):41.5,72.m19257:100.0):100.0):100.0,
2252	72.m19424	AN6229.1	AO070304000080	FG06202.1	AFAO			((FG06202.1:100.0,((AO07030400:100.0,72.m19424:100.0):68.5,AN6229.1:100.0):100.0):100.0,
2253	54.m06594	AN0476.1	AO070328000164	FG08747.1	AFAO		yes	((FG08747.1:100.0,((AO07032800:100.0,54.m06594:100.0):87.3,AN0476.1:100.0):100.0):100.0,
2254	69.m15112	AN7524.1	AO070258000032	FG08746.1	AFAO			((FG08746.1:100.0,((AO07025800:100.0,69.m15112:100.0):70.5,AN7524.1:100.0):100.0):100.0,
2255	69.m14923	AN1909.1	AO070341000140	FG08629.1	AFAO			((FG08629.1:100.0,((69.m14923:100.0,AO07034100:100.0):63.7,AN1909.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2256	69.m15084	AN7537.1	AO070324000009	FG08631.1	AFAO	yes	yes	((FG08631.1:100.0,((AO07032400:100.0,69.m15084:100.0):94.0,AN7537.1:100.0):100.0):100.0,
2257	70.m15397	AN0787.1	AO070239000021	FG03922.1	AFAO	yes	yes	((FG03922.1:100.0,((AO07023900:100.0,70.m15397:100.0):92.5,AN0787.1:100.0):100.0):100.0,
2258	55.m03194	AN1290.1	AO070339000255	FG02820.1	ANAO			((FG02820.1:100.0,((AO07033900:100.0,AN1290.1:100.0):61.0,55.m03194:100.0):100.0):100.0,
2259	72.m19487	AN6374.1	AO070241000031	FG02752.1	AFAN		yes	((FG02752.1:100.0,(AO07024100:100.0,(AN6374.1:100.0,72.m19487:100.0):78.0):100.0):100.0,
2260	58.m07430	AN3669.1	AO070342000010	FG09275.1	ANAO		yes	((FG09275.1:100.0,(58.m07430:100.0,(AN3669.1:100.0,AO07034200:100.0):81.0):100.0):100.0,
2261	54.m06598	AN0471.1	AO070328000167	FG08758.1	ANAO			((FG08758.1:100.0,(54.m06598:100.0,(AN0471.1:100.0,AO07032800:100.0):61.5):100.0):100.0,
2262	54.m07063	AN0472.1	AO070328000166	FG08757.1	AFAO	yes	yes	((FG08757.1:100.0,((AO07032800:100.0,54.m07063:100.0):98.5,AN0472.1:100.0):100.0):100.0,
2263	72.m19417	AN6240.1	AO070304000091	FG08756.1	AFAO		yes	((FG08756.1:100.0,((AO07030400:100.0,72.m19417:100.0):83.5,AN6240.1:100.0):100.0):100.0,
2264	54.m06445	AN0313.1	AO070334000019	FG01975.1	ANAO			((FG01975.1:100.0,(54.m06445:100.0,(AN0313.1:100.0,AO07033400:100.0):47.5):100.0):100.0,
2265	54.m06444	AN0314.1	AO070334000018	FG01976.1	ANAO			((FG01976.1:100.0,((AO07033400:100.0,AN0314.1:100.0):60.5,54.m06444:100.0):100.0):100.0,
2266	66.m04793	AN1826.1	AO070275000025	FG11291.1				(((AO07027500:100.0,66.m04793:100.0):60.7,(AN1826.1:100.0,FG11291.1:100.0):49.0):100.0,
2267	66.m04732	AN8346.1	AO070275000024	FG03259.1	AFAO			((((AO07027500:100.0,66.m04732:100.0):92.0,AN8346.1:100.0):62.5,FG03259.1:100.0):100.0,
2268	72.m18952	AN5823.1	AO070260000021	FG05371.1	AFAO			((FG05371.1:100.0,((AO07026000:100.0,72.m18952:100.0):58.5,AN5823.1:100.0):100.0):100.0,
2269	71.m15297	AN7959.1	AO070314000099	FG10480.1	AFAN			((FG10480.1:100.0,(AO07031400:100.0,(AN7959.1:100.0,71.m15297:100.0):62.5):100.0):100.0,
2270	57.m05738	AN1878.1	AO070341000173	FG02232.1	AFAO		yes	((FG02232.1:100.0,((AO07034100:100.0,57.m05738:100.0):87.0,AN1878.1:100.0):100.0):100.0,
2271	69.m15419	AN3712.1	AO070341000341	FG02231.1	AFAO			((FG02231.1:100.0,((69.m15419:100.0,AO07034100:100.0):50.3,AN3712.1:100.0):100.0):100.0,
2272	57.m05818	AN2112.1	AO070341000294	FG11348.1	AFAN			((((AN2112.1:100.0,57.m05818:100.0):57.5,AO07034100:100.0):58.5,FG11348.1:100.0):100.0,
2273	59.m09320	AN3459.1	AO070265000036	FG09893.1	ANAO			((FG09893.1:100.0,((AO07026500:100.0,AN3459.1:100.0):57.0,59.m09320:100.0):100.0):100.0,
2274	57.m05914	AN7430.1	AO070229000001	FG09984.1	AFAO			((FG09984.1:100.0,((AO07022900:100.0,57.m05914:100.0):72.0,AN7430.1:100.0):100.0):100.0,
2275	57.m05889	AN7454.1	AO070287000072	FG09986.1	ANAO			((FG09986.1:100.0,((AO07028700:100.0,AN7454.1:100.0):63.5,57.m05889:100.0):100.0):100.0,
2276	70.m15270	AN0667.1	AO070343000553	FG04481.1	AFAN			((FG04481.1:100.0,(AO07034300:100.0,(AN0667.1:100.0,70.m15270:100.0):74.0):100.0):100.0,
2277	70.m15193	AN8968.1	AO070342000435	FG05942.1	ANAO		yes	((((AN8968.1:100.0,AO07034200:100.0):95.0,70.m15193:100.0):75.0,FG05942.1:100.0):100.0,
2278	70.m15784	AN8417.1	AO070343000540	FG04486.1	AFAO	yes	yes	((((AO07034300:100.0,70.m15784:100.0):100.0,AN8417.1:100.0):99.0,FG04486.1:100.0):100.0,
2279	70.m15275	AN0673.1	AO070343000547	FG04485.1	AFAO			((FG04485.1:100.0,((AO07034300:100.0,70.m15275:100.0):59.5,AN0673.1:100.0):100.0):100.0,
2280	59.m08500	AN2489.1	AO070312000131	FG04484.1	ANAO	yes	yes	((FG04484.1:100.0,(59.m08500:100.0,(AN2489.1:100.0,AO07031200:100.0):97.0):100.0):100.0,
2281	59.m09512	AN5020.1	AO070338000180	FG04483.1	AFAO		yes	((FG04483.1:100.0,((AO07033800:100.0,59.m09512:100.0):86.2,AN5020.1:100.0):100.0):100.0,
2282	70.m15272	AN0670.1	AO070343000550	FG04473.1	AFAO			((FG04473.1:100.0,((70.m15272:100.0,AO07034300:100.0):73.5,AN0670.1:100.0):100.0):100.0,
2283	70.m15077	AN8583.1	AO070339000078	FG11217.1				((((FG11217.1:100.0,AO07033900:100.0):54.5,70.m15077:100.0):96.0,AN8583.1:100.0):100.0,
2284	59.m09494	AN5022.1	AO070338000182	FG10315.1	AFAO	yes	yes	((FG10315.1:100.0,(AN5022.1:100.0,(59.m09494:100.0,AO07033800:100.0):100.0):100.0):100.0,
2285	69.m15744	AN6362.1	AO070337000045	FG00756.1	AFAO			(((AN6362.1:100.0,(69.m15744:100.0,AO07033700:100.0):43.5):92.5,FG00756.1:100.0):100.0,
2286	54.m06961	AN5101.1	AO070291000078	FG00028.1	AFAO	yes	yes	((FG00028.1:100.0,((AO07029100:100.0,54.m06961:100.0):94.0,AN5101.1:100.0):100.0):100.0,
2287	71.m15326	AN0055.1	AO070314000132	FG07700.1	ANAO	yes	yes	((FG07700.1:100.0,(71.m15326:100.0,(AN0055.1:100.0,AO07031400:100.0):98.5):100.0):100.0,
2288	53.m03978	AN8162.1	AO070322000035	FG11232.1	AFAN			((FG11232.1:100.0,(AO07032200:100.0,(AN8162.1:100.0,53.m03978:100.0):63.0):100.0):100.0,
2289	70.m15787	AN0675.1	AO070343000544	FG10216.1	AFAO			((FG10216.1:100.0,((70.m15787:100.0,AO07034300:100.0):61.0,AN0675.1:100.0):100.0):100.0,
2290	59.m08507	AN3154.1	AO070312000165	FG10384.1	AFAO	yes	yes	((FG10384.1:100.0,((AO07031200:100.0,59.m08507:100.0):98.0,AN3154.1:100.0):100.0):100.0,
2291	70.m15455	AN0871.1	AO070320000029	FG09635.1	ANAO			((FG09635.1:100.0,((AO07032000:100.0,AN0871.1:100.0):47.3,70.m15455:100.0):100.0):100.0,
2292	69.m15558	AN5346.1	AO070333000176	FG09631.1	AFAO	yes	yes	((FG09631.1:100.0,((AO07033300:100.0,69.m15558:100.0):94.0,AN5346.1:100.0):100.0):100.0,
2293	69.m15551	AN5356.1	AO070333000156	FG09633.1	AFAO			((FG09633.1:100.0,((AO07033300:100.0,69.m15551:100.0):68.0,AN5356.1:100.0):100.0):100.0,
2294	69.m15553	AN5351.1	AO070333000172	FG09630.1	AFAO			((FG09630.1:100.0,((AO07033300:100.0,69.m15553:100.0):45.8,AN5351.1:100.0):100.0):100.0,
2295	70.m15347	AN0714.1	AO070343000454	FG09629.1	AFAO			((FG09629.1:100.0,((70.m15347:100.0,AO07034300:100.0):48.3,AN0714.1:100.0):100.0):100.0,
2296	70.m15343	AN0720.1	AO070343000474	FG09628.1	AFAO			((FG09628.1:100.0,((AO07034300:100.0,70.m15343:100.0):69.5,AN0720.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2297	59.m08593	AN3132.1	AO070303000012	FG09261.1	AFAO			((FG09261.1:100.0,((AO07030300:100.0,59.m08593:100.0):66.0,AN3132.1:100.0):100.0):100.0,
2298	57.m05453	AN7676.1	AO070325000057	FG06565.1	AFAO	yes	yes	((FG06565.1:100.0,((AO07032500:100.0,57.m05453:100.0):98.5,AN7676.1:100.0):100.0):100.0,
2299	72.m19189	AN5973.1	AO070340000333	FG05845.1	AFAO	yes	yes	((FG05845.1:100.0,((AO07034000:100.0,72.m19189:100.0):99.0,AN5973.1:100.0):100.0):100.0,
2300	72.m19944	AN6037.1	AO070340000248	FG05843.1	AFAO	yes	yes	((FG05843.1:100.0,((AO07034000:100.0,72.m19944:100.0):93.0,AN6037.1:100.0):100.0):100.0,
2301	59.m08720	AN2872.1	AO070338000142	FG00591.1	AFAO			((FG00591.1:100.0,((59.m08720:100.0,AO07033800:100.0):59.0,AN2872.1:100.0):100.0):100.0,
2302	59.m08843	AN4939.1	AO070338000004	FG02758.1	AFAO	yes	yes	((FG02758.1:100.0,((AO07033800:100.0,59.m08843:100.0):98.0,AN4939.1:100.0):100.0):100.0,
2303	59.m08830	AN4928.1	AO070338000015	FG00597.1	AFAO	yes	yes	((FG00597.1:100.0,(AN4928.1:100.0,(59.m08830:100.0,AO07033800:100.0):100.0):100.0):100.0,
2304	54.m06802	AN4239.1	AO070324000175	FG01193.1	ANAO			((FG01193.1:100.0,(54.m06802:100.0,(AN4239.1:100.0,AO07032400:100.0):71.5):100.0):100.0,
2305	58.m07474	AN3685.1	AO070328000065	FG01189.1	AFAO		yes	((FG01189.1:100.0,((AO07032800:100.0,58.m07474:100.0):84.5,AN3685.1:100.0):100.0):100.0,
2306	58.m07475	AN5529.1	AO070328000064	FG01188.1	ANAO			((FG01188.1:100.0,(58.m07475:100.0,(AN5529.1:100.0,AO07032800:100.0):62.0):100.0):100.0,
2307	54.m06786	AN4230.1	AO070234000016	FG00600.1	AFAN			((FG00600.1:100.0,(AO07023400:100.0,(AN4230.1:100.0,54.m06786:100.0):41.0):100.0):100.0,
2308	58.m07476	AN5530.1	AO070328000063	FG01187.1	AFAO	yes	yes	((FG01187.1:100.0,((AO07032800:100.0,58.m07476:100.0):92.0,AN5530.1:100.0):100.0):100.0,
2309	58.m07423	AN3677.1	AO070194000005	FG00604.1	AFAO	yes	yes	((FG00604.1:100.0,((AO07019400:100.0,58.m07423:100.0):92.0,AN3677.1:100.0):100.0):100.0,
2310	58.m07422	AN3678.1	AO070194000003	FG00581.1	AFAO		yes	((FG00581.1:100.0,((AO07019400:100.0,58.m07422:100.0):85.5,AN3678.1:100.0):100.0):100.0,
2311	52.m04035	AN9408.1	AO070274000009	FG05322.1	AFAN			((FG05322.1:100.0,(AO07027400:100.0,(AN9408.1:100.0,52.m04035:100.0):65.5):100.0):100.0,
2312	52.m04034	AN9407.1	AO070274000010	FG05321.1	AFAO			((FG05321.1:100.0,((AO07027400:100.0,52.m04034:100.0):59.5,AN9407.1:100.0):100.0):100.0,
2313	72.m19188	AN5972.1	AO070340000330	FG05844.1	ANAO			((FG05844.1:100.0,(72.m19188:100.0,(AN5972.1:100.0,AO07034000:100.0):64.0):100.0):100.0,
2314	71.m15639	AN0243.1	AO070284000073	FG04985.1	ANAO	yes	yes	((FG04985.1:100.0,(71.m15639:100.0,(AO07028400:100.0,AN0243.1:100.0):93.5):100.0):100.0,
2315	69.m15451	AN5512.1	AO070341000384	FG04986.1	AFAO	yes	yes	((FG04986.1:100.0,((AO07034100:100.0,69.m15451:100.0):99.5,AN5512.1:100.0):100.0):100.0,
2316	69.m15570	AN5338.1	AO070333000229	FG06539.1	AFAO			((FG06539.1:100.0,((69.m15570:100.0,AO07033300:100.0):50.0,AN5338.1:100.0):100.0):100.0,
2317	70.m15781	AN0660.1	AO070343000564	FG05277.1	AFAO			((FG05277.1:100.0,((AO07034300:100.0,70.m15781:100.0):68.5,AN0660.1:100.0):100.0):100.0,
2318	69.m15544	AN7534.1	AO070330000186	FG08902.1		yes	yes	(((FG08902.1:100.0,AN7534.1:100.0):100.0,(AO07033000:100.0,69.m15544:100.0):95.0):100.0,
2319	69.m15310	AN0494.1	AO070285000063	FG00571.1	AFAO		yes	((FG00571.1:100.0,((AO07028500:100.0,69.m15310:100.0):86.0,AN0494.1:100.0):100.0):100.0,
2320	70.m15647	AN0635.1	AO070318000125	FG02806.1	AFAN			((((AN0635.1:100.0,70.m15647:100.0):52.3,AO07031800:100.0):92.5,FG02806.1:100.0):100.0,
2321	59.m08997	AN3024.1	AO070337000065	FG10915.1	AFAO		yes	((FG10915.1:100.0,((59.m08997:100.0,AO07033700:100.0):84.5,AN3024.1:100.0):100.0):100.0,
2322	71.m15143	AN9286.1	AO070279000041	FG03629.1	AFAO	yes	yes	(((AN9286.1:100.0,(AO07027900:100.0,71.m15143:100.0):99.0):95.0,FG03629.1:100.0):100.0,
2323	54.m06540	AN4051.1	AO070328000105	FG07925.1	ANAO			((FG07925.1:100.0,((AO07032800:100.0,AN4051.1:100.0):63.5,54.m06540:100.0):100.0):100.0,
2324	58.m08999	AN1961.1	AO070301000041	FG00976.1	ANAO			((FG00976.1:100.0,(58.m08999:100.0,(AN1961.1:100.0,AO07030100:100.0):62.5):100.0):100.0,
2325	55.m02972	AN1469.1	AO070306000092	FG01028.1	AFAO		yes	((FG01028.1:100.0,((55.m02972:100.0,AO07030600:100.0):86.5,AN1469.1:100.0):100.0):100.0,
2326	55.m03058	AN1539.1	AO070334000263	FG00623.1	AFAO			((FG00623.1:100.0,((AO07033400:100.0,55.m03058:100.0):73.0,AN1539.1:100.0):100.0):100.0,
2327	54.m07055	AN5146.1	AO070291000027	FG01027.1	AFAO			((FG01027.1:100.0,((AO07029100:100.0,54.m07055:100.0):47.5,AN5146.1:100.0):100.0):100.0,
2328	54.m06460	AN0301.1	AO070334000040	FG01026.1	AFAO	yes	yes	((FG01026.1:100.0,((AO07033400:100.0,54.m06460:100.0):90.5,AN0301.1:100.0):100.0):100.0,
2329	69.m14814	AN5783.1	AO070249000028	FG01200.1	AFAO		yes	((FG01200.1:100.0,((AO07024900:100.0,69.m14814:100.0):82.5,AN5783.1:100.0):100.0):100.0,
2330	69.m14845	AN5747.1	AO070341000004	FG01198.1	ANAO		yes	((FG01198.1:100.0,(69.m14845:100.0,(AN5747.1:100.0,AO07034100:100.0):81.5):100.0):100.0,
2331	72.m19194	AN5935.1	AO070340000335	FG01311.1	AFAO			((FG01311.1:100.0,((AO07034000:100.0,72.m19194:100.0):52.0,AN5935.1:100.0):100.0):100.0,
2332	72.m19591	AN7572.1	AO070343000419	FG01312.1	AFAO		yes	((FG01312.1:100.0,((AO07034300:100.0,72.m19591:100.0):82.0,AN7572.1:100.0):100.0):100.0,
2333	72.m19558	AN7542.1	AO070277000038	FG01313.1	ANAO			((FG01313.1:100.0,(72.m19558:100.0,(AN7542.1:100.0,AO07027700:100.0):65.7):100.0):100.0,
2334	72.m19557	AN7540.1	AO070277000037	FG01314.1	ANAO			((FG01314.1:100.0,(72.m19557:100.0,(AN7540.1:100.0,AO07027700:100.0):40.5):100.0):100.0,
2335	54.m06630	AN0440.1	AO070338000297	FG00741.1	ANAO			((FG00741.1:100.0,((AO07033800:100.0,AN0440.1:100.0):69.0,54.m06630:100.0):100.0):100.0,
2336	72.m19588	AN7569.1	AO070343000415	FG01038.1	ANAO			((((AN7569.1:100.0,AO07034300:100.0):46.0,72.m19588:100.0):98.0,FG01038.1:100.0):100.0,
2337	55.m02962	AN1458.1	AO070306000074	FG01039.1	AFAO	yes	yes	((FG01039.1:100.0,((AO07030600:100.0,55.m02962:100.0):98.5,AN1458.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2338	69.m14887	AN5148.1	AO070237000017	FG07069.1	AFAO	yes	yes	((FG07069.1:100.0,((AO07023700:100.0,69.m14887:100.0):98.5,AN5148.1:100.0):100.0):100.0,
2339	69.m14867	AN5169.1	AO070247000004	FG07068.1	AFAN	yes	yes	((FG07068.1:100.0,((AN5169.1:100.0,69.m14867:100.0):100.0,AO07024700:100.0):100.0):100.0,
2340	58.m07662	AN1848.1	AO070292000046	FG07067.1	ANAO			((FG07067.1:100.0,(58.m07662:100.0,(AN1848.1:100.0,AO07029200:100.0):64.5):100.0):100.0,
2341	57.m05411	AN7652.1	AO070268000009	FG06867.1	AFAN			((FG06867.1:100.0,((57.m05411:100.0,AN7652.1:100.0):38.5,AO07026800:100.0):100.0):100.0,
2342	55.m02978	AN1476.1	AO070306000099	FG02675.1	AFAO		yes	((FG02675.1:100.0,((AO07030600:100.0,55.m02978:100.0):75.5,AN1476.1:100.0):100.0):100.0,
2343	55.m02977	AN1475.1	AO070306000098	FG06823.1	ANAO			((FG06823.1:100.0,((AO07030600:100.0,AN1475.1:100.0):46.0,55.m02977:100.0):100.0):100.0,
2344	58.m07666	AN1845.1	AO070292000060	FG01033.1	ANAO			((FG01033.1:100.0,((AO07029200:100.0,AN1845.1:100.0):68.3,58.m07666:100.0):100.0):100.0,
2345	59.m09058	AN2936.1	AO070337000172	FG06831.1	AFAO	yes	yes	((FG06831.1:100.0,((AO07033700:100.0,59.m09058:100.0):97.0,AN2936.1:100.0):100.0):100.0,
2346	54.m06676	AN2734.1	AO070338000217	FG06827.1	AFAO			((FG06827.1:100.0,((54.m06676:100.0,AO07033800:100.0):47.5,AN2734.1:100.0):100.0):100.0,
2347	54.m07004	AN2735.1	AO070338000216	FG06826.1	AFAO	yes	yes	((FG06826.1:100.0,((AO07033800:100.0,54.m07004:100.0):96.5,AN2735.1:100.0):100.0):100.0,
2348	54.m06953	AN2739.1	AO070338000234	FG06834.1	AFAO	yes	yes	((FG06834.1:100.0,((AO07033800:100.0,54.m06953:100.0):90.5,AN2739.1:100.0):100.0):100.0,
2349	54.m06673	AN2731.1	AO070338000213	FG06825.1	AFAN			((FG06825.1:100.0,(AO07033800:100.0,(AN2731.1:100.0,54.m06673:100.0):72.5):100.0):100.0,
2350	57.m05795	AN2092.1	AO070341000250	FG06836.1	AFAN			((FG06836.1:100.0,(AO07034100:100.0,(AN2092.1:100.0,57.m05795:100.0):62.3):100.0):100.0,
2351	58.m07376	AN3578.1	AO070342000171	FG06839.1	AFAO			((FG06839.1:100.0,((AO07034200:100.0,58.m07376:100.0):55.0,AN3578.1:100.0):100.0):100.0,
2352	59.m09061	AN2933.1	AO070337000174	FG06840.1	AFAO		yes	((FG06840.1:100.0,((AO07033700:100.0,59.m09061:100.0):89.5,AN2933.1:100.0):100.0):100.0,
2353	62.m03394	AN8676.1	AO070315000096	FG08696.1	AFAO			((FG08696.1:100.0,((AO07031500:100.0,62.m03394:100.0):72.8,AN8676.1:100.0):100.0):100.0,
2354	62.m03357	AN8712.1	AO070315000138	FG08655.1	AFAO			(((AN8712.1:100.0,(AO07031500:100.0,62.m03357:100.0):37.3):97.0,FG08655.1:100.0):100.0,
2355	62.m03468	AN8713.1	AO070315000139	FG08658.1	AFAO		yes	((FG08658.1:100.0,((AO07031500:100.0,62.m03468:100.0):81.5,AN8713.1:100.0):100.0):100.0,
2356	62.m03467	AN6636.1	AO070326000087	FG08596.1	AFAO			((FG08596.1:100.0,((AO07032600:100.0,62.m03467:100.0):58.5,AN6636.1:100.0):100.0):100.0,
2357	62.m03398	AN8672.1	AO070315000089	FG08595.1	AFAO			((FG08595.1:100.0,((AO07031500:100.0,62.m03398:100.0):50.0,AN8672.1:100.0):100.0):100.0,
2358	62.m03396	AN8674.1	AO070315000092	FG08593.1	AFAO			((FG08593.1:100.0,((AO07031500:100.0,62.m03396:100.0):65.5,AN8674.1:100.0):100.0):100.0,
2359	70.m14843	AN1380.1	AO070343000393	FG08614.1	AFAN	yes	yes	((FG08614.1:100.0,((AN1380.1:100.0,70.m14843:100.0):100.0,AO07034300:100.0):100.0):100.0,
2360	54.m06785	AN4231.1	AO070234000015	FG01131.1	AFAO			((FG01131.1:100.0,((AO07023400:100.0,54.m06785:100.0):50.5,AN4231.1:100.0):100.0):100.0,
2361	59.m08619	AN3118.1	AO070303000030	FG01132.1	AFAO			((FG01132.1:100.0,((AO07030300:100.0,59.m08619:100.0):53.0,AN3118.1:100.0):100.0):100.0,
2362	54.m06782	AN4234.1	AO070234000012	FG01133.1	AFAN			((FG01133.1:100.0,(AO07023400:100.0,(AN4234.1:100.0,54.m06782:100.0):58.0):100.0):100.0,
2363	70.m14859	AN1370.1	AO070215000011	FG00518.1	AFAO		yes	((FG00518.1:100.0,((AO07021500:100.0,70.m14859:100.0):84.0,AN1370.1:100.0):100.0):100.0,
2364	70.m14988	AN1231.1	AO070331000243	FG00621.1	AFAO		yes	((FG00621.1:100.0,((AO07033100:100.0,70.m14988:100.0):85.0,AN1231.1:100.0):100.0):100.0,
2365	59.m09424	AN2977.1	AO070337000144	FG01230.1	AFAO			((FG01230.1:100.0,((59.m09424:100.0,AO07033700:100.0):60.0,AN2977.1:100.0):100.0):100.0,
2366	59.m09037	AN2976.1	AO070337000145	FG01229.1	AFAO	yes	yes	((FG01229.1:100.0,((AO07033700:100.0,59.m09037:100.0):97.0,AN2976.1:100.0):100.0):100.0,
2367	58.m07390	AN3590.1	AO070342000142	FG01228.1	AFAO			((FG01228.1:100.0,((AO07034200:100.0,58.m07390:100.0):62.0,AN3590.1:100.0):100.0):100.0,
2368	54.m06529	AN0254.1	AO070334000106	FG01227.1	ANAO			((FG01227.1:100.0,(54.m06529:100.0,(AN0254.1:100.0,AO07033400:100.0):61.5):100.0):100.0,
2369	54.m06489	AN0290.1	AO070334000051	FG01226.1	AFAN		yes	((FG01226.1:100.0,((54.m06489:100.0,AN0290.1:100.0):82.8,AO07033400:100.0):100.0):100.0,
2370	58.m07388	AN3588.1	AO070342000139	FG01233.1	AFAO		yes	((FG01233.1:100.0,((AO07034200:100.0,58.m07388:100.0):83.5,AN3588.1:100.0):100.0):100.0,
2371	55.m03177	AN1607.1	AO070309000147	FG01530.1	AFAO			((FG01530.1:100.0,((AO07030900:100.0,55.m03177:100.0):68.5,AN1607.1:100.0):100.0):100.0,
2372	72.m19077	AN6087.1	AO070340000139	FG09323.1	ANAO			((FG09323.1:100.0,(72.m19077:100.0,(AN6087.1:100.0,AO07034000:100.0):64.0):100.0):100.0,
2373	59.m09031	AN2983.1	AO070337000139	FG00910.1	AFAO		yes	((FG00910.1:100.0,((AO07033700:100.0,59.m09031:100.0):81.5,AN2983.1:100.0):100.0):100.0,
2374	57.m05905	AN7435.1	AO070229000009	FG00911.1	AFAN			((FG00911.1:100.0,(AO07022900:100.0,(AN7435.1:100.0,57.m05905:100.0):68.5):100.0):100.0,
2375	72.m19548	AN1796.1	AO070309000135	FG00283.1	AFAN			((FG00283.1:100.0,(AO07030900:100.0,(AN1796.1:100.0,72.m19548:100.0):54.5):100.0):100.0,
2376	71.m15838	AN2227.1	AO070326000160	FG00088.1	AFAO	yes	yes	((FG00088.1:100.0,(AN2227.1:100.0,(71.m15838:100.0,AO07032600:100.0):100.0):100.0):100.0,
2377	57.m05691	AN3793.1	AO070337000236	FG00852.1	AFAO		yes	((FG00852.1:100.0,((AO07033700:100.0,57.m05691:100.0):79.5,AN3793.1:100.0):100.0):100.0,
2378	69.m14911	AN5213.1	AO070337000268	FG00849.1	AFAO			((FG00849.1:100.0,((AO07033700:100.0,69.m14911:100.0):59.0,AN5213.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2379	69.m14913	AN5215.1	AO070337000264	FG00848.1	AFAO	yes	yes	((FG00848.1:100.0,((AO07033700:100.0,69.m14913:100.0):99.0,AN5215.1:100.0):100.0):100.0,
2380	69.m14916	AN5217.1	AO070337000262	FG00900.1	ANAO			((FG00900.1:100.0,(69.m14916:100.0,(AN5217.1:100.0,AO07033700:100.0):62.0):100.0):100.0,
2381	57.m05908	AN7437.1	AO070229000007	FG01225.1	AFAO		yes	((FG01225.1:100.0,((AO07022900:100.0,57.m05908:100.0):80.5,AN7437.1:100.0):100.0):100.0,
2382	69.m14815	AN5782.1	AO070249000027	FG11179.1	ANAO			((FG11179.1:100.0,(69.m14815:100.0,(AN5782.1:100.0,AO07024900:100.0):52.3):100.0):100.0,
2383	65.m07387	AN3747.1	AO070309000075	FG07110.1	AFAO			((FG07110.1:100.0,((AO07030900:100.0,65.m07387:100.0):62.0,AN3747.1:100.0):100.0):100.0,
2384	72.m19030	AN6132.1	AO070340000067	FG06568.1	AFAO	yes	yes	((FG06568.1:100.0,((AO07034000:100.0,72.m19030:100.0):99.0,AN6132.1:100.0):100.0):100.0,
2385	55.m02974	AN1472.1	AO070306000093	FG03643.1	ANAO		yes	((FG03643.1:100.0,(55.m02974:100.0,(AN1472.1:100.0,AO07030600:100.0):79.0):100.0):100.0,
2386	59.m08707	AN2861.1	AO070338000161	FG06615.1	AFAO	yes	yes	((FG06615.1:100.0,(AN2861.1:100.0,(59.m08707:100.0,AO07033800:100.0):100.0):100.0):100.0,
2387	72.m19014	AN6165.1	AO070340000051	FG06586.1	AFAN		yes	((FG06586.1:100.0,(AO07034000:100.0,(AN6165.1:100.0,72.m19014:100.0):75.0):100.0):100.0,
2388	58.m07557	AN5633.1	AO070301000032	FG10466.1	AFAO	yes	yes	((FG10466.1:100.0,(AN5633.1:100.0,(58.m07557:100.0,AO07030100:100.0):100.0):100.0):100.0,
2389	71.m15953	AN2304.1	AO070271000061	FG06767.1	AFAO	yes	yes	((FG06767.1:100.0,(AN2304.1:100.0,(71.m15953:100.0,AO07027100:100.0):100.0):100.0):100.0,
2390	62.m03168	AN6574.1	AO070326000017	FG06769.1	AFAO	yes	yes	((FG06769.1:100.0,((AO07032600:100.0,62.m03168:100.0):96.0,AN6574.1:100.0):100.0):100.0,
2391	71.m15234	AN6902.1	AO070314000013	FG06705.1	AFAN			((FG06705.1:100.0,(AO07031400:100.0,(AN6902.1:100.0,71.m15234:100.0):65.0):100.0):100.0,
2392	71.m15232	AN6904.1	AO070314000010	FG06703.1	ANAO			((FG06703.1:100.0,(71.m15232:100.0,(AN6904.1:100.0,AO07031400:100.0):48.0):100.0):100.0,
2393	71.m15236	AN6900.1	AO070314000015	FG06702.1	ANAO			((FG06702.1:100.0,(71.m15236:100.0,(AN6900.1:100.0,AO07031400:100.0):74.5):100.0):100.0,
2394	72.m19496	AN6364.1	AO070279000050	FG06754.1	ANAO			((FG06754.1:100.0,((AO07027900:100.0,AN6364.1:100.0):63.0,72.m19496:100.0):100.0):100.0,
2395	72.m19320	AN6313.1	AO070308000069	FG06759.1	AFAO		yes	((FG06759.1:100.0,((AO07030800:100.0,72.m19320:100.0):88.0,AN6313.1:100.0):100.0):100.0,
2396	72.m19781	AN7284.1	AO070297000024	FG06755.1	AFAO	yes	yes	((FG06755.1:100.0,((AO07029700:100.0,72.m19781:100.0):98.0,AN7284.1:100.0):100.0):100.0,
2397	72.m19772	AN7294.1	AO070297000036	FG06756.1	AFAO			((FG06756.1:100.0,((AO07029700:100.0,72.m19772:100.0):46.8,AN7294.1:100.0):100.0):100.0,
2398	72.m19774	AN7293.1	AO070297000034	FG06758.1	AFAO	yes	yes	((FG06758.1:100.0,((AO07029700:100.0,72.m19774:100.0):97.0,AN7293.1:100.0):100.0):100.0,
2399	69.m14865	AN5167.1	AO070247000001	FG06762.1	AFAO	yes	yes	((FG06762.1:100.0,((AO07024700:100.0,69.m14865:100.0):94.0,AN5167.1:100.0):100.0):100.0,
2400	58.m07660	AN1851.1	AO070292000043	FG06761.1	AFAO	yes	yes	((FG06761.1:100.0,((AO07029200:100.0,58.m07660:100.0):99.0,AN1851.1:100.0):100.0):100.0,
2401	70.m15511	AN0902.1	AO070320000074	FG06382.1	ANAO			((FG06382.1:100.0,(70.m15511:100.0,(AN0902.1:100.0,AO07032000:100.0):60.5):100.0):100.0,
2402	72.m19039	AN2184.1	AO070340000082	FG05395.1	AFAO	yes	yes	((FG05395.1:100.0,(AN2184.1:100.0,(72.m19039:100.0,AO07034000:100.0):100.0):100.0):100.0,
2403	53.m03696	AN8261.1	AO070310000040	FG05393.1	ANAO			((FG05393.1:100.0,(53.m03696:100.0,(AN8261.1:100.0,AO07031000:100.0):47.3):100.0):100.0,
2404	59.m08521	AN3144.1	AO070256000047	FG04221.1	AFAO		yes	((FG04221.1:100.0,((AO07025600:100.0,59.m08521:100.0):85.0,AN3144.1:100.0):100.0):100.0,
2405	65.m07269	AN6715.1	AO070339000143	FG04220.1	AFAO		yes	((FG04220.1:100.0,((AO07033900:100.0,65.m07269:100.0):82.5,AN6715.1:100.0):100.0):100.0,
2406	69.m15573	AN5336.1	AO070333000217	FG04235.1	AFAN			((FG04235.1:100.0,((69.m15573:100.0,AN5336.1:100.0):45.0,AO07033300:100.0):100.0):100.0,
2407	69.m15225	AN2434.1	AO070264000045	FG04211.1	AFAN			((FG04211.1:100.0,(AO07026400:100.0,(AN2434.1:100.0,69.m15225:100.0):43.5):100.0):100.0,
2408	65.m07276	AN6703.1	AO070339000139	FG04204.1	AFAO			((FG04204.1:100.0,((AO07033900:100.0,65.m07276:100.0):66.5,AN6703.1:100.0):100.0):100.0,
2409	69.m15218	AN2440.1	AO070264000039	FG02480.1	ANAO			((FG02480.1:100.0,((AO07026400:100.0,AN2440.1:100.0):43.0,69.m15218:100.0):100.0):100.0,
2410	72.m19977	AN6230.1	AO070304000083	FG02471.1	ANAO			((FG02471.1:100.0,((AO07030400:100.0,AN6230.1:100.0):60.0,72.m19977:100.0):100.0):100.0,
2411	57.m05681	AN3799.1	AO070337000228	FG02589.1	AFAO			((FG02589.1:100.0,((AO07033700:100.0,57.m05681:100.0):66.5,AN3799.1:100.0):100.0):100.0,
2412	69.m15305	AN8943.1	AO070226000019	FG09370.1	ANAO			((FG09370.1:100.0,(69.m15305:100.0,(AN8943.1:100.0,AO07022600:100.0):62.0):100.0):100.0,
2413	65.m07261	AN6709.1	AO070339000154	FG04168.1	AFAO			((FG04168.1:100.0,((AO07033900:100.0,65.m07261:100.0):74.5,AN6709.1:100.0):100.0):100.0,
2414	65.m07259	AN6708.1	AO070339000155	FG04171.1	ANAO			((FG04171.1:100.0,(65.m07259:100.0,(AN6708.1:100.0,AO07033900:100.0):54.5):100.0):100.0,
2415	70.m15483	AN0880.1	AO070320000040	FG05109.1	AFAO		yes	((FG05109.1:100.0,((AO07032000:100.0,70.m15483:100.0):80.0,AN0880.1:100.0):100.0):100.0,
2416	70.m15484	AN0881.1	AO070320000049	FG05110.1	AFAO		yes	((FG05110.1:100.0,((AO07032000:100.0,70.m15484:100.0):87.0,AN0881.1:100.0):100.0):100.0,
2417	70.m15490	AN0891.1	AO070320000062	FG05120.1	AFAO			((FG05120.1:100.0,((AO07032000:100.0,70.m15490:100.0):74.0,AN0891.1:100.0):100.0):100.0,
2418	70.m15505	AN0894.1	AO070320000067	FG05108.1	AFAO	yes	yes	((FG05108.1:100.0,((AO07032000:100.0,70.m15505:100.0):96.0,AN0894.1:100.0):100.0):100.0,
2419	72.m19230	AN5900.1	AO070248000034	FG05099.1	AFAO			((FG05099.1:100.0,((AO07024800:100.0,72.m19230:100.0):67.2,AN5900.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2420	72.m19288	AN6190.1	AO070308000111	FG05101.1	ANAO		yes	((FG05101.1:100.0,(72.m19288:100.0,(AN6190.1:100.0,AO07030800:100.0):84.0):100.0):100.0,
2421	72.m19231	AN5899.1	AO070248000035	FG05105.1	AFAO			((FG05105.1:100.0,((AO07024800:100.0,72.m19231:100.0):49.5,AN5899.1:100.0):100.0):100.0,
2422	72.m19267	AN5867.1	AO070308000132	FG01939.1	ANAO			((FG01939.1:100.0,(72.m19267:100.0,(AN5867.1:100.0,AO07030800:100.0):72.0):100.0):100.0,
2423	70.m15210	AN1025.1	AO070312000120	FG06193.1	ANAO			((FG06193.1:100.0,(70.m15210:100.0,(AN1025.1:100.0,AO07031200:100.0):49.8):100.0):100.0,
2424	72.m19248	AN5883.1	AO070245000025	FG09572.1	ANAO		yes	((FG09572.1:100.0,(72.m19248:100.0,(AN5883.1:100.0,AO07024500:100.0):81.0):100.0):100.0,
2425	70.m15221	AN1003.1	AO070312000031	FG09580.1	AFAO	yes	yes	((FG09580.1:100.0,((AO07031200:100.0,70.m15221:100.0):96.5,AN1003.1:100.0):100.0):100.0,
2426	70.m15220	AN1002.1	AO070312000032	FG09579.1	AFAO	yes	yes	((FG09579.1:100.0,(AN1002.1:100.0,(70.m15220:100.0,AO07031200:100.0):100.0):100.0):100.0,
2427	72.m19449	AN6330.1	AO070304000108	FG09574.1	AFAN	yes	yes	((FG09574.1:100.0,(AO07030400:100.0,(AN6330.1:100.0,72.m19449:100.0):94.5):100.0):100.0,
2428	72.m19447	AN6328.1	AO070304000106	FG09576.1	ANAO			((FG09576.1:100.0,(72.m19447:100.0,(AN6328.1:100.0,AO07030400:100.0):67.5):100.0):100.0,
2429	72.m19448	AN6329.1	AO070304000107	FG09575.1	AFAO		yes	((FG09575.1:100.0,((AO07030400:100.0,72.m19448:100.0):88.0,AN6329.1:100.0):100.0):100.0,
2430	72.m18938	AN5808.1	AO070260000039	FG05068.1	ANAO			((FG05068.1:100.0,((AO07026000:100.0,AN5808.1:100.0):57.3,72.m18938:100.0):100.0):100.0,
2431	57.m05835	AN7504.1	AO070287000007	FG09765.1	AFAO			((FG09765.1:100.0,((AO07028700:100.0,57.m05835:100.0):65.0,AN7504.1:100.0):100.0):100.0,
2432	69.m15265	AN0583.1	AO070280000005	FG09766.1	AFAO	yes	yes	((FG09766.1:100.0,((AO07028000:100.0,69.m15265:100.0):95.0,AN0583.1:100.0):100.0):100.0,
2433	69.m15259	AN0590.1	AO070280000012	FG09767.1	AFAO			((FG09767.1:100.0,((AO07028000:100.0,69.m15259:100.0):70.0,AN0590.1:100.0):100.0):100.0,
2434	69.m15266	AN0582.1	AO070280000004	FG09724.1	ANAO			((FG09724.1:100.0,((AO07028000:100.0,AN0582.1:100.0):48.5,69.m15266:100.0):100.0):100.0,
2435	69.m15690	AN0579.1	AO070280000001	FG09722.1	AFAO		yes	((FG09722.1:100.0,((AO07028000:100.0,69.m15690:100.0):84.0,AN0579.1:100.0):100.0):100.0,
2436	71.m15406	AN0125.1	AO070311000087	FG09783.1	AFAO			((FG09783.1:100.0,((AO07031100:100.0,71.m15406:100.0):65.5,AN0125.1:100.0):100.0):100.0,
2437	71.m15405	AN0124.1	AO070311000088	FG09784.1	AFAO		yes	((FG09784.1:100.0,((AO07031100:100.0,71.m15405:100.0):80.0,AN0124.1:100.0):100.0):100.0,
2438	72.m19243	AN5887.1	AO070245000020	FG00053.1	AFAO		yes	((FG00053.1:100.0,((AO07024500:100.0,72.m19243:100.0):86.5,AN5887.1:100.0):100.0):100.0,
2439	71.m15266	AN6866.1	AO070314000070	FG09602.1	AFAO			((FG09602.1:100.0,((71.m15266:100.0,AO07031400:100.0):44.8,AN6866.1:100.0):100.0):100.0,
2440	71.m15267	AN6865.1	AO070314000071	FG09601.1	AFAO	yes	yes	((FG09601.1:100.0,((AO07031400:100.0,71.m15267:100.0):93.0,AN6865.1:100.0):100.0):100.0,
2441	71.m15877	AN2243.1	AO070326000130	FG09554.1	AFAO		yes	((FG09554.1:100.0,((AO07032600:100.0,71.m15877:100.0):84.0,AN2243.1:100.0):100.0):100.0,
2442	71.m15948	AN2299.1	AO070295000080	FG02008.1	AFAO			((FG02008.1:100.0,((AO07029500:100.0,71.m15948:100.0):62.5,AN2299.1:100.0):100.0):100.0,
2443	66.m04728	AN8089.1	AO070332000054	FG10823.1	AFAN	yes	yes	((FG10823.1:100.0,(AO07033200:100.0,(AN8089.1:100.0,66.m04728:100.0):95.0):100.0):100.0,
2444	71.m15968	AN8837.1	AO070271000041	FG02072.1	AFAO		yes	((FG02072.1:100.0,((AO07027100:100.0,71.m15968:100.0):80.5,AN8837.1:100.0):100.0):100.0,
2445	58.m07723	AN1631.1	AO070299000043	FG02145.1	AFAN			((FG02145.1:100.0,((58.m07723:100.0,AN1631.1:100.0):46.0,AO07029900:100.0):100.0):100.0,
2446	71.m15510	AN0057.1	AO070253000025	FG07436.1		yes	yes	(((AO07025300:100.0,AN0057.1:100.0):100.0,(FG07436.1:100.0,71.m15510:100.0):99.0):100.0,
2447	71.m15600	AN8793.1	AO070276000066	FG09012.1	AFAO			((FG09012.1:100.0,((71.m15600:100.0,AO07027600:100.0):53.5,AN8793.1:100.0):100.0):100.0,
2448	53.m03737	AN8232.1	AO070310000076	FG09011.1	AFAO	yes	yes	((FG09011.1:100.0,((AO07031000:100.0,53.m03737:100.0):95.0,AN8232.1:100.0):100.0):100.0,
2449	62.m03432	AN6534.1	AO070270000051	FG03803.1	AFAO	yes	yes	((FG03803.1:100.0,((AO07027000:100.0,62.m03432:100.0):91.0,AN6534.1:100.0):100.0):100.0,
2450	53.m03851	AN7996.1	AO070322000049	FG08969.1	AFAO	yes	yes	((FG08969.1:100.0,((AO07032200:100.0,53.m03851:100.0):96.5,AN7996.1:100.0):100.0):100.0,
2451	58.m07396	AN3597.1	AO070342000150	FG02047.1	AFAO		yes	((FG02047.1:100.0,((58.m07396:100.0,AO07034200:100.0):88.5,AN3597.1:100.0):100.0):100.0,
2452	58.m07399	AN3602.1	AO070342000154	FG02043.1	AFAO		yes	((FG02043.1:100.0,((AO07034200:100.0,58.m07399:100.0):83.0,AN3602.1:100.0):100.0):100.0,
2453	58.m07398	AN3600.1	AO070342000153	FG02044.1	AFAN			((FG02044.1:100.0,(AO07034200:100.0,(AN3600.1:100.0,58.m07398:100.0):60.0):100.0):100.0,
2454	72.m19370	AN6273.1	AO070304000011	FG11205.1	ANAO	yes	yes	((FG11205.1:100.0,(72.m19370:100.0,(AN6273.1:100.0,AO07030400:100.0):94.0):100.0):100.0,
2455	53.m03717	AN8248.1	AO070310000058	FG06111.1	ANAO			((FG06111.1:100.0,(53.m03717:100.0,(AN8248.1:100.0,AO07031000:100.0):62.0):100.0):100.0,
2456	59.m08724	AN2875.1	AO070338000136	FG02770.1	AFAO			((FG02770.1:100.0,((59.m08724:100.0,AO07033800:100.0):57.8,AN2875.1:100.0):100.0):100.0,
2457	56.m03091	AN8945.1	AO070319000047	FG04837.1	ANAO			((FG04837.1:100.0,(56.m03091:100.0,(AN8945.1:100.0,AO07031900:100.0):52.5):100.0):100.0,
2458	63.m00629	AN0362.1	AO070318000042	FG02190.1	ANAO			(((63.m00629:100.0,(AN0362.1:100.0,AO07031800:100.0):52.5):79.5,FG02190.1:100.0):100.0,
2459	52.m03714	AN4111.1	AO070342000382	FG04667.1	AFAO			((FG04667.1:100.0,((52.m03714:100.0,AO07034200:100.0):64.8,AN4111.1:100.0):100.0):100.0,
2460	52.m04073	AN4109.1	AO070342000385	FG11475.1	AFAO		yes	((FG11475.1:100.0,((AO07034200:100.0,52.m04073:100.0):75.5,AN4109.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2461	71.m15235	AN6901.1	AO070314000014	FG02590.1	AFAO			((FG02590.1:100.0,((71.m15235:100.0,AO07031400:100.0):48.5,AN6901.1:100.0):100.0):100.0,
2462	54.m06703	AN4060.1	AO070342000045	FG02588.1	AFAO		yes	((FG02588.1:100.0,((AO07034200:100.0,54.m06703:100.0):79.5,AN4060.1:100.0):100.0):100.0,
2463	72.m19174	AN5960.1	AO070340000311	FG02541.1	ANAO	yes	yes	((FG02541.1:100.0,(72.m19174:100.0,(AO07034000:100.0,AN5960.1:100.0):90.0):100.0):100.0,
2464	72.m19792	AN7258.1	AO070297000014	FG04119.1	AFAO	yes	yes	((FG04119.1:100.0,((AO07029700:100.0,72.m19792:100.0):93.0,AN7258.1:100.0):100.0):100.0,
2465	72.m19945	AN6046.1	AO070340000236	FG04123.1	ANAO			((FG04123.1:100.0,((AO07034000:100.0,AN6046.1:100.0):55.5,72.m19945:100.0):100.0):100.0,
2466	72.m19114	AN6045.1	AO070340000237	FG04124.1	AFAN			((FG04124.1:100.0,(AO07034000:100.0,(AN6045.1:100.0,72.m19114:100.0):58.0):100.0):100.0,
2467	72.m19180	AN9469.1	AO070340000318	FG04125.1	ANAO			((FG04125.1:100.0,(72.m19180:100.0,(AN9469.1:100.0,AO07034000:100.0):60.5):100.0):100.0,
2468	72.m19181	AN9470.1	AO070340000319	FG04126.1	ANAO			((FG04126.1:100.0,(72.m19181:100.0,(AN9470.1:100.0,AO07034000:100.0):59.0):100.0):100.0,
2469	72.m19176	AN5958.1	AO070340000315	FG04127.1	AFAO	yes	yes	((FG04127.1:100.0,((72.m19176:100.0,AO07034000:100.0):92.0,AN5958.1:100.0):100.0):100.0,
2470	65.m07414	AN5688.1	AO070309000104	FG05593.1	ANAO		yes	((FG05593.1:100.0,(65.m07414:100.0,(AN5688.1:100.0,AO07030900:100.0):80.0):100.0):100.0,
2471	59.m09135	AN4843.1	AO070327000126	FG01235.1	ANAO			((FG01235.1:100.0,((AO07032700:100.0,AN4843.1:100.0):56.0,59.m09135:100.0):100.0):100.0,
2472	58.m07861	AN4471.1	AO070305000130	FG05585.1	ANAO			((FG05585.1:100.0,(58.m07861:100.0,(AN4471.1:100.0,AO07030500:100.0):74.5):100.0):100.0,
2473	72.m19197	AN5932.1	AO070340000348	FG05421.1	AFAO	yes	yes	((FG05421.1:100.0,((AO07034000:100.0,72.m19197:100.0):97.0,AN5932.1:100.0):100.0):100.0,
2474	70.m15141	AN1091.1	AO070285000058	FG05417.1	ANAO			((FG05417.1:100.0,(70.m15141:100.0,(AN1091.1:100.0,AO07028500:100.0):65.5):100.0):100.0,
2475	71.m15585	AN8791.1	AO070276000072	FG05506.1	AFAN		yes	((FG05506.1:100.0,(AO07027600:100.0,(AN8791.1:100.0,71.m15585:100.0):77.3):100.0):100.0,
2476	71.m15343	AN0066.1	AO070314000155	FG05414.1	ANAO			((FG05414.1:100.0,(71.m15343:100.0,(AN0066.1:100.0,AO07031400:100.0):60.0):100.0):100.0,
2477	71.m15342	AN0065.1	AO070314000154	FG05413.1	AFAO		yes	((FG05413.1:100.0,((AO07031400:100.0,71.m15342:100.0):83.5,AN0065.1:100.0):100.0):100.0,
2478	71.m15344	AN0067.1	AO070314000157	FG05409.1	ANAO			((FG05409.1:100.0,((AO07031400:100.0,AN0067.1:100.0):70.8,71.m15344:100.0):100.0):100.0,
2479	71.m15337	AN0061.1	AO070314000148	FG05410.1	AFAO	yes	yes	((FG05410.1:100.0,((AO07031400:100.0,71.m15337:100.0):99.0,AN0061.1:100.0):100.0):100.0,
2480	70.m14975	AN1244.1	AO070223000006	FG03979.1	AFAO	yes	yes	((FG03979.1:100.0,((AO07022300:100.0,70.m14975:100.0):94.0,AN1244.1:100.0):100.0):100.0,
2481	70.m14974	AN1246.1	AO070223000009	FG03992.1	AFAO			((FG03992.1:100.0,((AO07022300:100.0,70.m14974:100.0):62.0,AN1246.1:100.0):100.0):100.0,
2482	70.m15739	AN1247.1	AO070223000010	FG03994.1	AFAO			((FG03994.1:100.0,((AO07022300:100.0,70.m15739:100.0):61.0,AN1247.1:100.0):100.0):100.0,
2483	65.m07265	AN6700.1	AO070339000147	FG04181.1	ANAO			((FG04181.1:100.0,(65.m07265:100.0,(AN6700.1:100.0,AO07033900:100.0):60.0):100.0):100.0,
2484	57.m05493	AN9157.1	AO070286000083	FG02555.1				((((AO07028600:100.0,FG02555.1:100.0):46.5,AN9157.1:100.0):49.5,57.m05493:100.0):100.0,
2485	70.m14958	AN1261.1	AO070214000004	FG05613.1	AFAO	yes	yes	((FG05613.1:100.0,((AO07021400:100.0,70.m14958:100.0):97.5,AN1261.1:100.0):100.0):100.0,
2486	70.m14937	AN1270.1	AO070332000019	FG05614.1	AFAN			((FG05614.1:100.0,(AO07033200:100.0,(AN1270.1:100.0,70.m14937:100.0):56.5):100.0):100.0,
2487	70.m14953	AN1263.1	AO070332000001	FG05615.1	AFAO			((FG05615.1:100.0,((AO07033200:100.0,70.m14953:100.0):50.8,AN1263.1:100.0):100.0):100.0,
2488	58.m07480	AN5534.1	AO070328000057	FG04024.1	AFAO	yes	yes	((FG04024.1:100.0,((AO07032800:100.0,58.m07480:100.0):94.5,AN5534.1:100.0):100.0):100.0,
2489	52.m03894	AN8767.1	AO070299000022	FG02772.1	AFAO	yes	yes	((FG02772.1:100.0,((AO07029900:100.0,52.m03894:100.0):98.5,AN8767.1:100.0):100.0):100.0,
2490	58.m07473	AN3628.1	AO070328000066	FG02774.1	AFAO			((FG02774.1:100.0,((AO07032800:100.0,58.m07473:100.0):50.5,AN3628.1:100.0):100.0):100.0,
2491	72.m19946	AN6047.1	AO070340000229	FG09738.1	AFAN			((FG09738.1:100.0,(AO07034000:100.0,(AN6047.1:100.0,72.m19946:100.0):66.0):100.0):100.0,
2492	72.m19935	AN6048.1	AO070340000228	FG09739.1	AFAO			((FG09739.1:100.0,((AO07034000:100.0,72.m19935:100.0):61.5,AN6048.1:100.0):100.0):100.0,
2493	66.m04595	AN1239.1	AO070315000009	FG01385.1	ANAO		yes	((((AO07031500:100.0,AN1239.1:100.0):100.0,66.m04595:100.0):78.0,FG01385.1:100.0):100.0,
2494	59.m08516	AN3147.1	AO070256000043	FG01974.1	AFAO			(((AN3147.1:100.0,(AO07025600:100.0,59.m08516:100.0):55.5):94.5,FG01974.1:100.0):100.0,
2495	69.m15760	AN5353.1	AO070302000060	FG03674.1	AFAN		yes	((((AN5353.1:100.0,69.m15760:100.0):100.0,AO07030200:100.0):78.5,FG03674.1:100.0):100.0,
2496	54.m06846	AN5726.1	AO070324000125	FG01341.1	ANAO	yes	yes	((FG01341.1:100.0,(54.m06846:100.0,(AN5726.1:100.0,AO07032400:100.0):90.0):100.0):100.0,
2497	57.m05801	AN2099.1	AO070341000258	FG01342.1	ANAO			((FG01342.1:100.0,(57.m05801:100.0,(AN2099.1:100.0,AO07034100:100.0):50.5):100.0):100.0,
2498	69.m14811	AN5786.1	AO070249000032	FG01344.1	ANAO			((FG01344.1:100.0,((AO07024900:100.0,AN5786.1:100.0):54.0,69.m14811:100.0):100.0):100.0,
2499	69.m14812	AN5785.1	AO070249000030	FG01345.1	AFAN			((FG01345.1:100.0,((69.m14812:100.0,AN5785.1:100.0):51.5,AO07024900:100.0):100.0):100.0,
2500	71.m15812	AN7770.1	AO070286000023	FG00407.1	ANAO		yes	((FG00407.1:100.0,(71.m15812:100.0,(AN7770.1:100.0,AO07028600:100.0):89.5):100.0):100.0,
2501	53.m03914	AN8063.1	AO070330000019	FG00406.1	AFAO			((FG00406.1:100.0,((AO07033000:100.0,53.m03914:100.0):62.0,AN8063.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2502	69.m15632	AN5763.1	AO070193000009	FG00405.1	AFAO	yes	yes	((FG00405.1:100.0,((AO07019300:100.0,69.m15632:100.0):98.5,AN5763.1:100.0):100.0):100.0,
2503	59.m08852	AN4947.1	AO070166000003	FG04044.1	AFAN		yes	((FG04044.1:100.0,(AO07016600:100.0,(AN4947.1:100.0,59.m08852:100.0):83.2):100.0):100.0,
2504	59.m08727	AN2880.1	AO070338000135	FG04042.1	AFAO			((FG04042.1:100.0,((AO07033800:100.0,59.m08727:100.0):66.0,AN2880.1:100.0):100.0):100.0,
2505	71.m15896	AN2256.1	AO070326000107	FG09828.1	AFAO	yes	yes	((FG09828.1:100.0,((AO07032600:100.0,71.m15896:100.0):96.0,AN2256.1:100.0):100.0):100.0,
2506	59.m08861	AN4956.1	AO070288000018	FG01086.1	AFAO		yes	((FG01086.1:100.0,((AO07028800:100.0,59.m08861:100.0):81.0,AN4956.1:100.0):100.0):100.0,
2507	72.m19436	AN9491.1	AO070304000051	FG01931.1	AFAO			((FG01931.1:100.0,((AO07030400:100.0,72.m19436:100.0):56.0,AN9491.1:100.0):100.0):100.0,
2508	54.m07018	AN4035.1	AO070328000127	FG06915.1	ANAO		yes	((FG06915.1:100.0,(54.m07018:100.0,(AN4035.1:100.0,AO07032800:100.0):84.5):100.0):100.0,
2509	72.m19293	AN6194.1	AO070308000104	FG05329.1	AFAO	yes	yes	((FG05329.1:100.0,((AO07030800:100.0,72.m19293:100.0):97.0,AN6194.1:100.0):100.0):100.0,
2510	72.m19361	AN6279.1	AO070308000038	FG01924.1	AFAO		yes	((FG01924.1:100.0,((AO07030800:100.0,72.m19361:100.0):84.0,AN6279.1:100.0):100.0):100.0,
2511	65.m07280	AN6705.1	AO070339000135	FG01925.1	AFAO	yes	yes	((FG01925.1:100.0,((AO07033900:100.0,65.m07280:100.0):96.0,AN6705.1:100.0):100.0):100.0,
2512	72.m19369	AN6272.1	AO070304000012	FG01927.1	AFAN			((FG01927.1:100.0,((72.m19369:100.0,AN6272.1:100.0):72.5,AO07030400:100.0):100.0):100.0,
2513	70.m15632	AN0991.1	AO070318000146	FG02168.1	ANAO			((FG02168.1:100.0,((AO07031800:100.0,AN0991.1:100.0):67.5,70.m15632:100.0):100.0):100.0,
2514	54.m06427	AN0331.1	AO070318000004	FG03940.1	AFAO			((FG03940.1:100.0,(AN0331.1:100.0,(54.m06427:100.0,AO07031800:100.0):83.0):59.8):100.0,
2515	72.m19751	AN7312.1	AO070297000060	FG04282.1	AFAO		yes	((FG04282.1:100.0,((AO07029700:100.0,72.m19751:100.0):85.0,AN7312.1:100.0):100.0):100.0,
2516	71.m15387	AN0112.1	AO070311000096	FG04279.1	ANAO			((FG04279.1:100.0,(71.m15387:100.0,(AN0112.1:100.0,AO07031100:100.0):62.5):100.0):100.0,
2517	72.m19688	AN2153.1	AO070343000202	FG04277.1	AFAO	yes	yes	((FG04277.1:100.0,((AO07034300:100.0,72.m19688:100.0):92.5,AN2153.1:100.0):100.0):100.0,
2518	71.m15473	AN0210.1	AO070321000034	FG04270.1	AFAO		yes	((FG04270.1:100.0,((AO07032100:100.0,71.m15473:100.0):86.5,AN0210.1:100.0):100.0):100.0,
2519	71.m15463	AN0193.1	AO070321000051	FG04272.1	AFAO			((FG04272.1:100.0,((AO07032100:100.0,71.m15463:100.0):50.2,AN0193.1:100.0):100.0):100.0,
2520	71.m15461	AN0191.1	AO070321000052	FG04274.1	ANAO			((FG04274.1:100.0,((AO07032100:100.0,AN0191.1:100.0):39.2,71.m15461:100.0):100.0):100.0,
2521	71.m15460	AN0190.1	AO070321000053	FG04275.1	AFAN			((FG04275.1:100.0,(AO07032100:100.0,(AN0190.1:100.0,71.m15460:100.0):66.0):100.0):100.0,
2522	69.m15216	AN2442.1	AO070264000033	FG04276.1	AFAO	yes	yes	((FG04276.1:100.0,((AO07026400:100.0,69.m15216:100.0):99.0,AN2442.1:100.0):100.0):100.0,
2523	71.m16048	AN0109.1	AO070311000111	FG04286.1	ANAO			((FG04286.1:100.0,(71.m16048:100.0,(AN0109.1:100.0,AO07031100:100.0):72.5):100.0):100.0,
2524	71.m15386	AN0111.1	AO070311000109	FG04284.1	AFAO			((FG04284.1:100.0,((AO07031100:100.0,71.m15386:100.0):47.0,AN0111.1:100.0):100.0):100.0,
2525	69.m15217	AN2441.1	AO070264000038	FG04268.1	AFAO		yes	((FG04268.1:100.0,((69.m15217:100.0,AO07026400:100.0):84.0,AN2441.1:100.0):100.0):100.0,
2526	71.m16064	AN0179.1	AO070321000059	FG04260.1	AFAO		yes	((FG04260.1:100.0,((AO07032100:100.0,71.m16064:100.0):83.5,AN0179.1:100.0):100.0):100.0,
2527	72.m20002	AN2154.1	AO070343000203	FG05066.1	AFAO		yes	((FG05066.1:100.0,((AO07034300:100.0,72.m20002:100.0):78.5,AN2154.1:100.0):100.0):100.0,
2528	62.m03252	AN6652.1	AO070269000016	FG00166.1	AFAO		yes	((FG00166.1:100.0,((AO07026900:100.0,62.m03252:100.0):89.5,AN6652.1:100.0):100.0):100.0,
2529	62.m03171	AN6581.1	AO070326000030	FG07383.1	AFAO	yes	yes	((FG07383.1:100.0,(AN6581.1:100.0,(62.m03171:100.0,AO07032600:100.0):100.0):100.0):100.0,
2530	71.m15562	AN3862.1	AO070308000044	FG02137.1	ANAO	yes	yes	((((AN3862.1:100.0,AO07030800:100.0):91.0,71.m15562:100.0):94.5,FG02137.1:100.0):100.0,
2531	71.m16097	AN2754.1	AO070276000006	FG09437.1	AFAO			((FG09437.1:100.0,((AO07027600:100.0,71.m16097:100.0):65.0,AN2754.1:100.0):100.0):100.0,
2532	71.m15720	AN7698.1	AO070325000103	FG09435.1	AFAO		yes	((FG09435.1:100.0,((AO07032500:100.0,71.m15720:100.0):84.0,AN7698.1:100.0):100.0):100.0,
2533	57.m05529	AN4612.1	AO070267000028	FG09434.1	AFAO	yes	yes	((FG09434.1:100.0,((AO07026700:100.0,57.m05529:100.0):90.5,AN4612.1:100.0):100.0):100.0,
2534	71.m15727	AN7701.1	AO070325000108	FG09438.1	ANAO			((FG09438.1:100.0,(71.m15727:100.0,(AN7701.1:100.0,AO07032500:100.0):43.3):100.0):100.0,
2535	59.m09204	AN4779.1	AO070329000071	FG09429.1	AFAO	yes	yes	((FG09429.1:100.0,((AO07032900:100.0,59.m09204:100.0):90.0,AN4779.1:100.0):100.0):100.0,
2536	59.m09207	AN4776.1	AO070329000076	FG09431.1	AFAO	yes	yes	((FG09431.1:100.0,((AO07032900:100.0,59.m09207:100.0):97.5,AN4776.1:100.0):100.0):100.0,
2537	72.m19948	AN6072.1	AO070340000116	FG00501.1	AFAN	yes	yes	((FG00501.1:100.0,(AO07034000:100.0,(AN6072.1:100.0,72.m19948:100.0):96.0):100.0):100.0,
2538	69.m15595	AN0013.1	AO070333000040	FG11495.1	AFAN			((((69.m15595:100.0,AN0013.1:100.0):39.3,AO07033300:100.0):65.5,FG11495.1:100.0):100.0,
2539	65.m07385	AN3749.1	AO070309000073	FG07112.1	AFAO			((FG07112.1:100.0,((65.m07385:100.0,AO07030900:100.0):57.0,AN3749.1:100.0):100.0):100.0,
2540	72.m19149	AN5991.1	AO070340000286	FG07104.1	AFAO	yes	yes	((FG07104.1:100.0,((AO07034000:100.0,72.m19149:100.0):99.0,AN5991.1:100.0):100.0):100.0,
2541	72.m19148	AN5992.1	AO070340000285	FG07105.1	AFAO			((FG07105.1:100.0,((AO07034000:100.0,72.m19148:100.0):68.0,AN5992.1:100.0):100.0):100.0,
2542	65.m07391	AN3744.1	AO070309000079	FG07106.1	AFAO	yes	yes	((FG07106.1:100.0,((AO07030900:100.0,65.m07391:100.0):99.0,AN3744.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2543	65.m07390	AN3745.1	AO070309000078	FG07107.1	AFAO			((FG07107.1:100.0,((AO07030900:100.0,65.m07390:100.0):64.0,AN3745.1:100.0):100.0):100.0,
2544	70.m15829	AN8317.1	AO070323000152	FG08715.1	AFAN	yes	yes	((((AN8317.1:100.0,70.m15829:100.0):99.0,AO07032300:100.0):98.0,FG08715.1:100.0):100.0,
2545	58.m07794	AN1708.1	AO070305000041	FG07549.1	AFAO			((FG07549.1:100.0,((AO07030500:100.0,58.m07794:100.0):61.5,AN1708.1:100.0):100.0):100.0,
2546	69.m14851	AN5753.1	AO070329000011	FG10755.1	AFAN		yes	((FG10755.1:100.0,(AO07032900:100.0,(AN5753.1:100.0,69.m14851:100.0):80.3):100.0):100.0,
2547	58.m07904	AN4415.1	AO070273000036	FG10422.1	AFAO		yes	((FG10422.1:100.0,((AO07027300:100.0,58.m07904:100.0):87.0,AN4415.1:100.0):100.0):100.0,
2548	52.m04017	AN9394.1	AO070274000022	FG02146.1	AFAO	yes	yes	((FG02146.1:100.0,((AO07027400:100.0,52.m04017:100.0):92.5,AN9394.1:100.0):100.0):100.0,
2549	57.m05434	AN7664.1	AO070268000037	FG04995.1	ANAO			((FG04995.1:100.0,(57.m05434:100.0,(AN7664.1:100.0,AO07026800:100.0):60.0):100.0):100.0,
2550	69.m15460	AN5493.1	AO070341000392	FG10531.1	AFAO		yes	((FG10531.1:100.0,((AO07034100:100.0,69.m15460:100.0):87.0,AN5493.1:100.0):100.0):100.0,
2551	69.m14849	AN5751.1	AO070341000008	FG10482.1	AFAO	yes	yes	((FG10482.1:100.0,((AO07034100:100.0,69.m14849:100.0):97.0,AN5751.1:100.0):100.0):100.0,
2552	59.m08483	AN6923.1	AO070318000108	FG01734.1	AFAO		yes	((FG01734.1:100.0,((AO07031800:100.0,59.m08483:100.0):79.5,AN6923.1:100.0):100.0):100.0,
2553	69.m15032	AN8622.1	AO070289000005	FG06610.1			yes	((69.m15032:100.0,(FG06610.1:100.0,(AO07028900:100.0,AN8622.1:100.0):89.0):98.5):100.0,
2554	58.m07908	AN4419.1	AO070273000041	FG10516.1	AFAO			((FG10516.1:100.0,((AO07027300:100.0,58.m07908:100.0):53.7,AN4419.1:100.0):100.0):100.0,
2555	69.m14855	AN5758.1	AO070341000017	FG10514.1	AFAO		yes	((FG10514.1:100.0,((69.m14855:100.0,AO07034100:100.0):75.5,AN5758.1:100.0):100.0):100.0,
2556	59.m09099	AN2914.1	AO070329000158	FG03694.1	AFAO	yes	yes	((FG03694.1:100.0,((AO07032900:100.0,59.m09099:100.0):95.0,AN2914.1:100.0):100.0):100.0,
2557	56.m02532	AN1783.1	AO070329000184	FG01586.1				(((56.m02532:100.0,FG01586.1:100.0):32.2,(AN1783.1:100.0,AO07032900:100.0):34.7):100.0,
2558	58.m07611	AN2003.1	AO070301000104	FG10425.1	AFAO	yes	yes	((FG10425.1:100.0,((AO07030100:100.0,58.m07611:100.0):91.5,AN2003.1:100.0):100.0):100.0,
2559	54.m06616	AN0455.1	AO070328000183	FG10426.1	ANAO			((FG10426.1:100.0,((AO07032800:100.0,AN0455.1:100.0):56.3,54.m06616:100.0):100.0):100.0,
2560	58.m07728	AN1633.1	AO070299000055	FG07485.1	AFAN			((FG07485.1:100.0,(AO07029900:100.0,(AN1633.1:100.0,58.m07728:100.0):49.5):100.0):100.0,
2561	55.m03098	AN3337.1	AO070293000073	FG02386.1	AFAN			((((AN3337.1:100.0,55.m03098:100.0):65.0,AO07029300:100.0):91.0,FG02386.1:100.0):100.0,
2562	58.m07733	AN1665.1	AO070299000047	FG07520.1	AFAO	yes	yes	((FG07520.1:100.0,((AO07029900:100.0,58.m07733:100.0):98.5,AN1665.1:100.0):100.0):100.0,
2563	57.m05385	AN5537.1	AO070294000074	FG07519.1	AFAO		yes	((FG07519.1:100.0,((AO07029400:100.0,57.m05385:100.0):85.5,AN5537.1:100.0):100.0):100.0,
2564	72.m19492	AN6368.1	AO070279000054	FG06576.1	AFAO		yes	((FG06576.1:100.0,((AO07027900:100.0,72.m19492:100.0):88.0,AN6368.1:100.0):100.0):100.0,
2565	69.m15764	AN3268.1	AO070304000069	FG06556.1	AFAO	yes	yes	((FG06556.1:100.0,(AN3268.1:100.0,(69.m15764:100.0,AO07030400:100.0):100.0):100.0):100.0,
2566	72.m18947	AN5820.1	AO070260000026	FG06544.1	AFAN			((FG06544.1:100.0,(AO07026000:100.0,(AN5820.1:100.0,72.m18947:100.0):53.0):100.0):100.0,
2567	72.m18946	AN5819.1	AO070260000028	FG06543.1	AFAO		yes	((FG06543.1:100.0,((AO07026000:100.0,72.m18946:100.0):89.5,AN5819.1:100.0):100.0):100.0,
2568	72.m18951	AN5824.1	AO070260000022	FG06542.1	AFAO	yes	yes	((FG06542.1:100.0,((AO07026000:100.0,72.m18951:100.0):96.5,AN5824.1:100.0):100.0):100.0,
2569	72.m19044	AN6115.1	AO070340000089	FG06513.1	AFAO	yes	yes	((FG06513.1:100.0,((AO07034000:100.0,72.m19044:100.0):92.5,AN6115.1:100.0):100.0):100.0,
2570	56.m02468	AN9172.1	AO070317000027	FG04232.1	AFAO	yes	yes	((FG04232.1:100.0,((AO07031700:100.0,56.m02468:100.0):91.5,AN9172.1:100.0):100.0):100.0,
2571	56.m02469	AN9159.1	AO070317000031	FG01701.1	AFAO			((((AO07031700:100.0,56.m02469:100.0):72.5,AN9159.1:100.0):99.0,FG01701.1:100.0):100.0,
2572	71.m15400	AN0120.1	AO070311000093	FG09800.1	AFAO		yes	((FG09800.1:100.0,((AO07031100:100.0,71.m15400:100.0):85.2,AN0120.1:100.0):100.0):100.0,
2573	52.m03833	AN2357.1	AO070307000082	FG05295.1	AFAO	yes	yes	((FG05295.1:100.0,(AN2357.1:100.0,(52.m03833:100.0,AO07030700:100.0):100.0):100.0):100.0,
2574	59.m08547	AN3156.1	AO070256000036	FG06220.1	ANAO			((FG06220.1:100.0,((AO07025600:100.0,AN3156.1:100.0):38.3,59.m08547:100.0):100.0):100.0,
2575	65.m07291	AN6690.1	AO070339000097	FG06222.1	AFAO			((FG06222.1:100.0,((65.m07291:100.0,AO07033900:100.0):57.0,AN6690.1:100.0):100.0):100.0,
2576	69.m15281	AN0565.1	AO070272000043	FG09638.1	AFAO	yes	yes	((FG09638.1:100.0,((AO07027200:100.0,69.m15281:100.0):97.0,AN0565.1:100.0):100.0):100.0,
2577	71.m15784	AN7752.1	AO070325000184	FG05316.1	AFAO	yes	yes	((FG05316.1:100.0,((AO07032500:100.0,71.m15784:100.0):90.0,AN7752.1:100.0):100.0):100.0,
2578	70.m15201	AN1045.1	AO070336000078	FG01968.1	AFAO	yes	yes	((FG01968.1:100.0,(AN1045.1:100.0,(70.m15201:100.0,AO07033600:100.0):100.0):100.0):100.0,
2579	54.m06854	AN5164.1	AO070291000003	FG05327.1	AFAO	yes	yes	((FG05327.1:100.0,((AO07029100:100.0,54.m06854:100.0):91.0,AN5164.1:100.0):100.0):100.0,
2580	65.m07502	AN6688.1	AO070339000095	FG05315.1	AFAO			((FG05315.1:100.0,((AO07033900:100.0,65.m07502:100.0):40.3,AN6688.1:100.0):100.0):100.0,
2581	72.m19309	AN6211.1	AO070308000082	FG01969.1	AFAO	yes	yes	((FG01969.1:100.0,((AO07030800:100.0,72.m19309:100.0):96.5,AN6211.1:100.0):100.0):100.0,
2582	70.m15214	AN0997.1	AO070312000043	FG01970.1	AFAO	yes	yes	((FG01970.1:100.0,((AO07031200:100.0,70.m15214:100.0):95.0,AN0997.1:100.0):100.0):100.0,
2583	71.m15403	AN0122.1	AO070311000090	FG09725.1	AFAN			((FG09725.1:100.0,(AO07031100:100.0,(AN0122.1:100.0,71.m15403:100.0):52.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2584	71.m15408	AN0126.1	AO070311000085	FG09728.1	AFAO	yes	yes	((FG09728.1:100.0,((AO07031100:100.0,71.m15408:100.0):97.5,AN0126.1:100.0):100.0):100.0,
2585	71.m15493	AN4724.1	AO070323000060	FG09686.1	ANAO			((FG09686.1:100.0,(71.m15493:100.0,(AN4724.1:100.0,AO07032300:100.0):58.5):100.0):100.0,
2586	57.m05496	AN4576.1	AO070316000158	FG05063.1	AFAO	yes	yes	((FG05063.1:100.0,(AN4576.1:100.0,(57.m05496:100.0,AO07031600:100.0):100.0):100.0):100.0,
2587	72.m19237	AN5893.1	AO070245000013	FG06228.1	AFAO	yes	yes	((FG06228.1:100.0,((AO07024500:100.0,72.m19237:100.0):97.0,AN5893.1:100.0):100.0):100.0,
2588	52.m04024	AN9398.1	AO070274000018	FG05229.1	ANAO			((FG05229.1:100.0,((AO07027400:100.0,AN9398.1:100.0):48.0,52.m04024:100.0):100.0):100.0,
2589	52.m04039	AN9409.1	AO070274000006	FG05230.1	ANAO			((FG05230.1:100.0,((AO07027400:100.0,AN9409.1:100.0):60.8,52.m04039:100.0):100.0):100.0,
2590	72.m20022	AN7304.1	AO070297000051	FG06226.1	AFAO			((FG06226.1:100.0,((AO07029700:100.0,72.m20022:100.0):52.0,AN7304.1:100.0):100.0):100.0,
2591	71.m15404	AN0123.1	AO070311000089	FG06224.1	AFAO		yes	((FG06224.1:100.0,((AO07031100:100.0,71.m15404:100.0):85.0,AN0123.1:100.0):100.0):100.0,
2592	54.m06579	AN4015.1	AO070328000151	FG01955.1	AFAO			(((AN4015.1:100.0,(AO07032800:100.0,54.m06579:100.0):53.5):58.6,FG01955.1:100.0):100.0,
2593	70.m15107	AN1128.1	AO070331000120	FG09914.1	AFAO			((FG09914.1:100.0,((AO07033100:100.0,70.m15107:100.0):64.0,AN1128.1:100.0):100.0):100.0,
2594	70.m15114	AN1126.1	AO070331000119	FG01014.1	AFAO	yes	yes	((FG01014.1:100.0,((AO07033100:100.0,70.m15114:100.0):96.0,AN1126.1:100.0):100.0):100.0,
2595	58.m07411	AN3624.1	AO070342000127	FG01501.1	AFAO	yes	yes	((FG01501.1:100.0,((AO07034200:100.0,58.m07411:100.0):97.0,AN3624.1:100.0):100.0):100.0,
2596	58.m07409	AN3622.1	AO070342000129	FG01503.1	AFAO		yes	((FG01503.1:100.0,((AO07034200:100.0,58.m07409:100.0):89.0,AN3622.1:100.0):100.0):100.0,
2597	69.m15458	AN5495.1	AO070341000391	FG01505.1	ANAO		yes	((FG01505.1:100.0,(69.m15458:100.0,(AN5495.1:100.0,AO07034100:100.0):87.0):100.0):100.0,
2598	69.m15722	AN5494.1	AO070341000390	FG01506.1	AFAO	yes	yes	((FG01506.1:100.0,((AO07034100:100.0,69.m15722:100.0):99.0,AN5494.1:100.0):100.0):100.0,
2599	69.m15723	AN5496.1	AO070341000389	FG00923.1	AFAO			((FG00923.1:100.0,((69.m15723:100.0,AO07034100:100.0):68.5,AN5496.1:100.0):100.0):100.0,
2600	58.m07379	AN3581.1	AO070342000168	FG00871.1	AFAO	yes	yes	((FG00871.1:100.0,((AO07034200:100.0,58.m07379:100.0):98.0,AN3581.1:100.0):100.0):100.0,
2601	54.m06455	AN0303.1	AO070334000035	FG00955.1	AFAO			((FG00955.1:100.0,((54.m06455:100.0,AO07033400:100.0):63.3,AN0303.1:100.0):100.0):100.0,
2602	57.m05971	AN3785.1	AO070337000246	FG00667.1	ANAO			((FG00667.1:100.0,((AO07033700:100.0,AN3785.1:100.0):54.0,57.m05971:100.0):100.0):100.0,
2603	71.m15746	AN8957.1	AO070319000071	FG00669.1	ANAO	yes	yes	((FG00669.1:100.0,((AN8957.1:100.0,AO07031900:100.0):100.0,71.m15746:100.0):100.0):100.0,
2604	70.m15715	AN2721.1	AO070309000062	FG02280.1				(((AO07030900:100.0,70.m15715:100.0):99.5,(FG02280.1:100.0,AN2721.1:100.0):53.0):100.0,
2605	58.m07788	AN1721.1	AO070305000036	FG00276.1	AFAO		yes	((FG00276.1:100.0,((AO07030500:100.0,58.m07788:100.0):82.0,AN1721.1:100.0):100.0):100.0,
2606	69.m15483	AN5449.1	AO070239000028	FG01496.1	AFAO			((FG01496.1:100.0,((AO07023900:100.0,69.m15483:100.0):55.5,AN5449.1:100.0):100.0):100.0,
2607	58.m08961	AN1720.1	AO070305000035	FG01495.1	AFAO	yes	yes	((FG01495.1:100.0,((AO07030500:100.0,58.m08961:100.0):97.0,AN1720.1:100.0):100.0):100.0,
2608	58.m07772	AN1696.1	AO070305000020	FG10081.1	AFAO			((FG10081.1:100.0,((58.m07772:100.0,AO07030500:100.0):51.0,AN1696.1:100.0):100.0):100.0,
2609	55.m02992	AN1486.1	AO070334000193	FG01490.1	AFAO			((FG01490.1:100.0,((AO07033400:100.0,55.m02992:100.0):62.5,AN1486.1:100.0):100.0):100.0,
2610	58.m07605	AN1996.1	AO070301000091	FG01498.1	AFAO		yes	((FG01498.1:100.0,((AO07030100:100.0,58.m07605:100.0):84.0,AN1996.1:100.0):100.0):100.0,
2611	72.m19550	AN1798.1	AO070309000133	FG05597.1	AFAN		yes	((FG05597.1:100.0,(AO07030900:100.0,(AN1798.1:100.0,72.m19550:100.0):89.5):100.0):100.0,
2612	59.m09078	AN2925.1	AO070337000214	FG05596.1	AFAO			((FG05596.1:100.0,((59.m09078:100.0,AO07033700:100.0):63.0,AN2925.1:100.0):100.0):100.0,
2613	58.m07389	AN3589.1	AO070342000140	FG01263.1	AFAN			((FG01263.1:100.0,(AO07034200:100.0,(AN3589.1:100.0,58.m07389:100.0):42.3):100.0):100.0,
2614	69.m15016	AN3913.1	AO070324000100	FG01234.1	AFAO			((FG01234.1:100.0,((AO07032400:100.0,69.m15016:100.0):47.5,AN3913.1:100.0):100.0):100.0,
2615	54.m06650	AN0426.1	AO070338000276	FG01526.1	ANAO			((FG01526.1:100.0,((AO07033800:100.0,AN0426.1:100.0):57.5,54.m06650:100.0):100.0):100.0,
2616	54.m06624	AN0433.1	AO070338000284	FG01516.1	ANAO			((FG01516.1:100.0,(54.m06624:100.0,(AN0433.1:100.0,AO07033800:100.0):46.0):100.0):100.0,
2617	70.m15627	AN0987.1	AO070317000115	FG01514.1	AFAN			((FG01514.1:100.0,((70.m15627:100.0,AN0987.1:100.0):70.5,AO07031700:100.0):99.0):100.0,
2618	56.m02506	AN8412.1	AO070336000018	FG10464.1		yes	yes	((56.m02506:100.0,(FG10464.1:100.0,(AN8412.1:100.0,AO07033600:100.0):99.5):100.0):100.0,
2619	52.m03823	AN8731.1	AO070327000127	FG04229.1				(((AO07032700:100.0,(FG04229.1:100.0,52.m03823:100.0):46.8):41.5,AN8731.1:100.0):100.0,
2620	52.m03867	AN5653.1	AO070335000212	FG10989.1	AFAO		yes	(((AN5653.1:100.0,(AO07033500:100.0,52.m03867:100.0):76.5):98.5,FG10989.1:100.0):100.0,
2621	72.m19978	AN6231.1	AO070304000084	FG10743.1	AFAO	yes	yes	((FG10743.1:100.0,((AO07030400:100.0,72.m19978:100.0):99.5,AN6231.1:100.0):100.0):100.0,
2622	58.m07603	AN1993.1	AO070301000084	FG10746.1	AFAN			((FG10746.1:100.0,(AO07030100:100.0,(AN1993.1:100.0,58.m07603:100.0):68.5):100.0):100.0,
2623	52.m04014	AN9393.1	AO070274000027	FG03330.1	AFAO	yes	yes	((FG03330.1:100.0,((AO07027400:100.0,52.m04014:100.0):93.0,AN9393.1:100.0):100.0):100.0,
2624	53.m03915	AN8064.1	AO070330000020	FG06027.1	AFAO	yes	yes	((FG06027.1:100.0,((AO07033000:100.0,53.m03915:100.0):97.0,AN8064.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2625	59.m08688	AN5019.1	AO070338000179	FG07880.1	AFAO	yes	yes	((FG07880.1:100.0,((AO07033800:100.0,59.m08688:100.0):94.0,AN5019.1:100.0):100.0):100.0,
2626	69.m15306	AN4179.1	AO070226000020	FG01581.1	AFAO	yes	yes	((FG01581.1:100.0,(AN4179.1:100.0,(69.m15306:100.0,AO07022600:100.0):100.0):100.0):100.0,
2627	52.m03954	AN6237.1	AO070302000118	FG04336.1	ANAO		yes	((FG04336.1:100.0,(52.m03954:100.0,(AN6237.1:100.0,AO07030200:100.0):84.5):100.0):100.0,
2628	52.m03953	AN6236.1	AO070302000119	FG03747.1	ANAO			((FG03747.1:100.0,(52.m03953:100.0,(AN6236.1:100.0,AO07030200:100.0):65.5):100.0):100.0,
2629	70.m14907	AN1324.1	AO070303000087	FG04366.1	AFAN	yes	yes	((FG04366.1:100.0,(AO07030300:100.0,(AN1324.1:100.0,70.m14907:100.0):92.0):100.0):100.0,
2630	53.m03676	AN4281.1	AO070310000015	FG10873.1	AFAO			((FG10873.1:100.0,((AO07031000:100.0,53.m03676:100.0):51.2,AN4281.1:100.0):100.0):100.0,
2631	54.m07054	AN5139.1	AO070291000038	FG10869.1	AFAO	yes	yes	((FG10869.1:100.0,((AO07029100:100.0,54.m07054:100.0):99.0,AN5139.1:100.0):100.0):100.0,
2632	70.m15179	AN1056.1	AO070336000055	FG10870.1	AFAN			((FG10870.1:100.0,((70.m15179:100.0,AN1056.1:100.0):49.0,AO07033600:100.0):100.0):100.0,
2633	58.m08946	AN1980.1	AO070301000065	FG00632.1	AFAO		yes	((FG00632.1:100.0,((AO07030100:100.0,58.m08946:100.0):87.5,AN1980.1:100.0):100.0):100.0,
2634	54.m06603	AN0465.1	AO070328000172	FG00631.1	ANAO			((FG00631.1:100.0,(54.m06603:100.0,(AN0465.1:100.0,AO07032800:100.0):46.3):100.0):100.0,
2635	58.m07569	AN1964.1	AO070301000045	FG00634.1	AFAO	yes	yes	((FG00634.1:100.0,((AO07030100:100.0,58.m07569:100.0):92.0,AN1964.1:100.0):100.0):100.0,
2636	69.m15204	AN2455.1	AO070264000021	FG01470.1	AFAO			((FG01470.1:100.0,((AO07026400:100.0,69.m15204:100.0):54.5,AN2455.1:100.0):100.0):100.0,
2637	69.m15211	AN2449.1	AO070264000029	FG01480.1	AFAO	yes	yes	((FG01480.1:100.0,((AO07026400:100.0,69.m15211:100.0):95.0,AN2449.1:100.0):100.0):100.0,
2638	69.m15212	AN2447.1	AO070264000030	FG01481.1	AFAN			((FG01481.1:100.0,(AO07026400:100.0,(AN2447.1:100.0,69.m15212:100.0):67.3):100.0):100.0,
2639	53.m03912	AN8035.1	AO070330000012	FG00946.1	AFAO	yes	yes	((FG00946.1:100.0,(AN8035.1:100.0,(53.m03912:100.0,AO07033000:100.0):100.0):100.0):100.0,
2640	53.m03913	AN8061.1	AO070330000013	FG00945.1	AFAO		yes	((FG00945.1:100.0,((AO07033000:100.0,53.m03913:100.0):86.0,AN8061.1:100.0):100.0):100.0,
2641	72.m19422	AN6232.1	AO070304000085	FG00637.1	ANAO			((FG00637.1:100.0,(72.m19422:100.0,(AN6232.1:100.0,AO07030400:100.0):73.5):100.0):100.0,
2642	59.m08570	AN3184.1	AO070256000010	FG01829.1	AFAO	yes	yes	((FG01829.1:100.0,((AO07025600:100.0,59.m08570:100.0):97.0,AN3184.1:100.0):100.0):100.0,
2643	72.m19031	AN6126.1	AO070340000068	FG06580.1	AFAO		yes	((FG06580.1:100.0,((AO07034000:100.0,72.m19031:100.0):79.0,AN6126.1:100.0):100.0):100.0,
2644	72.m18941	AN5811.1	AO070260000036	FG06524.1	AFAO		yes	((FG06524.1:100.0,((AO07026000:100.0,72.m18941:100.0):82.0,AN5811.1:100.0):100.0):100.0,
2645	72.m19777	AN7287.1	AO070297000028	FG06566.1	AFAO	yes	yes	((FG06566.1:100.0,((AO07029700:100.0,72.m19777:100.0):96.0,AN7287.1:100.0):100.0):100.0,
2646	72.m19499	AN6359.1	AO070279000047	FG05455.1	ANAO			((FG05455.1:100.0,((AO07027900:100.0,AN6359.1:100.0):68.0,72.m19499:100.0):100.0):100.0,
2647	59.m08718	AN2877.1	AO070338000146	FG02771.1	AFAO			((FG02771.1:100.0,((59.m08718:100.0,AO07033800:100.0):53.5,AN2877.1:100.0):100.0):100.0,
2648	59.m08723	AN2873.1	AO070338000139	FG00380.1	AFAO		yes	((FG00380.1:100.0,((59.m08723:100.0,AO07033800:100.0):85.5,AN2873.1:100.0):100.0):100.0,
2649	57.m05803	AN2101.1	AO070341000259	FG00552.1	AFAO	yes	yes	((FG00552.1:100.0,((AO07034100:100.0,57.m05803:100.0):90.5,AN2101.1:100.0):100.0):100.0,
2650	67.m02865	AN8562.1	AO070332000127	FG00550.1	AFAN	yes	yes	((FG00550.1:100.0,(AO07033200:100.0,(AN8562.1:100.0,67.m02865:100.0):96.0):100.0):100.0,
2651	57.m05786	AN2085.1	AO070341000243	FG00367.1	ANAO			((FG00367.1:100.0,((AO07034100:100.0,AN2085.1:100.0):56.3,57.m05786:100.0):100.0):100.0,
2652	54.m06459	AN0302.1	AO070334000037	FG00368.1	ANAO		yes	((FG00368.1:100.0,(54.m06459:100.0,(AN0302.1:100.0,AO07033400:100.0):80.0):100.0):100.0,
2653	54.m06679	AN2738.1	AO070338000220	FG00369.1	AFAO	yes	yes	((FG00369.1:100.0,((AO07033800:100.0,54.m06679:100.0):95.0,AN2738.1:100.0):100.0):100.0,
2654	69.m14994	AN3933.1	AO070341000044	FG05627.1	AFAO	yes	yes	((FG05627.1:100.0,(AN3933.1:100.0,(69.m14994:100.0,AO07034100:100.0):100.0):100.0):100.0,
2655	72.m19967	AN9468.1	AO070340000317	FG04136.1	AFAO	yes	yes	((((AO07034000:100.0,72.m19967:100.0):99.5,AN9468.1:100.0):99.0,FG04136.1:100.0):100.0,
2656	54.m06351	AN0387.1	AO070290000083	FG00797.1	ANAO			((FG00797.1:100.0,(54.m06351:100.0,(AN0387.1:100.0,AO07029000:100.0):44.5):100.0):100.0,
2657	57.m05609	AN4519.1	AO070321000125	FG00796.1	AFAO			((FG00796.1:100.0,((AO07032100:100.0,57.m05609:100.0):70.0,AN4519.1:100.0):100.0):100.0,
2658	57.m05618	AN4510.1	AO070311000065	FG00816.1	ANAO	yes	yes	((FG00816.1:100.0,(57.m05618:100.0,(AN4510.1:100.0,AO07031100:100.0):91.0):100.0):100.0,
2659	66.m04689	AN2360.1	AO070298000079	FG04504.1	AFAO			(((AN2360.1:100.0,(AO07029800:100.0,66.m04689:100.0):64.0):82.5,FG04504.1:100.0):100.0,
2660	71.m15459	AN0189.1	AO070321000054	FG04185.1	ANAO	yes	yes	((FG04185.1:100.0,(71.m15459:100.0,(AN0189.1:100.0,AO07032100:100.0):94.5):100.0):100.0,
2661	71.m15470	AN0205.1	AO070321000039	FG04187.1	AFAO	yes	yes	((FG04187.1:100.0,((AO07032100:100.0,71.m15470:100.0):96.5,AN0205.1:100.0):100.0):100.0,
2662	72.m19761	AN1711.1	AO070297000053	FG09760.1	AFAO	yes	yes	((FG09760.1:100.0,(AN1711.1:100.0,(72.m19761:100.0,AO07029700:100.0):100.0):100.0):100.0,
2663	69.m15234	AN9498.1	AO070188000007	FG04190.1	AFAO	yes	yes	((FG04190.1:100.0,(AN9498.1:100.0,(69.m15234:100.0,AO07018800:100.0):100.0):100.0):100.0,
2664	69.m15233	AN9497.1	AO070188000006	FG04189.1	AFAO	yes	yes	((FG04189.1:100.0,((AO07018800:100.0,69.m15233:100.0):98.5,AN9497.1:100.0):100.0):100.0,
2665	72.m19762	AN7305.1	AO070297000052	FG09761.1	ANAO	yes	yes	((FG09761.1:100.0,(72.m19762:100.0,(AN7305.1:100.0,AO07029700:100.0):94.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2666	71.m15506	AN2311.1	AO070323000049	FG09764.1	ANAO			((FG09764.1:100.0,(71.m15506:100.0,(AN2311.1:100.0,AO07032300:100.0):50.5):100.0):100.0,
2667	71.m15811	AN7771.1	AO070286000022	FG00549.1	AFAO		yes	((FG00549.1:100.0,((AO07028600:100.0,71.m15811:100.0):81.0,AN7771.1:100.0):100.0):100.0,
2668	59.m08858	AN4953.1	AO070288000006	FG04068.1	ANAO			((FG04068.1:100.0,((AO07028800:100.0,AN4953.1:100.0):62.3,59.m08858:100.0):100.0):100.0,
2669	53.m03832	AN8121.1	AO070322000029	FG09440.1	AFAO		yes	((FG09440.1:100.0,((AO07032200:100.0,53.m03832:100.0):86.8,AN8121.1:100.0):100.0):100.0,
2670	59.m08862	AN4957.1	AO070288000019	FG04085.1	AFAO		yes	((FG04085.1:100.0,((AO07028800:100.0,59.m08862:100.0):83.0,AN4957.1:100.0):100.0):100.0,
2671	72.m19749	AN7314.1	AO070297000067	FG04280.1	AFAO			((FG04280.1:100.0,((AO07029700:100.0,72.m19749:100.0):67.0,AN7314.1:100.0):100.0):100.0,
2672	72.m19133	AN6010.1	AO070340000269	FG06154.1	AFAN		yes	((FG06154.1:100.0,(AO07034000:100.0,(AN6010.1:100.0,72.m19133:100.0):86.0):100.0):100.0,
2673	58.m07580	AN1975.1	AO070301000060	FG10890.1	ANAO			((FG10890.1:100.0,((AO07030100:100.0,AN1975.1:100.0):74.5,58.m07580:100.0):100.0):100.0,
2674	54.m06612	AN0458.1	AO070328000180	FG10749.1	AFAO	yes	yes	((FG10749.1:100.0,(AN0458.1:100.0,(54.m06612:100.0,AO07032800:100.0):100.0):100.0):100.0,
2675	71.m15432	AN0154.1	AO070321000096	FG01623.1	AFAO	yes	yes	((FG01623.1:100.0,((AO07032100:100.0,71.m15432:100.0):98.0,AN0154.1:100.0):100.0):100.0,
2676	58.m07886	AN4439.1	AO070273000015	FG01611.1	AFAO			((FG01611.1:100.0,((AO07027300:100.0,58.m07886:100.0):36.8,AN4439.1:100.0):100.0):100.0,
2677	71.m15251	AN6888.1	AO070314000034	FG07775.1	ANAO			((FG07775.1:100.0,((AO07031400:100.0,AN6888.1:100.0):55.0,71.m15251:100.0):100.0):100.0,
2678	53.m03924	AN8071.1	AO070330000029	FG01665.1	AFAO		yes	((FG01665.1:100.0,((AO07033000:100.0,53.m03924:100.0):81.5,AN8071.1:100.0):100.0):100.0,
2679	53.m03922	AN3784.1	AO070330000028	FG01666.1	AFAO	yes	yes	((FG01666.1:100.0,((AO07033000:100.0,53.m03922:100.0):96.5,AN3784.1:100.0):100.0):100.0,
2680	54.m06742	AN4102.1	AO070342000101	FG06605.1	AFAO	yes	yes	((FG06605.1:100.0,((AO07034200:100.0,54.m06742:100.0):96.5,AN4102.1:100.0):100.0):100.0,
2681	55.m03185	AN1602.1	AO070339000250	FG06397.1	AFAO			(((AN1602.1:100.0,(55.m03185:100.0,AO07033900:100.0):96.5):65.0,FG06397.1:100.0):100.0,
2682	54.m06738	AN4095.1	AO070342000096	FG06607.1	AFAO		yes	((FG06607.1:100.0,((AO07034200:100.0,54.m06738:100.0):75.0,AN4095.1:100.0):100.0):100.0,
2683	54.m06498	AN4094.1	AO070342000095	FG06606.1	AFAO	yes	yes	((FG06606.1:100.0,(AN4094.1:100.0,(54.m06498:100.0,AO07034200:100.0):100.0):100.0):100.0,
2684	72.m19498	AN6360.1	AO070279000048	FG06510.1	AFAN			((FG06510.1:100.0,(AO07027900:100.0,(AN6360.1:100.0,72.m19498:100.0):53.0):100.0):100.0,
2685	72.m19497	AN6363.1	AO070279000049	FG06502.1	AFAO			((FG06502.1:100.0,((AO07027900:100.0,72.m19497:100.0):60.5,AN6363.1:100.0):100.0):100.0,
2686	72.m19523	AN8829.1	AO070271000051	FG06585.1	AFAN		yes	((FG06585.1:100.0,(AO07027100:100.0,(AN8829.1:100.0,72.m19523:100.0):83.5):100.0):100.0,
2687	72.m19456	AN6336.1	AO070236000020	FG06557.1	AFAO		yes	((FG06557.1:100.0,((AO07023600:100.0,72.m19456:100.0):89.5,AN6336.1:100.0):100.0):100.0,
2688	72.m19478	AN2425.1	AO070241000006	FG06493.1	AFAO		yes	((FG06493.1:100.0,((72.m19478:100.0,AO07024100:100.0):77.0,AN2425.1:100.0):100.0):100.0,
2689	59.m09446	AN3017.1	AO070337000098	FG01765.1	AFAO		yes	((FG01765.1:100.0,((AO07033700:100.0,59.m09446:100.0):85.5,AN3017.1:100.0):100.0):100.0,
2690	62.m03219	AN8637.1	AO070326000073	FG06554.1	AFAO	yes	yes	((FG06554.1:100.0,((AO07032600:100.0,62.m03219:100.0):98.5,AN8637.1:100.0):100.0):100.0,
2691	54.m06604	AN0464.1	AO070328000173	FG08553.1	ANAO			((FG08553.1:100.0,(54.m06604:100.0,(AN0464.1:100.0,AO07032800:100.0):50.0):100.0):100.0,
2692	69.m14963	AN3957.1	AO070341000077	FG03963.1	AFAO		yes	((FG03963.1:100.0,((AO07034100:100.0,69.m14963:100.0):82.0,AN3957.1:100.0):100.0):100.0,
2693	71.m16044	AN6845.1	AO070314000094	FG05096.1	AFAO			((FG05096.1:100.0,((71.m16044:100.0,AO07031400:100.0):53.5,AN6845.1:100.0):100.0):100.0,
2694	72.m19295	AN6195.1	AO070308000098	FG09715.1	AFAO			((FG09715.1:100.0,((AO07030800:100.0,72.m19295:100.0):72.5,AN6195.1:100.0):100.0):100.0,
2695	72.m19950	AN6034.1	AO070340000254	FG09713.1	AFAO		yes	((FG09713.1:100.0,((AO07034000:100.0,72.m19950:100.0):80.0,AN6034.1:100.0):100.0):100.0,
2696	72.m19123	AN6033.1	AO070340000255	FG09712.1	AFAO			((FG09712.1:100.0,((AO07034000:100.0,72.m19123:100.0):60.3,AN6033.1:100.0):100.0):100.0,
2697	71.m15454	AN0183.1	AO070321000057	FG09776.1	AFAO		yes	((FG09776.1:100.0,((AO07032100:100.0,71.m15454:100.0):84.5,AN0183.1:100.0):100.0):100.0,
2698	72.m19686	AN2155.1	AO070343000207	FG09774.1	AFAO		yes	((FG09774.1:100.0,((AO07034300:100.0,72.m19686:100.0):81.0,AN2155.1:100.0):100.0):100.0,
2699	71.m15827	AN3129.1	AO070341000298	FG05924.1	AFAN			((FG05924.1:100.0,(AO07034100:100.0,(AN3129.1:100.0,71.m15827:100.0):43.0):100.0):100.0,
2700	72.m19156	AN5985.1	AO070340000294	FG02751.1			yes	((AN5985.1:100.0,((72.m19156:100.0,AO07034000:100.0):89.5,FG02751.1:100.0):89.0):100.0,
2701	58.m07219	AN2957.1	AO070307000048	FG11338.1				(((FG11338.1:100.0,(58.m07219:100.0,AO07030700:100.0):99.0):64.0,AN2957.1:100.0):100.0,
2702	72.m19214	AN5917.1	AO070340000369	FG10747.1	AFAO			((FG10747.1:100.0,((72.m19214:100.0,AO07034000:100.0):52.5,AN5917.1:100.0):99.0):100.0,
2703	53.m03735	AN8234.1	AO070310000074	FG08986.1	ANAO		yes	((FG08986.1:100.0,(53.m03735:100.0,(AN8234.1:100.0,AO07031000:100.0):77.5):100.0):100.0,
2704	72.m19512	AN6343.1	AO070298000012	FG02048.1	AFAO	yes	yes	((FG02048.1:100.0,((AO07029800:100.0,72.m19512:100.0):98.0,AN6343.1:100.0):100.0):100.0,
2705	71.m15291	AN6825.1	AO070314000105	FG05888.1	AFAO	yes	yes	((FG05888.1:100.0,((AO07031400:100.0,71.m15291:100.0):92.0,AN6825.1:100.0):100.0):100.0,
2706	69.m15196	AN2458.1	AO070264000020	FG05884.1	AFAO	yes	yes	((FG05884.1:100.0,((AO07026400:100.0,69.m15196:100.0):99.0,AN2458.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2707	70.m15148	AN1074.1	AO070285000074	FG08351.1	AFAN			((FG08351.1:100.0,(AO07028500:100.0,(AN1074.1:100.0,70.m15148:100.0):65.3):100.0):100.0,
2708	70.m15020	AN1199.1	AO070331000204	FG10375.1	AFAO		yes	((FG10375.1:100.0,((AO07033100:100.0,70.m15020:100.0):87.5,AN1199.1:100.0):100.0):100.0,
2709	71.m15856	AN2208.1	AO070294000014	FG02075.1	ANAO			((FG02075.1:100.0,(71.m15856:100.0,(AN2208.1:100.0,AO07029400:100.0):53.5):100.0):100.0,
2710	62.m03237	AN6640.1	AO070295000024	FG02121.1	AFAO	yes	yes	((FG02121.1:100.0,(AN6640.1:100.0,(62.m03237:100.0,AO07029500:100.0):100.0):100.0):100.0,
2711	54.m06727	AN4086.1	AO070342000079	FG05431.1	AFAO			((FG05431.1:100.0,((AO07034200:100.0,54.m06727:100.0):47.5,AN4086.1:100.0):100.0):100.0,
2712	53.m03749	AN8225.1	AO070310000087	FG05932.1	AFAO	yes	yes	((FG05932.1:100.0,((AO07031000:100.0,53.m03749:100.0):98.5,AN8225.1:100.0):100.0):100.0,
2713	53.m03750	AN8224.1	AO070310000088	FG04582.1	AFAO	yes	yes	((FG04582.1:100.0,(AN8224.1:100.0,(53.m03750:100.0,AO07031000:100.0):100.0):100.0):100.0,
2714	59.m08597	AN3128.1	AO070303000018	FG06509.1	AFAO			((FG06509.1:100.0,((59.m08597:100.0,AO07030300:100.0):53.5,AN3128.1:100.0):100.0):100.0,
2715	71.m15748	AN7721.1	AO070325000136	FG09016.1	AFAO		yes	((FG09016.1:100.0,((AO07032500:100.0,71.m15748:100.0):82.5,AN7721.1:100.0):100.0):100.0,
2716	71.m15675	AN6521.1	AO070270000019	FG10949.1	ANAO	yes	yes	((FG10949.1:100.0,((AN6521.1:100.0,AO07027000:100.0):100.0,71.m15675:100.0):100.0):100.0,
2717	72.m19901	AN6167.1	AO070343000365	FG04755.1	AFAN	yes	yes	((FG04755.1:100.0,((AN6167.1:100.0,72.m19901:100.0):100.0,AO07034300:100.0):100.0):100.0,
2718	53.m03902	AN8043.1	AO070330000003	FG04735.1				((AN8043.1:100.0,(FG04735.1:100.0,(AO07033000:100.0,53.m03902:100.0):95.0):65.0):100.0,
2719	69.m15387	AN3730.1	AO070342000284	FG02022.1	AFAO	yes	yes	((FG02022.1:100.0,(AN3730.1:100.0,(69.m15387:100.0,AO07034200:100.0):100.0):100.0):100.0,
2720	71.m15855	AN2210.1	AO070294000012	FG02025.1	AFAO		yes	((FG02025.1:100.0,((AO07029400:100.0,71.m15855:100.0):88.0,AN2210.1:100.0):100.0):100.0,
2721	54.m06911	AN5111.1	AO070291000068	FG10286.1	AFAO		yes	((FG10286.1:100.0,((AO07029100:100.0,54.m06911:100.0):82.5,AN5111.1:100.0):100.0):100.0,
2722	69.m15243	AN6394.1	AO070343000149	FG10285.1	AFAO		yes	((FG10285.1:100.0,((AO07034300:100.0,69.m15243:100.0):84.0,AN6394.1:100.0):100.0):100.0,
2723	59.m08679	AN5025.1	AO070338000186	FG10284.1	AFAO	yes	yes	((FG10284.1:100.0,((AO07033800:100.0,59.m08679:100.0):96.5,AN5025.1:100.0):100.0):100.0,
2724	69.m15461	AN5491.1	AO070341000394	FG10283.1	AFAO		yes	((FG10283.1:100.0,((AO07034100:100.0,69.m15461:100.0):89.0,AN5491.1:100.0):100.0):100.0,
2725	58.m07921	AN4405.1	AO070261000048	FG10374.1	AFAO	yes	yes	((FG10374.1:100.0,(AN4405.1:100.0,(58.m07921:100.0,AO07026100:100.0):100.0):100.0):100.0,
2726	72.m18954	AN5827.1	AO070260000019	FG10391.1	AFAO			((FG10391.1:100.0,((72.m18954:100.0,AO07026000:100.0):59.5,AN5827.1:100.0):100.0):100.0,
2727	58.m07930	AN4397.1	AO070261000042	FG10362.1	ANAO		yes	((FG10362.1:100.0,(58.m07930:100.0,(AN4397.1:100.0,AO07026100:100.0):85.0):100.0):100.0,
2728	58.m07933	AN4390.1	AO070261000036	FG10089.1	AFAO	yes	yes	((FG10089.1:100.0,((AO07026100:100.0,58.m07933:100.0):98.0,AN4390.1:100.0):100.0):100.0,
2729	58.m07935	AN4389.1	AO070261000034	FG10090.1	AFAO		yes	((FG10090.1:100.0,((AO07026100:100.0,58.m07935:100.0):76.0,AN4389.1:100.0):100.0):100.0,
2730	58.m07928	AN4395.1	AO070261000040	FG10091.1	AFAO			((FG10091.1:100.0,((AO07026100:100.0,58.m07928:100.0):54.0,AN4395.1:100.0):100.0):100.0,
2731	58.m07937	AN4387.1	AO070261000033	FG10295.1	AFAO		yes	((FG10295.1:100.0,((AO07026100:100.0,58.m07937:100.0):85.0,AN4387.1:100.0):100.0):100.0,
2732	70.m14950	AN1264.1	AO070332000010	FG10026.1	AFAO			(((AN1264.1:100.0,(AO07033200:100.0,70.m14950:100.0):79.5):61.5,FG10026.1:100.0):100.0,
2733	70.m14903	AN1328.1	AO070303000092	FG10299.1	AFAO			((FG10299.1:100.0,((AO07030300:100.0,70.m14903:100.0):58.3,AN1328.1:100.0):100.0):100.0,
2734	59.m08664	AN5013.1	AO070334000121	FG10307.1	AFAO	yes	yes	((FG10307.1:100.0,(AN5013.1:100.0,(59.m08664:100.0,AO07033400:100.0):100.0):100.0):100.0,
2735	70.m15288	AN0686.1	AO070343000532	FG10306.1	AFAO			((FG10306.1:100.0,((70.m15288:100.0,AO07034300:100.0):71.0,AN0686.1:100.0):100.0):100.0,
2736	70.m14890	AN1343.1	AO070247000021	FG10302.1	ANAO			((FG10302.1:100.0,((AO07024700:100.0,AN1343.1:100.0):70.3,70.m14890:100.0):100.0):100.0,
2737	58.m09011	AN4299.1	AO070207000001	FG10303.1	AFAO			((FG10303.1:100.0,((AO07020700:100.0,58.m09011:100.0):54.0,AN4299.1:100.0):100.0):100.0,
2738	70.m14889	AN1344.1	AO070247000020	FG10301.1	AFAO			((FG10301.1:100.0,((70.m14889:100.0,AO07024700:100.0):60.5,AN1344.1:100.0):100.0):100.0,
2739	58.m07920	AN4406.1	AO070261000049	FG10373.1	AFAO		yes	((FG10373.1:100.0,((AO07026100:100.0,58.m07920:100.0):76.5,AN4406.1:100.0):100.0):100.0,
2740	54.m06840	AN5719.1	AO070324000131	FG10368.1	ANAO			(((54.m06840:100.0,(AN5719.1:100.0,AO07032400:100.0):92.2):68.7,FG10368.1:100.0):100.0,
2741	72.m19926	AN6081.1	AO070340000131	FG10244.1	AFAO			((FG10244.1:100.0,((AO07034000:100.0,72.m19926:100.0):48.0,AN6081.1:100.0):100.0):100.0,
2742	72.m19923	AN6082.1	AO070340000132	FG10245.1	AFAO		yes	((((AO07034000:100.0,72.m19923:100.0):80.0,AN6082.1:100.0):97.5,FG10245.1:100.0):100.0,
2743	72.m19924	AN6083.1	AO070340000133	FG10246.1	AFAO			((FG10246.1:100.0,((AO07034000:100.0,72.m19924:100.0):71.7,AN6083.1:100.0):100.0):100.0,
2744	72.m19074	AN6084.1	AO070340000134	FG10247.1	AFAO	yes	yes	((FG10247.1:100.0,((AO07034000:100.0,72.m19074:100.0):98.0,AN6084.1:100.0):100.0):100.0,
2745	65.m07345	AN3313.1	AO070339000070	FG05049.1	ANAO			((FG05049.1:100.0,((AO07033900:100.0,AN3313.1:100.0):67.0,65.m07345:100.0):100.0):100.0,
2746	59.m08765	AN4870.1	AO070338000090	FG10254.1	AFAN		yes	((FG10254.1:100.0,(AO07033800:100.0,(AN4870.1:100.0,59.m08765:100.0):87.0):100.0):100.0,
2747	70.m15658	AN0627.1	AO070280000079	FG06897.1	AFAN			((FG06897.1:100.0,(AO07028000:100.0,(AN0627.1:100.0,70.m15658:100.0):55.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2748	70.m15622	AN0981.1	AO070318000167	FG06896.1	AFAO			((FG06896.1:100.0,((70.m15622:100.0,AO07031800:100.0):55.0,AN0981.1:100.0):100.0):100.0,
2749	70.m15662	AN0623.1	AO070280000074	FG06918.1	ANAO			((FG06918.1:100.0,(70.m15662:100.0,(AN0623.1:100.0,AO07028000:100.0):61.0):100.0):100.0,
2750	70.m15137	AN1094.1	AO070285000053	FG04130.1	AFAO	yes	yes	((FG04130.1:100.0,((AO07028500:100.0,70.m15137:100.0):94.0,AN1094.1:100.0):100.0):100.0,
2751	70.m15448	AN0848.1	AO070216000007	FG05390.1	AFAO		yes	((FG05390.1:100.0,((AO07021600:100.0,70.m15448:100.0):81.5,AN0848.1:100.0):100.0):100.0,
2752	70.m15477	AN0874.1	AO070320000033	FG05389.1	AFAO	yes	yes	((FG05389.1:100.0,((AO07032000:100.0,70.m15477:100.0):92.0,AN0874.1:100.0):100.0):100.0,
2753	70.m15144	AN1068.1	AO070285000068	FG07305.1	AFAO	yes	yes	((FG07305.1:100.0,((AO07028500:100.0,70.m15144:100.0):98.0,AN1068.1:100.0):100.0):100.0,
2754	72.m19957	AN5912.1	AO070248000038	FG06920.1	ANAO			((FG06920.1:100.0,(72.m19957:100.0,(AN5912.1:100.0,AO07024800:100.0):69.0):100.0):100.0,
2755	71.m15951	AN2302.1	AO070271000063	FG06922.1	AFAO	yes	yes	((((AO07027100:100.0,71.m15951:100.0):100.0,AN2302.1:100.0):93.0,FG06922.1:100.0):100.0,
2756	62.m03431	AN6598.1	AO070326000047	FG06903.1	AFAO		yes	((FG06903.1:100.0,((AO07032600:100.0,62.m03431:100.0):84.0,AN6598.1:100.0):100.0):100.0,
2757	54.m06534	AN4057.1	AO070342000044	FG04151.1	AFAO			((FG04151.1:100.0,((54.m06534:100.0,AO07034200:100.0):54.3,AN4057.1:100.0):100.0):100.0,
2758	57.m05613	AN4516.1	AO070311000077	FG04152.1	AFAO		yes	((FG04152.1:100.0,((AO07031100:100.0,57.m05613:100.0):82.5,AN4516.1:100.0):100.0):100.0,
2759	71.m15887	AN2248.1	AO070326000122	FG05554.1	AFAO			((FG05554.1:100.0,((AO07032600:100.0,71.m15887:100.0):60.5,AN2248.1:100.0):100.0):100.0,
2760	71.m15985	AN8850.1	AO070271000026	FG05566.1	AFAO		yes	((FG05566.1:100.0,((71.m15985:100.0,AO07027100:100.0):81.0,AN8850.1:100.0):100.0):100.0,
2761	71.m15822	AN7628.1	AO070294000038	FG05565.1	AFAO	yes	yes	((FG05565.1:100.0,((AO07029400:100.0,71.m15822:100.0):92.0,AN7628.1:100.0):100.0):100.0,
2762	71.m15821	AN7629.1	AO070294000039	FG05564.1	AFAO		yes	(((AN7629.1:100.0,(71.m15821:100.0,AO07029400:100.0):75.8):95.8,FG05564.1:100.0):100.0,
2763	71.m15747	AN7720.1	AO070325000135	FG05563.1	AFAO		yes	((FG05563.1:100.0,((AO07032500:100.0,71.m15747:100.0):82.0,AN7720.1:100.0):100.0):100.0,
2764	71.m15956	AN8824.1	AO070271000057	FG05428.1	AFAN			((FG05428.1:100.0,(AO07027100:100.0,(AN8824.1:100.0,71.m15956:100.0):60.0):100.0):100.0,
2765	71.m15947	AN2298.1	AO070295000079	FG05561.1	AFAO	yes	yes	((FG05561.1:100.0,((AO07029500:100.0,71.m15947:100.0):98.0,AN2298.1:100.0):100.0):100.0,
2766	71.m15765	AN7729.1	AO070325000156	FG05571.1	AFAO	yes	yes	((FG05571.1:100.0,((AO07032500:100.0,71.m15765:100.0):96.0,AN7729.1:100.0):100.0):100.0,
2767	53.m03894	AN8050.1	AO070292000100	FG06908.1	AFAN			((((AN8050.1:100.0,53.m03894:100.0):48.8,AO07029200:100.0):76.7,FG06908.1:100.0):100.0,
2768	53.m03898	AN8045.1	AO070292000104	FG06907.1	AFAO	yes	yes	((FG06907.1:100.0,((AO07029200:100.0,53.m03898:100.0):91.5,AN8045.1:100.0):100.0):100.0,
2769	58.m07796	AN1706.1	AO070305000044	FG09401.1	AFAO	yes	yes	((FG09401.1:100.0,((AO07030500:100.0,58.m07796:100.0):90.0,AN1706.1:100.0):100.0):100.0,
2770	59.m08750	AN2900.1	AO070338000107	FG06078.1	AFAO		yes	((FG06078.1:100.0,((AO07033800:100.0,59.m08750:100.0):79.5,AN2900.1:100.0):100.0):100.0,
2771	69.m15064	AN1772.1	AO070324000030	FG02133.1	AFAO	yes	yes	((FG02133.1:100.0,((AO07032400:100.0,69.m15064:100.0):95.5,AN1772.1:100.0):100.0):100.0,
2772	65.m07399	AN5673.1	AO070309000086	FG09884.1	AFAO			((FG09884.1:100.0,((AO07030900:100.0,65.m07399:100.0):64.5,AN5673.1:100.0):100.0):100.0,
2773	65.m07398	AN5672.1	AO070309000085	FG09883.1	AFAO		yes	((FG09883.1:100.0,((AO07030900:100.0,65.m07398:100.0):84.0,AN5672.1:100.0):100.0):100.0,
2774	65.m07397	AN4186.1	AO070309000084	FG09882.1	ANAO			((FG09882.1:100.0,((AO07030900:100.0,AN4186.1:100.0):55.5,65.m07397:100.0):100.0):100.0,
2775	70.m15504	AN0895.1	AO070320000068	FG00150.1	ANAO			((FG00150.1:100.0,((AO07032000:100.0,AN0895.1:100.0):58.0,70.m15504:100.0):100.0):100.0,
2776	72.m19633	AN7590.1	AO070343000286	FG04826.1	AFAO	yes	yes	((FG04826.1:100.0,((AO07034300:100.0,72.m19633:100.0):96.5,AN7590.1:100.0):100.0):100.0,
2777	67.m02987	AN2824.1	AO070330000093	FG02314.1	AFAO	yes	yes	((FG02314.1:100.0,(AN2824.1:100.0,(67.m02987:100.0,AO07033000:100.0):100.0):100.0):100.0,
2778	59.m09486	AN2773.1	AO070327000015	FG10788.1	AFAO		yes	((FG10788.1:100.0,((AO07032700:100.0,59.m09486:100.0):89.5,AN2773.1:100.0):100.0):100.0,
2779	59.m08746	AN2896.1	AO070338000112	FG06084.1	AFAN		yes	((((59.m08746:100.0,AN2896.1:100.0):100.0,AO07033800:100.0):76.5,FG06084.1:100.0):100.0,
2780	57.m05519	AN4597.1	AO070267000013	FG10944.1	AFAO	yes	yes	((FG10944.1:100.0,((AO07026700:100.0,57.m05519:100.0):97.0,AN4597.1:100.0):100.0):100.0,
2781	62.m03338	AN8742.1	AO070250000039	FG08702.1	AFAO	yes	yes	((FG08702.1:100.0,(AN8742.1:100.0,(62.m03338:100.0,AO07025000:100.0):100.0):100.0):100.0,
2782	62.m03407	AN8667.1	AO070269000068	FG08634.1	AFAO			((FG08634.1:100.0,((AO07026900:100.0,62.m03407:100.0):54.5,AN8667.1:100.0):100.0):100.0,
2783	62.m03324	AN8751.1	AO070250000011	FG08635.1	AFAO	yes	yes	((FG08635.1:100.0,((AO07025000:100.0,62.m03324:100.0):90.0,AN8751.1:100.0):100.0):100.0,
2784	59.m09147	AN4830.1	AO070327000152	FG08803.1	AFAO		yes	((FG08803.1:100.0,((AO07032700:100.0,59.m09147:100.0):84.5,AN4830.1:100.0):100.0):100.0,
2785	62.m03405	AN8668.1	AO070269000064	FG08598.1	AFAO	yes	yes	((FG08598.1:100.0,(AN8668.1:100.0,(62.m03405:100.0,AO07026900:100.0):100.0):100.0):100.0,
2786	54.m06882	AN5140.1	AO070291000036	FG08810.1	AFAO	yes	yes	((FG08810.1:100.0,((AO07029100:100.0,54.m06882:100.0):99.0,AN5140.1:100.0):100.0):100.0,
2787	59.m09142	AN4836.1	AO070327000142	FG08805.1	ANAO			((FG08805.1:100.0,(59.m09142:100.0,(AN4836.1:100.0,AO07032700:100.0):68.5):100.0):100.0,
2788	70.m15086	AN1156.1	AO070331000145	FG08786.1	AFAO		yes	((FG08786.1:100.0,((70.m15086:100.0,AO07033100:100.0):77.5,AN1156.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2789	59.m09039	AN2973.1	AO070337000148	FG01275.1	AFAO	yes	yes	((FG01275.1:100.0,((AO07033700:100.0,59.m09039:100.0):90.0,AN2973.1:100.0):100.0):100.0,
2790	59.m09038	AN2975.1	AO070337000146	FG01276.1	ANAO			((FG01276.1:100.0,(59.m09038:100.0,(AN2975.1:100.0,AO07033700:100.0):70.8):100.0):100.0,
2791	59.m09034	AN2980.1	AO070337000142	FG01278.1	AFAO			((FG01278.1:100.0,((AO07033700:100.0,59.m09034:100.0):66.2,AN2980.1:100.0):100.0):100.0,
2792	59.m09033	AN2981.1	AO070337000141	FG01279.1	AFAO			((FG01279.1:100.0,((AO07033700:100.0,59.m09033:100.0):60.0,AN2981.1:100.0):100.0):100.0,
2793	72.m19971	AN6338.1	AO070236000016	FG01285.1	ANAO		yes	((FG01285.1:100.0,(72.m19971:100.0,(AN6338.1:100.0,AO07023600:100.0):89.5):100.0):100.0,
2794	54.m06530	AN0253.1	AO070334000107	FG06874.1	AFAO			((FG06874.1:100.0,((AO07033400:100.0,54.m06530:100.0):52.0,AN0253.1:100.0):100.0):100.0,
2795	54.m06531	AN0252.1	AO070334000108	FG06875.1	ANAO			((FG06875.1:100.0,((AO07033400:100.0,AN0252.1:100.0):46.5,54.m06531:100.0):100.0):100.0,
2796	72.m19463	AN2412.1	AO070236000002	FG06878.1	AFAO		yes	((FG06878.1:100.0,((AO07023600:100.0,72.m19463:100.0):76.3,AN2412.1:100.0):100.0):100.0,
2797	55.m02954	AN1452.1	AO070302000017	FG00398.1	AFAN			((FG00398.1:100.0,(AO07030200:100.0,(AN1452.1:100.0,55.m02954:100.0):49.0):100.0):100.0,
2798	58.m07465	AN3636.1	AO070328000080	FG00423.1	AFAO	yes	yes	((FG00423.1:100.0,((AO07032800:100.0,58.m07465:100.0):99.0,AN3636.1:100.0):100.0):100.0,
2799	53.m04034	AN2577.1	AO070234000010	FG04688.1	AFAO		yes	((FG04688.1:100.0,((AO07023400:100.0,53.m04034:100.0):87.0,AN2577.1:100.0):100.0):100.0,
2800	58.m07477	AN5531.1	AO070328000062	FG00425.1	AFAO	yes	yes	((FG00425.1:100.0,(AN5531.1:100.0,(58.m07477:100.0,AO07032800:100.0):100.0):100.0):100.0,
2801	55.m02959	AN1454.1	AO070302000024	FG00428.1	AFAO			((FG00428.1:100.0,((AO07030200:100.0,55.m02959:100.0):69.0,AN1454.1:100.0):100.0):100.0,
2802	57.m05596	AN4530.1	AO070321000140	FG02702.1	AFAO	yes	yes	((FG02702.1:100.0,((AO07032100:100.0,57.m05596:100.0):99.0,AN4530.1:100.0):100.0):100.0,
2803	65.m07143	AN4608.1	AO070337000243	FG09372.1	AFAN	yes	yes	((FG09372.1:100.0,((AN4608.1:100.0,65.m07143:100.0):100.0,AO07033700:100.0):100.0):100.0,
2804	52.m03778	AN2533.1	AO070325000028	FG03049.1				((((AO07032500:100.0,FG03049.1:100.0):44.0,52.m03778:100.0):74.8,AN2533.1:100.0):100.0,
2805	71.m15661	AN4673.1	AO070284000033	FG05679.1	AFAO	yes	yes	((FG05679.1:100.0,((AO07028400:100.0,71.m15661:100.0):90.5,AN4673.1:100.0):100.0):100.0,
2806	58.m07651	AN1857.1	AO070292000034	FG04829.1	AFAO	yes	yes	((FG04829.1:100.0,((AO07029200:100.0,58.m07651:100.0):93.0,AN1857.1:100.0):100.0):100.0,
2807	65.m07256	AN6718.1	AO070339000158	FG04177.1	AFAO			((FG04177.1:100.0,((AO07033900:100.0,65.m07256:100.0):67.5,AN6718.1:100.0):100.0):100.0,
2808	72.m19071	AN6079.1	AO070340000129	FG08738.1	AFAO	yes	yes	((FG08738.1:100.0,(AN6079.1:100.0,(72.m19071:100.0,AO07034000:100.0):100.0):100.0):100.0,
2809	70.m15522	AN0913.1	AO070320000094	FG05154.1	AFAN			((FG05154.1:100.0,(AO07032000:100.0,(AN0913.1:100.0,70.m15522:100.0):68.0):100.0):100.0,
2810	54.m07022	AN5720.1	AO070324000130	FG08496.1	AFAO		yes	((FG08496.1:100.0,((AO07032400:100.0,54.m07022:100.0):87.0,AN5720.1:100.0):100.0):100.0,
2811	52.m03720	AN5311.1	AO070285000028	FG11450.1				((((52.m03720:100.0,AN5311.1:100.0):98.0,FG11450.1:100.0):49.5,AO07028500:100.0):100.0,
2812	70.m15167	AN1065.1	AO070218000010	FG02797.1	AFAO	yes	yes	((FG02797.1:100.0,((AO07021800:100.0,70.m15167:100.0):92.0,AN1065.1:100.0):100.0):100.0,
2813	57.m05648	AN4483.1	AO070311000032	FG00786.1	AFAO			((FG00786.1:100.0,((AO07031100:100.0,57.m05648:100.0):68.0,AN4483.1:100.0):100.0):100.0,
2814	69.m15659	AN9511.1	AO070324000090	FG07093.1	AFAO			((FG07093.1:100.0,((AO07032400:100.0,69.m15659:100.0):59.5,AN9511.1:100.0):100.0):100.0,
2815	57.m05797	AN2094.1	AO070341000252	FG07084.1	AFAO			((FG07084.1:100.0,((57.m05797:100.0,AO07034100:100.0):52.0,AN2094.1:100.0):100.0):100.0,
2816	57.m05792	AN2090.1	AO070341000248	FG07094.1	AFAN			((FG07094.1:100.0,(AO07034100:100.0,(AN2090.1:100.0,57.m05792:100.0):59.5):100.0):100.0,
2817	58.m07724	AN1638.1	AO070299000044	FG08340.1	AFAO			((FG08340.1:100.0,((AO07029900:100.0,58.m07724:100.0):55.0,AN1638.1:100.0):100.0):100.0,
2818	55.m02949	AN1446.1	AO070302000003	FG01177.1	AFAN			((FG01177.1:100.0,(AO07030200:100.0,(AN1446.1:100.0,55.m02949:100.0):68.5):100.0):100.0,
2819	69.m15257	AN0591.1	AO070280000017	FG10410.1	AFAO	yes	yes	((FG10410.1:100.0,((AO07028000:100.0,69.m15257:100.0):97.5,AN0591.1:100.0):100.0):100.0,
2820	57.m05789	AN2089.1	AO070341000245	FG01055.1	AFAO		yes	((FG01055.1:100.0,((AO07034100:100.0,57.m05789:100.0):75.0,AN2089.1:100.0):100.0):100.0,
2821	57.m05790	AN2088.1	AO070341000246	FG01054.1	AFAO	yes	yes	((FG01054.1:100.0,((AO07034100:100.0,57.m05790:100.0):98.0,AN2088.1:100.0):100.0):100.0,
2822	57.m05807	AN2107.1	AO070341000264	FG01359.1	AFAO			((FG01359.1:100.0,((AO07034100:100.0,57.m05807:100.0):74.0,AN2107.1:100.0):100.0):100.0,
2823	54.m06982	AN0312.1	AO070334000021	FG07086.1	AFAO	yes	yes	((FG07086.1:100.0,((AO07033400:100.0,54.m06982:100.0):90.0,AN0312.1:100.0):100.0):100.0,
2824	54.m06562	AN4034.1	AO070328000126	FG07087.1	ANAO			((FG07087.1:100.0,((AO07032800:100.0,AN4034.1:100.0):65.5,54.m06562:100.0):100.0):100.0,
2825	55.m03263	AN1437.1	AO070232000002	FG00584.1	AFAO	yes	yes	((FG00584.1:100.0,((AO07023200:100.0,55.m03263:100.0):93.0,AN1437.1:100.0):100.0):100.0,
2826	57.m05901	AN7443.1	AO070229000015	FG00583.1	AFAO	yes	yes	((FG00583.1:100.0,((AO07022900:100.0,57.m05901:100.0):99.0,AN7443.1:100.0):100.0):100.0,
2827	72.m19075	AN6085.1	AO070340000136	FG01357.1	AFAO		yes	((FG01357.1:100.0,((72.m19075:100.0,AO07034000:100.0):76.0,AN6085.1:100.0):100.0):100.0,
2828	55.m03039	AN1520.1	AO070334000238	FG00614.1	AFAO	yes	yes	((FG00614.1:100.0,((AO07033400:100.0,55.m03039:100.0):92.5,AN1520.1:100.0):100.0):100.0,
2829	69.m14984	AN3940.1	AO070341000052	FG00482.1	AFAO	yes	yes	((FG00482.1:100.0,(AN3940.1:100.0,(69.m14984:100.0,AO07034100:100.0):100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2830	59.m08374	AN2369.1	AO070289000068	FG07869.1	AFAN			((FG07869.1:100.0,((59.m08374:100.0,AN2369.1:100.0):58.0,AO07028900:100.0):87.5):100.0,
2831	58.m08903	AN3593.1	AO070342000145	FG00493.1	AFAO			((FG00493.1:100.0,((AO07034200:100.0,58.m08903:100.0):65.0,AN3593.1:100.0):100.0):100.0,
2832	58.m07392	AN3592.1	AO070342000144	FG00491.1	ANAO			((FG00491.1:100.0,(58.m07392:100.0,(AN3592.1:100.0,AO07034200:100.0):57.0):100.0):100.0,
2833	58.m07391	AN3591.1	AO070342000143	FG00490.1	AFAO		yes	((FG00490.1:100.0,((AO07034200:100.0,58.m07391:100.0):86.0,AN3591.1:100.0):100.0):100.0,
2834	69.m15746	AN5482.1	AO070341000403	FG01099.1	AFAO			((FG01099.1:100.0,((AO07034100:100.0,69.m15746:100.0):43.5,AN5482.1:100.0):100.0):100.0,
2835	53.m03795	AN8184.1	AO070310000141	FG11536.1	ANAO			((FG11536.1:100.0,((AO07031000:100.0,AN8184.1:100.0):46.0,53.m03795:100.0):100.0):100.0,
2836	55.m03218	AN6881.1	AO070342000371	FG07895.1	AFAN			((FG07895.1:100.0,(AO07034200:100.0,(55.m03218:100.0,AN6881.1:100.0):61.3):99.0):100.0,
2837	58.m08992	AN3873.1	AO070305000057	FG00236.1	AFAO			(((AN3873.1:100.0,(58.m08992:100.0,AO07030500:100.0):46.5):70.7,FG00236.1:100.0):100.0,
2838	59.m08714	AN2869.1	AO070338000153	FG00830.1	AFAO	yes	yes	((FG00830.1:100.0,((AO07033800:100.0,59.m08714:100.0):98.0,AN2869.1:100.0):100.0):100.0,
2839	65.m07368	AN3756.1	AO070309000050	FG05631.1	AFAO		yes	((FG05631.1:100.0,((AO07030900:100.0,65.m07368:100.0):87.0,AN3756.1:100.0):100.0):100.0,
2840	53.m04165	AN8047.1	AO070330000001	FG06574.1	AFAN			((FG06574.1:100.0,(AO07033000:100.0,(AN8047.1:100.0,53.m04165:100.0):69.5):100.0):100.0,
2841	59.m09314	AN3451.1	AO070265000026	FG07854.1	ANAO			((FG07854.1:100.0,(59.m09314:100.0,(AN3451.1:100.0,AO07026500:100.0):66.0):100.0):100.0,
2842	59.m09309	AN3444.1	AO070265000020	FG07857.1	AFAO		yes	((FG07857.1:100.0,((AO07026500:100.0,59.m09309:100.0):78.0,AN3444.1:100.0):100.0):100.0,
2843	59.m08753	AN2902.1	AO070338000104	FG07853.1	AFAO	yes	yes	((FG07853.1:100.0,((AO07033800:100.0,59.m08753:100.0):99.0,AN2902.1:100.0):100.0):100.0,
2844	57.m05524	AN4601.1	AO070267000018	FG07850.1	AFAO	yes	yes	((FG07850.1:100.0,((AO07026700:100.0,57.m05524:100.0):91.0,AN4601.1:100.0):100.0):100.0,
2845	69.m15379	AN3737.1	AO070342000271	FG07849.1	AFAO	yes	yes	((FG07849.1:100.0,((AO07034200:100.0,69.m15379:100.0):92.0,AN3737.1:100.0):100.0):100.0,
2846	69.m14995	AN3932.1	AO070341000043	FG06886.1	ANAO			((FG06886.1:100.0,(69.m14995:100.0,(AO07034100:100.0,AN3932.1:100.0):61.0):100.0):100.0,
2847	56.m02296	AN8884.1	AO070293000016	FG01252.1	AFAO		yes	((FG01252.1:100.0,((AO07029300:100.0,56.m02296:100.0):78.5,AN8884.1:100.0):100.0):100.0,
2848	56.m02289	AN8878.1	AO070293000007	FG01256.1	AFAO	yes	yes	((FG01256.1:100.0,((AO07029300:100.0,56.m02289:100.0):91.0,AN8878.1:100.0):100.0):100.0,
2849	56.m02290	AN8879.1	AO070293000008	FG01257.1	AFAO	yes	yes	((FG01257.1:100.0,((AO07029300:100.0,56.m02290:100.0):98.0,AN8879.1:100.0):100.0):100.0,
2850	53.m03690	AN8271.1	AO070310000030	FG00545.1	AFAO	yes	yes	((FG00545.1:100.0,((AO07031000:100.0,53.m03690:100.0):98.0,AN8271.1:100.0):100.0):100.0,
2851	54.m06678	AN2737.1	AO070338000219	FG00547.1	AFAO	yes	yes	((FG00547.1:100.0,(AN2737.1:100.0,(54.m06678:100.0,AO07033800:100.0):100.0):100.0):100.0,
2852	69.m15017	AN3910.1	AO070324000099	FG00374.1	AFAO	yes	yes	((FG00374.1:100.0,((AO07032400:100.0,69.m15017:100.0):98.5,AN3910.1:100.0):100.0):100.0,
2853	55.m03071	AN1554.1	AO070339000300	FG01273.1	ANAO			((FG01273.1:100.0,(55.m03071:100.0,(AN1554.1:100.0,AO07033900:100.0):54.0):100.0):100.0,
2854	55.m03072	AN1555.1	AO070339000298	FG01272.1	ANAO		yes	((FG01272.1:100.0,(55.m03072:100.0,(AN1555.1:100.0,AO07033900:100.0):79.5):100.0):100.0,
2855	66.m04614	AN9151.1	AO070332000109	FG01251.1	AFAO	yes	yes	((FG01251.1:100.0,(AN9151.1:100.0,(66.m04614:100.0,AO07033200:100.0):100.0):100.0):100.0,
2856	55.m02963	AN1459.1	AO070306000075	FG00608.1	AFAO		yes	((FG00608.1:100.0,((AO07030600:100.0,55.m02963:100.0):88.0,AN1459.1:100.0):100.0):100.0,
2857	72.m19608	AN7583.1	AO070343000298	FG04452.1	AFAO			((FG04452.1:100.0,((AO07034300:100.0,72.m19608:100.0):69.0,AN7583.1:100.0):100.0):100.0,
2858	58.m07537	AN5614.1	AO070301000013	FG10742.1	AFAO		yes	((FG10742.1:100.0,((AO07030100:100.0,58.m07537:100.0):80.5,AN5614.1:100.0):100.0):100.0,
2859	53.m03858	AN8009.1	AO070322000058	FG01672.1	AFAO		yes	((FG01672.1:100.0,((AO07032200:100.0,53.m03858:100.0):88.5,AN8009.1:100.0):100.0):100.0,
2860	58.m07347	AN1949.1	AO070342000215	FG04350.1	AFAN			((FG04350.1:100.0,(AO07034200:100.0,(AN1949.1:100.0,58.m07347:100.0):48.8):100.0):100.0,
2861	52.m03735	AN8102.1	AO070319000053	FG04345.1	ANAO		yes	((((AN8102.1:100.0,AO07031900:100.0):77.5,52.m03735:100.0):89.0,FG04345.1:100.0):100.0,
2862	69.m14813	AN5784.1	AO070249000029	FG01160.1	AFAO	yes	yes	((FG01160.1:100.0,((AO07024900:100.0,69.m14813:100.0):96.5,AN5784.1:100.0):100.0):100.0,
2863	65.m07508	AN4278.1	AO070277000007	FG01161.1	AFAO	yes	yes	((FG01161.1:100.0,((AO07027700:100.0,65.m07508:100.0):99.0,AN4278.1:100.0):100.0):100.0,
2864	63.m00628	AN5049.1	AO070338000189	FG01162.1	AFAO			((FG01162.1:100.0,((AO07033800:100.0,63.m00628:100.0):60.5,AN5049.1:100.0):100.0):100.0,
2865	66.m04608	AN9146.1	AO070332000116	FG01166.1	AFAO	yes	yes	((FG01166.1:100.0,((AO07033200:100.0,66.m04608:100.0):91.5,AN9146.1:100.0):100.0):100.0,
2866	55.m03064	AN1545.1	AO070339000309	FG01369.1	AFAO	yes	yes	((FG01369.1:100.0,((AO07033900:100.0,55.m03064:100.0):93.0,AN1545.1:100.0):100.0):100.0,
2867	70.m14984	AN1235.1	AO070331000248	FG01128.1	AFAO	yes	yes	((FG01128.1:100.0,(AN1235.1:100.0,(70.m14984:100.0,AO07033100:100.0):100.0):100.0):100.0,
2868	58.m07456	AN3646.1	AO070328000091	FG01129.1	AFAO			((FG01129.1:100.0,((AO07032800:100.0,58.m07456:100.0):52.0,AN3646.1:100.0):100.0):100.0,
2869	58.m07429	AN3668.1	AO070342000007	FG01365.1	AFAO		yes	((FG01365.1:100.0,((AO07034200:100.0,58.m07429:100.0):85.5,AN3668.1:100.0):100.0):100.0,
2870	72.m19066	AN6075.1	AO070340000119	FG09311.1	AFAO	yes	yes	((FG09311.1:100.0,(AN6075.1:100.0,(72.m19066:100.0,AO07034000:100.0):100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2871	69.m15536	AN8144.1	AO070340000167	FG04461.1	AFAO	yes	yes	((FG04461.1:100.0,((AO07034000:100.0,69.m15536:100.0):93.0,AN8144.1:100.0):100.0):100.0,
2872	58.m07780	AN1713.1	AO070305000029	FG07555.1	AFAO			((FG07555.1:100.0,((AO07030500:100.0,58.m07780:100.0):72.0,AN1713.1:100.0):100.0):100.0,
2873	57.m05357	AN6422.1	AO070337000266	FG03612.1				((((AO07033700:100.0,AN6422.1:100.0):56.0,FG03612.1:100.0):82.0,57.m05357:100.0):100.0,
2874	57.m05728	AN1884.1	AO070341000165	FG01048.1	AFAN			((FG01048.1:100.0,(AO07034100:100.0,(AN1884.1:100.0,57.m05728:100.0):66.5):100.0):100.0,
2875	59.m08787	AN4890.1	AO070338000068	FG00343.1	AFAO	yes	yes	((FG00343.1:100.0,((AO07033800:100.0,59.m08787:100.0):96.0,AN4890.1:100.0):100.0):100.0,
2876	59.m08790	AN4892.1	AO070338000064	FG00349.1	AFAO	yes	yes	((FG00349.1:100.0,((AO07033800:100.0,59.m08790:100.0):99.0,AN4892.1:100.0):100.0):100.0,
2877	59.m09317	AN3455.1	AO070265000031	FG06340.1	AFAO		yes	((FG06340.1:100.0,((59.m09317:100.0,AO07026500:100.0):75.0,AN3455.1:100.0):100.0):100.0,
2878	59.m09004	AN3014.1	AO070337000102	FG06322.1	ANAO			((FG06322.1:100.0,(59.m09004:100.0,(AN3014.1:100.0,AO07033700:100.0):40.0):100.0):100.0,
2879	58.m07743	AN1662.1	AO070299000024	FG07515.1	AFAN			((((AN1662.1:100.0,58.m07743:100.0):54.5,AO07029900:100.0):99.5,FG07515.1:100.0):100.0,
2880	52.m03741	AN9315.1	AO070315000078	FG07389.1			yes	(((AO07031500:100.0,AN9315.1:100.0):100.0,(FG07389.1:100.0,52.m03741:100.0):79.0):100.0,
2881	58.m07776	AN1700.1	AO070305000026	FG07499.1	AFAO		yes	((FG07499.1:100.0,((AO07030500:100.0,58.m07776:100.0):89.5,AN1700.1:100.0):100.0):100.0,
2882	69.m15725	AN5519.1	AO070341000374	FG06007.1	AFAO			((FG06007.1:100.0,((AO07034100:100.0,69.m15725:100.0):73.5,AN5519.1:100.0):100.0):100.0,
2883	69.m15408	AN3702.1	AO070341000324	FG06009.1	AFAO			((FG06009.1:100.0,((AO07034100:100.0,69.m15408:100.0):52.0,AN3702.1:100.0):100.0):100.0,
2884	70.m15661	AN0624.1	AO070280000076	FG06026.1	AFAN		yes	((FG06026.1:100.0,(AO07028000:100.0,(AN0624.1:100.0,70.m15661:100.0):76.5):100.0):100.0,
2885	54.m06442	AN0316.1	AO070334000016	FG00639.1	AFAO	yes	yes	((FG00639.1:100.0,((54.m06442:100.0,AO07033400:100.0):93.5,AN0316.1:100.0):100.0):100.0,
2886	54.m06441	AN0317.1	AO070334000015	FG05182.1	ANAO		yes	((FG05182.1:100.0,(54.m06441:100.0,(AN0317.1:100.0,AO07033400:100.0):78.5):100.0):100.0,
2887	70.m15443	AN0843.1	AO070216000003	FG06019.1	AFAO		yes	((FG06019.1:100.0,((AO07021600:100.0,70.m15443:100.0):76.5,AN0843.1:100.0):100.0):100.0,
2888	54.m06707	AN4064.1	AO070342000052	FG06021.1	ANAO		yes	((FG06021.1:100.0,(54.m06707:100.0,(AN4064.1:100.0,AO07034200:100.0):80.5):100.0):100.0,
2889	70.m15601	AN0954.1	AO070320000155	FG06024.1	AFAO	yes	yes	((FG06024.1:100.0,((AO07032000:100.0,70.m15601:100.0):96.0,AN0954.1:100.0):100.0):100.0,
2890	70.m15446	AN0847.1	AO070216000006	FG10819.1	ANAO			((FG10819.1:100.0,((AO07021600:100.0,AN0847.1:100.0):66.5,70.m15446:100.0):100.0):100.0,
2891	54.m06605	AN0463.1	AO070328000174	FG06016.1	ANAO		yes	((FG06016.1:100.0,(54.m06605:100.0,(AN0463.1:100.0,AO07032800:100.0):83.0):100.0):100.0,
2892	72.m19804	AN9492.1	AO070297000001	FG02743.1	AFAO			((FG02743.1:100.0,((AO07029700:100.0,72.m19804:100.0):73.5,AN9492.1:100.0):100.0):100.0,
2893	72.m19802	AN7248.1	AO070297000002	FG02733.1	AFAO			((FG02733.1:100.0,((AO07029700:100.0,72.m19802:100.0):74.5,AN7248.1:100.0):100.0):100.0,
2894	71.m15322	AN0048.1	AO070314000127	FG02735.1	ANAO			((FG02735.1:100.0,((AO07031400:100.0,AN0048.1:100.0):57.0,71.m15322:100.0):100.0):100.0,
2895	71.m16041	AN0047.1	AO070314000125	FG02736.1	AFAO		yes	((FG02736.1:100.0,((AO07031400:100.0,71.m16041:100.0):75.0,AN0047.1:100.0):100.0):100.0,
2896	71.m15325	AN0056.1	AO070314000131	FG02489.1	AFAO	yes	yes	((FG02489.1:100.0,((AO07031400:100.0,71.m15325:100.0):97.0,AN0056.1:100.0):100.0):100.0,
2897	71.m15319	AN0044.1	AO070314000123	FG02724.1	AFAO	yes	yes	((FG02724.1:100.0,((AO07031400:100.0,71.m15319:100.0):90.0,AN0044.1:100.0):100.0):100.0,
2898	71.m15318	AN0043.1	AO070314000122	FG02725.1	ANAO			((FG02725.1:100.0,((AO07031400:100.0,AN0043.1:100.0):59.0,71.m15318:100.0):100.0):100.0,
2899	59.m08473	AN2515.1	AO070263000051	FG02703.1	ANAO		yes	((FG02703.1:100.0,(59.m08473:100.0,(AN2515.1:100.0,AO07026300:100.0):75.5):100.0):100.0,
2900	59.m08702	AN2859.1	AO070338000163	FG05128.1	AFAO	yes	yes	((FG05128.1:100.0,(AN2859.1:100.0,(59.m08702:100.0,AO07033800:100.0):100.0):100.0):100.0,
2901	59.m08701	AN2858.1	AO070338000164	FG05130.1	AFAO			((FG05130.1:100.0,((AO07033800:100.0,59.m08701:100.0):74.0,AN2858.1:100.0):100.0):100.0,
2902	59.m08667	AN2846.1	AO070334000118	FG06150.1	AFAN		yes	((FG06150.1:100.0,(AO07033400:100.0,(AN2846.1:100.0,59.m08667:100.0):86.5):100.0):100.0,
2903	69.m15127	AN0224.1	AO070336000254	FG07437.1	ANAO	yes	yes	((FG07437.1:100.0,(69.m15127:100.0,(AN0224.1:100.0,AO07033600:100.0):98.5):100.0):100.0,
2904	53.m03816	AN8165.1	AO070266000010	FG07006.1	ANAO		yes	((FG07006.1:100.0,((AO07026600:100.0,AN8165.1:100.0):86.0,53.m03816:100.0):100.0):100.0,
2905	53.m03799	AN8181.1	AO070310000145	FG07005.1	ANAO			((FG07005.1:100.0,(53.m03799:100.0,(AN8181.1:100.0,AO07031000:100.0):51.0):100.0):100.0,
2906	53.m03758	AN8215.1	AO070310000097	FG07127.1	AFAO		yes	((FG07127.1:100.0,((AO07031000:100.0,53.m03758:100.0):86.5,AN8215.1:100.0):100.0):100.0,
2907	58.m07866	AN4458.1	AO070305000135	FG06789.1	AFAO			((FG06789.1:100.0,((AO07030500:100.0,58.m07866:100.0):50.5,AN4458.1:100.0):100.0):100.0,
2908	63.m00650	AN7332.1	AO070342000220	FG00625.1				((((63.m00650:100.0,FG00625.1:100.0):43.0,AN7332.1:100.0):46.5,AO07034200:100.0):100.0,
2909	55.m03202	AN1820.1	AO070333000048	FG04170.1	ANAO	yes	yes	((FG04170.1:100.0,(55.m03202:100.0,(AN1820.1:100.0,AO07033300:100.0):92.5):100.0):100.0,
2910	69.m15071	AN1766.1	AO070324000026	FG05127.1	AFAO	yes	yes	((FG05127.1:100.0,((AO07032400:100.0,69.m15071:100.0):97.0,AN1766.1:100.0):100.0):100.0,
2911	59.m08684	AN5021.1	AO070338000181	FG04456.1	AFAO	yes	yes	((FG04456.1:100.0,((AO07033800:100.0,59.m08684:100.0):97.0,AN5021.1:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2912	58.m07504	AN5577.1	AO070328000027	FG04454.1	AFAO	yes	yes	((FG04454.1:100.0,((AO07032800:100.0,58.m07504:100.0):98.5,AN5577.1:100.0):100.0):100.0,
2913	58.m07500	AN5574.1	AO070328000032	FG04453.1	AFAN		yes	((FG04453.1:100.0,(AO07032800:100.0,(AN5574.1:100.0,58.m07500:100.0):84.5):100.0):100.0,
2914	56.m02375	AN8956.1	AO070319000056	FG02426.1	AFAO			((FG02426.1:100.0,((AO07031900:100.0,56.m02375:100.0):73.5,AN8956.1:100.0):100.0):100.0,
2915	52.m03911	AN2812.1	AO070303000084	FG02426.1	AFAO	yes	yes	((FG02426.1:100.0,((AO07030300:100.0,52.m03911:100.0):99.0,AN2812.1:100.0):100.0):100.0,
2916	53.m03917	AN8066.1	AO070330000022	FG01601.1	AFAO		yes	((FG01601.1:100.0,((AO07033000:100.0,53.m03917:100.0):85.5,AN8066.1:100.0):100.0):100.0,
2917	59.m08511	AN5321.1	AO070191000002	FG03687.1	AFAO	yes	yes	((FG03687.1:100.0,((AO07019100:100.0,59.m08511:100.0):99.0,AN5321.1:100.0):100.0):100.0,
2918	57.m05965	AN2813.1	AO070251000001	FG07852.1	AFAN	yes	yes	((FG07852.1:100.0,((57.m05965:100.0,AN2813.1:100.0):95.0,AO07025100:100.0):98.5):100.0,
2919	70.m14976	AN1243.1	AO070223000005	FG03033.1	AFAO		yes	((FG03033.1:100.0,((AO07022300:100.0,70.m14976:100.0):89.5,AN1243.1:100.0):100.0):100.0,
2920	72.m19105	AN6053.1	AO070340000201	FG00831.1	AFAO	yes	yes	((FG00831.1:100.0,((AO07034000:100.0,72.m19105:100.0):97.0,AN6053.1:100.0):100.0):100.0,
2921	54.m06886	AN5137.1	AO070291000040	FG00836.1	AFAO	yes	yes	((FG00836.1:100.0,((AO07029100:100.0,54.m06886:100.0):95.0,AN5137.1:100.0):100.0):100.0,
2922	54.m06894	AN5129.1	AO070291000048	FG00838.1	AFAO			((FG00838.1:100.0,((AO07029100:100.0,54.m06894:100.0):71.5,AN5129.1:100.0):100.0):100.0,
2923	54.m06909	AN5114.1	AO070291000065	FG00834.1	AFAO	yes	yes	((FG00834.1:100.0,(AN5114.1:100.0,(54.m06909:100.0,AO07029100:100.0):100.0):100.0):100.0,
2924	70.m15159	AN1085.1	AO070285000085	FG00833.1	AFAO		yes	((FG00833.1:100.0,((AO07028500:100.0,70.m15159:100.0):75.0,AN1085.1:100.0):100.0):100.0,
2925	69.m15180	AN6815.1	AO070252000017	FG02941.1		yes	yes	(((AN6815.1:100.0,FG02941.1:100.0):100.0,(AO07025200:100.0,69.m15180:100.0):99.5):100.0,
2926	70.m15204	AN8095.1	AO070298000078	FG08749.1	AFAO			((FG08749.1:100.0,((70.m15204:100.0,AO07029800:100.0):59.0,AN8095.1:100.0):100.0):100.0,
2927	59.m08548	AN3157.1	AO070256000037	FG04242.1	AFAO	yes	yes	((FG04242.1:100.0,((AO07025600:100.0,59.m08548:100.0):96.0,AN3157.1:100.0):100.0):100.0,
2928	54.m06857	AN5166.1	AO070291000006	FG04237.1	AFAO			((FG04237.1:100.0,((54.m06857:100.0,AO07029100:100.0):62.8,AN5166.1:100.0):100.0):100.0,
2929	70.m15207	AN1050.1	AO070312000117	FG04243.1	AFAN	yes	yes	((FG04243.1:100.0,(AO07031200:100.0,(AN1050.1:100.0,70.m15207:100.0):95.5):100.0):100.0,
2930	56.m03099	AN3205.1	AO070336000134	FG02220.1				(((AO07033600:100.0,AN3205.1:100.0):56.5,(56.m03099:100.0,FG02220.1:100.0):57.0):100.0,
2931	52.m03795	AN3776.1	AO070302000047	FG03956.1	AFAO			((FG03956.1:100.0,((AO07030200:100.0,52.m03795:100.0):65.5,AN3776.1:100.0):100.0):100.0,
2932	69.m15731	AN5376.1	AO070333000163	FG02819.1	AFAO			((FG02819.1:100.0,((AO07033300:100.0,69.m15731:100.0):67.0,AN5376.1:100.0):100.0):100.0,
2933	72.m19426	AN6228.1	AO070304000079	FG04184.1	ANAO			((FG04184.1:100.0,(72.m19426:100.0,(AN6228.1:100.0,AO07030400:100.0):72.0):100.0):100.0,
2934	65.m07271	AN6714.1	AO070339000148	FG04183.1	AFAO	yes	yes	((FG04183.1:100.0,((AO07033900:100.0,65.m07271:100.0):99.0,AN6714.1:100.0):100.0):100.0,
2935	71.m16099	AN7741.1	AO070325000162	FG02105.1	AFAO		yes	((FG02105.1:100.0,((AO07032500:100.0,71.m16099:100.0):75.0,AN7741.1:100.0):100.0):100.0,
2936	71.m15889	AN2251.1	AO070326000115	FG06575.1	ANAO			((FG06575.1:100.0,(71.m15889:100.0,(AN2251.1:100.0,AO07032600:100.0):72.5):100.0):100.0,
2937	69.m15282	AN0993.1	AO070272000042	FG04668.1	AFAO			((FG04668.1:100.0,((AO07027200:100.0,69.m15282:100.0):73.5,AN0993.1:100.0):100.0):100.0,
2938	57.m05494	AN4572.1	AO070316000155	FG04016.1	AFAO	yes	yes	((FG04016.1:100.0,(AN4572.1:100.0,(57.m05494:100.0,AO07031600:100.0):100.0):100.0):100.0,
2939	71.m15602	AN8795.1	AO070276000071	FG08982.1	AFAO		yes	((FG08982.1:100.0,((71.m15602:100.0,AO07027600:100.0):87.0,AN8795.1:100.0):99.0):100.0,
2940	53.m04204	AN8246.1	AO070310000061	FG08964.1	AFAO	yes	yes	((FG08964.1:100.0,(AN8246.1:100.0,(53.m04204:100.0,AO07031000:100.0):100.0):100.0):100.0,
2941	54.m06828	AN5713.1	AO070324000145	FG06306.1	ANAO			((FG06306.1:100.0,(54.m06828:100.0,(AN5713.1:100.0,AO07032400:100.0):63.0):100.0):100.0,
2942	59.m09292	AN3432.1	AO070265000009	FG06059.1	ANAO	yes	yes	((FG06059.1:100.0,(59.m09292:100.0,(AN3432.1:100.0,AO07026500:100.0):96.5):100.0):100.0,
2943	59.m08777	AN4883.1	AO070338000077	FG06316.1	AFAO	yes	yes	((FG06316.1:100.0,((AO07033800:100.0,59.m08777:100.0):97.5,AN4883.1:100.0):100.0):100.0,
2944	59.m08960	AN3055.1	AO070337000019	FG06315.1	AFAO		yes	((FG06315.1:100.0,((AO07033700:100.0,59.m08960:100.0):80.0,AN3055.1:100.0):100.0):100.0,
2945	59.m08955	AN3056.1	AO070337000018	FG06314.1	AFAO	yes	yes	((FG06314.1:100.0,((AO07033700:100.0,59.m08955:100.0):97.0,AN3056.1:100.0):100.0):100.0,
2946	59.m08929	AN3070.1	AO070337000004	FG06313.1	AFAO			((FG06313.1:100.0,((AO07033700:100.0,59.m08929:100.0):53.0,AN3070.1:100.0):100.0):100.0,
2947	59.m09009	AN3005.1	AO070337000107	FG06052.1	ANAO			((FG06052.1:100.0,((AO07033700:100.0,AN3005.1:100.0):51.5,59.m09009:100.0):100.0):100.0,
2948	69.m15435	AN5523.1	AO070341000366	FG06051.1	AFAO			((FG06051.1:100.0,((AO07034100:100.0,69.m15435:100.0):54.0,AN5523.1:100.0):100.0):100.0,
2949	59.m08990	AN3029.1	AO070337000071	FG06317.1	AFAO			((FG06317.1:100.0,((AO07033700:100.0,59.m08990:100.0):65.5,AN3029.1:100.0):100.0):100.0,
2950	71.m15830	AN2239.1	AO070326000142	FG09557.1	ANAO			((FG09557.1:100.0,(71.m15830:100.0,(AN2239.1:100.0,AO07032600:100.0):60.0):100.0):100.0,
2951	69.m15563	AN5343.1	AO070333000181	FG05088.1	AFAO		yes	((FG05088.1:100.0,((AO07033300:100.0,69.m15563:100.0):89.5,AN5343.1:100.0):100.0):100.0,
2952	72.m19758	AN7307.1	AO070297000055	FG04255.1	ANAO		yes	((FG04255.1:100.0,((AO07029700:100.0,AN7307.1:100.0):80.5,72.m19758:100.0):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2953	69.m15254	AN0594.1	AO070280000020	FG09787.1	AFAO	yes	yes	((FG09787.1:100.0,((AO07028000:100.0,69.m15254:100.0):97.0,AN0594.1:100.0):100.0):100.0,
2954	69.m15252	AN0595.1	AO070280000021	FG09786.1	ANAO			((FG09786.1:100.0,(69.m15252:100.0,(AN0595.1:100.0,AO07028000:100.0):68.5):100.0):100.0,
2955	69.m15219	AN2439.1	AO070264000040	FG06219.1	AFAO			((FG06219.1:100.0,((AO07026400:100.0,69.m15219:100.0):67.5,AN2439.1:100.0):100.0):100.0,
2956	69.m15220	AN2438.1	AO070264000041	FG05298.1	AFAN		yes	((FG05298.1:100.0,(AO07026400:100.0,(AN2438.1:100.0,69.m15220:100.0):76.3):100.0):100.0,
2957	72.m19643	AN3778.1	AO070343000274	FG05299.1	AFAO			((FG05299.1:100.0,((72.m19643:100.0,AO07034300:100.0):60.5,AN3778.1:100.0):100.0):100.0,
2958	72.m19644	AN7603.1	AO070343000273	FG05300.1	AFAN			((FG05300.1:100.0,((72.m19644:100.0,AN7603.1:100.0):67.5,AO07034300:100.0):99.0):100.0,
2959	72.m19657	AN2181.1	AO070343000260	FG05301.1	AFAO			(((AN2181.1:100.0,(AO07034300:100.0,72.m19657:100.0):73.3):99.5,FG05301.1:100.0):100.0,
2960	58.m07593	AN1986.1	AO070301000073	FG06006.1	AFAO	yes	yes	((FG06006.1:100.0,((AO07030100:100.0,58.m07593:100.0):93.5,AN1986.1:100.0):100.0):100.0,
2961	70.m15646	AN0636.1	AO070318000126	FG00960.1	AFAN	yes	yes	((FG00960.1:100.0,(AO07031800:100.0,(AN0636.1:100.0,70.m15646:100.0):90.0):100.0):100.0,
2962	58.m07958	AN4369.1	AO070261000009	FG10889.1	AFAO			((FG10889.1:100.0,((AO07026100:100.0,58.m07958:100.0):67.0,AN4369.1:100.0):100.0):100.0,
2963	54.m06345	AN0392.1	AO070278000009	FG03365.1	AFAN		yes	((((AN0392.1:100.0,54.m06345:100.0):83.5,AO07027800:100.0):95.0,FG03365.1:100.0):100.0,
2964	55.m03067	AN1547.1	AO070339000307	FG08266.1	AFAO		yes	((FG08266.1:100.0,((55.m03067:100.0,AO07033900:100.0):78.5,AN1547.1:100.0):100.0):100.0,
2965	55.m02928	AN1427.1	AO070242000025	FG07917.1	AFAO	yes	yes	((FG07917.1:100.0,(AN1427.1:100.0,(55.m02928:100.0,AO07024200:100.0):100.0):100.0):100.0,
2966	72.m19543	AN5267.1	AO070275000042	FG11036.1	ANAO	yes	yes	((FG11036.1:100.0,(72.m19543:100.0,(AO07027500:100.0,AN5267.1:100.0):99.5):100.0):100.0,
2967	69.m15602	AN1571.1	AO070298000116	FG03813.1				((AN1571.1:100.0,((AO07029800:100.0,69.m15602:100.0):99.5,FG03813.1:100.0):52.5):100.0,
2968	69.m14961	AN4182.1	AO070341000081	FG08468.1	AFAO			((FG08468.1:100.0,((AO07034100:100.0,69.m14961:100.0):47.8,AN4182.1:100.0):100.0):100.0,
2969	70.m15488	AN0893.1	AO070320000065	FG05187.1	AFAO	yes	yes	((FG05187.1:100.0,((AO07032000:100.0,70.m15488:100.0):99.3,AN0893.1:100.0):100.0):100.0,
2970	69.m15446	AN5515.1	AO070341000381	FG05346.1	ANAO			((FG05346.1:100.0,(69.m15446:100.0,(AN5515.1:100.0,AO07034100:100.0):72.0):100.0):100.0,
2971	72.m20007	AN7353.1	AO070278000047	FG02628.1	ANAO			((FG02628.1:100.0,((AO07027800:100.0,AN7353.1:100.0):55.0,72.m20007:100.0):100.0):100.0,
2972	67.m02964	AN8329.1	AO070330000092	FG03475.1	AFAO		yes	((((67.m02964:100.0,AO07033000:100.0):100.0,AN8329.1:100.0):79.5,FG03475.1:100.0):100.0,
2973	53.m04191	AN8018.1	AO070322000067	FG03429.1	AFAO	yes	yes	((FG03429.1:100.0,((AO07032200:100.0,53.m04191:100.0):99.0,AN8018.1:100.0):100.0):100.0,
2974	70.m15668	AN8594.1	AO070280000033	FG07590.1	AFAO			((FG07590.1:100.0,((AO07028000:100.0,70.m15668:100.0):67.5,AN8594.1:100.0):100.0):100.0,
2975	72.m19586	AN7567.1	AO070343000413	FG01317.1	AFAN	yes	yes	((FG01317.1:100.0,(AO07034300:100.0,(AN7567.1:100.0,72.m19586:100.0):92.0):100.0):100.0,
2976	56.m02287	AN8874.1	AO070293000003	FG01320.1	AFAO		yes	((FG01320.1:100.0,((AO07029300:100.0,56.m02287:100.0):76.5,AN8874.1:100.0):100.0):100.0,
2977	58.m07442	AN3658.1	AO070342000030	FG09376.1	AFAO			((FG09376.1:100.0,((58.m07442:100.0,AO07034200:100.0):51.5,AN3658.1:100.0):100.0):100.0,
2978	70.m15030	AN1191.1	AO070331000192	FG01322.1	ANAO		yes	((((AN1191.1:100.0,AO07033100:100.0):76.4,70.m15030:100.0):93.5,FG01322.1:100.0):100.0,
2979	70.m15031	AN1190.1	AO070331000190	FG01323.1	AFAO	yes	yes	((FG01323.1:100.0,((AO07033100:100.0,70.m15031:100.0):92.0,AN1190.1:100.0):100.0):100.0,
2980	54.m06397	AN0357.1	AO070318000033	FG00561.1	ANAO		yes	((FG00561.1:100.0,(54.m06397:100.0,(AN0357.1:100.0,AO07031800:100.0):89.5):100.0):100.0,
2981	54.m06940	AN0354.1	AO070318000031	FG00478.1	AFAO			((FG00478.1:100.0,((AO07031800:100.0,54.m06940:100.0):50.5,AN0354.1:100.0):100.0):100.0,
2982	54.m06366	AN0380.1	AO070318000064	FG00480.1	ANAO			((FG00480.1:100.0,(54.m06366:100.0,(AO07031800:100.0,AN0380.1:100.0):58.5):90.5):100.0,
2983	58.m08026	AN3679.1	AO070189000006	FG00578.1	AFAO	yes	yes	((FG00578.1:100.0,(AN3679.1:100.0,(58.m08026:100.0,AO07018900:100.0):100.0):100.0):100.0,
2984	71.m15601	AN8794.1	AO070276000069	FG09009.1	AFAO	yes	yes	((FG09009.1:100.0,((AO07027600:100.0,71.m15601:100.0):92.5,AN8794.1:100.0):100.0):100.0,
2985	52.m03751	AN8489.1	AO070342000405	FG08830.1	AFAO			((FG08830.1:100.0,((52.m03751:100.0,AO07034200:100.0):47.0,AN8489.1:100.0):100.0):100.0,
2986	71.m15775	AN7747.1	AO070325000174	FG02078.1	AFAO			((FG02078.1:100.0,((AO07032500:100.0,71.m15775:100.0):48.0,AN7747.1:100.0):100.0):100.0,
2987	57.m05479	AN4648.1	AO070316000120	FG10060.1	AFAO		yes	((FG10060.1:100.0,((AO07031600:100.0,57.m05479:100.0):89.0,AN4648.1:100.0):100.0):100.0,
2988	52.m03801	AN5085.1	AO070246000035	FG03582.1	ANAO		yes	((((AO07024600:100.0,AN5085.1:100.0):82.3,52.m03801:100.0):80.3,FG03582.1:100.0):100.0,
2989	69.m15046	AN1743.1	AO070324000053	FG09239.1	AFAO			((FG09239.1:100.0,((AO07032400:100.0,69.m15046:100.0):64.5,AN1743.1:100.0):100.0):100.0,
2990	69.m15044	AN1726.1	AO070324000057	FG09240.1	AFAO	yes	yes	((FG09240.1:100.0,(AN1726.1:100.0,(69.m15044:100.0,AO07032400:100.0):100.0):100.0):100.0,
2991	54.m06607	AN0462.1	AO070328000176	FG09244.1	AFAO	yes	yes	((FG09244.1:100.0,(AN0462.1:100.0,(54.m06607:100.0,AO07032800:100.0):100.0):100.0):100.0,
2992	69.m14936	AN1918.1	AO070341000122	FG08601.1	AFAO			((FG08601.1:100.0,((69.m14936:100.0,AO07034100:100.0):56.0,AN1918.1:100.0):100.0):100.0,
2993	70.m15303	AN0700.1	AO070343000510	FG10719.1	ANAO	yes	yes	((FG10719.1:100.0,(70.m15303:100.0,(AN0700.1:100.0,AO07034300:100.0):92.5):100.0):100.0,

ID	AFgene	ANgene	AOgene	FGgene	Topo	Boot90	Boot75	tree
2994	65.m07180	AN6761.1	AO070339000213	FG10950.1	AFAO	yes	yes	((((AO07033900:100.0,65.m07180:100.0):92.0,AN6761.1:100.0):93.5,FG10950.1:100.0):100.0,
2995	69.m15628	AN5191.1	AO070237000021	FG10948.1	AFAO		yes	((FG10948.1:100.0,((AO07023700:100.0,69.m15628:100.0):78.0,AN5191.1:100.0):100.0):100.0,
2996	70.m15018	AN1201.1	AO070331000207	FG01333.1	AFAO	yes	yes	((FG01333.1:100.0,((AO07033100:100.0,70.m15018:100.0):98.5,AN1201.1:100.0):100.0):100.0,
2997	70.m15019	AN1200.1	AO070331000206	FG01332.1	AFAO			((FG01332.1:100.0,((70.m15019:100.0,AO07033100:100.0):65.5,AN1200.1:100.0):100.0):100.0,
2998	69.m15050	AN1747.1	AO070324000049	FG01330.1	AFAO			((FG01330.1:100.0,((AO07032400:100.0,69.m15050:100.0):59.5,AN1747.1:100.0):100.0):100.0,
2999	70.m15024	AN1196.1	AO070331000200	FG01330.1	AFAO	yes	yes	(((AN1196.1:100.0,(70.m15024:100.0,AO07033100:100.0):93.5):96.5,FG01330.1:100.0):100.0,
3000	70.m15765	AN1194.1	AO070331000198	FG01329.1	AFAO	yes	yes	((FG01329.1:100.0,((70.m15765:100.0,AO07033100:100.0):98.5,AN1194.1:100.0):100.0):100.0,
3001	70.m15025	AN1195.1	AO070331000199	FG01328.1	AFAO			((FG01328.1:100.0,((70.m15025:100.0,AO07033100:100.0):54.0,AN1195.1:100.0):100.0):100.0,
3002	70.m14915	AN1293.1	AO070303000055	FG01324.1	AFAO	yes	yes	((FG01324.1:100.0,((AO07030300:100.0,70.m14915:100.0):90.0,AN1293.1:100.0):100.0):100.0,
3003	62.m03251	AN6651.1	AO070269000002	FG08532.1	AFAO		yes	((FG08532.1:100.0,((62.m03251:100.0,AO07026900:100.0):78.5,AN6651.1:100.0):100.0):100.0,
3004	54.m06657	AN0418.1	AO070338000266	FG03111.1	AFAO	yes	yes	((FG03111.1:100.0,((AO07033800:100.0,54.m06657:100.0):99.0,AN0418.1:100.0):100.0):100.0,
3005	69.m15311	AN0495.1	AO070226000029	FG08971.1	AFAN		yes	((FG08971.1:100.0,(AO07022600:100.0,(AN0495.1:100.0,69.m15311:100.0):78.5):100.0):100.0,
3006	62.m03222	AN6623.1	AO070326000077	FG00152.1	ANAO			((FG00152.1:100.0,(62.m03222:100.0,(AN6623.1:100.0,AO07032600:100.0):59.0):100.0):100.0,
3007	52.m03820	AN8401.1	AO070302000072	FG07993.1	ANAO			((FG07993.1:100.0,((AO07030200:100.0,AN8401.1:100.0):66.0,52.m03820:100.0):100.0):100.0,
3008	57.m05964	AN2060.1	AO070328000072	FG03054.1	ANAO	yes	yes	((FG03054.1:100.0,(57.m05964:100.0,(AN2060.1:100.0,AO07032800:100.0):95.5):100.0):100.0,
3009	72.m19949	AN6032.1	AO070340000256	FG09710.1	AFAO	yes	yes	((FG09710.1:100.0,(AN6032.1:100.0,(72.m19949:100.0,AO07034000:100.0):100.0):100.0):100.0,
3010	52.m04032	AN9405.1	AO070274000012	FG02789.1	ANAO			((FG02789.1:100.0,(52.m04032:100.0,(AN9405.1:100.0,AO07027400:100.0):64.5):100.0):100.0,
3011	53.m03817	AN8164.1	AO070266000011	FG02787.1	ANAO			((FG02787.1:100.0,(53.m03817:100.0,(AN8164.1:100.0,AO07026600:100.0):62.5):100.0):100.0,
3012	59.m08451	AN2528.1	AO070300000123	FG04848.1	AFAO			((FG04848.1:100.0,((59.m08451:100.0,AO07030000:100.0):46.0,AN2528.1:100.0):100.0):100.0,
3013	70.m15178	AN1057.1	AO070336000001	FG09417.1	AFAO		yes	((FG09417.1:100.0,((AO07033600:100.0,70.m15178:100.0):80.0,AN1057.1:100.0):100.0):100.0,
3014	59.m08733	AN2886.1	AO070338000128	FG00383.1	ANAO			((FG00383.1:100.0,(59.m08733:100.0,(AN2886.1:100.0,AO07033800:100.0):64.5):100.0):100.0,
3015	59.m08734	AN2887.1	AO070338000127	FG00382.1	ANAO			((FG00382.1:100.0,((AO07033800:100.0,AN2887.1:100.0):51.0,59.m08734:100.0):100.0):100.0,
3016	62.m03255	AN6653.1	AO070269000013	FG08700.1	AFAO	yes	yes	((FG08700.1:100.0,((AO07026900:100.0,62.m03255:100.0):94.5,AN6653.1:100.0):100.0):100.0,
3017	62.m03362	AN8707.1	AO070315000134	FG08712.1	ANAO		yes	((FG08712.1:100.0,(62.m03362:100.0,(AN8707.1:100.0,AO07031500:100.0):87.5):100.0):100.0,
3018	58.m08951	AN5631.1	AO070301000030	FG10524.1	ANAO	yes	yes	((FG10524.1:100.0,(58.m08951:100.0,(AN5631.1:100.0,AO07030100:100.0):93.5):100.0):100.0,
3019	57.m05978	AN4514.1	AO070311000070	FG00815.1	AFAN			((FG00815.1:100.0,(AO07031100:100.0,(AN4514.1:100.0,57.m05978:100.0):68.0):100.0):100.0,
3020	58.m07982	AN4342.1	AO070240000017	FG04395.1	AFAO	yes	yes	((FG04395.1:100.0,((AO07024000:100.0,58.m07982:100.0):90.0,AN4342.1:100.0):100.0):100.0,
3021	58.m09007	AN4333.1	AO070240000012	FG04394.1	AFAO	yes	yes	((FG04394.1:100.0,(AN4333.1:100.0,(58.m09007:100.0,AO07024000:100.0):100.0):100.0):100.0,
3022	69.m14844	AN5746.1	AO070341000003	FG01346.1	AFAO	yes	yes	((FG01346.1:100.0,((AO07034100:100.0,69.m14844:100.0):94.0,AN5746.1:100.0):100.0):100.0,
3023	69.m14975	AN3946.1	AO070341000066	FG01347.1	AFAO			((FG01347.1:100.0,((69.m14975:100.0,AO07034100:100.0):61.0,AN3946.1:100.0):100.0):100.0,
3024	55.m03190	AN3390.1	AO070290000088	FG03406.1	AFAO			((FG03406.1:100.0,((AO07029000:100.0,55.m03190:100.0):56.5,AN3390.1:100.0):100.0):100.0,
3025	69.m15654	AN1761.1	AO070324000020	FG09313.1	AFAO			((FG09313.1:100.0,((69.m15654:100.0,AO07032400:100.0):47.0,AN1761.1:100.0):100.0):100.0,
3026	69.m15077	AN1778.1	AO070324000018	FG09312.1	AFAO		yes	((((AO07032400:100.0,69.m15077:100.0):85.0,AN1778.1:100.0):99.0,FG09312.1:100.0):100.0,
3027	66.m04779	AN3361.1	AO070281000037	FG07554.1	ANAO		yes	((FG07554.1:100.0,(66.m04779:100.0,(AN3361.1:100.0,AO07028100:100.0):82.5):100.0):100.0,
3028	59.m08711	AN2867.1	AO070338000157	FG00387.1	AFAO	yes	yes	((FG00387.1:100.0,((AO07033800:100.0,59.m08711:100.0):90.0,AN2867.1:100.0):100.0):100.0,
3029	59.m08710	AN2866.1	AO070338000158	FG00389.1	AFAO	yes	yes	((FG00389.1:100.0,(AN2866.1:100.0,(59.m08710:100.0,AO07033800:100.0):100.0):100.0):100.0,
3030	59.m08764	AN4869.1	AO070338000091	FG10255.1	AFAO		yes	((FG10255.1:100.0,((AO07033800:100.0,59.m08764:100.0):88.0,AN4869.1:100.0):100.0):100.0,
3031	59.m09001	AN3026.1	AO070337000068	FG07939.1	AFAN			((FG07939.1:100.0,(AO07033700:100.0,(AN3026.1:100.0,59.m09001:100.0):53.0):100.0):100.0,
3032	59.m09445	AN3019.1	AO070337000095	FG07938.1	AFAO		yes	((FG07938.1:100.0,((AO07033700:100.0,59.m09445:100.0):88.0,AN3019.1:100.0):100.0):100.0,
3033	56.m02286	AN8873.1	AO070293000002	FG01316.1	AFAO		yes	((FG01316.1:100.0,((AO07029300:100.0,56.m02286:100.0):82.5,AN8873.1:100.0):100.0):100.0,
3034	54.m07033	AN4247.1	AO070324000165	FG07924.1	AFAO			((FG07924.1:100.0,((AO07032400:100.0,54.m07033:100.0):54.5,AN4247.1:100.0):100.0):100.0,

§S2. Synteny Analysis

§S2.1. Hierarchical Synteny Clustering Method

Blocks of snyteny were predicted using a hierarchical clustering technique (Figure S2.1A). The algorithm is initiated by detecting clusters of sequence anchors with conserved order and orientation. These regions are then merged in to successively larger syntenic clusters by tolerating successively larger rearrangements within blocks. Specifically:

Given: two genome sequences with a set of pairwise alignments defined on a two-dimensional coordinate system formed by the concatenation of the contigs of each genome.

Step1: Calculate Exact Syntenic Clusters. Find blocks of anchors with exact conservation of order and orientation and cluster them. The orientation of each cluster is either "+" or "-" (defined as expected from the given coordinate system). Create a list, L, of these seed clusters.

Step2: Initialize the Cluster Distance Matrix. Define the bounds of a cluster as its endpoints on each axis of the coordinate system (this defines a box). Define the asymmetric distance between cluster X and cluster Y as the cartesian distance between the two nearest points on the bounds if (a) these clusters are on the same supercontig, (b) the distance is less than a scale factor D, and (c) *only if cluster X is oriented toward cluster Y* (see Figure S2.1). Otherwise the distance is infinity. Calculate the complete distance matrix, d_{ij}, between all pairs of clusters (in practice only one half of the matrix is required).

Step3: Merge Nearest Cluster. Find the minimum entry in the distance matrix and merge the two corresponding clusters into a new cluster. Create pointers in the new cluster to the merged clusters. Remove the merged clusters from L, and add the new cluster.

Step4: Calculate Merged Cluster Orientation. The orientation of the new cluster is defined according to the slope of the line through the merged clusters.

Step5: Update Distance Matrix. Remove the entries in d_{ij} for the merged clusters and create an entry for the new cluster. Recalculate those entries impacted by this procedure. Increase the scale factor D and repeat steps 3-5 until D exceeds the size of the largest supercontig.

Output: When no new clusters can be merged, output L. Each cluster in L is a tree defining a hierarchical relationship between merged clusters.

An example of the algorithm applied to a 1Mb region of synteny between *A. nidulans* and *A. fumigatus* is shown in Figure S2.1B. The clustering function produces a tree-based data structure that can be manipulated by standard tree traversal algorithms. Using these structures, the number of rearrangement events (at a any given level of resolution) in pairwise comparisons can be calculated. Given multiple pairwise comparisons, branch specific rearrangements can be calculated as described in the methods.

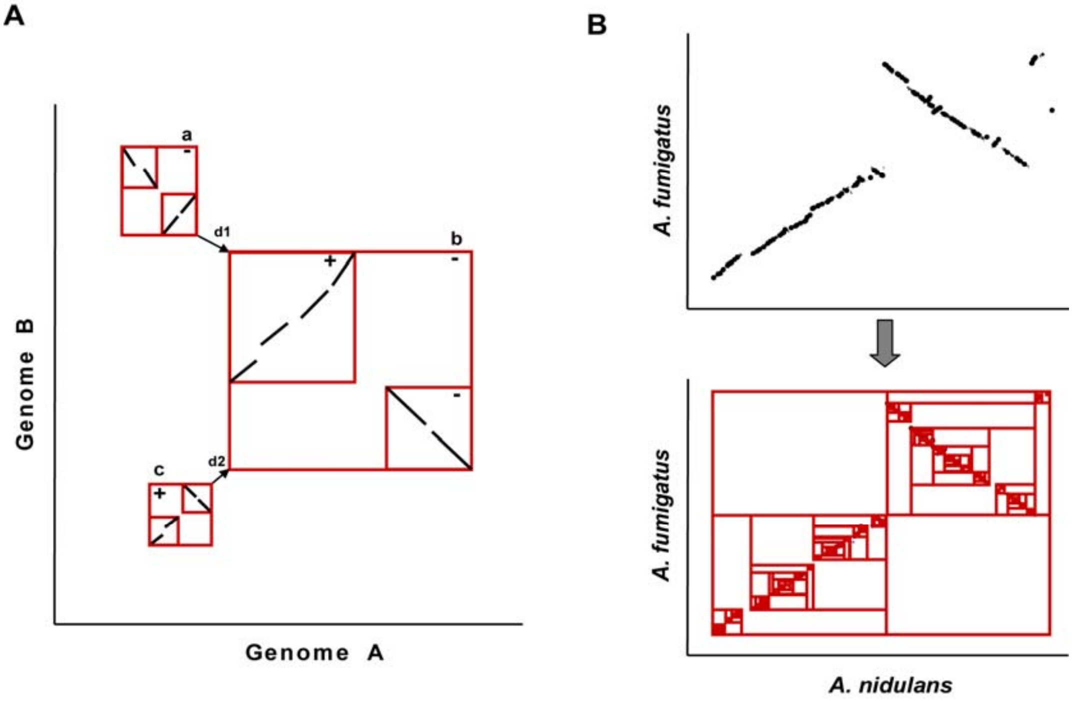

Figure S2.1. Hierarchical clustering algorithm for whole genome synteny mapping. (A) Algorithm schematic. Each cluster (boxes) is associated with an orientation ('+' or '-' symbols). An asymmetric distance is defined between all pairs of clusters. If a cluster is oriented "toward" another, the distance is defined to be the cartesian distance (e.g. d_{ab}=d1). Otherwise the distance is infinity (e.g. $d_{ba}=\infty$). The method merges the closest pair of clusters at each iteration. Information about merged clusters is maintained (boxes within boxes). See text for more details. (B) Application to 1Mb region of synteny between *A. nidulans* and *A. fumigatus*. The method identifies the large inversion, as well as rearrangements within rearrangements (boxes within boxes).

§S2.2. Syntenic breaks are associated with repeats and telomeres

As described in the main text, an examination of the pattern of pairwise syteny between the three Aspergilli reveals large regions lacking detectable long range synteny. Repeat sequences are enriched in these non-syntenic regions, with 40% of *A. nidulans* repeats sequences in breaks with both *A. fumigatus* and *A. oryzae*, compared to 27% expected ($p<1e-116$ – similar enrichments for *A. fumigatus* and *A. oryzae*). Extensive rearrangement is also observed at the ends of Aspergillus chromosomes. This association of large-scale genome rearrangement with repeats and chromosome ends has been observed for a number organisms including mammals, nematodes, and yeasts[7,9-13], and our data confirm these trends for the Aspergilli.

In addition, the observed subtelomeric rearrangement may have specific implications for fungi. Growing evidence suggests that subtelomeric regions in fungi contain genes with roles in niche adaptation and virulence. It is thus noteworthy that sub-telomeric regions in both *A. nidulans* and *A. fumigatus* show enrichment for gene clusters with predicted roles in secondary metabolism. In *A. fumigatus*, 8 of 24 secondary metabolite clusters are found within 100Kb of the nearest telomere ($p<1e5$), while in *A. nidulans*, 11 different secondary metabolite gene clusters, including a penicillin and a sterigmatocystin cluster, are situated within 100 kb of the nearest telomere. Further, over 30% of predicted non ribosomal peptide synthetases and polyketide synthases genes in *A. nidulans* and *A. fumigatus* reside within just 100 kb of a telomere (a 5.5-fold enrichment). This enrichment suggests that these genes may play an important role in the ecology of these fungi. The rapid rearrangement of subtelomeric regions may facilitate the species specific evolution of these genes, and in this regard it is conspicuous that *A. nidulans* and *A. fumigatus* do not have any telomere-associated secondary metabolite gene clusters in common.

§S2.3. The Random Breakage Model of Genome Evolution

As described in the main text, it has long been proposed that genomes evolve according to random breakage model which predicts that distances between breakpoints should follow an exponential distribution of the form $f(x) = 1/L\ e^{-x/L}$, where L is the average size of all unbroken segments[14,15]. To determine whether conserved syntenic blocks in Aspergilli follow random breakage, we analyzed the distribution of lengths of unbroken regions between micro-rearrangements within pairwise syntenic blocks (see Methods). As shown in XXXXX, although the mean breakpoint length differs between the three pairwise comparisons, in all three cases the distribution of lengths shows close agreement with the model prediction. It thus appears that syntenic blocks, comprising the majority of the Aspergillus chromosomes, are evolving in a manner consistent with random breakage.

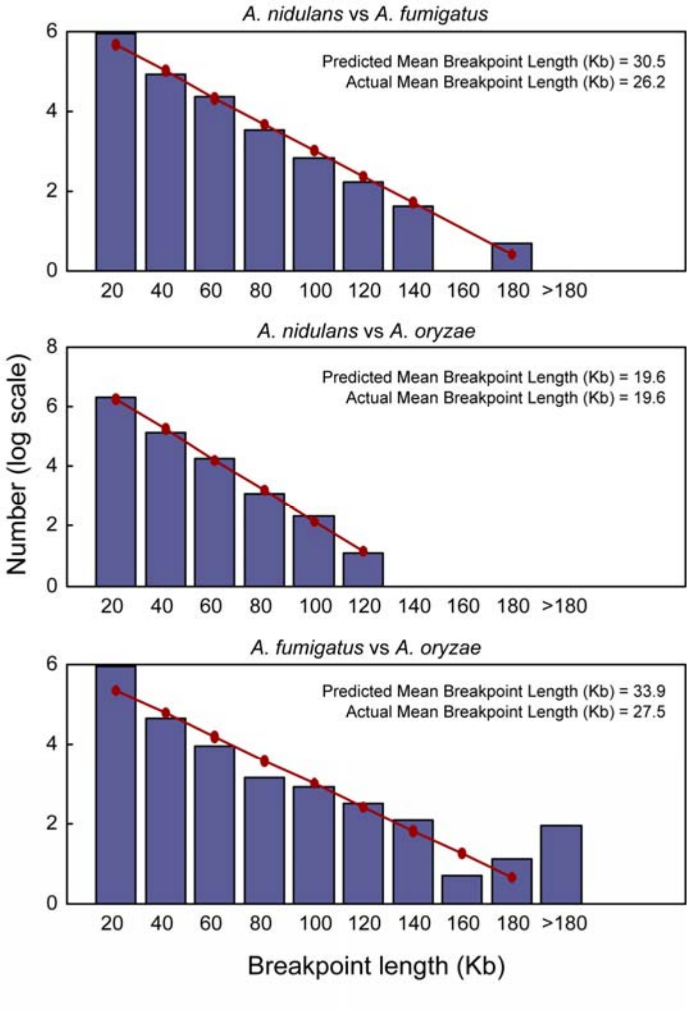

Figure S2.2 Random Distribution of Breakpoints in Conserved Syntenic Blocks. Histogram of length distributions between microrearrangement breakpoints within conserved pairwise syntenic blocks. Red line indicates fit to random breakage model which predicts an exponential distribution of breakpoint lengths of the form $f(x)=e^{-x/L}$ where L is the predicted mean breakpoint length.

§S2.4. No Deceleration of Rearrangement in A. fumigatus

The data in Figure 4 reveal a greater rate of rearrangement in *A. oryzae* relative to *A. fumigatus*. In principle, this could be due to a deceleration in breakage in *A. fumigatus*, possibly consistent with parasitic lifestyle. However, if this were the case, and the rate remained constant in *A. oryzae* and *A. nidulans*, syntenic blocks between *A. fumigatus* and *A. oryzae* would be larger than those between *A. fumigatus* and *A. nidulans*. Instead the opposite is observed Table 2. We note also that a greater rate of rearrangement is consistent with the smaller average syntenic block sizes for *A. oryzae* (Table 2).

§S2.5. Similar Rates of Protein Evolution in A. fumigatus and A. oryzae

We compared the rates of molecular evolution in *A. oryzae* and *A. fumigatus* with *A. nidulans* as an outgroup using a number of different but related methods. First, an examination of threeway orthologs revealed the distribution of amino acid identity to be nearly identical for both *A. oryzae* and *A. fumigatus*, relative to *A. nidulans*. Equivalently, a scatter plot of non-synonymous divergences of *A. fumigatus* and *A. oryzae* threeway orthologs relative to A. nidulans reveales a strong correlation between *A. fumigatus* and *A. oryzae* divergences with an overall slope of nearly 1. Finally, branch lengths predicted from both single gene and concatenated gene phylogenies indicate a comparable rate of substitution in both the *A. oryzae* and *A. fumigatus* lineages.

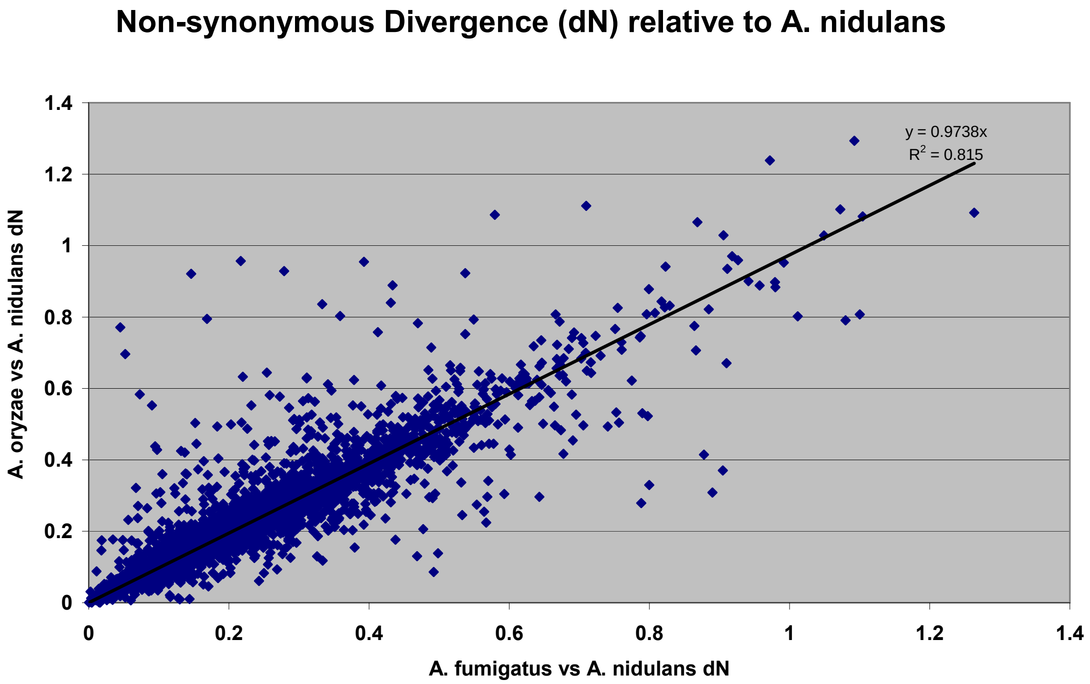

Figure S2.3. Correlation between non-synonymous divergence rates (substitutions/site) of three way orthologs in *A. fumigatus* and *A. oryzae* relative to *A. nidulans*.

§S3 Upstream open reading frames (uORFs)

Method:

To search for uORFs conserved between the three Aspergillus species, we started with the set of 4936 ortholog triplets and 1000bp upstream regions multiply aligned using MLAGAN. For the 25% of A. nidulans genes with EST alignments indicating 5’ UTRs, the entire length of the EST alignment was searched for uORFs. Otherwise the search was conservatively constrained to the upstream 60bp region, since 60% of all 5’ partial ESTs extend beyond 60bp (considering only the final UTR exon that overlaps the gene start). Additionally, to avoid annotation errors if there were no ESTs, we limited the search to those unambiguous intergenic regions upstream of the 2372 orthologs with all three annotated start codons aligned within 40bp. For each species, we identified all upstream open reading frames >= 12bp, with a maximum 1bp overlap with the protein-coding gene’s ATG. *Conserved uORFs* were

We also include here, under the "extended_data_300bp" tab, those uORFs not within 60bp or in UTRs, but within 300bp of aligned upstream sequence. These may not be within the mRNA transcript.

For each data set, we also search for uORFs in the An gene's ortholog in other fully-sequenced fungi: Neurospora crassa (Nc), Fusarium graminearum (Fg), Magnaporthe grisea (Mg), Saccharomyces cerevisiae (Sc), Saccharomyces bayanus (Sb), Saccharomyces mikatae (Sm), and Saccharomyces paradoxus (Sp). Orthologs are defined as best bidirectional hit within an all-vs-all blastp analysis (expect < 1e-5, coverage > 60% of each gene). For the filamentous fungi Nc, Fg, and Mg, we search for uORFs only within known UTRs (defined by unique EST blat alignments) or within 60bp since these genomes often have 5' UTR introns. For Sc, since introns are rare and ESTs are not available, we search within 100bp upstream of the gene start. For Sc orthologs, we also check whether a uORF co-occurs upstream of the 4 closely related yeast species (Sc,Sb,Sm,Sp) based on the 4-way

The 38 uORFs mentioned in the text that are conserved in all three Aspergilli are provided in the tab "Aspergillus

Abbreviations:

an: *Aspergillus nidulans*
af: *Aspergillus fumigatus*
ao: *Aspergillus oryzae*

Data fields: (use tab "data" below)

uORF_id: unique identifier for each uORF

ortholog_cluster_id: unique identifier for each 3-way ortholog

species: species that contains the uORF; "conserved" indicates uORF is found in all 3 species with the start and stop codons aligned

an_gene,af_gene,ao_gene: locus identifier for each of the 3-way orthologs

in_utr: 1 if the location of the uORF overlaps a 5' An UTR (as defined by an EST alignment)

an_rel_start, af_rel_start, ao_rel_start: coordinate of the uORF's ATG relative to the protein-coding gene's start codon

an_rel_stop, af_rel_stop, ao_rel_stop: coordinate of the stop codon relative to the protein-coding gene's start codon (1 indicates that the "A" of the stop codon's TGA/TAA overlaps with the gene's ATG) consensus_dna: uORF consensus DNA sequence, using the degenerate DNA code if the uORF is conserved

an_dna,af_dna,ao_dna: DNA sequence of the uORF in each species

consensus_aa: uORF amino acid sequence from An, with capital letters representing 3-way conserved amino acids (if not conserved, use the species specific amino acid sequence)

an_aa, af_aa, ao_aa : uORF amino acid sequence in each species

context_up_consensus: 10bp upstream of uORF start codon, in degenerate code if the uORF is conserved

context_down_consensus: 10bp down of uORF stop codon, in degenerate code if the uORF is conserved

within_60bp : 1 if the uORF is within 60bp of the protein-coding gene's start codon

COG category: functional category designation of the An gene

fg_uorf_utr: name of Fusarium ortholog with a uORF contained within the 5' UTR (defined by EST alignment)

mg_uorf_utr: name of Magnaporthe ortholog with a uORF contained within the 5' UTR (defined by EST alignment)

nc_uorf_utr: name of Neurospora ortholog with a uORF contained within the 5' UTR (defined by EST alignment)

sc_uorf_utr: name of S.cerevisiae ortholog with a uORF contained within the upstream 100bp

sc_cooccur_orf_100bp: name of S.cerevisiae ortholog with a uORF contained within the upstream 100bp, where uORF is also found upstream of orthologs in Sb, Sm, and Sp

Genes with conserved upstream ORFs

***A. nidulans* Locus**	**Predicted function**	**uORF pos[†]**	**Length (aa)**
AN8076.1	Splicing coactivator SRm160/300 subunit SRm300	-11	3
AN0244.1	**Vacuolar assembly/sorting protein VPS8**	**-23**	**7**
AN2905.1	DNA-binding proteins Bright/BRCAA1/RBP1	-23	3
AN3144.1	FYVE finger-containing protein	-23	3
AN4486.1	hypothetical protein	-26	8
AN1179.1	**Vacuolar import and degradation protein**	**-27***	**5**
AN4864.1	Glucosyltransferase - Alg6p	-30	4
AN1341.1	Membrane coat complex Retromer subunit VPS29	-31*	3
AN5627.1	Nuclear pore complex, Nup98 component	-33	3
AN0877.1	hypothetical protein	-34	6
AN0118.1	Dyneins, heavy chain	-36	8
AN5885.1	Glycogen synthase	-36	4
AN1168.1	Voltage-gated Ca2+ channels, alpha1 subunits	-37[§]	5
AN4597.1	Structural maintenance of chromosome protein 4	-38	12
AN5151.1	Predicted membrane protein	-48*	3
AN4460.1	18S rRNA processing complex subunit	-52	3
AN9125.1	RNA polymerase III, subunit C34	-52*	8
AN1854.1	hypothetical protein	-57	17
AN1494.1	TATA binding protein associated factor	-60	15
AN1014.1	Peroxisomal long-chain acyl-CoA transporter	-67*[§]	8
AN6642.1	Ca2+ transporting ATPase	-68*	4
AN5528.1	Mitochondrial Fe/S cluster exporter	-69*	3
AN8846.1	Protein involved in beta-1,3-glucan synthesis	-87*	7
AN8723.1	predicted protein	-93*	17
AN5966.1	FOG: Zn-finger	-100*	5
AN6642.1	Ca2+ transporting ATPase	-101*	15
AN5452.1	Splicing factor 3b, subunit 3	-105*	6
AN2902.1	TFIIF-interacting CTD phosphatases	-143*	3
AN4670.1	FOG: WD40 repeat	-171*	3
AN1779.1	Protein kinase (DNA replication initiation)	-177*	4
AN1546.1	Histone deacetylase complex, SIN3 component	-185*	3
AN8009.1	ABC-type nitrate/sulfonate/bicarbonate transport	-191*	21
AN1521.1	DNA-directed RNA polymerase subunit E'	-207*	3
AN0412.1	FOG: Immunoglobin and related proteins	-228*	5
AN4984.1	Cyclin	-236*	4
AN1082.1	Nucleoside phosphatase	-243*	8
AN1349.1	mRNA-binding protein Encore	-254*	17
AN6843.1	Mitochondrial/chloroplast ribosomal protein L4	-278*[§]	13
AN1349.1	mRNA-binding protein Encore	-418*	5

[†] uORF start position relative to gene start codon. * uORF overlaps 5' EST alignment. Bold rows indicate experimentally tested loci. [§] Predicted orthologs in S. cerevisiae contain uORFs conserved in 4 related yeast species[18]. Also note that AN1349.1 has two uORFs.

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
5	4	conserved	AN0877.1	70.m15480	AO070320000036	0	-34	-14	-34	-14	-34	-14	ATGTGTkGTGAyCACGGmTGA	ATGTGTTGTGATCACGGATGA	ATGTGTTGTGACCACGGCTGA	ATGTGTGGTGACCACGGATGA	MCcDHG*	MCCDHG*	MCCDHG*	MCGDHG*	yrrrTGysmv	hhAyTyGCTC	1		0	0	0	0	0
7	4	an	AN0877.1	70.m15480	AO070320000036	0	-41	-24					ATGCCCGATGTGTTGTGA	ATGCCCGATGTGTTGTGA			MPDVL*	MPDVL*			CAACGCTCAA	TCACGGATGA	1		0	0	0	0	0
22	19	af	AN6250.1	72.m19408	AO070304000038	1			-568	-557			ATGGATACCTAA		ATGGATACCTAA		MDT*		MDT*		GGTCTTGAGG	GGCTGCTTCA	0	O	0	MG06681.1	0	0	0
23	19	af	AN6250.1	72.m19408	AO070304000038	1			-501	-451			ATGGAGAGTAGTGAGCAATCTATTATTTTTCTCTACTCCGTAATCTACTAG		ATGGAGAGTAGTGAGCAATCTATTATTTTTCTCTACTCCGTAATCTACTAG		MESSEQSIIFLYSVIY*		MESSEQSIIFLYSVIY*		GGCTGGCCGT	ACATCAACGA	0	O	0	MG06681.1	0	0	0
24	19	af	AN6250.1	72.m19408	AO070304000038	1			-398	-219			ATGGTCAACCGTCATCGTCGTAACCAAGTACAGCGCGACCAGCTCATCGTTGTTAGTCCCTCCTCGTGGCTCTCTTTTTGCCGCCTCCGACCTCCAATACTCATTATTTCTTCCCTTCCCGCCTTGAGCGCTGGCAATAATATAACTGATCCGCGACTTCCACCGCCATCTTTTCTCTGA		ATGGTCAACCGTCATCGTCGTAACCAAGTACAGCGCGACCAGCTCATCGTTGTTAGTCCCTCCTCGTGGCTCTCTTTTTGCCGCCTCCGACCTCCAATACTCATTATTTCTTCCCTTCCCGCCTTGAGCGCTGGCAATAATATAACTGATCCGCGACTTCCACCGCCATCTTTTCTCTGA		MVNRHRRNQVQRDQLIVVSPSSWLSFCRLRPPILIISSLPALSAGNNITDPRLPPPSFL*		MVNRHRRNQVQRDQLIVVSPSSWLSFCRLRPPILIISSLPALSAGNNITDPRLPPPSFL*		TCTCCATCCT	ACGATCCGAT	0	O	0	MG06681.1	0	0	0
46	46	an	AN2446.1	69.m15213	AO070264000031	0	-41	-18					ATGCCGTCTGAATCACGTCCATAG	ATGCCGTCTGAATCACGTCCATAG			MPSESRP*	MPSESRP*			AAACGATTAT	ATTCAGATCT	1		0	0	0	0	0
66	51	ao	AN1507.1	55.m03019	AO070334000226	0					-47	-30	ATGACTTGGATCGTGTGA			ATGACTTGGATCGTGTGA	MTWIV*			MTWIV*	GTATTCACGC	GTAGGTTTGT	1		0	0	0	0	0
75	61	an	AN8809.1	71.m15615	AO070276000049	0	-40	-20					ATGAAGGCAAAGGGCCTTTGA	ATGAAGGCAAAGGGCCTTTGA			MKAKGL*	MKAKGL*			TATTTCCCGC	TCGTCATCGG	1	R	0	0	0	0	0
77	61	af	AN8809.1	71.m15615	AO070276000049	0			-43	-32			ATGAAGTTATAA		ATGAAGTTATAA		MKL*		MKL*		TGAACACCCT	TACCATCAAC	1	R	0	0	0	0	0
82	61	ao	AN8809.1	71.m15615	AO070276000049	0					-42	-22	ATGAGGCCGACATTTCCGTGA			ATGAGGCCGACATTTCCGTGA	MRPTFP*			MRPTFP*	TCGTGACTGC	AACACAGGCG	1	R	0	0	0	0	0
116	85	conserved	AN1521.1	55.m03040	AO070334000239	1	-207	-196	-283	-272	-282	-271	ATGArybryTrA	ATGAATCATTAA	ATGAGCGACTGA	ATGAGCTGCTGA	Mnh*	MNH*	MSD*	MSC*	kmbwsykryC	khTyhbddyh	0	K	0	0	0	0	0
117	85	af	AN1521.1	55.m03040	AO070334000239	1			-363	-337			ATGTCTCGGTTCTATACCCTCCATTAG		ATGTCTCGGTTCTATACCCTCCATTAG		MSRFYTLH*		MSRFYTLH*		TCTGTTCTTG	CGTTTTTCAA	0	K	0	0	0	0	0
119	92	af	AN8843.1	71.m15975	AO070271000034	0			-55	-44			ATGCCTTTCTAA		ATGCCTTTCTAA		MPF*		MPF*		ACTTTCTTTC	TCAGACCGTT	1	E	FG10211.1	0	0	YHR025W	YHR025W
140	109	af	AN2928.1	59.m09067	AO070337000181	1			-342	-316			ATGCTAGACAAAGGGTGGCGCTGGTAG		ATGCTAGACAAAGGGTGGCGCTGGTAG		MLDKGWRW*		MLDKGWRW*		TTTGGCACCA	TGGTCCGCCA	0	WV	0	0	0	0	0
141	109	af	AN2928.1	59.m09067	AO070337000181	1			-298	-275			ATGAGACTGGGGAGTGCTTTCTAG		ATGAGACTGGGGAGTGCTTTCTAG		MRLGSAF*		MRLGSAF*		CCAATCGTGT	TCTCTCCATC	0	WV	0	0	0	0	0
142	109	af	AN2928.1	59.m09067	AO070337000181	1			-264	-232			ATGGCCGGCCATACTTGCATCCCCCAGGGGTAG		ATGGCCGGCCATACTTGCATCCCCCAGGGGTAG		MAGHTCIPQG*		MAGHTCIPQG*		TCTCTCCATC	TATATATACC	0	WV	0	0	0	0	0
143	109	af	AN2928.1	59.m09067	AO070337000181	1			-215	-195			ATGATCTACCTTTCCGATTGA		ATGATCTACCTTTCCGATTGA		MIYLSD*		MIYLSD*		TACCTGGATA	TCATCAACTC	0	WV	0	0	0	0	0
148	115	an	AN8288.1	65.m07464	AO070190000002	1	-368	-348					ATGGGACTCAGAATACGTTAA	ATGGGACTCAGAATACGTTAA			MGLRIR*	MGLRIR*			TGACACACGC	TGGACTGCTT	0	U	0	0	0	0	0
149	115	an	AN8288.1	65.m07464	AO070190000002	1	-348	-316					ATGGACTGCTTATTGATACGTACTCTAGCCTAA	ATGGACTGCTTATTGATACGTACTCTAGCCTAA			MDCLLIRTLA*	MDCLLIRTLA*			GAATACGTTA	TCACTACGGA	0	U	0	0	0	0	0
150	115	an	AN8288.1	65.m07464	AO070190000002	1	-262	-218					ATGTCAAGCCGCGCTTCTGAAGGGCTGAGCAGTCGCCAGTGTTAG	ATGTCAAGCCGCGCTTCTGAAGGGCTGAGCAGTCGCCAGTGTTAG			MSSRASEGLSSRQC*	MSSRASEGLSSRQC*			CCCGTTATCG	CCAATTCAAC	0	U	0	0	0	0	0
151	115	an	AN8288.1	65.m07464	AO070190000002	1	-35	-3					ATGCTCAAAGTCATCATTCAGGATCTCAATTGA	ATGCTCAAAGTCATCATTCAGGATCTCAATTGA			MLKVIIQDLN*	MLKVIIQDLN*			GCTGCCCGCC	TAATGCCTAG	1	U	0	0	0	0	0
152	115	af	AN8288.1	65.m07464	AO070190000002	1			-299	-285			ATGAGGTCTCCTTAG		ATGAGGTCTCCTTAG		MRSP*		MRSP*		GCCCCAAAGT	GGCCTTGGCG	0	U	0	0	0	0	0
153	115	af	AN8288.1	65.m07464	AO070190000002	1			-249	-160			ATGACCTTCCATATTCATCACGAATATAACACTCAACTTACTGAGACTAATATATTATTTCCAGATACTAATATTGACTCTTTTACCTAG		ATGACCTTCCATATTCATCACGAATATAACACTCAACTTACTGAGACTAATATATTATTTCCAGATACTAATATTGACTCTTTTACCTAG		MTFHIHHEYNTQLTETNILFPDTNIDSFT*		MTFHIHHEYNTQLTETNILFPDTNIDSFT*		CCAAATCTTA	ACTAATAGTC	0	U	0	0	0	0	0
154	115	af	AN8288.1	65.m07464	AO070190000002	1			-139	-128			ATGTGCTGTTAA		ATGTGCTGTTAA		MCC*		MCC*		AAGCATTATA	TCATTTAAGT	0	U	0	0	0	0	0
155	115	ao	AN8288.1	65.m07464	AO070190000002	1					-38	-9	ATGAAAATGGTCATTAGATACGTTGGATAG			ATGAAAATGGTCATTAGATACGTTGGATAG	MKMVIRYVG*			MKMVIRYVG*	TTAAGCCTGT	CCTATAACAT	1	U	0	0	0	0	0
156	115	ao	AN8288.1	65.m07464	AO070190000002	1					-32	-9	ATGGTCATTAGATACGTTGGATAG			ATGGTCATTAGATACGTTGGATAG	MVIRYVG*			MVIRYVG*	CTGTATGAAA	CCTATAACAT	1	U	0	0	0	0	0
160	120	af	AN0668.1	70.m15271	AO070343000552	0			-57	-31			ATGCTACCTTACTGGACACGGGCTTGA		ATGCTACCTTACTGGACACGGGCTTGA		MLPYWTRA*		MLPYWTRA*		GCTTGTTTCT	TCCGTCCCGA	1	R	0	0	0	0	0
173	138	conserved	AN5627.1	58.m08920	AO070301000027	0	-33	-22	-37	-26	-34	-23	ATGAAbCywTAA	ATGAAGCTATAA	ATGAATCCTTAA	ATGAACCTATAA	Mkl*	MKL*	MNP*	MNL*	bwhhsAACvd	kmhyCrmwkw	1	YU	0	0	0	0	0
176	140	an	AN8891.1	56.m02304	AO070293000026	0	-20	-6					ATGCGCCAACGCTGA	ATGCGCCAACGCTGA			MRQR*	MRQR*			CTCGACGCGA	TCACCATGAG	1	M	0	0	0	0	0
184	141	ao	AN4461.1	58.m07863	AO070305000132	0					-54	-31	ATGGGTCTACGTCATTTTACTTAA			ATGGGTCTACGTCATTTTACTTAA	MGLRHFT*			MGLRHFT*	CCTATCTGGC	CTGTCGCGAT	1	K	0	0	0	0	0
200	150	ao	AN0287.1	54.m06482	AO070334000066	0					-56	-33	ATGATCCAAACCCAAGCAGATTGA			ATGATCCAAACCCAAGCAGATTGA	MIQTQAD*			MIQTQAD*	GTTGCGCGCA	ACACCGTCTG	1	R	0	0	0	0	0
217	166	ao	AN2105.1	57.m05806	AO070341000263	1					-220	-197	ATGCGATTAATGCCCGCACTATGA			ATGCGATTAATGCCCGCACTATGA	MRLMPAL*			MRLMPAL*	TGACTAAGCT	GTAACGTGAG	0	A	FG00358.1	MG04741.1	NCU00505.1	YGR074W	0
218	166	ao	AN2105.1	57.m05806	AO070341000263	1					-211	-197	ATGCCCGCACTATGA			ATGCCCGCACTATGA	MPAL*			MPAL*	TATGCGATTA	GTAACGTGAG	0	A	FG00358.1	MG04741.1	NCU00505.1	YGR074W	0
219	166	ao	AN2105.1	57.m05806	AO070341000263	1					-200	-174	ATGAGTAACGTGAGGATGGGTGACTAA			ATGAGTAACGTGAGGATGGGTGACTAA	MSNVRMGD*			MSNVRMGD*	TGCCCGCACT	GCAGAACCAC	0	A	FG00358.1	MG04741.1	NCU00505.1	YGR074W	0
220	166	ao	AN2105.1	57.m05806	AO070341000263	1					-185	-174	ATGGGTGACTAA			ATGGGTGACTAA	MGD*			MGD*	TAACGTGAGG	GCAGAACCAC	0	A	FG00358.1	MG04741.1	NCU00505.1	YGR074W	0
238	182	an	AN4899.1	59.m08798	AO070338000053	1	-128	-81					ATGCAGCAGAAGTTATCCAAAAGCTTGCATTCTTCTTTCTCTCTTTAG	ATGCAGCAGAAGTTATCCAAAAGCTTGCATTCTTCTTTCTCTCTTTAG			MQQKLSKSLHSSFSL*	MQQKLSKSLHSSFSL*			CAACCAACAA	TCTATTATTA	0	U	0	0	0	0	0
240	182	af	AN4899.1	59.m08798	AO070338000053	1			-99	-13			ATGCGTGCGTCTGCCAAACTCCCCTTTCACCACAGCGCTGGTCTCTCCTTTCCAGTCATTTCCTCAGAATTGTTCAGGAGTATATGA		ATGCGTGCGTCTGCCAAACTCCCCTTTCACCACAGCGCTGGTCTCTCCTTTCCAGTCATTTCCTCAGAATTGTTCAGGAGTATATGA		MRASAKLPFHHSAGLSFPVISSELFRSI*		MRASAKLPFHHSAGLSFPVISSELFRSI*		TCTTCTTCAC	CTTTCAGACA	0	U	0	0	0	0	0
270	212	af	AN1798.1	72.m19550	AO070309000133	1			-117	-49			ATGACCTCTTCTGTGGTCACTTGTTCACTTCAGCTTTCCTTCTTCCATCTTTGGCCCTGGCCAAAATGA		ATGACCTCTTCTGTGGTCACTTGTTCACTTCAGCTTTCCTTCTTCCATCTTTGGCCCTGGCCAAAATGA		MTSSVVTCSLQLSFFHLWPWPK*		MTSSVVTCSLQLSFFHLWPWPK*		AACGCTCACC	GGCCTTTTGC	0	I	0	0	0	0	0
271	212	af	AN1798.1	72.m19550	AO070309000133	1			-52	-5			ATGAGGCCTTTTGCAGTCTTTACTACATTCACATTCACAAGCCCCTGA		ATGAGGCCTTTTGCAGTCTTTACTACATTCACATTCACAAGCCCCTGA		MRPFAVFTTFTFTSP*		MRPFAVFTTFTFTSP*		CCTGGCCAAA	CACCATGTTG	1	I	0	0	0	0	0
273	214	af	AN6864.1	71.m15275	AO070314000084	0			-46	-17			ATGCCCCTCTCCCTTTCGCGGTCGCGTTAA		ATGCCCCTCTCCCTTTCGCGGTCGCGTTAA		MPLSLSRSR*		MPLSLSRSR*		AAAGTCGCCA	ATTAGTTGAG	1	J	0	0	0	0	0
276	214	ao	AN6864.1	71.m15275	AO070314000084	0					-49	-17	ATGCCCCTCCGCTCCGTCGTCATCGTCATTTAG			ATGCCCCTCCGCTCCGTCGTCATCGTCATTTAG	MPLRSVVIVI*			MPLRSVVIVI*	AAAGTCGCCA	TCCGCTTCTT	1	J	0	0	0	0	0
277	221	af	AN6588.1	62.m03177	AO070326000036	1			-197	-30			ATGATGATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGATGATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MMMMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MMMMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		AGTGTAAGTG	GGTACACCTG	0		0	MG04986.1	0	0	0
278	221	af	AN6588.1	62.m03177	AO070326000036	1			-194	-30			ATGATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MMMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MMMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		GTAAGTGATG	GGTACACCTG	0		0	MG04986.1	0	0	0
279	221	af	AN6588.1	62.m03177	AO070326000036	1			-191	-30			ATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MMMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		AGTGATGATG	GGTACACCTG	0		0	MG04986.1	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
280	221	af	AN6588.1	62.m03177	AO070326000036	1			-188	-30			ATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MMMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		GATGATGATG	GGTACACCTG	0		0	MG04986.1	0	0	0
281	221	af	AN6588.1	62.m03177	AO070326000036	1			-185	-30			ATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MMGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		GATGATGATG	GGTACACCTG	0		0	MG04986.1	0	0	0
282	221	af	AN6588.1	62.m03177	AO070326000036	1			-182	-30			ATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		ATGGGAAGACTGCCTGACGTCCTTGGACTGGTCATTGACGGGAAGGGAAATGTGACAGCACGACCGCCTTTTTTTGGATTCAATACACTCGTTCATCGAATACTCGAGCTCGTTAAAGAGCCAGCAAGAATCGGTGGCGAGACGCGTCGCTAG		MGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		MGRLPDVLGLVIDGKGNVTARPPFFGFNTLVHRILELVKEPARIGGETRR*		GATGATGATG	GGTACACCTG	0		0	MG04986.1	0	0	0
283	225	an	AN2288.1	71.m15935	AO070295000067	1	-91	-41					ATGTGCGCATCGTATTGGCGTCAGAAAATCGCCGCTGGAGTAAACCGCTAG	ATGTGCGCATCGTATTGGCGTCAGAAAATCGCCGCTGGAGTAAACCGCTAG			MCASYWRQKIAAGVNR*	MCASYWRQKIAAGVNR*			GTGGACTATT	GGAGCGTCAA	0	P	0	0	0	0	0
285	225	ao	AN2288.1	71.m15935	AO070295000067	1					-240	-154	ATGTGCGCCTTGGTCTGGCGCCAGAGACTCGCAGCTGGAGCTAACCGCTTGGTGTCATCCGCTGTCGTGGTTGCGTGGCCTTCGTAA			ATGTGCGCCTTGGTCTGGCGCCAGAGACTCGCAGCTGGAGCTAACCGCTTGGTGTCATCCGCTGTCGTGGTTGCGTGGCCTTCGTAA	MCALVWRQRLAAGANRLVSSAVVVAWPS*			MCALVWRQRLAAGANRLVSSAVVVAWPS*	CCAGTGGATT	GCATGGCTAG	0	P	0	0	0	0	0
308	241	an	AN5631.1	58.m08951	AO070301000030	0	-32	-12					ATGAATCGTTTCTTCCGGTAA	ATGAATCGTTTCTTCCGGTAA			MNRFFR*	MNRFFR*			CTTTTTTTAC	TTTAATCCAA	1	D	0	0	0	0	0
309	241	af	AN5631.1	58.m08951	AO070301000030	0			-27	-4			ATGACGATTTTCTCTCTGATCTAG		ATGACGATTTTCTCTCTGATCTAG		MTIFSLI*		MTIFSLI*		CTTGTTTTCC	TTCATGATGT	1	D	0	0	0	0	0
310	249	af	AN2741.1	54.m06957	AO070338000230	1			-176	-144			ATGCGCGATTTCAGAAATCCGCCGACTCGCTGA		ATGCGCGATTTCAGAAATCCGCCGACTCGCTGA		MRDFRNPPTR*		MRDFRNPPTR*		CAACGTAACC	CATCATCAAC	0	O	0	0	0	0	0
311	249	af	AN2741.1	54.m06957	AO070338000230	1			-127	-80			ATGCAACTAAATACCACCTTTGCATCTCACCAGCTCTCCAGTCAATAA		ATGCAACTAAATACCACCTTTGCATCTCACCAGCTCTCCAGTCAATAA		MQLNTTFASHQLSSQ*		MQLNTTFASHQLSSQ*		CAACCACCTC	TCAAATCACC	0	O	0	0	0	0	0
312	249	ao	AN2741.1	54.m06957	AO070338000230	1					-237	-193	ATGGACGAAATCCACACGAAGAAGAGCCTCAAGCTCTTCTTTTAG			ATGGACGAAATCCACACGAAGAAGAGCCTCAAGCTCTTCTTTTAG	MDEIHTKKSLKLFF*			MDEIHTKKSLKLFF*	AGAGCCCGCC	TTGTCCTCGC	0	O	0	0	0	0	0
318	254	af	AN0331.1	54.m06427	AO070318000004	0			-54	-31			ATGACACCAGCCTCGTTATACTAG		ATGACACCAGCCTCGTTATACTAG		MTPASLY*		MTPASLY*		TGCTCGTGAA	ATCGAATCTC	1		0	0	0	0	0
336	270	af	AN6412.1	56.m02547	AO070339000013	1			-52	-41			ATGCAGGTCTAA		ATGCAGGTCTAA		MQV*		MQV*		TTTCAGGACG	TTTCTCCATT	1	U	0	0	0	0	0
352	284	ao	AN3081.1	59.m08917	AO070224000005	1					-247	-230	ATGTCGGTACTGTTTTAA			ATGTCGGTACTGTTTTAA	MSVLF*			MSVLF*	ATATCAGACT	GATCAGCGGG	0	E	0	0	0	0	0
353	284	ao	AN3081.1	59.m08917	AO070224000005	1					-179	-117	ATGCATTCACGTCTTCGTCCATTGACACGCGTTATATTAAACTTGAGCATAAAGTGCTGTTAA			ATGCATTCACGTCTTCGTCCATTGACACGCGTTATATTAAACTTGAGCATAAAGTGCTGTTAA	MHSRLRPLTRVILNLSIKCC*			MHSRLRPLTRVILNLSIKCC*	CACAGCTGTA	CTCTCAGCGA	0	E	0	0	0	0	0
370	299	af	AN4305.1	58.m08019	AO070330000015	0			-60	-46			ATGATAACCAACTAA		ATGATAACCAACTAA		MITN*		MITN*		ATCGTCGCAT	TAGTTCCTGT	1	PD	0	0	0	0	0
375	301	an	AN1114.1	70.m15121	AO070285000024	1	-286	-245					ATGGCTGCTGCGCTGTTTTCTCTCGAGTGCGCCACCAGTTGA	ATGGCTGCTGCGCTGTTTTCTCTCGAGTGCGCCACCAGTTGA			MAAALFSLECATS*	MAAALFSLECATS*			AAAGGGTACC	GCACGGTGCC	0	K	0	0	0	0	0
376	301	an	AN1114.1	70.m15121	AO070285000024	1	-219	-118					ATGCCTGCTCGGGTACAAGGAAGAATATCCTCCCCGGTCTCATTAATATCCCGTTCTTTGCATCTCAAGGCAAGAAAATTGTACAACACCCGTGACAAGTGA	ATGCCTGCTCGGGTACAAGGAAGAATATCCTCCCCGGTCTCATTAATATCCCGTTCTTTGCATCTCAAGGCAAGAAAATTGTACAACACCCGTGACAAGTGA			MPARVQGRISSPVSLISRSLHLKARKLYNTRDK*	MPARVQGRISSPVSLISRSLHLKARKLYNTRDK*			TATACATTGG	ACCTGCCCGT	0	K	0	0	0	0	0
377	301	af	AN1114.1	70.m15121	AO070285000024	1			-432	-328			ATGTCTTCCGGCTGGTCGAATCATCTTCTCAGGAAGAGGCAGCACGCCTCTTCCTTCCGCTATCAGCACGGTATTCGCATCTACACCGTGTTTCCGGCTTGGTGA		ATGTCTTCCGGCTGGTCGAATCATCTTCTCAGGAAGAGGCAGCACGCCTCTTCCTTCCGCTATCAGCACGGTATTCGCATCTACACCGTGTTTCCGGCTTGGTGA		MSSGWSNHLLRKRQHASSFRYQHGIRIYTVFPAW*		MSSGWSNHLLRKRQHASSFRYQHGIRIYTVFPAW*		CTCTCTGCAC	ACAATGTCCC	0	K	0	0	0	0	0
378	301	af	AN1114.1	70.m15121	AO070285000024	1			-324	-310			ATGTCCCAGATTTGA		ATGTCCCAGATTTGA		MSQI*		MSQI*		TTGGTGAACA	AGTGTCTTAG	0	K	0	0	0	0	0
379	301	af	AN1114.1	70.m15121	AO070285000024	1			-265	-134			ATGAGTACAGAATACGCAATTGACCCGTTCTTAAGAGGCCTGAGGCTGCTGTCTCTTTTTCTTCGGGTTCCGTCTTTCTCTTACTCCCTTGTTGCCCGTCTCACACGTGTCTCTTCTACGGTCAATTTGTAA		ATGAGTACAGAATACGCAATTGACCCGTTCTTAAGAGGCCTGAGGCTGCTGTCTCTTTTTCTTCGGGTTCCGTCTTTCTCTTACTCCCTTGTTGCCCGTCTCACACGTGTCTCTTCTACGGTCAATTTGTAA		MSTEYAIDPFLRGLRLLSLFLRVPSFSYSLVARLTRVSSTVNL*		MSTEYAIDPFLRGLRLLSLFLRVPSFSYSLVARLTRVSSTVNL*		TTTCTCCTAT	AACGACAATT	0	K	0	0	0	0	0
380	301	ao	AN1114.1	70.m15121	AO070285000024	1					-360	-307	ATGCCGGTGCCTCTTGGATCCGTTTATCCAATTTATTCCTGTTCTATTGGGTAA			ATGCCGGTGCCTCTTGGATCCGTTTATCCAATTTATTCCTGTTCTATTGGGTAA	MPVPLGSVYPIYSCSIG*			MPVPLGSVYPIYSCSIG*	GCTCTCCACC	TCTCTCCCCA	0	K	0	0	0	0	0
381	301	ao	AN1114.1	70.m15121	AO070285000024	1					-297	-280	ATGTATCCGTACCTTTAA			ATGTATCCGTACCTTTAA	MYPYL*			MYPYL*	ATCTCTCCCC	GGGAGTTAAA	0	K	0	0	0	0	0
409	329	af	AN7950.1	52.m03642	AO070342000340	1			-127	-98			ATGTTCAATTCAGTCGTTCTCTCCCTCTAG		ATGTTCAATTCAGTCGTTCTCTCCCTCTAG		MFNSVVLSL*		MFNSVVLSL*		CTGACATCCG	GTTCATTCTT	0	G	0	0	0	0	0
413	332	an	AN5724.1	54.m06844	AO070324000127	0	-46	-26					ATGCAGTTGCCCTTAATTTGA	ATGCAGTTGCCCTTAATTTGA			MQLPLI*	MQLPLI*			TTCGTTCTGC	AAGAAGAGAC	1	OU	0	0	0	0	0
423	340	an	AN6680.1	65.m07300	AO070289000022	1	-73	-14					ATGACCAACACGCTCAACGTCGCATCGGCCGCATCAGTTACGTTTCAAGAATTGCAATAG	ATGACCAACACGCTCAACGTCGCATCGGCCGCATCAGTTACGTTTCAAGAATTGCAATAG			MTNTLNVASAASVTFQELQ*	MTNTLNVASAASVTFQELQ*			CACCCGAGAT	TGACACTTGC	0		0	0	0	0	0
424	340	af	AN6680.1	65.m07300	AO070289000022	1			-115	-104			ATGGCCGTTTAG		ATGGCCGTTTAG		MAV*		MAV*		GGTAGAGTTC	GTGCCCCGCC	0		0	0	0	0	0
425	341	af	AN5866.1	72.m19268	AO070308000130	1			-267	-124			ATGTTCTCTCATATCACCCGCATTGAGCTGCTCCACAAGTCCACTCACTCACTTTTTCTAGGCTTTCCCGCCGAACCGGAAACCCCTCTAATTTTCAGCCCTTCCCCGTCATCTCCGCCATCGCTGTTACTACGGTCTACCTAG		ATGTTCTCTCATATCACCCGCATTGAGCTGCTCCACAAGTCCACTCACTCACTTTTTCTAGGCTTTCCCGCCGAACCGGAAACCCCTCTAATTTTCAGCCCTTCCCCGTCATCTCCGCCATCGCTGTTACTACGGTCTACCTAG		MFSHITRIELLHKSTHSLFLGFPAEPETPLIFSPSPSSPPSLLLRST*		MFSHITRIELLHKSTHSLFLGFPAEPETPLIFSPSPSSPPSLLLRST*		CATTCCACTA	GTACCCGTGC	0	R	0	0	0	0	0
427	343	an	AN6277.1	72.m19363	AO070304000003	0	-37	-11					ATGCTAACGTGGGCCCGACAGTGGTGA	ATGCTAACGTGGGCCCGACAGTGGTGA			MLTWARQW*	MLTWARQW*			TATAAGGGCA	TTCAACCAAG	1	R	0	MG04158.1	NCU06519.1	0	0
455	364	af	AN7677.1	57.m05454	AO070325000067	1			-423	-385			ATGTTTCAACTCTCTATCTCGACGCAGATTCTAGCTTAG		ATGTTTCAACTCTCTATCTCGACGCAGATTCTAGCTTAG		MFQLSISTQILA*		MFQLSISTQILA*		ATGCAGCTTC	GGCATGATGG	0		0	0	0	YDR479C	0
456	364	ao	AN7677.1	57.m05454	AO070325000067	1					-44	-12	ATGTCTTTGCTTACTATCAATCTCTTTCGGTAG			ATGTCTTTGCTTACTATCAATCTCTTTCGGTAG	MSLLTINLFR*			MSLLTINLFR*	GCTGTCGGAA	CTGAATCTAT	1		0	0	0	YDR479C	0
465	369	af	AN3650.1	58.m07449	AO070328000098	1			-146	-66			ATGCTGTATTGGTATGTCTTTTCGTTCTTCGTCATTGAGGTCGTGAAACCTCCGTTCTTGCGCGTTTGTCGAGTCGCATAG		ATGCTGTATTGGTATGTCTTTTCGTTCTTCGTCATTGAGGTCGTGAAACCTCCGTTCTTGCGCGTTTGTCGAGTCGCATAG		MLYWYVFSFFVIEVVKPPFLRVCRVA*		MLYWYVFSFFVIEVVKPPFLRVCRVA*		ACGCCTTCCA	TCCCGAGAGC	0		0	0	0	0	0
466	369	af	AN3650.1	58.m07449	AO070328000098	1			-133	-101			ATGTCTTTTCGTTCTTCGTCATTGAGGTCGTGA		ATGTCTTTTCGTTCTTCGTCATTGAGGTCGTGA		MSFRSSSLRS*		MSFRSSSLRS*		CTGTATTGGT	AACCTCCGTT	0		0	0	0	0	0
467	369	ao	AN3650.1	58.m07449	AO070328000098	1					-229	-143	ATGCTCCTGGCGCTGCCTGTCTTTAATAGTTGCGTTATTGGGGTTTGGCGCCTCCTATCTGCCGACGGGTATCCAACCTTTACTTAA			ATGCTCCTGGCGCTGCCTGTCTTTAATAGTTGCGTTATTGGGGTTTGGCGCCTCCTATCTGCCGACGGGTATCCAACCTTTACTTAA	MLLALPVFNSCVIGVWRLLSADGYPTFT*			MLLALPVFNSCVIGVWRLLSADGYPTFT*	TTGCCGTCCA	TCGCAATCCG	0		0	0	0	0	0
481	387	ao	AN7754.1	71.m15786	AO070325000185	0					-58	-23	ATGCGCTACTGGATATCTCTAGTACCCGAGTACTAA			ATGCGCTACTGGATATCTCTAGTACCCGAGTACTAA	MRYWISLVPEY*			MRYWISLVPEY*	ACCCCCCTTG	TCACCGTGTG	1		0	0	0	0	0
482	390	an	AN4408.1	58.m07896	AO070273000028	1	-162	-139					ATGCGTTCATCTCTATTTATCTAA	ATGCGTTCATCTCTATTTATCTAA			MRSSLFI*	MRSSLFI*			CAATTATTGC	TTTATGTAAA	0		0	0	0	0	0
483	390	an	AN4408.1	58.m07896	AO070273000028	1	-118	-74					ATGAGGCCTCTAAACTGGTCATATCTGGCCCGATTCGCCGTCTGA	ATGAGGCCTCTAAACTGGTCATATCTGGCCCGATTCGCCGTCTGA			MRPLNWSYLARFAV*	MRPLNWSYLARFAV*			TTATAGTCAA	TCAGCCTCAA	0		0	0	0	0	0

§S3 Upstream open reading frames (uORFs)

Tab 2 - data

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
484	390	af	AN4408.1	58.m07896	AO070273000028	1			-200	-102			ATGCTTCAAGTATGGATACCTTACTTAACAGTCCATCAACTTATTCTTGTTCTGCTCTTCTTTGATCCTATTATTGTTATAGATTGCATCTTTCTATAG		ATGCTTCAAGTATGGATACCTTACTTAACAGTCCATCAACTTATTCTTGTTCTGCTCTTCTTTGATCCTATTATTGTTATAGATTGCATCTTTCTATAG		MLQVWIPYLTVHQLILVLLFFDPIIVIDCIFL*		MLQVWIPYLTVHQLILVLLFFDPIIVIDCIFL*		AGTCTATCCG	TACTTGTGTA	0		0	0	0	0	0
485	390	af	AN4408.1	58.m07896	AO070273000028	1			-189	-136			ATGGATACCTTACTTAACAGTCCATCAACTTATTCTTGTTCTGCTCTTCTTTGA		ATGGATACCTTACTTAACAGTCCATCAACTTATTCTTGTTCTGCTCTTCTTTGA		MDTLLNSPSTYSCSALL*		MDTLLNSPSTYSCSALL*		TGCTTCAAGT	TCCTATTATT	0		0	0	0	0	0
486	390	ao	AN4408.1	58.m07896	AO070273000028	1					-278	-246	ATGATTGCCGATCATCACGGTGATTCAAACTGA			ATGATTGCCGATCATCACGGTGATTCAAACTGA	MIADHHGDSN*			MIADHHGDSN*	TTAGCGTGGT	TAGGCTATAC	0		0	0	0	0	0
489	396	ao	AN1342.1	70.m14891	AO070247000022	1					-251	-210	ATGGATATATGCAATTGTGTCGTTGGAGTTAGCTTCTACTAG			ATGGATATATGCAATTGTGTCGTTGGAGTTAGCTTCTACTAG	MDICNCVVGVSFY*			MDICNCVVGVSFY*	ATAACTTGAG	TGGAAATTGG	0	R	0	0	0	0	0
490	396	ao	AN1342.1	70.m14891	AO070247000022	1					-243	-220	ATGCAATTGTGTCGTTGGAGTTAG			ATGCAATTGTGTCGTTGGAGTTAG	MQLCRWS*			MQLCRWS*	AGATGGATAT	CTTCTACTAG	0	R	0	0	0	0	0
491	396	ao	AN1342.1	70.m14891	AO070247000022	1					-126	-49	ATGTTGGATAAATATATAATTCTCCGCAGCATACGGGTTCCGAATGTTCTAAAACCCAGACGCAACAATGGAATATGA			ATGTTGGATAAATATATAATTCTCCGCAGCATACGGGTTCCGAATGTTCTAAAACCCAGACGCAACAATGGAATATGA	MLDKYIILRSIRVPNVLKPRRNNGI*			MLDKYIILRSIRVPNVLKPRRNNGI*	ATACACAATT	TGTTTTCATT	0	R	0	0	0	0	0
492	397	an	AN3450.1	59.m09313	AO070265000025	1	-115	-50					ATGATTTATTTTCATAACAGACCTTTTCCCTCCCTTCCATACGGCGGCGAAACCCATCGAGTGTAA	ATGATTTATTTTCATAACAGACCTTTTCCCTCCCTTCCATACGGCGGCGAAACCCATCGAGTGTAA			MIYFHNRPFPSLPYGGETHRV*	MIYFHNRPFPSLPYGGETHRV*			TTGATTCTTT	TCCGGCCGCT	0	L	0	0	0	0	0
494	397	af	AN3450.1	59.m09313	AO070265000025	1			-238	-176			ATGGATCATACACAATTACATACGCGCCTACCCGTGGCCATCAACCGCGAAATTGATGATTTGA		ATGGATCATACACAATTACATACGCGCCTACCGTGGCCATCAACCGCGAAATTGATGATTTGA		MDHTQLHTRLPWPSTAKLMI*		MDHTQLHTRLPWPSTAKLMI*		GACCATTTTG	GAAATCCTCG	0	L	0	0	0	0	0
495	397	af	AN3450.1	59.m09313	AO070265000025	1			-81	-67			ATGCAAGATATTTGA		ATGCAAGATATTTGA		MQDI*		MQDI*		ACCTCAGTCC	GGAACCCCTC	0	L	0	0	0	0	0
505	400	af	AN8262.1	53.m04209	AO070310000038	0			-57	-46			ATGGATCTGTGA		ATGGATCTGTGA		MDL*		MDL*		CGTTCCTTGC	AGATCCTTCG	1		0	0	0	0	0
565	429	af	AN3001.1	59.m09013	AO070337000111	1			-355	-284			ATGCGCCTTGGTTGCCCGTTGTCTACCTATTACTTACTCGCTTATTGCGTCAGACATCTATATAATTTCTGA		ATGCGCCTTGGTTGCCCGTTGTCTACCTATTACTTACTCGCTTATTGCGTCAGACATCTATATAATTTCTGA		MRLGCPLSTYYLLAYCVRHLYNF*		MRLGCPLSTYYLLAYCVRHLYNF*		AATCCAGAGT	CGCATATAAC	0	T	0	0	0	0	0
579	433	an	AN6824.1	71.m15292	AO070314000104	0	-59	-27					ATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG	ATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG			MRASSTCSQV*	MRASSTCSQV*			TTGTTCTAAT	GACTCGCTCT	1	G	0	0	0	YJR049C	YJR049C
587	441	an	AN7485.1	57.m05867	AO070287000048	1	-183	-148					ATGGTTGCCTTGTCACATCTGGCTTTCGGCAGCTGA	ATGGTTGCCTTGTCACATCTGGCTTTCGGCAGCTGA			MVALSHLAFGS*	MVALSHLAFGS*			CTTCGGTCTT	TCTCGTTTGC	0	R	0	0	NCU07564.1	0	0
588	441	af	AN7485.1	57.m05867	AO070287000048	1			-259	-164			ATGGCACAATCGACCAAATGGAACAACACAGCGATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		ATGGCACAATCGACCAAATGGAACAACACAGCGATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		MAQSTKWNNTAMMKANGFSRNSVILADLVVT*		MAQSTKWNNTAMMKANGFSRNSVILADLVVT*		GGACCCTCTT	CGTCAATTTC	0	R	0	0	NCU07564.1	0	0
589	441	af	AN7485.1	57.m05867	AO070287000048	1			-242	-30			ATGGAACAACACAGCGATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAACGTCAATTTCGGAAGATTCGGTGCAGGAAGGCGTTAGAAAAATCGAAGCGATCAATTTGACTTGGACTGCACGGTCTCTGGTCATAGCATATGTCAGGTCGGTCCCTCTGGGACACGTGCGGCGCGTCTTATAA		ATGGAACAACACAGCGATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAACGTCAATTTCGGAAGATTCGGTGCAGGAAGGCGTTAGAAAAATCGAAGCGATCAATTTGACTTGGACTGCACGGTCTCTGGTCATAGCATATGTCAGGTCGGTCCCTCTGGGACACGTGCGGCGCGTCTTATAA		MEQHSDDEGERFLQEQCDTGRFSSDITSISEDSVQEGVRKIEAINLTWTARSLVIAYVRSVPLGHVRRVL*		MEQHSDDEGERFLQEQCDTGRFSSDITSISEDSVQEGVRKIEAINLTWTARSLVIAYVRSVPLGHVRRVL*		AATCGACCAA	TACTGACATA	0	R	0	0	NCU07564.1	0	0
590	441	af	AN7485.1	57.m05867	AO070287000048	1			-226	-164			ATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		ATGATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		MMKANGFSRNSVILADLVVT*		MMKANGFSRNSVILADLVVT*		CAACACAGCG	CGTCAATTTC	0	R	0	0	NCU07564.1	0	0
591	441	af	AN7485.1	57.m05867	AO070287000048	1			-223	-164			ATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		ATGAAGGCGAACGGTTTCTCCAGGAACAGTGTGATACTGGCAGATTTAGTAGTGACATAA		MKANGFSRNSVILADLVVT*		MKANGFSRNSVILADLVVT*		CACAGCGATG	CGTCAATTTC	0	R	0	0	NCU07564.1	0	0
594	443	an	AN8039.1	53.m03907	AO070330000007	1	-278	-219					ATGCCCTGGCATTCATCATCTCGAGTCATGGCCATAGCTGGGCTTCGGTTGGGATGGTGA	ATGCCCTGGCATTCATCATCTCGAGTCATGGCCATAGCTGGGCTTCGGTTGGGATGGTGA			MPWHSSSRVMAIAGLRLGW*	MPWHSSSRVMAIAGLRLGW*			CGGCACGCCG	GGTGGTTCCC	0	B	FG01627.1	0	NCU05347.1	0	0
595	443	an	AN8039.1	53.m03907	AO070330000007	1	-251	-219					ATGGCCATAGCTGGGCTTCGGTTGGGATGGTGA	ATGGCCATAGCTGGGCTTCGGTTGGGATGGTGA			MAIAGLRLGW*	MAIAGLRLGW*			ATCTCGAGTC	GGTGGTTCCC	0	B	FG01627.1	0	NCU05347.1	0	0
596	443	an	AN8039.1	53.m03907	AO070330000007	1	-225	-196					ATGGTGAGGTGGTTCCCTAATCTGGACTAG	ATGGTGAGGTGGTTCCCTAATCTGGACTAG			MVRWFPNLD*	MVRWFPNLD*			TTCGGTTGGG	CGGCGTTTGA	0	B	FG01627.1	0	NCU05347.1	0	0
597	443	af	AN8039.1	53.m03907	AO070330000007	1			-259	-227			ATGCCTTCTCAGCTCGCCTTTGGAAGCATCTGA		ATGCCTTCTCAGCTCGCCTTTGGAAGCATCTGA		MPSQLAFGSI*		MPSQLAFGSI*		CTTGCTCAGT	GTCGAAGTTG	0	B	FG01627.1	0	NCU05347.1	0	0
598	443	ao	AN8039.1	53.m03907	AO070330000007	1					-318	-298	ATGCAATTGAAATCTGCTTAG			ATGCAATTGAAATCTGCTTAG	MQLKSA*			MQLKSA*	TGGATATGCA	CTGCTTTGCT	0	B	FG01627.1	0	NCU05347.1	0	0
599	443	ao	AN8039.1	53.m03907	AO070330000007	1					-225	-205	ATGATGTTCTTGGTTTCCTAA			ATGATGTTCTTGGTTTCCTAA	MMFLVS*			MMFLVS*	GAGACTTGGG	TCAGGACTAG	0	B	FG01627.1	0	NCU05347.1	0	0
600	443	ao	AN8039.1	53.m03907	AO070330000007	1					-222	-205	ATGTTCTTGGTTTCCTAA			ATGTTCTTGGTTTCCTAA	MFLVS*			MFLVS*	ACTTGGGATG	TCAGGACTAG	0	B	FG01627.1	0	NCU05347.1	0	0
601	443	ao	AN8039.1	53.m03907	AO070330000007	1					-157	-47	ATGGCTTTGACATTTCTGACTCCTTCATCCATCAACAACGCGCGTGCCGCTGGTGTATCGAATCGCTTCAACGTCCACCATCGTGCTCTATCACTTCAAACACCCGTTTGA			ATGGCTTTGACATTTCTGACTCCTTCATCCATCAACAACGCGCGTGCCGCTGGTGTATCGAATCGCTTCAACGTCCACCATCGTGCTCTATCACTTCAAACACCCGTTTGA	MALTFLTPSSINNARAAGVSNRFNVHHRALSLQTPV*			MALTFLTPSSINNARAAGVSNRFNVHHRALSLQTPV*	AGCGACCAGG	CGCGACATTT	0	B	FG01627.1	0	NCU05347.1	0	0
614	458	an	AN0315.1	54.m06443	AO070334000017	1	-164	-138					ATGACGCTGATGGATAACTGCCTTTGA	ATGACGCTGATGGATAACTGCCTTTGA			MTLMDNCL*	MTLMDNCL*			CTTCGCAGCC	GAGCCATCAT	0		0	0	0	0	0
615	458	an	AN0315.1	54.m06443	AO070334000017	1	-155	-138					ATGGATAACTGCCTTTGA	ATGGATAACTGCCTTTGA			MDNCL*	MDNCL*			CATGACGCTG	GAGCCATCAT	0		0	0	0	0	0
616	458	an	AN0315.1	54.m06443	AO070334000017	1	-65	-54					ATGCTGAATTGA	ATGCTGAATTGA			MLN*	MLN*			ACAGATCTCA	ACGAATCGGC	0		0	0	0	0	0
617	458	af	AN0315.1	54.m06443	AO070334000017	1			-346	-224			ATGTTGTCTGTCAATCTTCCTTGGCATTTTGATAGTATTGCTGTAGTATCTGTCAATTCATTGATGCGGTGTCACCATTTGCTGCGGGAGTTCCCAAACTGGCAATGGAAACCCAAGCAATGA		ATGTTGTCTGTCAATCTTCCTTGGCATTTTGATAGTATTGCTGTAGTATCTGTCAATTCATTGATGCGGTGTCACCATTTGCTGCGGGAGTTCCCAAACTGGCAATGGAAACCCAAGCAATGA		MLSVNLPWHFDSIAVVSVNSLMRCHHLLREFPNWQWKPKQ*		MLSVNLPWHFDSIAVVSVNSLMRCHHLLREFPNWQWKPKQ*		GATAGAAGGT	ATAGCTCTGC	0		0	0	0	0	0
618	458	af	AN0315.1	54.m06443	AO070334000017	1			-283	-224			ATGCGGTGTCACCATTTGCTGCGGGAGTTCCCAAACTGGCAATGGAAACCCAAGCAATGA		ATGCGGTGTCACCATTTGCTGCGGGAGTTCCCAAACTGGCAATGGAAACCCAAGCAATGA		MRCHHLLREFPNWQWKPKQ*		MRCHHLLREFPNWQWKPKQ*		CAATTCATTG	ATAGCTCTGC	0		0	0	0	0	0
619	458	af	AN0315.1	54.m06443	AO070334000017	1			-242	-54			ATGGAAACCCAAGCAATGAATAGCTCTGCATATGATATAGAATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAGACGAGTTTTAATTTATTCAGAGACATATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGACCATATAG		ATGGAAACCCAAGCAATGAATAGCTCTGCATATGATATAGAATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAGACGAGTTTTAATTTATTCAGAGACATATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGACCATATAG		METQAMNSSAYDIECIRDLASLLHAVICSSNCIPRRVLIYSETYANSLFRSTLSHIKPNMTI*		METQAMNSSAYDIECIRDLASLLHAVICSSNCIPRRVLIYSETYANSLFRSTLSHIKPNMTI*		CAAACTGGCA	ACCACTTTTA	0		0	0	0	0	0
620	458	af	AN0315.1	54.m06443	AO070334000017	1			-227	-54			ATGAATAGCTCTGCATATGATATAGAATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAGACGAGTTTTAATTTATTCAGAGACATATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGACCATATAG		ATGAATAGCTCTGCATATGATATAGAATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAGACGAGTTTTAATTTATTCAGAGACATATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGACCATATAG		MNSSAYDIECIRDLASLLHAVICSSNCIPRRVLIYSETYANSLFRSTLSHIKPNMTI*		MNSSAYDIECIRDLASLLHAVICSSNCIPRRVLIYSETYANSLFRSTLSHIKPNMTI*		AACCCAAGCA	ACCACTTTTA	0		0	0	0	0	0
621	458	af	AN0315.1	54.m06443	AO070334000017	1			-201	-139			ATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAG		ATGTATTCGAGATTTGGCATCCTTGCTCCATGCTGTAATCTGCTCTTCCAATTGTATCCCTAG		MYSRFGILAPCCNLLFQLYP*		MYSRFGILAPCCNLLFQLYP*		ATGATATAGA	ACGAGTTTTA	0		0	0	0	0	0
622	458	af	AN0315.1	54.m06443	AO070334000017	1			-112	-62			ATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGA		ATGCTAACAGCTTGTTTAGATCTACTCTATCTCATATCAAGCCCAACATGA		MLTACLDLLYLISSPT*		MLTACLDLLYLISSPT*		TCAGAGACAT	CCATATAGAC	0		0	0	0	0	0
623	458	af	AN0315.1	54.m06443	AO070334000017	1			-65	-54			ATGACCATATAG		ATGACCATATAG		MTI*		MTI*		CAAGCCCAAC	ACCACTTTTA	0		0	0	0	0	0
624	458	ao	AN0315.1	54.m06443	AO070334000017	1					-188	-171	ATGGTAAGATCGTATTGA			ATGGTAAGATCGTATTGA	MVRSY*			MVRSY*	GGCCTAATTT	CATTGAATCA	0		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
625	458	ao	AN0315.1	54.m06443	AO070334000017	1					-50	-39	ATGACCGTCTAG			ATGACCGTCTAG	MTV*			MTV*	GACTAGAACC	CAGCAGCGTC	1		0	0	0	0	0
632	460	ao	AN4206.1	54.m06765	AO070231000018	1					-36	-13	ATGATCAATTTATGTATTCATTGA			ATGATCAATTTATGTATTCATTGA	MINLCIH*			MINLCIH*	ACAAGTTTGG	GTTGTCCAAA	1	A	0	0	0	0	0
642	464	an	AN0082.1	71.m15360	AO070311000135	1	-285	-271					ATGAAACACCGTTGA	ATGAAACACCGTTGA			MKHR*	MKHR*			CGGGGCACAG	GTTGTCACAA	0	T	0	0	0	0	0
643	464	an	AN0082.1	71.m15360	AO070311000135	1	-66	-43					ATGCTGCAGACCTTACGTATATAA	ATGCTGCAGACCTTACGTATATAA			MLQTLRI*	MLQTLRI*			CTGCTCACGG	GTGTTTCACC	0	T	0	0	0	0	0
648	466	af	AN4505.1	57.m05626	AO070311000058	1			-29	-9			ATGACAGCATATCCTATATAA		ATGACAGCATATCCTATATAA		MTAYPI*		MTAYPI*		TTACCATCTT	ACATCACCAT	1	R	0	0	0	0	0
656	472	af	AN9090.1	66.m04770	AO070332000188	1			-59	-6			ATGTTCCCAGATAGCATTAACGCGATTCCCATCTTTACGACTGTCGGAGTTTAG		ATGTTCCCAGATAGCATTAACGCGATTCCCATCTTTACGACTGTCGGAGTTTAG		MFPDSINAIPIFTTVGV*		MFPDSINAIPIFTTVGV*		ACTAATTACT	TCAACATGTC	1	R	0	0	0	0	0
673	485	an	AN8293.1	52.m04044	AO070274000002	0	-41	-21					ATGTTGAACCAATTTAGGTAG	ATGTTGAACCAATTTAGGTAG			MLNQFR*	MLNQFR*			AAAAACTTCA	TGAATAGTAC	1	R	0	MG06038.1	NCU07011.1	YLR409C	YLR409C
674	485	af	AN8293.1	52.m04044	AO070274000002	0			-31	-5			ATGCTACGGAGACCCGACCCGAATTAA		ATGCTACGGAGACCCGACCCGAATTAA		MLRRPDPN*		MLRRPDPN*		GAAACTGGTA	CATGATGCCT	1	R	0	MG06038.1	NCU07011.1	YLR409C	YLR409C
680	492	ao	AN8710.1	62.m03358	AO070315000137	0					-45	-31	ATGCGCCATCAATAA			ATGCGCCATCAATAA	MRHQ*			MRHQ*	TCTTTCTTTT	TCGATTAACT	1	S	0	0	0	0	0
693	513	an	AN6881.1	55.m03218	AO070342000371	1	-54	-31					ATGTATCTCTGGAGGACGTCCTAA	ATGTATCTCTGGAGGACGTCCTAA			MYLWRTS*	MYLWRTS*			GCTCTTATTT	ACCTCAAAAT	1		0	0	0	0	0
698	516	conserved	AN5151.1	69.m14882	AO070237000013	1	-48	-37	-365	-354	-101	-90	ATGydsvTTTGA	ATGTACCTTTGA	ATGCGGGTTTGA	ATGCTGATTTGA	Myl*	MYL*	MRV*	MLI*	mhhsmAGrhy	TmTbsmmdwd	0	RT	0	0	0	0	0
711	522	an	AN1559.1	55.m03275	AO070339000294	1	-76	-50					ATGGATATACTGTTGACATATACTTGA	ATGGATATACTGTTGACATATACTTGA			MDILLTYT*	MDILLTYT*			GAAACCTGCG	ATTGAACACA	0	R	0	0	0	0	0
712	522	ao	AN1559.1	55.m03275	AO070339000294	1					-241	-191	ATGGACTTGTGCTACCCGCTTATTTCCTCACTCCCTATCCTTAACTTGTAA			ATGGACTTGTGCTACCCGCTTATTTCCTCACTCCCTATCCTTAACTTGTAA	MDLCYPLISSLPILNL*			MDLCYPLISSLPILNL*	TTTGAGAGTC	CTCTTCTTCG	0	R	0	0	0	0	0
713	533	an	AN5527.1	69.m15430	AO070341000362	1	-324	-211					ATGTTATTCCACCAGCAAAATATAATCCCCTCCAGCCGCGAGTCCGAACGATATCCTTGGCGACTGTCCACGATGAGACTCCCGGGCAAGCGTCAAGCTGTGCTCGGCATTTGA	ATGTTATTCCACCAGCAAAATATAATCCCCTCCAGCCGCGAGTCCGAACGATATCCTTGGCGACTGTCCACGATGAGACTCCCGGGCAAGCGTCAAGCTGTGCTCGGCATTTGA			MLFHQQNIIPSSRESERYPWRLSTMRLPGKRQAVLGI*	MLFHQQNIIPSSRESERYPWRLSTMRLPGKRQAVLGI*			TCTCTAGCAC	TGAATTCTGT	0	L	0	0	0	0	0
714	533	an	AN5527.1	69.m15430	AO070341000362	1	-252	-211					ATGAGACTCCCGGGCAAGCGTCAAGCTGTGCTCGGCATTTGA	ATGAGACTCCCGGGCAAGCGTCAAGCTGTGCTCGGCATTTGA			MRLPGKRQAVLGI*	MRLPGKRQAVLGI*			ACTGTCCACG	TGAATTCTGT	0	L	0	0	0	0	0
715	533	an	AN5527.1	69.m15430	AO070341000362	1	-211	-125					ATGAATTCTGTTGGGGAGGAAACTGTCCAGCTGGCAATTCCGCCTAAGGCCCCAGCAAGCCAAAGTTTATATAGAGCACAATTTTGA	ATGAATTCTGTTGGGGAGGAAACTGTCCAGCTGGCAATTCCGCCTAAGGCCCCAGCAAGCCAAAGTTTATATAGAGCACAATTTTGA			MNSVGEETVQLAIPPKAPASQSLYRAQF*	MNSVGEETVQLAIPPKAPASQSLYRAQF*			TCGGCATTTG	GGGTTGGTGG	0	L	0	0	0	0	0
718	533	ao	AN5527.1	69.m15430	AO070341000362	1					-491	-474	ATGGCTCCTCCGAAATAA			ATGGCTCCTCCGAAATAA	MAPPK*			MAPPK*	AGCACAGGTT	AGCCCCCTCC	0	L	0	0	0	0	0
719	533	ao	AN5527.1	69.m15430	AO070341000362	1					-424	-383	ATGACGCTCCCGGGCGTGAGTCAAGTTGCGTTCGGCATTTGA			ATGACGCTCCCGGGCGTGAGTCAAGTTGCGTTCGGCATTTGA	MTLPGVSQVAFGI*			MTLPGVSQVAFGI*	ACGGTCCAAG	TAAACTCAGT	0	L	0	0	0	0	0
745	550	ao	AN5596.1	58.m07520	AO070328000008	0					-31	-11	ATGTTGAAGAGAAATAACTAG			ATGTTGAAGAGAAATAACTAG	MLKRNN*			MLKRNN*	TAGAGGAATT	CCCTCCCATC	1	R	0	0	0	0	0
763	565	af	AN0768.1	70.m15371	AO070316000076	0			-34	-23			ATGTTTCTGTAA		ATGTTTCTGTAA		MFL*		MFL*		TCTTGTGTAT	AGAGAAGTTA	1	M	0	0	0	0	0
771	570	ao	AN3020.1	59.m09444	AO070337000094	0					-54	-28	ATGTTCCTTCTGAAGCGGGTTGACTAG			ATGTTCCTTCTGAAGCGGGTTGACTAG	MFLLKRVD*			MFLLKRVD*	ATCTCCCGGT	GCTTTATCTG	1	O	0	0	0	0	0
791	586	af	AN2750.1	54.m06682	AO070338000222	0			-31	-17			ATGAGCAGTGGCTGA		ATGAGCAGTGGCTGA		MSSG*		MSSG*		GAAACCTCCA	GCCTTTTGTG	1		0	0	0	0	0
796	610	an	AN5790.1	69.m14806	AO070249000036	1	-188	-174					ATGATCCTTAGATAA	ATGATCCTTAGATAA			MILR*	MILR*			GCAGATTGAG	GATCGGGCCG	0	E	FG05733.1	MG01995.1	0	0	0
797	610	af	AN5790.1	69.m14806	AO070249000036	1			-269	-237			ATGATATTATGGCGCGGAGAGGGGGAAAGATAA		ATGATATTATGGCGCGGAGAGGGGGAAAGATAA		MILWRGEGER*		MILWRGEGER*		TTGAGGACTG	GATCGGGCCG	0	E	FG05733.1	MG01995.1	0	0	0
798	610	af	AN5790.1	69.m14806	AO070249000036	1			-261	-160			ATGGCGCGGAGAGGGGGAAAGATAAGATCGGGCCGTGTTCTGAGACAGGTTGGTGCGCAAATTATACATGGAAGGACGGCACCTTGGTGGATGCCGAGATGA		ATGGCGCGGAGAGGGGGAAAGATAAGATCGGGCCGTGTTCTGAGACAGGTTGGTGCGCAAATTATACATGGAAGGACGGCACCTTGGTGGATGCCGAGATGA		MARRGGKIRSGRVLRQVGAQIIHGRTAPWWMPR*		MARRGGKIRSGRVLRQVGAQIIHGRTAPWWMPR*		TGATGATATT	TCCGCCGTTT	0	E	FG05733.1	MG01995.1	0	0	0
799	610	af	AN5790.1	69.m14806	AO070249000036	1			-171	-160			ATGCCGAGATGA		ATGCCGAGATGA		MPR*		MPR*		ACCTTGGTGG	TCCGCCGTTT	0	E	FG05733.1	MG01995.1	0	0	0
800	610	af	AN5790.1	69.m14806	AO070249000036	1			-163	-107			ATGATCCGCCGTTTTTTCCGGCGCCCCCTTCTTGTGGCCCTGCATCTCGTTTTCTAA		ATGATCCGCCGTTTTTTCCGGCGCCCCCTTCTTGTGGCCCTGCATCTCGTTTTCTAA		MIRRFFRRPLLVALHLVF*		MIRRFFRRPLLVALHLVF*		GGATGCCGAG	CTCCATCTGT	0	E	FG05733.1	MG01995.1	0	0	0
801	610	ao	AN5790.1	69.m14806	AO070249000036	1					-247	-236	ATGGGACCCTAA			ATGGGACCCTAA	MGP*			MGP*	TAATTGAGTG	AGATAAGATC	0	E	FG05733.1	MG01995.1	0	0	0
802	610	ao	AN5790.1	69.m14806	AO070249000036	1					-187	-2	ATGGATGCCGAGACGATCCGCCGTTTTTTCCGGCGTCTCGTGCACTCCCTGTCCTTAGCCTTGGCCGCCTTTCTTTCCCGTCCTCCGTCTCTCTTCCCTCTGCACGCCTTTTTCTCTCCTCTAGCTAGATTCGCTTTTCGCCTCTCTCCTCTCCCTCCCTTCCCCCACCCCCTGGTTCATTGTTAA			ATGGATGCCGAGACGATCCGCCGTTTTTTCCGGCGTCTCGTGCACTCCCTGTCCTTAGCCTTGGCCGCCTTTCTTTCCCGTCCTCCGTCTCTCTTCCCTCTGCACGCCTTTTTCTCTCCTCTAGCTAGATTCGCTTTTCGCCTCTCTCCTCTCCCTCCCTTCCCCCACCCCCTGGTTCATTGTTAA	MDAETIRRFFRRLVHSLSLALAAFLSRPPSLFPLHAFFSPLARFAFRLSPLPPFPHPLVHC*			MDAETIRRFFRRLVHSLSLALAAFLSRPPSLFPLHAFFSPLARFAFRLSPLPPFPHPLVHC*	GTTGGCTTTC	GATGTTTTCC	0	E	FG05733.1	MG01995.1	0	0	0
803	610	ao	AN5790.1	69.m14806	AO070249000036	1					-183	-130	ATGCCGAGACGATCCGCCGTTTTTTCCGGCGTCTCGTGCACTCCCTGTCCTTAG			ATGCCGAGACGATCCGCCGTTTTTTCCGGCGTCTCGTGCACTCCCTGTCCTTAG	MPRRSAVFSGVSCTPCP*			MPRRSAVFSGVSCTPCP*	GCTTTCATGG	CCTTGGCCGC	0	E	FG05733.1	MG01995.1	0	0	0
812	613	af	AN2919.1	59.m09077	AO070337000216	1			-663	-613			ATGCTCAACTTGGCCCTCCCTCCTATCCTCGATATTCGCTTTTTGAAGTGA		ATGCTCAACTTGGCCCTCCCTCCTATCCTCGATATTCGCTTTTTGAAGTGA		MLNLALPPILDIRFLK*		MLNLALPPILDIRFLK*		CCTTACCTGT	TTCTTAACGT	0	R	0	0	0	0	0
813	613	af	AN2919.1	59.m09077	AO070337000216	1			-289	-212			ATGTGTTTGCACCTTCGGTTTAGATTTTATGCTTTTCATCGGGTGCTTCATCCTCGTTGCTTGTCTGGGATTAAATAG		ATGTGTTTGCACCTTCGGTTTAGATTTTATGCTTTTCATCGGGTGCTTCATCCTCGTTGCTTGTCTGGGATTAAATAG		MCLHLRFRFYAFHRVLHPRCLSGIK*		MCLHLRFRFYAFHRVLHPRCLSGIK*		TCATCACGGT	CTAATTCTTG	0	R	0	0	0	0	0
817	613	ao	AN2919.1	59.m09077	AO070337000216	0					-56	-45	ATGGACCACTAG			ATGGACCACTAG	MDH*			MDH*	CTACTTATCA	ACATTTAAAT	1	R	0	0	0	0	0
828	630	an	AN6166.1	72.m19013	AO070340000049	1	-200	-177					ATGGCAGCTTCTCCCAGTTCATAA	ATGGCAGCTTCTCCCAGTTCATAA			MAASPSS*	MAASPSS*			CTGTGAACGG	TCCCATTTCT	0	K	0	0	0	0	0
829	630	an	AN6166.1	72.m19013	AO070340000049	1	-122	-96					ATGCTAAAGTTTGAAAGTCAGGTCTAG	ATGCTAAAGTTTGAAAGTCAGGTCTAG			MLKFESQV*	MLKFESQV*			AAACGGAGAT	TACCTCATTA	0	K	0	0	0	0	0
830	630	af	AN6166.1	72.m19013	AO070340000049	1			-135	-115			ATGTCCCTCGTCTCTCGTTAA		ATGTCCCTCGTCTCTCGTTAA		MSLVSR*		MSLVSR*		ACGGAAAAGA	AGCTCTGTCC	0	K	0	0	0	0	0
831	630	ao	AN6166.1	72.m19013	AO070340000049	1					-819	-799	ATGCTACTCGTTTTGCGCTGA			ATGCTACTCGTTTTGCGCTGA	MLLVLR*			MLLVLR*	AAAAAAAGCC	CCTTAGTACG	0	K	0	0	0	0	0
835	640	af	AN4324.1	58.m07999	AO070240000001	1			-103	-80			ATGCTCTGTCTGAGCTTCGGTTAA		ATGCTCTGTCTGAGCTTCGGTTAA		MLCLSFG*		MLCLSFG*		CCTCGGTTCT	TCTTTCCAAA	0		0	0	0	0	0
876	660	af	AN4732.1	71.m15501	AO070323000052	1			-202	-164			ATGTATTCGTCGGTTGCCTCCTTCCCACACCTCGTTTAA		ATGTATTCGTCGGTTGCCTCCTTCCCACACCTCGTTTAA		MYSSVASFPHLV*		MYSSVASFPHLV*		GATTTCTTGA	AGCGACTCTC	0		0	0	0	0	0
877	660	ao	AN4732.1	71.m15501	AO070323000052	1					-554	-525	ATGGCCCCCTTCATCCTTCTCCCGAAATAG			ATGGCCCCCTTCATCCTTCTCCCGAAATAG	MAPFILLPK*			MAPFILLPK*	CGTCGGTCGC	AACCACTCCG	0		0	0	0	0	0
878	665	an	AN4515.1	57.m05614	AO070311000076	0	-39	-19					ATGATTCTCGGCCTATCCTGA	ATGATTCTCGGCCTATCCTGA			MILGLS*	MILGLS*			TTCTCTGTAT	CCCCATCACG	1	G	0	0	0	0	0
887	677	an	AN4071.1	54.m06996	AO070342000060	1	-332	-315					ATGCAGTCATCCAACTGA	ATGCAGTCATCCAACTGA			MQSSN*	MQSSN*			TAGCACCATT	TCTTAACCGT	0	I	0	0	0	0	0
888	677	an	AN4071.1	54.m06996	AO070342000060	1	-280	-236					ATGCTGACAATGGGCACTCTTTGTTCAGTTCATGGGAAGAAATGA	ATGCTGACAATGGGCACTCTTTGTTCAGTTCATGGGAAGAAATGA			MLTMGTLCSVHGKK*	MLTMGTLCSVHGKK*			ACTTTTCAGC	TGTGTCCGAC	0	I	0	0	0	0	0
889	677	an	AN4071.1	54.m06996	AO070342000060	1	-271	-236					ATGGGCACTCTTTGTTCAGTTCATGGGAAGAAATGA	ATGGGCACTCTTTGTTCAGTTCATGGGAAGAAATGA			MGTLCSVHGKK*	MGTLCSVHGKK*			CATGCTGACA	TGTGTCCGAC	0	I	0	0	0	0	0
890	677	an	AN4071.1	54.m06996	AO070342000060	1	-249	-184					ATGGGAAGAAATGATGTGTCCGACGTGATGCTCAAGTTGCGAAACCTCGCTTGCGGCGTATCGTAA	ATGGGAAGAAATGATGTGTCCGACGTGATGCTCAAGTTGCGAAACCTCGCTTGCGGCGTATCGTAA			MGRNDVSDVMLKLRNLACGVS*	MGRNDVSDVMLKLRNLACGVS*			TGTTCAGTTC	TCAAACCTCA	0	I	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
891	677	an	AN4071.1	54.m06996	AO070342000060	1	-239	-222					ATGATGTGTCCGACGTGA	ATGATGTGTCCGACGTGA			MMCPT*	MMCPT*			ATGGGAAGAA	TGCTCAAGTT	0	I	0	0	0	0	0
892	677	an	AN4071.1	54.m06996	AO070342000060	1	-236	-222					ATGTGTCCGACGTGA	ATGTGTCCGACGTGA			MCPT*	MCPT*			GGAAGAAATG	TGCTCAAGTT	0	I	0	0	0	0	0
893	677	an	AN4071.1	54.m06996	AO070342000060	1	-222	-184					ATGCTCAAGTTGCGAAACCTCGCTTGCGGCGTATCGTAA	ATGCTCAAGTTGCGAAACCTCGCTTGCGGCGTATCGTAA			MLKLRNLACGVS*	MLKLRNLACGVS*			GTCCGACGTG	TCAAACCTCA	0	I	0	0	0	0	0
894	677	an	AN4071.1	54.m06996	AO070342000060	1	-139	-68					ATGGTCATTTTTACCACCACAATTGTTGGCACTAACCTGGCAATTATCGCAACTTTGATCGCAGTTCTTTGA	ATGGTCATTTTTACCACCACAATTGTTGGCACTAACCTGGCAATTATCGCAACTTTGATCGCAGTTCTTTGA			MVIFTTTIVGTNLAIIATLIAVL*	MVIFTTTIVGTNLAIIATLIAVL*			CCTGGTCTTG	GAGAGTAGGG	0	I	0	0	0	0	0
895	677	af	AN4071.1	54.m06996	AO070342000060	1			-341	-321			ATGTCCGCAGCGCAAGAATAA		ATGTCCGCAGCGCAAGAATAA		MSAAQE*		MSAAQE*		GGCGATTGCA	CTAGATTTAG	0	I	0	0	0	0	0
896	677	af	AN4071.1	54.m06996	AO070342000060	1			-250	-239			ATGGTATGGTGA		ATGGTATGGTGA		MVW*		MVW*		GCCAAATTCT	TCCGCTCGGT	0	I	0	0	0	0	0
897	677	af	AN4071.1	54.m06996	AO070342000060	1			-245	-222			ATGGTGATCCGCTCGGTTGCGTGA		ATGGTGATCCGCTCGGTTGCGTGA		MVIRSVA*		MVIRSVA*		ATTCTATGGT	TCCGCTCGCT	0	I	0	0	0	0	0
898	677	ao	AN4071.1	54.m06996	AO070342000060	1					-479	-429	ATGTGTTGTTTACCTACAACTTTACTGACTAATAATTACTTTACTCCATGA			ATGTGTTGTTTACCTACAACTTTACTGACTAATAATTACTTTACTCCATGA	MCCLPTTLLTNNYFTP*			MCCLPTTLLTNNYFTP*	TCAAAATGAA	ATACCAAACA	0	I	0	0	0	0	0
899	677	ao	AN4071.1	54.m06996	AO070342000060	1					-432	-403	ATGAATACCAAACAAAGAGGCGAAATTTAG			ATGAATACCAAACAAAGAGGCGAAATTTAG	MNTKQRGEI*			MNTKQRGEI*	ACTTTACTCC	AGCTAGTTCA	0	I	0	0	0	0	0
900	677	ao	AN4071.1	54.m06996	AO070342000060	1					-393	-301	ATGTTATTTTCTACTGGCTTCTCACGAGACCACGGTGGAACCCAAAGGATGCCGATTATTACTCGGTTTGGGGGTTTGTTTATGATTTTATGA			ATGTTATTTTCTACTGGCTTCTCACGAGACCACGGTGGAACCCAAAGGATGCCGATTATTACTCGGTTTGGGGGTTTGTTTATGATTTTATGA	MLFSTGFSRDHGGTQRMPIITRFGGLFMIL*			MLFSTGFSRDHGGTQRMPIITRFGGLFMIL*	GAGCTAGTTC	CTGCTCATCT	0	I	0	0	0	0	0
901	677	ao	AN4071.1	54.m06996	AO070342000060	1					-345	-301	ATGCCGATTATTACTCGGTTTGGGGGTTTGTTTATGATTTTATGA			ATGCCGATTATTACTCGGTTTGGGGGTTTGTTTATGATTTTATGA	MPIITRFGGLFMIL*			MPIITRFGGLFMIL*	AACCCAAAGG	CTGCTCATCT	0	I	0	0	0	0	0
902	677	ao	AN4071.1	54.m06996	AO070342000060	1					-312	-301	ATGATTTTATGA			ATGATTTTATGA	MIL*			MIL*	GGGTTTGTTT	CTGCTCATCT	0	I	0	0	0	0	0
903	677	ao	AN4071.1	54.m06996	AO070342000060	1					-304	-128	ATGACTGCTCATCTTGCCTTGGCCTGTGGAGTCTCGGTGGTTTTTGTTCTCCACAAACAGCAGTCGAACGTGTCTCATCGTTGTGACAGAACAGGGACCATCGTCAGTGTAAGTAATGCGAATACGAGGTTTCACCTGCGGGCAAAGTCCAGATCGCGTCCTGGAACCATTCCATGA			ATGACTGCTCATCTTGCCTTGGCCTGTGGAGTCTCGGTGGTTTTTGTTCTCCACAAACAGCAGTCGAACGTGTCTCATCGTTGTGACAGAACAGGGACCATCGTCAGTGTAAGTAATGCGAATACGAGGTTTCACCTGCGGGCAAAGTCCAGATCGCGTCCTGGAACCATTCCATGA	MTAHLALACGVSVVFVLHKQQSNVSHRCDRTGTIVSVSNANTRFHLRAKSRSRPGTIP*			MTAHLALACGVSVVFVLHKQQSNVSHRCDRTGTIVSVSNANTRFHLRAKSRSRPGTIP*	TTATGATTTT	GCAAAACAAA	0	I	0	0	0	0	0
904	677	ao	AN4071.1	54.m06996	AO070342000060	1					-189	-16	ATGCGAATACGAGGTTTCACCTGCGGGCAAAGTCCAGATCGCGTCCTGGAACCATTCCATGAGCAAAACAAACCCCAGAGTGGTGTGCTGTCTGTCGAACTAGTCTTTTCAAGTTTTTTTTGATCTTCAATCAATTTCCCTCCGCCCATCATCTGCGGGTTCCCTCCACGTAG			ATGCGAATACGAGGTTTCACCTGCGGGCAAAGTCCAGATCGCGTCCTGGAACCATTCCATGAGCAAAACAAACCCCAGAGTGGTGTGCTGTCTGTCGAACTAGTCTTTTCAAGTTTTTTTTGATCTTCAATCAATTTCCCTCCGCCCATCATCTGCGGGTTCCCTCCACGTAG	MRIRGFTCGQSPDRVLEPFHEQNKPQSGVLSVELVFSSFFLIFNQFPSAHHLRVPST*			MRIRGFTCGQSPDRVLEPFHEQNKPQSGVLSVELVFSSFFLIFNQFPSAHHLRVPST*	AGTGTAAGTA	GGGACAAGAA	0	I	0	0	0	0	0
905	677	ao	AN4071.1	54.m06996	AO070342000060	1					-131	-87	ATGAGCAAAACAAACCCCAGAGTGGTGTGCTGTCTGTCGAACTAG			ATGAGCAAAACAAACCCCAGAGTGGTGTGCTGTCTGTCGAACTAG	MSKTNPRVVCCLSN*			MSKTNPRVVCCLSN*	GAACCATTCC	TCTTTTCAAG	0	I	0	0	0	0	0
920	690	an	AN6119.1	72.m19041	AO070340000085	0	-27	-16					ATGGCTTATTGA	ATGGCTTATTGA			MAY*	MAY*			TGACAGAACC	TACGAGTGTC	1	S	FG01898.1	0	0	YHR132C	YHR132C
923	690	af	AN6119.1	72.m19041	AO070340000085	0			-37	-26			ATGACAGCATAA		ATGACAGCATAA		MTA*		MTA*		GACAGAAACA	TTGTTGTCTC	1	S	FG01898.1	0	0	YHR132C	YHR132C
930	690	ao	AN6119.1	72.m19041	AO070340000085	0					-45	-28	ATGAAGATTTTGGCATAG			ATGAAGATTTTGGCATAG	MKILA*			MKILA*	GGATCTGACA	CTTTTCTGCG	1	S	FG01898.1	0	0	YHR132C	YHR132C
937	694	an	AN3035.1	59.m08982	AO070337000077	0	-60	-40					ATGCCTCCCTCGAGTCTGTGA	ATGCCTCCCTCGAGTCTGTGA			MPPSSL*	MPPSSL*			TATCCCACTG	AAAACACGAG	1	L	0	0	0	0	0
943	694	ao	AN3035.1	59.m08982	AO070337000077	0					-54	-34	ATGTTCAACTTGACGACCTAA			ATGTTCAACTTGACGACCTAA	MFNLTT*			MFNLTT*	CCCGTTTTGG	CGAGGAGCAG	1	L	0	0	0	0	0
955	699	an	AN0476.1	54.m06594	AO070328000164	0	-54	-31					ATGATAACTGTTATTCCAAGGTGA	ATGATAACTGTTATTCCAAGGTGA			MITVIPR*	MITVIPR*			ATCTCCGTCG	ATTTGTTCGT	1	J	0	0	0	0	0
958	700	conserved	AN8076.1	53.m03929	AO070330000034	0	-11		-11		-11		ATGryCyGGTGA	ATGGTCCGGTGA	ATGACCTGGTGA	ATGACCTGGTGA	Mvr*	MVR*	MTW*	MTW*	myyTTywrky	TGTCTkCrCG	1	A	0	0	0	0	0
966	700	af	AN8076.1	53.m03929	AO070330000034	1			-899	-864			ATGTTGCATCTCCATTTTTCATGCTCGGCGAGCTAA		ATGTTGCATCTCCATTTTTCATGCTCGGCGAGCTAA		MLHLHFSCSAS*		MLHLHFSCSAS*		AATTTAATAC	AGTGAAGGAT	0	A	0	0	0	0	0
967	700	af	AN8076.1	53.m03929	AO070330000034	1			-879	-859			ATGCTCGGCGAGCTAAAGTGA		ATGCTCGGCGAGCTAAAGTGA		MLGELK*		MLGELK*		TCCATTTTTC	AGGATCACCT	0	A	0	0	0	0	0
977	709	an	AN7770.1	71.m15812	AO070286000023	0	-57	-19					ATGCCCATCCTACACTTGCCTCATACTCATTCCTTTTGA	ATGCCCATCCTACACTTGCCTCATACTCATTCCTTTTGA			MPILHLPHTHSF*	MPILHLPHTHSF*			TTTCAGGTTT	TTTCTGTGAC	1	R	FG00407.1	MG05138.1	NCU07958.1	0	0
979	710	an	AN3071.1	59.m08927	AO070337000003	0	-47	-18					ATGCCGGTTACGTTTCACCTGAGTTCATGA	ATGCCGGTTACGTTTCACCTGAGTTCATGA			MPVTFHLSS*	MPVTFHLSS*			AAACGCGTGG	TAGATCTCTT	1	B	0	0	0	0	0
1005	733	an	AN8291.1	65.m07469	AO070190000007	1	-327	-292					ATGCCCTCGTTATCCAACGAATTGGCGTATACGTAA	ATGCCCTCGTTATCCAACGAATTGGCGTATACGTAA			MPSLSNELAYT*	MPSLSNELAYT*			CTGTCGACCT	AGAATTTCGC	0	U	0	0	0	0	0
1007	733	an	AN8291.1	65.m07469	AO070190000007	1	-207	-193					ATGGGGTACAATTAA	ATGGGGTACAATTAA			MGYN*	MGYN*			CATTCCACGC	CAAAGCCTCC	0	U	0	0	0	0	0
1008	737	af	AN4615.1	57.m05532	AO070267000032	1			-158	-126			ATGTTCGAAATCTTCTTCACGACTCTGTTCTGA		ATGTTCGAAATCTTCTTCACGACTCTGTTCTGA		MFEIFFTTLF*		MFEIFFTTLF*		TCTGCGGCAC	CCGTCTAAAT	0		0	0	0	0	0
1009	737	af	AN4615.1	57.m05532	AO070267000032	1			-96	-82			ATGCTAGTTTCTTAG		ATGCTAGTTTCTTAG		MLVS*		MLVS*		TGGGCCTTTG	CTTTACCAAG	0		0	0	0	0	0
1010	737	ao	AN4615.1	57.m05532	AO070267000032	1					-231	-79	ATGGGTCGCCGGGACTGCCGGAATTTCGCTTTAATACCTAAAGCCCTAGCTGTGTTCTCCCACTTTCATCGTCTTCGACTCCTCTTCCTTCCTTTTCGCCTTCAACTCTTCCCATTGTATACCCAAACTGGCCAGTTGAACATTTGGGATTGA			ATGGGTCGCCGGGACTGCCGGAATTTCGCTTTAATACCTAAAGCCCTAGCTGTGTTCTCCCACTTTCATCGTCTTCGACTCCTCTTCCTTCCTTTTCGCCTTCAACTCTTCCCATTGTATACCCAAACTGGCCAGTTGAACATTTGGGATTGA	MGRRDCRNFALIPKALAVFSHFHRLRLLFLPFRLQLFPLYTQTGQLNIWD*			MGRRDCRNFALIPKALAVFSHFHRLRLLFLPFRLQLFPLYTQTGQLNIWD*	CCCCGTGAAC	ACCATATTGA	0		0	0	0	0	0
1011	739	an	AN8881.1	56.m02292	AO070293000011	1	-244	-227					ATGCTTTCTAGTTTCTGA	ATGCTTTCTAGTTTCTGA			MLSSF*	MLSSF*			CTTGCAAGCG	GCTCTTCAGG	0	C	0	0	0	0	0
1012	739	an	AN8881.1	56.m02292	AO070293000011	1	-123	-109					ATGCTTTCCCGATAA	ATGCTTTCCCGATAA			MLSR*	MLSR*			CCTTTCTACG	AATCTACCAA	0	C	0	0	0	0	0
1013	739	af	AN8881.1	56.m02292	AO070293000011	1			-450	-433			ATGTGCATTGGCCTTTGA		ATGTGCATTGGCCTTTGA		MCIGL*		MCIGL*		TGAATCAATC	GGCCTAATCC	0	C	0	0	0	0	0
1014	739	af	AN8881.1	56.m02292	AO070293000011	1			-410	-399			ATGCACACTTAG		ATGCACACTTAG		MHT*		MHT*		CTCATAAGCG	TTGCTTCACC	0	C	0	0	0	0	0
1015	739	af	AN8881.1	56.m02292	AO070293000011	1			-292	-278			ATGCTTCACCAATAA		ATGCTTCACCAATAA		MLHQ*		MLHQ*		GACTTATACA	GTCTTACACT	0	C	0	0	0	0	0
1016	739	ao	AN8881.1	56.m02292	AO070293000011	1					-250	-236	ATGCTCACTTGCTGA			ATGCTCACTTGCTGA	MLTC*			MLTC*	TCTGCAGGCG	TTTTATCGCG	0	C	0	0	0	0	0
1017	739	ao	AN8881.1	56.m02292	AO070293000011	1					-99	-85	ATGTCCTGCCGATAG			ATGTCCTGCCGATAG	MSCR*			MSCR*	GAACCATACA	GGTTTCGTCT	0	C	0	0	0	0	0
1051	757	conserved	AN1854.1	58.m08938	AO070292000029	0	-57	-4	-51	-4	-51	-4	ATGsTkywThyvmsvArrrhdrkhhymmkwmmhhvhCwvvmmACkwvrACGTGA	ATGGTGTTTTCCAGAAAGGTTGGATCAAGAACAACTCAACACACGACGACGTGA	ATGGTTCATATACGGAGAGCGAGTACCATACATCGACTGGCCACTTGA	ATGCTTCTTCCGCCCAAAAAAATCCTACTTCACTACCTCACAACTTAA	MvfsrkvgsrttqhTtt*	MVFSRKVGSRTTQHTTT*	MVHIRRASTIHRLAT*	MLLPPKKILLHYLTT*	yvvbGwGrCm	CsrATGACvm	1		0	0	0	0	0
1057	759	ao	AN1712.1	58.m07778	AO070305000028	0					-56	-45	ATGTTGCTATAG			ATGTTGCTATAG	MLL*			MLL*	TCTACTCCGT	ATTCAACATA	1		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
1058	760	an	AN8234.1	53.m03735	AO070310000074	1	-234	-175					ATGCGACCTGATTCAGCTCTGCGGTTAGACCCTTCAGCTGACTTGGGATCTGGTATATAG	ATGCGACCTGATTCAGCTCTGCGGTTAGACCCTTCAGCTGACTTGGGATCTGGTATATAG			MRPDSALRLDPSADLGSGI*	MRPDSALRLDPSADLGSGI*			AGGAGGGTGA	GTACAAACAG	0		0	0	0	0	0
1059	760	ao	AN8234.1	53.m03735	AO070310000074	1					-157	-131	ATGATCTTTGCGATCTCAGCTGACTAG			ATGATCTTTGCGATCTCAGCTGACTAG	MIFAISAD*			MIFAISAD*	CCTCAGTTTC	GTTTTCCTTG	0		0	0	0	0	0
1063	762	an	AN4036.1	54.m06576	AO070328000140	0	-57	-25					ATGCATTTCTTCTTTGCAGGCCGAGGCTATTGA	ATGCATTTCTTCTTTGCAGGCCGAGGCTATTGA			MHFFFAGRGY*	MHFFFAGRGY*			GCCCCTATCT	TTTACGTGCA	1	T	0	0	0	0	0
1066	762	af	AN4036.1	54.m06576	AO070328000140	0			-55	-32			ATGAGATTTTGTGTCTTCTATTAA		ATGAGATTTTGTGTCTTCTATTAA		MRFCVFY*		MRFCVFY*		CTGTTAAGAG	GGAGCGAGCT	1	T	0	0	0	0	0
1070	763	an	AN4707.1	71.m15695	AO070329000169	1	-259	-182					ATGAGTAGCGTCCGTCATGAGCATTACCTAAGAAATGCCTCAAATTCGTTTGATGCTGGCGGTGTCTATAGAGCTTGA	ATGAGTAGCGTCCGTCATGAGCATTACCTAAGAAATGCCTCAAATTCGTTTGATGCTGGCGGTGTCTATAGAGCTTGA			MSSVRHEHYLRNASNSFDAGGVYRA*	MSSVRHEHYLRNASNSFDAGGVYRA*			AGCCAATCCG	AGTGCTGTTT	0	A	0	0	0	0	0
1071	763	an	AN4707.1	71.m15695	AO070329000169	1	-243	-229					ATGAGCATTACCTAA	ATGAGCATTACCTAA			MSIT*	MSIT*			AGCGTCCGTC	GAAATGCCTC	0	A	0	0	0	0	0
1072	763	ao	AN4707.1	71.m15695	AO070329000169	1					-232	-218	ATGAACTTGCAGTAA			ATGAACTTGCAGTAA	MNLQ*			MNLQ*	CCTACAAATA	GTTTATTCAC	0	A	0	0	0	0	0
1073	763	ao	AN4707.1	71.m15695	AO070329000169	1					-78	-25	ATGAGGGCATATTTCTTCCACCCCCATCTCTTGTCCCCTCCAGATTTGCATTGA			ATGAGGGCATATTTCTTCCACCCCCATCTCTTGTCCCCTCCAGATTTGCATTGA	MRAYFFHPHLLSPPDLH*			MRAYFFHPHLLSPPDLH*	TTGCCATGAC	GATCGACTCG	0	A	0	0	0	0	0
1101	786	af	AN1358.1	70.m15731	AO070237000002	1			-541	-494			ATGCGTGACTTGTGGCCCGAGAAAAAAAATTTCTCTCACCATCTTTGA		ATGCGTGACTTGTGGCCCGAGAAAAAAAATTTCTCTCACCATCTTTGA		MRDLWPEKKNFSHHL*		MRDLWPEKKNFSHHL*		ACTTTTGTGG	TATTCTCAAG	0	T	0	0	0	0	0
1102	786	ao	AN1358.1	70.m15731	AO070237000002	1					-58	-20	ATGTGCATTTCTGGCCTACAGTCTTCCCAGAACCTCTAA			ATGTGCATTTCTGGCCTACAGTCTTCCCAGAACCTCTAA	MCISGLQSSQNL*			MCISGLQSSQNL*	TGAGTTGTGC	ATCGTGATCA	1	T	0	0	0	0	0
1107	789	an	AN4501.1	57.m05629	AO070311000054	0	-57	-31					ATGTGCATACTTGGTGACAGCCGCTAA	ATGTGCATACTTGGTGACAGCCGCTAA			MCILGDSR*	MCILGDSR*			TTGCCAACGA	CTTTCGTCTA	1	O	0	0	0	0	0
1144	803	ao	AN5959.1	72.m19175	AO070340000312	1					-82	-71	ATGTTGTGTTAA			ATGTTGTGTTAA	MLC*			MLC*	CAACGATTTG	TTGCTCTGGC	0	E	0	0	NCU00468.1	0	0
1154	806	af	AN8276.1	53.m03684	AO070310000024	0			-46	-26			ATGTCTTTCGTACTGCGCTGA		ATGTCTTTCGTACTGCGCTGA		MSFVLR*		MSFVLR*		TGGTAATTGT	GATCCCTGAA	1	AK	0	0	0	0	0
1155	813	an	AN5660.1	58.m07314	AO070342000252	1	-271	-245					ATGGGCATCGACTCCAAGGGATACTGA	ATGGGCATCGACTCCAAGGGATACTGA			MGIDSKGY*	MGIDSKGY*			GCGACCGTTA	AACACACTAA	0	GO	0	0	0	0	0
1156	813	af	AN5660.1	58.m07314	AO070342000252	1			-643	-575			ATGTTCGAAGGTTTCGACTCCAGTAACCACCCTTATTGCATTCTTTGTCAACGTCCTTGTCGTTTCTAG		ATGTTCGAAGGTTTCGACTCCAGTAACCACCCTTATTGCATTCTTTGTCAACGTCCTTGTCGTTTCTAG		MFEGFDSSNHPYCILCQRPCRF*		MFEGFDSSNHPYCILCQRPCRF*		TTTCTACTGT	ATTTCATCTT	0	GO	0	0	0	0	0
1164	820	an	AN2318.1	71.m15516	AO070323000040	1	-222	-205					ATGATATTTCGCTTCTGA	ATGATATTTCGCTTCTGA			MIFRF*	MIFRF*			GTTTTCGCCA	AACTGAGCCC	0		0	0	0	0	0
1165	820	an	AN2318.1	71.m15516	AO070323000040	1	-103	-74					ATGATCGGGCGCTGCGGCCAATTTGCTTAA	ATGATCGGGCGCTGCGGCCAATTTGCTTAA			MIGRCGQFA*	MIGRCGQFA*			AGGATACAAC	GAGGTTGACC	0		0	0	0	0	0
1166	820	af	AN2318.1	71.m15516	AO070323000040	1			-401	-372			ATGAGAACCGAGTTTGGTTACTTCGCTTGA		ATGAGAACCGAGTTTGGTTACTTCGCTTGA		MRTEFGYFA*		MRTEFGYFA*		AGACACCACC	TAACGCATCT	0		0	0	0	0	0
1167	820	ao	AN2318.1	71.m15516	AO070323000040	1					-161	-141	ATGAGAGAGTCTGCCGACTAA			ATGAGAGAGTCTGCCGACTAA	MRESAD*			MRESAD*	AAGCAGCAAC	ATTATTGGCC	0		0	0	0	0	0
1168	823	an	AN0448.1	54.m06640	AO070338000312	0	-48	-16					ATGGAACGGACAGGGCGACGGTCACTTAACTGA	ATGGAACGGACAGGGCGACGGTCACTTAACTGA			MERTGRRSLN*	MERTGRRSLN*			ACTAGCAGTC	CAATACTCAA	1		0	0	0	0	0
1169	823	af	AN0448.1	54.m06640	AO070338000312	0			-57	-40			ATGCTTGACGAAGTTTGA		ATGCTTGACGAAGTTTGA		MLDEV*		MLDEV*		GCTACAAACC	TCGCAGCTCA	1		0	0	0	0	0
1182	825	an	AN5890.1	72.m19240	AO070245000018	0	-55	-44					ATGTGTCTATGA	ATGTGTCTATGA			MCL*	MCL*			ACCTCCCCTC	CTTTACCCCT	1	E	0	0	0	0	0
1199	847	an	AN4488.1	57.m05643	AO070311000040	0	-35	-3					ATGCCTTTGTTTCATTCAATGTGCCTTGATTGA	ATGCCTTTGTTTCATTCAATGTGCCTTGATTGA			MPLFHSMCLD*	MPLFHSMCLD*			GATCTCGGAT	ATATGGTGGA	1		0	0	0	0	0
1200	847	an	AN4488.1	57.m05643	AO070311000040	0	-17	-3					ATGTGCCTTGATTGA	ATGTGCCTTGATTGA			MCLD*	MCLD*			GTTTCATTCA	ATATGGTGGA	1		0	0	0	0	0
1202	847	af	AN4488.1	57.m05643	AO070311000040	0			-46	-23			ATGGTCTTATTCTACCAGACGTAG		ATGGTCTTATTCTACCAGACGTAG		MVLFYQT*		MVLFYQT*		GGCTACAGAA	ATGTCTCCAT	1		0	0	0	0	0
1215	867	af	AN5191.1	69.m15628	AO070237000021	0			-25	-5			ATGTTGCTTCCTTGTCAATGA		ATGTTGCTTCCTTGTCAATGA		MLLPCQ*		MLLPCQ*		ACTGACATTT	CCTCATGAAC	1	S	0	0	0	0	0
1222	875	an	AN8129.1	53.m03824	AO070266000018	1	-84	-64					ATGTTTTTCCTCTTCTGTTAA	ATGTTTTTCCTCTTCTGTTAA			MFFLFC*	MFFLFC*			TCTCATCAAG	TCGTCTCTTG	0		0	0	0	0	0
1223	875	af	AN8129.1	53.m03824	AO070266000018	1			-239	-225			ATGGTGTATCACTAA		ATGGTGTATCACTAA		MVYH*		MVYH*		GTACTTTTGA	GTTTGCCGTA	0		0	0	0	0	0
1224	875	af	AN8129.1	53.m03824	AO070266000018	1			-158	-129			ATGATTATTACCGGTCAAATCAATCGTTAA		ATGATTATTACCGGTCAAATCAATCGTTAA		MIITGQINR*		MIITGQINR*		TTCTCTAGCT	TTGTGCCCCA	0		0	0	0	0	0
1225	875	ao	AN8129.1	53.m03824	AO070266000018	1					-137	-111	ATGTTCTTCCCCTCAATGAGGTGTTAA			ATGTTCTTCCCCTCAATGAGGTGTTAA	MFFPSMRC*			MFFPSMRC*	CTCTCCCCCA	TTCTTATTCC	0		0	0	0	0	0
1226	875	ao	AN8129.1	53.m03824	AO070266000018	1					-122	-111	ATGAGGTGTTAA			ATGAGGTGTTAA	MRC*			MRC*	CTTCCCCTCA	TTCTTATTCC	0		0	0	0	0	0
1265	899	af	AN6913.1	71.m15219	AO070219000018	0			-32	-3			ATGCTGTCGTCGTTCTTTTCTTCTGGTTAG		ATGCTGTCGTCGTTCTTTTCTTCTGGTTAG		MLSSFFSSG*		MLSSFFSSG*		AAAAGCCTCT	CCATGAATGC	1	O	0	0	0	0	0
1285	910	an	AN7658.1	57.m05422	AO070268000027	1	-34	-5					ATGTGCCAAAGTCACTGGTACAGTTGTTAG	ATGTGCCAAAGTCACTGGTACAGTTGTTAG			MCQSHWYSC*	MCQSHWYSC*			CGCAGGTCGC	AACAATGGCA	1	Z	0	0	0	0	0
1286	910	af	AN7658.1	57.m05422	AO070268000027	1			-639	-604			ATGCCCGCACCAACAACGGAGTTTAACATGAGATGA		ATGCCCGCACCAACAACGGAGTTTAACATGAGATGA		MPAPTTEFNMR*		MPAPTTEFNMR*		CGCTTCCGCA	CAATACCCTT	0	Z	0	0	0	0	0
1287	910	af	AN7658.1	57.m05422	AO070268000027	1			-607	-551			ATGACAATACCCTTTTGGTCGTGTCTTATCAGACATTTCCTATTTTTATTAACTTAG		ATGACAATACCCTTTTGGTCGTGTCTTATCAGACATTTCCTATTTTTATTAACTTAG		MTIPFWSCLIRHFLFLLT*		MTIPFWSCLIRHFLFLLT*		TTAACATGAG	CGACTTGTGA	0	Z	0	0	0	0	0
1288	910	af	AN7658.1	57.m05422	AO070268000027	1			-397	-368			ATGCGCCGAGCTACACCAGAGGCCCTCTAA		ATGCGCCGAGCTACACCAGAGGCCCTCTAA		MRRATPEAL*		MRRATPEAL*		ACTGTGTCTT	AAGATGGCAA	0	Z	0	0	0	0	0
1289	910	ao	AN7658.1	57.m05422	AO070268000027	1					-249	-94	ATGCCCCCTTCAGGTAGCCTGATAGATTGTCAGGTACAGATCCGCTTAGCGGTTGGTCACTCCTTTATATCCAGAGCGAAATCACGACGAATCATTCGTGTCGCACAAGAAAAGACAGCACGTGGAGGTACGTGGCTAAGCCAGTCCCAATCATAG			ATGCCCCCTTCAGGTAGCCTGATAGATTGTCAGGTACAGATCCGCTTAGCGGTTGGTCACTCCTTTATATCCAGAGCGAAATCACGACGAATCATTCGTGTCGCACAAGAAAAGACAGCACGTGGAGGTACGTGGCTAAGCCAGTCCCAATCATAG	MPPSGSLIDCQVQIRLAVGHSFISRAKSRRIIRVAQEKTARGGTWLSQSQS*			MPPSGSLIDCQVQIRLAVGHSFISRAKSRRIIRVAQEKTARGGTWLSQSQS*	CCGCTTCCGC	CTGCCTAAGT	0	Z	0	0	0	0	0
1296	916	an	AN1524.1	55.m03268	AO070334000242	0	-59	-45					ATGAAACGGCATTAA	ATGAAACGGCATTAA			MKRH*	MKRH*			TCCATCACCC	CTCATTCTCA	1	H	FG00417.1	0	0	0	0
1303	917	conserved	AN4670.1	71.m15658	AO070284000036	1	-171	-160	-308	-297	-158	-147	ATGArbCyhTrA	ATGAGGCTCTGA	ATGAGTCCATAA	ATGAACCCTTGA	Mrl*	MRL*	MSP*	MNP*	bhmksArGCC	wyTsssvrsd	0	R	0	0	0	0	0
1304	917	an	AN4670.1	71.m15658	AO070284000036	1	-254	-222					ATGTCAACCGTCTCTTTATTTTTCTTCTCCTGA	ATGTCAACCGTCTCTTTATTTTTCTTCTCCTGA			MSTVSLFFFS*	MSTVSLFFFS*			TTGAACTCTT	CAGCAGATCT	0	R	0	0	0	0	0
1305	917	af	AN4670.1	71.m15658	AO070284000036	1			-418	-380			ATGTGGTGCATGAATCGAAAAGCCTTGTTTCGACTTTAG		ATGTGGTGCATGAATCGAAAAGCCTTGTTTCGACTTTAG		MWCMNRKALFRL*		MWCMNRKALFRL*		TCCTGGCTTC	GGGTTCTACT	0	R	0	0	0	0	0
1306	917	af	AN4670.1	71.m15658	AO070284000036	1			-409	-380			ATGAATCGAAAAGCCTTGTTTCGACTTTAG		ATGAATCGAAAAGCCTTGTTTCGACTTTAG		MNRKALFRL*		MNRKALFRL*		CATGTGGTGC	GGGTTCTACT	0	R	0	0	0	0	0
1307	917	ao	AN4670.1	71.m15658	AO070284000036	1					-123	-112	ATGGGCCATTGA			ATGGGCCATTGA	MGH*			MGH*	CCACCGAGAG	GAAAGAGCTC	0	R	0	0	0	0	0
1314	918	af	AN7240.1	72.m19809	AO070290000007	0			-60	-40			ATGCGGTGGATCTTCCAGTGA		ATGCGGTGGATCTTCCAGTGA		MRWIFQ*		MRWIFQ*		TACATATATA	GAAAGAAGCA	1	G	0	0	0	0	0
1354	935	af	AN0657.1	70.m15789	AO070343000569	1			-110	-99			ATGCTAGTCTGA		ATGCTAGTCTGA		MLV*		MLV*		GGTATCTTTT	CGTGAGATAC	0	U	0	0	0	0	0
1355	936	conserved	AN1082.1	70.m15156	AO070285000082	1	-243	-217	-285	-259	-116	-90	ATGrTyyyhvykyvyTTyrryysyTAA	ATGATTCTAGCGTCCTTCAATTCCTAA	ATGGTCCTCACTCGTTTTAGTCGCTAA	ATGGTTTCTCTTCATTTCGACCGTTAA	MilasFns*	MILASFNS*	MVLTRFSR*	MVSLHFDR*	ysvwGvmyCk	hhwvTCTyTC	0	F	FG05143.1	MG08146.1	0	0	0
1356	936	af	AN1082.1	70.m15156	AO070285000082	1			-293	-255			ATGAATCGATGGTCCTCACTCGTTTTAGTCGCTAATTAG		ATGAATCGATGGTCCTCACTCGTTTTAGTCGCTAATTAG		MNRWSSLVLVAN*		MNRWSSLVLVAN*		GAGGCTTCTG	TCTCTCATTT	0	F	FG05143.1	MG08146.1	0	0	0
1357	939	an	AN8655.1	55.m03152	AO070296000035	1	-253	-206					ATGCGTGCGAAGTTCTTGCTAGTGGTAGTGCCGGTGTTGTCATGTTGA	ATGCGTGCGAAGTTCTTGCTAGTGGTAGTGCCGGTGTTGTCATGTTGA			MRAKFLLVVVPVLSC*	MRAKFLLVVVPVLSC*			TGGAAGGCCA	TGTTTCCCTC	0		0	0	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
1358	939	an	AN8655.1	55.m03152	AO070296000035	1	-212	-141					ATGTTGATGTTTCCCTCCCCTCTTCTCCTTCCCTTCCTCATCGCCCTCTCTTATTGCACCAGCGCGTTCTAG	ATGTTGATGTTTCCCTCCCCTCTTCTCCTTCCCTTCCTCATCGCCCTCTCTTATTGCACCAGCGCGTTCTAG			MLMFPSPLLLPFLIALSYCTSAF*	MLMFPSPLLLPFLIALSYCTSAF*			CGGTGTTGTC	CGCCTCAAGC	0		0	0	0	0	0
1359	939	an	AN8655.1	55.m03152	AO070296000035	1	-206	-141					ATGTTTCCCTCCCCTCTTCTCCTTCCCTTCCTCATCGCCCTCTCTTATTGCACCAGCGCGTTCTAG	ATGTTTCCCTCCCCTCTTCTCCTTCCCTTCCTCATCGCCCTCTCTTATTGCACCAGCGCGTTCTAG			MFPSPLLLPFLIALSYCTSAF*	MFPSPLLLPFLIALSYCTSAF*			TGTCATGTTG	CGCCTCAAGC	0		0	0	0	0	0
1360	939	af	AN8655.1	55.m03152	AO070296000035	1			-475	-365			ATGGTTGATCTCGCTCCTCAGCGAGATTTGAACGTCATCATCATCGTCATATTCTTCTATTGCTCTTTGGTGCATATAGTTTACGAGCTCGTCTTGACATATTCAAGCTGA		ATGGTTGATCTCGCTCCTCAGCGAGATTTGAACGTCATCATCATCGTCATATTCTTCTATTGCTCTTTGGTGCATATAGTTTACGAGCTCGTCTTGACATATTCAAGCTGA		MVDLAPQRDLNVIIIVIFFYCSLVHIVYELVLTYSS*		MVDLAPQRDLNVIIIVIFFYCSLVHIVYELVLTYSS*		CCCTACTTGG	TTCGGTATAA	0		0	0	0	0	0
1361	939	ao	AN8655.1	55.m03152	AO070296000035	1					-264	-205	ATGGCAAAAGTATTCGGGATCTCATCGGGAATTCTCCTACCTTCCTTTGCATTGGAATGA			ATGGCAAAAGTATTCGGGATCTCATCGGGAATTCTCCTACCTTCCTTTGCATTGGAATGA	MAKVFGISSGILLPSFALE*			MAKVFGISSGILLPSFALE*	CTTCAACTCC	AGATTTTATT	0		0	0	0	0	0
1362	939	ao	AN8655.1	55.m03152	AO070296000035	1					-208	-44	ATGAAGATTTTATTTTTATTATCATTTTCTTACATTATTTTTTCTTTTTCCTTCTTCCCCCCCCTCCGTCCTTCCCTGCTACACGCTGGATTCACCATGACTGGCCGTTGCGGGGGTATTTATCATAACCCCTTACATCACCGCAGAGCTATATCCTTTGATTAA			ATGAAGATTTTATTTTTATTATCATTTTCTTACATTATTTTTTCTTTTTCCTTCTTCCCCCCCCTCCGTCCTTCCCTGCTACACGCTGGATTCACCATGACTGGCCGTTGCGGGGGTATTTATCATAACCCCTTACATCACCGCAGAGCTATATCCTTTGATTAA	MKILFLLSFSYIIFSFSFFPPLRPSLLHAGFTMTGRCGGIYHNPLHHRRAISFD*			MKILFLLSFSYIIFSFSFFPPLRPSLLHAGFTMTGRCGGIYHNPLHHRRAISFD*	TTGCATTGGA	CTTTCTCTAT	0		0	0	0	0	0
1363	939	ao	AN8655.1	55.m03152	AO070296000035	1					-112	-44	ATGACTGGCCGTTGCGGGGGTATTTATCATAACCCCTTACATCACCGCAGAGCTATATCCTTTGATTAA			ATGACTGGCCGTTGCGGGGGTATTTATCATAACCCCTTACATCACCGCAGAGCTATATCCTTTGATTAA	MTGRCGGIYHNPLHHRRAISFD*			MTGRCGGIYHNPLHHRRAISFD*	TGGATTCACC	CTTTCTCTAT	0		0	0	0	0	0
1372	952	an	AN1604.1	55.m03110	AO070339000257	0	-38	-18					ATGATTATCAGTCCAATCTGA	ATGATTATCAGTCCAATCTGA			MIISPI*	MIISPI*			TTTCTCCGAC	AGCGAACCTG	1		0	0	0	0	0
1387	958	ao	AN1634.1	58.m09021	AO070299000045	0					-57	-40	ATGGTCATCCATTGGTGA			ATGGTCATCCATTGGTGA	MVIHW*			MVIHW*	AAGCCGCGGC	TTCCGAAACA	1	A	0	0	0	0	0
1390	960	an	AN5694.1	65.m07419	AO070309000110	0	-54	-43					ATGCTTCCGTGA	ATGCTTCCGTGA			MLP*	MLP*			ATTCATATCT	TCCTTCTGGT	1	L	0	0	0	0	0
1406	965	an	AN8604.1	66.m04790	AO070340000151	0	-56	-33					ATGTATAAACGTCCCGGACCGTGA	ATGTATAAACGTCCCGGACCGTGA			MYKRPGP*	MYKRPGP*			CCATCCAGCA	AAATGTGTCC	1	J	0	0	0	YIR042C	0
1430	982	an	AN1564.1	55.m03090	AO070339000288	0	-50	-6					ATGCGTATATGTCTCATACATGACGAGCCAATTTTACCCTCGTGA	ATGCGTATATGTCTCATACATGACGAGCCAATTTTACCCTCGTGA			MRICLIHDEPILPS*	MRICLIHDEPILPS*			TGCAGTTAAT	CGGAAATGCC	1	L	0	0	0	0	0
1431	982	an	AN1564.1	55.m03090	AO070339000288	0	-42	-28					ATGTCTCATACATGA	ATGTCTCATACATGA			MSHT*	MSHT*			ATATGCGTAT	CGAGCCAATT	1	L	0	0	0	0	0
1432	982	af	AN1564.1	55.m03090	AO070339000288	0			-58	-29			ATGAAAGGGATCAATACATCTAGAGGATGA		ATGAAAGGGATCAATACATCTAGAGGATGA		MKGINTSRG*		MKGINTSRG*		ATCAATAAAA	TCCGAGAATC	1	L	0	0	0	0	0
1433	982	af	AN1564.1	55.m03090	AO070339000288	0			-32	-3			ATGATCCGAGAATCCCGTCATCGCCGTTGA		ATGATCCGAGAATCCCGTCATCGCCGTTGA		MIRESRHRR*		MIRESRHRR*		CATCTAGAGG	GGATGCCGAT	1	L	0	0	0	0	0
1434	982	ao	AN1564.1	55.m03090	AO070339000288	0					-35	-3	ATGGTCTCTCGTTTGCATAAGTACAATCTCTAA			ATGGTCTCTCGTTTGCATAAGTACAATCTCTAA	MVSRLHKYNL*			MVSRLHKYNL*	TATAGGAGCA	AGATGCCGAT	1	L	0	0	0	0	0
1460	997	af	AN7258.1	72.m19792	AO070297000014	1			-453	-421			ATGCACATAACTCTCCGGAGCTGCTGCAAGTAA		ATGCACATAACTCTCCGGAGCTGCTGCAAGTAA		MHITLRSCCK*		MHITLRSCCK*		GATCAATTGC	GACATTTTGG	0	R	0	0	0	0	0
1461	997	ao	AN7258.1	72.m19792	AO070297000014	1					-526	-512	ATGACCTGCATATAG			ATGACCTGCATATAG	MTCI*			MTCI*	TTTTCGATAC	GAAGAAACCC	0	R	0	0	0	0	0
1471	1011	af	AN0990.1	70.m15631	AO070318000147	0			-40	-11			ATGAGATTGAGCCCTCAGCTCATACTCTAG		ATGAGATTGAGCCCTCAGCTCATACTCTAG		MRLSPQLIL*		MRLSPQLIL*		TTCCAATGCT	GCCTTACTCC	1	A	0	0	0	0	0
1474	1011	ao	AN0990.1	70.m15631	AO070318000147	0					-39	-13	ATGAATTGTCTTAACAAAACTTGCTAA			ATGAATTGTCTTAACAAAACTTGCTAA	MNCLNKTC*			MNCLNKTC*	CAAAAGATAG	ATACAGTGCA	1	A	0	0	0	0	0
1487	1023	af	AN4871.1	59.m08766	AO070338000089	1			-159	-145			ATGCCCTTTAAATAA		ATGCCCTTTAAATAA		MPFK*		MPFK*		TGGTAACGCC	TTTCTTCTCC	0	G	0	0	0	YDR371W	0
1510	1035	af	AN3747.1	65.m07387	AO070309000075	1			-151	-77			ATGCTTCTGCTATCATCTAGCCGTGGAGGGACCGCACAGAATCTGCTTCGCCTACCTGAACCTGTTTCGAGCTAA		ATGCTTCTGCTATCATCTAGCCGTGGAGGGACCGCACAGAATCTGCTTCGCCTACCTGAACCTGTTTCGAGCTAA		MLLLSSSRGGTAQNLLRLPEPVSS*		MLLLSSSRGGTAQNLLRLPEPVSS*		GGTGCTTTCA	TACGAACCTC	0	O	0	0	0	0	0
1528	1046	conserved	AN1494.1	55.m03004	AO070334000211	0	-60	-13	-60	-13	-60	-13	ATGACGGTrGAkGryCAGskwrGCGCTCGyGGCGCAGTrCACGAyTGA	ATGACGGTGGATGGTCAGCTTGGCGCTCGTGGCGCAGTACACGACTGA	ATGACGGTGGATGGTCAGCGTGGCGCTCGCGGCGCAGTGCACGATTGA	ATGACGGTAGAGGACCAGGGAAGCGCTCGCGGCGCAGTGCACGACTGA	MTVdgQlgARGAVHD*	MTVDGQLGARGAVHD*	MTVDGQRGARGAVHD*	MTVEDQGSARGAVHD*	krrsyTGGAC	GTAyyyTGCG	1	K	0	0	NCU02052.1	0	0
1532	1051	an	AN9467.1	53.m03848	AO070322000047	0	-26	-3					ATGTGGCTTTCTTACCAGTGGTGA	ATGTGGCTTTCTTACCAGTGGTGA			MWLSYQW*	MWLSYQW*			GTCCGAGTAC	CAATGAAGGG	1	T	0	0	0	0	0
1570	1064	an	AN5100.1	54.m06960	AO070291000079	1	-24	-7					ATGGAATGGGTCTTATGA	ATGGAATGGGTCTTATGA			MEWVL*	MEWVL*			ATATTTCTCT	GAAACTATGT	1	DKT	0	0	0	0	0
1585	1083	af	AN2143.1	72.m19698	AO070343000190	0			-57	-40			ATGCAGCTTACTGACTGA		ATGCAGCTTACTGACTGA		MQLTD*		MQLTD*		GGGTCAGCTT	TAATTTATTC	1	D	FG07139.1	MG07070.1	0	0	0
1586	1083	ao	AN2143.1	72.m19698	AO070343000190	0					-47	-33	ATGCATCTACGATGA			ATGCATCTACGATGA	MHLR*			MHLR*	ATGTGAACTA	CTATCTAGTG	1	D	FG07139.1	MG07070.1	0	0	0
1587	1083	ao	AN2143.1	72.m19698	AO070343000190	0					-36	-25	ATGACTATCTAG			ATGACTATCTAG	MTI*			MTI*	TGCATCTACG	TGTTCTAAAT	1	D	FG07139.1	MG07070.1	0	0	0
1619	1104	af	AN5328.1	52.m03790	AO070339000247	0			-54	-10			ATGAGAGGACACACAAGCGTCCCTTCCGAGTCTACAGTCCGATAG		ATGAGAGGACACACAAGCGTCCCTTCCGAGTCTACAGTCCGATAG		MRGHTSVPSESTVR*		MRGHTSVPSESTVR*		TTATGCCAGT	CAAAAGAAGA	1	Q	0	0	0	0	0
1638	1112	an	AN4268.1	65.m07446	AO070343000043	1	-211	-200					ATGAATCATTGA	ATGAATCATTGA			MNH*	MNH*			CAAAGGAAAG	TGCCTACGAG	0	R	0	0	NCU03949.1	0	0
1639	1112	an	AN4268.1	65.m07446	AO070343000043	1	-200	-165					ATGCCTACGAGTACGAGTGATGCAAATACTTATTAG	ATGCCTACGAGTACGAGTGATGCAAATACTTATTAG			MPTSTSDANTY*	MPTSTSDANTY*			TGAATCATTG	ACTGTTCAAC	0	R	0	0	NCU03949.1	0	0
1640	1112	an	AN4268.1	65.m07446	AO070343000043	1	-181	-116					ATGCAAATACTTATTAGACTGTTCAACGAGAAGACGCCCGAACATCTCCGCGCGTGGTTGATTTGA	ATGCAAATACTTATTAGACTGTTCAACGAGAAGACGCCCGAACATCTCCGCGCGTGGTTGATTTGA			MQILIRLFNEKTPEHLRAWLI*	MQILIRLFNEKTPEHLRAWLI*			AGTACGAGTG	CTCAAATGCC	0	R	0	0	NCU03949.1	0	0
1641	1112	an	AN4268.1	65.m07446	AO070343000043	1	-110	-81					ATGCCCCCGCGGCCGAATATTCCCGACTGA	ATGCCCCCGCGGCCGAATATTCCCGACTGA			MPPRPNIPD*	MPPRPNIPD*			TTTGACTCAA	CAATTATATA	0	R	0	0	NCU03949.1	0	0
1642	1112	an	AN4268.1	65.m07446	AO070343000043	1	-71	-42					ATGCTCATCCAATACTACTCGTGTAAATAA	ATGCTCATCCAATACTACTCGTGTAAATAA			MLIQYYSCK*	MLIQYYSCK*			ACAATTATAT	CCCCTCCACA	0	R	0	0	NCU03949.1	0	0
1643	1112	af	AN4268.1	65.m07446	AO070343000043	1			-125	-78			ATGTGGAACAACATCGGGATGGCGGGTGGAAGCGATCCGCAAGTTTAA		ATGTGGAACAACATCGGGATGGCGGGTGGAAGCGATCCGCAAGTTTAA		MWNNIGMAGGSDPQV*		MWNNIGMAGGSDPQV*		AGTCCAGAGG	TATAGTATCT	0	R	0	0	NCU03949.1	0	0
1644	1112	af	AN4268.1	65.m07446	AO070343000043	1			-107	-78			ATGGCGGGTGGAAGCGATCCGCAAGTTTAA		ATGGCGGGTGGAAGCGATCCGCAAGTTTAA		MAGGSDPQV*		MAGGSDPQV*		CAACATCGGG	TATAGTATCT	0	R	0	0	NCU03949.1	0	0
1652	1125	conserved	AN1546.1	55.m03274	AO070339000308	1	-185	-174	-657	-646	-177	-166	ATGkykyTGTGA	ATGTTTCTGTGA	ATGGCTTTGTGA	ATGTCGCTGTGA	MfL*	MFL*	MAL*	MSL*	yArymCAGTG	rATGAsydGG	0	B	0	0	0	0	0
1653	1125	an	AN1546.1	55.m03274	AO070339000308	1	-172	-152					ATGAGTGGGAAGAGAAACTGA	ATGAGTGGGAAGAGAAACTGA			MSGKRN*	MSGKRN*			TTTCTGTGAG	TCCGTGCGAA	0	B	0	0	0	0	0
1654	1125	af	AN1546.1	55.m03274	AO070339000308	1			-644	-621			ATGACCAGGAGCAAGATCACTTGA		ATGACCAGGAGCAAGATCACTTGA		MTRSKIT*		MTRSKIT*		GCTTTGTGAA	GAGTGCAAAA	0	B	0	0	0	0	0
1655	1125	ao	AN1546.1	55.m03274	AO070339000308	1					-164	-123	ATGACTTGGAGAAAGAGTACTCAACCGTGCGAAAAGGAATAA			ATGACTTGGAGAAAGAGTACTCAACCGTGCGAAAAGGAATAA	MTWRKSTQPCEKE*			MTWRKSTQPCEKE*	TCGCTGTGAA	CAGATCAAGA	0	B	0	0	0	0	0
1660	1127	af	AN0847.1	70.m15446	AO070216000006	0			-52	-32			ATGGTGCTCAGCTTTGTCTGA		ATGGTGCTCAGCTTTGTCTGA		MVLSFV*		MVLSFV*		CTCTTCCTCC	CCTCTATTAT	1	O	0	MG06648.1	NCU09485.1	0	0
1674	1133	af	AN3539.1	56.m02549	AO070331000053	1			-287	-270			ATGGTTAAAATGCCTTGA		ATGGTTAAAATGCCTTGA		MVKMP*		MVKMP*		GTTTGAAGCC	TCACCCTGGA	0		0	0	0	0	0
1675	1133	af	AN3539.1	56.m02549	AO070331000053	1			-221	-207			ATGAACCCTTACTAG		ATGAACCCTTACTAG		MNPY*		MNPY*		CCACCAATGC	TTTGTACTCG	0		0	0	0	0	0
1676	1133	ao	AN3539.1	56.m02549	AO070331000053	1					-256	-191	ATGGTATGTTCAGCTAGGCAAATGGCAAGGAAGCTTGGCGCATGTCCAAGTAATATTAAAACATAA			ATGGTATGTTCAGCTAGGCAAATGGCAAGGAAGCTTGGCGCATGTCCAAGTAATATTAAAACATAA	MVCSARQMARKLGACPSNIKT*			MVCSARQMARKLGACPSNIKT*	GCACTTGTCA	TAATATTGTA	0		0	0	0	0	0
1677	1133	ao	AN3539.1	56.m02549	AO070331000053	1					-251	-240	ATGTTCAGCTAG			ATGTTCAGCTAG	MFS*			MFS*	TGTCAATGGT	GCAAATGGCA	0		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
1678	1133	ao	AN3539.1	56.m02549	AO070331000053	1					-235	-191	ATGGCAAGGAAGCTTGGCGCATGTCCAAGTAATATTAAAACATAA			ATGGCAAGGAAGCTTGGCGCATGTCCAAGTAATATTAAAACATAA	MARKLGACPSNIKT*			MARKLGACPSNIKT*	AGCTAGGCAA	TAATATTGTA	0		0	0	0	0	0
1679	1133	ao	AN3539.1	56.m02549	AO070331000053	1					-215	-204	ATGTCCAAGTAA			ATGTCCAAGTAA	MSK*			MSK*	AGCTTGGCGC	TATTAAAACA	0		0	0	0	0	0
1691	1144	af	AN6528.1	62.m03116	AO070270000028	1			-399	-364			ATGCATCACATTTCAGCACCTACAGTCTCAGGATAA		ATGCATCACATTTCAGCACCTACAGTCTCAGGATAA		MHHISAPTVSG*		MHHISAPTVSG*		AGCTGGCCTG	TCATCAATCG	0	O	0	0	0	0	0
1697	1152	an	AN4517.1	57.m05611	AO070321000123	1	-518	-489					ATGCTCGTTGCATTCTATCCTCTTGGGTAG	ATGCTCGTTGCATTCTATCCTCTTGGGTAG			MLVAFYPLG*	MLVAFYPLG*			CTTCCTTCTC	TCTTTGCTTC	0	P	0	0	NCU00010.1	0	0
1698	1152	an	AN4517.1	57.m05611	AO070321000123	1	-68	-54					ATGGAAATACTTTAA	ATGGAAATACTTTAA			MEIL*	MEIL*			TCGTCGTGCC	TCGACGGTCT	0	P	0	0	NCU00010.1	0	0
1699	1152	af	AN4517.1	57.m05611	AO070321000123	1			-665	-642			ATGGCCCAATGCTTCACCATATAG		ATGGCCCAATGCTTCACCATATAG		MAQCFTI*		MAQCFTI*		TATTTCTTGT	TAGGGGTTTT	0	P	0	0	NCU00010.1	0	0
1700	1152	af	AN4517.1	57.m05611	AO070321000123	1			-657	-595			ATGCTTCACCATATAGTAGGGGTTTTTCCTTCATCCCTGTTCGTGTCCTCGTCCCACATATAG		ATGCTTCACCATATAGTAGGGGTTTTTCCTTCATCCCTGTTCGTGTCCTCGTCCCACATATAG		MLHHIVGVFPSSLFVSSSHI*		MLHHIVGVFPSSLFVSSSHI*		GTATGGCCCA	CTTTTTAATC	0	P	0	0	NCU00010.1	0	0
1701	1152	af	AN4517.1	57.m05611	AO070321000123	1			-251	-237			ATGGAAACATTTTGA		ATGGAAACATTTTGA		METF*		METF*		CAATTGTGTC	TGAACGTGTG	0	P	0	0	NCU00010.1	0	0
1702	1152	af	AN4517.1	57.m05611	AO070321000123	1			-237	-226			ATGAACGTGTGA		ATGAACGTGTGA		MNV*		MNV*		AAACATTTTG	TTGTGTCGGA	0	P	0	0	NCU00010.1	0	0
1703	1152	ao	AN4517.1	57.m05611	AO070321000123	1					-63	-34	ATGGAAATACCCTATGGTGGTTTGATCTGA			ATGGAAATACCCTATGGTGGTTTGATCTGA	MEIPYGGLI*			MEIPYGGLI*	TTGTCGTGTC	GCTTGTTGGA	0	P	0	0	NCU00010.1	0	0
1704	1152	ao	AN4517.1	57.m05611	AO070321000123	1					-50	-39	ATGGTGGTTTGA			ATGGTGGTTTGA	MVV*			MVV*	GAAATACCCT	TCTGAGCTTG	1	P	0	0	NCU00010.1	0	0
1715	1165	an	AN0414.1	54.m06661	AO070338000256	0	-41	-12					ATGAGACAAAGATTGTTTTGCATTTTCTAA	ATGAGACAAAGATTGTTTTGCATTTTCTAA			MRQRLFCIF*	MRQRLFCIF*			TTATTGATTG	AGAAGTATAC	1	Z	0	0	0	0	0
1718	1165	ao	AN0414.1	54.m06661	AO070338000256	0					-57	-19	ATGCCTTATATTGCACCATACTCACTTCAGATCGGTTAG			ATGCCTTATATTGCACCATACTCACTTCAGATCGGTTAG	MPYIAPYSLQIG*			MPYIAPYSLQIG*	ATAAGGTCTT	ACACTGTTCA	1	Z	0	0	0	0	0
1733	1173	an	AN9065.1	66.m04528	AO070332000209	0	-59	-9					ATGTGCCAGCCAGTACATCATACGATTCCCAACTCAGAGCCATACTTTTAA	ATGTGCCAGCCAGTACATCATACGATTCCCAACTCAGAGCCATACTTTTAA			MCQPVHHTIPNSEPYF*	MCQPVHHTIPNSEPYF*			GGCGAAATAA	CCAACGAAAT	1		0	0	0	0	0
1745	1176	af	AN2336.1	65.m07340	AO070343000082	0			-51	-28			ATGGCCAAACTGCTCAGCAAGTGA		ATGGCCAAACTGCTCAGCAAGTGA		MAKLLSK*		MAKLLSK*		AGTATAAAAG	CAATGGGTAA	1	M	0	0	0	0	0
1751	1177	ao	AN7587.1	72.m19609	AO070343000300	0					-14	-3	ATGGCGAGCTGA			ATGGCGAGCTGA	MAS*			MAS*	TGGAACGAGT	GAATGCAGGT	1	S	0	0	0	0	0
1752	1179	ao	AN8870.1	71.m16010	AO070271000001	1					-397	-386	ATGCTTAATTAG			ATGCTTAATTAG	MLN*			MLN*	TCATTGTCAT	AGATTCACGC	0	J	FG07480.1	0	NCU01452.1	0	0
1775	1186	ao	AN1722.1	58.m07789	AO070305000037	0					-51	-37	ATGAGGGTTCAATGA			ATGAGGGTTCAATGA	MRVQ*			MRVQ*	ACCTCGTTCT	CAGTTCAAAC	1	H	0	0	0	0	0
1776	1186	ao	AN1722.1	58.m07789	AO070305000037	0					-40	-14	ATGACAGTTCAAACAGATCCTTCTTAA			ATGACAGTTCAAACAGATCCTTCTTAA	MTVQTDPS*			MTVQTDPS*	TGAGGGTTCA	TGTCCTTCTC	1	H	0	0	0	0	0
1777	1189	an	AN0772.1	70.m15377	AO070316000067	0	-51	-25					ATGGCGTTATCACTACTTCAGCTCTAG	ATGGCGTTATCACTACTTCAGCTCTAG			MALSLLQL*	MALSLLQL*			AGCACTGAAA	ATCTGGTTTG	1	IQR	0	0	0	0	0
1782	1189	af	AN0772.1	70.m15377	AO070316000067	0			-57	-25			ATGTGCTACTGTTACCAAAATTTAGCACTCTGA		ATGTGCTACTGTTACCAAAATTTAGCACTCTGA		MCYCYQNLAL*		MCYCYQNLAL*		AATATGGCCC	GTTGAATCTG	1	IQR	0	0	0	0	0
1821	1215	an	AN6725.1	65.m07245	AO070339000169	0	-42	-28					ATGCGGCCACCCTGA	ATGCGGCCACCCTGA			MRPP*	MRPP*			TATTCATACT	ATCGACAGTA	1	A	0	MG07164.1	NCU06763.1	0	0
1827	1215	ao	AN6725.1	65.m07245	AO070339000169	0					-40	-29	ATGACCGCATAA			ATGACCGCATAA	MTA*			MTA*	TCACTGTGAC	TCGCGAGAGA	1	A	0	MG07164.1	NCU06763.1	0	0
1858	1224	an	AN8565.1	71.m15702	AO070311000007	0	-45	-31					ATGCGGCGGCCATGA	ATGCGGCGGCCATGA			MRRP*	MRRP*			TGCAAATGCA	TCCGTTCACA	1	E	0	0	0	0	0
1859	1224	an	AN8565.1	71.m15702	AO070311000007	0	-34	-2					ATGATCCGTTCACATCGCCCTCGTGCCTGCTGA	ATGATCCGTTCACATCGCCCTCGTGCCTGCTGA			MIRSHRPRAC*	MIRSHRPRAC*			TGCGGCGGCC	AATGAGTCCG	1	E	0	0	0	0	0
1866	1231	an	AN4162.1	58.m07363	AO070342000192	1	-41	-15					ATGAGTCGATATATATTTGCAAGTTAA	ATGAGTCGATATATATTTGCAAGTTAA			MSRYIFAS*	MSRYIFAS*			GGATCCCTTG	AGTTCGCTTC	1		0	0	0	0	0
1892	1240	an	AN4861.1	59.m09110	AO070329000146	1	-122	-105					ATGCTTCATGCACCTTGA	ATGCTTCATGCACCTTGA			MLHAP*	MLHAP*			TGAAACTCCC	TTCCAACATA	0	K	0	0	0	0	0
1905	1243	an	AN2884.1	59.m08731	AO070338000130	0	-25	-8					ATGGCCTGTCATATGTGA	ATGGCCTGTCATATGTGA			MACHM*	MACHM*			CCGGCCTTAC	CCTCACGATG	1		0	0	0	0	0
1907	1243	ao	AN2884.1	59.m08731	AO070338000130	0					-27	-16	ATGGCTCATTAG			ATGGCTCATTAG	MAH*			MAH*	ATGTATATGT	AGGTAAACGT	1		0	0	0	0	0
1947	1264	af	AN5588.1	58.m07509	AO070328000021	1			-246	-220			ATGGCAGTCATCCCGATCAAAGATTGA		ATGGCAGTCATCCCGATCAAAGATTGA		MAVIPIKD*		MAVIPIKD*		CTCGTTGGCG	GCTACCATCT	0	O	FG01475.1	0	0	0	0
1948	1264	ao	AN5588.1	58.m07509	AO070328000021	1					-113	-87	ATGGCATTTGCGTTCACTAAGAGATAA			ATGGCATTTGCGTTCACTAAGAGATAA	MAFAFTKR*			MAFAFTKR*	CTGATCAGTG	TCTCGTCTCA	0	O	FG01475.1	0	0	0	0
1958	1276	an	AN7470.1	57.m05874	AO070287000056	0	-60	-19					ATGATCTACCCATCAATTGACCTTTACATCCAGCTCAATTGA	ATGATCTACCCATCAATTGACCTTTACATCCAGCTCAATTGA			MIYPSIDLYIQLN*	MIYPSIDLYIQLN*			GCGTGAACGA	GATAGTCTTT	1		0	0	0	0	0
1963	1276	af	AN7470.1	57.m05874	AO070287000056	1			-159	-79			ATGCCAGCAGTATTTGCCAGTGAGGATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAA		ATGCCAGCAGTATTTGCCAGTGAGGATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAA		MPAVFASEDVESFSEYTANLQRSKIL*		MPAVFASEDVESFSEYTANLQRSKIL*		TATTATATAA	TTATCAGCAT	0		0	0	0	0	0
1964	1276	af	AN7470.1	57.m05874	AO070287000056	1			-134	-66			ATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAATTATCAGCATTGA		ATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAATTATCAGCATTGA		MSSRSASTLLIYKGQKYYNYQH*		MSSRSASTLLIYKGQKYYNYQH*		GCCAGTGAGG	GATTTCCCAA	0		0	0	0	0	0
1970	1279	an	AN0905.1	70.m15514	AO070320000080	0	-33	-22					ATGATGGCCTAG	ATGATGGCCTAG			MMA*	MMA*			CTCGTATTAT	AGCACTTTGG	1	DO	0	0	0	0	0
1982	1283	af	AN2447.1	69.m15212	AO070264000030	1			-37	-14			ATGCGATTAAGCGGGACCGCCTGA		ATGCGATTAAGCGGGACCGCCTGA		MRLSGTA*		MRLSGTA*		CTTGGCGCAG	TCGCCCGGCC	1		FG01481.1	MG03241.1	0	0	0
1983	1287	conserved	AN6642.1	62.m03239	AO070295000022	1	-101	-54	-86	-39	-139	-92	ATGGACTCkCAyTssyTkGwdGAyACrATmTAyATGrAGCCTCCyTAr	ATGGACTCGCATTCCTTGGTTGACACGATCTATATGGAGCCTCCCTAA	ATGGACTCTCACTCGCTTGAAGATACGATATACATGAAGCCTCCTTAG	ATGGACTCGCATTGCCTGGAGGATACAATCTATATGGAGCCTCCCTAA	MDSHsLvDTIYMePP*	MDSHSLVDTIYMEPP*	MDSHSLEDTIYMKPP*	MDSHCLEDTIYMEPP*	sTbbwkGTGy	rrdmmmbsmh	0	P	0	0	0	0	0
1984	1287	conserved	AN6642.1	62.m03239	AO070295000022	1	-68	-54	-53	-39	-106	-92	ATGrAGCCTCCyTAr	ATGGAGCCTCCCTAA	ATGAAGCCTCCTTAG	ATGGAGCCTCCCTAA	MePP*	MEPP*	MKPP*	MEPP*	yACrATmTAy	rrdmmmbsmh	0	P	0	0	0	0	0
1992	1294	an	AN5549.1	69.m14939	AO070341000115	1	-300	-226					ATGACAAAATGGACCAAATCCTGGATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGA	ATGACAAAATGGACCAAATCCTGGATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGA			MTKWTKSWMKWQRYLALSLQRRWA*	MTKWTKSWMKWQRYLALSLQRRWA*			GAGGAGTGGA	AAATTCCATC	0	P	0	0	0	0	0
1993	1294	an	AN5549.1	69.m14939	AO070341000115	1	-292	-176					ATGGACCAAATCCTGGATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGAAAATTCCATCAGATTCCGCAGGATTGACAGGCCCCAGCAGCCCAATTTGA	ATGGACCAAATCCTGGATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGAAAATTCCATCAGATTCCGCAGGATTGACAGGCCCCAGCAGCCCAATTTGA			MDQILDEMAEIPCSLFTATLGLKIPSDSAGLTGPSSPI*	MDQILDEMAEIPCSLFTATLGLKIPSDSAGLTGPSSPI*			GAATGACAAA	TCCTACCTAG	0	P	0	0	0	0	0
1994	1294	an	AN5549.1	69.m14939	AO070341000115	1	-276	-226					ATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGA	ATGAAATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGA			MKWQRYLALSLQRRWA*	MKWQRYLALSLQRRWA*			CAAATCCTGG	AAATTCCATC	0	P	0	0	0	0	0
1995	1294	an	AN5549.1	69.m14939	AO070341000115	1	-271	-176					ATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGAAAATTCCATCAGATTCCGCAGGATTGACAGGCCCCAGCAGCCCAATTTGA	ATGGCAGAGATACCTTGCTCTCTCTTTACAGCGACGCTGGGCCTGAAAATTCCATCAGATTCCGCAGGATTGACAGGCCCCAGCAGCCCAATTTGA			MAEIPCSLFTATLGLKIPSDSAGLTGPSSPI*	MAEIPCSLFTATLGLKIPSDSAGLTGPSSPI*			CCTGGATGAA	TCCTACCTAG	0	P	0	0	0	0	0
1996	1295	an	AN4401.1	58.m07925	AO070261000045	1	-275	-255					ATGACGCCGCTGGGAATGTAG	ATGACGCCGCTGGGAATGTAG			MTPLGM*	MTPLGM*			TTGCCGGCCA	CTGTTATCTT	0	E	0	0	0	0	0
1997	1295	an	AN4401.1	58.m07925	AO070261000045	1	-238	-137					ATGAGTCAGTTCTGTCAGTGTCCCTCTTTCACCCAGATTTTTTTGGAGGCCGAAATCGCCCCTCGATTCCGCCCCGCCGACGGGACCGGGACCCTACCTTGA	ATGAGTCAGTTCTGTCAGTGTCCCTCTTTCACCCAGATTTTTTTGGAGGCCGAAATCGCCCCTCGATTCCGCCCCGCCGACGGGACCGGGACCCTACCTTGA			MSQFCQCPSFTQIFLEAEIAPRFRPADGTGTLP*	MSQFCQCPSFTQIFLEAEIAPRFRPADGTGTLP*			TCTTATCGAG	CATTTTAAAA	0	E	0	0	0	0	0
1998	1295	af	AN4401.1	58.m07925	AO070261000045	1			-240	-226			ATGAAATGTGGTTAG		ATGAAATGTGGTTAG		MKCG*		MKCG*		AAAAACTCCG	TGTAGGGACG	0	E	0	0	0	0	0
1999	1295	af	AN4401.1	58.m07925	AO070261000045	1			-235	-221			ATGTGGTTAGTGTAG		ATGTGGTTAGTGTAG		MWLV*		MWLV*		CTCCGATGAA	GGACGGCAGT	0	E	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
2000	1295	af	AN4401.1	58.m07925	AO070261000045	1			-191	-114			ATGAGTCAAAGATTTGTGGCCGAAATCGCCTCTCGGTCATTGTTCTGCCCCGCCAGTCTGGCTCCAGCTTTCCTTTAA		ATGAGTCAAAGATTTGTGGCCGAAATCGCCTCTCGGTCATTGTTCTGCCCCGCCAGTCTGGCTCCAGCTTTCCTTTAA		MSQRFVAEIASRSLFCPASLAPAFL*		MSQRFVAEIASRSLFCPASLAPAFL*		TATCGGGGGT	AATTTCCCTC	0	E	0	0	0	0	0
2015	1300	ao	AN3123.1	59.m08613	AO070303000024	0					-38	-9	ATGTCTGGAATCTTCCTGCAGCCTGAATAA			ATGTCTGGAATCTTCCTGCAGCCTGAATAA	MSGIFLQPE*			MSGIFLQPE*	CTTGTTACCG	ACTGCAACAT	1	PT	FG04030.1	0	NCU04512.1	0	0
2020	1301	ao	AN8251.1	53.m03716	AO070310000057	0					-59	-48	ATGACCCGCTGA			ATGACCCGCTGA	MTR*			MTR*	ACCCGGGGAC	CTTCTACCCA	1		0	0	0	0	0
2039	1311	af	AN8363.1	52.m04104	AO070274000030	1			-165	-61			ATGTTCCGCATAGGACAGGACGTTCACGCGATGTGGATCCCCTCGGCAGACGTCTTAGTCTGGTCTCCTGAAAATCTCCCTTCTGCTTTCACAAGCCACAGGTAA		ATGTTCCGCATAGGACAGGACGTTCACGCGATGTGGATCCCCTCGGCAGACGTCTTAGTCTGGTCTCCTGAAAATCTCCCTTCTGCTTTCACAAGCCACAGGTAA		MFRIGQDVHAMWIPSADVLVWSPENLPSAFTSHR*		MFRIGQDVHAMWIPSADVLVWSPENLPSAFTSHR*		ATCAACAAGG	CCAACAACTC	0	R	0	0	0	0	0
2040	1311	af	AN8363.1	52.m04104	AO070274000030	1			-135	-61			ATGTGGATCCCCTCGGCAGACGTCTTAGTCTGGTCTCCTGAAAATCTCCCTTCTGCTTTCACAAGCCACAGGTAA		ATGTGGATCCCCTCGGCAGACGTCTTAGTCTGGTCTCCTGAAAATCTCCCTTCTGCTTTCACAAGCCACAGGTAA		MWIPSADVLVWSPENLPSAFTSHR*		MWIPSADVLVWSPENLPSAFTSHR*		CGTTCACGCG	CCAACAACTC	0	R	0	0	0	0	0
2042	1311	ao	AN8363.1	52.m04104	AO070274000030	1					-146	-108	ATGAAAGAATATCCCGAGCGAAGCAGCCGTCACATGTAA			ATGAAAGAATATCCCGAGCGAAGCAGCCGTCACATGTAA	MKEYPERSSRHM*			MKEYPERSSRHM*	GGTGCCCTGT	TGTGAGAAAA	0	R	0	0	0	0	0
2043	1321	af	AN1451.1	55.m02953	AO070302000016	1			-225	-193			ATGAGACTTGTCTATCTTCGTCCAAATCTATAG		ATGAGACTTGTCTATCTTCGTCCAAATCTATAG		MRLVYLRPNL*		MRLVYLRPNL*		GGAGACATCT	CCACCGGGTT	0		FG00185.1	0	NCU00537.1	0	0
2044	1321	ao	AN1451.1	55.m02953	AO070302000016	1					-294	-232	ATGCACGGCTTGAGTCAGTGGACTTGTAATTTGATCCAGTTTTCGTTATTGTCTTCAGCTTGA			ATGCACGGCTTGAGTCAGTGGACTTGTAATTTGATCCAGTTTTCGTTATTGTCTTCAGCTTGA	MHGLSQWTCNLIQFSLLSSA*			MHGLSQWTCNLIQFSLLSSA*	TCGAATCTGT	CTTAATTGAG	0		FG00185.1	0	NCU00537.1	0	0
2055	1323	an	AN4495.1	57.m05636	AO070311000047	0	-47	-36					ATGATATTATAA	ATGATATTATAA			MIL*	MIL*			AACATTGAAC	TAAATATCAT	1	L	0	0	0	0	0
2074	1331	an	AN4270.1	65.m07444	AO070277000018	0	-20						ATGCCGGTGCATCTTAACTAA	ATGCCGGTGCATCTTAACTAA			MPVHLN*	MPVHLN*			TCTGCTGTTG	TGTATTCTTC	1	TU	0	0	0	0	0
2075	1331	af	AN4270.1	65.m07444	AO070277000018	0			-14				ATGCGAGCGCTGTGA		ATGCGAGCGCTGTGA		MRAL*		MRAL*		TCCCACTCTA	TGTACTCGTC	1	TU	0	0	0	0	0
2078	1331	ao	AN4270.1	65.m07444	AO070277000018	0					-43	-32	ATGGCTGCTTGA			ATGGCTGCTTGA	MAA*			MAA*	TCTTTCTTAT	TTGTTTTTCT	1	TU	0	0	0	0	0
2079	1331	ao	AN4270.1	65.m07444	AO070277000018	0					-20		ATGCAAGGGCTGTGTTGGTAA			ATGCAAGGGCTGTGTTGGTAA	MQGLCW*			MQGLCW*	TGTTTTTCTA	TGTACTCTTC	1	TU	0	0	0	0	0
2081	1333	an	AN7481.1	57.m05862	AO070287000038	0	-48	-28					ATGTTCATTGCGTCTATCTGA	ATGTTCATTGCGTCTATCTGA			MFIASI*	MFIASI*			AACATCCTTT	CTGGGCTGAA	1	D	0	0	0	0	0
2089	1341	an	AN4878.1	59.m09408	AO070338000082	1	-287	-252					ATGATTGCGCGATTGCCGGCTTCATTTATCATCTAA	ATGATTGCGCGATTGCCGGCTTCATTTATCATCTAA			MIARLPASFII*	MIARLPASFII*			CGGTCGTACA	TCTATACCTA	0	K	0	0	0	0	0
2090	1341	af	AN4878.1	59.m09408	AO070338000082	1			-413	-354			ATGCTGAGTCTAGCGGCGATTCGTCGATCACCGTTCTTGTCAACCGTCAATTCCGCTTGA		ATGCTGAGTCTAGCGGCGATTCGTCGATCACCGTTCTTGTCAACCGTCAATTCCGCTTGA		MLSLAAIRRSPFLSTVNSA*		MLSLAAIRRSPFLSTVNSA*		CCTGATCCGA	CTCTTTAGCT	0	K	0	0	0	0	0
2091	1341	ao	AN4878.1	59.m09408	AO070338000082	1					-105	-25	ATGTTATCTTTATTGGCACTCCCTTCTTCACCTCTTCCCAGCTTTCAGCCCCCATCCCTGGGCCTACCGTCTGGGTACTAA			ATGTTATCTTTATTGGCACTCCCTTCTTCACCTCTTCCCAGCTTTCAGCCCCCATCCCTGGGCCTACCGTCTGGGTACTAA	MLSLLALPSSPLPSFQPPSLGLPSGY*			MLSLLALPSSPLPSFQPPSLGLPSGY*	CTTGAGCCGG	ATACACGCCC	0	K	0	0	0	0	0
2117	1358	an	AN4915.1	59.m09401	AO070338000028	1	-320	-303					ATGTTGCAAGGCATCTAA	ATGTTGCAAGGCATCTAA			MLQGI*	MLQGI*			TGCCTTACCT	AATTCTGCAG	0	U	FG05501.1	MG06241.1	NCU06410.1	0	YOR089C
2118	1359	an	AN3600.1	58.m07398	AO070342000153	1	-182	-141					ATGCTTTCATTGTGCTCGCGTGGTGGGTCTGCAGGACAATGA	ATGCTTTCATTGTGCTCGCGTGGTGGGTCTGCAGGACAATGA			MLSLCSRGGSAGQ*	MLSLCSRGGSAGQ*			TGAGCGATAC	ATATCCCTGC	0		0	0	0	0	0
2119	1359	an	AN3600.1	58.m07398	AO070342000153	1	-144	-103					ATGAATATCCCTGCCAACGGTTCAGGCGATTCTGTGAATTGA	ATGAATATCCCTGCCAACGGTTCAGGCGATTCTGTGAATTGA			MNIPANGSGDSVN*	MNIPANGSGDSVN*			CTGCAGGACA	GCTTGACGAT	0		0	0	0	0	0
2120	1359	an	AN3600.1	58.m07398	AO070342000153	1	-74	-54					ATGCGCACAGGTTCTCGGTGA	ATGCGCACAGGTTCTCGGTGA			MRTGSR*	MRTGSR*			ACCCCTTGCC	CCTACTTTTA	0		0	0	0	0	0
2121	1359	af	AN3600.1	58.m07398	AO070342000153	1			-65	-27			ATGGCTCATTGCAGAATTTCCTCATTTTTCGACTGGTGA		ATGGCTCATTGCAGAATTTCCTCATTTTTCGACTGGTGA		MAHCRISSFFDW*		MAHCRISSFFDW*		CGGAAAGCAT	AGAAATAGAG	0		0	0	0	0	0
2122	1359	ao	AN3600.1	58.m07398	AO070342000153	1					-225	-193	ATGGATCATTCTCTGCGTCGGACTGCGTCCTGA			ATGGATCATTCTCTGCGTCGGACTGCGTCCTGA	MDHSLRRTAS*			MDHSLRRTAS*	TCTCTCTTCC	CATAATTCTT	0		0	0	0	0	0
2123	1359	ao	AN3600.1	58.m07398	AO070342000153	1					-67	-23	ATGCAAACCATCCCTGGCAGATCCACCTTAACGCTCGACCGATGA			ATGCAAACCATCCCTGGCAGATCCACCTTAACGCTCGACCGATGA	MQTIPGRSTLTLDR*			MQTIPGRSTLTLDR*	GTGCACGAGA	GAACAGGGAT	0		0	0	0	0	0
2124	1359	ao	AN3600.1	58.m07398	AO070342000153	1					-26	-3	ATGAGAACAGGGATTTTGTTTTAG			ATGAGAACAGGGATTTTGTTTTAG	MRTGILF*			MRTGILF*	CGCTCGACCG	AAATGGATAT	1		0	0	0	0	0
2125	1364	af	AN1090.1	70.m15142	AO070285000059	1			-368	-357			ATGATACTCTGA		ATGATACTCTGA		MIL*		MIL*		GAGCTCTTCA	CCGAATAAAT	0	R	0	0	0	0	0
2126	1364	af	AN1090.1	70.m15142	AO070285000059	1			-333	-247			ATGTATCTTATGCATCATCTGTTTCGATCAATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		ATGTATCTTATGCATCATCTGTTTCGATCAATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		MYLMHHLFRSMHSRRQCLSSTQRRDTQT*		MYLMHHLFRSMHSRRQCLSSTQRRDTQT*		GTGTCCTTAT	GAGAACCATA	0	R	0	0	0	0	0
2127	1364	af	AN1090.1	70.m15142	AO070285000059	1			-324	-247			ATGCATCATCTGTTTCGATCAATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		ATGCATCATCTGTTTCGATCAATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		MHHLFRSMHSRRQCLSSTQRRDTQT*		MHHLFRSMHSRRQCLSSTQRRDTQT*		TATGTATCTT	GAGAACCATA	0	R	0	0	0	0	0
2128	1364	af	AN1090.1	70.m15142	AO070285000059	1			-303	-247			ATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		ATGCATAGTCGTCGTCAGTGTTTGTCCTCGACTCAGCGACGAGATACCCAAACATGA		MHSRRQCLSSTQRRDTQT*		MHSRRQCLSSTQRRDTQT*		GTTTCGATCA	GAGAACCATA	0	R	0	0	0	0	0
2129	1364	af	AN1090.1	70.m15142	AO070285000059	1			-250	-236			ATGAGAGAACCATAG		ATGAGAGAACCATAG		MREP*		MREP*		ATACCCAAAC	ACATGCTGCC	0	R	0	0	0	0	0
2130	1364	af	AN1090.1	70.m15142	AO070285000059	1			-233	-213			ATGCTGCCAGAAACAAACTAA		ATGCTGCCAGAAACAAACTAA		MLPETN*		MLPETN*		AACCATAGAC	CTTTGTCGCA	0	R	0	0	0	0	0
2131	1364	ao	AN1090.1	70.m15142	AO070285000059	1					-350	-183	ATGATATTCTTTGTCCTTTCGTGCAGAACGTCAAAATTGCCTACGATCTTACATCGTCATGATTGCGCTCCTCCTGGCCCTTTCATTGGTCTCATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAA			ATGATATTCTTTGTCCTTTCGTGCAGAACGTCAAAATTGCCTACGATCTTACATCGTCATGATTGCGCTCCTCCTGGCCCTTTCATTGGTCTCATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAA	MIFFVLSCRTSKLPTILHRHDCAPPGPFIGLMWSQKPVVPTQVPAWRECYWSCCV*			MIFFVLSCRTSKLPTILHRHDCAPPGPFIGLMWSQKPVVPTQVPAWRECYWSCCV*	GTGGTAGGTA	TCTATCTCCC	0	R	0	0	0	0	0
2132	1364	ao	AN1090.1	70.m15142	AO070285000059	1					-292	-116	ATGATTGCGCTCCTCCTGGCCCTTTCATTGGTCTCATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAATCTATCTCCCGTCTCATTCCAGGTTTTCAGGCACCCCTGTTACAACTTGCGTCAGCTGCGGACCTGA			ATGATTGCGCTCCTCCTGGCCCTTTCATTGGTCTCATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAATCTATCTCCCGTCTCATTCCAGGTTTTCAGGCACCCCTGTTACAACTTGCGTCAGCTGCGGACCTGA	MIALLLALSLVSCGLRNQWYLLRYLPGGSAIGVAAFNLSPVSFQVFRHPCYNLRQLRT*			MIALLLALSLVSCGLRNQWYLLRYLPGGSAIGVAAFNLSPVSFQVFRHPCYNLRQLRT*	TTACATCGTC	CTTGATCAAC	0	R	0	0	0	0	0
2133	1364	ao	AN1090.1	70.m15142	AO070285000059	1					-257	-183	ATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAA			ATGTGGTCTCAGAAACCAGTGGTACCTACTCAGGTACCTGCCTGGCGGGAGTGCTATTGGAGTTGCTGCGTTTAA	MWSQKPVVPTQVPAWRECYWSCCV*			MWSQKPVVPTQVPAWRECYWSCCV*	CATTGGTCTC	TCTATCTCCC	0	R	0	0	0	0	0
2149	1381	af	AN4390.1	58.m07933	AO070261000036	0			-50	-27			ATGACATTACTGACCTTGCTTTGA		ATGACATTACTGACCTTGCTTTGA		MTLLTLL*		MTLLTLL*		AAGCCTGCTA	GAATCTAGTA	1		0	0	0	0	0
2152	1381	ao	AN4390.1	58.m07933	AO070261000036	0					-47	-3	ATGTCCAACGTGCTAACAGTATCTCCATTAGAAGAAATCACATAA			ATGTCCAACGTGCTAACAGTATCTCCATTAGAAGAAATCACATAA	MSNVLTVSPLEEIT*			MSNVLTVSPLEEIT*	GACCTTGATC	CAATGTTCAT	1		0	0	0	0	0
2171	1387	af	AN1832.1	58.m07674	AO070318000085	0			-50	-21			ATGCAAGAGTCACGCACCATCCAACCTTGA		ATGCAAGAGTCACGCACCATCCAACCTTGA		MQESRTIQP*		MQESRTIQP*		TCTGGCTACA	AAAAGAAAAT	1		0	0	0	0	0
2179	1396	conserved	AN5452.1	69.m15743	AO070239000031	1	-105	-85	-103	-83	-106	-86	ATGGGAdTrvTwyyAywhTrA	ATGGGAGTACTTTTATTATAA	ATGGGATTGATTCTATTCTGA	ATGGGAATGGTATCACATTAA	MGvlll*	MGVLLL*	MGLILF*	MGMVSH*	mTCTGCAGCA	AGwCAmmywd	0	A	0	MG06457.1	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
2181	1396	ao	AN5452.1	69.m15743	AO070239000031	1					-100	-86	ATGGTATCACATTAA			ATGGTATCACATTAA	MVSH*			MVSH*	AGCAATGGGA	AGTCAACTTT	0	A	0	MG06457.1	0	0	0
2185	1399	an	AN6524.1	62.m03113	AO070270000023	0	-58	-23					ATGGGCTCTAAGTTATTGAAACTGTGCCGCCCGTAG	ATGGGCTCTAAGTTATTGAAACTGTGCCGCCCGTAG			MGSKLLKLCRP*	MGSKLLKLCRP*			AGGTCGGTAG	GATTACGAAT	1		0	0	0	0	0
2194	1400	af	AN4674.1	71.m15664	AO070284000032	1			-251	-222			ATGCTCTTAGCGTCTTATAGCTTGCCGTAA		ATGCTCTTAGCGTCTTATAGCTTGCCGTAA		MLLASYSLP*		MLLASYSLP*		CACGGAGCAG	ACGCTTCGTC	0	GO	0	0	0	0	0
2197	1400	ao	AN4674.1	71.m15664	AO070284000032	1					-380	-345	ATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAA			ATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAA	MCSWSVADRRQ*			MCSWSVADRRQ*	GCCCATTTCC	TTAACTGCCA	0	GO	0	0	0	0	0
2200	1407	af	AN5983.1	72.m19943	AO070340000297	0			-24	-4			ATGCTTGCCCGAAGTCGATGA		ATGCTTGCCCGAAGTCGATGA		MLARSR*		MLARSR*		GTCTATTTTG	ACCATGACGC	1	S	0	0	0	0	0
2201	1407	ao	AN5983.1	72.m19943	AO070340000297	0					-54	-43	ATGTATATCTAA			ATGTATATCTAA	MYI*			MYI*	GCATCTCACA	ATACATGTGC	1	S	0	0	0	0	0
2202	1407	ao	AN5983.1	72.m19943	AO070340000297	0					-38	-27	ATGTGCCCTTAG			ATGTGCCCTTAG	MCP*			MCP*	ATCTAAATAC	ACTTTTTGAA	1	S	0	0	0	0	0
2203	1408	conserved	AN5966.1	72.m19965	AO070340000323	1	-100	-83	-175	-158	-77	-60	ATGAwCGGGATACCGTGA	ATGATCGGGATACCGTGA	ATGAACGGGATACCGTGA	ATGATCGGGATACCGTGA	MiGIP*	MIGIP*	MNGIP*	MIGIP*	TyTGyrATCr	AmyyydysyC	0	R	0	0	0	0	0
2211	1421	an	AN6730.1	65.m07240	AO070339000174	0	-34	-17					ATGATACGTCGAGATTGA	ATGATACGTCGAGATTGA			MIRRD*	MIRRD*			AGGCTCCCGC	TCGTTCAACG	1	F	0	0	0	0	0
2213	1433	af	AN5725.1	54.m06845	AO070324000126	0			-23	-3			ATGTCTCTTGTCTCGTGTTGA		ATGTCTCTTGTCTCGTGTTGA		MSLVSC*		MSLVSC*		TTCATTGACT	TCATGATGCT	1	M	0	0	NCU06779.1	YNL048W	YNL048W
2215	1433	ao	AN5725.1	54.m06845	AO070324000126	0					-43	-29	ATGAGACTACAATAG			ATGAGACTACAATAG	MRLQ*			MRLQ*	CAACGTACGG	TGATGTCCGT	1	M	0	0	NCU06779.1	YNL048W	YNL048W
2216	1433	ao	AN5725.1	54.m06845	AO070324000126	0					-26	-6	ATGTCCGTTGTCTTTTGTTAG			ATGTCCGTTGTCTTTTGTTAG	MSVVFC*			MSVVFC*	TACAATAGTG	CCATGATGCT	1	M	0	0	NCU06779.1	YNL048W	YNL048W
2217	1436	an	AN1510.1	55.m03022	AO070334000228	1	-146	-132					ATGGCCACGTTCTGA	ATGGCCACGTTCTGA			MATF*	MATF*			TTGGACGTTT	TTAGCCACTC	0	OU	0	0	0	0	0
2218	1436	af	AN1510.1	55.m03022	AO070334000228	1			-227	-186			ATGGTCTTCCAGTCTCCTTGGCTCCGTCTTTGCTTTGATTGA		ATGGTCTTCCAGTCTCCTTGGCTCCGTCTTTGCTTTGATTGA		MVFQSPWLRLCFD*		MVFQSPWLRLCFD*		TTGCTATTGC	TAATCCTCGA	0	OU	0	0	0	0	0
2219	1436	af	AN1510.1	55.m03022	AO070334000228	1			-85	-74			ATGCATTTCTGA		ATGCATTTCTGA		MHF*		MHF*		TTACTAGTAT	GAACTTGATC	0	OU	0	0	0	0	0
2220	1436	ao	AN1510.1	55.m03022	AO070334000228	1					-289	-248	ATGATTTTCTCGGTCGCATTGGATTTTGTTGCGTCTTTTTAA			ATGATTTTCTCGGTCGCATTGGATTTTGTTGCGTCTTTTTA	MIFSVALDFVASF*			MIFSVALDFVASF*	TCTCTTTTTT	TTTTTTCGTT	0	OU	0	0	0	0	0
2221	1436	ao	AN1510.1	55.m03022	AO070334000228	1					-166	-140	ATGAGTTTGTTTAGACCCTTGATCTGA			ATGAGTTTGTTTAGACCCTTGATCTGA	MSLFRPLI*			MSLFRPLI*	ACAGAAGATC	TTGACAATTT	0	OU	0	0	0	0	0
2235	1441	an	AN8445.1	52.m03678	AO070341000302	0	-51	-25					ATGAAACAAGGGCGATCAGGGCTTTAG	ATGAAACAAGGGCGATCAGGGCTTTAG			MKQGRSGL*	MKQGRSGL*			CCCTTCCTGC	GACACGTCCG	1	R	0	0	0	0	0
2281	1457	af	AN7418.1	57.m05460	AO070323000154	0			-54	-34			ATGCCTACTCTTCTTTATTGA		ATGCCTACTCTTCTTTATTGA		MPTLLY*		MPTLLY*		TTGCAAGCAC	TATGCAAACT	1	HC	0	0	0	0	0
2287	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-55	-35	ATGTTACGCTTCCGGCCATAG			ATGTTACGCTTCCGGCCATAG	MLRFRP*			MLRFRP*	GGCACTTTAA	CTCAGATAAG	1	HC	0	0	0	0	0
2312	1473	an	AN5307.1	70.m15393	AO070316000053	0	-36	-19					ATGCAGGTGAAAGGATGA	ATGCAGGTGAAAGGATGA			MQVKG*	MQVKG*			CAGCGGAAGG	ATCAAGCCAG	1	C	0	0	0	0	0
2322	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-57	-16	ATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA			ATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA	MSVSATPPGEAGS*			MSVSATPPGEAGS*	TTCGATCAAT	AATAATATAC	1	C	0	0	0	0	0
2332	1488	an	AN1097.1	70.m15134	AO070285000045	1	-173	-162					ATGGCTCGATAA	ATGGCTCGATAA			MAR*	MAR*			CCGATAGTCG	GATACTCCAC	0	T	0	0	0	0	0
2333	1488	an	AN1097.1	70.m15134	AO070285000045	1	-49	-29					ATGACTTATAACTCTTTCTAA	ATGACTTATAACTCTTTCTAA			MTYNSF*	MTYNSF*			TACATACTTC	AGGCCTTCTT	1	T	0	0	0	0	0
2359	1510	an	AN7759.1	71.m15791	AO070286000006	1	-129	-13					ATGCTCTCCGCATCTCTAATCTTTGCTCTCCCCTCCTTCACTGCTTCTGAACATCTCGCTACACCCGACCCAATGCTCTGCCCACGGCGAATCACCACTCATCAGCCTTGGGCTTGA	ATGCTCTCCGCATCTCTAATCTTTGCTCTCCCCTCCTTCACTGCTTCTGAACATCTCGCTACACCCGACCCAATGCTCTGCCCACGGCGAATCACCACTCATCAGCCTTGGGCTTGA			MLSASLIFALPSFTASEHLATPDPMLCPRRITTHQPWA*	MLSASLIFALPSFTASEHLATPDPMLCPRRITTHQPWA*			TGAACATCTA	ACCCCGCTCA	0	WV	0	0	0	0	0
2360	1510	an	AN7759.1	71.m15791	AO070286000006	1	-57	-13					ATGCTCTGCCCACGGCGAATCACCACTCATCAGCCTTGGGCTTGA	ATGCTCTGCCCACGGCGAATCACCACTCATCAGCCTTGGGCTTGA			MLCPRRITTHQPWA*	MLCPRRITTHQPWA*			ACCCGACCCA	ACCCCGCTCA	1	WV	0	0	0	0	0
2386	1523	ao	AN3015.1	59.m09005	AO070337000100	0					-49	-20	ATGAGTATACAGAACCTACACACTCACTAG			ATGAGTATACAGAACCTACACACTCACTAG	MSIQNLHTH*			MSIQNLHTH*	GTGTTTATAT	ACTCCCTCAA	1	S	0	0	0	0	0
2390	1529	an	AN9384.1	54.m06360	AO070253000015	0	-59	-30					ATGCCCAGGACCAACGGACTGACTGACTGA	ATGCCCAGGACCAACGGACTGACTGACTGA			MPRTNGLTD*	MPRTNGLTD*			ATTCGCCAGG	CTGACGAACT	1	QI	0	0	0	0	0
2396	1533	an	AN2053.1	58.m07641	AO070292000020	1	-76	-50					ATGGGCCTAGCTCTGTTACACTCCTAA	ATGGGCCTAGCTCTGTTACACTCCTAA			MGLALLHS*	MGLALLHS*			ACTTTTGATA	TTACAATTCG	0	F	0	0	NCU00356.1	0	0
2400	1533	af	AN2053.1	58.m07641	AO070292000020	1			-115	-53			ATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGATTGCCGCCGTTTGA		ATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGATTGCCGCCGTTTGA		MVGSGSCKPRNVNHDLIAAV*		MVGSGSCKPRNVNHDLIAAV*		CCTTGGCTTC	TTTATCCACT	0	F	0	0	NCU00356.1	0	0
2401	1533	af	AN2053.1	58.m07641	AO070292000020	1			-84	-67			ATGTTAACCATGACTTGA		ATGTTAACCATGACTTGA		MLTMT*		MLTMT*		AAGCCACGAA	TTGCCGCCGT	0	F	0	0	NCU00356.1	0	0
2403	1533	ao	AN2053.1	58.m07641	AO070292000020	0					-54	-10	ATGTCCCGTTTCTACCTCCAGGAAGGGACTTATATCACACTATAA			ATGTCCCGTTTCTACCTCCAGGAAGGGACTTATATCACACTATAA	MSRFYLQEGTYITL*			MSRFYLQEGTYITL*	GTCCCATTTT	TCGAAAGCAA	1	F	0	0	NCU00356.1	0	0
2410	1534	af	AN2534.1	59.m08439	AO070300000048	0			-50	-27			ATGCCTCTTTTCTCACCATTGTGA		ATGCCTCTTTTCTCACCATTGTGA		MPLFSPL*		MPLFSPL*		CCCTCCTACC	AATTGACTGG	1	G	0	0	0	0	0
2412	1536	af	AN7710.1	71.m15734	AO070325000117	1			-233	-90			ATGTTTGCCACTTGCGTCCTACTTTATCCCGGTCCAATCCACTCCAACGATTCGTTCCCTTTCCGCTTAACCCAAACAGCTCCCATATTTGCCTTTCTTTACGGCTACTTTTACCCACTTCCTCTCCCTTCATCTCTCCTCTAG		ATGTTTGCCACTTGCGTCCTACTTTATCCCGGTCCAATCCACTCCAACGATTCGTTCCCTTTCCGCTTAACCCAAACAGCTCCCATATTTGCCTTTCTTTACGGCTACTTTTACCCACTTCCTCTCCCTTCATCTCTCCTCTAG		MFATCVLLYPGPIHSNDSFPFRLTQTAPIFAFLYGYFYPLPLPSSLL*		MFATCVLLYPGPIHSNDSFPFRLTQTAPIFAFLYGYFYPLPLPSSLL*		CAGCCCGTTG	CAGACTTCTT	0	R	FG05132.1	MG08166.1	0	0	0
2438	1561	ao	AN2060.1	57.m05964	AO070328000072	0					-52	-32	ATGAGAGAAGTATGCTTCTGA			ATGAGAGAAGTATGCTTCTGA	MREVCF*			MREVCF*	TGTCTTTGTT	CTAGACTTGT	1		0	0	0	0	0
2465	1603	an	AN5720.1	54.m07022	AO070324000130	1	-92	-18					ATGTTGGAAATCTCTGCGCGGCGCTCTCGCACCAGCTATTATCTCATGCGACCTTTTCAATACTCATATAATTGA	ATGTTGGAAATCTCTGCGCGGCGCTCTCGCACCAGCTATTATCTCATGCGACCTTTTCAATACTCATATAATTGA			MLEISARRSRTSYYLMRPFQYSYN*	MLEISARRSRTSYYLMRPFQYSYN*			CAAGTTTCAA	GTGTCTACCC	0	S	0	MG02855.1	0	YOL092W	0
2466	1603	an	AN5720.1	54.m07022	AO070324000130	1	-47	-18					ATGCGACCTTTTCAATACTCATATAATTGA	ATGCGACCTTTTCAATACTCATATAATTGA			MRPFQYSYN*	MRPFQYSYN*			CTATTATCTC	GTGTCTACCC	1	S	0	MG02855.1	0	YOL092W	0
2467	1603	af	AN5720.1	54.m07022	AO070324000130	1			-274	-245			ATGCGGCCACCAAACGGGAAGAGCTGCTAA		ATGCGGCCACCAAACGGGAAGAGCTGCTAA		MRPPNGKSC*		MRPPNGKSC*		CTCTTATCGG	GAGCTGCTAT	0	S	0	MG02855.1	0	YOL092W	0
2468	1603	af	AN5720.1	54.m07022	AO070324000130	1			-236	-129			ATGAATAGAGTCGCAGCAAGGAAAATCTTCATTTTTCGCTTTGACAACTTTTTTTGGTTTCAGATAGCCGAAAGTCGAAAAGCTGGATGTACTTTGGCTAGTGACTAG		ATGAATAGAGTCGCAGCAAGGAAAATCTTCATTTTTCGCTTTGACAACTTTTTTTGGTTTCAGATAGCCGAAAGTCGAAAAGCTGGATGTACTTTGGCTAGTGACTAG		MNRVAARKIFIFRFDNFFWFQIAESRKAGCTLASD*		MNRVAARKIFIFRFDNFFWFQIAESRKAGCTLASD*		AAGAGCTGCT	AACTCGTTCC	0	S	0	MG02855.1	0	YOL092W	0
2469	1603	af	AN5720.1	54.m07022	AO070324000130	1			-150	-136			ATGTACTTTGGCTAG		ATGTACTTTGGCTAG		MYFG*		MYFG*		GAAAAGCTGG	TGACTAGAAC	0	S	0	MG02855.1	0	YOL092W	0
2470	1603	ao	AN5720.1	54.m07022	AO070324000130	1					-338	-246	ATGCCCCCTCACAATTCTCGCAGCTTAGTAAAACATTCTCCGAGAGGCAGCGGTTCCGCCCCGTAACTATAATAAAATCCTACTTCGACCGTGA			ATGCCCCCTCACAATTCTCGCAGCTTAGTAAAACATTCTCCGAGAGGCAGCGGTTCCGCCCGTAACTATAATAAAATCCTACTTCGACCGTGA	MPPHNSRSLVKHSPRGSGSARNYNKILLRP*			MPPHNSRSLVKHSPRGSGSARNYNKILLRP*	GGTGAAAAAG	CACTTGCTTC	0	S	0	MG02855.1	0	YOL092W	0
2471	1603	ao	AN5720.1	54.m07022	AO070324000130	1					-231	-142	ATGCGTGGGATTGTCCATATCTTGTTCGATGAGAACACTATCGGGAAAATTTCAATCATTAGATTGGATTTCGCCACTGCACTATATTAG			ATGCGTGGGATTGTCCATATCTTGTTCGATGAGAACACTATCGGGAAAATTTCAATCATTAGATTGGATTTCGCCACTGCACTATATTAG	MRGIVHILFDENTIGKISIIRLDFATALY*			MRGIVHILFDENTIGKISIIRLDFATALY*	TGCTTCTGCC	TGACTCATGT	0	S	0	MG02855.1	0	YOL092W	0
2472	1603	ao	AN5720.1	54.m07022	AO070324000130	1					-203	-93	ATGAGAACACTATCGGGAAAATTTCAATCATTAGATTGGATTTCGCCACTGCACTATATTAGTGACTCATGTGCTATCACGTTACATCCGAGCGCTTCGCGAGATAGCTAA			ATGAGAACACTATCGGGAAAATTTCAATCATTAGATTGGATTTCGCCACTGCACTATATTAGTGACTCATGTGCTATCACGTTACATCCGAGCGCTTCGCGAGATAGCTAA	MRTLSGKFQSLDWISPLHYISDSCAITLHPSASRDS*			MRTLSGKFQSLDWISPLHYISDSCAITLHPSASRDS*	ATCTTGTTCG	CTTTTTCCTT	0	S	0	MG02855.1	0	YOL092W	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
2473	1603	ao	AN5720.1	54.m07022	AO070324000130	1					-135	-97	ATGTGCTATCACGTTACATCCGAGCGCTTCGCGAGATAG			ATGTGCTATCACGTTACATCCGAGCGCTTCGCGAGATAG	MCYHVTSERFAR*			MCYHVTSERFAR*	TTAGTGACTC	CTAACTTTTT	0	S	0	MG02855.1	0	YOL092W	0
2479	1613	an	AN3460.1	59.m09482	AO070265000037	1	-71	-51					ATGCCTGCCCCGCAAATTTAG	ATGCCTGCCCCGCAAATTTAG			MPAPQI*	MPAPQI*			TTTCGATTCT	TATGACCGGT	0	A	0	0	NCU02402.1	0	0
2480	1613	af	AN3460.1	59.m09482	AO070265000037	1			-226	-161			ATGGAGATAAATTTCGGACTTAAGAAGGTAGCTAACAAGACACGCGGCGACGCGACTCAGCAATAG		ATGGAGATAAATTTCGGACTTAAGAAGGTAGCTAACAAGACACGCGGCGACGCGACTCAGCAATAG		MEINFGLKKVANKTRGDATQQ*		MEINFGLKKVANKTRGDATQQ*		ACTTGACCCG	ATGCTAATTA	0	A	0	0	NCU02402.1	0	0
2481	1613	af	AN3460.1	59.m09482	AO070265000037	1			-160	-47			ATGCTAATTATTGCGCTGAGCTCCATATTAAGTCTCACCTTGGGATTCTTTCAGGCGCAGCCGTGTCCCGTTTTTGCAAATGCTCTGCAGCGGGAAGACTTGACGCATCGCTAG		ATGCTAATTATTGCGCTGAGCTCCATATTAAGTCTCACCTTGGGATTCTTTCAGGCGCAGCCGTGTCCCGTTTTTGCAAATGCTCTGCAGCGGGAAGACTTGACGCATCGCTAG		MLIIALSSILSLTLGFFQAQPCPVFANALQREDLTHR*		MLIIALSSILSLTLGFFQAQPCPVFANALQREDLTHR*		TCAGCAATAG	GCTAGCATGA	0	A	0	0	NCU02402.1	0	0
2482	1613	af	AN3460.1	59.m09482	AO070265000037	1			-81	-58			ATGCTCTGCAGCGGGAAGACTTGA		ATGCTCTGCAGCGGGAAGACTTGA		MLCSGKT*		MLCSGKT*		GTTTTTGCAA	CGCATCGCTA	0	A	0	0	NCU02402.1	0	0
2483	1613	af	AN3460.1	59.m09482	AO070265000037	1			-40	-23			ATGATTACAATTTCATGA		ATGATTACAATTTCATGA		MITIS*		MITIS*		CTAGGCTAGC	CCAAAAACTT	1	A	0	0	NCU02402.1	0	0
2484	1613	af	AN3460.1	59.m09482	AO070265000037	0			-26				ATGACCAAAAACTTATCCGCTCCTTGA		ATGACCAAAAACTTATCCGCTCCTTGA		MTKNLSAP*		MTKNLSAP*		TTACAATTTC	TGATGGCGTC	1	A	0	0	NCU02402.1	0	0
2485	1613	ao	AN3460.1	59.m09482	AO070265000037	1					-136	-89	ATGGGTTTTTATTTGACCTTGATCGGAAGGCCGCTAGATCCTGTGTAG			ATGGGTTTTTATTTGACCTTGATCGGAAGGCCGCTAGATCCTGTGTAG	MGFYLTLIGRPLDPV*			MGFYLTLIGRPLDPV*	TTCGCATCCA	TGGCTCTTGA	0	A	0	0	NCU02402.1	0	0
2486	1613	ao	AN3460.1	59.m09482	AO070265000037	1					-45	-19	ATGAATAATTACTGTTCATTTGTATGA			ATGAATAATTACTGTTCATTTGTATGA	MNNYCSFV*			MNNYCSFV*	TACTTCTAGT	CCCGGTCGCA	1	A	0	0	NCU02402.1	0	0
2487	1615	an	AN5114.1	54.m06909	AO070291000065	1	-234	-193					ATGGCTGATACAGTGAAGAAACATTGTTATTCTTGCTTCTAA	ATGGCTGATACAGTGAAGAAACATTGTTATTCTTGCTTCTAA			MADTVKKHCYSCF*	MADTVKKHCYSCF*			TCCGCCTTCG	TTCAGTCTCG	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2488	1615	an	AN5114.1	54.m06909	AO070291000065	1	-174	-130					ATGCACCATTGTACGAGTTTGTCTTTTCGAACCAGCCAAATTTAA	ATGCACCATTGTACGAGTTTGTCTTTTCGAACCAGCCAAATTTAA			MHHCTSLSFRTSQI*	MHHCTSLSFRTSQI*			CGTCACATGC	GTGGAACGCG	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2489	1615	af	AN5114.1	54.m06909	AO070291000065	1			-310	-278			ATGCAGGGGAACACCCTGTGCCTCGTGCACTAA		ATGCAGGGGAACACCCTGTGCCTCGTGCACTAA		MQGNTLCLVH*		MQGNTLCLVH*		GACGTATCTC	TAGGATGTTA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2490	1615	af	AN5114.1	54.m06909	AO070291000065	1			-273	-235			ATGTTAAGGGAGGGGAGTTTAAGCGTTGGGCAAGAGTAA		ATGTTAAGGGAGGGGAGTTTAAGCGTTGGGCAAGAGTAA		MLREGSLSVGQE*		MLREGSLSVGQE*		CACTAATAGG	AGATGATGGT	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2491	1615	af	AN5114.1	54.m06909	AO070291000065	1			-232	-92			ATGATGGTTACTTGGGAGGGGAATTACATTGGTATTCATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGACGCGTCCAAACCCTCCCAAAGTGCAGTCGCCAGGCCATACAAGCATGTGA		ATGATGGTTACTTGGGAGGGGAATTACATTGGTATTCATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGACGCGTCCAAACCCTCCCAAAGTGCAGTCGCCAGGCCATACAAGCATGTGA		MMVTWEGNYIGIHDGRRTTRGSAASPERFLTRPNPPKVQSPGHTSM*		MMVTWEGNYIGIHDGRRTTRGSAASPERFLTRPNPPKVQSPGHTSM*		AAGAGTAAAG	GTGTCTTCCA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2492	1615	af	AN5114.1	54.m06909	AO070291000065	1			-229	-92			ATGGTTACTTGGGAGGGGAATTACATTGGTATTCATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGACGCGTCCAAACCCTCCCAAAGTGCAGTCGCCAGGCCATACAAGCATGTGA		ATGGTTACTTGGGAGGGGAATTACATTGGTATTCATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGACGCGTCCAAACCCTCCCAAAGTGCAGTCGCCAGGCCATACAAGCATGTGA		MVTWEGNYIGIHDGRRTTRGSAASPERFLTRPNPPKVQSPGHTSM*		MVTWEGNYIGIHDGRRTTRGSAASPERFLTRPNPPKVQSPGHTSM*		AGTAAAGATG	GTGTCTTCCA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2493	1615	af	AN5114.1	54.m06909	AO070291000065	1			-195	-142			ATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGA		ATGATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGA		MMGGEQRAEVPLVRNGS*		MMGGEQRAEVPLVRNGS*		ATTGGTATTC	CGCGTCCAAA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2494	1615	af	AN5114.1	54.m06909	AO070291000065	1			-192	-142			ATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGA		ATGGGCGGCGAACAACGCGCGGAAGTGCCGCTAGTCCGGAACGGTTCTTGA		MGGEQRAEVPLVRNGS*		MGGEQRAEVPLVRNGS*		GGTATTCATG	CGCGTCCAAA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2495	1615	ao	AN5114.1	54.m06909	AO070291000065	1					-129	-94	ATGGTTTGGGACGCGTCTAGAGCTCAACCTTCATAG			ATGGTTTGGGACGCGTCTAGAGCTCAACCTTCATAG	MVWDASRAQPS*			MVWDASRAQPS*	CTAGTCCGGA	CTTACAACTA	0	L	FG00834.1	MG06959.1	0	YNL072W	0
2497	1617	an	AN1488.1	55.m02995	AO070334000200	1	-82	-44					ATGCTTGCGTTGAAGCGACTACGGCCTTCCACATCTTGA	ATGCTTGCGTTGAAGCGACTACGGCCTTCCACATCTTGA			MLALKRLRPSTS*	MLALKRLRPSTS*			ACATCTGTCA	CGTCGTCAAT	0	O	0	0	0	0	0
2498	1617	af	AN1488.1	55.m02995	AO070334000200	1			-91	-74			ATGCCTTATTGCACTTGA		ATGCCTTATTGCACTTGA		MPYCT*		MPYCT*		AGACTTTCTA	CTTTGGCTGC	0	O	0	0	0	0	0
2499	1617	ao	AN1488.1	55.m02995	AO070334000200	1					-79	-68	ATGTCCCTCTGA			ATGTCCCTCTGA	MSL*			MSL*	GCCGCTGTCG	CAACCTTACT	0	O	0	0	0	0	0
2539	1634	an	AN3759.1	65.m07497	AO070309000045	0	-59	-33					ATGGCATGCTTCTTCAGCACAACTTAA	ATGGCATGCTTCTTCAGCACAACTTAA			MACFFSTT*	MACFFSTT*			CGTTCGCCGC	TCAGGGAACC	1	O	0	0	0	0	0
2548	1635	af	AN6894.1	71.m16019	AO070314000028	0			-60	-25			ATGAAATCAACTACACAGATTGATTTGGCCAAATAA		ATGAAATCAACTACACAGATTGATTTGGCCAAATAA		MKSTTQIDLAK*		MKSTTQIDLAK*		GCTGAAGATC	ATCCTAACTC	1	O	FG05403.1	0	NCU00181.1	0	0
2589	1659	af	AN3620.1	58.m07407	AO070342000132	0			-43	-5			ATGCGTTTCTCCGGCTATCTGTACAGACAAGAGTCCTAG		ATGCGTTTCTCCGGCTATCTGTACAGACAAGAGTCCTAG		MRFSGYLYRQES*		MRFSGYLYRQES*		TCATTGTTTT	GGCCATGGAA	1	DL	FG00281.1	MG03676.1	0	0	0
2596	1668	an	AN5633.1	58.m07557	AO070301000032	1	-174	-160					ATGTCGGGACTTTGA	ATGTCGGGACTTTGA			MSGL*	MSGL*			CGTTCGGGCA	AGTGCAACTC	0	P	0	0	0	0	0
2597	1668	af	AN5633.1	58.m07557	AO070301000032	1			-228	-211			ATGGACGTAGGATATTGA		ATGGACGTAGGATATTGA		MDVGY*		MDVGY*		CGTCAACCTC	TGCGCAACTG	0	P	0	0	0	0	0
2598	1668	af	AN5633.1	58.m07557	AO070301000032	1			-211	-137			ATGCGCAACTGTCTACAAGGAACAACTGCAATCGGGAAGTTTCGGGCCTTCTTTCCCGCAGGCCCCCAGCTTTGA		ATGCGCAACTGTCTACAAGGAACAACTGCAATCGGGAAGTTTCGGGCCTTCTTTCCCGCAGGCCCCCAGCTTTGA		MRNCLQGTTAIGKFRAFFPAGPQL*		MRNCLQGTTAIGKFRAFFPAGPQL*		TAGGATATTG	TTCCGGCGTA	0	P	0	0	0	0	0
2599	1668	ao	AN5633.1	58.m07557	AO070301000032	1					-216	-166	ATGTACCCACTTTGTAGTGAATGTGTCGCACTGGGACTGGGACTACCGTAG			ATGTACCCACTTTGTAGTGAATGTGTCGCACTGGGACTGGGACTACCGTAG	MYPLCSECVALGLGLP*			MYPLCSECVALGLGLP*	CTCTTACTGC	CCGGGGAAAT	0	P	0	0	0	0	0
2600	1668	ao	AN5633.1	58.m07557	AO070301000032	1					-196	-125	ATGTGTCGCACTGGGACTGGGACTACCGTAGCCGGGGAAATTCGGCCATTCGTTCCCGCACGTTACTCTTGA			ATGTGTCGCACTGGGACTGGGACTACCGTAGCCGGGGAAATTCGGCCATTCGTTCCCGCACGTTACTCTTGA	MCRTGTGTTVAGEIRPFVPARYS*			MCRTGTGTTVAGEIRPFVPARYS*	TTTGTAGTGA	TTTGGTTTCC	0	P	0	0	0	0	0
2613	1669	ao	AN1986.1	58.m07593	AO070301000073	0					-57	-40	ATGATATCCATCTCCTAG			ATGATATCCATCTCCTAG	MISIS*			MISIS*	CCCTCTTCGA	AAGACAGTCT	1	P	0	0	0	0	0
2616	1671	ao	AN6626.1	62.m03217	AO070315000108	0					-52	-35	ATGCTCACCACCTCCTGA			ATGCTCACCACCTCCTGA	MLTTS*			MLTTS*	AAAATACATA	ACATCATCAT	1	R	0	0	0	0	0
2620	1675	ao	AN3308.1	52.m03702	AO070330000181	0					-52	-29	ATGAACTGGGGTTACACGAGTTAA			ATGAACTGGGGTTACACGAGTTAA	MNWGYTS*			MNWGYTS*	TCATCACTCT	GGATCCACCG	1	G	0	0	0	0	0
2624	1679	an	AN1923.1	69.m14941	AO070341000112	1	-444	-415					ATGTGCGGACACCGCTGCGGCGGGCAGTGA	ATGTGCGGACACCGCTGCGGCGGGCAGTGA			MCGHRCGGQ*	MCGHRCGGQ*			ATCGCAACCC	CTTTCCAGCC	0	E	0	0	0	0	0
2625	1679	an	AN1923.1	69.m14941	AO070341000112	1	-399	-337					ATGCTCGGCTCGCGCGACAGAGCCAGATTTATCAGTCTCGTTCGTTCTCTCGAGCAGCGTTAG	ATGCTCGGCTCGCGCGACAGAGCCAGATTTATCAGTCTCGTTCGTTCTCTCGAGCAGCGTTAG			MLGSRDRARFISLVRSLEQR*	MLGSRDRARFISLVRSLEQR*			CAGCCGAATA	CCGCGGGAAG	0	E	0	0	0	0	0
2639	1679	ao	AN1923.1	69.m14941	AO070341000112	1					-375	-292	ATGCTCACTTTCCCGGCCGAATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAG			ATGCTCACTTTCCCGGCCGAATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAG	MLTFPAEWSVAYPAGVFQQHKVPRRGF*			MLTFPAEWSVAYPAGVFQQHKVPRRGF*	CTCCGCTACG	GCCTTCTTCA	0	E	0	0	0	0	0
2646	1679	ao	AN1923.1	69.m14941	AO070341000112	1					-77	-30	ATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA			ATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA	MLHPGERSTPSKQDN*			MLHPGERSTPSKQDN*	TATCCAATGG	CCCCTCTCGA	0	E	0	0	0	0	0
2660	1685	af	AN8755.1	62.m03322	AO070250000017	0			-31	-11			ATGCTCATACCGGAAATCTAA		ATGCTCATACCGGAAATCTAA		MLIPEI*		MLIPEI*		TTTCCCCCTC	TTAGGACAAG	1	C	0	MG02616.1	0	0	0
2664	1688	an	AN2531.1	59.m08446	AO070300000119	0	-50	-18					ATGGGCGATTTCTCCAGATTATTGAATATTTGA	ATGGGCGATTTCTCCAGATTATTGAATATTTGA			MGDFSRLLNI*	MGDFSRLLNI*			CATTCGTCCA	AAATTCATAC	1	R	0	MG07444.1	0	0	0
2674	1695	af	AN6009.1	72.m19134	AO070340000270	1			-612	-595			ATGTCAGCGCGATCTTGA		ATGTCAGCGCGATCTTGA		MSARS*		MSARS*		CACTTCAACA	CGAACCATCA	0	R	0	0	0	0	0
2675	1695	ao	AN6009.1	72.m19134	AO070340000270	1					-875	-864	ATGTCACCTTAG			ATGTCACCTTAG	MSP*			MSP*	CTTTCCAACG	TCTAGCCTCG	0	R	0	0	0	0	0
2700	1704	ao	AN1087.1	52.m04007	AO070293000079	0					-57	-37	ATGGATCTTCACAAAGCCTAA			ATGGATCTTCACAAAGCCTAA	MDLHKA*			MDLHKA*	GTCACGACTG	GACTTCAACA	1	Q	0	0	0	0	0
2712	1723	an	AN4479.1	57.m05654	AO070311000025	0	-34	-20					ATGTCCGATTTTTAA	ATGTCCGATTTTTAA			MSDF*	MSDF*			CTACCTTGAC	CTGAGTATCC	1	T	0	0	0	0	0
2716	1723	af	AN4479.1	57.m05654	AO070311000025	0			-33	-16			ATGTCCCAAGTTAACTAA		ATGTCCCAAGTTAACTAA		MSQVN*		MSQVN*		GGCTATCCCT	TTTACAACAG	1	T	0	0	0	0	0
2718	1723	ao	AN4479.1	57.m05654	AO070311000025	0					-34	-20	ATGTCCCGTTTGTGA			ATGTCCCGTTTGTGA	MSRL*			MSRL*	AACACTACTT	TTGAGTCGTC	1	T	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
2719	1726	an	AN7741.1	71.m16099	AO070325000162	0	-55	-26					ATGTACATCTCCAGTCCCCTCACCCCCTAA	ATGTACATCTCCAGTCCCCTCACCCCCTAA			MYISSPLTP*	MYISSPLTP*			TCACGGCTGA	CCTTACCACC	1	U	0	MG05484.1	NCU09673.1	YOL062C	0
2722	1727	an	AN4014.1	54.m06948	AO070328000150	1	-33	-19					ATGATATCCTCCTAA	ATGATATCCTCCTAA			MISS*	MISS*			CCTCTTTAAC	TATCCTTCGC	1	UZ	0	0	0	0	0
2723	1727	af	AN4014.1	54.m06948	AO070328000150	1			-245	-222			ATGTTGTGCATGACAGTCCTCTAA		ATGTTGTGCATGACAGTCCTCTAA		MLCMTVL*		MLCMTVL*		AGGGTGGAGT	TTCTGGCGAG	0	UZ	0	0	0	0	0
2724	1727	af	AN4014.1	54.m06948	AO070328000150	1			-236	-222			ATGACAGTCCTCTAA		ATGACAGTCCTCTAA		MTVL*		MTVL*		TATGTTGTGC	TTCTGGCGAG	0	UZ	0	0	0	0	0
2725	1727	af	AN4014.1	54.m06948	AO070328000150	1			-200	-165			ATGCCTCTATGTCTACAAGCTGTCTTTCTTGAATAG		ATGCCTCTATGTCTACAAGCTGTCTTTCTTGAATAG		MPLCLQAVFLE*		MPLCLQAVFLE*		CGGCTGAGAT	CCTGAGTTGC	0	UZ	0	0	0	0	0
2726	1727	af	AN4014.1	54.m06948	AO070328000150	1			-192	-169			ATGTCTACAAGCTGTCTTTCTTGA		ATGTCTACAAGCTGTCTTTCTTGA		MSTSCLS*		MSTSCLS*		ATATGCCTCT	ATAGCCTGAG	0	UZ	0	0	0	0	0
2727	1727	af	AN4014.1	54.m06948	AO070328000150	1			-125	-93			ATGCCACCAGTGTGGAGAGCTTGCCAGGCATAG		ATGCCACCAGTGTGGAGAGCTTGCCAGGCATAG		MPPVWRACQA*		MPPVWRACQA*		ATTGCATTGC	ATCTATAAAC	0	UZ	0	0	0	0	0
2742	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-57	-37	ATGAGATTTTCCCTTCGATAA			ATGAGATTTTCCCTTCGATAA	MRFSLR*			MRFSLR*	TTTAGCTGCA	CGACCATCTT	1	Q	0	0	0	0	0
2765	1740	an	AN5197.1	69.m14896	AO070237000027	0	-41	-21					ATGGTGAATCATTTTGTCTAG	ATGGTGAATCATTTTGTCTAG			MVNHFV*	MVNHFV*			AGTTGTAATA	TATTTCCACA	1	S	0	0	0	0	0
2767	1740	af	AN5197.1	69.m14896	AO070237000027	0			-58	-35			ATGATAATGATATCAACCACCTAA		ATGATAATGATATCAACCACCTAA		MIMISTT*		MIMISTT*		ATGACTAGTG	TCTCTGCAGC	1	S	0	0	0	0	0
2768	1740	af	AN5197.1	69.m14896	AO070237000027	0			-52	-35			ATGATATCAACCACCTAA		ATGATATCAACCACCTAA		MISTT*		MISTT*		AGTGATGATA	TCTCTGCAGC	1	S	0	0	0	0	0
2769	1740	ao	AN5197.1	69.m14896	AO070237000027	0					-55	-26	ATGAGAATGACCCAATTCAATAGCCCATAG			ATGAGAATGACCCAATTCAATAGCCCATAG	MRMTQFNSP*			MRMTQFNSP*	CACATTCACG	CTCTTTCGCC	1	S	0	0	0	0	0
2770	1740	ao	AN5197.1	69.m14896	AO070237000027	0					-49	-26	ATGACCCAATTCAATAGCCCATAG			ATGACCCAATTCAATAGCCCATAG	MTQFNSP*			MTQFNSP*	CACGATGAGA	CTCTTTCGCC	1	S	0	0	0	0	0
2811	1770	af	AN1292.1	70.m14916	AO070303000054	1			-70	-56			ATGTCAACAGAATAA		ATGTCAACAGAATAA		MSTE*		MSTE*		CTTGACTCAG	TTGCTTGCGT	0	I	0	0	0	0	0
2815	1772	ao	AN8707.1	62.m03362	AO070315000134	1					-43	-8	ATGAGTACAAAACTAAACAAAATCATCCTTGTCTAG			ATGAGTACAAAACTAAACAAAATCATCCTTGTCTAG	MSTKLNKIILV*			MSTKLNKIILV*	CATTGACCTA	CTCCATCATG	1	C	0	0	0	0	0
2817	1776	af	AN3010.1	59.m09008	AO070337000106	0			-60	-49			ATGTCCCAATAG		ATGTCCCAATAG		MSQ*		MSQ*		GTATTATCTT	GACATAGCTT	1	S	0	0	0	YOL093W	YOL093W
2846	1792	conserved	AN8723.1	62.m03343	AO070315000151	1	-93	-40	-93	-40	-93	-40	ATGAAmTysGGTCCrTysyvTCymymCrswTysAGAwCGryyGGyGCwTCyTAG	ATGAACTTCGGTCCGTCCTGTCCATCCACATTGAGATCGGCTGGTGCATCCTAG	ATGAAATCGGGTCCATTGTCTCTATACGGTTCCAGATCGATCGGCGCTTCTTAG	ATGAAATTCGGTCCGTCCCATCTCCACACATCGAGAACGACCGGCGCTTCCTAG	MnfGPscpstlRsaGAS*	MNFGPSCPSTLRSAGAS*	MKSGPLSLYGSRSIGAS*	MKFGPSHLHTSRTTGAS*	vvyhAsCATC	ACTybwGTCr	0		0	0	0	0	0
2850	1792	af	AN8723.1	62.m03343	AO070315000151	1			-538	-458			ATGTTCCTGTGCATGTCTGATAAGCTCCATCATCATCAATCAACTCAGATCAGATCGACCTCGCGCGCCTCGTCAGTGTAA		ATGTTCCTGTGCATGTCTGATAAGCTCCATCATCATCAATCAACTCAGATCAGATCGACCTCGCGCGCCTCGTCAGTGTAA		MFLCMSDKLHHHQSTQIRSTSRASSV*		MFLCMSDKLHHHQSTQIRSTSRASSV*		AAGATTCGAC	CCTGACAGGC	0		0	0	0	0	0
2851	1792	af	AN8723.1	62.m03343	AO070315000151	1			-526	-458			ATGTCTGATAAGCTCCATCATCATCAATCAACTCAGATCAGATCGACCTCGCGCGCCTCGTCAGTGTAA		ATGTCTGATAAGCTCCATCATCATCAATCAACTCAGATCAGATCGACCTCGCGCGCCTCGTCAGTGTAA		MSDKLHHHQSTQIRSTSRASSV*		MSDKLHHHQSTQIRSTSRASSV*		GTTCCTGTGC	CCTGACAGGC	0		0	0	0	0	0
2854	1797	af	AN6577.1	62.m03163	AO070326000023	0			-60	-16			ATGGCAATAATGCAGTTTCACTGTTCTGGTGTAGAGTCGTCCTGA		ATGGCAATAATGCAGTTTCACTGTTCTGGTGTAGAGTCGTCCTGA		MAIMQFHCSGVESS*		MAIMQFHCSGVESS*		GTATTTTTCC	CTAAAAAGTA	1	J	0	0	0	0	0
2855	1797	af	AN6577.1	62.m03163	AO070326000023	0			-51	-16			ATGCAGTTTCACTGTTCTGGTGTAGAGTCGTCCTGA		ATGCAGTTTCACTGTTCTGGTGTAGAGTCGTCCTGA		MQFHCSGVESS*		MQFHCSGVESS*		CATGGCAATA	CTAAAAAGTA	1	J	0	0	0	0	0
2858	1809	af	AN7661.1	57.m05428	AO070268000032	0			-27	-7			ATGGTCCAAGACCAGCAGTGA		ATGGTCCAAGACCAGCAGTGA		MVQDQQ*		MVQDQQ*		AGTACATCTG	AACACGATGT	1	K	0	0	0	0	0
2901	1817	af	AN2723.1	70.m15716	AO070309000061	0			-60	-46			ATGCGCAAATTCTAA		ATGCGCAAATTCTAA		MRKF*		MRKF*		GATCAATGAA	GTGCAATCTT	1	E	0	0	0	0	0
2914	1821	af	AN8018.1	53.m04191	AO070322000067	0			-48	-34			ATGAGCCAAAATTGA		ATGAGCCAAAATTGA		MSQN*		MSQN*		CGCCATTGGG	TTTCAGCGCT	1	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2916	1838	an	AN6186.1	72.m19284	AO070308000114	0	-56	-27					ATGCATGTTCTTCTATCCTTTTCCGATTAA	ATGCATGTTCTTCTATCCTTTTCCGATTAA			MHVLLSFSD*	MHVLLSFSD*			ACACCTTCAA	TTACCTTTAT	1	L	FG05269.1	MG01699.1	0	0	0
2923	1844	conserved	AN4864.1	59.m09108	AO070329000150	0	-30	-16	-27	-13	-35	-21	ATGGrwsACmvbTrA	ATGGAAGACCACTGA	ATGGGAGACAGGTGA	ATGGGTCACCCTTAA	Medh*	MEDH*	MGDR*	MGHP*	TwyksrGyCA	whvydhyhhv	1	GE	0	MG09310.1	0	YOR002W	0
2927	1846	an	AN5748.1	69.m14846	AO070341000005	1	-173	-162					ATGCCGGCTTAA	ATGCCGGCTTAA			MPA*	MPA*			GGATCTATCC	GCTGCAGTTA	0	G	0	0	0	YJR131W	0
2928	1846	an	AN5748.1	69.m14846	AO070341000005	1	-82	-68					ATGACTACCGCCTAG	ATGACTACCGCCTAG			MTTA*	MTTA*			GTTATCATCT	CTGGAGCATC	0	G	0	0	0	YJR131W	0
2930	1846	af	AN5748.1	69.m14846	AO070341000005	1			-258	-175			ATGTTTGTTTGTGTCTGCGGGACGGAGAATTTAGCGAGCTCAATCACCAAGCTCAAGACTGGTGTCGAATTCCAAGGTTGCTAA		ATGTTTGTTTGTGTCTGCGGGACGGAGAATTTAGCGAGCTCAATCACCAAGCTCAAGACTGGTGTCGAATTCCAAGGTTGCTAA		MFVCVCGTENLASSITKLKTGVEFQGC*		MFVCVCGTENLASSITKLKTGVEFQGC*		GTACATTGAT	CGTTTCGTCT	0	G	0	0	0	YJR131W	0
2931	1846	af	AN5748.1	69.m14846	AO070341000005	1			-100	-86			ATGCGATCCCATTGA		ATGCGATCCCATTGA		MRSH*		MRSH*		TCGCGCATCT	TTTCTCTTCG	0	G	0	0	0	YJR131W	0
2932	1846	ao	AN5748.1	69.m14846	AO070341000005	1					-508	-488	ATGAATCCCCCATTGCAATAA			ATGAATCCCCCATTGCAATAA	MNPPLQ*			MNPPLQ*	AAATCCCAGA	TTGTCTAACC	0	G	0	0	0	YJR131W	0
2936	1846	ao	AN5748.1	69.m14846	AO070341000005	1					-278	-174	ATGGTTGTAAGCAATATTTCTAACGTTTCCTCCCCCATCTATGTAGGAATTATTCTCCCGTCACCAATTTGCCCTATAGATAGTTGTACCTTGTTCAAGAGTTGA			ATGGTTGTAAGCAATATTTCTAACGTTTCCTCCCCCATCTATGTAGGAATTATTCTCCCGTCACCAATTTGCCCTATAGATAGTTGTACCTTGTTCAAGAGTTGA	MVVSNISNVSSPIYVGIILPSPICPIDSCTLFKS*			MVVSNISNVSSPIYVGIILPSPICPIDSCTLFKS*	TATGTGAACC	CACCGATCGG	0	G	0	0	0	YJR131W	0
2937	1846	ao	AN5748.1	69.m14846	AO070341000005	1					-103	-71	ATGCCGATTGACTGTTCACTTTCTTCGCTATAG			ATGCCGATTGACTGTTCACTTTCTTCGCTATAG	MPIDCSLSSL*			MPIDCSLSSL*	GCTAGCGCCT	CGAGTGGGTT	0	G	0	0	0	YJR131W	0
2958	1857	af	AN0998.1	70.m15216	AO070312000041	1			-82	-35			ATGAGCGACATACCTAGTACAGTTCGACTTTTGGCTGGATACCGTTAG		ATGAGCGACATACCTAGTACAGTTCGACTTTTGGCTGGATACCGTTAG		MSDIPSTVRLLAGYR*		MSDIPSTVRLLAGYR*		CTACCTGAGG	GTGTTGAGCT	0		0	0	0	0	0
2964	1858	an	AN8706.1	62.m03363	AO070315000133	1	-125	-96					ATGGTGACATTGTTCACATACTTAGTCTGA	ATGGTGACATTGTTCACATACTTAGTCTGA			MVTLFTYLV*	MVTLFTYLV*			ACGACTCCGT	AACTCAATCT	0	M	0	0	0	0	0
2965	1863	an	AN5048.1	59.m08678	AO070338000188	1	-112	-74					ATGGTGCCAGTGTTTTTTCTCGCATTCTCTTCTTTTTAG	ATGGTGCCAGTGTTTTTTCTCGCATTCTCTTCTTTTTAG			MVPVFFLAFSSF*	MVPVFFLAFSSF*			CTTCCACGCA	CTCTAATTGT	0	R	0	0	0	0	0
2966	1863	an	AN5048.1	59.m08678	AO070338000188	1	-42	-13					ATGCTGCCGTTCCGTGTCGACTCTACATAA	ATGCTGCCGTTCCGTGTCGACTCTACATAA			MLPFRVDST*	MLPFRVDST*			CTTCGTCCTT	CCACCACCCA	1	R	0	0	0	0	0
2968	1863	af	AN5048.1	59.m08678	AO070338000188	1			-124	-110			ATGTCAATGTTCTGA		ATGTCAATGTTCTGA		MSMF*		MSMF*		ATTCTCCTCC	TCCTTTTTAT	0	R	0	0	0	0	0
2969	1863	af	AN5048.1	59.m08678	AO070338000188	1			-48	-31			ATGTCACACCGATCTTGA		ATGTCACACCGATCTTGA		MSHRS*		MSHRS*		CAATTCCCCC	ATCCTATCGA	1	R	0	0	0	0	0
2971	1863	ao	AN5048.1	59.m08678	AO070338000188	1					-30	-16	ATGCTTTTATCCTAA			ATGCTTTTATCCTAA	MLLS*			MLLS*	TCTAGCCCTC	CCTATCAACT	1	R	0	0	0	0	0
2987	1871	ao	AN6290.1	72.m19345	AO070308000002	0					-24	-13	ATGATTATTTGA			ATGATTATTTGA	MII*			MII*	TCGCTCCTCT	AGAGACTTAG	1		0	0	0	0	0
2989	1874	ao	AN0874.1	70.m15477	AO070320000033	0					-31	-14	ATGATCCTGTACCTTTAA			ATGATCCTGTACCTTTAA	MILYL*			MILYL*	TAAGCACCGC	CTAGACAGTC	1	A	0	MG06313.1	0	0	0
3012	1889	af	AN6438.1	58.m07697	AO070299000087	0			-38	-12			ATGCAAGTACCTCGCTGTGGCTGCTAG		ATGCAAGTACCTCGCTGTGGCTGCTAG		MQVPRCGC*		MQVPRCGC*		CAGGGAGGCG	CCGCAGTCAA	1	O	0	0	NCU02515.1	0	0
3046	1907	conserved	AN4597.1	57.m05519	AO070267000013	0	-38		-38		-38		ATGmGryhyyyybwwdCvdryydyAbyhyhmydhymTAA	ATGCGATACCTTCTATCATACTTTAGTCTACCTCTCTAA	ATGAGGCTTTCTGATACCAGTTGCATTTTTACGACATAA	ATGAGGCCCTCCTTTGCGGACCATACCACCATATCATAA	MRyllsyfslpl*	MRYLLSYFSLPL*	MRLSDTSCIFTT*	MRPSFADHTTIS*	mhyyGsCTTs	TGwCrTCwwy	1	BD	0	0	0	0	0
3106	1928	an	AN1487.1	55.m02993	AO070334000194	1	-288	-262					ATGCTTCTGTCTGTTCGCAGGGGTTAA	ATGCTTCTGTCTGTTCGCAGGGGTTAA			MLLSVRRG*	MLLSVRRG*			ACAGCTTCAT	CAATGCGATT	0		0	0	0	0	0
3107	1928	an	AN1487.1	55.m02993	AO070334000194	1	-259	-248					ATGCGATTCTAA	ATGCGATTCTAA			MRF*	MRF*			GGGGTTAACA	TGCATGCCTC	0		0	0	0	0	0
3108	1928	an	AN1487.1	55.m02993	AO070334000194	1	-248	-225					ATGCATGCCTCTCGCTCCGTTTAA	ATGCATGCCTCTCGCTCCGTTTAA			MHASRSV*	MHASRSV*			TGCGATTCTA	CTTGCTGGTA	0		0	0	0	0	0
3124	1939	af	AN4230.1	54.m06786	AO070234000016	0			-55	-41			ATGCACATCGGCTAA		ATGCACATCGGCTAA		MHIG*		MHIG*		ACTGTCATAC	GCCTTGAAAG	1	I	0	MG09516.1	0	0	0
3128	1939	ao	AN4230.1	54.m06786	AO070234000016	0					-24	-7	ATGTACCGCTTCAAGTGA			ATGTACCGCTTCAAGTGA	MYRFK*			MYRFK*	TGGAAACCAC	AGGACAATGA	1	I	0	MG09516.1	0	0	0
3142	1951	an	AN0868.1	70.m15459	AO070320000019	0	-48	-37					ATGCCATACTAG	ATGCCATACTAG			MPY*	MPY*			AACTCACTTG	CCCTTGCGAC	1	I	0	MG02999.1	NCU00580.1	0	0
3165	1961	an	AN3927.1	69.m15001	AO070341000039	0	-60	-16					ATGGATGGGGAGCTTTATCTCATCTCCACACTCAATTCTCTATGA	ATGGATGGGGAGCTTTATCTCATCTCCACACTCAATTCTCTATGA			MDGELYLISTLNSL*	MDGELYLISTLNSL*			TTACTATTAC	TGTAGACTCC	1	T	0	0	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
3170	1961	af	AN3927.1	69.m15001	AO070341000039	0			-49	-17			ATGCGTTTCTTACGGCTCTCGTCGATCATTTGA		ATGCGTTTCTTACGGCTCTCGTCGATCATTTGA		MRFLRLSSII*		MRFLRLSSII*		CAATCTGAGA	TATACTGACA	1	T	0	0	0	0	0
3198	1965	an	AN9405.1	52.m04032	AO070274000012	1	-58	-44					ATGATTTCATCCTAA	ATGATTTCATCCTAA			MISS*	MISS*			AAAAATTGCA	CATACTGTCT	1		0	0	0	0	0
3202	1965	af	AN9405.1	52.m04032	AO070274000012	1			-102	-82			ATGATGATGACGATGCGATGA		ATGATGATGACGATGCGATGA		MMMTMR*		MMMTMR*		AGGCTTGATC	ACTTATGAGT	0		0	0	0	0	0
3203	1965	af	AN9405.1	52.m04032	AO070274000012	1			-99	-82			ATGATGACGATGCGATGA		ATGATGACGATGCGATGA		MMTMR*		MMTMR*		CTTGATCATG	ACTTATGAGT	0		0	0	0	0	0
3204	1965	af	AN9405.1	52.m04032	AO070274000012	1			-96	-82			ATGACGATGCGATGA		ATGACGATGCGATGA		MTMR*		MTMR*		GATCATGATG	ACTTATGAGT	0		0	0	0	0	0
3205	1965	af	AN9405.1	52.m04032	AO070274000012	1			-85	-74			ATGAACTTATGA		ATGAACTTATGA		MNL*		MNL*		TGACGATGCG	GTCGTTTAAT	0		0	0	0	0	0
3206	1965	af	AN9405.1	52.m04032	AO070274000012	1			-77	-30			ATGAGTCGTTTAATATTCATTGCAATTATTCATCTGACTCGGTTTTAG		ATGAGTCGTTTAATATTCATTGCAATTATTCATCTGACTCGGTTTTAG		MSRLIFIAIIHLTRF*		MSRLIFIAIIHLTRF*		CGATGAACTT	CTAGAGATAT	0		0	0	0	0	0
3213	1966	an	AN8796.1	71.m15603	AO070276000064	1	-123	-91					ATGTCAATGGAAACCAGGAGCATCGGATGCTGA	ATGTCAATGGAAACCAGGAGCATCGGATGCTGA			MSMETRSIGC*	MSMETRSIGC*			TGACTTCTCA	ACTTACCCCC	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3214	1966	an	AN8796.1	71.m15603	AO070276000064	1	-117	-91					ATGGAAACCAGGAGCATCGGATGCTGA	ATGGAAACCAGGAGCATCGGATGCTGA			METRSIGC*	METRSIGC*			CTCAATGTCA	ACTTACCCCC	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3215	1966	an	AN8796.1	71.m15603	AO070276000064	1	-97	-11					ATGCTGAACTTACCCCCTGCGAGAGCTGTTTCTCCCTTCGATGGCAGCTGCGGGGTACCGGTTGAACTAAGCAGCATCTCCAATTGA	ATGCTGAACTTACCCCCTGCGAGAGCTGTTTCTCCCTTCGATGGCAGCTGCGGGGTACCGGTTGAACTAAGCAGCATCTCCAATTGA			MLNLPPARAVSPFDGSCGVPVELSSISN*	MLNLPPARAVSPFDGSCGVPVELSSISN*			GGAGCATCGG	GTGAGCAACG	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3216	1966	an	AN8796.1	71.m15603	AO070276000064	1	-57	-28					ATGGCAGCTGCGGGGTACCGGTTGAACTAA	ATGGCAGCTGCGGGGTACCGGTTGAACTAA			MAAAGYRLN*	MAAAGYRLN*			TCTCCCTTCG	GCAGCATCTC	1	T	FG05865.1	0	NCU01099.1	YML121W	0
3219	1966	af	AN8796.1	71.m15603	AO070276000064	1			-143	-102			ATGTATATGAGGAGCCTACAGAACCCGCACCTCACACGATAG		ATGTATATGAGGAGCCTACAGAACCCGCACCTCACACGATAG		MYMRSLQNPHLTR*		MYMRSLQNPHLTR*		AGTTGCACAT	CGCTGCAGGT	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3220	1966	af	AN8796.1	71.m15603	AO070276000064	1			-137	-102			ATGAGGAGCCTACAGAACCCGCACCTCACACGATAG		ATGAGGAGCCTACAGAACCCGCACCTCACACGATAG		MRSLQNPHLTR*		MRSLQNPHLTR*		ACATATGTAT	CGCTGCAGGT	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3223	1966	ao	AN8796.1	71.m15603	AO070276000064	1					-113	-72	ATGTCCGGAACCAGTCCACCACGCCCCCCTCTCCCCCATTGA			ATGTCCGGAACCAGTCCACCACGCCCCCCTCTCCCCCATTGA	MSGTSPPRPPLPH*			MSGTSPPRPPLPH*	AACTCAACCG	ACTAAAAGAA	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3234	1973	an	AN0954.1	70.m15601	AO070320000155	0	-17						ATGCCAATCTACTCATGA	ATGCCAATCTACTCATGA			MPIYS*	MPIYS*			AACATCTCAG	TGTCTGAAGT	1	R	0	0	0	0	0
3235	1973	af	AN0954.1	70.m15601	AO070320000155	1			-198	-157			ATGAATTCAAATTATATACCAGTTGCACGTCGCGCTCCATAA		ATGAATTCAAATTATATACCAGTTGCACGTCGCGCTCCATAA		MNSNYIPVARRAP*		MNSNYIPVARRAP*		GCAGCTCTGA	TTGTGAAACC	0	R	0	0	0	0	0
3236	1973	af	AN0954.1	70.m15601	AO070320000155	1			-36	-16			ATGCCATCCAGCATTATCTGA		ATGCCATCCAGCATTATCTGA		MPSSII*		MPSSII*		AACAAACCAA	ACAACAACCA	1	R	0	0	0	0	0
3237	1973	ao	AN0954.1	70.m15601	AO070320000155	1					-250	-236	ATGAACATAAGTTGA			ATGAACATAAGTTGA	MNIS*			MNIS*	TGAGTTCAAA	AACTCGAGAT	0	R	0	0	0	0	0
3238	1973	ao	AN0954.1	70.m15601	AO070320000155	1					-52	-41	ATGCCACCTTAA			ATGCCACCTTAA	MPP*			MPP*	TGCACTTTCC	CCAAACCAAA	1	R	0	0	0	0	0
3254	1980	an	AN3957.1	69.m14963	AO070341000077	1	-370	-260					ATGTATTATGATAACGCTACGAGCTTTCGTCGGTGCTCCAGGCTGATAGACTGTCTGATGCACTCAACTGATAAGATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA	ATGTATTATGATAACGCTACGAGCTTTCGTCGGTGCTCCAGGCTGATAGACTGTCTGATGCACTCAACTGATAAGATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA			MYYDNATSFRRCSRLIDCLMHSTDKMGVPHHPARAR*	MYYDNATSFRRCSRLIDCLMHSTDKMGVPHHPARAR*			TTCGAATAAT	ATAGTACAAA	0	JIT	0	0	0	0	0
3255	1980	an	AN3957.1	69.m14963	AO070341000077	1	-363	-325					ATGATAACGCTACGAGCTTTCGTCGGTGCTCCAGGCTGA	ATGATAACGCTACGAGCTTTCGTCGGTGCTCCAGGCTGA			MITLRAFVGAPG*	MITLRAFVGAPG*			AATATGTATT	TAGACTGTCT	0	JIT	0	0	0	0	0
3256	1980	an	AN3957.1	69.m14963	AO070341000077	1	-313	-260					ATGCACTCAACTGATAAGATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA	ATGCACTCAACTGATAAGATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA			MHSTDKMGVPHHPARAR*	MHSTDKMGVPHHPARAR*			AGACTGTCTG	ATAGTACAAA	0	JIT	0	0	0	0	0
3257	1980	an	AN3957.1	69.m14963	AO070341000077	1	-295	-260					ATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA	ATGGGTGTTCCCCACCACCCCGCCAGAGCCCGGTAA			MGVPHHPARAR*	MGVPHHPARAR*			AACTGATAAG	ATAGTACAAA	0	JIT	0	0	0	0	0
3258	1980	an	AN3957.1	69.m14963	AO070341000077	1	-203	-165					ATGGACATGAACTTATCGACCTGCCGTTTTAAGGGCTAG	ATGGACATGAACTTATCGACCTGCCGTTTTAAGGGCTAG			MDMNLSTCRFKG*	MDMNLSTCRFKG*			GAGCTCTTCC	TTTCGTCCAA	0	JIT	0	0	0	0	0
3259	1980	an	AN3957.1	69.m14963	AO070341000077	1	-197	-165					ATGAACTTATCGACCTGCCGTTTTAAGGGCTAG	ATGAACTTATCGACCTGCCGTTTTAAGGGCTAG			MNLSTCRFKG*	MNLSTCRFKG*			TTCCATGGAC	TTTCGTCCAA	0	JIT	0	0	0	0	0
3260	1980	an	AN3957.1	69.m14963	AO070341000077	1	-145	-110					ATGTCTACCTATCGTAGTTTCCGATGGAGGGGTTGA	ATGTCTACCTATCGTAGTTTCCGATGGAGGGGTTGA			MSTYRSFRWRG*	MSTYRSFRWRG*			ATCTTCGCCG	GATCTTGATA	0	JIT	0	0	0	0	0
3261	1980	an	AN3957.1	69.m14963	AO070341000077	1	-122	-102					ATGGAGGGGTTGAGATCTTGA	ATGGAGGGGTTGAGATCTTGA			MEGLRS*	MEGLRS*			GTAGTTTCCG	TACGAGGAGT	0	JIT	0	0	0	0	0
3262	1980	an	AN3957.1	69.m14963	AO070341000077	1	-89	-27					ATGGGTATATATATATTGATACAGTTACCCCTCTCATGTCTTGAAGACAGGTCTAATGCCTGA	ATGGGTATATATATATTGATACAGTTACCCCTCTCATGTCTTGAAGACAGGTCTAATGCCTGA			MGIYILIQLPLSCLEDRSNA*	MGIYILIQLPLSCLEDRSNA*			CGAGGAGTCT	ACTTACATTA	0	JIT	0	0	0	0	0
3263	1980	af	AN3957.1	69.m14963	AO070341000077	1			-508	-446			ATGTTCATAGTGCCGATATCCATTGCGGGAAAAAGCAAGAGATTCGCCAGGCCTAGGTACTAG		ATGTTCATAGTGCCGATATCCATTGCGGGAAAAAGCAAGAGATTCGCCAGGCCTAGGTACTAG		MFIVPISIAGKSKRFARPRY*		MFIVPISIAGKSKRFARPRY*		TACCTTCTAA	CCAACCTACT	0	JIT	0	0	0	0	0
3264	1980	af	AN3957.1	69.m14963	AO070341000077	1			-411	-373			ATGCCGAATATGTACCATAGGACTCCAACTACTCCATAG		ATGCCGAATATGTACCATAGGACTCCAACTACTCCATAG		MPNMYHRTPTTP*		MPNMYHRTPTTP*		AGCTTCCCCA	GCTCACATCC	0	JIT	0	0	0	0	0
3265	1980	af	AN3957.1	69.m14963	AO070341000077	1			-402	-373			ATGTACCATAGGACTCCAACTACTCCATAG		ATGTACCATAGGACTCCAACTACTCCATAG		MYHRTPTTP*		MYHRTPTTP*		AATGCCGAAT	GCTCACATCC	0	JIT	0	0	0	0	0
3266	1980	af	AN3957.1	69.m14963	AO070341000077	1			-361	-326			ATGGTTCTCCAACTTTATATTTCTGTTGGAGAATAG		ATGGTTCTCCAACTTTATATTTCTGTTGGAGAATAG		MVLQLYISVGE*		MVLQLYISVGE*		CTCACATCCA	GTAGAATACG	0	JIT	0	0	0	0	0
3267	1980	af	AN3957.1	69.m14963	AO070341000077	1			-302	-285			ATGTTAGTGGACAGATAA		ATGTTAGTGGACAGATAA		MLVDR*		MLVDR*		TGCATCTCAG	CGCTGCCCCA	0	JIT	0	0	0	0	0
3268	1980	af	AN3957.1	69.m14963	AO070341000077	1			-183	-133			ATGTCTCTCGACCTGCCTAATCGGAAAAGATATGAGGTTCCTGACACCTAA		ATGTCTCTCGACCTGCCTAATCGGAAAAGATATGAGGTTCCTGACACCTAA		MSLDLPNRKRYEVPDT*		MSLDLPNRKRYEVPDT*		AGTCCAGGGC	GATAAGGAGA	0	JIT	0	0	0	0	0
3269	1980	af	AN3957.1	69.m14963	AO070341000077	1			-152	-120			ATGAGGTTCCTGACACCTAAGATAAGGAGATGA		ATGAGGTTCCTGACACCTAAGATAAGGAGATGA		MRFLTPKIRR*		MRFLTPKIRR*		CGGAAAAGAT	CCCCATTCTC	0	JIT	0	0	0	0	0
3270	1980	af	AN3957.1	69.m14963	AO070341000077	1			-123	-88			ATGACCCCATTCTCCAACTGCCTGCACCCGATTTAA		ATGACCCCATTCTCCAACTGCCTGCACCCGATTTAA		MTPFSNCLHPI*		MTPFSNCLHPI*		AGATAAGGAG	GGCAGCCGTT	0	JIT	0	0	0	0	0
3271	1980	ao	AN3957.1	69.m14963	AO070341000077	1					-318	-304	ATGTGTTTTGCGTAA			ATGTGTTTTGCGTAA	MCFA*			MCFA*	AAAGCGTGTG	CAGATAACTC	0	JIT	0	0	0	0	0
3272	1980	ao	AN3957.1	69.m14963	AO070341000077	1					-70	-11	ATGTGTTTCATAGCGCAACATCATATACCTCCTACCTTCCCCTTAGTTGATCCCCAATAG			ATGTGTTTCATAGCGCAACATCATATACCTCCTACCTTCCCCTTAGTTGATCCCCAATAG	MCFIAQHHIPPTFPLVDPQ*			MCFIAQHHIPPTFPLVDPQ*	GCTTCCTTTG	CTTACTGACT	0	JIT	0	0	0	0	0
3312	1999	ao	AN2748.1	54.m06683	AO070338000223	0					-45	-34	ATGAAACCATAG			ATGAAACCATAG	MKP*			MKP*	ATTGTCTTGG	GCTTGGGGGC	1	R	0	0	0	YPR186C	0
3323	2005	an	AN6512.1	62.m03099	AO070270000007	0	-52	-29					ATGACTTGGGCTGTTCCTAATTAA	ATGACTTGGGCTGTTCCTAATTAA			MTWAVPN*	MTWAVPN*			CTACTGATTT	ACTGAGTTCA	1	RK	FG07165.1	0	0	YFL028C	0
3330	2007	an	AN7483.1	57.m05865	AO070287000044	1	-83	-66					ATGACTTGCCATGCCTGA	ATGACTTGCCATGCCTGA			MTCHA*	MTCHA*			TATCTGTGCA	GGAATGGGTG	0		0	0	0	0	0
3331	2007	an	AN7483.1	57.m05865	AO070287000044	1	-73	-26					ATGCCTGAGGAATGGGTGCCCTTTTCATGCTGTTTTTTCCACCTTTGA	ATGCCTGAGGAATGGGTGCCCTTTTCATGCTGTTTTTTCCACCTTTGA			MPEEWVPFSCCFFHL*	MPEEWVPFSCCFFHL*			ATGACTTGCC	CTGTGACCAG	0		0	0	0	0	0
3335	2007	af	AN7483.1	57.m05865	AO070287000044	1			-45	-16			ATGTGTCGGCAAATCACTTCCAGCAGCTGA		ATGTGTCGGCAAATCACTTCCAGCAGCTGA		MCRQITSSS*		MCRQITSSS*		CATTCGAGGA	TGACGATTCT	1		0	0	0	0	0
3338	2007	ao	AN7483.1	57.m05865	AO070287000044	1					-33	-13	ATGTTTTCTTCATTCATGTGA			ATGTTTTCTTCATTCATGTGA	MFSSFM*			MFSSFM*	GGCTAGGCGG	CGATCATTCG	1		0	0	0	0	0
3356	2013	ao	AN6870.1	71.m15261	AO070314000052	0					-47	-30	ATGTACAGTACTGTTTAA			ATGTACAGTACTGTTTAA	MYSTV*			MYSTV*	ATTCTCTTGT	CTAGTTTACC	1	R	FG02207.1	MG10534.1	0	0	0
3357	2016	conserved	AN1779.1	69.m15647	AO070324000017	1	-177	-163	-188	-174	-129	-115	ATGrCbTyTyTsTrA	ATGGCCTTTCTCTGA	ATGACTTCTCTCTAA	ATGGCGTCTTTGTGA	MafL*	MAFL*	MTSL*	MASL*	mryryswACA	kykAmvvTyy	0	LD	0	0	0	0	0
3358	2017	an	AN2243.1	71.m15877	AO070326000130	1	-296	-285					ATGTCCTTCTAA	ATGTCCTTCTAA			MSF*	MSF*			ACGAAAGCCC	AACAACATCC	0	R	0	MG01743.1	0	0	0
3363	2017	af	AN2243.1	71.m15877	AO070326000130	1			-303	-292			ATGTCTTTTTAG		ATGTCTTTTTAG		MSF*		MSF*		TGATCGATTC	ACACCACACC	0	R	0	MG01743.1	0	0	0
3369	2017	ao	AN2243.1	71.m15877	AO070326000130	1					-337	-326	ATGTCGATCTAA			ATGTCGATCTAA	MSI*			MSI*	CATCTCGTCG	TCAACCCTTT	0	R	0	MG01743.1	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
3384	2032	conserved	AN8846.1	71.m15980	AO070271000030	1	-87	-64	-260	-237	-89	-66	ATGAyCmrybkbyGsTwydCdTrA	ATGATCCGTTGGCGCTTTGCATAA	ATGACCCACCTTCGGTACACTTGA	ATGATCAGTGTCTGGTACTCGTAA	Mirwrfa*	MIRWRFA*	MTHLRYT*	MISVWYS*	CmkywATymA	rwwyyysrAr	0	G	0	0	0	0	0
3385	2032	an	AN8846.1	71.m15980	AO070271000030	1	-318	-295					ATGCCATTCCAGCCAGTGCTTTAA	ATGCCATTCCAGCCAGTGCTTTAA			MPFQPVL*	MPFQPVL*			TTTCTATCGC	CTTCTCTTTC	0	G	0	0	0	0	0
3386	2032	an	AN8846.1	71.m15980	AO070271000030	1	-101	-84					ATGCCCTTTATCCAATGA	ATGCCCTTTATCCAATGA			MPFIQ*	MPFIQ*			CCCCTCTTGC	TCCGTTGGCG	0	G	0	0	0	0	0
3393	2034	an	AN3376.1	66.m04646	AO070281000020	1	-155	-108					ATGTACATTACTTCTCTATTGTGTACTAATACGCCAATTTGCTGCTAA	ATGTACATTACTTCTCTATTGTGTACTAATACGCCAATTTGCTGCTAA			MYITSLLCTNTPICC*	MYITSLLCTNTPICC*			AGAGAGCCTT	TTTTGCCTCC	0	I	0	0	0	0	0
3394	2034	ao	AN3376.1	66.m04646	AO070281000020	1					-103	-86	ATGACTATCTCCTTTTGA			ATGACTATCTCCTTTTGA	MTISF*			MTISF*	TATTTTCTGT	CACAGCGTAT	0	I	0	0	0	0	0
3401	2036	af	AN8767.1	52.m03894	AO070299000022	0			-31	-17			ATGAACAGACGATAA		ATGAACAGACGATAA		MNRR*		MNRR*		ATACTCACTT	CACTTCGTTT	1	M	0	0	0	0	0
3412	2040	ao	AN3233.1	58.m07220	AO070307000047	0					-48	-16	ATGTCCCCGGACTCATCTTCCTTCGCTACATGA			ATGTCCCCGGACTCATCTTCCTTCGCTACATGA	MSPDSSSFAT*			MSPDSSSFAT*	CTTCCCCGGA	AAACCCCTTG	1	R	0	0	0	0	0
3428	2045	an	AN0770.1	70.m15373	AO070316000074	0	-58	-44					ATGAACACCTGGTGA	ATGAACACCTGGTGA			MNTW*	MNTW*			TACCTGCTGA	CTCCAGTTCG	1	T	0	0	NCU01928.1	0	0
3430	2045	af	AN0770.1	70.m15373	AO070316000074	0			-23	-3			ATGGATCACGACTCTCATTAA		ATGGATCACGACTCTCATTAA		MDHDSH*		MDHDSH*		CTGTCGTTGT	CTATGTCCTC	1	T	0	0	NCU01928.1	0	0
3431	2045	ao	AN0770.1	70.m15373	AO070316000074	0					-23	-3	ATGGATCGAGCCATTGATTGA			ATGGATCGAGCCATTGATTGA	MDRAID*			MDRAID*	CCCAATTTGT	CAATGTCCTC	1	T	0	0	NCU01928.1	0	0
3432	2046	an	AN0766.1	70.m15369	AO070316000078	1	-336	-199					ATGACCCCCGCTTGTTTCTCGTCGTTTTGCAGGTCCCTCTCTGCCCGCCGCCTTCTGGCCGAATCTAAACCCGCATTGGAGCGTCCGGCTCCGCCATCGGTAGCACCTCCTCTGCCAGCGTTTCCTATTACTCAATAA	ATGACCCCCGCTTGTTTCTCGTCGTTTTGCAGGTCCCTCTCTGCCCGCCGCCTTCTGGCCGAATCTAAACCCGCATTGGAGCGTCCGGCTCCGCCATCGGTAGCACCTCCTCTGCCAGCGTTTCCTATTACTCAATAA			MTPACFSSFCRSLSARRLLAESKPALERPAPPSVAPPLPAFPITQ*	MTPACFSSFCRSLSARRLLAESKPALERPAPPSVAPPLPAFPITQ*			TCGCTATCCT	CCACCCGCCT	0		0	0	0	0	0
3433	2046	af	AN0766.1	70.m15369	AO070316000078	1			-209	-174			ATGCTCCGCCGTCACTCACCATCGATCGCCATTTGA		ATGCTCCGCCGTCACTCACCATCGATCGCCATTTGA		MLRRHSPSIAI*		MLRRHSPSIAI*		CTGGAGCCTT	CTTTTTTTTC	0		0	0	0	0	0
3437	2047	an	AN9511.1	69.m15659	AO070324000090	0	-25	-8					ATGTCTTGGTCACGCTAG	ATGTCTTGGTCACGCTAG			MSWSR*	MSWSR*			TACTTCACCC	AGCCACCATG	1	R	0	0	0	0	0
3441	2047	af	AN9511.1	69.m15659	AO070324000090	0			-58	-2			ATGGACGAGCATTGGAACATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		ATGGACGAGCATTGGAACATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		MDEHWNMGLDALSLIWST*		MDEHWNMGLDALSLIWST*		CCGTTTCATG	CATGGCGAGC	1	R	0	0	0	0	0
3442	2047	af	AN9511.1	69.m15659	AO070324000090	0			-40	-2			ATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		ATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		MGLDALSLIWST*		MGLDALSLIWST*		GCATTGGAAC	CATGGCGAGC	1	R	0	0	0	0	0
3499	2082	af	AN5742.1	69.m14840	AO070193000003	0			-59	-18			ATGAAGGATTCCTTTACAAGACACCATCAGGCCTGCCATTAA		ATGAAGGATTCCTTTACAAGACACCATCAGGCCTGCCATTAA		MKDSFTRHHQACH*		MKDSFTRHHQACH*		GCGTTTCTTT	CCTCCGCAAT	1	G	FG01593.1	0	0	0	0
3512	2083	af	AN1397.1	70.m14825	AO070233000013	0			-36	-25			ATGAGCAACTGA		ATGAGCAACTGA		MSN*		MSN*		AACATTGACC	ATTTCTGTTG	1	Q	0	0	0	0	0
3560	2107	af	AN6697.1	65.m07286	AO070339000128	1			-52	-26			ATGAATATAAGATTACCGACATTGTGA		ATGAATATAAGATTACCGACATTGTGA		MNIRLPTL*		MNIRLPTL*		GCTAATTGGC	GCGCAGTATT	1		FG01351.1	0	NCU02668.1	0	0
3575	2110	ao	AN2153.1	72.m19688	AO070343000202	0					-17		ATGCCAAGTAATGTGTAA			ATGCCAAGTAATGTGTAA	MPSNV*			MPSNV*	ATTTTATCGG	TGACTGACCG	1	J	0	MG07084.1	NCU08026.1	0	0
3578	2111	an	AN7437.1	57.m05908	AO070229000007	0	-53	-33					ATGTGTTCCAAACCCAAGTGA	ATGTGTTCCAAACCCAAGTGA			MCSKPK*	MCSKPK*			AGCGCCTCGA	TTACTATAAG	1	R	0	0	NCU07504.1	0	0
3587	2113	ao	AN6655.1	62.m03451	AO070269000011	0					-59	-30	ATGTCCCCGCCGAGGATAACTACTCACTGA			ATGTCCCCGCCGAGGATAACTACTCACTGA	MSPPRITTH*			MSPPRITTH*	CAGAAGTCCG	GAATCGCTTG	1	IQR	FG00177.1	0	0	0	0
3608	2121	an	AN0213.1	71.m15479	AO070323000085	1	-180	-166					ATGGAACTGGCCTAG	ATGGAACTGGCCTAG			MELA*	MELA*			CTCCTGACCC	GGTGCCGCCC	0		0	0	0	0	0
3609	2121	an	AN0213.1	71.m15479	AO070323000085	1	-83	-57					ATGATACCACGACGGAACGAATTTTGA	ATGATACCACGACGGAACGAATTTTGA			MIPRRNEF*	MIPRRNEF*			CATCGAGCTG	TTCCATCGAT	0		0	0	0	0	0
3610	2121	af	AN0213.1	71.m15479	AO070323000085	1			-393	-319			ATGACGGCCATCCCTCAGCTATTTGCCGTTTTCTATCCTGCCATACGATTTGCGGCCTTTCAGTTCCTACATTGA		ATGACGGCCATCCCTCAGCTATTTGCCGTTTTCTATCCTGCCATACGATTTGCGGCCTTTCAGTTCCTACATTGA		MTAIPQLFAVFYPAIRFAAFQFLH*		MTAIPQLFAVFYPAIRFAAFQFLH*		ACTTTGCTGC	GGACGATATT	0		0	0	0	0	0
3611	2121	af	AN0213.1	71.m15479	AO070323000085	1			-248	-117			ATGATCATTTTCTCCGCCTCATGGGAGGATCCTGAGGAACCAGCAGGTTCCGACCGCGGTCAACGGTACTCGCCACTAGTCTATCGAACCTCACGACTCACGACGGCACGATTATTTGAATACCATTTCTAA		ATGATCATTTTCTCCGCCTCATGGGAGGATCCTGAGGAACCAGCAGGTTCCGACCGCGGTCAACGGTACTCGCCACTAGTCTATCGAACCTCACGACTCACGACGGCACGATTATTTGAATACCATTTCTAA		MIIFSASWEDPEEPAGSDRGQRYSPLVYRTSRLTTARLFEYHF*		MIIFSASWEDPEEPAGSDRGQRYSPLVYRTSRLTTARLFEYHF*		TCACTGTTTG	ATAGGATTGG	0		0	0	0	0	0
3612	2121	af	AN0213.1	71.m15479	AO070323000085	1			-228	-214			ATGGGAGGATCCTGA		ATGGGAGGATCCTGA		MGGS*		MGGS*		TCTCCGCCTC	GGAACCAGCA	0		0	0	0	0	0
3613	2121	ao	AN0213.1	71.m15479	AO070323000085	1					-375	-364	ATGTTCTTTTAG			ATGTTCTTTTAG	MFF*			MFF*	CCTTTTCTTT	CTAGTCTCTC	0		0	0	0	0	0
3614	2121	ao	AN0213.1	71.m15479	AO070323000085	1					-235	-224	ATGGAACTGTAG			ATGGAACTGTAG	MEL*			MEL*	TCGTCATTCC	TGAGGACCCA	0		0	0	0	0	0
3632	2131	an	AN6711.1	65.m07264	AO070339000151	1	-75	-58					ATGACACTCATTTCTTGA	ATGACACTCATTTCTTGA			MTLIS*	MTLIS*			TTCCCTTGAG	CCGGCTCATT	0	FE	FG04261.1	0	NCU05254.1	0	0
3633	2131	an	AN6711.1	65.m07264	AO070339000151	1	-34	-17					ATGTCTATGATTCTTTGA	ATGTCTATGATTCTTTGA			MSMIL*	MSMIL*			TTTCAGCTTG	TCCGCTCGAT	1	FE	FG04261.1	0	NCU05254.1	0	0
3634	2131	an	AN6711.1	65.m07264	AO070339000151	1	-28	-17					ATGATTCTTTGA	ATGATTCTTTGA			MIL*	MIL*			CTTGATGTCT	TCCGCTCGAT	1	FE	FG04261.1	0	NCU05254.1	0	0
3635	2131	af	AN6711.1	65.m07264	AO070339000151	1			-90	-10			ATGCCCTTCACAACCCCTACCTCCTTTCTACTCTCCCCTCTCGTCTCCTCATTGTACATGCCTTCATTTCGCAGTACTTAA		ATGCCCTTCACAACCCCTACCTCCTTTCTACTCTCCCCTCTCGTCTCCTCATTGTACATGCCTTCATTTCGCAGTACTTAA		MPFTTPTSFLLSPLVSSLYMPSFRST*		MPFTTPTSFLLSPLVSSLYMPSFRST*		GCCATTTGAA	TAGGTCACAA	0	FE	FG04261.1	0	NCU05254.1	0	0
3636	2131	af	AN6711.1	65.m07264	AO070339000151	1			-33	-10			ATGCCTTCATTTCGCAGTACTTAA		ATGCCTTCATTTCGCAGTACTTAA		MPSFRST*		MPSFRST*		CTCATTGTAC	TAGGTCACAA	1	FE	FG04261.1	0	NCU05254.1	0	0
3637	2131	ao	AN6711.1	65.m07264	AO070339000151	1					-479	-459	ATGTCTTATTCTAGCACATAA			ATGTCTTATTCTAGCACATAA	MSYSST*			MSYSST*	TCCCTTGTCC	TTACACCAAA	0	FE	FG04261.1	0	NCU05254.1	0	0
3647	2138	af	AN5005.1	59.m08905	AO070255000035	0			-58	-29			ATGCTCCTACCTTACTATCCTATCTTTTAA		ATGCTCCTACCTTACTATCCTATCTTTTAA		MLLPYYPIF*		MLLPYYPIF*		TTAACCACAT	TCCCACCATT	1		0	0	0	0	0
3649	2138	ao	AN5005.1	59.m08905	AO070255000035	0					-59	-45	ATGTTCCTTCCATAA			ATGTTCCTTCCATAA	MFLP*			MFLP*	AATTGTCTAT	TCTATATCTC	1		0	0	0	0	0
3650	2143	an	AN8886.1	56.m03088	AO070293000018	1	-253	-173					ATGACAGCTGCCTCCGACCACTCCCTGCCCGAAACCTCCTTCACTCCGCATTGCGCTTATCGTTCCCCGGTTTCCCCTTAA	ATGACAGCTGCCTCCGACCACTCCCTGCCCGAAACCTCCTTCACTCCGCATTGCGCTTATCGTTCCCCGGTTTCCCCTTAA			MTAASDHSLPETSFTPHCAYRSPVSP*	MTAASDHSLPETSFTPHCAYRSPVSP*			CCATTGCAGC	GATATGGGAG	0	E	0	0	NCU04358.1	0	0
3651	2143	an	AN8886.1	56.m03088	AO070293000018	1	-169	-158					ATGGGAGTTTAG	ATGGGAGTTTAG			MGV*	MGV*			CCCTTAAGAT	GAGATGAATC	0	E	0	0	NCU04358.1	0	0
3652	2143	af	AN8886.1	56.m03088	AO070293000018	1			-362	-255			ATGTTTCTTACTGTACCCCATACCTCCTCATCCCCTCGTCCTTCCAAATCTCCACGCGTGCCGCAGCTGTGCAGTTGTGAGACTTTTCTATTCGCAGCACGTTAACTGA		ATGTTTCTTACTGTACCCCATACCTCCTCATCCCCTCGTCCTTCCAAATCTCCACGCGTGCCGCAGCTGTGCAGTTGTGAGACTTTTCTATTCGCAGCACGTTAACTGA		MFLTVPHTSSSLVLPNLHACRSCAVVRLFYSQHVN*		MFLTVPHTSSSLVLPNLHACRSCAVVRLFYSQHVN*		AATCACTAAT	GACTGAGAGA	0	E	0	0	NCU04358.1	0	0
3653	2143	af	AN8886.1	56.m03088	AO070293000018	1			-96	-64			ATGGCGCCTAAAAAAGAAAACAACTTTGGATAA		ATGGCGCCTAAAAAAGAAAACAACTTTGGATAA		MAPKKENNFG*		MAPKKENNFG*		TTATCGAGAG	ATTGGGACAA	0	E	0	0	NCU04358.1	0	0
3654	2143	ao	AN8886.1	56.m03088	AO070293000018	1					-267	-181	ATGCTCGCTGTGAATCGTTGCATCGTCTCAAGGCATATGCGCCCCGATTATCTACTACGTCCTTATCTCGTTATCAAGCTCGAGTAG			ATGCTCGCTGTGAATCGTTGCATCGTCTCAAGGCATATGCGCCCCGATTATCTACTACGTCCTTATCTCGTTATCAAGCTCGAGTAG	MLAVNRCIVSRHMRPDYLLRPYLVIKLE*			MLAVNRCIVSRHMRPDYLLRPYLVIKLE*	CAGTCACAGC	TGGATTCAGG	0	E	0	0	NCU04358.1	0	0
3655	2143	ao	AN8886.1	56.m03088	AO070293000018	1					-231	-181	ATGCGCCCCGATTATCTACTACGTCCTTATCTCGTTATCAAGCTCGAGTAG			ATGCGCCCCGATTATCTACTACGTCCTTATCTCGTTATCAAGCTCGAGTAG	MRPDYLLRPYLVIKLE*			MRPDYLLRPYLVIKLE*	CTCAAGGCAT	TGGATTCAGG	0	E	0	0	NCU04358.1	0	0
3656	2143	ao	AN8886.1	56.m03088	AO070293000018	1					-134	-108	ATGGTTCCACTTATGATTGTTCGCTGA			ATGGTTCCACTTATGATTGTTCGCTGA	MVPLMIVR*			MVPLMIVR*	CAGCTGAATC	AGATAGTGAG	0	E	0	0	NCU04358.1	0	0
3657	2143	ao	AN8886.1	56.m03088	AO070293000018	1					-122	-108	ATGATTGTTCGCTGA			ATGATTGTTCGCTGA	MIVR*			MIVR*	GGTTCCACTT	AGATAGTGAG	0	E	0	0	NCU04358.1	0	0
3681	2153	af	AN9526.1	59.m09117	AO070327000084	1			-171	-145			ATGTTTACTTATTCTGCCCCTATTTGA		ATGTTTACTTATTCTGCCCCTATTTGA		MFTYSAPI*		MFTYSAPI*		GACTCACTCG	CTAACGCCGC	0	U	0	0	0	0	0
3695	2156	ao	AN2830.1	71.m15507	AO070330000102	0					-52	-20	ATGGGGTGCAACGTTTTCCCTAACCGATCATAA			ATGGGGTGCAACGTTTTCCCTAACCGATCATAA	MGCNVFPNRS*			MGCNVFPNRS*	CCCCCTCCCC	CATAGCAGAA	1	I	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
3699	2157	af	AN6721.1	53.m03953	AO070335000072	0			-51	-34			ATGGCAACAGTAGATTGA		ATGGCAACAGTAGATTGA		MATVD*		MATVD*		TATATTATAT	TTCGCTGGAT	1	R	0	0	0	0	0
3764	2186	ao	AN2236.1	71.m15828	AO070326000140	0					-42	-28	ATGTGTGGCGCATAG			ATGTGTGGCGCATAG	MCGA*			MCGA*	CTCTTTCTTT	ACGGTAGGCG	1	S	0	0	0	0	0
3770	2191	ao	AN3793.1	57.m05691	AO070337000236	1					-505	-419	ATGTGGTGCATGATATCGACATCGCTAACCGTCGTATCGCAGAAGCTTACTTCGGGCGAATCGGAACTTTCCCTTCCGACCAACTAG			ATGTGGTGCATGATATCGACATCGCTAACCGTCGTATCGCAGAAGCTTACTTCGGGCGAATCGGAACTTTCCCTTCCGACCAACTAG	MWCMISTSLTVVSQKLTSGESELSLPTN*			MWCMISTSLTVVSQKLTSGESELSLPTN*	TGTTGGTCCC	TTCGCCGGTG	0	TR	0	0	0	0	0
3771	2191	ao	AN3793.1	57.m05691	AO070337000236	1					-496	-419	ATGATATCGACATCGCTAACCGTCGTATCGCAGAAGCTTACTTCGGGCGAATCGGAACTTTCCCTTCCGACCAACTAG			ATGATATCGACATCGCTAACCGTCGTATCGCAGAAGCTTACTTCGGGCGAATCGGAACTTTCCCTTCCGACCAACTAG	MISTSLTVVSQKLTSGESELSLPTN*			MISTSLTVVSQKLTSGESELSLPTN*	CATGTGGTGC	TTCGCCGGTG	0	TR	0	0	0	0	0
3775	2192	ao	AN5992.1	72.m19148	AO070340000285	1					-80	-69	ATGCGAGTCTAG			ATGCGAGTCTAG	MRV*			MRV*	CCCCCGATCG	TACTGTCGCC	0	L	0	0	0	0	0
3796	2204	an	AN6779.1	71.m15523	AO070292000024	0	-36	-7					ATGGTTCTTCTTTCTACGGACAGCAGCTGA	ATGGTTCTTCTTTCTACGGACAGCAGCTGA			MVLLSTDSS*	MVLLSTDSS*			TGCCAGCGTT	TTGACAATGT	1	Q	0	0	0	0	0
3814	2215	af	AN4763.1	59.m09489	AO070327000053	0			-54	-31			ATGATCAATCGGCGTTCCTGCTAA		ATGATCAATCGGCGTTCCTGCTAA		MINRRSC*		MINRRSC*		AAACTATGCC	GTAGAGATTC	1	R	0	0	0	0	0
3824	2218	an	AN9144.1	66.m04609	AO070332000114	0	-55	-26					ATGCGCCATAGTAGATTTGACAAGTTTTGA	ATGCGCCATAGTAGATTTGACAAGTTTTGA			MRHSRFDKF*	MRHSRFDKF*			TACCCCTGCA	GAATTTACGC	1	E	0	0	0	0	0
3827	2218	af	AN9144.1	66.m04609	AO070332000114	0			-58	-41			ATGCTTATAGCATTCTAG		ATGCTTATAGCATTCTAG		MLIAF*		MLIAF*		CTCGCTTGCG	TATCATCCCG	1	E	0	0	0	0	0
3828	2218	ao	AN9144.1	66.m04609	AO070332000114	0					-49	-38	ATGCTTCTATAG			ATGCTTCTATAG	MLL*			MLL*	CGAACTTGCT	TAAACTATAC	1	E	0	0	0	0	0
3832	2222	af	AN1555.1	55.m03072	AO070339000298	0			-59	-30			ATGTTGATGGATACCGGCCAGGGTCACTGA		ATGTTGATGGATACCGGCCAGGGTCACTGA		MLMDTGQGH*		MLMDTGQGH*		GTTCTGTCAG	CAATGTCTTT	1	M	0	0	0	0	0
3833	2222	af	AN1555.1	55.m03072	AO070339000298	0			-53	-30			ATGGATACCGGCCAGGGTCACTGA		ATGGATACCGGCCAGGGTCACTGA		MDTGQGH*		MDTGQGH*		TCAGATGTTG	CAATGTCTTT	1	M	0	0	0	0	0
3834	2222	af	AN1555.1	55.m03072	AO070339000298	0			-27	-16			ATGTCTTTCTGA		ATGTCTTTCTGA		MSF*		MSF*		GTCACTGACA	ATCCATAGAA	1	M	0	0	0	0	0
3838	2222	ao	AN1555.1	55.m03072	AO070339000298	0					-30	-16	ATGCTCACACTCTAG			ATGCTCACACTCTAG	MLTL*			MLTL*	GCATCTCGCC	TTCCTTAGAA	1	M	0	0	0	0	0
3852	2228	an	AN5657.1	58.m07322	AO070342000247	0	-35	-18					ATGCTTGTCTATCTTTGA	ATGCTTGTCTATCTTTGA			MLVYL*	MLVYL*			TCAGGGCTCT	ACTATTTTAC	1		0	0	0	0	0
3864	2229	af	AN4111.1	52.m03714	AO070342000382	0			-22	-5			ATGCTCATCAAAGACTAG		ATGCTCATCAAAGACTAG		MLIKD*		MLIKD*		CAAGGTTGTT	CACCATGGCT	1	Q	0	0	0	0	0
3957	2274	af	AN3220.1	67.m02928	AO070330000070	1			-117	-103			ATGCACGGGGTATAA		ATGCACGGGGTATAA		MHGV*		MHGV*		CGCAGTGTTC	AGCTGGGAAG	0	GEPR	FG10483.1	MG05600.1	0	0	0
3990	2291	an	AN5333.1	69.m15580	AO070290000026	0	-39	-25					ATGAAACCCAGGTGA	ATGAAACCCAGGTGA			MKPR*	MKPR*			GACATAGGCC	ATCGCAAAAA	1		0	0	0	0	0
4001	2294	an	AN8726.1	66.m04723	AO070300000100	0	-36	-16					ATGTTTCGTGGCCTTATGTAA	ATGTTTCGTGGCCTTATGTAA			MFRGLM*	MFRGLM*			TCTTCCTTTC	TTGATCGTTG	1	E	0	0	0	0	0
4002	2300	an	AN8689.1	62.m03383	AO070315000110	1	-311	-261					ATGAAATTATCTCGGCCTTGCTTCATTTTACCTCTTTATGAATTATTATAA	ATGAAATTATCTCGGCCTTGCTTCATTTTACCTCTTTATGAATTATTATAA			MKLSRPCFILPLYELL*	MKLSRPCFILPLYELL*			CTCCGTGTCG	TCGTCCGTTC	0	G	0	0	0	0	0
4005	2300	ao	AN8689.1	62.m03383	AO070315000110	1					-234	-190	ATGCGCCCTCAATATTATCGCTTGGATACCATGCAACCTATATAA			ATGCGCCCTCAATATTATCGCTTGGATACCATGCAACCTATATAA	MRPQYYRLDTMQPI*			MRPQYYRLDTMQPI*	TTCCCTACGT	TTCCAAGAAA	0	G	0	0	0	0	0
4006	2300	ao	AN8689.1	62.m03383	AO070315000110	1					-204	-190	ATGCAACCTATATAA			ATGCAACCTATATAA	MQPI*			MQPI*	CTTGGATACC	TTCCAAGAAA	0	G	0	0	0	0	0
4038	2310	an	AN1176.1	70.m15041	AO070331000171	1	-39	-7					ATGCTCTCTCTCCTATGTTCTTGTCCCTCCTAG	ATGCTCTCTCTCCTATGTTCTTGTCCCTCCTAG			MLSLLCSCPS*	MLSLLCSCPS*			TTTAAATCCT	GAAAAAATGG	1	IT	0	0	0	0	0
4039	2310	af	AN1176.1	70.m15041	AO070331000171	1			-169	-146			ATGAAGTACCTATGTCAAAGCTGA		ATGAAGTACCTATGTCAAAGCTGA		MKYLCQS*		MKYLCQS*		CTAAGAAATA	CTCTACCTCA	0	IT	0	0	0	0	0
4040	2310	af	AN1176.1	70.m15041	AO070331000171	1			-158	-87			ATGTCAAAGCTGACTCTACCTCAATCTCGAACATCCTACAAGGAGTTCTTGCCTTTTTCATTCTTATATTGA		ATGTCAAAGCTGACTCTACCTCAATCTCGAACATCCTACAAGGAGTTCTTGCCTTTTTCATTCTTATATTGA		MSKLTLPQSRTSYKEFLPFSFLY*		MSKLTLPQSRTSYKEFLPFSFLY*		TGAAGTACCT	CTATCATTAT	0	IT	0	0	0	0	0
4041	2310	ao	AN1176.1	70.m15041	AO070331000171	1					-247	-215	ATGAAACCAAGTCAGCCAATTCTTTTTTATTAA			ATGAAACCAAGTCAGCCAATTCTTTTTTATTAA	MKPSQPILFY*			MKPSQPILFY*	CAACATTTAA	TTTTTCGACA	0	IT	0	0	0	0	0
4042	2310	ao	AN1176.1	70.m15041	AO070331000171	1					-201	-175	ATGATCATCTATTTAGCCTTTTCCTGA			ATGATCATCTATTTAGCCTTTTCCTGA	MIIYLAFS*			MIIYLAFS*	TTCGACATTT	ACCTCCGCCC	0	IT	0	0	0	0	0
4045	2311	an	AN1198.1	70.m15021	AO070331000203	0	-20						ATGCTACGAATTAACCCATAA	ATGCTACGAATTAACCCATAA			MLRINP*	MLRINP*			TTTTTTTCAT	TGTCTGCTTT	1	E	0	MG04826.1	NCU02727.1	0	0
4054	2314	an	AN0247.1	54.m06700	AO070338000240	0	-60	-4					ATGCAGAGACTTCGCGTGCAGTATCTTCTAGAGTTCAGAGATCTAGCGGTTGCATGA	ATGCAGAGACTTCGCGTGCAGTATCTTCTAGAGTTCAGAGATCTAGCGGTTGCATGA			MQRLRVQYLLEFRDLAVA*	MQRLRVQYLLEFRDLAVA*			TTTTTTTTTA	AAGATGCCTC	1	R	FG00732.1	0	0	0	0
4071	2318	ao	AN8968.1	70.m15193	AO070342000435	0					-33	-22	ATGCATGTATGA			ATGCATGTATGA	MHV*			MHV*	AAGCATCTAC	TCTCAAGAAA	1		0	0	0	0	0
4072	2318	ao	AN8968.1	70.m15193	AO070342000435	0					-25	-5	ATGATCTCAAGAAACAGATGA			ATGATCTCAAGAAACAGATGA	MISRNR*			MISRNR*	ACATGCATGT	CAAAATGGCT	1		0	0	0	0	0
4111	2326	an	AN3363.1	66.m04629	AO070281000032	0	-48	-22					ATGTCCAATTATTGTTTCTGTACCTAA	ATGTCCAATTATTGTTTCTGTACCTAA			MSNYCFCT*	MSNYCFCT*			GTTTGGTCTT	TTCCTACCGT	1	Z	FG00697.1	0	0	0	0
4120	2333	an	AN6890.1	71.m15249	AO070314000031	0	-52	-38					ATGACGACTGGATGA	ATGACGACTGGATGA			MTTG*	MTTG*			ATTGACTTGC	AGACAGAAGT	1	R	0	0	0	0	0
4122	2333	af	AN6890.1	71.m15249	AO070314000031	0			-56	-18			ATGATCGGACGAATACAACACTCGCACTGCTATTGCTGA		ATGATCGGACGAATACAACACTCGCACTGCTATTGCTGA		MIGRIQHSHCYC*		MIGRIQHSHCYC*		GCTCACTAGA	GTCCTTAACC	1	R	0	0	0	0	0
4127	2333	ao	AN6890.1	71.m15249	AO070314000031	0					-38	-18	ATGACTGCGCACATCAACTAA			ATGACTGCGCACATCAACTAA	MTAHIN*			MTAHIN*	TGCACATATA	ACAATCAAGC	1	R	0	0	0	0	0
4154	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-53		ATGCCGGAAACAGTTGGGCTTGCGTCGCCGTTTCGCCCCAATCCCTGCTCATGA			ATGCCGGAAACAGTTGGGCTTGCGTCGCCGTTTCGCCCCAATCCCTGCTCATGA	MPETVGLASPFRPNPCS*			MPETVGLASPFRPNPCS*	ATTTATTGAT	TGACTGGATT	1	H	0	0	0	0	0
4167	2345	an	AN6147.1	72.m19018	AO070340000055	0	-29	-15					ATGGGACTTCTGTGA	ATGGGACTTCTGTGA			MGLL*	MGLL*			GCTTGATTAC	TAAGCTATCT	1	B	0	0	0	0	0
4169	2345	ao	AN6147.1	72.m19018	AO070340000055	0					-29	-15	ATGGGAAATCTGTGA			ATGGGAAATCTGTGA	MGNL*			MGNL*	CAATCTTTAT	TCTCGCAGAT	1	B	0	0	0	0	0
4175	2347	ao	AN3590.1	58.m07390	AO070342000142	1					-459	-304	ATGAATGTGACTTGCTCTTTCCCTGACATCAATTCATTTAAATACCATCCCCTCATAACCTCTCACTACCCCAGTGGTTCCCTCAGATTATTATTACTCGCATCCTCCTCCTCAGCACTAACTGTGGCTAACCTCCATCCATTTTTTATTTCTTGA			ATGAATGTGACTTGCTCTTTCCCTGACATCAATTCATTTAAATACCATCCCCTCATAACCTCTCACTACCCCAGTGGTTCCCTCAGATTATTATTACTCGCATCCTCCTCCTCAGCACTAACTGTGGCTAACCTCCATCCATTTTTTATTTCTTGA	MNVTCSFPDINSFKYHPLITSHYPSGSLRLLLLASSSALTVANLHPFFIS*			MNVTCSFPDINSFKYHPLITSHYPSGSLRLLLLASSSALTVANLHPFFIS*	GGAAAGGCAC	CTTGTATACT	0		0	MG09900.1	0	0	0
4198	2350	ao	AN0646.1	70.m15248	AO070343000583	1					-143	-129	ATGACCGATTCGTGA			ATGACCGATTCGTGA	MTDS*			MTDS*	AAGCTCGTGT	TTTTGATCTG	0	A	0	0	0	0	0
4203	2352	ao	AN1427.1	55.m02928	AO070242000025	1					-397	-353	ATGATACCCTTCGATTTGTTCCTGCCATTCACTTGCTTCCGGTAG			ATGATACCCTTCGATTTGTTCCTGCCATTCACTTGCTTCCGGTAG	MIPFDLFLPFTCFR*			MIPFDLFLPFTCFR*	CTACACATTG	CTTCCCTTTT	0	S	0	0	0	0	0
4204	2352	ao	AN1427.1	55.m02928	AO070242000025	1					-326	-144	ATGTGTGTATCCTTCTCCAAGTTCTCCTTCCCTCCCTCTTCCTTCTGTTTACCTTGCTCCACCTATTTGCCCCCCCTTTTCCTCCTCCTACATTCTTCCTCATCCCTCTTCCTTTCAAGCTTGACCCACCACCAAACTCTCCTCCATTCTTGTCTCTCTTTCTCCCCTTTCAATATTTCTTTGA			ATGTGTGTATCCTTCTCCAAGTTCTCCTTCCCTCCCTCTTCCTTCTGTTTACCTTGCTCCACCTATTTGCCCCCCCTTTTCCTCCTCCTACATTCTTCCTCATCCCTCTTCCTTTCAAGCTTGACCACCACCAAACTCTCCTCCATTCTTGTCTCTCTTTCTCCCCTTTCAATATTTCTTTGA	MCVSFSKFSFPPSSFCLPCSTYLPPLFLLLHSSSSLFLSSLTTTKLSSILVSLSPLSIFL*			MCVSFSKFSFPPSSFCLPCSTYLPPLFLLLHSSSSLFLSSLTTTKLSSILVSLSPLSIFL*	ATTTATTTTC	TCCACTATTG	0	S	0	0	0	0	0
4211	2355	ao	AN6409.1	67.m02948	AO070276000080	0					-55	-26	ATGTGCACTATCGTCTCCTCAATCTACTAG			ATGTGCACTATCGTCTCCTCAATCTACTAG	MCTIVSSIY*			MCTIVSSIY*	TCTTTATTTT	CAACCCATCC	1		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
4214	2359	ao	AN8880.1	56.m02291	AO070293000010	0					-20	-6	ATGTTTCAAGAGTAG			ATGTTTCAAGAGTAG	MFQE*			MFQE*	GTTGTTTCAA	CGGTCATGAT	1	R	FG00615.1	0	0	0	0
4223	2364	an	AN3828.1	58.m07804	AO070305000065	0	-28	-11					ATGTTCATACTCCCATGA	ATGTTCATACTCCCATGA			MFILP*	MFILP*			GCGGCCGTTG	ATCTCGAGGC	1		0	0	0	0	0
4229	2364	af	AN3828.1	58.m07804	AO070305000065	0			-23	-6			ATGACTCTCTTAGACTGA		ATGACTCTCTTAGACTGA		MTLLD*		MTLLD*		TAGGAGACGC	AAACAATGTC	1		0	0	0	0	0
4259	2373	ao	AN1772.1	69.m15064	AO070324000030	0					-34	-23	ATGTCTCCGTGA			ATGTCTCCGTGA	MSP*			MSP*	GCAGAGGAAA	ACAACAACCA	1		0	0	0	0	0
4261	2374	af	AN6618.1	62.m03214	AO070326000068	0			-58	-38			ATGATGAGAACTTTTCTCTGA		ATGATGAGAACTTTTCTCTGA		MMRTFL*		MMRTFL*		AGTCTTTCGC	AAAAACATCT	1	T	0	0	0	0	0
4262	2374	af	AN6618.1	62.m03214	AO070326000068	0			-55	-38			ATGAGAACTTTTCTCTGA		ATGAGAACTTTTCTCTGA		MRTFL*		MRTFL*		CTTTCGCATG	AAAAACATCT	1	T	0	0	0	0	0
4272	2377	an	AN0484.1	69.m15370	AO070336000183	1	-143	-99					ATGTGTGGAAGCCGCCAAGGATACCAAGGCGGGCCATGGAGATAA	ATGTGTGGAAGCCGCCAAGGATACCAAGGCGGGCCATGGAGATAA			MCGSRQGYQGGPWR*	MCGSRQGYQGGPWR*			TGCTGACTGC	GTATGTGCTA	0		0	0	0	0	0
4276	2377	af	AN0484.1	69.m15370	AO070336000183	1			-139	-122			ATGCGAACTGGGGAGTGA		ATGCGAACTGGGGAGTGA		MRTGE*		MRTGE*		TACTGCTGCC	ACGGTTTTTC	0		0	0	0	0	0
4277	2377	ao	AN0484.1	69.m15370	AO070336000183	1					-185	-108	ATGGGAAGCAAGGGACGGAATTGTGATATGCTCCAACCTCGTGAACCGGGCCGACAGAGGCTTCCGGTTCGAGGATAA			ATGGGAAGCAAGGGACGGAATTGTGATATGCTCCAACCTCGTGAACCGGGCCGACAGAGGCTTCCGGTTCGAGGATAA	MGSKGRNCDMLQPREPGRQRLPVRG*			MGSKGRNCDMLQPREPGRQRLPVRG*	CTTATCAGAT	ATAGGAGCTT	0		0	0	0	0	0
4278	2377	ao	AN0484.1	69.m15370	AO070336000183	1					-158	-108	ATGCTCCAACCTCGTGAACCGGGCCGACAGAGGCTTCCGGTTCGAGGATAA			ATGCTCCAACCTCGTGAACCGGGCCGACAGAGGCTTCCGGTTCGAGGATAA	MLQPREPGRQRLPVRG*			MLQPREPGRQRLPVRG*	GAATTGTGAT	ATAGGAGCTT	0		0	0	0	0	0
4285	2379	af	AN0249.1	54.m06702	AO070338000242	0			-47	-27			ATGACCTTTAATTGCTGCTAG		ATGACCTTTAATTGCTGCTAG		MTFNCC*		MTFNCC*		TCTTCTGGTG	ATACTCTCCC	1		0	0	0	0	0
4286	2379	af	AN0249.1	54.m06702	AO070338000242	0			-16	-2			ATGCACCACAGTTAA		ATGCACCACAGTTAA		MHHS*		MHHS*		ATACTCTCCC	AATGATGGCG	1		0	0	0	0	0
4292	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-60	-34	ATGCTTGACTCTCCTCTGCGCTCGTGA			ATGCTTGACTCTCCTCTGCGCTCGTGA	MLDSPLRS*			MLDSPLRS*	CATTTTCTCT	ACAGAAGCTC	1		0	0	0	0	0
4301	2383	an	AN3711.1	69.m15416	AO070341000337	1	-190	-140					ATGCTCTCGGACGGCGCGATATATTCAATTCAAATCCGTCAAGTTATTTGA	ATGCTCTCGGACGGCGCGATATATTCAATTCAAATCCGTCAAGTTATTTGA			MLSDGAIYSIQIRQVI*	MLSDGAIYSIQIRQVI*			AAGACGCACA	AGCCGAAGTA	0	O	0	0	0	0	0
4302	2383	an	AN3711.1	69.m15416	AO070341000337	1	-126	-109					ATGTTTAACCTGCTCTGA	ATGTTTAACCTGCTCTGA			MFNLL*	MFNLL*			CGAAGTATAC	GCCGTGTATG	0	O	0	0	0	0	0
4306	2383	af	AN3711.1	69.m15416	AO070341000337	1			-238	-194			ATGCTCTGGCACCTAGGCCCTTACCTCTGTTTCCTAAGCCTTTGA		ATGCTCTGGCACCTAGGCCCTTACCTCTGTTTCCTAAGCCTTTGA		MLWHLGPYLCFLSL*		MLWHLGPYLCFLSL*		AAAACGCACA	CGGTGGATGA	0	O	0	0	0	0	0
4307	2383	af	AN3711.1	69.m15416	AO070341000337	1			-187	-140			ATGATCTCCCAAAGCAAAAGGGAGGCCTGCGTACTGCTTCTCTGCTAA		ATGATCTCCCAAAGCAAAAGGGAGGCCTGCGTACTGCTTCTCTGCTAA		MISQSKREACVLLLC*		MISQSKREACVLLLC*		TTGACGGTGG	GGCCAAAGTA	0	O	0	0	0	0	0
4311	2383	ao	AN3711.1	69.m15416	AO070341000337	1					-491	-417	ATGCTTTGGCTCCTCGCTCCAGATCCGGGGAATCGGCTACTACACAAAAAGGCCTACGTACAACTAGCTTTTTAA			ATGCTTTGGCTCCTCGCTCCAGATCCGGGGAATCGGCTACTACACAAAAAGGCCTACGTACAACTAGCTTTTTAA	MLWLLAPDPGNRLLHKKAYVQLAF*			MLWLLAPDPGNRLLHKKAYVQLAF*	AAGACACATA	AACCAAAGTA	0	O	0	0	0	0	0
4351	2394	af	AN3432.1	59.m09292	AO070265000009	1			-86	-75			ATGCCCAATTGA		ATGCCCAATTGA		MPN*		MPN*		AACAACTCGC	ACTACTTAAC	0	G	FG06059.1	MG03853.1	NCU09705.1	YNR071C	0
4352	2394	af	AN3432.1	59.m09292	AO070265000009	1			-52	-38			ATGTCCAACCAGTGA		ATGTCCAACCAGTGA		MSNQ*		MSNQ*		CATTAAGTCC	CAAGATCCCA	1	G	FG06059.1	MG03853.1	NCU09705.1	YNR071C	0
4370	2399	af	AN4991.1	59.m08894	AO070288000071	1			-389	-366			ATGCAGCGCCTCCTAGCGATTTAA		ATGCAGCGCCTCCTAGCGATTTAA		MQRLLAI*		MQRLLAI*		AAATTGTTTT	CCTCGTTCTC	0		0	0	0	0	0
4409	2407	an	AN6923.1	59.m08483	AO070318000108	0	-52	-32					ATGCTTTTCTTCATTGATTAG	ATGCTTTTCTTCATTGATTAG			MLFFID*	MLFFID*			CTTCTTCCTG	TGTGCTGTTG	1	R	0	0	NCU08152.1	0	0
4412	2407	ao	AN6923.1	59.m08483	AO070318000108	0					-55	-41	ATGTTCTCTGCTTGA			ATGTTCTCTGCTTGA	MFSA*			MFSA*	CTTTCTTCAC	TCCGACCTTG	1	R	0	0	NCU08152.1	0	0
4420	2408	ao	AN2342.1	71.m15578	AO070319000156	0					-53	-30	ATGTCTCTGAGTACAGTTCAGTAA			ATGTCTCTGAGTACAGTTCAGTAA	MSLSTVQ*			MSLSTVQ*	CTTTTCATTA	ATTAGCACAT	1		0	0	0	0	0
4469	2422	an	AN2176.1	72.m19664	AO070343000248	1	-145	-83					ATGACTCAACTCCGCACTTCTCGACTGCAGCAATTGCTCCCTATCACGCTCCCTTGTGGATAA	ATGACTCAACTCCGCACTTCTCGACTGCAGCAATTGCTCCCTATCACGCTCCCTTGTGGATAA			MTQLRTSRLQQLLPITLPCG*	MTQLRTSRLQQLLPITLPCG*			ACCATTGCCC	TCTCACGCGT	0		0	0	0	0	0
4470	2422	af	AN2176.1	72.m19664	AO070343000248	1			-364	-296			ATGGTGATGACAGCTGCAAGGGTGGATTCAGGCTGCCATAAGTTCATGATGCGTATACTGGATGATTGA		ATGGTGATGACAGCTGCAAGGGTGGATTCAGGCTGCCATAAGTTCATGATGCGTATACTGGATGATTGA		MVMTAARVDSGCHKFMMRILDD*		MVMTAARVDSGCHKFMMRILDD*		CCTAGGAGTG	CTCAACCCAG	0		0	0	0	0	0
4471	2422	af	AN2176.1	72.m19664	AO070343000248	1			-358	-296			ATGACAGCTGCAAGGGTGGATTCAGGCTGCCATAAGTTCATGATGCGTATACTGGATGATTGA		ATGACAGCTGCAAGGGTGGATTCAGGCTGCCATAAGTTCATGATGCGTATACTGGATGATTGA		MTAARVDSGCHKFMMRILDD*		MTAARVDSGCHKFMMRILDD*		AGTGATGGTG	CTCAACCCAG	0		0	0	0	0	0
4472	2422	af	AN2176.1	72.m19664	AO070343000248	1			-319	-296			ATGATGCGTATACTGGATGATTGA		ATGATGCGTATACTGGATGATTGA		MMRILDD*		MMRILDD*		CCATAAGTTC	CTCAACCCAG	0		0	0	0	0	0
4473	2422	af	AN2176.1	72.m19664	AO070343000248	1			-316	-296			ATGCGTATACTGGATGATTGA		ATGCGTATACTGGATGATTGA		MRILDD*		MRILDD*		TAAGTTCATG	CTCAACCCAG	0		0	0	0	0	0
4474	2422	af	AN2176.1	72.m19664	AO070343000248	1			-303	-259			ATGATTGACTCAACCCAGCGGTGCCCACACTCATTTCTCGAGTGA		ATGATTGACTCAACCCAGCGGTGCCCACACTCATTTCTCGAGTGA		MIDSTQRCPHSFLE*		MIDSTQRCPHSFLE*		CGTATACTGG	CATTGAATTG	0		0	0	0	0	0
4475	2422	ao	AN2176.1	72.m19664	AO070343000248	1					-413	-354	ATGGGAGCTCAATTGAGGGCGGTGACGGAAATAATGATGACGGGTACAATGGGTAACTGA			ATGGGAGCTCAATTGAGGGCGGTGACGGAAATAATGATGACGGGTACAATGGGTAACTGA	MGAQLRAVTEIMMTGTMGN*			MGAQLRAVTEIMMTGTMGN*	TACACCTAGT	AGGTATCTAA	0		0	0	0	0	0
4476	2422	ao	AN2176.1	72.m19664	AO070343000248	1					-380	-354	ATGATGACGGGTACAATGGGTAACTGA			ATGATGACGGGTACAATGGGTAACTGA	MMTGTMGN*			MMTGTMGN*	GACGGAAATA	AGGTATCTAA	0		0	0	0	0	0
4477	2422	ao	AN2176.1	72.m19664	AO070343000248	1					-377	-354	ATGACGGGTACAATGGGTAACTGA			ATGACGGGTACAATGGGTAACTGA	MTGTMGN*			MTGTMGN*	GGAAATAATG	AGGTATCTAA	0		0	0	0	0	0
4478	2422	ao	AN2176.1	72.m19664	AO070343000248	1					-365	-354	ATGGGTAACTGA			ATGGGTAACTGA	MGN*			MGN*	GACGGGTACA	AGGTATCTAA	0		0	0	0	0	0
4482	2424	an	AN5883.1	72.m19248	AO070245000025	0	-30	-13					ATGGCTCGAGCAGAATAA	ATGGCTCGAGCAGAATAA			MARAE*	MARAE*			AACAGTGCTG	GCAGCCCGCA	1	E	0	0	NCU07690.1	0	0
4493	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-164	-129	ATGCTGTACTTCTTGGCAAGGTATGAGAACCCATAA			ATGCTGTACTTCTTGGCAAGGTATGAGAACCCATAA	MLYFLARYENP*			MLYFLARYENP*	TGCCCTGCAT	ATAATTCGGT	0		0	0	0	0	0
4494	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-142	-125	ATGAGAACCCATAAATAA			ATGAGAACCCATAAATAA	MRTHK*			MRTHK*	TTGGCAAGGT	TTCGGTAGAG	0		0	0	0	0	0
4495	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-103	-32	ATGATGAACCATGCCTTGTTTTGGGTACGGAGGAGATTAGTAAGGTTCGAGATAACCCTTTGCAACCACTGA			ATGATGAACCATGCCTTGTTTTGGGTACGGAGGAGATTAGTAAGGTTCGAGATAACCCTTTGCAACCACTGA	MMNHALFWVRRRLVRFEITLCNH*			MMNHALFWVRRRLVRFEITLCNH*	AGTCGGTTTC	ATGACGGTAG	0		0	0	0	0	0
4496	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-100	-32	ATGAACCATGCCTTGTTTTGGGTACGGAGGAGATTAGTAAGGTTCGAGATAACCCTTTGCAACCACTGA			ATGAACCATGCCTTGTTTTGGGTACGGAGGAGATTAGTAAGGTTCGAGATAACCCTTTGCAACCACTGA	MNHALFWVRRRLVRFEITLCNH*			MNHALFWVRRRLVRFEITLCNH*	CGGTTTCATG	ATGACGGTAG	0		0	0	0	0	0
4497	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-93	-64	ATGCCTTGTTTTGGGTACGGAGGAGATTAG			ATGCCTTGTTTTGGGTACGGAGGAGATTAG	MPCFGYGGD*			MPCFGYGGD*	ATGATGAACC	TAAGGTTCGA	0		0	0	0	0	0
4498	2426	ao	AN7511.1	57.m05828	AO070258000009	1					-31	-17	ATGACGGTAGAATAG			ATGACGGTAGAATAG	MTVE*			MTVE*	CAACCACTGA	AGGAGAAGAT	1		0	0	0	0	0
4509	2429	an	AN3459.1	59.m09320	AO070265000036	1	-188	-150					ATGTATCCAGCAGAATGCCCCTCACCCTGCGTAGCATAA	ATGTATCCAGCAGAATGCCCCTCACCCTGCGTAGCATAA			MYPAECPSPCVA*	MYPAECPSPCVA*			AGAAGACTGC	CGACTTCCTT	0	E	FG09893.1	MG00256.1	0	0	0
4510	2429	af	AN3459.1	59.m09320	AO070265000036	1			-226	-125			ATGATTCATCCGTCAACCATAGGTGATTCCTACTGTAGCCGCCCAAATGCCCCTCCCCCTCCGTCGCATTGCAACGTCCCTGACAGACCAAACTCTTCATAA		ATGATTCATCCGTCAACCATAGGTGATTCCTACTGTAGCCGCCCAAATGCCCCTCCCCCTCCGTCGCATTGCAACGTCCCTGACAGACCAAACTCTTCATAA		MIHPSTIGDSYCSRPNAPPPSHCNVPDRPNSS*		MIHPSTIGDSYCSRPNAPPPSHCNVPDRPNSS*		TCATCCAATA	GCTCTACAAA	0	E	FG09893.1	MG00256.1	0	0	0
4511	2430	an	AN8832.1	71.m15963	AO070271000047	1	-184	-146					ATGGCCAGATTCTGTTCCCCACACGCCAAAGAGCTCTGA	ATGGCCAGATTCTGTTCCCCACACGCCAAAGAGCTCTGA			MARFCSPHAKEL*	MARFCSPHAKEL*			AAGCTCCGTG	CCTGACGATC	0	J	FG02093.1	0	0	0	0
4512	2430	an	AN8832.1	71.m15963	AO070271000047	1	-120	-79					ATGGGTCAGACCTTTCAGAATTTGTCAAACATCAATCAATAA	ATGGGTCAGACCTTTCAGAATTTGTCAAACATCAATCAATAA			MGQTFQNLSNINQ*	MGQTFQNLSNINQ*			TACAGAGATC	CAGCTTCAAC	0	J	FG02093.1	0	0	0	0
4513	2430	af	AN8832.1	71.m15963	AO070271000047	1			-240	-202			ATGCAATTGAGCTCCTGGTTCGCTCATTGCATTACCTGA		ATGCAATTGAGCTCCTGGTTCGCTCATTGCATTACCTGA		MQLSSWFAHCIT*		MQLSSWFAHCIT*		CGACGAATTT	TTTGGCTCTC	0	J	FG02093.1	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
4514	2430	ao	AN8832.1	71.m15963	AO071000047	1					-204	-163	ATGGACACTTTTCCTTTTCAATTGTACACCTACGTTCTCTGA			ATGGACACTTTTCCTTTTCAATTGTACACCTACGTTCTCTGA	MDTFPFQLYTYVL*			MDTFPFQLYTYVL*	ACGACATCCC	TGGTGTACTG	0	J	FG02093.1	0	0	0	0
4515	2430	ao	AN8832.1	71.m15963	AO070271000047	1					-163	-152	ATGGTGTACTGA			ATGGTGTACTGA	MVY*			MVY*	ACGTTCTCTG	TTCCGTCCTC	0	J	FG02093.1	0	0	0	0
4521	2431	ao	AN8829.1	72.m19523	AO070271000051	0					-60	-19	ATGTACCCATCACAAGTACATTCTATATCGTCTCTAAAATAG			ATGTACCCATCACAAGTACATTCTATATCGTCTCTAAAATAG	MYPSQVHSISSLK*			MYPSQVHSISSLK*	CATTCCTCAT	CTATTAGTTT	1		0	0	0	0	0
4526	2436	an	AN4684.1	71.m15668	AO070284000040	0	-44	-27					ATGCATCTCAGTAACTAG	ATGCATCTCAGTAACTAG			MHLSN*	MHLSN*			TAACCAAGTT	CTAACTGTTG	1	I	FG08571.1	MG02622.1	0	0	0
4559	2446	ao	AN6330.1	72.m19449	AO070304000108	1					-280	-260	ATGCATGCTCCCGTGTATTGA			ATGCATGCTCCCGTGTATTGA	MHAPVY*			MHAPVY*	AGCCTGCGTC	TTGATTAGAT	0	J	0	MG01742.1	0	0	0
4560	2446	ao	AN6330.1	72.m19449	AO070304000108	1					-276	-256	ATGCTCCCGTGTATTGATTGA			ATGCTCCCGTGTATTGATTGA	MLPCID*			MLPCID*	TGCGTCATGC	TTAGATTTGG	0	J	0	MG01742.1	0	0	0
4561	2446	ao	AN6330.1	72.m19449	AO070304000108	1					-196	-182	ATGATACGCATATAG			ATGATACGCATATAG	MIRI*			MIRI*	ACGGTACATA	ACATACATGC	0	J	0	MG01742.1	0	0	0
4592	2468	an	AN2173.1	72.m19667	AO070343000244	1	-125	-21					ATGCCCCTGCTATTCATACGCCAAAACTCCCCTACTTCGCCGGGGATACACTCAGTTCGCGCGTTCTTGAGCCCCTCGTTCAAAATAATGACGGAAGCCCGATAA	ATGCCCCTGCTATTCATACGCCAAAACTCCCCTACTTCGCCGGGGATACACTCAGTTCGCGCGTTCTTGAGCCCCTCGTTCAAAATAATGACGGAAGCCCGATAA			MPLLFIRQNSPTSPGIHSVRAFLSPSFKIMTEAR*	MPLLFIRQNSPTSPGIHSVRAFLSPSFKIMTEAR*			CGCAGATTCG	TAATCTTATA	0	F	0	0	0	YNL083W	YNL083W
4593	2468	an	AN2173.1	72.m19667	AO070343000244	1	-38	-21					ATGACGGAAGCCCGATAA	ATGACGGAAGCCCGATAA			MTEAR*	MTEAR*			GTTCAAAATA	TAATCTTATA	1	F	0	0	0	YNL083W	YNL083W
4595	2468	af	AN2173.1	72.m19667	AO070343000244	1			-176	-162			ATGCACAGCATATAG		ATGCACAGCATATAG		MHSI*		MHSI*		TGCAATAATA	CGGTTTTTTC	0	F	0	0	0	YNL083W	YNL083W
4596	2468	af	AN2173.1	72.m19667	AO070343000244	1			-123	-52			ATGCACCAGTCATCACGAAAACATACGAACCCCTGCCCTCACAGGGAAAGCTCCGACCTCAAATTTTTGTGA		ATGCACCAGTCATCACGAAAACATACGAACCCCTGCCCTCACAGGGAAAGCTCCGACCTCAAATTTTTGTGA		MHQSSRKHTNPCPHRESSDLKFL*		MHQSSRKHTNPCPHRESSDLKFL*		TACGGATTCG	CCTCTCCGAA	0	F	0	0	0	YNL083W	YNL083W
4597	2468	af	AN2173.1	72.m19667	AO070343000244	1			-37	-17			ATGACGGGTCCTCGGCTATAG		ATGACGGGTCCTCGGCTATAG		MTGPRL*		MTGPRL*		TCCGAAAATA	TCGATAAACA	1	F	0	0	0	YNL083W	YNL083W
4598	2468	ao	AN2173.1	72.m19667	AO070343000244	1					-177	-148	ATGTATGCGGAACCTCTCCTCTCTTTATAA			ATGTATGCGGAACCTCTCCTCTCTTTATAA	MYAEPLLSL*			MYAEPLLSL*	AGACATACCA	ACTAGCTCCA	0	F	0	0	0	YNL083W	YNL083W
4599	2468	ao	AN2173.1	72.m19667	AO070343000244	1					-173	-42	ATGCGGAACCTCTCCTCTCTTTATAAACTAGCTCCACAGATTCGATGCACAAGCTATTATCGCAGTCTACCCTACTACCACCCTGTTTTGACAGGGACACCTCCGCTCTCAAGTCCCGTGACCCCTCCTTGA			ATGCGGAACCTCTCCTCTCTTTATAAACTAGCTCCACAGATTCGATGCACAAGCTATTATCGCAGTCTACCCTACTACCACCCTGTTTTGACAGGGACACCTCCGCTCTCAAGTCCCGTGACCCCTCCTTGA	MRNLSSLYKLAPQIRCTSYYRSLPYYHPVLTGTPPLSSPVTPP*			MRNLSSLYKLAPQIRCTSYYRSLPYYHPVLTGTPPLSSPVTPP*	ATACCAATGT	AAATAATGTC	0	F	0	0	0	YNL083W	YNL083W
4600	2468	ao	AN2173.1	72.m19667	AO070343000244	1					-129	-19	ATGCACAAGCTATTATCGCAGTCTACCCTACTACCACCCTGTTTTGACAGGGACACCTCCGCTCTCAAGTCCCGTGACCCCTCCTTGAAAATAATGTCGGATAGCCGATGA			ATGCACAAGCTATTATCGCAGTCTACCCTACTACCACCCTGTTTTGACAGGGACACCTCCGCTCTCAAGTCCCGTGACCCCTCCTTGAAAATAATGTCGGATAGCCGATGA	MHKLLSQSTLLPPCFDRDTSALKSRDPSLKIMSDSR*			MHKLLSQSTLLPPCFDRDTSALKSRDPSLKIMSDSR*	CACAGATTCG	TAAATTTACA	0	F	0	0	0	YNL083W	YNL083W
4601	2468	ao	AN2173.1	72.m19667	AO070343000244	1					-36	-19	ATGTCGGATAGCCGATGA			ATGTCGGATAGCCGATGA	MSDSR*			MSDSR*	CTTGAAAATA	TAAATTTACA	1	F	0	0	0	YNL083W	YNL083W
4610	2472	ao	AN2016.1	58.m07624	AO070202000009	0					-47	-15	ATGATTTCTAAAGGCTCCACATCGGCGAGATAG			ATGATTTCTAAAGGCTCCACATCGGCGAGATAG	MISKGSTSAR*			MISKGSTSAR*	GCGGGATGCC	TATCCTATCC	1		0	0	0	0	0
4614	2474	af	AN0842.1	70.m15442	AO070216000002	0			-56	-3			ATGTGGACCCGAATGAGAGACGTCGTGATCTGTTCTTACCAAGCGCTTCTGTGA		ATGTGGACCCGAATGAGAGACGTCGTGATCTGTTCTTACCAAGCGCTTCTGTGA		MWTRMRDVVICSYQALL*		MWTRMRDVVICSYQALL*		AACTTCTCAT	ACATGGCGGA	1	R	0	0	0	0	0
4615	2474	af	AN0842.1	70.m15442	AO070216000002	0			-44	-3			ATGAGAGACGTCGTGATCTGTTCTTACCAAGCGCTTCTGTGA		ATGAGAGACGTCGTGATCTGTTCTTACCAAGCGCTTCTGTGA		MRDVVICSYQALL*		MRDVVICSYQALL*		GTGGACCCGA	ACATGGCGGA	1	R	0	0	0	0	0
4617	2474	ao	AN0842.1	70.m15442	AO070216000002	0					-40	-23	ATGAGAGCCCCTCATTAA			ATGAGAGCCCCTCATTAA	MRAPH*			MRAPH*	GCGGATTCGC	GTTCATATTC	1	R	0	0	0	0	0
4638	2493	af	AN3812.1	57.m05670	AO070311000009	1			-49	-11			ATGAAGAAAAGAAATTGGTGGACGATAACAATAATTTGA		ATGAAGAAAAGAAATTGGTGGACGATAACAATAATTTGA		MKKRNWWTITII*		MKKRNWWTITII*		AAGCCGGTTG	ACAACTCAGG	1	J	FG09363.1	MG06785.1	0	0	0
4643	2494	af	AN8344.1	53.m04018	AO070312000017	0			-47	-9			ATGCCGGAACAGTACGAACGTGATCCTCACCTCGGTTGA		ATGCCGGAACAGTACGAACGTGATCCTCACCTCGGTTGA		MPEQYERDPHLG*		MPEQYERDPHLG*		TACATTCCTG	TCGACCCTAT	1	Q	0	0	0	0	0
4656	2496	an	AN3359.1	66.m04660	AO070317000081	0	-36	-22					ATGAGCTTTCAATGA	ATGAGCTTTCAATGA			MSFQ*	MSFQ*			CCTCTACATC	ATATCTACAC	1	E	0	0	0	0	0
4688	2508	an	AN5455.1	69.m15477	AO070341000411	0	-44	-21					ATGGACACATTGCTCGAATTTTAA	ATGGACACATTGCTCGAATTTTAA			MDTLLEF*	MDTLLEF*			TTATCGAGGG	AAAGGATTTG	1	S	FG07262.1	MG04995.1	0	0	0
4690	2508	af	AN5455.1	69.m15477	AO070341000411	0			-48	-37			ATGGCCGTCTAA		ATGGCCGTCTAA		MAV*		MAV*		TCGTTGAGCG	TCTGATTGCC	1	S	FG07262.1	MG04995.1	0	0	0
4691	2508	ao	AN5455.1	69.m15477	AO070341000411	0					-47	-21	ATGGGTTACTATTGTAAATACGGTTAA			ATGGGTTACTATTGTAAATACGGTTAA	MGYYCKYG*			MGYYCKYG*	TTTCTGAGGG	GAAACAATTT	1	S	FG07262.1	MG04995.1	0	0	0
4716	2517	an	AN2278.1	71.m15923	AO070295000054	0	-27	-13					ATGAATAGACAATAA	ATGAATAGACAATAA			MNRQ*	MNRQ*			TCTTATATTT	ACGCGCTCGA	1	BK	0	0	0	0	0
4718	2517	ao	AN2278.1	71.m15923	AO070295000054	0					-27	-4	ATGAACAGTAAAACTACGCGCTAA			ATGAACAGTAAAACTACGCGCTAA	MNSKTTR*			MNSKTTR*	TACTCCGTCT	ATCATGGCTT	1	BK	0	0	0	0	0
4724	2521	af	AN1685.1	58.m07761	AO070305000004	0			-56	-12			ATGGTTTCCCGATCAGATTCAACGACGGAGGAATCGCAACCCTAA		ATGGTTTCCCGATCAGATTCAACGACGGAGGAATCGCAACCCTAA		MVSRSDSTTEESQP*		MVSRSDSTTEESQP*		CGAGGGGAGG	TTGTCGGTAT	1	R	0	0	0	0	0
4734	2524	an	AN8206.1	53.m03768	AO070310000111	0	-55	-20					ATGACAGAACACTTCTACCTCAATCATCTACGCTGA	ATGACAGAACACTTCTACCTCAATCATCTACGCTGA			MTEHFYLNHLR*	MTEHFYLNHLR*			GGTCTCCAAA	GAGGCGATGC	1	Q	0	0	0	0	0
4757	2532	af	AN4007.1	54.m06583	AO070328000146	0			-25	-14			ATGAGCAACTGA		ATGAGCAACTGA		MSN*		MSN*		ACTCATTTGA	TCCAGGTCCG	1	C	0	0	0	0	0
4778	2535	af	AN1129.1	70.m15106	AO070331000121	0			-43	-17			ATGTTGCTAGATCGTGGAACTGACTGA		ATGTTGCTAGATCGTGGAACTGACTGA		MLLDRGTD*		MLLDRGTD*		TATATTTAGA	ACACATCATC	1	P	0	0	0	0	0
4785	2541	an	AN2985.1	59.m09028	AO070337000137	0	-13	-2					ATGTGCTGGTGA	ATGTGCTGGTGA			MCW*	MCW*			TCGTACTATT	AATGGCGGCA	1	R	0	0	0	0	0
4787	2545	an	AN2895.1	59.m08744	AO070338000115	1	-72	-25					ATGATTTTTCTAAGCCATTCAAGGCTCTGCCTAGCGTCTCCGCACTAA	ATGATTTTTCTAAGCCATTCAAGGCTCTGCCTAGCGTCTCCGCACTAA			MIFLSHSRLCLASPH*	MIFLSHSRLCLASPH*			CTTGTTATTC	GAAGGCCCTA	0	S	0	0	0	0	0
4817	2556	an	AN4323.1	58.m08000	AO070230000015	1	-61	-38					ATGATCCCTTCGCTGTTTTGCTGA	ATGATCCCTTCGCTGTTTTGCTGA			MIPSLFC*	MIPSLFC*			CGGCATTGAT	GAATTGACTA	0	E	0	MG02489.1	0	YHR208W	0
4855	2566	ao	AN0590.1	69.m15259	AO070280000012	1					-98	-78	ATGCGGAGCTTTTATCAGTAG			ATGCGGAGCTTTTATCAGTAG	MRSFYQ*			MRSFYQ*	TCTATTCTCC	CATCCGAATC	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4856	2569	af	AN5154.1	54.m06864	AO070291000014	0			-44	-6			ATGTCACTTGGGAGGTCGCCTTTTATTGTGGTGAGCTGA		ATGTCACTTGGGAGGTCGCCTTTTATTGTGGTGAGCTGA		MSLGRSPFIVVS*		MSLGRSPFIVVS*		TAGAGCTTGG	CAGAAATGTC	1	A	0	0	0	0	0
4930	2592	af	AN9086.1	66.m04759	AO070332000191	0			-14	-3			ATGCAAAGCTAG		ATGCAAAGCTAG		MQS*		MQS*		AAACATTTAG	ACATGTCGTC	1	U	FG02649.1	MG04694.1	0	YKR068C	0
4940	2597	an	AN6722.1	65.m07248	AO070339000165	1	-299	-270					ATGAACGTACTGCCCTATTTCCGAAACTAG	ATGAACGTACTGCCCTATTTCCGAAACTAG			MNVLPYFRN*	MNVLPYFRN*			ATATTGCGGA	GTGGGCCCTC	0	R	0	0	0	0	0
4941	2597	an	AN6722.1	65.m07248	AO070339000165	1	-156	-61					ATGAGCTCGATCTTGCGTTATTCGAGCTCCGATACGGGAACCTATCGATTGCCAATGTTACCGTGCCATTCGTTAGTGGAGGTGTCGTTAGTTTGA	ATGAGCTCGATCTTGCGTTATTCGAGCTCCGATACGGGAACCTATCGATTGCCAATGTTACCGTGCCATTCGTTAGTGGAGGTGTCGTTAGTTTGA			MSSILRYSSSDTGTYRLPMLPCHSLVEVSLV*	MSSILRYSSSDTGTYRLPMLPCHSLVEVSLV*			GTCGCTTTCA	TATAACAGTC	0	R	0	0	0	0	0
4942	2597	an	AN6722.1	65.m07248	AO070339000165	1	-102	-61					ATGTTACCGTGCCATTCGTTAGTGGAGGTGTCGTTAGTTTGA	ATGTTACCGTGCCATTCGTTAGTGGAGGTGTCGTTAGTTTGA			MLPCHSLVEVSLV*	MLPCHSLVEVSLV*			TCGATTGCCA	TATAACAGTC	0	R	0	0	0	0	0
4943	2597	af	AN6722.1	65.m07248	AO070339000165	1			-227	-180			ATGCTATCCAACTCTACCATAAATCTACTCTGCATGCAAATCGTGTGA		ATGCTATCCAACTCTACCATAAATCTACTCTGCATGCAAATCGTGTGA		MLSNSTINLLCMQIV*		MLSNSTINLLCMQIV*		TTTTTCTTTG	GATTTCAAAT	0	R	0	0	0	0	0
4944	2597	af	AN6722.1	65.m07248	AO070339000165	1			-194	-180			ATGCAAATCGTGTGA		ATGCAAATCGTGTGA		MQIV*		MQIV*		TCTACTCTGC	GATTTCAAAT	0	R	0	0	0	0	0
4945	2597	af	AN6722.1	65.m07248	AO070339000165	1			-157	-119			ATGATCTCCTCCTGGATATACCGTATTAGTGTGCACTGA		ATGATCTCCTCCTGGATATACCGTATTAGTGTGCACTGA		MISSWIYRISVH*		MISSWIYRISVH*		ATCAACTTGC	TGTAATTATA	0	R	0	0	0	0	0
4946	2597	ao	AN6722.1	65.m07248	AO070339000165	1					-322	-281	ATGGGACCTCGGTTATATTTCGTGAATGTTTCAATCCCTTGA			ATGGGACCTCGGTTATATTTCGTGAATGTTTCAATCCCTTGA	MGPRLYFVNVSIP*			MGPRLYFVNVSIP*	TGTAAACCAA	ACTTCATAGT	0	R	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
4947	2597	ao	AN6722.1	65.m07248	AO070339000165	1					-297	-235	ATGTTTCAATCCCTTGAACTTCATAGTGGCTGCTGGTTCTTTGTTGGCTTCCGGCGCACCTGA			ATGTTTCAATCCCTTGAACTTCATAGTGGCTGCTGGTTCTTTGTTGGCTTCCGGCGCACCTGA	MFQSLELHSGCWFFVGFRRT*			MFQSLELHSGCWFFVGFRRT*	TATTTCGTGA	GCAACCGCTG	0	R	0	0	0	0	0
4952	2599	an	AN5932.1	72.m19197	AO070340000348	0	-49	-26					ATGCCTATCATTTCTATGGAATAA	ATGCCTATCATTTCTATGGAATAA			MPIISME*	MPIISME*			ATCACATTCC	TTGCCAGGCT	1	L	FG05421.1	MG06397.1	0	0	0
4955	2599	af	AN5932.1	72.m19197	AO070340000348	0			-39	-22			ATGACCACCCATCGATAA		ATGACCACCCATCGATAA		MTTHR*		MTTHR*		GAGGTCATTG	GTCGGCTAGA	1	L	FG05421.1	MG06397.1	0	0	0
4958	2599	ao	AN5932.1	72.m19197	AO070340000348	0					-38	-21	ATGGACGCCAATTCTTAG			ATGGACGCCAATTCTTAG	MDANS*			MDANS*	AAGGTGTTTA	GGATCTTCTA	1	L	FG05421.1	MG06397.1	0	0	0
4973	2603	an	AN0673.1	70.m15275	AO070343000547	1	-78	-43					ATGATCTCTTTTGTCTCTCTCTCTCGAATTGATTGA	ATGATCTCTTTTGTCTCTCTCTCTCGAATTGATTGA			MISFVSLSRID*	MISFVSLSRID*			CCTCATATTC	CATATCTTCA	0	Z	0	0	NCU07171.1	0	0
4979	2603	ao	AN0673.1	70.m15275	AO070343000547	1					-67	-32	ATGATCGCATTTGTTTGTTACTCTGGAATTATTTGA			ATGATCGCATTTGTTTGTTACTCTGGAATTATTTGA	MIAFVCYSGII*			MIAFVCYSGII*	CTACATCCCC	GCATTTACTA	0	Z	0	0	NCU07171.1	0	0
4989	2604	af	AN0654.1	70.m15258	AO070343000572	0			-60	-22			ATGTTTGACACCTCGTGGGCAGAGCACGTTCTAAAGTGA		ATGTTTGACACCTCGTGGGCAGAGCACGTTCTAAAGTGA		MFDTSWAEHVLK*		MFDTSWAEHVLK*		TTTCACGTGC	GAGCCGTTGA	1	H	FG10097.1	0	0	0	0
5002	2608	af	AN5908.1	72.m19223	AO070245000002	1			-442	-425			ATGACTAGCAGATATTGA		ATGACTAGCAGATATTGA		MTSRY*		MTSRY*		GAAGCATCCC	CAAGACAAGT	0	G	FG06702.1	0	NCU07550.1	0	0
5007	2608	af	AN5908.1	72.m19223	AO070245000002	1			-196	-38			ATGACATTCCTGTCATTCCCCAGAATGCTTACTCCCCTCATTGGCAGCCAAATTGTACCTATCCTAGAGCCTATCCGAGGGGCATCCGAGCTCGCATCCTGCCTTCGCTACCAGTCGCTCAATCAACAACAGAGGACCAGAATCAACAGAGAACAATAA		ATGACATTCCTGTCATTCCCCAGAATGCTTACTCCCCTCATTGGCAGCCAAATTGTACCTATCCTAGAGCCTATCCGAGGGGCATCCGAGCTCGCATCCTGCCTTCGCTACCAGTCGCTCAATCAACAACAGAGGACCAGAATCAACAGAGAACAATAA		MTFLSFPRMLTPLIGSQIVPILEPIRGASELASCLRYQSLNQQQRTRINREQ*		MTFLSFPRMLTPLIGSQIVPILEPIRGASELASCLRYQSLNQQQRTRINREQ*		GAAGAGTGGC	ATACTCAAGC	0	G	FG06702.1	0	NCU07550.1	0	0
5008	2608	af	AN5908.1	72.m19223	AO070245000002	1			-172	-38			ATGCTTACTCCCCTCATTGGCAGCCAAATTGTACCTATCCTAGAGCCTATCCGAGGGGCATCCGAGCTCGCATCCTGCCTTCGCTACCAGTCGCTCAATCAACAACAGAGGACCAGAATCAACAGAGAACAATAA		ATGCTTACTCCCCTCATTGGCAGCCAAATTGTACCTATCCTAGAGCCTATCCGAGGGGCATCCGAGCTCGCATCCTGCCTTCGCTACCAGTCGCTCAATCAACAACAGAGGACCAGAATCAACAGAGAACAATAA		MLTPLIGSQIVPILEPIRGASELASCLRYQSLNQQQRTRINREQ*		MLTPLIGSQIVPILEPIRGASELASCLRYQSLNQQQRTRINREQ*		ATTCCCCAGA	ATACTCAAGC	0	G	FG06702.1	0	NCU07550.1	0	0
5009	2608	ao	AN5908.1	72.m19223	AO070245000002	1					-516	-436	ATGCATTCGCGTGGGACGATCGACTGTCTCCTCTTTCTGTCGCTGGGGAAGCCCACTTGGTTACCGAAACTCATGTTTTAG			ATGCATTCGCGTGGGACGATCGACTGTCTCCTCTTTCTGTCGCTGGGGAAGCCCACTTGGTTACCGAAACTCATGTTTTAG	MHSRGTIDCLLFLSLGKPTWLPKLMF*			MHSRGTIDCLLFLSLGKPTWLPKLMF*	CCGCCGGGGG	TCCCAGACTT	0	G	FG06702.1	0	NCU07550.1	0	0
5014	2609	an	AN0827.1	70.m15428	AO070255000018	0	-56	-45					ATGACCCCTTAA	ATGACCCCTTAA			MTP*	MTP*			TCGATCAACA	CGACGGTCTG	1	S	0	0	NCU00913.1	YJL091C	0
5036	2616	af	AN3970.1	54.m06355	AO070286000067	1			-67	-56			ATGTTGACTTAA		ATGTTGACTTAA		MLT*		MLT*		GCTATTTCCA	ATTCAAGTTG	0	Z	0	0	0	0	0
5070	2627	af	AN3829.1	58.m07805	AO070305000066	1			-376	-221			ATGCGTGCTGTTCTAAGAATGACGTCGACCCACGTGATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		ATGCGTGCTGTTCTAAGAATGACGTCGACCCACGTGATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		MRAVLRMTSTHVMDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		MRAVLRMTSTHVMDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		TGGAGAATAG	AGTATAAAGA	0	C	FG06752.1	0	0	0	0
5071	2627	af	AN3829.1	58.m07805	AO070305000066	1			-358	-221			ATGACGTCGACCCACGTGATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		ATGACGTCGACCCACGTGATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		MTSTHVMDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		MTSTHVMDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		TGTTCTAAGA	AGTATAAAGA	0	C	FG06752.1	0	0	0	0
5072	2627	af	AN3829.1	58.m07805	AO070305000066	1			-340	-221			ATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		ATGGACATCTCTCCCCGCTTAGAGGAAACTGGTGGTAATGAATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAA		MDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		MDISPRLEETGGNECLTSSEIRLALLYILHRWIHPSLDL*		GACCCACGTG	AGTATAAAGA	0	C	FG06752.1	0	0	0	0
5073	2627	af	AN3829.1	58.m07805	AO070305000066	1			-303	-292			ATGAATGCTTGA		ATGAATGCTTGA		MNA*		MNA*		ACTGGTGGTA	CAAGCTCGGA	0	C	FG06752.1	0	0	0	0
5074	2627	af	AN3829.1	58.m07805	AO070305000066	1			-299	-189			ATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAAAGTATAAAGATAACTTTTTCCTCCTCCCGTAG		ATGCTTGACAAGCTCGGAGATACGATTAGCATTACTTTACATACTCCATCGTTGGATCCATCCTTCCCTGGATTTATAAAGTATAAAGATAACTTTTTCCTCCTCCCGTAG		MLDKLGDTISITLHTPSLDPSFPGFIKYKDNFFLLP*		MLDKLGDTISITLHTPSLDPSFPGFIKYKDNFFLLP*		GTGGTAATGA	ATAAAGCCCT	0	C	FG06752.1	0	0	0	0
5075	2627	ao	AN3829.1	58.m07805	AO070305000066	1					-440	-357	ATGACGTCGATACACGTGACGCGGAGCTTCCCCGCTGGACGGCATTACAGGGAGCAGCTCGGAGGCATTCTCAACAATGATTAG			ATGACGTCGATACACGTGACGCGGAGCTTCCCCGCTGGACGGCATTACAGGGAGCAGCTCGGAGGCATTCTCAACAATGATTAG	MTSIHVTRSFPAGRHYREQLGGILNND*			MTSIHVTRSFPAGRHYREQLGGILNND*	AAATAGAGAA	TCTCCACGCG	0	C	FG06752.1	0	0	0	0
5076	2627	ao	AN3829.1	58.m07805	AO070305000066	1					-364	-317	ATGATTAGTCTCCACGCGATGGATCAACCTCGCTCCTGCAGTATATAA			ATGATTAGTCTCCACGCGATGGATCAACCTCGCTCCTGCAGTATATAA	MISLHAMDQPRSCSI*			MISLHAMDQPRSCSI*	ATTCTCAACA	GTCTGAAGCA	0	C	FG06752.1	0	0	0	0
5077	2627	ao	AN3829.1	58.m07805	AO070305000066	1					-346	-317	ATGGATCAACCTCGCTCCTGCAGTATATAA			ATGGATCAACCTCGCTCCTGCAGTATATAA	MDQPRSCSI*			MDQPRSCSI*	TCTCCACGCG	GTCTGAAGCA	0	C	FG06752.1	0	0	0	0
5111	2649	an	AN6720.1	65.m07477	AO070339000162	1	-253	-197					ATGACCTCACCGCAATCCAGGTCCGCATCGACTTCCACCCTGTTCTGCTGCTATTGA	ATGACCTCACCGCAATCCAGGTCCGCATCGACTTCCACCCTGTTCTGCTGCTATTGA			MTSPQSRSASTSTLFCCY*	MTSPQSRSASTSTLFCCY*			GCGTTACTCA	TCGTGTGATA	0	G	0	0	0	0	0
5127	2654	af	AN1918.1	69.m14936	AO070341000122	1			-339	-289			ATGCATGTACCCGTGCGTTATCATCCATTATCCACGAGTCATCAAGAATAA		ATGCATGTACCCGTGCGTTATCATCCATTATCCACGAGTCATCAAGAATAA		MHVPVRYHPLSTSHQE*		MHVPVRYHPLSTSHQE*		TCTCAGCCCG	TTTATCCCTT	0	C	FG08601.1	0	NCU09873.1	0	0
5128	2654	af	AN1918.1	69.m14936	AO070341000122	1			-335	-252			ATGTACCCGTGCGTTATCATCCATTATCCACGAGTCATCAAGAATAATTTATCCCTTCCCGATCAGTCCTCCCTGCAGCACTAA		ATGTACCCGTGCGTTATCATCCATTATCCACGAGTCATCAAGAATAATTTATCCCTTCCCGATCAGTCCTCCCTGCAGCACTAA		MYPCVIIHYPRVIKNNLSLPDQSSLQH*		MYPCVIIHYPRVIKNNLSLPDQSSLQH*		AGCCCGATGC	GTACGTCGTC	0	C	FG08601.1	0	NCU09873.1	0	0
5129	2654	af	AN1918.1	69.m14936	AO070341000122	1			-143	-3			ATGAGAGGCATTTTTGTTCACTCCACGGCTAACCATCATCGCTGCAGACTCATTCCTCAACCCCCGACATCACCCGCGGAACTGTGGAGAAGTAGATCGGAGAGGATCCTTGAAACTGCCCTTGAGACCTGTATCATCGTGA		ATGAGAGGCATTTTTGTTCACTCCACGGCTAACCATCATCGCTGCAGACTCATTCCTCAACCCCCGACATCACCCGCGGAACTGTGGAGAAGTAGATCGGAGAGGATCCTTGAAACTGCCCTTGAGACCTGTATCATCGTGA		MRGIFVHSTANHHRCRLIPQPRHHPRNCGEVDRRGSLKLPLRPVSS*		MRGIFVHSTANHHRCRLIPQPRHHPRNCGEVDRRGSLKLPLRPVSS*		CGGACAGTCT	GCATGGCTCC	0	C	FG08601.1	0	NCU09873.1	0	0
5130	2654	ao	AN1918.1	69.m14936	AO070341000122	1					-449	-135	ATGAGACATTTCTTGACTGGATACCATCCGCGCGTTATCATAATCCAGAGACACACCCCTTTATTTTCATTCCGAAAATCGCATTTTCTTGCTTCTAGTTGGTGCACCCGACCGGTTTTCCCGGAACCACTTCGTGCCTACATCTGGGGTTCGGAACAAGTCGGAGAACCCACAAGAGGCATTTTACACACTCCAGAGTCCACGGTTACCAACGCTGCCTCAGCCCGGTCTTCAGCCCCGACATCTCCCGTCAAACTGTGGAGAAGCATATCGGAGTCGAAGACTGAAACGCCTTCTGGACTTACTTTGCTGTGA			ATGAGACATTTCTTGACTGGATACCATCCGCGCGTTATCATAATCCAGAGACACACCCCTTTATTTTCATTCCGAAAATCGCATTTTCTTGCTTCTAGTTGGTGCACCCGACCGGTTTTCCCGGAACCACTTCGTGCCTACATCTGGGGTTCGGAACAAGTCGGAGAACCCACAAGAGGCATTTTACACACTCCAGAGTCCACGGTTACCAACGCTGCCTCAGCCCGGTCTTCAGCCCCGACATCTCCCGTCAAACTGTGGAGAAGCATATCGGAGTCGAAGACTGAAACGCCTTCTGGACTTACTTTGCTGTGA	MRHFLTGYHPRVIIQRHTPLFSFRKSHFLASSWCTRPVFPEPLRAYIWGSEQVGEPTRGILHTPESTVTNAASARSSAPTSPVKLWRSISESKTETPSGLTLL*			MRHFLTGYHPRVIIQRHTPLFSFRKSHFLASSWCTRPVFPEPLRAYIWGSEQVGEPTRGILHTPESTVTNAASARSSAPTSPVKLWRSISESKTETPSGLTLL*	TTGCTCCTGC	TCATGGCTCC	0	C	FG08601.1	0	NCU09873.1	0	0
5131	2655	conserved	AN5528.1	69.m15427	AO070341000360	1	-69	-58	-59	-48	-67	-56	ATGsTyyCyTGA	ATGCTCCCCTGA	ATGGTCTCTTGA	ATGGTTCCTTGA	Mlp*	MLP*	MVS*	MVP*	CrCkmywAhr	skAhAvrbhG	0	U	0	0	NCU05029.1	0	0
5133	2655	af	AN5528.1	69.m15427	AO070341000360	1			-62	-48			ATGATGGTCTCTTGA		ATGATGGTCTCTTGA		MMVS*		MMVS*		ACACACGCCT	CGATACATCG	0	U	0	0	NCU05029.1	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_coocu
5139	2662	ao	AN7387.1	71.m15107	AO070343000118	1					-203	-75	ATGTTTATATCCAACCCCGCCCTGCAACTCCCATCCCGGCACCGCCTTCCCTATTTCAGGACAAGTAATGCCAACTTCGGCGGGCGGTCGGTTTGTGCCCCGCCTTTTGACCGAGTGGGGGAATTTTAG			ATGTTTATATCCAACCCCGCCCTGCAACTCCCATCCCGGCACCGCCTTCCCTATTTCAGGACAAGTAATGCCAACTTCGGCGGGCGGTCGGTTTGTGCCCCGCCTTTTGACCGAGTGGGGGAATTTTAG	MFISNPALQLPSRHRLPYFRTSNANFGGRSVCAPPFDRVGEF*			MFISNPALQLPSRHRLPYFRTSNANFGGRSVCAPPFDRVGEF*	TTTTTACGTC	GATCATGTCC	0	E	0	0	0	0	0
5142	2664	af	AN2163.1	72.m19677	AO070343000222	1			-700	-665			ATGTCCCCTGTTTCAAAACTTGTTGTCTGTATGTAA		ATGTCCCCTGTTTCAAAACTTGTTGTCTGTATGTAA		MSPVSKLVVCM*		MSPVSKLVVCM*		CTTTCTTTGC	GTATCAATCA	0	D	0	0	0	0	0
5164	2669	af	AN4333.1	58.m09007	AO070240000012	0			-39	-19			ATGTGGCAGCCAGGTTGTTGA		ATGTGGCAGCCAGGTTGTTGA		MWQPGC*		MWQPGC*		CTCAAAGGAC	AATAAATTGA	1		0	0	NCU10035.1	0	0
5165	2671	conserved	AN3144.1	59.m08521	AO070256000047	0	-23	-12	-25	-14	-23	-12	ATGCTCymmTAA	ATGCTCCCATAA	ATGCTCCCATAA	ATGCTCTACTAA	MLp*	MLP*	MLP*	MLY*	TyyhyyTCCC	yCbrmdyCwm	1	R	FG04221.1	MG09837.1	0	YDR323C	0
5173	2672	an	AN5808.1	72.m18938	AO070260000039	1	-310	-281					ATGCCGAACCATCGCAGTTACCCATGTTGA	ATGCCGAACCATCGCAGTTACCCATGTTGA			MPNHRSYPC*	MPNHRSYPC*			GTCTAGAGAC	CCTGGGCTAC	0		0	0	0	0	0
5177	2672	af	AN5808.1	72.m18938	AO070260000039	1			-277	-266			ATGGGCTTCTAA		ATGGGCTTCTAA		MGF*		MGF*		AAATCTCACC	TCGTTGTGTA	0		0	0	0	0	0
5178	2672	af	AN5808.1	72.m18938	AO070260000039	1			-179	-144			ATGTTCCAAGCCACAGGACAGAGAGTTTGGTCTTAG		ATGTTCCAAGCCACAGGACAGAGAGTTTGGTCTTAG		MFQATGQRVWS*		MFQATGQRVWS*		CATTTCGAGG	GTGACGGGTA	0		0	0	0	0	0
5180	2672	ao	AN5808.1	72.m18938	AO070260000039	1					-277	-248	ATGAATTTACCCCAGTATTATGATAATTAA			ATGAATTTACCCCAGTATTATGATAATTAA	MNLPQYYDN*			MNLPQYYDN*	ACTGACTAGA	GTGCTCAAAT	0		0	0	0	0	0
5182	2672	ao	AN5808.1	72.m18938	AO070260000039	1					-239	-201	ATGAACTTCTGTCCTTATTTTCGTCCAATGCAGCTATGA			ATGAACTTCTGTCCTTATTTTCGTCCAATGCAGCTATGA	MNFCPYFRPMQL*			MNFCPYFRPMQL*	AAGTGCTCAA	GACACTCCAC	0		0	0	0	0	0
5183	2672	ao	AN5808.1	72.m18938	AO070260000039	1					-212	-201	ATGCAGCTATGA			ATGCAGCTATGA	MQL*			MQL*	TTTTCGTCCA	GACACTCCAC	0		0	0	0	0	0
5185	2672	ao	AN5808.1	72.m18938	AO070260000039	1					-161	-114	ATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGA			ATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGA	MVIQLLLTSLVPHTY*			MVIQLLLTSLVPHTY*	ACCGTCGGTT	TGAACAACAG	0		0	0	0	0	0
5188	2673	an	AN3439.1	59.m09299	AO070265000013	0	-45	-16					ATGAAAGTCCCTTCTATGTTCGCGTCCTAG	ATGAAAGTCCCTTCTATGTTCGCGTCCTAG			MKVPSMFAS*	MKVPSMFAS*			CACGCCGTAT	GAAATCTGAC	1	S	0	0	0	0	0
5189	2673	an	AN3439.1	59.m09299	AO070265000013	0	-30	-16					ATGTTCGCGTCCTAG	ATGTTCGCGTCCTAG			MFAS*	MFAS*			AGTCCCTTCT	GAAATCTGAC	1	S	0	0	0	0	0
5194	2679	an	AN7785.1	71.m15814	AO070286000027	1	-26	-6					ATGTTTGTTTCTAATCTCTGA	ATGTTTGTTTCTAATCTCTGA			MFVSNL*	MFVSNL*			TTTTCTTTCC	TCGCTATGAC	1		0	0	0	0	0
5195	2679	af	AN7785.1	71.m15814	AO070286000027	1			-33	-19			ATGTGTGCTTTTTAA		ATGTGTGCTTTTTAA		MCAF*		MCAF*		CTTTTACCTC	AACTTGTTGC	1		0	0	0	0	0
5196	2679	ao	AN7785.1	71.m15814	AO070286000027	1					-32	-18	ATGTCCATCCTCTAA			ATGTCCATCCTCTAA	MSIL*			MSIL*	TCCAACTCTC	CTCCTTCCAC	1		0	0	0	0	0
5238	2688	an	AN6182.1	72.m19274	AO070308000124	0	-32	-18					ATGTTAATTCAATAA	ATGTTAATTCAATAA			MLIQ*	MLIQ*			CTGTATCTTG	TCAATATCCT	1	C	FG05668.1	MG05098.1	0	0	0
5264	2704	an	AN2764.1	59.m09260	AO070327000027	1	-233	-174					ATGTGGCTGTGGCAGTTCTCAGGTCTAGTACTTCAGGGCTCCGTAGAGGACTTAGTCTAG	ATGTGGCTGTGGCAGTTCTCAGGTCTAGTACTTCAGGGCTCCGTAGAGGACTTAGTCTAG			MWLWQFSGLVLQGSVEDLV*	MWLWQFSGLVLQGSVEDLV*			TGTCGAGCCA	ATAGGTAGGA	0	L	0	0	0	0	0
5265	2704	an	AN2764.1	59.m09260	AO070327000027	1	-129	-58					ATGACGCTATACCAAATGCAGTCTAATGGTGTCAGCGCGTTCAACGCGTTTCATGCCCGCCACCGTGCTTGA	ATGACGCTATACCAAATGCAGTCTAATGGTGTCAGCGCGTTCAACGCGTTTCATGCCCGCCACCGTGCTTGA			MTLYQMQSNGVSAFNAFHARHRA*	MTLYQMQSNGVSAFNAFHARHRA*			TATATATCGC	CTGCTCTGCT	0	L	0	0	0	0	0
5266	2704	an	AN2764.1	59.m09260	AO070327000027	1	-114	-58					ATGCAGTCTAATGGTGTCAGCGCGTTCAACGCGTTTCATGCCCGCCACCGTGCTTGA	ATGCAGTCTAATGGTGTCAGCGCGTTCAACGCGTTTCATGCCCGCCACCGTGCTTGA			MQSNGVSAFNAFHARHRA*	MQSNGVSAFNAFHARHRA*			GCTATACCAA	CTGCTCTGCT	0	L	0	0	0	0	0
5267	2704	ao	AN2764.1	59.m09260	AO070327000027	1					-543	-385	ATGGGGTTTTCTAGCGGGGAAGTCACGTGGAATGTGTGTCGCCGGAAGCTAACCCCGAAGAGGTCTAATGATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAA			ATGGGGTTTTCTAGCGGGGAAGTCACGTGGAATGTGTGTCGCCGGAAGCTAACCCCGAAGAGGTCTAATGATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAA	MGFSSGEVTWNVCRRKLTPKRSNDVFPPVARSRSSARVWSRYHSRNLFCDLG*			MGFSSGEVTWNVCRRKLTPKRSNDVFPPVARSRSSARVWSRYHSRNLFCDLG*	GGCGAAAGGA	ACCAAGGGAG	0	L	0	0	0	0	0
5268	2704	ao	AN2764.1	59.m09260	AO070327000027	1					-512	-492	ATGTGTGTCGCCGGAAGCTAA			ATGTGTGTCGCCGGAAGCTAA	MCVAGS*			MCVAGS*	GTCACGTGGA	CCCCGAAGAG	0	L	0	0	0	0	0
5269	2704	ao	AN2764.1	59.m09260	AO070327000027	1					-476	-372	ATGATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAAACCAAGGGAGTAG			ATGATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAAACCAAGGGAGTAG	MMYSRPSRVLEARRAFGRGITLETFSVILVKPRE*			MMYSRPSRVLEARRAFGRGITLETFSVILVKPRE*	AAGAGGTCTA	TTCTGACTGG	0	L	0	0	0	0	0
5270	2704	ao	AN2764.1	59.m09260	AO070327000027	1					-473	-372	ATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAAACCAAGGGAGTAG			ATGTATTCCCGCCCGTCGCGCGTTCTCGAAGCTCGGCGCGCGTTTGGTCGCGGTATCACTCTAGAAACCTTTTCTGTGATCTTGGTTAAACCAAGGGAGTAG	MYSRPSRVLEARRAFGRGITLETFSVILVKPRE*			MYSRPSRVLEARRAFGRGITLETFSVILVKPRE*	AGGTCTAATG	TTCTGACTGG	0	L	0	0	0	0	0
5282	2715	an	AN5228.1	57.m05703	AO070337000249	1	-137	-63					ATGTCTCGTAGTCTCCAATCTTCCCTAAAACTACACCACACTACTCTACACAACTTTACATTACTACATACTTAA	ATGTCTCGTAGTCTCCAATCTTCCCTAAAACTACACCACACTACTCTACACAACTTTACATTACTACATACTTAA			MSRSLQSSLKLHHTTLHNFTLLHT*	MSRSLQSSLKLHHTTLHNFTLLHT*			CTTGCTCAGA	CTCCTGCTCC	0	CR	0	0	0	0	0
5294	2719	an	AN5925.1	72.m19206	AO070340000359	1	-545	-507					ATGCGACAAGGTTCCATTCAGCTTCGAATTCGTCATTGA	ATGCGACAAGGTTCCATTCAGCTTCGAATTCGTCATTGA			MRQGSIQLRIRH*	MRQGSIQLRIRH*			ATATTTTCCT	TTGAGCCTTG	0	A	0	0	NCU06365.1	YDR291W	0
5300	2719	an	AN5925.1	72.m19206	AO070340000359	1	-67	-32					ATGTGCTCCTTCTCTCTTCTTGCCACATTAAGTTAG	ATGTGCTCCTTCTCTCTTCTTGCCACATTAAGTTAG			MCSFSLLATLS*	MCSFSLLATLS*			ACACCCCTGC	GAAGCTCAGG	0	A	0	0	NCU06365.1	YDR291W	0
5339	2730	af	AN5175.1	69.m14872	AO070247000006	1			-161	-111			ATGGATTACACTGCTTGTCGTCGCGTCACTTTTAGGTCATTGCTTCATTAG		ATGGATTACACTGCTTGTCGTCGCGTCACTTTTAGGTCATTGCTTCATTAG		MDYTACRRVTFRSLLH*		MDYTACRRVTFRSLLH*		AGCGTCTTTA	TATTTGGCTA	0	R	0	0	0	0	0
5371	2743	ao	AN1701.1	58.m07777	AO070305000027	0					-58	-47	ATGTCCGAGTAG			ATGTCCGAGTAG	MSE*			MSE*	TATAGTTTTA	CTTCTATCTA	1	S	0	0	0	0	0
5394	2755	an	AN4645.1	57.m05476	AO070316000119	1	-226	-194					ATGCGCGGAGAACGACAAATACAGTGCAGGTGA	ATGCGCGGAGAACGACAAATACAGTGCAGGTGA			MRGERQIQCR*	MRGERQIQCR*			AGGACTAGGC	TGAGGGCTTC	0	P	0	0	NCU01356.1	0	0
5395	2755	an	AN4645.1	57.m05476	AO070316000119	1	-194	-180					ATGAGGGCTTCCTGA	ATGAGGGCTTCCTGA			MRAS*	MRAS*			AGTGCAGGTG	GTAGCGAAAA	0	P	0	0	NCU01356.1	0	0
5396	2755	an	AN4645.1	57.m05476	AO070316000119	1	-152	-6					ATGCACATAGCAACTTCTCGAGATATATTCTCAACGCGGTACTTCCGCACGCTTTTCCTAGACTCAGTACGTCAGATCCATCATTTCGAAATAATCGATAGTCATTCTTTGAGCTCCACAACTTCCATATCCTCTGGAGCTGAATGA	ATGCACATAGCAACTTCTCGAGATATATTCTCAACGCGGTACTTCCGCACGCTTTTCCTAGACTCAGTACGTCAGATCCATCATTTCGAAATAATCGATAGTCATTCTTTGAGCTCCACAACTTCCATATCCTCTGGAGCTGAATGA			MHIATSRDIFSTRYFRTLFLDSVRQIHHFEIIDSHSLSSTTSISSGAE*	MHIATSRDIFSTRYFRTLFLDSVRQIHHFEIIDSHSLSSTTSISSGAE*			GTTGCTGGGA	ACATAATGCT	0	P	0	0	NCU01356.1	0	0
5397	2755	af	AN4645.1	57.m05476	AO070316000119	1			-590	-555			ATGAGCCACTGCCCGTTCAACGAGTTGGCTACCTAG		ATGAGCCACTGCCCGTTCAACGAGTTGGCTACCTAG		MSHCPFNELAT*		MSHCPFNELAT*		ACTGGAATAC	TTGCCGTCCA	0	P	0	0	NCU01356.1	0	0
5398	2755	af	AN4645.1	57.m05476	AO070316000119	1			-530	-489			ATGTCTAGTTTCCCACCCTTGTCACTCGCTTCTCTGCAGTGA		ATGTCTAGTTTCCCACCCTTGTCACTCGCTTCTCTGCAGTGA		MSSFPPLSLASLQ*		MSSFPPLSLASLQ*		TTACCTCGCT	GTTTAAACTG	0	P	0	0	NCU01356.1	0	0
5399	2755	ao	AN4645.1	57.m05476	AO070316000119	1					-573	-562	ATGCGTGCATGA			ATGCGTGCATGA	MRA*			MRA*	TGTGGGGAGA	GGGTAGTTGG	0	P	0	0	NCU01356.1	0	0
5400	2755	ao	AN4645.1	57.m05476	AO070316000119	1					-565	-440	ATGAGGGTAGTTGGCGAGGCCTTGGGCTTTTTCAGGTGGGAGGAAGAAGGCCGAACCGTTGGACATGTTGAGAATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAA			ATGAGGGTAGTTGGCGAGGCCTTGGGCTTTTTCAGGTGGGAGGAAGAAGGCCGAACCGTTGGACATGTTGAGAATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAA	MRVVGEALGFFRWEEEGRTVGHVENDRIKITTRAVSGGFRR*			MRVVGEALGFFRWEEEGRTVGHVENDRIKITTRAVSGGFRR*	GAATGCGTGC	ATCAATTTAA	0	P	0	0	NCU01356.1	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
5401	2755	ao	AN4645.1	57.m05476	AO070316000119	1					-501	-430	ATGTTGAGAATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAAATCAATTTAA			ATGTTGAGAATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAAATCAATTTAA	MLRMIELKLPLGLYLEVLGDKSI*			MLRMIELKLPLGLYLEVLGDKSI*	ACCGTTGGAC	AAAAGGCGGG	0	P	0	0	NCU01356.1	0	0
5402	2755	ao	AN4645.1	57.m05476	AO070316000119	1					-492	-430	ATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAAATCAATTTAA			ATGATCGAATTAAAATTACCACTAGGGCTGTATCTGGAGGTTTTAGGCGATAAATCAATTTAA	MIELKLPLGLYLEVLGDKSI*			MIELKLPLGLYLEVLGDKSI*	CATGTTGAGA	AAAAGGCGGG	0	P	0	0	NCU01356.1	0	0
5438	2761	af	AN8056.1	53.m03887	AO070322000144	1			-82	-68			ATGAGATGCAAATGA		ATGAGATGCAAATGA		MRCK*		MRCK*		ACAGCAATAA	CTGTCTGAGA	0	BD	0	MG08841.1	0	0	0
5439	2761	af	AN8056.1	53.m03887	AO070322000144	1			-77	-60			ATGCAAATGACTGTCTGA		ATGCAAATGACTGTCTGA		MQMTV*		MQMTV*		AATAAATGAG	GATGACCTAA	0	BD	0	MG08841.1	0	0	0
5440	2761	af	AN8056.1	53.m03887	AO070322000144	1			-71	-60			ATGACTGTCTGA		ATGACTGTCTGA		MTV*		MTV*		TGAGATGCAA	GATGACCTAA	0	BD	0	MG08841.1	0	0	0
5441	2761	ao	AN8056.1	53.m03887	AO070322000144	1					-99	-85	ATGACACGATTTTGA			ATGACACGATTTTGA	MTRF*			MTRF*	AATCTATGCT	GATGTTATCT	0	BD	0	MG08841.1	0	0	0
5442	2761	ao	AN8056.1	53.m03887	AO070322000144	1					-83	-69	ATGTTATCTGACTGA			ATGTTATCTGACTGA	MLSD*			MLSD*	CGATTTTGAG	CTTATGCGAC	0	BD	0	MG08841.1	0	0	0
5443	2761	ao	AN8056.1	53.m03887	AO070322000144	1					-65	-45	ATGCGACAACTCCTTACTTGA			ATGCGACAACTCCTTACTTGA	MRQLLT*			MRQLLT*	TGACTGACTT	CCGACACATT	0	BD	0	MG08841.1	0	0	0
5450	2762	ao	AN1735.1	69.m15034	AO070324000065	0					-33	-10	ATGACTCTTTTTCTTCCAGAGTAA			ATGACTCTTTTTCTTCCAGAGTAA	MTLFLPE*			MTLFLPE*	AACTCTTTAG	AGCGCGACAA	1	F	0	0	0	0	0
5453	2764	af	AN7751.1	71.m15782	AO070325000182	0			-59	-45			ATGCTTCGCAGGTGA		ATGCTTCGCAGGTGA		MLRR*		MLRR*		GTTTATATCA	CGCCCATAGA	1	I	0	0	0	0	0
5456	2764	ao	AN7751.1	71.m15782	AO070325000182	0					-59	-45	ATGCTCTATCAGTGA			ATGCTCTATCAGTGA	MLYQ*			MLYQ*	AATTCCCCTG	TATCTCAATT	1	I	0	0	0	0	0
5460	2766	an	AN4836.1	59.m09142	AO070327000142	1	-235	-161					ATGTCCAGGATCTTTACCGTCGCGGCTCTCCCACTACCCACCCGAACGCCGACGAGGTCGAGCTTCAGAATCTAG	ATGTCCAGGATCTTTACCGTCGCGGCTCTCCCACTACCCACCCGAACGCCGACGAGGTCGAGCTTCAGAATCTAG			MSRIFTVAALPLPTRTPTRSSFRI*	MSRIFTVAALPLPTRTPTRSSFRI*			TCCTCTATCC	CATGCAGGAT	0	P	0	0	0	0	0
5461	2766	an	AN4836.1	59.m09142	AO070327000142	1	-159	-142					ATGCAGGATCAGAGATAA	ATGCAGGATCAGAGATAA			MQDQR*	MQDQR*			AGAATCTAGC	ATCACAAACA	0	P	0	0	0	0	0
5462	2766	af	AN4836.1	59.m09142	AO070327000142	1			-245	-198			ATGTACCTACAGTTAGGCTGCAAAAGACGCGAAGAAAAGAGCTGCTAG		ATGTACCTACAGTTAGGCTGCAAAAGACGCGAAGAAAAGAGCTGCTAG		MYLQLGCKRREEKSC*		MYLQLGCKRREEKSC*		TCAAGATCGG	CCTTTTCCAT	0	P	0	0	0	0	0
5463	2766	af	AN4836.1	59.m09142	AO070327000142	1			-189	-160			ATGATCCCCCAGTCCCTGGACTATTATTAG		ATGATCCCCCAGTCCCTGGACTATTATTAG		MIPQSLDYY*		MIPQSLDYY*		AGCCTTTTCC	CCGACCTCCG	0	P	0	0	0	0	0
5464	2766	ao	AN4836.1	59.m09142	AO070327000142	1					-232	-221	ATGCAGAATTGA			ATGCAGAATTGA	MQN*			MQN*	ATCGACTAGT	CCAGGGGCCA	0	P	0	0	0	0	0
5466	2767	ao	AN4834.1	59.m09144	AO070327000147	0					-35		ATGTTTTCTGCGGATCAAATTCCTCCAATCGCATGA			ATGTTTTCTGCGGATCAAATTCCTCCAATCGCATGA	MFSADQIPPIA*			MFSADQIPPIA*	TCTGCGCCGT	TGCAGTCCAG	1		0	0	0	0	0
5469	2768	af	AN3634.1	58.m07467	AO070328000078	1			-119	-54			ATGACTCCTCCGGTGATACAAGCTGAGGGGCTGTTTGCTACTTCCACCTTCCTTTGTCATTGCTGA		ATGACTCCTCCGGTGATACAAGCTGAGGGGCTGTTTGCTACTTCCACCTTCCTTTGTCATTGCTGA		MTPPVIQAEGLFATSTFLCHC*		MTPPVIQAEGLFATSTFLCHC*		CCGAGTGCCG	CATTTGGAGT	0	E	FG00598.1	MG05168.1	NCU04411.1	0	0
5470	2768	ao	AN3634.1	58.m07467	AO070328000078	1					-122	-105	ATGACGGATTCTATATGA			ATGACGGATTCTATATGA	MTDSI*			MTDSI*	GCCTACGCCG	GGGGTGCATT	0	E	FG00598.1	MG05168.1	NCU04411.1	0	0
5471	2768	ao	AN3634.1	58.m07467	AO070328000078	1					-108	-91	ATGAGGGGTGCATTTTGA			ATGAGGGGTGCATTTTGA	MRGAF*			MRGAF*	CGGATTCTAT	GTCAGAGATT	0	E	FG00598.1	MG05168.1	NCU04411.1	0	0
5480	2774	af	AN3498.1	58.m07225	AO070333000036	0			-60	-43			ATGGACTCGGGCGTCTGA		ATGGACTCGGGCGTCTGA		MDSGV*		MDSGV*		CGGCCTTTGA	ATCTTTCACC	1	R	0	0	0	0	0
5506	2778	ao	AN3061.1	59.m08953	AO070337000012	1					-198	-178	ATGGGTCCGGCTTTTGTCTAG			ATGGGTCCGGCTTTTGTCTAG	MGPAFV*			MGPAFV*	CTGGAGTCGA	TCTTTATCTG	0	O	FG10964.1	0	NCU06942.1	YPR173C	0
5509	2780	af	AN5216.1	69.m14914	AO070337000263	0			-60	-25			ATGTTGCCTTTTATGCCAGATATTTCTTGGCAATAG		ATGTTGCCTTTTATGCCAGATATTTCTTGGCAATAG		MLPFMPDISWQ*		MLPFMPDISWQ*		TACATCAGCT	TATCGCTTCA	1	L	0	0	0	0	0
5510	2780	af	AN5216.1	69.m14914	AO070337000263	0			-48	-25			ATGCCAGATATTTCTTGGCAATAG		ATGCCAGATATTTCTTGGCAATAG		MPDISWQ*		MPDISWQ*		GTTGCCTTTT	TATCGCTTCA	1	L	0	0	0	0	0
5513	2780	ao	AN5216.1	69.m14914	AO070337000263	0					-56	-33	ATGTCGTCGAGAGTACTACTATGA			ATGTCGTCGAGAGTACTACTATGA	MSSRVLL*			MSSRVLL*	TCACAAGGTC	CGCAACCTTA	1	L	0	0	0	0	0
5514	2780	ao	AN5216.1	69.m14914	AO070337000263	0					-36	-22	ATGACGCAACCTTAG			ATGACGCAACCTTAG	MTQP*			MTQP*	GAGTACTACT	ATCCGCCATT	1	L	0	0	0	0	0
5516	2782	an	AN2872.1	59.m08720	AO070338000142	0	-47	-18					ATGCCAATCACCGACACCTCTGAAATTTGA	ATGCCAATCACCGACACCTCTGAAATTTGA			MPITDTSEI*	MPITDTSEI*			AAAATCCCCA	CAGATTTATC	1		0	0	0	0	0
5528	2789	an	AN2090.1	57.m05792	AO070341000248	0	-55	-29					ATGCTGCTAGATCGAACCCATCACTAA	ATGCTGCTAGATCGAACCCATCACTAA			MLLDRTHH*	MLLDRTHH*			TCCAAGGGTG	CAAACTCCAT	1	R	0	0	0	YPL263C	0
5531	2794	an	AN7443.1	57.m05901	AO070229000015	1	-46	-23					ATGCGGTTTCGCCTGAGATCATAA	ATGCGGTTTCGCCTGAGATCATAA			MRFRLRS*	MRFRLRS*			TAAGGACCTC	ATTACAACCC	1		0	0	0	0	0
5532	2794	ao	AN7443.1	57.m05901	AO070229000015	1					-47	-21	ATGTTGGCACTTGAACTTAAGTATTAG			ATGTTGGCACTTGAACTTAAGTATTAG	MLALELKY*			MLALELKY*	AACACGTTTG	AAAAGATTGT	1		0	0	0	0	0
5535	2801	an	AN1660.1	58.m08995	AO070299000020	0	-48	-4					ATGTTCCGTTTTCTCTCCTCCTTCTACCACTGCTTCTTGTCTTGA	ATGTTCCGTTTTCTCTCCTCCTTCTACCACTGCTTCTTGTCTTGA			MFRFLSSFYHCFLS*	MFRFLSSFYHCFLS*			CCGTCTCGCA	ACTATGGTTG	1	RP	0	0	0	0	0
5542	2802	an	AN1665.1	58.m07733	AO070299000047	0	-57	-7					ATGGTTACGGGCTTTTACCCTCTTGCCTTATTGGGAGATATGCCGCCTTGA	ATGGTTACGGGCTTTTACCCTCTTGCCTTATTGGGAGATATGCCGCCTTGA			MVTGFYPLALLGDMPP*	MVTGFYPLALLGDMPP*			TAAATCTCTC	TTGATAATGG	1	T	FG07520.1	MG00700.1	0	YJL057C	0
5543	2802	an	AN1665.1	58.m07733	AO070299000047	0	-18	-7					ATGCCGCCTTGA	ATGCCGCCTTGA			MPP*	MPP*			ATTGGGAGAT	TTGATAATGG	1	T	FG07520.1	MG00700.1	0	YJL057C	0
5548	2802	ao	AN1665.1	58.m07733	AO070299000047	0					-53	-24	ATGATATTCTCTTGTTCCCCTAATTCTTGA			ATGATATTCTCTTGTTCCCCTAATTCTTGA	MIFSCSPNS*			MIFSCSPNS*	CTCTTCGAGA	GATGCGCGTG	1	T	FG07520.1	MG00700.1	0	YJL057C	0
5549	2804	conserved	AN4460.1	58.m07864	AO070305000133	0	-52	-41	-49	-38	-51	-40	ATGGCGCGmTAr	ATGGCGCGCTAA	ATGGCGCGCTAG	ATGGCGCGATAG	MAR*	MAR*	MAR*	MAR*	krkwyrkrks	wwhbywyrsm	1	A	FG06788.1	0	NCU03628.1	0	0
5552	2804	af	AN4460.1	58.m07864	AO070305000133	0			-52	-38			ATGATGGCGCGCTAG		ATGATGGCGCGCTAG		MMAR*		MMAR*		TTCTGGACGT	TTCTCTTGCA	1	A	FG06788.1	0	NCU03628.1	0	0
5585	2820	ao	AN0756.1	70.m15358	AO070343000444	0					-51	-34	ATGGGAAATCTGCTGTAA			ATGGGAAATCTGCTGTAA	MGNLL*			MGNLL*	CCCCCGAAAC	GCTCTCACTG	1	G	0	0	0	0	0
5599	2827	an	AN2015.1	58.m07623	AO070202000008	1	-70	-56					ATGCGTATGCGATAG	ATGCGTATGCGATAG			MRMR*	MRMR*			AGCGCTCGCG	TGTCGTATTC	0	G	0	0	0	0	0
5600	2827	af	AN2015.1	58.m07623	AO070202000008	1			-123	-7			ATGGTCGGTCGGGATGTACATGCTGTTGTCGACACGGTAATCGGTTTCTGTCTCTATCGTCGCTGGTTAATCGAGCTTGGGTTTGAACGAGGGAAAGCGGAACACATACAGGAATAA		ATGGTCGGTCGGGATGTACATGCTGTTGTCGACACGGTAATCGGTTTCTGTCTCTATCGTCGCTGGTTAATCGAGCTTGGGTTTGAACGAGGGAAAGCGGAACACATACAGGAATAA		MVGRDVHAVVDTVIGFCLYRRWLIELGFERGKAEHIQE*		MVGRDVHAVVDTVIGFCLYRRWLIELGFERGKAEHIQE*		CAGTTTCTTC	ACTCAAATGT	0	G	0	0	0	0	0
5601	2827	af	AN2015.1	58.m07623	AO070202000008	1			-110	-84			ATGTACATGCTGTTGTCGACACGGTAA		ATGTACATGCTGTTGTCGACACGGTAA		MYMLLSTR*		MYMLLSTR*		GTCGGTCGGG	TCGGTTTCTG	0	G	0	0	0	0	0
5602	2827	af	AN2015.1	58.m07623	AO070202000008	1			-104	-84			ATGCTGTTGTCGACACGGTAA		ATGCTGTTGTCGACACGGTAA		MLLSTR*		MLLSTR*		CGGGATGTAC	TCGGTTTCTG	0	G	0	0	0	0	0
5603	2827	ao	AN2015.1	58.m07623	AO070202000008	1					-89	-63	ATGATCGAGATGCTTATGCTTTTCTAG			ATGATCGAGATGCTTATGCTTTTCTAG	MIEMLMLF*			MIEMLMLF*	GCCGTGCTGG	TGCGGTACCT	0	G	0	0	0	0	0
5604	2827	ao	AN2015.1	58.m07623	AO070202000008	1					-80	-63	ATGCTTATGCTTTTCTAG			ATGCTTATGCTTTTCTAG	MLMLF*			MLMLF*	GATGATCGAG	TGCGGTACCT	0	G	0	0	0	0	0
5605	2827	ao	AN2015.1	58.m07623	AO070202000008	1					-74	-63	ATGCTTTTCTAG			ATGCTTTTCTAG	MLF*			MLF*	CGAGATGCTT	TGCGGTACCT	0	G	0	0	0	0	0
5616	2833	af	AN6911.1	71.m15221	AO070219000015	0			-23				ATGAATACAAGTAAACACAATTAA		ATGAATACAAGTAAACACAATTAA		MNTSKHN*		MNTSKHN*		CTTTTTATTA	TGGCGCCATC	1	U	0	0	0	0	0
5626	2838	af	AN4316.1	58.m08008	AO070230000004	0			-33	-4			ATGTCTAGCGGTGGAAAGAAAGAAGCTTAA		ATGTCTAGCGGTGGAAAGAAAGAAGCTTAA		MSSGGKKEA*		MSSGGKKEA*		TATACTACCA	GCGATGAATC	1	R	0	0	0	0	0
5687	2862	conserved	AN1341.1	70.m15733	AO070247000023	1	-31	-20	-46	-35	-34	-23	ATGGGCyGTTGA	ATGGGCCGTTGA	ATGGGCCGTTGA	ATGGGCTGTTGA	MGr*	MGR*	MGR*	MGC*	TkdyyTTGGA	vyyvyymrhw	1	U	FG01552.1	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
5690	2866	an	AN5783.1	69.m14814	AO070249000028	1	-217	-65					ATGAATATCCCTTGTCCATCCTTTCTATATCTGCGATGTAATAGTCTGAGAGATTATATTACCCATCATCTATACTTCTACTGCAACATTGATATCGGACATCAGCTTTCCCAGGGACTATTTGGAAATGATGCTGGGACTTGGGAATTATGA	ATGAATATCCCTTGTCCATCCTTTCTATATCTGCGATGTAATAGTCTGAGAGATTATATTACCCATCATCTATACTTCTACTGCAACATTGATATCGGACATCAGCTTTCCCAGGGACTATTTGGAAATGATGCTGGGACTTGGGAATTATGA			MNIPCPSFLYLRCNSLRDYITHHLYFYCNIDIGHQLSQGLFGNDAGTWEL*	MNIPCPSFLYLRCNSLRDYITHHLYFYCNIDIGHQLSQGLFGNDAGTWEL*			CTCTGCCTTA	AAGCAGTAGT	0	O	0	0	0	0	0
5691	2866	af	AN5783.1	69.m14814	AO070249000028	1			-289	-248			ATGATTTTAATGGTAGTTATGGTGAAGGACAACATGCTTTGA		ATGATTTTAATGGTAGTTATGGTGAAGGACAACATGCTTTGA		MILMVVMVKDNML*		MILMVVMVKDNML*		TTCTGATCTC	ATGGATTGAC	0	O	0	0	0	0	0
5692	2866	af	AN5783.1	69.m14814	AO070249000028	1			-280	-248			ATGGTAGTTATGGTGAAGGACAACATGCTTTGA		ATGGTAGTTATGGTGAAGGACAACATGCTTTGA		MVVMVKDNML*		MVVMVKDNML*		CATGATTTTA	ATGGATTGAC	0	O	0	0	0	0	0
5693	2866	af	AN5783.1	69.m14814	AO070249000028	1			-271	-248			ATGGTGAAGGACAACATGCTTTGA		ATGGTGAAGGACAACATGCTTTGA		MVKDNML*		MVKDNML*		AATGGTAGTT	ATGGATTGAC	0	O	0	0	0	0	0
5694	2866	ao	AN5783.1	69.m14814	AO070249000028	1					-448	-401	ATGAGTACTCAAAGGCAACTGTATATATCTAGTATTCGTGGAGTTTAA			ATGAGTACTCAAAGGCAACTGTATATATCTAGTATTCGTGGAGTTTAA	MSTQRQLYISSIRGV*			MSTQRQLYISSIRGV*	ATCGTAATCC	CAAAGGAGCA	0	O	0	0	0	0	0
5701	2868	af	AN8745.1	62.m03335	AO070250000030	0			-59	-9			ATGATACAAGACTTGGTTTCTTTATATTTAAAATCGGCACCCTATAAGTGA		ATGATACAAGACTTGGTTTCTTTATATTTAAAATCGGCACCCTATAAGTGA		MIQDLVSLYLKSAPYK*		MIQDLVSLYLKSAPYK*		TCCTTCATAT	CCCGCGCAAT	1	G	0	0	0	0	0
5716	2870	af	AN7201.1	69.m15184	AO070252000010	0			-59	-30			ATGAAGCGGTTCCCCAGGCCGTCTTGCTAG		ATGAAGCGGTTCCCCAGGCCGTCTTGCTAG		MKRFPRPSC*		MKRFPRPSC*		AAACATTTAT	GTACACACAA	1	O	0	0	0	0	0
5741	2876	af	AN3153.1	59.m08513	AO070256000033	1			-72	-4			ATGAAACCTCCAAGCTACCTACATTTGTTGAATAGCTTTCCAATTCATCAAAAGCGTCAAACTCCTTAA		ATGAAACCTCCAAGCTACCTACATTTGTTGAATAGCTTTCCAATTCATCAAAAGCGTCAAACTCCTTAA		MKPPSYLHLLNSFPIHQKRQTP*		MKPPSYLHLLNSFPIHQKRQTP*		CTTTCAGCAT	ACAATGTCAC	0	BK	0	0	0	0	0
5775	2892	an	AN7663.1	57.m05430	AO070268000034	0	-32	-21					ATGATTCTCTGA	ATGATTCTCTGA			MIL*	MIL*			CAACTGGCTA	AAAACAACAA	1	C	0	0	0	0	0
5778	2892	af	AN7663.1	57.m05430	AO070268000034	0			-57	-40			ATGGAGGACAAGCCGTAG		ATGGAGGACAAGCCGTAG		MEDKP*		MEDKP*		GACAACTCCC	CCCTAGTATA	1	C	0	0	0	0	0
5806	2899	an	AN6546.1	62.m03127	AO070270000039	1	-159	-148					ATGATTGAGTAG	ATGATTGAGTAG			MIE*	MIE*			GATTAATCTG	ATTGGTCGAG	0	T	0	0	0	0	0
5807	2899	an	AN6546.1	62.m03127	AO070270000039	1	-103	-35					ATGCAGTCGCTTGCTTTCCGCACAAGACAGTCCTACAACAACTTCCTTTGCCCGCTGCCCGCTGCCTGA	ATGCAGTCGCTTGCTTTCCGCACAAGACAGTCCTACAACAACTTCCTTTGCCCGCTGCCCGCTGCCTGA			MQSLAFRTRQSYNNFLCPLPAA*	MQSLAFRTRQSYNNFLCPLPAA*			GAGGAGTTAT	AGCTTGAGCT	0	T	0	0	0	0	0
5808	2899	af	AN6546.1	62.m03127	AO070270000039	1			-137	-114			ATGCAGACAAAACAGTCCCTGTGA		ATGCAGACAAAACAGTCCCTGTGA		MQTKQSL*		MQTKQSL*		GACCGTCTCG	TTTAGATCAT	0	T	0	0	0	0	0
5809	2899	ao	AN6546.1	62.m03127	AO070270000039	1					-140	-117	ATGCTGAAGGAGCGTTGTCTATAA			ATGCTGAAGGAGCGTTGTCTATAA	MLKERCL*			MLKERCL*	CAACGTCTCC	ATCAAGCTTC	0	T	0	0	0	0	0
5860	2922	ao	AN1133.1	71.m15635	AO070276000007	1					-50	-33	ATGCTGCACTTTTCCTAG			ATGCTGCACTTTTCCTAG	MLHFS*			MLHFS*	ATCGACGTGC	AATAGTCAAC	1	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5861	2923	an	AN8820.1	71.m15631	AO070276000022	1	-315	-289					ATGCTTCTCGAGCAGCCTATCGCGTGA	ATGCTTCTCGAGCAGCCTATCGCGTGA			MLLEQPIA*	MLLEQPIA*			GCGACAGAAC	TCAACAAGAG	0	R	0	0	0	0	0
5864	2924	an	AN8810.1	71.m15616	AO070276000047	1	-45	-31					ATGCTTCCTCTTTGA	ATGCTTCCTCTTTGA			MLPL*	MLPL*			TAATAAACTG	AGTGACAGTT	1		FG06805.1	0	0	YHR045W	0
5867	2924	ao	AN8810.1	71.m15616	AO070276000047	0					-35	-12	ATGACGACGTATTGTCGATCATAA			ATGACGACGTATTGTCGATCATAA	MTTYCRS*			MTTYCRS*	CACATCCTAC	GTAAACCAAA	1		FG06805.1	0	0	YHR045W	0
5875	2926	ao	AN8283.1	65.m07459	AO070277000005	0					-52	-20	ATGTCATTATTCCCCCTTTCGTCTACCTGTTGA			ATGTCATTATTCCCCCTTTCGTCTACCTGTTGA	MSLFPLSSTC*			MSLFPLSSTC*	TTTCCTTTTC	CCCCTACTGT	1	Q	0	MG04432.1	0	0	0
5883	2930	an	AN7354.1	72.m19725	AO070278000046	0	-20	-3					ATGCTAACAATTGCGTGA	ATGCTAACAATTGCGTGA			MLTIA*	MLTIA*			AGGTTCATTG	AGATGGTCCT	1	J	0	MG05248.1	0	0	0
5884	2930	af	AN7354.1	72.m19725	AO070278000046	0			-56	-30			ATGTTCATTCTGCATATTTGCGTCTGA		ATGTTCATTCTGCATATTTGCGTCTGA		MFILHICV*		MFILHICV*		CCGACAAGGT	TGCATTGAGG	1	J	0	MG05248.1	0	0	0
5886	2930	ao	AN7354.1	72.m19725	AO070278000046	0					-55	-44	ATGCCGGGATGA			ATGCCGGGATGA	MPG*			MPG*	GGTATGTTCT	TGGCTTTATA	1	J	0	MG05248.1	0	0	0
5887	2930	ao	AN7354.1	72.m19725	AO070278000046	0					-47	-18	ATGATGGCTTTATATTGTCGTTATTCTTGA			ATGATGGCTTTATATTGTCGTTATTCTTGA	MMALYCRYS*			MMALYCRYS*	CTATGCCGGG	TACTAATTGG	1	J	0	MG05248.1	0	0	0
5888	2930	ao	AN7354.1	72.m19725	AO070278000046	0					-44	-18	ATGGCTTTATATTGTCGTTATTCTTGA			ATGGCTTTATATTGTCGTTATTCTTGA	MALYCRYS*			MALYCRYS*	TGCCGGGATG	TACTAATTGG	1	J	0	MG05248.1	0	0	0
5891	2931	af	AN6364.1	72.m19496	AO070279000050	0			-53	-36			ATGTTCTGGATGCAATAG		ATGTTCTGGATGCAATAG		MFWMQ*		MFWMQ*		TGGCTGCGTG	CTGTCATTTA	1	D	0	MG04988.1	NCU07554.1	YJL074C	YJL074C
5892	2931	ao	AN6364.1	72.m19496	AO070279000050	0					-55	-29	ATGATCTGGTTGTTGTGCCTGCCATAA			ATGATCTGGTTGTTGTGCCTGCCATAA	MIWLLCLP*			MIWLLCLP*	CGGTCGCGTG	CTTCCCGTGT	1	D	0	MG04988.1	NCU07554.1	YJL074C	YJL074C
5898	2939	an	AN1069.1	70.m15145	AO070285000067	0	-60	-43					ATGACCAGAGTTCATTGA	ATGACCAGAGTTCATTGA			MTRVH*	MTRVH*			GGGGAACTGC	TCGAGTCGAG	1		0	0	0	0	0
5955	2961	af	AN8877.1	56.m03107	AO070293000006	0			-46	-2			ATGGCATACTACGACGCTCGGTCACACACGGAGCAACTCGTCTGA		ATGGCATACTACGACGCTCGGTCACACACGGAGCAACTCGTCTGA		MAYYDARSHTEQLV*		MAYYDARSHTEQLV*		TGGATGTCCG	AATGGAGGGC	1	T	0	0	NCU03264.1	0	0
5963	2962	an	AN8896.1	56.m02307	AO070293000029	0	-56	-33					ATGCCACCTGATTACTCTTCCTAG	ATGCCACCTGATTACTCTTCCTAG			MPPDYSS*	MPPDYSS*			CAATCTAGTC	TTTTCGCATC	1	Q	0	0	0	0	0
6012	2970	af	AN4336.1	70.m15045	AO070295000006	0			-45	-31			ATGGAGCCTGATTGA		ATGGAGCCTGATTGA		MEPD*		MEPD*		CGATTCCAGA	TCACCAAACT	1	Q	0	MG01231.1	NCU00643.1	0	0
6079	2990	an	AN1965.1	58.m07570	AO070301000046	1	-136	-104					ATGGTTATATCCAGGTCTTTGCAGCTGCTCTAG	ATGGTTATATCCAGGTCTTTGCAGCTGCTCTAG			MVISRSLQLL*	MVISRSLQLL*			TCGACACTGC	CATCACTCTA	0	FE	0	MG07148.1	0	0	0
6081	2990	af	AN1965.1	58.m07570	AO070301000046	1			-144	-121			ATGACTCTACGTCTCTTCTTCTGA		ATGACTCTACGTCTCTTCTTCTGA		MTLRLFF*		MTLRLFF*		GTTCCCTGAC	ATATACATTC	0	FE	0	MG07148.1	0	0	0
6082	2990	ao	AN1965.1	58.m07570	AO070301000046	1					-152	-120	ATGTATCACCTTTTGTTTGACTCTGGGGTTTGA			ATGTATCACCTTTTGTTTGACTCTGGGGTTTGA	MYHLLFDSGV*			MYHLLFDSGV*	CGGGGCATTT	TTGTCCTCAG	0	FE	0	MG07148.1	0	0	0
6098	2992	an	AN1970.1	58.m07575	AO070301000054	0	-59	-42					ATGCTCCAGCTTGTTTGA	ATGCTCCAGCTTGTTTGA			MLQLV*	MLQLV*			TGACCTTGCC	GACTCTATTC	1	J	0	0	0	0	0
6102	2992	af	AN1970.1	58.m07575	AO070301000054	0			-40	-14			ATGCCATTGCTCATGCAGTTTCTATAA		ATGCCATTGCTCATGCAGTTTCTATAA		MPLLMQFL*		MPLLMQFL*		TCCTACTGTC	CTTGATTATC	1	J	0	0	0	0	0
6103	2992	af	AN1970.1	58.m07575	AO070301000054	0			-28	-14			ATGCAGTTTCTATAA		ATGCAGTTTCTATAA		MQFL*		MQFL*		GCCATTGCTC	CTTGATTATC	1	J	0	0	0	0	0
6107	2992	ao	AN1970.1	58.m07575	AO070301000054	0					-35	-9	ATGGTCGATACGATATCGACCTTTTGA			ATGGTCGATACGATATCGACCTTTTGA	MVDTISTF*			MVDTISTF*	TTTCCCTGTC	TCAAGACAAT	1	J	0	0	0	0	0
6109	2993	af	AN1971.1	58.m07576	AO070301000055	1			-107	-81			ATGACCCTCCTTCGCAACCCTTTCTAA		ATGACCCTCCTTCGCAACCCTTTCTAA		MTLLRNPF*		MTLLRNPF*		TTTCCTTTGC	TACCTGATCA	0	L	0	0	0	YDR190C	YDR190C
6125	3008	af	AN6256.1	72.m19400	AO070304000032	1			-45	-34			ATGGCTCAATAA		ATGGCTCAATAA		MAQ*		MAQ*		CGGTTCTCAT	TCAGTCTCAT	1	O	0	MG01109.1	NCU06739.1	0	0
6126	3008	ao	AN6256.1	72.m19400	AO070304000032	1					-55	-44	ATGGTGCGATAA			ATGGTGCGATAA	MVR*			MVR*	CTACAACTCT	GCTCTCCGGC	1	O	0	MG01109.1	NCU06739.1	0	0
6140	3017	ao	AN4464.1	58.m07849	AO070305000118	1					-179	-42	ATGTTGTTGTGGTTCTTGTTCCCCGGGTGTGCCCCTCCGACTGCTTGCAGTGTTGATTGTGGAGGGGTCGTGGGGATAAATTTTTCCCCTCCTTCAATTTTCTTTTCCCTTCCTTTTTCTTGTCTTTCTGGTCCCTGA			ATGTTGTTGTGGTTCTTGTTCCCCGGGTGTGCCCCTCCGACTGCTTGCAGTGTTGATTGTGGAGGGGTCGTGGGGATAAATTTTTCCCCTCCTTCAATTTTCTTTTCCCTTCCTTTTTCTTGTCTTTCTGGTCCCTGA	MLLWFLFPGCAPPTACSVDCGGVVGINFSPPSIFFSLPFSCLSGP*			MLLWFLFPGCAPPTACSVDCGGVVGINFSPPSIFFSLPFSCLSGP*	CTTCCCTTCG	CCTTGACGTG	0	F	0	MG04435.1	NCU02629.1	0	0
6221	3048	conserved	AN1014.1	70.m15232	AO070312000004	1	-67	-41	-120	-94	-73	-47	ATGTTvbCyywmGyyGAyyCyGGmTrr	ATGTTGCCTTACGTTGATTCCGGATAA	ATGTTCGCCTTCGCCGACCCTGGATAG	ATGTTATCCCAAGTTGACTCTGGCTGA	MlpyvDsG*	MLPYVDSG*	MFAFADPG*	MLSQVDSG*	bhbbmTrGhy	wvyywwwwby	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6227	3048	ao	AN1014.1	70.m15232	AO070312000004	1					-79	-47	ATGGCCATGTTATCCCAAGTTGACTCTGGCTGA			ATGGCCATGTTATCCCAAGTTGACTCTGGCTGA	MAMLSQVDSG*			MAMLSQVDSG*	AATCCGCTTC	AATTAATTCT	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6232	3051	ao	AN2500.1	59.m09384	AO070312000055	0					-56	-21	ATGACAATTTTGCACCACCTGATCCCCCGTGAATAG			ATGACAATTTTGCACCACCTGATCCCCCGTGAATAG	MTILHHLIPRE*			MTILHHLIPRE*	TCTGGTTCGA	GGGGCGCGAC	1	R	0	0	0	YLR285W	YLR285W
6233	3053	af	AN6920.1	71.m15192	AO070313000059	1			-141	-127			ATGCTTTTGCGATAA		ATGCTTTTGCGATAA		MLLR*		MLLR*		ACACAACTTG	CGTAGCCTTG	0	U	0	0	0	0	0
6271	3060	an	AN6841.1	71.m15298	AO070314000098	0	-43	-32					ATGACGACCTGA	ATGACGACCTGA			MTT*	MTT*			AAAGAATGAA	AGCATACAAT	1	O	0	0	0	YMR150C	YMR150C
6300	3071	ao	AN8698.1	62.m03470	AO070315000125	1					-52	-35	ATGGTACCAGCGGAGTAA			ATGGTACCAGCGGAGTAA	MVPAE*			MVPAE*	TAAGTTGTTG	CAACGGAGAC	1	Z	0	0	0	0	0
6329	3083	an	AN0633.1	70.m15649	AO070318000123	1	-338	-303					ATGGCACGTCAGACCATTGTCCATTCCTTCTCCTAA	ATGGCACGTCAGACCATTGTCCATTCCTTCTCCTAA			MARQTIVHSFS*	MARQTIVHSFS*			CCTTCCCCTC	TGTAACGACG	0		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
6330	3083	an	AN0633.1	70.m15649	AO070318000123	1	-286	-224					ATGGCTGTCCAGTTACCTCCCCGTCGCTCGAGGGTAGTACTGGTCTCCGGTTTTTGGCTTTAA	ATGGCTGTCCAGTTACCTCCCCGTCGCTCGAGGGTAGTACTGGTCTCCGGTTTTTGGCTTTAA			MAVQLPPRRSRVVLVSGFWL*	MAVQLPPRRSRVVLVSGFWL*			GACGTCTCTC	CTTCTCTGTT	0		0	0	0	0	0
6331	3083	af	AN0633.1	70.m15649	AO070318000123	1			-198	-88			ATGGCCAAACCCAAACCCAAACCCCCAATCCGAGCCTCCATAAACTCCCCTCATGTAATCACTACTGATCAGATTATGATCTTGTTTGCTTCTCCATGGCCTTCCAGTTGA		ATGGCCAAACCCAAACCCAAACCCCCAATCCGAGCCTCCATAAACTCCCCTCATGTAATCACTACTGATCAGATTATGATCTTGTTTGCTTCTCCATGGCCTTCCAGTTGA		MAKPKPKPPIRASINSPHVITTDQIMILFASPWPSS*		MAKPKPKPPIRASINSPHVITTDQIMILFASPWPSS*		ACCCCCGTTT	TCAACCTTCA	0		0	0	0	0	0
6332	3083	af	AN0633.1	70.m15649	AO070318000123	1			-123	-88			ATGATCTTGTTTGCTTCTCCATGGCCTTCCAGTTGA		ATGATCTTGTTTGCTTCTCCATGGCCTTCCAGTTGA		MILFASPWPSS*		MILFASPWPSS*		TGATCAGATT	TCAACCTTCA	0		0	0	0	0	0
6333	3083	af	AN0633.1	70.m15649	AO070318000123	1			-103	-47			ATGGCCTTCCAGTTGATCAACCTTCATGTGAAGGTAGTAAACAGGTTCGCCGGTTGA		ATGGCCTTCCAGTTGATCAACCTTCATGTGAAGGTAGTAAACAGGTTCGCCGGTTGA		MAFQLINLHVKVVNRFAG*		MAFQLINLHVKVVNRFAG*		TTGCTTCTCC	TCGGGGCCAC	0		0	0	0	0	0
6334	3083	ao	AN0633.1	70.m15649	AO070318000123	1					-171	-118	ATGTGCGCCTCTCACGCCATCTTCCTGCAGCAATTTCTGCCATCTCAGATGTAA			ATGTGCGCCTCTCACGCCATCTTCCTGCAGCAATTTCTGCCATCTCAGATGTAA	MCASHAIFLQQFLPSQM*			MCASHAIFLQQFLPSQM*	GATCCGCTCA	CCTCTTTCGA	0		0	0	0	0	0
6335	3083	ao	AN0633.1	70.m15649	AO070318000123	1					-92	-72	ATGTCCTTCACAGGAAGGTAG			ATGTCCTTCACAGGAAGGTAG	MSFTGR*			MSFTGR*	TAACGGCTTC	TGGTGCCGTG	0		0	0	0	0	0
6359	3088	af	AN0873.1	70.m15476	AO070320000032	0			-60	-7			ATGGAGACGCTCAATTCCTTCATTCTCATAGAAATATCTCTTTTTGTATACTAA		ATGGAGACGCTCAATTCCTTCATTCTCATAGAAATATCTCTTTTTGTATACTAA		METLNSFILIEISLFVY*		METLNSFILIEISLFVY*		ATTTGAGAGC	GTCAACATGT	1	R	0	0	0	0	0
6402	3102	an	AN0189.1	71.m15459	AO070321000054	0	-60	-22					ATGCATTTTCTCGAACCGAACTCAGGGAATCAAATTTAA	ATGCATTTTCTCGAACCGAACTCAGGGAATCAAATTTAA			MHFLEPNSGNQI*	MHFLEPNSGNQI*			ATAAATCTGA	CTACGATAAT	1	A	0	MG01893.1	0	0	0
6407	3103	an	AN0182.1	71.m16065	AO070321000058	1	-342	-283					ATGCTAAGTCGAGGCAGCCAAGCGAATCGCGTCCCGGCTCACACTCAATTCCGCCTGTGA	ATGCTAAGTCGAGGCAGCCAAGCGAATCGCGTCCCGGCTCACACTCAATTCCGCCTGTGA			MLSRGSQANRVPAHTQFRL*	MLSRGSQANRVPAHTQFRL*			AAAACCTTGC	CAGAGTTCCA	0	R	0	0	0	0	0
6413	3109	af	AN4539.1	57.m05582	AO070321000157	1			-380	-291			ATGATCCCTTTCACCCGGTGCTACAGCCGCTGTTTCCGAATTCCCCCATATATACTTTCCTACTTCCAAAGTTGTACAGTCAGTCCATAA		ATGATCCCTTTCACCCGGTGCTACAGCCGCTGTTTCCGAATTCCCCCATATATACTTTCCTACTTCCAAAGTTGTACAGTCAGTCCATAA		MIPFTRCYSRCFRIPPYILSYFQSCTVSP*		MIPFTRCYSRCFRIPPYILSYFQSCTVSP*		GTCAACATAC	AGCGGGGAGC	0	R	0	0	0	0	0
6416	3115	conserved	AN8009.1	53.m03858	AO070322000058	1	-191	-126	-317	-141	-325	-125	ATGACAGGTGTTCGdyykGGryywvhsyykGwhGhyykGhsmTyhyhsTdybdyAwsyTsdhCydsysTGTskkTmTyyyTTTrrsskkkrkrsmCsyCkmrsrrrmsGwkrGACrmwsssmrwmGkCwGwswGrArssskryCGkkykkAsrwkryAswGTCmkrwCkTkmTswrrTTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGGCCGGGGTCAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGATCTGGGTTTCTGTCTGAAGACTGGTGCTTTTTGTTCGGTATGCTCGACTGCTCTGTGGTTATTTTTTTGACCTGGAGAGACGCCTCGCAGACGGATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGTCTTGGACCTGCCCTGGTTGCCTGGCCATCCCCCTACTTCATGCTGTCCCTGCGTGTCTGTCTCCCTTTAGGGGTTGTGCCCCTCGAAGGAGACGTGAGACAAAGGGCAAAGGCTGAGTGGAGGGGTACCGGGTGTACGAGGCAGAGTCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	MTGVRpGsnpvvlrlychnLi*	MTGVRPGSNPVVLRLYCHNLI*	MTGVRSGFLSEDWCFLFGMLDCSVVIFLTWRDASQTDGRSQSSVRNPVVLRLYCHNLI*	MTGVRLGPALVAWPSPYFMLSLRVCLPLGVVPLEGDVRQRAKAEWRGTGCTRQSPVVLRLYCHNLI*	ywGCwysCGC	ATAATACTAG	0	P	FG01672.1	0	0	0	0
6417	3115	an	AN8009.1	53.m03858	AO070322000058	1	-248	-126					ATGGGTTCAGACGGGTCAAGGTATCGTACAGATTATCCAAACAGTCACTGCATCCGCATGACAGGTGTTCGGCCGGGGTCAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	ATGGGTTCAGACGGGTCAAGGTATCGTACAGATTATCCAAACAGTCACTGCATCCGCATGACAGGTGTTCGGCCGGGGTCAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG			MGSDGSRYRTDYPNSHCIRMTGVRPGSNPVVLRLYCHNLI*	MGSDGSRYRTDYPNSHCIRMTGVRPGSNPVVLRLYCHNLI*			GACTTTCGCT	ATAATACTAG	0	P	FG01672.1	0	0	0	0
6418	3115	an	AN8009.1	53.m03858	AO070322000058	1	-106	-62					ATGCGTTGCATTGATTGCCCCCTTTTTGAAAGGAAGAGAGCATAG	ATGCGTTGCATTGATTGCCCCCTTTTTGAAAGGAAGAGAGCATAG			MRCIDCPLFERKRA*	MRCIDCPLFERKRA*			GCGAAAGGAC	TCTCTCATGC	0	P	FG01672.1	0	0	0	0
6419	3115	an	AN8009.1	53.m03858	AO070322000058	1	-55	-26					ATGCTGACAACTTCTAGTCACCCGATCTGA	ATGCTGACAACTTCTAGTCACCCGATCTGA			MLTTSSHPI*	MLTTSSHPI*			ATAGTCTCTC	TCCTATCTGA	1	P	FG01672.1	0	0	0	0
6420	3115	af	AN8009.1	53.m03858	AO070322000058	1			-417	-373			ATGGGGCCGCGCAGTCAAGATGACCCTCGGGGTCATTTTCGCTAG		ATGGGGCCGCGCAGTCAAGATGACCCTCGGGGTCATTTTCGCTAG		MGPRSQDDPRGHFR*		MGPRSQDDPRGHFR*		AGGACTCACC	GGGTTGAGAT	0	P	FG01672.1	0	0	0	0
6421	3115	af	AN8009.1	53.m03858	AO070322000058	1			-398	-366			ATGACCCTCGGGGTCATTTTCGCTAGGGGTTGA		ATGACCCTCGGGGTCATTTTCGCTAGGGGTTGA		MTLGVIFARG*		MTLGVIFARG*		CGCAGTCAAG	GATGGGTCAA	0	P	FG01672.1	0	0	0	0
6422	3115	af	AN8009.1	53.m03858	AO070322000058	1			-364	-314			ATGGGTCAAGGTATCGTACATTGTATAATAACAGTCACTGCTCGCGCATGA		ATGGGTCAAGGTATCGTACATTGTATAATAACAGTCACTGCTCGCGCATGA		MGQGIVHCIITVTARA*		MGQGIVHCIITVTARA*		AGGGGTTGAG	CAGGTGTTCG	0	P	FG01672.1	0	0	0	0
6423	3115	af	AN8009.1	53.m03858	AO070322000058	1			-263	-141			ATGCTCGACTGCTCTGTGGTTATTTTTTTGACCTGGAGAGACGCCTCGCAGACGGATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG		ATGCTCGACTGCTCTGTGGTTATTTTTTTGACCTGGAGAGACGCCTCGCAGACGGATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG		MLDCSVVIFLTWRDASQTDGRSQSSVRNPVVLRLYCHNLI*		MLDCSVVIFLTWRDASQTDGRSQSSVRNPVVLRLYCHNLI*		TTTGTTCGGT	ATAATACTAG	0	P	FG01672.1	0	0	0	0
6424	3115	af	AN8009.1	53.m03858	AO070322000058	1			-208	-167			ATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGA		ATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGA		MDAPSRQSETRSF*		MDAPSRQSETRSF*		TCGCAGACGG	GATTATACTG	0	P	FG01672.1	0	0	0	0
6425	3115	af	AN8009.1	53.m03858	AO070322000058	1			-121	-83			ATGCGTGGCACTGATTGTCCCCCTTACCCCCTTCTGTGA		ATGCGTGGCACTGATTGTCCCCCTTACCCCCTTCTGTGA		MRGTDCPPYPLL*		MRGTDCPPYPLL*		GCGAAAGGAC	AAGATGAGGG	0	P	FG01672.1	0	0	0	0
6426	3115	af	AN8009.1	53.m03858	AO070322000058	1			-79	-47			ATGAGGGGCTTTGCCTCTCTGTTTGCTGACTGA		ATGAGGGGCTTTGCCTCTCTGTTTGCTGACTGA		MRGFASLFAD*		MRGFASLFAD*		TCTGTGAAAG	TTTTCAGAAC	0	P	FG01672.1	0	0	0	0
6427	3115	ao	AN8009.1	53.m03858	AO070322000058	1					-429	-379	ATGAGGCCGCGCAGCCAGAATGACCTTCTGGGTCGTTTCGCTATGGGTTAA			ATGAGGCCGCGCAGCCAGAATGACCTTCTGGGTCGTTTCGCTATGGGTTAA	MRPRSQNDLLGRFAMG*			MRPRSQNDLLGRFAMG*	ACGGCTCACT	TTTAACCACA	0	P	FG01672.1	0	0	0	0
6428	3115	ao	AN8009.1	53.m03858	AO070322000058	1					-410	-342	ATGACCTTCTGGGTCGTTTCGCTATGGGTTAATTTAACCACACGGGTCAAGGTATCGTACATAGTATAA			ATGACCTTCTGGGTCGTTTCGCTATGGGTTAATTTAACCACACGGGTCAAGGTATCGTACATAGTATAA	MTFWVVSLWVNLTTRVKVSYIV*			MTFWVVSLWVNLTTRVKVSYIV*	CGCAGCCAGA	CAGTCATAGC	0	P	FG01672.1	0	0	0	0
6429	3115	ao	AN8009.1	53.m03858	AO070322000058	1					-271	-125	ATGCTGTCCCTGCGTGTCTGTCTCCCTTTAGGGGTTGTGCCCCTCGAAGGAGACGTGAGACAAAGGGCAAAGGCTGAGTGGAGGGGTACCGGGTGTACGAGGCAGAGTCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG			ATGCTGTCCCTGCGTGTCTGTCTCCCTTTAGGGGTTGTGCCCCTCGAAGGAGACGTGAGACAAAGGGCAAAGGCTGAGTGGAGGGGTACCGGGTGTACGAGGCAGAGTCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	MLSLRVCLPLGVVPLEGDVRQRAKAEWRGTGCTRQSPVVLRLYCHNLI*			MLSLRVCLPLGVVPLEGDVRQRAKAEWRGTGCTRQSPVVLRLYCHNLI*	CCCCTACTTC	ATAATACTAG	0	P	FG01672.1	0	0	0	0
6430	3115	ao	AN8009.1	53.m03858	AO070322000058	1					-105	-37	ATGCGTGGCATTGATTGTTCCCCTTTATATCTCTTGTCACAGAAGAGGGACTTCGGTCCCCTTTACTAA			ATGCGTGGCATTGATTGTTCCCCTTTATATCTCTTGTCACAGAAGAGGGACTTCGGTCCCCTTTACTAA	MRGIDCSPLYLLSQKRDFGPLY*			MRGIDCSPLYLLSQKRDFGPLY*	GCGAAAGGAC	CAAGTTTCAG	0	P	FG01672.1	0	0	0	0
6457	3124	af	AN1782.1	69.m15081	AO070324000013	0			-38	-6			ATGAAACATAGCAGTTCGAGAGCAGTGACGTGA		ATGAAACATAGCAGTTCGAGAGCAGTGACGTGA		MKHSSSRAVT*		MKHSSSRAVT*		TTGCGTCTTC	ACATTATGGC	1	BK	0	0	0	0	0
6470	3136	an	AN6569.1	62.m03156	AO070326000012	0	-43	-26					ATGAGTTTTTCCCCCTAA	ATGAGTTTTTCCCCCTAA			MSFSP*	MSFSP*			TACTATCTTA	TTGTCAGCAG	1	O	0	0	0	0	0
6477	3137	ao	AN6589.1	62.m03178	AO070326000037	0					-41		ATGAATACGGCCTCGACAGACTCGGCGACCTCCTACCCGTGA			ATGAATACGGCCTCGACAGACTCGGCGACCTCCTACCCGTGA	MNTASTDSATSYP*			MNTASTDSATSYP*	GTCGCTTTAG	TGGCATCCGG	1	T	FG05591.1	0	0	0	0
6484	3140	an	AN6637.1	62.m03232	AO070326000089	1	-327	-313					ATGTCTTCGTCATAG	ATGTCTTCGTCATAG			MSSS*	MSSS*			ACATCCCTTG	CAGATCTCTC	0	F	0	0	0	0	0
6485	3140	an	AN6637.1	62.m03232	AO070326000089	1	-170	-42					ATGATGATCTTTCCGTTTTTTATAGATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAAACTATAACATATCGCATATTCTTTTATCTCGCTTGAGCTGGGTGCGCGTTTGCTGA	ATGATGATCTTTCCGTTTTTTATAGATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAAACTATAACATATCGCATATTCTTTTATCTCGCTTGAGCTGGGTGCGCGTTTGCTGA			MMIFPFFIDVRLPKHIADTFRPDLNYNISHILLSRLSWVRVC*	MMIFPFFIDVRLPKHIADTFRPDLNYNISHILLSRLSWVRVC*			CCTCCCTTTC	TAAATCACAC	0	F	0	0	0	0	0
6486	3140	an	AN6637.1	62.m03232	AO070326000089	1	-167	-42					ATGATCTTTCCGTTTTTTATAGATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAAACTATAACATATCGCATATTCTTTTATCTCGCTTGAGCTGGGTGCGCGTTTGCTGA	ATGATCTTTCCGTTTTTTATAGATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAAACTATAACATATCGCATATTCTTTTATCTCGCTTGAGCTGGGTGCGCGTTTGCTGA			MIFPFFIDVRLPKHIADTFRPDLNYNISHILLSRLSWVRVC*	MIFPFFIDVRLPKHIADTFRPDLNYNISHILLSRLSWVRVC*			CCCTTTCATG	TAAATCACAC	0	F	0	0	0	0	0
6487	3140	an	AN6637.1	62.m03232	AO070326000089	1	-145	-98					ATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAA	ATGTTAGACTTCCTAAGCATATTGCGGACACTTTCCGGCCTGACCTAA			MLDFLSILRTLSGLT*	MLDFLSILRTLSGLT*			TTTTTTATAG	ACTATAACAT	0	F	0	0	0	0	0
6488	3140	af	AN6637.1	62.m03232	AO070326000089	1			-350	-339			ATGTCTCAATAA		ATGTCTCAATAA		MSQ*		MSQ*		GGCTATTGTT	GAGAGTCGTT	0	F	0	0	0	0	0
6489	3140	af	AN6637.1	62.m03232	AO070326000089	1			-167	-99			ATGAATTTCGGTTTTTTTTTTATAGATGTTAGACTTCCTAAGCATCCTTGCGGAGAAAATCCGATCTGA		ATGAATTTCGGTTTTTTTTTTATAGATGTTAGACTTCCTAAGCATCCTTGCGGAGAAAATCCGATCTGA		MNFGFFFIDVRLPKHPCGENPI*		MNFGFFFIDVRLPKHPCGENPI*		CTCTTTTGTG	CTTAAATGCT	0	F	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
6490	3140	af	AN6637.1	62.m03232	AO070326000089	1			-142	-80			ATGTTAGACTTCCTAAGCATCCTTGCGGAGAAAATCCGATCTGACTTAAATGCTTCACCTTGA		ATGTTAGACTTCCTAAGCATCCTTGCGGAGAAAATCCGATCTGACTTAAATGCTTCACCTTGA		MLDFLSILAEKIRSDLNASP*		MLDFLSILAEKIRSDLNASP*		TTTTTTATAG	TTTGTCTTAC	0	F	0	0	0	0	0
6491	3140	af	AN6637.1	62.m03232	AO070326000089	1			-93	-58			ATGCTTCACCTTGATTTGTCTTACCATTCAGTCTGA		ATGCTTCACCTTGATTTGTCTTACCATTCAGTCTGA		MLHLDLSYHSV*		MLHLDLSYHSV*		TCTGACTTAA	TTCCCAGGCC	0	F	0	0	0	0	0
6492	3140	af	AN6637.1	62.m03232	AO070326000089	1			-45	-31			ATGCTGATATCATGA		ATGCTGATATCATGA		MLIS*		MLIS*		CCCAGGCCCA	ATACTTCTAG	1	F	0	0	0	0	0
6493	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-334	-311	ATGACTATTGTTATGTTTCGATAG			ATGACTATTGTTATGTTTCGATAG	MTIVMFR*			MTIVMFR*	CTTATCCTCT	AGTCAAAAAC	0	F	0	0	0	0	0
6494	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-322	-311	ATGTTTCGATAG			ATGTTTCGATAG	MFR*			MFR*	GACTATTGTT	AGTCAAAAAC	0	F	0	0	0	0	0
6495	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-185	-168	ATGCCCCTCCTTTCATGA			ATGCCCCTCCTTTCATGA	MPLLS*			MPLLS*	ATCAATCAAT	TGAATTTCGG	0	F	0	0	0	0	0
6496	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-171	-100	ATGATGAATTTCGGTTTTTTTATTATAGATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGA			ATGATGAATTTCGGTTTTTTTATTATAGATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGA	MMNFGFFIIDVRLPKHFCGENPT*			MMNFGFFIIDVRLPKHFCGENPT*	CCCTCCTTTC	TCTCATATTC	0	F	0	0	0	0	0
6497	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-168	-100	ATGAATTTCGGTTTTTTTATTATAGATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGA			ATGAATTTCGGTTTTTTTATTATAGATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGA	MNFGFFIIDVRLPKHFCGENPT*			MNFGFFIIDVRLPKHFCGENPT*	TCCTTTCATG	TCTCATATTC	0	F	0	0	0	0	0
6498	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-143	-51	ATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGATCTCATATTCGATGCTGTTTATATTGTCTCACAGCTCATCCATTTGTGA			ATGTTAGACTTCCTAAGCATTTTTGCGGAGAAAATCCGACCTGATCTCATATTCGATGCTGTTTATATTGTCTCACAGCTCATCCATTTGTGA	MLDFLSIFAEKIRPDLIFDAVYIVSQLIHL*			MLDFLSIFAEKIRPDLIFDAVYIVSQLIHL*	TTTATTATAG	GAGCCTTGGT	0	F	0	0	0	0	0
6499	3140	ao	AN6637.1	62.m03232	AO070326000089	1					-88	-38	ATGCTGTTTATATTGTCTCACAGCTCATCCATTTGTGAGAGCCTTGGTTAA			ATGCTGTTTATATTGTCTCACAGCTCATCCATTTGTGAGAGCCTTGGTTAA	MLFILSHSSSICESLG*			MLFILSHSSSICESLG*	CTCATATTCG	TCATAAGCAT	0	F	0	0	0	0	0
6500	3141	ao	AN2244.1	71.m15878	AO070326000129	1					-321	-310	ATGATGGAATAG			ATGATGGAATAG	MME*			MME*	TTTCCAATAC	ATACTATCAT	0	T	0	MG08640.1	NCU01183.1	0	0
6521	3153	ao	AN5563.1	58.m07489	AO070328000044	1					-212	-198	ATGGAACTTAACTAA			ATGGAACTTAACTAA	MELN*			MELN*	AGATTAATTA	ACCCCTCCCT	0	R	FG07908.1	MG00097.1	NCU04923.1	0	0
6564	3170	af	AN4709.1	71.m15697	AO070329000166	0			-27	-13			ATGAGGGACTTATAG		ATGAGGGACTTATAG		MRDL*		MRDL*		AATTCTGGTG	GTCTCTGGAC	1	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6565	3170	ao	AN4709.1	71.m15697	AO070329000166	0					-51	-28	ATGAAGGACTCCAAGAGTCAATGA			ATGAAGGACTCCAAGAGTCAATGA	MKDSKSQ*			MKDSKSQ*	GATATATGTA	GGGCTAATTC	1	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6568	3175	af	AN1117.1	70.m15118	AO070331000109	1			-127	-101			ATGAATTCTGCTCCGGAGTTTCGTTGA		ATGAATTCTGCTCCGGAGTTTCGTTGA		MNSAPEFR*		MNSAPEFR*		TCGGATCCTT	ATTTACCCTC	0	U	0	0	0	0	0
6578	3178	conserved	AN1179.1	70.m15038	AO070331000175	1	-27	-10	-27	-10	-27	-10	ATGTCATyCCbTybyTrA	ATGTCATCCCCTCGTTAA	ATGTCATCCCGTCCTTGA	ATGTCATTCCTTTTCTGA	MSspr*	MSSPR*	MSSRP*	MSFLF*	dyhvGATCCG	yTmGyCTCAA	0	U	0	0	0	0	0
6579	3178	an	AN1179.1	70.m15038	AO070331000176	1	-93	-10					ATGCATTGTCTGGCTGTTCACTCGCCTTCTTTCGTTCGCCACCCATCCAACAGTCAGTTCGATCCGATGTCATCCCCTCGTTAA	ATGCATTGTCTGGCTGTTCACTCGCCTTCTTTCGTTCGCCACCCATCCAACAGTCAGTTCGATCCGATGTCATCCCCTCGTTAA			MHCLAVHSPSFVRHPSNSQFDPMSSPR*	MHCLAVHSPSFVRHPSNSQFDPMSSPR*			TGCTCCTTGT	CTCGTCTCAA	0	U	0	0	0	0	0
6585	3181	af	AN1222.1	70.m15003	AO070331000222	1			-219	-196			ATGGCGCAATCGGGGCCTCATTAA		ATGGCGCAATCGGGGCCTCATTAA		MAQSGPH*		MAQSGPH*		CCGGAGCAAG	TACGGCCAAA	0	H	0	MG00383.1	0	0	0
6587	3181	ao	AN1222.1	70.m15003	AO070331000222	1					-247	-185	ATGCGCACTTTTTCTGCCGAGGGTGACCGCCGGAGGAAGATGGCGCCATCGGCGGCACATTAA			ATGCGCACTTTTTCTGCCGAGGGTGACCGCCGGAGGAAGATGGCGCCATCGGCGGCACATTAA	MRTFSAEGDRRRKMAPSAAH*			MRTFSAEGDRRRKMAPSAAH*	AGATGTCAGA	TACGGCCAGA	0	H	0	MG00383.1	0	0	0
6588	3181	ao	AN1222.1	70.m15003	AO070331000222	1					-208	-185	ATGGCGCCATCGGCGGCACATTAA			ATGGCGCCATCGGCGGCACATTAA	MAPSAAH*			MAPSAAH*	CCGGAGGAAG	TACGGCCAGA	0	H	0	MG00383.1	0	0	0
6597	3186	conserved	AN9125.1	66.m04585	AO070332000149	1	-52	-26	-62	-36	-65	-39	ATGChmdyTywymAdsvybTbCGGTGA	ATGCAATTTTACCAACGCCTGCGGTGA	ATGCTCACTTTCAATGCCGTCCGGTGA	ATGCCAGTTCATAAGCATTTTCGGTGA	MqfyqrlR*	MQFYQRLR*	MLTFNAVR*	MPVHKHFR*	mkmwyykAmh	ywbbwCkCyy	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
6599	3186	af	AN9125.1	66.m04585	AO070332000149	1			-49	-11			ATGCCGTCCGGTGATATTTCTCTCTCTCTCTGTGACTGA		ATGCCGTCCGGTGATATTTCTCTCTCTCTCTGTGACTGA		MPSGDISLSLCD*		MPSGDISLSLCD*		CTCACTTTCA	CGGCTCAAAA	1	K	FG00778.1	0	NCU00727.1	YNR003C	0
6601	3186	ao	AN9125.1	66.m04585	AO070332000149	1					-92	-81	ATGCTGGTCTAA			ATGCTGGTCTAA	MLV*			MLV*	GTATAGATAG	TATGCATCTC	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
6602	3186	ao	AN9125.1	66.m04585	AO070332000149	1					-79	-68	ATGCATCTCTGA			ATGCATCTCTGA	MHL*			MHL*	CTGGTCTAAT	ATATGCCAGT	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
6620	3189	ao	AN9085.1	66.m04772	AO070332000192	1					-93	-43	ATGCCATTTTTTCTGTACAATCCAGAGCCTTTTCTCATTACAAGTTTCTAA			ATGCCATTTTTTCTGTACAATCCAGAGCCTTTTCTCATTACAAGTTTCTAA	MPFFLYNPEPFLITSF*			MPFFLYNPEPFLITSF*	TGCTATCTTC	AAATTGTCAT	0	A	0	0	0	0	0
6622	3190	af	AN9078.1	66.m04536	AO070332000201	0			-47	-24			ATGTCGAATTCTATGACCCCTTAA		ATGTCGAATTCTATGACCCCTTAA		MSNSMTP*		MSNSMTP*		GCCTACTTCA	CTGTCGCTAA	1		0	0	0	0	0
6623	3190	af	AN9078.1	66.m04536	AO070332000201	0			-35	-24			ATGACCCCTTAA		ATGACCCCTTAA		MTP*		MTP*		GTCGAATTCT	CTGTCGCTAA	1		0	0	0	0	0
6681	3220	ao	AN3013.1	59.m09003	AO070337000103	0					-57	-25	ATGCTATTTAAATCAGGACAAATTGATTCATAG			ATGCTATTTAAATCAGGACAAATTGATTCATAG	MLFKSGQIDS*			MLFKSGQIDS*	CTTCTATTCT	TTCTACTCGC	1		FG06325.1	MG00882.1	0	0	0
6714	3237	an	AN2886.1	59.m08733	AO070338000128	0	-42	-22					ATGCTTCCTTTGAGTCTCTGA	ATGCTTCCTTTGAGTCTCTGA			MLPLSL*	MLPLSL*			AGATCACGAG	CCTGCCACGA	1		0	0	0	0	0
6716	3239	ao	AN2859.1	59.m08702	AO070338000163	0					-54	-16	ATGTATACTATCACACCATTCAGTACTAATATCTGGTAG			ATGTATACTATCACACCATTCAGTACTAATATCTGGTAG	MYTITPFSTNIW*			MYTITPFSTNIW*	CGACGGCACT	AAAAGAAGCA	1	EM	0	MG07462.1	NCU09532.1	0	0
6730	3246	af	AN0411.1	54.m06663	AO070338000254	1			-58	-38			ATGATCGTCAGCTATATTTAA		ATGATCGTCAGCTATATTTAA		MIVSYI*		MIVSYI*		TCTTTTCCTT	ATTTCTTTCA	1	U	0	0	0	0	0
6737	3249	an	AN0443.1	54.m06633	AO070338000300	1	-243	-223					ATGCAGAATACTCCGGGCTGA	ATGCAGAATACTCCGGGCTGA			MQNTPG*	MQNTPG*			CAGAAGAAGG	TTCGCAGAAG	0	ER	FG04922.1	0	0	0	0
6738	3249	an	AN0443.1	54.m06633	AO070338000300	1	-177	-127					ATGTCTGGTGTAGAAGCTGGACTGCCCTCAGCTCACCCGCACTCTATTTAG	ATGTCTGGTGTAGAAGCTGGACTGCCCTCAGCTCACCCGCACTCTATTTAG			MSGVEAGLPSAHPHSI*	MSGVEAGLPSAHPHSI*			CCCAGTTGGC	ACCGGCCCAG	0	ER	FG04922.1	0	0	0	0
6762	3256	an	AN6176.1	72.m18993	AO070340000023	0	-50	-12					ATGATATACTTATACATAATCAGGCATAAAACATCATAA	ATGATATACTTATACATAATCAGGCATAAAACATCATAA			MIYLYIIRHKTS*	MIYLYIIRHKTS*			TTACAAGACG	TCGTTATCAT	1		0	0	0	0	0
6769	3256	af	AN6176.1	72.m18993	AO070340000023	0			-48	-34			ATGGTTAGTTGCTAG		ATGGTTAGTTGCTAG		MVSC*		MVSC*		AGTGAACGCT	ATTACTGACA	1		0	0	0	0	0
6773	3256	ao	AN6176.1	72.m18993	AO070340000023	0					-32	-21	ATGGCTAACTAA			ATGGCTAACTAA	MAN*			MAN*	CCGTGAGTTA	GTCTTTAGAC	1		0	0	0	0	0
6780	3259	an	AN6126.1	72.m19031	AO070340000068	0	-44	-30					ATGGGAAGCGTTTAA	ATGGGAAGCGTTTAA			MGSV*	MGSV*			TATATATCGC	TACATAATAC	1	I	0	0	0	0	0
6781	3259	ao	AN6126.1	72.m19031	AO070340000068	0					-37	-23	ATGGGAATTGTATAA			ATGGGAATTGTATAA	MGIV*			MGIV*	GATATTTCGC	TCTATAATTC	1	I	0	0	0	0	0
6813	3269	af	AN6034.1	72.m19950	AO070340000254	1			-194	-108			ATGTTGGAACAAGGCTTCCCACGTGACCCACTGTATCCAGGGCCGTCCCCACATGGCCGAGTTTCGATATCGCATGCAATGCTTTGA		ATGTTGGAACAAGGCTTCCCACGTGACCCACTGTATCCAGGGCCGTCCCCACATGGCCGAGTTTCGATATCGCATGCAATGCTTTGA		MLEQGFPRDPLYPGPSPHGRVSISHAML*		MLEQGFPRDPLYPGPSPHGRVSISHAML*		TTTCGAACCG	TGGATTATTT	0		0	0	0	0	0
6814	3269	af	AN6034.1	72.m19950	AO070340000254	1			-142	-59			ATGGCCGAGTTTCGATATCGCATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		ATGGCCGAGTTTCGATATCGCATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		MAEFRYRMQCFDGLFAGFETNGNTIQA*		MAEFRYRMQCFDGLFAGFETNGNTIQA*		CCGTCCCCAC	CGTTGGACTT	0		0	0	0	0	0
6815	3269	af	AN6034.1	72.m19950	AO070340000254	1			-121	-59			ATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		ATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		MQCFDGLFAGFETNGNTIQA*		MQCFDGLFAGFETNGNTIQA*		TCGATATCGC	CGTTGGACTT	0		0	0	0	0	0
6816	3269	af	AN6034.1	72.m19950	AO070340000254	1			-108	-25			ATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGACGTTGGACTTGGGACTTTGTTTTCTGATGAATAG		ATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGACGTTGGACTTGGGACTTTGTTTTCTGATGAATAG		MDYLPDLKRMVIQFRLDVGLGTLFSDE*		MDYLPDLKRMVIQFRLDVGLGTLFSDE*		CAATGCTTTG	TCGCCTGCTC	0		0	0	0	0	0
6817	3269	af	AN6034.1	72.m19950	AO070340000254	1			-81	-25			ATGGTAATACAATTCAGGCTTGACGTTGGACTTGGGACTTTGTTTTCTGATGAATAG		ATGGTAATACAATTCAGGCTTGACGTTGGACTTGGGACTTTGTTTTCTGATGAATAG		MVIQFRLDVGLGTLFSDE*		MVIQFRLDVGLGTLFSDE*		TTTGAAACGA	TCGCCTGCTC	0		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
6818	3269	ao	AN6034.1	72.m19950	AO070340000254	1					-153	-37	ATGGACCGAGTCTCAATTGAATGCCGACCACGGCTCAGCGCATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGA			ATGGACCGAGTCTCAATTGAATGCCGACCACGGCTCAGCGCATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGA	MDRVSIECRPRLSAWNFMRSFSSSCSNLPCSRPPCDTV*			MDRVSIECRPRLSAWNFMRSFSSSCSNLPCSRPPCDTV*	GTCTCCCCAC	TCCGACTGGA	0		0	0	0	0	0
6819	3269	ao	AN6034.1	72.m19950	AO070340000254	1					-133	-17	ATGCCGACCACGGCTCAGCGCATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA			ATGCCGACCACGGCTCAGCGCATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA	MPTTAQRMEFYEIIQQFLLESPMLTTAVRYSLIRLEPG*			MPTTAQRMEFYEIIQQFLLESPMLTTAVRYSLIRLEPG*	TCTCAATTGA	TGTTCGATAT	0		0	0	0	0	0
6820	3269	ao	AN6034.1	72.m19950	AO070340000254	1					-112	-17	ATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA			ATGGAATTTTATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA	MEFYEIIQQFLLESPMLTTAVRYSLIRLEPG*			MEFYEIIQQFLLESPMLTTAVRYSLIRLEPG*	GGCTCAGCGC	TGTTCGATAT	0		0	0	0	0	0
6821	3269	ao	AN6034.1	72.m19950	AO070340000254	1					-102	-37	ATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGA			ATGAGATCATTCAGCAGTTCTTGCTCGAATCTCCCATGCTCACGACCGCCGTGCGATACAGTTTGA	MRSFSSSCSNLPCSRPPCDTV*			MRSFSSSCSNLPCSRPPCDTV*	ATGGAATTTT	TCCGACTGGA	0		0	0	0	0	0
6822	3269	ao	AN6034.1	72.m19950	AO070340000254	1					-67	-17	ATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA			ATGCTCACGACCGCCGTGCGATACAGTTTGATCCGACTGGAACCCGGGTGA	MLTTAVRYSLIRLEPG*			MLTTAVRYSLIRLEPG*	CGAATCTCCC	TGTTCGATAT	0		0	0	0	0	0
6845	3279	an	AN5915.1	72.m19953	AO070340000372	1	-89	-69					ATGCCGTATAGCTGGTGCTGA	ATGCCGTATAGCTGGTGCTGA			MPYSWC*	MPYSWC*			GACCTCTTGG	GAGTGCGCCC	0	U	0	MG06273.1	0	0	0
6846	3279	ao	AN5915.1	72.m19953	AO070340000372	1					-91	-62	ATGAGAAGTACGAATATCAGGGGCTTCTGA			ATGAGAAGTACGAATATCAGGGGCTTCTGA	MRSTNIRGF*			MRSTNIRGF*	CATATCGTGC	GATATTTTAC	0	U	0	MG06273.1	0	0	0
6883	3289	af	AN4174.1	69.m14956	AO070341000088	0			-40	-14			ATGAGCCGTTGCAGGAACCTCTACTAG		ATGAGCCGTTGCAGGAACCTCTACTAG		MSRCRNLY*		MSRCRNLY*		TCATTTGCTA	ATTGTTGGCA	1	G	0	0	0	YML004C	0
6910	3297	ao	AN7967.1	57.m05767	AO070341000216	0					-29	-12	ATGCTTGTTAGTACATGA			ATGCTTGTTAGTACATGA	MLVST*			MLVST*	TTTACACATT	CCATTCGCAA	1	F	0	0	0	0	0
7071	3345	ao	AN6551.1	62.m03122	AO070270000034	0					-52	-35	ATGCAGTGGCACCCATGA			ATGCAGTGGCACCCATGA	MQWHP*			MQWHP*	TCTCAACCAT	GAGGTTTCTA	1		0	0	0	0	0
7072	3345	ao	AN6551.1	62.m03122	AO070270000034	0					-38	-24	ATGAGAGGTTTCTAG			ATGAGAGGTTTCTAG	MRGF*			MRGF*	AGTGGCACCC	CATGGTATGA	1		0	0	0	0	0
7073	3345	ao	AN6551.1	62.m03122	AO070270000034	0					-17		ATGACTTTGATGGCATAA			ATGACTTTGATGGCATAA	MTLMA*			MTLMA*	CTAGCATGGT	TGACGCAGAA	1		0	0	0	0	0
7081	3348	af	AN6359.1	72.m19499	AO070279000047	1			-20	-9			ATGAGTGGTTGA		ATGAGTGGTTGA		MSG*		MSG*		AATATACCAG	GTGCCGCTAT	1	R	0	0	0	0	0
7085	3350	an	AN1075.1	70.m15149	AO070285000075	1	-71	-48					ATGAAATCCAGTTTCGCGACGTAA	ATGAAATCCAGTTTCGCGACGTAA			MKSSFAT*	MKSSFAT*			AACTTTAGCA	GGTGGCTTGA	0	O	0	0	0	0	0
7086	3350	af	AN1075.1	70.m15149	AO070285000075	1			-100	-83			ATGGAAACTCCGTCATAA		ATGGAAACTCCGTCATAA		METPS*		METPS*		TCCTGTCTAA	ACTGGAGATG	0	O	0	0	0	0	0
7087	3350	af	AN1075.1	70.m15149	AO070285000075	1			-75	-61			ATGCGATCAACATAG		ATGCGATCAACATAG		MRST*		MRST*		TAAACTGGAG	GTCGTTTTCA	0	O	0	0	0	0	0
7088	3350	ao	AN1075.1	70.m15149	AO070285000075	1					-69	-40	ATGCAGCACAACGTACGCCGTTCCATTTGA			ATGCAGCACAACGTACGCCGTTCCATTTGA	MQHNVRRSI*			MQHNVRRSI*	TGGACTGGCA	GGAGACTCCA	0	O	0	0	0	0	0
7093	3355	an	AN7325.1	72.m19745	AO070297000077	0	-21	-10					ATGCGTCTATGA	ATGCGTCTATGA			MRL*	MRL*			TGTATTATAT	GTGTTCATCA	1	L	0	MG08071.1	0	0	0
7117	3371	af	AN0314.1	54.m06444	AO070334000018	1			-71	-21			ATGATGAAAACTGGCCACCTGCCTAACTGTACACGTCCAGTGACAATCTAG		ATGATGAAAACTGGCCACCTGCCTAACTGTACACGTCCAGTGACAATCTAG		MMKTGHLPNCTRPVTI*		MMKTGHLPNCTRPVTI*		CCGGTCTCGG	GTGGTCTCTC	0	J	0	MG04681.1	0	0	0
7118	3371	af	AN0314.1	54.m06444	AO070334000018	1			-68	-21			ATGAAAACTGGCCACCTGCCTAACTGTACACGTCCAGTGACAATCTAG		ATGAAAACTGGCCACCTGCCTAACTGTACACGTCCAGTGACAATCTAG		MKTGHLPNCTRPVTI*		MKTGHLPNCTRPVTI*		GTCTCGGATG	GTGGTCTCTC	0	J	0	MG04681.1	0	0	0
7136	3377	an	AN3933.1	69.m14994	AO070341000044	0	-50	-30					ATGCAAACTTTATCTCAGTAA	ATGCAAACTTTATCTCAGTAA			MQTLSQ*	MQTLSQ*			TCACTATCGC	AAGCCGGGAA	1	K	0	MG01572.1	0	0	0
7158	3387	af	AN5774.1	69.m14823	AO070249000018	0			-43	-8			ATGCGCCAGGTTAAGCATATTTTTTTCTCTATCTGA		ATGCGCCAGGTTAAGCATATTTTTTTCTCTATCTGA		MRQVKHIFFSI*		MRQVKHIFFSI*		CACATTATCC	ATTCGTTATG	1	S	FG05736.1	0	NCU00770.1	0	0
7170	3395	ao	AN6541.1	62.m03133	AO070270000044	0					-44	-27	ATGTTCCCCTTCAATTAG			ATGTTCCCCTTCAATTAG	MFPFN*			MFPFN*	TCAGTTCCTA	GTTTACTCGA	1	F	0	0	0	0	0
7186	3402	an	AN0239.1	71.m15643	AO070284000068	0	-54	-37					ATGTCTGATGGTCTCTAG	ATGTCTGATGGTCTCTAG			MSDGL*	MSDGL*			GTGATTGTTC	CCGTCAGGTA	1	TU	FG00191.1	0	NCU00671.1	0	0
7189	3402	af	AN0239.1	71.m15643	AO070284000068	0			-51	-22			ATGGTTGTTGGCCATCAGGTCGATAGTTGA		ATGGTTGTTGGCCATCAGGTCGATAGTTGA		MVVGHQVDS*		MVVGHQVDS*		ATGGTGTCTG	GGGTAAAGCT	1	TU	FG00191.1	0	NCU00671.1	0	0
7193	3402	ao	AN0239.1	71.m15643	AO070284000068	0					-60	-25	ATGGTGTCTGATGGTCTCTGGCCATCGAATAGGTAG			ATGGTGTCTGATGGTCTCTGGCCATCGAATAGGTAG	MVSDGLWPSNR*			MVSDGLWPSNR*	GTGCTGGCTC	TCGGGGATAA	1	TU	FG00191.1	0	NCU00671.1	0	0
7194	3402	ao	AN0239.1	71.m15643	AO070284000068	0					-50	-15	ATGGTCTCTGGCCATCGAATAGGTAGTCGGGGATAA			ATGGTCTCTGGCCATCGAATAGGTAGTCGGGGATAA	MVSGHRIGSRG*			MVSGHRIGSRG*	ATGGTGTCTG	GCTTCAGCGG	1	TU	FG00191.1	0	NCU00671.1	0	0
7195	3403	ao	AN2523.1	59.m08459	AO070286000091	1					-181	-155	ATGTTTGTTGTCACGTTGACCGAGTAG			ATGTTTGTTGTCACGTTGACCGAGTAG	MFVVTLTE*			MFVVTLTE*	GGTTCGGTTC	TATACAATTG	0	M	0	0	0	0	0
7200	3406	an	AN5139.1	54.m07054	AO070291000038	1	-62	-42					ATGCTGAAAAGAGTACGGTGA	ATGCTGAAAAGAGTACGGTGA			MLKRVR*	MLKRVR*			TAGTTACGAC	TTTACTCGGT	0	R	0	0	NCU08484.1	YPR135W	0
7201	3406	af	AN5139.1	54.m07054	AO070291000038	1			-71	-51			ATGTATAGCTCAGTGTTATGA		ATGTATAGCTCAGTGTTATGA		MYSSVL*		MYSSVL*		CTGGATTTAG	TTGTGCTTCC	0	R	0	0	NCU08484.1	YPR135W	0
7202	3406	af	AN5139.1	54.m07054	AO070291000038	1			-54	-13			ATGATTGTGCTTCCAGCGCTGACCCTTACCGGCATTTACTGA		ATGATTGTGCTTCCAGCGCTGACCCTTACCGGCATTTACTGA		MIVLPALTLTGIY*		MIVLPALTLTGIY*		GCTCAGTGTT	TCGGTATCTA	1	R	0	0	NCU08484.1	YPR135W	0
7203	3406	ao	AN5139.1	54.m07054	AO070291000038	1					-92	-45	ATGCGTCGGGTTGATCTCTCTGAGTGTTTCACGTTCAATTCCCGGTAA			ATGCGTCGGGTTGATCTCTCTGAGTGTTTCACGTTCAATTCCCGGTAA	MRRVDLSECFTFNSR*			MRRVDLSECFTFNSR*	ATTTTGATAG	CTCTATTTTC	0	R	0	0	NCU08484.1	YPR135W	0
7207	3407	af	AN8051.1	53.m03891	AO070292000094	0			-55	-20			ATGTCGTCTTTTTTCCACTGCGCAATCTCCCTCTAG		ATGTCGTCTTTTTTCCACTGCGCAATCTCCCTCTAG		MSSFFHCAISL*		MSSFFHCAISL*		TCCTTTACCA	CAATAATATC	1		0	0	0	0	0
7224	3416	af	AN6247.1	72.m19980	AO070304000102	1			-273	-142			ATGTCTTGCATCTTCCCGTTGCTGCTTCTTGCATTCGACTTACTAAACTCTTTACTTCTTATCCGAACTTCTGATTCTTTGCCTCGTCGTTCATTCCCGACAGCACATAGATCAGACCTCACTGGATCTTAG		ATGTCTTGCATCTTCCCGTTGCTGCTTCTTGCATTCGACTTACTAAACTCTTTACTTCTTATCCGAACTTCTGATTCTTTGCCTCGTCGTTCATTCCCGACAGCACATAGATCAGACCTCACTGGATCTTAG		MSCIFPLLLLAFDLLNSLLLIRTSDSLPRRSFPTAHRSDLTGS*		MSCIFPLLLLAFDLLNSLLLIRTSDSLPRRSFPTAHRSDLTGS*		ACGCATTCCC	CGCGCTTGCG	0		0	0	0	0	0
7225	3416	ao	AN6247.1	72.m19980	AO070304000102	1					-290	-147	ATGTCTTGCGTCTGCCCATTCCAGTACCTTCGTTCTGACCTGCAGACTACTCTTCGTTACTTGTCTTTCCCTACCTACCACTTATTTACTTTCTCCCCACCTCTTATCGCGACAGCGCATAAGGCCCATCCCACCTCGTCTTAG			ATGTCTTGCGTCTGCCCATTCCAGTACCTTCGTTCTGACCTGCAGACTACTCTTCGTTACTTGTCTTTCCCTACCTACCACTTATTTACTTTCTCCCCACCTCTTATCGCGACAGCGCATAAGGCCCATCCCACCTCGTCTTAG	MSCVCPFQYLRSDLQTTLRYLSFPTYHLFTFSPPLIATAHKAHPTSS*			MSCVCPFQYLRSDLQTTLRYLSFPTYHLFTFSPPLIATAHKAHPTSS*	TCGCATTCCC	TGCGCTTGCG	0		0	0	0	0	0
7227	3417	an	AN1715.1	58.m08959	AO070305000031	1	-151	-47					ATGACGAAAGATCTCTCGATTTGGGTGCTGAGTGTCCTGTCATGTCATGCATGCGGTTACAGGTACATAAAAGGCCTATCCAGGTCCACGTCGCAGTGGCATTAA	ATGACGAAAGATCTCTCGATTTGGGTGCTGAGTGTCCTGTCATGTCATGCATGCGGTTACAGGTACATAAAAGGCCTATCCAGGTCCACGTCGCAGTGGCATTAA			MTKDLSIWVLSVLSCHACGYRYIKGLSRSTSQWH*	MTKDLSIWVLSVLSCHACGYRYIKGLSRSTSQWH*			TTGCTGGATC	ACCATCAATA	0	G	0	MG10677.1	0	0	0
7228	3417	an	AN1715.1	58.m08959	AO070305000031	1	-105	-82					ATGCATGCGGTTACAGGTACATAA	ATGCATGCGGTTACAGGTACATAA			MHAVTGT*	MHAVTGT*			CTGTCATGTC	AAGGCCTATC	0	G	0	MG10677.1	0	0	0
7229	3417	af	AN1715.1	58.m08959	AO070305000031	1			-238	-53			ATGGTGGATTTAGTTTTATACCAGATTCCCTGTTATATCGTCTGTTCCACTGGGTATACCAACAATGACGCCATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGAATCGTTCGCTTGAGGATCAGTAA		ATGGTGGATTTAGTTTTATACCAGATTCCCTGTTATATCGTCTGTTCCACTGGGTATACCAACAATGACGCCATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGAATCGTTCGCTTGAGGATCAGTAA		MVDLVLYQIPCYIVCSTGYTNNDAMPTHYTLSLLQSPIIFAAFCIAHDYYPYCLNRSLEDQ*		MVDLVLYQIPCYIVCSTGYTNNDAMPTHYTLSLLQSPIIFAAFCIAHDYYPYCLNRSLEDQ*		ATATTAGGCA	TAACAACTAT	0	G	0	MG10677.1	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
7230	3417	af	AN1715.1	58.m08959	AO070305000031	1			-174	-76			ATGACGCCATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGA		ATGACGCCATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGA		MTPCPRITPYRCCKVRLSSLLSASLTIIIPIA*		MTPCPRITPYRCCKVRLSSLLSASLTIIIPIA*		TATACCAACA	ATCGTTCGCT	0	G	0	MG10677.1	0	0	0
7231	3417	af	AN1715.1	58.m08959	AO070305000031	1			-166	-53			ATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGAATCGTTCGCTTGAGGATCAGTAA		ATGCCCACGCATTACACCTTATCGCTGTTGCAAAGTCCGATTATCTTCGCTGCTTTCTGCATCGCTCACGATTATTATCCCTATTGCTTGAATCGTTCGCTTGAGGATCAGTAA		MPTHYTLSLLQSPIIFAAFCIAHDYYPYCLNRSLEDQ*		MPTHYTLSLLQSPIIFAAFCIAHDYYPYCLNRSLEDQ*		CAATGACGCC	TAACAACTAT	0	G	0	MG10677.1	0	0	0
7233	3417	ao	AN1715.1	58.m08959	AO070305000031	1					-232	-221	ATGAAGTCATGA			ATGAAGTCATGA	MKS*			MKS*	CTCGGTGGGT	CCAGGAATTT	0	G	0	MG10677.1	0	0	0
7234	3417	ao	AN1715.1	58.m08959	AO070305000031	1					-224	-123	ATGACCAGGAATTTCCCAAAAAGGAAGTTGCGATCAGTTCCAGGCGCACCTTCCCTCCATGACGACATGTTAACGCAGGGCTGCATTTCATCCTACACATAA			ATGACCAGGAATTTCCCAAAAAGGAAGTTGCGATCAGTTCCAGGCGCACCTTCCCTCCATGACGACATGTTAACGCAGGGCTGCATTTCATCCTACACATAA	MTRNFPKRKLRSVPGAPSLHDDMLTQGCISSYT*			MTRNFPKRKLRSVPGAPSLHDDMLTQGCISSYT*	GTATGAAGTC	ATACTCTCTT	0	G	0	MG10677.1	0	0	0
7235	3417	ao	AN1715.1	58.m08959	AO070305000031	1					-166	-152	ATGACGACATGTTAA			ATGACGACATGTTAA	MTTC*			MTTC*	CCTTCCCTCC	CGCAGGGCTG	0	G	0	MG10677.1	0	0	0
7236	3417	ao	AN1715.1	58.m08959	AO070305000031	1					-158	-123	ATGTTAACGCAGGGCTGCATTTCATCCTACACATAA			ATGTTAACGCAGGGCTGCATTTCATCCTACACATAA	MLTQGCISSYT*			MLTQGCISSYT*	CCATGACGAC	ATACTCTCTT	0	G	0	MG10677.1	0	0	0
7258	3425	an	AN2692.1	71.m15179	AO070313000096	1	-150	-127					ATGGACCTCGGAAGCTGTTGTTAG	ATGGACCTCGGAAGCTGTTGTTAG			MDLGSCC*	MDLGSCC*			CATCGTCAAA	AGACTTGATG	0		0	0	0	0	0
7259	3425	af	AN2692.1	71.m15179	AO070313000096	1			-130	-110			ATGGATATCCATTGCATATGA		ATGGATATCCATTGCATATGA		MDIHCI*		MDIHCI*		TATCATCAAA	ATCGATCTGT	0		0	0	0	0	0
7260	3425	ao	AN2692.1	71.m15179	AO070313000096	1					-405	-385	ATGGACCTCATATCTTGTTGA			ATGGACCTCATATCTTGTTGA	MDLISC*			MDLISC*	CATCGCCAAA	ATGAATGTAG	0		0	0	0	0	0
7262	3427	an	AN6857.1	71.m15270	AO070314000074	0	-30	-4					ATGCAACAGTTTCCAGTGCGAACCTAA	ATGCAACAGTTTCCAGTGCGAACCTAA			MQQFPVRT*	MQQFPVRT*			AGACCAGATC	GTCATGCCCA	1		0	0	0	0	0
7285	3431	an	AN4526.1	57.m05980	AO070321000134	1	-178	-143					ATGATGACCGGTGTTCGACGACTGCGTGCCAACTGA	ATGATGACCGGTGTTCGACGACTGCGTGCCAACTGA			MMTGVRRLRAN*	MMTGVRRLRAN*			ATCTGCCTGC	GCCTGCCATT	0	F	0	0	0	0	0
7286	3431	an	AN4526.1	57.m05980	AO070321000134	1	-175	-143					ATGACCGGTGTTCGACGACTGCGTGCCAACTGA	ATGACCGGTGTTCGACGACTGCGTGCCAACTGA			MTGVRRLRAN*	MTGVRRLRAN*			TGCCTGCATG	GCCTGCCATT	0	F	0	0	0	0	0
7287	3431	an	AN4526.1	57.m05980	AO070321000134	1	-56	-15					ATGCGCGCGACCCCTTACTTATTATCGCGAACCAAATGCTAA	ATGCGCGCGACCCCTTACTTATTATCGCGAACCAAATGCTAA			MRATPYLLSRTKC*	MRATPYLLSRTKC*			GAAAGAACTC	TCAATCCATC	1	F	0	0	0	0	0
7288	3431	af	AN4526.1	57.m05980	AO070321000134	1			-236	-96			ATGAAGACCGGTGTTCGGCTTCAGTGTTGCGTTTCACATATCATCCGGTGGTCATTGTCGCTAGTCGCATCGTCAGATTATCGCCAATGGTTCCTGGGTACATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGA		ATGAAGACCGGTGTTCGGCTTCAGTGTTGCGTTTCACATATCATCCGGTGGTCATTGTCGCTAGTCGCATCGTCAGATTATCGCCAATGGTTCCTGGGTACATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGA		MKTGVRLQCCVSHIIRWSLSLVASSDYRQWFLGTCGVAVVVLRSYG*		MKTGVRLQCCVSHIIRWSLSLVASSDYRQWFLGTCGVAVVVLRSYG*		ATCTACCCGC	ACTTGATCTG	0	F	0	0	0	0	0
7289	3431	af	AN4526.1	57.m05980	AO070321000134	1			-150	-22			ATGGTTCCTGGGTACATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGAACTTGATCTGGATAATTCCAGCGAAAGGACTCATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		ATGGTTCCTGGGTACATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGAACTTGATCTGGATAATTCCAGCGAAAGGACTCATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		MVPGYMWRRCCRSEIIRLNLIWIIPAKGLMRALSASSPFKCI*		MVPGYMWRRCCRSEIIRLNLIWIIPAKGLMRALSASSPFKCI*		ATTATCGCCA	AGACTAACTC	0	F	0	0	0	0	0
7290	3431	af	AN4526.1	57.m05980	AO070321000134	1			-135	-22			ATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGAACTTGATCTGGATAATTCCAGCGAAAGGACTCATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		ATGTGGCGTCGCTGTTGTCGTTCTGAGATCATACGGTTGAACTTGATCTGGATAATTCCAGCGAAAGGACTCATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		MWRRCCRSEIIRLNLIWIIPAKGLMRALSASSPFKCI*		MWRRCCRSEIIRLNLIWIIPAKGLMRALSASSPFKCI*		TCCTGGGTAC	AGACTAACTC	0	F	0	0	0	0	0
7291	3431	af	AN4526.1	57.m05980	AO070321000134	1			-63	-22			ATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		ATGCGCGCTCTTTCAGCTTCAAGCCCTTTCAAATGTATATGA		MRALSASSPFKCI*		MRALSASSPFKCI*		GAAAGGACTC	AGACTAACTC	0	F	0	0	0	0	0
7292	3431	af	AN4526.1	57.m05980	AO070321000134	1			-31	-5			ATGTATATGAAGACTAACTCAGGATAA		ATGTATATGAAGACTAACTCAGGATAA		MYMKTNSG*		MYMKTNSG*		GCCCTTTCAA	CAGCATGTCG	1	F	0	0	0	0	0
7293	3431	af	AN4526.1	57.m05980	AO070321000134	1			-25	-5			ATGAAGACTAACTCAGGATAA		ATGAAGACTAACTCAGGATAA		MKTNSG*		MKTNSG*		TCAAATGTAT	CAGCATGTCG	1	F	0	0	0	0	0
7294	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-237	-196	ATGATGACCGGTGTTCGGCAACGCTGTGACACAGAGATCTGA			ATGATGACCGGTGTTCGGCAACGCTGTGACACAGAGATCTGA	MMTGVRQRCDTEI*			MMTGVRQRCDTEI*	ATACGCCTGC	TGCAATATGC	0	F	0	0	0	0	0
7295	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-234	-196	ATGACCGGTGTTCGGCAACGCTGTGACACAGAGATCTGA			ATGACCGGTGTTCGGCAACGCTGTGACACAGAGATCTGA	MTGVRQRCDTEI*			MTGVRQRCDTEI*	CGCCTGCATG	TGCAATATGC	0	F	0	0	0	0	0
7296	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-196	-176	ATGCAATATGCCCGGCCATGA			ATGCAATATGCCCGGCCATGA	MQYARP*			MQYARP*	CAGAGATCTG	CTCGCGTGTT	0	F	0	0	0	0	0
7297	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-189	-130	ATGCCCGGCCATGACTCGCGTGTTTCTTGGCTTGTTGTCTCCGAACCTGGGTACAGATGA			ATGCCCGGCCATGACTCGCGTGTTTCTTGGCTTGTTGTCTCCGAACCTGGGTACAGATGA	MPGHDSRVSWLVVSEPGYR*			MPGHDSRVSWLVVSEPGYR*	CTGATGCAAT	TGTGGCAGCA	0	F	0	0	0	0	0
7298	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-179	-93	ATGACTCGCGTGTTTCTTGGCTTGTTGTCTCCGAACCTGGGTACAGATGATGTGGCAGCAGTTGTCGTTCTGAGAATATACGGTTGA			ATGACTCGCGTGTTTCTTGGCTTGTTGTCTCCGAACCTGGGTACAGATGATGTGGCAGCAGTTGTCGTTCTGAGAATATACGGTTGA	MTRVFLGLLSPNLGTDDVAAVVVLRIYG*			MTRVFLGLLSPNLGTDDVAAVVVLRIYG*	ATGCCCGGCC	ACTTGATCTG	0	F	0	0	0	0	0
7299	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-133	-107	ATGATGTGGCAGCAGTTGTCGTTCTGA			ATGATGTGGCAGCAGTTGTCGTTCTGA	MMWQQLSF*			MMWQQLSF*	CTGGGTACAG	GAATATACGG	0	F	0	0	0	0	0
7300	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-130	-107	ATGTGGCAGCAGTTGTCGTTCTGA			ATGTGGCAGCAGTTGTCGTTCTGA	MWQQLSF*			MWQQLSF*	GGTACAGATG	GAATATACGG	0	F	0	0	0	0	0
7301	3431	ao	AN4526.1	57.m05980	AO070321000134	1					-60	-22	ATGCGCGCTTTTTTAGCCCTCAGTTTCTTCATGAGCTGA			ATGCGCGCTTTTTTAGCCCTCAGTTTCTTCATGAGCTGA	MRAFLALSFFMS*			MRAFLALSFFMS*	GAAAGGACTC	TACTAACTGG	1	F	0	0	0	0	0
7321	3441	an	AN4706.1	71.m15694	AO070329000170	0	-38						ATGCATATAATGAGCTGTCAACGATACCCACAGCAATAA	ATGCATATAATGAGCTGTCAACGATACCCACAGCAATAA			MHIMSCQRYPQQ*	MHIMSCQRYPQQ*			AGCCTTTTTG	TGCTCCCCTC	1	Z	0	0	0	0	0
7322	3441	an	AN4706.1	71.m15694	AO070329000170	0	-29						ATGAGCTGTCAACGATACCCACAGCAATAA	ATGAGCTGTCAACGATACCCACAGCAATAA			MSCQRYPQQ*	MSCQRYPQQ*			GATGCATATA	TGCTCCCCTC	1	Z	0	0	0	0	0
7330	3441	af	AN4706.1	71.m15694	AO070329000170	0			-27	-13			ATGATGCTCCATTGA		ATGATGCTCCATTGA		MMLH*		MMLH*		CTGTTTACAA	ATCAACGACA	1	Z	0	0	0	0	0
7331	3441	af	AN4706.1	71.m15694	AO070329000170	0			-24	-13			ATGCTCCATTGA		ATGCTCCATTGA		MLH*		MLH*		TTTACAAATG	ATCAACGACA	1	Z	0	0	0	0	0
7333	3441	ao	AN4706.1	71.m15694	AO070329000170	0					-27	-13	ATGATGACCTATTGA			ATGATGACCTATTGA	MMTY*			MMTY*	AAACACTTGA	ATTAACGACG	1	Z	0	0	0	0	0
7334	3441	ao	AN4706.1	71.m15694	AO070329000170	0					-24	-13	ATGACCTATTGA			ATGACCTATTGA	MTY*			MTY*	CACTTGAATG	ATTAACGACG	1	Z	0	0	0	0	0
7336	3442	af	AN1208.1	70.m15013	AO070331000214	1			-188	-33			ATGACACATCACGGATGCGGTGACTTTAATCAAGCAAATTCCACCACCAATCAGGCCCTTCGAACAGGGTTCAGGACGCGTACTGCACGTCCTCTCTGGCGACCTGCGTCAGTCTTCAACGCCCGCAACGCCCAGGATAATCATTCGGCCTTCTGA		ATGACACATCACGGATGCGGTGACTTTAATCAAGCAAATTCCACCACCAATCAGGCCCTTCGAACAGGGTTCAGGACGCGTACTGCACGTCCTCTCTGGCGACCTGCGTCAGTCTTCAACGCCCGCAACGCCCAGGATAATCATTCGGCCTTCTGA		MTHHGCGDFNQANSTTNQALRTGFRTRTARPLWRPASVFNARNAQDNHSAF*		MTHHGCGDFNQANSTTNQALRTGFRTRTARPLWRPASVFNARNAQDNHSAF*		CTTTCCTTGT	AATCTGGGTC	0	A	FG01337.1	MG05616.1	NCU02966.1	0	0
7337	3442	ao	AN1208.1	70.m15013	AO070331000214	1					-171	-160	ATGAGGCAGTAA			ATGAGGCAGTAA	MRQ*			MRQ*	TAGATTTTGA	TTTGCTGCTA	0	A	FG01337.1	MG05616.1	NCU02966.1	0	0
7343	3447	af	AN0304.1	54.m06978	AO070334000034	1			-111	-91			ATGCTCTTTGAAAGAGCTTGA		ATGCTCTTTGAAAGAGCTTGA		MLFERA*		MLFERA*		CCAGGCATAT	GTTCTCAAGC	0	P	0	0	0	0	0
7348	3451	conserved	AN2905.1	59.m08756	AO070338000100	0	-23	-12	-23	-12	-23	-12	ATGGGTTGGTAA	ATGGGTTGGTAA	ATGGGTTGGTAA	ATGGGTTGGTAA	MGW*	MGW*	MGW*	MGW*	sdCyTTGCAG	rACCrCACGA	1	K	0	0	0	0	0
7359	3451	ao	AN2905.1	59.m08756	AO070338000100	0					-58	-41	ATGTCTCATAAAGTCTGA			ATGTCTCATAAAGTCTGA	MSHKV*			MSHKV*	CTCTATTCTT	CAGCTTTCAC	1	K	0	0	0	0	0
7385	3464	af	AN3586.1	58.m07385	AO070342000163	0			-43	-8			ATGATCGACTTTCAGACTGTACTCCGTACGCTTTAG		ATGATCGACTTTCAGACTGTACTCCGTACGCTTTAG		MIDFQTVLRTL*		MIDFQTVLRTL*		AGGTGATCTG	GCTCACCATG	1	HC	0	0	0	0	0
7435	3480	af	AN3157.1	59.m08548	AO070256000037	1			-65	-48			ATGGCGGTTTTTGGATGA		ATGGCGGTTTTTGGATGA		MAVFG*		MAVFG*		TCGCCCGATC	TTGTTTATGT	0	P	0	0	0	YPR003C	0
7436	3480	af	AN3157.1	59.m08548	AO070256000037	1			-41	-24			ATGTCCCAGGATTATTGA		ATGTCCCAGGATTATTGA		MSQDY*		MSQDY*		ATGATTGTTT	GTGATCATTA	1	P	0	0	0	YPR003C	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
7437	3480	ao	AN3157.1	59.m08548	AO070256000037	1					-259	-212	ATGATATTTACTTACTTCTTCCGTCTTCATGCTTCCCATCCCCGCTAA			ATGATATTTACTTACTTCTTCCGTCTTCATGCTTCCCATCCCCGCTAA	MIFTYFFRLHASHPR*			MIFTYFFRLHASHPR*	CTCTTGAATA	CTACCAATCG	0	P	0	0	0	YPR003C	0
7438	3480	ao	AN3157.1	59.m08548	AO070256000037	1					-231	-199	ATGCTTCCCATCCCCGCTAACTACCAATCGTAG			ATGCTTCCCATCCCCGCTAACTACCAATCGTAG	MLPIPANYQS*			MLPIPANYQS*	TTCCGTCTTC	CCACCGCCTG	0	P	0	0	0	YPR003C	0
7439	3480	ao	AN3157.1	59.m08548	AO070256000037	1					-65	-33	ATGGCGAGTGCTGAGTTACTCTGCACATCATAG			ATGGCGAGTGCTGAGTTACTCTGCACATCATAG	MASAELLCTS*			MASAELLCTS*	CGTAGCACTC	CGATACTGAC	0	P	0	0	0	YPR003C	0
7454	3485	af	AN6532.1	62.m03120	AO070270000032	0			-52	-35			ATGGACACACTCCCCTGA		ATGGACACACTCCCCTGA		MDTLP*		MDTLP*		CAGCCATGGC	CTCCCATATC	1	IQR	0	MG08857.1	NCU00148.1	0	0
7461	3491	an	AN7495.1	57.m05848	AO070287000021	1	-54	-28					ATGTTTGATTATCGTGATCTGGTTTAG	ATGTTTGATTATCGTGATCTGGTTTAG			MFDYRDLV*	MFDYRDLV*			ACGCAAATTT	CAACGGTTTC	1	AD	0	0	0	0	0
7472	3496	af	AN2295.1	71.m15944	AO070295000075	1			-113	-102			ATGTCATTTTGA		ATGTCATTTTGA		MSF*		MSF*		GAAGTGTCCC	TATATTCTGC	0	C	0	MG05480.1	0	0	0
7501	3503	an	AN3827.1	58.m07803	AO070305000064	0	-56	-3					ATGACTAGAAGACCTTCCTCCCATCATTCTTCCATTCTACCATCAAAGTCGTAA	ATGACTAGAAGACCTTCCTCCCATCATTCTTCCATTCTACCATCAAAGTCGTAA			MTRRPSSHHSSILPSKS*	MTRRPSSHHSSILPSKS*			AAATTTTTGG	TCATGGCGAA	1	A	0	0	0	YGR103W	0
7504	3507	an	AN8242.1	53.m03728	AO070310000066	0	-29	-18					ATGCTGTCTTGA	ATGCTGTCTTGA			MLS*	MLS*			CTAGTAGTTT	TGCAACCTAT	1	V	0	0	0	0	0
7508	3511	an	AN1016.1	70.m15234	AO070312000002	0	-39	-4					ATGGTTCCACCGGACGCTGTCGAAGGCAGTATCTAG	ATGGTTCCACCGGACGCTGTCGAAGGCAGTATCTAG			MVPPDAVEGSI*	MVPPDAVEGSI*			CGAACAGCGT	AAAATGGGGT	1	DT	0	0	0	0	0
7547	3522	ao	AN8126.1	70.m15699	AO070322000018	0					-46	-11	ATGTCAGTCTCTAGCGGCATCGCGTGCAGTCACTAA			ATGTCAGTCTCTAGCGGCATCGCGTGCAGTCACTAA	MSVSSGIACSH*			MSVSSGIACSH*	ATACAAACCC	ACTCCAGACC	1	R	0	0	0	0	0
7557	3529	af	AN4003.1	54.m06586	AO070328000160	0			-30	-7			ATGAACTTATTTAGCAGAGAATAA		ATGAACTTATTTAGCAGAGAATAA		MNLFSRE*		MNLFSRE*		TCCCATCCAT	AAGCAAATGG	1	CE	0	0	0	0	0
7575	3531	af	AN8066.1	53.m03917	AO070330000022	0			-51	-37			ATGTGTGACTGCTGA		ATGTGTGACTGCTGA		MCDC*		MCDC*		ATCGCGAGAC	AGCTTGAATT	1	J	0	MG00308.1	NCU09571.1	0	0
7590	3538	an	AN5013.1	59.m08664	AO070334000121	1	-205	-179					ATGATCTCGTTATGTGATATCTCATGA	ATGATCTCGTTATGTGATATCTCATGA			MISLCDIS*	MISLCDIS*			GTCCAACGTC	ACCTCCTCCG	0	L	0	MG06005.1	0	0	0
7591	3538	an	AN5013.1	59.m08664	AO070334000121	1	-182	-120					ATGAACCTCCTCCGCTACAATAATCAAGTATCCGGACAGCTAAACAATCGCGGAGACTCCTGA	ATGAACCTCCTCCGCTACAATAATCAAGTATCCGGACAGCTAAACAATCGCGGAGACTCCTGA			MNLLRYNNQVSGQLNNRGDS*	MNLLRYNNQVSGQLNNRGDS*			GTGATATCTC	GCTACGTCTT	0	L	0	MG06005.1	0	0	0
7592	3538	an	AN5013.1	59.m08664	AO070334000121	1	-107	-90					ATGAGCGCTAATCTCTGA	ATGAGCGCTAATCTCTGA			MSANL*	MSANL*			TACGTCTTCT	ATTCTGTACT	0	L	0	MG06005.1	0	0	0
7595	3542	af	AN5215.1	69.m14913	AO070337000264	0			-60	-46			ATGCGTGATTCCTGA		ATGCGTGATTCCTGA		MRDS*		MRDS*		GAATTGATCA	ATTAGATTTT	1	R	FG00848.1	0	NCU07492.1	YPL183C	YPL183C
7627	3551	an	AN2099.1	57.m05801	AO070341000258	1	-96	-64					ATGTATGTCAAAGCAACATCTTATCTTGACTAA	ATGTATGTCAAAGCAACATCTTATCTTGACTAA			MYVKATSYLD*	MYVKATSYLD*			TCAACTCCTT	GTACAGTTCG	0		0	0	0	0	0
7628	3551	an	AN2099.1	57.m05801	AO070341000258	1	-92	-24					ATGTCAAAGCAACATCTTATCTTGACTAAGTACAGTTCGTCAGAATTGACAGCACCTTTTCAACAATAA	ATGTCAAAGCAACATCTTATCTTGACTAAGTACAGTTCGTCAGAATTGACAGCACCTTTTCAACAATAA			MSKQHLILTKYSSSELTAPFQQ*	MSKQHLILTKYSSSELTAPFQQ*			CTCCTTATGT	ACAATATCAG	0		0	0	0	0	0
7659	3558	af	AN0661.1	70.m15264	AO070343000559	0			-60	-49			ATGAATCCCTGA		ATGAATCCCTGA		MNP*		MNP*		AAAACGATCC	GACTGCATCA	1		0	0	0	0	0
7699	3569	an	AN4360.1	58.m07961	AO070261000003	0	-31	-17					ATGAGTCTGAAGTGA	ATGAGTCTGAAGTGA			MSLK*	MSLK*			GTTTACAGAC	TCCTAGATTA	1		0	0	0	0	0
7702	3569	af	AN4360.1	58.m07961	AO070261000003	0			-48	-28			ATGGTTATGCTTAGTCAATAG		ATGGTTATGCTTAGTCAATAG		MVMLSQ*		MVMLSQ*		ACTCAGCCTC	TATAAAGAGG	1		0	0	0	0	0
7703	3569	af	AN4360.1	58.m07961	AO070261000003	0			-42	-28			ATGCTTAGTCAATAG		ATGCTTAGTCAATAG		MLSQ*		MLSQ*		CCTCATGGTT	TATAAAGAGG	1		0	0	0	0	0
7709	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-54	-28	ATGCGCAAGAACTCCGTGCAACTATAG			ATGCGCAAGAACTCCGTGCAACTATAG	MRKNSVQL*			MRKNSVQL*	CGGCGGGATA	ACGCCACATC	1		0	0	0	0	0
7711	3573	ao	AN6934.1	62.m03423	AO070269000048	0					-40	-20	ATGTTCCTTGCTGAGTTCTAG			ATGTTCCTTGCTGAGTTCTAG	MFLAEF*			MFLAEF*	TGCCCTCAGA	AAAGACGCTC	1	G	0	0	0	0	0
7735	3585	an	AN2290.1	71.m15938	AO070295000069	0	-56	-27					ATGGTCCCATGCTCGAAACCTGGCTTCTGA	ATGGTCCCATGCTCGAAACCTGGCTTCTGA			MVPCSKPGF*	MVPCSKPGF*			CGCATAGTGG	CGCTTCTAAT	1	R	0	0	0	0	0
7736	3585	an	AN2290.1	71.m15938	AO070295000069	0	-48	-10					ATGCTCGAAACCTGGCTTCTGACGCTTCTAATCCTCTAG	ATGCTCGAAACCTGGCTTCTGACGCTTCTAATCCTCTAG			MLETWLLTLLIL*	MLETWLLTLLIL*			GGATGGTCCC	GTCACGAATA	1	R	0	0	0	0	0
7820	3610	ao	AN4639.1	57.m05552	AO070321000194	0					-53	-39	ATGATACCTGCATAA			ATGATACCTGCATAA	MIPA*			MIPA*	CTTGCACACG	TGAAGGATCC	1	D	0	MG02874.1	0	0	0
7833	3616	af	AN3923.1	69.m15006	AO070324000119	0			-33	-1			ATGAGAGTTGGATCTGTATTCATACCAAGCTGA		ATGAGAGTTGGATCTGTATTCATACCAAGCTGA		MRVGSVFIPS*		MRVGSVFIPS*		GGGGAGCTGA	ATGATGCTCA	1	O	0	0	0	0	0
7834	3616	ao	AN3923.1	69.m15006	AO070324000119	0					-36	-13	ATGCGTCTCGTCTTCTCAGACTAG			ATGCGTCTCGTCTTCTCAGACTAG	MRLVFSD*			MRLVFSD*	TGCAAATTGG	AGACGATAAA	1	O	0	0	0	0	0
7835	3619	an	AN6634.1	62.m03229	AO070326000086	0	-55	-29					ATGGTTGCTTGGATAACTTCTCTGTAG	ATGGTTGCTTGGATAACTTCTCTGTAG			MVAWITSL*	MVAWITSL*			ACCTGACGCG	TCTCAGACAT	1		0	0	0	0	0
7836	3619	an	AN6634.1	62.m03229	AO070326000086	0	-20	-6					ATGATTTCTTCATAG	ATGATTTCTTCATAG			MISS*	MISS*			AGTCTCAGAC	ACGGCATGCC	1		0	0	0	0	0
7841	3619	ao	AN6634.1	62.m03229	AO070326000086	0					-56	-33	ATGGCCCGCGACAACAAAATTTGA			ATGGCCCGCGACAACAAAATTTGA	MARDNKI*			MARDNKI*	CTCCCATCCA	GTGACAAGAC	1		0	0	0	0	0
7846	3622	an	AN4050.1	54.m06541	AO070328000106	1	-215	-171					ATGAGTGGCTCACTAGCACTCCTGGCTTCACGTTTCGCTAATTAA	ATGAGTGGCTCACTAGCACTCCTGGCTTCACGTTTCGCTAATTAA			MSGSLALLASRFAN*	MSGSLALLASRFAN*			TCTTTCTCAT	TGGATAGGAC	0	C	0	MG00652.1	NCU02056.1	0	0
7847	3622	an	AN4050.1	54.m06541	AO070328000106	1	-171	-139					ATGGATAGGACCTTCACAGTGCCTTCCGGATAA	ATGGATAGGACCTTCACAGTGCCTTCCGGATAA			MDRTFTVPSG*	MDRTFTVPSG*			TCGCTAATTA	AGGTTCTGGG	0	C	0	MG00652.1	NCU02056.1	0	0
7848	3622	an	AN4050.1	54.m06541	AO070328000106	1	-114	-100					ATGGGCCATACTTGA	ATGGGCCATACTTGA			MGHT*	MGHT*			TGAATGGGTC	GAGCAGAGCT	0	C	0	MG00652.1	NCU02056.1	0	0
7849	3622	ao	AN4050.1	54.m06541	AO070328000106	1					-232	-89	ATGCTTATTGCGAACCGTCTGTCTTTTATGGCTTTTATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA			ATGCTTATTGCGAACCGTCTGTCTTTTATGGCTTTTATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA	MLIANRLSFMAFMVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*			MLIANRLSFMAFMVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*	TCCAACGGGT	AGCCGTTCAC	0	C	0	MG00652.1	NCU02056.1	0	0
7850	3622	ao	AN4050.1	54.m06541	AO070328000106	1					-205	-89	ATGGCTTTTATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA			ATGGCTTTTATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA	MAFMVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*			MAFMVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*	TCTGTCTTTT	AGCCGTTCAC	0	C	0	MG00652.1	NCU02056.1	0	0
7851	3622	ao	AN4050.1	54.m06541	AO070328000106	1					-196	-89	ATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA			ATGGTGGCGCCGTCGGTCTGTGATCATCCTTTGCTCTCCCGCCCTTCTTCCCCTTTTGTATATAATACACCTCTCCCCCCTCGCTACCCTACTTTAGTTCCTTTATAA	MVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*			MVAPSVCDHPLLSRPSSPFVYNTPLPPRYPTLVPL*	TATGGCTTTT	AGCCGTTCAC	0	C	0	MG00652.1	NCU02056.1	0	0
7869	3633	af	AN2880.1	59.m08727	AO070338000135	0			-24	-13			ATGCCGCAGTAG		ATGCCGCAGTAG		MPQ*		MPQ*		CTCTCTGTCC	ATTTTAGATA	1	R	0	0	0	0	0
7871	3633	ao	AN2880.1	59.m08727	AO070338000135	0					-25	-14	ATGTCGCCTTGA			ATGTCGCCTTGA	MSP*			MSP*	CCCTTAATCC	CTGTCAAGGC	1	R	0	0	0	0	0
7882	3635	ao	AN6136.1	72.m19029	AO070340000066	0					-60	-37	ATGATATCTTGCTATCGCTATTAA			ATGATATCTTGCTATCGCTATTAA	MISCYRY*			MISCYRY*	AACTATAGAT	TGACGATCGG	1	A	0	0	0	0	0
7883	3636	af	AN5972.1	72.m19188	AO070340000330	1			-203	-102			ATGTTTGTGACAACTCCGCGGGCCATTTTGTCCGGGGACTCTCGATATTTTATTTGTCCACCACTTTTTCATCTCAAACCCTCTCACTCAGGTCCTCTTTAA		ATGTTTGTGACAACTCCGCGGGCCATTTTGTCCGGGGACTCTCGATATTTTATTTGTCCACCACTTTTTCATCTCAAACCCTCTCACTCAGGTCCTCTTTAA		MFVTTPRAILSGDSRYFICPPLFHLKPSHSGPL*		MFVTTPRAILSGDSRYFICPPLFHLKPSHSGPL*		CAGTCCCTGA	TCCCAAGCTG	0	U	0	0	0	YGL137W	YGL137W
7884	3637	an	AN3958.1	69.m14962	AO070341000080	1	-56	-42					ATGGAATATTTATGA	ATGGAATATTTATGA			MEYL*	MEYL*			CGTCGAAATC	CTGCATGATA	1	A	0	0	0	0	0
7885	3637	an	AN3958.1	69.m14962	AO070341000080	1	-45	-34					ATGACTGCATGA	ATGACTGCATGA			MTA*	MTA*			TGGAATATTT	TATAAGCTGT	1	A	0	0	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
7886	3637	ao	AN3958.1	69.m14962	AO070341000080	1					-406	-386	ATGTTAAATGCAGTGAACTGA			ATGTTAAATGCAGTGAACTGA	MLNAVN*			MLNAVN*	ACTGGGACTA	TTCACCGAGT	0	A	0	0	0	0	0
7939	3651	conserved	AN1349.1	70.m14884	AO070237000012	1	-418	-401	-398	-381	-430	-413	ATGAwmmArTCkyTyTGA	ATGATCAAATCTCTTTGA	ATGAAACAGTCGTTTTGA	ATGAACAAGTCGCTCTGA	MikSl*	MIKSL*	MKQSF*	MNKSL*	srsAAAAryC	CmAymGTGTA	0	A	0	0	0	0	0
7940	3651	conserved	AN1349.1	70.m14884	AO070237000012	1	-254	-201	-250	-197	-260	-207	ATGGCGAAyTwCsyTkTyhmrAGATATGyCGTCwTTCyTTTTkGGCTTGTGTGA	ATGGCGAATTACGTTGTCTCAAGATATGTCGTCTTTCCTTTTTGGCTTGTGTGA	ATGGCGAACTTCCCTTTTCAGAGATATGTCGTCATTCTTTTTGGGCTTGTGTGA	ATGGCGAATTACGTTTTCAAGAGATATGCCGTCTTTCTTTTTGGGCTTGTGTGA	MANyvvsRYvVfpFwLV*	MANYVVSRYVVFPFWLV*	MANFPFQRYVVILFGLV*	MANYVFKRYAVFLFGLV*	AGCTTTCChT	AGTGGGATyT	0	A	0	0	0	0	0
7942	3651	an	AN1349.1	70.m14884	AO070237000012	1	-229	-146					ATGTCGTCTTTCCTTTTTGGCTTGTGTGAAGTGGGATTTCTTAGTGGCCTTTTCTCCATTCGAATTTCGGTTTCGTCGTCTTGA	ATGTCGTCTTTCCTTTTTGGCTTGTGTGAAGTGGGATTTCTTAGTGGCCTTTTCTCCATTCGAATTTCGGTTTCGTCGTCTTGA			MSSFLFGLCEVGFLSGLFSIRISVSSS*	MSSFLFGLCEVGFLSGLFSIRISVSSS*			GTCTCAAGAT	AATCCTGCAA	0	A	0	0	0	0	0
7943	3651	af	AN1349.1	70.m14884	AO070237000012	1			-533	-513			ATGACCCTTCATCTTTATTAG		ATGACCCTTCATCTTTATTAG		MTLHLY*		MTLHLY*		TGGGCTTTTT	CAGGGTAACA	0	A	0	0	0	0	0
7945	3651	af	AN1349.1	70.m14884	AO070237000012	1			-225	-142			ATGTCGTCATTCTTTTTGGGCTTGTGTGAAGTGGGATTTCTGAGTGGCTTCTTCTCAATTCGAAATTCGGTTTCGTCCTGTTAA		ATGTCGTCATTCTTTTTGGGCTTGTGTGAAGTGGGATTTCTGAGTGGCTTCTTCTCAATTCGAAATTCGGTTTCGTCCTGTTAA		MSSFFLGLCEVGFLSGFFSIRNSVSSC*		MSSFFLGLCEVGFLSGFFSIRNSVSSC*		TTTCAGAGAT	AAATCGAGCA	0	A	0	0	0	0	0
7946	3651	ao	AN1349.1	70.m14884	AO070237000012	1					-442	-413	ATGGGAAAAGCCATGAACAAGTCGCTCTGA			ATGGGAAAAGCCATGAACAAGTCGCTCTGA	MGKAMNKSL*			MGKAMNKSL*	AAAATAATCA	CCATCGTGTA	0	A	0	0	0	0	0
7947	3651	ao	AN1349.1	70.m14884	AO070237000012	1					-235	-173	ATGCCGTCTTTCTTTTTGGCTTGTGTGAAGTGGGATCTTTGAGTGGCTTATTGTCGTCTTAA			ATGCCGTCTTTCTTTTTGGGCTTGTGTGAAGTGGGATCTTTGAGTGGCTTATTGTCGTCTTAA	MPSFFLGLCEVGSLSGLLSS*			MPSFFLGLCEVGSLSGLLSS*	TTCAAGAGAT	ATTTCGGTTT	0	A	0	0	0	0	0
7948	3652	an	AN9421.1	55.m02908	AO070242000003	1	-346	-260					ATGGAAGCGGCGACTTCCCTTTCTGAACTCAACAACGGAAAACAGTACGCAGACGCCGAAAGAGAGAAAAAAAAAGGGCGATATTAG	ATGGAAGCGGCGACTTCCCTTTCTGAACTCAACAACGGAAAACAGTACGCAGACGCCGAAAGAGAGAAAAAAAAAGGGCGATATTAG			MEAATSLSELNNGKQYADAEREKKKGRY*	MEAATSLSELNNGKQYADAEREKKKGRY*			GCCATTACCC	GGCCGTCGCA	0	O	0	0	0	0	0
7949	3652	an	AN9421.1	55.m02908	AO070242000003	1	-224	-105					ATGCCCCGTCAGGTGTTCATTCCTAGGTCTCCCCGACTCGATGAATTGAACTGTGACTCCCGACACCTTCTGTTGAGGTTTCCAGCGTGGTACTCCCGTCTTTCGAGGCGGGAAATTTGA	ATGCCCCGTCAGGTGTTCATTCCTAGGTCTCCCCGACTCGATGAATTGAACTGTGACTCCCGACACCTTCTGTTGAGGTTTCCAGCGTGGTACTCCCGTCTTTCGAGGCGGGAAATTTGA			MPRQVFIPRSPRLDELNCDSRHLLLRFPAWYSRLSRREI*	MPRQVFIPRSPRLDELNCDSRHLLLRFPAWYSRLSRREI*			GCTAACAGTG	AACTACAATT	0	O	0	0	0	0	0
7950	3652	af	AN9421.1	55.m02908	AO070242000003	1			-398	-318			ATGAGAACATACAGAGGGACTCAGTGCCAAACAGAGAAGGGCAAGAAGGAAGATAGAGAACCCTTCAGCAAGTTGACCTAA		ATGAGAACATACAGAGGGACTCAGTGCCAAACAGAGAAGGGCAAGAAGGAAGATAGAGAACCCTTCAGCAAGTTGACCTAA		MRTYRGTQCQTEKGKKEDREPFSKLT*		MRTYRGTQCQTEKGKKEDREPFSKLT*		CTTGGAGAGT	ACACACATCA	0	O	0	0	0	0	0
7951	3652	af	AN9421.1	55.m02908	AO070242000003	1			-308	-273			ATGTTGAGTGATGACTCCCCAGATGCACATCTCTAA		ATGTTGAGTGATGACTCCCCAGATGCACATCTCTAA		MLSDDSPDAHL*		MLSDDSPDAHL*		AACACACATC	GTATAATTGG	0	O	0	0	0	0	0
7952	3652	af	AN9421.1	55.m02908	AO070242000003	1			-298	-113			ATGACTCCCCAGATGCACATCTCTAAGTATAATTGGAGTCATACGCTTCCCCCAGATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGATCTACCTATCCTCTCTCGGTCAATGA		ATGACTCCCCAGATGCACATCTCTAAGTATAATTGGAGTCATACGCTTCCCCCAGATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGATCTACCTATCCTCTCTCGGTCAATGA		MTPQMHISKYNWSHTLPPDEWIFTIVIYKSIATFKGLHTLSNCLERTEILLAVIYLSSLGQ*		MTPQMHISKYNWSHTLPPDEWIFTIVIYKSIATFKGLHTLSNCLERTEILLAVIYLSSLGQ*		ATGTTGAGTG	ACAAACAATC	0	O	0	0	0	0	0
7953	3652	af	AN9421.1	55.m02908	AO070242000003	1			-286	-113			ATGCACATCTCTAAGTATAATTGGAGTCATACGCTTCCCCCAGATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGATCTACCTATCCTCTCTCGGTCAATGA		ATGCACATCTCTAAGTATAATTGGAGTCATACGCTTCCCCCAGATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGATCTACCTATCCTCTCTCGGTCAATGA		MHISKYNWSHTLPPDEWIFTIVIYKSIATFKGLHTLSNCLERTEILLAVIYLSSLGQ*		MHISKYNWSHTLPPDEWIFTIVIYKSIATFKGLHTLSNCLERTEILLAVIYLSSLGQ*		GACTCCCCAG	ACAAACAATC	0	O	0	0	0	0	0
7954	3652	af	AN9421.1	55.m02908	AO070242000003	1			-243	-139			ATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGA		ATGAGTGGATATTCACAATCGTCATCTATAAAAGCATCGCTACCTTTAAAGGTCTCCATACACTCTCGAACTGTCTGGAAAGAACTGAAATCTTACTCGCAGTGA		MSGYSQSSSIKASLPLKVSIHSRTVWKELKSYSQ*		MSGYSQSSSIKASLPLKVSIHSRTVWKELKSYSQ*		CTTCCCCCAG	TCTACCTATC	0	O	0	0	0	0	0
7955	3652	af	AN9421.1	55.m02908	AO070242000003	1			-116	-57			ATGAACAAACAATCGGAGTGGTCCCTTCCACCTTTCAATACGTTCATTTTCTTTTATTAG		ATGAACAAACAATCGGAGTGGTCCCTTCCACCTTTCAATACGTTCATTTTCTTTTATTAG		MNKQSEWSLPPFNTFIFFY*		MNKQSEWSLPPFNTFIFFY*		CTCTCGGTCA	TAACTGATAC	0	O	0	0	0	0	0
7956	3652	ao	AN9421.1	55.m02908	AO070242000003	1					-543	-481	ATGTGGAGTATCGTCAACGGCATTCTAGACTCAAATGCGATATACGTCCCTGGTTTACAATAA			ATGTGGAGTATCGTCAACGGCATTCTAGACTCAAATGCGATATACGTCCCTGGTTTACAATAA	MWSIVNGILDSNAIYVPGLQ*			MWSIVNGILDSNAIYVPGLQ*	TTACGGAGTA	GAACCATTCT	0	O	0	0	0	0	0
7957	3652	ao	AN9421.1	55.m02908	AO070242000003	1					-509	-438	ATGCGATATACGTCCCTGGTTTACAATAAGAACCATTCTTTCAGCAGCCCCAGGCGCAGCTGCCGCCAGTGA			ATGCGATATACGTCCCTGGTTTACAATAAGAACCATTCTTTCAGCAGCCCCAGGCGCAGCTGCCGCCAGTGA	MRYTSLVYNKNHSFSSPRRSCRQ*			MRYTSLVYNKNHSFSSPRRSCRQ*	CTAGACTCAA	TGATCCACCG	0	O	0	0	0	0	0
7958	3652	ao	AN9421.1	55.m02908	AO070242000003	1					-438	-340	ATGATCCACCGCGTTCGCATTTTGGTGTGTGCCTTGTATCGCTACCCTGAAGTAGATGAATCGGGTTGCTCCCATCGCTTTTGCGTGTTAGAGCCATAA			ATGATCCACCGCGTTCGCATTTTGGTGTGTGCCTTGTATCGCTACCCTGAAGTAGATGAATCGGGTTGCTCCCATCGCTTTTGCGTGTTAGAGCCATAA	MIHRVRILVCALYRYPEVDESGCSHRFCVLEP*			MIHRVRILVCALYRYPEVDESGCSHRFCVLEP*	GCCGCCAGTG	CGTTGCTTCA	0	O	0	0	0	0	0
7959	3652	ao	AN9421.1	55.m02908	AO070242000003	1					-383	-348	ATGAATCGGGTTGCTCCCATCGCTTTTGCGTGTTAG			ATGAATCGGGTTGCTCCCATCGCTTTTGCGTGTTAG	MNRVAPIAFAC*			MNRVAPIAFAC*	CCTGAAGTAG	AGCCATAACG	0	O	0	0	0	0	0
7995	3667	af	AN1706.1	58.m07796	AO070305000044	0			-33	-19			ATGAAAGCCTGCTAG		ATGAAAGCCTGCTAG		MKAC*		MKAC*		ATCACTTGCC	CATCACCCTA	1	O	0	0	0	0	0
7998	3669	an	AN1476.1	55.m02978	AO070306000099	0	-29	-18					ATGCTGAATTGA	ATGCTGAATTGA			MLN*	MLN*			GCTCTTTGAA	CTGTCAATAC	1	R	0	0	0	0	0
8000	3669	ao	AN1476.1	55.m02978	AO070306000099	0					-25	-11	ATGTTACGAGCGTGA			ATGTTACGAGCGTGA	MLRA*			MLRA*	GTCTAGCTGG	TCAATTGAAA	1	R	0	0	0	0	0
8001	3673	conserved	AN0118.1	71.m15397	AO070311000095	0	-36	-10	-39	-13	-39	-13	ATGmTmmmsdysrGyydmTwCyyrTAr	ATGATACAGTCGGGTTACTTCTCATAG	ATGCTAACCGTGGGTCGCTACCTGTAA	ATGATCACCACCAGCTTATTCTCATAA	Miqsgyfs*	MIQSGYFS*	MLTVGRYL*	MITTSLFS*	yvrmmymTys	rkwrTyryvr	1	Z	0	0	0	0	0
8013	3674	ao	AN8145.1	71.m15392	AO070311000100	1					-103	-65	ATGATTTATAGACGTCTGGGCGAGTTCCGTCTTACATAG			ATGATTTATAGACGTCTGGGCGAGTTCCGTCTTACATAG	MIYRRLGEFRLT*			MIYRRLGEFRLT*	ATTTATAAGC	TATGCTCCAA	0	S	0	0	0	YML079W	0
8014	3674	ao	AN8145.1	71.m15392	AO070311000100	1					-63	-16	ATGCTCCAACTAAACCTTTCTCCTCAAGAAGAACAGACAAGACAGTAG			ATGCTCCAACTAAACCTTTCTCCTCAAGAAGAACAGACAAGACAGTAG	MLQLNLSPQEEQTRQ*			MLQLNLSPQEEQTRQ*	CTTACATAGT	TAAATAAAAG	0	S	0	0	0	YML079W	0
8022	3675	af	AN1007.1	70.m15225	AO070312000026	0			-39	-13			ATGAGCTGTGGTCAATACTGGCGTTGA		ATGAGCTGTGGTCAATACTGGCGTTGA		MSCGQYWR*		MSCGQYWR*		CATTCTGGTA	GACTTCGTCA	1	C	0	0	0	0	0
8029	3677	af	AN6853.1	71.m15279	AO070314000087	0			-45	-22			ATGAGATATAGAAATCTGGTTTGA		ATGAGATATAGAAATCTGGTTTGA		MRYRNLV*		MRYRNLV*		GCTTAGATTT	AAGCTTAAAC	1	I	FG05890.1	0	0	0	0
8036	3678	af	AN0043.1	71.m15318	AO070314000122	0			-55	-38			ATGCCAGCGATCCTCTGA		ATGCCAGCGATCCTCTGA		MPAIL*		MPAIL*		GGCTATGTGC	AGCAGAAACG	1	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8041	3679	af	AN8672.1	62.m03398	AO070315000089	0			-33	-1			ATGCCCTTCTCACAAGGGCTTGAAGCCGCGTAA		ATGCCCTTCTCACAAGGGCTTGAAGCCGCGTAA		MPFSQGLEAA*		MPFSQGLEAA*		CCTCCGGTTT	ATGGCGTCAG	1	R	0	0	0	0	0
8043	3679	ao	AN8672.1	62.m03398	AO070315000089	0					-30	-1	ATGCCCTTTCGAGGGTTAGAAGTAGCCTAA			ATGCCCTTTCGAGGGTTAGAAGTAGCCTAA	MPFRGLEVA*			MPFRGLEVA*	CACACATTGC	ATGGCTTCCA	1	R	0	0	0	0	0
8048	3680	af	AN4581.1	57.m05499	AO070316000164	0			-47	-30			ATGTGTTGCGCAGCCTAA		ATGTGTTGCGCAGCCTAA		MCCAA*		MCCAA*		CAGCGGACAT	CAATAATAAT	1	T	0	0	0	0	0
8053	3685	an	AN4245.1	54.m06807	AO070324000167	1	-431	-366					ATGCTGAAGATCGCCGCTGCCTTCAGTGCGCATTTCTCCGCACAAGGCCAGGAGATCAGCAGATGA	ATGCTGAAGATCGCCGCTGCCTTCAGTGCGCATTTCTCCGCACAAGGCCAGGAGATCAGCAGATGA			MLKIAAAFSAHFSAQGQEISR*	MLKIAAAFSAHFSAQGQEISR*			GCGACAGCAC	CCCTCGCTTC	0	T	0	MG07051.1	0	0	0
8054	3685	an	AN4245.1	54.m06807	AO070324000167	1	-369	-352					ATGACCCTCGCTTCTTGA	ATGACCCTCGCTTCTTGA			MTLAS*	MTLAS*			AGATCAGCAG	GAAATCCTTC	0	T	0	MG07051.1	0	0	0
8055	3685	an	AN4245.1	54.m06807	AO070324000167	1	-283	-224					ATGCAATCTGAACCGGGGGATAAGCAGGTTCAGGCTTCGATGCTATCTTCAACAAACTGA	ATGCAATCTGAACCGGGGGATAAGCAGGTTCAGGCTTCGATGCTATCTTCAACAAACTGA			MQSEPGDKQVQASMLSSTN*	MQSEPGDKQVQASMLSSTN*			AGGAACGCGA	ACGCCAATCA	0	T	0	MG07051.1	0	0	0
8056	3685	an	AN4245.1	54.m06807	AO070324000167	1	-244	-224					ATGCTATCTTCAACAAACTGA	ATGCTATCTTCAACAAACTGA			MLSSTN*	MLSSTN*			TCAGGCTTCG	ACGCCAATCA	0	T	0	MG07051.1	0	0	0
8057	3685	af	AN4245.1	54.m06807	AO070324000167	1			-460	-440			ATGGTTTTCCATCAACCATAG		ATGGTTTTCCATCAACCATAG		MVFHQP*		MVFHQP*		CGGGCCCCAT	ACGACACAGT	0	T	0	MG07051.1	0	0	0
8058	3685	af	AN4245.1	54.m06807	AO070324000167	1			-388	-356			ATGCCGCCTTCTGCATATCTCACGGCATTTTGA		ATGCCGCCTTCTGCATATCTCACGGCATTTTGA		MPPSAYLTAF*		MPPSAYLTAF*		CCACCAATAA	GGAAGCGGGG	0	T	0	MG07051.1	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
8059	3685	af	AN4245.1	54.m06807	AO070324000167	1			-344	-315			ATGAACGATCACGTACCCAATAAAGTATAG		ATGAACGATCACGTACCCAATAAAGTATAG		MNDHVPNKV*		MNDHVPNKV*		GAAGCGGGGA	CGGCAGAGGA	0	T	0	MG07051.1	0	0	0
8060	3685	af	AN4245.1	54.m06807	AO070324000167	1			-305	-294			ATGGCAGCGTGA		ATGGCAGCGTGA		MAA*		MAA*		GCGGCAGAGG	CGACGGCCAC	0	T	0	MG07051.1	0	0	0
8061	3685	af	AN4245.1	54.m06807	AO070324000167	1			-278	-126			ATGCTACCCTCCTGCTGCATTCCTGTCGATCTGCTGGTCATGCGCTCCCTTGCTGTACGTACCTGTACGGGGTCATTCCTGTTCCTATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGATCGATAA		ATGCTACCCTCCTGCTGCATTCCTGTCGATCTGCTGGTCATGCGCTCCCTTGCTGTACGTACCTGTACGGGGTCATTCCTGTTCCTATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGATCGATAA		MLPSCCIPVDLLVMRSLAVRTCTGSFLFLCGLCLNPVSQAIRRITMRSDR*		MLPSCCIPVDLLVMRSLAVRTCTGSFLFLCGLCLNPVSQAIRRITMRSDR*		GCCACAAGCG	GAAGACTGCA	0	T	0	MG07051.1	0	0	0
8062	3685	af	AN4245.1	54.m06807	AO070324000167	1			-239	-126			ATGCGCTCCCTTGCTGTACGTACCTGTACGGGGTCATTCCTGTTCCTATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGATCGATAA		ATGCGCTCCCTTGCTGTACGTACCTGTACGGGGTCATTCCTGTTCCTATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGATCGATAA		MRSLAVRTCTGSFLFLCGLCLNPVSQAIRRITMRSDR*		MRSLAVRTCTGSFLFLCGLCLNPVSQAIRRITMRSDR*		TCTGCTGGTC	GAAGACTGCA	0	T	0	MG07051.1	0	0	0
8063	3685	af	AN4245.1	54.m06807	AO070324000167	1			-192	-133			ATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGA		ATGTGGCCTTTGCTTGAACCCTGTCAGCCAGGCCATTCGGAGAATAACAATGCGATCTGA		MWPLLEPCQPGHSENNNAI*		MWPLLEPCQPGHSENNNAI*		TCCTGTTCCT	TCGATAAGAA	0	T	0	MG07051.1	0	0	0
8064	3685	af	AN4245.1	54.m06807	AO070324000167	1			-143	-126			ATGCGATCTGATCGATAA		ATGCGATCTGATCGATAA		MRSDR*		MRSDR*		GAGAATAACA	GAAGACTGCA	0	T	0	MG07051.1	0	0	0
8065	3685	af	AN4245.1	54.m06807	AO070324000167	1			-73	-59			ATGTCATCAACATAA		ATGTCATCAACATAA		MSST*		MSST*		ATACTTTCTG	CAGGTCACAA	0	T	0	MG07051.1	0	0	0
8066	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-420	-340	ATGGAATGGTCTATCACAATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG			ATGGAATGGTCTATCACAATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG	MEWSITMLIIAFVMRCYLVPCQLLHP*			MEWSITMLIIAFVMRCYLVPCQLLHP*	TCCCCGCCCT	GGTTCAAGAG	0	T	0	MG07051.1	0	0	0
8067	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-415	-293	ATGGTCTATCACAATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAGGGTTCAAGAGAGCGGGGGATGAAGAGGACGTGCCCAATTCAGTTTAG			ATGGTCTATCACAATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAGGGTTCAAGAGAGCGGGGGATGAAGAGGACGTGCCCAATTCAGTTTAG	MVYHNAHHCFCHALLPCALSITPSLGFKRAGDEEDVPNSV*			MVYHNAHHCFCHALLPCALSITPSLGFKRAGDEEDVPNSV*	GCCCTATGGA	GGCCGGCAAG	0	T	0	MG07051.1	0	0	0
8068	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-402	-340	ATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG			ATGCTCATCATTGCTTTTGTCATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG	MLIIAFVMRCYLVPCQLLHP*			MLIIAFVMRCYLVPCQLLHP*	GTCTATCACA	GGTTCAAGAG	0	T	0	MG07051.1	0	0	0
8069	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-381	-340	ATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG			ATGCGCTGTTACCTTGTGCCTTGTCAATTACTCCATCCTTAG	MRCYLVPCQLLHP*			MRCYLVPCQLLHP*	TGCTTTTGTC	GGTTCAAGAG	0	T	0	MG07051.1	0	0	0
8070	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-321	-187	ATGAAGAGGACGTGCCCAATTCAGTTTAGGGCCGGCAAGTCATCATCCAAACTACGGACAGACGATGTCACCCTTCCTTCAACTCTACACCAATCGTACTATTTCATCCCCTTCCTTCCGGGGCATCGCAACTGA			ATGAAGAGGACGTGCCCAATTCAGTTTAGGGCCGGCAAGTCATCATCCAAACTACGGACAGACGATGTCACCCTTCCTTCAACTCTACACCAATCGTACTATTTCATCCCCTTCCTTCCGGGGCATCGCAACTGA	MKRTCPIQFRAGKSSSKLRTDDVTLPSTLHQSYYFIPFLPGHRN*			MKRTCPIQFRAGKSSSKLRTDDVTLPSTLHQSYYFIPFLPGHRN*	AGAGCGGGGG	AATTTGATTT	0	T	0	MG07051.1	0	0	0
8071	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-257	-180	ATGTCACCCTTCCTTCAACTCTACACCAATCGTACTATTTCATCCCCTTCCTTCCGGGGCATCGCAACTGAAATTTGA			ATGTCACCCTTCCTTCAACTCTACACCAATCGTACTATTTCATCCCCTTCCTTCCGGGGCATCGCAACTGAAATTTGA	MSPFLQLYTNRTISSPSFRGIATEI*			MSPFLQLYTNRTISSPSFRGIATEI*	CGGACAGACG	TTTGTGATCG	0	T	0	MG07051.1	0	0	0
8072	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-145	-110	ATGCGCATGCAGAGTGATCGATTCGCCTCGGCTTGA			ATGCGCATGCAGAGTGATCGATTCGCCTCGGCTTGA	MRMQSDRFASA*			MRMQSDRFASA*	ATACTCGGTC	AGCGATTCAC	0	T	0	MG07051.1	0	0	0
8073	3685	ao	AN4245.1	54.m06807	AO070324000167	1					-139	-110	ATGCAGAGTGATCGATTCGCCTCGGCTTGA			ATGCAGAGTGATCGATTCGCCTCGGCTTGA	MQSDRFASA*			MQSDRFASA*	GGTCATGCGC	AGCGATTCAC	0	T	0	MG07051.1	0	0	0
8086	3689	an	AN2772.1	59.m09271	AO070327000014	0	-56	-15					ATGGCGTCTACTGCCCGACGGCTTTCTCCCCGCAATACATGA	ATGGCGTCTACTGCCCGACGGCTTTCTCCCCGCAATACATGA			MASTARRLSPRNT*	MASTARRLSPRNT*			CGAACCGACG	ACGCCGCCTC	1	DO	FG06074.1	MG03314.1	0	0	0
8095	3691	ao	AN5568.1	58.m07492	AO070328000040	1					-654	-586	ATGCCATTTACTCCGCTGGTACGACTAAGGTTTTTTTTTCCTTTGGAATCTCCATTACGCCTTACTTAA			ATGCCATTTACTCCGCTGGTACGACTAAGGTTTTTTTTTCCTTTGGAATCTCCATTACGCCTTACTTAA	MPFTPLVRLRFFFPLESPLRLT*			MPFTPLVRLRFFFPLESPLRLT*	TACCTATTTA	TAAAATTTGA	0		0	0	0	0	0
8103	3695	af	AN9486.1	59.m09213	AO070329000083	0			-55	-20			ATGGTCACTCTGCCAATCCTCATATCGTCCACATAA		ATGGTCACTCTGCCAATCCTCATATCGTCCACATAA		MVTLPILISST*		MVTLPILISST*		GATATCATCG	CCACTCCAGG	1	H	0	0	0	YOR196C	0
8118	3699	ao	AN1516.1	55.m03035	AO070334000235	0					-39	-28	ATGCTATATTGA			ATGCTATATTGA	MLY*			MLY*	GCCCCTATTT	ATCCGGTTAC	1	EH	0	0	0	0	0
8119	3700	af	AN3056.1	59.m08955	AO070337000018	1			-66	-46			ATGCAATTTCTGGAAATATAA		ATGCAATTTCTGGAAATATAA		MQFLEI*		MQFLEI*		GTTTTTTTAT	GCTCAATCTG	0	R	0	0	0	YOL022C	0
8121	3700	ao	AN3056.1	59.m08955	AO070337000018	1					-133	-71	ATGAGGGGCCGATTGCTTTTATCTGTTGACCTTCTGTGCACACTTATTGTCGACTACTTATGA			ATGAGGGGCCGATTGCTTTTATCTGTTGACCTTCTGTGCACACTTATTGTCGACTACTTATGA	MRGRLLLSVDLLCTLIVDYL*			MRGRLLLSVDLLCTLIVDYL*	TGCTGGACTG	ATCAATATAG	0	R	0	0	0	YOL022C	0
8122	3700	ao	AN3056.1	59.m08955	AO070337000018	1					-74	-48	ATGAATCAATATAGTCAATTATTCTAG			ATGAATCAATATAGTCAATTATTCTAG	MNQYSQLF*			MNQYSQLF*	TCGACTACTT	ACCAGGTTTC	0	R	0	0	0	YOL022C	0
8130	3705	an	AN2738.1	54.m06679	AO070338000220	0	-27	-4					ATGATCGACGTTCGATTGCCATAA	ATGATCGACGTTCGATTGCCATAA			MIDVRLP*	MIDVRLP*			CCGCCCTCGT	GCCATGGCGG	1	U	0	MG01245.1	0	0	0
8134	3705	af	AN2738.1	54.m06679	AO070338000220	0			-22	-5			ATGATCGTCGCTCCTTGA		ATGATCGTCGCTCCTTGA		MIVAP*		MIVAP*		TTTCGACCTT	AGAGATGCCT	1	U	0	MG01245.1	0	0	0
8145	3709	an	AN2065.1	57.m05763	AO070341000211	0	-57	-43					ATGATAACACCTTAA	ATGATAACACCTTAA			MITP*	MITP*			CACCGAGGGC	AGCTTGGATC	1	L	0	0	0	0	0
8163	3716	an	AN1061.1	70.m15172	AO070218000005	0	-52	-38					ATGCTGTGGTTGTAA	ATGCTGTGGTTGTAA			MLWL*	MLWL*			TACTTGATTC	TTATACGAGA	1	E	0	MG01385.1	0	0	0
8169	3716	ao	AN1061.1	70.m15172	AO070218000005	0					-59	-12	ATGACTCTGGATTCCTTCTATACCTGCCCCGTGTCTCAGAGCTCTTAA			ATGACTCTGGATTCCTTCTATACCTGCCCCGTGTCTCAGAGCTCTTAA	MTLDSFYTCPVSQSS*			MTLDSFYTCPVSQSS*	CCCTTTCGTG	CTCCCACAAT	1	E	0	MG01385.1	0	0	0
8229	3733	an	AN3110.1	59.m08628	AO070303000041	1	-304	-269					ATGCATTCTCCGCCCCGTCTCCGACCGCGGCCATAG	ATGCATTCTCCGCCCCGTCTCCGACCGCGGCCATAG			MHSPPRLRPRP*	MHSPPRLRPRP*			GCCCTGGATC	TCAACTTGGC	0	T	0	0	0	0	0
8230	3735	an	AN5675.1	65.m07401	AO070309000090	1	-181	-86					ATGATAGAATACATGCTGAGACCCTTTCGGCCCTCGACCAAACTTGGTGGGATTCACGTTTGTCTGCAGCTCTTCGCTTTCAAGCTTGTGGTTTGA	ATGATAGAATACATGCTGAGACCCTTTCGGCCCTCGACCAAACTTGGTGGGATTCACGTTTGTCTGCAGCTCTTCGCTTTCAAGCTTGTGGTTTGA			MIEYMLRPFRPSTKLGGIHVCLQLFAFKLVV*	MIEYMLRPFRPSTKLGGIHVCLQLFAFKLVV*			CCTCTCTTAG	ATTCGTATAA	0	O	FG05735.1	0	0	YDR330W	0
8231	3735	an	AN5675.1	65.m07401	AO070309000090	1	-169	-86					ATGCTGAGACCCTTTCGGCCCTCGACCAAACTTGGTGGGATTCACGTTTGTCTGCAGCTCTTCGCTTTCAAGCTTGTGGTTTGA	ATGCTGAGACCCTTTCGGCCCTCGACCAAACTTGGTGGGATTCACGTTTGTCTGCAGCTCTTCGCTTTCAAGCTTGTGGTTTGA			MLRPFRPSTKLGGIHVCLQLFAFKLVV*	MLRPFRPSTKLGGIHVCLQLFAFKLVV*			GATAGAATAC	ATTCGTATAA	0	O	FG05735.1	0	0	YDR330W	0
8232	3735	ao	AN5675.1	65.m07401	AO070309000090	1					-247	-203	ATGCTGGGTTCATTCCTCTTACCACATAACTGCGATCATTGTTAA			ATGCTGGGTTCATTCCTCTTACCACATAACTGCGATCATTGTTAA	MLGSFLLPHNCDHC*			MLGSFLLPHNCDHC*	AAAAGCTCGT	TTATTAAGAC	0	O	FG05735.1	0	0	YDR330W	0
8235	3736	af	AN5687.1	65.m07413	AO070309000102	1			-68	-30			ATGATCAACCACGACGCATACACGGCCATTTCGATTTGA		ATGATCAACCACGACGCATACACGGCCATTTCGATTTGA		MINHDAYTAISI*		MINHDAYTAISI*		CTAGCGACTG	ATGAGTATCA	0		0	0	0	0	0
8244	3738	af	AN9413.1	53.m03669	AO070310000006	0			-49	-2			ATGATAGTCTCTCCTGTCGCCACCGGTTCTTCGAGAAGCTGTCCGTAA		ATGATAGTCTCTCCTGTCGCCACCGGTTCTTCGAGAAGCTGTCCGTAA		MIVSPVATGSSRSCP*		MIVSPVATGSSRSCP*		TTAAATTTAC	CATGGAGTCA	1		0	0	0	0	0
8249	3741	af	AN0112.1	71.m15387	AO070311000096	0			-59	-39			ATGAGATTGCTCTGTCATTGA		ATGAGATTGCTCTGTCATTGA		MRLLCH*		MRLLCH*		AGGCTATGGT	GCAACCTCCC	1	U	0	0	0	0	0
8254	3742	af	AN1005.1	70.m15223	AO070312000029	0			-39	-7			ATGCTGATAAGGAGTCGAGAATTATATGCATGA		ATGCTGATAAGGAGTCGAGAATTATATGCATGA		MLIRSRELYA*		MLIRSRELYA*		GAAGCTCAGG	AATAGCATGA	1	Z	FG09793.1	0	NCU05282.1	0	0
8278	3752	af	AN5535.1	58.m07481	AO070328000056	0			-26	-12			ATGGACTCGTCTTGA		ATGGACTCGTCTTGA		MDSS*		MDSS*		CGAAAGCTCT	CAGAACTCAA	1	S	0	MG00102.1	NCU04505.1	0	0
8316	3762	an	AN2927.1	59.m09068	AO070337000182	0	-39	-7					ATGCAGCCCAATGCGTCTGGTGGCTGCTCATGA	ATGCAGCCCAATGCGTCTGGTGGCTGCTCATGA			MQPNASGGCS*	MQPNASGGCS*			ATTGCGACGG	ACGACAATGG	1	D	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
8325	3762	ao	AN2927.1	59.m09068	AO070337000182	0					-26		ATGTGGCCTCGCTTTGAATCGCTATGA			ATGTGGCCTCGCTTTGAATCGCTATGA	MWPRFESL*			MWPRFESL*	GGACGCGTCC	TGGCTTCTAC	1	D	0	0	0	0	0
8331	3763	af	AN3797.1	57.m05686	AO070337000231	0			-49	-35			ATGAAGTGCATGTAA		ATGAAGTGCATGTAA		MKCM*		MKCM*		CCTGTCGGGG	CACTAAACAA	1	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8333	3765	conserved	AN0244.1	54.m06697	AO070338000236	0	-23		-23		-23		ATGrwyATkCGrACrThyyGCTGA	ATGAACATTCGGACATACCGCTGA	ATGGTTATGCGAACGTCCTGCTGA	ATGGTCATTCGAACATTTTGCTGA	MniRTyr*	MNIRTYR*	MVMRTSC*	MVIRTFC*	wbwbrrAGmr	TGAGCTCCAh	1	U	0	0	0	0	0
8336	3765	af	AN0244.1	54.m06697	AO070338000236	0			-17				ATGCGAACGTCCTGCTGA		ATGCGAACGTCCTGCTGA		MRTSC*		MRTSC*		AGAGATGGTT	TGAGCTCCAA	1	U	0	0	0	0	0
8365	3782	an	AN8836.1	71.m15967	AO070271000042	0	-59	-36					ATGGGAAGACATTTAGACTTTTAG	ATGGGAAGACATTTAGACTTTTAG			MGRHLDF*	MGRHLDF*			ATTTCGTCGT	TGTACTATGG	1	T	0	0	0	0	0
8366	3782	an	AN8836.1	71.m15967	AO070271000042	0	-29	-18					ATGGCTAACTGA	ATGGCTAACTGA			MAN*	MAN*			TTAGTGTACT	CTCCCTTGTC	1	T	0	0	0	0	0
8393	3790	ao	AN8879.1	56.m02290	AO070293000008	0					-32	-9	ATGCCGACGAAGCCTTGCCGTTAG			ATGCCGACGAAGCCTTGCCGTTAG	MPTKPCR*			MPTKPCR*	TAATAGCCCG	CTAGAACGAT	1	U	0	0	NCU09313.1	0	0
8404	3794	af	AN8389.1	59.m08445	AO070300000072	0			-52	-35			ATGGAGTGTCTATCATGA		ATGGAGTGTCTATCATGA		MECLS*		MECLS*		TAATGCGGTT	TCATACCATC	1		0	0	0	0	0
8409	3798	an	AN1708.1	58.m07794	AO070305000041	0	-50	-39					ATGATTCAATAA	ATGATTCAATAA			MIQ*	MIQ*			AGTTCATGAC	TAGGCTCAGC	1	L	0	0	0	0	0
8414	3798	ao	AN1708.1	58.m07794	AO070305000041	0					-49	-38	ATGTTCTATTAG			ATGTTCTATTAG	MFY*			MFY*	TATCTACGGC	AGTTTTAAAT	1	L	0	0	0	0	0
8415	3799	ao	AN8269.1	53.m03692	AO070310000033	0					-51	-16	ATGACTAACACAACATTGACGTGGAATAGAATATAA			ATGACTAACACAACATTGACGTGGAATAGAATATAA	MTNTTLTWNRI*			MTNTTLTWNRI*	CAGTAGACCT	CTCACATCCC	1	O	0	0	0	0	0
8439	3809	an	AN5234.1	54.m06837	AO070324000133	1	-179	-108					ATGTTGCCCGCCGTATGTGCCAGTAGTATATCGGATCTGCTCCTACCTCATACACGGTTCAATTCTCCATGA	ATGTTGCCCGCCGTATGTGCCAGTAGTATATCGGATCTGCTCCTACCTCATACACGGTTCAATTCTCCATGA			MLPAVCASSISDLLLPHTRFNSP*	MLPAVCASSISDLLLPHTRFNSP*			CCTTCGTCGT	GCCCCACATC	0	C	0	0	0	0	0
8440	3809	an	AN5234.1	54.m06837	AO070324000133	1	-165	-154					ATGTGCCAGTAG	ATGTGCCAGTAG			MCQ*	MCQ*			TGCCCGCCGT	TATATCGGAT	0	C	0	0	0	0	0
8441	3809	an	AN5234.1	54.m06837	AO070324000133	1	-111	-37					ATGAGCCCCACATCCCCACATTACTGGCAGTATTACTGTAGTTTACTTAAGGTGAGGTCATCTCGGCCACCATAG	ATGAGCCCCACATCCCCACATTACTGGCAGTATTACTGTAGTTTACTTAAGGTGAGGTCATCTCGGCCACCATAG			MSPTSPHYWQYYCSLLKVRSSRPP*	MSPTSPHYWQYYCSLLKVRSSRPP*			TCAATTCTCC	GCTCGAAACG	0	C	0	0	0	0	0
8442	3809	af	AN5234.1	54.m06837	AO070324000133	1			-251	-123			ATGTACGTTTTGTCTGTTATAAGATATCCAATCGAACAGTTTGAATTCAATCTTGGGCCATGCATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		ATGTACGTTTTGTCTGTTATAAGATATCCAATCGAACAGTTTGAATTCAATCTTGGGCCATGCATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		MYVLSVIRYPIEQFEFNLGPCMMQFSQASLFCLRPEVKEESP*		MYVLSVIRYPIEQFEFNLGPCMMQFSQASLFCLRPEVKEESP*		GTTCGCGTGT	CCCCGCACCT	0	C	0	0	0	0	0
8443	3809	af	AN5234.1	54.m06837	AO070324000133	1			-192	-88			ATGCATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAGCCCCGCACCTTATCCACCGGCCTACAACTGTATGA		ATGCATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAGCCCCGCACCTTATCCACCGGCCTACAACTGTATGA		MHDAILTGVIILLEARSQGGISLAPHLIHRPTTV*		MHDAILTGVIILLEARSQGGISLAPHLIHRPTTV*		ATCTTGGGCC	CCTTTCTGTT	0	C	0	0	0	0	0
8444	3809	af	AN5234.1	54.m06837	AO070324000133	1			-188	-123			ATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		ATGATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		MMQFSQASLFCLRPEVKEESP*		MMQFSQASLFCLRPEVKEESP*		TGGGCCATGC	CCCCGCACCT	0	C	0	0	0	0	0
8445	3809	af	AN5234.1	54.m06837	AO070324000133	1			-185	-123			ATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		ATGCAATTCTCACAGGCGTCATTATTTTGCTTGAGGCCAGAAGTCAAGGAGGAATCTCCCTAG		MQFSQASLFCLRPEVKEESP*		MQFSQASLFCLRPEVKEESP*		GCCATGCATG	CCCCGCACCT	0	C	0	0	0	0	0
8446	3809	af	AN5234.1	54.m06837	AO070324000133	1			-91	-56			ATGACCTTTCTGTTCCCTCACCGATTATACAAGTAG		ATGACCTTTCTGTTCCCTCACCGATTATACAAGTAG		MTFLFPHRLYK*		MTFLFPHRLYK*		CTACAACTGT	TACGTCAACT	0	C	0	0	0	0	0
8447	3809	ao	AN5234.1	54.m06837	AO070324000133	1					-299	-252	ATGTCAATGTCAAATTTTCTTAAGACAGCTGTTTCCTCGTACTATTGA			ATGTCAATGTCAAATTTTCTTAAGACAGCTGTTTCCTCGTACTATTGA	MSMSNFLKTAVSSYY*			MSMSNFLKTAVSSYY*	TTATTTTATT	TCTACTGCGA	0	C	0	0	0	0	0
8448	3809	ao	AN5234.1	54.m06837	AO070324000133	1					-293	-252	ATGTCAAATTTTCTTAAGACAGCTGTTTCCTCGTACTATTGA			ATGTCAAATTTTCTTAAGACAGCTGTTTCCTCGTACTATTGA	MSNFLKTAVSSYY*			MSNFLKTAVSSYY*	TATTATGTCA	TCTACTGCGA	0	C	0	0	0	0	0
8469	3821	ao	AN3063.1	59.m08951	AO070337000010	0					-57	-43	ATGGAGCGAAACTGA			ATGGAGCGAAACTGA	MERN*			MERN*	TTTTCTTTTG	CTTCTTGCGC	1	K	0	0	NCU02401.1	0	0
8517	3838	ao	AN8743.1	62.m03337	AO070250000032	0					-45	-19	ATGCAATACGAAAGAAAGTTCAAGTGA			ATGCAATACGAAAGAAAGTTCAAGTGA	MQYERKFK*			MQYERKFK*	CACTCTTTTA	ACAGTTTAAT	1	IOT	0	0	0	0	0
8537	3841	af	AN3430.1	59.m09287	AO070265000004	0			-27	-13			ATGTCTGTGGTCTGA		ATGTCTGTGGTCTGA		MSVV*		MSVV*		TCTTGCCGAT	GGTGCTTTAA	1		0	0	0	0	0
8585	3855	an	AN3920.1	69.m15008	AO070324000116	0	-48	-28					ATGTTCTTCATTTCTCAATGA	ATGTTCTTCATTTCTCAATGA			MFFISQ*	MFFISQ*			CCCCTACCAG	CTTTCGCTAC	1	H	0	0	0	0	0
8586	3855	an	AN3920.1	69.m15008	AO070324000116	0	-31	-2					ATGACTTTCGCTACTACTCATTTTCGCTGA	ATGACTTTCGCTACTACTCATTTTCGCTGA			MTFATTHFR*	MTFATTHFR*			TCATTTCTCA	AATGCGTGGA	1	H	0	0	0	0	0
8587	3855	ao	AN3920.1	69.m15008	AO070324000116	0					-50	-9	ATGCTCTTCTTTTGTCCTCACTCGCAGTTTCATCCTCTCTAA			ATGCTCTTCTTTTGTCCTCACTCGCAGTTTCATCCTCTCTAA	MLFFCPHSQFHPL*			MLFFCPHSQFHPL*	TTTTCCAACC	TTGCGGAGAT	1	H	0	0	0	0	0
8640	3865	an	AN1132.1	70.m15104	AO070331000124	0	-54	-43					ATGTCAGCCTAA	ATGTCAGCCTAA			MSA*	MSA*			AATATATAAC	CATGATTTCC	1	E	0	0	0	0	0
8641	3865	an	AN1132.1	70.m15104	AO070331000124	0	-41	-15					ATGATTTCCACCTTTGCTGTGGTATAA	ATGATTTCCACCTTTGCTGTGGTATAA			MISTFAVV*	MISTFAVV*			TCAGCCTAAC	TCCGTCGTCT	1	E	0	0	0	0	0
8646	3865	ao	AN1132.1	70.m15104	AO070331000124	0					-49	-5	ATGCTCCTCCTCGCCGAAGACATAGACGCTACTTCTTCGGTGTGA			ATGCTCCTCCTCGCCGAAGACATAGACGCTACTTCTTCGGTGTGA	MLLLAEDIDATSSV*			MLLLAEDIDATSSV*	TAATCCAGGA	CAATATGTCT	1	E	0	0	0	0	0
8652	3867	an	AN0311.1	54.m06980	AO070334000022	0	-57	-46					ATGTGCTATTAG	ATGTGCTATTAG			MCY*	MCY*			CCAGCTCTCG	TTCTCGACTT	1		0	0	0	0	0
8656	3871	an	AN1038.1	70.m15196	AO070336000073	0	-48	-13					ATGCTCCTCGCGCGCAGACAGCTTCCCCCTGAATAG	ATGCTCCTCGCGCGCAGACAGCTTCCCCCTGAATAG			MLLARRQLPPE*	MLLARRQLPPE*			GCCGACCGGA	TGCGCGGGAA	1	R	0	0	0	0	0
8662	3871	af	AN1038.1	70.m15196	AO070336000073	0			-48	-13			ATGTCACTAAGGTTGCTTGTGTTACATCCCGAATAG		ATGTCACTAAGGTTGCTTGTGTTACATCCCGAATAG		MSLRLLVLHPE*		MSLRLLVLHPE*		CTAAAGCGGA	CGCTCGGGAA	1	R	0	0	0	0	0
8664	3871	ao	AN1038.1	70.m15196	AO070336000073	0					-52	-35	ATGCTTCTTGGAAGCTAG			ATGCTTCTTGGAAGCTAG	MLLGS*			MLLGS*	CTCCAACGGC	TCTTCTGTCA	1	R	0	0	0	0	0
8674	3880	an	AN0407.1	54.m06667	AO070338000247	0	-33	-13					ATGATGGTCGCCAAAGTATGA	ATGATGGTCGCCAAAGTATGA			MMVAKV*	MMVAKV*			CAATCGTCCA	TAACAAGCCA	1	K	FG05376.1	0	NCU00310.1	YGR047C	0
8675	3880	an	AN0407.1	54.m06667	AO070338000247	0	-30	-13					ATGGTCGCCAAAGTATGA	ATGGTCGCCAAAGTATGA			MVAKV*	MVAKV*			TCGTCCAATG	TAACAAGCCA	1	K	FG05376.1	0	NCU00310.1	YGR047C	0
8715	3892	ao	AN1421.1	55.m02935	AO070232000017	0					-24	-4	ATGGTCCATCATCAGTCATAA			ATGGTCCATCATCAGTCATAA	MVHHQS*			MVHHQS*	CCATCGCTAT	CAAATGACGA	1	K	0	0	0	0	0
8717	3893	an	AN5198.1	69.m14897	AO070237000028	0	-34	-2					ATGGAGGTGCTAGGTGATCCGACTCGCTTGTAG	ATGGAGGTGCTAGGTGATCCGACTCGCTTGTAG			MEVLGDPTRL*	MEVLGDPTRL*			TTTTCAGTTG	CATGTCGTCA	1	R	0	0	0	0	0
8730	3896	af	AN2464.1	69.m15203	AO070264000006	1			-259	-233			ATGAAAATGGGAAAAAACCCTTTTTGA		ATGAAAATGGGAAAAAACCCTTTTTGA		MKMGKNPF*		MKMGKNPF*		GCGGAGAAAA	CATCAATGTA	0	U	0	MG05189.1	0	0	0
8731	3896	af	AN2464.1	69.m15203	AO070264000006	1			-253	-233			ATGGGAAAAAACCCTTTTTGA		ATGGGAAAAAACCCTTTTTGA		MGKNPF*		MGKNPF*		AAAAATGAAA	CATCAATGTA	0	U	0	MG05189.1	0	0	0
8737	3902	an	AN4951.1	59.m08856	AO070288000003	1	-179	-69					ATGGAATCTGAAAGCAGTCAAATCTCTTCCGTTCCAGTGTTTTCCCTCCGATATTATCATAGTTTCATCTCTCCCCTCCCTTTTGAGCCATTCCAGCTGCTTACCGCCTAA	ATGGAATCTGAAAGCAGTCAAATCTCTTCCGTTCCAGTGTTTTCCCTCCGATATTATCATAGTTTCATCTCTCCCCTCCCTTTTGAGCCATTCCAGCTGCTTACCGCCTAA			MESESSQISSVPVFSLRYYHSFISPLPFEPFQLLTA*	MESESSQISSVPVFSLRYYHSFISPLPFEPFQLLTA*			TCTCTGTTCT	ACCCAAGCCG	0	U	0	0	NCU06284.1	0	0
8740	3902	ao	AN4951.1	59.m08856	AO070288000003	1					-162	-127	ATGGACCAGGAGTTCCCTGATCCTTTTCCCTTTTAG			ATGGACCAGGAGTTCCCTGATCCTTTTCCCTTTTAG	MDQEFPDPFPF*			MDQEFPDPFPF*	CCTCCTGTCT	CGCTATTACC	0	U	0	0	NCU06284.1	0	0
8754	3905	an	AN3752.1	65.m07375	AO070309000065	1	-193	-164					ATGGCCCTGTGCCTCCTTGTGGAATATTAG	ATGGCCCTGTGCCTCCTTGTGGAATATTAG			MALCLLVEY*	MALCLLVEY*			TGGTAAATTA	TACAGCGTGG	0	TR	0	0	0	0	0
8755	3905	ao	AN3752.1	65.m07375	AO070309000065	1					-371	-342	ATGTTTGACGACCATCTACATATGTCCTAG			ATGTTTGACGACCATCTACATATGTCCTAG	MFDDHLHMS*			MFDDHLHMS*	CTCCTATTCG	TCTGTCTCCT	0	TR	0	0	0	0	0
8756	3905	ao	AN3752.1	65.m07375	AO070309000065	1					-254	-216	ATGATTCTTAGTGTCACGTTCAATAGTCGATTATCTTAA			ATGATTCTTAGTGTCACGTTCAATAGTCGATTATCTTAA	MILSVTFNSRLS*			MILSVTFNSRLS*	CGGGTTCTGG	TATCGCCTGG	0	TR	0	0	0	0	0
8766	3911	an	AN0135.1	71.m15419	AO070321000117	1	-215	-165					ATGACTGCTGTCTTCCGTTATTTATCCACTGTCTCGGAGTGCGTGGGTTAA	ATGACTGCTGTCTTCCGTTATTTATCCACTGTCTCGGAGTGCGTGGGTTAA			MTAVFRYLSTVSECVG*	MTAVFRYLSTVSECVG*			CTTTCTCTCC	TCTATCTTCT	0	ODR	FG10861.1	MG03876.1	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
8781	3920	af	AN2967.1	59.m09040	AO070337000149	0			-29	-18			ATGCTATGCTAA		ATGCTATGCTAA		MLC*		MLC*		AAAGTCAATA	GATTTCTCCG	1	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8802	3924	af	AN1560.1	55.m03076	AO070339000293	0			-58	-17			ATGCGACAATTGATGCCCACACACTGTAAGGAAACCGATTGA		ATGCGACAATTGATGCCCACACACTGTAAGGAAACCGATTGA		MRQLMPTHCKETD*		MRQLMPTHCKETD*		TTGATCTCCA	AGGACTGGAA	1	D	0	0	0	0	0
8803	3924	af	AN1560.1	55.m03076	AO070339000293	0			-46	-17			ATGCCCACACACTGTAAGGAAACCGATTGA		ATGCCCACACACTGTAAGGAAACCGATTGA		MPTHCKETD*		MPTHCKETD*		GCGACAATTG	AGGACTGGAA	1	D	0	0	0	0	0
8826	3936	an	AN2508.1	59.m08476	AO070263000056	1	-28	-14					ATGTGGAGGCTATAA	ATGTGGAGGCTATAA			MWRL*	MWRL*			TGACTCTTTT	ACTGCTTTCC	1	E	FG10049.1	0	0	0	0
8831	3936	af	AN2508.1	59.m08476	AO070263000056	1			-27	-4			ATGGTACGGTTGAGCAACATCTAA		ATGGTACGGTTGAGCAACATCTAA		MVRLSNI*		MVRLSNI*		CAAGCCATTC	ATTATGTCTA	1	E	FG10049.1	0	0	0	0
8849	3943	af	AN4728.1	71.m15638	AO070284000080	0			-22	-5			ATGACCGTTTGGAGCTGA		ATGACCGTTTGGAGCTGA		MTVWS*		MTVWS*		TGAACCTCCA	GGTTATGAAA	1	S	FG00261.1	MG02867.1	0	0	0
8850	3943	ao	AN4728.1	71.m15638	AO070284000080	0					-29	-6	ATGACCAGTTTTCTGTCGAGGTAA			ATGACCAGTTTTCTGTCGAGGTAA	MTSFLSR*			MTSFLSR*	TCGCGACCCC	TAACCATGCG	1	S	FG00261.1	MG02867.1	0	0	0
8885	3960	af	AN6630.1	62.m03226	AO070326000082	1			-283	-200			ATGGCATTCACACAGCTTTGCGACCTTCCACTTACAACAAGACAAAAAAACCCCCAATCATCCCCAACAGCCCTCTATCCGTGA		ATGGCATTCACACAGCTTTGCGACCTTCCACTTACAACAAGACAAAAAAACCCCCAATCATCCCCAACAGCCCTCTATCCGTGA		MAFTQLCDLPLTTRQKNPQSSPTALYP*		MAFTQLCDLPLTTRQKNPQSSPTALYP*		TTTCGGCAGC	ACTAGGTATG	0	K	0	0	0	YHR193C	0
8887	3960	ao	AN6630.1	62.m03226	AO070326000082	1					-282	-211	ATGACATTCACACAGCTTTGCGCCTTTCCAACTTCAACCAGACCAAAAAAACCCCCTCATCCACCACAGTAA			ATGACATTCACACAGCTTTGCGCCTTTCCAACTTCAACCAGACCAAAAAAACCCCCTCATCCACCACAGTAA	MTFTQLCAFPTSTRPKKPPHPPQ*			MTFTQLCAFPTSTRPKKPPHPPQ*	TTCGGCAGCC	TCTTTTCTGT	0	K	0	0	0	YHR193C	0
8916	3977	conserved	AN5885.1	72.m19245	AO070245000022	0	-36	-22	-60	-46	-56	-42	ATGyyGsyykywTrA	ATGTCGGTTGTTTGA	ATGCTGCTCTCATAA	ATGCCGGCTGTTTGA	Msvv*	MSVV*	MLLS*	MPAV*	CbTkrrvCAC	drmvrTvsbd	1	G	0	0	0	0	0
8918	3978	an	AN3168.1	59.m08557	AO070256000022	0	-41	-18					ATGTCGATGCGGAGAGCCGTCTGA	ATGTCGATGCGGAGAGCCGTCTGA			MSMRRAV*	MSMRRAV*			GGAGCTCTCC	TCTGCTAGAG	1	C	FG10907.1	MG07007.1	0	0	0
8919	3978	an	AN3168.1	59.m08557	AO070256000022	0	-35	-18					ATGCGGAGAGCCGTCTGA	ATGCGGAGAGCCGTCTGA			MRRAV*	MRRAV*			CTCCATGTCG	TCTGCTAGAG	1	C	FG10907.1	MG07007.1	0	0	0
8960	3995	af	AN1461.1	55.m03257	AO070306000077	1			-216	-169			ATGACATACCTCTGCATTCTGAGATCTGAATTCTATATGCTGCTGTAA		ATGACATACCTCTGCATTCTGAGATCTGAATTCTATATGCTGCTGTAA		MTYLCILRSEFYMLL*		MTYLCILRSEFYMLL*		ACAACTTCTA	TCATGAGAAC	0	R	0	0	0	0	0
8961	3995	af	AN1461.1	55.m03257	AO070306000077	1			-180	-169			ATGCTGCTGTAA		ATGCTGCTGTAA		MLL*		MLL*		TGAATTCTAT	TCATGAGAAC	0	R	0	0	0	0	0
8962	3995	af	AN1461.1	55.m03257	AO070306000077	1			-166	-134			ATGAGAACGAACTGCTGCCCTTCACTTCATTGA		ATGAGAACGAACTGCTGCCCTTCACTTCATTGA		MRTNCCPSLH*		MRTNCCPSLH*		TGCTGTAATC	CCCGGGCACC	0	R	0	0	0	0	0
8964	3995	ao	AN1461.1	55.m03257	AO070306000077	1					-188	-174	ATGATGACCAATTGA			ATGATGACCAATTGA	MMTN*			MMTN*	ATATAGTACC	ACTATCTTTT	0	R	0	0	0	0	0
8965	3995	ao	AN1461.1	55.m03257	AO070306000077	1					-185	-174	ATGACCAATTGA			ATGACCAATTGA	MTN*			MTN*	TAGTACCATG	ACTATCTTTT	0	R	0	0	0	0	0
8974	3997	ao	AN3749.1	65.m07385	AO070309000073	0					-33	-4	ATGTGGCTTATAAAAACACCCGGGCAGTAA			ATGTGGCTTATAAAAACACCCGGGCAGTAA	MWLIKTPGQ*			MWLIKTPGQ*	GTTGAAGTCT	ACGATGCCTT	1	L	FG07112.1	MG09306.1	0	0	0
8979	4003	an	AN0910.1	70.m15519	AO070320000091	0	-42	-25					ATGTCCCGTTCGGGATGA	ATGTCCCGTTCGGGATGA			MSRSG*	MSRSG*			TACCTGTTTC	CTTTCATGGT	1	I	0	0	0	0	0
8980	4003	an	AN0910.1	70.m15519	AO070320000091	0	-28	-11					ATGACTTTCATGGTGTGA	ATGACTTTCATGGTGTGA			MTFMV*	MTFMV*			CCCGTTCGGG	CGCTCGCATT	1	I	0	0	0	0	0
8982	4003	af	AN0910.1	70.m15519	AO070320000091	0			-28	-11			ATGATGTCTCTGGAGTAG		ATGATGTCTCTGGAGTAG		MMSLE*		MMSLE*		CCCGTAAGGG	ATCAGTGATT	1	I	0	0	0	0	0
8983	4003	af	AN0910.1	70.m15519	AO070320000091	0			-25	-11			ATGTCTCTGGAGTAG		ATGTCTCTGGAGTAG		MSLE*		MSLE*		GTAAGGGATG	ATCAGTGATT	1	I	0	0	0	0	0
8998	4007	an	AN7672.1	57.m05448	AO070325000052	1	-118	-83					ATGAGTCACTTGACCCACCGCCGATTCGTTAATTGA	ATGAGTCACTTGACCCACCGCCGATTCGTTAATTGA			MSHLTHRRFVN*	MSHLTHRRFVN*			CTTTGGAGTG	CCACATACGA	0		0	0	NCU02635.1	0	0
8999	4007	af	AN7672.1	57.m05448	AO070325000052	1			-208	-164			ATGTCGGGGCGCAGGTCGGAGAGAATTGACTTCATTACTGGCTAA		ATGTCGGGGCGCAGGTCGGAGAGAATTGACTTCATTACTGGCTAA		MSGRRSERIDFITG*		MSGRRSERIDFITG*		CGATCCCGCT	GTATTTTCTC	0		0	0	NCU02635.1	0	0
9000	4007	ao	AN7672.1	57.m05448	AO070325000052	1					-173	-132	ATGTCAGGGGCCAGGCACAGCACTGCTTTTATCGCTGGCTAA			ATGTCAGGGGCCAGGCACAGCACTGCTTTTATCGCTGGCTAA	MSGARHSTAFIAG*			MSGARHSTAFIAG*	CGAATTCGCT	CGAGGATTCG	0		0	0	NCU02635.1	0	0
9002	4008	an	AN7723.1	71.m15750	AO070325000138	0	-50	-6					ATGGTACCTTGCTACTGTCCTCTCCACAGATTCCTGCAGCATTAG	ATGGTACCTTGCTACTGTCCTCTCCACAGATTCCTGCAGCATTAG			MVPCYCPLHRFLQH*	MVPCYCPLHRFLQH*			CATTGCAGCA	CTAAAATGAA	1	L	FG06122.1	0	NCU01370.1	0	0
9004	4008	ao	AN7723.1	71.m15750	AO070325000138	0					-52	-2	ATGGTATTTAGTTTCCTGCTATCAATTGCGTTTGTTCTTCGAACATACTGA			ATGGTATTTAGTTTCCTGCTATCAATTGCGTTTGTTCTTCGAACATACTGA	MVFSFLLSIAFVLRTY*			MVFSFLLSIAFVLRTY*	TCGCGTCCTG	CATGAAGCGC	1	L	FG06122.1	0	NCU01370.1	0	0
9022	4010	af	AN9038.1	59.m08392	AO070330000171	1			-89	-48			ATGATCTTACAAACACGACATGACCCTATCATAAGATATTGA		ATGATCTTACAAACACGACATGACCCTATCATAAGATATTGA		MILQTRHDPIIRY*		MILQTRHDPIIRY*		AATCTCCCCC	CATTATAGTA	0	H	FG05299.1	0	0	0	0
9023	4010	af	AN9038.1	59.m08392	AO070330000171	1			-70	-56			ATGACCCTATCATAA		ATGACCCTATCATAA		MTLS*		MTLS*		CAAACACGAC	GATATTGACA	0	H	FG05299.1	0	0	0	0
9032	4011	af	AN2879.1	53.m04051	AO070330000208	0			-31	-17			ATGCCATTATCATGA		ATGCCATTATCATGA		MPLS*		MPLS*		CAGTCGAGCC	TATCTACCGA	1	JIT	0	0	0	0	0
9035	4015	af	AN2992.1	59.m09022	AO070337000126	1			-441	-316			ATGTCTCTACCAATATATCAACCTCTCGTCAGGCTACCTATAGGCAAGTCTTTACTGCTAGATAACATTCTTCCTGACTGTTATCATATTTGGAAGTGCCTACTGCTGCAGAAAGGACATATATAA		ATGTCTCTACCAATATATCAACCTCTCGTCAGGCTACCTATAGGCAAGTCTTTACTGCTAGATAACATTCTTCCTGACTGTTATCATATTTGGAAGTGCCTACTGCTGCAGAAAGGACATATATAA		MSLPIYQPLVRLPIGKSLLLDNILPDCYHIWKCLLLQKGHI*		MSLPIYQPLVRLPIGKSLLLDNILPDCYHIWKCLLLQKGHI*		ACCCAAAGAT	TATGGCGGAT	0	J	0	0	0	0	0
9060	4027	conserved	AN4984.1	59.m08886	AO070288000052	1	-236	-222	-265	-251	-629	-615	ATGyywwTywwCTAA	ATGCTTTTCAACTAA	ATGTCAATCATCTAA	ATGTTATTTTACTAA	Mlfn*	MLFN*	MSII*	MLFY*	kwdTCyCyyC	GmGAhwyymA	0	R	0	0	0	0	0
9102	4038	conserved	AN6843.1	71.m15300	AO070314000096	1	-278	-237	-157	-116	-166	-125	ATGGCTbTCbCGmAGCwCwrGkGGbyTkyTbwCdGGvdCTGA	ATGGCTGTCTCGCAGCTCAAGGGGTCTTCTTTCTGGAACTGA	ATGGCTTTCGCGAAGCTCAAGTGGCCTGTTGACAGGCGCTGA	ATGGCTCTCCCGAAGCACTGGTGGGTTGCTCTCGGGGTCTGA	MAvsqlkgssfwn*	MAVSQLKGSSFWN*	MAFAKLKWPVDRR*	MALPKHWWVALGV*	GhrCyyTmAG	rrCCAChACr	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9109	4040	an	AN0211.1	71.m15474	AO070321000033	0	-25	-11					ATGAACCGCTCATAA	ATGAACCGCTCATAA			MNRS*	MNRS*			TGCTCCGTTT	TTCCGTCACT	1	A	0	0	0	0	0
9111	4040	af	AN0211.1	71.m15474	AO070321000033	0			-44	-30			ATGATACCCCAATAG		ATGATACCCCAATAG		MIPQ*		MIPQ*		ACTTGCGTGC	AGAAGCAGCA	1	A	0	0	0	0	0
9157	4058	an	AN7559.1	72.m19579	AO070343000399	0	-42	-28					ATGACCCACGATTGA	ATGACCCACGATTGA			MTHD*	MTHD*			TTTCTCATAC	CTACGTTTAC	1	K	0	0	0	0	0
9162	4064	ao	AN3464.1	59.m09325	AO070265000042	0					-44	-33	ATGCACATCTAG			ATGCACATCTAG	MHI*			MHI*	GGTTCTCTAA	TGCTGTGGAA	1	O	0	0	0	0	0
9179	4070	an	AN6823.1	71.m15293	AO070314000102	1	-211	-173					ATGCCGCAGTGGGCATCCATGGCTCCGCTCCGTGTTTGA	ATGCCGCAGTGGGCATCCATGGCTCCGCTCCGTGTTTGA			MPQWASMAPLRV*	MPQWASMAPLRV*			TCCTGTGCAT	TATACATACA	0		0	0	0	0	0
9180	4070	an	AN6823.1	71.m15293	AO070314000102	1	-193	-173					ATGGCTCCGCTCCGTGTTTGA	ATGGCTCCGCTCCGTGTTTGA			MAPLRV*	MAPLRV*			GTGGGCATCC	TATACATACA	0		0	0	0	0	0
9181	4070	af	AN6823.1	71.m15293	AO070314000102	1			-257	-228			ATGACTACTCGGCTTGGTACCTTGCCATGA		ATGACTACTCGGCTTGGTACCTTGCCATGA		MTTRLGTLP*		MTTRLGTLP*		TCCTCCTGCA	GCGCCCTGTG	0		0	0	0	0	0
9182	4070	af	AN6823.1	71.m15293	AO070314000102	1			-231	-217			ATGAGCGCCCTGTGA		ATGAGCGCCCTGTGA		MSAL*		MSAL*		GTACCTTGCC	CCCCTTGTGT	0		0	0	0	0	0
9183	4070	af	AN6823.1	71.m15293	AO070314000102	1			-197	-78			ATGACGAGTTCTCGATCTCTGACCTTTATTGTGCATCTTACTGCAGCCATCCATGGATTTCAATCTACCTCCATCTGTCATATAACCTACACTCTACTTGTTCCTCTTTCGCCATTATAA		ATGACGAGTTCTCGATCTCTGACCTTTATTGTGCATCTTACTGCAGCCATCCATGGATTTCAATCTACCTCCATCTGTCATATAACCTACACTCTACTTGTTCCTCTTTCGCCATTATAA		MTSSRSLTFIVHLTAAIHGFQSTSICHITYTLLVPLSPL*		MTSSRSLTFIVHLTAAIHGFQSTSICHITYTLLVPLSPL*		TCATCTTTAT	CCGACACCTC	0		0	0	0	0	0
9184	4070	af	AN6823.1	71.m15293	AO070314000102	1			-145	-113			ATGGATTTCAATCTACCTCCATCTGTCATATAA		ATGGATTTCAATCTACCTCCATCTGTCATATAA		MDFNLPPSVI*		MDFNLPPSVI*		GCAGCCATCC	CCTACACTCT	0		0	0	0	0	0
9185	4070	ao	AN6823.1	71.m15293	AO070314000102	1					-350	-333	ATGGATCCTATGGATTGA			ATGGATCCTATGGATTGA	MDPMD*			MDPMD*	CCTTCCCTTC	CTTCCCCCGT	0		0	0	0	0	0
9186	4070	ao	AN6823.1	71.m15293	AO070314000102	1					-274	-239	ATGGAAAAGTCCCGATCTTTATTACAGATCCTTTGA			ATGGAAAAGTCCCGATCTTTATTACAGATCCTTTGA	MEKSRSLLQIL*			MEKSRSLLQIL*	TCATCTTTGA	TCCTTTGCAT	0		0	0	0	0	0
9187	4070	ao	AN6823.1	71.m15293	AO070314000102	1					-207	-187	ATGGGGCTTATCCGCACTTGA			ATGGGGCTTATCCGCACTTGA	MGLIRT*			MGLIRT*	GCAGTCACCC	TATTCCATAC	0		0	0	0	0	0
9188	4070	ao	AN6823.1	71.m15293	AO070314000102	1					-114	-70	ATGTATGTTCACATCTACCATCTCACCCCTCTCAACCCAAACTGA			ATGTATGTTCACATCTACCATCTCACCCCTCTCAACCCAAACTGA	MYVHIYHLTPLNPN*			MYVHIYHLTPLNPN*	TCATACAAAT	TTATCTCTCC	0		0	0	0	0	0
9191	4072	ao	AN2312.1	71.m15515	AO070323000042	0					-46	-23	ATGAGAGCAAGTTCATTCAGATAG			ATGAGAGCAAGTTCATTCAGATAG	MRASSFR*			MRASSFR*	CGGTTTCTGC	TACCGAGTAT	1	R	0	0	0	0	0
9193	4076	conserved	AN1168.1	70.m15052	AO070331000162	0	-37	-20	-37	-20	-37	-20	ATGTCTrCmTTCGGyTAG	ATGTCTGCATTCGGCTAG	ATGTCTACATTCGGCTAG	ATGTCTGCCTTCGGTTAG	MSaFG*	MSAFG*	MSTFG*	MSAFG*	GCrGyyTGCr	ysvAyyrwwy	1	PT	FG01364.1	0	0	YGR217W	YGR217W

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
9202	4079	af	AN4901.1	59.m08801	AO070338000047	0			-58	-47			ATGCGGATTTGA		ATGCGGATTTGA		MRI*		MRI*		CTTTCTCTGC	TTGTAGACCT	1		0	0	0	0	0
9231	4086	an	AN7781.1	57.m05368	AO070343000355	0	-51	-7					ATGACCAGATCCCATTTCTGCCCAATTGAGCTAGACCCTGAATAA	ATGACCAGATCCCATTTCTGCCCAATTGAGCTAGACCCTGAATAA			MTRSHFCPIELDPE*	MTRSHFCPIELDPE*			ATGAGTTCGA	AGCAAAATGA	1		0	0	0	0	0
9291	4111	an	AN0055.1	71.m15326	AO070314000132	1	-306	-268					ATGTGGACCCCAGGTTGCAAAGAGGAACGATGGGCCTAG	ATGTGGACCCCAGGTTGCAAAGAGGAACGATGGGCCTAG			MWTPGCKEERWA*	MWTPGCKEERWA*			GGACCGTCTA	GGCACGGCTG	0		0	0	0	0	0
9292	4111	an	AN0055.1	71.m15326	AO070314000132	1	-277	-215					ATGGGCCTAGGGCACGGCTGGAAAGCCCGATGCAGGCCAACCCTCTGGGAAATGTCTCGTTAG	ATGGGCCTAGGGCACGGCTGGAAAGCCCGATGCAGGCCAACCCTCTGGGAAATGTCTCGTTAG			MGLGHGWKARCRPTLWEMSR*	MGLGHGWKARCRPTLWEMSR*			AAGAGGAACG	CTAAACCAGA	0		0	0	0	0	0
9293	4111	an	AN0055.1	71.m15326	AO070314000132	1	-248	-117					ATGCAGGCCAACCCTCTGGGAAATGTCTCGTTAGCTAAACCAGATGGCGCTATGCATTCAAAAGACTCATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA	ATGCAGGCCAACCCTCTGGGAAATGTCTCGTTAGCTAAACCAGATGGCGCTATGCATTCAAAAGACTCATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA			MQANPLGNVSLAKPDGAMHSKDSCILHGTPDIPMVGLVLYSSV*	MQANPLGNVSLAKPDGAMHSKDSCILHGTPDIPMVGLVLYSSV*			GGAAAGCCCG	GTGCAAGCCA	0		0	0	0	0	0
9294	4111	an	AN0055.1	71.m15326	AO070314000132	1	-226	-215					ATGTCTCGTTAG	ATGTCTCGTTAG			MSR*	MSR*			CCTCTGGGAA	CTAAACCAGA	0		0	0	0	0	0
9295	4111	an	AN0055.1	71.m15326	AO070314000132	1	-197	-117					ATGCATTCAAAAGACTCATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA	ATGCATTCAAAAGACTCATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA			MHSKDSCILHGTPDIPMVGLVLYSSV*	MHSKDSCILHGTPDIPMVGLVLYSSV*			AGATGGCGCT	GTGCAAGCCA	0		0	0	0	0	0
9296	4111	an	AN0055.1	71.m15326	AO070314000132	1	-180	-124					ATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAG	ATGCATCCTGCATGGAACGCCAGACATCCCAATGGTTGGCTTGGTCCTGTATTCTAG			MHPAWNARHPNGWLGPVF*	MHPAWNARHPNGWLGPVF*			CAAAAGACTC	TGTATGAGTG	0		0	0	0	0	0
9297	4111	an	AN0055.1	71.m15326	AO070314000132	1	-149	-117					ATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA	ATGGTTGGCTTGGTCCTGTATTCTAGTGTATGA			MVGLVLYSSV*	MVGLVLYSSV*			AGACATCCCA	GTGCAAGCCA	0		0	0	0	0	0
9298	4111	an	AN0055.1	71.m15326	AO070314000132	1	-120	-34					ATGAGTGCAAGCCACACATCGCTGCTCTTCACCACTTACCTCACCCATTTCACTGCTACACCATACGACCCATATATCCTCTGTTGA	ATGAGTGCAAGCCACACATCGCTGCTCTTCACCACTTACCTCACCCATTTCACTGCTACACCATACGACCCATATATCCTCTGTTGA			MSASHTSLLFTTYLTHFTATPYDPYILC*	MSASHTSLLFTTYLTHFTATPYDPYILC*			ATTCTAGTGT	CTCGAGGTGT	0		0	0	0	0	0
9299	4111	af	AN0055.1	71.m15326	AO070314000132	1			-264	-193			ATGCATGCGGCACAGTGCCATAGCGGATGCCACGAACTTTACGAATGGCCTAGAGACTATTCGATTGTCTAA		ATGCATGCGGCACAGTGCCATAGCGGATGCCACGAACTTTACGAATGGCCTAGAGACTATTCGATTGTCTAA		MHAAQCHSGCHELYEWPRDYSIV*		MHAAQCHSGCHELYEWPRDYSIV*		GCCGAGGTCC	TGTAGGTGCA	0		0	0	0	0	0
9300	4111	af	AN0055.1	71.m15326	AO070314000132	1			-260	-168			ATGCGGCACAGTGCCATAGCGGATGCCACGAACTTTACGAATGGCCTAGAGACTATTCGATTGTCTAATGTAGGTGCACAGTTCGGGCAATAG		ATGCGGCACAGTGCCATAGCGGATGCCACGAACTTTACGAATGGCCTAGAGACTATTCGATTGTCTAATGTAGGTGCACAGTTCGGGCAATAG		MRHSAIADATNFTNGLETIRLSNVGAQFGQ*		MRHSAIADATNFTNGLETIRLSNVGAQFGQ*		AGGTCCATGC	CTCCATCTGG	0		0	0	0	0	0
9301	4111	af	AN0055.1	71.m15326	AO070314000132	1			-238	-212			ATGCCACGAACTTTACGAATGGCCTAG		ATGCCACGAACTTTACGAATGGCCTAG		MPRTLRMA*		MPRTLRMA*		GCCATAGCGG	AGACTATTCG	0		0	0	0	0	0
9302	4111	ao	AN0055.1	71.m15326	AO070314000132	1					-324	-268	ATGGTCCCTTTGTCTAATGTACGATCACGCTTTAGGAAAGAGAGAGAAGATGCCTGA			ATGGTCCCTTTGTCTAATGTACGATCACGCTTTAGGAAAGAGAGAGAAGATGCCTGA	MVPLSNVRSRFRKEREDA*			MVPLSNVRSRFRKEREDA*	CTATCAAGCG	GGGGAAGCGA	0		0	0	0	0	0
9303	4111	ao	AN0055.1	71.m15326	AO070314000132	1					-308	-213	ATGTACGATCACGCTTTAGGAAAGAGAGAGAAGATGCCTGAGGGGAAGCGACATCATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGA			ATGTACGATCACGCTTTAGGAAAGAGAGAGAAGATGCCTGAGGGGAAGCGACATCATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGA	MYDHALGKREKMPEGKRHHVPTQKAACALHH*			MYDHALGKREKMPEGKRHHVPTQKAACALHH*	CCTTTGTCTA	TTGATTGAGC	0		0	0	0	0	0
9304	4111	ao	AN0055.1	71.m15326	AO070314000132	1					-275	-213	ATGCCTGAGGGGAAGCGACATCATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGA			ATGCCTGAGGGGAAGCGACATCATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGA	MPEGKRHHVPTQKAACALHH*			MPEGKRHHVPTQKAACALHH*	GAGAGAGAAG	TTGATTGAGC	0		0	0	0	0	0
9305	4111	ao	AN0055.1	71.m15326	AO070314000132	1					-253	-209	ATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGATTGA			ATGTGCCAACTCAAAAGGCTGCATGTGCCCTGCATCATTGATTGA	MCQLKRLHVPCIID*			MCQLKRLHVPCIID*	AAGCGACATC	TTGAGCTTCA	0		0	0	0	0	0
9306	4111	ao	AN0055.1	71.m15326	AO070314000132	1					-231	-205	ATGTGCCCTGCATCATTGATTGATTGA			ATGTGCCCTGCATCATTGATTGATTGA	MCPASLID*			MCPASLID*	AAAAGGCTGC	GCTTCACAAG	0		0	0	0	0	0
9330	4117	af	AN6597.1	62.m03201	AO070326000046	0			-31	-17			ATGATCTTGCGGTAG		ATGATCTTGCGGTAG		MILR*		MILR*		GCTCTCTCGA	CCCCAACTCT	1	R	0	0	0	0	0
9334	4117	ao	AN6597.1	62.m03201	AO070326000046	0					-53	-15	ATGTTTCCCACACTGTCTTTCCTTGGACAAACTCCATAA			ATGTTTCCCACACTGTCTTTCCTTGGACAAACTCCATAA	MFPTLSFLGQTP*			MFPTLSFLGQTP*	CACCTGCTCC	TCGTTCTCTT	1	R	0	0	0	0	0
9362	4122	af	AN3018.1	59.m08991	AO070337000096	0			-54	-37			ATGGGCGTTCAGAAGTAG		ATGGGCGTTCAGAAGTAG		MGVQK*		MGVQK*		AAAAACTTGT	CAAAATTAAA	1	E	0	MG03562.1	0	0	0
9380	4128	an	AN2148.1	72.m19693	AO070343000197	0	-42	-22					ATGTATAATGTCGTTGTATGA	ATGTATAATGTCGTTGTATGA			MYNVVV*	MYNVVV*			ATCCTTGCGA	TTGTTTTGTT	1	S	0	0	0	0	0
9382	4128	af	AN2148.1	72.m19693	AO070343000197	1			-27	-7			ATGTCTTTCGTTTGCCTATAA		ATGTCTTTCGTTTGCCTATAA		MSFVCL*		MSFVCL*		ATGCCTTTGT	CCCACAATGG	1	S	0	0	0	0	0
9385	4128	ao	AN2148.1	72.m19693	AO070343000197	0					-34	-8	ATGTCTCTGTCTGCCTGCTTCTCTTGA			ATGTCTCTGTCTGCCTGCTTCTCTTGA	MSLSACFS*			MSLSACFS*	TTCCTGTAGA	TGGCACAATG	1	S	0	0	0	0	0
9389	4130	an	AN5902.1	72.m19228	AO070248000040	0	-17	-6					ATGGTCCATTGA	ATGGTCCATTGA			MVH*	MVH*			GCACCTTTGA	GAACTATGAA	1	OKIT	0	0	0	0	0
9400	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-58	-26	ATGATTCTACTCTTTACTTTAATTCCAGCTTGA			ATGATTCTACTCTTTACTTTAATTCCAGCTTGA	MILLFTLIPA*			MILLFTLIPA*	CACTGACTCC	TGGTCAATTA	1	OKIT	0	0	0	0	0
9401	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-26	-15	ATGGTCAATTAG			ATGGTCAATTAG	MVN*			MVN*	TTCCAGCTTG	CCCAAATCAA	1	OKIT	0	0	0	0	0
9404	4132	an	AN7652.1	57.m05411	AO070268000009	0	-41	-12					ATGCTTCTGGAAACCGACACTGCCTTTTAA	ATGCTTCTGGAAACCGACACTGCCTTTTAA			MLLETDTAF*	MLLETDTAF*			AAACCACTAC	ACAAGCCCTC	1	L	0	0	0	0	0
9411	4132	ao	AN7652.1	57.m05411	AO070268000009	0					-56	-21	ATGAATCTCATTGACACGAAACTAATGCTTATATGA			ATGAATCTCATTGACACGAAACTAATGCTTATATGA	MNLIDTKLMLI*			MNLIDTKLMLI*	AGGAACACAC	ATACCAAGGA	1	L	0	0	0	0	0
9412	4132	ao	AN7652.1	57.m05411	AO070268000009	0					-32	-21	ATGCTTATATGA			ATGCTTATATGA	MLI*			MLI*	CACGAAACTA	ATACCAAGGA	1	L	0	0	0	0	0
9422	4135	ao	AN6345.1	72.m19510	AO070275000008	0					-50	-39	ATGGCCACATGA			ATGGCCACATGA	MAT*			MAT*	AATCCAGGGG	AACGTACTGT	1	I	FG02055.1	0	0	0	0
9423	4135	ao	AN6345.1	72.m19510	AO070275000008	0					-42	-4	ATGAAACGTACTGTGATCGCAACACCACACCGTCGTTGA			ATGAAACGTACTGTGATCGCAACACCACACCGTCGTTGA	MKRTVIATPHRR*			MKRTVIATPHRR*	GGATGGCCAC	AACATGGAGA	1	I	FG02055.1	0	0	0	0
9451	4144	an	AN4557.1	57.m05569	AO070321000171	1	-92	-69					ATGGCTTGCTGTGCTAGATTATAA	ATGGCTTGCTGTGCTAGATTATAA			MACCARL*	MACCARL*			GAGGGCTTCC	ACTCTATATA	0	O	0	0	0	0	0
9453	4144	af	AN4557.1	57.m05569	AO070321000171	1			-83	-54			ATGGCTTCTGCGGACTTTTTTTCTAACTGA		ATGGCTTCTGCGGACTTTTTTTCTAACTGA		MASADFFSN*		MASADFFSN*		TAGAGCCTCT	AGTGAGCCTA	0	O	0	0	0	0	0
9455	4144	ao	AN4557.1	57.m05569	AO070321000171	1					-83	-54	ATGGATTCGGCAGTCTGCCATTGTCCCTGA			ATGGATTCGGCAGTCTGCCATTGTCCCTGA	MDSAVCHCP*			MDSAVCHCP*	GAGGACTTAT	ATCTCGATTG	0	O	0	0	0	0	0
9460	4147	af	AN6598.1	62.m03431	AO070326000047	0			-33	-19			ATGGGTAATGCCTGA		ATGGGTAATGCCTGA		MGNA*		MGNA*		TACATTATTG	CAGAGCCCGT	1	S	0	0	0	0	0
9480	4152	an	AN6087.1	72.m19077	AO070340000139	1	-205	-188					ATGCGCTGGATGAATTAA	ATGCGCTGGATGAATTAA			MRWMN*	MRWMN*			CAACTACCCA	GATAGGAATT	0	C	0	0	0	0	0
9481	4155	an	AN3928.1	69.m15000	AO070341000038	1	-284	-24					ATGAATAGCCTTTGGCTGGCATTCAATTCAATCATCAAGGTATCTCAGGTAATGTCTGGGCGTGGCCGGTGTTCGTTCTTATCCTTAGCATATCCCTACCTCAACTGTACTGGCCTTTATCCAGCGTTGAAGGGGACTGCCAAAGGCTCTGGGTTCGTTCTGAGAATATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTTGCCTCTTCCTATAGTTAGTGGAATGGCTAACAGTCTATAG	ATGAATAGCCTTTGGCTGGCATTCAATTCAATCATCAAGGTATCTCAGGTAATGTCTGGGCGTGGCCGGTGTTCGTTCTTATCCTTAGCATATCCCTACCTCAACTGTACTGGCCTTTATCCAGCGTTGAAGGGGACTGCCAAAGGCTCTGGGTTCGTTCTGAGAATATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTTGCCTCTTCCTATAGTTAGTGGAATGGCTAACAGTCTATAG			MNSLWLAFNSIIKVSQVMSGRGRCSFLSLAYPYLNCTGLYPALKGTAKGSGFVLRIYGQNLIWIIPAKGSCLPLPLPIVSGMANSL*	MNSLWLAFNSIIKVSQVMSGRGRCSFLSLAYPYLNCTGLYPALKGTAKGSGFVLRIYGQNLIWIIPAKGSCLPLPLPIVSGMANSL*			TACGGAAGTC	TCGAACCATT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
9482	4155	an	AN3928.1	69.m15000	AO070341000038	1	-233	-24					ATGTCTGGGCGTGGCCGGTGTTCGTTCTTATCCTTAGCATATCCCTACCTCAACTGTACTGGCCTTTATCCAGCGTTGAAGGGGACTGCCAAAGGCTCTGGGTTCGTTCTGAGAATATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTTGCCTCTTCCTATAGTTAGTGGAATGGCTAACAGTCTATAG	ATGTCTGGGCGTGGCCGGTGTTCGTTCTTATCCTTAGCATATCCCTACCTCAACTGTACTGGCCTTTATCCAGCGTTGAAGGGGACTGCCAAAGGCTCTGGGTTCGTTCTGAGAATATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTTGCCTCTTCCTATAGTTAGTGGAATGGCTAACAGTCTATAG			MSGRGRCSFLSLAYPYLNCTGLYPALKGTAKGSGFVLRIYGQNLIWIIPAKGSCLPLPLPIVSGMANSL*	MSGRGRCSFLSLAYPYLNCTGLYPALKGTAKGSGFVLRIYGQNLIWIIPAKGSCLPLPLPIVSGMANSL*			ATCTCAGGTA	TCGAACCATT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9483	4155	an	AN3928.1	69.m15000	AO070341000038	1	-75	-46					ATGCCTTCCCTTGCCTCTTCCTATAGTTAG	ATGCCTTCCCTTGCCTCTTCCTATAGTTAG			MPSLASSYS*	MPSLASSYS*			CGAAAGGATC	TGGAATGGCT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9484	4155	an	AN3928.1	69.m15000	AO070341000038	1	-41	-24					ATGGCTAACAGTCTATAG	ATGGCTAACAGTCTATAG			MANSL*	MANSL*			AGTTAGTGGA	TCGAACCATT	1	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9485	4155	af	AN3928.1	69.m15000	AO070341000038	1			-301	-167			ATGGAAGCCATGGAATCACTTTGGCTGGGCTGTTCATTCAATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAA		ATGGAAGCCATGGAATCACTTTGGCTGGGCTGTTCATTCAATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAA		MEAMESLWLGCSFNDQGISGKSWAWAGVRSHSLAQQRLSLFRSS*		MEAMESLWLGCSFNDQGISGKSWAWAGVRSHSLAQQRLSLFRSS*		TTTTCTATCG	CTCTTGACTG	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9486	4155	af	AN3928.1	69.m15000	AO070341000038	1			-292	-167			ATGGAATCACTTTGGCTGGGCTGTTCATTCAATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAA		ATGGAATCACTTTGGCTGGGCTGTTCATTCAATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAA		MESLWLGCSFNDQGISGKSWAWAGVRSHSLAQQRLSLFRSS*		MESLWLGCSFNDQGISGKSWAWAGVRSHSLAQQRLSLFRSS*		GATGGAAGCC	CTCTTGACTG	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9487	4155	af	AN3928.1	69.m15000	AO070341000038	1			-261	-160			ATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAACTCTTGA		ATGATCAAGGTATCTCAGGTAAATCTTGGGCGTGGGCCGGTGTTCGTTCTCATTCATTGGCACAACAACGTTTATCTCTTTTTCGGAGCTCGTAACTCTTGA		MIKVSQVNLGRGPVFVLIHWHNNVYLFFGARNS*		MIKVSQVNLGRGPVFVLIHWHNNVYLFFGARNS*		TGTTCATTCA	CTGGAGTGCA	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9488	4155	af	AN3928.1	69.m15000	AO070341000038	1			-128	-18			ATGGATGGGTTCGTTCTGAGATTATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTCCGTTCTGTGTTGTCCACGTTCGTGGAATAGCTAA		ATGGATGGGTTCGTTCTGAGATTATACGGTCAAAACTTGATCTGGATAATACCAGCGAAAGGATCATGCCTTCCCTCCGTTCTGTGTTGTCCACGTTCGTGGAATAGCTAA		MDGFVLRLYGQNLIWIIPAKGSCLPSVLCCPRSWNS*		MDGFVLRLYGQNLIWIIPAKGSCLPSVLCCPRSWNS*		CACGGTGCCA	CCAGTTACAG	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9489	4155	af	AN3928.1	69.m15000	AO070341000038	1			-124	-110			ATGGGTTCGTTCTGA		ATGGGTTCGTTCTGA		MGSF*		MGSF*		GTGCCAATGG	GATTATACGG	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9490	4155	af	AN3928.1	69.m15000	AO070341000038	1			-63	-22			ATGCCTTCCCTCCGTTCTGTGTTGTCCACGTTCGTGGAATAG		ATGCCTTCCCTCCGTTCTGTGTTGTCCACGTTCGTGGAATAG		MPSLRSVLSTFVE*		MPSLRSVLSTFVE*		CGAAAGGATC	CTAACCAGTT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9491	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-299	-180	ATGGAAGTCATGGAATACTTTTGGCTGGACTCTCACAATGATCAAGGTATCTTAGGTAACGTCTTTGGCGTGGGCCGGTGTTCGTTCCCAGTCATCGATGCATTCACATGCCCTCCCTAA			ATGGAAGTCATGGAATACTTTTGGCTGGACTCTCACAATGATCAAGGTATCTTAGGTAACGTCTTTGGCGTGGGCCGGTGTTCGTTCCCAGTCATCGATGCATTCACATGCCCTCCCTAA	MEVMEYFWLDSHNDQGILGNVFGVGRCSFPVIDAFTCPP*			MEVMEYFWLDSHNDQGILGNVFGVGRCSFPVIDAFTCPP*	AGGGCATACG	GCTGGGCCCT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9492	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-290	-180	ATGGAATACTTTTGGCTGGACTCTCACAATGATCAAGGTATCTTAGGTAACGTCTTTGGCGTGGGCCGGTGTTCGTTCCCAGTCATCGATGCATTCACATGCCCTCCCTAA			ATGGAATACTTTTGGCTGGACTCTCACAATGATCAAGGTATCTTAGGTAACGTCTTTGGCGTGGGCCGGTGTTCGTTCCCAGTCATCGATGCATTCACATGCCCTCCCTAA	MEYFWLDSHNDQGILGNVFGVGRCSFPVIDAFTCPP*			MEYFWLDSHNDQGILGNVFGVGRCSFPVIDAFTCPP*	GATGGAAGTC	GCTGGGCCCT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9493	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-262	-245	ATGATCAAGGTATCTTAG			ATGATCAAGGTATCTTAG	MIKVS*			MIKVS*	GACTCTCACA	GTAACGTCTT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9494	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-202	-161	ATGCATTCACATGCCCTCCCTAAGCTGGGCCCTAGACTCTAG			ATGCATTCACATGCCCTCCCTAAGCTGGGCCCTAGACTCTAG	MHSHALPKLGPRL*			MHSHALPKLGPRL*	CCAGTCATCG	GATCCTAGTC	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9495	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-192	-148	ATGCCCTCCCTAAGCTGGGCCCTAGACTCTAGGATCCTAGTCTAG			ATGCCCTCCCTAAGCTGGGCCCTAGACTCTAGGATCCTAGTCTAG	MPSLSWALDSRILV*			MPSLSWALDSRILV*	ATGCATTCAC	AAGGACATGG	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9496	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-141	-40	ATGGCATCGATGGACTGGGTTCGTTCTGAGATTATACGGCTAAAACTTGATCTGGATAATACCAGCGAAAAGGATCATGCCTTCTCTCGTTCTTCCTGTTGA			ATGGCATCGATGGACTGGGTTCGTTCTGAGATTATACGGCTAAAACTTGATCTGGATAATACCAGCGAAAAGGATCATGCCTTCTCTCGTTCTTCCTGTTGA	MASMDWVRSEIIRLKLDLDNTSEKDHAFSRSSC*			MASMDWVRSEIIRLKLDLDNTSEKDHAFSRSSC*	CTAGAAGGAC	TGGAATGGCT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9497	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-132	-40	ATGGACTGGGTTCGTTCTGAGATTATACGGCTAAAACTTGATCTGGATAATACCAGCGAAAAGGATCATGCCTTCTCTCGTTCTTCCTGTTGA			ATGGACTGGGTTCGTTCTGAGATTATACGGCTAAAACTTGATCTGGATAATACCAGCGAAAAGGATCATGCCTTCTCTCGTTCTTCCTGTTGA	MDWVRSEIIRLKLDLDNTSEKDHAFSRSSC*			MDWVRSEIIRLKLDLDNTSEKDHAFSRSSC*	CATGGCATCG	TGGAATGGCT	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9498	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-65	-21	ATGCCTTCTCTCGTTCTTCCTGTTGATGGAATGGCTAACAGATGA			ATGCCTTCTCTCGTTCTTCCTGTTGATGGAATGGCTAACAGATGA	MPSLVLPVDGMANR*			MPSLVLPVDGMANR*	GAAAAGGATC	TAGTCATTGC	0	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9499	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-35	-21	ATGGCTAACAGATGA			ATGGCTAACAGATGA	MANR*			MANR*	TGTTGATGGA	TAGTCATTGC	1	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9500	4155	ao	AN3928.1	69.m15000	AO070341000038	1					-24	-4	ATGATAGTCATTGCAACTTGA			ATGATAGTCATTGCAACTTGA	MIVIAT*			MIVIAT*	TGGCTAACAG	AACATGTCTC	1	R	FG02469.1	MG03098.1	NCU06110.1	0	0
9524	4160	af	AN8165.1	53.m03816	AO070266000010	0			-55	-41			ATGCGCCATTCATAG		ATGCGCCATTCATAG		MRHS*		MRHS*		CATAACTGCT	CGATCTGTAT	1	A	0	0	0	0	0
9553	4172	af	AN7733.1	71.m15761	AO070325000151	0			-37	-17			ATGCTTAGCACAGGTATCTAG		ATGCTTAGCACAGGTATCTAG		MLSTGI*		MLSTGI*		TCACTCTCTC	ACTCCAACAT	1	E	0	0	0	YJR062C	0
9564	4179	an	AN1052.1	70.m15191	AO070336000059	0	-24	-7					ATGCAACAAGTCTTCTAG	ATGCAACAAGTCTTCTAG			MQQVF*	MQQVF*			CTAACAAGGA	AGCATTTTGT	1	WV	0	0	0	0	0
9565	4179	af	AN1052.1	70.m15191	AO070336000059	1			-347	-264			ATGTTTCTCTATCTTCTTTTCCTTACACTTTTCTTCCATCGAATATTTCCCCAGGCTTTATACGTCAGCCAACTGACTACCTAG		ATGTTTCTCTATCTTCTTTTCCTTACACTTTTCTTCCATCGAATATTTCCCCAGGCTTTATACGTCAGCCAACTGACTACCTAG		MFLYLLFLTLFFHRIFPQALYVSQLTT*		MFLYLLFLTLFFHRIFPQALYVSQLTT*		CCCTTGTTCT	TCCGTCATCC	0	WV	0	0	0	0	0
9566	4179	af	AN1052.1	70.m15191	AO070336000059	1			-199	-179			ATGCACGTTCCGGGTCGTTGA		ATGCACGTTCCGGGTCGTTGA		MHVPGR*		MHVPGR*		AGCTAGCTTG	TATTATAAGA	0	WV	0	0	0	0	0
9602	4189	af	AN6443.1	58.m08930	AO070238000002	0			-54	-34			ATGATGGTGTCGGAAATTTAA		ATGATGGTGTCGGAAATTTAA		MMVSEI*		MMVSEI*		GTTTCGATAC	TGTCATTTCA	1	Q	0	0	0	YGR281W	0
9603	4189	af	AN6443.1	58.m08930	AO070238000002	0			-51	-34			ATGGTGTCGGAAATTTAA		ATGGTGTCGGAAATTTAA		MVSEI*		MVSEI*		TCGATACATG	TGTCATTTCA	1	Q	0	0	0	YGR281W	0
9609	4192	ao	AN5776.1	69.m14821	AO070249000021	0					-52	-23	ATGTTTGACAACAGAATTGACGTAACATAG			ATGTTTGACAACAGAATTGACGTAACATAG	MFDNRIDVT*			MFDNRIDVT*	CACATTGACC	CTTATTCGTA	1	B	0	0	0	0	0
9613	4193	ao	AN8742.1	62.m03338	AO070250000039	0					-55	-29	ATGAATACCAGATGCGCCCGGGCCTAA			ATGAATACCAGATGCGCCCGGGCCTAA	MNTRCARA*			MNTRCARA*	ATATTTATCC	CAAGAAGCCA	1	BDL	0	0	0	0	0
9632	4199	af	AN0869.1	70.m15458	AO070320000020	0			-17	-3			ATGTCTCGCCGATAA		ATGTCTCGCCGATAA		MSRR*		MSRR*		TTTGGGATTA	AAATGTCTTC	1		0	0	0	0	0
9640	4201	ao	AN3909.1	69.m15021	AO070324000094	0					-24	-7	ATGAGAACCGGTCTCTAG			ATGAGAACCGGTCTCTAG	MRTGL*			MRTGL*	GGTCAGTATC	CCCATCATGG	1	L	0	0	0	0	0
9668	4206	af	AN2239.1	71.m15830	AO070326000142	0			-49	-14			ATGGTAACAATCCTGCCCCGCGCAGCAATTGTATGA		ATGGTAACAATCCTGCCCCGCGCAGCAATTGTATGA		MVTILPRAAIV*		MVTILPRAAIV*		AGGGGCAGAT	CTTATATCCC	1	C	0	0	0	0	0
9672	4206	ao	AN2239.1	71.m15830	AO070326000142	0					-58	-14	ATGGAGGGGTTATCAAACCCCAATACAAGACGAGCAGCGCGGTAA			ATGGAGGGGTTATCAAACCCCAATACAAGACGAGCAGCGCGGTAA	MEGLSNPNTRRAAR*			MEGLSNPNTRRAAR*	AACCGCAAAA	AAGCACCTGC	1	C	0	0	0	0	0
9680	4208	af	AN9066.1	66.m04520	AO070332000218	1			-78	-58			ATGCCTTTCTATCCGACTTAA		ATGCCTTTCTATCCGACTTAA		MPFYPT*		MPFYPT*		GAGAAAACAA	CTGAAGGTCG	0	C	FG00706.1	0	0	0	0
9717	4224	af	AN0854.1	70.m15453	AO070320000001	1			-266	-246			ATGCTTTTGTACAAGCCGTGA		ATGCTTTTGTACAAGCCGTGA		MLLYKP*		MLLYKP*		CAGTCCTGTA	GTGAGTGCGC	0	A	0	0	0	0	0
9723	4228	an	AN2757.1	59.m09254	AO070327000036	0	-51	-16					ATGGTCGTCGCGAAATCCTCGCTAAAACGGGTTTGA	ATGGTCGTCGCGAAATCCTCGCTAAAACGGGTTTGA			MVVAKSSLKRV*	MVVAKSSLKRV*			GCGGCAGCCG	TTGAACGGGC	1	R	0	0	0	0	0
9725	4228	ao	AN2757.1	59.m09254	AO070327000036	0					-44	-15	ATGATGGACCTTTCGATGTTGCTATTGTGA			ATGATGGACCTTTCGATGTTGCTATTGTGA	MMDLSMLLL*			MMDLSMLLL*	TCATATCCTC	TTGACCGGCT	1	R	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
9726	4228	ao	AN2757.1	59.m09254	AO070327000036	0					-29	-15	ATGTTGCTATTGTGA			ATGTTGCTATTGTGA	MLLL*			MLLL*	GGACCTTTCG	TTGACCGGCT	1	R	0	0	0	0	0
9739	4234	an	AN3038.1	59.m08979	AO070337000055	1	-59	-42					ATGCCCCTCGAGCAATGA	ATGCCCCTCGAGCAATGA			MPLEQ*	MPLEQ*			CAGCGCTACC	TCAAGAGGTC	1		0	0	0	0	0
9740	4234	af	AN3038.1	59.m08979	AO070337000055	1			-398	-384			ATGGTGGGAAAATGA		ATGGTGGGAAAATGA		MVGK*		MVGK*		CGCTGAAACC	TGAGGTCTGC	0		0	0	0	0	0
9753	4240	an	AN1408.1	55.m02915	AO070242000011	0	-57	-40					ATGCACTACCGACATTGA	ATGCACTACCGACATTGA			MHYRH*	MHYRH*			AGAAAAAGTA	GAGCTTTGGT	1	J	0	0	0	0	0
9754	4240	ao	AN1408.1	55.m02915	AO070242000011	0					-59	-21	ATGCGACAGCTCACTGGTGACAAGTTTTTGGCAGCTTGA			ATGCGACAGCTCACTGGTGACAAGTTTTTGGCAGCTTGA	MRQLTGDKFLAA*			MRQLTGDKFLAA*	ACAAAAAGAG	ACCACCTTTC	1	J	0	0	0	0	0
9774	4244	an	AN0576.1	69.m15269	AO070272000056	0	-49	-35					ATGATTGTTTTATGA	ATGATTGTTTTATGA			MIVL*	MIVL*			TTTCCTAAAC	ACCTATTCTT	1	T	FG05306.1	MG06100.1	0	0	0
9775	4244	an	AN0576.1	69.m15269	AO070272000056	0	-38	-21					ATGAACCTATTCTTATGA	ATGAACCTATTCTTATGA			MNLFL*	MNLFL*			TGATTGTTTT	AATGAAGACG	1	T	FG05306.1	MG06100.1	0	0	0
9779	4244	af	AN0576.1	69.m15269	AO070272000056	0			-50	-21			ATGAAATTCATTGTTCTTGTTAGCTCTTGA		ATGAAATTCATTGTTCTTGTTAGCTCTTGA		MKFIVLVSS*		MKFIVLVSS*		CTCTTAGTGG	GATGAGGTCG	1	T	FG05306.1	MG06100.1	0	0	0
9803	4248	af	AN1669.1	58.m07734	AO070299000051	0			-53	-12			ATGTTATGGTTTTATCTCCCCCTATATAAGATAGATACCTGA		ATGTTATGGTTTTATCTCCCCCTATATAAGATAGATACCTGA		MLWFYLPLYKIDT*		MLWFYLPLYKIDT*		ACAAAGTTCT	AAACCTCTAC	1	RP	0	0	0	0	0
9804	4248	af	AN1669.1	58.m07734	AO070299000051	0			-48	-25			ATGGTTTTATCTCCCCCTATATAA		ATGGTTTTATCTCCCCCTATATAA		MVLSPPI*		MVLSPPI*		GTTCTATGTT	GATAGATACC	1	RP	0	0	0	0	0
9815	4250	af	AN6245.1	72.m19412	AO070304000099	0			-57	-28			ATGCACCTCGCCACAAAATACCCTCTTTAA		ATGCACCTCGCCACAAAATACCCTCTTTAA		MHLATKYPL*		MHLATKYPL*		CACAAAGTAT	GACCCTCACT	1		0	0	0	0	0
9817	4251	af	AN3754.1	65.m07373	AO070309000055	0			-51	-34			ATGCAAACGTCCGGATAA		ATGCAAACGTCCGGATAA		MQTSG*		MQTSG*		TAATTGCGGA	CCGAACGCTG	1	T	0	0	0	0	0
9842	4263	an	AN4322.1	58.m08001	AO070230000013	0	-53	-6					ATGATAGCGAATCTTGTGGCAGATACCCCGAGACTCGGATCGCTTTAA	ATGATAGCGAATCTTGTGGCAGATACCCCGAGACTCGGATCGCTTTAA			MIANLVADTPRLGSL*	MIANLVADTPRLGSL*			AAGAATTACT	CGAAGATGTT	1	T	0	0	0	0	0
9845	4265	ao	AN3433.1	59.m09290	AO070265000008	1					-222	-178	ATGAAGAACAGCTGGAATAATATCACGTACAAGTCCGACTTTTAA			ATGAAGAACAGCTGGAATAATATCACGTACAAGTCCGACTTTTAA	MKNSWNNITYKSDF*			MKNSWNNITYKSDF*	CAGAACGCGA	TTTCCAGTGG	0		0	0	0	0	0
9867	4272	af	AN8202.1	53.m03772	AO070310000115	1			-45	-34			ATGCAAGTCTGA		ATGCAAGTCTGA		MQV*		MQV*		CACACGTTCG	ACTACGTACG	1		0	0	0	0	0
9869	4273	an	AN6859.1	71.m15272	AO070314000076	0	-14						ATGCTCTTGCGATAA	ATGCTCTTGCGATAA			MLLR*	MLLR*			ATCGATATTC	TGTACCACTA	1	AK	0	0	0	0	0
9870	4273	af	AN6859.1	71.m15272	AO070314000076	0			-14				ATGCTTTGGCGATAA		ATGCTTTGGCGATAA		MLWR*		MLWR*		TCGATTTTCC	TGTATCACTA	1	AK	0	0	0	0	0
9881	4277	ao	AN0925.1	70.m15533	AO070320000104	1					-177	-109	ATGACATACTCTTGGCTTGCGGAGGGTTTCTTGCGAACGACGGTATGGACTATTAGTTTCATTGAATAA			ATGACATACTCTTGGCTTGCGGAGGGTTTCTTGCGAACGACGGTATGGACTATTAGTTTCATTGAATAA	MTYSWLAEGFLRTTVWTISFIE*			MTYSWLAEGFLRTTVWTISFIE*	TTTTTTCCTC	TGCAAGCTCG	0	I	0	0	0	0	0
9882	4277	ao	AN0925.1	70.m15533	AO070320000104	1					-133	-122	ATGGACTATTAG			ATGGACTATTAG	MDY*			MDY*	GAACGACGGT	TTTCATTGAA	0	I	0	0	0	0	0
9886	4279	ao	AN8034.1	53.m03883	AO070322000125	0					-60	-10	ATGATCTTATCTTTGCCCCGGTTCTTCACACTCCCTGAATCCCGACTGTAA			ATGATCTTATCTTTGCCCCGGTTCTTCACACTCCCTGAATCCCGACTGTAA	MILSLPRFFTLPESRL*			MILSLPRFFTLPESRL*	TGTTTATGTC	TCCAACGTCA	1	A	0	0	0	0	0
9903	4283	ao	AN4751.1	59.m09234	AO070327000068	0					-50	-27	ATGTTTCTTTTTCTTTTCTCTTAG			ATGTTTCTTTTTCTTTTCTCTTAG	MFLFLFS*			MFLFLFS*	TAACCATTGA	AGGATCGATA	1	R	0	0	0	0	0
9933	4298	ao	AN3051.1	59.m09447	AO070285000008	0					-27	-16	ATGACCAAGTAA			ATGACCAAGTAA	MTK*			MTK*	ATCCATATCA	TATCCATCAT	1		0	0	0	0	0
9957	4308	an	AN2307.1	71.m15512	AO070323000045	1	-451	-440					ATGAATTTATAA	ATGAATTTATAA			MNL*	MNL*			TTAGCAGTAC	CTTTTGGTTT	0		0	0	0	0	0
9958	4308	an	AN2307.1	71.m15512	AO070323000045	1	-316	-248					ATGCGTAAACGCGCCCGAGCCGCTTCGTCCACGATCACCAGAATTACCGCGTCCTTCAGTTCGAACTAA	ATGCGTAAACGCGCCCGAGCCGCTTCGTCCACGATCACCAGAATTACCGCGTCCTTCAGTTCGAACTAA			MRKRARAASSTITRITASFSSN*	MRKRARAASSTITRITASFSSN*			GCGATATTGT	GCGTGCTTAT	0		0	0	0	0	0
9959	4308	an	AN2307.1	71.m15512	AO070323000045	1	-178	-47					ATGCCTACCAAAGATACCAGAACCGCGTCCGGCTTGGGTGCGTCTCCAGAGATCACAGGTCAAAGCTCTCTTCCTAGTACGTCCAACGTACCCTTGATGTCCGTATATATCCACTTGCTAAGGCTTTGTTAG	ATGCCTACCAAAGATACCAGAACCGCGTCCGGCTTGGGTGCGTCTCCAGAGATCACAGGTCAAAGCTCTCTTCCTAGTACGTCCAACGTACCCTTGATGTCCGTATATATCCACTTGCTAAGGCTTTGTTAG			MPTKDTRTASGLGASPEITGQSSLPSTSNVPLMSVYIHLLRLC*	MPTKDTRTASGLGASPEITGQSSLPSTSNVPLMSVYIHLLRLC*			TTGCGTCGCC	TCTCTCGTAT	0		0	0	0	0	0
9960	4308	an	AN2307.1	71.m15512	AO070323000045	1	-82	-47					ATGTCCGTATATATCCACTTGCTAAGGCTTTGTTAG	ATGTCCGTATATATCCACTTGCTAAGGCTTTGTTAG			MSVYIHLLRLC*	MSVYIHLLRLC*			CGTACCCTTG	TCTCTCGTAT	0		0	0	0	0	0
9961	4308	af	AN2307.1	71.m15512	AO070323000045	1			-537	-460			ATGCAAGCATATTCTACATCATTTGCGGAGAACATCTACACGCCGCGCGCTCTTGATTTCTACCCGCACGCGGTGTAG		ATGCAAGCATATTCTACATCATTTGCGGAGAACATCTACACGCCGCGCGCTCTTGATTTCTACCCGCACGCGGTGTAG		MQAYSTSFAENIYTPRALDFYPHAV*		MQAYSTSFAENIYTPRALDFYPHAV*		GTCAAAGCAC	CAGTAATTTC	0		0	0	0	0	0
9962	4308	af	AN2307.1	71.m15512	AO070323000045	1			-179	-159			ATGCCACAGTTACACGAATAA		ATGCCACAGTTACACGAATAA		MPQLHE*		MPQLHE*		AGGGGCTTAC	AGAAAATCAT	0		0	0	0	0	0
9963	4308	ao	AN2307.1	71.m15512	AO070323000045	1					-505	-431	ATGCGTATTTTATCGGCACTGACGCCACGCGCTATATGGATTTCCACGCCGCACGCGCCAGGCTCAATTGCCTAA			ATGCGTATTTTATCGGCACTGACGCCACGCGCTATATGGATTTCCACGCCGCACGCGCCAGGCTCAATTGCCTAA	MRILSALTPRAIWISTPHAPGSIA*			MRILSALTPRAIWISTPHAPGSIA*	AGATAACTAA	CACTTCCTGC	0		0	0	0	0	0
9964	4308	ao	AN2307.1	71.m15512	AO070323000045	1					-470	-408	ATGGATTTCCACGCCGCACGCGCCAGGCTCAATTGCCTAACACTTCCTGCACACTTCAAATAA			ATGGATTTCCACGCCGCACGCGCCAGGCTCAATTGCCTAACACTTCCTGCACACTTCAAATAA	MDFHAARARLNCLTLPAHFK*			MDFHAARARLNCLTLPAHFK*	CACGCGCTAT	TTATCAAGTT	0		0	0	0	0	0
9965	4308	ao	AN2307.1	71.m15512	AO070323000045	1					-274	-161	ATGCCTCCCAAGGAGAAGTCCACTCCGGACTCTGCGCCATCCCACGAGATCACCGGCCAGAGCGCTCTTCCTAGTACGCAGAATACACCCATCGTAATGGATATCGCCGGTTGA			ATGCCTCCCAAGGAGAAGTCCACTCCGGACTCTGCGCCATCCCACGAGATCACCGGCCAGAGCGCTCTTCCTAGTACGCAGAATACACCCATCGTAATGGATATCGCCGGTTGA	MPPKEKSTPDSAPSHEITGQSALPSTQNTPIVMDIAG*			MPPKEKSTPDSAPSHEITGQSALPSTQNTPIVMDIAG*	CGACCCCACG	CTGGTTCTGC	0		0	0	0	0	0
9966	4308	ao	AN2307.1	71.m15512	AO070323000045	1					-178	-161	ATGGATATCGCCGGTTGA			ATGGATATCGCCGGTTGA	MDIAG*			MDIAG*	ACCCATCGTA	CTGGTTCTGC	0		0	0	0	0	0
9985	4320	an	AN4378.1	58.m08998	AO070261000021	0	-38	-12					ATGGATTTCTCGCACTTTCCTAAGTGA	ATGGATTTCTCGCACTTTCCTAAGTGA			MDFSHFPK*	MDFSHFPK*			TCTAGCGGCC	GCCGTTACAC	1	G	0	0	0	0	0
10005	4324	ao	AN1847.1	58.m07663	AO070292000057	1					-182	-123	ATGGTCTGCTCCATCCATTGCATGACTCCTACTATGCTGTCTACTTCCACGCACGTGTAA			ATGGTCTGCTCCATCCATTGCATGACTCCTACTATGCTGTCTACTTCCACGCACGTGTAA	MVCSIHCMTPTMLSTSTHV*			MVCSIHCMTPTMLSTSTHV*	CCTGACTTGT	AGGTCAGGCG	0		0	0	0	0	0
10006	4324	ao	AN1847.1	58.m07663	AO070292000057	1					-161	-123	ATGACTCCTACTATGCTGTCTACTTCCACGCACGTGTAA			ATGACTCCTACTATGCTGTCTACTTCCACGCACGTGTAA	MTPTMLSTSTHV*			MTPTMLSTSTHV*	CATCCATTGC	AGGTCAGGCG	0		0	0	0	0	0
10007	4324	ao	AN1847.1	58.m07663	AO070292000057	1					-149	-123	ATGCTGTCTACTTCCACGCACGTGTAA			ATGCTGTCTACTTCCACGCACGTGTAA	MLSTSTHV*			MLSTSTHV*	GACTCCTACT	AGGTCAGGCG	0		0	0	0	0	0
10016	4329	af	AN3377.1	66.m04648	AO070317000062	0			-57	-34			ATGACGGGAAAGCCGCATCGTTAG		ATGACGGGAAAGCCGCATCGTTAG		MTGKPHR*		MTGKPHR*		CCCGCAGATT	CCCTGTTCAG	1		0	0	0	0	0
10034	4334	ao	AN6615.1	62.m03212	AO070326000064	0					-58	-38	ATGCGAGCTATAAAAAGCTGA			ATGCGAGCTATAAAAAGCTGA	MRAIKS*			MRAIKS*	AAAACGTGTC	CATTTTACCG	1	K	0	0	0	0	0
10035	4335	af	AN2238.1	71.m15825	AO070326000135	1			-122	-99			ATGACGGGTGCCATTGTGGCCTGA		ATGACGGGTGCCATTGTGGCCTGA		MTGAIVA*		MTGAIVA*		GCAATATCGC	TCCTTTCCCC	0	O	0	0	0	0	0
10039	4338	an	AN2966.1	59.m09423	AO070337000161	1	-182	-78					ATGTATTATGGGCTTCTGACCCAGATCAAAATGTTGTTGTTCAGCTGTTTATTCCTCAGGCCAACACGAATAACGTCTCCCCATCAACGCAACAACATCGCCTAG	ATGTATTATGGGCTTCTGACCCAGATCAAAATGTTGTTGTTCAGCTGTTTATTCCTCAGGCCAACACGAATAACGTCTCCCCATCAACGCAACAACATCGCCTAG			MYYGLLTQIKMLLFSCLFLRPTRITSPHQRNNIA*	MYYGLLTQIKMLLFSCLFLRPTRITSPHQRNNIA*			CGAGACAGCA	CTCTATCAGT	0	E	0	0	0	0	0
10040	4338	an	AN2966.1	59.m09423	AO070337000161	1	-175	-164					ATGGGCTTCTGA	ATGGGCTTCTGA			MGF*	MGF*			GCAATGTATT	CCCAGATCAA	0	E	0	0	0	0	0
10041	4338	an	AN2966.1	59.m09423	AO070337000161	1	-152	-78					ATGTTGTTGTTCAGCTGTTTATTCCTCAGGCCAACACGAATAACGTCTCCCCATCAACGCAACAACATCGCCTAG	ATGTTGTTGTTCAGCTGTTTATTCCTCAGGCCAACACGAATAACGTCTCCCCATCAACGCAACAACATCGCCTAG			MLLFSCLFLRPTRITSPHQRNNIA*	MLLFSCLFLRPTRITSPHQRNNIA*			CCAGATCAAA	CTCTATCAGT	0	E	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
10042	4339	conserved	AN2902.1	59.m08753	AO070338000104	1	-143	-132	-159	-148	-143	-132	ATGGmkCCmTAG	ATGGCTCCATAG	ATGGATCCCTAG	ATGGCGCCATAG	MaP*	MAP*	MDP*	MAP*	mkCkwCGGGC	Ckrybrrrmv	0	K	0	MG03485.1	NCU09300.1	0	0
10043	4339	an	AN2902.1	59.m08753	AO070338000104	1	-311	-282					ATGTACCTCCTCTTCTCAGCACAACCTTAA	ATGTACCTCCTCTTCTCAGCACAACCTTAA			MYLLFSAQP*	MYLLFSAQP*			GCAACCACTC	AGCGAAATAA	0	K	0	MG03485.1	NCU09300.1	0	0
10044	4339	af	AN2902.1	59.m08753	AO070338000104	1			-504	-415			ATGCATCACCAACGTTCCTCTCTCTCGTCTCATCATCTTCTTTTTTGGCCCCCAATTTTGATAGGAGTCAAACTTCATCGCATTGAATAA		ATGCATCACCAACGTTCCTCTCTCTCGTCTCATCATCTTCTTTTTTGGCCCCCAATTTTGATAGGAGTCAAACTTCATCGCATTGAATAA		MHHQRSSLSSHHLLFWPPILIGVKLHRIE*		MHHQRSSLSSHHLLFWPPILIGVKLHRIE*		CATTTCTTTC	TAACTCTCGC	0	K	0	MG03485.1	NCU09300.1	0	0
10045	4339	ao	AN2902.1	59.m08753	AO070338000104	1					-101	-42	ATGCATATTACCCCGTTGTCAATTGCTATTGTCAATAGAGGTAGGGTCATCAAGCATTAA			ATGCATATTACCCCGTTGTCAATTGCTATTGTCAATAGAGGTAGGGTCATCAAGCATTAA	MHITPLSIAIVNRGRVIKH*			MHITPLSIAIVNRGRVIKH*	CTCGCAATTC	ATCATTCAAA	0	K	0	MG03485.1	NCU09300.1	0	0
10061	4348	af	AN8783.1	71.m15597	AO070289000008	0			-59	-33			ATGACCGTAACTCATGGTCACATCTAA		ATGACCGTAACTCATGGTCACATCTAA		MTVTHGHI*		MTVTHGHI*		CAATGCGTCT	CATTACAGGA	1	D	FG05504.1	0	0	0	0
10068	4351	an	AN1652.1	58.m07719	AO070299000039	0	-58	-41					ATGTCGGGTCAATACTAA	ATGTCGGGTCAATACTAA			MSGQY*	MSGQY*			GCCAGGGTCC	TGCAGTACAG	1	R	0	0	0	0	0
10069	4351	ao	AN1652.1	58.m07719	AO070299000039	1					-53	-21	ATGACTATATATCATACAGGATGCCCATACTGA			ATGACTATATATCATACAGGATGCCCATACTGA	MTIYHTGCPY*			MTIYHTGCPY*	TCGTGGAAGG	TCCCTCGTCT	1	R	0	0	0	0	0
10075	4355	af	AN3391.1	70.m15714	AO070309000063	0			-39	-10			ATGGCCCCCCCGCGTTCGGAGCTGCGTTAG		ATGGCCCCCCCGCGTTCGGAGCTGCGTTAG		MAPPRSELR*		MAPPRSELR*		TGTTCCACCC	CTAGGCACCA	1	R	0	0	0	0	0
10076	4355	ao	AN3391.1	70.m15714	AO070309000063	0					-47	-3	ATGCACTCCACGCTCGGGCTGTATACAGCCTTGGATATTGCCTGA			ATGCACTCCACGCTCGGGCTGTATACAGCCTTGGATATTGCCTGA	MHSTLGLYTALDIA*			MHSTLGLYTALDIA*	TAGGTGCCAA	CCATGGCCTC	1	R	0	0	0	0	0
10118	4374	an	AN8271.1	53.m03690	AO070310000030	1	-274	-254					ATGCTTGCCTGTTGCTCCTGA	ATGCTTGCCTGTTGCTCCTGA			MLACCS*	MLACCS*			ACAACCGGCC	ACCTCGACGC	0	B	0	MG04359.1	0	0	0
10119	4374	af	AN8271.1	53.m03690	AO070310000030	1			-138	-79			ATGTTCTTCGGGATAAAACCATCGGCTGGGGATAAAGTACACAGGCTTGCCACTCATTGA		ATGTTCTTCGGGATAAAACCATCGGCTGGGGATAAAGTACACAGGCTTGCCACTCATTGA		MFFGIKPSAGDKVHRLATH*		MFFGIKPSAGDKVHRLATH*		CATTAACATG	AGCCCCCCAA	0	B	0	MG04359.1	0	0	0
10120	4378	an	AN4785.1	59.m09463	AO070329000062	1	-380	-351					ATGGGACCAATGATAAGCATCTGTGCTTGA	ATGGGACCAATGATAAGCATCTGTGCTTGA			MGPMISICA*	MGPMISICA*			AACGCCTCTA	TGCATCTTTC	0		0	0	0	0	0
10121	4378	an	AN4785.1	59.m09463	AO070329000062	1	-371	-351					ATGATAAGCATCTGTGCTTGA	ATGATAAGCATCTGTGCTTGA			MISICA*	MISICA*			AATGGGACCA	TGCATCTTTC	0		0	0	0	0	0
10122	4378	an	AN4785.1	59.m09463	AO070329000062	1	-351	-337					ATGCATCTTTCATGA	ATGCATCTTTCATGA			MHLS*	MHLS*			TCTGTGCTTG	GTTATCCCTG	0		0	0	0	0	0
10123	4378	an	AN4785.1	59.m09463	AO070329000062	1	-340	-326					ATGAGTTATCCCTGA	ATGAGTTATCCCTGA			MSYP*	MSYP*			TGCATCTTTC	AGCGTGCATA	0		0	0	0	0	0
10124	4378	af	AN4785.1	59.m09463	AO070329000062	1			-381	-361			ATGGGTTCGGTGACTGCATGA		ATGGGTTCGGTGACTGCATGA		MGSVTA*		MGSVTA*		TGACCTTCTC	GTTTATGACT	0		0	0	0	0	0
10125	4378	af	AN4785.1	59.m09463	AO070329000062	1			-364	-353			ATGAGTTTATGA		ATGAGTTTATGA		MSL*		MSL*		CGGTGACTGC	CTTCTGGTTG	0		0	0	0	0	0
10126	4378	ao	AN4785.1	59.m09463	AO070329000062	1					-576	-547	ATGGGTTCGGGGGTTTACATCTGTCGCTGA			ATGGGTTCGGGGGTTTACATCTGTCGCTGA	MGSGVYICR*			MGSGVYICR*	CTTCTTGTAT	TTTCTCTCCA	0		0	0	0	0	0
10127	4378	ao	AN4785.1	59.m09463	AO070329000062	1					-520	-509	ATGAACAATTGA			ATGAACAATTGA	MNN*			MNN*	TCCCAGGGAC	TTCCTTTCCA	0		0	0	0	0	0
10155	4394	an	AN2049.1	58.m07637	AO070292000016	1	-229	-194					ATGAGTCGAGGCCCATTCGTTATCTCTTTTAATTGA	ATGAGTCGAGGCCCATTCGTTATCTCTTTTAATTGA			MSRGPFVISFN*	MSRGPFVISFN*			CTCAAAGTCA	TACGCAAGTA	0	A	0	0	0	0	0
10158	4394	af	AN2049.1	58.m07637	AO070292000016	1			-176	-153			ATGCTGTTTTTGTTTCTCAACTAA		ATGCTGTTTTTGTTTCTCAACTAA		MLFLFLN*		MLFLFLN*		GAAAGCGTTT	CCCGACGCCA	0	A	0	0	0	0	0
10159	4394	ao	AN2049.1	58.m07637	AO070292000016	1					-168	-145	ATGTATTCCATTCACTTGTTATAG			ATGTATTCCATTCACTTGTTATAG	MYSIHLL*			MYSIHLL*	CTTATTGCTT	TATCGAAGAC	0	A	0	0	0	0	0
10164	4397	ao	AN0077.1	71.m16046	AO070311000138	0					-41	-30	ATGTCAATTTAA			ATGTCAATTTAA	MSI*			MSI*	TGCAGAATCC	CATATCCGTG	1	QR	0	MG08311.1	0	0	0
10182	4406	af	AN5829.1	72.m18956	AO070260000017	0			-47	-6			ATGGTTGAAAGCTACGACTCGTCTGTTCCGTCTGAAAGATAG		ATGGTTGAAAGCTACGACTCGTCTGTTCCGTCTGAAAGATAG		MVESYDSSVPSER*		MVESYDSSVPSER*		CTTTGTGTTG	GATTCATGGC	1	Z	0	0	0	0	0
10199	4413	conserved	AN4486.1	57.m05645	AO070311000037	0	-26		-26		-26		ATGCTyCTGyyGyyrCCrGyCCCGTrA	ATGCTTCTGTCGTCACCAGCCCCGTGA	ATGCTTCTGCTGCTGCCGGCCCCGTAA	ATGCTCCTGCTGCCACCAGTCCCGTAA	MLLssPaP*	MLLSSPAP*	MLLLLPAP*	MLLLPPVP*	vmdvskAATA	TGGGAGGTry	1		0	0	0	0	0
10202	4417	an	AN2852.1	59.m08695	AO070338000173	0	-21	-4					ATGCGGCGGTTCGATTGA	ATGCGGCGGTTCGATTGA			MRRFD*	MRRFD*			GTCAATTTGC	GTCATGGAAA	1		0	0	0	0	0
10206	4418	conserved	AN0412.1	54.m06662	AO070338000255	1	-228	-211	-292	-275	-300	-283	ATGysTykTATATyATrr	ATGTCTCTTATATTATAG	ATGCGTTGTATATCATGA	ATGCCTTGTATATCATGA	MslII*	MSLIL*	MRCIS*	MPCIS*	CmyhmmCAyC	ymvTChTysk	0	RP	0	0	0	0	0
10207	4418	af	AN0412.1	54.m06662	AO070338000255	1			-278	-246			ATGACAATCATCGTCCTGCCGAGGACAACCTAA		ATGACAATCATCGTCCTGCCGAGGACAACCTAA		MTIIVLPRTT*		MTIIVLPRTT*		GTTGTATATC	TCTCCCGCCC	0	RP	0	0	0	0	0
10208	4418	ao	AN0412.1	54.m06662	AO070338000255	1					-286	-218	ATGACCGTCTTCGTCCTTTTTGGGACCCCATTCTCTTCTGCCCTCTGGCTCGATCGGTTACACGATTGA			ATGACCGTCTTCGTCCTTTTTGGGACCCCATTCTCTTCTGCCCTCTGGCTCGATCGGTTACACGATTGA	MTVFVLFGTPFSSALWLDRLHD*			MTVFVLFGTPFSSALWLDRLHD*	CTTGTATATC	TCGATACTGA	0	RP	0	0	0	0	0
10209	4418	ao	AN0412.1	54.m06662	AO070338000255	1					-175	-11	ATGAAATTATCGGATTATATTCTTTCCAAGCAATTGAATCCTCCAATCCTCGCCGTCGCCACGATCCTTTCCACCGTTCACCATACTACTACCTACCGAACTGTCTCTCTATCCTCACTTACCTTGTTTCTCTCACATACTCTTTTGTCGTCAGTATTAATTTAA			ATGAAATTATCGGATTATATTCTTTCCAAGCAATTGAATCCTCCAATCCTCGCCGTCGCCACGATCCTTTCCACCGTTCACCATACTACTACCTACCGAACTGTCTCTCTATCCTCACTTACCTTGTTTCTCTCACATACTCTTTTGTCGTCAGTATTAATTTAA	MKLSDYILSKQLNPPILAVATILSTVHHTTTYRTVSLSSLTLFLSHTLLSSVLI*			MKLSDYILSKQLNPPILAVATILSTVHHTTTYRTVSLSSLTLFLSHTLLSSVLI*	TATTTGATTG	TCGTAAAGTG	0	RP	0	0	0	0	0
10214	4420	af	AN2083.1	57.m05782	AO070341000236	0			-58	-35			ATGGTTTTGTTTCGTTCTTTTTAG		ATGGTTTTGTTTCGTTCTTTTTAG		MVLFRSF*		MVLFRSF*		ACTTAGACTC	TTCCAAAATA	1	S	0	0	0	0	0
10233	4429	an	AN7628.1	71.m15822	AO070294000038	0	-49	-2					ATGACCAGCCCCTCGAGTCGCAGTCGACACCGATTCACATACCGCTAA	ATGACCAGCCCCTCGAGTCGCAGTCGACACCGATTCACATACCGCTAA			MTSPSSRSRHRFTYR*	MTSPSSRSRHRFTYR*			TCTCAGATGC	TATGCCCCCT	1	A	0	0	0	0	0
10310	4452	an	AN8675.1	62.m03480	AO070315000094	0	-20						ATGCATGAGGTTGCTCCGTAA	ATGCATGAGGTTGCTCCGTAA			MHEVAP*	MHEVAP*			TCTGCCACCG	TGGGCAATCT	1	S	0	0	NCU07447.1	0	0
10339	4461	af	AN3623.1	58.m07410	AO070342000128	0			-49	-32			ATGTCCTACAGCAGCTGA		ATGTCCTACAGCAGCTGA		MSYSS*		MSYSS*		GTCTCGCCCA	CCTCCATTAA	1	OT	0	0	0	0	0
10379	4481	af	AN1500.1	55.m03010	AO070334000217	1			-111	-76			ATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		ATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		MVGTSTVDYRA*		MVGTSTVDYRA*		CTTTTACCGA	GACGTCTGCA	0	R	0	0	0	0	0
10385	4483	an	AN4030.1	54.m06559	AO070328000122	1	-58	-26					ATGAAATCGCAGAGATCTTGGCCGCAAAGTTAA	ATGAAATCGCAGAGATCTTGGCCGCAAAGTTAA			MKSQRSWPQS*	MKSQRSWPQS*			CGTGTTCCGT	GGCTAGAACG	1		0	0	0	0	0
10386	4483	af	AN4030.1	54.m06559	AO070328000122	1			-649	-617			ATGGGAAGTCATCTGATAACTTTACAGCGATGA		ATGGGAAGTCATCTGATAACTTTACAGCGATGA		MGSHLITLQR*		MGSHLITLQR*		CGAATGTTTT	CTGTGCTAAT	0		0	0	0	0	0
10422	4494	ao	AN6279.1	72.m19361	AO070308000038	0					-34	-23	ATGGCATGTTAA			ATGGCATGTTAA	MAC*			MAC*	TTGGATTCGA	CTGGCATATG	1	I	0	MG01721.1	0	0	0
10427	4495	af	AN5673.1	65.m07399	AO070309000086	0			-40	-23			ATGGAAGCTTTCCCATAA		ATGGAAGCTTTCCCATAA		MEAFP*		MEAFP*		GCTCTTGCTT	CCCCGAAACT	1		0	0	0	0	0
10429	4495	ao	AN5673.1	65.m07399	AO070309000086	0					-59	-48	ATGATGCAGTAG			ATGATGCAGTAG	MMQ*			MMQ*	GGTCCCCGTC	GGGCTTGACC	1		0	0	0	0	0
10438	4497	af	AN6572.1	62.m03169	AO070326000015	1			-50	-36			ATGCGATTAAGCTAG		ATGCGATTAAGCTAG		MRLS*		MRLS*		GCATTACATC	ACCAAGAGCT	1	R	0	0	0	0	0
10440	4497	ao	AN6572.1	62.m03169	AO070326000015	0					-50	-36	ATGCGAGCTCATTAG			ATGCGAGCTCATTAG	MRAH*			MRAH*	CCCGTTCGTC	ACCGGACACA	1	R	0	0	0	0	0
10441	4500	an	AN5836.1	72.m19916	AO070340000001	1	-500	-489					ATGAGTTTCTGA	ATGAGTTTCTGA			MSF*	MSF*			TTCCTATCTC	AAACAGCACG	0	K	0	0	0	0	0
10442	4500	ao	AN5836.1	72.m19916	AO070340000001	1					-556	-527	ATGTCGACGACTCGCTCTTTCGTGATCTGA			ATGTCGACGACTCGCTCTTTCGTGATCTGA	MSTTRSFVI*			MSTTRSFVI*	CATCACTTGC	CCGGTACCAC	0	K	0	0	0	0	0
10443	4501	af	AN5525.1	69.m15433	AO070341000364	1			-42	-13			ATGTATTGCGGCATTGCCCAACTCACATAG		ATGTATTGCGGCATTGCCCAACTCACATAG		MYCGIAQLT*		MYCGIAQLT*		CTCTCGTTGG	AGAGCTTCCA	1	CE	FG07953.1	0	NCU02366.1	0	0
10444	4501	ao	AN5525.1	69.m15433	AO070341000364	1					-42	-13	ATGTGTTGCGGCCTTGCTCACCTCGCATAG			ATGTGTTGCGGCCTTGCTCACCTCGCATAG	MCCGLAHLA*			MCCGLAHLA*	CTCTTCTTGG	AGAGCTTTCA	1	CE	FG07953.1	0	NCU02366.1	0	0
10445	4502	an	AN5491.1	69.m15461	AO070341000394	0	-52	-32					ATGACTTCTAATGTCTTCTAA	ATGACTTCTAATGTCTTCTAA			MTSNVF*	MTSNVF*			TTCTTTTCCG	GTGAGCCCCG	1	U	0	0	0	0	0
10446	4502	an	AN5491.1	69.m15461	AO070341000394	0	-42	-28					ATGTCTTCTAAGTGA	ATGTCTTCTAAGTGA			MSSK*	MSSK*			ATGACTTCTA	GCCCCGGTCG	1	U	0	0	0	0	0
10448	4502	af	AN5491.1	69.m15461	AO070341000394	0			-51	-28			ATGACATTCGAAACTCCTAAATGA		ATGACATTCGAAACTCCTAAATGA		MTFETPK*		MTFETPK*		CCCTGCTCCG	GCCGCTGGTT	1	U	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
10450	4502	ao	AN5491.1	69.m15461	AO070341000394	0					-52	-29	ATGACACCTGCGGTCTTTAAATGA			ATGACACCTGCGGTCTTTAAATGA	MTPAVFK*			MTPAVFK*	TACCCACCCG	GCCCCGGTCG	1	U	0	0	0	0	0
10457	4515	af	AN1175.1	70.m15042	AO070331000170	0			-31	-11			ATGAATAAAACAAAACCTTAG		ATGAATAAAACAAAACCTTAG		MNKTKP*		MNKTKP*		TTCTTCCTGC	ATCACCAGTC	1	A	0	0	0	0	0
10462	4522	ao	AN6644.1	62.m03242	AO070295000021	0					-39	-28	ATGTGTGCTTAG			ATGTGTGCTTAG	MCA*			MCA*	CGATCATTCG	TAGTACCATC	1	E	0	0	0	0	0
10482	4530	an	AN5749.1	69.m14847	AO070341000006	0	-23	-9					ATGCCCATCCCGTAA	ATGCCCATCCCGTAA			MPIP*	MPIP*			GACCCAGAGA	AAGCAGCAAT	1	E	0	0	0	0	0
10491	4532	af	AN4341.1	58.m07983	AO070240000016	0			-28	-14			ATGTGGTCCAGATAA		ATGTGGTCCAGATAA		MWSR*		MWSR*		TACACTGCCA	CAGGGACACC	1		0	0	0	0	0
10495	4532	ao	AN4341.1	58.m07983	AO070240000016	0					-52	-35	ATGGTAAATGACGGTTGA			ATGGTAAATGACGGTTGA	MVNDG*			MVNDG*	TGTCAACGCC	CTAGTTCAAT	1		0	0	0	0	0
10496	4532	ao	AN4341.1	58.m07983	AO070240000016	0					-45	-31	ATGACGGTTGACTAG			ATGACGGTTGACTAG	MTVD*			MTVD*	GCCATGGTAA	TTCAATGATG	1		0	0	0	0	0
10497	4533	ao	AN6371.1	72.m19489	AO070279000075	1					-88	-56	ATGTCATATCTCTTCATCGGACATACCAACTGA			ATGTCATATCTCTTCATCGGACATACCAACTGA	MSYLFIGHTN*			MSYLFIGHTN*	GCAATCTGGA	CCGCATCAGA	0		0	0	0	0	0
10500	4534	an	AN9010.1	52.m03996	AO070289000056	0	-60	-40					ATGCCAACGCTGGCCTCCTGA	ATGCCAACGCTGGCCTCCTGA			MPTLAS*	MPTLAS*			CTCTTTAAGA	GTGTAATTCC	1	G	0	0	0	0	0
10505	4535	an	AN2281.1	71.m15926	AO070295000058	1	-63	-31					ATGATGAACTGCATTGATCGGATACTTGCCTGA	ATGATGAACTGCATTGATCGGATACTTGCCTGA			MMNCIDRILA*	MMNCIDRILA*			ACCGAGTTAT	AGCTAACACC	0	MU	0	0	0	0	0
10506	4535	an	AN2281.1	71.m15926	AO070295000058	1	-60	-31					ATGAACTGCATTGATCGGATACTTGCCTGA	ATGAACTGCATTGATCGGATACTTGCCTGA			MNCIDRILA*	MNCIDRILA*			GAGTTATATG	AGCTAACACC	1	MU	0	0	0	0	0
10507	4535	af	AN2281.1	71.m15926	AO070295000058	1			-64	-41			ATGATATGTAATGAATTATTTTGA		ATGATATGTAATGAATTATTTTGA		MICNELF*		MICNELF*		TTTCAATCTC	ATGATTTGAC	0	MU	0	0	0	0	0
10508	4535	af	AN2281.1	71.m15926	AO070295000058	1			-54	-37			ATGAATTATTTTGAATGA		ATGAATTATTTTGAATGA		MNYFE*		MNYFE*		ATGATATGTA	TTTGACTTTC	1	MU	0	0	0	0	0
10512	4535	ao	AN2281.1	71.m15926	AO070295000058	1					-64	-53	ATGATGAGCTGA			ATGATGAGCTGA	MMS*			MMS*	TTTATACTTT	ATTGATTCAT	0	MU	0	0	0	0	0
10524	4538	an	AN1796.1	72.m19548	AO070309000135	0	-46	-32					ATGTGCCGACCTTGA	ATGTGCCGACCTTGA			MCRP*	MCRP*			CCGCGGAGCA	GCGCCTTTCA	1	L	0	0	0	YDR182W	0
10526	4538	af	AN1796.1	72.m19548	AO070309000135	0			-54	-37			ATGCAGCCTGCACATTAA		ATGCAGCCTGCACATTAA		MQPAH*		MQPAH*		AGTTCGAGCA	GCCACCTGCT	1	L	0	0	0	YDR182W	0
10530	4538	ao	AN1796.1	72.m19548	AO070309000135	0					-49	-11	ATGCCGCAGACAGCTTCGCTTTGGCCACTTTCGGGTTGA			ATGCCGCAGACAGCTTCGCTTTGGCCACTTTCGGGTTGA	MPQTASLWPLSG*			MPQTASLWPLSG*	AGGCGGAGCA	CACAGCAAGC	1	L	0	0	0	YDR182W	0
10543	4541	an	AN8120.1	53.m03831	AO070322000028	0	-35	-3					ATGGGGCTTTATTCTGGCATCGTACAGATGTAA	ATGGGGCTTTATTCTGGCATCGTACAGATGTAA			MGLYSGIVQM*	MGLYSGIVQM*			AGAATAAATT	TTATGGCGGC	1	S	0	0	0	0	0
10547	4543	an	AN1221.1	70.m15002	AO070331000223	0	-24	-13					ATGTATGAGTAG	ATGTATGAGTAG			MYE*	MYE*			CTGCAGTACA	ACCGACGCGT	1	T	0	0	0	0	0
10549	4543	af	AN1221.1	70.m15002	AO070331000223	0			-26	-9			ATGCTTGATGCCCGATAG		ATGCTTGATGCCCGATAG		MLDAR*		MLDAR*		CAAAATCATA	ACGCGTCCAT	1	T	0	0	0	0	0
10552	4543	ao	AN1221.1	70.m15002	AO070331000223	0					-24	-13	ATGCTTGCTTAA			ATGCTTGCTTAA	MLA*			MLA*	AAAGCACACA	CTAGACGCGT	1	T	0	0	0	0	0
10555	4545	af	AN2184.1	72.m19039	AO070340000082	0			-30	-19			ATGCGCCGATAA		ATGCGCCGATAA		MRR*		MRR*		CCGGAGATCA	ATACCACCAC	1	S	0	MG04663.1	NCU07577.1	0	0
10558	4545	ao	AN2184.1	72.m19039	AO070340000082	0					-39	-28	ATGTCCTTTTAG			ATGTCCTTTTAG	MSF*			MSF*	CTCCCACTCC	GTATTCAGCC	1	S	0	MG04663.1	NCU07577.1	0	0
10570	4552	af	AN7538.1	69.m15082	AO070324000011	0			-58	-35			ATGACAACTGCTATTTACATCTGA		ATGACAACTGCTATTTACATCTGA		MTTAIYI*		MTTAIYI*		ACATAACCGG	CGGAGTTCAG	1	KL	0	0	0	0	0
10571	4553	an	AN2760.1	59.m09264	AO070327000022	1	-290	-252					ATGGCATGGGCATGCTTTGGGTGTAACTCCAATGCTTAG	ATGGCATGGGCATGCTTTGGGTGTAACTCCAATGCTTAG			MAWACFGCNSNA*	MAWACFGCNSNA*			TTCTGGTTGG	GGTACTTAGG	0	E	0	0	0	0	0
10572	4553	an	AN2760.1	59.m09264	AO070327000022	1	-285	-265					ATGGGCATGCTTTGGGTGTAA	ATGGGCATGCTTTGGGTGTAA			MGMLWV*	MGMLWV*			GTTGGATGGC	CTCCAATGCT	0	E	0	0	0	0	0
10573	4553	an	AN2760.1	59.m09264	AO070327000022	1	-279	-265					ATGCTTTGGGTGTAA	ATGCTTTGGGTGTAA			MLWV*	MLWV*			TGGCATGGGC	CTCCAATGCT	0	E	0	0	0	0	0
10574	4553	an	AN2760.1	59.m09264	AO070327000022	1	-259	-203					ATGCTTAGGGTACTTAGGGAGCTTTATCCTGTTCTTTATCAGCCCGCTTCTTCCTGA	ATGCTTAGGGTACTTAGGGAGCTTTATCCTGTTCTTTATCAGCCCGCTTCTTCCTGA			MLRVLRELYPVLYQPASS*	MLRVLRELYPVLYQPASS*			TGTAACTCCA	CTCACCGTCT	0	E	0	0	0	0	0
10575	4553	af	AN2760.1	59.m09264	AO070327000022	1			-331	-158			ATGCTTGGGTCTCTCCATCTGTACAGCAAGACCTGCCTTGAAATAGCACCGTCAGTCCTCTTTCGTGCTTCTGAACTGTGTCCTCTTCGCCTTGAAAGTGTCATTCAATCATCAGCGTTCTGCACCCAAGGATTCGAGCATTATATATACGCTGTCCTCTACTTAGGGGATTAG		ATGCTTGGGTCTCTCCATCTGTACAGCAAGACCTGCCTTGAAATAGCACCGTCAGTCCTCTTTCGTGCTTCTGAACTGTGTCCTCTTCGCCTTGAAAGTGTCATTCAATCATCAGCGTTCTGCACCCAAGGATTCGAGCATTATATATACGCTGTCCTCTACTTAGGGGATTAG		MLGSLHLYSKTCLEIAPSVLFRASELCPLRLESVIQSSAFCTQGFEHYIYAVLYLGD*		MLGSLHLYSKTCLEIAPSVLFRASELCPLRLESVIQSSAFCTQGFEHYIYAVLYLGD*		TCGGTTGGGC	GAATCTCAGC	0	E	0	0	0	0	0
10576	4553	af	AN2760.1	59.m09264	AO070327000022	1			-123	-94			ATGTTGTTCATAGACATCCTTGTTTCGTGA		ATGTTGTTCATAGACATCCTTGTTTCGTGA		MLFIDILVS*		MLFIDILVS*		CTTTCCTTGG	CTCAACTTTA	0	E	0	0	0	0	0
10581	4556	an	AN1118.1	70.m15117	AO070331000110	1	-156	-58					ATGCCCTTCATGTGGTCCTCGATCGCCTTGACTACGGATCTCTGCTCTCACATCGCGGCACACCAGTGTCAATCTTGCTTTGCGTTATCGGACTACTAG	ATGCCCTTCATGTGGTCCTCGATCGCCTTGACTACGGATCTCTGCTCTCACATCGCGGCACACCAGTGTCAATCTTGCTTTGCGTTATCGGACTACTAG			MPFMWSSIALTTDLCSHIAAHQCQSCFALSDY*	MPFMWSSIALTTDLCSHIAAHQCQSCFALSDY*			CCTTATACCG	ATCATAACGG	0		0	0	0	0	0
10582	4556	an	AN1118.1	70.m15117	AO070331000110	1	-147	-58					ATGTGGTCCTCGATCGCCTTGACTACGGATCTCTGCTCTCACATCGCGGCACACCAGTGTCAATCTTGCTTTGCGTTATCGGACTACTAG	ATGTGGTCCTCGATCGCCTTGACTACGGATCTCTGCTCTCACATCGCGGCACACCAGTGTCAATCTTGCTTTGCGTTATCGGACTACTAG			MWSSIALTTDLCSHIAAHQCQSCFALSDY*	MWSSIALTTDLCSHIAAHQCQSCFALSDY*			GATGCCCTTC	ATCATAACGG	0		0	0	0	0	0
10583	4556	af	AN1118.1	70.m15117	AO070331000110	1			-163	-101			ATGTTGTCGTTAGCGCCACAGCAAACATTGAGATCAAACTACAAGTGCCTCCGGGCCAAATAG		ATGTTGTCGTTAGCGCCACAGCAAACATTGAGATCAAACTACAAGTGCCTCCGGGCCAAATAG		MLSLAPQQTLRSNYKCLRAK*		MLSLAPQQTLRSNYKCLRAK*		AACGCCCTTC	ATACTCAGAC	0		0	0	0	0	0
10584	4556	ao	AN1118.1	70.m15117	AO070331000110	1					-163	-92	ATGTTGCTGTCAGCGACACGACAAACATCGAGACATATTTACCGGTGTCCTCGGGCCTATCTGTTCTCGTGA			ATGTTGCTGTCAGCGACACGACAAACATCGAGACATATTTACCGGTGTCCTCGGGCCTATCTGTTCTCGTGA	MLLSATRQTSRHIYRCPRAYLFS*			MLLSATRQTSRHIYRCPRAYLFS*	TACGCCCTTC	GTGCCATAGT	0		0	0	0	0	0
10595	4562	af	AN1948.1	58.m07348	AO070342000213	0			-45	-28			ATGATCTTGTTTGGCTGA		ATGATCTTGTTTGGCTGA		MILFG*		MILFG*		ACAGGCTACT	GGACCTCACA	1	A	0	0	0	0	0
10596	4562	ao	AN1948.1	58.m07348	AO070342000213	0					-44	-27	ATGATCGGGTCTGGTTGA			ATGATCGGGTCTGGTTGA	MIGSG*			MIGSG*	GACAGGGGTA	AAGGAGAGTC	1	A	0	0	0	0	0
10617	4567	an	AN0889.1	70.m15493	AO070320000058	0	-26	-12					ATGAGCGACACCTAG	ATGAGCGACACCTAG			MSDT*	MSDT*			TTGTTGCAGG	CACAATATAC	1	R	FG09745.1	MG06080.1	0	YHR168W	0
10622	4567	af	AN0889.1	70.m15493	AO070320000058	0			-31	-5			ATGAATCAGGCCAAGGCTGCGATCTGA		ATGAATCAGGCCAAGGCTGCGATCTGA		MNQAKAAI*		MNQAKAAI*		GTTCTCCAGG	AATAATGACT	1	R	FG09745.1	MG06080.1	0	YHR168W	0
10639	4569	af	AN3421.1	67.m02958	AO070323000200	0			-36	-16			ATGATCTCAAGCCGGAGTTGA		ATGATCTCAAGCCGGAGTTGA		MISSRS*		MISSRS*		CTTCCCTTGA	TCGAGAGTCA	1		FG08465.1	MG09333.1	0	0	0
10642	4569	ao	AN3421.1	67.m02958	AO070323000200	0					-52	-14	ATGGTGTACATACTTCCGACTAGCAATTACATTCTATAA			ATGGTGTACATACTTCCGACTAGCAATTACATTCTATAA	MVYILPTSNYIL*			MVYILPTSNYIL*	GTACTATTTT	TTCTACATAC	1		FG08465.1	MG09333.1	0	0	0
10664	4577	ao	AN4365.1	58.m09005	AO070261000008	0					-27	-16	ATGTACCTTTGA			ATGTACCTTTGA	MYL*			MYL*	TCTGTAAACC	TTTTGACCAT	1	L	0	0	0	0	0
10668	4582	an	AN6261.1	72.m19396	AO070304000028	0	-42	-31					ATGGAACTCTAG	ATGGAACTCTAG			MEL*	MEL*			TTTTCGAAGA	AGACATGGGC	1		0	0	0	0	0
10669	4582	af	AN6261.1	72.m19396	AO070304000028	0			-42	-31			ATGGACAAATAA		ATGGACAAATAA		MDK*		MDK*		TGGACGAAGC	GGAAATGGGC	1		0	0	0	0	0
10671	4582	ao	AN6261.1	72.m19396	AO070304000028	0					-42	-31	ATGGGGTATTAA			ATGGGGTATTAA	MGY*			MGY*	CTACGAAGTA	GGAGATGGGC	1		0	0	0	0	0
10677	4583	af	AN6254.1	72.m19981	AO070304000034	0			-32	-6			ATGGCTGGAATGTCCACACCTTGTTGA		ATGGCTGGAATGTCCACACCTTGTTGA		MAGMSTPC*		MAGMSTPC*		TTTTTGATCT	TCAAGATGGC	1	C	0	0	0	YLR348C	0
10678	4583	af	AN6254.1	72.m19981	AO070304000034	0			-23	-6			ATGTCCACACCTTGTTGA		ATGTCCACACCTTGTTGA		MSTPC*		MSTPC*		TATGGCTGGA	TCAAGATGGC	1	C	0	0	0	YLR348C	0
10706	4592	an	AN0440.1	54.m06630	AO070338000297	0	-29	-3					ATGCTTAGCAGTCCAGTTACAACTTGA	ATGCTTAGCAGTCCAGTTACAACTTGA			MLSSPVTT*	MLSSPVTT*			CCACTAGCTT	AGATGCCCTC	1	B	0	0	0	YDR176W	0
10711	4593	an	AN3083.1	52.m03887	AO070339000016	1	-278	-261					ATGCATGGTGACAGTTGA	ATGCATGGTGACAGTTGA			MHGDS*	MHGDS*			CACACCGAGA	ATGGAGATTT	0	C	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
10712	4593	an	AN3083.1	52.m03887	AO070339000016	1	-274	-218					ATGGTGACAGTTGAATGGAGATTTTATTTCAGCAGAGAATCATCATATCATGACTAA	ATGGTGACAGTTGAATGGAGATTTTATTTCAGCAGAGAATCATCATATCATGACTAA			MVTVEWRFYFSRESSYHD*	MVTVEWRFYFSRESSYHD*			CCGAGAATGC	CATGAAGGTA	0	C	0	0	0	0	0
10713	4593	an	AN3083.1	52.m03887	AO070339000016	1	-260	-222					ATGGAGATTTTATTTCAGCAGAGAATCATCATATCATGA	ATGGAGATTTTATTTCAGCAGAGAATCATCATATCATGA			MEILFQQRIIIS*	MEILFQQRIIIS*			TGACAGTTGA	CTAACATGAA	0	C	0	0	0	0	0
10714	4593	an	AN3083.1	52.m03887	AO070339000016	1	-225	-187					ATGACTAACATGAAGGTAACATCCCATCTGCTCCATTAG	ATGACTAACATGAAGGTAACATCCCATCTGCTCCATTAG			MTNMKVTSHLLH*	MTNMKVTSHLLH*			TCATCATATC	GAAAAGGTGA	0	C	0	0	0	0	0
10715	4593	an	AN3083.1	52.m03887	AO070339000016	1	-216	-187					ATGAAGGTAACATCCCATCTGCTCCATTAG	ATGAAGGTAACATCCCATCTGCTCCATTAG			MKVTSHLLH*	MKVTSHLLH*			CATGACTAAC	GAAAAGGTGA	0	C	0	0	0	0	0
10716	4593	af	AN3083.1	52.m03887	AO070339000016	1			-371	-351			ATGTTCACGTCAATGTGGTAG		ATGTTCACGTCAATGTGGTAG		MFTSMW*		MFTSMW*		ACCGTAAGGT	TACAGACTGG	0	C	0	0	0	0	0
10717	4593	af	AN3083.1	52.m03887	AO070339000016	1			-268	-242			ATGTGCCTTGCGCCAGAACGGCAATGA		ATGTGCCTTGCGCCAGAACGGCAATGA		MCLAPERQ*		MCLAPERQ*		AATTGCCAGC	TGGGAATGCT	0	C	0	0	0	0	0
10718	4593	af	AN3083.1	52.m03887	AO070339000016	1			-245	-195			ATGATGGGAATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		ATGATGGGAATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		MMGMLHVTCQSDVARW*		MMGMLHVTCQSDVARW*		CAGAACGGCA	GCACTAGCTT	0	C	0	0	0	0	0
10719	4593	af	AN3083.1	52.m03887	AO070339000016	1			-242	-195			ATGGGAATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		ATGGGAATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		MGMLHVTCQSDVARW*		MGMLHVTCQSDVARW*		AACGGCAATG	GCACTAGCTT	0	C	0	0	0	0	0
10720	4593	af	AN3083.1	52.m03887	AO070339000016	1			-236	-195			ATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		ATGCTTCATGTAACATGTCAGAGTGATGTAGCACGCTGGTAA		MLHVTCQSDVARW*		MLHVTCQSDVARW*		AATGATGGGA	GCACTAGCTT	0	C	0	0	0	0	0
10721	4593	af	AN3083.1	52.m03887	AO070339000016	1			-222	-211			ATGTCAGAGTGA		ATGTCAGAGTGA		MSE*		MSE*		TTCATGTAAC	TGTAGCACGC	0	C	0	0	0	0	0
10722	4593	af	AN3083.1	52.m03887	AO070339000016	1			-174	-61			ATGCTCATAGGGCAGGGCTTCTCGTCGTATGAAAGGTGTGCATTAGTGTCAGACTTCCTCGTGTCAAGCTCATATTCGACAAGGGAATTGGACCATATGTATCCTCGTCAGTGA		ATGCTCATAGGGCAGGGCTTCTCGTCGTATGAAAGGTGTGCATTAGTGTCAGACTTCCTCGTGTCAAGCTCATATTCGACAAGGGAATTGGACCATATGTATCCTCGTCAGTGA		MLIGQGFSSYERCALVSDFLVSSSYSTRELDHMYPRQ*		MLIGQGFSSYERCALVSDFLVSSSYSTRELDHMYPRQ*		CGTATTATCA	CACCCACCTT	0	C	0	0	0	0	0
10723	4593	af	AN3083.1	52.m03887	AO070339000016	1			-146	-129			ATGAAAGGTGTGCATTAG		ATGAAAGGTGTGCATTAG		MKGVH*		MKGVH*		TTCTCGTCGT	TGTCAGACTT	0	C	0	0	0	0	0
10724	4593	af	AN3083.1	52.m03887	AO070339000016	1			-78	-61			ATGTATCCTCGTCAGTGA		ATGTATCCTCGTCAGTGA		MYPRQ*		MYPRQ*		ATTGGACCAT	CACCCACCTT	0	C	0	0	0	0	0
10725	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-307	-290	ATGCTCCATGCGAACTAG			ATGCTCCATGCGAACTAG	MLHAN*			MLHAN*	TCATTAGTGC	CTGCATCGAA	0	C	0	0	0	0	0
10726	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-300	-121	ATGCGAACTAGCTGCATCGAAACGTGGCATATGGGGCCAGGCTGCGTTGCATCCTTCCTGCACCGTCATCCTTCAGCAGCACAAAGTTCGCTGGTGGATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAGTCCATCACTACACCAGATGA			ATGCGAACTAGCTGCATCGAAACGTGGCATATGGGGCCAGGCTGCGTTGCATCCTTCCTGCACCGTCATCCTTCAGCAGCACAAAGTTCGCTGGTGGATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAGTCCATCACTACACCAGATGA	MRTSCIETWHMGPGCVASFLHRHPSAAQSSLVDGPIHTTRHIYRSDLSPSRNVVHHYTR*			MRTSCIETWHMGPGCVASFLHRHPSAAQSSLVDGPIHTTRHIYRSDLSPSRNVVHHYTR*	TGCATGCTCC	TCCTTTTATG	0	C	0	0	0	0	0
10727	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-270	-121	ATGGGGCCAGGCTGCGTTGCATCCTTCCTGCACCGTCATCCTTCAGCAGCACAAAGTTCGCTGGTGGATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAGTCCATCACTACACCAGATGA			ATGGGGCCAGGCTGCGTTGCATCCTTCCTGCACCGTCATCCTTCAGCAGCACAAAGTTCGCTGGTGGATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAGTCCATCACTACACCAGATGA	MGPGCVASFLHRHPSAAQSSLVDGPIHTTRHIYRSDLSPSRNVVHHYTR*			MGPGCVASFLHRHPSAAQSSLVDGPIHTTRHIYRSDLSPSRNVVHHYTR*	AACGTGGCAT	TCCTTTTATG	0	C	0	0	0	0	0
10728	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-203	-141	ATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAG			ATGGGCCAATCCACACAACTCGGCATATTTATAGATCTGATCTATCTCCCTCTCGCAATGTAG	MGQSTQLGIFIDLIYLPLAM*			MGQSTQLGIFIDLIYLPLAM*	TCGCTGGTGG	TCCATCACTA	0	C	0	0	0	0	0
10729	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-124	-101	ATGATCCTTTTATGCTTCCATTGA			ATGATCCTTTTATGCTTCCATTGA	MILLCFH*			MILLCFH*	ACTACACCAG	TGTTGTTTTA	0	C	0	0	0	0	0
10730	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-113	-63	ATGCTTCCATTGATGTTGTTTTATTATATATATTTCTCTCCACACCGTTAG			ATGCTTCCATTGATGTTGTTTTATTATATATATTTCTCTCCACACCGTTAG	MLPLMLFYYIYFSPHR*			MLPLMLFYYIYFSPHR*	TGATCCTTTT	GCTTATCTGT	0	C	0	0	0	0	0
10731	4593	ao	AN3083.1	52.m03887	AO070339000016	1					-101	-63	ATGTTGTTTTATTATATATATTTCTCTCCACACCGTTAG			ATGTTGTTTTATTATATATATTTCTCTCCACACCGTTAG	MLFYYIYFSPHR*			MLFYYIYFSPHR*	GCTTCCATTG	GCTTATCTGT	0	C	0	0	0	0	0
10733	4594	ao	AN5489.1	69.m15463	AO070341000396	1					-188	-165	ATGTCCCCATCCGAGCGGCATTGA			ATGTCCCCATCCGAGCGGCATTGA	MSPSERH*			MSPSERH*	ACCCAACCCT	TATACCACAC	0	Z	0	0	0	0	0
10734	4594	ao	AN5489.1	69.m15463	AO070341000396	1					-120	-79	ATGCTGGGAGAGACAATAGTCCTTACAAGTCACCGCGTCTGA			ATGCTGGGAGAGACAATAGTCCTTACAAGTCACCGCGTCTGA	MLGETIVLTSHRV*			MLGETIVLTSHRV*	ACAACATTGA	TTCTTCGAAA	0	Z	0	0	0	0	0
10746	4601	af	AN2470.1	53.m03715	AO070310000056	1			-158	-99			ATGTCAGTGCCACGATCGACTCCTATAAGAACTACAACAATGCAAGAGACTCCATCATGA		ATGTCAGTGCCACGATCGACTCCTATAAGAACTACAACAATGCAAGAGACTCCATCATGA		MSVPRSTPIRTTTMQETPS*		MSVPRSTPIRTTTMQETPS*		CGAAGGGGTG	CGGAAAGGAA	0	ER	0	0	0	0	0
10747	4601	af	AN2470.1	53.m03715	AO070310000056	1			-119	-99			ATGCAAGAGACTCCATCATGA		ATGCAAGAGACTCCATCATGA		MQETPS*		MQETPS*		AACTACAACA	CGGAAAGGAA	0	ER	0	0	0	0	0
10748	4601	af	AN2470.1	53.m03715	AO070310000056	1			-102	-70			ATGACGGAAAGGAATCGATCATTTCAACTATAG		ATGACGGAAAGGAATCGATCATTTCAACTATAG		MTERNRSFQL*		MTERNRSFQL*		AGACTCCATC	CTGATATCTT	0	ER	0	0	0	0	0
10753	4601	ao	AN2470.1	53.m03715	AO070310000056	1					-126	-52	ATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MSVLMMYSTTTIEISPFNPRMHHP*			MSVLMMYSTTTIEISPFNPRMHHP*	ATTCATAGTG	TTGAAGCCGT	0	ER	0	0	0	0	0
10754	4601	ao	AN2470.1	53.m03715	AO070310000056	1					-114	-52	ATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MMYSTTTIEISPFNPRMHHP*			MMYSTTTIEISPFNPRMHHP*	GTCAGTCCTG	TTGAAGCCGT	0	ER	0	0	0	0	0
10755	4601	ao	AN2470.1	53.m03715	AO070310000056	1					-111	-52	ATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MYSTTTIEISPFNPRMHHP*			MYSTTTIEISPFNPRMHHP*	AGTCCTGATG	TTGAAGCCGT	0	ER	0	0	0	0	0
10756	4601	ao	AN2470.1	53.m03715	AO070310000056	1					-66	-52	ATGCACCATCCATAA			ATGCACCATCCATAA	MHHP*			MHHP*	TAATCCACGC	TTGAAGCCGT	0	ER	0	0	0	0	0
10770	4603	ao	AN4177.1	56.m02500	AO070319000001	0					-57	-13	ATGTTCAACTCATTACTGAACTACATACTATACTTCGTTGCCTGA			ATGTTCAACTCATTACTGAACTACATACTATACTTCGTTGCCTGA	MFNSLLNYILYFVA*			MFNSLLNYILYFVA*	TTACTTTAGT	ACGTACTAGA	1		0	0	0	0	0
10772	4604	an	AN0977.1	70.m15615	AO070320000180	0	-33	-19					ATGCGCAGCCTGTAA	ATGCGCAGCCTGTAA			MRSL*	MRSL*			ACGTGGATCT	TTGTTATCGT	1		0	0	0	0	0
10773	4604	ao	AN0977.1	70.m15615	AO070320000180	0					-33	-19	ATGCGCCAGCCCTAA			ATGCGCCAGCCCTAA	MRQP*			MRQP*	ATCTGTTTTT	TTGACCTCAG	1		0	0	0	0	0
10794	4620	af	AN6104.1	72.m19098	AO070340000185	1			-296	-213			ATGTCACATCGCAAATCGGACGAACACATCTGCGCCAATTCTTTGATTCAGTGTACGAATCGATCTGGGGAACAGAAAAGATAA		ATGTCACATCGCAAATCGGACGAACACATCTGCGCCAATTCTTTGATTCAGTGTACGAATCGATCTGGGGAACAGAAAAGATAA		MSHRKSDEHICANSLIQCTNRSGEQKR*		MSHRKSDEHICANSLIQCTNRSGEQKR*		CAACCAGTGG	GGGGACTATT	0	AJ	0	0	0	0	0
10800	4626	an	AN1511.1	55.m03024	AO070334000229	1	-30	-19					ATGCAGCACTGA	ATGCAGCACTGA			MQH*	MQH*			ACACCGCTTC	GTTTTCCTCG	1	U	0	0	0	0	0
10801	4626	af	AN1511.1	55.m03024	AO070334000229	1			-37	-23			ATGCGAGGCTGGTAA		ATGCGAGGCTGGTAA		MRGW*		MRGW*		CTGGGCTCAA	TAATTCTCCC	1	U	0	0	0	0	0
10804	4638	af	AN1467.1	55.m02969	AO070306000090	1			-99	-19			ATGGTCCAGCAGACAATATCGTTGTACAGAAGTATTCTGCTGGAGGGTCTTGGTATTCTGAGGGACAGGGCCCTCCGGTGA		ATGGTCCAGCAGACAATATCGTTGTACAGAAGTATTCTGCTGGAGGGTCTTGGTATTCTGAGGGACAGGGCCCTCCGGTGA		MVQQTISLYRSILLEGLGILRDRALR*		MVQQTISLYRSILLEGLGILRDRALR*		CGTTCTTCAA	CGATCCTGCT	0	T	0	MG00166.1	NCU00958.1	0	0
10805	4638	ao	AN1467.1	55.m02969	AO070306000090	1					-102	-31	ATGTTCCCAACAGACGGGTCAAAGGAAAATTCCCTATCGCTCTTTCGCGAGGGCTTGAATTGCGTTACTTAG			ATGTTCCCAACAGACGGGTCAAAGGAAAATTCCCTATCGCTCTTTCGCGAGGGCTTGAATTGCGTTACTTAG	MFPTDGSKENSLSLFREGLNCVT*			MFPTDGSKENSLSLFREGLNCVT*	ATTCTGTTGC	CGCCCTTCGG	0	T	0	MG00166.1	NCU00958.1	0	0
10809	4647	an	AN8884.1	56.m02296	AO070293000016	1	-13	-2					ATGCTTCGCTAA	ATGCTTCGCTAA			MLR*	MLR*			TCTGAGGCTG	TATGACCGCT	1		0	0	0	0	0
10811	4647	ao	AN8884.1	56.m02296	AO070293000016	1					-218	-201	ATGCACGTCTGGTCCTGA			ATGCACGTCTGGTCCTGA	MHVWS*			MHVWS*	TGTCTCAAAC	AACCTCTCAT	0		0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
10812	4647	ao	AN8884.1	56.m02296	AO070293000016	1					-23	-3	ATGATTACCATTTGCCCGTGA			ATGATTACCATTTGCCCGTGA	MITICP*			MITICP*	TTTAACTCCA	AGATGGCTGC	1		0	0	0	0	0
10834	4661	af	AN6707.1	65.m07278	AO070339000137	0			-53	-30			ATGAGAGTGCCATCTCTCACATGA		ATGAGAGTGCCATCTCTCACATGA		MRVPSLT*		MRVPSLT*		GAGGCGAGCG	CTGACATGCC	1	KL	0	0	0	0	0
10859	4674	ao	AN0560.1	69.m15287	AO070272000037	0					-43	-11	ATGAATCTGAAGCGTTCCCTCCTGGCTTCGTGA			ATGAATCTGAAGCGTTCCCTCCTGGCTTCGTGA	MNLKRSLLAS*			MNLKRSLLAS*	CCTCTTCCTC	TCCAGACAAG	1	U	FG09816.1	0	0	0	0
10880	4680	af	AN6074.1	72.m19065	AO070340000118	1			-175	-155			ATGAAATTGTTACTTATCTAG		ATGAAATTGTTACTTATCTAG		MKLLLI*		MKLLLI*		CTTTGAACTG	AACATCCTAC	0	A	0	0	0	0	0
10881	4681	an	AN5730.1	54.m06849	AO070341000031	1	-346	-311					ATGCATACGTACTCCAGACTCACTTTGTTTACATGA	ATGCATACGTACTCCAGACTCACTTTGTTTACATGA			MHTYSRLTLFT*	MHTYSRLTLFT*			GACGATTGAG	CTGGCTTCAC	0		0	0	0	0	0
10882	4681	an	AN5730.1	54.m06849	AO070341000031	1	-314	-201					ATGACTGGCTTCACCATCGCCCTTGCTCATTACCTTCAAAACCACGCTGGCCAGATCCTTGACCAGCATCGGGTTCGCTACATCACTCAGGATTGCCATTGTACGAACTCTTGA	ATGACTGGCTTCACCATCGCCCTTGCTCATTACCTTCAAAACCACGCTGGCCAGATCCTTGACCAGCATCGGGTTCGCTACATCACTCAGGATTGCCATTGTACGAACTCTTGA			MTGFTIALAHYLQNHAGQILDQHRVRYITQDCHCTNS*	MTGFTIALAHYLQNHAGQILDQHRVRYITQDCHCTNS*			CTTTGTTTAC	AGGTGTTAAC	0		0	0	0	0	0
10883	4681	an	AN5730.1	54.m06849	AO070341000031	1	-96	-49					ATGTCTCAAAGTCGGGCTGCTCATTGCACCTCTGCCTACGTTGCCTGA	ATGTCTCAAAGTCGGGCTGCTCATTGCACCTCTGCCTACGTTGCCTGA			MSQSRAAHCTSAYVA*	MSQSRAAHCTSAYVA*			ACAGCCTCCA	AATCTCGTGC	0		0	0	0	0	0
10884	4681	af	AN5730.1	54.m06849	AO070341000031	1			-333	-244			ATGTTTACTGTTGCTGTTACCTTCATTTTTGCCTCTCGCTCCTACACTCTTGATACTTTCTTCGCAAGGGCGTCTTCACTCGAACCTTAA		ATGTTTACTGTTGCTGTTACCTTCATTTTTGCCTCTCGCTCCTACACTCTTGATACTTTCTTCGCAAGGGCGTCTTCACTCGAACCTTAA		MFTVAVTFIFASRSYTLDTFFARASSLEP*		MFTVAVTFIFASRSYTLDTFFARASSLEP*		ATTGCCTGTG	TGCAGAACAG	0		0	0	0	0	0
10885	4681	af	AN5730.1	54.m06849	AO070341000031	1			-244	-113			ATGCAGAACAGCCTACTAAATCCATCGAATTTATCGATCCCCTCCCATGAAACAGAGGAACTTCAAGATCGTCCCACTGTACAGTTCTGCTCCATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAA		ATGCAGAACAGCCTACTAAATCCATCGAATTTATCGATCCCCTCCCATGAAACAGAGGAACTTCAAGATCGTCCCACTGTACAGTTCTGCTCCATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAA		MQNSLLNPSNLSIPSHETEELQDRPTVQFCSMSVDLVSGPRLL*		MQNSLLNPSNLSIPSHETEELQDRPTVQFCSMSVDLVSGPRLL*		TCGAACCTTA	ATATAATCGT	0		0	0	0	0	0
10886	4681	af	AN5730.1	54.m06849	AO070341000031	1			-198	-31			ATGAAACAGAGGAACTTCAAGATCGTCCCACTGTACAGTTCTGCTCCATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAAATATAATCGTGACAAGCTAAGATCATCGATCTCGCTAGATGCCTCGCGCATCATCTCAGATCGCAGTCTTCGTATCCACTAG		ATGAAACAGAGGAACTTCAAGATCGTCCCACTGTACAGTTCTGCTCCATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAAATATAATCGTGACAAGCTAAGATCATCGATCTCGCTAGATGCCTCGCGCATCATCTCAGATCGCAGTCTTCGTATCCACTAG		MKQRNFKIVPLYSSAPCRSIWCLARAYSKYNRDKLRSSISLDASRIISDRSLRIH*		MKQRNFKIVPLYSSAPCRSIWCLARAYSKYNRDKLRSSISLDASRIISDRSLRIH*		ATCCCCTCCC	ACACTCTGAC	0		0	0	0	0	0
10887	4681	af	AN5730.1	54.m06849	AO070341000031	1			-151	-113			ATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAA		ATGTCGGTCGATCTGGTGTCTGGCCCGCGCCTACTCTAA		MSVDLVSGPRLL*		MSVDLVSGPRLL*		GTTCTGCTCC	ATATAATCGT	0		0	0	0	0	0
10888	4681	ao	AN5730.1	54.m06849	AO070341000031	1					-461	-258	ATGCTCGATCATCTCACGTTTCCGACTTCACTTCTGGATTCTGCCCTAATCCCTCCCCTCGTATACAGAATCCCTTCTCTTCAGAACCTTCAAAACGTGCACCCTAGATTTATTTACTCCTCTCCATGCCGGCCTACCCTGCCTCCACACACCCCCGCTGCGAGTCAATCTAGAAAACGCCGATCAACGGTCTTTCTGGCATAG			ATGCTCGATCATCTCACGTTTCCGACTTCACTTCTGGATTCTGCCCTAATCCCTCCCCTCGTATACAGAATCCCTTCTCTTCAGAACCTTCAAAACGTGCACCCTAGATTTATTTACTCCTCTCCATGCCGGCCTACCCTGCCTCCACACACCCCCGCTGCGAGTCAATCTAGAAAACGCCGATCAACGGTCTTTCTGGCATAG	MLDHLTFPTSLLDSALIPPLVYRIPSLQNLQNVHPRFIYSSPCRPTLPPHTPAASQSRKRRSTVFLA*			MLDHLTFPTSLLDSALIPPLVYRIPSLQNLQNVHPRFIYSSPCRPTLPPHTPAASQSRKRRSTVFLA*	TCTGTTTACC	GCGTTGACGG	0		0	0	0	0	0
10889	4681	ao	AN5730.1	54.m06849	AO070341000031	1					-336	-289	ATGCCGGCCTACCCTGCCTCCACACACCCCCGCTGCGAGTCAATCTAG			ATGCCGGCCTACCCTGCCTCCACACACCCCCGCTGCGAGTCAATCTAG	MPAYPASTHPRCESI*			MPAYPASTHPRCESI*	ACTCCTCTCC	AAAACGCCGA	0		0	0	0	0	0
10890	4681	ao	AN5730.1	54.m06849	AO070341000031	1					-243	-214	ATGCCACTTGGGATAGATATATCTTCATAG			ATGCCACTTGGGATAGATATATCTTCATAG	MPLGIDISS*			MPLGIDISS*	TGACGGTCTT	CAATATCGAA	0		0	0	0	0	0
10891	4681	ao	AN5730.1	54.m06849	AO070341000031	1					-115	-104	ATGTGCACTTGA			ATGTGCACTTGA	MCT*			MCT*	TTTGTCTCAA	CGAAGAAGAG	0		0	0	0	0	0
10896	4682	af	AN1151.1	69.m15307	AO070226000022	0			-39	-28			ATGTTACTTTGA		ATGTTACTTTGA		MLL*		MLL*		TTCATCAATT	GATCCAATCG	1	G	FG09485.1	MG01335.1	NCU04071.1	0	0
10923	4689	ao	AN6132.1	72.m19030	AO070340000067	1					-93	-76	ATGCATTTCCACTGGTAA			ATGCATTTCCACTGGTAA	MHFHW*			MHFHW*	CTTTGAGATC	CGGCGGCGTG	0		0	0	0	0	0
10924	4693	an	AN0709.1	70.m15316	AO070343000497	1	-340	-281					ATGACACCCGATCCCCACTGCTGCCATATCGGCCATACGGAGACCTGCTCATCACCGTGA	ATGACACCCGATCCCCACTGCTGCCATATCGGCCATACGGAGACCTGCTCATCACCGTGA			MTPDPHCCHIGHTETCSSP*	MTPDPHCCHIGHTETCSSP*			TTATTCAACT	CAAAGTCCAG	0	R	0	0	0	0	0
10925	4693	an	AN0709.1	70.m15316	AO070343000497	1	-244	-206					ATGCTAGACCCAAACATCTGGTCCCTCGACTCGATTTAA	ATGCTAGACCCAAACATCTGGTCCCTCGACTCGATTTAA			MLDPNIWSLDSI*	MLDPNIWSLDSI*			CCTAATCACT	AACCAGCATC	0	R	0	0	0	0	0
10991	4716	af	AN4540.1	57.m05981	AO070321000158	0			-54	-7			ATGTCTACCATTGAGGCCTATTGCAAGAACAGTAGCTCGTCATATTGA		ATGTCTACCATTGAGGCCTATTGCAAGAACAGTAGCTCGTCATATTGA		MSTIEAYCKNSSSSY*		MSTIEAYCKNSSSSY*		TCATATGTAG	CACAGCATGG	1	ER	0	0	0	0	0
11005	4720	ao	AN1362.1	70.m14867	AO070243000002	1					-102	-64	ATGTCGGGCTCAGCAGCACGCTTCTTCTCGTGCTTGTAG			ATGTCGGGCTCAGCAGCACGCTTCTTCTCGTGCTTGTAG	MSGSAARFFSCL*			MSGSAARFFSCL*	TGCTTTCTGC	ACGATATCTT	0		0	0	0	0	0
11007	4722	af	AN3826.1	58.m07802	AO070305000062	0			-57	-43			ATGGTCAATTATTGA		ATGGTCAATTATTGA		MVNY*		MVNY*		TTAGATAACG	TAATTGCTAT	1	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11008	4722	af	AN3826.1	58.m07802	AO070305000062	0			-34	-8			ATGCTACAATCTTCAATTTTTTGTTGA		ATGCTACAATCTTCAATTTTTTGTTGA		MLQSSIFC*		MLQSSIFC*		GATAATTGCT	ACACATTATG	1	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11011	4722	ao	AN3826.1	58.m07802	AO070305000062	0					-34	-8	ATGTACAGCACTAGGAATATTTCCTGA			ATGTACAGCACTAGGAATATTTCCTGA	MYSTRNIS*			MYSTRNIS*	CCGTTCGGCT	TAGTGTCATG	1	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11014	4728	an	AN1795.1	72.m19547	AO070309000136	1	-134	-90					ATGTATCCTTTGTATCGCCTCCACAGCCATCAATCTCCTTTTTAA	ATGTATCCTTTGTATCGCCTCCACAGCCATCAATCTCCTTTTTAA			MYPLYRLHSHQSPF*	MYPLYRLHSHQSPF*			TTCTCTCCTC	TACCTAACTG	0	P	0	0	0	0	0
11015	4728	af	AN1795.1	72.m19547	AO070309000136	1			-119	-6			ATGGTGTGTTTGGTATCTGCCACACCTGGGTCGGCCCCGTCACACTTATTCAATCAGCATCATCTATCTCTCTCTACCGATAATCGCGCCACTGTGCGCGTCGCAAGGCTATAG		ATGGTGTGTTTGGTATCTGCCACACCTGGGTCGGCCCCGTCACACTTATTCAATCAGCATCATCTATCTCTCTCTACCGATAATCGCGCCACTGTGCGCGTCGCAAGGCTATAG		MVCLVSATPGSAPSHLFNQHHLSLSTDNRATVRVARL*		MVCLVSATPGSAPSHLFNQHHLSLSTDNRATVRVARL*		TCCTCGTCCG	CAATCATGGG	0	P	0	0	0	0	0
11041	4738	af	AN0888.1	70.m15494	AO070320000057	0			-29	-18			ATGACTCTCTAA		ATGACTCTCTAA		MTL*		MTL*		CTCTGACTTC	TCCTTCCTTG	1	BT	0	0	0	0	0
11079	4749	af	AN6114.1	72.m19045	AO070340000090	1			-61	-41			ATGCAGCGAGTGATCGCCTAA		ATGCAGCGAGTGATCGCCTAA		MQRVIA*		MQRVIA*		ATCACCCTCA	TTGTCAGATA	0	L	FG01896.1	0	NCU01321.1	0	0
11097	4755	af	AN1871.1	57.m05746	AO070341000188	0			-30	-16			ATGTTCACGCCGTAG		ATGTTCACGCCGTAG		MFTP*		MFTP*		TTCTCATTGA	CGATATCCAT	1		0	0	0	0	0
11127	4765	af	AN3802.1	57.m05972	AO070337000226	0			-45	-28			ATGCAGCTGGTCAACTGA		ATGCAGCTGGTCAACTGA		MQLVN*		MQLVN*		GCAAGAACAG	CTGTGACGGC	1		0	0	0	0	0
11129	4766	af	AN5205.1	69.m14902	AO070199000004	0			-55	-44			ATGTCTCTCTGA		ATGTCTCTCTGA		MSL*		MSL*		GGGCTGGTCT	TATCGGGTCT	1	RP	0	0	0	0	0
11140	4768	af	AN1045.1	70.m15201	AO070336000078	1			-124	-92			ATGTCGAGAATTTTTCGTTGTATGCTGACCTAG		ATGTCGAGAATTTTTCGTTGTATGCTGACCTAG		MSRIFRCMLT*		MSRIFRCMLT*		TTTAAATCGG	TCTGATCGAG	0	R	0	0	0	0	0
11141	4768	af	AN1045.1	70.m15201	AO070336000078	1			-103	-92			ATGCTGACCTAG		ATGCTGACCTAG		MLT*		MLT*		TTTTCGTTGT	TCTGATCGAG	0	R	0	0	0	0	0
11160	4782	af	AN8400.1	59.m09197	AO070329000063	0			-60	-43			ATGAGTATGGTCGCATAG		ATGAGTATGGTCGCATAG		MSMVA*		MSMVA*		TCACTTGCTG	AACAAGATCA	1	GEPR	0	0	0	0	0
11161	4782	af	AN8400.1	59.m09197	AO070329000063	0			-54	-43			ATGGTCGCATAG		ATGGTCGCATAG		MVA*		MVA*		GCTGATGAGT	AACAAGATCA	1	GEPR	0	0	0	0	0
11164	4782	ao	AN8400.1	59.m09197	AO070329000063	0					-30	-7	ATGTGCCACTATACAATACGCTGA			ATGTGCCACTATACAATACGCTGA	MCHYTIR*			MCHYTIR*	CTACTTCGTT	GTAGCAATGG	1	GEPR	0	0	0	0	0
11170	4791	af	AN5881.1	72.m19250	AO070245000027	0			-48	-31			ATGCAACGTCCCTGGTAG		ATGCAACGTCCCTGGTAG		MQRPW*		MQRPW*		GTGAAGGGTA	CGATCAAAAT	1		0	0	0	0	0
11184	4793	an	AN5970.1	72.m19186	AO070340000328	1	-98	-84					ATGTGCCACCTTTAA	ATGTGCCACCTTTAA			MCHL*	MCHL*			TTGTTCCCCC	ATAAATCCGA	0	O	0	0	0	0	0
11185	4793	af	AN5970.1	72.m19186	AO070340000328	1			-129	-19			ATGTGGAGTTTGGACCAATGTGCCTATTGTGAAATCTACTTCAGCCCCTTCTTCTTTAACAATTCTCGACTTTCGTTTTCAGTCTTAACCTGTTGCTTTCCGGGTCTTTGA		ATGTGGAGTTTGGACCAATGTGCCTATTGTGAAATCTACTTCAGCCCCTTCTTCTTTAACAATTCTCGACTTTCGTTTTCAGTCTTAACCTGTTGCTTTCCGGGTCTTTGA		MWSLDQCAYCEIYFSPFFFNNSRLSFSVLTCCFPGL*		MWSLDQCAYCEIYFSPFFFNNSRLSFSVLTCCFPGL*		GGTTCGATAA	CCTTGAACGC	0	O	0	0	0	0	0
11186	4793	af	AN5970.1	72.m19186	AO070340000328	1			-112	-98			ATGTGCCTATTGTGA		ATGTGCCTATTGTGA		MCLL*		MCLL*		GTTTGGACCA	AATCTACTTC	0	O	0	0	0	0	0
11187	4793	ao	AN5970.1	72.m19186	AO070340000328	1					-100	-86	ATGTGCCACCCGTAA			ATGTGCCACCCGTAA	MCHP*			MCHP*	CTAGGTCTTC	TTTCTTTGGC	0	O	0	0	0	0	0
11188	4794	af	AN1532.1	55.m03049	AO070334000248	1			-68	-24			ATGTTGGTGCCTCTCCTGCCCGAGCGATTGATCGCTGGCGGCTAA		ATGTTGGTGCCTCTCCTGCCCGAGCGATTGATCGCTGGCGGCTAA		MLVPLLPERLIAGG*		MLVPLLPERLIAGG*		TCTTGCTTTG	TTCTGATAGC	0		0	0	0	0	0

§S3 Upstream open reading frames (uORFs)

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG categ	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
11189	4794	ao	AN1532.1	55.m03049	AO070334000248	1					-143	-21	ATGAAGTTCTTTTCATATCACTTTTCTTGCATTGTAATCAACTCTTATTGTACCGTGTCGCTGTCCTTGCTCTATTGCTTGCATACTTCAAGTGGTTTATCTCACCCATTATCTAACGCTTAA			ATGAAGTTCTTTTCATATCACTTTTCTTGCATTGTAATCAACTCTTATTGTACCGTGTCGCTGTCCTTGCTCTATTGCTTGCATACTTCAAGTGGTTTATCTCACCCATTATCTAACGCTTAA	MKFFSYHFSCIVINSYCTVSLSLLYCLHTSSGLSHPLSNA*			MKFFSYHFSCIVINSYCTVSLSLLYCLHTSSGLSHPLSNA*	TCGGACGTGG	GAAGGTATAA	0		0	0	0	0	0
11219	4820	af	AN4209.1	54.m07042	AO070231000015	0			-40	-8			ATGTCCTTCTGGTTCATAACTACCTCCCAATAG		ATGTCCTTCTGGTTCATAACTACCTCCCAATAG		MSFWFITTSQ*		MSFWFITTSQ*		CGCAGTACAT	GTGCAAGATG	1	R	FG05384.1	0	0	0	0
11235	4831	an	AN5517.1	69.m15442	AO070341000376	1	-304	-290					ATGATCATGTTCTAA	ATGATCATGTTCTAA			MIMF*	MIMF*			CACCACTGTG	CGATTACTGT	0	R	0	0	0	0	0
11236	4831	an	AN5517.1	69.m15442	AO070341000376	1	-227	-189					ATGCTGACAAGCCCCCATTTTGCCTGCTCCCAAGACTAG	ATGCTGACAAGCCCCCATTTTGCCTGCTCCCAAGACTAG			MLTSPHFACSQD*	MLTSPHFACSQD*			ACCGAGTATC	ACACTTCCTC	0	R	0	0	0	0	0
11237	4831	an	AN5517.1	69.m15442	AO070341000376	1	-141	-31					ATGATACTCAAAAGTACGCGTGACGTATATCGACTTTTGAACAGAGACGACGATAACGGTCCAGTTTCCACCGCCTCGAAGACGCGTCTCTGTGCTAGCATATCCCGATAA	ATGATACTCAAAAGTACGCGTGACGTATATCGACTTTTGAACAGAGACGACGATAACGGTCCAGTTTCCACCGCCTCGAAGACGCGTCTCTGTGCTAGCATATCCCGATAA			MILKSTRDVYRLLNRDDDNGPVSTASKTRLCASISR*	MILKSTRDVYRLLNRDDDNGPVSTASKTRLCASISR*			TTCTTCTCGC	CGCAGCCGAA	0	R	0	0	0	0	0
11238	4831	af	AN5517.1	69.m15442	AO070341000376	1			-329	-312			ATGACAATCATGTTCTGA		ATGACAATCATGTTCTGA		MTIMF*		MTIMF*		GAACTCTCTT	ATTATTCTCT	0	R	0	0	0	0	0
11239	4831	ao	AN5517.1	69.m15442	AO070341000376	1					-320	-306	ATGGCCGTGCTTTAA			ATGGCCGTGCTTTAA	MAVL*			MAVL*	CGCCGTCCTT	TCACCGCTTT	0	R	0	0	0	0	0
11240	4831	ao	AN5517.1	69.m15442	AO070341000376	1					-276	-244	ATGGTTCTTACAGGCGTGTATGTACCGTGCTGA			ATGGTTCTTACAGGCGTGTATGTACCGTGCTGA	MVLTGVYVPC*			MVLTGVYVPC*	CGGCACTTAG	CCGCCCTCGA	0	R	0	0	0	0	0
11241	4831	ao	AN5517.1	69.m15442	AO070341000376	1					-257	-210	ATGTACCGTGCTGACCGCCCTCGATATACCGGATCGTTTCCCTGTTGA			ATGTACCGTGCTGACCGCCCTCGATATACCGGATCGTTTCCCTGTTGA	MYRADRPRYTGSFPC*			MYRADRPRYTGSFPC*	ACAGGCGTGT	GCATCGCCGG	0	R	0	0	0	0	0
11242	4831	ao	AN5517.1	69.m15442	AO070341000376	1					-125	-114	ATGTCCCTATAA			ATGTCCCTATAA	MSL*			MSL*	TAGTATCTTG	CCGCCGACGT	0	R	0	0	0	0	0
11247	4839	an	AN4528.1	57.m05598	AO070321000138	1	-431	-390					ATGTCACTGACGCCCGGTAGCGTCCTATCAATCTCAATCTAG	ATGTCACTGACGCCCGGTAGCGTCCTATCAATCTCAATCTAG			MSLTPGSVLSISI*	MSLTPGSVLSISI*			GTCTTGTGCA	CTTTCAGCGT	0	U	0	0	0	0	0
11248	4839	af	AN4528.1	57.m05598	AO070321000138	1			-369	-340			ATGCACTATCAGCATTTGATTCTTTTTTAA		ATGCACTATCAGCATTTGATTCTTTTTTAA		MHYQHLILF*		MHYQHLILF*		ATCAGTCACC	GTGATTATCT	0	U	0	0	0	0	0
11249	4839	ao	AN4528.1	57.m05598	AO070321000138	1					-684	-670	ATGACACATCTGTAG			ATGACACATCTGTAG	MTHL*			MTHL*	ACCGAGATAC	GACAGAATCT	0	U	0	0	0	0	0
11250	4839	ao	AN4528.1	57.m05598	AO070321000138	1					-418	-392	ATGGCTATTGCTTGGATGGTGTCGTGA			ATGGCTATTGCTTGGATGGTGTCGTGA	MAIAWMVS*			MAIAWMVS*	AACTGTCTTG	TTCGTGAACA	0	U	0	0	0	0	0
11251	4839	ao	AN4528.1	57.m05598	AO070321000138	1					-403	-392	ATGGTGTCGTGA			ATGGTGTCGTGA	MVS*			MVS*	TATTGCTTGG	TTCGTGAACA	0	U	0	0	0	0	0
11261	4845	ao	AN1830.1	52.m03901	AO070292000077	0					-56	-3	ATGTTTCTCCGCGGTAAACACGTAAGTCACGACTTGAATAAGGACCAGCGGTAA			ATGTTTCTCCGCGGTAAACACGTAAGTCACGACTTGAATAAGGACCAGCGGTAA	MFLRGKHVSHDLNKDQR*			MFLRGKHVSHDLNKDQR*	ATGAACTTGG	CAATGACATT	1	R	0	0	0	0	0
11263	4849	an	AN0671.1	70.m15273	AO070343000549	1	-220	-185					ATGCTCTCATATCATCTCGACCTGAGTCTTTCCTGA	ATGCTCTCATATCATCTCGACCTGAGTCTTTCCTGA			MLSYHLDLSLS*	MLSYHLDLSLS*			TCTTATTTTA	TCTTGCTCGT	0		0	0	0	0	0
11264	4849	an	AN0671.1	70.m15273	AO070343000549	1	-135	-112					ATGCCGCTAAGCTTCTTCCGCTGA	ATGCCGCTAAGCTTCTTCCGCTGA			MPLSFFR*	MPLSFFR*			AAGCTCCCCA	TCAAGGAGAT	0		0	0	0	0	0
11265	4849	af	AN0671.1	70.m15273	AO070343000549	1			-334	-260			ATGGGCTCGAATCCTGAACGACTGTGGGAATTATGCGACCTCCATGTCAAACAGCATCTGGCTCAACAACAGTAG		ATGGGCTCGAATCCTGAACGACTGTGGGAATTATGCGACCTCCATGTCAAACAGCATCTGGCTCAACAACAGTAG		MGSNPERLWELCDLHVKQHLAQQQ*		MGSNPERLWELCDLHVKQHLAQQQ*		CTCTGAAGGA	AAGCAGCAGC	0		0	0	0	0	0
11266	4849	af	AN0671.1	70.m15273	AO070343000549	1			-302	-204			ATGCGACCTCCATGTCAAACAGCATCTGGCTCAACAACAGTAGAAGCAGCAGCAACGCCGAAGGAAGAGGAGGAGGACGACGATCCTGAATCGAGCTGA		ATGCGACCTCCATGTCAAACAGCATCTGGCTCAACAACAGTAGAAGCAGCAGCAACGCCGAAGGAAGAGGAGGAGGACGACGATCCTGAATCGAGCTGA		MRPPCQTASGSTTVEAAATPKEEEEDDDPESS*		MRPPCQTASGSTTVEAAATPKEEEEDDDPESS*		TGTGGGAATT	GGTAGAAAAA	0		0	0	0	0	0
11267	4849	af	AN0671.1	70.m15273	AO070343000549	1			-291	-214			ATGTCAAACAGCATCTGGCTCAACAACAGTAGAAGCAGCAGCAACGCCGAAGGAAGAGGAGGAGGACGACGATCCTGA		ATGTCAAACAGCATCTGGCTCAACAACAGTAGAAGCAGCAGCAACGCCGAAGGAAGAGGAGGAGGACGACGATCCTGA		MSNSIWLNNSRSSSNAEGRGGGRRS*		MSNSIWLNNSRSSSNAEGRGGGRRS*		TGCGACCTCC	ATCGAGCTGA	0		0	0	0	0	0
11268	4849	af	AN0671.1	70.m15273	AO070343000549	1			-152	-126			ATGTCGAGTCTTCCGTATTCCCACTGA		ATGTCGAGTCTTCCGTATTCCCACTGA		MSSLPYSH*		MSSLPYSH*		TCCATTCCAA	CACAATTCCC	0		0	0	0	0	0
11269	4849	af	AN0671.1	70.m15273	AO070343000549	1			-38	-18			ATGGCCGTTGGCGTCAGCTAG		ATGGCCGTTGGCGTCAGCTAG		MAVGVS*		MAVGVS*		GCCGCTTTGA	ACGCGCCAGT	1		0	0	0	0	0
11270	4849	ao	AN0671.1	70.m15273	AO070343000549	1					-191	-108	ATGTCGAAACGTCGTCGGCTGAAAAAGTATCGTTCTTCTTCTCTCACACCACATCATTCTTTTCGTTTACGACATCGATGCTGA			ATGTCGAAACGTCGTCGGCTGAAAAAGTATCGTTCTTCTTCTCTCACACCACATCATTCTTTTCGTTTACGACATCGATGCTGA	MSKRRRLKKYRSSSLTPHHSFRLRHRC*			MSKRRRLKKYRSSSLTPHHSFRLRHRC*	ACTCGTAGTC	TCCTCTTGAG	0		0	0	0	0	0
11271	4849	ao	AN0671.1	70.m15273	AO070343000549	1					-114	-58	ATGCTGATCCTCTTGAGTTCCTGCAGACCCAGGTATTATCCTGGAAGACACCTTTAA			ATGCTGATCCTCTTGAGTTCCTGCAGACCCAGGTATTATCCTGGAAGACACCTTTAA	MLILLSSCRPRYYPGRHL*			MLILLSSCRPRYYPGRHL*	TACGACATCG	ATTTTGCGGC	0		0	0	0	0	0
11272	4849	ao	AN0671.1	70.m15273	AO070343000549	1					-39	-22	ATGGCCGTTACGTTTTGA			ATGGCCGTTACGTTTTGA	MAVTF*			MAVTF*	GCCGTCTTGA	TAACAAATTG	1		0	0	0	0	0
11288	4855	ao	AN0326.1	54.m06429	AO070318000002	1					-223	-200	ATGAGGTGCCACCAGACTTGGTGA			ATGAGGTGCCACCAGACTTGGTGA	MRCHQTW*			MRCHQTW*	CTCACTGTAA	AATAAGCACG	0	Z	0	0	0	0	0
11295	4860	an	AN6241.1	72.m19416	AO070304000092	1	-36	-22					ATGGTTCTGAAATAA	ATGGTTCTGAAATAA			MVLK*	MVLK*			TCCTCGTCGG	AGCGTGAACC	1	T	0	0	0	0	0
11307	4865	an	AN2109.1	57.m05963	AO070341000274	1	-176	-159					ATGGGAGCGTTCGTCTGA	ATGGGAGCGTTCGTCTGA			MGAFV*	MGAFV*			TTCAGACTCC	AGGTCTGTGC	0	DO	0	0	0	0	0
11309	4867	an	AN5980.1	72.m19163	AO070340000300	0	-21	-4					ATGACCAAAAAATTTTGA	ATGACCAAAAAATTTTGA			MTKKF*	MTKKF*			CTCTCCATAT	ATCATGTCTT	1		0	0	0	0	0
11312	4867	ao	AN5980.1	72.m19163	AO070340000300	0					-53	-18	ATGCCCAACCACTTTTCTCACCCTCTACACCATTGA			ATGCCCAACCACTTTTCTCACCCTCTACACCATTGA	MPNHFSHPLHH*			MPNHFSHPLHH*	ACCGTCTTCA	CAGAATTACC	1		0	0	0	0	0
11327	4872	af	AN5346.1	69.m15558	AO070333000176	0			-42	-28			ATGATCGCACGTTAG		ATGATCGCACGTTAG		MIAR*		MIAR*		TTACAACACA	ACTAGATTTC	1	O	0	MG10494.1	0	0	0
11331	4872	ao	AN5346.1	69.m15558	AO070333000176	0					-50	-36	ATGATTGATATCTAA			ATGATTGATATCTAA	MIDI*			MIDI*	TTTGCGCATT	ACTATCTAAT	1	O	0	MG10494.1	0	0	0
11346	4876	af	AN5400.1	69.m15773	AO070333000134	0			-32	-15			ATGGTCAGTGAAAAGTGA		ATGGTCAGTGAAAAGTGA		MVSEK*		MVSEK*		GTTCCCGATC	CAACTACCAG	1	P	0	0	0	0	0
11351	4878	ao	AN0564.1	69.m15283	AO070272000041	0					-57	-43	ATGTATTCTTGTTAA			ATGTATTCTTGTTAA	MYSC*			MYSC*	CCCTTTCACT	GTCCAGCAAT	1	R	0	0	0	0	0
11352	4879	an	AN6305.1	72.m19329	AO070308000060	0	-52	-11					ATGCTTCCAGTTTGTCTTACATCGACCGTTGTCTCATCTTAA	ATGCTTCCAGTTTGTCTTACATCGACCGTTGTCTCATCTTAA			MLPVCLTSTVVSS*	MLPVCLTSTVVSS*			CTAGCGCTGC	ACCGTCCTCG	1	T	0	0	0	0	0
11353	4879	af	AN6305.1	72.m19329	AO070308000060	0			-57	-31			ATGGTCCATGTTTCACCTTATCTCTGA		ATGGTCCATGTTTCACCTTATCTCTGA		MVHVSPYL*		MVHVSPYL*		CACCAATCCT	CCTCTTATAC	1	T	0	0	0	0	0
11354	4879	af	AN6305.1	72.m19329	AO070308000060	0			-50	-15			ATGTTTCACCTTATCTCTGACCTCTTATACTTTTAA		ATGTTTCACCTTATCTCTGACCTCTTATACTTTTAA		MFHLISDLLYF*		MFHLISDLLYF*		CCTATGGTCC	CTCTCGTTTC	1	T	0	0	0	0	0
11371	4884	af	AN1981.1	58.m08945	AO070301000066	0			-25	-14			ATGCTGATGTGA		ATGCTGATGTGA		MLM*		MLM*		CGACCTGCAT	CTATTACTTC	1	O	0	0	0	YJL031C	0
11374	4885	an	AN6208.1	72.m19306	AO070308000085	1	-84	-49					ATGGACAAGGATTACACGCCTTCAACTCACAAATGA	ATGGACAAGGATTACACGCCTTCAACTCACAAATGA			MDKDYTPSTHK*	MDKDYTPSTHK*			CAGGCAGCCT	GCTTTCGCTT	0		0	0	0	0	0
11375	4885	ao	AN6208.1	72.m19306	AO070308000085	1					-90	-76	ATGCATCATTTCTAA			ATGCATCATTTCTAA	MHHF*			MHHF*	TCCTGAACAG	GCTTGCATCG	0		0	0	0	0	0
11388	4890	an	AN8696.1	62.m03488	AO070315000121	0	-47	-36					ATGCAAAATTAG	ATGCAAAATTAG			MQN*	MQN*			CTATCATAAG	CAACGGTGGT	1	S	0	0	0	0	0
11395	4892	ao	AN4781.1	59.m09202	AO070329000069	0					-45	-34	ATGCGCCACTAA			ATGCGCCACTAA	MRH*			MRH*	CAGCCAGACA	TCAGATATAT	1	CH	0	0	0	0	0
11396	4893	af	AN1544.1	55.m03062	AO070339000310	0			-41	-3			ATGTGCACGGAGTGTCGTACAGATAATCCCCGCTATTGA		ATGTGCACGGAGTGTCGTACAGATAATCCCCGCTATTGA		MCTECRTDNPRY*		MCTECRTDNPRY*		AACCCCTTGA	CCATGTCCGA	1		0	0	0	0	0
11444	4911	an	AN5103.1	54.m06964	AO070291000076	1	-87	-40					ATGTTTCTACCTAAGGCCAATGTTGAGCGCTCCAAATCATCTTATTGA	ATGTTTCTACCTAAGGCCAATGTTGAGCGCTCCAAATCATCTTATTGA			MFLPKANVERSKSSY*	MFLPKANVERSKSSY*			GGTCACTACA	ACTTCAGCGT	0	C	0	0	0	0	0
11447	4911	af	AN5103.1	54.m06964	AO070291000076	1			-176	-129			ATGTTTTTAAACTTGTTTTGTCCTTCATGTCGATTCTTTTCTCCATAA		ATGTTTTTAAACTTGTTTTGTCCTTCATGTCGATTCTTTTCTCCATAA		MFLNLFCPSCRFFSP*		MFLNLFCPSCRFFSP*		TGATATCTCA	TCTGTACTCT	0	C	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_conser	context_down_co	within 60b	COG cate	fg_uorf_utr	mg_uorf_u	nc_uorf_ut	sc_uorf_10	sc_cooccu
11448	4911	af	AN5103.1	54.m06964	AO070291000076	1			-150	-115			ATGTCGATTCTTTTCTCCATAATCTGTACTCTATAG		ATGTCGATTCTTTTCTCCATAATCTGTACTCTATAG		MSILFSIICTL*		MSILFSIICTL*		TTTGTCCTTC	GCGAGCATTG	0	C	0	0	0	0	0
11449	4911	af	AN5103.1	54.m06964	AO070291000076	1			-83	-48			ATGGTATCATCCTCCCCGCGAATATTTGTGATCTGA		ATGGTATCATCCTCCCCGCGAATATTTGTGATCTGA		MVSSSPRIFVI*		MVSSSPRIFVI*		AGATACCCAA	ATGCATATAC	0	C	0	0	0	0	0
11450	4911	af	AN5103.1	54.m06964	AO070291000076	1			-47	-12			ATGCATATACGTCCCGATGGAGAAGGGTGCGCTTAG		ATGCATATACGTCCCGATGGAGAAGGGTGCGCTTAG		MHIRPDGEGCA*		MHIRPDGEGCA*		TGTGATCTGA	ATATCCGCAT	1	C	0	0	0	0	0
11478	4924	af	AN3814.1	57.m05668	AO070311000012	1			-598	-509			ATGGATGGACATCCGACTGACTCCGAGGAATCTCCCTTTCTTTCTCCCTTGTTCCTGAATCATTGTGCCGTCCAGGTTATCATTATATAA		ATGGATGGACATCCGACTGACTCCGAGGAATCTCCCTTTCTTTCTCCCTTGTTCCTGAATCATTGTGCCGTCCAGGTTATCATTATATAA		MDGHPTDSEESPFLSPLFLNHCAVQVIII*		MDGHPTDSEESPFLSPLFLNHCAVQVIII*		CACGTGATTT	TCAAAAATTT	0	O	0	0	0	0	0
11479	4924	af	AN3814.1	57.m05668	AO070311000012	1			-594	-541			ATGGACATCCGACTGACTCCGAGGAATCTCCCTTTCTTTCTCCCTTGTTCCTGA		ATGGACATCCGACTGACTCCGAGGAATCTCCCTTTCTTTCTCCCTTGTTCCTGA		MDIRLTPRNLPFFLPCS*		MDIRLTPRNLPFFLPCS*		TGATTTATGG	ATCATTGTGC	0	O	0	0	0	0	0
11495	4925	ao	AN0454.1	54.m06615	AO070328000182	1					-63	-43	ATGTTCACAATCATTTTGTAA			ATGTTCACAATCATTTTGTAA	MFTIIL*			MFTIIL*	TCTTCTTTCG	TCTGTGGTGA	0	E	0	0	0	0	0

1	2	af	AN5593.1	58.m07517	AO070328000010	0			-199	-137			ATGATCCCCTGTTCTGATCAATTATCATATTCTCTGACTGCACGAACAACGAAAACGTCCTAG		ATGATCCCCTGTTCTGATCAATTATCATATTCTCTGACTGCACGAACAACGAAAACGTCCTAG		MIPCSDQLSYSLTARTTKTS*		MIPCSDQLSYSLTARTTKTS*		CTTGATTGGC	CTCTGTCTAT	0	S	0	0	0	0	0
2	2	af	AN5593.1	58.m07517	AO070328000010	0			-89	-48			ATGCCAACCAAGCTCATACTGGACGACGAAGATTCGTTATAG		ATGCCAACCAAGCTCATACTGGACGACGAAGATTCGTTATAG		MPTKLILDDEDSL*		MPTKLILDDEDSL*		TCCTAACCCA	GGACAATAAT	0	S	0	0	0	0	0
3	2	ao	AN5593.1	58.m07517	AO070328000010	0					-240	-199	ATGCTAAGTTTCGATATAAGTCTCGTTCATGCTTGCACTTGA			ATGCTAAGTTTCGATATAAGTCTCGTTCATGCTTGCACTTGA	MLSFDISLVHACT*			MLSFDISLVHACT*	AGGCCCTTCA	AAGCGTGACG	0	S	0	0	0	0	0
4	2	ao	AN5593.1	58.m07517	AO070328000010	0					-212	-132	ATGCTTGCACTTGAAAGCGTGACGCGGTCGACTTACAGGGACACAAGCAGTCCAATATCCGCCTGTTTTGCTGCCAAGTAA			ATGCTTGCACTTGAAAGCGTGACGCGGTCGACTTACAGGGACACAAGCAGTCCAATATCCGCCTGTTTTGCTGCCAAGTAA	MLALESVTRSTYRDTSSPISACFAAK*			MLALESVTRSTYRDTSSPISACFAAK*	AGTCTCGTTC	GAAGACAAAC	0	S	0	0	0	0	0
8	4	af	AN0877.1	70.m15480	AO070320000036	0			-196	-119			ATGGAGTTTTCTCTTCTGCTGGTGCTCCGTCCCATCGATTATCCTCATCTGTGTCGCCGGAATCTACGGAAATCCTAG		ATGGAGTTTTCTCTTCTGCTGGTGCTCCGTCCCATCGATTATCCTCATCTGTGTCGCCGGAATCTACGGAAATCCTAG		MEFSLLLVLRPIDYPHLCRRNLRKS*		MEFSLLLVLRPIDYPHLCRRNLRKS*		AACAACGTCC	CGCCCCTCGC	0		0	0	0	0	0
6	4	an	AN0877.1	70.m15480	AO070320000036	0	-184	-62					ATGGACTTTTCGCCTGGACAAGTTCTGCCATCAAGACACTTCCCGCGCTACGTATACCTTCGACCGCTGGTCCCTTCTGTCGCGATACCAGAAGCGCATCACCGCCGAAGCTTGATTGCTTAG	ATGGACTTTTCGCCTGGACAAGTTCTGCCATCAAGACACTTCCCGCGCTACGTATACCTTCGACCGCTGGTCCCTTCTGTCGCGATACCAGAAGCGCATCACCGCCGAAGCTTGATTGCTTAG			MDFSPGQVLPSRHFPRYVYLRPLVPSVAIPEAHHRRSLIA*	MDFSPGQVLPSRHFPRYVYLRPLVPSVAIPEAHHRRSLIA*			AGTCACGCCC	ACCTGTTTGA	0		0	0	0	0	0
9	4	ao	AN0877.1	70.m15480	AO070320000036	0					-183	-58	ATGGATTTTTCTCTTTACCTAGTGCTTTTTCCGAAAGATATTCCGTATCGCCGCTTTTCCCGTCTATTGTCTTCTTCTTTTGCGACTCCCCCGGACACCGTTACCGGTGACGTTCGATTGCTATAG			ATGGATTTTTCTCTTTACCTAGTGCTTTTTCCGAAAGATATTCCGTATCGCCGCTTTTCCCGTCTATTGTCTTCTTCTTTTGCGACTCCCCCGGACACCGTTACCGGTGACGTTCGATTGCTATAG	MDFSLYLVLFPKDIPYRRFSRLLSSSFATPPDTVTGDVRLL*			MDFSLYLVLFPKDIPYRRFSRLLSSSFATPPDTVTGDVRLL*	CCCATTGTCC	AGCGAGGAAG	0		0	0	0	0	0
10	9	an	AN3785.1	57.m05971	AO070337000246	0	-218	-174					ATGTGGCTCCCCCTCTCGCGACCCCCGTCCCTCGTCGGCCCCTGA	ATGTGGCTCCCCCTCTCGCGACCCCCGTCCCTCGTCGGCCCCTGA			MWLPLSRPPSLVGP*	MWLPLSRPPSLVGP*			GTTGCTTTTG	TATCCGCATC	0	BL	0	0	0	0	0
16	13	af	AN2751.1	71.m15497	AO070323000056	0			-218	-192			ATGAAGGAATCTCTCCGCATTGTATGA		ATGAAGGAATCTCTCCGCATTGTATGA		MKESLRIV*		MKESLRIV*		TTTCGTTTGC	AATGTGTCCT	0	S	0	0	0	0	0
17	13	af	AN2751.1	71.m15497	AO070323000056	0			-195	-142			ATGAAATGTGTCCTGTGGCGGTGTGCTGTGACGACTGTCTGCCTCAGGCAGTAA		ATGAAATGTGTCCTGTGGCGGTGTGCTGTGACGACTGTCTGCCTCAGGCAGTAA		MKCVLWRCAVTTVCLRQ*		MKCVLWRCAVTTVCLRQ*		TCCGCATTGT	TTCCACTAAC	0	S	0	0	0	0	0
18	13	af	AN2751.1	71.m15497	AO070323000056	0			-63	-52			ATGCCGTGGTAG		ATGCCGTGGTAG		MPW*		MPW*		CACTACGAGA	ATCTTGCCAT	0	S	0	0	0	0	0
11	13	an	AN2751.1	71.m15497	AO070323000056	0	-232	-209					ATGTCATCGGGCTCCTATTTGTGA	ATGTCATCGGGCTCCTATTTGTGA			MSSGSYL*	MSSGSYL*			ACCATGCCCA	CCTAGATCAG	0	S	0	0	0	0	0
12	13	an	AN2751.1	71.m15497	AO070323000056	0	-151	-140					ATGCTGGGGTGA	ATGCTGGGGTGA			MLG*	MLG*			GGTCTTTTCA	ATGAGCGACA	0	S	0	0	0	0	0
13	13	an	AN2751.1	71.m15497	AO070323000056	0	-139	-110					ATGAGCGACAAATGGTGCCTTAGGCTGTAA	ATGAGCGACAAATGGTGCCTTAGGCTGTAA			MSDKWCLRL*	MSDKWCLRL*			GCTGGGGTGA	GGCAGAAAAC	0	S	0	0	0	0	0
14	13	an	AN2751.1	71.m15497	AO070323000056	0	-128	-117					ATGGTGCCTTAG	ATGGTGCCTTAG			MVP*	MVP*			TGAGCGACAA	GCTGTAAGGC	0	S	0	0	0	0	0
15	13	an	AN2751.1	71.m15497	AO070323000056	0	-89	-57					ATGATCCCGCACCACAATTATGATGAGTGCTAA	ATGATCCCGCACCACAATTATGATGAGTGCTAA			MIPHHNYDEC*	MIPHHNYDEC*			GTGACCCGTC	ATCTCCCGAG	0	S	0	0	0	0	0
19	13	ao	AN2751.1	71.m15497	AO070323000056	0					-159	-100	ATGTGTTGCCTTAGGCATCAATACCTCTCCGGCACTAACCTGGAGTCGGTAAGCGGGTGA			ATGTGTTGCCTTAGGCATCAATACCTCTCCGGCACTAACCTGGAGTCGGTAAGCGGGTGA	MCCLRHQYLSGTNLESVSG*			MCCLRHQYLSGTNLESVSG*	AACCGGTATA	TATCAGACCG	0	S	0	0	0	0	0
20	13	ao	AN2751.1	71.m15497	AO070323000056	0					-61	-50	ATGCGGCGGTAA			ATGCGGCGGTAA	MRR*			MRR*	CACTACATTT	ATCTCGCTCC	0	S	0	0	0	0	0
21	14	ao	AN0228.1	71.m15484	AO070323000081	0					-238	-197	ATGTCTTTTCCGACGCGTTCGCGTCGCCAACGCGTTTCTTGA			ATGTCTTTTCCGACGCGTTCGCGTCGCCAACGCGTTTCTTGA	MSFPTRSRRQRVS*			MSFPTRSRRQRVS*	GAACCGCGAT	AAAAGAAAGT	0	L	0	0	0	0	0
25	26	an	AN8236.1	53.m04127	AO070310000072	0	-219	-175					ATGTCCTTTTGTCCACTTCCATTTGAGGCTACATCCACTCATTGA	ATGTCCTTTTGTCCACTTCCATTTGAGGCTACATCCACTCATTGA			MSFCPLPFEATSTH*	MSFCPLPFEATSTH*			GGATCGGCCC	ATGTTTCTTA	0	T	0	0	0	0	0
26	26	an	AN8236.1	53.m04127	AO070310000072	0	-174	-121					ATGTTTCTTAATGACTTCAAGGATTGTCTGGTTTTGATTGATTGGGTTATTTGA	ATGTTTCTTAATGACTTCAAGGATTGTCTGGTTTTGATTGATTGGGTTATTTGA			MFLNDFKDCLVLIDWVI*	MFLNDFKDCLVLIDWVI*			CACTCATTGA	ACTTGGTACC	0	T	0	0	0	0	0
27	26	an	AN8236.1	53.m04127	AO070310000072	0	-164	-138					ATGACTTCAAGGATTGTCTGGTTTTGA	ATGACTTCAAGGATTGTCTGGTTTTGA			MTSRIVWF*	MTSRIVWF*			ATGTTTCTTA	TTGATTGGGT	0	T	0	0	0	0	0
28	26	an	AN8236.1	53.m04127	AO070310000072	0	-93	-52					ATGTACGAGGGTCACGGGCGAGTTCTGATCGTCCCTTCCTGA	ATGTACGAGGGTCACGGGCGAGTTCTGATCGTCCCTTCCTGA			MYEGHGRVLIVPS*	MYEGHGRVLIVPS*			AGCTGTCTTG	ATCGTTGCTT	0	T	0	0	0	0	0
29	26	ao	AN8236.1	53.m04127	AO070310000072	0					-149	-123	ATGTGTGAGAGTAGTTTCCACCCTTGA			ATGTGTGAGAGTAGTTTCCACCCTTGA	MCESSFHP*			MCESSFHP*	GATTTGTTCG	TTTCTAGATT	0	T	0	0	0	0	0
31	36	af	AN8197.1	53.m03776	AO070310000122	0			-207	-160			ATGAGCGGTAAAATGAGTCCTGAGAACGCCCACGTTTGCCCTTTTTAG		ATGAGCGGTAAAATGAGTCCTGAGAACGCCCACGTTTGCCCTTTTTAG		MSGKMSPENAHVCPF*		MSGKMSPENAHVCPF*		GAAAAAGGAC	GGCCTTCAGC	0	R	0	0	0	0	0
32	36	af	AN8197.1	53.m03776	AO070310000122	0			-195	-160			ATGAGTCCTGAGAACGCCCACGTTTGCCCTTTTTAG		ATGAGTCCTGAGAACGCCCACGTTTGCCCTTTTTAG		MSPENAHVCPF*		MSPENAHVCPF*		GAGCGGTAAA	GGCCTTCAGC	0	R	0	0	0	0	0
33	36	af	AN8197.1	53.m03776	AO070310000122	0			-122	-93			ATGAGCAATGTACTGTCAGGTCACGTGTAA		ATGAGCAATGTACTGTCAGGTCACGTGTAA		MSNVLSGHV*		MSNVLSGHV*		TGCGAGAACT	CAGGACAGAT	0	R	0	0	0	0	0
30	36	an	AN8197.1	53.m03776	AO070310000122	0	-145	-128					ATGAACTGCAGCGCATAA	ATGAACTGCAGCGCATAA			MNCSA*	MNCSA*			GTAGTGGAAG	CAAGCTGAGT	0	R	0	0	0	0	0
34	36	ao	AN8197.1	53.m03776	AO070310000122	0					-238	-221	ATGACGCAACGAGGATAA			ATGACGCAACGAGGATAA	MTQRG*			MTQRG*	AAGGAAACAG	CCATGCTCTG	0	R	0	0	0	0	0
35	36	ao	AN8197.1	53.m03776	AO070310000122	0					-199	-143	ATGATGTTATGCATCAAAGTCAATCTGCACAAAGATTTTGATTCCATGTATGATTAA			ATGATGTTATGCATCAAAGTCAATCTGCACAAAGATTTTGATTCCATGTATGATTAA	MMLCIKVNLHKDFDSMYD*			MMLCIKVNLHKDFDSMYD*	CCTGCATTAC	TGTGTAGGAG	0	R	0	0	0	0	0
36	36	ao	AN8197.1	53.m03776	AO070310000122	0					-196	-143	ATGTTATGCATCAAAGTCAATCTGCACAAAGATTTTGATTCCATGTATGATTAA			ATGTTATGCATCAAAGTCAATCTGCACAAAGATTTTGATTCCATGTATGATTAA	MLCIKVNLHKDFDSMYD*			MLCIKVNLHKDFDSMYD*	GCATTACATG	TGTGTAGGAG	0	R	0	0	0	0	0
37	36	ao	AN8197.1	53.m03776	AO070310000122	0					-191	-159	ATGCATCAAAGTCAATCTGCACAAAGATTTTGA			ATGCATCAAAGTCAATCTGCACAAAGATTTTGA	MHQSQSAQRF*			MHQSQSAQRF*	ACATGATGTT	TTCCATGTAT	0	R	0	0	0	0	0
38	36	ao	AN8197.1	53.m03776	AO070310000122	0					-154	-143	ATGTATGATTAA			ATGTATGATTAA	MYD*			MYD*	TTTTGATTCC	TGTGTAGGAG	0	R	0	0	0	0	0
39	36	ao	AN8197.1	53.m03776	AO070310000122	0					-150	-136	ATGATTAATGTGTAG			ATGATTAATGTGTAG	MINV*			MINV*	GATTCCATGT	GAGATGGAAA	0	R	0	0	0	0	0
40	36	ao	AN8197.1	53.m03776	AO070310000122	0					-132	-118	ATGGAAAGGGAATAG			ATGGAAAGGGAATAG	MERE*			MERE*	TGTGTAGGAG	TACGGAAATA	0	R	0	0	0	0	0
41	37	an	AN4988.1	59.m08891	AO070288000057	0	-220	-65					ATGCTAAATCCTCCGAAAGACAAGTTGCGCGACCGCCACCCCGCTTTGGCCCAAAGCTGCCTGCTGCCGGCACCGCAAATCCAATCCCAGCCCCCTCACGCTTTATCAGTGCAGCACCCCAAAGCTCCGTCCTGTTCTTTGCTATATTACTCGTAA	ATGCTAAATCCTCCGAAAGACAAGTTGCGCGACCGCCACCCCGCTTTGGCCCAAAGCTGCCTGCTGCCGGCACCGCAAATCCAATCCCAGCCCCCTCACGCTTTATCAGTGCAGCACCCCAAAGCTCCGTCCTGTTCTTTGCTATATTACTCGTAA			MLNPPKDKLRDRHPALAQSCLLPAPQIQSQPPHALSVQHPKAPSCSLLYYS*	MLNPPKDKLRDRHPALAQSCLLPAPQIQSQPPHALSVQHPKAPSCSLLYYS*			GGCGTTGTCA	TCTTGGACGC	0	G	0	0	0	0	0
42	37	ao	AN4988.1	59.m08891	AO070288000057	0					-254	-144	ATGGATTCCCTAATCTTACTTCCCCGCCCCAGAAAATACTATAAAGAATCTCATCTTTCACGTCAGCATGTCGTTGCATTGGATCCACTAACGTCTTTCCACTCTATCTAA			ATGGATTCCCTAATCTTACTTCCCCGCCCCAGAAAATACTATAAAGAATCTCATCTTTCACGTCAGCATGTCGTTGCATTGGATCCACTAACGTCTTTCCACTCTATCTAA	MDSLILLPRPRKYYKESHLSRQHVVALDPLTSFHSI*			MDSLILLPRPRKYYKESHLSRQHVVALDPLTSFHSI*	TCAGGCTCCC	AGTTTGTCGT	0	G	0	0	0	0	0
43	37	ao	AN4988.1	59.m08891	AO070288000057	0					-187	-164	ATGTCGTTGCATTGGATCCACTAA			ATGTCGTTGCATTGGATCCACTAA	MSLHWIH*			MSLHWIH*	TCACGTCAGC	CGTCTTTCCA	0	G	0	0	0	0	0
44	39	af	AN7526.1	69.m15144	AO070258000030	0			-62	-42			ATGAGTTGGACCAAAACTTAA		ATGAGTTGGACCAAAACTTAA		MSWTKT*		MSWTKT*		TAAAAAAAAA	CAGCAACCAC	0	KU	0	0	0	YDR299W	0
47	46	af	AN2446.1	69.m15213	AO070264000031	0			-198	-46			ATGTGCCTCCGTCCAGTGGTTGATGGTCGAGAGTTGACGGTTCGGTTGCCATGTGCAACGCCCACAATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAA		ATGTGCCTCCGTCCAGTGGTTGATGGTCGAGAGTTGACGGTTCGGTTGCCATGTGCAACGCCCACAATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAA		MCLRPVVDGRELTVRLPCATPTMTSPSPHPPEPDLKTASCNKLSASNGLS*		MCLRPVVDGRELTVRLPCATPTMTSPSPHPPEPDLKTASCNKLSASNGLS*		GGCTTAGAGT	TACAAAAATA	0		0	0	0	0	0
48	46	af	AN2446.1	69.m15213	AO070264000031	0			-176	-162			ATGGTCGAGAGTTGA		ATGGTCGAGAGTTGA		MVES*		MVES*		CCAGTGGTTG	CGGTTCGGTT	0		0	0	0	0	0
49	46	af	AN2446.1	69.m15213	AO070264000031	0			-148	-11			ATGTGCAACGCCCACAATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAATACAAAAATACAGAAATTACATTCATATCCTGTAA		ATGTGCAACGCCCACAATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAATACAAAAATACAGAAATTACATTCATATCCTGTAA		MCNAHNDIAFSTSTRTRSQNCKLQQAISLKRSLLIQKYRNYIHIL*		MCNAHNDIAFSTSTRTRSQNCKLQQAISLKRSLLIQKYRNYIHIL*		TTCGGTTGCC	TAAATTGAAT	0		0	0	0	0	0
50	46	af	AN2446.1	69.m15213	AO070264000031	0			-132	-46			ATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAA		ATGACATCGCCTTCTCCACATCCACCAGAACCAGATCTCAAAACTGCAAGTTGCAACAAGCTATCAGCCTCAAACGGTCTCTCTTAA		MTSPSPHPPEPDLKTASCNKLSASNGLS*		MTSPSPHPPEPDLKTASCNKLSASNGLS*		AACGCCCACA	TACAAAAATA	0		0	0	0	0	0
45	46	an	AN2446.1	69.m15213	AO070264000031	0	-142	-50					ATGACATCGTTCCCCCACAGGCCGGAGCCAGACTTCACCTCCGCACACTCGTCAATCCTGAATCTCGACAACATTTTCCAGCGTGATTTTTAA	ATGACATCGTTCCCCCACAGGCCGGAGCCAGACTTCACCTCCGCACACTCGTCAATCCTGAATCTCGACAACATTTTCCAGCGTGATTTTTAA			MTSFPHRPEPDFTSAHSSILNLDNIFQRDF*	MTSFPHRPEPDFTSAHSSILNLDNIFQRDF*			AACGAAAGGA	ACGATTATAT	0		0	0	0	0	0
51	46	ao	AN2446.1	69.m15213	AO070264000031	0					-175	-56	ATGTGCAACAACCAACCCAAACTTTATGACATCGATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGACCCCAGACCCGATCTTTCTCTCCACCCTGCACATTAGTACCTTGTAG			ATGTGCAACAACCAACCCAAACTTTATGACATCGATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGACCCCAGACCCGATCTTTCTCTCCACCCTGCACATTAGTACCTTGTAG	MCNNQPKLYDIDVPTIFELHSTGLTPDPIFLSTLHISTL*			MCNNQPKLYDIDVPTIFELHSTGLTPDPIFLSTLHISTL*	TTCGGTTGCC	ACTCCGACTA	0		0	0	0	0	0
52	46	ao	AN2446.1	69.m15213	AO070264000031	0					-150	-103	ATGACATCGATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGA			ATGACATCGATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGA	MTSMSPLSSNYTVPV*			MTSMSPLSSNYTVPV*	CCCAAACTTT	CCCCAGACCC	0		0	0	0	0	0
53	46	ao	AN2446.1	69.m15213	AO070264000031	0					-141	-103	ATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGA			ATGTCCCCACTATCTTCGAACTACACAGTACCGGTTTGA	MSPLSSNYTVPV*			MSPLSSNYTVPV*	TATGACATCG	CCCCAGACCC	0		0	0	0	0	0
56	50	af	AN1157.1	70.m15085	AO070331000147	0			-227	-207			ATGTTCTATCTCATGAATTGA		ATGTTCTATCTCATGAATTGA		MFYLMN*		MFYLMN*		GACGTTCGCT	TCGCCATTCG	0	A	0	0	0	0	0
57	50	af	AN1157.1	70.m15085	AO070331000147	0			-193	-170			ATGACCTCGCACAACACGCATTGA		ATGACCTCGCACAACACGCATTGA		MTSHNTH*		MTSHNTH*		CCATTCGCAG	TCTTCTCTTA	0	A	0	0	0	0	0
54	50	an	AN1157.1	70.m15085	AO070331000147	0	-242	-225					ATGGTTTCCGAACTCTAA	ATGGTTTCCGAACTCTAA			MVSEL*	MVSEL*			CACCAGAAGA	GGAGTCATTT	0	A	0	0	0	0	0
55	50	an	AN1157.1	70.m15085	AO070331000147	0	-111	-16					ATGATCCGTTGCGCTTATATCTGCGCCACCATAGAACCCATCAAGCTGCAGCGTGAAGCTCCAACTTCACTCTGTCTGATTGCCAACCGCAACTGA	ATGATCCGTTGCGCTTATATCTGCGCCACCATAGAACCCATCAAGCTGCAGCGTGAAGCTCCAACTTCACTCTGTCTGATTGCCAACCGCAACTGA			MIRCAYICATIEPIKLQREAPTSLCLIANRN*	MIRCAYICATIEPIKLQREAPTSLCLIANRN*			CGTGCGGTTT	AGCACTACCG	0	A	0	0	0	0	0
60	51	af	AN1507.1	55.m03019	AO070334000226	0			-261	-214			ATGCAAGATTTGAAATTCTGGAAAGAGGTAGTCCCCTCAAGATACTGA		ATGCAAGATTTGAAATTCTGGAAAGAGGTAGTCCCCTCAAGATACTGA		MQDLKFWKEVVPSRY*		MQDLKFWKEVVPSRY*		GCAGTGAACA	ACTTCAACGC	0		0	0	0	0	0
58	51	an	AN1507.1	55.m03019	AO070334000226	0	-152	-78					ATGTCGTCCTTCATGGACTGGTACGAGACTTATGTAAAATACCGTAATAATACAAACCGCAGTCGCGCTTCTTGA	ATGTCGTCCTTCATGGACTGGTACGAGACTTATGTAAAATACCGTAATAATACAAACCGCAGTCGCGCTTCTTGA			MSSFMDWYETYVKYRNNTNRSRAS*	MSSFMDWYETYVKYRNNTNRSRAS*			GCCTTTCTAA	GCCTCATCTC	0		0	0	0	0	0
59	51	an	AN1507.1	55.m03019	AO070334000226	0	-140	-78					ATGGACTGGTACGAGACTTATGTAAAATACCGTAATAATACAAACCGCAGTCGCGCTTCTTGA	ATGGACTGGTACGAGACTTATGTAAAATACCGTAATAATACAAACCGCAGTCGCGCTTCTTGA			MDWYETYVKYRNNTNRSRAS*	MDWYETYVKYRNNTNRSRAS*			GTCGTCCTTC	GCCTCATCTC	0		0	0	0	0	0
61	51	ao	AN1507.1	55.m03019	AO070334000226	0					-255	-118	ATGTTAGACATCATTTCAATGGAATCTCTGCAGAGGGAAAATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAAGATTACAGACCTTGGTTGTCGCGCCAAGAGACGCGTCCTTTTGA			ATGTTAGACATCATTTCAATGGAATCTCTGCAGAGGGAAAATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAAGATTACAGACCTTGGTTGTCGCGCCAAGAGACGCGTCCTTTTGA	MLDIISMESLQRENVRDICGCLRIHKYGKDVRLQTLVVAPRDASF*			MLDIISMESLQRENVRDICGCLRIHKYGKDVRLQTLVVAPRDASF*	GGACCTTTTA	TTTCCTCCCG	0		0	0	0	0	0

62	51	ao	AN1507.1	55.m03019	AO070334000226	0					-237	-118	ATGGAATCTCTGCAGAGGGAAAATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAAGATTACAGACCTTGGTTGTCGCGCCAAGAGACGCGTCCTTTTGA			ATGGAATCTCTGCAGAGGGAAAATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAAGATTACAGACCTTGGTTGTCGCGCCAAGAGACGCGTCCTTTTGA	MESLQRENVRDICGCLRIHKYGKDVRLQTLVVAPRDASF*			MESLQRENVRDICGCLRIHKYGKDVRLQTLVVAPRDASF*	CATCATTTCA	TTTCCTCCCG	0		0	0	0	0	0
63	51	ao	AN1507.1	55.m03019	AO070334000226	0					-215	-162	ATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAA			ATGTACGAGATATATGTGGATGCCTCAGGATACATAAATACGGGAAAGACGTAA	MYEIYVDASGYINTGKT*			MYEIYVDASGYINTGKT*	CAGAGGGAAA	GATTACAGAC	0		0	0	0	0	0
64	51	ao	AN1507.1	55.m03019	AO070334000226	0					-202	-179	ATGTGGATGCCTCAGGATACATAA			ATGTGGATGCCTCAGGATACATAA	MWMPQDT*			MWMPQDT*	TACGAGATAT	ATACGGGAAA	0		0	0	0	0	0
65	51	ao	AN1507.1	55.m03019	AO070334000226	0					-196	-179	ATGCCTCAGGATACATAA			ATGCCTCAGGATACATAA	MPQDT*			MPQDT*	ATATATGTGG	ATACGGGAAA	0		0	0	0	0	0
67	52	an	AN5580.1	58.m07507	AO070328000024	0	-116	-24					ATGCCGCTACCCCGCGTCAATTGGTGCGGGACATCGTGGGCCGAGCTCTATCCGGGCTTTCCAACGGCGGTTGCTAACGTGAGTTTCCGGTGA	ATGCCGCTACCCCGCGTCAATTGGTGCGGGACATCGTGGGCCGAGCTCTATCCGGGCTTTCCAACGGCGGTTGCTAACGTGAGTTTCCGGTGA			MPLPRVNWCGTSWAELYPGFPTAVANVSFR*	MPLPRVNWCGTSWAELYPGFPTAVANVSFR*			TCCCTGTCAA	AAAAATTAGC	0		0	0	0	0	0
70	54	af	AN6896.1	71.m16024	AO070314000025	0			-275	-201			ATGACGCAAGTCGTAATACTTTCCAGGATCATTCCCGCGATTGTTAAAGCCAGGAAGCAACTCAAAATCGACTGA		ATGACGCAAGTCGTAATACTTTCCAGGATCATTCCCGCGATTGTTAAAGCCAGGAAGCAACTCAAAATCGACTGA		MTQVVILSRIIPAIVKARKQLKID*		MTQVVILSRIIPAIVKARKQLKID*		TACCCAACCA	TCAATCCGAT	0	L	0	0	0	0	0
71	54	af	AN6896.1	71.m16024	AO070314000025	0			-192	-178			ATGAAGCTCTCCTGA		ATGAAGCTCTCCTGA		MKLS*		MKLS*		GATCAATCCG	TTTAATCAGC	0	L	0	0	0	0	0
68	54	an	AN6896.1	71.m16024	AO070314000025	0	-122	-111					ATGGCAACTTGA	ATGGCAACTTGA			MAT*	MAT*			CTCGCAGTCC	ATATACTATA	0	L	0	0	0	0	0
69	54	an	AN6896.1	71.m16024	AO070314000025	0	-95	-78					ATGACTGTCACGCGATAA	ATGACTGTCACGCGATAA			MTVTR*	MTVTR*			CTATAAATAC	TACAATATCG	0	L	0	0	0	0	0
72	54	ao	AN6896.1	71.m16024	AO070314000025	0					-68	-36	ATGCGGCATCGGAAGTATCAAATCAATCCATGA			ATGCGGCATCGGAAGTATCAAATCAATCCATGA	MRHRKYQINP*			MRHRKYQINP*	AAACGCGCCA	GCAAGCCTGT	0	L	0	0	0	0	0
73	56	ao	AN8074.1	53.m04162	AO070330000032	0					-260	-246	ATGTTTGGTTTTTGA			ATGTTTGGTTTTTGA	MFGF*			MFGF*	TTGTGCCTAG	GTTTTGCTTA	0	O	0	0	0	0	0
74	57	ao	AN9142.1	66.m04612	AO070332000112	0					-226	-185	ATGGGAGATAGGAAAGATCAGATCATCGCATTCTTTATTTAA			ATGGGAGATAGGAAAGATCAGATCATCGCATTCTTTATTTAA	MGDRKDQIIAFFI*			MGDRKDQIIAFFI*	TCTTGGGGAG	TACTACGTCG	0		0	0	0	0	0
76	61	af	AN8809.1	71.m15615	AO070276000049	0			-232	-197			ATGGCCGCGCTCCATCTCCGTTGGTCCAAGAGGTAA		ATGGCCGCGCTCCATCTCCGTTGGTCCAAGAGGTAA		MAALHLRWSKR*		MAALHLRWSKR*		AGCTCGCATC	CTTCCCGCTG	0	R	0	0	0	0	0
78	61	ao	AN8809.1	71.m15615	AO070276000049	0					-282	-259	ATGGACCGCACAATACGCAACTAG			ATGGACCGCACAATACGCAACTAG	MDRTIRN*			MDRTIRN*	AAAAATAAGC	GCAGCTTTTT	0	R	0	0	0	0	0
79	61	ao	AN8809.1	71.m15615	AO070276000049	0					-231	-208	ATGTCGGAGTCTCCGCGGGTCTAG			ATGTCGGAGTCTCCGCGGGTCTAG	MSESPRV*			MSESPRV*	TCCCCAGTTC	TACCAAGTTC	0	R	0	0	0	0	0
80	61	ao	AN8809.1	71.m15615	AO070276000049	0					-184	-149	ATGCATTGGCCCAAGAATGCCAACTACCTCCATTGA			ATGCATTGGCCCAAGAATGCCAACTACCTCCATTGA	MHWPKNANYLH*			MHWPKNANYLH*	TTCCCGCTTT	CATTCATCCA	0	R	0	0	0	0	0
81	61	ao	AN8809.1	71.m15615	AO070276000049	0					-168	-70	ATGCCAACTACCTCCATTGACATTCATCCACACGCGGCACTCACCGATTGGAGTATTTTCCAAAGCACCGTTTTTGAAAAGCGTCATATTCAACCCTGA			ATGCCAACTACCTCCATTGACATTCATCCACACGCGGCACTCACCGATTGGAGTATTTTCCAAAGCACCGTTTTTGAAAAGCGTCATATTCAACCCTGA	MPTTSIDIHPHAALTDWSIFQSTVFEKRHIQP*			MPTTSIDIHPHAALTDWSIFQSTVFEKRHIQP*	TGGCCCAAGA	ATTTCGATCA	0	R	0	0	0	0	0
83	64	an	AN1549.1	55.m03069	AO070339000302	0	-238	-197					ATGGCTGCTATCCGACCTCGTCCAATGGACGAATATAAATGA	ATGGCTGCTATCCGACCTCGTCCAATGGACGAATATAAATGA			MAAIRPRPMDEYK*	MAAIRPRPMDEYK*			TCAGTTTGCC	TAGATCTTTG	0		0	0	0	0	0
84	64	an	AN1549.1	55.m03069	AO070339000302	0	-214	-197					ATGGACGAATATAAATGA	ATGGACGAATATAAATGA			MDEYK*	MDEYK*			ACCTCGTCCA	TAGATCTTTG	0		0	0	0	0	0
85	64	an	AN1549.1	55.m03069	AO070339000302	0	-200	-186					ATGATAGATCTTTGA	ATGATAGATCTTTGA			MIDL*	MIDL*			ACGAATATAA	AGCAAGAAGT	0		0	0	0	0	0
86	64	ao	AN1549.1	55.m03069	AO070339000302	0					-261	-241	ATGTGGCATCATGGATGGTGA			ATGTGGCATCATGGATGGTGA	MWHHGW*			MWHHGW*	TGGTGCTGGG	GAGGCTTGGG	0		0	0	0	0	0
87	64	ao	AN1549.1	55.m03069	AO070339000302	0					-251	-228	ATGGATGGTGAGAGGCTTGGGTGA			ATGGATGGTGAGAGGCTTGGGTGA	MDGERLG*			MDGERLG*	ATGTGGCATC	TCGATGTTGC	0		0	0	0	0	0
88	64	ao	AN1549.1	55.m03069	AO070339000302	0					-247	-194	ATGGTGAGAGGCTTGGGTGATCGATGTTGCTGGACATGGATGTTGGGTATATAA			ATGGTGAGAGGCTTGGGTGATCGATGTTGCTGGACATGGATGTTGGGTATATAA	MVRGLGDRCCWTWMLGI*			MVRGLGDRCCWTWMLGI*	GGCATCATGG	GGGATTGGAG	0		0	0	0	0	0
89	64	ao	AN1549.1	55.m03069	AO070339000302	0					-224	-87	ATGTTGCTGGACATGGATGTTGGGTATATAAGGGATTGGAGCATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA			ATGTTGCTGGACATGGATGTTGGGTATATAAGGGATTGGAGCATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA	MLLDMDVGYIRDWSMDGLGVYSSSSEQHNKASKSILQQLLSCSLR*			MLLDMDVGYIRDWSMDGLGVYSSSSEQHNKASKSILQQLLSCSLR*	TGGGTGATCG	ATAACCTCTT	0		0	0	0	0	0
90	64	ao	AN1549.1	55.m03069	AO070339000302	0					-212	-87	ATGGATGTTGGGTATATAAGGGATTGGAGCATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA			ATGGATGTTGGGTATATAAGGGATTGGAGCATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA	MDVGYIRDWSMDGLGVYSSSSEQHNKASKSILQQLLSCSLR*			MDVGYIRDWSMDGLGVYSSSSEQHNKASKSILQQLLSCSLR*	GTTGCTGGAC	ATAACCTCTT	0		0	0	0	0	0
91	64	ao	AN1549.1	55.m03069	AO070339000302	0					-208	-194	ATGTTGGGTATATAA			ATGTTGGGTATATAA	MLGI*			MLGI*	CTGGACATGG	GGGATTGGAG	0		0	0	0	0	0
92	64	ao	AN1549.1	55.m03069	AO070339000302	0					-182	-87	ATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA			ATGGATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGA	MDGLGVYSSSSEQHNKASKSILQQLLSCSLR*			MDGLGVYSSSSEQHNKASKSILQQLLSCSLR*	GGATTGGAGC	ATAACCTCTT	0		0	0	0	0	0
93	64	ao	AN1549.1	55.m03069	AO070339000302	0					-178	-83	ATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGAATAA			ATGGACTTGGTGTCTATTCTTCATCATCAGAACAACATAACAAAGCAAGCAAGTCTATCTTACAGCAACTACTATCTTGTTCACTGCGCTGAATAA	MDLVSILHHQNNITKQASLSYSNYYLVHCAE*			MDLVSILHHQNNITKQASLSYSNYYLVHCAE*	TGGAGCATGG	CCTCTTGGGT	0		0	0	0	0	0
94	70	conserved	AN3169.1	59.m09379	AO070256000021	0	-262	-212	-281	-225	-266	-216	ATGTyyyyTymryyChwkymvTyGrrshbyGTyywhGmhyyysmkyCwysrCCATGA	ATGTCTCTTTCGTCCTTGCCCTTGAAGCGTGTTCAAGACTCCCCGCCATGA	ATGTCTCCTCAGTCCAATTCGTCGGGCTTCGTCTACGCTCTTGATTCTCCGCCATGA	ATGTTCTCTCCACTCCATCAATCGGACACCGTTCTTGAATCCCCGCCATGA	MslsslplkrVqdspp*	MSLSSLPLKRVQDSPP*	MSPQSNSSGFVYALDSPP*	MFSPLHQSDTVLESPP*	mhyThmTyCm	ksTAGTkbyy	0	FE	0	0	0	0	0
95	79	af	AN8759.1	62.m03461	AO070312000139	0			-161	-126			ATGCGGGGTACGGCACAATTCCGCTGTAGCCTATAA		ATGCGGGGTACGGCACAATTCCGCTGTAGCCTATAA		MRGTAQFRCSL*		MRGTAQFRCSL*		CCAGGAGTAT	CCTGTACAAT	0	IR	0	0	0	0	0
96	79	af	AN8759.1	62.m03461	AO070312000139	0			-117	-76			ATGACCGTCAAGAGAGATTACGGGGTTTGTACGGTGTATTAG		ATGACCGTCAAGAGAGATTACGGGGTTTGTACGGTGTATTAG		MTVKRDYGVCTVY*		MTVKRDYGVCTVY*		AACCTGTACA	AATGAGGGTA	0	IR	0	0	0	0	0
97	79	af	AN8759.1	62.m03461	AO070312000139	0			-74	-36			ATGAGGGTATTGGTATTTGTATATCAACCACGCCGTTAG		ATGAGGGTATTGGTATTTGTATATCAACCACGCCGTTAG		MRVLVFVYQPRR*		MRVLVFVYQPRR*		GTGTATTAGA	AAGTTTACCC	0	IR	0	0	0	0	0
98	79	ao	AN8759.1	62.m03461	AO070312000139	0					-287	-246	ATGCCACCTTACGTGCCAGTTTCCACATTTCACACTCCATGA			ATGCCACCTTACGTGCCAGTTTCCACATTTCACACTCCATGA	MPPYVPVSTFHTP*			MPPYVPVSTFHTP*	ACAGAGATTC	TGCCATTAAT	0	IR	0	0	0	0	0
99	79	ao	AN8759.1	62.m03461	AO070312000139	0					-249	-181	ATGATGCCATTAATTCCGCGCCATCGGCTCGTCCTGCATGCAGGATCCGGGGCACACTCATCCCCGTGA			ATGATGCCATTAATTCCGCGCCATCGGCTCGTCCTGCATGCAGGATCCGGGGCACACTCATCCCCGTGA	MMPLIPRHRLVLHAGSGAHSSP*			MMPLIPRHRLVLHAGSGAHSSP*	TTCACACTCC	TCTCGAAAGC	0	IR	0	0	0	0	0
100	79	ao	AN8759.1	62.m03461	AO070312000139	0					-246	-181	ATGCCATTAATTCCGCGCCATCGGCTCGTCCTGCATGCAGGATCCGGGGCACACTCATCCCCGTGA			ATGCCATTAATTCCGCGCCATCGGCTCGTCCTGCATGCAGGATCCGGGGCACACTCATCCCCGTGA	MPLIPRHRLVLHAGSGAHSSP*			MPLIPRHRLVLHAGSGAHSSP*	ACACTCCATG	TCTCGAAAGC	0	IR	0	0	0	0	0
101	79	ao	AN8759.1	62.m03461	AO070312000139	0					-212	-69	ATGCAGGATCCGGGGCACACTCATCCCCGTGATCTCGAAAGCATCGAGACCGCCGATCTCGGGAATACCCCAGCAGCGATGTGGAGAACTGTCAAGGAGGGGTTTGGAATCAGTACCAGAGATTGTCGCCGATGTGAAATATGA			ATGCAGGATCCGGGGCACACTCATCCCCGTGATCTCGAAAGCATCGAGACCGCCGATCTCGGGAATACCCCAGCAGCGATGTGGAGAACTGTCAAGGAGGGGTTTGGAATCAGTACCAGAGATTGTCGCCGATGTGAAATATGA	MQDPGHTHPRDLESIETADLGNTPAAMWRTVKEGFGISTRDCRRCEI*			MQDPGHTHPRDLESIETADLGNTPAAMWRTVKEGFGISTRDCRRCEI*	CTCGTCCTGC	GAGATGCCAG	0	IR	0	0	0	0	0
102	79	ao	AN8759.1	62.m03461	AO070312000139	0					-134	-69	ATGTGGAGAACTGTCAAGGAGGGGTTTGGAATCAGTACCAGAGATTGTCGCCGATGTGAAATATGA			ATGTGGAGAACTGTCAAGGAGGGGTTTGGAATCAGTACCAGAGATTGTCGCCGATGTGAAATATGA	MWRTVKEGFGISTRDCRRCEI*			MWRTVKEGFGISTRDCRRCEI*	CCCAGCAGCG	GAGATGCCAG	0	IR	0	0	0	0	0
103	79	ao	AN8759.1	62.m03461	AO070312000139	0					-72	-31	ATGAGAGATGCCAGAGGATATAGCCACCGAATCCAAGATTAG			ATGAGAGATGCCAGAGGATATAGCCACCGAATCCAAGATTAG	MRDARGYSHRIQD*			MRDARGYSHRIQD*	GATGTGAAAT	CCTCATTCAC	0	IR	0	0	0	0	0
104	79	ao	AN8759.1	62.m03461	AO070312000139	0					-65	-18	ATGCCAGAGGATATAGCCACCGAATCCAAGATTAGCCTCATTCACTGA			ATGCCAGAGGATATAGCCACCGAATCCAAGATTAGCCTCATTCACTGA	MPEDIATESKISLIH*			MPEDIATESKISLIH*	AATATGAGAG	ACTCTACCCA	0	IR	0	0	0	0	0
107	84	af	AN0635.1	70.m15647	AO070318000125	0			-230	-159			ATGACTATGAAGTCACTTCATCAGCTTGACGTAATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		ATGACTATGAAGTCACTTCATCAGCTTGACGTAATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		MTMKSLHQLDVMFWLYLWTPAHE*		MTMKSLHQLDVMFWLYLWTPAHE*		AGCGTATGAT	ATAGATGAGA	0		0	0	0	0	0
108	84	af	AN0635.1	70.m15647	AO070318000125	0			-224	-159			ATGAAGTCACTTCATCAGCTTGACGTAATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		ATGAAGTCACTTCATCAGCTTGACGTAATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		MKSLHQLDVMFWLYLWTPAHE*		MKSLHQLDVMFWLYLWTPAHE*		TGATATGACT	ATAGATGAGA	0		0	0	0	0	0
109	84	af	AN0635.1	70.m15647	AO070318000125	0			-197	-159			ATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		ATGTTCTGGTTGTATCTTTGGACCCCTGCACATGAGTAA		MFWLYLWTPAHE*		MFWLYLWTPAHE*		GCTTGACGTA	ATAGATGAGA	0		0	0	0	0	0
110	84	af	AN0635.1	70.m15647	AO070318000125	0			-166	-155			ATGAGTAAATAG		ATGAGTAAATAG		MSK*		MSK*		ACCCCTGCAC	ATGAGATGAT	0		0	0	0	0	0
105	84	an	AN0635.1	70.m15647	AO070318000125	0	-170	-147					ATGAAGTCAGCAGTGGTTGGTTGA	ATGAAGTCAGCAGTGGTTGGTTGA			MKSAVVG*	MKSAVVG*			TGATCTGATT	CGTCACGCCT	0		0	0	0	0	0
106	84	an	AN0635.1	70.m15647	AO070318000125	0	-104	-93					ATGCAGAGTTAG	ATGCAGAGTTAG			MQS*	MQS*			CCGCATATAT	CTTAATCTAT	0		0	0	0	0	0
111	84	ao	AN0635.1	70.m15647	AO070318000125	0					-238	-179	ATGGATGTCGATGGTGGTGAGTTAAGTATGAAGTCAACCCCATCAGCCTTGACGTCATAG			ATGGATGTCGATGGTGGTGAGTTAAGTATGAAGTCAACCCCATCAGCCTTGACGTCATAG	MDVDGGELSMKSTPSALTS*			MDVDGGELSMKSTPSALTS*	GAATTAAATC	GGTTACTGGC	0		0	0	0	0	0
112	84	ao	AN0635.1	70.m15647	AO070318000125	0					-234	-214	ATGTCGATGGTGGTGAGTTAA			ATGTCGATGGTGGTGAGTTAA	MSMVVS*			MSMVVS*	TAAATCATGG	GTATGAAGTC	0		0	0	0	0	0
113	84	ao	AN0635.1	70.m15647	AO070318000125	0					-228	-214	ATGGTGGTGAGTTAA			ATGGTGGTGAGTTAA	MVVS*			MVVS*	ATGGATGTCG	GTATGAAGTC	0		0	0	0	0	0
114	84	ao	AN0635.1	70.m15647	AO070318000125	0					-211	-179	ATGAAGTCAACCCCATCAGCCTTGACGTCATAG			ATGAAGTCAACCCCATCAGCCTTGACGTCATAG	MKSTPSALTS*			MKSTPSALTS*	TGAGTTAAGT	GGTTACTGGC	0		0	0	0	0	0
115	84	ao	AN0635.1	70.m15647	AO070318000125	0					-168	-151	ATGCATCGAGTAGGTTGA			ATGCATCGAGTAGGTTGA	MHRVG*			MHRVG*	GGTTACTGGC	AGGGTTATAA	0		0	0	0	0	0
118	86	an	AN7302.1	72.m19765	AO070297000048	0	-258	-247					ATGTTTTTGTGA	ATGTTTTTGTGA			MFL*	MFL*			AAAGACCCCA	TCGCCCTTGG	0	U	0	0	0	0	0
120	92	ao	AN8843.1	71.m15975	AO070271000034	0					-262	-251	ATGACAGGTTAA			ATGACAGGTTAA	MTG*			MTG*	TCGGATTGAT	CCCATCTCTT	0	E	FG10211.1	0	0	YHR025W	YHR025W
124	95	af	AN3687.1	69.m15395	AO070342000308	0			-251	-180			ATGGAGAACTTAGATGGCTCCATGTTGCCATACCAGCCAGAGGAGACCATGACGAAATACGTTCAGTGGTGA		ATGGAGAACTTAGATGGCTCCATGTTGCCATACCAGCCAGAGGAGACCATGACGAAATACGTTCAGTGGTGA		MENLDGSMLPYQPEETMTKYVQW*		MENLDGSMLPYQPEETMTKYVQW*		AAAAGTGTTG	AGCGCCTCGG	0	O	0	0	0	0	0
125	95	af	AN3687.1	69.m15395	AO070342000308	0			-238	-200			ATGGCTCCATGTTGCCATACCAGCCAGAGGAGACCATGA		ATGGCTCCATGTTGCCATACCAGCCAGAGGAGACCATGA		MAPCCHTSQRRP*		MAPCCHTSQRRP*		GAGAACTTAG	CGAAATACGT	0	O	0	0	0	0	0
126	95	af	AN3687.1	69.m15395	AO070342000308	0			-230	-180			ATGTTGCCATACCAGCCAGAGGAGACCATGACGAAATACGTTCAGTGGTGA		ATGTTGCCATACCAGCCAGAGGAGACCATGACGAAATACGTTCAGTGGTGA		MLPYQPEETMTKYVQW*		MLPYQPEETMTKYVQW*		AGATGGCTCC	AGCGCCTCGG	0	O	0	0	0	0	0
127	95	af	AN3687.1	69.m15395	AO070342000308	0			-203	-180			ATGACGAAATACGTTCAGTGGTGA		ATGACGAAATACGTTCAGTGGTGA		MTKYVQW*		MTKYVQW*		AGAGGAGACC	AGCGCCTCGG	0	O	0	0	0	0	0
128	95	af	AN3687.1	69.m15395	AO070342000308	0			-82	-47			ATGTCAATTGAATTAGCACATTTAAATATCTCATAG		ATGTCAATTGAATTAGCACATTTAAATATCTCATAG		MSIELAHLNIS*		MSIELAHLNIS*		GAACCATTAT	CCGCTATAAC	0	O	0	0	0	0	0
121	95	an	AN3687.1	69.m15395	AO070342000308	0	-233	-216					ATGTTGCTGTTAGATTGA	ATGTTGCTGTTAGATTGA			MLLLD*	MLLLD*			ATACAGTTAG	GAAGATGAAG	0	O	0	0	0	0	0
122	95	an	AN3687.1	69.m15395	AO070342000308	0	-211	-188					ATGAAGTCTTCTTCTGACAGTTAA	ATGAAGTCTTCTTCTGACAGTTAA			MKSSSDS*	MKSSSDS*			GATTGAGAAG	CGGTTGCCGG	0	O	0	0	0	0	0

123	95	an	AN3687.1	69.m15395	AO070342000308	0	-155	-45					ATGACGTGCGTAGCTGACTCAGGCCACCGCAAGTTCCTCGCGTCCTCGAGCTCATCCGCATCACAGCTCCCAGGGACAATTACCTCGAATTCCCTATCATTATCTTATTAG	ATGACGTGCGTAGCTGACTCAGGCCACCGCAAGTTCCTCGCGTCCTCGAGCTCATCCGCATCACAGCTCCCAGGGACAATTACCTCGAATTCCCTATCATTATCTTATTAG			MTCVADSGHRKFLASSSSASQLPGTITSNSLSLSY*	MTCVADSGHRKFLASSSSASQLPGTITSNSLSLSY*			TAACTAAACA	CATAACAACA	0	O	0	0	0	0	0
129	95	ao	AN3687.1	69.m15395	AO070342000308	0					-211	-197	ATGACGCAATGCTGA			ATGACGCAATGCTGA	MTQC*			MTQC*	GAAACGCGCT	GTAATGGGAA	0	O	0	0	0	0	0
130	95	ao	AN3687.1	69.m15395	AO070342000308	0					-203	-126	ATGCTGAGTAATGGGAATCATACCCCTCAGCGACCAATCAGGATGCACGGGTACCTTGCCGATGACGGACGATGTTGA			ATGCTGAGTAATGGGAATCATACCCCTCAGCGACCAATCAGGATGCACGGGTACCTTGCCGATGACGGACGATGTTGA	MLSNGNHTPQRPIRMHGYLADDGRC*			MLSNGNHTPQRPIRMHGYLADDGRC*	CTATGACGCA	ACCTCCTCCA	0	O	0	0	0	0	0
131	95	ao	AN3687.1	69.m15395	AO070342000308	0					-193	-77	ATGGGAATCATACCCCTCAGCGACCAATCAGGATGCACGGGTACCTTGCCGATGACGGACGATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAAACAACAACTACTCCGGGTGA			ATGGGAATCATACCCCTCAGCGACCAATCAGGATGCACGGGTACCTTGCCGATGACGGACGATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAAACAACAACTACTCCGGGTGA	MGIIPLSDQSGCTGTLPMTDDVEPPPICISNLNNNYSG*			MGIIPLSDQSGCTGTLPMTDDVEPPPICISNLNNNYSG*	ATGCTGAGTA	AGACGTCTAC	0	O	0	0	0	0	0
132	95	ao	AN3687.1	69.m15395	AO070342000308	0					-161	-126	ATGCACGGGTACCTTGCCGATGACGGACGATGTTGA			ATGCACGGGTACCTTGCCGATGACGGACGATGTTGA	MHGYLADDGRC*			MHGYLADDGRC*	ACCAATCAGG	ACCTCCTCCA	0	O	0	0	0	0	0
133	95	ao	AN3687.1	69.m15395	AO070342000308	0					-142	-77	ATGACGGACGATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAAACAACAACTACTCCGGGTGA			ATGACGGACGATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAAACAACAACTACTCCGGGTGA	MTDDVEPPPICISNLNNNYSG*			MTDDVEPPPICISNLNNNYSG*	TACCTTGCCG	AGACGTCTAC	0	O	0	0	0	0	0
134	95	ao	AN3687.1	69.m15395	AO070342000308	0					-132	-97	ATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAA			ATGTTGAACCTCCTCCAATCTGCATCAGCAACTTAA	MLNLLQSASAT*			MLNLLQSASAT*	ATGACGGACG	ACAACAACTA	0	O	0	0	0	0	0
135	100	af	AN6568.1	62.m03155	AO070326000011	0			-204	-85			ATGCATTTCCCCTCCCACAACGGTGGATTGCCTTTGGATATCCCTCCATTGCCTTGGAGATCTACTGAGAGTTACTTCCTCTCTTTATCTCCTCGATACCCCCCTCCTCTACCTTGTTGA		ATGCATTTCCCCTCCCACAACGGTGGATTGCCTTTGGATATCCCTCCATTGCCTTGGAGATCTACTGAGAGTTACTTCCTCTCTTTATCTCCTCGATACCCCCCTCCTCTACCTTGTTGA		MHFPSHNGGLPLDIPPLPWRSTESYFLSLSPRYPPPLPC*		MHFPSHNGGLPLDIPPLPWRSTESYFLSLSPRYPPPLPC*		AACCCACTCC	AATCGTCTGT	0	S	0	0	0	YDR257C	YDR257C
137	103	af	AN8857.1	71.m15995	AO070271000016	0			-207	-136			ATGGACCATTGTCATTTTTCCATGCCTGGAGGGGGTGCCATTTCATGTATTATCTACTTTCAGAAATCATAA		ATGGACCATTGTCATTTTTCCATGCCTGGAGGGGGTGCCATTTCATGTATTATCTACTTTCAGAAATCATAA		MDHCHFSMPGGGAISCIIYFQKS*		MDHCHFSMPGGGAISCIIYFQKS*		CGCGGCAGAA	CGCCACCGGG	0	K	0	MG06309.1	0	0	0
138	103	af	AN8857.1	71.m15995	AO070271000016	0			-186	-136			ATGCCTGGAGGGGGTGCCATTTCATGTATTATCTACTTTCAGAAATCATAA		ATGCCTGGAGGGGGTGCCATTTCATGTATTATCTACTTTCAGAAATCATAA		MPGGGAISCIIYFQKS*		MPGGGAISCIIYFQKS*		TCATTTTTCC	CGCCACCGGG	0	K	0	MG06309.1	0	0	0
139	103	af	AN8857.1	71.m15995	AO070271000016	0			-163	-110			ATGTATTATCTACTTTCAGAAATCATAACGCCACCGGGTCCTCTGGAAGACTAA		ATGTATTATCTACTTTCAGAAATCATAACGCCACCGGGTCCTCTGGAAGACTAA		MYYLLSEIITPPGPLED*		MYYLLSEIITPPGPLED*		GTGCCATTTC	AGCGAAAAAC	0	K	0	MG06309.1	0	0	0
136	103	an	AN8857.1	71.m15995	AO070271000016	0	-172	-149					ATGCACTATCTGATAAGGTCTTAG	ATGCACTATCTGATAAGGTCTTAG			MHYLIRS*	MHYLIRS*			CGGTGAGAGC	CCTGGTTCTT	0	K	0	MG06309.1	0	0	0
146	113	af	AN5335.1	69.m15576	AO070333000215	0			-206	-57			ATGAAGACTTGTCGTGTGGGGGGAAAAAATGAGCCACTGGCCTCTCCCCGGTTCTTTTTCTCGGTTCAGGACATTGCGGTTAAACAAGGAGACGGAGTGTGGTGTCATGTTAGGTTGCTTCTTCGACCTCCAAAGGTGGTTTTCTACTGA		ATGAAGACTTGTCGTGTGGGGGGAAAAAATGAGCCACTGGCCTCTCCCCGGTTCTTTTTCTCGGTTCAGGACATTGCGGTTAAACAAGGAGACGGAGTGTGGTGTCATGTTAGGTTGCTTCTTCGACCTCCAAAGGTGGTTTTCTACTGA		MKTCRVGGKNEPLASPRFFFSVQDIAVKQGDGVWCHVRLLLRPPKVVFY*		MKTCRVGGKNEPLASPRFFFSVQDIAVKQGDGVWCHVRLLLRPPKVVFY*		AGTTCTAGCA	TTTCTTTCAA	0	Q	0	0	0	0	0
144	113	an	AN5335.1	69.m15576	AO070333000215	0	-98	-66					ATGCCACTTGGTTTAGTCAAGACGACTCAATGA	ATGCCACTTGGTTTAGTCAAGACGACTCAATGA			MPLGLVKTTQ*	MPLGLVKTTQ*			CTCATAAATC	TTAGGATACT	0	Q	0	0	0	0	0
145	113	an	AN5335.1	69.m15576	AO070333000215	0	-69	-37					ATGATTAGGATACTTCCGCCACTGCTCACTTAA	ATGATTAGGATACTTCCGCCACTGCTCACTTAA			MIRILPPLLT*	MIRILPPLLT*			AGACGACTCA	TAATGCTCTT	0	Q	0	0	0	0	0
147	113	ao	AN5335.1	69.m15576	AO070333000215	0					-186	-34	ATGCCACCTGCCAATTTCCGGCTATTTTTCTTCGTTCGGGTTCCCTCTCGGAATATTGCGGCCCAAGAAAAGGGGACAATTTGGCAACGGTTGGGCTTTGTACTCGCAAATTCGAAAGCCAACAAACCTCGGCCGCTTCTACAGGATCTTTAG			ATGCCACCTGCCAATTTCCGGCTATTTTTCTTCGTTCGGGTTCCCTCTCGGAATATTGCGGCCCAAGAAAAGGGGACAATTTGGCAACGGTTGGGCTTTGTACTCGCAAATTCGAAAGCCAACAAACCTCGGCCGCTTCTACAGGATCTTTAG	MPPANFRLFFFVRVPSRNIAAQEKGTIWQRLGFVLANSKANKPRPLLQDL*			MPPANFRLFFFVRVPSRNIAAQEKGTIWQRLGFVLANSKANKPRPLLQDL*	GTGAACCAAA	GAAGATGTGC	0	Q	0	0	0	0	0
157	117	an	AN4192.1	54.m06754	AO070342000112	0	-207	-166					ATGAGATTCTCTGACAGCTCAGCGAAGCGGGCCTGGATTTAG	ATGAGATTCTCTGACAGCTCAGCGAAGCGGGCCTGGATTTAG			MRFSDSSAKRAWI*	MRFSDSSAKRAWI*			TCGGAGTTCG	ATATCTGCTT	0	O	0	0	0	0	0
159	120	af	AN0668.1	70.m15271	AO070343000552	0			-69	-31			ATGCTTGTTTCTATGCTACCTTACTGGACACGGGCTTGA		ATGCTTGTTTCTATGCTACCTTACTGGACACGGGCTTGA		MLVSMLPYWTRA*		MLVSMLPYWTRA*		TCCCCTCCAA	TCCGTCCCGA	0	R	0	0	0	0	0
158	120	an	AN0668.1	70.m15271	AO070343000552	0	-207	-85					ATGTTGTTTTTTACTCTTGACGCCGCCTCTGTGTTTCTCCTGCGTACAGAAGCTGTCTGCCTTTTATCTGGACTGGTAGAATTAGCAGAGCTGGCTAAGCTTGTCTTCTACCCCTCGAAATAA	ATGTTGTTTTTTACTCTTGACGCCGCCTCTGTGTTTCTCCTGCGTACAGAAGCTGTCTGCCTTTTATCTGGACTGGTAGAATTAGCAGAGCTGGCTAAGCTTGTCTTCTACCCCTCGAAATAA			MLFFTLDAASVFLLRTEAVCLLSGLVELAELAKLVFYPSK*	MLFFTLDAASVFLLRTEAVCLLSGLVELAELAKLVFYPSK*			CTGCTCAAAT	ACAAGACCTA	0	R	0	0	0	0	0
161	120	ao	AN0668.1	70.m15271	AO070343000552	0					-208	-152	ATGTGTTTGAACAAGAAAGAAGATGGAAATAGAAAGGATCTTTTCCACAGATTGTGA			ATGTGTTTGAACAAGAAAGAAGATGGAAATAGAAAGGATCTTTTCCACAGATTGTGA	MCLNKKEDGNRKDLFHRL*			MCLNKKEDGNRKDLFHRL*	ATTCACTGAA	AAGTGAGTCT	0	R	0	0	0	0	0
162	120	ao	AN0668.1	70.m15271	AO070343000552	0					-186	-43	ATGGAAATAGAAAGGATCTTTTCCACAGATTGTGAAAGTGAGTCTTTTCTCGTTTTTAAAATAATTCCCCTGCGTCTCCAAGTCCCATCTTCCAAGAAAGTCAACCCACTTTCCCTTCACGTCTGCCCCTCCATTCAATACTAA			ATGGAAATAGAAAGGATCTTTTCCACAGATTGTGAAAGTGAGTCTTTTCTCGTTTTTAAAATAATTCCCCTGCGTCTCCAAGTCCCATCTTCCAAGAAAGTCAACCCACTTTCCCTTCACGTCTGCCCCTCCATTCAATACTAA	MEIERIFSTDCESESFLVFKIIPLRLQVPSSKKVNPLSLHVCPSIQY*			MEIERIFSTDCESESFLVFKIIPLRLQVPSSKKVNPLSLHVCPSIQY*	AAGAAAGAAG	TTATACCCAA	0	R	0	0	0	0	0
166	126	af	AN8860.1	71.m15999	AO070271000011	0			-193	-92			ATGAAGCTTCTACATAAGCAGTACCTTCACTGTACCTGTGATTTTGAGTTCGCCTTTGTTGCGAATTTATGCCTGAGGCCCAAAGAAGTGCCGCCCCGCTGA		ATGAAGCTTCTACATAAGCAGTACCTTCACTGTACCTGTGATTTTGAGTTCGCCTTTGTTGCGAATTTATGCCTGAGGCCCAAAGAAGTGCCGCCCCGCTGA		MKLLHKQYLHCTCDFEFAFVANLCLRPKEVPPR*		MKLLHKQYLHCTCDFEFAFVANLCLRPKEVPPR*		TAGAGAATTA	AAAATTCCCC	0	F	0	0	0	0	0
167	126	af	AN8860.1	71.m15999	AO070271000011	0			-61	-41			ATGGTACCAGACACGACTTAA		ATGGTACCAGACACGACTTAA		MVPDTT*		MVPDTT*		ATTCCGTTGC	TCATCACTCT	0	F	0	0	0	0	0
163	126	an	AN8860.1	71.m15999	AO070271000011	0	-150	-130					ATGCCCCACTCTCCGAGTTGA	ATGCCCCACTCTCCGAGTTGA			MPHSPS*	MPHSPS*			ATACTTTAAA	TGCCCCAGGA	0	F	0	0	0	0	0
164	126	an	AN8860.1	71.m15999	AO070271000011	0	-130	-56					ATGCCCCAGGAACTAACACCCCGCCAAAATTTTCTCTTGGCATATGAGCTGCTGGTCACTAGAATCAGATTCTAA	ATGCCCCAGGAACTAACACCCCGCCAAAATTTTCTCTTGGCATATGAGCTGCTGGTCACTAGAATCAGATTCTAA			MPQELTPRQNFLLAYELLVTRIRF*	MPQELTPRQNFLLAYELLVTRIRF*			CTCCGAGTTG	CGGCGGTCAT	0	F	0	0	0	0	0
165	126	an	AN8860.1	71.m15999	AO070271000011	0	-87	-16					ATGAGCTGCTGGTCACTAGAATCAGATTCTAACGGCGGTCATTCAAATCCTTTCTCTCAATCACTTTATTGA	ATGAGCTGCTGGTCACTAGAATCAGATTCTAACGGCGGTCATTCAAATCCTTTCTCTCAATCACTTTATTGA			MSCWSLESDSNGGHSNPFSQSLY*	MSCWSLESDSNGGHSNPFSQSLY*			CTCTTGGCAT	TAACCATAAT	0	F	0	0	0	0	0
168	126	ao	AN8860.1	71.m15999	AO070271000011	0					-176	-123	ATGTGCTATATCCGTCGGATCGGACCCACTTTTCCCGCTGAAATAGGTGCCTGA			ATGTGCTATATCCGTCGGATCGGACCCACTTTTCCCGCTGAAATAGGTGCCTGA	MCYIRRIGPTFPAEIGA*			MCYIRRIGPTFPAEIGA*	CTAGTATTTA	GGTGTTCGTT	0	F	0	0	0	0	0
169	130	ao	AN7742.1	71.m15770	AO070325000166	0					-124	-86	ATGACAGTTAAACCTCTGGGAGAAGCAGTTGACATTTGA			ATGACAGTTAAACCTCTGGGAGAAGCAGTTGACATTTGA	MTVKPLGEAVDI*			MTVKPLGEAVDI*	AAGCAACGTA	CTTCCATTTT	0	L	0	0	0	0	0
172	134	af	AN8746.1	62.m03333	AO070250000027	0			-313	-182			ATGCGCATCATTAGCAACTTCAACCTCCTCCCACCAGACACCACCTCAGTCACGGTAAGTCAACCCAAACCTCATCTCAGCCCTCGTCCTTCGGTTCACCATTACGACGGTGTTTCATCTGTCTCTCCCTGA		ATGCGCATCATTAGCAACTTCAACCTCCTCCCACCAGACACCACCTCAGTCACGGTAAGTCAACCCAAACCTCATCTCAGCCCTCGTCCTTCGGTTCACCATTACGACGGTGTTTCATCTGTCTCTCCCTGA		MRIISNFNLLPPDTTSVTVSQPKPHLSPRPSVHHYDGVSSVSP*		MRIISNFNLLPPDTTSVTVSQPKPHLSPRPSVHHYDGVSSVSP*		GGGAGCCGAG	CCCGGTACCG	0	K	FG08675.1	0	NCU03148.1	0	0
170	134	an	AN8746.1	62.m03333	AO070250000027	0	-236	-192					ATGCCCGTTCTTAATTCAACGAGCGATCGATTGCCTTTCAGATAG	ATGCCCGTTCTTAATTCAACGAGCGATCGATTGCCTTTCAGATAG			MPVLNSTSDRLPFR*	MPVLNSTSDRLPFR*			GTAGGTCAAT	CACCACAAAA	0	K	FG08675.1	0	NCU03148.1	0	0
171	134	an	AN8746.1	62.m03333	AO070250000027	0	-156	-142					ATGGACATCGTCTGA	ATGGACATCGTCTGA			MDIV*	MDIV*			TGATCGTGGA	CGTCGTGAAA	0	K	FG08675.1	0	NCU03148.1	0	0
177	140	af	AN8891.1	56.m02304	AO070293000026	0			-238	-176			ATGGACGGATTTTATAGGCGGATAAACTCTCTCTTCTTGCGTCTTGACAGGCACTTCCTCTAG		ATGGACGGATTTTATAGGCGGATAAACTCTCTCTTCTTGCGTCTTGACAGGCACTTCCTCTAG		MDGFYRRINSLFLRLDRHFL*		MDGFYRRINSLFLRLDRHFL*		GGCAGCCGCA	CTCATAATCC	0	M	0	0	0	0	0
178	140	af	AN8891.1	56.m02304	AO070293000026	0			-81	-64			ATGGGCAGGTCGGAGTGA		ATGGGCAGGTCGGAGTGA		MGRSE*		MGRSE*		GAGGGCCATC	AAGTGCCAGC	0	M	0	0	0	0	0
174	140	an	AN8891.1	56.m02304	AO070293000026	0	-146	-75					ATGGCCCGCTACAGGCGGAGAAATTGCTGTGACAATTATGCATGGCACGAGCTCATTAATCTATCCTTATAA	ATGGCCCGCTACAGGCGGAGAAATTGCTGTGACAATTATGCATGGCACGAGCTCATTAATCTATCCTTATAA			MARYRRRNCCDNYAWHELINLSL*	MARYRRRNCCDNYAWHELINLSL*			TGGTCCGACT	AGCACACTCA	0	M	0	0	0	0	0
175	140	an	AN8891.1	56.m02304	AO070293000026	0	-105	-88					ATGGCACGAGCTCATTAA	ATGGCACGAGCTCATTAA			MARAH*	MARAH*			ACAATTATGC	TCTATCCTTA	0	M	0	0	0	0	0
179	140	ao	AN8891.1	56.m02304	AO070293000026	0					-232	-221	ATGGCACGGTAA			ATGGCACGGTAA	MAR*			MAR*	GAAGCATTTG	TTCCGGAGGT	0	M	0	0	0	0	0
181	141	af	AN4461.1	58.m07863	AO070305000132	0			-244	-197			ATGTTGTGTCTTCAACACTTGTACATAGTGCAGCACAAACGAGACTAA		ATGTTGTGTCTTCAACACTTGTACATAGTGCAGCACAAACGAGACTAA		MLCLQHLYIVQHKRD*		MLCLQHLYIVQHKRD*		ATTCCTATTC	GCGCGCGCTT	0	K	0	0	0	0	0
182	141	af	AN4461.1	58.m07863	AO070305000132	0			-70	-53			ATGGGCTGTCCTATATAA		ATGGGCTGTCCTATATAA		MGCPI*		MGCPI*		ATTATCATAA	GCACATTTTG	0	K	0	0	0	0	0
180	141	an	AN4461.1	58.m07863	AO070305000132	0	-217	-179					ATGAAGTTTGATCTTCAGTCTAGCACTCATACCAACTGA	ATGAAGTTTGATCTTCAGTCTAGCACTCATACCAACTGA			MKFDLQSSTHTN*	MKFDLQSSTHTN*			CAGGCTTAGG	GTTATCACCC	0	K	0	0	0	0	0
183	141	ao	AN4461.1	58.m07863	AO070305000132	0					-131	-99	ATGCGACCGTCCAAGCTGAATCTTACTCAATAA			ATGCGACCGTCCAAGCTGAATCTTACTCAATAA	MRPSKLNLTQ*			MRPSKLNLTQ*	TTCTTTAGGG	TCTTCGTGCG	0	K	0	0	0	0	0
185	144	an	AN3451.1	59.m09314	AO070265000026	0	-206	-189					ATGTTTTTGTTCACATGA	ATGTTTTTGTTCACATGA			MFLFT*	MFLFT*			AGTCGTTACT	CTTACAGCGG	0	BD	0	0	0	0	0
186	144	an	AN3451.1	59.m09314	AO070265000026	0	-192	-148					ATGACTTACAGCGGCGAATCTGGTCGGCGGGAAAACGGCGCCTAA	ATGACTTACAGCGGCGAATCTGGTCGGCGGGAAAACGGCGCCTAA			MTYSGESGRRENGA*	MTYSGESGRRENGA*			TTTTGTTCAC	ATCGGAAAGA	0	BD	0	0	0	0	0
187	145	af	AN1801.1	72.m19552	AO070309000126	0			-207	-157			ATGGCGGTACACTTAATACTCCGTAGTAGCAAAGCCACAGCCACCTCGTGA		ATGGCGGTACACTTAATACTCCGTAGTAGCAAAGCCACAGCCACCTCGTGA		MAVHLILRSSKATATS*		MAVHLILRSSKATATS*		GCTAATAGCA	CAAACGATGA	0		0	0	0	0	0
188	145	af	AN1801.1	72.m19552	AO070309000126	0			-150	-25			ATGAATAATAGCCAGTCGCAATGTATATTTCTTGCTGGAACCAGGCCGTCAGCAACCAGGCAGCCATATTCCAGAACACATATCTTCACCATCATCTGTCTCCTCATCGATCATCAGCAACGCTAG		ATGAATAATAGCCAGTCGCAATGTATATTTCTTGCTGGAACCAGGCCGTCAGCAACCAGGCAGCCATATTCCAGAACACATATCTTCACCATCATCTGTCTCCTCATCGATCATCAGCAACGCTAG		MNNSQSQCIFLAGTRPSATRQPYSRTHIFTIICLLIDHQQR*		MNNSQSQCIFLAGTRPSATRQPYSRTHIFTIICLLIDHQQR*		GTGACAAACG	AAGAGAGACA	0		0	0	0	0	0
189	145	ao	AN1801.1	72.m19552	AO070309000126	0					-145	-122	ATGACACTCTCGTATAAGCAGTAG			ATGACACTCTCGTATAAGCAGTAG	MTLSYKQ*			MTLSYKQ*	CAACACTGAG	GCAGCAGAAT	0		0	0	0	0	0
191	147	af	AN6609.1	62.m03184	AO070326000058	0			-120	-67			ATGGTTGGGTTTGGTATAACTCCGTTCCAAACTCCGCTTCGCCACCAGATATAA		ATGGTTGGGTTTGGTATAACTCCGTTCCAAACTCCGCTTCGCCACCAGATATAA		MVGFGITPFQTPLRHQI*		MVGFGITPFQTPLRHQI*		ATTTTATACT	CCTCTGATCT	0	O	FG07155.1	0	0	0	0
190	147	an	AN6609.1	62.m03184	AO070326000058	0	-120	-94					ATGATTACACTCGTTGCTCATCACTGA	ATGATTACACTCGTTGCTCATCACTGA			MITLVAHH*	MITLVAHH*			GGAGTCTAAT	TCAGCCCATC	0	O	FG07155.1	0	0	0	0
192	147	ao	AN6609.1	62.m03184	AO070326000058	0					-155	-102	ATGATATTTTTAAGCGATACATATACCATGGTTGTGTCAGGAATATTCCATTAA			ATGATATTTTTAAGCGATACATATACCATGGTTGTGTCAGGAATATTCCATTAA	MIFLSDTYTMVVSGIFH*			MIFLSDTYTMVVSGIFH*	TCTCGAAGGC	AGAATCTTCC	0	O	FG07155.1	0	0	0	0
193	147	ao	AN6609.1	62.m03184	AO070326000058	0					-128	-102	ATGGTTGTGTCAGGAATATTCCATTAA			ATGGTTGTGTCAGGAATATTCCATTAA	MVVSGIFH*			MVVSGIFH*	TACATATACC	AGAATCTTCC	0	O	FG07155.1	0	0	0	0
194	148	an	AN8828.1	71.m15960	AO070271000052	0	-286	-263					ATGACATCGTCCGTCCACCGCTGA	ATGACATCGTCCGTCCACCGCTGA			MTSSVHR*	MTSSVHR*			TTCCTACGTT	AAATCCCTTC	0	U	0	0	0	0	0

195	148	an	AN8828.1	71.m15960	AO070271000052	0	-225	-70					ATGTCCAAGGAAGCGCTTAGGACATACCTAGAGTGTTTGTCCCATGTAAACATCGGTTCACCGCCCAATTCATCCCCGACACATCTCCTTATCGCGACATCGTCACCCCTAAACCAGTCCATCAGCCATCAACCAAACCAATCGATATTGGAATAG	ATGTCCAAGGAAGCGCTTAGGACATACCTAGAGTGTTTGTCCCATGTAAACATCGGTTCACCGCCCAATTCATCCCCGACACATCTCCTTATCGCGACATCGTCACCCCTAAACCAGTCCATCAGCCATCAACCAAACCAATCGATATTGGAATAG			MSKEALRTYLECLSHVNIGSPPNSSPTHLLIATSSPLNQSISHQPNQSILE*	MSKEALRTYLECLSHVNIGSPPNSSPTHLLIATSSPLNQSISHQPNQSILE*			CTTCTACTCT	ACTCATCAAG	0	U	0	0	0	0	0
196	148	ao	AN8828.1	71.m15960	AO070271000052	0					-69	-28	ATGCCCTCTTCATCAAGTCAGATCCCGTGTATTCTTCTGTAG			ATGCCCTCTTCATCAAGTCAGATCCCGTGTATTCTTCTGTAG	MPSSSSQIPCILL*			MPSSSSQIPCILL*	CCGCACCTTA	TGAATTGTCT	0	U	0	0	0	0	0
198	150	af	AN0287.1	54.m06482	AO070334000066	0			-82	-59			ATGGTCCACACGCCAGGAGACTAG		ATGGTCCACACGCCAGGAGACTAG		MVHTPGD*		MVHTPGD*		CCGGGTCGAG	AAAACCGCCC	0	R	0	0	0	0	0
197	150	an	AN0287.1	54.m06482	AO070334000066	0	-72	-58					ATGACCCAATCCTAA	ATGACCCAATCCTAA			MTQS*	MTQS*			TGGTCGTAAG	ACACTCAAGC	0	R	0	0	0	0	0
199	150	ao	AN0287.1	54.m06482	AO070334000066	0					-216	-193	ATGAACCTCCGCCGACGACTTTGA			ATGAACCTCCGCCGACGACTTTGA	MNLRRRL*			MNLRRRL*	TAGCCTTCTT	CTTTTGGTCC	0	R	0	0	0	0	0
202	152	af	AN7594.1	72.m19619	AO070343000316	0			-167	-48			ATGGCTGGTGGTTCCAAATCAGATGGAGAAGGAGGTGAGAGATTTGGGGGTATAAATAACCCCCCTCATCGCCATTTCTCTACAAAGGTACTCAACTTTGAGCACCCTGTTGACTCTTAA		ATGGCTGGTGGTTCCAAATCAGATGGAGAAGGAGGTGAGAGATTTGGGGGTATAAATAACCCCCCTCATCGCCATTTCTCTACAAAGGTACTCAACTTTGAGCACCCTGTTGACTCTTAA		MAGGSKSDGEGGERFGGINNPPHRHFSTKVLNFEHPVDS*		MAGGSKSDGEGGERFGGINNPPHRHFSTKVLNFEHPVDS*		TGTCAAATTA	CGTGATACAT	0	S	0	0	0	0	0
203	152	af	AN7594.1	72.m19619	AO070343000316	0			-145	-113			ATGGAGAAGGAGGTGAGAGATTTGGGGGTATAA		ATGGAGAAGGAGGTGAGAGATTTGGGGGTATAA		MEKEVRDLGV*		MEKEVRDLGV*		TCCAAATCAG	ATAACCCCCC	0	S	0	0	0	0	0
201	152	an	AN7594.1	72.m19619	AO070343000316	0	-179	-141					ATGGATTCCTATCAGAAGCAGAACTCTGCAGAAGAGTGA	ATGGATTCCTATCAGAAGCAGAACTCTGCAGAAGAGTGA			MDSYQKQNSAEE*	MDSYQKQNSAEE*			CCGCATTCCC	CATTGCCCAT	0	S	0	0	0	0	0
204	152	ao	AN7594.1	72.m19619	AO070343000316	0					-148	-137	ATGCTCAGGTGA			ATGCTCAGGTGA	MLR*			MLR*	CAAGGAATCG	ATGACCGGGG	0	S	0	0	0	0	0
205	152	ao	AN7594.1	72.m19619	AO070343000316	0					-136	-62	ATGACCGGGGGACCATGGAGGCCTATAAATACCCCGCTGAGGTGCCATCATTCTTCGAAGGTCCCCAACCCATGA			ATGACCGGGGGACCATGGAGGCCTATAAATACCCCGCTGAGGTGCCATCATTCTTCGAAGGTCCCCAACCCATGA	MTGGPWRPINTPLRCHHSSKVPNP*			MTGGPWRPINTPLRCHHSSKVPNP*	GCTCAGGTGA	GCACCTTGTT	0	S	0	0	0	0	0
206	152	ao	AN7594.1	72.m19619	AO070343000316	0					-122	-45	ATGGAGGCCTATAAATACCCCGCTGAGGTGCCATCATTCTTCGAAGGTCCCCAACCCATGAGCACCTTGTTCGCTTGA			ATGGAGGCCTATAAATACCCCGCTGAGGTGCCATCATTCTTCGAAGGTCCCCAACCCATGAGCACCTTGTTCGCTTGA	MEAYKYPAEVPSFFEGPQPMSTLFA*			MEAYKYPAEVPSFFEGPQPMSTLFA*	CCGGGGGACC	CTCTACACCA	0	S	0	0	0	0	0
207	152	ao	AN7594.1	72.m19619	AO070343000316	0					-65	-45	ATGAGCACCTTGTTCGCTTGA			ATGAGCACCTTGTTCGCTTGA	MSTLFA*			MSTLFA*	TCCCCAACCC	CTCTACACCA	0	S	0	0	0	0	0
208	154	an	AN3079.1	59.m08919	AO070224000007	0	-219	-190					ATGTCAGGCTGGGTTCTCAGGTATAAATAG	ATGTCAGGCTGGGTTCTCAGGTATAAATAG			MSGWVLRYK*	MSGWVLRYK*			GAAAGACCCT	GGCTGAGGAT	0		0	0	0	0	0
209	154	ao	AN3079.1	59.m08919	AO070224000007	0					-262	-200	ATGTCCGTCCTAAATCGACTCTTTTCTTCTTCAACCATCCACATTCTCTTATACATTCTCTAG			ATGTCCGTCCTAAATCGACTCTTTTCTTCTTCAACCATCCACATTCTCTTATACATTCTCTAG	MSVLNRLFSSSTIHILLYIL*			MSVLNRLFSSSTIHILLYIL*	AACCCTGACG	ACAAGCTCTG	0		0	0	0	0	0
212	155	af	AN1719.1	58.m08960	AO070305000034	0			-107	-51			ATGCCCGGCTATCGAACCTCCGGCGTGTCGCCTATTTTCCCCTCGAACTTACAGTAA		ATGCCCGGCTATCGAACCTCCGGCGTGTCGCCTATTTTCCCCTCGAACTTACAGTAA		MPGYRTSGVSPIFPSNLQ*		MPGYRTSGVSPIFPSNLQ*		TGCCATTTCG	TAGATTGACT	0		0	0	0	0	0
210	155	an	AN1719.1	58.m08960	AO070305000034	0	-241	-224					ATGTCGGTTGGGCGCTGA	ATGTCGGTTGGGCGCTGA			MSVGR*	MSVGR*			TCGAGTTCGG	TCGTGCGACT	0		0	0	0	0	0
211	155	an	AN1719.1	58.m08960	AO070305000034	0	-88	-26					ATGCCAGAAAGGTCTGCCAACGATTGCGCGGCTCTTCTGGGTTTGAGATTCGCTGCGGTTTGA	ATGCCAGAAAGGTCTGCCAACGATTGCGCGGCTCTTCTGGGTTTGAGATTCGCTGCGGTTTGA			MPERSANDCAALLGLRFAAV*	MPERSANDCAALLGLRFAAV*			GTCGGATTCG	TTTGTGCTGC	0		0	0	0	0	0
213	155	ao	AN1719.1	58.m08960	AO070305000034	0					-78	-37	ATGCCAGCACTGCGGACAAGCTTTGCTTCTTGGCTGTCATAG			ATGCCAGCACTGCGGACAAGCTTTGCTTCTTGGCTGTCATAG	MPALRTSFASWLS*			MPALRTSFASWLS*	TGAGTATTAA	TGCAGGCAGT	0		0	0	0	0	0
214	158	an	AN2167.1	72.m19673	AO070343000229	0	-237	-166					ATGGCAATGTTGACAACTTCTTATTTTCGTAAACTTTGTAGCCTCGGTATAATACCATCCTTTCTGTTATAG	ATGGCAATGTTGACAACTTCTTATTTTCGTAAACTTTGTAGCCTCGGTATAATACCATCCTTTCTGTTATAG			MAMLTTSYFRKLCSLGIIPSFLL*	MAMLTTSYFRKLCSLGIIPSFLL*			AGTGAGGCAG	GGCTGCAGTG	0	U	0	0	0	0	0
215	158	an	AN2167.1	72.m19673	AO070343000229	0	-231	-166					ATGTTGACAACTTCTTATTTTCGTAAACTTTGTAGCCTCGGTATAATACCATCCTTTCTGTTATAG	ATGTTGACAACTTCTTATTTTCGTAAACTTTGTAGCCTCGGTATAATACCATCCTTTCTGTTATAG			MLTTSYFRKLCSLGIIPSFLL*	MLTTSYFRKLCSLGIIPSFLL*			GCAGATGGCA	GGCTGCAGTG	0	U	0	0	0	0	0
216	158	an	AN2167.1	72.m19673	AO070343000229	0	-137	-60					ATGAATCTGAGGTCATCTTCCTCCGCTCATGTGAGTTCAGCTTTCTTGACCAAAACAAAACTCTCGCCGCCTTCGTAA	ATGAATCTGAGGTCATCTTCCTCCGCTCATGTGAGTTCAGCTTTCTTGACCAAAACAAAACTCTCGCCGCCTTCGTAA			MNLRSSSSAHVSSAFLTKTKLSPPS*	MNLRSSSSAHVSSAFLTKTKLSPPS*			GGCAGGGCAT	CTCAACCCAC	0	U	0	0	0	0	0
226	172	af	AN0821.1	70.m15420	AO070255000026	0			-150	-31			ATGCAGACAGCCGAGGAATGTCCGTTATGGCGTCAGTCATTATTTCTTGAGCTGACTGATTCTCGCCTGCGTCATAGTCAAATTTGGAAAACGCTTCCTCGCATCAAGACCAACAAATAG		ATGCAGACAGCCGAGGAATGTCCGTTATGGCGTCAGTCATTATTTCTTGAGCTGACTGATTCTCGCCTGCGTCATAGTCAAATTTGGAAAACGCTTCCTCGCATCAAGACCAACAAATAG		MQTAEECPLWRQSLFLELTDSRLRHSQIWKTLPRIKTNK*		MQTAEECPLWRQSLFLELTDSRLRHSQIWKTLPRIKTNK*		GTGACTCAAC	CTGCGCAGGT	0		0	0	0	0	0
227	172	af	AN0821.1	70.m15420	AO070255000026	0			-133	-101			ATGTCCGTTATGGCGTCAGTCATTATTTCTTGA		ATGTCCGTTATGGCGTCAGTCATTATTTCTTGA		MSVMASVIIS*		MSVMASVIIS*		CAGCCGAGGA	GCTGACTGAT	0		0	0	0	0	0
228	172	af	AN0821.1	70.m15420	AO070255000026	0			-124	-101			ATGGCGTCAGTCATTATTTCTTGA		ATGGCGTCAGTCATTATTTCTTGA		MASVIIS*		MASVIIS*		AATGTCCGTT	GCTGACTGAT	0		0	0	0	0	0
221	172	an	AN0821.1	70.m15420	AO070255000026	0	-188	-156					ATGGAGCTTGATCTTTGTTGTCGTTGGGGTTAA	ATGGAGCTTGATCTTTGTTGTCGTTGGGGTTAA			MELDLCCRWG*	MELDLCCRWG*			CGAGTCAGCA	TCAGAATGAT	0		0	0	0	0	0
222	172	an	AN0821.1	70.m15420	AO070255000026	0	-150	-130					ATGATGCAAGTTCAAAGTTGA	ATGATGCAAGTTCAAAGTTGA			MMQVQS*	MMQVQS*			GTTAATCAGA	GGCTGTTGAG	0		0	0	0	0	0
223	172	an	AN0821.1	70.m15420	AO070255000026	0	-147	-130					ATGCAAGTTCAAAGTTGA	ATGCAAGTTCAAAGTTGA			MQVQS*	MQVQS*			AATCAGAATG	GGCTGTTGAG	0		0	0	0	0	0
224	172	an	AN0821.1	70.m15420	AO070255000026	0	-98						ATGGCCCTTGCTCAATCACGTGATATGCCGGACAATACTGGCCTTCCTTTTGTCAATTGCTTCAACAGTCAGTCAACTCCCTTTCACCTCCACATGTGA	ATGGCCCTTGCTCAATCACGTGATATGCCGGACAATACTGGCCTTCCTTTTGTCAATTGCTTCAACAGTCAGTCAACTCCCTTTCACCTCCACATGTGA			MALAQSRDMPDNTGLPFVNCFNSQSTPFHLHM*	MALAQSRDMPDNTGLPFVNCFNSQSTPFHLHM*			GGATCGCTCG	TGTCCATCGA	0		0	0	0	0	0
225	172	an	AN0821.1	70.m15420	AO070255000026	0	-74						ATGCCGGACAATACTGGCCTTCCTTTTGTCAATTGCTTCAACAGTCAGTCAACTCCCTTTCACCTCCACATGTGA	ATGCCGGACAATACTGGCCTTCCTTTTGTCAATTGCTTCAACAGTCAGTCAACTCCCTTTCACCTCCACATGTGA			MPDNTGLPFVNCFNSQSTPFHLHM*	MPDNTGLPFVNCFNSQSTPFHLHM*			ATCACGTGAT	TGTCCATCGA	0		0	0	0	0	0
229	172	ao	AN0821.1	70.m15420	AO070255000026	0					-245	-138	ATGAGAAGACGTCCATTGCTGATTTACAATGTCATCGATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAAATTAA			ATGAGAAGACGTCCATTGCTGATTTACAATGTCATCGATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAAATTAA	MRRRPLLIYNVIDEVTSTSRDLHGTRVGPRRLRLN*			MRRRPLLIYNVIDEVTSTSRDLHGTRVGPRRLRLN*	GAGATATGCC	TCCCTGTGGA	0		0	0	0	0	0
230	172	ao	AN0821.1	70.m15420	AO070255000026	0					-217	-143	ATGTCATCGATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAA			ATGTCATCGATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAA	MSSMRLLQHHVICTGRELVRGDCA*			MSSMRLLQHHVICTGRELVRGDCA*	CTGATTTACA	ATTAATCCCT	0		0	0	0	0	0
231	172	ao	AN0821.1	70.m15420	AO070255000026	0					-208	-143	ATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAA			ATGAGGTTACTTCAACATCACGTGATTTGCACGGGACGCGAGTTGGTCCGCGGCGACTGCGCCTAA	MRLLQHHVICTGRELVRGDCA*			MRLLQHHVICTGRELVRGDCA*	AATGTCATCG	ATTAATCCCT	0		0	0	0	0	0
232	177	af	AN3469.1	59.m09329	AO070265000045	0			-289	-272			ATGGTTTGTATTACTTGA		ATGGTTTGTATTACTTGA		MVCIT*		MVCIT*		GCTGTGCCCT	ACGTGTTTAC	0	B	FG11626.1	0	0	0	0
234	178	af	AN3503.1	54.m07029	AO070306000124	0			-156	-64			ATGCTCGCAGATCCCACAGTGACCTCGGCGACGTATACTATCAAAATCACGCCCTCTCCTTTCTCCTTGTCACCTCGTCTTTTGGACCTCTAG		ATGCTCGCAGATCCCACAGTGACCTCGGCGACGTATACTATCAAAATCACGCCCTCTCCTTTCTCCTTGTCACCTCGTCTTTTGGACCTCTAG		MLADPTVTSATYTIKITPSPFSLSPRLLDL*		MLADPTVTSATYTIKITPSPFSLSPRLLDL*		TCAAGTTTGT	GCACGTGAAA	0	G	0	0	NCU09654.1	YLR004C	0
233	178	an	AN3503.1	54.m07029	AO070306000124	0	-177	-145					ATGTATCTTCCTGACCTGTACCTCAACGGCTGA	ATGTATCTTCCTGACCTGTACCTCAACGGCTGA			MYLPDLYLNG*	MYLPDLYLNG*			TCGCCAGGAT	CTTGGGCCTT	0	G	0	0	NCU09654.1	YLR004C	0
235	178	ao	AN3503.1	54.m07029	AO070306000124	0					-125	-84	ATGTGCTTATCACCATCTGTTCTAAGCACTGGAGAAATTTGA			ATGTGCTTATCACCATCTGTTCTAAGCACTGGAGAAATTTGA	MCLSPSVLSTGEI*			MCLSPSVLSTGEI*	TCACTACTTC	AGCTCTCCCC	0	G	0	0	NCU09654.1	YLR004C	0
236	179	an	AN6921.1	71.m16029	AO070313000060	0	-237	-172					ATGAGGGGAGCGAGGCAAACACTACAAACACACTCAGCAGGTTCCAGTACTTTCCAGAGTTTCTAG	ATGAGGGGAGCGAGGCAAACACTACAAACACACTCAGCAGGTTCCAGTACTTTCCAGAGTTTCTAG			MRGARQTLQTHSAGSSTFQSF*	MRGARQTLQTHSAGSSTFQSF*			TCCGCCCTGA	CACTCATTTG	0	O	0	0	0	0	0
239	182	af	AN4899.1	59.m08798	AO070338000053	0			-159	-13			ATGCCGCGGCGATCGGCTTTCGGTTCCCCGCCAAAAGAGACCCCAACATTTCTTCTTCACATGCGTGCGTCTGCCAAACTCCCCTTTCACCACAGCGCTGGTCTCTCCTTTCCAGTCATTTCCTCAGAATTGTTCAGGAGTATATGA		ATGCCGCGGCGATCGGCTTTCGGTTCCCCGCCAAAAGAGACCCCAACATTTCTTCTTCACATGCGTGCGTCTGCCAAACTCCCCTTTCACCACAGCGCTGGTCTCTCCTTTCCAGTCATTTCCTCAGAATTGTTCAGGAGTATATGA		MPRRSAFGSPPKETPTFLLHMRASAKLPFHHSAGLSFPVISSELFRSI*		MPRRSAFGSPPKETPTFLLHMRASAKLPFHHSAGLSFPVISSELFRSI*		AGTACTGGCG	CTTTCAGACA	0	U	0	0	0	0	0
237	182	an	AN4899.1	59.m08798	AO070338000053	0	-156	-64					ATGATCCCGGAATCGACGCAACCAACAAATGCAGCAGAAGTTATCCAAAAGCTTGCATTCTTCTTTCTCTCTTTAGTCTATTATTATCGCTAA	ATGATCCCGGAATCGACGCAACCAACAAATGCAGCAGAAGTTATCCAAAAGCTTGCATTCTTCTTTCTCTCTTTAGTCTATTATTATCGCTAA			MIPESTQPTNAAEVIQKLAFFFLSLVYYYR*	MIPESTQPTNAAEVIQKLAFFFLSLVYYYR*			TTCACATGAA	CGTTACTTCG	0	U	0	0	0	0	0
242	186	af	AN0159.1	71.m15436	AO070321000088	0			-153	-97			ATGCAAACCGCCACCAGGAAAGGGTATCTAATCAGCCGTGTCACTGCCACAAGATAG		ATGCAAACCGCCACCAGGAAAGGGTATCTAATCAGCCGTGTCACTGCCACAAGATAG		MQTATRKGYLISRVTATR*		MQTATRKGYLISRVTATR*		GAGCCATACC	CCTTTGCCCG	0	AR	0	0	0	0	0
241	186	an	AN0159.1	71.m15436	AO070321000088	0	-136	-83					ATGAACACTGACTGGGATTTGACTGAACCTGACTACATCGCCGCGACCGGATAA	ATGAACACTGACTGGGATTTGACTGAACCTGACTACATCGCCGCGACCGGATAA			MNTDWDLTEPDYIAATG*	MNTDWDLTEPDYIAATG*			ACAGACTACC	CTGCTTCTCT	0	AR	0	0	0	0	0
243	186	ao	AN0159.1	71.m15436	AO070321000088	0					-184	-131	ATGCCAGCTTCCAGGAAAGAGTCTCTAATCCACCGCGCCGCTGCAATAGGATAG			ATGCCAGCTTCCAGGAAAGAGTCTCTAATCCACCGCGCCGCTGCAATAGGATAG	MPASRKESLIHRAAAIG*			MPASRKESLIHRAAAIG*	CGAACATAAT	CCCTTGGCTT	0	AR	0	0	0	0	0
244	191	af	AN6054.1	72.m19104	AO070340000200	0			-179	-147			ATGCCATCATACCACTATTGTAATCATATCTGA		ATGCCATCATACCACTATTGTAATCATATCTGA		MPSYHYCNHI*		MPSYHYCNHI*		TGTACTATAG	ACCATCACCA	0		0	0	0	YJR144W	0
245	191	ao	AN6054.1	72.m19104	AO070340000200	0					-197	-111	ATGTACTACTATACTCTGTACAATAATCCAATGCAATCCATCTCCCCTCCCGCCTTTGTTCAGAACATTGAAAGCCCCGTCACGTGA			ATGTACTACTATACTCTGTACAATAATCCAATGCAATCCATCTCCCCTCCCGCCTTTGTTCAGAACATTGAAAGCCCCGTCACGTGA	MYYYTLYNNPMQSISPPAFVQNIESPVT*			MYYYTLYNNPMQSISPPAFVQNIESPVT*	CTTAGAGCCT	TCATATCAAG	0		0	0	0	YJR144W	0
246	191	ao	AN6054.1	72.m19104	AO070340000200	0					-167	-111	ATGCAATCCATCTCCCCTCCCGCCTTTGTTCAGAACATTGAAAGCCCCGTCACGTGA			ATGCAATCCATCTCCCCTCCCGCCTTTGTTCAGAACATTGAAAGCCCCGTCACGTGA	MQSISPPAFVQNIESPVT*			MQSISPPAFVQNIESPVT*	CAATAATCCA	TCATATCAAG	0		0	0	0	YJR144W	0
247	194	an	AN6735.1	65.m07233	AO070339000181	0	-227	-186					ATGGTGGTGACTGACGATCCGCTCCCAAGGAAAAGTTGGTGA	ATGGTGGTGACTGACGATCCGCTCCCAAGGAAAAGTTGGTGA			MVVTDDPLPRKSW*	MVVTDDPLPRKSW*			TGAAAGTGGG	GCCGCAACAA	0	A	0	0	0	YOR159C	0
250	197	af	AN6743.1	66.m04708	AO070313000143	0			-274	-242			ATGTCCACCCTTCGGCAAGCCTCATGCCATTGA		ATGTCCACCCTTCGGCAAGCCTCATGCCATTGA		MSTLRQASCH*		MSTLRQASCH*		CAGCAGTGAC	CACCGCGTCA	0	R	0	MG08785.1	0	0	0
251	197	af	AN6743.1	66.m04708	AO070313000143	0			-251	-123			ATGCCATTGACACCGCGTCATCGAGGAAGATTTGAGGAAAGATCGCGGTCGAGCCATCGGCTCCGCATCTCGGCTCCACATGCGGAGAGGAACAGAGAGCAGTGGCTCGCCCGCCTGATGCGGACGTAA		ATGCCATTGACACCGCGTCATCGAGGAAGATTTGAGGAAAGATCGCGGTCGAGCCATCGGCTCCGCATCTCGGCTCCACATGCGGAGAGGAACAGAGAGCAGTGGCTCGCCCGCCTGATGCGGACGTAA		MPLTPRHRGRFEERSRSSHRLRISAPHAERNREQWLARLMRT*		MPLTPRHRGRFEERSRSSHRLRISAPHAERNREQWLARLMRT*		GGCAAGCCTC	GCCCTTTGAC	0	R	0	MG08785.1	0	0	0
252	197	af	AN6743.1	66.m04708	AO070313000143	0			-172	-134			ATGCGGAGAGGAACAGAGAGCAGTGGCTCGCCCGCCTGA		ATGCGGAGAGGAACAGAGAGCAGTGGCTCGCCCGCCTGA		MRRGTESSGSPA*		MRRGTESSGSPA*		TCGGCTCCAC	TGCGGACGTA	0	R	0	MG08785.1	0	0	0
253	197	af	AN6743.1	66.m04708	AO070313000143	0			-134	-123			ATGCGGACGTAA		ATGCGGACGTAA		MRT*		MRT*		CGCCCGCCTG	GCCCTTTGAC	0	R	0	MG08785.1	0	0	0
248	197	an	AN6743.1	66.m04708	AO070313000143	0	-121	-47					ATGCATTCCAAAGAGGGGAATGCAAATATTTATCCCACATGCCGGATCTTACGATCTTCTTCTGATAATCTTTGA	ATGCATTCCAAAGAGGGGAATGCAAATATTTATCCCACATGCCGGATCTTACGATCTTCTTCTGATAATCTTTGA			MHSKEGNANIYPTCRILRSSSDNL*	MHSKEGNANIYPTCRILRSSSDNL*			ATCGCGCGAT	TCATCAGAAT	0	R	0	MG08785.1	0	0	0
249	197	an	AN6743.1	66.m04708	AO070313000143	0	-83	-57					ATGCCGGATCTTACGATCTTCTTCTGA	ATGCCGGATCTTACGATCTTCTTCTGA			MPDLTIFF*	MPDLTIFF*			TTTATCCCAC	TAATCTTTGA	0	R	0	MG08785.1	0	0	0
254	197	ao	AN6743.1	66.m04708	AO070313000143	0					-196	-110	ATGCGTTCGGATCGAACATTTCGGCTCCACATACGGTCGGGGGCCCATGGTCCCGGTCGTATGAACACAGCTAGAGACATTATTTAG			ATGCGTTCGGATCGAACATTTCGGCTCCACATACGGTCGGGGGCCCATGGTCCCGGTCGTATGAACACAGCTAGAGACATTATTTAG	MRSDRTFRLHIRSGAHGPGRMNTARDII*			MRSDRTFRLHIRSGAHGPGRMNTARDII*	CTGTGCCTCA	AGCAGGCAAG	0	R	0	MG08785.1	0	0	0
255	197	ao	AN6743.1	66.m04708	AO070313000143	0					-150	-133	ATGGTCCCGGTCGTATGA			ATGGTCCCGGTCGTATGA	MVPVV*			MVPVV*	TCGGGGGCCC	ACACAGCTAG	0	R	0	MG08785.1	0	0	0

256	197	ao	AN6743.1	66.m04708	AO070313000143	0					-136	-110	ATGAACACAGCTAGAGACATTATTTAG			ATGAACACAGCTAGAGACATTATTTAG	MNTARDII*			MNTARDII*	TCCCGGTCGT	AGCAGGCAAG	0	R	0	MG08785.1	0	0	0
258	205	af	AN9067.1	66.m04519	AO070332000219	0			-224	-186			ATGGCGGGGTACTCATTCTATTCCTCTCCCCCTCCTTGA		ATGGCGGGGTACTCATTCTATTCCTCTCCCCCTCCTTGA		MAGYSFYSSPPP*		MAGYSFYSSPPP*		ATTAAAACCT	GCAGGTACAC	0	R	0	0	0	0	0
257	205	an	AN9067.1	66.m04519	AO070332000219	0	-153	-97					ATGGCGGGGCAGCTGAATCCCCCGCCATGTTTCAGCTTCGTCAACTTGTCTTCCTGA	ATGGCGGGGCAGCTGAATCCCCCGCCATGTTTCAGCTTCGTCAACTTGTCTTCCTGA			MAGQLNPPPCFSFVNLSS*	MAGQLNPPPCFSFVNLSS*			TGTGCACCTG	ACTTTCTCCC	0	R	0	0	0	0	0
259	205	ao	AN9067.1	66.m04519	AO070332000219	0					-241	-230	ATGATAATATAA			ATGATAATATAA	MII*			MII*	TTGATATAGT	TTTGTCCTTG	0	R	0	0	0	0	0
260	205	ao	AN9067.1	66.m04519	AO070332000219	0					-208	-197	ATGATAATGTGA			ATGATAATGTGA	MIM*			MIM*	CAAGCTGGCA	GACTGCATGG	0	R	0	0	0	0	0
261	205	ao	AN9067.1	66.m04519	AO070332000219	0					-190	-128	ATGGCGGGGCACCTGTATTTCTGTCGGCTAGCTTGCTCTTTCACAGTGCAAAGGCGCCCCTAG			ATGGCGGGGCACCTGTATTTCTGTCGGCTAGCTTGCTCTTTCACAGTGCAAAGGCGCCCCTAG	MAGHLYFCRLACSFTVQRRP*			MAGHLYFCRLACSFTVQRRP*	GTGAGACTGC	GGAGCTGGGC	0	R	0	0	0	0	0
265	210	af	AN9533.1	54.m06731	AO070342000087	0			-218	-192			ATGATGGAGTGTCCGATCCTTTTTTGA		ATGATGGAGTGTCCGATCCTTTTTTGA		MMECPILF*		MMECPILF*		TGTAACCGAA	ATTCCCCATA	0		0	0	0	0	0
266	210	af	AN9533.1	54.m06731	AO070342000087	0			-215	-192			ATGGAGTGTCCGATCCTTTTTTGA		ATGGAGTGTCCGATCCTTTTTTGA		MECPILF*		MECPILF*		AACCGAAATG	ATTCCCCATA	0		0	0	0	0	0
262	210	an	AN9533.1	54.m06731	AO070342000087	0	-160	-29					ATGCACGCGGCCTTCATGGTATCTCGTACAAAGATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA	ATGCACGCGGCCTTCATGGTATCTCGTACAAAGATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA			MHAAFMVSRTKMDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*	MHAAFMVSRTKMDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*			GCTTTGTGTG	TTCAACAAGA	0		0	0	0	0	0
263	210	an	AN9533.1	54.m06731	AO070342000087	0	-145	-29					ATGGTATCTCGTACAAAGATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA	ATGGTATCTCGTACAAAGATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA			MVSRTKMDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*	MVSRTKMDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*			CGCGGCCTTC	TTCAACAAGA	0		0	0	0	0	0
264	210	an	AN9533.1	54.m06731	AO070342000087	0	-127	-29					ATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA	ATGGATCCCCGCAAGTACGATAACGCTCACGTGACAGTATCTAGCTTCGTAATCGCTAAATTTCCCGGGCAAGTTGAAAGCTCAATAGTCCAGATATAA			MDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*	MDPRKYDNAHVTVSSFVIAKFPGQVESSIVQI*			TCGTACAAAG	TTCAACAAGA	0		0	0	0	0	0
267	210	ao	AN9533.1	54.m06731	AO070342000087	0					-241	-95	ATGCCAATATCGTATAGGCTCCTCTCGGTCACAGATGACAGTTCGATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGAAATACGTTCTGCAGAAACTGACCGCCTTGAACGTCTTCCCGGCGCTGCGGAGGTAA			ATGCCAATATCGTATAGGCTCCTCTCGGTCACAGATGACAGTTCGATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGAAATACGTTCTGCAGAAACTGACCGCCTTGAACGTCTTCCCGGCGCTGCGGAGGTAA	MPISYRLLSVTDDSSMLLVSPHSAPRRALLKYVLQKLTALNVFPALRR*			MPISYRLLSVTDDSSMLLVSPHSAPRRALLKYVLQKLTALNVFPALRR*	TTCCTCAATT	AATCCACGGA	0		0	0	0	0	0
268	210	ao	AN9533.1	54.m06731	AO070342000087	0					-207	-151	ATGACAGTTCGATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGA			ATGACAGTTCGATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGA	MTVRCFWFPHTPRQGGRY*			MTVRCFWFPHTPRQGGRY*	TCGGTCACAG	AATACGTTCT	0		0	0	0	0	0
269	210	ao	AN9533.1	54.m06731	AO070342000087	0					-196	-95	ATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGAAATACGTTCTGCAGAAACTGACCGCCTTGAACGTCTTCCCGGCGCTGCGGAGGTAA			ATGCTTCTGGTTTCCCCACACTCCGCGCCAAGGCGGGCGTTATTGAAATACGTTCTGCAGAAACTGACCGCCTTGAACGTCTTCCCGGCGCTGCGGAGGTAA	MLLVSPHSAPRRALLKYVLQKLTALNVFPALRR*			MLLVSPHSAPRRALLKYVLQKLTALNVFPALRR*	TGACAGTTCG	AATCCACGGA	0		0	0	0	0	0
272	214	af	AN6864.1	71.m15275	AO070314000084	0			-194	-177			ATGCAGCCTGAATTTTAG		ATGCAGCCTGAATTTTAG		MQPEF*		MQPEF*		AAGTGCGAGT	GGCTGGTTTA	0	J	0	0	0	0	0
274	214	ao	AN6864.1	71.m15275	AO070314000084	0					-248	-231	ATGAAACTATTTGAATAG			ATGAAACTATTTGAATAG	MKLFE*			MKLFE*	GTCTTAAGAT	GTGAATAGCA	0	J	0	0	0	0	0
275	214	ao	AN6864.1	71.m15275	AO070314000084	0					-145	-122	ATGGCATCATGCCGAATTTGGTGA			ATGGCATCATGCCGAATTTGGTGA	MASCRIW*			MASCRIW*	GTGTCGGCTT	GTCAAAGTCA	0	J	0	0	0	0	0
284	225	af	AN2288.1	71.m15935	AO070295000067	0			-463	-392			ATGTGCGCCTTGGTTTGGCGTCAGAGACTCGCAGCTGGGGTTAACTGCTTAGTGGTTGTGTGCACTTCATAA		ATGTGCGCCTTGGTTTGGCGTCAGAGACTCGCAGCTGGGGTTAACTGCTTAGTGGTTGTGTGCACTTCATAA		MCALVWRQRLAAGVNCLVVVCTS*		MCALVWRQRLAAGVNCLVVVCTS*		AGTTATTATT	TGGCGAGCCA	0	P	0	0	0	0	0
286	226	an	AN2987.1	59.m09026	AO070337000135	0	-262	-221					ATGCGGTTGGATACCGGATACCTGCCGTATCCGTATATATAA	ATGCGGTTGGATACCGGATACCTGCCGTATCCGTATATATAA			MRLDTGYLPYPYI*	MRLDTGYLPYPYI*			TACTTTGCGA	GCTCTTTTGG	0	Q	0	0	0	0	0
287	226	an	AN2987.1	59.m09026	AO070337000135	0	-150	-133					ATGCCAGGCTTCGTCTAA	ATGCCAGGCTTCGTCTAA			MPGFV*	MPGFV*			GGGTCCGCAA	ATTATTCTCC	0	Q	0	0	0	0	0
288	236	af	AN2430.1	69.m15231	AO070188000004	0			-145	-71			ATGAAAAGCGTGGAGGACAAGTCTCTGCAGCTCTCCTTTTGTTCTCGCATGGTTCCGAACGGTCTTCGAATTTGA		ATGAAAAGCGTGGAGGACAAGTCTCTGCAGCTCTCCTTTTGTTCTCGCATGGTTCCGAACGGTCTTCGAATTTGA		MKSVEDKSLQLSFCSRMVPNGLRI*		MKSVEDKSLQLSFCSRMVPNGLRI*		AAGTGAAGCG	GGCATCCTAG	0	R	0	0	0	0	0
289	236	af	AN2430.1	69.m15231	AO070188000004	0			-97	-71			ATGGTTCCGAACGGTCTTCGAATTTGA		ATGGTTCCGAACGGTCTTCGAATTTGA		MVPNGLRI*		MVPNGLRI*		TTGTTCTCGC	GGCATCCTAG	0	R	0	0	0	0	0
290	236	ao	AN2430.1	69.m15231	AO070188000004	0					-267	-247	ATGTCGGATATCTTCTGCTGA			ATGTCGGATATCTTCTGCTGA	MSDIFC*			MSDIFC*	TAGGCTTAAT	ACTCATTGAT	0	R	0	0	0	0	0
291	236	ao	AN2430.1	69.m15231	AO070188000004	0					-238	-212	ATGGCGTTATATGAAAGTTCAAAGTGA			ATGGCGTTATATGAAAGTTCAAAGTGA	MALYESSK*			MALYESSK*	GAACTCATTG	TTTGCCAAAA	0	R	0	0	0	0	0
292	236	ao	AN2430.1	69.m15231	AO070188000004	0					-228	-82	ATGAAAGTTCAAAGTGATTTGCCAAAAGGAGAGATCCCCCGCATTTTGAGCTACTGGTATCGTATTTGGATATCAAGTATAAGGTCAACTTCATCCGCAACATTCTTTTTACTCTTGTCATATTGGTCTGTCATGTCTCTTGATTAG			ATGAAAGTTCAAAGTGATTTGCCAAAAGGAGAGATCCCCCGCATTTTGAGCTACTGGTATCGTATTTGGATATCAAGTATAAGGTCAACTTCATCCGCAACATTCTTTTTACTCTTGTCATATTGGTCTGTCATGTCTCTTGATTAG	MKVQSDLPKGEIPRILSYWYRIWISSIRSTSSATFFLLLSYWSVMSLD*			MKVQSDLPKGEIPRILSYWYRIWISSIRSTSSATFFLLLSYWSVMSLD*	ATGGCGTTAT	CGTTCTTGGT	0	R	0	0	0	0	0
293	236	ao	AN2430.1	69.m15231	AO070188000004	0					-96	-82	ATGTCTCTTGATTAG			ATGTCTCTTGATTAG	MSLD*			MSLD*	TTGGTCTGTC	CGTTCTTGGT	0	R	0	0	0	0	0
297	238	af	AN3508.1	53.m03968	AO070296000076	0			-217	-92			ATGAGATATACGCAGCATCTGTGTGGAGCATCAGGAGCACAAGATGGCCTTCGTTATTATATCTGTGTCCAAAACCCGCCCTTTCATTCTTTGATGGCCAAATCTAAATCTGCACGTCAGCAGTAA		ATGAGATATACGCAGCATCTGTGTGGAGCATCAGGAGCACAAGATGGCCTTCGTTATTATATCTGTGTCCAAAACCCGCCCTTTCATTCTTTGATGGCCAAATCTAAATCTGCACGTCAGCAGTAA		MRYTQHLCGASGAQDGLRYYICVQNPPFHSLMAKSKSARQQ*		MRYTQHLCGASGAQDGLRYYICVQNPPFHSLMAKSKSARQQ*		CAGCTCTAAA	GCTGCTTTTA	0		0	0	0	0	0
298	238	af	AN3508.1	53.m03968	AO070296000076	0			-174	-124			ATGGCCTTCGTTATTATATCTGTGTCCAAAACCCGCCCTTTCATTCTTTGA		ATGGCCTTCGTTATTATATCTGTGTCCAAAACCCGCCCTTTCATTCTTTGA		MAFVIISVSKTRPFIL*		MAFVIISVSKTRPFIL*		GGAGCACAAG	TGGCCAAATC	0		0	0	0	0	0
299	238	af	AN3508.1	53.m03968	AO070296000076	0			-124	-92			ATGGCCAAATCTAAATCTGCACGTCAGCAGTAA		ATGGCCAAATCTAAATCTGCACGTCAGCAGTAA		MAKSKSARQQ*		MAKSKSARQQ*		TCATTCTTTG	GCTGCTTTTA	0		0	0	0	0	0
294	238	an	AN3508.1	53.m03968	AO070296000076	0	-169	-83					ATGGAGATCCGAGTAGGGTTATGCCTGGGTGGAGTGCTTCTATTCCGATCTGACTTCCCTTGTGCACCTGGTGCCCACCCATCATGA	ATGGAGATCCGAGTAGGGTTATGCCTGGGTGGAGTGCTTCTATTCCGATCTGACTTCCCTTGTGCACCTGGTGCCCACCCATCATGA			MEIRVGLCLGGVLLFRSDFPCAPGAHPS*	MEIRVGLCLGGVLLFRSDFPCAPGAHPS*			CGTACTTCGT	GCGATGCAGC	0		0	0	0	0	0
295	238	an	AN3508.1	53.m03968	AO070296000076	0	-149	-117					ATGCCTGGGTGGAGTGCTTCTATTCCGATCTGA	ATGCCTGGGTGGAGTGCTTCTATTCCGATCTGA			MPGWSASIPI*	MPGWSASIPI*			GAGTAGGGTT	CTTCCCTTGT	0		0	0	0	0	0
296	238	an	AN3508.1	53.m03968	AO070296000076	0	-86	-63					ATGAGCGATGCAGCGAATACATAA	ATGAGCGATGCAGCGAATACATAA			MSDAANT*	MSDAANT*			CCCACCCATC	ACGGGACCTG	0		0	0	0	0	0
301	240	af	AN5938.1	53.m03962	AO070300000043	0			-228	-208			ATGGTCGTCCGTGGTGAGTAG		ATGGTCGTCCGTGGTGAGTAG		MVVRGE*		MVVRGE*		ATCGGGTGGA	TCCAAGCTGT	0	G	0	0	0	0	0
302	240	af	AN5938.1	53.m03962	AO070300000043	0			-156	-121			ATGAATATTACGATATCTGAATGTGCGGTCAGCTAG		ATGAATATTACGATATCTGAATGTGCGGTCAGCTAG		MNITISECAVS*		MNITISECAVS*		TGATAATAGT	AATGCTCTGA	0	G	0	0	0	0	0
300	240	an	AN5938.1	53.m03962	AO070300000043	0	-128	-105					ATGGTCGTAGAGATTCCGCACTAG	ATGGTCGTAGAGATTCCGCACTAG			MVVEIPH*	MVVEIPH*			CTAGCAGGAA	TTAATCTGCC	0	G	0	0	0	0	0
303	240	ao	AN5938.1	53.m03962	AO070300000043	0					-272	-258	ATGCAAAGTTCATGA			ATGCAAAGTTCATGA	MQSS*			MQSS*	TACGCAGGAG	GTTCAGACTC	0	G	0	0	0	0	0
304	240	ao	AN5938.1	53.m03962	AO070300000043	0					-261	-199	ATGAGTTCAGACTCAGATTTGCATCCCTTAATGTCCTATAGTATACATAGTGCCTCAGAATAA			ATGAGTTCAGACTCAGATTTGCATCCCTTAATGTCCTATAGTATACATAGTGCCTCAGAATAA	MSSDSDLHPLMSYSIHSASE*			MSSDSDLHPLMSYSIHSASE*	TGCAAAGTTC	ACCATGTATA	0	G	0	0	0	0	0
305	240	ao	AN5938.1	53.m03962	AO070300000043	0					-231	-199	ATGTCCTATAGTATACATAGTGCCTCAGAATAA			ATGTCCTATAGTATACATAGTGCCTCAGAATAA	MSYSIHSASE*			MSYSIHSASE*	GCATCCCTTA	ACCATGTATA	0	G	0	0	0	0	0
306	240	ao	AN5938.1	53.m03962	AO070300000043	0					-195	-118	ATGTATACTCCGATATTCACTAAGCTTTGCTACATAAAGACAAAAGACCCTAACTTCAATCCTTCCCAATCGGGCTAA			ATGTATACTCCGATATTCACTAAGCTTTGCTACATAAAGACAAAAGACCCTAACTTCAATCCTTCCCAATCGGGCTAA	MYTPIFTKLCYIKTKDPNFNPSQSG*			MYTPIFTKLCYIKTKDPNFNPSQSG*	AGAATAAACC	TTCCCGATAC	0	G	0	0	0	0	0
307	241	an	AN5631.1	58.m08951	AO070301000030	0	-199	-149					ATGAGAGCGCCTTCTACACGTGTATCCTGTGCATCACACGAGGACCCATAG	ATGAGAGCGCCTTCTACACGTGTATCCTGTGCATCACACGAGGACCCATAG			MRAPSTRVSCASHEDP*	MRAPSTRVSCASHEDP*			AGCGTGATAT	ATCGATCCTC	0	D	0	0	0	0	0
316	254	af	AN0331.1	54.m06427	AO070318000004	0			-177	-31			ATGCACCACTCCCGAGGGGAAAATGCGGATACAACTGCTGCGGTAGACACAAACATCCGTGGCTATCTCCGAGTATTGAAGATCTCCCTTGGTTTAAAGAGCTGGGAAGTCGCTGCTCGTGAAATGACACCAGCCTCGTTATACTAG		ATGCACCACTCCCGAGGGGAAAATGCGGATACAACTGCTGCGGTAGACACAAACATCCGTGGCTATCTCCGAGTATTGAAGATCTCCCTTGGTTTAAAGAGCTGGGAAGTCGCTGCTCGTGAAATGACACCAGCCTCGTTATACTAG		MHHSRGENADTTAAVDTNIRGYLRVLKISLGLKSWEVAAREMTPASLY*		MHHSRGENADTTAAVDTNIRGYLRVLKISLGLKSWEVAAREMTPASLY*		AATTGTGGGG	ATCGAATCTC	0		0	0	0	0	0
317	254	af	AN0331.1	54.m06427	AO070318000004	0			-155	-132			ATGCGGATACAACTGCTGCGGTAG		ATGCGGATACAACTGCTGCGGTAG		MRIQLLR*		MRIQLLR*		CGAGGGGAAA	ACACAAACAT	0		0	0	0	0	0
313	254	an	AN0331.1	54.m06427	AO070318000004	0	-214	-194					ATGCGCCGACAAGTGTACTGA	ATGCGCCGACAAGTGTACTGA			MRRQVY*	MRRQVY*			AAAGCGATAT	CAAATAGGTC	0		0	0	0	0	0
314	254	an	AN0331.1	54.m06427	AO070318000004	0	-168	-70					ATGTACATACCTCGGATTATCCGTGCTAATGCAGTGTGGGGAGAATCGTGGGGATGTGGGAGGGGGACAATCCGTATACCAATACCCCAGGCTCTTTAA	ATGTACATACCTCGGATTATCCGTGCTAATGCAGTGTGGGGAGAATCGTGGGGATGTGGGAGGGGGACAATCCGTATACCAATACCCCAGGCTCTTTAA			MYIPRIIRANAVWGESWGCGRGTIRIPIPQAL*	MYIPRIIRANAVWGESWGCGRGTIRIPIPQAL*			GGCATAACAT	GCTTCGCTAT	0		0	0	0	0	0
315	254	an	AN0331.1	54.m06427	AO070318000004	0	-140	-36					ATGCAGTGTGGGGAGAATCGTGGGGATGTGGGAGGGGGACAATCCGTATACCAATACCCCAGGCTCTTTAAGCTTCGCTATTCCAACAAACCCAACTTCTCCTGA	ATGCAGTGTGGGGAGAATCGTGGGGATGTGGGAGGGGGACAATCCGTATACCAATACCCCAGGCTCTTTAAGCTTCGCTATTCCAACAAACCCAACTTCTCCTGA			MQCGENRGDVGGGQSVYQYPRLFKLRYSNKPNFS*	MQCGENRGDVGGGQSVYQYPRLFKLRYSNKPNFS*			ATCCGTGCTA	CACACAACTA	0		0	0	0	0	0
319	254	ao	AN0331.1	54.m06427	AO070318000004	0					-113	-78	ATGTCGGCCGGCTGCTCAAGGAACTTCTTCATTTAA			ATGTCGGCCGGCTGCTCAAGGAACTTCTTCATTTAA	MSAGCSRNFFI*			MSAGCSRNFFI*	TCAGCGCCGG	AAGCTGATAG	0		0	0	0	0	0
324	259	af	AN2559.1	59.m08405	AO070268000057	0			-161	-135			ATGCGGAGCCAGAAAGTCAATACCTGA		ATGCGGAGCCAGAAAGTCAATACCTGA		MRSQKVNT*		MRSQKVNT*		ACACAGCGAT	TGGGGAAAAC	0	CR	0	0	0	0	0
325	259	af	AN2559.1	59.m08405	AO070268000057	0			-135	-82			ATGGGGAAAACCGCAGATAATATTTGGTCAGCGTGTAAGCGCACGGCGTCGTAG		ATGGGGAAAACCGCAGATAATATTTGGTCAGCGTGTAAGCGCACGGCGTCGTAG		MGKTADNIWSACKRTAS*		MGKTADNIWSACKRTAS*		TCAATACCTG	TGGTGTTTTG	0	CR	0	0	0	0	0
320	259	an	AN2559.1	59.m08405	AO070268000057	0	-247	-191					ATGTTACGCTCTCGTGCGAGAGATGCGCTCCATATCTCCGATGGCCGGCCAGATTAG	ATGTTACGCTCTCGTGCGAGAGATGCGCTCCATATCTCCGATGGCCGGCCAGATTAG			MLRSRARDALHISDGRPD*	MLRSRARDALHISDGRPD*			GCCGACTAAT	ATGGAGAGCA	0	CR	0	0	0	0	0
321	259	an	AN2559.1	59.m08405	AO070268000057	0	-225	-163					ATGCGCTCCATATCTCCGATGGCCGGCCAGATTAGATGGAGAGCACAGAGCACGCAAGATTAG	ATGCGCTCCATATCTCCGATGGCCGGCCAGATTAGATGGAGAGCACAGAGCACGCAAGATTAG			MRSISPMAGQIRWRAQSTQD*	MRSISPMAGQIRWRAQSTQD*			CGTGCGAGAG	ATCCAGTGCA	0	CR	0	0	0	0	0
322	259	an	AN2559.1	59.m08405	AO070268000057	0	-207	-163					ATGGCCGGCCAGATTAGATGGAGAGCACAGAGCACGCAAGATTAG	ATGGCCGGCCAGATTAGATGGAGAGCACAGAGCACGCAAGATTAG			MAGQIRWRAQSTQD*	MAGQIRWRAQSTQD*			CATATCTCCG	ATCCAGTGCA	0	CR	0	0	0	0	0
323	259	an	AN2559.1	59.m08405	AO070268000057	0	-190	-128					ATGGAGAGCACAGAGCACGCAAGATTAGATCCAGTGCAAAGCCCTTGGCTCATTACCCTCTGA	ATGGAGAGCACAGAGCACGCAAGATTAGATCCAGTGCAAAGCCCTTGGCTCATTACCCTCTGA			MESTEHARLDPVQSPWLITL*	MESTEHARLDPVQSPWLITL*			GCCAGATTAG	ACTTGAAGTT	0	CR	0	0	0	0	0
326	259	ao	AN2559.1	59.m08405	AO070268000057	0					-185	-69	ATGGATGGATCCATTATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA			ATGGATGGATCCATTATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA	MDGSIMSRVATPMLGSAPLSLTRRWSSAVPIAGLPLYM*			MDGSIMSRVATPMLGSAPLSLTRRWSSAVPIAGLPLYM*	TGTAACTTGG	CTGGAAGTGA	0	CR	0	0	0	0	0

327	259	ao	AN2559.1	59.m08405	AO070268000057	0					-181	-92	ATGGATCCATTATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAG			ATGGATCCATTATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAG	MDPLCLAWRLQCWDRLLYLLLDAGRVRCR*			MDPLCLAWRLQCWDRLLYLLLDAGRVRCR*	ACTTGGATGG	CCGGTCTACC	0	CR	0	0	0	0	0
328	259	ao	AN2559.1	59.m08405	AO070268000057	0					-170	-69	ATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA			ATGTCTCGCGTGGCGACTCCAATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA	MSRVATPMLGSAPLSLTRRWSSAVPIAGLPLYM*			MSRVATPMLGSAPLSLTRRWSSAVPIAGLPLYM*	TGGATCCATT	CTGGAAGTGA	0	CR	0	0	0	0	0
329	259	ao	AN2559.1	59.m08405	AO070268000057	0					-149	-69	ATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA			ATGCTGGGATCGGCTCCTCTATCTCTTACTAGACGCTGGTCGAGTGCGGTGCCGATAGCCGGTCTACCTCTATATATGTGA	MLGSAPLSLTRRWSSAVPIAGLPLYM*			MLGSAPLSLTRRWSSAVPIAGLPLYM*	GGCGACTCCA	CTGGAAGTGA	0	CR	0	0	0	0	0
330	262	an	AN5828.1	72.m18955	AO070260000018	0	-207	-100					ATGAGTCCGGAATTCCAGAGCCGAGGTTCGACTCCAGTCCCAGCGGTCGGTCCAGCCAACTGTCCCGCATCTTCCCCATCCGTCATCCCCATCCACCTGTACCTCTAA	ATGAGTCCGGAATTCCAGAGCCGAGGTTCGACTCCAGTCCCAGCGGTCGGTCCAGCCAACTGTCCCGCATCTTCCCCATCCGTCATCCCCATCCACCTGTACCTCTAA			MSPEFQSRGSTPVPAVGPANCPASSPSVIPIHLYL*	MSPEFQSRGSTPVPAVGPANCPASSPSVIPIHLYL*			AGACCGCGGC	ATACTTCAGC	0	C	0	0	0	0	0
332	270	af	AN6412.1	56.m02547	AO070339000013	0			-181	-161			ATGGGACATTACCCGAACTGA		ATGGGACATTACCCGAACTGA		MGHYPN*		MGHYPN*		ATAGCGTTAC	CTATTTTATC	0	U	0	0	0	0	0
333	270	af	AN6412.1	56.m02547	AO070339000013	0			-145	-41			ATGAAGATCGCATTCCCGTGGTGTATCCCTGTACTCTGTACCGCTAATCCTTCGTTCAATGCACTTATGATCTCCCTGCAGACTTTCAGGACGATGCAGGTCTAA		ATGAAGATCGCATTCCCGTGGTGTATCCCTGTACTCTGTACCGCTAATCCTTCGTTCAATGCACTTATGATCTCCCTGCAGACTTTCAGGACGATGCAGGTCTAA		MKIAFPWCIPVLCTANPSFNALMISLQTFRTMQV*		MKIAFPWCIPVLCTANPSFNALMISLQTFRTMQV*		TTATCCTTGC	TTTCTCCATT	0	U	0	0	0	0	0
334	270	af	AN6412.1	56.m02547	AO070339000013	0			-87	-76			ATGCACTTATGA		ATGCACTTATGA		MHL*		MHL*		CCTTCGTTCA	TCTCCCTGCA	0	U	0	0	0	0	0
335	270	af	AN6412.1	56.m02547	AO070339000013	0			-79	-41			ATGATCTCCCTGCAGACTTTCAGGACGATGCAGGTCTAA		ATGATCTCCCTGCAGACTTTCAGGACGATGCAGGTCTAA		MISLQTFRTMQV*		MISLQTFRTMQV*		CAATGCACTT	TTTCTCCATT	0	U	0	0	0	0	0
331	270	an	AN6412.1	56.m02547	AO070339000013	0	-187	-158					ATGTCCGGCCTGAACCAACGAGACAACTAG	ATGTCCGGCCTGAACCAACGAGACAACTAG			MSGLNQRDN*	MSGLNQRDN*			GCCCGCCCAG	CGATCGCGAA	0	U	0	0	0	0	0
337	270	ao	AN6412.1	56.m02547	AO070339000013	0					-260	-195	ATGCATAATTTTCTTTCTCTCGTTGGTCCGACAGGGATGATCGGATTTGGGGATTGCCTCGTTTAG			ATGCATAATTTTCTTTCTCTCGTTGGTCCGACAGGGATGATCGGATTTGGGGATTGCCTCGTTTAG	MHNFLSLVGPTGMIGFGDCLV*			MHNFLSLVGPTGMIGFGDCLV*	CGCGGGTCGG	CGACTACAAA	0	U	0	0	0	0	0
338	270	ao	AN6412.1	56.m02547	AO070339000013	0					-224	-195	ATGATCGGATTTGGGGATTGCCTCGTTTAG			ATGATCGGATTTGGGGATTGCCTCGTTTAG	MIGFGDCLV*			MIGFGDCLV*	TCCGACAGGG	CGACTACAAA	0	U	0	0	0	0	0
339	270	ao	AN6412.1	56.m02547	AO070339000013	0					-181	-164	ATGAACTTGAACTATTGA			ATGAACTTGAACTATTGA	MNLNY*			MNLNY*	CTACAAATTA	CCTGCTGATC	0	U	0	0	0	0	0
340	270	ao	AN6412.1	56.m02547	AO070339000013	0					-97	-80	ATGTTTCTCGTATTATAA			ATGTTTCTCGTATTATAA	MFLVL*			MFLVL*	AATTCCAGGC	GACAAGAGGG	0	U	0	0	0	0	0
341	274	ao	AN2080.1	57.m05779	AO070341000233	0					-167	-48	ATGGCTGAGTCAGCGCCTGCAAAATCGACGCTTTCCAAAGGCCCCTCACTATCTAAACTACTCTTCGTTCGTCAACTTTTAGATCCACCTCCAGACTTGCCCTTTTTTGCTCTTCAATAG			ATGGCTGAGTCAGCGCCTGCAAAATCGACGCTTTCCAAAGGCCCCTCACTATCTAAACTACTCTTCGTTCGTCAACTTTTAGATCCACCTCCAGACTTGCCCTTTTTTGCTCTTCAATAG	MAESAPAKSTLSKGPSLSKLLFVRQLLDPPPDLPFFALQ*			MAESAPAKSTLSKGPSLSKLLFVRQLLDPPPDLPFFALQ*	AGCCCGTTTT	AGACGTGTTT	0	J	0	0	0	0	0
342	278	af	AN9521.1	53.m03730	AO070310000069	0			-240	-214			ATGGATCCGCATCCTGGAGGAAACTAG		ATGGATCCGCATCCTGGAGGAAACTAG		MDPHPGGN*		MDPHPGGN*		CACTTCCCCT	GATAGATAGT	0	T	0	0	0	0	0
343	278	af	AN9521.1	53.m03730	AO070310000069	0			-150	-55			ATGCAACGTATAAATATCGAGAACGGACCCTCCTTAGCTGGCGTGATTGGAGTCCAGTCTACCTTCCCCCCTCTCTCAGATCCCCCCTGCTCGTGA		ATGCAACGTATAAATATCGAGAACGGACCCTCCTTAGCTGGCGTGATTGGAGTCCAGTCTACCTTCCCCCCTCTCTCAGATCCCCCCTGCTCGTGA		MQRINIENGPSLAGVIGVQSTFPPLSDPPCS*		MQRINIENGPSLAGVIGVQSTFPPLSDPPCS*		GAGTAAACAA	ACTATCAGTT	0	T	0	0	0	0	0
344	278	ao	AN9521.1	53.m03730	AO070310000069	0					-158	-123	ATGGCAGTGCTTAATCCAATCCCTTTTTGCCCTTAA			ATGGCAGTGCTTAATCCAATCCCTTTTTGCCCTTAA	MAVLNPIPFCP*			MAVLNPIPFCP*	CTTAGCCCCG	TTACCCCTCC	0	T	0	0	0	0	0
348	283	af	AN6795.1	67.m02939	AO070335000198	0			-109	-8			ATGAAGACCGGGAGGTCACGATGCAGTGCAGGGTATAAATTCCCCTGGTCAACTTCTTCAACAAACACAGGCAGTAAACATCATCTCAACATCACCACCTGA		ATGAAGACCGGGAGGTCACGATGCAGTGCAGGGTATAAATTCCCCTGGTCAACTTCTTCAACAAACACAGGCAGTAAACATCATCTCAACATCACCACCTGA		MKTGRSRCSAGYKFPWSTSSTNTGSKHHLNITT*		MKTGRSRCSAGYKFPWSTSSTNTGSKHHLNITT*		TTGCAAGATC	AGTGAAGATG	0		0	0	0	0	0
349	283	af	AN6795.1	67.m02939	AO070335000198	0			-89	-72			ATGCAGTGCAGGGTATAA		ATGCAGTGCAGGGTATAA		MQCRV*		MQCRV*		GGAGGTCACG	ATTCCCCTGG	0		0	0	0	0	0
345	283	an	AN6795.1	67.m02939	AO070335000198	0	-226	-194					ATGCGGGGAGGGGGCAATTTAGACTGCCACTAG	ATGCGGGGAGGGGGCAATTTAGACTGCCACTAG			MRGGGNLDCH*	MRGGGNLDCH*			TCCTTTTCTG	GGTGAGGATT	0		0	0	0	0	0
346	283	an	AN6795.1	67.m02939	AO070335000198	0	-153	-127					ATGAGGGCTCAATGCGGTGGTAATTGA	ATGAGGGCTCAATGCGGTGGTAATTGA			MRAQCGGN*	MRAQCGGN*			TTGGGATCTC	GATAAATCCC	0		0	0	0	0	0
347	283	an	AN6795.1	67.m02939	AO070335000198	0	-142	-131					ATGCGGTGGTAA	ATGCGGTGGTAA			MRW*	MRW*			TGAGGGCTCA	TTGAGATAAA	0		0	0	0	0	0
350	283	ao	AN6795.1	67.m02939	AO070335000198	0					-218	-201	ATGGGCTTTTCAGGCTAA			ATGGGCTTTTCAGGCTAA	MGFSG*			MGFSG*	AAACAGGGAG	AGACTAGCAG	0		0	0	0	0	0
351	283	ao	AN6795.1	67.m02939	AO070335000198	0					-158	-93	ATGTGGGAATTCTCCACGGCGGCATTGTGTCTTCCACAGTTAATCAGGATCCAAAGCTTGTGCTGA			ATGTGGGAATTCTCCACGGCGGCATTGTGTCTTCCACAGTTAATCAGGATCCAAAGCTTGTGCTGA	MWEFSTAALCLPQLIRIQSLC*			MWEFSTAALCLPQLIRIQSLC*	CGAGCATATA	ACCATACCTT	0		0	0	0	0	0
356	287	af	AN8233.1	53.m03736	AO070310000075	0			-214	-182			ATGTACTCTGTAGAAGGGAATAGGAGTAGATAG		ATGTACTCTGTAGAAGGGAATAGGAGTAGATAG		MYSVEGNRSR*		MYSVEGNRSR*		TACGCAGTAT	GGAATTTGTC	0	I	0	0	0	0	0
354	287	an	AN8233.1	53.m03736	AO070310000075	0	-271	-203					ATGAGGGATCGTACGACCGGATCCATGAGACTAGTCTTGAAAGAGAAGTGGTCTAGATGTGATAAATAG	ATGAGGGATCGTACGACCGGATCCATGAGACTAGTCTTGAAAGAGAAGTGGTCTAGATGTGATAAATAG			MRDRTTGSMRLVLKEKWSRCDK*	MRDRTTGSMRLVLKEKWSRCDK*			TTCACAAATC	ATTTGTATGA	0	I	0	0	0	0	0
355	287	an	AN8233.1	53.m03736	AO070310000075	0	-247	-203					ATGAGACTAGTCTTGAAAGAGAAGTGGTCTAGATGTGATAAATAG	ATGAGACTAGTCTTGAAAGAGAAGTGGTCTAGATGTGATAAATAG			MRLVLKEKWSRCDK*	MRLVLKEKWSRCDK*			GACCGGATCC	ATTTGTATGA	0	I	0	0	0	0	0
358	292	af	AN7273.1	72.m19783	AO070297000022	0			-108	-28			ATGCAGCTTCGACACTTGCATCGAGAAAGACAGAGCTCGACTGCAAGTAAAACGCTCATAAGGCAATCATCCCTAATTTGA		ATGCAGCTTCGACACTTGCATCGAGAAAGACAGAGCTCGACTGCAAGTAAAACGCTCATAAGGCAATCATCCCTAATTTGA		MQLRHLHRERQSSTASKTLIRQSSLI*		MQLRHLHRERQSSTASKTLIRQSSLI*		AGGAATTTCC	AACACTTTCG	0		0	MG00114.1	0	0	0
357	292	an	AN7273.1	72.m19783	AO070297000022	0	-104	-87					ATGCGCTCAGCCATTTAA	ATGCGCTCAGCCATTTAA			MRSAI*	MRSAI*			GCAATTTTTG	TATACTCGGC	0		0	MG00114.1	0	0	0
359	292	ao	AN7273.1	72.m19783	AO070297000022	0					-234	-172	ATGCTCACGCTGCTGAAAAATACGGAAACCGCGCGTGCAGCTTGTCGACACCTCAGAAGCTGA			ATGCTCACGCTGCTGAAAAATACGGAAACCGCGCGTGCAGCTTGTCGACACCTCAGAAGCTGA	MLTLLKNTETARAACRHLRS*			MLTLLKNTETARAACRHLRS*	CCAATTTTCT	CGTTAGAGAA	0		0	MG00114.1	0	0	0
363	294	af	AN2276.1	71.m15921	AO070295000052	0			-169	-47			ATGGAAACGAGGGTCTGCTCTCAAAGTGGCCAATCAGCAGCGCAGACTGCACAAAGAGGGTTCAAGTTGTCGTATTCAATCAACAATCCCAAGTGTTGCAAAAATCCCATAACCCATCACTAA		ATGGAAACGAGGGTCTGCTCTCAAAGTGGCCAATCAGCAGCGCAGACTGCACAAAGAGGGTTCAAGTTGTCGTATTCAATCAACAATCCCAAGTGTTGCAAAAATCCCATAACCCATCACTAA		METRVCSQSGQSAAQTAQRGFKLSYSINNPKCCKNPITHH*		METRVCSQSGQSAAQTAQRGFKLSYSINNPKCCKNPITHH*		CTGGCAACTG	TGTCCTGGGT	0	F	0	0	0	0	0
360	294	an	AN2276.1	71.m15921	AO070295000052	0	-203	-192					ATGTGTCTTTGA	ATGTGTCTTTGA			MCL*	MCL*			GCTGGCGCCT	AATGGCATTG	0	F	0	0	0	0	0
361	294	an	AN2276.1	71.m15921	AO070295000052	0	-190	-140					ATGGCATTGATACGTCGGATTTTCGAACATTGGAAGTTGCTCTCAAAGTAA	ATGGCATTGATACGTCGGATTTTCGAACATTGGAAGTTGCTCTCAAAGTAA			MALIRRIFEHWKLLSK*	MALIRRIFEHWKLLSK*			TGTCTTTGAA	CCAATCAGCG	0	F	0	0	0	0	0
362	294	an	AN2276.1	71.m15921	AO070295000052	0	-98	-78					ATGAGTCTCATCACTTATTAA	ATGAGTCTCATCACTTATTAA			MSLITY*	MSLITY*			TACGAGTCTC	GGTGTTGAAA	0	F	0	0	0	0	0
364	294	ao	AN2276.1	71.m15921	AO070295000052	0					-206	-147	ATGGCGGATGTCATGTACGCCCGGAGCTCTGTAGGGGTAAAAAGACTGATCTTGAACTGA			ATGGCGGATGTCATGTACGCCCGGAGCTCTGTAGGGGTAAAAAGACTGATCTTGAACTGA	MADVMYARSSVGVKRLILN*			MADVMYARSSVGVKRLILN*	TATACACAGT	CCAATCAGCG	0	F	0	0	0	0	0
365	294	ao	AN2276.1	71.m15921	AO070295000052	0					-199	-173	ATGTCATGTACGCCCGGAGCTCTGTAG			ATGTCATGTACGCCCGGAGCTCTGTAG	MSCTPGAL*			MSCTPGAL*	AGTATGGCGG	GGGTAAAAAG	0	F	0	0	0	0	0
366	294	ao	AN2276.1	71.m15921	AO070295000052	0					-194	-147	ATGTACGCCCGGAGCTCTGTAGGGGTAAAAAGACTGATCTTGAACTGA			ATGTACGCCCGGAGCTCTGTAGGGGTAAAAAGACTGATCTTGAACTGA	MYARSSVGVKRLILN*			MYARSSVGVKRLILN*	GGCGGATGTC	CCAATCAGCG	0	F	0	0	0	0	0
368	299	af	AN4305.1	58.m08019	AO070330000015	0			-206	-153			ATGTCCGAATTGCATCACCGGCAGCCTTGGATCGTCACCGATCTACTTGAATAA		ATGTCCGAATTGCATCACCGGCAGCCTTGGATCGTCACCGATCTACTTGAATAA		MSELHHRQPWIVTDLLE*		MSELHHRQPWIVTDLLE*		TAAAAAAGCA	AGGGCGGTGC	0	PD	0	0	0	0	0
369	299	af	AN4305.1	58.m08019	AO070330000015	0			-125	-72			ATGCTTGGAGGGCGTCGGCAGTCCTGCTTGATCACTCGCATTCACGACAGCTGA		ATGCTTGGAGGGCGTCGGCAGTCCTGCTTGATCACTCGCATTCACGACAGCTGA		MLGGRRQSCLITRIHDS*		MLGGRRQSCLITRIHDS*		TATCAGTTAG	CATCGTCGCA	0	PD	0	0	0	0	0
367	299	an	AN4305.1	58.m08019	AO070330000015	0	-94	-77					ATGGTTTATTTCTCATAA	ATGGTTTATTTCTCATAA			MVYFS*	MVYFS*			GCTATAAAGA	CCTCGCCACA	0	PD	0	0	0	0	0
371	299	ao	AN4305.1	58.m08019	AO070330000015	0					-295	-242	ATGAAGTTATTTCATGGATCATACTCCATCGCAGGCCAGCAAACTTATTGTTAA			ATGAAGTTATTTCATGGATCATACTCCATCGCAGGCCAGCAAACTTATTGTTAA	MKLFHGSYSIAGQQTYC*			MKLFHGSYSIAGQQTYC*	TCTCGGCTAT	CGTAAGTTAT	0	PD	0	0	0	0	0
372	299	ao	AN4305.1	58.m08019	AO070330000015	0					-282	-193	ATGGATCATACTCCATCGCAGGCCAGCAAACTTATTGTTAACGTAAGTTATTCAACAGTTTTACTAAGTATAGATGACTTAAGAGAATGA			ATGGATCATACTCCATCGCAGGCCAGCAAACTTATTGTTAACGTAAGTTATTCAACAGTTTTACTAAGTATAGATGACTTAAGAGAATGA	MDHTPSQASKLIVNVSYSTVLLSIDDLRE*			MDHTPSQASKLIVNVSYSTVLLSIDDLRE*	AAGTTATTTC	AAGGACGTAA	0	PD	0	0	0	0	0
373	299	ao	AN4305.1	58.m08019	AO070330000015	0					-196	-125	ATGAAAGGACGTAAATTAAACTTATTCTTTCTGGGAGAGCATCTCGAGTCAAACATGATTTTCTATAGTTAA			ATGAAAGGACGTAAATTAAACTTATTCTTTCTGGGAGAGCATCTCGAGTCAAACATGATTTTCTATAGTTAA	MKGRKLNLFFLGEHLESNMIFYS*			MKGRKLNLFFLGEHLESNMIFYS*	ACTTAAGAGA	CTCTGCACAA	0	PD	0	0	0	0	0
374	299	ao	AN4305.1	58.m08019	AO070330000015	0					-142	-125	ATGATTTTCTATAGTTAA			ATGATTTTCTATAGTTAA	MIFYS*			MIFYS*	CGAGTCAAAC	CTCTGCACAA	0	PD	0	0	0	0	0
387	305	af	AN5403.1	69.m15504	AO070333000092	0			-275	-63			ATGCCAGCAAAATCAGGCAGACTTCATGATGTAGAGCATCACGTGATCTGGCGGGACTCACGCGTCCGAGATGTTTTGATGTTGACTTCAGCCAACGACGAGAGACCGCAGCACATTGTTCTCCAACAAACATTAGCCGCACCACGCCATAAATCGATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		ATGCCAGCAAAATCAGGCAGACTTCATGATGTAGAGCATCACGTGATCTGGCGGGACTCACGCGTCCGAGATGTTTTGATGTTGACTTCAGCCAACGACGAGAGACCGCAGCACATTGTTCTCCAACAAACATTAGCCGCACCACGCCATAAATCGATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		MPAKSGRLHDVEHHVIWRDSRVRDVLMLTSANDERPQHIVLQQTLAAPRHKSMITSPGPDSSERAFWPFT*		MPAKSGRLHDVEHHVIWRDSRVRDVLMLTSANDERPQHIVLQQTLAAPRHKSMITSPGPDSSERAFWPFT*		TACGGAGTAG	TTACACTGAT	0	S	0	0	0	0	0
388	305	af	AN5403.1	69.m15504	AO070333000092	0			-197	-63			ATGTTGACTTCAGCCAACGACGAGAGACCGCAGCACATTGTTCTCCAACAAACATTAGCCGCACCACGCCATAAATCGATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		ATGTTGACTTCAGCCAACGACGAGAGACCGCAGCACATTGTTCTCCAACAAACATTAGCCGCACCACGCCATAAATCGATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		MLTSANDERPQHIVLQQTLAAPRHKSMITSPGPDSSERAFWPFT*		MLTSANDERPQHIVLQQTLAAPRHKSMITSPGPDSSERAFWPFT*		AGATGTTTTG	TTACACTGAT	0	S	0	0	0	0	0
389	305	af	AN5403.1	69.m15504	AO070333000092	0			-119	-63			ATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		ATGATTACCTCGCCTGGTCCTGACTCCTCAGAACGGGCGTTTTGGCCCTTTACGTGA		MITSPGPDSSERAFWPFT*		MITSPGPDSSERAFWPFT*		CCATAAATCG	TTACACTGAT	0	S	0	0	0	0	0
382	305	an	AN5403.1	69.m15504	AO070333000092	0	-261	-229					ATGCCTGAAATTTATGGCTATATACTCACGTGA	ATGCCTGAAATTTATGGCTATATACTCACGTGA			MPEIYGYILT*	MPEIYGYILT*			CCAGGTATAT	TGTAGTGGTG	0	S	0	0	0	0	0
383	305	an	AN5403.1	69.m15504	AO070333000092	0	-248	-102					ATGGCTATATACTCACGTGATGTAGTGGTGGGACGCGTAGCCGATGTTTTGATGCTGGGCTCTCCCGCGGCATCGTCAACCTCAATCGCCGAGTCAACCACCGCCACCAACCGTCCACATCGAGATTCAATGAATTGCTTCTGTTAA	ATGGCTATATACTCACGTGATGTAGTGGTGGGACGCGTAGCCGATGTTTTGATGCTGGGCTCTCCCGCGGCATCGTCAACCTCAATCGCCGAGTCAACCACCGCCACCAACCGTCCACATCGAGATTCAATGAATTGCTTCTGTTAA			MAIYSRDVVVGRVADVLMLGSPAASSTSIAESTTATNRPHRDSMNCFC*	MAIYSRDVVVGRVADVLMLGSPAASSTSIAESTTATNRPHRDSMNCFC*			CCTGAAATTT	CAGATTTTAT	0	S	0	0	0	0	0

384	305	an	AN5403.1	69.m15504	AO070333000092	0	-197	-102					ATGCTGGGCTCTCCCGCGGCATCGTCAACCTCAATCGCCGAGTCAACCACCGCCACCAACCGTCCACATCGAGATTCAATGAATTGCTTCTGTTAA	ATGCTGGGCTCTCCCGCGGCATCGTCAACCTCAATCGCCGAGTCAACCACCGCCACCAACCGTCCACATCGAGATTCAATGAATTGCTTCTGTTAA			MLGSPAASSTSIAESTTATNRPHRDSMNCFC*	MLGSPAASSTSIAESTTATNRPHRDSMNCFC*			CGATGTTTTG	CAGATTTTAT	0	S	0	0	0	0	0
385	305	an	AN5403.1	69.m15504	AO070333000092	0	-119	-102					ATGAATTGCTTCTGTTAA	ATGAATTGCTTCTGTTAA			MNCFC*	MNCFC*			TCGAGATTCA	CAGATTTTAT	0	S	0	0	0	0	0
386	305	an	AN5403.1	69.m15504	AO070333000092	0	-89	-66					ATGGACTTCCTTATCCTGAGCTAG	ATGGACTTCCTTATCCTGAGCTAG			MDFLILS*	MDFLILS*			GATTTTATAG	ATTTTTTTTT	0	S	0	0	0	0	0
390	305	ao	AN5403.1	69.m15504	AO070333000092	0					-274	-230	ATGCCTGTAAAGTCAGGCATACATGATGTAAAGTCACGTGTGTAG			ATGCCTGTAAAGTCAGGCATACATGATGTAAAGTCACGTGTGTAG	MPVKSGIHDVKSRV*			MPVKSGIHDVKSRV*	CTGCATATTT	GTGGGACTCA	0	S	0	0	0	0	0
391	305	ao	AN5403.1	69.m15504	AO070333000092	0					-201	-52	ATGCCTCGACTCTTGCCGACGACGGACATCCTCAGCCCACCGACGATAATCAATATCCACCGACTCCACGCCAACTTTCAATGCCGTTGTCGCCCCGGTTGCTATCCTAATTCGGGCTTTGTCGCCCTCGATTTCATTCGCTTAATCTGA			ATGCCTCGACTCTTGCCGACGACGGACATCCTCAGCCCACCGACGATAATCAATATCCACCGACTCCACGCCAACTTTCAATGCCGTTGTCGCCCCGGTTGCTATCCTAATTCGGGCTTTGTCGCCCTCGATTTCATTCGCTTAATCTGA	MPRLLPTTDILSPPTIINIHRLHANFQCRCRPGCYPNSGFVALDFIRLI*			MPRLLPTTDILSPPTIINIHRLHANFQCRCRPGCYPNSGFVALDFIRLI*	CGATGTTTTG	ATATCGACCT	0	S	0	0	0	0	0
392	305	ao	AN5403.1	69.m15504	AO070333000092	0					-121	-92	ATGCCGTTGTCGCCCCGGTTGCTATCCTAA			ATGCCGTTGTCGCCCCGGTTGCTATCCTAA	MPLSPRLLS*			MPLSPRLLS*	CCAACTTTCA	TTCGGGCTTT	0	S	0	0	0	0	0
393	310	af	AN1662.1	58.m07743	AO070299000024	0			-198	-76			ATGACGTACGGTCTTAGCCTGGTGGGGCTCGCGACCACCATGCAAAAATCTCCAGCAAGAAAAAAGATTGCGGGGCACACTTATCACCAGCGTGAACTTTTCACATATTTGACACCAATTTGA		ATGACGTACGGTCTTAGCCTGGTGGGGCTCGCGACCACCATGCAAAAATCTCCAGCAAGAAAAAAGATTGCGGGGCACACTTATCACCAGCGTGAACTTTTCACATATTTGACACCAATTTGA		MTYGLSLVGLATTMQKSPARKKIAGHTYHQRELFTYLTPI*		MTYGLSLVGLATTMQKSPARKKIAGHTYHQRELFTYLTPI*		GAGATAGCCG	GAACCTTCCT	0	S	FG07515.1	MG04898.1	NCU09442.1	YPL225W	0
394	310	af	AN1662.1	58.m07743	AO070299000024	0			-159	-76			ATGCAAAAATCTCCAGCAAGAAAAAAGATTGCGGGGCACACTTATCACCAGCGTGAACTTTTCACATATTTGACACCAATTTGA		ATGCAAAAATCTCCAGCAAGAAAAAAGATTGCGGGGCACACTTATCACCAGCGTGAACTTTTCACATATTTGACACCAATTTGA		MQKSPARKKIAGHTYHQRELFTYLTPI*		MQKSPARKKIAGHTYHQRELFTYLTPI*		CGCGACCACC	GAACCTTCCT	0	S	FG07515.1	MG04898.1	NCU09442.1	YPL225W	0
395	310	ao	AN1662.1	58.m07743	AO070299000024	0					-176	-162	ATGACGTACCGATAA			ATGACGTACCGATAA	MTYR*			MTYR*	GGTGGATTAA	AGCGGGACTG	0	S	FG07515.1	MG04898.1	NCU09442.1	YPL225W	0
396	312	an	AN3004.1	59.m09010	AO070337000108	0	-69	-28					ATGATCCACCCTTCATCAAGGGACGATCACTCTGCCGATTGA	ATGATCCACCCTTCATCAAGGGACGATCACTCTGCCGATTGA			MIHPSSRDDHSAD*	MIHPSSRDDHSAD*			AGTTGAACTC	ACCCGAATCA	0	L	0	0	0	0	0
397	312	ao	AN3004.1	59.m09010	AO070337000108	0					-74	-42	ATGACTTGGATATCTCGTTCCCTGGATTCGTGA			ATGACTTGGATATCTCGTTCCCTGGATTCGTGA	MTWISRSLDS*			MTWISRSLDS*	AGCCAATTGA	GCTCCTCCAT	0	L	0	0	0	0	0
398	316	af	AN5806.1	72.m18936	AO070260000042	0			-190	-98			ATGTTCATCATTTCTGACATGATTATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		ATGTTCATCATTTCTGACATGATTATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		MFIISDMIMTRPVFTRPLNHLIPENRYLCI*		MFIISDMIMTRPVFTRPLNHLIPENRYLCI*		TGCTACTCCA	AACCACTGTG	0	K	0	0	0	0	0
399	316	af	AN5806.1	72.m18936	AO070260000042	0			-172	-98			ATGATTATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		ATGATTATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		MIMTRPVFTRPLNHLIPENRYLCI*		MIMTRPVFTRPLNHLIPENRYLCI*		CATTTCTGAC	AACCACTGTG	0	K	0	0	0	0	0
400	316	af	AN5806.1	72.m18936	AO070260000042	0			-166	-98			ATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		ATGACGCGTCCTGTATTCACGCGTCCATTAAATCATCTTATACCAGAGAATCGTTATTTATGCATTTGA		MTRPVFTRPLNHLIPENRYLCI*		MTRPVFTRPLNHLIPENRYLCI*		TGACATGATT	AACCACTGTG	0	K	0	0	0	0	0
401	316	af	AN5806.1	72.m18936	AO070260000042	0			-107	-87			ATGCATTTGAAACCACTGTGA		ATGCATTTGAAACCACTGTGA		MHLKPL*		MHLKPL*		ATCGTTATTT	ACAATTTATT	0	K	0	0	0	0	0
403	327	af	AN2092.1	57.m05795	AO070341000250	0			-234	-223			ATGGATGATTGA		ATGGATGATTGA		MDD*		MDD*		GCAAGAATTG	ACTCTTTCGA	0	R	0	0	0	0	0
404	327	af	AN2092.1	57.m05795	AO070341000250	0			-230	-156			ATGATTGAACTCTTTCGAATTGAGTCTGCTTGTGTTCTTAGCATGGATACTAGTCCAGGCTGTTTCATTCATTGA		ATGATTGAACTCTTTCGAATTGAGTCTGCTTGTGTTCTTAGCATGGATACTAGTCCAGGCTGTTTCATTCATTGA		MIELFRIESACVLSMDTSPGCFIH*		MIELFRIESACVLSMDTSPGCFIH*		GAATTGATGG	TGCGGTTGAT	0	R	0	0	0	0	0
405	327	af	AN2092.1	57.m05795	AO070341000250	0			-188	-156			ATGGATACTAGTCCAGGCTGTTTCATTCATTGA		ATGGATACTAGTCCAGGCTGTTTCATTCATTGA		MDTSPGCFIH*		MDTSPGCFIH*		TGTTCTTAGC	TGCGGTTGAT	0	R	0	0	0	0	0
406	327	af	AN2092.1	57.m05795	AO070341000250	0			-156	-124			ATGCGGTTGATCGTCCCGTTGCAGCCCTCCTAG		ATGCGGTTGATCGTCCCGTTGCAGCCCTCCTAG		MRLIVPLQPS*		MRLIVPLQPS*		TCATTCATTG	TGATCTCCGC	0	R	0	0	0	0	0
402	327	an	AN2092.1	57.m05795	AO070341000250	0	-109	-95					ATGGTGGAAGTCTGA	ATGGTGGAAGTCTGA			MVEV*	MVEV*			AGGAAGTTGT	GAAACGATCC	0	R	0	0	0	0	0
407	327	ao	AN2092.1	57.m05795	AO070341000250	0					-281	-261	ATGCAGAGTCAAACCCCGTGA			ATGCAGAGTCAAACCCCGTGA	MQSQTP*			MQSQTP*	ACATATATTA	GTCACCGTGA	0	R	0	0	0	0	0
408	327	ao	AN2092.1	57.m05795	AO070341000250	0					-207	-178	ATGGATTCCGTCGGGTGGACTAGACGTTAA			ATGGATTCCGTCGGGTGGACTAGACGTTAA	MDSVGWTRR*			MDSVGWTRR*	TAGTGGTTGA	GGGACTAGCC	0	R	0	0	0	0	0
414	332	af	AN5724.1	54.m06844	AO070324000127	0			-268	-197			ATGTATGTAATGTGTCGTCTTGTTTGGTTTGATACTATACCGTCAAGTATCGCACCTCAAAACGCCACGTGA		ATGTATGTAATGTGTCGTCTTGTTTGGTTTGATACTATACCGTCAAGTATCGCACCTCAAAACGCCACGTGA		MYVMCRLVWFDTIPSSIAPQNAT*		MYVMCRLVWFDTIPSSIAPQNAT*		GGTGTATGTA	TATGCTCACT	0	OU	0	0	0	0	0
415	332	af	AN5724.1	54.m06844	AO070324000127	0			-259	-197			ATGTGTCGTCTTGTTTGGTTTGATACTATACCGTCAAGTATCGCACCTCAAAACGCCACGTGA		ATGTGTCGTCTTGTTTGGTTTGATACTATACCGTCAAGTATCGCACCTCAAAACGCCACGTGA		MCRLVWFDTIPSSIAPQNAT*		MCRLVWFDTIPSSIAPQNAT*		AATGTATGTA	TATGCTCACT	0	OU	0	0	0	0	0
416	332	af	AN5724.1	54.m06844	AO070324000127	0			-195	-76			ATGCTCACTGGAGCTTCTGCAGCATCACACTGTTTTTTTTTCTCAGTGTATACCGGCAGAACCACACATGCACTGCTCCACTGTAAGTGTATGTTAATCTATCTTATTTCCTATTCTTGA		ATGCTCACTGGAGCTTCTGCAGCATCACACTGTTTTTTTTTCTCAGTGTATACCGGCAGAACCACACATGCACTGCTCCACTGTAAGTGTATGTTAATCTATCTTATTTCCTATTCTTGA		MLTGASAASHCFFFSVYTGRTTHALLHCKCMLIYLISYS*		MLTGASAASHCFFFSVYTGRTTHALLHCKCMLIYLISYS*		GCCACGTGAT	GATATATATT	0	OU	0	0	0	0	0
417	332	af	AN5724.1	54.m06844	AO070324000127	0			-128	-99			ATGCACTGCTCCACTGTAAGTGTATGTTAA		ATGCACTGCTCCACTGTAAGTGTATGTTAA		MHCSTVSVC*		MHCSTVSVC*		AGAACCACAC	TCTATCTTAT	0	OU	0	0	0	0	0
418	332	af	AN5724.1	54.m06844	AO070324000127	0			-105	-76			ATGTTAATCTATCTTATTTCCTATTCTTGA		ATGTTAATCTATCTTATTTCCTATTCTTGA		MLIYLISYS*		MLIYLISYS*		CTGTAAGTGT	GATATATATT	0	OU	0	0	0	0	0
410	332	an	AN5724.1	54.m06844	AO070324000127	0	-207	-31					ATGGTACGGTATGGTATAGTTGGTATTATTTCTAACTATAGCATGGTCACCGCCCACGTGATAAATCGCATCAGATGGCACAGCTCGGAATCTTTCTGCCATAGAACTCTTTTGTGTTGTTTACCTCTGTGTGAGACTACTGTTCTTGTCTTTCGTTCTGCATGCAGTTGCCCTTAA	ATGGTACGGTATGGTATAGTTGGTATTATTTCTAACTATAGCATGGTCACCGCCCACGTGATAAATCGCATCAGATGGCACAGCTCGGAATCTTTCTGCCATAGAACTCTTTTGTGTTGTTTACCTCTGTGTGAGACTACTGTTCTTGTCTTTCGTTCTGCATGCAGTTGCCCTTAA			MVRYGIVGIISNYSMVTAHVINRIRWHSSESFCHRTLLCCLPLCETTVLVFRSACSCP*	MVRYGIVGIISNYSMVTAHVINRIRWHSSESFCHRTLLCCLPLCETTVLVFRSACSCP*			TAAGCCCTGT	TTTGAAAGAA	0	OU	0	0	0	0	0
411	332	an	AN5724.1	54.m06844	AO070324000127	0	-165	-31					ATGGTCACCGCCCACGTGATAAATCGCATCAGATGGCACAGCTCGGAATCTTTCTGCCATAGAACTCTTTTGTGTTGTTTACCTCTGTGTGAGACTACTGTTCTTGTCTTTCGTTCTGCATGCAGTTGCCCTTAA	ATGGTCACCGCCCACGTGATAAATCGCATCAGATGGCACAGCTCGGAATCTTTCTGCCATAGAACTCTTTTGTGTTGTTTACCTCTGTGTGAGACTACTGTTCTTGTCTTTCGTTCTGCATGCAGTTGCCCTTAA			MVTAHVINRIRWHSSESFCHRTLLCCLPLCETTVLVFRSACSCP*	MVTAHVINRIRWHSSESFCHRTLLCCLPLCETTVLVFRSACSCP*			TAACTATAGC	TTTGAAAGAA	0	OU	0	0	0	0	0
412	332	an	AN5724.1	54.m06844	AO070324000127	0	-133	-104					ATGGCACAGCTCGGAATCTTTCTGCCATAG	ATGGCACAGCTCGGAATCTTTCTGCCATAG			MAQLGIFLP*	MAQLGIFLP*			ATCGCATCAG	AACTCTTTTG	0	OU	0	0	0	0	0
419	332	ao	AN5724.1	54.m06844	AO070324000127	0					-225	-172	ATGGTATTGTATGGTATGACTTTCATCAAAGCCCACGTGATATCAATCAAATGA			ATGGTATTGTATGGTATGACTTTCATCAAAGCCCACGTGATATCAATCAAATGA	MVLYGMTFIKAHVISIK*			MVLYGMTFIKAHVISIK*	ACAGTTCGGT	TTTATTCTTT	0	OU	0	0	0	0	0
420	332	ao	AN5724.1	54.m06844	AO070324000127	0					-210	-172	ATGACTTTCATCAAAGCCCACGTGATATCAATCAAATGA			ATGACTTTCATCAAAGCCCACGTGATATCAATCAAATGA	MTFIKAHVISIK*			MTFIKAHVISIK*	ATTGTATGGT	TTTATTCTTT	0	OU	0	0	0	0	0
421	332	ao	AN5724.1	54.m06844	AO070324000127	0					-175	-29	ATGATTTATTCTTTTGTTTTTCTGATGTCTCCGGAGATACTACATCTATTCAGTGCGCCAATCGCCTTGTATACTACTGTACTTATATCCTTTTTTTGTTTCCTCACCTCTCCATCTTGTGTAATCGCATATATCGGACGCTCATAA			ATGATTTATTCTTTTGTTTTTCTGATGTCTCCGGAGATACTACATCTATTCAGTGCGCCAATCGCCTTGTATACTACTGTACTTATATCCTTTTTTTGTTTCCTCACCTCTCCATCTTGTGTAATCGCATATATCGGACGCTCATAA	MIYSFVFLMSPEILHLFSAPIALYTTVLISFFCFLTSPSCVIAYIGRS*			MIYSFVFLMSPEILHLFSAPIALYTTVLISFFCFLTSPSCVIAYIGRS*	TATCAATCAA	AGCAATCAGC	0	OU	0	0	0	0	0
422	332	ao	AN5724.1	54.m06844	AO070324000127	0					-151	-29	ATGTCTCCGGAGATACTACATCTATTCAGTGCGCCAATCGCCTTGTATACTACTGTACTTATATCCTTTTTTTGTTTCCTCACCTCTCCATCTTGTGTAATCGCATATATCGGACGCTCATAA			ATGTCTCCGGAGATACTACATCTATTCAGTGCGCCAATCGCCTTGTATACTACTGTACTTATATCCTTTTTTTGTTTCCTCACCTCTCCATCTTGTGTAATCGCATATATCGGACGCTCATAA	MSPEILHLFSAPIALYTTVLISFFCFLTSPSCVIAYIGRS*			MSPEILHLFSAPIALYTTVLISFFCFLTSPSCVIAYIGRS*	TGTTTTTCTG	AGCAATCAGC	0	OU	0	0	0	0	0
428	343	af	AN6277.1	72.m19363	AO070304000003	0			-77	-51			ATGGTTGCTACGCGTTCACACCTCTAA		ATGGTTGCTACGCGTTCACACCTCTAA		MVATRSHL*		MVATRSHL*		TGTTTCCCTA	CCGTCTTTTA	0	R	0	MG04158.1	NCU06519.1	0	0
426	343	an	AN6277.1	72.m19363	AO070304000003	0	-145	-98					ATGCGTCTGTTGCTTTCGGTGCTCTTGACCATCTGTTACTCTGGATGA	ATGCGTCTGTTGCTTTCGGTGCTCTTGACCATCTGTTACTCTGGATGA			MRLLLSVLLTICYSG*	MRLLLSVLLTICYSG*			GTAGTATCTC	CCTCGCACTG	0	R	0	MG04158.1	NCU06519.1	0	0
429	345	af	AN3745.1	65.m07390	AO070309000078	0			-255	-196			ATGCGGCTGGGGTCTCAGAGCAACATTTTCGAACTTCTCCTGTTACTATTTAGGGCTTAG		ATGCGGCTGGGGTCTCAGAGCAACATTTTCGAACTTCTCCTGTTACTATTTAGGGCTTAG		MRLGSQSNIFELLLLLFRA*		MRLGSQSNIFELLLLLFRA*		ATTAATTCCA	CGCAGTGGCC	0	J	FG07107.1	MG09302.1	0	YOR294W	0
432	349	af	AN5914.1	72.m19959	AO070248000032	0			-259	-137			ATGTGTGGTCCTGATAGGATATGGCGGCCCATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGA		ATGTGTGGTCCTGATAGGATATGGCGGCCCATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGA		MCGPDRIWRPMLLRYWEPTFTSEGSWWGIFMMHSIALVPN*		MCGPDRIWRPMLLRYWEPTFTSEGSWWGIFMMHSIALVPN*		AGTCAGGACC	TAGTTGCGCC	0	I	0	0	0	0	0
433	349	af	AN5914.1	72.m19959	AO070248000032	0			-239	-30			ATGGCGGCCCATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGATAGTTGCGCCGTTGATTGAAGAACGCGCCCCTTTCTCTCCAGTGCCCTTCTCTCTTGAGGTTGCTTTCAGTCAACTCCTGTTCCTTTCAGTCTCACGTTGGGGATTGA		ATGGCGGCCCATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGATAGTTGCGCCGTTGATTGAAGAACGCGCCCCTTTCTCTCCAGTGCCCTTCTCTCTTGAGGTTGCTTTCAGTCAACTCCTGTTCCTTTCAGTCTCACGTTGGGGATTGA		MAAHAAPILGANVYVRRVMVGHLYDAFNCPCPELIVAPLIEERALSLQCPSLLRLLSVNSCSFQSHVGD*		MAAHAAPILGANVYVRRVMVGHLYDAFNCPCPELIVAPLIEERALSLQCPSLLRLLSVNSCSFQSHVGD*		CTGATAGGAT	TACCTTGAGC	0	I	0	0	0	0	0
434	349	af	AN5914.1	72.m19959	AO070248000032	0			-229	-137			ATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGA		ATGCTGCTCCGATATTGGGAGCCAACGTTTACGTCCGAAGGGTCATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGA		MLLRYWEPTFTSEGSWWGIFMMHSIALVPN*		MLLRYWEPTFTSEGSWWGIFMMHSIALVPN*		ATGGCGGCCC	TAGTTGCGCC	0	I	0	0	0	0	0
435	349	af	AN5914.1	72.m19959	AO070248000032	0			-185	-30			ATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGATAGTTGCGCCGTTGATTGAAGAACGCGCCCCTTTCTCTCCAGTGCCCTTCTCTCTTGAGGTTGCTTTCAGTCAACTCCTGTTCCTTTCAGTCTCACGTTGGGGATTGA		ATGGTGGGGCATCTTTATGATGCATTCAATTGCCCTTGTCCCGAACTGATAGTTGCGCCGTTGATTGAAGAACGCGCCCCTTTCTCTCCAGTGCCCTTCTCTCTTGAGGTTGCTTTCAGTCAACTCCTGTTCCTTTCAGTCTCACGTTGGGGATTGA		MVGHLYDAFNCPCPELIVAPLIEERALSLQCPSLLRLLSVNSCSFQSHVGD*		MVGHLYDAFNCPCPELIVAPLIEERALSLQCPSLLRLLSVNSCSFQSHVGD*		CCGAAGGGTC	TACCTTGAGC	0	I	0	0	0	0	0
436	349	af	AN5914.1	72.m19959	AO070248000032	0			-169	-137			ATGATGCATTCAATTGCCCTTGTCCCGAACTGA		ATGATGCATTCAATTGCCCTTGTCCCGAACTGA		MMHSIALVPN*		MMHSIALVPN*		GGGCATCTTT	TAGTTGCGCC	0	I	0	0	0	0	0
437	349	af	AN5914.1	72.m19959	AO070248000032	0			-166	-137			ATGCATTCAATTGCCCTTGTCCCGAACTGA		ATGCATTCAATTGCCCTTGTCCCGAACTGA		MHSIALVPN*		MHSIALVPN*		CATCTTTATG	TAGTTGCGCC	0	I	0	0	0	0	0
430	349	an	AN5914.1	72.m19959	AO070248000032	0	-242	-132					ATGTGTGCTCCTGATAGGGCGTCATGTCCTTTGCACTCTTCCTCGTTCCCTTACATTAGGAACCAACGCTGTCGACAGACAGTCCTGGTGGGTCAAAAGGGGCAAGCTTAG	ATGTGTGCTCCTGATAGGGCGTCATGTCCTTTGCACTCTTCCTCGTTCCCTTACATTAGGAACCAACGCTGTCGACAGACAGTCCTGGTGGGTCAAAAGGGGCAAGCTTAG			MCAPDRASCPLHSSSFPYIRNQRCRQTVLVGQKGQA*	MCAPDRASCPLHSSSFPYIRNQRCRQTVLVGQKGQA*			CGCCGGGCCC	CTCCTCTTCC	0	I	0	0	0	0	0
431	349	an	AN5914.1	72.m19959	AO070248000032	0	-219	-184					ATGTCCTTTGCACTCTTCCTCGTTCCCTTACATTAG	ATGTCCTTTGCACTCTTCCTCGTTCCCTTACATTAG			MSFALFLVPLH*	MSFALFLVPLH*			ATAGGGCGTC	GAACCAACGC	0	I	0	0	0	0	0

438	349	ao	AN5914.1	72.m19959	AO070248000032	0					-251	-192	ATGTGTGTCTCTGATAGGACATCGCATTGCTATCCCTTCGTTTGGATCCGGCCTTTGTAA			ATGTGTGTCTCTGATAGGACATCGCATTGCTATCCCTTCGTTTGGATCCGGCCTTTGTAA	MCVSDRTSHCYPFVWIRPL*			MCVSDRTSHCYPFVWIRPL*	TGCCACGCCC	TGGAGAGAGG	0	I	0	0	0	0	0
439	349	ao	AN5914.1	72.m19959	AO070248000032	0					-192	-112	ATGGAGAGAGGGGCATGGTGGGGCACTAGAACGATGCATTCAACGCAGTTCTCCTGCTGGTGGTCTGGTGGAGGCGTTTGA			ATGGAGAGAGGGGCATGGTGGGGCACTAGAACGATGCATTCAACGCAGTTCTCCTGCTGGTGGTCTGGTGGAGGCGTTTGA	MERGAWWGTRTMHSTQFSCWWSGGGV*			MERGAWWGTRTMHSTQFSCWWSGGGV*	GGCCTTTGTA	TTCAAGAAGG	0	I	0	0	0	0	0
440	349	ao	AN5914.1	72.m19959	AO070248000032	0					-178	-164	ATGGTGGGGCACTAG			ATGGTGGGGCACTAG	MVGH*			MVGH*	AGAGAGGGGC	AACGATGCAT	0	I	0	0	0	0	0
441	349	ao	AN5914.1	72.m19959	AO070248000032	0					-159	-112	ATGCATTCAACGCAGTTCTCCTGCTGGTGGTCTGGTGGAGGCGTTTGA			ATGCATTCAACGCAGTTCTCCTGCTGGTGGTCTGGTGGAGGCGTTTGA	MHSTQFSCWWSGGGV*			MHSTQFSCWWSGGGV*	CACTAGAACG	TTCAAGAAGG	0	I	0	0	0	0	0
442	351	an	AN0298.1	54.m06464	AO070334000044	0	-175	-137					ATGTTTTCCCATAATAAACGACCAGCTGCCGTTTGGTGA	ATGTTTTCCCATAATAAACGACCAGCTGCCGTTTGGTGA			MFSHNKRPAAVW*	MFSHNKRPAAVW*			GTGTGGGTCC	CACCGCTTTC	0	A	0	0	0	0	0
443	351	an	AN0298.1	54.m06464	AO070334000044	0	-121	-83					ATGTCAGCATTTCTTGACCGCGTCAAGCTCGACGGATAG	ATGTCAGCATTTCTTGACCGCGTCAAGCTCGACGGATAG			MSAFLDRVKLDG*	MSAFLDRVKLDG*			CTTTCCCCAT	TCAATTGCTG	0	A	0	0	0	0	0
444	352	an	AN0734.1	70.m15319	AO070343000495	0	-244	-221					ATGGTCACGTTACCGCCCGTCTAG	ATGGTCACGTTACCGCCCGTCTAG			MVTLPPV*	MVTLPPV*			CAACTGCGTC	GGCCGCGCAT	0	B	FG05491.1	0	0	0	0
445	352	an	AN0734.1	70.m15319	AO070343000495	0	-201	-160					ATGCCCCGCCCTCTGATTGGTCGATCCTCCGACAGTGAGTGA	ATGCCCCGCCCTCTGATTGGTCGATCCTCCGACAGTGAGTGA			MPRPLIGRSSDSE*	MPRPLIGRSSDSE*			TCAGATCAAC	TTCCAGCTCT	0	B	FG05491.1	0	0	0	0
446	352	ao	AN0734.1	70.m15319	AO070343000495	0					-122	-66	ATGGCAGCTGTCCCAATCTTTCCCTTCCCATCTCTCTCACATCTGTCATCCAATTAA			ATGGCAGCTGTCCCAATCTTTCCCTTCCCATCTCTCTCACATCTGTCATCCAATTAA	MAAVPIFPFPSLSHLSSN*			MAAVPIFPFPSLSHLSSN*	CACCCGTCCC	CCACCTATCT	0	B	FG05491.1	0	0	0	0
450	354	af	AN5758.1	69.m14855	AO070341000017	0			-258	-67			ATGAAACACCATAGCATGAACACAATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTTCTGACACATAA		ATGAAACACCATAGCATGAACACAATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTTCTGACACATAA		MKHHSMNTMEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSISLSLSLPFFSDT*		MKHHSMNTMEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSISLSLSLPFFSDT*		GGCTTATCAA	AAAAGTTCAG	0	U	0	0	NCU08161.1	0	0
451	354	af	AN5758.1	69.m14855	AO070341000017	0			-243	-67			ATGAACACAATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTCTGACACATAA		ATGAACACAATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTTCTGACACATAA		MNTMEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSLSISLSLSLPFFSDT*		MNTMEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSISLSLSLPFFSDT*		ACACCATAGC	AAAAGTTCAG	0	U	0	0	NCU08161.1	0	0
452	354	af	AN5758.1	69.m14855	AO070341000017	0			-234	-67			ATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTTCTGACACATAA		ATGGAGATAGAGGAGAGTCATCTCGAGCGATCTGCCGCCGGGGAGGGCCCGTGGTCTTTATCTCCCATTCCATCTATCCGCACTCTGATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCTCTCTCTCTCTCTCTCTTCCTTTTTTTTTCTGACACATAA		MEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSLSISLSLSLPFFSDT*		MEIEESHLERSAAGEGPWSLSPIPSIRTLILSLSLSLSLSISLSLSLPFFSDT*		CATGAACACA	AAAAGTTCAG	0	U	0	0	NCU08161.1	0	0
447	354	an	AN5758.1	69.m14855	AO070341000017	0	-249	-193					ATGAGGAGTCCCAGACTTCGTTTAGCTGGGCGAATGATAAGTCTCATTGCATGTTAA	ATGAGGAGTCCCAGACTTCGTTTAGCTGGGCGAATGATAAGTCTCATTGCATGTTAA			MRSPRLRLAGRMISLIAC*	MRSPRLRLAGRMISLIAC*			TAAAACAGCT	TCACAAACAT	0	U	0	0	NCU08161.1	0	0
448	354	an	AN5758.1	69.m14855	AO070341000017	0	-216	-193					ATGATAAGTCTCATTGCATGTTAA	ATGATAAGTCTCATTGCATGTTAA			MISLIAC*	MISLIAC*			AGCTGGGCGA	TCACAAACAT	0	U	0	0	NCU08161.1	0	0
449	354	an	AN5758.1	69.m14855	AO070341000017	0	-199	-164					ATGTTAATCACAAACATTTGCAGCGTATTCGACTAA	ATGTTAATCACAAACATTTGCAGCGTATTCGACTAA			MLITNICSVFD*	MLITNICSVFD*			GTCTCATTGC	TCCCTGGGCG	0	U	0	0	NCU08161.1	0	0
453	354	ao	AN5758.1	69.m14855	AO070341000017	0					-208	-191	ATGACTGGTCGCTATTAA			ATGACTGGTCGCTATTAA	MTGRY*			MTGRY*	AATAGGGCTA	GCCCCCGATT	0	U	0	0	NCU08161.1	0	0
454	361	an	AN1297.1	70.m15735	AO070303000057	0	-187	-143					ATGCAGATCATCTGCACGCAAAAGACCAGCTTCCGTTGTGCATAG	ATGCAGATCATCTGCACGCAAAAGACCAGCTTCCGTTGTGCATAG			MQIICTQKTSFRCA*	MQIICTQKTSFRCA*			TCCGAGATAT	TCCCTGCAGC	0	U	0	0	0	0	0
458	366	af	AN6141.1	72.m19023	AO070340000061	0			-218	-171			ATGATATTCAATGCGTATGCTATGAAACATCTGTGGATCGTCTGTTGA		ATGATATTCAATGCGTATGCTATGAAACATCTGTGGATCGTCTGTTGA		MIFNAYAMKHLWIVC*		MIFNAYAMKHLWIVC*		ATTACCCAAC	CAGTTCACCG	0	H	0	MG05981.1	0	YMR095C	0
459	366	af	AN6141.1	72.m19023	AO070340000061	0			-208	-194			ATGCGTATGCTATGA		ATGCGTATGCTATGA		MRML*		MRML*		ATGATATTCA	AACATCTGTG	0	H	0	MG05981.1	0	YMR095C	0
460	366	af	AN6141.1	72.m19023	AO070340000061	0			-197	-171			ATGAAACATCTGTGGATCGTCTGTTGA		ATGAAACATCTGTGGATCGTCTGTTGA		MKHLWIVC*		MKHLWIVC*		TGCGTATGCT	CAGTTCACCG	0	H	0	MG05981.1	0	YMR095C	0
461	366	af	AN6141.1	72.m19023	AO070340000061	0			-96	-28			ATGTTAACCCGCTTAGGTAATGGCTGTATACACGACGAAGAGAGTGGCCAAGGTGTGAGTCAAAAATGA		ATGTTAACCCGCTTAGGTAATGGCTGTATACACGACGAAGAGAGTGGCCAAGGTGTGAGTCAAAAATGA		MLTRLGNGCIHDEESGQGVSQK*		MLTRLGNGCIHDEESGQGVSQK*		TACCGGCCAA	TATTGTTTTC	0	H	0	MG05981.1	0	YMR095C	0
462	366	af	AN6141.1	72.m19023	AO070340000061	0			-77	-39			ATGGCTGTATACACGACGAAGAGAGTGGCCAAGGTGTGA		ATGGCTGTATACACGACGAAGAGAGTGGCCAAGGTGTGA		MAVYTTKRVAKV*		MAVYTTKRVAKV*		CGCTTAGGTA	GTCAAAAATG	0	H	0	MG05981.1	0	YMR095C	0
457	366	an	AN6141.1	72.m19023	AO070340000061	0	-232	-206					ATGCGTAATGTCGTGACCCTCTATTAA	ATGCGTAATGTCGTGACCCTCTATTAA			MRNVVTLY*	MRNVVTLY*			CGCTTGGAAA	TTATAAAGTG	0	H	0	MG05981.1	0	YMR095C	0
463	366	ao	AN6141.1	72.m19023	AO070340000061	0					-174	-154	ATGATTCCCCGTACAGAATAA			ATGATTCCCCGTACAGAATAA	MIPRTE*			MIPRTE*	GCAGAGATTC	GCTGAGGTTA	0	H	0	MG05981.1	0	YMR095C	0
464	366	ao	AN6141.1	72.m19023	AO070340000061	0					-72	-31	ATGTTGATCCGGCGATATATACAGGCCGTGGCCAACACTTGA			ATGTTGATCCGGCGATATATACAGGCCGTGGCCAACACTTGA	MLIRRYIQAVANT*			MLIRRYIQAVANT*	ACTCGGATAT	CTCATCTTCT	0	H	0	MG05981.1	0	YMR095C	0
468	370	ao	AN2185.1	72.m19038	AO070340000081	0					-207	-157	ATGTTCTATGTGTGGTACCTGAGACACCGTGCCTGGATCATCATCATCTGA			ATGTTCTATGTGTGGTACCTGAGACACCGTGCCTGGATCATCATCATCTGA	MFYVWYLRHRAWIIII*			MFYVWYLRHRAWIIII*	TTTGTCCTGT	TCTCCGCCAT	0	F	FG06686.1	0	0	0	0
469	370	ao	AN2185.1	72.m19038	AO070340000081	0					-200	-186	ATGTGTGGTACCTGA			ATGTGTGGTACCTGA	MCGT*			MCGT*	TGTATGTTCT	GACACCGTGC	0	F	FG06686.1	0	0	0	0
470	385	af	AN8333.1	52.m03916	AO070330000167	0			-261	-241			ATGACCACATATCCAGCGTAG		ATGACCACATATCCAGCGTAG		MTTYPA*		MTTYPA*		CACAGAAGGT	AACAGGCTGC	0		0	0	0	0	0
471	385	af	AN8333.1	52.m03916	AO070330000167	0			-207	-94			ATGTTAGCACAGTCACTGGCTCGTATTCTGGTTTTCAGGATGTGTAGGGGAACCTTCGGATGTCGAGGATCTCCTTGGGGGTATAAAGGCTCAATGCTAGCCTTGTCCCTTTGA		ATGTTAGCACAGTCACTGGCTCGTATTCTGGTTTTCAGGATGTGTAGGGGAACCTTCGGATGTCGAGGATCTCCTTGGGGGTATAAAGGCTCAATGCTAGCCTTGTCCCTTTGA		MLAQSLARILVFRMCRGTFGCRGSPWGYKGSMLALSL*		MLAQSLARILVFRMCRGTFGCRGSPWGYKGSMLALSL*		TTGCTTGGCG	CAATCATCAT	0		0	0	0	0	0
472	385	af	AN8333.1	52.m03916	AO070330000167	0			-168	-94			ATGTGTAGGGGAACCTTCGGATGTCGAGGATCTCCTTGGGGGTATAAAGGCTCAATGCTAGCCTTGTCCCTTTGA		ATGTGTAGGGGAACCTTCGGATGTCGAGGATCTCCTTGGGGGTATAAAGGCTCAATGCTAGCCTTGTCCCTTTGA		MCRGTFGCRGSPWGYKGSMLALSL*		MCRGTFGCRGSPWGYKGSMLALSL*		GGTTTTCAGG	CAATCATCAT	0		0	0	0	0	0
473	385	af	AN8333.1	52.m03916	AO070330000167	0			-148	-122			ATGTCGAGGATCTCCTTGGGGGTATAA		ATGTCGAGGATCTCCTTGGGGGTATAA		MSRISLGV*		MSRISLGV*		GAACCTTCGG	AGGCTCAATG	0		0	0	0	0	0
474	385	af	AN8333.1	52.m03916	AO070330000167	0			-114	-94			ATGCTAGCCTTGTCCCTTTGA		ATGCTAGCCTTGTCCCTTTGA		MLALSL*		MLALSL*		TAAAGGCTCA	CAATCATCAT	0		0	0	0	0	0
475	385	ao	AN8333.1	52.m03916	AO070330000167	0					-181	-149	ATGTCTTGGAAGAGACTCCATCGACTTGATTAG			ATGTCTTGGAAGAGACTCCATCGACTTGATTAG	MSWKRLHRLD*			MSWKRLHRLD*	GTTGACATCA	GTTGTCATTG	0		0	0	0	0	0
478	387	af	AN7754.1	71.m15786	AO070325000185	0			-123	-103			ATGGCTATATTTTGGCGTTGA		ATGGCTATATTTTGGCGTTGA		MAIFWR*		MAIFWR*		CCCGAACTCA	TCTCAGGGTG	0		0	0	0	0	0
479	387	af	AN7754.1	71.m15786	AO070325000185	0			-70	-50			ATGCCTTGGTGGTTGGCATAG		ATGCCTTGGTGGTTGGCATAG		MPWWLA*		MPWWLA*		TACACCGTAT	CGAGTCATCA	0		0	0	0	0	0
476	387	an	AN7754.1	71.m15786	AO070325000185	0	-203	-72					ATGGTCCAGCTCTTGAACCCTTCGCCTTCCTACTGTCCTTTATCAGTCTTCATTCTCAGCTCCGGGGCCATTGACACCATTTCGTTCTCTCGAAACCCATCACCCATTCGCTTGATCGACATGGTTGGCTGA	ATGGTCCAGCTCTTGAACCCTTCGCCTTCCTACTGTCCTTTATCAGTCTTCATTCTCAGCTCCGGGGCCATTGACACCATTTCGTTCTCTCGAAACCCATCACCCATTCGCTTGATCGACATGGTTGGCTGA			MVQLLNPSPSYCPLSVFILSSGAIDTISFSRNPSPIRLIDMVG*	MVQLLNPSPSYCPLSVFILSSGAIDTISFSRNPSPIRLIDMVG*			TACTGCGCCA	ATAAAAGAAT	0		0	0	0	0	0
477	387	an	AN7754.1	71.m15786	AO070325000185	0	-83	-72					ATGGTTGGCTGA	ATGGTTGGCTGA			MVG*	MVG*			CTTGATCGAC	ATAAAAGAAT	0		0	0	0	0	0
480	387	ao	AN7754.1	71.m15786	AO070325000185	0					-142	-122	ATGCATACCAATCGCCAGTGA			ATGCATACCAATCGCCAGTGA	MHTNRQ*			MHTNRQ*	CAGTTCTTAC	ACGCTCAGTA	0		0	0	0	0	0
487	393	af	AN0369.1	57.m05477	AO070311000035	0			-199	-68			ATGTCTCGATTTGTATCCGAGAGCAAAAACATGCAAACCAGACCTTTTAAGGCAAGGGATTGTCAGGCAACCGTCAGCAGTCAAACAGTCAGCCACATTCCATCCCCGCTTTTTCTTTTTTCTGACAACTGA		ATGTCTCGATTTGTATCCGAGAGCAAAAACATGCAAACCAGACCTTTTAAGGCAAGGGATTGTCAGGCAACCGTCAGCAGTCAAACAGTCAGCCACATTCCATCCCCGCTTTTTCTTTTTTCTGACAACTGA		MSRFVSESKNMQTRPFKARDCQATVSSQTVSHIPSPLFLFSDN*		MSRFVSESKNMQTRPFKARDCQATVSSQTVSHIPSPLFLFSDN*		CTCGGCATAA	CAACCGACAA	0	R	0	0	0	0	0
488	393	af	AN0369.1	57.m05477	AO070311000035	0			-169	-68			ATGCAAACCAGACCTTTTAAGGCAAGGGATTGTCAGGCAACCGTCAGCAGTCAAACAGTCAGCCACATTCCATCCCCGCTTTTTCTTTTTTCTGACAACTGA		ATGCAAACCAGACCTTTTAAGGCAAGGGATTGTCAGGCAACCGTCAGCAGTCAAACAGTCAGCCACATTCCATCCCCGCTTTTTCTTTTTTCTGACAACTGA		MQTRPFKARDCQATVSSQTVSHIPSPLFLFSDN*		MQTRPFKARDCQATVSSQTVSHIPSPLFLFSDN*		GAGCAAAAAC	CAACCGACAA	0	R	0	0	0	0	0
493	397	af	AN3450.1	59.m09313	AO070265000025	0			-275	-51			ATGCTGCTTTCACTATCTTTAAACCCCGACCATTTTGATGGATCATACACAATTACATACGCGCCTACCGTGGCCATCAACCGCGAAATTGATGATTTGAGAAATCCTCGACGCGCTGTCCTGCAAAATCCATTTCCAGAGCGCATTGCCAGCCCCGTGTCTGGGGCCCCTGATCCAGTCGATCACCTCAGTCCATGCAAGATATTTGAGGAACCCCTCACTTAG		ATGCTGCTTTCACTATCTTTAAACCCCGACCATTTTGATGGATCATACACAATTACATACGCGCCTACCGTGGCCATCAACCGCGAAATTGATGATTTGAGAAATCCTCGACGCGCTGTCCTGCAAAATCCATTTCCAGAGCGCATTGCCAGCCCCGTGTCTGGGGCCCCTGATCCAGTCGATCACCTCAGTCCATGCAAGATATTTGAGGAACCCCTCACTTAG		MLLSLSLNPDHFDGSYTITYAPTVAINREIDDLRNPRRAVLQNPFPERIASPVSGAPDPVDHLSPCKIFEEPLT*		MLLSLSLNPDHFDGSYTITYAPTVAINREIDDLRNPRRAVLQNPFPERIASPVSGAPDPVDHLSPCKIFEEPLT*		GACAATTTGC	CTTCGGTCAT	0	L	0	0	0	0	0
496	397	ao	AN3450.1	59.m09313	AO070265000025	0					-238	-224	ATGAACCATTTCTGA			ATGAACCATTTCTGA	MNHF*			MNHF*	GTACTTGTTC	AACGTAGAAA	0	L	0	0	0	0	0
501	399	af	AN6300.1	72.m19334	AO070308000056	0			-223	-122			ATGGCTTTGGACTTTAAGACAGGCAACTTCATCTCGATCACGTGGGATTCCACTAAAACTGTTCTCATAGGTATGACCAATGGGGCACGGGCCACTAATTAA		ATGGCTTTGGACTTTAAGACAGGCAACTTCATCTCGATCACGTGGGATTCCACTAAAACTGTTCTCATAGGTATGACCAATGGGGCACGGGCCACTAATTAA		MALDFKTGNFISITWDSTKTVLIGMTNGARATN*		MALDFKTGNFISITWDSTKTVLIGMTNGARATN*		CTAATTGTTC	GCTCACGCGT	0	DL	0	0	NCU06769.1	0	0
502	399	af	AN6300.1	72.m19334	AO070308000056	0			-151	-122			ATGACCAATGGGGCACGGGCCACTAATTAA		ATGACCAATGGGGCACGGGCCACTAATTAA		MTNGARATN*		MTNGARATN*		TCTCATAGGT	GCTCACGCGT	0	DL	0	0	NCU06769.1	0	0
503	399	af	AN6300.1	72.m19334	AO070308000056	0			-144	-103			ATGGGGCACGGGCCACTAATTAAGCTCACGCGTCACGAATAG		ATGGGGCACGGGCCACTAATTAAGCTCACGCGTCACGAATAG		MGHGPLIKLTRHE*		MGHGPLIKLTRHE*		GGTATGACCA	ACGCGTATCA	0	DL	0	0	NCU06769.1	0	0
497	399	an	AN6300.1	72.m19334	AO070308000056	0	-243	-187					ATGTTGAACTCTAGAACGTGGATTCCTCAAGTTCATATCTTTCCATGTGGTGTATAA	ATGTTGAACTCTAGAACGTGGATTCCTCAAGTTCATATCTTTCCATGTGGTGTATAA			MLNSRTWIPQVHIFPCGV*	MLNSRTWIPQVHIFPCGV*			CGGCTTGTTA	ATCGTGGTAT	0	DL	0	0	NCU06769.1	0	0
498	399	an	AN6300.1	72.m19334	AO070308000056	0	-199	-164					ATGTGGTGTATAAATCGTGGTATGCTAGTTATGTAG	ATGTGGTGTATAAATCGTGGTATGCTAGTTATGTAG			MWCINRGMLVM*	MWCINRGMLVM*			ATATCTTTCC	AGTCATTAGT	0	DL	0	0	NCU06769.1	0	0
499	399	an	AN6300.1	72.m19334	AO070308000056	0	-178	-164					ATGCTAGTTATGTAG	ATGCTAGTTATGTAG			MLVM*	MLVM*			AAATCGTGGT	AGTCATTAGT	0	DL	0	0	NCU06769.1	0	0
500	399	an	AN6300.1	72.m19334	AO070308000056	0	-150	-85					ATGCATAAATATCAATTAAGCTCGCGTCACGACGCGTCTGCAACTCCAACTTTCGTGATTTCGTGA	ATGCATAAATATCAATTAAGCTCGCGTCACGACGCGTCTGCAACTCCAACTTTCGTGATTTCGTGA			MHKYQLSSRHDASATPTFVIS*	MHKYQLSSRHDASATPTFVIS*			CATTAGTCAT	GCTTTTGGAT	0	DL	0	0	NCU06769.1	0	0
504	399	ao	AN6300.1	72.m19334	AO070308000056	0					-159	-70	ATGTACGATTGTAAGCACCCGTGCACGGACCACCAATTAAGCTCGCGTGTCACGATCTTCCCGACGCGTCTTGCTCTCCGATCCATCTAA			ATGTACGATTGTAAGCACCCGTGCACGGACCACCAATTAAGCTCGCGTGTCACGATCTTCCCGACGCGTCTTGCTCTCCGATCCATCTAA	MYDCKHPCTDHQLSSRVTIFPTRLALRSI*			MYDCKHPCTDHQLSSRVTIFPTRLALRSI*	ACTGGTATCT	GCTATCTTTA	0	DL	0	0	NCU06769.1	0	0

506	400	ao	AN8262.1	53.m04209	AO070310000038	0					-159	-73	ATGACAAGGGGCTTGGTTCGTCCCTACGTATATGATACCGGATTTTGCTTCTGTATAGCTATTTGGATTGTGGCTTTCTGCGCGTGA			ATGACAAGGGGCTTGGTTCGTCCCTACGTATATGATACCGGATTTTGCTTCTGTATAGCTATTTGGATTGTGGCTTTCTGCGCGTGA	MTRGLVRPYVYDTGFCFCIAIWIVAFCA*			MTRGLVRPYVYDTGFCFCIAIWIVAFCA*	CGGGTGATAG	TACCCAGATA	0		0	0	0	0	0
507	400	ao	AN8262.1	53.m04209	AO070310000038	0					-128	-102	ATGATACCGGATTTTGCTTCTGTATAG			ATGATACCGGATTTTGCTTCTGTATAG	MIPDFASV*			MIPDFASV*	CCCTACGTAT	CTATTTGGAT	0		0	0	0	0	0
512	403	af	AN3565.1	52.m03643	AO070298000020	0			-291	-247			ATGGTCCGTATCACAGTCAGGCGGAGTCGATCCTCCCCGATCTAA		ATGGTCCGTATCACAGTCAGGCGGAGTCGATCCTCCCCGATCTAA		MVRITVRRSRSSPI*		MVRITVRRSRSSPI*		ATTGCCGGTG	AGCTGAGATG	0	R	0	0	0	0	0
513	403	af	AN3565.1	52.m03643	AO070298000020	0			-234	-163			ATGATTCTACATGCATGTACTGGGAGATTTCCGATGAGTTCGGAAGATGATGGTCGGCATAAGCGGGGCTAA		ATGATTCTACATGCATGTACTGGGAGATTTCCGATGAGTTCGGAAGATGATGGTCGGCATAAGCGGGGCTAA		MILHACTGRFPMSSEDDGRHKRG*		MILHACTGRFPMSSEDDGRHKRG*		CTGAGATGTG	GAATGAGGGG	0	R	0	0	0	0	0
514	403	af	AN3565.1	52.m03643	AO070298000020	0			-224	-198			ATGCATGTACTGGGAGATTTCCGATGA		ATGCATGTACTGGGAGATTTCCGATGA		MHVLGDFR*		MHVLGDFR*		ATGATTCTAC	GTTCGGAAGA	0	R	0	0	0	0	0
515	403	af	AN3565.1	52.m03643	AO070298000020	0			-220	-185			ATGTACTGGGAGATTTCCGATGAGTTCGGAAGATGA		ATGTACTGGGAGATTTCCGATGAGTTCGGAAGATGA		MYWEISDEFGR*		MYWEISDEFGR*		TTCTACATGC	TGGTCGGCAT	0	R	0	0	0	0	0
516	403	af	AN3565.1	52.m03643	AO070298000020	0			-201	-163			ATGAGTTCGGAAGATGATGGTCGGCATAAGCGGGGCTAA		ATGAGTTCGGAAGATGATGGTCGGCATAAGCGGGGCTAA		MSSEDDGRHKRG*		MSSEDDGRHKRG*		GAGATTTCCG	GAATGAGGGG	0	R	0	0	0	0	0
517	403	af	AN3565.1	52.m03643	AO070298000020	0			-188	-141			ATGATGGTCGGCATAAGCGGGGCTAAGAATGAGGGGAAACACGTATAG		ATGATGGTCGGCATAAGCGGGGCTAAGAATGAGGGGAAACACGTATAG		MMVGISGAKNEGKHV*		MMVGISGAKNEGKHV*		AGTTCGGAAG	GCTTCCAGCT	0	R	0	0	0	0	0
518	403	af	AN3565.1	52.m03643	AO070298000020	0			-185	-141			ATGGTCGGCATAAGCGGGGCTAAGAATGAGGGGAAACACGTATAG		ATGGTCGGCATAAGCGGGGCTAAGAATGAGGGGAAACACGTATAG		MVGISGAKNEGKHV*		MVGISGAKNEGKHV*		TCGGAAGATG	GCTTCCAGCT	0	R	0	0	0	0	0
508	403	an	AN3565.1	52.m03643	AO070298000020	0	-197	-168					ATGCTATTCAGCCAATGGATCAAGCGGTGA	ATGCTATTCAGCCAATGGATCAAGCGGTGA			MLFSQWIKR*	MLFSQWIKR*			TGCGGAACTG	TCGGCGCGAG	0	R	0	0	0	0	0
509	403	an	AN3565.1	52.m03643	AO070298000020	0	-183	-94					ATGGATCAAGCGGTGATCGGCGCGAGGGGTACCCCGCGCTGGGGATTTCCCGGGCATCCCCTCAATCGTCACGCGATCATGAGACTGTAG	ATGGATCAAGCGGTGATCGGCGCGAGGGGTACCCCGCGCTGGGGATTTCCCGGGCATCCCCTCAATCGTCACGCGATCATGAGACTGTAG			MDQAVIGARGTPRWGFPGHPLNRHAIMRL*	MDQAVIGARGTPRWGFPGHPLNRHAIMRL*			TATTCAGCCA	GGAGGTTATA	0	R	0	0	0	0	0
510	403	an	AN3565.1	52.m03643	AO070298000020	0	-105	-94					ATGAGACTGTAG	ATGAGACTGTAG			MRL*	MRL*			TCACGCGATC	GGAGGTTATA	0	R	0	0	0	0	0
511	403	an	AN3565.1	52.m03643	AO070298000020	0	-80	-39					ATGCAGAGGAGAAAGCGAGACCTGCCGATTATCCATTTTTAG	ATGCAGAGGAGAAAGCGAGACCTGCCGATTATCCATTTTTAG			MQRRKRDLPIIHF*	MQRRKRDLPIIHF*			GGTTATAAAT	GTCTACATCC	0	R	0	0	0	0	0
519	403	ao	AN3565.1	52.m03643	AO070298000020	0					-213	-193	ATGAGGATTAGTGATCAATAA			ATGAGGATTAGTGATCAATAA	MRISDQ*			MRISDQ*	TTTCATACTT	CCATAACCTC	0	R	0	0	0	0	0
520	403	ao	AN3565.1	52.m03643	AO070298000020	0					-132	-97	ATGCGGTTCACTACAGCGGAAGGTCTTTATAAATAA			ATGCGGTTCACTACAGCGGAAGGTCTTTATAAATAA	MRFTTAEGLYK*			MRFTTAEGLYK*	AGACAGAACA	ATTCATAAGT	0	R	0	0	0	0	0
522	408	af	AN4487.1	57.m05644	AO070311000038	0			-223	-134			ATGGACCGACTGCAGGCCAGCACGTGCTATGACCGGATCAGGTATTGCATGACCTTTATCGTTTCTATACTGAGGTTCTTGATGGCTTAG		ATGGACCGACTGCAGGCCAGCACGTGCTATGACCGGATCAGGTATTGCATGACCTTTATCGTTTCTATACTGAGGTTCTTGATGGCTTAG		MDRLQASTCYDRIRYCMTFIVSILRFLMA*		MDRLQASTCYDRIRYCMTFIVSILRFLMA*		GCACCCTGGA	CCTTAGTGAT	0	O	0	0	0	0	0
523	408	af	AN4487.1	57.m05644	AO070311000038	0			-195	-172			ATGACCGGATCAGGTATTGCATGA		ATGACCGGATCAGGTATTGCATGA		MTGSGIA*		MTGSGIA*		AGCACGTGCT	CCTTTATCGT	0	O	0	0	0	0	0
524	408	af	AN4487.1	57.m05644	AO070311000038	0			-175	-134			ATGACCTTTATCGTTTCTATACTGAGGTTCTTGATGGCTTAG		ATGACCTTTATCGTTTCTATACTGAGGTTCTTGATGGCTTAG		MTFIVSILRFLMA*		MTFIVSILRFLMA*		CAGGTATTGC	CCTTAGTGAT	0	O	0	0	0	0	0
525	408	af	AN4487.1	57.m05644	AO070311000038	0			-122	-87			ATGCTGTTGGCGTGCACCCGAAACCTGCTGAAGTAG		ATGCTGTTGGCGTGCACCCGAAACCTGCTGAAGTAG		MLLACTRNLLK*		MLLACTRNLLK*		CTTAGTGATC	AACATTTAAA	0	O	0	0	0	0	0
521	408	an	AN4487.1	57.m05644	AO070311000038	0	-192	-157					ATGATTAGACGAGTGAAGCGGGAGACGGCGCCCTGA	ATGATTAGACGAGTGAAGCGGGAGACGGCGCCCTGA			MIRRVKRETAP*	MIRRVKRETAP*			TTATCTCCAG	AATCCAGCTG	0	O	0	0	0	0	0
526	408	ao	AN4487.1	57.m05644	AO070311000038	0					-288	-277	ATGCTACACTAG			ATGCTACACTAG	MLH*			MLH*	TGTTGCTGCA	TGGGTTGCCC	0	O	0	0	0	0	0
527	408	ao	AN4487.1	57.m05644	AO070311000038	0					-251	-84	ATGTCTCTCCACAGATGCAGATGTATGATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA			ATGTCTCTCCACAGATGCAGATGTATGATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA	MSLHRCRCMMISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*			MSLHRCRCMMISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*	TCTAGAAACA	CTCCTTCCAT	0	O	0	0	0	0	0
528	408	ao	AN4487.1	57.m05644	AO070311000038	0					-237	-205	ATGCAGATGTATGATGATATCCTTGGCCTTTGA			ATGCAGATGTATGATGATATCCTTGGCCTTTGA	MQMYDDILGL*			MQMYDDILGL*	CTCTCCACAG	TTCGCTCATC	0	O	0	0	0	0	0
529	408	ao	AN4487.1	57.m05644	AO070311000038	0					-231	-205	ATGTATGATGATATCCTTGGCCTTTGA			ATGTATGATGATATCCTTGGCCTTTGA	MYDDILGL*			MYDDILGL*	ACAGATGCAG	TTCGCTCATC	0	O	0	0	0	0	0
530	408	ao	AN4487.1	57.m05644	AO070311000038	0					-227	-84	ATGATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA			ATGATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA	MMISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*			MMISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*	ATGCAGATGT	CTCCTTCCAT	0	O	0	0	0	0	0
531	408	ao	AN4487.1	57.m05644	AO070311000038	0					-224	-84	ATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA			ATGATATCCTTGGCCTTTGATTCGCTCATCCATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGAGCCATAATCTTACATCACAGGCCTCTAATATAAGTGTAGACATTACATATAAAGCAGCATGA	MISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*			MISLAFDSLIHGSSPPSYYLPGEALLSHNLTSQASNISVDITYKAA*	CAGATGTATG	CTCCTTCCAT	0	O	0	0	0	0	0
532	408	ao	AN4487.1	57.m05644	AO070311000038	0					-193	-146	ATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGA			ATGGATCATCGCCCCCATCTTACTATTTGCCCGGCGAGGCATTACTGA	MDHRPHLTICPARHY*			MDHRPHLTICPARHY*	TCGCTCATCC	GCCATAATCT	0	O	0	0	0	0	0
533	408	ao	AN4487.1	57.m05644	AO070311000038	0					-87	-22	ATGACTCCTTCCATGTTAATCGAACACCCTATCTCTTCTTTAGAATATGATACCTCAAGCATATGA			ATGACTCCTTCCATGTTAATCGAACACCCTATCTCTTCTTTAGAATATGATACCTCAAGCATATGA	MTPSMLIEHPISSLEYDTSSI*			MTPSMLIEHPISSLEYDTSSI*	ATAAAGCAGC	ACCTTCAGTC	0	O	0	0	0	0	0
534	408	ao	AN4487.1	57.m05644	AO070311000038	0					-75	-22	ATGTTAATCGAACACCCTATCTCTTCTTTAGAATATGATACCTCAAGCATATGA			ATGTTAATCGAACACCCTATCTCTTCTTTAGAATATGATACCTCAAGCATATGA	MLIEHPISSLEYDTSSI*			MLIEHPISSLEYDTSSI*	GACTCCTTCC	ACCTTCAGTC	0	O	0	0	0	0	0
535	413	af	AN4602.1	57.m05525	AO070267000019	0			-202	-164			ATGTATGTGATGACGGCTGATGGGACCTTGCCAGATTAG		ATGTATGTGATGACGGCTGATGGGACCTTGCCAGATTAG		MYVMTADGTLPD*		MYVMTADGTLPD*		TCGGACGATA	GGAAGTGAGC	0	O	FG06294.1	0	NCU02264.1	0	0
536	413	af	AN4602.1	57.m05525	AO070267000019	0			-193	-164			ATGACGGCTGATGGGACCTTGCCAGATTAG		ATGACGGCTGATGGGACCTTGCCAGATTAG		MTADGTLPD*		MTADGTLPD*		AATGTATGTG	GGAAGTGAGC	0	O	FG06294.1	0	NCU02264.1	0	0
537	413	af	AN4602.1	57.m05525	AO070267000019	0			-183	-49			ATGGGACCTTGCCAGATTAGGGAAGTGAGCTCCCCCCACATCCATCACCTTCAACTGATAATAAATATCACCAGCTTCATCGCCCGCCATCCTCAGATCGGCGCTCCTTCGCCATATCCCTCTCTAGTTGCATAA		ATGGGACCTTGCCAGATTAGGGAAGTGAGCTCCCCCCACATCCATCACCTTCAACTGATAATAAATATCACCAGCTTCATCGCCCGCCATCCTCAGATCGGCGCTCCTTCGCCATATCCCTCTCTAGTTGCATAA		MGPCQIREVSSPHIHHLQLIINITSFIARHPQIGAPSPYPSLVA*		MGPCQIREVSSPHIHHLQLIINITSFIARHPQIGAPSPYPSLVA*		ATGACGGCTG	TATCGTATTC	0	O	FG06294.1	0	NCU02264.1	0	0
538	413	ao	AN4602.1	57.m05525	AO070267000019	0					-229	-218	ATGGTTTACTAA			ATGGTTTACTAA	MVY*			MVY*	CCAGAGTTAT	AGCTCAGCCC	0	O	FG06294.1	0	NCU02264.1	0	0
544	414	af	AN8020.1	53.m03866	AO070322000068	0			-154	-131			ATGCCAGCAGCGCTGTATATATGA		ATGCCAGCAGCGCTGTATATATGA		MPAALYI*		MPAALYI*		GAGCAGGTGT	GAGGGATGTT	0		0	0	0	0	0
545	414	af	AN8020.1	53.m03866	AO070322000068	0			-134	-66			ATGAGAGGGATGTTTTCAGGTGGCCGGAATGGCTCAGTGGAAATAATTTTGCTGAACACCACATCATGA		ATGAGAGGGATGTTTTCAGGTGGCCGGAATGGCTCAGTGGAAATAATTTTGCTGAACACCACATCATGA		MRGMFSGGRNGSVEIILLNTTS*		MRGMFSGGRNGSVEIILLNTTS*		CGCTGTATAT	CAATACAGTA	0		0	0	0	0	0
546	414	af	AN8020.1	53.m03866	AO070322000068	0			-125	-66			ATGTTTTCAGGTGGCCGGAATGGCTCAGTGGAAATAATTTTGCTGAACACCACATCATGA		ATGTTTTCAGGTGGCCGGAATGGCTCAGTGGAAATAATTTTGCTGAACACCACATCATGA		MFSGGRNGSVEIILLNTTS*		MFSGGRNGSVEIILLNTTS*		TATGAGAGGG	CAATACAGTA	0		0	0	0	0	0
547	414	af	AN8020.1	53.m03866	AO070322000068	0			-106	-89			ATGGCTCAGTGGAAATAA		ATGGCTCAGTGGAAATAA		MAQWK*		MAQWK*		GGTGGCCGGA	TTTTGCTGAA	0		0	0	0	0	0
548	414	af	AN8020.1	53.m03866	AO070322000068	0			-69	-31			ATGACAATACAGTACGCTACGCTATATATCGAGACATAG		ATGACAATACAGTACGCTACGCTATATATCGAGACATAG		MTIQYATLYIET*		MTIQYATLYIET*		ACACCACATC	GGTGAGAGTT	0		0	0	0	0	0
539	414	an	AN8020.1	53.m03866	AO070322000068	0	-258	-247					ATGCTTAACTAA	ATGCTTAACTAA			MLN*	MLN*			TGCCTCGAGC	CTTCCTCGAT	0		0	0	0	0	0
540	414	an	AN8020.1	53.m03866	AO070322000068	0	-225	-190					ATGCCGAGAGGCGGCCCTTTGCCTCTTCGGGGATGA	ATGCCGAGAGGCGGCCCTTTGCCTCTTCGGGGATGA			MPRGGPLPLRG*	MPRGGPLPLRG*			CGTGGTTTGG	GCTTCGACAT	0		0	0	0	0	0
541	414	an	AN8020.1	53.m03866	AO070322000068	0	-193	-134					ATGAGCTTCGACATAGACGTGGTAAGGATGCTAGAAATGCTAGGAATAAAGCAGACTTGA	ATGAGCTTCGACATAGACGTGGTAAGGATGCTAGAAATGCTAGGAATAAAGCAGACTTGA			MSFDIDVVRMLEMLGIKQT*	MSFDIDVVRMLEMLGIKQT*			CTCTTCGGGG	AAGGGAGAGG	0		0	0	0	0	0
542	414	an	AN8020.1	53.m03866	AO070322000068	0	-166	-134					ATGCTAGAAATGCTAGGAATAAAGCAGACTTGA	ATGCTAGAAATGCTAGGAATAAAGCAGACTTGA			MLEMLGIKQT*	MLEMLGIKQT*			CGTGGTAAGG	AAGGGAGAGG	0		0	0	0	0	0
543	414	an	AN8020.1	53.m03866	AO070322000068	0	-157	-134					ATGCTAGGAATAAAGCAGACTTGA	ATGCTAGGAATAAAGCAGACTTGA			MLGIKQT*	MLGIKQT*			GATGCTAGAA	AAGGGAGAGG	0		0	0	0	0	0
549	414	ao	AN8020.1	53.m03866	AO070322000068	0					-216	-193	ATGAACAAGGACACTTGTTCATAG			ATGAACAAGGACACTTGTTCATAG	MNKDTCS*			MNKDTCS*	ATTGGAGGTC	ATGGCTACTA	0		0	0	0	0	0
550	414	ao	AN8020.1	53.m03866	AO070322000068	0					-192	-160	ATGGCTACTACCCTCGTGGTATCACTTCATTAA			ATGGCTACTACCCTCGTGGTATCACTTCATTAA	MATTLVVSLH*			MATTLVVSLH*	TTGTTCATAG	GTAAGGTACA	0		0	0	0	0	0
551	414	ao	AN8020.1	53.m03866	AO070322000068	0					-97	-86	ATGTATACCTAA			ATGTATACCTAA	MYT*			MYT*	TGCTCTATCA	GAATTTGTCA	0		0	0	0	0	0
552	415	af	AN0237.1	71.m15490	AO070323000064	0			-214	-152			ATGCATTTAAATCATTCCGCCTACAAAAGATACGGGATGGCTCGTCCTTCGGGTCAAAAATAA		ATGCATTTAAATCATTCCGCCTACAAAAGATACGGGATGGCTCGTCCTTCGGGTCAAAAATAA		MHLNHSAYKRYGMARPSGQK*		MHLNHSAYKRYGMARPSGQK*		TTTGTTCTCC	GTTGGTGTGA	0	S	0	0	0	0	0
553	415	af	AN0237.1	71.m15490	AO070323000064	0			-178	-152			ATGGCTCGTCCTTCGGGTCAAAAATAA		ATGGCTCGTCCTTCGGGTCAAAAATAA		MARPSGQK*		MARPSGQK*		AAGATACGGG	GTTGGTGTGA	0	S	0	0	0	0	0
554	415	ao	AN0237.1	71.m15490	AO070323000064	0					-179	-87	ATGGGGCTGTACTCCGTATTCCGTATTCATGCAAAGTTTCTTCGCTCCTTCCGTGGGGTCGCCGGCAGCCAATCAGATATCGCAAAATTTTGA			ATGGGGCTGTACTCCGTATTCCGTATTCATGCAAAGTTTCTTCGCTCCTTCCGTGGGGTCGCCGGCAGCCAATCAGATATCGCAAAATTTTGA	MGLYSVFRIHAKFLRSFRGVAGSQSDIAKF*			MGLYSVFRIHAKFLRSFRGVAGSQSDIAKF*	AGAACTTTTG	CGGGAACTGA	0	S	0	0	0	0	0
555	415	ao	AN0237.1	71.m15490	AO070323000064	0					-151	-77	ATGCAAAGTTTCTTCGCTCCTTCCGTGGGGTCGCCGGCAGCCAATCAGATATCGCAAAATTTTGACGGGAACTGA			ATGCAAAGTTTCTTCGCTCCTTCCGTGGGGTCGCCGGCAGCCAATCAGATATCGCAAAATTTTGACGGGAACTGA	MQSFFAPSVGSPAANQISQNFDGN*			MQSFFAPSVGSPAANQISQNFDGN*	TTCCGTATTC	GCTTTACATA	0	S	0	0	0	0	0
560	416	af	AN4232.1	54.m06784	AO070234000014	0			-253	-242			ATGCTCGGATAA		ATGCTCGGATAA		MLG*		MLG*		GTCCCGCATT	TTCTCACAGC	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
561	416	af	AN4232.1	54.m06784	AO070234000014	0			-201	-145			ATGTGCTCGTCTTTGTATCAGCAAAGGAAATATTTTTTGGCGCCGCAAAATTGTTGA		ATGTGCTCGTCTTTGTATCAGCAAAGGAAATATTTTTTGGCGCCGCAAAATTGTTGA		MCSSLYQQRKYFLAPQNC*		MCSSLYQQRKYFLAPQNC*		TGGATTTCTG	TCCGAGCTCC	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
556	416	an	AN4232.1	54.m06784	AO070234000014	0	-200	-186					ATGACCAGATTATGA	ATGACCAGATTATGA			MTRL*	MTRL*			TTGTGAATAA	TACAGTGAGG	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
557	416	an	AN4232.1	54.m06784	AO070234000014	0	-189	-178					ATGATACAGTGA	ATGATACAGTGA			MIQ*	MIQ*			TGACCAGATT	GGAAGACGGC	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
558	416	an	AN4232.1	54.m06784	AO070234000014	0	-165	-31					ATGCTCCGCAGACAAAAAATTATATGGGGACACCGCAGAAATATTGATCCGGACAATCTTTGCGGAGCCCGGGCTTTATCTTTTTTTTCCGCCCAGAAAAAAGATCAGCTAGACCATCGAAAGATACCTTGGTAA	ATGCTCCGCAGACAAAAAATTATATGGGGACACCGCAGAAATATTGATCCGGACAATCTTTGCGGAGCCCGGGCTTTATCTTTTTTTTCCGCCCAGAAAAAAGATCAGCTAGACCATCGAAAGATACCTTGGTAA			MLRRQKIIWGHRRNIDPDNLCGARALSFFSAQKKDQLDHRKIPW*	MLRRQKIIWGHRRNIDPDNLCGARALSFFSAQKKDQLDHRKIPW*			AAGACGGCTC	TTCTCTGCTT	0	J	0	MG00087.1	NCU04503.1	YHR066W	0

559	416	an	AN4232.1	54.m06784	AO070234000014	0	-142	-119					ATGGGGACACCGCAGAAATATTGA	ATGGGGACACCGCAGAAATATTGA			MGTPQKY*	MGTPQKY*			AAAAAATTAT	TCCGGACAAT	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
562	416	ao	AN4232.1	54.m06784	AO070234000014	0					-240	-205	ATGACACCAAAAGTTTGTACTCGGTGGACTGATTGA			ATGACACCAAAAGTTTGTACTCGGTGGACTGATTGA	MTPKVCTRWTD*			MTPKVCTRWTD*	GAATCAATAT	ATAGTTTCTT	0	J	0	MG00087.1	NCU04503.1	YHR066W	0
563	417	af	AN3140.1	59.m08585	AO070303000003	0			-135	-124			ATGTCTCGGTGA		ATGTCTCGGTGA		MSR*		MSR*		GGACAACGCA	CCTCTTCATT	0		0	0	0	0	0
564	417	ao	AN3140.1	59.m08585	AO070303000003	0					-239	-225	ATGACTGTCAGCTAG			ATGACTGTCAGCTAG	MTVS*			MTVS*	TCTGGTCTAG	GGATACCCTA	0		0	0	0	0	0
570	430	af	AN6004.1	72.m19138	AO070340000274	0			-221	-144			ATGCGCGACCAAAGCTACTCCACCGTGGCGGTGCATGCAACCCCTCACAACGTCATATGTGGCGCAATTATGGGCTAG		ATGCGCGACCAAAGCTACTCCACCGTGGCGGTGCATGCAACCCCTCACAACGTCATATGTGGCGCAATTATGGGCTAG		MRDQSYSTVAVHATPHNVICGAIMG*		MRDQSYSTVAVHATPHNVICGAIMG*		ACTTTTTCAC	GCTGCACGCC	0		FG08365.1	MG00444.1	0	0	0
571	430	af	AN6004.1	72.m19138	AO070340000274	0			-187	-44			ATGCAACCCCTCACAACGTCATATGTGGCGCAATTATGGGCTAGGCTGCACGCCAAAATAAATACAGCTTGTTGTCGTCCTGCACTTTCACATTTCGATCATCCTACAAGTTTCTGTGAAAATTGCGAATCCATAATTACTTAA		ATGCAACCCCTCACAACGTCATATGTGGCGCAATTATGGGCTAGGCTGCACGCCAAAATAAATACAGCTTGTTGTCGTCCTGCACTTTCACATTTCGATCATCCTACAAGTTTCTGTGAAAATTGCGAATCCATAATTACTTAA		MQPLTTSYVAQLWARLHAKINTACCRPALSHFDHPTSFCENCESIIT*		MQPLTTSYVAQLWARLHAKINTACCRPALSHFDHPTSFCENCESIIT*		GTGGCGGTGC	GCACATACTT	0		FG08365.1	MG00444.1	0	0	0
572	430	af	AN6004.1	72.m19138	AO070340000274	0			-165	-127			ATGTGGCGCAATTATGGGCTAGGCTGCACGCCAAAATAA		ATGTGGCGCAATTATGGGCTAGGCTGCACGCCAAAATAA		MWRNYGLGCTPK*		MWRNYGLGCTPK*		ACAACGTCAT	ATACAGCTTG	0		FG08365.1	MG00444.1	0	0	0
566	430	an	AN6004.1	72.m19138	AO070340000274	0	-223	-197					ATGTATCAACCTGACGTTTGCACATGA	ATGTATCAACCTGACGTTTGCACATGA			MYQPDVCT*	MYQPDVCT*			AACTAAAATA	AAGCAAGCTA	0		FG08365.1	MG00444.1	0	0	0
567	430	an	AN6004.1	72.m19138	AO070340000274	0	-200	-111					ATGAAAGCAAGCTATGACCATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAACGTACGGTGTGGCTGCGTTCGTCATCGTCTAG	ATGAAAGCAAGCTATGACCATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAACGTACGGTGTGGCTGCGTTCGTCATCGTCTAG			MKASYDHGPPHRGCAANVITYGVAAFVIV*	MKASYDHGPPHRGCAANVITYGVAAFVIV*			ACGTTTGCAC	AATAAATACC	0		FG08365.1	MG00444.1	0	0	0
568	430	an	AN6004.1	72.m19138	AO070340000274	0	-187	-143					ATGACCATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAA	ATGACCATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAA			MTMGHPTVAVPQTS*	MTMGHPTVAVPQTS*			AAAGCAAGCT	CGTACGGTGT	0		FG08365.1	MG00444.1	0	0	0
569	430	an	AN6004.1	72.m19138	AO070340000274	0	-181	-143					ATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAA	ATGGGCCACCCCACCGTGGCTGTGCCGCAAACGTCATAA			MGHPTVAVPQTS*	MGHPTVAVPQTS*			AGCTATGACC	CGTACGGTGT	0		FG08365.1	MG00444.1	0	0	0
573	430	ao	AN6004.1	72.m19138	AO070340000274	0					-198	-37	ATGTTGATGACGACTCCCCACTGTGGCTGTGCAACGTGCCCCTCTCTCCCACGTCATCTGTGGCTCGACTGCTCCGCTCAAATAAATACTCCTGAATTGTTCTTCCATTCCTATAACTCTCTATTATTTCAATTGCACCCCCTGCTGATATACCGATCTTGA			ATGTTGATGACGACTCCCCACTGTGGCTGTGCAACGTGCCCCTCTCTCCCACGTCATCTGTGGCTCGACTGCTCCGCTCAAATAAATACTCCTGAATTGTTCTTCCATTCCTATAACTCTCTATTATTTCAATTGCACCCCCTGCTGATATACCGATCTTGA	MLMTTPHCGCATCPSLPRHLWLDCSAQINTPELFFHSYNSLLFQLHPLLIYRS*			MLMTTPHCGCATCPSLPRHLWLDCSAQINTPELFFHSYNSLLFQLHPLLIYRS*	TTGCCGTCAC	TATATTCTCT	0		FG08365.1	MG00444.1	0	0	0
574	430	ao	AN6004.1	72.m19138	AO070340000274	0					-192	-37	ATGACGACTCCCCACTGTGGCTGTGCAACGTGCCCCTCTCTCCCACGTCATCTGTGGCTCGACTGCTCCGCTCAAATAAATACTCCTGAATTGTTCTTCCATTCCTATAACTCTCTATTATTTCAATTGCACCCCCTGCTGATATACCGATCTTGA			ATGACGACTCCCCACTGTGGCTGTGCAACGTGCCCCTCTCTCCCACGTCATCTGTGGCTCGACTGCTCCGCTCAAATAAATACTCCTGAATTGTTCTTCCATTCCTATAACTCTCTATTATTTCAATTGCACCCCCTGCTGATATACCGATCTTGA	MTTPHCGCATCPSLPRHLWLDCSAQINTPELFFHSYNSLLFQLHPLLIYRS*			MTTPHCGCATCPSLPRHLWLDCSAQINTPELFFHSYNSLLFQLHPLLIYRS*	TCACATGTTG	TATATTCTCT	0		FG08365.1	MG00444.1	0	0	0
580	433	af	AN6824.1	71.m15292	AO070314000104	0			-513	-499			ATGATGACTGTTTGA		ATGATGACTGTTTGA		MMTV*		MMTV*		AGGATCAGGT	GCCGTGCAAC	0	G	0	0	0	YJR049C	YJR049C
581	433	af	AN6824.1	71.m15292	AO070314000104	0			-510	-499			ATGACTGTTTGA		ATGACTGTTTGA		MTV*		MTV*		ATCAGGTATG	GCCGTGCAAC	0	G	0	0	0	YJR049C	YJR049C
575	433	an	AN6824.1	71.m15292	AO070314000104	0	-185	-27					ATGATGGTATCCCGTAGATATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG	ATGATGGTATCCCGTAGATATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG			MMVSRRYVDKGAAVSPEGFNVGAAGVGVELNLHLPEKWFCSNMRASSTCSQV*	MMVSRRYVDKGAAVSPEGFNVGAAGVGVELNLHLPEKWFCSNMRASSTCSQV*			GCCTCAGGGT	GACTCGCTCT	0	G	0	0	0	YJR049C	YJR049C
576	433	an	AN6824.1	71.m15292	AO070314000104	0	-182	-27					ATGGTATCCCGTAGATATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG	ATGGTATCCCGTAGATATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAG			MVSRRYVDKGAAVSPEGFNVGAAGVGVELNLHLPEKWFCSNMRASSTCSQV*	MVSRRYVDKGAAVSPEGFNVGAAGVGVELNLHLPEKWFCSNMRASSTCSQV*			TCAGGGTATG	GACTCGCTCT	0	G	0	0	0	YJR049C	YJR049C
577	433	an	AN6824.1	71.m15292	AO070314000104	0	-166	-8					ATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAGGACTCGCTCTTTGTGCTGA	ATGTCGATAAGGGAGCGGCGGTTTCTCCCGAAGGTTTCAACGTTGGTGCTGCCGGTGTTGGAGTCGAGCTCAACCTTCACCTTCCAGAGAAATGGTTTTGTTCTAATATGCGGGCGAGCAGTACATGCTCTCAAGTCTAGGACTCGCTCTTTGTGCTGA			MSIRERRFLPKVSTLVLPVLESSSTFTFQRNGFVLICGRAVHALKSRTRSLC*	MSIRERRFLPKVSTLVLPVLESSSTFTFQRNGFVLICGRAVHALKSRTRSLC*			TCCCGTAGAT	GTGCAAGATG	0	G	0	0	0	YJR049C	YJR049C
578	433	an	AN6824.1	71.m15292	AO070314000104	0	-75	-61					ATGGTTTTGTTCTAA	ATGGTTTTGTTCTAA			MVLF*	MVLF*			TTCCAGAGAA	TATGCGGGCG	0	G	0	0	0	YJR049C	YJR049C
584	437	af	AN4251.1	54.m07028	AO070324000161	0			-115	-50			ATGTGTGCCTCAGGCCTAAAACATCCGCCAAGCCCAACATCAAAAGTTCGATCGGCCGGAAACTGA		ATGTGTGCCTCAGGCCTAAAACATCCGCCAAGCCCAACATCAAAAGTTCGATCGGCCGGAAACTGA		MCASGLKHPPSPTSKVRSAGN*		MCASGLKHPPSPTSKVRSAGN*		AGCATACACT	GCATTTCGCA	0	J	0	0	0	0	0
582	437	an	AN4251.1	54.m07028	AO070324000161	0	-226	-206					ATGCGACTCAGGCTGACTTAA	ATGCGACTCAGGCTGACTTAA			MRLRLT*	MRLRLT*			TCCAGTAACT	TACGTACCTG	0	J	0	0	0	0	0
583	437	an	AN4251.1	54.m07028	AO070324000161	0	-179	-102					ATGGTTACGTGCGGAGTTGTCCGGGAGTGGTATTTTGAAGTAGATGGTAATAGGCCAGAACTGCTGCCTGAGGCATAA	ATGGTTACGTGCGGAGTTGTCCGGGAGTGGTATTTTGAAGTAGATGGTAATAGGCCAGAACTGCTGCCTGAGGCATAA			MVTCGVVREWYFEVDGNRPELLPEA*	MVTCGVVREWYFEVDGNRPELLPEA*			TGCCTGTCTT	AAGTACCGTG	0	J	0	0	0	0	0
585	437	ao	AN4251.1	54.m07028	AO070324000161	0					-168	-148	ATGGGGTACTCCGGAGATTGA			ATGGGGTACTCCGGAGATTGA	MGYSGD*			MGYSGD*	CAATAATAAT	AGTATGAATA	0	J	0	0	0	0	0
586	437	ao	AN4251.1	54.m07028	AO070324000161	0					-110	-54	ATGCCTCAGGCAGAAGGCTCGCCAAGCCCGACATCAAAAGTTCGAGCGGAAAGATAA			ATGCCTCAGGCAGAAGGCTCGCCAAGCCCGACATCAAAAGTTCGAGCGGAAAGATAA	MPQAEGSPSPTSKVRAER*			MPQAEGSPSPTSKVRAER*	CTGTTCCTGG	CCCAGGAAGT	0	J	0	0	0	0	0
593	442	af	AN2528.1	59.m08451	AO070300000123	0			-153	-70			ATGCGTTTGCTTGTAGTTGTAGGTTTCTCGTATGCGCATAGGAGTGAGGGACTACATAAAGGGAGTTGGTTGCTTAAGCCTTGA		ATGCGTTTGCTTGTAGTTGTAGGTTTCTCGTATGCGCATAGGAGTGAGGGACTACATAAAGGGAGTTGGTTGCTTAAGCCTTGA		MRLLVVVGFSYAHRSEGLHKGSWLLKP*		MRLLVVVGFSYAHRSEGLHKGSWLLKP*		TTTTCCACGT	GGAACAGAGC	0	E	0	0	0	0	0
592	442	an	AN2528.1	59.m08451	AO070300000123	0	-188	-174					ATGTTCCACGTATAG	ATGTTCCACGTATAG			MFHV*	MFHV*			GGCTGCCAAC	GACGTTCTAC	0	E	0	0	0	0	0
603	444	af	AN9204.1	58.m07216	AO070338000019	0			-244	-164			ATGAGAGGCGGAATCACGCCCGCAGATGTCGTCTCAATTCAGACTCCGCACAGGCTTAGCGGCCGTATTCTTATTGATTGA		ATGAGAGGCGGAATCACGCCCGCAGATGTCGTCTCAATTCAGACTCCGCACAGGCTTAGCGGCCGTATTCTTATTGATTGA		MRGGITPADVVSIQTPHRLSGRILID*		MRGGITPADVVSIQTPHRLSGRILID*		TCAGTATTGC	TGACTCATTA	0	J	0	0	0	0	0
604	444	af	AN9204.1	58.m07216	AO070338000019	0			-219	-130			ATGTCGTCTCAATTCAGACTCCGCACAGGCTTAGCGGCCGTATTCTTATTGATTGATGACTCATTATTATTTAGGCCCCCAGAGAGCTGA		ATGTCGTCTCAATTCAGACTCCGCACAGGCTTAGCGGCCGTATTCTTATTGATTGATGACTCATTATTATTTAGGCCCCCAGAGAGCTGA		MSSQFRLRTGLAAVFLLIDDSLLFRPPES*		MSSQFRLRTGLAAVFLLIDDSLLFRPPES*		ACGCCCGCAG	GCGCGAGAGC	0	J	0	0	0	0	0
605	444	af	AN9204.1	58.m07216	AO070338000019	0			-164	-60			ATGACTCATTATTATTTAGGCCCCCAGAGAGCTGAGCGCGAGAGCTCACCGATGAGAAATGTCTCCATATATATATCTCCGCTTGCTCTGTTGAATGTCGTTTGA		ATGACTCATTATTATTTAGGCCCCCAGAGAGCTGAGCGCGAGAGCTCACCGATGAGAAATGTCTCCATATATATATCTCCGCTTGCTCTGTTGAATGTCGTTTGA		MTHYYLGPQRAERESSPMRNVSIYISPLALLNVV*		MTHYYLGPQRAERESSPMRNVSIYISPLALLNVV*		TTATTGATTG	GATATCGCGC	0	J	0	0	0	0	0
606	444	af	AN9204.1	58.m07216	AO070338000019	0			-113	-60			ATGAGAAATGTCTCCATATATATATCTCCGCTTGCTCTGTTGAATGTCGTTTGA		ATGAGAAATGTCTCCATATATATATCTCCGCTTGCTCTGTTGAATGTCGTTTGA		MRNVSIYISPLALLNVV*		MRNVSIYISPLALLNVV*		GAGCTCACCG	GATATCGCGC	0	J	0	0	0	0	0
607	444	af	AN9204.1	58.m07216	AO070338000019	0			-106	-71			ATGTCTCCATATATATATCTCCGCTTGCTCTGTTGA		ATGTCTCCATATATATATCTCCGCTTGCTCTGTTGA		MSPYIYLRLLC*		MSPYIYLRLLC*		CCGATGAGAA	ATGTCGTTTG	0	J	0	0	0	0	0
602	444	an	AN9204.1	58.m07216	AO070338000019	0	-161	-150					ATGCGTTGGTAA	ATGCGTTGGTAA			MRW*	MRW*			TGTATATTAT	ACTGAAGGAT	0	J	0	0	0	0	0
608	444	ao	AN9204.1	58.m07216	AO070338000019	0					-239	-201	ATGAATTTCGATCTCTATATTTTCTGTCAAAGGACTTGA			ATGAATTTCGATCTCTATATTTTCTGTCAAAGGACTTGA	MNFDLYIFCQRT*			MNFDLYIFCQRT*	CTAAGTATTC	CCCACTGTTA	0	J	0	0	0	0	0
609	444	ao	AN9204.1	58.m07216	AO070338000019	0					-164	-117	ATGTCCATATCGGTTGTCCAATATATGGCGGGCACTCTTTCCGGTTAA			ATGTCCATATCGGTTGTCCAATATATGGCGGGCACTCTTTCCGGTTAA	MSISVVQYMAGTLSG*			MSISVVQYMAGTLSG*	TGTACATCCA	ATCTCAGATT	0	J	0	0	0	0	0
610	444	ao	AN9204.1	58.m07216	AO070338000019	0					-140	-117	ATGGCGGGCACTCTTTCCGGTTAA			ATGGCGGGCACTCTTTCCGGTTAA	MAGTLSG*			MAGTLSG*	TGTCCAATAT	ATCTCAGATT	0	J	0	0	0	0	0
611	448	an	AN0794.1	70.m15402	AO070239000017	0	-246	-229					ATGAACCTGTCGTCTTGA	ATGAACCTGTCGTCTTGA			MNLSS*	MNLSS*			TACTTCTACC	TCTTCGCCTT	0	K	0	0	0	0	0
612	448	an	AN0794.1	70.m15402	AO070239000017	0	-218	-126					ATGCCAATCCCAACCTCTTCGATATTCTCGCCGTTCCTGTCTTTCACCGGCTGCCTGAAACCCCACGCGCGACCTATTCTTGGAGCCCAATGA	ATGCCAATCCCAACCTCTTCGATATTCTCGCCGTTCCTGTCTTTCACCGGCTGCCTGAAACCCCACGCGCGACCTATTCTTGGAGCCCAATGA			MPIPTSSIFSPFLSFTGCLKPHARPILGAQ*	MPIPTSSIFSPFLSFTGCLKPHARPILGAQ*			TCTTCGCCTT	AACGAACTTG	0	K	0	0	0	0	0
613	448	an	AN0794.1	70.m15402	AO070239000017	0	-129	-112					ATGAAACGAACTTGCTGA	ATGAAACGAACTTGCTGA			MKRTC*	MKRTC*			TTGGAGCCCA	GCAGGTATCT	0	K	0	0	0	0	0
629	459	af	AN6162.1	72.m19009	AO070340000046	0			-100	-86			ATGACGCTTCTTTGA		ATGACGCTTCTTTGA		MTLL*		MTLL*		AATCCAGACT	GGCCATCACA	0	O	0	0	0	0	0
626	459	an	AN6162.1	72.m19009	AO070340000046	0	-262	-218					ATGTCGAGAACAATCCGGGCGCTGAACGAGGAACAAAGAAATAA	ATGTCGAGAACAATCCGGGCGCTGAACGAGGAACAAAGAAATAA			MSRTIRALNEEQKK*	MSRTIRALNEEQKK*			AGGGTTCTAT	AGCATGGCGC	0	O	0	0	0	0	0
627	459	an	AN6162.1	72.m19009	AO070340000046	0	-214	-194					ATGGCGCGCATTGGTCCCTGA	ATGGCGCGCATTGGTCCCTGA			MARIGP*	MARIGP*			GAAATAAAGC	GGCTCCAGCT	0	O	0	0	0	0	0
628	459	an	AN6162.1	72.m19009	AO070340000046	0	-75	-61					ATGCTTCTTCCCTGA	ATGCTTCTTCCCTGA			MLLP*	MLLP*			CTGCCACGCC	CACTACCTTA	0	O	0	0	0	0	0
630	459	ao	AN6162.1	72.m19009	AO070340000046	0					-146	-135	ATGACGCATTAA			ATGACGCATTAA	MTH*			MTH*	CCACTCAATC	ATCCCTGAGC	0	O	0	0	0	0	0
631	460	ao	AN4206.1	54.m06765	AO070231000018	0					-193	-152	ATGCCCAGACTGGTGTGCAACGCCACCGACCAGCAACACTAA			ATGCCCAGACTGGTGTGCAACGCCACCGACCAGCAACACTAA	MPRLVCNATDQQH*			MPRLVCNATDQQH*	TCCTTATTTT	ACATATATTA	0	A	0	0	0	0	0
635	463	af	AN3852.1	58.m07832	AO070305000091	0			-248	-84			ATGACATCGCAGAGCGGAGGCGGTGCCCTCATTCCTGAGGCAGTGAGGCACACCACTTCCCAACTATCGCATGCTGTCTACACGCCATATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGA		ATGACATCGCAGAGCGGAGGCGGTGCCCTCATTCCTGAGGCAGTGAGGCACACCACTTCCCAACTATCGCATGCTGTCTACACGCCATATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGA		MTSQSGGGALIPEAVRHTTSQLSHAVYTPYGHIDGADDRATNCRYHSFHRFISM*		MTSQSGGGALIPEAVRHTTSQLSHAVYTPYGHIDGADDRATNCRYHSFHRFISM*		AAGTCCGGAA	TTCTTTTGGG	0		0	0	0	0	0
636	463	af	AN3852.1	58.m07832	AO070305000091	0			-178	-35			ATGCTGTCTACACGCCATATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		ATGCTGTCTACACGCCATATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		MLSTRHMDISMGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		MLSTRHMDISMGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		CAACTATCGC	GCGTCATACC	0		0	0	0	0	0
637	463	af	AN3852.1	58.m07832	AO070305000091	0			-160	-35			ATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		ATGGACATATCGATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		MDISMGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		MDISMGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		TACACGCCAT	GCGTCATACC	0		0	0	0	0	0
638	463	af	AN3852.1	58.m07832	AO070305000091	0			-148	-35			ATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		ATGGGGCTGACGATCGAGCCACCAATTGCCGATATCATTCATTCCATCGATTCATTTCGATGTGATTCTTTTGGGACAGACTTAAAGCATCTCAAAGCCTCCGCCGTTGCCTGA		MGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		MGLTIEPPIADIIHSIDSFRCDSFGTDLKHLKASAVA*		GGACATATCG	GCGTCATACC	0		0	0	0	0	0
633	463	an	AN3852.1	58.m07832	AO070305000091	0	-87	-70					ATGGGGCCTCCTGGATGA	ATGGGGCCTCCTGGATGA			MGPPG*	MGPPG*			CATTCTGCAT	GGTTGAAGGA	0		0	0	0	0	0

634	463	an	AN3852.1	58.m07832	AO070305000091	0	-73	-14					ATGAGGTTGAAGGAACATACTTTCTCTTTCCCAGTGTCTGGAGTTCAGAGCTCCTACTAA	ATGAGGTTGAAGGAACATACTTTCTCTTTCCCAGTGTCTGGAGTTCAGAGCTCCTACTAA			MRLKEHTFSFPVSGVQSSY*	MRLKEHTFSFPVSGVQSSY*			GGCCTCCTGG	CCGCCATTTC	0		0	0	0	0	0
639	463	ao	AN3852.1	58.m07832	AO070305000091	0					-248	-105	ATGACATCGTGGAGATCGATCGGAGGAGCGTTCCTCAGGCCTCATCTTGACCCTAGGATCACCTCACATACTTTTATTGGATATCTTAGAAGCTTGCGGATGGGCATCGGCAGCAGAAAAATATCTCATCAACTATCCCGATAA			ATGACATCGTGGAGATCGATCGGAGGAGCGTTCCTCAGGCCTCATCTTGACCCTAGGATCACCTCACATACTTTTATTGGATATCTTAGAAGCTTGCGGATGGGCATCGGCAGCAGAAAAATATCTCATCAACTATCCCGATAA	MTSWRSIGGAFLRPHLDPRITSHTFIGYLRSLRMGIGSRKISHQLSR*			MTSWRSIGGAFLRPHLDPRITSHTFIGYLRSLRMGIGSRKISHQLSR*	GGCGAGGGTG	TTCAATGGGG	0		0	0	0	0	0
640	463	ao	AN3852.1	58.m07832	AO070305000091	0					-149	-105	ATGGGCATCGGCAGCAGAAAAATATCTCATCAACTATCCCGATAA			ATGGGCATCGGCAGCAGAAAAATATCTCATCAACTATCCCGATAA	MGIGSRKISHQLSR*			MGIGSRKISHQLSR*	AAGCTTGCGG	TTCAATGGGG	0		0	0	0	0	0
641	463	ao	AN3852.1	58.m07832	AO070305000091	0					-100	-83	ATGGGGCCTCTTAGGTGA			ATGGGGCCTCTTAGGTGA	MGPLR*			MGPLR*	CGATAATTCA	CGTTGGAGTG	0		0	0	0	0	0
646	466	af	AN4505.1	57.m05626	AO070311000058	0			-201	-178			ATGTTCTCCCAGGCCTCAGGCTGA		ATGTTCTCCCAGGCCTCAGGCTGA		MFSQASG*		MFSQASG*		TGTCATTTGT	ACCGCTAAAG	0	R	0	0	0	0	0
647	466	af	AN4505.1	57.m05626	AO070311000058	0			-136	-86			ATGGCGCCAAGCTTCCGCAATGCCAATTATTGTGGTTGCTGTATCCGCTAG		ATGGCGCCAAGCTTCCGCAATGCCAATTATTGTGGTTGCTGTATCCGCTAG		MAPSFRNANYCGCCIR*		MAPSFRNANYCGCCIR*		CACATCACCC	AAGCGTTCTC	0	R	0	0	0	0	0
644	466	an	AN4505.1	57.m05626	AO070311000058	0	-214	-146					ATGCAGACTATAGTGTTCTTTTTGATATGGAAGATAAGTTGTGGTCTGGTTATATCCTTGATTATATAA	ATGCAGACTATAGTGTTCTTTTTGATATGGAAGATAAGTTGTGGTCTGGTTATATCCTTGATTATATAA			MQTIVFFLIWKISCGLVISLII*	MQTIVFFLIWKISCGLVISLII*			CCTTTATTTT	TCACACCGAA	0	R	0	0	0	0	0
645	466	an	AN4505.1	57.m05626	AO070311000058	0	-188						ATGGAAGATAAGTTGTGGTCTGGTTATATCCTTGATTATATAATCACACCGAAGCGGGTTGACCTAACTCAACTCTCAATCTATCGCGACTCGACATTCACAAGCTTTGCCTTGCCGCCGATTCCCCGTCATCTCTTTTTTGCCGCGCCCCTTTCAACGAAAAGGAATTTGCTTTCTCATTTGGCATAA	ATGGAAGATAAGTTGTGGTCTGGTTATATCCTTGATTATATAATCACACCGAAGCGGGTTGACCTAACTCAACTCTCAATCTATCGCGACTCGACATTCACAAGCTTTGCCTTGCCGCCGATTCCCCGTCATCTCTTTTTTGCCGCGCCCCTTTCAACGAAAAGGAATTTGCTTTCTCATTTGGCATAA			MEDKLWSGYILDYIITPKRVDLTQLSIYRDSTFTSFALPPIPRHLFFAAPLSTKRNLLSHLA*	MEDKLWSGYILDYIITPKRVDLTQLSIYRDSTFTSFALPPIPRHLFFAAPLSTKRNLLSHLA*			TCTTTTTGAT	TGTCTGGAGA	0	R	0	0	0	0	0
649	466	ao	AN4505.1	57.m05626	AO070311000058	0					-144	-34	ATGAATGATCGCTCCCAAGCTTCTCGCGACCCAAGGCATTGTGAACGATTTCGTCGAGCCGGAATTCACTTGGTTGTTTTTTTTTCCCGTGGCATCCTTTTCGATATATAA			ATGAATGATCGCTCCCAAGCTTCTCGCGACCCAAGGCATTGTGAACGATTTCGTCGAGCCGGAATTCACTTGGTTGTTTTTTTTTCCCGTGGCATCCTTTTCGATATATAA	MNDRSQASRDPRHCERFRRAGIHLVVFFSRGILFDI*			MNDRSQASRDPRHCERFRRAGIHLVVFFSRGILFDI*	ACCTCCGGCA	ACCTCTACCC	0	R	0	0	0	0	0
651	469	af	AN0422.1	54.m07010	AO070283000023	0			-209	-84			ATGGTTCCCTATAAACATCTTGTTGTTCGCACCCACATTCTCTTTCCCAGGTTCTTACATTCTCTTCCCATCATCTGCGTTCTTGATCGCTGCTTGGTGACTGCTGCGTTCTTAGCCAGGCAGTAA		ATGGTTCCCTATAAACATCTTGTTGTTCGCACCCACATTCTCTTTCCCAGGTTCTTACATTCTCTTCCCATCATCTGCGTTCTTGATCGCTGCTTGGTGACTGCTGCGTTCTTAGCCAGGCAGTAA		MVPYKHLVVRTHILFPRFLHSLPIICVLDRCLVTAAFLARQ*		MVPYKHLVVRTHILFPRFLHSLPIICVLDRCLVTAAFLARQ*		TCAAGGGAAA	GCATTTCGAG	0	K	0	0	0	0	0
650	469	an	AN0422.1	54.m07010	AO070283000023	0	-255	-205					ATGCTACTACTGGGGATACATTCACCCTCCCCTCTCCAGGGGGATTCCTGA	ATGCTACTACTGGGGATACATTCACCCTCCCCTCTCCAGGGGGATTCCTGA			MLLLGIHSPSPLQGDS*	MLLLGIHSPSPLQGDS*			TGATCCAGCA	GCTCTCCCGT	0	K	0	0	0	0	0
652	469	ao	AN0422.1	54.m07010	AO070283000023	0					-146	-123	ATGTGGCGAAATTCTATTCGATGA			ATGTGGCGAAATTCTATTCGATGA	MWRNSIR*			MWRNSIR*	TTGCGGCGCC	GATGATAGCC	0	K	0	0	0	0	0
653	469	ao	AN0422.1	54.m07010	AO070283000023	0					-121	-41	ATGATAGCCTCGTCAAGGGAAGTCGGTGTATATTATTTACTAGGCAAGAAATATTTCCCACCCTCGACACCTTCGGTTTAG			ATGATAGCCTCGTCAAGGGAAGTCGGTGTATATTATTTACTAGGCAAGAAATATTTCCCACCCTCGACACCTTCGGTTTAG	MIASSREVGVYYLLGKKYFPPSTPSV*			MIASSREVGVYYLLGKKYFPPSTPSV*	ATTCGATGAG	AATTTATCCT	0	K	0	0	0	0	0
655	472	af	AN9090.1	66.m04770	AO070332000188	0			-141	-46			ATGCCGACGCGACTTTTCTGCCACTTCTGCGCCATCGCACTGATAGAAATCATTTTCGTGTTTTTCGCTAATACTAATTACTATGTTCCCAGATAG		ATGCCGACGCGACTTTTCTGCCACTTCTGCGCCATCGCACTGATAGAAATCATTTTCGTGTTTTTCGCTAATACTAATTACTATGTTCCCAGATAG		MPTRLFCHFCAIALIEIIFVFFANTNYYVPR*		MPTRLFCHFCAIALIEIIFVFFANTNYYVPR*		GAGGTATGTA	CATTAACGCG	0	R	0	0	0	0	0
654	472	an	AN9090.1	66.m04770	AO070332000188	0	-117	-67					ATGCGAGGTCTCTATTCATATTCTGAACGCGCGAATAACACAGTAGGCTAA	ATGCGAGGTCTCTATTCATATTCTGAACGCGCGAATAACACAGTAGGCTAA			MRGLYSYSERANNTVG*	MRGLYSYSERANNTVG*			AACTTAAGGT	GCTAACACTG	0	R	0	0	0	0	0
657	472	ao	AN9090.1	66.m04770	AO070332000188	0					-154	-62	ATGCGCAAGAGTCTTCCTGTCCCCCGAGGGGCGTGGTTCGAGAACGAGGTGCTACAAATGGCGGAGTACTCGATCTCGGTCGAAGAAATCTAA			ATGCGCAAGAGTCTTCCTGTCCCCCGAGGGGCGTGGTTCGAGAACGAGGTGCTACAAATGGCGGAGTACTCGATCTCGGTCGAAGAAATCTAA	MRKSLPVPRGAWFENEVLQMAEYSISVEEI*			MRKSLPVPRGAWFENEVLQMAEYSISVEEI*	AATTTGAGGT	TTAACTGGGG	0	R	0	0	0	0	0
658	472	ao	AN9090.1	66.m04770	AO070332000188	0					-97	-62	ATGGCGGAGTACTCGATCTCGGTCGAAGAAATCTAA			ATGGCGGAGTACTCGATCTCGGTCGAAGAAATCTAA	MAEYSISVEEI*			MAEYSISVEEI*	GGTGCTACAA	TTAACTGGGG	0	R	0	0	0	0	0
659	474	af	AN6514.1	62.m03101	AO070270000009	0			-210	-187			ATGCATCGATCAATCGAGGTGTAG		ATGCATCGATCAATCGAGGTGTAG		MHRSIEV*		MHRSIEV*		CAAGTTTGAC	TTGTTCCTCA	0	L	0	0	0	YGL246C	0
660	474	af	AN6514.1	62.m03101	AO070270000009	0			-143	-78			ATGTACTGGTGTCTTTCTCTATTTAACAATCCGGATTGGTCGCAAGCAGCCTATATAGATGCCTGA		ATGTACTGGTGTCTTTCTCTATTTAACAATCCGGATTGGTCGCAAGCAGCCTATATAGATGCCTGA		MYWCLSLFNNPDWSQAAYIDA*		MYWCLSLFNNPDWSQAAYIDA*		AGACGATCAT	GCTTCAAATA	0	L	0	0	0	YGL246C	0
661	474	af	AN6514.1	62.m03101	AO070270000009	0			-85	-44			ATGCCTGAGCTTCAAATAGCTTCCCCTTGGAGAATCACTTGA		ATGCCTGAGCTTCAAATAGCTTCCCCTTGGAGAATCACTTGA		MPELQIASPWRIT*		MPELQIASPWRIT*		GCCTATATAG	TTTTCTTTAA	0	L	0	0	0	YGL246C	0
662	474	ao	AN6514.1	62.m03101	AO070270000009	0					-233	-213	ATGTCTGGGTCGACGCGATAG			ATGTCTGGGTCGACGCGATAG	MSGSTR*			MSGSTR*	TCCTAGCTGT	TTGTTCGTTT	0	L	0	0	0	YGL246C	0
663	474	ao	AN6514.1	62.m03101	AO070270000009	0					-189	-127	ATGTTGCGATCACTTAGATTTCCCTTTGGTTTATTTAATTTTTTCATGTTTGACTTTTACTAG			ATGTTGCGATCACTTAGATTTCCCTTTGGTTTATTTAATTTTTTCATGTTTGACTTTTACTAG	MLRSLRFPFGLFNFFMFDFY*			MLRSLRFPFGLFNFFMFDFY*	CTACTATTAG	CCACCATTCT	0	L	0	0	0	YGL246C	0
664	474	ao	AN6514.1	62.m03101	AO070270000009	0					-144	-127	ATGTTTGACTTTTACTAG			ATGTTTGACTTTTACTAG	MFDFY*			MFDFY*	TAATTTTTTC	CCACCATTCT	0	L	0	0	0	YGL246C	0
665	474	ao	AN6514.1	62.m03101	AO070270000009	0					-66	-49	ATGATTATCCGTTGTTGA			ATGATTATCCGTTGTTGA	MIIRC*			MIIRC*	CAACGTCCTG	TCTAGCTACA	0	L	0	0	0	YGL246C	0
670	478	af	AN3915.1	69.m15012	AO070324000102	0			-275	-120			ATGGGCTATAATCCGAATGTATACCAATGCCTATTACATACGGCAAGTTCCGCTTGTGAACGGTATTTTCCATCTAGTATCAGGTCTTGGTACACTGCCATTCACTTCCGTGCTCACCAGTCCCGGCCCTCCCCTCAGACCATTCCCTTGTGGTGA		ATGGGCTATAATCCGAATGTATACCAATGCCTATTACATACGGCAAGTTCCGCTTGTGAACGGTATTTTCCATCTAGTATCAGGTCTTGGTACACTGCCATTCACTTCCGTGCTCACCAGTCCCGGCCCTCCCCTCAGACCATTCCCTTGTGGTGA		MGYNPNVYQCLLHTASSACERYFPSSIRSWYTAIHFRAHQSRPSPQTIPLW*		MGYNPNVYQCLLHTASSACERYFPSSIRSWYTAIHFRAHQSRPSPQTIPLW*		GTCTGGGTAT	TATTTATACC	0	G	0	0	0	0	0
671	478	af	AN3915.1	69.m15012	AO070324000102	0			-259	-83			ATGTATACCAATGCCTATTACATACGGCAAGTTCCGCTTGTGAACGGTATTTTCCATCTAGTATCAGGTCTTGGTACACTGCCATTCACTTCCGTGCTCACCAGTCCCGGCCCTCCCCTCAGACCATTCCCTTGTGGTGATATTTATACCTTCCTACTTCAAATCTTGCCTCGATAG		ATGTATACCAATGCCTATTACATACGGCAAGTTCCGCTTGTGAACGGTATTTTCCATCTAGTATCAGGTCTTGGTACACTGCCATTCACTTCCGTGCTCACCAGTCCCGGCCCTCCCCTCAGACCATTCCCTTGTGGTGATATTTATACCTTCCTACTTCAAATCTTGCCTCGATAG		MYTNAYYIRQVPLVNGIFHLVSGLGTLPFTSVLTSPGPPLRPFPCGDIYTFLLQILPR*		MYTNAYYIRQVPLVNGIFHLVSGLGTLPFTSVLTSPGPPLRPFPCGDIYTFLLQILPR*		TATAATCCGA	CTTCAGCATT	0	G	0	0	0	0	0
672	478	af	AN3915.1	69.m15012	AO070324000102	0			-249	-217			ATGCCTATTACATACGGCAAGTTCCGCTTGTGA		ATGCCTATTACATACGGCAAGTTCCGCTTGTGA		MPITYGKFRL*		MPITYGKFRL*		ATGTATACCA	ACGGTATTTT	0	G	0	0	0	0	0
666	478	an	AN3915.1	69.m15012	AO070324000102	0	-178	-158					ATGTATGCTGATGATGTTTAG	ATGTATGCTGATGATGTTTAG			MYADDV*	MYADDV*			AGGTGACACC	ATGTAGGATA	0	G	0	0	0	0	0
667	478	an	AN3915.1	69.m15012	AO070324000102	0	-174	-88					ATGCTGATGATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA	ATGCTGATGATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA			MLMMFRCRICCTPCTKTPRHNPRRSLPI*	MLMMFRCRICCTPCTKTPRHNPRRSLPI*			GACACCATGT	ACACCTCGCC	0	G	0	0	0	0	0
668	478	an	AN3915.1	69.m15012	AO070324000102	0	-168	-88					ATGATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA	ATGATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA			MMFRCRICCTPCTKTPRHNPRRSLPI*	MMFRCRICCTPCTKTPRHNPRRSLPI*			ATGTATGCTG	ACACCTCGCC	0	G	0	0	0	0	0
669	478	an	AN3915.1	69.m15012	AO070324000102	0	-165	-88					ATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA	ATGTTTAGATGTAGGATATGTTGCACACCTTGCACGAAGACCCCGAGGCACAACCCACGGCGTTCCCTTCCTATTTGA			MFRCRICCTPCTKTPRHNPRRSLPI*	MFRCRICCTPCTKTPRHNPRRSLPI*			TATGCTGATG	ACACCTCGCC	0	G	0	0	0	0	0
675	485	ao	AN8293.1	52.m04044	AO070274000002	0					-225	-190	ATGGGAAACGCTAATGCCGATCTGCTTCGGTGCTAA			ATGGGAAACGCTAATGCCGATCTGCTTCGGTGCTAA	MGNANADLLRC*			MGNANADLLRC*	ATCCGTATCA	GACCGTTGTT	0	R	0	MG06038.1	NCU07011.1	YLR409C	YLR409C
676	485	ao	AN8293.1	52.m04044	AO070274000002	0					-212	-153	ATGCCGATCTGCTTCGGTGCTAAGACCGTTGTTCCGGGAGAAAAAAGAGGGAAGGGGTAA			ATGCCGATCTGCTTCGGTGCTAAGACCGTTGTTCCGGGAGAAAAAAGAGGGAAGGGGTAA	MPICFGAKTVVPGEKRGKG*			MPICFGAKTVVPGEKRGKG*	GGAAACGCTA	AAAAAAAAAA	0	R	0	MG06038.1	NCU07011.1	YLR409C	YLR409C
677	488	an	AN1538.1	55.m03057	AO070334000262	0	-139	-128					ATGTATTCCTGA	ATGTATTCCTGA			MYS*	MYS*			CGGTGCATGG	GCCGCCTTTG	0	K	0	0	0	YGR005C	0
678	488	ao	AN1538.1	55.m03057	AO070334000262	0					-218	-165	ATGCCGCCACCGCCTTTGGCTGACCCGCCGCTCGACAGCTCCCTCTGCAGTTAG			ATGCCGCCACCGCCTTTGGCTGACCCGCCGCTCGACAGCTCCCTCTGCAGTTAG	MPPPPLADPPLDSSLCS*			MPPPPLADPPLDSSLCS*	GCGGTTGAAG	AGCGGACGCA	0	K	0	0	0	YGR005C	0
679	492	af	AN8710.1	62.m03358	AO070315000137	0			-244	-161			ATGATCGATCTTGTCAAGTCCTTAAAAATAGCATTCCCGACCCCAAGTCTGGGCCACGCAGGCCGTGCCTTCTTGGCATGTTGA		ATGATCGATCTTGTCAAGTCCTTAAAAATAGCATTCCCGACCCCAAGTCTGGGCCACGCAGGCCGTGCCTTCTTGGCATGTTGA		MIDLVKSLKIAFPTPSLGHAGRAFLAC*		MIDLVKSLKIAFPTPSLGHAGRAFLAC*		TGAAGGCGTA	CAACTAAATT	0	S	0	0	0	0	0
681	494	an	AN9095.1	66.m04553	AO070332000180	0	-214	-131					ATGATGACGGCGGCTCCGCATTGGATCTTGTCCGGGGGACCTTTTTTCTTTGCTCCTTGCAGAGAAAAAATAATCCGATTGTGA	ATGATGACGGCGGCTCCGCATTGGATCTTGTCCGGGGGACCTTTTTTCTTTGCTCCTTGCAGAGAAAAAATAATCCGATTGTGA			MMTAAPHWILSGGPFFFAPCREKIIRL*	MMTAAPHWILSGGPFFFAPCREKIIRL*			GGCGGGCGGA	AGGCTACTGC	0	O	0	0	0	0	0
682	494	an	AN9095.1	66.m04553	AO070332000180	0	-211	-131					ATGACGGCGGCTCCGCATTGGATCTTGTCCGGGGGACCTTTTTTCTTTGCTCCTTGCAGAGAAAAAATAATCCGATTGTGA	ATGACGGCGGCTCCGCATTGGATCTTGTCCGGGGGACCTTTTTTCTTTGCTCCTTGCAGAGAAAAAATAATCCGATTGTGA			MTAAPHWILSGGPFFFAPCREKIIRL*	MTAAPHWILSGGPFFFAPCREKIIRL*			GGGCGGAATG	AGGCTACTGC	0	O	0	0	0	0	0
684	500	af	AN5311.1	52.m03720	AO070285000028	0			-215	-186			ATGCTAATTTTGCCCTTAGCCTGCATCTAG		ATGCTAATTTTGCCCTTAGCCTGCATCTAG		MLILPLACI*		MLILPLACI*		AAGTCATATC	GCAGATAGTT	0		0	0	0	0	0
685	500	af	AN5311.1	52.m03720	AO070285000028	0			-170	-105			ATGCTTCGGTGCCGAATTATCCACGTTGTTGAGGCATTATTTACTCCCAGCGATATGTTTAAATAG		ATGCTTCGGTGCCGAATTATCCACGTTGTTGAGGCATTATTTACTCCCAGCGATATGTTTAAATAG		MLRCRIIHVVEALFTPSDMFK*		MLRCRIIHVVEALFTPSDMFK*		TAGTTTTGAT	CCTGAAATCA	0		0	0	0	0	0
686	500	af	AN5311.1	52.m03720	AO070285000028	0			-116	-105			ATGTTTAAATAG		ATGTTTAAATAG		MFK*		MFK*		TCCCAGCGAT	CCTGAAATCA	0		0	0	0	0	0
683	500	an	AN5311.1	52.m03720	AO070285000028	0	-179	-165					ATGGAGAGAAAGTAG	ATGGAGAGAAAGTAG			MERK*	MERK*			CGTCGCGGCT	AAGAGCCGGT	0		0	0	0	0	0
687	500	ao	AN5311.1	52.m03720	AO070285000028	0					-277	-257	ATGGGCCTTCTTCGGAGCTGA			ATGGGCCTTCTTCGGAGCTGA	MGLLRS*			MGLLRS*	AGCTGCAGCA	ACCACCACTC	0		0	0	0	0	0
688	500	ao	AN5311.1	52.m03720	AO070285000028	0					-204	-193	ATGCATGCTTAG			ATGCATGCTTAG	MHA*			MHA*	CGATAGCTGG	CTCGGAAAGT	0		0	0	0	0	0
689	500	ao	AN5311.1	52.m03720	AO070285000028	0					-200	-60	ATGCTTAGCTCGGAAAGTTCAATACTTTGCATATTAGTTCGTGCGCCTGTGCGTCTCCAGAAATCTCACAGCATCGTAGGGAGTCGAAAGGCCCCCAACGCGGCGGTGACCAAAACCTTTATATTGACTATCATTCCCTAA			ATGCTTAGCTCGGAAAGTTCAATACTTTGCATATTAGTTCGTGCGCCTGTGCGTCTCCAGAAATCTCACAGCATCGTAGGGAGTCGAAAGGCCCCCAACGCGGCGGTGACCAAAACCTTTATATTGACTATCATTCCCTAA	MLSSESSILCILVRAPVRLQKSHSIVGSRKAPNAAVTKTFILTIIP*			MLSSESSILCILVRAPVRLQKSHSIVGSRKAPNAAVTKTFILTIIP*	AGCTGGATGC	TCCGTTCCGC	0		0	0	0	0	0
690	511	an	AN1205.1	70.m15017	AO070331000209	0	-187	-149					ATGGACAGCTTCGACTTTATCACAATTATTCCCGACTAA	ATGGACAGCTTCGACTTTATCACAATTATTCCCGACTAA			MDSFDFITIIPD*	MDSFDFITIIPD*			CTTTCAGCAC	AAAGACTTAA	0	O	0	0	0	0	0
691	511	ao	AN1205.1	70.m15017	AO070331000209	0					-160	-74	ATGATATCAACCAACGGACGAGGAAATAACCCAATCCCTCGCACCGTTGATATTCCAACCAAGGTCAACTTTTCCACATATACATAA			ATGATATCAACCAACGGACGAGGAAATAACCCAATCCCTCGCACCGTTGATATTCCAACCAAGGTCAACTTTTCCACATATACATAA	MISTNGRGNNPIPRTVDIPTKVNFSTYT*			MISTNGRGNNPIPRTVDIPTKVNFSTYT*	TCACAGCCAA	CTCGGGTTTA	0	O	0	0	0	0	0
694	513	af	AN6881.1	55.m03218	AO070342000371	0			-197	-114			ATGATTGATCTAAAGAAATTCACACACGTCATGGTGCTGGCCCACCATGTGGCGGACAGCCATACCCAAACCAGCATTATATAG		ATGATTGATCTAAAGAAATTCACACACGTCATGGTGCTGGCCCACCATGTGGCGGACAGCCATACCCAAACCAGCATTATATAG		MIDLKKFTHVMVLAHHVADSHTQTSII*		MIDLKKFTHVMVLAHHVADSHTQTSII*		GGATCGAGTA	AAGGCTATCG	0		0	0	0	0	0
695	513	af	AN6881.1	55.m03218	AO070342000371	0			-167	-114			ATGGTGCTGGCCCACCATGTGGCGGACAGCCATACCCAAACCAGCATTATATAG		ATGGTGCTGGCCCACCATGTGGCGGACAGCCATACCCAAACCAGCATTATATAG		MVLAHHVADSHTQTSII*		MVLAHHVADSHTQTSII*		CACACACGTC	AAGGCTATCG	0		0	0	0	0	0

696	513	af	AN6881.1	55.m03218	AO070342000371	0			-151	-95			ATGTGGCGGACAGCCATACCCAAACCAGCATTATATAGAAGGCTATCGCGACCTTAG		ATGTGGCGGACAGCCATACCCAAACCAGCATTATATAGAAGGCTATCGCGACCTTAG		MWRTAIPKPALYRRLSRP*		MWRTAIPKPALYRRLSRP*		CTGGCCCACC	TCTCATGAGA	0		0	0	0	0	0
697	513	af	AN6881.1	55.m03218	AO070342000371	0			-90	-73			ATGAGAATATCTGTTTAA		ATGAGAATATCTGTTTAA		MRISV*		MRISV*		CCTTAGTCTC	TAGCAAACTT	0		0	0	0	0	0
692	513	an	AN6881.1	55.m03218	AO070342000371	0	-124	-89					ATGCCCGCTTACTTATTCTCTATCGCAAGTTGGTAA	ATGCCCGCTTACTTATTCTCTATCGCAAGTTGGTAA			MPAYLFSIASW*	MPAYLFSIASW*			ATCTCAGAAA	CAAGTTCTAA	0		0	0	0	0	0
699	516	ao	AN5151.1	69.m14882	AO070237000013	0					-194	-129	ATGAATGCCGAGATTCCGATACCCGAACACCCCAAACATAAAATAAATCCACTTCGGACGATCTAA			ATGAATGCCGAGATTCCGATACCCGAACACCCCAAACATAAAATAAATCCACTTCGGACGATCTAA	MNAEIPIPEHPKHKINPLRTI*			MNAEIPIPEHPKHKINPLRTI*	CAGTCCTGGA	TGTTTTGGTT	0	RT	0	0	0	0	0
700	516	ao	AN5151.1	69.m14882	AO070237000013	0					-190	-149	ATGCCGAGATTCCGATACCCGAACACCCCAAACATAAAATAA			ATGCCGAGATTCCGATACCCGAACACCCCAAACATAAAATAA	MPRFRYPNTPNIK*			MPRFRYPNTPNIK*	CCTGGAATGA	ATCCACTTCG	0	RT	0	0	0	0	0
701	516	ao	AN5151.1	69.m14882	AO070237000013	0					-129	-67	ATGTTTTGGTTTGTCTACCTCCCAGGTCATGCTGATTTGATCTGGCCGAACCGAACCCTCTGA			ATGTTTTGGTTTGTCTACCTCCCAGGTCATGCTGATTTGATCTGGCCGAACCGAACCCTCTGA	MFWFVYLPGHADLIWPNRTL*			MFWFVYLPGHADLIWPNRTL*	GGACGATCTA	GGAATTGGTC	0	RT	0	0	0	0	0
703	517	af	AN5177.1	69.m14874	AO070247000008	0			-197	-69			ATGTCTCTGAGCTTGAGGACGGAGTTTAAATCATGGTTGAGAGTAGGAAGGCCAGTGCGCTTTTGGCATATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAA		ATGTCTCTGAGCTTGAGGACGGAGTTTAAATCATGGTTGAGAGTAGGAAGGCCAGTGCGCTTTTGGCATATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAA		MSLSLRTEFKSWLRVGRPVRFWHMIVKGTHKRNIHRPATYPF*		MSLSLRTEFKSWLRVGRPVRFWHMIVKGTHKRNIHRPATYPF*		ATATCCAGAG	ATGCCATCTA	0	R	0	MG08053.1	0	0	0
704	517	af	AN5177.1	69.m14874	AO070247000008	0			-165	-19			ATGGTTGAGAGTAGGAAGGCCAGTGCGCTTTTGGCATATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAAATGCCATCTATTCTAGAGCTCCTTCGAGGAGAAGTAAAGAAAGACCTTGA		ATGGTTGAGAGTAGGAAGGCCAGTGCGCTTTTGGCATATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAAATGCCATCTATTCTAGAGCTCCTTCGAGGAGAAGTAAAGAAAGACCTTGA		MVESRKASALLAYDSERNPQAEHSSARNVPILNAIYSRAPSRRSKERP*		MVESRKASALLAYDSERNPQAEHSSARNVPILNAIYSRAPSRRSKERP*		AGTTTAAATC	ATTACCTCTT	0	R	0	MG08053.1	0	0	0
705	517	af	AN5177.1	69.m14874	AO070247000008	0			-128	-69			ATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAA		ATGATAGTGAAAGGAACCCACAAGCGGAACATTCATCGGCCCGCAACGTACCCATTTTAA		MIVKGTHKRNIHRPATYPF*		MIVKGTHKRNIHRPATYPF*		CTTTTGGCAT	ATGCCATCTA	0	R	0	MG08053.1	0	0	0
702	517	an	AN5177.1	69.m14874	AO070247000008	0	-253	-230					ATGAAACCATTAGTGCGCTTGTAG	ATGAAACCATTAGTGCGCTTGTAG			MKPLVRL*	MKPLVRL*			ACAGGTGGAA	CAGTCTTTTC	0	R	0	MG08053.1	0	0	0
706	517	ao	AN5177.1	69.m14874	AO070247000008	0					-178	-149	ATGGTCGATCGGGAACGTGGTTACATTTGA			ATGGTCGATCGGGAACGTGGTTACATTTGA	MVDRERGYI*			MVDRERGYI*	GGAGTGGTAG	AATATATAAT	0	R	0	MG08053.1	0	0	0
708	518	af	AN8284.1	65.m07460	AO070277000004	0			-136	-53			ATGCCAAGAGAATCAGCAAAGAAAAAGTTATATCTGAGGGCAGCGTCCTTTTTCAAACCCTTCCAAAACAGTTATCAGCAATAA		ATGCCAAGAGAATCAGCAAAGAAAAAGTTATATCTGAGGGCAGCGTCCTTTTTCAAACCCTTCCAAAACAGTTATCAGCAATAA		MPRESAKKKLYLRAASFFKPFQNSYQQ*		MPRESAKKKLYLRAASFFKPFQNSYQQ*		AAATTCCTAG	GTTGTCTCCA	0		0	0	0	0	0
707	518	an	AN8284.1	65.m07460	AO070277000004	0	-249	-232					ATGGTTGGGATGATCTGA	ATGGTTGGGATGATCTGA			MVGMI*	MVGMI*			TCTCAGAAAA	AGAGATACGG	0		0	0	0	0	0
709	518	ao	AN8284.1	65.m07460	AO070277000004	0					-270	-232	ATGCCAGTGTGTTGTGGTTGGTGGCACTTACTGTATTAA			ATGCCAGTGTGTTGTGGTTGGTGGCACTTACTGTATTAA	MPVCCGWWHLLY*			MPVCCGWWHLLY*	TATAAGCTTA	GCATGCATTA	0		0	0	0	0	0
710	518	ao	AN8284.1	65.m07460	AO070277000004	0					-229	-200	ATGCATTACCAAGTCTCGGAGTTTTGTTGA			ATGCATTACCAAGTCTCGGAGTTTTGTTGA	MHYQVSEFC*			MHYQVSEFC*	TGTATTAAGC	TCCTGAACAT	0		0	0	0	0	0
716	533	ao	AN5527.1	69.m15430	AO070341000362	0					-593	-576	ATGGTGCGCTCCAAGTAG			ATGGTGCGCTCCAAGTAG	MVRSK*			MVRSK*	AGATAAGTAA	AACATGCGGG	0	L	0	0	0	0	0
717	533	ao	AN5527.1	69.m15430	AO070341000362	0					-572	-525	ATGCGGGGCGAGGGGAGAGGAAATCCGGGGAAATATTGTGCGTACTAA			ATGCGGGGCGAGGGGAGAGGAAATCCGGGGAAATATTGTGCGTACTAA	MRGEGRGNPGKYCAY*			MRGEGRGNPGKYCAY*	CAAGTAGAAC	AATCCATAGC	0	L	0	0	0	0	0
721	540	af	AN5318.1	71.m15558	AO070334000168	0			-216	-205			ATGATCATCTAA		ATGATCATCTAA		MII*		MII*		GCCTCATCGG	CATTGCCCAC	0	Q	0	0	0	0	0
720	540	an	AN5318.1	71.m15558	AO070334000168	0	-164	-123					ATGCACCCTCATCCCACATTCTACTGTGATCCTTTTCATTGA	ATGCACCCTCATCCCACATTCTACTGTGATCCTTTTCATTGA			MHPHPTFYCDPFH*	MHPHPTFYCDPFH*			GGGCCTACCG	GCGTTCGAGC	0	Q	0	0	0	0	0
722	540	ao	AN5318.1	71.m15558	AO070334000168	0					-169	-152	ATGAACAATTCACGCTGA			ATGAACAATTCACGCTGA	MNNSR*			MNNSR*	CCAGTGACTA	CTCCTAGATC	0	Q	0	0	0	0	0
723	544	af	AN8467.1	70.m15048	AO070317000134	0			-203	-93			ATGGGGCCTCAAGAGCAGAATCCCGGGGAACAGACACCCCGGACTCCTCCATCGCCACCGGGGGATTGTGGGGAGACAAGTTTCTATGTCCATCTAGCCACAGTTCTGTGA		ATGGGGCCTCAAGAGCAGAATCCCGGGGAACAGACACCCCGGACTCCTCCATCGCCACCGGGGGATTGTGGGGAGACAAGTTTCTATGTCCATCTAGCCACAGTTCTGTGA		MGPQEQNPGEQTPRTPPSPPGDCGETSFYVHLATVL*		MGPQEQNPGEQTPRTPPSPPGDCGETSFYVHLATVL*		GATCCCGCAG	GGGAACCAGG	0	R	0	0	0	0	0
724	544	af	AN8467.1	70.m15048	AO070317000134	0			-118	-107			ATGTCCATCTAG		ATGTCCATCTAG		MSI*		MSI*		ACAAGTTTCT	CCACAGTTCT	0	R	0	0	0	0	0
725	544	ao	AN8467.1	70.m15048	AO070317000134	0					-182	-162	ATGTACTATACAAGTAGTTGA			ATGTACTATACAAGTAGTTGA	MYYTSS*			MYYTSS*	CAAACGGCCG	GTGGATCTTC	0	R	0	0	0	0	0
726	544	ao	AN8467.1	70.m15048	AO070317000134	0					-126	-25	ATGTCAATCCCACCTTATATAAGATGCGATGGGTCCCGAAAAATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGATCATAATTGA			ATGTCAATCCCACCTTATATAAGATGCGATGGGTCCCGAAAAATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGATCATAATTGA	MSIPPYIRCDGSRKMRGFTWFVGSSTPGQIDHN*			MSIPPYIRCDGSRKMRGFTWFVGSSTPGQIDHN*	GGGAATTGGG	CCCGCTGGAG	0	R	0	0	0	0	0
727	544	ao	AN8467.1	70.m15048	AO070317000134	0					-103	-35	ATGCGATGGGTCCCGAAAAATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGA			ATGCGATGGGTCCCGAAAAATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGA	MRWVPKNARFHVVRWFQHARAD*			MRWVPKNARFHVVRWFQHARAD*	CTTATATAAG	TCATAATTGA	0	R	0	0	0	0	0
728	544	ao	AN8467.1	70.m15048	AO070317000134	0					-84	-25	ATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGATCATAATTGA			ATGCGCGGTTTCACGTGGTTCGTTGGTTCCAGCACGCCAGGGCAGATTGATCATAATTGA	MRGFTWFVGSSTPGQIDHN*			MRGFTWFVGSSTPGQIDHN*	GTCCCGAAAA	CCCGCTGGAG	0	R	0	0	0	0	0
731	545	af	AN0160.1	71.m16052	AO070321000087	0			-211	-122			ATGTTTCCAATAGCTTATTGCGACCTCAGCAAGTTTAACCACCTTATAACTATCCCTATAGTTAACTCCTATGATTATTTACATGATTAA		ATGTTTCCAATAGCTTATTGCGACCTCAGCAAGTTTAACCACCTTATAACTATCCCTATAGTTAACTCCTATGATTATTTACATGATTAA		MFPIAYCDLSKFNHLITIPIVNSYDYLHD*		MFPIAYCDLSKFNHLITIPIVNSYDYLHD*		ATCTTGTATA	CTCAAAAAAC	0	G	FG00452.1	0	0	0	0
732	545	af	AN0160.1	71.m16052	AO070321000087	0			-141	-85			ATGATTATTTACATGATTAACTCAAAAAACACTACTCCCTGCTCATGTGGCTGTTGA		ATGATTATTTACATGATTAACTCAAAAAACACTACTCCCTGCTCATGTGGCTGTTGA		MIIYMINSKNTTPCSCGC*		MIIYMINSKNTTPCSCGC*		GTTAACTCCT	CGCGTACAAC	0	G	FG00452.1	0	0	0	0
733	545	af	AN0160.1	71.m16052	AO070321000087	0			-129	-85			ATGATTAACTCAAAAAACACTACTCCCTGCTCATGTGGCTGTTGA		ATGATTAACTCAAAAAACACTACTCCCTGCTCATGTGGCTGTTGA		MINSKNTTPCSCGC*		MINSKNTTPCSCGC*		GATTATTTAC	CGCGTACAAC	0	G	FG00452.1	0	0	0	0
729	545	an	AN0160.1	71.m16052	AO070321000087	0	-168	-145					ATGGATTCGGAACCTCCACCATGA	ATGGATTCGGAACCTCCACCATGA			MDSEPPP*	MDSEPPP*			GTATCCTCAA	CCCTTTTCCG	0	G	FG00452.1	0	0	0	0
730	545	an	AN0160.1	71.m16052	AO070321000087	0	-148	-74					ATGACCCTTTTCCGTCCCTCTCTTTCCCTCTTACATCACTCCTCACCTATTTTCATACATCTCTCCCTCCCCTAA	ATGACCCTTTTCCGTCCCTCTCTTTCCCTCTTACATCACTCCTCACCTATTTTCATACATCTCTCCCTCCCCTAA			MTLFRPSLSLLHHSSPIFIHLSLP*	MTLFRPSLSLLHHSSPIFIHLSLP*			AACCTCCACC	ACTCCCAACT	0	G	FG00452.1	0	0	0	0
736	547	af	AN7475.1	57.m05856	AO070287000029	0			-127	-83			ATGACTGTGAATGCAATAGAGCGAATGTCTTCTACGGGAACGTGA		ATGACTGTGAATGCAATAGAGCGAATGTCTTCTACGGGAACGTGA		MTVNAIERMSSTGT*		MTVNAIERMSSTGT*		TCATTTATTA	TACTTCACAT	0	R	0	0	0	0	0
737	547	af	AN7475.1	57.m05856	AO070287000029	0			-103	-83			ATGTCTTCTACGGGAACGTGA		ATGTCTTCTACGGGAACGTGA		MSSTGT*		MSSTGT*		AATAGAGCGA	TACTTCACAT	0	R	0	0	0	0	0
734	547	an	AN7475.1	57.m05856	AO070287000029	0	-206	-192					ATGATTTGCTGTTGA	ATGATTTGCTGTTGA			MICC*	MICC*			CCTTATCTGA	CTATCGTCCT	0	R	0	0	0	0	0
735	547	an	AN7475.1	57.m05856	AO070287000029	0	-135	-112					ATGATATTGTTGGAGTGGAGTTAG	ATGATATTGTTGGAGTGGAGTTAG			MILLEWS*	MILLEWS*			CAGAAATTAA	GTCATCCGTT	0	R	0	0	0	0	0
738	547	ao	AN7475.1	57.m05856	AO070287000029	0					-153	-49	ATGATAACAAGCTCTGCGAATTTCCTGAATCGAGCGGAACTAAACGCCACGCCGGATCCTCTCACATCCGTTTTCTTCGGACGTATTTCCGTGACTAGCTTCTGA			ATGATAACAAGCTCTGCGAATTTCCTGAATCGAGCGGAACTAAACGCCACGCCGGATCCTCTCACATCCGTTTTCTTCGGACGTATTTCCGTGACTAGCTTCTGA	MITSSANFLNRAELNATPDPLTSVFFGRISVTSF*			MITSSANFLNRAELNATPDPLTSVFFGRISVTSF*	TCTGACCTTT	AACAGGCCAT	0	R	0	0	0	0	0
742	550	af	AN5596.1	58.m07520	AO070328000008	0			-226	-206			ATGAGACTTTCTCTGAAATAA		ATGAGACTTTCTCTGAAATAA		MRLSLK*		MRLSLK*		AGTGGAGGAA	CGCCAGCGTT	0	R	0	0	0	0	0
743	550	af	AN5596.1	58.m07520	AO070328000008	0			-181	-167			ATGTCGACGAACTAA		ATGTCGACGAACTAA		MSTN*		MSTN*		ACCGACAAGG	AGCAACTAAC	0	R	0	0	0	0	0
739	550	an	AN5596.1	58.m07520	AO070328000008	0	-254	-204					ATGAGAAGGGGCACACAGGAATGCCAATGCGGAGAAGCCCACGAACTGTGA	ATGAGAAGGGGCACACAGGAATGCCAATGCGGAGAAGCCCACGAACTGTGA			MRRGTQECQCGEAHEL*	MRRGTQECQCGEAHEL*			GCGGAATTTG	CGAACACCTG	0	R	0	0	0	0	0
740	550	an	AN5596.1	58.m07520	AO070328000008	0	-234	-193					ATGCCAATGCGGAGAAGCCCACGAACTGTGACGAACACCTGA	ATGCCAATGCGGAGAAGCCCACGAACTGTGACGAACACCTGA			MPMRRSPRTVTNT*	MPMRRSPRTVTNT*			GCACACAGGA	TCGAACGTGA	0	R	0	0	0	0	0
741	550	an	AN5596.1	58.m07520	AO070328000008	0	-228	-193					ATGCGGAGAAGCCCACGAACTGTGACGAACACCTGA	ATGCGGAGAAGCCCACGAACTGTGACGAACACCTGA			MRRSPRTVTNT*	MRRSPRTVTNT*			AGGAATGCCA	TCGAACGTGA	0	R	0	0	0	0	0
744	550	ao	AN5596.1	58.m07520	AO070328000008	0					-142	-74	ATGCGCTGTAACCCTCGTCGGATCATTCCCAACGGCGTCCTCCGGCTCTTCAAGAATACCTACTTATAA			ATGCGCTGTAACCCTCGTCGGATCATTCCCAACGGCGTCCTCCGGCTCTTCAAGAATACCTACTTATAA	MRCNPRRIIPNGVLRLFKNTYL*			MRCNPRRIIPNGVLRLFKNTYL*	TGCGCCACAT	TTGATTGCTA	0	R	0	0	0	0	0
748	557	af	AN3044.1	70.m15683	AO070337000034	0			-230	-63			ATGGATCAGCGGATCATTTATATCGTGTCGAACATGTTGGTGTTGGTGTTGGTGTTGGTGTTGGATATCAATTACCAACAGATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		ATGGATCAGCGGATCATTTATATCGTGTCGAACATGTTGGTGTTGGTGTTGGTGTTGGTGTTGGATATCAATTACCAACAGATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		MDQRIIYIVSNMLVLVLVLVLDINYQQMSHRRRMSLSWSNGFKIQLRCGKYINNP*		MDQRIIYIVSNMLVLVLVLVLDINYQQMSHRRRMSLSWSNGFKIQLRCGKYINNP*		TGAGCTTGGC	ACATTGGATA	0	G	0	0	0	0	0
749	557	af	AN3044.1	70.m15683	AO070337000034	0			-197	-63			ATGTTGGTGTTGGTGTTGGTGTTGGTGTTGGATATCAATTACCAACAGATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		ATGTTGGTGTTGGTGTTGGTGTTGGTGTTGGATATCAATTACCAACAGATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		MLVLVLVLVLDINYQQMSHRRRMSLSWSNGFKIQLRCGKYINNP*		MLVLVLVLVLDINYQQMSHRRRMSLSWSNGFKIQLRCGKYINNP*		CGTGTCGAAC	ACATTGGATA	0	G	0	0	0	0	0
750	557	af	AN3044.1	70.m15683	AO070337000034	0			-149	-63			ATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		ATGAGCCACAGGAGGAGAATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		MSHRRRMSLSWSNGFKIQLRCGKYINNP*		MSHRRRMSLSWSNGFKIQLRCGKYINNP*		TTACCAACAG	ACATTGGATA	0	G	0	0	0	0	0
751	557	af	AN3044.1	70.m15683	AO070337000034	0			-131	-63			ATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		ATGAGCCTGAGTTGGAGCAATGGCTTCAAGATACAATTAAGATGTGGAAAGTATATAAATAATCCCTGA		MSLSWSNGFKIQLRCGKYINNP*		MSLSWSNGFKIQLRCGKYINNP*		CAGGAGGAGA	ACATTGGATA	0	G	0	0	0	0	0
752	557	af	AN3044.1	70.m15683	AO070337000034	0			-112	-92			ATGGCTTCAAGATACAATTAA		ATGGCTTCAAGATACAATTAA		MASRYN*		MASRYN*		AGTTGGAGCA	GATGTGGAAA	0	G	0	0	0	0	0
753	557	af	AN3044.1	70.m15683	AO070337000034	0			-90	-70			ATGTGGAAAGTATATAAATAA		ATGTGGAAAGTATATAAATAA		MWKVYK*		MWKVYK*		TACAATTAAG	TCCCTGAACA	0	G	0	0	0	0	0
746	557	an	AN3044.1	70.m15683	AO070337000034	0	-203	-183					ATGTTGCTGCCTGGCTGGTAA	ATGTTGCTGCCTGGCTGGTAA			MLLPGW*	MLLPGW*			GGTATAGCGC	ATCATCCTGT	0	G	0	0	0	0	0
747	557	an	AN3044.1	70.m15683	AO070337000034	0	-118	-104					ATGTTGGAGCTATGA	ATGTTGGAGCTATGA			MLEL*	MLEL*			GCTTGGAGCT	CGATGGCCAG	0	G	0	0	0	0	0
754	564	conserved	AN1048.1	70.m15205	AO070313000110	0	-63	-46	-79	-62	-79	-62	ATGCrmACvrArrCGTGA	ATGCGAACGAAAACGTGA	ATGCAAACAGAGACGTGA	ATGCGCACCGAGGCGTGA	MrTkt*	MRTKT*	MQTET*	MRTEA*	hmmvdsCAsd	yhkyysyvsk	0		0	0	0	0	0
757	565	af	AN0768.1	70.m15371	AO070316000076	0			-283	-209			ATGAGAATTTATGGGAATTCATGCAATCATCCTTGTTCGATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGA		ATGAGAATTTATGGGAATTCATGCAATCATCCTTGTTCGATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGA		MRIYGNSCNHPCSMKVWLLFSNAP*		MRIYGNSCNHPCSMKVWLLFSNAP*		TGTCACTGGC	TTGTTTTGAT	0	M	0	0	0	0	0
758	565	af	AN0768.1	70.m15371	AO070316000076	0			-273	-241			ATGGGAATTCATGCAATCATCCTTGTTCGATGA		ATGGGAATTCATGCAATCATCCTTGTTCGATGA		MGIHAIILVR*		MGIHAIILVR*		ATGAGAATTT	AAGTCTGGCT	0	M	0	0	0	0	0
759	565	af	AN0768.1	70.m15371	AO070316000076	0			-263	-120			ATGCAATCATCCTTGTTCGATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGATTGTTTTGATTGGGTTGGGTGATCTATGCACTGTAAGCGCTTCCGAAGATTCCACATCAGCTTCGTCATCATACTACAATATGTCATGA		ATGCAATCATCCTTGTTCGATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGATTGTTTTGATTGGGTTGGGTGATCTATGCACTGTAAGCGCTTCCGAAGATTCCACATCAGCTTCGTCATCATACTACAATATGTCATGA		MQSSLFDESLAALFERPLIVLIGLGDLCTVSASEDSTSASSSYYNMS*		MQSSLFDESLAALFERPLIVLIGLGDLCTVSASEDSTSASSSYYNMS*		ATGGGAATTC	TGTGATTGAG	0	M	0	0	0	0	0

760	565	af	AN0768.1	70.m15371	AO070316000076	0			-244	-209			ATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGA		ATGAAAGTCTGGCTGCTCTTTTCGAACGCCCCTTGA		MKVWLLFSNAP*		MKVWLLFSNAP*		TCCTTGTTCG	TTGTTTTGAT	0	M	0	0	0	0	0
761	565	af	AN0768.1	70.m15371	AO070316000076	0			-183	-115			ATGCACTGTAAGCGCTTCCGAAGATTCCACATCAGCTTCGTCATCATACTACAATATGTCATGATGTGA		ATGCACTGTAAGCGCTTCCGAAGATTCCACATCAGCTTCGTCATCATACTACAATATGTCATGATGTGA		MHCKRFRRFHISFVIILQYVMM*		MHCKRFRRFHISFVIILQYVMM*		TGGGTGATCT	TTGAGGTTGC	0	M	0	0	0	0	0
762	565	af	AN0768.1	70.m15371	AO070316000076	0			-97	-23			ATGATCTGTGGCGCTGGTAAGAATAAGTTTCTTGATCATATCATATTTCATCTTCTTGTGTATATGTTTCTGTAA		ATGATCTGTGGCGCTGGTAAGAATAAGTTTCTTGATCATATCATATTTCATCTTCTTGTGTATATGTTTCTGTAA		MICGAGKNKFLDHIIFHLLVYMFL*		MICGAGKNKFLDHIIFHLLVYMFL*		TGCCTTAAAT	AGAGAAGTTA	0	M	0	0	0	0	0
755	565	an	AN0768.1	70.m15371	AO070316000076	0	-149	-102					ATGATGAACCTCGCTAGGTCAGCTTCCATCGCCCAGGCTGGACGCTGA	ATGATGAACCTCGCTAGGTCAGCTTCCATCGCCCAGGCTGGACGCTGA			MMNLARSASIAQAGR*	MMNLARSASIAQAGR*			TTGCGCCAGA	TCCAGCTCTA	0	M	0	0	0	0	0
756	565	an	AN0768.1	70.m15371	AO070316000076	0	-146	-102					ATGAACCTCGCTAGGTCAGCTTCCATCGCCCAGGCTGGACGCTGA	ATGAACCTCGCTAGGTCAGCTTCCATCGCCCAGGCTGGACGCTGA			MNLARSASIAQAGR*	MNLARSASIAQAGR*			CGCCAGAATG	TCCAGCTCTA	0	M	0	0	0	0	0
764	570	af	AN3020.1	59.m09444	AO070337000094	0			-242	-111			ATGTACTGTTTACACAAACGGGTTTGCGACCGGCGTACACATGGACCGCGAGCCACGGTTCCAAGACGACCCTTATATTGGTCACTTGCAGCCATTGTTTATATGCTACTCCACAGGAAACGGGGATACTGA		ATGTACTGTTTACACAAACGGGTTTGCGACCGGCGTACACATGGACCGCGAGCCACGGTTCCAAGACGACCCTTATATTGGTCACTTGCAGCCATTGTTTATATGCTACTCCACAGGAAACGGGGATACTGA		MYCLHKRVCDRRTHGPRATVPRRPLYWSLAAIVYMLLHRKRGY*		MYCLHKRVCDRRTHGPRATVPRRPLYWSLAAIVYMLLHRKRGY*		CAGCACAAGG	CGTCCCCACA	0	O	0	0	0	0	0
765	570	af	AN3020.1	59.m09444	AO070337000094	0			-202	-83			ATGGACCGCGAGCCACGGTTCCAAGACGACCCTTATATTGGTCACTTGCAGCCATTGTTTATATGCTACTCCACAGGAAACGGGGATACTGACGTCCCCACATCTTTAAGTGACAGATAA		ATGGACCGCGAGCCACGGTTCCAAGACGACCCTTATATTGGTCACTTGCAGCCATTGTTTATATGCTACTCCACAGGAAACGGGGATACTGACGTCCCCACATCTTTAAGTGACAGATAA		MDREPRFQDDPYIGHLQPLFICYSTGNGDTDVPTSLSDR*		MDREPRFQDDPYIGHLQPLFICYSTGNGDTDVPTSLSDR*		CGGCGTACAC	AGCGGAGTCG	0	O	0	0	0	0	0
766	570	af	AN3020.1	59.m09444	AO070337000094	0			-140	-111			ATGCTACTCCACAGGAAACGGGGATACTGA		ATGCTACTCCACAGGAAACGGGGATACTGA		MLLHRKRGY*		MLLHRKRGY*		CATTGTTTAT	CGTCCCCACA	0	O	0	0	0	0	0
767	570	ao	AN3020.1	59.m09444	AO070337000094	0					-172	-146	ATGGCAATAGGTCTTGAACGCGACTGA			ATGGCAATAGGTCTTGAACGCGACTGA	MAIGLERD*			MAIGLERD*	ACTAATCAGA	TACCTGGGCT	0	O	0	0	0	0	0
768	570	ao	AN3020.1	59.m09444	AO070337000094	0					-96	-79	ATGTGTGAGGGTGGTTAG			ATGTGTGAGGGTGGTTAG	MCEGG*			MCEGG*	ACCTCTACAT	CTTCCAATGA	0	O	0	0	0	0	0
769	570	ao	AN3020.1	59.m09444	AO070337000094	0					-72	-28	ATGAATGCATCTCCCGGTATGTTCCTTCTGAAGCGGGTTGACTAG			ATGAATGCATCTCCCGGTATGTTCCTTCTGAAGCGGGTTGACTAG	MNASPGMFLLKRVD*			MNASPGMFLLKRVD*	TTAGCTTCCA	GCTTTATCTG	0	O	0	0	0	0	0
770	570	ao	AN3020.1	59.m09444	AO070337000094	0					-68	-42	ATGCATCTCCCGGTATGTTCCTTCTGA			ATGCATCTCCCGGTATGTTCCTTCTGA	MHLPVCSF*			MHLPVCSF*	CTTCCAATGA	AGCGGGTTGA	0	O	0	0	0	0	0
773	572	af	AN4224.1	54.m06793	AO070234000026	0			-188	-165			ATGGCTGATCTCGAGTTGGCTTGA		ATGGCTGATCTCGAGTTGGCTTGA		MADLELA*		MADLELA*		CTCCTGCATC	CCAGTATCTA	0	TR	0	0	0	0	0
772	572	an	AN4224.1	54.m06793	AO070234000026	0	-190	-176					ATGGCCAGGCTCTAG	ATGGCCAGGCTCTAG			MARL*	MARL*			TCTTACCAAG	GCTTCTCGCA	0	TR	0	0	0	0	0
774	572	ao	AN4224.1	54.m06793	AO070234000026	0					-229	-191	ATGGCTAGCCTGGGGTCCCGTCTAGACACCGCCGTTTGA			ATGGCTAGCCTGGGGTCCCGTCTAGACACCGCCGTTTGA	MASLGSRLDTAV*			MASLGSRLDTAV*	GCTCGAGACC	CCGTCCCCTT	0	TR	0	0	0	0	0
775	574	af	AN1811.1	58.m07714	AO070299000060	0			-151	-29			ATGACCGGGGCGGATCCCGTCGCTTTTTGCCGGCCCGGACACTTTGTCCTCTTGGCCGCTCTATTAGGTAGTTTATTGATTTTGTTACTCTCTTGCTGGCATCGGAGGTTATCACGGGGTTAG		ATGACCGGGGCGGATCCCGTCGCTTTTTGCCGGCCCGGACACTTTGTCCTCTTGGCCGCTCTATTAGGTAGTTTATTGATTTTGTTACTCTCTTGCTGGCATCGGAGGTTATCACGGGGTTAG		MTGADPVAFCRPGHFVLLAALLGSLLILLLSCWHRRLSRG*		MTGADPVAFCRPGHFVLLAALLGSLLILLLSCWHRRLSRG*		CCTCCACTGC	ATACGCCCGG	0	MO	0	0	0	YGL142C	0
776	574	ao	AN1811.1	58.m07714	AO070299000060	0					-227	-114	ATGGCTCTCGCGCGATCCACTCTTGCCTTCGCTCTCCCACTCACAATTCGTTCATTACCACTTGGAAGGACTCGCCCTTCTTCCGCCTTTCCGTTTTCGGTTAAGCCCCGTTAG			ATGGCTCTCGCGCGATCCACTCTTGCCTTCGCTCTCCCACTCACAATTCGTTCATTACCACTTGGAAGGACTCGCCCTTCTTCCGCCTTTCCGTTTTCGGTTAAGCCCCGTTAG	MALARSTLAFALPLTIRSLPLGRTRPSSAFPFSVKPR*			MALARSTLAFALPLTIRSLPLGRTRPSSAFPFSVKPR*	AAACCGTCCC	ACTCTCGCTC	0	MO	0	0	0	YGL142C	0
782	577	af	AN9110.1	66.m04575	AO070332000160	0			-230	-144			ATGTCGATCATTCGGGCAATCAAATGGGCATTGCCTTCCTTTCGATTTACCGGAAACGGAAATTTTCCTTCAGATCGAGATGAATAG		ATGTCGATCATTCGGGCAATCAAATGGGCATTGCCTTCCTTTCGATTTACCGGAAACGGAAATTTTCCTTCAGATCGAGATGAATAG		MSIIRAIKWALPSFRFTGNGNFPSDRDE*		MSIIRAIKWALPSFRFTGNGNFPSDRDE*		AGAGCAGCCG	TGTTTAAACC	0		0	0	0	0	0
783	577	af	AN9110.1	66.m04575	AO070332000160	0			-207	-148			ATGGGCATTGCCTTCCTTTCGATTTACCGGAAACGGAAATTTTCCTTCAGATCGAGATGA		ATGGGCATTGCCTTCCTTTCGATTTACCGGAAACGGAAATTTTCCTTCAGATCGAGATGA		MGIAFLSIYRKRKFSFRSR*		MGIAFLSIYRKRKFSFRSR*		GGGCAATCAA	ATAGTGTTTA	0		0	0	0	0	0
784	577	af	AN9110.1	66.m04575	AO070332000160	0			-151	-137			ATGAATAGTGTTTAA		ATGAATAGTGTTTAA		MNSV*		MNSV*		TCAGATCGAG	ACCAAGCCTT	0		0	0	0	0	0
785	577	af	AN9110.1	66.m04575	AO070332000160	0			-111	-37			ATGGTTCAACTCAAGAACGCTTCGTATTCACTAACCGGCCAGCAGACTATAAAGATTCTTGGTCTTCCTGGATAA		ATGGTTCAACTCAAGAACGCTTCGTATTCACTAACCGGCCAGCAGACTATAAAGATTCTTGGTCTTCCTGGATAA		MVQLKNASYSLTGQQTIKILGLPG*		MVQLKNASYSLTGQQTIKILGLPG*		GGAGTGATCA	TTCAGATCTT	0		0	0	0	0	0
777	577	an	AN9110.1	66.m04575	AO070332000160	0	-213	-103					ATGACGAATCGTCTTTGGGAAAGAATCGTCTTATCCATGGATATACAAACACCAATAATAAGATTGACGGCTCAGCCTCCATGCCAAGCTCGTATTTCCAGTTTCGGGTGA	ATGACGAATCGTCTTTGGGAAAGAATCGTCTTATCCATGGATATACAAACACCAATAATAAGATTGACGGCTCAGCCTCCATGCCAAGCTCGTATTTCCAGTTTCGGGTGA			MTNRLWERIVLSMDIQTPIIRLTAQPPCQARISSFG*	MTNRLWERIVLSMDIQTPIIRLTAQPPCQARISSFG*			GATCATCCCT	TCGAGGGATG	0		0	0	0	0	0
778	577	an	AN9110.1	66.m04575	AO070332000160	0	-177	-103					ATGGATATACAAACACCAATAATAAGATTGACGGCTCAGCCTCCATGCCAAGCTCGTATTTCCAGTTTCGGGTGA	ATGGATATACAAACACCAATAATAAGATTGACGGCTCAGCCTCCATGCCAAGCTCGTATTTCCAGTTTCGGGTGA			MDIQTPIIRLTAQPPCQARISSFG*	MDIQTPIIRLTAQPPCQARISSFG*			CGTCTTATCC	TCGAGGGATG	0		0	0	0	0	0
779	577	an	AN9110.1	66.m04575	AO070332000160	0	-133	-83					ATGCCAAGCTCGTATTTCCAGTTTCGGGTGATCGAGGGATGGTACCTCTAG	ATGCCAAGCTCGTATTTCCAGTTTCGGGTGATCGAGGGATGGTACCTCTAG			MPSSYFQFRVIEGWYL*	MPSSYFQFRVIEGWYL*			CTCAGCCTCC	GATGGCGAGA	0		0	0	0	0	0
780	577	an	AN9110.1	66.m04575	AO070332000160	0	-95	-63					ATGGTACCTCTAGGATGGCGAGAGAGCATATAA	ATGGTACCTCTAGGATGGCGAGAGAGCATATAA			MVPLGWRESI*	MVPLGWRESI*			TGATCGAGGG	GGAGGGCGCA	0		0	0	0	0	0
781	577	an	AN9110.1	66.m04575	AO070332000160	0	-81	-40					ATGGCGAGAGAGCATATAAGGAGGGCGCAGCCTGCCTCCTGA	ATGGCGAGAGAGCATATAAGGAGGGCGCAGCCTGCCTCCTGA			MAREHIRRAQPAS*	MAREHIRRAQPAS*			TACCTCTAGG	TCAAAACACA	0		0	0	0	0	0
786	577	ao	AN9110.1	66.m04575	AO070332000160	0					-222	-154	ATGGCATTCCTTCACATTGTTCTTTTTTTAAGTTATCCCTTGGAACCTCATGATGATGATCAACGCTAA			ATGGCATTCCTTCACATTGTTCTTTTTTTAAGTTATCCCTTGGAACCTCATGATGATGATCAACGCTAA	MAFLHIVLFLSYPLEPHDDDQR*			MAFLHIVLFLSYPLEPHDDDQR*	TAATAATTGG	GCCTTGTGCT	0		0	0	0	0	0
787	577	ao	AN9110.1	66.m04575	AO070332000160	0					-84	-22	ATGCGTAGAAAACGCCCCTCGAATAACCCTGTATCCTATCTCTTATTCCTCACTCATGTGTAA			ATGCGTAGAAAACGCCCCTCGAATAACCCTGTATCCTATCTCTTATTCCTCACTCATGTGTAA	MRRKRPSNNPVSYLLFLTHV*			MRRKRPSNNPVSYLLFLTHV*	GATATATAAG	CAAGATCTTG	0		0	0	0	0	0
788	579	af	AN3100.1	59.m08644	AO070334000141	0			-238	-125			ATGAATCTTCCTCCTTCTTCCCTTTCCATTCCTTCATCCCAGGTCCTGTTCTTCAAGCCTGACTTGACCATACTCCTCCCTGATCTTACTCATATCACATCTCTACACCTTTGA		ATGAATCTTCCTCCTTCTTCCCTTTCCATTCCTTCATCCCAGGTCCTGTTCTTCAAGCCTGACTTGACCATACTCCTCCCTGATCTTACTCATATCACATCTCTACACCTTTGA		MNLPPSSLSIPSSQVLFFKPDLTILLPDLTHITSLHL*		MNLPPSSLSIPSSQVLFFKPDLTILLPDLTHITSLHL*		TTCTTTCATC	GCAAGCAAAG	0		0	0	0	0	0
789	586	an	AN2750.1	54.m06682	AO070338000222	0	-260	-162					ATGTTTATGTTTCTCCAAGGCAGCAGCTTCTTTATCTGCCTCGCCTATTCAGCTCCATTTATTCATTATCTACAACACCCGGTCTCGGCAATGACTTAG	ATGTTTATGTTTCTCCAAGGCAGCAGCTTCTTTATCTGCCTCGCCTATTCAGCTCCATTTATTCATTATCTACAACACCCGGTCTCGGCAATGACTTAG			MFMFLQGSSFFICLAYSAPFIHYLQHPVSAMT*	MFMFLQGSSFFICLAYSAPFIHYLQHPVSAMT*			TGTTCTCAAC	TGCTCAAGGC	0		0	0	0	0	0
790	586	an	AN2750.1	54.m06682	AO070338000222	0	-254	-162					ATGTTTCTCCAAGGCAGCAGCTTCTTTATCTGCCTCGCCTATTCAGCTCCATTTATTCATTATCTACAACACCCGGTCTCGGCAATGACTTAG	ATGTTTCTCCAAGGCAGCAGCTTCTTTATCTGCCTCGCCTATTCAGCTCCATTTATTCATTATCTACAACACCCGGTCTCGGCAATGACTTAG			MFLQGSSFFICLAYSAPFIHYLQHPVSAMT*	MFLQGSSFFICLAYSAPFIHYLQHPVSAMT*			CAACATGTTT	TGCTCAAGGC	0		0	0	0	0	0
792	586	ao	AN2750.1	54.m06682	AO070338000222	0					-104	-63	ATGCACTCTACTGTTTCTTGGCTTGCTTTTATTAAAGCATAG			ATGCACTCTACTGTTTCTTGGCTTGCTTTTATTAAAGCATAG	MHSTVSWLAFIKA*			MHSTVSWLAFIKA*	TGCTGGTTCC	CAAAACGTGA	0		0	0	0	0	0
793	595	af	AN8059.1	53.m03884	AO070322000124	0			-152	-33			ATGTCCGAGATGGTTATCTGTAGCCAGCGACTTGATTTCCATTCAGCGACGTGCGTTTCATCTTTCCTTGCGAGAATTCTAGTGGCAGAATATCTGCGCATACATTACAGCACTCGATAG		ATGTCCGAGATGGTTATCTGTAGCCAGCGACTTGATTTCCATTCAGCGACGTGCGTTTCATCTTTCCTTGCGAGAATTCTAGTGGCAGAATATCTGCGCATACATTACAGCACTCGATAG		MSEMVICSQRLDFHSATCVSSFLARILVAEYLRIHYSTR*		MSEMVICSQRLDFHSATCVSSFLARILVAEYLRIHYSTR*		TCTCCGCAAA	TATCTACGCC	0	U	FG06120.1	0	0	0	0
794	595	af	AN8059.1	53.m03884	AO070322000124	0			-143	-33			ATGGTTATCTGTAGCCAGCGACTTGATTTCCATTCAGCGACGTGCGTTTCATCTTTCCTTGCGAGAATTCTAGTGGCAGAATATCTGCGCATACATTACAGCACTCGATAG		ATGGTTATCTGTAGCCAGCGACTTGATTTCCATTCAGCGACGTGCGTTTCATCTTTCCTTGCGAGAATTCTAGTGGCAGAATATCTGCGCATACATTACAGCACTCGATAG		MVICSQRLDFHSATCVSSFLARILVAEYLRIHYSTR*		MVICSQRLDFHSATCVSSFLARILVAEYLRIHYSTR*		AATGTCCGAG	TATCTACGCC	0	U	FG06120.1	0	0	0	0
795	595	ao	AN8059.1	53.m03884	AO070322000124	0					-248	-117	ATGCTGCACAAAAGGTGCGCTCCGACCACCGTAAATAAATTTGCAAGTCGCCATCTCATCTCCGCAAAAAGTCCGGGGATCGCACTCTCACCTCCGGTCCTTCTCGAGCTACACACTCCTTTTGAGCTCTGA			ATGCTGCACAAAAGGTGCGCTCCGACCACCGTAAATAAATTTGCAAGTCGCCATCTCATCTCCGCAAAAAGTCCGGGGATCGCACTCTCACCTCCGGTCCTTCTCGAGCTACACACTCCTTTTGAGCTCTGA	MLHKRCAPTTVNKFASRHLISAKSPGIALSPPVLLELHTPFEL*			MLHKRCAPTTVNKFASRHLISAKSPGIALSPPVLLELHTPFEL*	TCACGTGATT	TAACCTCCGC	0	U	FG06120.1	0	0	0	0
805	611	af	AN5875.1	72.m19257	AO070308000144	0			-183	-142			ATGGCGCAAATCATGTGCTGTCGCAGCCTTACTGGTGCCTGA		ATGGCGCAAATCATGTGCTGTCGCAGCCTTACTGGTGCCTGA		MAQIMCCRSLTGA*		MAQIMCCRSLTGA*		TTGGGCGCTT	ATAACGAGGC	0	JD	FG06203.1	0	0	0	0
806	611	af	AN5875.1	72.m19257	AO070308000144	0			-171	-142			ATGTGCTGTCGCAGCCTTACTGGTGCCTGA		ATGTGCTGTCGCAGCCTTACTGGTGCCTGA		MCCRSLTGA*		MCCRSLTGA*		GGCGCAAATC	ATAACGAGGC	0	JD	FG06203.1	0	0	0	0
804	611	an	AN5875.1	72.m19257	AO070308000144	0	-165	-121					ATGTTGGGAGTCTTAGCCGCCAGTTGGTGCCTTATTTATGCCTAA	ATGTTGGGAGTCTTAGCCGCCAGTTGGTGCCTTATTTATGCCTAA			MLGVLAASWCLIYA*	MLGVLAASWCLIYA*			GAAGGATCGA	TTATACAGGC	0	JD	FG06203.1	0	0	0	0
807	611	ao	AN5875.1	72.m19257	AO070308000144	0					-117	-46	ATGCCAAACATGGTAAGTCTCCGCGCGGATCAGAAAAAAGTTGGCGGCCAATTCAGATCCGTCGAAGAATAA			ATGCCAAACATGGTAAGTCTCCGCGCGGATCAGAAAAAAGTTGGCGGCCAATTCAGATCCGTCGAAGAATAA	MPNMVSLRADQKKVGGQFRSVEE*			MPNMVSLRADQKKVGGQFRSVEE*	GGCGCGCTAA	TCCTGTACCA	0	JD	FG06203.1	0	0	0	0
808	611	ao	AN5875.1	72.m19257	AO070308000144	0					-108	-46	ATGGTAAGTCTCCGCGCGGATCAGAAAAAAGTTGGCGGCCAATTCAGATCCGTCGAAGAATAA			ATGGTAAGTCTCCGCGCGGATCAGAAAAAAGTTGGCGGCCAATTCAGATCCGTCGAAGAATAA	MVSLRADQKKVGGQFRSVEE*			MVSLRADQKKVGGQFRSVEE*	AATGCCAAAC	TCCTGTACCA	0	JD	FG06203.1	0	0	0	0
810	612	af	AN1817.1	58.m07686	AO070318000115	0			-123	-112			ATGATCATGTAG		ATGATCATGTAG		MIM*		MIM*		CGTCTGGGTC	ACTACGTCCC	0		0	0	0	0	0
809	612	an	AN1817.1	58.m07686	AO070318000115	0	-279	-172					ATGTCGACTGGCCTGCACTGCCTCGTTTCTTGTTTTTCATCTTCATCTTTATATTATCGATCTCCCATCACCAACTCCAGCTCCAGCTCAGTTTCTTCCATCATATAA	ATGTCGACTGGCCTGCACTGCCTCGTTTCTTGTTTTTCATCTTCATCTTTATATTATCGATCTCCCATCACCAACTCCAGCTCCAGCTCAGTTTCTTCCATCATATAA			MSTGLHCLVSCFSSSSLYYRSPITNSSSSSVSSII*	MSTGLHCLVSCFSSSSLYYRSPITNSSSSSVSSII*			CCCGGTCTGA	CCATCGACCT	0		0	0	0	0	0
814	613	af	AN2919.1	59.m09077	AO070337000216	0			-261	-208			ATGCTTTTCATCGGGTGCTTCATCCTCGTTGCTTGTCTGGGATTAAATAGCTAA		ATGCTTTTCATCGGGTGCTTCATCCTCGTTGCTTGTCTGGGATTAAATAGCTAA		MLFIGCFILVACLGLNS*		MLFIGCFILVACLGLNS*		TTTAGATTTT	TTCTTGATTG	0	R	0	0	0	0	0
815	613	af	AN2919.1	59.m09077	AO070337000216	0			-177	-163			ATGTACGTCATTTGA		ATGTACGTCATTTGA		MYVI*		MYVI*		ATTGACTCGC	ATCACCAGGG	0	R	0	0	0	0	0
811	613	an	AN2919.1	59.m09077	AO070337000216	0	-246	-166					ATGTATTTCATCAACGCCCCGTCGCCCGACCGTCTACGAAGAGTCGATATATTCCCAACCTTGCTCTTGTGTACATTCTAA	ATGTATTTCATCAACGCCCCGTCGCCCGACCGTCTACGAAGAGTCGATATATTCCCAACCTTGCTCTTGTGTACATTCTAA			MYFINAPSPDRLRRVDIFPTLLLCTF*	MYFINAPSPDRLRRVDIFPTLLLCTF*			CGACCTCTGT	CAATCGTCAA	0	R	0	0	0	0	0
816	613	ao	AN2919.1	59.m09077	AO070337000216	0					-222	-79	ATGACCGGTTATCGCTCTATACCCACTACTTCACTTTGGCGTCATAACAATACCAAGAAGAGTAAGAACCCCTCCTCAACCACGACTACCTTTTTATATCTTCTTTTTCTATTGCGCCTTTTCGTACTGTGCTACGGGTGGTAA			ATGACCGGTTATCGCTCTATACCCACTACTTCACTTTGGCGTCATAACAATACCAAGAAGAGTAAGAACCCCTCCTCAACCACGACTACCTTTTTATATCTTCTTTTTCTATTGCGCCTTTTCGTACTGTGCTACGGGTGGTAA	MTGYRSIPTTSLWRHNNTKKSKNPSSTTTTFLYLLFLLRLFVLCYGW*			MTGYRSIPTTSLWRHNNTKKSKNPSSTTTTFLYLLFLLRLFVLCYGW*	TCGAATTTGA	TCTATAGAAT	0	R	0	0	0	0	0
818	616	af	AN1371.1	70.m14858	AO070215000010	0			-124	-89			ATGGGCCTTCTGGGTGATGAGGCATCCCAGATATGA		ATGGGCCTTCTGGGTGATGAGGCATCCCAGATATGA		MGLLGDEASQI*		MGLLGDEASQI*		AAGATTGACC	CAACAAGTAG	0		0	0	0	0	0
819	616	af	AN1371.1	70.m14858	AO070215000010	0			-108	-79			ATGAGGCATCCCAGATATGACAACAAGTAG		ATGAGGCATCCCAGATATGACAACAAGTAG		MRHPRYDNK*		MRHPRYDNK*		CTTCTGGGTG	TCACTTTAAA	0		0	0	0	0	0

820	616	af	AN1371.1	70.m14858	AO070215000010	0			-92	-6			ATGACAACAAGTAGTCACTTTAAAAGAAAACGAGAACCCTTGGTATCTGTTATTACTCAAGCTCAAGAAGATTTGTTCCACAGCTAG		ATGACAACAAGTAGTCACTTTAAAAGAAAACGAGAACCCTTGGTATCTGTTATTACTCAAGCTCAAGAAGATTTGTTCCACAGCTAG		MTTSSHFKRKREPLVSVITQAQEDLFHS*		MTTSSHFKRKREPLVSVITQAQEDLFHS*		CATCCCAGAT	CCGAAATGTC	0		0	0	0	0	0
821	616	ao	AN1371.1	70.m14858	AO070215000010	0					-106	-50	ATGTGTCACGTGGAGATAGAAACAAGCAATGATAAACAGTTGCCATGTTTGTGTTAA			ATGTGTCACGTGGAGATAGAAACAAGCAATGATAAACAGTTGCCATGTTTGTGTTAA	MCHVEIETSNDKQLPCLC*			MCHVEIETSNDKQLPCLC*	AGTACAGGTA	ACATCACACA	0		0	0	0	0	0
822	616	ao	AN1371.1	70.m14858	AO070215000010	0					-62	-15	ATGTTTGTGTTAAACATCACACAGCGCAGGAGAAGGAAAATCCAGTAG			ATGTTTGTGTTAAACATCACACAGCGCAGGAGAAGGAAAATCCAGTAG	MFVLNITQRRRRKIQ*			MFVLNITQRRRRKIQ*	AACAGTTGCC	AGACAACCGA	0		0	0	0	0	0
823	618	af	AN9143.1	66.m04611	AO070327000186	0			-216	-124			ATGCTGAGGTGTGGAGTCGCGATTGGCGATAAGAGTTACCCCACACCAGCTTCATCACTCAGCACCATCCTCATGATCCTCCAAATAGACTGA		ATGCTGAGGTGTGGAGTCGCGATTGGCGATAAGAGTTACCCCACACCAGCTTCATCACTCAGCACCATCCTCATGATCCTCCAAATAGACTGA		MLRCGVAIGDKSYPTPASSLSTILMILQID*		MLRCGVAIGDKSYPTPASSLSTILMILQID*		GTACTGTGTG	AAAGAGCATC	0		0	0	0	0	0
824	618	af	AN9143.1	66.m04611	AO070327000186	0			-144	-124			ATGATCCTCCAAATAGACTGA		ATGATCCTCCAAATAGACTGA		MILQID*		MILQID*		CACCATCCTC	AAAGAGCATC	0		0	0	0	0	0
825	629	af	AN4804.1	59.m09172	AO070329000035	0			-279	-256			ATGGCCAGTGCCAAAATAAAGTAA		ATGGCCAGTGCCAAAATAAAGTAA		MASAKIK*		MASAKIK*		CAACTCGCTC	GGCAGTGACT	0		0	0	0	0	0
826	629	af	AN4804.1	59.m09172	AO070329000035	0			-217	-17			ATGGCAATCAAAGCGGTGTCCCTTGGAAATTGTCTGATAAGCTTTTGTTTACTTTTCCGTTATCTACCAGCCAACACGCAGTCAAGGGTATCCGTTCTGAGGATAACCAAGATTATCAGGCAAAGAAATCTTTTAATATTCCAACTCAGGGCTTCGAACATAGGACTCACACATATCGCTGCCATACGTACCTCATTTTGA		ATGGCAATCAAAGCGGTGTCCCTTGGAAATTGTCTGATAAGCTTTTGTTTACTTTTCCGTTATCTACCAGCCAACACGCAGTCAAGGGTATCCGTTCTGAGGATAACCAAGATTATCAGGCAAAGAAATCTTTTAATATTCCAACTCAGGGCTTCGAACATAGGACTCACACATATCGCTGCCATACGTACCTCATTTTGA		MAIKAVSLGNCLISFCLLFRYLPANTQSRVSVLRITKIIRQRNLLIFQLRASNIGLTHIAAIRTSF*		MAIKAVSLGNCLISFCLLFRYLPANTQSRVSVLRITKIIRQRNLLIFQLRASNIGLTHIAAIRTSF*		GCCGCACTAG	AGAGACCGCC	0		0	0	0	0	0
827	629	ao	AN4804.1	59.m09172	AO070329000035	0					-250	-239	ATGGCGAATTAG			ATGGCGAATTAG	MAN*			MAN*	TATCAGGGAA	TCCATCATAC	0		0	0	0	0	0
833	640	af	AN4324.1	58.m07999	AO070240000001	0			-218	-150			ATGCTTCCTGTTCCTTCTGATGGATCCTGTCTGTTGATTCTCAGTTACCTGTTGCAACTTTATCATTAG		ATGCTTCCTGTTCCTTCTGATGGATCCTGTCTGTTGATTCTCAGTTACCTGTTGCAACTTTATCATTAG		MLPVPSDGSCLLILSYLLQLYH*		MLPVPSDGSCLLILSYLLQLYH*		AAATACTCTG	TCTACATTCT	0		0	0	0	0	0
834	640	af	AN4324.1	58.m07999	AO070240000001	0			-199	-182			ATGGATCCTGTCTGTTGA		ATGGATCCTGTCTGTTGA		MDPVC*		MDPVC*		GTTCCTTCTG	TTCTCAGTTA	0		0	0	0	0	0
832	640	an	AN4324.1	58.m07999	AO070240000001	0	-181	-119					ATGCGCCTCTGGGCTGGCTTTCGATTCAAACCTCCACCAAGCCTACGGAGCTGGACTATATAG	ATGCGCCTCTGGGCTGGCTTTCGATTCAAACCTCCACCAAGCCTACGGAGCTGGACTATATAG			MRLWAGFRFKPPPSLRSWTI*	MRLWAGFRFKPPPSLRSWTI*			AATACTCGCA	CCCCTTCCTT	0		0	0	0	0	0
840	645	af	AN6698.1	65.m07285	AO070339000130	0			-169	-131			ATGTCGCTTGGTGCTAGTTATCTTGATGATGAGACATGA		ATGTCGCTTGGTGCTAGTTATCTTGATGATGAGACATGA		MSLGASYLDDET*		MSLGASYLDDET*		TAGTGAATCG	CTAAGCAGAT	0	S	0	0	0	0	0
841	645	af	AN6698.1	65.m07285	AO070339000130	0			-144	-127			ATGATGAGACATGACTAA		ATGATGAGACATGACTAA		MMRHD*		MMRHD*		AGTTATCTTG	GCAGATCCAT	0	S	0	0	0	0	0
842	645	af	AN6698.1	65.m07285	AO070339000130	0			-141	-127			ATGAGACATGACTAA		ATGAGACATGACTAA		MRHD*		MRHD*		TATCTTGATG	GCAGATCCAT	0	S	0	0	0	0	0
843	645	af	AN6698.1	65.m07285	AO070339000130	0			-134	-75			ATGACTAAGCAGATCCATACACGCCAAGACCGGACAAATTTGCCTACCGCCTTCCCGTGA		ATGACTAAGCAGATCCATACACGCCAAGACCGGACAAATTTGCCTACCGCCTTCCCGTGA		MTKQIHTRQDRTNLPTAFP*		MTKQIHTRQDRTNLPTAFP*		ATGATGAGAC	ATTTTTTTGA	0	S	0	0	0	0	0
836	645	an	AN6698.1	65.m07285	AO070339000130	0	-205	-191					ATGCTCAATACATGA	ATGCTCAATACATGA			MLNT*	MLNT*			CGTACAATAG	TACTCGTAGT	0	S	0	0	0	0	0
837	645	an	AN6698.1	65.m07285	AO070339000130	0	-194	-150					ATGATACTCGTAGTCTGCAATCCATCCTCTGATAATACATACTAA	ATGATACTCGTAGTCTGCAATCCATCCTCTGATAATACATACTAA			MILVVCNPSSDNTY*	MILVVCNPSSDNTY*			TGCTCAATAC	GATCACATGA	0	S	0	0	0	0	0
838	645	an	AN6698.1	65.m07285	AO070339000130	0	-143	-117					ATGACCACAATAGTGACTAATCAATGA	ATGACCACAATAGTGACTAATCAATGA			MTTIVTNQ*	MTTIVTNQ*			CTAAGATCAC	CAGGCAGAAA	0	S	0	0	0	0	0
839	645	an	AN6698.1	65.m07285	AO070339000130	0	-120	-40					ATGACAGGCAGAAACTCTCACCGCTTTCTGAGATCCGACTTTTTTTTATCGGTCGATATCGCGGATTTTCAGGCCGGTAG	ATGACAGGCAGAAACTCTCACCGCTTTCTGAGATCCGACTTTTTTTTATCGGTCGATATCGCGGATTTTCAGGCCGGTAG			MTGRNSHRFLRSDFFFIGRYRGFSGR*	MTGRNSHRFLRSDFFFIGRYRGFSGR*			TGACTAATCA	AAATTGTCTG	0	S	0	0	0	0	0
844	645	ao	AN6698.1	65.m07285	AO070339000130	0					-140	-129	ATGAATGACTAA			ATGAATGACTAA	MND*			MND*	CATTGGGAGC	TCCACGATCT	0	S	0	0	0	0	0
845	645	ao	AN6698.1	65.m07285	AO070339000130	0					-136	-5	ATGACTAATCCACGATCTAGGTCGATGCCAAGACCGGACAAATTTGCCCACCGCCTTCCCGTGAATTTTTTTGATCTCCATTATCGCAGAATTCGAGACGAGTCGAAATCTGCAGCAACCGACACAAAATAG			ATGACTAATCCACGATCTAGGTCGATGCCAAGACCGGACAAATTTGCCCACCGCCTTCCCGTGAATTTTTTTGATCTCCATTATCGCAGAATTCGAGACGAGTCGAAATCTGCAGCAACCGACACAAAATAG	MTNPRSRSMPRPDKFAHRLPVNFFDLHYRRIRDESKSAATDTK*			MTNPRSRSMPRPDKFAHRLPVNFFDLHYRRIRDESKSAATDTK*	GGGAGCATGA	CAAAATGGTG	0	S	0	0	0	0	0
846	645	ao	AN6698.1	65.m07285	AO070339000130	0					-112	-5	ATGCCAAGACCGGACAAATTTGCCCACCGCCTTCCCGTGAATTTTTTTGATCTCCATTATCGCAGAATTCGAGACGAGTCGAAATCTGCAGCAACCGACACAAAATAG			ATGCCAAGACCGGACAAATTTGCCCACCGCCTTCCCGTGAATTTTTTTGATCTCCATTATCGCAGAATTCGAGACGAGTCGAAATCTGCAGCAACCGACACAAAATAG	MPRPDKFAHRLPVNFFDLHYRRIRDESKSAATDTK*			MPRPDKFAHRLPVNFFDLHYRRIRDESKSAATDTK*	ATCTAGGTCG	CAAAATGGTG	0	S	0	0	0	0	0
848	650	af	AN4735.1	59.m09246	AO070327000042	0			-148	-80			ATGCAGAGAACGCGCCGATGGTCTCATCGCTCAGTGAAGTTTCAGCATAGTCCTTCCATTGTTGGATGA		ATGCAGAGAACGCGCCGATGGTCTCATCGCTCAGTGAAGTTTCAGCATAGTCCTTCCATTGTTGGATGA		MQRTRRWSHRSVKFQHSPSIVG*		MQRTRRWSHRSVKFQHSPSIVG*		GCGTGGTCGT	AACCCTCTCC	0	DO	0	0	0	0	0
849	650	af	AN4735.1	59.m09246	AO070327000042	0			-131	-99			ATGGTCTCATCGCTCAGTGAAGTTTCAGCATAG		ATGGTCTCATCGCTCAGTGAAGTTTCAGCATAG		MVSSLSEVSA*		MVSSLSEVSA*		GAACGCGCCG	TCCTTCCATT	0	DO	0	0	0	0	0
850	650	af	AN4735.1	59.m09246	AO070327000042	0			-61	-47			ATGTTGACTATGTGA		ATGTTGACTATGTGA		MLTM*		MLTM*		CCGGCAAAGG	AAAAGGAATT	0	DO	0	0	0	0	0
847	650	an	AN4735.1	59.m09246	AO070327000042	0	-151	-110					ATGGGCGAAGTATCCAGTCTAGGGTCGATAGCAATTCTTTGA	ATGGGCGAAGTATCCAGTCTAGGGTCGATAGCAATTCTTTGA			MGEVSSLGSIAIL*	MGEVSSLGSIAIL*			TCCATTGGAG	TCTTGTTTAT	0	DO	0	0	0	0	0
851	650	ao	AN4735.1	59.m09246	AO070327000042	0					-248	-45	ATGAGTACCAAAAAGTTACTATCAAAAAAGCTATCATGCTCCCCACGTTTTGCTCCTTTGCCGTTGCTCATACCGCGTAGCCTGCACAGCGTGCGATTTGGGACAAACGATTCGGTGGGGTTGCTGGATTTAGTTGTCACGAACCAGAAATCCCATTTTACTAAGGCTGTCCGAAGTGTTTGTTGTCTTGACGCGTCGCAGTGA			ATGAGTACCAAAAAGTTACTATCAAAAAAGCTATCATGCTCCCCACGTTTTGCTCCTTTGCCGTTGCTCATACCGCGTAGCCTGCACAGCGTGCGATTTGGGACAAACGATTCGGTGGGGTTGCTGGATTTAGTTGTCACGAACCAGAAATCCCATTTTACTAAGGCTGTCCGAAGTGTTTGTTGTCTTGACGCGTCGCAGTGA	MSTKKLLSKKLSCSPRFAPLPLLIPRSLHSVRFGTNDSVGLLDLVVTNQKSHFTKAVRSVCCLDASQ*			MSTKKLLSKKLSCSPRFAPLPLLIPRSLHSVRFGTNDSVGLLDLVVTNQKSHFTKAVRSVCCLDASQ*	CTAATACCAA	CAATATCAGC	0	DO	0	0	0	0	0
852	650	ao	AN4735.1	59.m09246	AO070327000042	0					-213	-169	ATGCTCCCCACGTTTTGCTCCTTTGCCGTTGCTCATACCGCGTAG			ATGCTCCCCACGTTTTGCTCCTTTGCCGTTGCTCATACCGCGTAG	MLPTFCSFAVAHTA*			MLPTFCSFAVAHTA*	AAAAGCTATC	CCTGCACAGC	0	DO	0	0	0	0	0
853	652	an	AN7782.1	71.m16017	AO070336000097	0	-289	-206					ATGTATGCCCATATTGTGCACAGGCTGTTAGGTTTCGCTTCCAACTGCCAGCTTCTAGCCTCAACCTATATAAACTATATATAG	ATGTATGCCCATATTGTGCACAGGCTGTTAGGTTTCGCTTCCAACTGCCAGCTTCTAGCCTCAACCTATATAAACTATATATAG			MYAHIVHRLLGFASNCQLLASTYINYI*	MYAHIVHRLLGFASNCQLLASTYINYI*			TGTGCCTGCT	CTGACACTGA	0	L	0	0	0	0	0
854	652	an	AN7782.1	71.m16017	AO070336000097	0	-285	-259					ATGCCCATATTGTGCACAGGCTGTTAG	ATGCCCATATTGTGCACAGGCTGTTAG			MPILCTGC*	MPILCTGC*			CCTGCTATGT	GTTTCGCTTC	0	L	0	0	0	0	0
855	652	an	AN7782.1	71.m16017	AO070336000097	0	-164	-93					ATGCATAGAATCAAACTCGAGATATTTCAGATAATTCTTGGTCTAGCACGAATTTCGAGGACGTTGCAGTGA	ATGCATAGAATCAAACTCGAGATATTTCAGATAATTCTTGGTCTAGCACGAATTTCGAGGACGTTGCAGTGA			MHRIKLEIFQIILGLARISRTLQ*	MHRIKLEIFQIILGLARISRTLQ*			AGTCCAAAAC	CATCATCCAT	0	L	0	0	0	0	0
856	652	ao	AN7782.1	71.m16017	AO070336000097	0					-90	-34	ATGACATCATGCTCTATTCCTACATCTTCATATAAATCCTATACATGTCCCTTTTGA			ATGACATCATGCTCTATTCCTACATCTTCATATAAATCCTATACATGTCCCTTTTGA	MTSCSIPTSSYKSYTCPF*			MTSCSIPTSSYKSYTCPF*	GAGATCACAT	CAAAATTAAT	0	L	0	0	0	0	0
857	652	ao	AN7782.1	71.m16017	AO070336000097	0					-82	-56	ATGCTCTATTCCTACATCTTCATATAA			ATGCTCTATTCCTACATCTTCATATAA	MLYSYIFI*			MLYSYIFI*	ATATGACATC	ATCCTATACA	0	L	0	0	0	0	0
862	657	af	AN9412.1	53.m03670	AO070310000007	0			-196	-143			ATGCCTAGTTGGCTTGCCATTCTTATGGAAACAAGAATGAATAGGCAGCAATAA		ATGCCTAGTTGGCTTGCCATTCTTATGGAAACAAGAATGAATAGGCAGCAATAA		MPSWLAILMETRMNRQQ*		MPSWLAILMETRMNRQQ*		GGTGACGTTG	CGGCTCCATT	0		0	0	0	0	0
863	657	af	AN9412.1	53.m03670	AO070310000007	0			-172	-143			ATGGAAACAAGAATGAATAGGCAGCAATAA		ATGGAAACAAGAATGAATAGGCAGCAATAA		METRMNRQQ*		METRMNRQQ*		TGCCATTCTT	CGGCTCCATT	0		0	0	0	0	0
864	657	af	AN9412.1	53.m03670	AO070310000007	0			-160	-143			ATGAATAGGCAGCAATAA		ATGAATAGGCAGCAATAA		MNRQQ*		MNRQQ*		GGAAACAAGA	CGGCTCCATT	0		0	0	0	0	0
865	657	af	AN9412.1	53.m03670	AO070310000007	0			-130	-116			ATGAAAGACACATAG		ATGAAAGACACATAG		MKDT*		MKDT*		GCTCCATTCA	TTTCTGAGAA	0		0	0	0	0	0
858	657	an	AN9412.1	53.m03670	AO070310000007	0	-290	-276					ATGACGACCATCTAA	ATGACGACCATCTAA			MTTI*	MTTI*			ACCTGAGAGG	ACATAGCGTG	0		0	0	0	0	0
859	657	an	AN9412.1	53.m03670	AO070310000007	0	-176	-132					ATGAAATGTCAGATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAA	ATGAAATGTCAGATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAA			MKCQMSVSVPSLVL*	MKCQMSVSVPSLVL*			GATACTGGTC	TTTGGGAAGG	0		0	0	0	0	0
860	657	an	AN9412.1	53.m03670	AO070310000007	0	-171	-112					ATGTCAGATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAATTTGGGAAGGCAGCAGTTAG	ATGTCAGATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAATTTGGGAAGGCAGCAGTTAG			MSDVCQRAKPSIVIWEGSS*	MSDVCQRAKPSIVIWEGSS*			TGGTCATGAA	AGAACAAGGC	0		0	0	0	0	0
861	657	an	AN9412.1	53.m03670	AO070310000007	0	-164	-132					ATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAA	ATGTCTGTCAGCGTGCCAAGCCTAGTATTGTAA			MSVSVPSLVL*	MSVSVPSLVL*			GAAATGTCAG	TTTGGGAAGG	0		0	0	0	0	0
866	657	ao	AN9412.1	53.m03670	AO070310000007	0					-172	-134	ATGAATCAGTACCTAGCAGGCAGCTATCTCTATACCTAG			ATGAATCAGTACCTAGCAGGCAGCTATCTCTATACCTAG	MNQYLAGSYLYT*			MNQYLAGSYLYT*	GTACCCTTTG	CCTGTAGCCT	0		0	0	0	0	0
867	657	ao	AN9412.1	53.m03670	AO070310000007	0					-123	-91	ATGATGACCCACCGCAGCGTTAAGTTACCTTAA			ATGATGACCCACCGCAGCGTTAAGTTACCTTAA	MMTHRSVKLP*			MMTHRSVKLP*	CCTGTAGCCT	TAACGGCAAT	0		0	0	0	0	0
868	657	ao	AN9412.1	53.m03670	AO070310000007	0					-120	-91	ATGACCCACCGCAGCGTTAAGTTACCTTAA			ATGACCCACCGCAGCGTTAAGTTACCTTAA	MTHRSVKLP*			MTHRSVKLP*	GTAGCCTATG	TAACGGCAAT	0		0	0	0	0	0
870	658	af	AN0455.1	54.m06616	AO070328000183	0			-250	-224			ATGATGGCGGGGTTCCCCTCCGTCTAA		ATGATGGCGGGGTTCCCCTCCGTCTAA		MMAGFPSV*		MMAGFPSV*		ATTCTTGTAT	CATTTCCTGT	0	J	0	0	0	0	0
871	658	af	AN0455.1	54.m06616	AO070328000183	0			-247	-224			ATGGCGGGGTTCCCCTCCGTCTAA		ATGGCGGGGTTCCCCTCCGTCTAA		MAGFPSV*		MAGFPSV*		CTTGTATATG	CATTTCCTGT	0	J	0	0	0	0	0
872	658	af	AN0455.1	54.m06616	AO070328000183	0			-172	-56			ATGAGCGGCAAGGAAAATCATCCCACTTGCACTGTGGGATTGCCATCGGCTCATGTATCCGCCCTTGTCTCCATACTTCAATCTACTCTTTCAGCTCATGTTTGCCTGATTCTCTGA		ATGAGCGGCAAGGAAAATCATCCCACTTGCACTGTGGGATTGCCATCGGCTCATGTATCCGCCCTTGTCTCCATACTTCAATCTACTCTTTCAGCTCATGTTTGCCTGATTCTCTGA		MSGKENHPTCTVGLPSAHVSALVSILQSTLSAHVCLIL*		MSGKENHPTCTVGLPSAHVSALVSILQSTLSAHVCLIL*		TTCGTCATCG	GCCTTGTGTC	0	J	0	0	0	0	0
873	658	af	AN0455.1	54.m06616	AO070328000183	0			-120	-64			ATGTATCCGCCCTTGTCTCCATACTTCAATCTACTCTTTCAGCTCATGTTTGCCTGA		ATGTATCCGCCCTTGTCTCCATACTTCAATCTACTCTTTCAGCTCATGTTTGCCTGA		MYPPLSPYFNLLFQLMFA*		MYPPLSPYFNLLFQLMFA*		CCATCGGCTC	TTCTCTGAGC	0	J	0	0	0	0	0
874	658	af	AN0455.1	54.m06616	AO070328000183	0			-75	-64			ATGTTTGCCTGA		ATGTTTGCCTGA		MFA*		MFA*		CTTTCAGCTC	TTCTCTGAGC	0	J	0	0	0	0	0
869	658	an	AN0455.1	54.m06616	AO070328000183	0	-139	-32					ATGCAGGAGCCCTCGCCAGCGCTTTTCTTTTTACTTGTTCACTTTACGTTTTACATCTATTTAAGACTCCGAGACAGGTCCTGTTTCTCTCTTCCGTACTCCGAGTGA	ATGCAGGAGCCCTCGCCAGCGCTTTTCTTTTTACTTGTTCACTTTACGTTTTACATCTATTTAAGACTCCGAGACAGGTCCTGTTTCTCTCTTCCGTACTCCGAGTGA			MQEPSPALFFLLVHFTFYIYLRLRDRSCFSLPYSE*	MQEPSPALFFLLVHFTFYIYLRLRDRSCFSLPYSE*			GACGGCTCGT	TCGCATTCGC	0	J	0	0	0	0	0
875	658	ao	AN0455.1	54.m06616	AO070328000183	0					-128	-84	ATGGGGAGGATCATCCCACTCGTCTCCACGCCGGACCTTTTCTGA			ATGGGGAGGATCATCCCACTCGTCTCCACGCCGGACCTTTTCTGA	MGRIIPLVSTPDLF*			MGRIIPLVSTPDLF*	TTGAGGGGCA	ATTCTGCACA	0	J	0	0	0	0	0
879	665	af	AN4515.1	57.m05614	AO070311000076	0			-180	-142			ATGTTCCATGCATCAAAAGATCCCAAAAATAATTCGTAA		ATGTTCCATGCATCAAAAGATCCCAAAAATAATTCGTAA		MFHASKDPKNNS*		MFHASKDPKNNS*		ATCGTTTGGT	TCAGATGGGT	0	G	0	0	0	0	0
880	665	af	AN4515.1	57.m05614	AO070311000076	0			-173	-75			ATGCATCAAAAGATCCCAAAAATAATTCGTAATCAGATGGGTTCTGTGGTTCTCATTACTGATTCTTCACAGTCCTCCATCCGTTCACCCTCCTGGTGA		ATGCATCAAAAGATCCCAAAAATAATTCGTAATCAGATGGGTTCTGTGGTTCTCATTACTGATTCTTCACAGTCCTCCATCCGTTCACCCTCCTGGTGA		MHQKIPKIIRNQMGSVVLITDSSQSSIRSPSW*		MHQKIPKIIRNQMGSVVLITDSSQSSIRSPSW*		GGTATGTTCC	TCTTTCTTTG	0	G	0	0	0	0	0
881	665	af	AN4515.1	57.m05614	AO070311000076	0			-137	-75			ATGGGTTCTGTGGTTCTCATTACTGATTCTTCACAGTCCTCCATCCGTTCACCCTCCTGGTGA		ATGGGTTCTGTGGTTCTCATTACTGATTCTTCACAGTCCTCCATCCGTTCACCCTCCTGGTGA		MGSVVLITDSSQSSIRSPSW*		MGSVVLITDSSQSSIRSPSW*		TCGTAATCAG	TCTTTCTTTG	0	G	0	0	0	0	0
882	667	an	AN4087.1	54.m06728	AO070342000080	0	-239	-210					ATGGTTGTTGGGATTGATGTCTTGGCATAA	ATGGTTGTTGGGATTGATGTCTTGGCATAA			MVVGIDVLA*	MVVGIDVLA*			CTGCCTAGTC	CTTAAACAGG	0	J	FG05433.1	0	NCU00489.1	0	0
883	667	an	AN4087.1	54.m06728	AO070342000080	0	-223	-92					ATGTCTTGGCATAACTTAAACAGGAAAAGTGTAGGCGGAGAGCAAGCGAGGGTTTGCCCTGACCAGATTAGGAAAGCAAAGCCCTACACCCAAAATTCCCCACTAACGCCGAACTTCTCAAAACTGACCTGA	ATGTCTTGGCATAACTTAAACAGGAAAAGTGTAGGCGGAGAGCAAGCGAGGGTTTGCCCTGACCAGATTAGGAAAGCAAAGCCCTACACCCAAAATTCCCCACTAACGCCGAACTTCTCAAAACTGACCTGA			MSWHNLNRKSVGGEQARVCPDQIRKAKPYTQNSPLTPNFSKLT*	MSWHNLNRKSVGGEQARVCPDQIRKAKPYTQNSPLTPNFSKLT*			GTTGGGATTG	ACCTCGAGCG	0	J	FG05433.1	0	NCU00489.1	0	0

884	674	an	AN5203.1	69.m15625	AO070199000002	0	-103	-23					ATGCCAACCATGCGCAATTTGTCTCCCCCAACTGATCGCCTGCTTGTTACAGAACTCCGTCCCATCGGCCATCCGGTTTGA	ATGCCAACCATGCGCAATTTGTCTCCCCCAACTGATCGCCTGCTTGTTACAGAACTCCGTCCCATCGGCCATCCGGTTTGA			MPTMRNLSPPTDRLLVTELRPIGHPV*	MPTMRNLSPPTDRLLVTELRPIGHPV*			GGTACTACCA	TTGCGCCAGT	0	J	0	0	0	YMR158W	0
885	674	an	AN5203.1	69.m15625	AO070199000002	0	-94	-23					ATGCGCAATTTGTCTCCCCCAACTGATCGCCTGCTTGTTACAGAACTCCGTCCCATCGGCCATCCGGTTTGA	ATGCGCAATTTGTCTCCCCCAACTGATCGCCTGCTTGTTACAGAACTCCGTCCCATCGGCCATCCGGTTTGA			MRNLSPPTDRLLVTELRPIGHPV*	MRNLSPPTDRLLVTELRPIGHPV*			AATGCCAACC	TTGCGCCAGT	0	J	0	0	0	YMR158W	0
886	674	ao	AN5203.1	69.m15625	AO070199000002	0					-123	-52	ATGAAAAAGTATTGCTCATACCTCCTCTTCCCCGTAACCAGTGATTTATCGGCTCTCCCGCACACCGTCTGA			ATGAAAAAGTATTGCTCATACCTCCTCTTCCCCGTAACCAGTGATTTATCGGCTCTCCCGCACACCGTCTGA	MKKYCSYLLFPVTSDLSALPHTV*			MKKYCSYLLFPVTSDLSALPHTV*	TCTTATCTCA	ACACTTAAGG	0	J	0	0	0	YMR158W	0
907	678	af	AN6233.1	72.m19420	AO070304000087	0			-299	-273			ATGTGGGTGAGGCTCTCCAGACGGTGA		ATGTGGGTGAGGCTCTCCAGACGGTGA		MWVRLSRR*		MWVRLSRR*		CTGCTTCGCT	AACTATGACG	0	O	0	0	0	0	0
908	678	af	AN6233.1	72.m19420	AO070304000087	0			-268	-224			ATGACGAAAGCTGATAAGCTAGGGAGTACCTCCAGTCTAACCTGA		ATGACGAAAGCTGATAAGCTAGGGAGTACCTCCAGTCTAACCTGA		MTKADKLGSTSSLT*		MTKADKLGSTSSLT*		CGGTGAAACT	TAAGGTAATC	0	O	0	0	0	0	0
909	678	af	AN6233.1	72.m19420	AO070304000087	0			-189	-97			ATGTCGCGTTTCCTCTGTCAGGAAATACATTTCACTATATCAAAGCAAACTTGCTGCTTGACGCTTCTTTCATCCTTTTTTTTTTTTCATTGA		ATGTCGCGTTTCCTCTGTCAGGAAATACATTTCACTATATCAAAGCAAACTTGCTGCTTGACGCTTCTTTCATCCTTTTTTTTTTTTCATTGA		MSRFLCQEIHFTISKQTCCLTLLSSFFFFH*		MSRFLCQEIHFTISKQTCCLTLLSSFFFFH*		TCGCGTCCGA	ATTTTGGGGG	0	O	0	0	0	0	0
906	678	an	AN6233.1	72.m19420	AO070304000087	0	-159	-136					ATGTTTTGGTCTAAACCTAATTAG	ATGTTTTGGTCTAAACCTAATTAG			MFWSKPN*	MFWSKPN*			CAAGTAGGTA	GAAAGCAAAG	0	O	0	0	0	0	0
910	678	ao	AN6233.1	72.m19420	AO070304000087	0					-257	-156	ATGACATCGAAGGCGGGGAGAGCTCCATTGGCAGCTCTAACCCAATCGGGTAAGCAAAATGGTTTTCCAATGGACGCGTCGCAACGCGTCTGTTGCCAGTGA			ATGACATCGAAGGCGGGGAGAGCTCCATTGGCAGCTCTAACCCAATCGGGTAAGCAAAATGGTTTTCCAATGGACGCGTCGCAACGCGTCTGTTGCCAGTGA	MTSKAGRAPLAALTQSGKQNGFPMDASQRVCCQ*			MTSKAGRAPLAALTQSGKQNGFPMDASQRVCCQ*	TTCAAGATCA	ATCAATTCAC	0	O	0	0	0	0	0
911	678	ao	AN6233.1	72.m19420	AO070304000087	0					-199	-59	ATGGTTTTCCAATGGACGCGTCGCAACGCGTCTGTTGCCAGTGAATCAATTCACTCCTCCTTTTCTATTTGTGTTTTCTTGTCTTTTGCTCTCATTCCTTCTCTACTCTTTCTGTCTTATTGGATCTTTGGAAGGCGGTGA			ATGGTTTTCCAATGGACGCGTCGCAACGCGTCTGTTGCCAGTGAATCAATTCACTCCTCCTTTTCTATTTGTGTTTTCTTGTCTTTTGCTCTCATTCCTTCTCTACTCTTTCTGTCTTATTGGATCTTTGGAAGGCGGTGA	MVFQWTRRNASVASESIHSSFSICVFLSFALIPSLLFLSYWIFGRR*			MVFQWTRRNASVASESIHSSFSICVFLSFALIPSLLFLSYWIFGRR*	GGTAAGCAAA	ACTGTGATAC	0	O	0	0	0	0	0
912	678	ao	AN6233.1	72.m19420	AO070304000087	0					-188	-156	ATGGACGCGTCGCAACGCGTCTGTTGCCAGTGA			ATGGACGCGTCGCAACGCGTCTGTTGCCAGTGA	MDASQRVCCQ*			MDASQRVCCQ*	TGGTTTTCCA	ATCAATTCAC	0	O	0	0	0	0	0
913	686	an	AN8863.1	71.m16001	AO070271000008	0	-229	-14					ATGTGGTTGGTGACAATTTCTGCGTCGCCGATTGATTCTGTTTCTCAACAGCCTTCGTCGCGCCAAGCCCCTCGGCCCAAAGGCGCTAAGATCCCACCAAGCCAGGATTCCAGACCCCAAAATCTCAGCGTATCAAATTCTTTCAACCCTCAACCTCCCTCTCCGCGACAACCTCTCAACGGATTCTTGTACTGGCAGCTTCCGTATACTTTCTGA	ATGTGGTTGGTGACAATTTCTGCGTCGCCGATTGATTCTGTTTCTCAACAGCCTTCGTCGCGCCAAGCCCCTCGGCCCAAAGGCGCTAAGATCCCACCAAGCCAGGATTCCAGACCCCAAAATCTCAGCGTATCAAATTCTTTCAACCCTCAACCTCCCTCTCCGCGACAACCTCTCAACGGATTCTTGTACTGGCAGCTTCCGTATACTTTCTGA			MWLVTISASPIDSVSQQPSSRQAPRPKGAKIPPSQDSRPQNLSVSNSFNPQPPSPRQPLNGFLYWQLPYTF*	MWLVTISASPIDSVSQQPSSRQAPRPKGAKIPPSQDSRPQNLSVSNSFNPQPPSPRQPLNGFLYWQLPYTF*			AGCATCAATC	TCAACTTTTC	0	BD	0	0	0	0	0
915	688	af	AN3413.1	66.m04623	AO070281000039	0			-236	-192			ATGATGCGGGTCTCATCGGCTTACCGTATTGGGACTACCCGCTAG		ATGATGCGGGTCTCATCGGCTTACCGTATTGGGACTACCCGCTAG		MMRVSSAYRIGTTR*		MMRVSSAYRIGTTR*		CACCCGTCAC	GGCATAGGGT	0	J	0	MG09222.1	NCU06047.1	0	0
916	688	af	AN3413.1	66.m04623	AO070281000039	0			-233	-192			ATGCGGGTCTCATCGGCTTACCGTATTGGGACTACCCGCTAG		ATGCGGGTCTCATCGGCTTACCGTATTGGGACTACCCGCTAG		MRVSSAYRIGTTR*		MRVSSAYRIGTTR*		CCGTCACATG	GGCATAGGGT	0	J	0	MG09222.1	NCU06047.1	0	0
914	688	an	AN3413.1	66.m04623	AO070281000039	0	-269	-213					ATGACGAGCCCCCTGGTGCTGGCCCGTGCGCCGGCGGGGCTAGAGCGGATTTCCTAA	ATGACGAGCCCCCTGGTGCTGGCCCGTGCGCCGGCGGGGCTAGAGCGGATTTCCTAA			MTSPLVLARAPAGLERIS*	MTSPLVLARAPAGLERIS*			GCCCCATCAC	AGTAGATACA	0	J	0	MG09222.1	NCU06047.1	0	0
917	688	ao	AN3413.1	66.m04623	AO070281000039	0					-218	-174	ATGATGCGGGCGTCAGCGGGTTGCCCAAACGGGTTCACCGCCTAG			ATGATGCGGGCGTCAGCGGGTTGCCCAAACGGGTTCACCGCCTAG	MMRASAGCPNGFTA*			MMRASAGCPNGFTA*	GCGAAGTCAC	GGTATAGGGT	0	J	0	MG09222.1	NCU06047.1	0	0
918	688	ao	AN3413.1	66.m04623	AO070281000039	0					-215	-174	ATGCGGGCGTCAGCGGGTTGCCCAAACGGGTTCACCGCCTAG			ATGCGGGCGTCAGCGGGTTGCCCAAACGGGTTCACCGCCTAG	MRASAGCPNGFTA*			MRASAGCPNGFTA*	AAGTCACATG	GGTATAGGGT	0	J	0	MG09222.1	NCU06047.1	0	0
921	690	af	AN6119.1	72.m19041	AO070340000085	0			-233	-222			ATGTGGTCCTGA		ATGTGGTCCTGA		MWS*		MWS*		AAAAACTCTC	TATTGCCCAG	0	S	FG01898.1	0	0	YHR132C	YHR132C
922	690	af	AN6119.1	72.m19041	AO070340000085	0			-177	-70			ATGGTAAAGTCGGAGTGCCTTCTGCCTGAGGCATCCATAGGCGTCCGCCATTCGCCCAATCTAATATTGTCACTCGTCCATCCTGATCCGTCCTCGTTCACCTTCTAG		ATGGTAAAGTCGGAGTGCCTTCTGCCTGAGGCATCCATAGGCGTCCGCCATTCGCCCAATCTAATATTGTCACTCGTCCATCCTGATCCGTCCTCGTTCACCTTCTAG		MVKSECLLPEASIGVRHSPNLILSLVHPDPSSFTF*		MVKSECLLPEASIGVRHSPNLILSLVHPDPSSFTF*		ATCAGGGAAA	GAGACTAGAC	0	S	FG01898.1	0	0	YHR132C	YHR132C
919	690	an	AN6119.1	72.m19041	AO070340000085	0	-143	-111					ATGACATTGCGGCTGCCTTCCACGGTTACTTAG	ATGACATTGCGGCTGCCTTCCACGGTTACTTAG			MTLRLPSTVT*	MTLRLPSTVT*			CAGGCGCCGA	TCTCCTCTCC	0	S	FG01898.1	0	0	YHR132C	YHR132C
924	690	ao	AN6119.1	72.m19041	AO070340000085	0					-247	-230	ATGACATGGATCTGTTAG			ATGACATGGATCTGTTAG	MTWIC*			MTWIC*	AGGGTTCGAT	GGTGGTATTA	0	S	FG01898.1	0	0	YHR132C	YHR132C
925	690	ao	AN6119.1	72.m19041	AO070340000085	0					-242	-219	ATGGATCTGTTAGGGTGGTATTAG			ATGGATCTGTTAGGGTGGTATTAG	MDLLGWY*			MDLLGWY*	TCGATATGAC	GCTTTATACT	0	S	FG01898.1	0	0	YHR132C	YHR132C
926	690	ao	AN6119.1	72.m19041	AO070340000085	0					-183	-28	ATGTCAGCCTTAGGCATCAGCCGCGGTCCATGGCTCACCATCACATCTCATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAAAGGATCTGACAATGAAGATTTTGGCATAG			ATGTCAGCCTTAGGCATCAGCCGCGGTCCATGGCTCACCATCACATCTCATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAAAGGATCTGACAATGAAGATTTTGGCATAG	MSALGISRGPWLTITSHVTSLHASSILPSPVAVWSRSIEIHLKDLTMKILA*			MSALGISRGPWLTITSHVTSLHASSILPSPVAVWSRSIEIHLKDLTMKILA*	GCACGATCAT	CTTTTCTGCG	0	S	FG01898.1	0	0	YHR132C	YHR132C
927	690	ao	AN6119.1	72.m19041	AO070340000085	0					-154	-68	ATGGCTCACCATCACATCTCATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGA			ATGGCTCACCATCACATCTCATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGA	MAHHHISCHFTPCFFHPSFPRRCLVALD*			MAHHHISCHFTPCFFHPSFPRRCLVALD*	GCCGCGGTCC	AATTCACTTA	0	S	FG01898.1	0	0	YHR132C	YHR132C
928	690	ao	AN6119.1	72.m19041	AO070340000085	0					-134	-57	ATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAA			ATGTCACTTCACTCCATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAA	MSLHSMLLPSFLPPSLSGRARLKFT*			MSLHSMLLPSFLPPSLSGRARLKFT*	ATCACATCTC	AGGATCTGAC	0	S	FG01898.1	0	0	YHR132C	YHR132C
929	690	ao	AN6119.1	72.m19041	AO070340000085	0					-119	-57	ATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAA			ATGCTTCTTCCATCCTTCCTTCCCCCGTCGCTGTCTGGTCGCGCTCGATTGAAATTCACTTAA	MLLPSFLPPSLSGRARLKFT*			MLLPSFLPPSLSGRARLKFT*	ACTTCACTCC	AGGATCTGAC	0	S	FG01898.1	0	0	YHR132C	YHR132C
931	693	an	AN5410.1	67.m02915	AO070334000166	0	-95	-33					ATGGCCCCATTCCCGTCCCAGTGCCTCTCATCTTCTTCTCTCAAGATTCCCAGACGCAAATAG	ATGGCCCCATTCCCGTCCCAGTGCCTCTCATCTTCTTCTCTCAAGATTCCCAGACGCAAATAG			MAPFPSQCLSSSSLKIPRRK*	MAPFPSQCLSSSSLKIPRRK*			AATCATAAGA	CAAAGACTTC	0		0	0	0	0	0
932	693	ao	AN5410.1	67.m02915	AO070334000166	0					-262	-92	ATGGCCGGCGACTGTGCATGGGTGTGGGCTGAGGGGGATGCTTGCTTTCTGGGTCTTTTAAGAGGGGGTTTTGGGCTTTTATCTCCTGTACTTCTGTGTTCCTGTGCTTCATTCTCTTTGTGCTGGGTGTTTCAAGTGTGTTACTCAGATACTACTGTGTCGTCACTATAA			ATGGCCGGCGACTGTGCATGGGTGTGGGCTGAGGGGGATGCTTGCTTTCTGGGTCTTTTAAGAGGGGGTTTTGGGCTTTTATCTCCTGTACTTCTGTGTTCCTGTGCTTCATTCTCTTTGTGCTGGGTGTTTCAAGTGTGTTACTCAGATACTACTGTGTCGTCACTATAA	MAGDCAWVWAEGDACFLGLLRGGFGLLSPVLLCSCASFSLCWVFQVCYSDTTVSSL*			MAGDCAWVWAEGDACFLGLLRGGFGLLSPVLLCSCASFSLCWVFQVCYSDTTVSSL*	GGATGAGAAA	AAACCCATAT	0		0	0	0	0	0
933	693	ao	AN5410.1	67.m02915	AO070334000166	0					-245	-231	ATGGGTGTGGGCTGA			ATGGGTGTGGGCTGA	MGVG*			MGVG*	GCGACTGTGC	GGGGGATGCT	0		0	0	0	0	0
934	693	ao	AN5410.1	67.m02915	AO070334000166	0					-225	-202	ATGCTTGCTTTCTGGGTCTTTTAA			ATGCTTGCTTTCTGGGTCTTTTAA	MLAFWVF*			MLAFWVF*	GCTGAGGGGG	GAGGGGGTTT	0		0	0	0	0	0
938	694	af	AN3035.1	59.m08982	AO070337000077	0			-240	-157			ATGGTGAACGAGAAGGAACGAACATTCCAGCCTCGTTGTCAGGGCCCAGAATCTTGTCTCTGGGTTGTTGGTCAGGGTGGCTGA		ATGGTGAACGAGAAGGAACGAACATTCCAGCCTCGTTGTCAGGGCCCAGAATCTTGTCTCTGGGTTGTTGGTCAGGGTGGCTGA		MVNEKERTFQPRCQGPESCLWVVGQGG*		MVNEKERTFQPRCQGPESCLWVVGQGG*		TCACGCGTCG	CTACTGTCAT	0	L	0	0	0	0	0
939	694	af	AN3035.1	59.m08982	AO070337000077	0			-62	-42			ATGCCCGTCTTGGCCAGTTAG		ATGCCCGTCTTGGCCAGTTAG		MPVLAS*		MPVLAS*		GTCAGAGCCG	GTGAACGGCA	0	L	0	0	0	0	0
935	694	an	AN3035.1	59.m08982	AO070337000077	0	-264	-163					ATGGCCTGCAATCGCGTTCCTGGCGCGTTCTGGGAAGAACGAGGAAGTCGATCGTTGCAAGCATTCCATCCTTGCTGCCGGGGTTCGTTCACCGTCTTATGA	ATGGCCTGCAATCGCGTTCCTGGCGCGTTCTGGGAAGAACGAGGAAGTCGATCGTTGCAAGCATTCCATCCTTGCTGCCGGGGTTCGTTCACCGTCTTATGA			MACNRVPGAFWEERGSRSLQAFHPCCRGSFTVL*	MACNRVPGAFWEERGSRSLQAFHPCCRGSFTVL*			AATCAAAGCC	TACCTGGGCG	0	L	0	0	0	0	0
936	694	an	AN3035.1	59.m08982	AO070337000077	0	-111	-40					ATGTCCTTCGCCCCCAGCCTGACTTTGTCCCGCTCGCAGAATATCCCACTGATGCCTCCCTCGAGTCTGTGA	ATGTCCTTCGCCCCCAGCCTGACTTTGTCCCGCTCGCAGAATATCCCACTGATGCCTCCCTCGAGTCTGTGA			MSFAPSLTLSRSQNIPLMPPSSL*	MSFAPSLTLSRSQNIPLMPPSSL*			CGGGAGTTTC	AAAACACGAG	0	L	0	0	0	0	0
940	694	ao	AN3035.1	59.m08982	AO070337000077	0					-277	-197	ATGCATCAACCTATCGCGTTTCTGTTGCGCGTCGGAGGGTTGATACTGGCAGTCAACTTACATTCCAGTCTCGTTGTCTAG			ATGCATCAACCTATCGCGTTTCTGTTGCGCGTCGGAGGGTTGATACTGGCAGTCAACTTACATTCCAGTCTCGTTGTCTAG	MHQPIAFLLRVGGLILAVNLHSSLVV*			MHQPIAFLLRVGGLILAVNLHSSLVV*	CTTCCTCTGT	GTCATACATA	0	L	0	0	0	0	0
941	694	ao	AN3035.1	59.m08982	AO070337000077	0					-181	-161	ATGACCCGCCAAGTTGGTTGA			ATGACCCGCCAAGTTGGTTGA	MTRQVG*			MTRQVG*	ACATAACTCA	TTGGCTTCCA	0	L	0	0	0	0	0
942	694	ao	AN3035.1	59.m08982	AO070337000077	0					-122	-87	ATGGTTCTCGTGCCCACCGCTCCTCCTGAGTCCTAA			ATGGTTCTCGTGCCCACCGCTCCTCCTGAGTCCTAA	MVLVPTAPPES*			MVLVPTAPPES*	GTTTCTCCTC	CCGTCGACTG	0	L	0	0	0	0	0
944	697	af	AN2329.1	71.m15527	AO070323000028	0			-104	-63			ATGGACATGTCGACGATCCTCCCTAGTCTACTGAGAGAGTGA		ATGGACATGTCGACGATCCTCCCTAGTCTACTGAGAGAGTGA		MDMSTILPSLLRE*		MDMSTILPSLLRE*		CGTTGATCAC	GATCTCGACT	0	GEPR	0	0	0	0	0
945	697	af	AN2329.1	71.m15527	AO070323000028	0			-98	-63			ATGTCGACGATCCTCCCTAGTCTACTGAGAGAGTGA		ATGTCGACGATCCTCCCTAGTCTACTGAGAGAGTGA		MSTILPSLLRE*		MSTILPSLLRE*		TCACATGGAC	GATCTCGACT	0	GEPR	0	0	0	0	0
946	697	ao	AN2329.1	71.m15527	AO070323000028	0					-158	-90	ATGGTTTCATGGGAAATCGCTTCACGTCTGTCACCCGGTCACGTGTTTCGAGACGGCTGTTATCGATGA			ATGGTTTCATGGGAAATCGCTTCACGTCTGTCACCCGGTCACGTGTTTCGAGACGGCTGTTATCGATGA	MVSWEIASRLSPGHVFRDGCYR*			MVSWEIASRLSPGHVFRDGCYR*	GCGAACTTGA	GGGGTTTCTG	0	GEPR	0	0	0	0	0
947	697	ao	AN2329.1	71.m15527	AO070323000028	0					-150	-79	ATGGGAAATCGCTTCACGTCTGTCACCCGGTCACGTGTTTCGAGACGGCTGTTATCGATGAGGGGTTTCTGA			ATGGGAAATCGCTTCACGTCTGTCACCCGGTCACGTGTTTCGAGACGGCTGTTATCGATGAGGGGTTTCTGA	MGNRFTSVTRSRVSRRLLSMRGF*			MGNRFTSVTRSRVSRRLLSMRGF*	GAATGGTTTC	TCGGCATTGT	0	GEPR	0	0	0	0	0
948	697	ao	AN2329.1	71.m15527	AO070323000028	0					-93	-79	ATGAGGGGTTTCTGA			ATGAGGGGTTTCTGA	MRGF*			MRGF*	GCTGTTATCG	TCGGCATTGT	0	GEPR	0	0	0	0	0
949	697	ao	AN2329.1	71.m15527	AO070323000028	0					-66	-19	ATGATCCAAAATTGCCGAGTGTCGGAAAGGATAGAGGGTGCCCAGTAG			ATGATCCAAAATTGCCGAGTGTCGGAAAGGATAGAGGGTGCCCAGTAG	MIQNCRVSERIEGAQ*			MIQNCRVSERIEGAQ*	GGCATTGTTC	AGCACGACGC	0	GEPR	0	0	0	0	0
950	698	an	AN7724.1	71.m15751	AO070325000139	0	-224	-204					ATGATCTGCGGATTAAAGTAA	ATGATCTGCGGATTAAAGTAA			MICGLK*	MICGLK*			TTGCCGGATC	CACCGACTGC	0		0	0	0	0	0
951	698	an	AN7724.1	71.m15751	AO070325000139	0	-136	-77					ATGTTACTCCGCACAGGGCAGATGCTGCTTGTTGACATCTACAAGAATCCCACCCTATAG	ATGTTACTCCGCACAGGGCAGATGCTGCTTGTTGACATCTACAAGAATCCCACCCTATAG			MLLRTGQMLLVDIYKNPTL*	MLLRTGQMLLVDIYKNPTL*			CGTAAAGGCC	GTTTATAATC	0		0	0	0	0	0
952	698	an	AN7724.1	71.m15751	AO070325000139	0	-115	-77					ATGCTGCTTGTTGACATCTACAAGAATCCCACCCTATAG	ATGCTGCTTGTTGACATCTACAAGAATCCCACCCTATAG			MLLVDIYKNPTL*	MLLVDIYKNPTL*			CACAGGGCAG	GTTTATAATC	0		0	0	0	0	0
953	698	ao	AN7724.1	71.m15751	AO070325000139	0					-178	-107	ATGACGTCACCCCATCTCCTCCGTCCAACATCTCCTTCAATAGCTGTTACATTCCCACCTCCAATCCCTTGA			ATGACGTCACCCCATCTCCTCCGTCCAACATCTCCTTCAATAGCTGTTACATTCCCACCTCCAATCCCTTGA	MTSPHLLRPTSPSIAVTFPPIP*			MTSPHLLRPTSPSIAVTFPPIP*	TGGCCTTCCG	AAGAAGCTTC	0		0	0	0	0	0
956	699	af	AN0476.1	54.m06594	AO070328000164	0			-232	-221			ATGAGAGACTGA		ATGAGAGACTGA		MRD*		MRD*		AAAAGTAAAT	AAATGTGGCT	0	J	0	0	0	0	0
954	699	an	AN0476.1	54.m06594	AO070328000164	0	-137	-93					ATGGCGGCAGAAAAAAATAATTTCTTGGCAAGGCGGAGAGCTTGA	ATGGCGGCAGAAAAAAATAATTTCTTGGCAAGGCGGAGAGCTTGA			MAAEKNNFLARRRA*	MAAEKNNFLARRRA*			TTGCTTATCG	CCGACCGCCA	0	J	0	0	0	0	0
957	699	ao	AN0476.1	54.m06594	AO070328000164	0					-232	-185	ATGCACTGCTCAACAAGTAAGAGTGTGGAGTGTGGTAGTTGGAATTAA			ATGCACTGCTCAACAAGTAAGAGTGTGGAGTGTGGTAGTTGGAATTAA	MHCSTSKSVECGSWN*			MHCSTSKSVECGSWN*	AAACCTTCGT	TATTTTTTTT	0	J	0	0	0	0	0

968	700	af	AN8076.1	53.m03929	AO070330000034	0			-659	-504			ATGAGTGCTTCGACCAAGTCCAGGTCGAGGTCAAGTCGTGGGCCGCAGCTGAGTCTGAAGGGACGGGTCCAGGCAGATAACTGCTCTGCGATTATCATCCTACATATTGAATTTGCTACAGAGATACGTACGATGGTTGCAAGGTCCCGTTGCTGA		ATGAGTGCTTCGACCAAGTCCAGGTCGAGGTCAAGTCGTGGGCCGCAGCTGAGTCTGAAGGGACGGGTCCAGGCAGATAACTGCTCTGCGATTATCATCCTACATATTGAATTTGCTACAGAGATACGTACGATGGTTGCAAGGTCCCGTTGCTGA		MSASTKSRSRSSRGPQLSLKGRVQADNCSAIIILHIEFATEIRTMVARSRC*		MSASTKSRSRSSRGPQLSLKGRVQADNCSAIIILHIEFATEIRTMVARSRC*		GGCGTTGTCG	CTTGGTTTGG	0	A	0	0	0	0	0
969	700	af	AN8076.1	53.m03929	AO070330000034	0			-527	-504			ATGGTTGCAAGGTCCCGTTGCTGA		ATGGTTGCAAGGTCCCGTTGCTGA		MVARSRC*		MVARSRC*		GATACGTACG	CTTGGTTTGG	0	A	0	0	0	0	0
970	700	af	AN8076.1	53.m03929	AO070330000034	0			-278	-267			ATGTTTACGTAA		ATGTTTACGTAA		MFT*		MFT*		GGCCTGGTGC	ACGCTTCAAG	0	A	0	0	0	0	0
971	700	af	AN8076.1	53.m03929	AO070330000034	0			-231	-97			ATGTGTGTGTGTGTGCACGCTCTTCACGATCACGTGCCTCTCCACACCAATTCAGGTGGCCTGAGGCCTCACGCTTGGTCATTATTGGGTCGTTTCCAATTTCGGATTGTTCTCGCCTCACCTTCGAATCACTGA		ATGTGTGTGTGTGTGCACGCTCTTCACGATCACGTGCCTCTCCACACCAATTCAGGTGGCCTGAGGCCTCACGCTTGGTCATTATTGGGTCGTTTCCAATTTCGGATTGTTCTCGCCTCACCTTCGAATCACTGA		MCVCVHALHDHVPLHTNSGGLRPHAWSLLGRFQFRIVLASPSNH*		MCVCVHALHDHVPLHTNSGGLRPHAWSLLGRFQFRIVLASPSNH*		GTGTTTGTGT	AAGTCTCCAA	0	A	0	0	0	0	0
959	700	an	AN8076.1	53.m03929	AO070330000034	0	-584	-351					ATGTCTTTTCATCTTTGTATTTTTTCCACTGTCGATGTCTTGGTCGGGGTCGATTCGGATCTGCCATCTTTGTCACACATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA	ATGTCTTTTCATCTTTGTATTTTTTCCACTGTCGATGTCTTGGTCGGGGTCGATTCGGATCTGCCATCTTTGTCACACATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA			MSFHLCIFSTVDVLVGVDSDLPSLSHMARRFLFDWQPKRHPVMETTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*	MSFHLCIFSTVDVLVGVDSDLPSLSHMARRFLFDWQPKRHPVMETTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*			GTTGAATTCT	GACAAAACAA	0	A	0	0	0	0	0
960	700	an	AN8076.1	53.m03929	AO070330000034	0	-550	-248					ATGTCTTGGTCGGGGTCGATTCGGATCTGCCATCTTTGTCACACATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGAGACAAAACAATGCCAAGTCGAGTCCAAGCTGCATCGTTCATCAACTTTCAGCTCTTCCTGGGGTTTGAGGCGCCTCTGCAATTTCCTGATTTGGCTGGACTGA	ATGTCTTGGTCGGGGTCGATTCGGATCTGCCATCTTTGTCACACATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGAGACAAAACAATGCCAAGTCGAGTCCAAGCTGCATCGTTCATCAACTTTCAGCTCTTCCTGGGGTTTGAGGCGCCTCTGCAATTTCCTGATTTGGCTGGACTGA			MSWSGSIRICHLCHTWHVDSYLTGSRNAIPSWKRPSGGRDVYYSLTVPRPVLCASTTSSFSSRPSSETKQCQVESKLHRSSTFSSSWGLRRLCNFLIWLD*	MSWSGSIRICHLCHTWHVDSYLTGSRNAIPSWKRPSGGRDVYYSLTVPRPVLCASTTSSFSSRPSSETKQCQVESKLHRSSTFSSSWGLRRLCNFLIWLD*			TCCACTGTCG	TTAGATAATT	0	A	0	0	0	0	0
961	700	an	AN8076.1	53.m03929	AO070330000034	0	-506	-351					ATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA	ATGGCACGTCGATTCTTATTTGACTGGCAGCCGAAACGCCATCCCGTCATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA			MARRFLFDWQPKRHPVMETTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*	MARRFLFDWQPKRHPVMETTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*			TTTGTCACAC	GACAAAACAA	0	A	0	0	0	0	0
962	700	an	AN8076.1	53.m03929	AO070330000034	0	-458	-351					ATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA	ATGGAAACGACCGTCGGGTGGGAGAGACGTTTATTATTCTTTGACTGTTCCACGGCCAGTCCTATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA			METTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*	METTVGWERRLLFFDCSTASPMRFHNILIFLSSEL*			CCATCCCGTC	GACAAAACAA	0	A	0	0	0	0	0
963	700	an	AN8076.1	53.m03929	AO070330000034	0	-395	-351					ATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA	ATGCGCTTCCACAACATCCTCATTTTCCTCTCGTCCGAGCTCTGA			MRFHNILIFLSSEL*	MRFHNILIFLSSEL*			GGCCAGTCCT	GACAAAACAA	0	A	0	0	0	0	0
964	700	an	AN8076.1	53.m03929	AO070330000034	0	-341	-240					ATGCCAAGTCGAGTCCAAGCTGCATCGTTCATCAACTTTCAGCTCTTCCTGGGGTTTGAGGCGCCTCTGCAATTTCCTGATTTGGCTGGACTGATTAGATAA	ATGCCAAGTCGAGTCCAAGCTGCATCGTTCATCAACTTTCAGCTCTTCCTGGGGTTTGAGGCGCCTCTGCAATTTCCTGATTTGGCTGGACTGATTAGATAA			MPSRVQAASFINFQLFLGFEAPLQFPDLAGLIR*	MPSRVQAASFINFQLFLGFEAPLQFPDLAGLIR*			AGACAAAACA	TTTCGAACAT	0	A	0	0	0	0	0
965	700	an	AN8076.1	53.m03929	AO070330000034	0	-231	-151					ATGGCCCGTGCTTCTTTATTTCAAGATCACGTGTTCCCCACATCTTTTAGCCCTGCGCAGTGTTGGCGACCAGGCGCCTGA	ATGGCCCGTGCTTCTTTATTTCAAGATCACGTGTTCCCCACATCTTTTAGCCCTGCGCAGTGTTGGCGACCAGGCGCCTGA			MARASLFQDHVFPTSFSPAQCWRPGA*	MARASLFQDHVFPTSFSPAQCWRPGA*			AATTTCGAAC	CGCCCCTGCC	0	A	0	0	0	0	0
972	700	ao	AN8076.1	53.m03929	AO070330000034	0					-616	-587	ATGGTTTTTAATTTCTTTATTCTATTTTGA			ATGGTTTTTAATTTCTTTATTCTATTTTGA	MVFNFFILF*			MVFNFFILF*	GCGCACTGTT	TCTTTTCCCC	0	A	0	0	0	0	0
973	700	ao	AN8076.1	53.m03929	AO070330000034	0					-531	-502	ATGGAGATCACCATATGTGCACGTAAATAG			ATGGAGATCACCATATGTGCACGTAAATAG	MEITICARK*			MEITICARK*	GAATTTTGGG	CCACGCGGCT	0	A	0	0	0	0	0
974	700	ao	AN8076.1	53.m03929	AO070330000034	0					-517	-506	ATGTGCACGTAA			ATGTGCACGTAA	MCT*			MCT*	AGATCACCAT	ATAGCCACGC	0	A	0	0	0	0	0
975	700	ao	AN8076.1	53.m03929	AO070330000034	0					-488	-390	ATGATTTGGTGGTGGATCGCAGTACCAAGGGCATTTGCACGCATCCAATCCAGCGATTCCAGTTCCCAGGAAAAAATTTGGATACTCATGGCGTCCTGA			ATGATTTGGTGGTGGATCGCAGTACCAAGGGCATTTGCACGCATCCAATCCAGCGATTCCAGTTCCCAGGAAAAAATTTGGATACTCATGGCGTCCTGA	MIWWWIAVPRAFARIQSSDSSSQEKIWILMAS*			MIWWWIAVPRAFARIQSSDSSSQEKIWILMAS*	CGCGGCTGCG	CTCCTCGTTC	0	A	0	0	0	0	0
976	700	ao	AN8076.1	53.m03929	AO070330000034	0					-401	-390	ATGGCGTCCTGA			ATGGCGTCCTGA	MAS*			MAS*	TTGGATACTC	CTCCTCGTTC	0	A	0	0	0	0	0
980	710	af	AN3071.1	59.m08927	AO070337000003	0			-247	-155			ATGGGTAGCGACTCTCGGTGTTATCATTTCCCCCACAGGACTCCATTGGGAATATCTCTTCTGAACATTATTGTCTTGCACGCTGGAACTTAA		ATGGGTAGCGACTCTCGGTGTTATCATTTCCCCCACAGGACTCCATTGGGAATATCTCTTCTGAACATTATTGTCTTGCACGCTGGAACTTAA		MGSDSRCYHFPHRTPLGISLLNIIVLHAGT*		MGSDSRCYHFPHRTPLGISLLNIIVLHAGT*		ATTATCTTGC	ACCACACCCT	0	B	0	0	0	0	0
981	710	af	AN3071.1	59.m08927	AO070337000003	0			-100	-35			ATGGCTCAGCATCAGAGGAAGCGTCGCATACATACCGTTGCAACTGTCTCTTTCACACAGCCTTGA		ATGGCTCAGCATCAGAGGAAGCGTCGCATACATACCGTTGCAACTGTCTCTTTCACACAGCCTTGA		MAQHQRKRRIHTVATVSFTQP*		MAQHQRKRRIHTVATVSFTQP*		AGCTACGCAG	ACCTCAATAC	0	B	0	0	0	0	0
978	710	an	AN3071.1	59.m08927	AO070337000003	0	-130	-56					ATGGCCTCGCAGCGCGACTTCTTCCGACGCGTTCTCATCCCAGGCGCGAAACCTACCCTCCCCGAACACGCCTAA	ATGGCCTCGCAGCGCGACTTCTTCCGACGCGTTCTCATCCCAGGCGCGAAACCTACCCTCCCCGAACACGCCTAA			MASQRDFFRRVLIPGAKPTLPEHA*	MASQRDFFRRVLIPGAKPTLPEHA*			CCGATCGTCA	ACGCGTGGAT	0	B	0	0	0	0	0
982	710	ao	AN3071.1	59.m08927	AO070337000003	0					-117	-73	ATGGCCAGAGATACGCATCAAAAGCAGATATACACTTATAGCTAA			ATGGCCAGAGATACGCATCAAAAGCAGATATACACTTATAGCTAA	MARDTHQKQIYTYS*			MARDTHQKQIYTYS*	AACAACGCCA	CCGGACGGAG	0	B	0	0	0	0	0
985	715	af	AN4541.1	70.m15825	AO070321000164	0			-258	-196			ATGGCAAAGCAGATCAAACACCAACACTCTCCTCTATGGCTTAAGAATGAATCATGTGACTGA		ATGGCAAAGCAGATCAAACACCAACACTCTCCTCTATGGCTTAAGAATGAATCATGTGACTGA		MAKQIKHQHSPLWLKNESCD*		MAKQIKHQHSPLWLKNESCD*		GCTCCTGCAC	ACAGAAGGGT	0	R	0	0	0	0	0
986	715	af	AN4541.1	70.m15825	AO070321000164	0			-212	-132			ATGAATCATGTGACTGAACAGAAGGGTTCCATTACCAGATTCTCACCGCCAAAATATCCGCCAACCAGAATATGCCAATGA		ATGAATCATGTGACTGAACAGAAGGGTTCCATTACCAGATTCTCACCGCCAAAATATCCGCCAACCAGAATATGCCAATGA		MNHVTEQKGSITRFSPPKYPPTRICQ*		MNHVTEQKGSITRFSPPKYPPTRICQ*		TGGCTTAAGA	TCCTCCAAAA	0	R	0	0	0	0	0
983	715	an	AN4541.1	70.m15825	AO070321000164	0	-131	-63					ATGGATATACAAAATGCACGTGATCTGATTTTTCCAGCTCAACAGCACAACAAACTCCTCCGGCCTTGA	ATGGATATACAAAATGCACGTGATCTGATTTTTCCAGCTCAACAGCACAACAAACTCCTCCGGCCTTGA			MDIQNARDLIFPAQQHNKLLRP*	MDIQNARDLIFPAQQHNKLLRP*			GATTGGCGGG	TAATACTTTC	0	R	0	0	0	0	0
984	715	an	AN4541.1	70.m15825	AO070321000164	0	-118	-104					ATGCACGTGATCTGA	ATGCACGTGATCTGA			MHVI*	MHVI*			GATATACAAA	TTTTTCCAGC	0	R	0	0	0	0	0
987	715	ao	AN4541.1	70.m15825	AO070321000164	0					-300	-229	ATGTCTCGTGGACAAAAGTGCTGGGATGATCCCAAGATCAAGCAGGCGTTCGAGATCCAAACCGATCATTGA			ATGTCTCGTGGACAAAAGTGCTGGGATGATCCCAAGATCAAGCAGGCGTTCGAGATCCAAACCGATCATTGA	MSRGQKCWDDPKIKQAFEIQTDH*			MSRGQKCWDDPKIKQAFEIQTDH*	GATATGACCA	AACATGTGAC	0	R	0	0	0	0	0
988	715	ao	AN4541.1	70.m15825	AO070321000164	0					-275	-213	ATGATCCCAAGATCAAGCAGGCGTTCGAGATCCAAACCGATCATTGAAACATGTGACCCATGA			ATGATCCCAAGATCAAGCAGGCGTTCGAGATCCAAACCGATCATTGAAACATGTGACCCATGA	MIPRSSRRSRSKPIIETCDP*			MIPRSSRRSRSKPIIETCDP*	AAGTGCTGGG	CTTGCAGGCG	0	R	0	0	0	0	0
989	715	ao	AN4541.1	70.m15825	AO070321000164	0					-216	-145	ATGACTTGCAGGCGGAGTATTCTGCCGACACAAATGACGACCGCCTATCCCCAAACCAATCAGAAGATTTGA			ATGACTTGCAGGCGGAGTATTCTGCCGACACAAATGACGACCGCCTATCCCCAAACCAATCAGAAGATTTGA	MTCRRSILPTQMTTAYPQTNQKI*			MTCRRSILPTQMTTAYPQTNQKI*	CATGTGACCC	AGCATACAAC	0	R	0	0	0	0	0
990	715	ao	AN4541.1	70.m15825	AO070321000164	0					-183	-145	ATGACGACCGCCTATCCCCAAACCAATCAGAAGATTTGA			ATGACGACCGCCTATCCCCAAACCAATCAGAAGATTTGA	MTTAYPQTNQKI*			MTTAYPQTNQKI*	GCCGACACAA	AGCATACAAC	0	R	0	0	0	0	0
995	728	af	AN7366.1	55.m03188	AO070290000078	0			-226	-110			ATGACCCTGAAGAATGGCAATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAAGGGGGCATATATAG		ATGACCCTGAAGAATGGCAATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAAGGGGGCATATATAG		MTLKNGNGENNLQGMSYRPTRTTDPRFLAFCSTVRGHI*		MTLKNGNGENNLQGMSYRPTRTTDPRFLAFCSTVRGHI*		ATTGGCGGAG	ATCTTCAGGA	0		0	0	0	0	0
996	728	af	AN7366.1	55.m03188	AO070290000078	0			-213	-124			ATGGCAATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAA		ATGGCAATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAA		MAMEKTISRECLTVRPELQTPDSWRFAPP*		MAMEKTISRECLTVRPELQTPDSWRFAPP*		ACCCTGAAGA	GGGGGCATAT	0		0	0	0	0	0
997	728	af	AN7366.1	55.m03188	AO070290000078	0			-207	-124			ATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAA		ATGGAGAAAACAATCTCCAGGGAATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAA		MEKTISRECLTVRPELQTPDSWRFAPP*		MEKTISRECLTVRPELQTPDSWRFAPP*		AAGAATGGCA	GGGGGCATAT	0		0	0	0	0	0
998	728	af	AN7366.1	55.m03188	AO070290000078	0			-184	-110			ATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAAGGGGGCATATATAG		ATGTCTTACCGTCCGACCAGAACTACAGACCCCCGATTCTTGGCGTTTTGCTCCACCGTAAGGGGGCATATATAG		MSYRPTRTTDPRFLAFCSTVRGHI*		MSYRPTRTTDPRFLAFCSTVRGHI*		TCTCCAGGGA	ATCTTCAGGA	0		0	0	0	0	0
991	728	an	AN7366.1	55.m03188	AO070290000078	0	-183	-139					ATGTCCAGCCGCTCCTGTCTGGCCGAGAGATGCTGCCAAGCATAA	ATGTCCAGCCGCTCCTGTCTGGCCGAGAGATGCTGCCAAGCATAA			MSSRSCLAERCCQA*	MSSRSCLAERCCQA*			ATATGGCTTC	GGAAAAGCGT	0		0	0	0	0	0
992	728	an	AN7366.1	55.m03188	AO070290000078	0	-154	-104					ATGCTGCCAAGCATAAGGAAAAGCGTTCCCCAGACCCCTGTTTCAGGATGA	ATGCTGCCAAGCATAAGGAAAAGCGTTCCCCAGACCCCTGTTTCAGGATGA			MLPSIRKSVPQTPVSG*	MLPSIRKSVPQTPVSG*			TGGCCGAGAG	ATATTTATAT	0		0	0	0	0	0
993	728	an	AN7366.1	55.m03188	AO070290000078	0	-107	-33					ATGAATATTTATATAACTAATAAGCCCGCCAATGGAGGAAATCAAGCCATTCCCTTCTACATAGCTATTGAGTAG	ATGAATATTTATATAACTAATAAGCCCGCCAATGGAGGAAATCAAGCCATTCCCTTCTACATAGCTATTGAGTAG			MNIYITNKPANGGNQAIPFYIAIE*	MNIYITNKPANGGNQAIPFYIAIE*			CTGTTTCAGG	CTGCGTTTCC	0		0	0	0	0	0
994	728	an	AN7366.1	55.m03188	AO070290000078	0	-76	-44					ATGGAGGAAATCAAGCCATTCCCTTCTACATAG	ATGGAGGAAATCAAGCCATTCCCTTCTACATAG			MEEIKPFPST*	MEEIKPFPST*			AAGCCCGCCA	CTATTGAGTA	0		0	0	0	0	0
999	728	ao	AN7366.1	55.m03188	AO070290000078	0					-265	-230	ATGGCCCTATTCGTGTGCTTGATTGATGGAGAATAG			ATGGCCCTATTCGTGTGCTTGATTGATGGAGAATAG	MALFVCLIDGE*			MALFVCLIDGE*	TTCTGCAGGC	GACTTTAGAG	0		0	0	0	0	0
1000	728	ao	AN7366.1	55.m03188	AO070290000078	0					-240	-142	ATGGAGAATAGGACTTTAGAGCTGACTCTCCGACACTCCGCTTCTTTGCCTAGAAGCCGTTGTATCGGACAAATTGTGGATATTTTGACTAGTAGATAG			ATGGAGAATAGGACTTTAGAGCTGACTCTCCGACACTCCGCTTCTTTGCCTAGAAGCCGTTGTATCGGACAAATTGTGGATATTTTGACTAGTAGATAG	MENRTLELTLRHSASLPRSRCIGQIVDILTSR*			MENRTLELTLRHSASLPRSRCIGQIVDILTSR*	TGCTTGATTG	CCTCGAACGA	0		0	0	0	0	0
1001	728	ao	AN7366.1	55.m03188	AO070290000078	0					-115	-80	ATGCTCTCTACAGTCTTCGTATCGACATGTTTGTGA			ATGCTCTCTACAGTCTTCGTATCGACATGTTTGTGA	MLSTVFVSTCL*			MLSTVFVSTCL*	GAAAATATAA	TCAATTTTTC	0		0	0	0	0	0
1003	729	af	AN1633.1	58.m07728	AO070299000055	0			-145	-134			ATGACTTCGTAA		ATGACTTCGTAA		MTS*		MTS*		ACTGTCGCTG	CGACATTATC	0		0	0	0	0	0
1002	729	an	AN1633.1	58.m07728	AO070299000055	0	-107	-84					ATGCGATCACATTTCCACGCTTGA	ATGCGATCACATTTCCACGCTTGA			MRSHFHA*	MRSHFHA*			TATCCGTGCG	CCCTTGTCCC	0		0	0	0	0	0
1004	729	ao	AN1633.1	58.m07728	AO070299000055	0					-127	-116	ATGACGCTATAG			ATGACGCTATAG	MTL*			MTL*	CACATCTGGG	CTACTCAACT	0		0	0	0	0	0
1006	733	an	AN8291.1	65.m07469	AO070190000007	0	-235	-173					ATGTGGTTACGAGACACACATTCCACGCATGGGGTACAATTAACAAAGCCTCCTCAAGACTAA	ATGTGGTTACGAGACACACATTCCACGCATGGGGTACAATTAACAAAGCCTCCTCAAGACTAA			MWLRDTHSTHGVQLTKPPQD*	MWLRDTHSTHGVQLTKPPQD*			TTCAGACGCA	ATATTGCCTG	0	U	0	0	0	0	0

1022	740	af	AN8046.1	53.m04164	AO070336000153	0			-189	-178			ATGAATATTTGA		ATGAATATTTGA		MNI*		MNI*		ACAAGGCGCG	GAGTGGAGAG	0	I	0	0	0	YJR107W	0
1018	740	an	AN8046.1	53.m04164	AO070336000153	0	-217	-140					ATGTGCCTATGCGAGTACGTGGTGTCTTCTCGATTTTTGACTGGTCTGCCCTTTGACTGGAGACTGGAAGACGATTAG	ATGTGCCTATGCGAGTACGTGGTGTCTTCTCGATTTTTGACTGGTCTGCCCTTTGACTGGAGACTGGAAGACGATTAG			MCLCEYVVSSRFLTGLPFDWRLEDD*	MCLCEYVVSSRFLTGLPFDWRLEDD*			CAAGTGAGGA	TATATAAGTA	0	I	0	0	0	YJR107W	0
1019	740	an	AN8046.1	53.m04164	AO070336000153	0	-209	-162					ATGCGAGTACGTGGTGTCTTCTCGATTTTTGACTGGTCTGCCCTTTGA	ATGCGAGTACGTGGTGTCTTCTCGATTTTTGACTGGTCTGCCCTTTGA			MRVRGVFSIFDWSAL*	MRVRGVFSIFDWSAL*			GAATGTGCCT	CTGGAGACTG	0	I	0	0	0	YJR107W	0
1020	740	an	AN8046.1	53.m04164	AO070336000153	0	-124	-86					ATGTTCCTGATGATCAAACAAGAGGTTTCTGTGCCTTAG	ATGTTCCTGATGATCAAACAAGAGGTTTCTGTGCCTTAG			MFLMIKQEVSVP*	MFLMIKQEVSVP*			AAGTAGCAAA	TGCAGCGGCG	0	I	0	0	0	YJR107W	0
1021	740	an	AN8046.1	53.m04164	AO070336000153	0	-115	-86					ATGATCAAACAAGAGGTTTCTGTGCCTTAG	ATGATCAAACAAGAGGTTTCTGTGCCTTAG			MIKQEVSVP*	MIKQEVSVP*			AATGTTCCTG	TGCAGCGGCG	0	I	0	0	0	YJR107W	0
1024	745	af	AN6544.1	62.m03493	AO070270000040	0			-268	-188			ATGCCTCGCTGCACAGCAGTATTCGCACAAGCTTATCCCGGGAATACAGACGTGATTGTTTTAAACGTCCCGGCCACATAA		ATGCCTCGCTGCACAGCAGTATTCGCACAAGCTTATCCCGGGAATACAGACGTGATTGTTTTAAACGTCCCGGCCACATAA		MPRCTAVFAQAYPGNTDVIVLNVPAT*		MPRCTAVFAQAYPGNTDVIVLNVPAT*		AGCCGCCCAC	CCAAGTCAAA	0	S	0	MG03971.1	0	0	0
1025	745	af	AN6544.1	62.m03493	AO070270000040	0			-174	-88			ATGGAAGGGTATCCAAACGCTACACTATATGTCGGATATTGTGAATCTCCGAGCTCCGGGCACCGCCTGCATCATGACCCCAGATAG		ATGGAAGGGTATCCAAACGCTACACTATATGTCGGATATTGTGAATCTCCGAGCTCCGGGCACCGCCTGCATCATGACCCCAGATAG		MEGYPNATLYVGYCESPSSGHRLHHDPR*		MEGYPNATLYVGYCESPSSGHRLHHDPR*		AGTCAAAAAT	CTGCGTATGC	0	S	0	MG03971.1	0	0	0
1026	745	af	AN6544.1	62.m03493	AO070270000040	0			-81	-19			ATGCGGATGTCGATCGAGCGAACATACTTTTGTCATAGCACAGCTACTTTATACGGCATCTGA		ATGCGGATGTCGATCGAGCGAACATACTTTTGTCATAGCACAGCTACTTTATACGGCATCTGA		MRMSIERTYFCHSTATLYGI*		MRMSIERTYFCHSTATLYGI*		ATAGCTGCGT	CCCCAAAAAA	0	S	0	MG03971.1	0	0	0
1027	745	af	AN6544.1	62.m03493	AO070270000040	0			-75	-19			ATGTCGATCGAGCGAACATACTTTTGTCATAGCACAGCTACTTTATACGGCATCTGA		ATGTCGATCGAGCGAACATACTTTTGTCATAGCACAGCTACTTTATACGGCATCTGA		MSIERTYFCHSTATLYGI*		MSIERTYFCHSTATLYGI*		GCGTATGCGG	CCCCAAAAAA	0	S	0	MG03971.1	0	0	0
1023	745	an	AN6544.1	62.m03493	AO070270000040	0	-153	-73					ATGAGATTTTCCGAACCGAATAGCTGCACCCGTCATCCGGCCTCCAAGTCGAATCAAGCATATAGTCGACGACGATCGTGA	ATGAGATTTTCCGAACCGAATAGCTGCACCCGTCATCCGGCCTCCAAGTCGAATCAAGCATATAGTCGACGACGATCGTGA			MRFSEPNSCTRHPASKSNQAYSRRRS*	MRFSEPNSCTRHPASKSNQAYSRRRS*			ATACTCCGGA	ACATTACCGG	0	S	0	MG03971.1	0	0	0
1028	745	ao	AN6544.1	62.m03493	AO070270000040	0					-238	-170	ATGACATATGAGTATTCGGACTCTATAGACATCAAGAAAGTCATACGGGAGTACATTACATGGTTTTAG			ATGACATATGAGTATTCGGACTCTATAGACATCAAGAAAGTCATACGGGAGTACATTACATGGTTTTAG	MTYEYSDSIDIKKVIREYITWF*			MTYEYSDSIDIKKVIREYITWF*	CAAAGCCACC	CAAGATAGGC	0	S	0	MG03971.1	0	0	0
1029	745	ao	AN6544.1	62.m03493	AO070270000040	0					-231	-211	ATGAGTATTCGGACTCTATAG			ATGAGTATTCGGACTCTATAG	MSIRTL*			MSIRTL*	ACCATGACAT	ACATCAAGAA	0	S	0	MG03971.1	0	0	0
1030	745	ao	AN6544.1	62.m03493	AO070270000040	0					-179	-162	ATGGTTTTAGCAAGATAG			ATGGTTTTAGCAAGATAG	MVLAR*			MVLAR*	AGTACATTAC	GCTATGACGG	0	S	0	MG03971.1	0	0	0
1031	745	ao	AN6544.1	62.m03493	AO070270000040	0					-158	-138	ATGACGGTATCGGCTTTGTGA			ATGACGGTATCGGCTTTGTGA	MTVSAL*			MTVSAL*	AAGATAGGCT	TTTTCCGACC	0	S	0	MG03971.1	0	0	0
1034	746	af	AN8804.1	71.m15611	AO070276000054	0			-183	-166			ATGCCTCAGAGGGCGTAG		ATGCCTCAGAGGGCGTAG		MPQRA*		MPQRA*		CCTTGCATTG	ATGCACTAGT	0		FG06662.1	0	0	0	0
1035	746	af	AN8804.1	71.m15611	AO070276000054	0			-149	-132			ATGGCTAGCTATCGATGA		ATGGCTAGCTATCGATGA		MASYR*		MASYR*		TAGTCCCTAT	TGATTGTTGG	0		FG06662.1	0	0	0	0
1036	746	af	AN8804.1	71.m15611	AO070276000054	0			-135	-91			ATGATGATTGTTGGAGTTAAATCATCCGCAGCGGAATCTCTGTAA		ATGATGATTGTTGGAGTTAAATCATCCGCAGCGGAATCTCTGTAA		MMIVGVKSSAAESL*		MMIVGVKSSAAESL*		CTAGCTATCG	TGCGCAAGTA	0		FG06662.1	0	0	0	0
1037	746	af	AN8804.1	71.m15611	AO070276000054	0			-132	-91			ATGATTGTTGGAGTTAAATCATCCGCAGCGGAATCTCTGTAA		ATGATTGTTGGAGTTAAATCATCCGCAGCGGAATCTCTGTAA		MIVGVKSSAAESL*		MIVGVKSSAAESL*		GCTATCGATG	TGCGCAAGTA	0		FG06662.1	0	0	0	0
1038	746	af	AN8804.1	71.m15611	AO070276000054	0			-91	-80			ATGCGCAAGTAA		ATGCGCAAGTAA		MRK*		MRK*		AATCTCTGTA	TTCTCCTACG	0		FG06662.1	0	0	0	0
1032	746	an	AN8804.1	71.m15611	AO070276000054	0	-217	-206					ATGCATCAATAA	ATGCATCAATAA			MHQ*	MHQ*			CTCTTTAGGC	GGGTTGAGTT	0		FG06662.1	0	0	0	0
1033	746	an	AN8804.1	71.m15611	AO070276000054	0	-143	-114					ATGTTCACTAAGCGCACAATTTGTCATTAG	ATGTTCACTAAGCGCACAATTTGTCATTAG			MFTKRTICH*	MFTKRTICH*			GTTGCTGTTC	TAATCCCCCG	0		FG06662.1	0	0	0	0
1039	746	ao	AN8804.1	71.m15611	AO070276000054	0					-185	-24	ATGATGTTCATATTCGATACGATATACTGGGGAAGAAGGATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG			ATGATGTTCATATTCGATACGATATACTGGGGAAGAAGGATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG	MMFIFDTIYWGRRMASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*			MMFIFDTIYWGRRMASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*	TATTATGATC	GGAACAAGAA	0		FG06662.1	0	0	0	0
1040	746	ao	AN8804.1	71.m15611	AO070276000054	0					-182	-24	ATGTTCATATTCGATACGATATACTGGGGAAGAAGGATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG			ATGTTCATATTCGATACGATATACTGGGGAAGAAGGATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG	MFIFDTIYWGRRMASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*			MFIFDTIYWGRRMASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*	TATGATCATG	GGAACAAGAA	0		FG06662.1	0	0	0	0
1041	746	ao	AN8804.1	71.m15611	AO070276000054	0					-146	-24	ATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG			ATGGCTAGTCCCGATATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG	MASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*			MASPDMVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*	GGGAAGAAGG	GGAACAAGAA	0		FG06662.1	0	0	0	0
1042	746	ao	AN8804.1	71.m15611	AO070276000054	0					-131	-24	ATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG			ATGGTTAGCGTCGTCGCGATACGGCGTCGGCATAATTCAATTCAATCACTCACACTCAACCCGCAGTATCTCTGCACTTCAGCCACAGCTCTGACGCGCCCTTTCTAG	MVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*			MVSVVAIRRRHNSIQSLTLNPQYLCTSATALTRPF*	TAGTCCCGAT	GGAACAAGAA	0		FG06662.1	0	0	0	0
1043	747	an	AN8246.1	53.m04204	AO070310000061	0	-189	-175					ATGGTGCAGCCTTGA	ATGGTGCAGCCTTGA			MVQP*	MVQP*			AATTGCAAAG	ACTTTTTCTG	0	U	FG08964.1	MG05977.1	NCU09696.1	YPR088C	0
1044	747	ao	AN8246.1	53.m04204	AO070310000061	0					-251	-177	ATGGTCTTTTTTTTTTCTTGTAAGTCTCGAATACATTCAAAGGCGGAAGAAACAATGATGTCTCTGATTGGCTGA			ATGGTCTTTTTTTTTTCTTGTAAGTCTCGAATACATTCAAAGGCGGAAGAAACAATGATGTCTCTGATTGGCTGA	MVFFFSCKSRIHSKAEETMMSLIG*			MVFFFSCKSRIHSKAEETMMSLIG*	TAGGAATTGC	CCGCCCGCTC	0	U	FG08964.1	MG05977.1	NCU09696.1	YPR088C	0
1045	747	ao	AN8246.1	53.m04204	AO070310000061	0					-197	-177	ATGATGTCTCTGATTGGCTGA			ATGATGTCTCTGATTGGCTGA	MMSLIG*			MMSLIG*	GGAAGAAACA	CCGCCCGCTC	0	U	FG08964.1	MG05977.1	NCU09696.1	YPR088C	0
1046	747	ao	AN8246.1	53.m04204	AO070310000061	0					-194	-177	ATGTCTCTGATTGGCTGA			ATGTCTCTGATTGGCTGA	MSLIG*			MSLIG*	AGAAACAATG	CCGCCCGCTC	0	U	FG08964.1	MG05977.1	NCU09696.1	YPR088C	0
1047	747	ao	AN8246.1	53.m04204	AO070310000061	0					-147	-79	ATGATTGAGATTGGTGGCCTCTCCGACATTCTACCTGTCGATCAAGCATTGCCATTATTCGGTTTCTGA			ATGATTGAGATTGGTGGCCTCTCCGACATTCTACCTGTCGATCAAGCATTGCCATTATTCGGTTTCTGA	MIEIGGLSDILPVDQALPLFGF*			MIEIGGLSDILPVDQALPLFGF*	CGCACTGGAA	TCACCTAACT	0	U	FG08964.1	MG05977.1	NCU09696.1	YPR088C	0
1048	749	an	AN0365.1	54.m06384	AO070318000045	0	-170	-132					ATGTTGACGTCTTCGCACATAACCTCCGTTTCCATCTGA	ATGTTGACGTCTTCGCACATAACCTCCGTTTCCATCTGA			MLTSSHITSVSI*	MLTSSHITSVSI*			CCCCTGGCAT	GGGTCTAGCG	0		0	0	0	0	0
1049	755	af	AN6505.1	62.m03092	AO070222000021	0			-207	-193			ATGCGACAGGTTTGA		ATGCGACAGGTTTGA		MRQV*		MRQV*		TCGCGCTGTG	CCTGCGTTTC	0	R	0	0	0	0	0
1050	755	ao	AN6505.1	62.m03092	AO070222000021	0					-199	-185	ATGCGGCTGCATTGA			ATGCGGCTGCATTGA	MRLH*			MRLH*	GCGCGCTGTG	CTTTCTACCA	0	R	0	0	0	0	0
1052	759	af	AN1712.1	58.m07778	AO070305000028	0			-259	-119			ATGAATACTAGAAGGATCCGAATCCCTGCAAAGCCCACTGTACTAGCAAAAACCACCGGGTCAATCACCAACCGAAGCCTTGGAGCCATGAAAAGACCATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAG		ATGAATACTAGAAGGATCCGAATCCCTGCAAAGCCCACTGTACTAGCAAAAACCACCGGGTCAATCACCAACCGAAGCCTTGGAGCCATGAAAAGACCATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAG		MNTRRIRIPAKPTVLAKTTGSITNRSLGAMKRPCTNVSDSPCPSQH*		MNTRRIRIPAKPTVLAKTTGSITNRSLGAMKRPCTNVSDSPCPSQH*		GAAGGCGGTA	CCACAACTAT	0		0	0	0	0	0
1053	759	af	AN1712.1	58.m07778	AO070305000028	0			-172	-119			ATGAAAAGACCATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAG		ATGAAAAGACCATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAG		MKRPCTNVSDSPCPSQH*		MKRPCTNVSDSPCPSQH*		CCTTGGAGCC	CCACAACTAT	0		0	0	0	0	0
1054	759	af	AN1712.1	58.m07778	AO070305000028	0			-161	-45			ATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAGCCACAACTATATATATCAGCGTCTTCATCTTGACAACCCAACGGCTACAGATTGCCACAGCTAGTACTCATTAG		ATGCACGAATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAGCCACAACTATATATATCAGCGTCTTCATCTTGACAACCCAACGGCTACAGATTGCCACAGCTAGTACTCATTAG		MHECFRLALSLPTLATTIYISVFILTTQRLQIATASTH*		MHECFRLALSLPTLATTIYISVFILTTQRLQIATASTH*		TGAAAAGACC	CAAGGGCAGG	0		0	0	0	0	0
1055	759	af	AN1712.1	58.m07778	AO070305000028	0			-153	-55			ATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAGCCACAACTATATATATCAGCGTCTTCATCTTGACAACCCAACGGCTACAGATTGCCACAGCTAG		ATGTTTCCGACTCGCCTTGTCCCTCCCAACATTAGCCACAACTATATATATCAGCGTCTTCATCTTGACAACCCAACGGCTACAGATTGCCACAGCTAG		MFPTRLVPPNISHNYIYQRLHLDNPTATDCHS*		MFPTRLVPPNISHNYIYQRLHLDNPTATDCHS*		CCATGCACGA	TACTCATTAG	0		0	0	0	0	0
1056	759	ao	AN1712.1	58.m07778	AO070305000028	0					-242	-213	ATGATCTGGGCTCGTTGTCCAGGGTTGTAG			ATGATCTGGGCTCGTTGTCCAGGGTTGTAG	MIWARCPGL*			MIWARCPGL*	ATAATCGGTA	GGCTGGAAGC	0		0	0	0	0	0
1064	762	af	AN4036.1	54.m06576	AO070328000140	0			-207	-160			ATGACAATGTTTCGTTTCCAATTCAGGAGGCTCATCTTTACTGCGTAA		ATGACAATGTTTCGTTTCCAATTCAGGAGGCTCATCTTTACTGCGTAA		MTMFRFQFRRLIFTA*		MTMFRFQFRRLIFTA*		ATCCTCGCTT	TACCCAGCCT	0	T	0	0	0	0	0
1065	762	af	AN4036.1	54.m06576	AO070328000140	0			-201	-160			ATGTTTCGTTTCCAATTCAGGAGGCTCATCTTTACTGCGTAA		ATGTTTCGTTTCCAATTCAGGAGGCTCATCTTTACTGCGTAA		MFRFQFRRLIFTA*		MFRFQFRRLIFTA*		GCTTATGACA	TACCCAGCCT	0	T	0	0	0	0	0
1060	762	an	AN4036.1	54.m06576	AO070328000140	0	-232	-176					ATGATTCCAACTTTTCTTGTCTTCACTCGTCTTCTAGAAATTAATGTTACATTGTGA	ATGATTCCAACTTTTCTTGTCTTCACTCGTCTTCTAGAAATTAATGTTACATTGTGA			MIPTFLVFTRLLEINVTL*	MIPTFLVFTRLLEINVTL*			CGTTTTTGAC	GCCCTTGGAT	0	T	0	0	0	0	0
1061	762	an	AN4036.1	54.m06576	AO070328000140	0	-189	-151					ATGTTACATTGTGAGCCCTTGGATGAAAGCGACATCTGA	ATGTTACATTGTGAGCCCTTGGATGAAAGCGACATCTGA			MLHCEPLDESDI*	MLHCEPLDESDI*			CTAGAAATTA	ATAGCTAGGA	0	T	0	0	0	0	0
1062	762	an	AN4036.1	54.m06576	AO070328000140	0	-167	-147					ATGAAAGCGACATCTGAATAG	ATGAAAGCGACATCTGAATAG			MKATSE*	MKATSE*			GAGCCCTTGG	CTAGGATAGT	0	T	0	0	0	0	0
1067	762	ao	AN4036.1	54.m06576	AO070328000140	0					-266	-249	ATGCCAATCCTCTCCTGA			ATGCCAATCCTCTCCTGA	MPILS*			MPILS*	CCGCGCTAAA	TGCCCGCTGT	0	T	0	0	0	0	0
1068	762	ao	AN4036.1	54.m06576	AO070328000140	0					-249	-208	ATGCCCGCTGTCAACTATCAACCCAATTCCGCATCGGTCTGA			ATGCCCGCTGTCAACTATCAACCCAATTCCGCATCGGTCTGA	MPAVNYQPNSASV*			MPAVNYQPNSASV*	TCCTCTCCTG	CTTGGCACGT	0	T	0	0	0	0	0
1069	762	ao	AN4036.1	54.m06576	AO070328000140	0					-139	-110	ATGGCCAGCCTAGCAGACGAAAAATACTGA			ATGGCCAGCCTAGCAGACGAAAAATACTGA	MASLADEKY*			MASLADEKY*	TTTATCATCC	TAAATCCTAA	0	T	0	0	0	0	0
1076	775	af	AN7772.1	71.m15807	AO070286000021	0			-201	-187			ATGATTGAATCATAA		ATGATTGAATCATAA		MIES*		MIES*		ATCGTCTAGC	TCATACTAGG	0	Q	0	0	0	0	0
1077	775	af	AN7772.1	71.m15807	AO070286000021	0			-72	-43			ATGAGTGATTACGGAGTAGGATCCAGATAA		ATGAGTGATTACGGAGTAGGATCCAGATAA		MSDYGVGSR*		MSDYGVGSR*		TATATATTCC	ACAATCAAAA	0	Q	0	0	0	0	0
1074	775	an	AN7772.1	71.m15807	AO070286000021	0	-196	-167					ATGTTTTACTCCGCATCCCGATCGTTATGA	ATGTTTTACTCCGCATCCCGATCGTTATGA			MFYSASRSL*	MFYSASRSL*			AAGCTTTTAT	TCTCCGCAGT	0	Q	0	0	0	0	0
1075	775	an	AN7772.1	71.m15807	AO070286000021	0	-170	-108					ATGATCTCCGCAGTGGCGGTGGGGGCGGGGTTGATCTGCATCCGCTTACTCCGGCAACGCTGA	ATGATCTCCGCAGTGGCGGTGGGGGCGGGGTTGATCTGCATCCGCTTACTCCGGCAACGCTGA			MISAVAVGAGLICIRLLRQR*	MISAVAVGAGLICIRLLRQR*			CCCGATCGTT	CAGTATCAGA	0	Q	0	0	0	0	0
1078	775	ao	AN7772.1	71.m15807	AO070286000021	0					-268	-257	ATGAGATACTAG			ATGAGATACTAG	MRY*			MRY*	TAATATCACC	ACTCCAATAA	0	Q	0	0	0	0	0
1079	775	ao	AN7772.1	71.m15807	AO070286000021	0					-152	-78	ATGATCAAACCCATCCCCGGAACCAATAAACAAGCACACACCTGCATCCGGCCGATCTATATAACGCATGCGTAA			ATGATCAAACCCATCCCCGGAACCAATAAACAAGCACACACCTGCATCCGGCCGATCTATATAACGCATGCGTAA	MIKPIPGTNKQAHTCIRPIYITHA*			MIKPIPGTNKQAHTCIRPIYITHA*	AGAAGACCTG	GCCCATCTTG	0	Q	0	0	0	0	0
1080	779	af	AN3926.1	69.m15002	AO070341000040	0			-198	-142			ATGCAGAGCGCCGTCCTTCTTGCCAACGTCGACATTATTTGTATGCCTGGAAATTGA		ATGCAGAGCGCCGTCCTTCTTGCCAACGTCGACATTATTTGTATGCCTGGAAATTGA		MQSAVLLANVDIICMPGN*		MQSAVLLANVDIICMPGN*		CAGTAGATAG	GGACAACAAT	0	R	0	0	0	0	0
1081	779	af	AN3926.1	69.m15002	AO070341000040	0			-156	-142			ATGCCTGGAAATTGA		ATGCCTGGAAATTGA		MPGN*		MPGN*		CATTATTTGT	GGACAACAAT	0	R	0	0	0	0	0
1082	779	af	AN3926.1	69.m15002	AO070341000040	0			-133	-38			ATGAAGTCACGTCTTCACCGCCTCAGGCCGCAAGGCGTCATTGGCCCGCGTGATTTTCATTATCGCGGCGTTGTTATCACAAGTCTCTGCCATTGA		ATGAAGTCACGTCTTCACCGCCTCAGGCCGCAAGGCGTCATTGGCCCGCGTGATTTTCATTATCGCGGCGTTGTTATCACAAGTCTCTGCCATTGA		MKSRLHRLRPQGVIGPRDFHYRGVVITSLCH*		MKSRLHRLRPQGVIGPRDFHYRGVVITSLCH*		GAGGACAACA	AGATTCACAT	0	R	0	0	0	0	0
1083	779	ao	AN3926.1	69.m15002	AO070341000040	0					-294	-283	ATGAATTATTAA			ATGAATTATTAA	MNY*			MNY*	AATGATATCT	AATTAGGTAG	0	R	0	0	0	0	0
1084	779	ao	AN3926.1	69.m15002	AO070341000040	0					-213	-193	ATGAGCTTGAACATCGAATAA			ATGAGCTTGAACATCGAATAA	MSLNIE*			MSLNIE*	AAGTGCTTTC	CTTTTGTTGG	0	R	0	0	0	0	0

1087	782	af	AN8862.1	71.m16000	AO070271000009	0			-101	-63			ATGCCTCTCCCAGAACCTTGTATCATCTCCGACTCATAG		ATGCCTCTCCCAGAACCTTGTATCATCTCCGACTCATAG		MPLPEPCIISDS*		MPLPEPCIISDS*		TTCTCACTAG	CCCACCGATC	0	Z	0	0	0	YOR326W	0
1085	782	an	AN8862.1	71.m16000	AO070271000009	0	-199	-161					ATGGGAGCTCTTTTCTCAGAATCAGCAACTTCTTACTAG	ATGGGAGCTCTTTTCTCAGAATCAGCAACTTCTTACTAG			MGALFSESATSY*	MGALFSESATSY*			TCAGTGAAGC	TGCCCTGGAA	0	Z	0	0	0	YOR326W	0
1086	782	an	AN8862.1	71.m16000	AO070271000009	0	-76	-62					ATGCCTTTGACTTGA	ATGCCTTTGACTTGA			MPLT*	MPLT*			ACTTTTTTAA	GCAACGAACA	0	Z	0	0	0	YOR326W	0
1088	782	ao	AN8862.1	71.m16000	AO070271000009	0					-118	-104	ATGATTCGCTGCTAG			ATGATTCGCTGCTAG	MIRC*			MIRC*	TATCCAATTA	ATGCCTACAG	0	Z	0	0	0	YOR326W	0
1089	782	ao	AN8862.1	71.m16000	AO070271000009	0					-103	-59	ATGCCTACAGCAGTGCTCGCTCGGTGTCATATACATTCCGCATAG			ATGCCTACAGCAGTGCTCGCTCGGTGTCATATACATTCCGCATAG	MPTAVLARCHIHSA*			MPTAVLARCHIHSA*	TCGCTGCTAG	GTTCTGGTTC	0	Z	0	0	0	YOR326W	0
1090	784	an	AN4520.1	57.m05608	AO070321000126	0	-196	-149					ATGTCTATCACTTATCATTGTTGTACTCAGTACTGTATAGGCAGCTAG	ATGTCTATCACTTATCATTGTTGTACTCAGTACTGTATAGGCAGCTAG			MSITYHCCTQYCIGS*	MSITYHCCTQYCIGS*			GGGTGAGGCG	GTGAGGCAGC	0	T	0	0	0	0	0
1091	784	ao	AN4520.1	57.m05608	AO070321000126	0					-258	-247	ATGAAAATTTGA			ATGAAAATTTGA	MKI*			MKI*	GCATTAAGTC	ATACTATTAA	0	T	0	0	0	0	0
1092	784	ao	AN4520.1	57.m05608	AO070321000126	0					-234	-175	ATGACCGTAGCTGTGGTCCTAAGATATACAACCAGTAGTCTTACTAGGCGGCAGAGCTGA			ATGACCGTAGCTGTGGTCCTAAGATATACAACCAGTAGTCTTACTAGGCGGCAGAGCTGA	MTVAVVLRYTTSSLTRRQS*			MTVAVVLRYTTSSLTRRQS*	ACTATTAAGA	TAAGGCGGAA	0	T	0	0	0	0	0
1095	785	af	AN5760.1	69.m14838	AO070193000006	0			-120	-55			ATGACAACAATGAAGCGCAATTCAGAGCGACGGACTCAACGAACTCACGCCTTCGCTTATTCTTAG		ATGACAACAATGAAGCGCAATTCAGAGCGACGGACTCAACGAACTCACGCCTTCGCTTATTCTTAG		MTTMKRNSERRTQRTHAFAYS*		MTTMKRNSERRTQRTHAFAYS*		CAACAGAATA	TTTTACGCTT	0	O	0	0	0	0	0
1096	785	af	AN5760.1	69.m14838	AO070193000006	0			-111	-55			ATGAAGCGCAATTCAGAGCGACGGACTCAACGAACTCACGCCTTCGCTTATTCTTAG		ATGAAGCGCAATTCAGAGCGACGGACTCAACGAACTCACGCCTTCGCTTATTCTTAG		MKRNSERRTQRTHAFAYS*		MKRNSERRTQRTHAFAYS*		AATGACAACA	TTTTACGCTT	0	O	0	0	0	0	0
1093	785	an	AN5760.1	69.m14838	AO070193000006	0	-159	-100					ATGGATCATCATTATTCTTCCTCCACCAAGAAAAGCAAGAGAGTCATGAAAGTTCTTTAA	ATGGATCATCATTATTCTTCCTCCACCAAGAAAAGCAAGAGAGTCATGAAAGTTCTTTAA			MDHHYSSSTKKSKRVMKVL*	MDHHYSSSTKKSKRVMKVL*			AGCTACCTAC	CAACCGTGGG	0	O	0	0	0	0	0
1094	785	an	AN5760.1	69.m14838	AO070193000006	0	-114	-100					ATGAAAGTTCTTTAA	ATGAAAGTTCTTTAA			MKVL*	MKVL*			CAAGAGAGTC	CAACCGTGGG	0	O	0	0	0	0	0
1097	785	ao	AN5760.1	69.m14838	AO070193000006	0					-263	-189	ATGATTAAACCGGAGTTATTTATTATTAACCTAATTTTCTCTCCCTTTCGAACCAAGCAAATCGTGTGGGGTTAA			ATGATTAAACCGGAGTTATTTATTATTAACCTAATTTTCTCTCCCTTTCGAACCAAGCAAATCGTGTGGGGTTAA	MIKPELFIINLIFSPFRTKQIVWG*			MIKPELFIINLIFSPFRTKQIVWG*	TAAAGCTGCT	TTGGGCGGCA	0	O	0	0	0	0	0
1098	785	ao	AN5760.1	69.m14838	AO070193000006	0					-147	-130	ATGAGAAATCGAGATTAA			ATGAGAAATCGAGATTAA	MRNRD*			MRNRD*	CGCCCACCAA	GAAGATGACT	0	O	0	0	0	0	0
1099	785	ao	AN5760.1	69.m14838	AO070193000006	0					-125	-102	ATGACTGATGGCAGGATAACTTGA			ATGACTGATGGCAGGATAACTTGA	MTDGRIT*			MTDGRIT*	GATTAAGAAG	CAAAGTATCT	0	O	0	0	0	0	0
1100	785	ao	AN5760.1	69.m14838	AO070193000006	0					-118	-107	ATGGCAGGATAA			ATGGCAGGATAA	MAG*			MAG*	AAGATGACTG	CTTGACAAAG	0	O	0	0	0	0	0
1108	789	af	AN4501.1	57.m05629	AO070311000054	0			-642	-397			ATGTTTCCCCTCCTTTTCTCCCTGAGCCACTGCTTCCCAAATGATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAATCGCCGGATCAGATCTTGTTTTGACAACCGCTTCACACCCCTCCCATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGA		ATGTTTCCCCTCCTTTTCTCCCTGAGCCACTGCTTCCCAAATGATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAATCGCCGGATCAGATCTTGTTTTGACAACCGCTTCACACCCCTCCCATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGA		MFPLLFSLSHCFPNDGQPHHHHIATLPLLLQAAQKSRLGVQGWNLWPFNRQNCVIAGSDLVLTTASHPSHVCRNGTFQQRI*		MFPLLFSLSHCFPNDGQPHHHHIATLPLLLQAAQKSRLGVQGWNLWPFNRQNCVIAGSDLVLTTASHPSHVCRNGTFQQRI*		TTTCTTCTGC	ACGGATCTCC	0	O	0	0	0	0	0
1109	789	af	AN4501.1	57.m05629	AO070311000054	0			-602	-480			ATGATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAA		ATGATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAA		MMVNLIITTLQPYRYSCKPHKNLVWACRDGICGHSIAKTV*		MMVNLIITTLQPYRYSCKPHKNLVWACRDGICGHSIAKTV*		TGCTTCCCAA	TCGCCGGATC	0	O	0	0	0	0	0
1110	789	af	AN4501.1	57.m05629	AO070311000054	0			-599	-480			ATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAA		ATGGTCAACCTCATCATCACCACATTGCAACCTTACCGTTACTCTTGCAAGCCGCACAAAAATCTCGTCTGGGCGTGCAGGGATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAA		MVNLIITTLQPYRYSCKPHKNLVWACRDGICGHSIAKTV*		MVNLIITTLQPYRYSCKPHKNLVWACRDGICGHSIAKTV*		TTCCCAAATG	TCGCCGGATC	0	O	0	0	0	0	0
1111	789	af	AN4501.1	57.m05629	AO070311000054	0			-517	-383			ATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAATCGCCGGATCAGATCTTGTTTTGACAACCGCTTCACACCCCTCCCATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAA		ATGGAATTTGTGGCCATTCAATCGCCAAAACTGTGTAATCGCCGGATCAGATCTTGTTTTGACAACCGCTTCACACCCCTCCCATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAA		MEFVAIQSPKLCNRRIRSCFDNRFTPLPCLSEWDLPTTHMNGSP*		MEFVAIQSPKLCNRRIRSCFDNRFTPLPCLSEWDLPTTHMNGSP*		GCGTGCAGGG	GGGAGGCAGC	0	O	0	0	0	0	0
1112	789	af	AN4501.1	57.m05629	AO070311000054	0			-434	-318			ATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAAGGGAGGCAGCGCTAGCGCAGCCCAGAATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		ATGTCTGTCGGAATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAAGGGAGGCAGCGCTAGCGCAGCCCAGAATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		MSVGMGPSNNAYERISLREAALAQPRMSTIFHDFFQLP*		MSVGMGPSNNAYERISLREAALAQPRMSTIFHDFFQLP*		CACCCCTCCC	TTCCATAATC	0	O	0	0	0	0	0
1113	789	af	AN4501.1	57.m05629	AO070311000054	0			-422	-318			ATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAAGGGAGGCAGCGCTAGCGCAGCCCAGAATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		ATGGGACCTTCCAACAACGCATATGAACGGATCTCCTTAAGGGAGGCAGCGCTAGCGCAGCCCAGAATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		MGPSNNAYERISLREAALAQPRMSTIFHDFFQLP*		MGPSNNAYERISLREAALAQPRMSTIFHDFFQLP*		GTCTGTCGGA	TTCCATAATC	0	O	0	0	0	0	0
1114	789	af	AN4501.1	57.m05629	AO070311000054	0			-400	-383			ATGAACGGATCTCCTTAA		ATGAACGGATCTCCTTAA		MNGSP*		MNGSP*		AACAACGCAT	GGGAGGCAGC	0	O	0	0	0	0	0
1115	789	af	AN4501.1	57.m05629	AO070311000054	0			-356	-318			ATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		ATGTCAACAATATTCCATGACTTCTTCCAGCTGCCTTGA		MSTIFHDFFQLP*		MSTIFHDFFQLP*		GCAGCCCAGA	TTCCATAATC	0	O	0	0	0	0	0
1116	789	af	AN4501.1	57.m05629	AO070311000054	0			-340	-161			ATGACTTCTTCCAGCTGCCTTGATTCCATAATCTTGAAAAAATCGGCTGCAAAACACGATATTTTTGCCCAGGCTGTATCGAATGGGAGCCTCAAGATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGA		ATGACTTCTTCCAGCTGCCTTGATTCCATAATCTTGAAAAAATCGGCTGCAAAACACGATATTTTTGCCCAGGCTGTATCGAATGGGAGCCTCAAGATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGA		MTSSSCLDSIILKKSAAKHDIFAQAVSNGSLKMGEFVEGYCTRRPSNHQRDFAASLATL*		MTSSSCLDSIILKKSAAKHDIFAQAVSNGSLKMGEFVEGYCTRRPSNHQRDFAASLATL*		ACAATATTCC	CTGCCGTCAT	0	O	0	0	0	0	0
1117	789	af	AN4501.1	57.m05629	AO070311000054	0			-258	-31			ATGGGAGCCTCAAGATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGACTGCCGTCATATTGCCCCTCGCCCTTTTTTACACGATCAGTATCGCACGGCTCCCCGGACATCCCTCACAACCAGACGAGATTGCTTCTTGACCATTCATTTTGTTCATACTGATAAAAGCTGTTGCTAA		ATGGGAGCCTCAAGATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGACTGCCGTCATATTGCCCCTCGCCCTTTTTTACACGATCAGTATCGCACGGCTCCCCGGACATCCCTCACAACCAGACGAGATTGCTTCTTGACCATTCATTTTGTTCATACTGATAAAAGCTGTTGCTAA		MGASRWESSWRGIVLGARRITNVISQPHLRPCDCRHIAPRPFLHDQYRTAPRTSLTTRRDCFLTIHFVHTDKSCC*		MGASRWESSWRGIVLGARRITNVISQPHLRPCDCRHIAPRPFLHDQYRTAPRTSLTTRRDCFLTIHFVHTDKSCC*		GCTGTATCGA	CCGCCAGTGT	0	O	0	0	0	0	0
1118	789	af	AN4501.1	57.m05629	AO070311000054	0			-244	-161			ATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGA		ATGGGAGAGTTCGTGGAGGGGTATTGTACTCGGCGCCCGTCGAATCACCAACGTGATTTCGCAGCCTCACTTGCGACCCTGTGA		MGEFVEGYCTRRPSNHQRDFAASLATL*		MGEFVEGYCTRRPSNHQRDFAASLATL*		GAGCCTCAAG	CTGCCGTCAT	0	O	0	0	0	0	0
1103	789	an	AN4501.1	57.m05629	AO070311000054	0	-531	-466					ATGTGGTCTTGGGTCGAATTGCATGCCTGGAGTTCAAGCCGCCCCCGGCTACGCTGGACTCTATAA	ATGTGGTCTTGGGTCGAATTGCATGCCTGGAGTTCAAGCCGCCCCCGGCTACGCTGGACTCTATAA			MWSWVELHAWSSSRPRLRWTL*	MWSWVELHAWSSSRPRLRWTL*			CTCTCTACAA	CCGCGATGCT	0	O	0	0	0	0	0
1104	789	an	AN4501.1	57.m05629	AO070311000054	0	-509	-264					ATGCCTGGAGTTCAAGCCGCCCCCGGCTACGCTGGACTCTATAACCGCGATGCTGTTTACTCGCTACCAGCCGAGTGGAGGACTGGCGGAACAACAAGCTGCTCGACGTCTATACGGCTAATAGAATTTGCGATTCAGCCAACTTTTCGCGAAATCGTCAGTTATTCTCTTGACTTGAAAACGTGGTCTGCCGTTGGGTTTTGGAGTGTATCGTGCTATCAGCCGTGTGACAGCTGGGCCCCCTAG	ATGCCTGGAGTTCAAGCCGCCCCCGGCTACGCTGGACTCTATAACCGCGATGCTGTTTACTCGCTACCAGCCGAGTGGAGGACTGGCGGAACAACAAGCTGCTCGACGTCTATACGGCTAATAGAATTTGCGATTCAGCCAACTTTTCGCGAAATCGTCAGTTATTCTCTTGACTTGAAAACGTGGTCTGCCGTTGGGTTTTGGAGTGTATCGTGCTATCAGCCGTGTGACAGCTGGGCCCCCTAG			MPGVQAAPGYAGLYNRDAVYSLPAEWRTGGTTSCSTSIRLIEFAIQPTFREIVSYSLDLKTWSAVGFWSVSCYQPCDSWAP*	MPGVQAAPGYAGLYNRDAVYSLPAEWRTGGTTSCSTSIRLIEFAIQPTFREIVSYSLDLKTWSAVGFWSVSCYQPCDSWAP*			GTCGAATTGC	TGCAGGGCAG	0	O	0	0	0	0	0
1105	789	an	AN4501.1	57.m05629	AO070311000054	0	-460	-389					ATGCTGTTTACTCGCTACCAGCCGAGTGGAGGACTGGCGGAACAACAAGCTGCTCGACGTCTATACGGCTAA	ATGCTGTTTACTCGCTACCAGCCGAGTGGAGGACTGGCGGAACAACAAGCTGCTCGACGTCTATACGGCTAA			MLFTRYQPSGGLAEQQAARRLYG*	MLFTRYQPSGGLAEQQAARRLYG*			TATAACCGCG	TAGAATTTGC	0	O	0	0	0	0	0
1106	789	an	AN4501.1	57.m05629	AO070311000054	0	-186	-169					ATGTTTCTTACAGTCTAG	ATGTTTCTTACAGTCTAG			MFLTV*	MFLTV*			TACCCCACGC	GCCTTGTCAT	0	O	0	0	0	0	0
1119	789	ao	AN4501.1	57.m05629	AO070311000054	0					-448	-434	ATGATCTCCGTTTAG			ATGATCTCCGTTTAG	MISV*			MISV*	TGTCGCTGCC	ACTACCGCTC	0	O	0	0	0	0	0
1120	789	ao	AN4501.1	57.m05629	AO070311000054	0					-304	-260	ATGATAGTATTTTCTGGGTTGACAATATGCATGAAATTATTTTGA			ATGATAGTATTTTCTGGGTTGACAATATGCATGAAATTATTTTGA	MIVFSGLTICMKLF*			MIVFSGLTICMKLF*	CTGGAGTCGA	CAACCAACCT	0	O	0	0	0	0	0
1121	789	ao	AN4501.1	57.m05629	AO070311000054	0					-278	-207	ATGCATGAAATTATTTTGACAACCAACCTTCAGCGTACTTCCTTTTGGGGTACTAGAAGGAAAGAAAAATGA			ATGCATGAAATTATTTTGACAACCAACCTTCAGCGTACTTCCTTTTGGGGTACTAGAAGGAAAGAAAAATGA	MHEIILTTNLQRTSFWGTRRKEK*			MHEIILTTNLQRTSFWGTRRKEK*	GGTTGACAAT	TGACGGAGGG	0	O	0	0	0	0	0
1122	789	ao	AN4501.1	57.m05629	AO070311000054	0					-274	-260	ATGAAATTATTTTGA			ATGAAATTATTTTGA	MKLF*			MKLF*	GACAATATGC	CAACCAACCT	0	O	0	0	0	0	0
1123	789	ao	AN4501.1	57.m05629	AO070311000054	0					-210	-166	ATGATGACGGAGGGATCTAGAATTCGTGTTCTTCGGGCCACTTGA			ATGATGACGGAGGGATCTAGAATTCGTGTTCTTCGGGCCACTTGA	MMTEGSRIRVLRAT*			MMTEGSRIRVLRAT*	GGAAAGAAAA	CTATCACAGC	0	O	0	0	0	0	0
1124	789	ao	AN4501.1	57.m05629	AO070311000054	0					-207	-166	ATGACGGAGGGATCTAGAATTCGTGTTCTTCGGGCCACTTGA			ATGACGGAGGGATCTAGAATTCGTGTTCTTCGGGCCACTTGA	MTEGSRIRVLRAT*			MTEGSRIRVLRAT*	AAGAAAAATG	CTATCACAGC	0	O	0	0	0	0	0
1125	789	ao	AN4501.1	57.m05629	AO070311000054	0					-110	-24	ATGATTCCGGCTCCATTTCATACTTGCTTTTTCCGTTGCTTTTGGCCCTCATGTTTTTGTGTTCGAATTTTAAAACGTCTCCACTAA			ATGATTCCGGCTCCATTTCATACTTGCTTTTTCCGTTGCTTTTGGCCCTCATGTTTTTGTGTTCGAATTTTAAAACGTCTCCACTAA	MIPAPFHTCFFRCFWPSCFCVRILKRLH*			MIPAPFHTCFFRCFWPSCFCVRILKRLH*	CACGCCATTT	CAGTCGACCA	0	O	0	0	0	0	0
1130	791	af	AN4550.1	57.m05560	AO070321000181	0			-113	-78			ATGGGTTGGCGGGGTGAGTCGAAAGGATCTCATTGA		ATGGGTTGGCGGGGTGAGTCGAAAGGATCTCATTGA		MGWRGESKGSH*		MGWRGESKGSH*		CAGGGCTAGT	CTCATGAACT	0	J	0	MG06566.1	0	YLL018C	0
1126	791	an	AN4550.1	57.m05560	AO070321000181	0	-246	-175					ATGTCCTTACATGCTGAGCTGCAAGCATATATATATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGA	ATGTCCTTACATGCTGAGCTGCAAGCATATATATATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGA			MSLHAELQAYIYDVASGCSFFNT*	MSLHAELQAYIYDVASGCSFFNT*			TTATGTTATG	GCAGCCCCTC	0	J	0	MG06566.1	0	YLL018C	0
1127	791	an	AN4550.1	57.m05560	AO070321000181	0	-236	-135					ATGCTGAGCTGCAAGCATATATATATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA	ATGCTGAGCTGCAAGCATATATATATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA			MLSCKHIYMMSPQAALFLTREQPLVGLGPALAG*	MLSCKHIYMMSPQAALFLTREQPLVGLGPALAG*			ATGTCCTTAC	TCCAATTGAA	0	J	0	MG06566.1	0	YLL018C	0
1128	791	an	AN4550.1	57.m05560	AO070321000181	0	-212	-135					ATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA	ATGATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA			MMSPQAALFLTREQPLVGLGPALAG*	MMSPQAALFLTREQPLVGLGPALAG*			GCATATATAT	TCCAATTGAA	0	J	0	MG06566.1	0	YLL018C	0
1129	791	an	AN4550.1	57.m05560	AO070321000181	0	-209	-135					ATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA	ATGTCGCCTCAGGCTGCTCTTTTTTTAACACGTGAGCAGCCCCTCGTAGGGTTAGGCCCCGCCCTGGCGGGGTGA			MSPQAALFLTREQPLVGLGPALAG*	MSPQAALFLTREQPLVGLGPALAG*			TATATATATG	TCCAATTGAA	0	J	0	MG06566.1	0	YLL018C	0
1131	791	ao	AN4550.1	57.m05560	AO070321000181	0					-116	-90	ATGCGGTGGGGTGACTCAAAGTATTGA			ATGCGGTGGGGTGACTCAAAGTATTGA	MRWGDSKY*			MRWGDSKY*	GGTTGCCTCC	TTGAGGTTGC	0	J	0	MG06566.1	0	YLL018C	0
1133	792	af	AN5706.1	54.m06822	AO070324000152	0			-248	-219			ATGTTCAATACGATGCGGTGGGTTCAATGA		ATGTTCAATACGATGCGGTGGGTTCAATGA		MFNTMRWVQ*		MFNTMRWVQ*		CAGTCACTTG	TCAGGAGGAC	0	CR	0	0	0	0	0

1134	792	af	AN5706.1	54.m06822	AO070324000152	0			-236	-219			ATGCGGTGGGTTCAATGA		ATGCGGTGGGTTCAATGA		MRWVQ*		MRWVQ*		GTTCAATACG	TCAGGAGGAC	0	CR	0	0	0	0	0
1135	792	af	AN5706.1	54.m06822	AO070324000152	0			-222	-91			ATGATCAGGAGGACTAAGTCCCCAGATGATATAAAACCCAAAAACGCCATCTGGGTTCAGAGGGACCCTTATGACTGTTTGCGTTCCTTCCTCAGCCGTGTGCTTATTTTGAGCTATCCGACCTCTATATAA		ATGATCAGGAGGACTAAGTCCCCAGATGATATAAACCCAAAAACGCCATCTGGGTTCAGAGGGACCCTTATGACTGTTTGCGTTCCTTCCTCAGCCGTGTGCTTATTTTGAGCTATCCGACCTCTATATAA		MIRRTKSPDDIKPKNAIWVQRDPYDCLRSFLSRVLILSYPTSI*		MIRRTKSPDDIKPKNAIWVQRDPYDCLRSFLSRVLILSYPTSI*		GGTGGGTTCA	ATCCAACTTT	0	CR	0	0	0	0	0
1136	792	af	AN5706.1	54.m06822	AO070324000152	0			-152	-111			ATGACTGTTTGCGTTCCTTCCTCAGCCGTGTGCTTATTTTGA		ATGACTGTTTGCGTTCCTTCCTCAGCCGTGTGCTTATTTTGA		MTVCVPSSAVCLF*		MTVCVPSSAVCLF*		AGGGACCCTT	GCTATCCGAC	0	CR	0	0	0	0	0
1132	792	an	AN5706.1	54.m06822	AO070324000152	0	-179	-120					ATGAAGATCAGGCGGGCAGCTTGCCCCGGAATTCGGGGTCTGTATAAGAATCGCGTCTAG	ATGAAGATCAGGCGGGCAGCTTGCCCCGGAATTCGGGGTCTGTATAAGAATCGCGTCTAG			MKIRRAACPGIRGLYKNRV*	MKIRRAACPGIRGLYKNRV*			CTTCGTGAAT	GAAGGTATTA	0	CR	0	0	0	0	0
1137	792	ao	AN5706.1	54.m06822	AO070324000152	0					-249	-193	ATGAGGTGTATGCGCAGATCAGGAGGACTATCAGCCTTACACATATGTGCTAGGTGA			ATGAGGTGTATGCGCAGATCAGGAGGACTATCAGCCTTACACATATGTGCTAGGTGA	MRCMRRSGGLSALHICAR*			MRCMRRSGGLSALHICAR*	AACCAATACG	TATAAAAGAA	0	CR	0	0	0	0	0
1138	792	ao	AN5706.1	54.m06822	AO070324000152	0					-240	-193	ATGCGCAGATCAGGAGGACTATCAGCCTTACACATATGTGCTAGGTGA			ATGCGCAGATCAGGAGGACTATCAGCCTTACACATATGTGCTAGGTGA	MRRSGGLSALHICAR*			MRRSGGLSALHICAR*	GATGAGGTGT	TATAAAAGAA	0	CR	0	0	0	0	0
1141	802	af	AN6826.1	71.m15290	AO070314000106	0			-158	-60			ATGTTTGATCGGAGATATCGACTTTTTCCTCCACAGTATAGCCATTCCCACCGTCTGTGGACGATATACTATTTCCACGCTGCGCAATACCACAGATGA		ATGTTTGATCGGAGATATCGACTTTTTCCTCCACAGTATAGCCATTCCCACCGTCTGTGGACGATATACTATTTCCACGCTGCGCAATACCACAGATGA		MFDRRYRLFPPQYSHSHRLWTIYYFHAAQYHR*		MFDRRYRLFPPQYSHSHRLWTIYYFHAAQYHR*		CAATCGGCAG	GCTCATAGAG	0	Z	0	0	0	0	0
1142	802	af	AN6826.1	71.m15290	AO070314000106	0			-63	-52			ATGAGCTCATAG		ATGAGCTCATAG		MSS*		MSS*		AATACCACAG	AGTCACCGAC	0	Z	0	0	0	0	0
1139	802	an	AN6826.1	71.m15290	AO070314000106	0	-224	-195					ATGCGCCGTCAATGTCATAGCCTGTTTTAA	ATGCGCCGTCAATGTCATAGCCTGTTTTAA			MRRQCHSLF*	MRRQCHSLF*			AGAATGAGAT	AAGGATATTC	0	Z	0	0	0	0	0
1140	802	an	AN6826.1	71.m15290	AO070314000106	0	-117	-94					ATGCGACGCAGTGGAGCTCATTGA	ATGCGACGCAGTGGAGCTCATTGA			MRRSGAH*	MRRSGAH*			AGGAACTCGA	AACCACACCA	0	Z	0	0	0	0	0
1143	802	ao	AN6826.1	71.m15290	AO070314000106	0					-82	-56	ATGATCGCAGTGACTTGTCTAACATAA			ATGATCGCAGTGACTTGTCTAACATAA	MIAVTCLT*			MIAVTCLT*	CTAGTGTACT	TTAAATCTCA	0	Z	0	0	0	0	0
1147	804	af	AN5777.1	69.m14820	AO070249000022	0			-177	-4			ATGTGGATAGCTGATCTGTGCTGGAGTCACCTGACTACCCCGGATTCTCGAAAAACGTCACAAATCACGATGGCACATCACGAGCCCATTGTCACTATCTTCCTGGGAGGCCAAGGTCTGAGCAAAGTGCCTGTCTCACTGTTATTAGAGAGCACAGACGACGATGTTTACTAG		ATGTGGATAGCTGATCTGTGCTGGAGTCACCTGACTACCCCGGATTCTCGAAAAACGTCACAAATCACGATGGCACATCACGAGCCCATTGTCACTATCTTCCTGGGAGGCCAAGGTCTGAGCAAAGTGCCTGTCTCACTGTTATTAGAGAGCACAGACGACGATGTTTACTAG		MWIADLCWSHLTTPDSRKTSQITMAHHEPIVTIFLGGQGLSKVPVSLLLESTDDDVY*		MWIADLCWSHLTTPDSRKTSQITMAHHEPIVTIFLGGQGLSKVPVSLLLESTDDDVY*		CAGTGGAGCC	TCCATGAGAC	0	I	0	MG04555.1	0	0	0
1148	804	af	AN5777.1	69.m14820	AO070249000022	0			-108	-4			ATGGCACATCACGAGCCCATTGTCACTATCTTCCTGGGAGGCCAAGGTCTGAGCAAAGTGCCTGTCTCACTGTTATTAGAGAGCACAGACGACGATGTTTACTAG		ATGGCACATCACGAGCCCATTGTCACTATCTTCCTGGGAGGCCAAGGTCTGAGCAAAGTGCCTGTCTCACTGTTATTAGAGAGCACAGACGACGATGTTTACTAG		MAHHEPIVTIFLGGQGLSKVPVSLLLESTDDDVY*		MAHHEPIVTIFLGGQGLSKVPVSLLLESTDDDVY*		ACAAATCACG	TCCATGAGAC	0	I	0	MG04555.1	0	0	0
1145	804	an	AN5777.1	69.m14820	AO070249000022	0	-160	-47					ATGCATGTGGGGTTGTACATGTGGCCTGATCGGGATAAGCGCTGCACTAGCGTTACCCCAGATTCGCCGCTGTTATGTTCAAGAAGCAACGCCAACCACTCTATATCTACCTAG	ATGCATGTGGGGTTGTACATGTGGCCTGATCGGGATAAGCGCTGCACTAGCGTTACCCCAGATTCGCCGCTGTTATGTTCAAGAAGCAACGCCAACCACTCTATATCTACCTAG			MHVGLYMWPDRDKRCTSVTPDSPLLCSRSNANHSIST*	MHVGLYMWPDRDKRCTSVTPDSPLLCSRSNANHSIST*			GTGATACTCA	CCCCCGCCTC	0	I	0	MG04555.1	0	0	0
1146	804	an	AN5777.1	69.m14820	AO070249000022	0	-142	-47					ATGTGGCCTGATCGGGATAAGCGCTGCACTAGCGTTACCCCAGATTCGCCGCTGTTATGTTCAAGAAGCAACGCCAACCACTCTATATCTACCTAG	ATGTGGCCTGATCGGGATAAGCGCTGCACTAGCGTTACCCCAGATTCGCCGCTGTTATGTTCAAGAAGCAACGCCAACCACTCTATATCTACCTAG			MWPDRDKRCTSVTPDSPLLCSRSNANHSIST*	MWPDRDKRCTSVTPDSPLLCSRSNANHSIST*			GGGGTTGTAC	CCCCCGCCTC	0	I	0	MG04555.1	0	0	0
1149	804	ao	AN5777.1	69.m14820	AO070249000022	0					-292	-233	ATGAGATGGAAATGCTATCAAAATTACAGGGATGTTGACAGTTGCACATACCTTATGTAA			ATGAGATGGAAATGCTATCAAAATTACAGGGATGTTGACAGTTGCACATACCTTATGTAA	MRWKCYQNYRDVDSCTYLM*			MRWKCYQNYRDVDSCTYLM*	TAGCGGGTAT	CAGATGACAC	0	I	0	MG04555.1	0	0	0
1150	804	ao	AN5777.1	69.m14820	AO070249000022	0					-287	-255	ATGGAAATGCTATCAAAATTACAGGGATGTTGA			ATGGAAATGCTATCAAAATTACAGGGATGTTGA	MEMLSKLQGC*			MEMLSKLQGC*	GGTATATGAG	CAGTTGCACA	0	I	0	MG04555.1	0	0	0
1151	804	ao	AN5777.1	69.m14820	AO070249000022	0					-281	-255	ATGCTATCAAAATTACAGGGATGTTGA			ATGCTATCAAAATTACAGGGATGTTGA	MLSKLQGC*			MLSKLQGC*	TGAGATGGAA	CAGTTGCACA	0	I	0	MG04555.1	0	0	0
1152	804	ao	AN5777.1	69.m14820	AO070249000022	0					-261	-226	ATGTTGACAGTTGCACATACCTTATGTAACAGATGA			ATGTTGACAGTTGCACATACCTTATGTAACAGATGA	MLTVAHTLCNR*			MLTVAHTLCNR*	AATTACAGGG	CACAGTGCGC	0	I	0	MG04555.1	0	0	0
1153	804	ao	AN5777.1	69.m14820	AO070249000022	0					-229	-203	ATGACACAGTGCGCCACTGGTCTATAG			ATGACACAGTGCGCCACTGGTCTATAG	MTQCATGL*			MTQCATGL*	TATGTAACAG	TACCTGCGCA	0	I	0	MG04555.1	0	0	0
1157	816	an	AN1105.1	70.m15127	AO070285000033	0	-198	-169					ATGAATGAGATACGGGGGATCTCCAGCTGA	ATGAATGAGATACGGGGGATCTCCAGCTGA			MNEIRGISS*	MNEIRGISS*			AGTGGAGTTG	GGTAGTGCAG	0	U	0	0	0	0	0
1158	816	ao	AN1105.1	70.m15127	AO070285000033	0					-259	-248	ATGGCTAGATAA			ATGGCTAGATAA	MAR*			MAR*	TGGTAATTGT	AGTAGAGATT	0	U	0	0	0	0	0
1159	816	ao	AN1105.1	70.m15127	AO070285000033	0					-217	-182	ATGAGTACTGGGGCCGAAACTCATTGCCGCTTTTAG			ATGAGTACTGGGGCCGAAACTCATTGCCGCTTTTAG	MSTGAETHCRF*			MSTGAETHCRF*	GCGCTACAGT	CCCCGTTTGG	0	U	0	0	0	0	0
1160	819	af	AN2686.1	71.m15174	AO070313000102	0			-69	-49			ATGCTACACAGATTGAACTAA		ATGCTACACAGATTGAACTAA		MLHRLN*		MLHRLN*		CTTACAGCGG	GTGAAGAATT	0		0	0	0	0	0
1161	819	ao	AN2686.1	71.m15174	AO070313000102	0					-156	-109	ATGGTTGGGTATTCTCGAATGGATAACGTGCGTCAAGCGTACAAATGA			ATGGTTGGGTATTCTCGAATGGATAACGTGCGTCAAGCGTACAAATGA	MVGYSRMDNVRQAYK*			MVGYSRMDNVRQAYK*	GCGCCACATA	TCCCAAAACA	0		0	0	0	0	0
1162	819	ao	AN2686.1	71.m15174	AO070313000102	0					-138	-109	ATGGATAACGTGCGTCAAGCGTACAAATGA			ATGGATAACGTGCGTCAAGCGTACAAATGA	MDNVRQAYK*			MDNVRQAYK*	GTATTCTCGA	TCCCAAAACA	0		0	0	0	0	0
1163	819	ao	AN2686.1	71.m15174	AO070313000102	0					-112	-89	ATGATCCCAAAACAGTATAACTGA			ATGATCCCAAAACAGTATAACTGA	MIPKQYN*			MIPKQYN*	AAGCGTACAA	GGATATCTGC	0		0	0	0	0	0
1170	823	ao	AN0448.1	54.m06640	AO070338000312	0					-88	-71	ATGCTCAACCATGCTTGA			ATGCTCAACCATGCTTGA	MLNHA*			MLNHA*	TTGTGGTTGG	GGGGGTCTGA	0		0	0	0	0	0
1171	823	ao	AN0448.1	54.m06640	AO070338000312	0					-78	-61	ATGCTTGAGGGGGTCTGA			ATGCTTGAGGGGGTCTGA	MLEGV*			MLEGV*	ATGCTCAACC	TTGAATGCTG	0		0	0	0	0	0
1175	824	af	AN7233.1	65.m07169	AO070340000208	0			-121	-101			ATGGAGGGGTGGAGTCGGTGA		ATGGAGGGGTGGAGTCGGTGA		MEGWSR*		MEGWSR*		GGTCGTGTCC	CAGGTCCCTT	0	R	0	0	0	0	0
1172	824	an	AN7233.1	65.m07169	AO070340000208	0	-170	-108					ATGGCCCAGTGGGCCGATACCATTGGCCCCTCACTGATGCCGAGGGGCACCCTACATGATTAA	ATGGCCCAGTGGGCCGATACCATTGGCCCCTCACTGATGCCGAGGGGCACCCTACATGATTAA			MAQWADTIGPSLMPRGTLHD*	MAQWADTIGPSLMPRGTLHD*			TTCGAGTTTA	ACTCTCACCA	0	R	0	0	0	0	0
1173	824	an	AN7233.1	65.m07169	AO070340000208	0	-134	-108					ATGCCGAGGGGCACCCTACATGATTAA	ATGCCGAGGGGCACCCTACATGATTAA			MPRGTLHD*	MPRGTLHD*			CCCCTCACTG	ACTCTCACCA	0	R	0	0	0	0	0
1174	824	an	AN7233.1	65.m07169	AO070340000208	0	-115	-74					ATGATTAAACTCTCACCACCAGCAGTCTTCTTGCGCCCCTGA	ATGATTAAACTCTCACCACCAGCAGTCTTCTTGCGCCCCTGA			MIKLSPPAVFLRP*	MIKLSPPAVFLRP*			GGCACCCTAC	GCAGTGTTTA	0	R	0	0	0	0	0
1176	824	ao	AN7233.1	65.m07169	AO070340000208	0					-170	-87	ATGTTTTTGCAGAGGGGAAAATCTGGAGGGGCTATGTGCCGAAGCGAGGTGGCATGTTTAATCTCCCCTTCGGTTTATGAATGA			ATGTTTTTGCAGAGGGGAAAATCTGGAGGGGCTATGTGCCGAAGCGAGGTGGCATGTTTAATCTCCCCTTCGGTTTATGAATGA	MFLQRGKSGGAMCRSEVACLISPSVYE*			MFLQRGKSGGAMCRSEVACLISPSVYE*	GTTGGGATTT	TATGAGTCTG	0	R	0	0	0	0	0
1177	824	ao	AN7233.1	65.m07169	AO070340000208	0					-137	-87	ATGTGCCGAAGCGAGGTGGCATGTTTAATCTCCCCTTCGGTTTATGAATGA			ATGTGCCGAAGCGAGGTGGCATGTTTAATCTCCCCTTCGGTTTATGAATGA	MCRSEVACLISPSVYE*			MCRSEVACLISPSVYE*	TGGAGGGGCT	TATGAGTCTG	0	R	0	0	0	0	0
1178	824	ao	AN7233.1	65.m07169	AO070340000208	0					-117	-91	ATGTTTAATCTCCCCTTCGGTTTATGA			ATGTTTAATCTCCCCTTCGGTTTATGA	MFNLPFGL*			MFNLPFGL*	GCGAGGTGGC	ATGATATGAG	0	R	0	0	0	0	0
1179	824	ao	AN7233.1	65.m07169	AO070340000208	0					-94	-53	ATGAATGATATGAGTCTGGCCTCGCCTGGGAATACGAGCTGA			ATGAATGATATGAGTCTGGCCTCGCCTGGGAATACGAGCTGA	MNDMSLASPGNTS*			MNDMSLASPGNTS*	CCTTCGGTTT	AATCACACAC	0	R	0	0	0	0	0
1180	824	ao	AN7233.1	65.m07169	AO070340000208	0					-85	-53	ATGAGTCTGGCCTCGCCTGGGAATACGAGCTGA			ATGAGTCTGGCCTCGCCTGGGAATACGAGCTGA	MSLASPGNTS*			MSLASPGNTS*	TATGAATGAT	AATCACACAC	0	R	0	0	0	0	0
1183	825	af	AN5890.1	72.m19240	AO070245000018	0			-128	-57			ATGCGCACTATATCCTCTACGTATTCCAGCACCGTCCCTGGAGTATCCGATCCAATCAGGCGGACCTCCTAG		ATGCGCACTATATCCTCTACGTATTCCAGCACCGTCCCTGGAGTATCCGATCCAATCAGGCGGACCTCCTAG		MRTISSTYSSTVPGVSDPIRRTS*		MRTISSTYSSTVPGVSDPIRRTS*		ATCACTACCC	CTTCCTCGCT	0	E	0	0	0	0	0
1181	825	an	AN5890.1	72.m19240	AO070245000018	0	-133	-89					ATGGGGCGAAGGCACTCTAATCCTGAACCCTTCCTCTGCTTCTAG	ATGGGGCGAAGGCACTCTAATCCTGAACCCTTCCTCTGCTTCTAG			MGRRHSNPEPFLCF*	MGRRHSNPEPFLCF*			AGCGCGGATC	TGTTGACTTC	0	E	0	0	0	0	0
1186	839	af	AN5734.1	69.m14862	AO070341000025	0			-132	-115			ATGAGCGTGGAATTTTAG		ATGAGCGTGGAATTTTAG		MSVEF*		MSVEF*		CTTGTGAGGG	ACGCGTTCCA	0	R	0	MG04225.1	0	0	0
1184	839	an	AN5734.1	69.m14862	AO070341000025	0	-249	-175					ATGGCTCGCTTGAAGTCCTATAACTATGCGGGCCGACCCCCTGTCGGGACCTTTTTGGAACAGGATCTCATATAA	ATGGCTCGCTTGAAGTCCTATAACTATGCGGGCCGACCCCCTGTCGGGACCTTTTTGGAACAGGATCTCATATAA			MARLKSYNYAGRPPVGTFLEQDLI*	MARLKSYNYAGRPPVGTFLEQDLI*			GCTATCTAGC	ATCTGAGCCG	0	R	0	MG04225.1	0	0	0
1185	839	an	AN5734.1	69.m14862	AO070341000025	0	-224	-153					ATGCGGGCCGACCCCCTGTCGGGACCTTTTTGGAACAGGATCTCATATAAATCTGAGCCGGGGTCGCTTTGA	ATGCGGGCCGACCCCCTGTCGGGACCTTTTTGGAACAGGATCTCATATAAATCTGAGCCGGGGTCGCTTTGA			MRADPLSGPFWNRISYKSEPGSL*	MRADPLSGPFWNRISYKSEPGSL*			TCCTATAACT	GCTTTCAGAA	0	R	0	MG04225.1	0	0	0
1187	839	ao	AN5734.1	69.m14862	AO070341000025	0					-125	-87	ATGAGCCAGGATCGCGATCATCGTTGTTTCAGGCTTTGA			ATGAGCCAGGATCGCGATCATCGTTGTTTCAGGCTTTGA	MSQDRDHRCFRL*			MSQDRDHRCFRL*	ATTGTCTTAT	AACGACGTGT	0	R	0	MG04225.1	0	0	0
1188	841	conserved	AN3682.1	58.m07417	AO070342000120	0	-219	-205	-202	-188	-213	-199	ATGyGyGvhwwyTAG	ATGTGTGATTTCTAG	ATGCGCGGCATTTAG	ATGTGTGCATATTAG	Mcdf*	MCDF*	MRGI*	MCAY*	khTsATTGGm	rCGsyyGysk	0		0	0	0	0	0
1194	846	af	AN2037.1	55.m03233	AO070281000048	0			-165	-112			ATGCGAGAATGGCATGGAAGAGTGGATCACTGGCATCTAAAAGATATAAATTGA		ATGCGAGAATGGCATGGAAGAGTGGATCACTGGCATCTAAAAGATATAAATTGA		MREWHGRVDHWHLKDIN*		MREWHGRVDHWHLKDIN*		GTCACTAGCG	CGGTAATATC	0		0	0	0	0	0
1195	846	af	AN2037.1	55.m03233	AO070281000048	0			-157	-44			ATGGCATGGAAGAGTGGATCACTGGCATCTAAAAGATATAAATTGACGGTAATATCCAGATACCCACAGGCTCAAACGGCAACAAGAGCTATACAAACACGACTACAACGCTAG		ATGGCATGGAAGAGTGGATCACTGGCATCTAAAAGATATAAATTGACGGTAATATCCAGATACCCACAGGCTCAAACGGCAACAAGAGCTATACAAACACGACTACAACGCTAG		MAWKSGSLASKRYKLTVISRYPQAQTATRAIQTRLQR*		MAWKSGSLASKRYKLTVISRYPQAQTATRAIQTRLQR*		CGATGCGAGA	TATACATTAC	0		0	0	0	0	0
1196	846	af	AN2037.1	55.m03233	AO070281000048	0			-152	-126			ATGGAAGAGTGGATCACTGGCATCTAA		ATGGAAGAGTGGATCACTGGCATCTAA		MEEWITGI*		MEEWITGI*		CGAGAATGGC	AAGATATAAA	0		0	0	0	0	0
1189	846	an	AN2037.1	55.m03233	AO070281000048	0	-231	-79					ATGCTCCGTGTGTTTGTTTCATTTAAGAACTTAACGCCGCTCGGATGGATATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA	ATGCTCCGTGTGTTTGTTTCATTTAAGAACTTAACGCCGCTCGGATGGATATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA			MLRVFVSFKNLTPLGWIWSRYCGVTMLSTAMAGFQAAVPPLQRDHKPESI*	MLRVFVSFKNLTPLGWIWSRYCGVTMLSTAMAGFQAAVPPLQRDHKPESI*			CGGTGGGAAG	ATTTATCATG	0		0	0	0	0	0
1190	846	an	AN2037.1	55.m03233	AO070281000048	0	-187	-95					ATGGATATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAA	ATGGATATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAA			MDMEPLLRSYDVEHGYGGVSGCSAAAAARS*	MDMEPLLRSYDVEHGYGGVSGCSAAAAARS*			CGCCGCTCGG	GCCGGAATCA	0		0	0	0	0	0
1191	846	an	AN2037.1	55.m03233	AO070281000048	0	-181	-95					ATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAA	ATGGAGCCGCTATTGCGGAGTTACGATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAA			MEPLLRSYDVEHGYGGVSGCSAAAAARS*	MEPLLRSYDVEHGYGGVSGCSAAAAARS*			TCGGATGGAT	GCCGGAATCA	0		0	0	0	0	0
1192	846	an	AN2037.1	55.m03233	AO070281000048	0	-156	-79					ATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA	ATGTTGAGCACGGCTATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA			MLSTAMAGFQAAVPPLQRDHKPESI*	MLSTAMAGFQAAVPPLQRDHKPESI*			CGGAGTTACG	ATTTATCATG	0		0	0	0	0	0
1193	846	an	AN2037.1	55.m03233	AO070281000048	0	-141	-79					ATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA	ATGGCGGGGTTTCAGGCTGCAGTGCCGCCGCTGCAGCGAGATCATAAGCCGGAATCAATATAA			MAGFQAAVPPLQRDHKPESI*	MAGFQAAVPPLQRDHKPESI*			GAGCACGGCT	ATTTATCATG	0		0	0	0	0	0
1197	846	ao	AN2037.1	55.m03233	AO070281000048	0					-203	-177	ATGACAAGGCTGCGAAGAGAACCTTAG			ATGACAAGGCTGCGAAGAGAACCTTAG	MTRLRREP*			MTRLRREP*	ACGATCAAAT	AGAACTACAG	0		0	0	0	0	0
1201	847	af	AN4488.1	57.m05643	AO070311000040	0			-152	-141			ATGTCGCTCTAG		ATGTCGCTCTAG		MSL*		MSL*		ACAACGTCAA	GATTTTCTGC	0		0	0	0	0	0
1198	847	an	AN4488.1	57.m05643	AO070311000040	0	-61	-44					ATGTGTGCACGGAATTGA	ATGTGTGCACGGAATTGA			MCARN*	MCARN*			AGGGAAGATC	TCTCGGATAT	0		0	0	0	0	0
1203	847	ao	AN4488.1	57.m05643	AO070311000040	0					-210	-109	ATGTACGCGCTGGCACCAGATCATCGTTGCATTGGCGCTGGGAGACACAGCCACCGGGCCGCTAAGTTGGCGCCTCCGTCTTTCCACAAGCGCTCCGGTTGA			ATGTACGCGCTGGCACCAGATCATCGTTGCATTGGCGCTGGGAGACACAGCCACCGGGCCGCTAAGTTGGCGCCTCCGTCTTTCCACAAGCGCTCCGGTTGA	MYALAPDHRCIGAGRHSHRAAKLAPPSFHKRSG*			MYALAPDHRCIGAGRHSHRAAKLAPPSFHKRSG*	GTCTCATCTC	TTCTCCAAAC	0		0	0	0	0	0
1204	847	ao	AN4488.1	57.m05643	AO070311000040	0					-70	-53	ATGGCGATGTGCAATTGA			ATGGCGATGTGCAATTGA	MAMCN*			MAMCN*	AGAGACCCCC	ATCCGGTTGT	0		0	0	0	0	0

1205	847	ao	AN4488.1	57.m05643	AO070311000040	0					-64	-53	ATGTGCAATTGA			ATGTGCAATTGA	MCN*			MCN*	CCCCATGGCG	ATCCGGTTGT	0		0	0	0	0	0
1207	852	af	AN6298.1	72.m18969	AO070260000006	0			-214	-155			ATGGGTTATCAGCAGTGCTGTTCGCGTAGATATCCCTTGTTACTCCGTACTCCATTGTAG		ATGGGTTATCAGCAGTGCTGTTCGCGTAGATATCCCTTGTTACTCCGTACTCCATTGTAG		MGYQQCCSRRYPLLLRTPL*		MGYQQCCSRRYPLLLRTPL*		GACAAAATTG	TTGCAAGGCA	0		0	0	0	0	0
1206	852	an	AN6298.1	72.m18969	AO070260000006	0	-162	-100					ATGCCTCCTTCCCTATTGTCTATCGACCCGGCAACAGCAAACGACCAATTTTCTTATCGATAA	ATGCCTCCTTCCCTATTGTCTATCGACCCGGCAACAGCAAACGACCAATTTTCTTATCGATAA			MPPSLLSIDPATANDQFSYR*	MPPSLLSIDPATANDQFSYR*			TGCATACCTG	GCCTATCCAT	0		0	0	0	0	0
1208	852	ao	AN6298.1	72.m18969	AO070260000006	0					-246	-229	ATGACGCAATGCGATTAA			ATGACGCAATGCGATTAA	MTQCD*			MTQCD*	TTGTTTTGTC	TTTCACGTCT	0		0	0	0	0	0
1209	852	ao	AN6298.1	72.m18969	AO070260000006	0					-238	-155	ATGCGATTAATTTCACGTCTAAATCTCAGAGCTATTCCAACCCCACTAAACCGCATACCAAACCCGAAAGCGAAGCAAAGCTAG			ATGCGATTAATTTCACGTCTAAATCTCAGAGCTATTCCAACCCCACTAAACCGCATACCAAACCCGAAAGCGAAGCAAAGCTAG	MRLISRLNLRAIPTPLNRIPNPKAKQS*			MRLISRLNLRAIPTPLNRIPNPKAKQS*	TCATGACGCA	CTCAAAACAG	0		0	0	0	0	0
1210	861	af	AN8851.1	71.m15986	AO070271000025	0			-237	-220			ATGGATTACATTCGCTGA		ATGGATTACATTCGCTGA		MDYIR*		MDYIR*		TTTCAATAAT	AGGTCACGGG	0	J	0	0	0	YLR175W	0
1211	861	ao	AN8851.1	71.m15986	AO070271000025	0					-203	-108	ATGTCTATTCAATTGGTAAGGGATTTTGCGCTAGCCTGTTTTGTTGTTAGACCGGTCGCCGCACTTCAAAATTTCCCATTACTGCTTTCTCGCTAG			ATGTCTATTCAATTGGTAAGGGATTTTGCGCTAGCCTGTTTTGTTGTTAGACCGGTCGCCGCACTTCAAAATTTCCCATTACTGCTTTCTCGCTAG	MSIQLVRDFALACFVVRPVAALQNFPLLLSR*			MSIQLVRDFALACFVVRPVAALQNFPLLLSR*	AAGTCACGGG	CGCCCCCAAA	0	J	0	0	0	YLR175W	0
1212	866	an	AN2851.1	59.m08696	AO070338000172	0	-211	-167					ATGGAACCCTGCCAAATGCGCCAGATTGAGCTCGCCTTATCGTAA	ATGGAACCCTGCCAAATGCGCCAGATTGAGCTCGCCTTATCGTAA			MEPCQMRQIELALS*	MEPCQMRQIELALS*			CCTGCGGGAC	AGCTGTTTAA	0	E	0	0	0	0	0
1213	866	an	AN2851.1	59.m08696	AO070338000172	0	-196	-167					ATGCGCCAGATTGAGCTCGCCTTATCGTAA	ATGCGCCAGATTGAGCTCGCCTTATCGTAA			MRQIELALS*	MRQIELALS*			ACCCTGCCAA	AGCTGTTTAA	0	E	0	0	0	0	0
1214	867	an	AN5191.1	69.m15628	AO070237000021	0	-148	-80					ATGCTATATCTCGGTCTCGGAATTAGCAGCCGAGGCATCTTGAGCTATCTCCCCACAATCTCAAGATAG	ATGCTATATCTCGGTCTCGGAATTAGCAGCCGAGGCATCTTGAGCTATCTCCCCACAATCTCAAGATAG			MLYLGLGISSRGILSYLPTISR*	MLYLGLGISSRGILSYLPTISR*			AAACGGCTGT	CTCTTTAATA	0	S	0	0	0	0	0
1216	867	ao	AN5191.1	69.m15628	AO070237000021	0					-259	-56	ATGATTTCGAGTTCGTCTCGGCGAAAGAAAAAGTCGCCGATGTTAAGTTTGATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG			ATGATTTCGAGTTCGTCTCGGCGAAAGAAAAAGTCGCCGATGTTAAGTTTGATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG	MISSSSRRKKKSPMLSLMMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*			MISSSSRRKKKSPMLSLMMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*	TGTTAAGGAA	CAAGAAAGCC	0	S	0	0	0	0	0
1217	867	ao	AN5191.1	69.m15628	AO070237000021	0					-220	-56	ATGTTAAGTTTGATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG			ATGTTAAGTTTGATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG	MLSLMMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*			MLSLMMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*	AAAGTCGCCG	CAAGAAAGCC	0	S	0	0	0	0	0
1218	867	ao	AN5191.1	69.m15628	AO070237000021	0					-208	-56	ATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG			ATGATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG	MMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*			MMLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*	GTTAAGTTTG	CAAGAAAGCC	0	S	0	0	0	0	0
1219	867	ao	AN5191.1	69.m15628	AO070237000021	0					-205	-56	ATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG			ATGTTACTTCCTGATTCGGTTAGTACCTCGGAAACATCACTATCCAGGATTCCGAGACCGAGACCCATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG	MLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*			MLLPDSVSTSETSLSRIPRPRPMARVSEPPQPQLSRCSPSNPASKLLFN*	AAGTTTGATG	CAAGAAAGCC	0	S	0	0	0	0	0
1220	867	ao	AN5191.1	69.m15628	AO070237000021	0					-139	-56	ATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG			ATGGCCCGAGTTTCGGAACCCCCTCAACCCCAACTCTCGAGATGCTCCCCCAGTAACCCAGCTTCTAAACTCCTTTTTAATTAG	MARVSEPPQPQLSRCSPSNPASKLLFN*			MARVSEPPQPQLSRCSPSNPASKLLFN*	ACCGAGACCC	CAAGAAAGCC	0	S	0	0	0	0	0
1221	867	ao	AN5191.1	69.m15628	AO070237000021	0					-98	-84	ATGCTCCCCCAGTAA			ATGCTCCCCCAGTAA	MLPQ*			MLPQ*	AACTCTCGAG	CCCAGCTTCT	0	S	0	0	0	0	0
1229	880	af	AN8073.1	53.m03926	AO070330000031	0			-195	-169			ATGAGGCCAGAACCTCACAGGTCGTGA		ATGAGGCCAGAACCTCACAGGTCGTGA		MRPEPHRS*		MRPEPHRS*		TCGGGAGCTC	GATTAATGCC	0	A	0	0	0	0	0
1230	880	af	AN8073.1	53.m03926	AO070330000031	0			-163	-137			ATGCCTCAGGCCGCTCTAAGGGGCTAG		ATGCCTCAGGCCGCTCTAAGGGGCTAG		MPQAALRG*		MPQAALRG*		CGTGAGATTA	ACCGCCTTCC	0	A	0	0	0	0	0
1227	880	an	AN8073.1	53.m03926	AO070330000031	0	-177	-163					ATGTTCCAGCCTTAG	ATGTTCCAGCCTTAG			MFQP*	MFQP*			GGGTTCGCAA	TACTCAGGCA	0	A	0	0	0	0	0
1228	880	an	AN8073.1	53.m03926	AO070330000031	0	-103	-59					ATGATCTACCGCCCATTCGGCCGCAGGAAAAAAGAAAAAAGTTGA	ATGATCTACCGCCCATTCGGCCGCAGGAAAAAAGAAAAAAGTTGA			MIYRPFGRRKKEKS*	MIYRPFGRRKKEKS*			TCTTTCTGCC	AATTTCTCTC	0	A	0	0	0	0	0
1231	880	ao	AN8073.1	53.m03926	AO070330000031	0					-172	-122	ATGCTGGGCTCCGGCTTCCACCGCCTGCCAGGAACTATCTGCCGATGTTGA			ATGCTGGGCTCCGGCTTCCACCGCCTGCCAGGAACTATCTGCCGATGTTGA	MLGSGFHRLPGTICRC*			MLGSGFHRLPGTICRC*	TTAAGAAACA	CCGCCCGGAG	0	A	0	0	0	0	0
1232	880	ao	AN8073.1	53.m03926	AO070330000031	0					-128	-99	ATGTTGACCGCCCGGAGAAAAAAAAAGTGA			ATGTTGACCGCCCGGAGAAAAAAAAAGTGA	MLTARRKKK*			MLTARRKKK*	CTATCTGCCG	AAGGGTAAAA	0	A	0	0	0	0	0
1235	884	af	AN1378.1	70.m14845	AO070243000008	0			-111	-94			ATGTGGGCGAGAAGCTAA		ATGTGGGCGAGAAGCTAA		MWARS*		MWARS*		TACCGTTCTC	TCCAGGAGGG	0		FG08359.1	0	0	0	0
1233	884	an	AN1378.1	70.m14845	AO070243000008	0	-162	-112					ATGATGGTTACTGAGCATGCCCTGGAGTTGTCACCCTTTTTGTGTTCCTGA	ATGATGGTTACTGAGCATGCCCTGGAGTTGTCACCCTTTTTGTGTTCCTGA			MMVTEHALELSPFLCS*	MMVTEHALELSPFLCS*			CACATATTCA	GCAGTCATCA	0		FG08359.1	0	0	0	0
1234	884	an	AN1378.1	70.m14845	AO070243000008	0	-159	-112					ATGGTTACTGAGCATGCCCTGGAGTTGTCACCCTTTTTGTGTTCCTGA	ATGGTTACTGAGCATGCCCTGGAGTTGTCACCCTTTTTGTGTTCCTGA			MVTEHALELSPFLCS*	MVTEHALELSPFLCS*			ATATTCAATG	GCAGTCATCA	0		FG08359.1	0	0	0	0
1236	884	ao	AN1378.1	70.m14845	AO070243000008	0					-118	-83	ATGCAAAAGCTTCATACACCCTTTCCTAAACATTGA			ATGCAAAAGCTTCATACACCCTTTCCTAAACATTGA	MQKLHTPFPKH*			MQKLHTPFPKH*	TACACCATCA	CACTATCATG	0		FG08359.1	0	0	0	0
1237	884	ao	AN1378.1	70.m14845	AO070243000008	0					-75	-43	ATGACGTCCAACGCTTACTTTGGTCAGCAGTGA			ATGACGTCCAACGCTTACTTTGGTCAGCAGTGA	MTSNAYFGQQ*			MTSNAYFGQQ*	TGACACTATC	TCACCCTCTT	0		FG08359.1	0	0	0	0
1242	890	af	AN7962.1	58.m07307	AO070336000161	0			-80	-27			ATGGGGTTGATCCCAGGTCTGCCAGACGCATCAGCAAGAGCACAGCATCAGTAA		ATGGGGTTGATCCCAGGTCTGCCAGACGCATCAGCAAGAGCACAGCATCAGTAA		MGLIPGLPDASARAQHQ*		MGLIPGLPDASARAQHQ*		GTCTATAAAT	AGCAGCTCAG	0	GO	0	0	0	0	0
1238	890	an	AN7962.1	58.m07307	AO070336000161	0	-215	-123					ATGGCTCAATGCAGCATTGGCCGCGGATGTAGATATGAGTATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAA	ATGGCTCAATGCAGCATTGGCCGCGGATGTAGATATGAGTATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAA			MAQCSIGRGCRYEYAFCSLRVSVGEGEEKV*	MAQCSIGRGCRYEYAFCSLRVSVGEGEEKV*			GTCCTTGGCT	AGACGCTGTT	0	GO	0	0	0	0	0
1239	890	an	AN7962.1	58.m07307	AO070336000161	0	-207	-184					ATGCAGCATTGGCCGCGGATGTAG	ATGCAGCATTGGCCGCGGATGTAG			MQHWPRM*	MQHWPRM*			CTATGGCTCA	ATATGAGTAT	0	GO	0	0	0	0	0
1240	890	an	AN7962.1	58.m07307	AO070336000161	0	-181	-92					ATGAGTATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAAAGACGCTGTTGATCCCATCGATTGTTGTTGA	ATGAGTATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAAAGACGCTGTTGATCCCATCGATTGTTGTTGA			MSMPFVRLESVLGRGRRKYKDAVDPIDCC*	MSMPFVRLESVLGRGRRKYKDAVDPIDCC*			GGATGTAGAT	TCCCATAAGC	0	GO	0	0	0	0	0
1241	890	an	AN7962.1	58.m07307	AO070336000161	0	-175	-92					ATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAAAGACGCTGTTGATCCCATCGATTGTTGTTGA	ATGCCTTTTGTTCGCTTAGAGTCAGTGTTGGGGAGGGGGAGGAGAAAGTATAAAGACGCTGTTGATCCCATCGATTGTTGTTGA			MPFVRLESVLGRGRRKYKDAVDPIDCC*	MPFVRLESVLGRGRRKYKDAVDPIDCC*			AGATATGAGT	TCCCATAAGC	0	GO	0	0	0	0	0
1243	890	ao	AN7962.1	58.m07307	AO070336000161	0					-240	-193	ATGAAGCCATGCTCCCGGAAGATGCTAACAGTGCCAGGGACAGAGTAA			ATGAAGCCATGCTCCCGGAAGATGCTAACAGTGCCAGGGACAGAGTAA	MKPCSRKMLTVPGTE*			MKPCSRKMLTVPGTE*	CTTGAACACG	CTATCTCCGT	0	GO	0	0	0	0	0
1244	890	ao	AN7962.1	58.m07307	AO070336000161	0					-232	-140	ATGCTCCCGGAAGATGCTAACAGTGCCAGGGACAGAGTAACTATCTCCGTAGTCCATGACACTGCAGCATCAGGACGGAAAAGTGAGGGGTGA			ATGCTCCCGGAAGATGCTAACAGTGCCAGGGACAGAGTAACTATCTCCGTAGTCCATGACACTGCAGCATCAGGACGGAAAAGTGAGGGGTGA	MLPEDANSARDRVTISVVHDTAASGRKSEG*			MLPEDANSARDRVTISVVHDTAASGRKSEG*	CGATGAAGCC	CTGAAAGCCA	0	GO	0	0	0	0	0
1245	890	ao	AN7962.1	58.m07307	AO070336000161	0					-219	-193	ATGCTAACAGTGCCAGGGACAGAGTAA			ATGCTAACAGTGCCAGGGACAGAGTAA	MLTVPGTE*			MLTVPGTE*	CTCCCGGAAG	CTATCTCCGT	0	GO	0	0	0	0	0
1246	890	ao	AN7962.1	58.m07307	AO070336000161	0					-177	-136	ATGACACTGCAGCATCAGGACGGAAAAGTGAGGGGTGACTGA			ATGACACTGCAGCATCAGGACGGAAAAGTGAGGGGTGACTGA	MTLQHQDGKVRGD*			MTLQHQDGKVRGD*	TCCGTAGTCC	AAGCCAATTC	0	GO	0	0	0	0	0
1248	892	af	AN3375.1	66.m04645	AO070281000019	0			-195	-178			ATGGTTCCCCCACCATGA		ATGGTTCCCCCACCATGA		MVPPP*		MVPPP*		ACCCTGACAG	CGAAACTGCT	0	O	0	0	0	YIR004W	YIR004W
1249	892	af	AN3375.1	66.m04645	AO070281000019	0			-181	-80			ATGACGAAACTGCTGTCAGAAAGCATCATCAGGCAGATAAAAATTATTATTGTCTTGGGTCAGCCGACTATTCTGGCAGGTTACGATCTGCTTTCCTCCTGA		ATGACGAAACTGCTGTCAGAAAGCATCATCAGGCAGATAAAAATTATTATTGTCTTGGGTCAGCCGACTATTCTGGCAGGTTACGATCTGCTTTCCTCCTGA		MTKLLSESIIRQIKIIVLGQPTILAGYDLLSS*		MTKLLSESIIRQIKIIVLGQPTILAGYDLLSS*		TTCCCCCACC	TTTTCTCTGA	0	O	0	0	0	YIR004W	YIR004W
1247	892	an	AN3375.1	66.m04645	AO070281000019	0	-204	-160					ATGACGAAAGGCCCTTCGGAAGCTTCACCAGGCAGAAAAAAATAA	ATGACGAAAGGCCCTTCGGAAGCTTCACCAGGCAGAAAAAAATAA			MTKGPSEASPGRKK*	MTKGPSEASPGRKK*			TCTCCCCGCC	TAATCCTCGC	0	O	0	0	0	YIR004W	YIR004W
1250	892	ao	AN3375.1	66.m04645	AO070281000019	0					-241	-143	ATGGGCGCCCCGCGCATGACGAAACTCCCGTCGGAAAGCATCGTCAGGCAGAAAAAAAAAGTTAGTTGTGTATCAATACTCCTACTACTACACCGTTGA			ATGGGCGCCCCGCGCATGACGAAACTCCCGTCGGAAAGCATCGTCAGGCAGAAAAAAAAAGTTAGTTGTGTATCAATACTCCTACTACTACACCGTTGA	MGAPRMTKLPSESIVRQKKKVSCVSILLLLHR*			MGAPRMTKLPSESIVRQKKKVSCVSILLLLHR*	GACAAAAGTC	CTGTTTTGGC	0	O	0	0	0	YIR004W	YIR004W
1251	892	ao	AN3375.1	66.m04645	AO070281000019	0					-226	-143	ATGACGAAACTCCCGTCGGAAAGCATCGTCAGGCAGAAAAAAAAAGTTAGTTGTGTATCAATACTCCTACTACTACACCGTTGA			ATGACGAAACTCCCGTCGGAAAGCATCGTCAGGCAGAAAAAAAAAGTTAGTTGTGTATCAATACTCCTACTACTACACCGTTGA	MTKLPSESIVRQKKKVSCVSILLLLHR*			MTKLPSESIVRQKKKVSCVSILLLLHR*	CGCCCCGCGC	CTGTTTTGGC	0	O	0	0	0	YIR004W	YIR004W
1255	894	af	AN5127.1	54.m06892	AO070291000046	0			-166	-140			ATGCAGTTCGGGATCAGGCTGAAATAG		ATGCAGTTCGGGATCAGGCTGAAATAG		MQFGIRLK*		MQFGIRLK*		CGTTCAGACG	ACAAGCTAAC	0	U	0	0	NCU01741.1	0	0
1253	894	an	AN5127.1	54.m06892	AO070291000046	0	-219	-154					ATGTGGCAGCCACCGTTTTCTCGAAAGATAGTTGACTTTCCGCAATCAGACCGGAGCTTCCAATAA	ATGTGGCAGCCACCGTTTTCTCGAAAGATAGTTGACTTTCCGCAATCAGACCGGAGCTTCCAATAA			MWQPPFSRKIVDFPQSDRSFQ*	MWQPPFSRKIVDFPQSDRSFQ*			GGAGAGACCC	TCATTCAAGG	0	U	0	0	NCU01741.1	0	0
1254	894	an	AN5127.1	54.m06892	AO070291000046	0	-75	-61					ATGGCTATCACCTGA	ATGGCTATCACCTGA			MAIT*	MAIT*			CTAAGCGCGA	CCGCGTAAAC	0	U	0	0	NCU01741.1	0	0
1256	894	ao	AN5127.1	54.m06892	AO070291000046	0					-198	-139	ATGGAGTACTTGTCTATTGTTTGCCGCTACCAGACCACGGGATCGGGTTTATTCAGATAA			ATGGAGTACTTGTCTATTGTTTGCCGCTACCAGACCACGGGATCGGGTTTATTCAGATAA	MEYLSIVCRYQTTGSGLFR*			MEYLSIVCRYQTTGSGLFR*	TGCGGACTTA	GAGCGCTCGA	0	U	0	0	NCU01741.1	0	0
1252	894	conserved	AN5127.1	54.m06892	AO070291000046	0	-96	-82	-95	-81	-96	-82	ATGykbryhmACTAr	ATGTGTATTCACTAA	ATGCGCACAAACTAG	ATGCTGGCCAACTAG	Mcih*	MCIH*	MRTN*	MLAN*	hCyvwhCrys	vhkbbrrkrr	0	U	0	0	NCU01741.1	0	0
1257	895	af	AN1776.1	69.m15061	AO070324000035	0			-239	-213			ATGAGCATCATAATATTTTTGCAATAA		ATGAGCATCATAATATTTTTGCAATAA		MSIIIFLQ*		MSIIIFLQ*		TAATATTATC	TTAAGTCTCT	0	A	FG02192.1	MG03758.1	NCU05645.1	0	0
1258	895	af	AN1776.1	69.m15061	AO070324000035	0			-145	-125			ATGTGCCTTAAGCTCACATAA		ATGTGCCTTAAGCTCACATAA		MCLKLT*		MCLKLT*		AACGGAGTAG	GCGCAGCCGC	0	A	FG02192.1	MG03758.1	NCU05645.1	0	0
1259	895	ao	AN1776.1	69.m15061	AO070324000035	0					-170	-132	ATGCTCGGACACTTACCGAAAGGGGTCGATGACCTTTAG			ATGCTCGGACACTTACCGAAAGGGGTCGATGACCTTTAG	MLGHLPKGVDDL*			MLGHLPKGVDDL*	ATCTGGACTA	AGTAAGCGCA	0	A	FG02192.1	MG03758.1	NCU05645.1	0	0

1261	899	af	AN6913.1	71.m15219	AO070219000018	0			-263	-90			ATGATACTCAAAATGAAAAGTGAAAAAATAGTCCGGACAAAGTTGTTGATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		ATGATACTCAAAATGAAAAGTGAAAAAATAGTCCGGACAAAGTTGTTGATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		MILKMKSEKIVRTKLLMWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		MILKMKSEKIVRTKLLMWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		ATTTTCCGTT	CAGATGCAAC	0	O	0	0	0	0	0
1262	899	af	AN6913.1	71.m15219	AO070219000018	0			-251	-90			ATGAAAAGTGAAAAAATAGTCCGGACAAAGTTGTTGATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		ATGAAAAGTGAAAAAATAGTCCGGACAAAGTTGTTGATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		MKSEKIVRTKLLMWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		MKSEKIVRTKLLMWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		GATACTCAAA	CAGATGCAAC	0	O	0	0	0	0	0
1263	899	af	AN6913.1	71.m15219	AO070219000018	0			-215	-90			ATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		ATGTGGGTGGAGAAGCCGCTTATCGATAGAAGAAAAGCTCCGGTGGCCAACAGAGACCGCAACCGCAGCCCGCGGTTTCTTTTACAGAGGCTGACGCGAGCTGGCGTAAGACTCCTTGTCCCATAG		MWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		MWVEKPLIDRRKAPVANRDRNRSPRFLLQRLTRAGVRLLVP*		AAAGTTGTTG	CAGATGCAAC	0	O	0	0	0	0	0
1264	899	af	AN6913.1	71.m15219	AO070219000018	0			-86	-3			ATGCAACAGATCTTCTTCAACCTTCTCTTCTCATTTGATCCTCCAAAAGCCTCTATGCTGTCGTCGTTCTTTTCTTCTGGTTAG		ATGCAACAGATCTTCTTCAACCTTCTCTTCTCATTTGATCCTCCAAAAGCCTCTATGCTGTCGTCGTTCTTTTCTTCTGGTTAG		MQQIFFNLLFSFDPPKASMLSSFFSSG*		MQQIFFNLLFSFDPPKASMLSSFFSSG*		CCCATAGCAG	CCATGAATGC	0	O	0	0	0	0	0
1260	899	an	AN6913.1	71.m15219	AO070219000018	0	-106	-14					ATGCAGGCGATCTGCAGGTGCTTCCTCCTCCATACAACGTTTTCTGTAGTTGCCTGTGCTCCAGCATCGCTGTCTCTATGCGTCGTCTTATAA	ATGCAGGCGATCTGCAGGTGCTTCCTCCTCCATACAACGTTTTCTGTAGTTGCCTGTGCTCCAGCATCGCTGTCTCTATGCGTCGTCTTATAA			MQAICRCFLLHTTFSVVACAPASLSLCVVL*	MQAICRCFLLHTTFSVVACAPASLSLCVVL*			GGGCGCTTAC	CTCTTCATCA	0	O	0	0	0	0	0
1266	899	ao	AN6913.1	71.m15219	AO070219000018	0					-259	-173	ATGAGGACCGGAAAGTTTGTGTTTTATCACAGCCGTAGAATATTTTCAGTGGAGACAATAGTCGCTATCGATAACGAGTCCGGGTAG			ATGAGGACCGGAAAGTTTGTGTTTTATCACAGCCGTAGAATATTTTCAGTGGAGACAATAGTCGCTATCGATAACGAGTCCGGGTAG	MRTGKFVFYHSRRIFSVETIVAIDNESG*			MRTGKFVFYHSRRIFSVETIVAIDNESG*	AGCCATTGTG	CCACAGAAAC	0	O	0	0	0	0	0
1273	904	af	AN0452.1	54.m06644	AO070328000184	0			-243	-223			ATGGGATACCCAGTCCACTGA		ATGGGATACCCAGTCCACTGA		MGYPVH*		MGYPVH*		CCACCAGTCA	ATGAGTCTTG	0		0	0	0	0	0
1274	904	af	AN0452.1	54.m06644	AO070328000184	0			-222	-199			ATGAGTCTTGAAGATGGAGGGTGA		ATGAGTCTTGAAGATGGAGGGTGA		MSLEDGG*		MSLEDGG*		AGTCCACTGA	TGATCACCGC	0		0	0	0	0	0
1275	904	af	AN0452.1	54.m06644	AO070328000184	0			-199	-14			ATGATCACCGCATCAAAGAGGTTAAGCGTCGAAGAATCTGGCCATGGGTACTCTGTACAGGACAAAGGCCCAAATTGGGATTCCCCCGGGGCGGGTTCAGGAGAGGCAATTCAGGAAACTATAAGAGTCGGAGGCCAATTCGGTGTGCCGTTCTGTCAGTCAACAGATCATACTCCAAGAACTTGA		ATGATCACCGCATCAAAGAGGTTAAGCGTCGAAGAATCTGGCCATGGGTACTCTGTACAGGACAAAGGCCCAAATTGGGATTCCCCCGGGGCGGGTTCAGGAGAGGCAATTCAGGAAACTATAAGAGTCGGAGGCCAATTCGGTGTGCCGTTCTGTCAGTCAACAGATCATACTCCAAGAACTTGA		MITASKRLSVEESGHGYSVQDKGPNWDSPGAGSGEAIQETIRVGGQFGVPFCQSTDHTPRT*		MITASKRLSVEESGHGYSVQDKGPNWDSPGAGSGEAIQETIRVGGQFGVPFCQSTDHTPRT*		ATGGAGGGTG	ACCATTATTC	0		0	0	0	0	0
1276	904	af	AN0452.1	54.m06644	AO070328000184	0			-156	-76			ATGGGTACTCTGTACAGGACAAAGGCCCAAATTGGGATTCCCCCGGGGCGGGTTCAGGAGAGGCAATTCAGGAAACTATAA		ATGGGTACTCTGTACAGGACAAAGGCCCAAATTGGGATTCCCCCGGGGCGGGTTCAGGAGAGGCAATTCAGGAAACTATAA		MGTLYRTKAQIGIPPGRVQERQFRKL*		MGTLYRTKAQIGIPPGRVQERQFRKL*		GAATCTGGCC	GAGTCGGAGG	0		0	0	0	0	0
1267	904	an	AN0452.1	54.m06644	AO070328000184	0	-180	-160					ATGGCACAGCAGATTTGGTGA	ATGGCACAGCAGATTTGGTGA			MAQQIW*	MAQQIW*			TTTGTGACGA	TATATCCGAC	0		0	0	0	0	0
1268	904	an	AN0452.1	54.m06644	AO070328000184	0	-137	-87					ATGCGTTTCGGCTCACAGGATGGAGAATGTTGGCTCGATGGAGATAAATAG	ATGCGTTTCGGCTCACAGGATGGAGAATGTTGGCTCGATGGAGATAAATAG			MRFGSQDGECWLDGDK*	MRFGSQDGECWLDGDK*			AATATACTGA	CAGACGGCCC	0		0	0	0	0	0
1269	904	an	AN0452.1	54.m06644	AO070328000184	0	-118	-11					ATGGAGAATGTTGGCTCGATGGAGATAAATAGCAGACGGCCCATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA	ATGGAGAATGTTGGCTCGATGGAGATAAATAGCAGACGGCCCATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA			MENVGSMEINSRRPMARSKLLAVTSSSRNRLSIAC*	MENVGSMEINSRRPMARSKLLAVTSSSRNRLSIAC*			GGCTCACAGG	CTTTGACGAC	0		0	0	0	0	0
1270	904	an	AN0452.1	54.m06644	AO070328000184	0	-111	-91					ATGTTGGCTCGATGGAGATAA	ATGTTGGCTCGATGGAGATAA			MLARWR*	MLARWR*			AGGATGGAGA	ATAGCAGACG	0		0	0	0	0	0
1271	904	an	AN0452.1	54.m06644	AO070328000184	0	-100	-11					ATGGAGATAAATAGCAGACGGCCCATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA	ATGGAGATAAATAGCAGACGGCCCATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA			MEINSRRPMARSKLLAVTSSSRNRLSIAC*	MEINSRRPMARSKLLAVTSSSRNRLSIAC*			TGTTGGCTCG	CTTTGACGAC	0		0	0	0	0	0
1272	904	an	AN0452.1	54.m06644	AO070328000184	0	-76	-11					ATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA	ATGGCGAGAAGCAAGCTTTTGGCTGTGACATCTAGTTCACGGAATCGCTTGTCTATCGCCTGTTGA			MARSKLLAVTSSSRNRLSIAC*	MARSKLLAVTSSSRNRLSIAC*			CAGACGGCCC	CTTTGACGAC	0		0	0	0	0	0
1277	904	ao	AN0452.1	54.m06644	AO070328000184	0					-201	-154	ATGTGCCGAATTAACCGGAGATTAAACCACGGTTCAGTGTGTTTCTAG			ATGTGCCGAATTAACCGGAGATTAAACCACGGTTCAGTGTGTTTCTAG	MCRINRRLNHGSVCF*			MCRINRRLNHGSVCF*	TCTAATCCCA	CTGAGGGCAT	0		0	0	0	0	0
1278	906	an	AN2959.1	59.m09083	AO070337000209	0	-207	-181					ATGTTAGCAAATTGGATGTTTAGATGA	ATGTTAGCAAATTGGATGTTTAGATGA			MLANWMFR*	MLANWMFR*			GTCCTTTGAG	CGTGCTAGCA	0	G	0	0	0	0	0
1279	906	an	AN2959.1	59.m09083	AO070337000209	0	-192	-181					ATGTTTAGATGA	ATGTTTAGATGA			MFR*	MFR*			AGCAAATTGG	CGTGCTAGCA	0	G	0	0	0	0	0
1280	906	an	AN2959.1	59.m09083	AO070337000209	0	-184	-173					ATGACGTGCTAG	ATGACGTGCTAG			MTC*	MTC*			GGATGTTTAG	CATGGCAGAG	0	G	0	0	0	0	0
1281	906	an	AN2959.1	59.m09083	AO070337000209	0	-171	-43					ATGGCAGAGAGCAGAAGCAAGCAAAATCCCCAGCATGACAGGCGGATAAATCAAGCTTTAAATTCTCAGTTATCCCGTACTACTCCGCGGAAGAGTTCATCGCCAACTTTTCTTGGTCGACCACCCTAG	ATGGCAGAGAGCAGAAGCAAGCAAAATCCCCAGCATGACAGGCGGATAAATCAAGCTTTAAATTCTCAGTTATCCCGTACTACTCCGCGGAAGAGTTCATCGCCAACTTTTCTTGGTCGACCACCCTAG			MAESRSKQNPQHDRRINQALNSQLSRTTPRKSSSPTFLGRPP*	MAESRSKQNPQHDRRINQALNSQLSRTTPRKSSSPTFLGRPP*			ACGTGCTAGC	GCTCTTGATT	0	G	0	0	0	0	0
1282	906	an	AN2959.1	59.m09083	AO070337000209	0	-137	-123					ATGACAGGCGGATAA	ATGACAGGCGGATAA			MTGG*	MTGG*			AATCCCCAGC	ATCAAGCTTT	0	G	0	0	0	0	0
1283	906	ao	AN2959.1	59.m09083	AO070337000209	0					-201	-187	ATGCTCGTCGCGTAG			ATGCTCGTCGCGTAG	MLVA*			MLVA*	TTCACGGTGC	TCTCAACTAG	0	G	0	0	0	0	0
1284	906	ao	AN2959.1	59.m09083	AO070337000209	0					-84	-70	ATGCTGCCCTTGTAA			ATGCTGCCCTTGTAA	MLPL*			MLPL*	TTAATTGCAT	TTGAAACAGC	0	G	0	0	0	0	0
1291	915	af	AN0139.1	71.m15422	AO070321000113	0			-196	-173			ATGTTAGCGACTCGACTGCGGTGA		ATGTTAGCGACTCGACTGCGGTGA		MLATRLR*		MLATRLR*		CTGCGTTGAG	ATATCAATCG	0	E	0	0	0	0	0
1290	915	an	AN0139.1	71.m15422	AO070321000113	0	-88	-77					ATGCCCCAGTGA	ATGCCCCAGTGA			MPQ*	MPQ*			CAGCGGTGCA	CAACTCGGCA	0	E	0	0	0	0	0
1292	915	ao	AN0139.1	71.m15422	AO070321000113	0					-191	-159	ATGTTTCCCCGGTGTTTATTCTCTACACTCTAG			ATGTTTCCCCGGTGTTTATTCTCTACACTCTAG	MFPRCLFSTL*			MFPRCLFSTL*	AGCTGAAGTG	TAAATTGGAT	0	E	0	0	0	0	0
1297	916	af	AN1524.1	55.m03268	AO070334000242	0			-218	-171			ATGCGAGGGATATATTCTTTTGGCCTACAGCTATATCACTCAATTTGA		ATGCGAGGGATATATTCTTTTGGCCTACAGCTATATCACTCAATTTGA		MRGIYSFGLQLYHSI*		MRGIYSFGLQLYHSI*		AACCTCAGCA	CCTGGTCTCC	0	H	FG00417.1	0	0	0	0
1298	916	af	AN1524.1	55.m03268	AO070334000242	0			-137	-114			ATGCGGCGTCTGCTTTATCGATAA		ATGCGGCGTCTGCTTTATCGATAA		MRRLLYR*		MRRLLYR*		CGTGGGCCGA	GCGAGCAATC	0	H	FG00417.1	0	0	0	0
1299	916	af	AN1524.1	55.m03268	AO070334000242	0			-80	-9			ATGCCCCTCTGTAGTTTGATCTCCGCAGAATACCGACTACTTCTCACCTATCTCCAGATTATATCACAGTAA		ATGCCCCTCTGTAGTTTGATCTCCGCAGAATACCGACTACTTCTCACCTATCTCCAGATTATATCACAGTAA		MPLCSLISAEYRLLLTYLQIISQ*		MPLCSLISAEYRLLLTYLQIISQ*		AAATTTGTCA	CCGCACAGAT	0	H	FG00417.1	0	0	0	0
1293	916	an	AN1524.1	55.m03268	AO070334000242	0	-174	-16					ATGAGTCACAGCTGGAAATCGATACTGGCTGAATGCGGGATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGAAACGGCATTAACTCATTCTCACATCTTGTCTCGAGGATAA	ATGAGTCACAGCTGGAAATCGATACTGGCTGAATGCGGGATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGAAACGGCATTAACTCATTCTCACATCTTGTCTCGAGGATAA			MSHSWKSILAECGMLDYLSISEPWEVFPASNFQGPSITHETALTHSHILSRG*	MSHSWKSILAECGMLDYLSISEPWEVFPASNFQGPSITHETALTHSHILSRG*			CACAAGCTGG	TCTCGTTGCA	0	H	FG00417.1	0	0	0	0
1294	916	an	AN1524.1	55.m03268	AO070334000242	0	-142	-56					ATGCGGGATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGA	ATGCGGGATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGA			MRDAGLLIDKRTLGGFSRLKFSRPLHHP*	MRDAGLLIDKRTLGGFSRLKFSRPLHHP*			TACTGGCTGA	AACGGCATTA	0	H	FG00417.1	0	0	0	0
1295	916	an	AN1524.1	55.m03268	AO070334000242	0	-135	-16					ATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGAAACGGCATTAACTCATTCTCACATCTTGTCTCGAGGATAA	ATGCTGGATTACTTATCGATAAGCGAACCTTGGGAGGTTTTTCCCGCCTCAAATTTTCAAGGCCCCTCCATCACCCATGAAACGGCATTAACTCATTCTCACATCTTGTCTCGAGGATAA			MLDYLSISEPWEVFPASNFQGPSITHETALTHSHILSRG*	MLDYLSISEPWEVFPASNFQGPSITHETALTHSHILSRG*			TGAATGCGGG	TCTCGTTGCA	0	H	FG00417.1	0	0	0	0
1300	916	ao	AN1524.1	55.m03268	AO070334000242	0					-260	-219	ATGCTCTTCTACTTCGAATTTCCTGTGATCCACAGCTACTAA			ATGCTCTTCTACTTCGAATTTCCTGTGATCCACAGCTACTAA	MLFYFEFPVIHSY*			MLFYFEFPVIHSY*	GACAACGTGC	ATGCCAAATA	0	H	FG00417.1	0	0	0	0
1301	916	ao	AN1524.1	55.m03268	AO070334000242	0					-218	-117	ATGCCAAATAAAATTAGGCTCATACAGGATCAGGAGGGGCTGTCGTCTACCTCTTCATCCATGGTGACTCAGTGGGCCGAAAGCGGCCTTCTTTATCGATAA			ATGCCAAATAAAATTAGGCTCATACAGGATCAGGAGGGGCTGTCGTCTACCTCTTCATCCATGGTGACTCAGTGGGCCGAAAGCGGCCTTCTTTATCGATAA	MPNKIRLIQDQEGLSSTSSSMVTQWAESGLLYR*			MPNKIRLIQDQEGLSSTSSSMVTQWAESGLLYR*	CAGCTACTAA	GCGAGCAGTC	0	H	FG00417.1	0	0	0	0
1302	916	ao	AN1524.1	55.m03268	AO070334000242	0					-158	-117	ATGGTGACTCAGTGGGCCGAAAGCGGCCTTCTTTATCGATAA			ATGGTGACTCAGTGGGCCGAAAGCGGCCTTCTTTATCGATAA	MVTQWAESGLLYR*			MVTQWAESGLLYR*	CTCTTCATCC	GCGAGCAGTC	0	H	FG00417.1	0	0	0	0
1309	918	af	AN7240.1	72.m19809	AO070290000007	0			-212	-186			ATGTGTCATTTTTGCATATTTGCTTGA		ATGTGTCATTTTTGCATATTTGCTTGA		MCHFCIFA*		MCHFCIFA*		GCAATAAGCA	TGATGATCGA	0	G	0	0	0	0	0
1310	918	af	AN7240.1	72.m19809	AO070290000007	0			-186	-40			ATGATGATCGACAGTGCTCTCCGGATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		ATGATGATCGACAGTGCTCTCCGGATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		MMIDSALRMIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		MMIDSALRMIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		TATTTGCTTG	GAAAGAAGCA	0	G	0	0	0	0	0
1311	918	af	AN7240.1	72.m19809	AO070290000007	0			-183	-40			ATGATCGACAGTGCTCTCCGGATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		ATGATCGACAGTGCTCTCCGGATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		MIDSALRMIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		MIDSALRMIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		TTGCTTGATG	GAAAGAAGCA	0	G	0	0	0	0	0
1312	918	af	AN7240.1	72.m19809	AO070290000007	0			-162	-40			ATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		ATGATTGATTTTCGTGATGTGTCCTGCTGGCTGGTTTACCTGATTGGGCAAACCCGTGTAGTTGGGCCGCCTGCCTATTTGAGCATAGGCACTACATATATAATGCGGTGGATCTTCCAGTGA		MIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		MIDFRDVSCWLVYLIGQTRVVGPPAYLSIGTTYIMRWIFQ*		TGCTCTCCGG	GAAAGAAGCA	0	G	0	0	0	0	0
1313	918	af	AN7240.1	72.m19809	AO070290000007	0			-146	-120			ATGTGTCCTGCTGGCTGGTTTACCTGA		ATGTGTCCTGCTGGCTGGTTTACCTGA		MCPAGWFT*		MCPAGWFT*		GATTTTCGTG	TTGGGCAAAC	0	G	0	0	0	0	0
1308	918	an	AN7240.1	72.m19809	AO070290000007	0	-201	-160					ATGGCAGAGCCCTGGACGGCGCTGGCCACCTTTACGATTTAG	ATGGCAGAGCCCTGGACGGCGCTGGCCACCTTTACGATTTAG			MAEPWTALATFTI*	MAEPWTALATFTI*			TAGGGCAAGA	GCAGTTAATA	0	G	0	0	0	0	0
1315	918	ao	AN7240.1	72.m19809	AO070290000007	0					-176	-129	ATGTTTGTTTGCTCCGGTCTTTGCTGCAAATTTTACCGCTTTAGGTAA			ATGTTTGTTTGCTCCGGTCTTTGCTGCAAATTTTACCGCTTTAGGTAA	MFVCSGLCCKFYRFR*			MFVCSGLCCKFYRFR*	GAGGTGGTGG	TTTAATCAAC	0	G	0	0	0	0	0
1319	924	af	AN4753.1	59.m09232	AO070327000066	0			-201	-91			ATGGTTGCTTATGTGTCCTCAAGCGAGCCAAACCACGCCATATGGCCAGCACAGCTTATCGGGGAAAGTCGTTGGTCTCCGCCGATCACGGGTTCCTCTTCACGATCCTAA		ATGGTTGCTTATGTGTCCTCAAGCGAGCCAAACCACGCCATATGGCCAGCACAGCTTATCGGGGAAAGTCGTTGGTCTCCGCCGATCACGGGTTCCTCTTCACGATCCTAA		MVAYVSSSEPNHAIWPAQLIGESRWSPPITGSSSRS*		MVAYVSSSEPNHAIWPAQLIGESRWSPPITGSSSRS*		TGAACCGGGT	AGGTCCGTCC	0	C	0	0	0	0	0

1320	924	af	AN4753.1	59.m09232	AO070327000066	0			-191	-27			ATGTGTCCTCAAGCGAGCCAAACCACGCCATATGGCCAGCACAGCTTATCGGGGAAAGTCGTTGGTCTCCGCCGATCACGGGTTCCTCTTCACGATCCTAAAGGTCCGTCCCGCATGTTCTCCTCGTCATCAATTCTTCAAACAAAGCACCAAGGTCTGGTCTGA		ATGTGTCCTCAAGCGAGCCAAACCACGCCATATGGCCAGCACAGCTTATCGGGGAAAGTCGTTGGTCTCCGCCGATCACGGGTTCCTCTTCACGATCCTAAAGGTCCGTCCCGCATGTTCTCCTCGTCATCAATTCTTCAAACAAAGCACCAAGGTCTGGTCTGA		MCPQASQTTPYGQHSLSGKVVGLRRSRVPLHDPKGPSRMFSSSSILQTKHQGLV*		MCPQASQTTPYGQHSLSGKVVGLRRSRVPLHDPKGPSRMFSSSSILQTKHQGLV*		ATGGTTGCTT	GCGCAGAGGC	0	C	0	0	0	0	0
1321	924	af	AN4753.1	59.m09232	AO070327000066	0			-77	-27			ATGTTCTCCTCGTCATCAATTCTTCAAACAAAGCACCAAGGTCTGGTCTGA		ATGTTCTCCTCGTCATCAATTCTTCAAACAAAGCACCAAGGTCTGGTCTGA		MFSSSSILQTKHQGLV*		MFSSSSILQTKHQGLV*		TCCGTCCCGC	GCGCAGAGGC	0	C	0	0	0	0	0
1316	924	an	AN4753.1	59.m09232	AO070327000066	0	-232	-221					ATGCTGTTCTGA	ATGCTGTTCTGA			MLF*	MLF*			TGACTGTGGT	TTTGAGGATG	0	C	0	0	0	0	0
1317	924	an	AN4753.1	59.m09232	AO070327000066	0	-213	-124					ATGTTATGGATTCGAAGGTCAGCAGTAGTTGCTCGCGCATCAGCCGGTGCCGATCATTTGGGGTTCCGCAGCACGGCCGGGTCGGTTTGA	ATGTTATGGATTCGAAGGTCAGCAGTAGTTGCTCGCGCATCAGCCGGTGCCGATCATTTGGGGTTCCGCAGCACGGCCGGGTCGGTTTGA			MLWIRRSAVVARASAGADHLGFRSTAGSV*	MLWIRRSAVVARASAGADHLGFRSTAGSV*			TGATTTGAGG	ATCTCCTCCA	0	C	0	0	0	0	0
1318	924	an	AN4753.1	59.m09232	AO070327000066	0	-208	-83					ATGGATTCGAAGGTCAGCAGTAGTTGCTCGCGCATCAGCCGGTGCCGATCATTTGGGGTTCCGCAGCACGGCCGGGTCGGTTTGAATCTCCTCCATCGACCTACTTTTTGCTTCTACTTCTTCTAG	ATGGATTCGAAGGTCAGCAGTAGTTGCTCGCGCATCAGCCGGTGCCGATCATTTGGGGTTCCGCAGCACGGCCGGGTCGGTTTGAATCTCCTCCATCGACCTACTTTTTGCTTCTACTTCTTCTAG			MDSKVSSSCSRISRCRSFGVPQHGRVGLNLLHRPTFCFYFF*	MDSKVSSSCSRISRCRSFGVPQHGRVGLNLLHRPTFCFYFF*			TGAGGATGTT	CTCATCAACA	0	C	0	0	0	0	0
1322	924	ao	AN4753.1	59.m09232	AO070327000066	0					-207	-190	ATGAAGTATGGATCGTAA			ATGAAGTATGGATCGTAA	MKYGS*			MKYGS*	AAAGCGATGT	GTAAAGCGAT	0	C	0	0	0	0	0
1323	924	ao	AN4753.1	59.m09232	AO070327000066	0					-200	-186	ATGGATCGTAAGTAA			ATGGATCGTAAGTAA	MDRK*			MDRK*	TGTATGAAGT	AGCGATAGCT	0	C	0	0	0	0	0
1327	927	af	AN8444.1	56.m02492	AO070296000033	0			-185	-159			ATGGTGCCTTTCCAGGAAGATAAATAA		ATGGTGCCTTTCCAGGAAGATAAATAA		MVPFQEDK*		MVPFQEDK*		GCACTCGAAG	TTCGGCTTCA	0	M	0	0	0	0	0
1328	927	af	AN8444.1	56.m02492	AO070296000033	0			-98	-84			ATGCGGGTCCTTTAG		ATGCGGGTCCTTTAG		MRVL*		MRVL*		CTCAAGCATC	AGTACAGAAC	0	M	0	0	0	0	0
1324	927	an	AN8444.1	56.m02492	AO070296000033	0	-148	-119					ATGGAATCTCCCAGAACCTGGTATATATGA	ATGGAATCTCCCAGAACCTGGTATATATGA			MESPRTWYI*	MESPRTWYI*			AGCGGCAGCC	TCTGGGGGAG	0	M	0	0	0	0	0
1325	927	an	AN8444.1	56.m02492	AO070296000033	0	-122	-57					ATGATCTGGGGGAGATTCCCCAAATTTGTGCACAGCTCTGTTTACGCGTCCAAAATGCGCGCCTAA	ATGATCTGGGGGAGATTCCCCAAATTTGTGCACAGCTCTGTTTACGCGTCCAAAATGCGCGCCTAA			MIWGRFPKFVHSSVYASKMRA*	MIWGRFPKFVHSSVYASKMRA*			CCTGGTATAT	CATTCCAGCG	0	M	0	0	0	0	0
1326	927	an	AN8444.1	56.m02492	AO070296000033	0	-68	-57					ATGCGCGCCTAA	ATGCGCGCCTAA			MRA*	MRA*			CGCGTCCAAA	CATTCCAGCG	0	M	0	0	0	0	0
1329	927	ao	AN8444.1	56.m02492	AO070296000033	0					-149	-126	ATGTTCATCATGCGCGGTGTTTAG			ATGTTCATCATGCGCGGTGTTTAG	MFIMRGV*			MFIMRGV*	ATAGAGATTT	ACAAAGAACA	0	M	0	0	0	0	0
1330	927	ao	AN8444.1	56.m02492	AO070296000033	0					-140	-126	ATGCGCGGTGTTTAG			ATGCGCGGTGTTTAG	MRGV*			MRGV*	TATGTTCATC	ACAAAGAACA	0	M	0	0	0	0	0
1332	928	af	AN1289.1	70.m14919	AO070303000050	0			-282	-259			ATGAAAAGCATACTGATGCGCTGA		ATGAAAAGCATACTGATGCGCTGA		MKSILMR*		MKSILMR*		AAGAAGTCGA	CGGTAAATGT	0	S	0	0	0	0	0
1333	928	af	AN1289.1	70.m14919	AO070303000050	0			-252	-208			ATGTATTTTCAATTGAACACTATCCTGTCGATTTTTGGACGATAG		ATGTATTTTCAATTGAACACTATCCTGTCGATTTTTGGACGATAG		MYFQLNTILSIFGR*		MYFQLNTILSIFGR*		CTGACGGTAA	ATACCTATAG	0	S	0	0	0	0	0
1334	928	af	AN1289.1	70.m14919	AO070303000050	0			-151	-14			ATGCGGGGAAACTTCGATGTTATCCCGCGATCGATAACCCCAAAACGACCGCTCCTCGACGCTCCCAGGGTGCTCCAATTGGCTTGTTCTCAACCCTTTTTTTCCCCTACAAAAAGCCATACAGGACTAATGGAATAA		ATGCGGGGAAACTTCGATGTTATCCCGCGATCGATAACCCCAAAACGACCGCTCCTCGACGCTCCCAGGGTGCTCCAATTGGCTTGTTCTCAACCCTTTTTTTCCCCTACAAAAAGCCATACAGGACTAATGGAATAA		MRGNFDVIPRSITPKRPLLDAPRVLQLACSQPFFSPTKSHTGLME*		MRGNFDVIPRSITPKRPLLDAPRVLQLACSQPFFSPTKSHTGLME*		TGGATAGTTG	CCACTACCAT	0	S	0	0	0	0	0
1335	928	af	AN1289.1	70.m14919	AO070303000050	0			-135	-115			ATGTTATCCCGCGATCGATAA		ATGTTATCCCGCGATCGATAA		MLSRDR*		MLSRDR*		GGAAACTTCG	CCCCAAAACG	0	S	0	0	0	0	0
1331	928	an	AN1289.1	70.m14919	AO070303000050	0	-186	-139					ATGCCGGGGGATTTTCGATCGTCCATTCCGAGAGGTAGAAATTACTAG	ATGCCGGGGGATTTTCGATCGTCCATTCCGAGAGGTAGAAATTACTAG			MPGDFRSSIPRGRNY*	MPGDFRSSIPRGRNY*			TTGGTGGATA	CTCTACGAAA	0	S	0	0	0	0	0
1336	928	ao	AN1289.1	70.m14919	AO070303000050	0					-156	-58	ATGCAGATCAACCAGTTGACGCGAAGCCATGCGGGGAAAAGCCAAGTTGGGGTCCAGCGGACGGACAATCCAATGAGCGCATCCATCACCCTAGCTTGA			ATGCAGATCAACCAGTTGACGCGAAGCCATGCGGGGAAAAGCCAAGTTGGGGTCCAGCGGACGGACAATCCAATGAGCGCATCCATCACCCTAGCTTGA	MQINQLTRSHAGKSQVGVQRTDNPMSASITLA*			MQINQLTRSHAGKSQVGVQRTDNPMSASITLA*	AAGTTAAGCA	AAGTGCAAAC	0	S	0	0	0	0	0
1337	928	ao	AN1289.1	70.m14919	AO070303000050	0					-128	-81	ATGCGGGGAAAAGCCAAGTTGGGGTCCAGCGGACGGACAATCCAATGA			ATGCGGGGAAAAGCCAAGTTGGGGTCCAGCGGACGGACAATCCAATGA	MRGKAKLGSSGRTIQ*			MRGKAKLGSSGRTIQ*	ACGCGAAGCC	GCGCATCCAT	0	S	0	0	0	0	0
1338	928	ao	AN1289.1	70.m14919	AO070303000050	0					-84	-58	ATGAGCGCATCCATCACCCTAGCTTGA			ATGAGCGCATCCATCACCCTAGCTTGA	MSASITLA*			MSASITLA*	GGACAATCCA	AAGTGCAAAC	0	S	0	0	0	0	0
1340	929	af	AN1049.1	70.m15206	AO070312000116	0			-170	-156			ATGGAAGTCATGTGA		ATGGAAGTCATGTGA		MEVM*		MEVM*		AGGTCAAGCA	TCCTATCGGC	0	D	0	0	0	0	0
1339	929	an	AN1049.1	70.m15206	AO070312000116	0	-215	-48					ATGTGCCTCTGGGTCCCATTCTTCCAATTACTTCGACGTATTCACTCCGTATCCAAACTTGAATTATCTCCGTACAATCTCCGGCTGACTAACCGAGGGTGGAAGGTGATCGAAGATCGACAGATTCATCATCAACGCCTCTGCCTACCTGCTTCCACGTCTCTATAA	ATGTGCCTCTGGGTCCCATTCTTCCAATTACTTCGACGTATTCACTCCGTATCCAAACTTGAATTATCTCCGTACAATCTCCGGCTGACTAACCGAGGGTGGAAGGTGATCGAAGATCGACAGATTCATCATCAACGCCTCTGCCTACCTGCTTCCACGTCTCTATAA			MCLWVPFFQLLRRIHSVSKLELSPYNLRLTNRGWKVIEDRQIHHQRLCLPASTSL*	MCLWVPFFQLLRRIHSVSKLELSPYNLRLTNRGWKVIEDRQIHHQRLCLPASTSL*			TCACTGGGAG	GATCATGTCG	0	D	0	0	0	0	0
1341	929	ao	AN1049.1	70.m15206	AO070312000116	0					-111	-100	ATGCGCCGATAA			ATGCGCCGATAA	MRR*			MRR*	ATATAAAGCA	GCCCCAAGCA	0	D	0	0	0	0	0
1344	932	af	AN5323.1	55.m03189	AO070333000254	0			-216	-91			ATGGAGGTAACCCCCCCCCCCCCCCATGTTTGAAACAATGCCCCAGAGCATATAAGACTGGAACAATCCCCACAACTGATCCGGAGGAGGCATGGTGCCCGATTACCCCAGGTTATATACCTTGA		ATGGAGGTAACCCCCCCCCCCCCCCATGTTTGAAACAATGCCCCAGAGCATATAAGACTGGAACAATCCCCACAACTGATCCGGAGGAGGCATGGTGCCCGATTACCCCAGGTTATATACCTTGA		MEVTPPPPPCLKQCPRAYKTGTIPTTDPEEAWCPITPGYIP*		MEVTPPPPPCLKQCPRAYKTGTIPTTDPEEAWCPITPGYIP*		ATCAGTCGGC	CCGAAGCCGA	0	R	0	0	0	0	0
1345	932	af	AN5323.1	55.m03189	AO070333000254	0			-190	-161			ATGTTTGAAACAATGCCCCAGAGCATATAA		ATGTTTGAAACAATGCCCCAGAGCATATAA		MFETMPQSI*		MFETMPQSI*		CCCCCCCCCC	GACTGGAACA	0	R	0	0	0	0	0
1346	932	af	AN5323.1	55.m03189	AO070333000254	0			-178	-161			ATGCCCCAGAGCATATAA		ATGCCCCAGAGCATATAA		MPQSI*		MPQSI*		GTTTGAAACA	GACTGGAACA	0	R	0	0	0	0	0
1347	932	af	AN5323.1	55.m03189	AO070333000254	0			-124	-53			ATGGTGCCCGATTACCCCAGGTTATATACCTTGACCGAAGCCGACGCGGAGAAGAGAGAGAAGACCCTGTAG		ATGGTGCCCGATTACCCCAGGTTATATACCTTGACCGAAGCCGACGCGGAGAAGAGAGAGAAGACCCTGTAG		MVPDYPRLYTLTEADAEKREKTL*		MVPDYPRLYTLTEADAEKREKTL*		CGGAGGAGGC	ACTTTGTTTA	0	R	0	0	0	0	0
1342	932	an	AN5323.1	55.m03189	AO070333000254	0	-131	-120					ATGGAATGGTGA	ATGGAATGGTGA			MEW*	MEW*			TAGCAGCGTC	TATCAGCCGC	0	R	0	0	0	0	0
1343	932	an	AN5323.1	55.m03189	AO070333000254	0	-126	-64					ATGGTGATATCAGCCGCAGTGCCATTGTCGGATTGCAGACAGGCGGGGATCGATAAATTCTAG	ATGGTGATATCAGCCGCAGTGCCATTGTCGGATTGCAGACAGGCGGGGATCGATAAATTCTAG			MVISAAVPLSDCRQAGIDKF*	MVISAAVPLSDCRQAGIDKF*			GCGTCATGGA	CCTGTCCCAT	0	R	0	0	0	0	0
1348	932	ao	AN5323.1	55.m03189	AO070333000254	0					-276	-235	ATGAAGACATTCGCTGAGGCTGTTACCCAATATGTCCTATAA			ATGAAGACATTCGCTGAGGCTGTTACCCAATATGTCCTATAA	MKTFAEAVTQYVL*			MKTFAEAVTQYVL*	GATTGGCCGT	AGCCAGACAC	0	R	0	0	0	0	0
1349	932	ao	AN5323.1	55.m03189	AO070333000254	0					-245	-171	ATGTCCTATAAAGCCAGACACGCATCCCCGCATCTCACGGTGGACACCTTACCTTGTTCTTGTGAGGTATCATAG			ATGTCCTATAAAGCCAGACACGCATCCCCGCATCTCACGGTGGACACCTTACCTTGTTCTTGTGAGGTATCATAG	MSYKARHASPHLTVDTLPCSCEVS*			MSYKARHASPHLTVDTLPCSCEVS*	GTTACCCAAT	CTATTTCCGC	0	R	0	0	0	0	0
1350	932	ao	AN5323.1	55.m03189	AO070333000254	0					-154	-89	ATGCTAACTACCTGGAAGCCACTCCAGAAATTAGAACTACTGTGTTTCTGTAGTTTGGATACCTGA			ATGCTAACTACCTGGAAGCCACTCCAGAAATTAGAACTACTGTGTTTCTGTAGTTTGGATACCTGA	MLTTWKPLQKLELLCFCSLDT*			MLTTWKPLQKLELLCFCSLDT*	CCGCCAAGCT	TACTCATTTG	0	R	0	0	0	0	0
1351	935	af	AN0657.1	70.m15789	AO070343000569	0			-247	-170			ATGCCTGAGGTATTGTCGCGGAGTTTATCAAAATATGCTAGAAACAAGTGGATGCGTTGCCAATCGAGCTGCGACTAG		ATGCCTGAGGTATTGTCGCGGAGTTTATCAAAATATGCTAGAAACAAGTGGATGCGTTGCCAATCGAGCTGCGACTAG		MPEVLSRSLSKYARNKWMRCQSSCD*		MPEVLSRSLSKYARNKWMRCQSSCD*		CTGTCCCTGG	CTTCAGGAAC	0	U	0	0	0	0	0
1352	935	af	AN0657.1	70.m15789	AO070343000569	0			-213	-94			ATGCTAGAAACAAGTGGATGCGTTGCCAATCGAGCTGCGACTAGCTTCAGGAACCATTCATTCCCGCCCCCGGCGTTTCTTAGCTATTGTATAGGTATCTTTTATGCTAGTCTGACGTGA		ATGCTAGAAACAAGTGGATGCGTTGCCAATCGAGCTGCGACTAGCTTCAGGAACCATTCATTCCCGCCCCCGGCGTTTCTTAGCTATTGTATAGGTATCTTTTATGCTAGTCTGACGTGA		MLETSGCVANRAATSFRNHSFPPPAFLSYCIGIFYASLT*		MLETSGCVANRAATSFRNHSFPPPAFLSYCIGIFYASLT*		TTATCAAAAT	GATACTTCTT	0	U	0	0	0	0	0
1353	935	af	AN0657.1	70.m15789	AO070343000569	0			-196	-170			ATGCGTTGCCAATCGAGCTGCGACTAG		ATGCGTTGCCAATCGAGCTGCGACTAG		MRCQSSCD*		MRCQSSCD*		AAACAAGTGG	CTTCAGGAAC	0	U	0	0	0	0	0
1364	949	af	AN1348.1	70.m14885	AO070247000017	0			-246	-199			ATGAATCTTTCCATCCGCCATCACAGACCAGCGTCGAGCGTCTCATAG		ATGAATCTTTCCATCCGCCATCACAGACCAGCGTCGAGCGTCTCATAG		MNLSIRHHRPASSVS*		MNLSIRHHRPASSVS*		GCGTGCCAAA	AAAAGCACAA	0	J	0	0	0	0	0
1365	951	an	AN0946.1	70.m15580	AO070320000143	0	-230	-186					ATGATCACCAGCGTCAAGAAGCGGGGAGAGGAGAGCTCTCTGTGA	ATGATCACCAGCGTCAAGAAGCGGGGAGAGGAGAGCTCTCTGTGA			MITSVKKRGEESSL*	MITSVKKRGEESSL*			TAAGATCGAT	AAAGGCCGAA	0	J	FG00292.1	0	0	YOR206W	0
1373	952	af	AN1604.1	55.m03110	AO070339000257	0			-230	-207			ATGTCTGACCGCTATGTGAGATAA		ATGTCTGACCGCTATGTGAGATAA		MSDRYVR*		MSDRYVR*		GCTTCCTGGA	ATGATATCAA	0		0	0	0	0	0
1374	952	af	AN1604.1	55.m03110	AO070339000257	0			-206	-192			ATGATATCAAGATGA		ATGATATCAAGATGA		MISR*		MISR*		TGTGAGATAA	AATGCCATGT	0		0	0	0	0	0
1375	952	af	AN1604.1	55.m03110	AO070339000257	0			-195	-127			ATGAAATGCCATGTTGGCATTCAATTGGCGCTAGGCAATCAATTGATCGAGGATCTGTGCAGATCATAA		ATGAAATGCCATGTTGGCATTCAATTGGCGCTAGGCAATCAATTGATCGAGGATCTGTGCAGATCATAA		MKCHVGIQLALGNQLIEDLCRS*		MKCHVGIQLALGNQLIEDLCRS*		TGATATCAAG	CAGAGATTTC	0		0	0	0	0	0
1376	952	af	AN1604.1	55.m03110	AO070339000257	0			-190	-38			ATGCCATGTTGGCATTCAATTGGCGCTAGGCAATCAATTGATCGAGGATCTGTGCAGATCATAACAGAGATTTCCTCCCATATCTTGACCAGGATGATCAGCAAGCCCATTTTCTTTCTTCTTAAACTTCCGATTGTCCATTGCCCTGTATAG		ATGCCATGTTGGCATTCAATTGGCGCTAGGCAATCAATTGATCGAGGATCTGTGCAGATCATAACAGAGATTTCCTCCCATATCTTGACCAGGATGATCAGCAAGCCCATTTTCTTTCTTCTTAAACTTCCGATTGTCCATTGCCCTGTATAG		MPCWHSIGARQSIDRGSVQIITEISSHILTRMISKPIFFLLKLPIVHCPV*		MPCWHSIGARQSIDRGSVQIITEISSHILTRMISKPIFFLLKLPIVHCPV*		TCAAGATGAA	TAGTCAGTAG	0		0	0	0	0	0
1377	952	af	AN1604.1	55.m03110	AO070339000257	0			-185	-162			ATGTTGGCATTCAATTGGCGCTAG		ATGTTGGCATTCAATTGGCGCTAG		MLAFNWR*		MLAFNWR*		ATGAAATGCC	GCAATCAATT	0		0	0	0	0	0
1378	952	af	AN1604.1	55.m03110	AO070339000257	0			-97	-38			ATGATCAGCAAGCCCATTTTCTTTCTTCTTAAACTTCCGATTGTCCATTGCCCTGTATAG		ATGATCAGCAAGCCCATTTTCTTTCTTCTTAAACTTCCGATTGTCCATTGCCCTGTATAG		MISKPIFFLLKLPIVHCPV*		MISKPIFFLLKLPIVHCPV*		CTTGACCAGG	TAGTCAGTAG	0		0	0	0	0	0
1366	952	an	AN1604.1	55.m03110	AO070339000257	0	-219	-196					ATGGCGTTCACAAGCATACTCTAA	ATGGCGTTCACAAGCATACTCTAA			MAFTSIL*	MAFTSIL*			TCCCACTCCC	TGGCCGGCCA	0		0	0	0	0	0
1367	952	an	AN1604.1	55.m03110	AO070339000257	0	-196	-149					ATGGCCGGCCAAGTGCGCCGAGTGAATAGTCTCTGCGAGATAGAGTAG	ATGGCCGGCCAAGTGCGCCGAGTGAATAGTCTCTGCGAGATAGAGTAG			MAGQVRRVNSLCEIE*	MAGQVRRVNSLCEIE*			GCATACTCTA	AACATGATAC	0		0	0	0	0	0
1368	952	an	AN1604.1	55.m03110	AO070339000257	0	-145	-83					ATGATACGCAGAAAAGGCTCCTGTCAACATGTTAATATATCCATAGACGCACTGCAATGTTAG	ATGATACGCAGAAAAGGCTCCTGTCAACATGTTAATATATCCATAGACGCACTGCAATGTTAG			MIRRKGSCQHVNISIDALQC*	MIRRKGSCQHVNISIDALQC*			AGAGTAGAAC	AATTTTGTCT	0		0	0	0	0	0
1369	952	an	AN1604.1	55.m03110	AO070339000257	0	-117	-100					ATGTTAATATATCCATAG	ATGTTAATATATCCATAG			MLIYP*	MLIYP*			TCCTGTCAAC	ACGCACTGCA	0		0	0	0	0	0
1370	952	an	AN1604.1	55.m03110	AO070339000257	0	-89	-18					ATGTTAGAATTTTGTCTGGCCATGGGTTTGGTATCCCTAGGTTTCTCCGACATGATTATCAGTCCAATCTGA	ATGTTAGAATTTTGTCTGGCCATGGGTTTGGTATCCCTAGGTTTCTCCGACATGATTATCAGTCCAATCTGA			MLEFCLAMGLVSLGFSDMIISPI*	MLEFCLAMGLVSLGFSDMIISPI*			ACGCACTGCA	AGCGAACCTG	0		0	0	0	0	0
1371	952	an	AN1604.1	55.m03110	AO070339000257	0	-68	-18					ATGGGTTTGGTATCCCTAGGTTTCTCCGACATGATTATCAGTCCAATCTGA	ATGGGTTTGGTATCCCTAGGTTTCTCCGACATGATTATCAGTCCAATCTGA			MGLVSLGFSDMIISPI*	MGLVSLGFSDMIISPI*			TTGTCTGGCC	AGCGAACCTG	0		0	0	0	0	0
1379	952	ao	AN1604.1	55.m03110	AO070339000257	0					-188	-174	ATGCTACTTGATTAG			ATGCTACTTGATTAG	MLLD*			MLLD*	AACGCTATTG	TTTGTGATAT	0		0	0	0	0	0
1380	952	ao	AN1604.1	55.m03110	AO070339000257	0					-132	-109	ATGTACTTTTTAGTTGGATTATAA			ATGTACTTTTTAGTTGGATTATAA	MYFLVGL*			MYFLVGL*	ACCCAAGGAT	AGATGGCCGT	0		0	0	0	0	0
1385	958	af	AN1634.1	58.m09021	AO070299000045	0			-221	-162			ATGGATTTGGACATTTCTTTTTCGATCGTGTACTCTAATTCTAGGTCGCAATGCCACTGA		ATGGATTTGGACATTTCTTTTTCGATCGTGTACTCTAATTCTAGGTCGCAATGCCACTGA		MDLDISFSIVYSNSRSQCH*		MDLDISFSIVYSNSRSQCH*		GGGTGGAATT	GACTTCATGT	0	A	0	0	0	0	0
1386	958	af	AN1634.1	58.m09021	AO070299000045	0			-171	-121			ATGCCACTGAGACTTCATGTACTCATTTGCTGGTATCCTTTCCACTGGTAA		ATGCCACTGAGACTTCATGTACTCATTTGCTGGTATCCTTTCCACTGGTAA		MPLRLHVLICWYPFHW*		MPLRLHVLICWYPFHW*		CTAGGTCGCA	TGTAGACAGA	0	A	0	0	0	0	0
1381	958	an	AN1634.1	58.m09021	AO070299000045	0	-229	-218					ATGACTAAGTAG	ATGACTAAGTAG			MTK*	MTK*			TTGTATTCCT	CAGGCTCATT	0	A	0	0	0	0	0
1382	958	an	AN1634.1	58.m09021	AO070299000045	0	-152	-141					ATGATCACGTGA	ATGATCACGTGA			MIT*	MIT*			TAGAAATCTA	TATGCACATA	0	A	0	0	0	0	0
1383	958	an	AN1634.1	58.m09021	AO070299000045	0	-139	-107					ATGCACATATGGTTTTCTTTGCCACCCGTATAA	ATGCACATATGGTTTTCTTTGCCACCCGTATAA			MHIWFSLPPV*	MHIWFSLPPV*			ATCACGTGAT	AATCGAGCCC	0	A	0	0	0	0	0
1384	958	an	AN1634.1	58.m09021	AO070299000045	0	-131	-30					ATGGTTTTCTTTGCCACCCGTATAAAATCGAGCCCATCTGCGGTCTTTCTACTCCGAGCAAGCTTAGATTCGTTTAATAGCAGACGCTTGCACTTTCTTTGA	ATGGTTTTCTTTGCCACCCGTATAAAATCGAGCCCATCTGCGGTCTTTCTACTCCGAGCAAGCTTAGATTCGTTTAATAGCAGACGCTTGCACTTTCTTTGA			MVFFATRIKSSPSAVFLLRASLDSFNSRRLHFL*	MVFFATRIKSSPSAVFLLRASLDSFNSRRLHFL*			ATATGCACAT	CAGTGCACCG	0	A	0	0	0	0	0

1391	960	af	AN5694.1	65.m07419	AO070309000110	0			-254	-222			ATGCTGAAAAGTTACTGTATACTCTGTAGGTAG		ATGCTGAAAAGTTACTGTATACTCTGTAGGTAG		MLKSYCILCR*		MLKSYCILCR*		TCTTAGCCGG	TTGTGATCAT	0	L	0	0	0	0	0
1392	960	af	AN5694.1	65.m07419	AO070309000110	0			-105	-49			ATGCATCATTGCTTTCTTTGGTGGTGCAACTTCCCGTCTCCGGTCCCTGTTTCATAA		ATGCATCATTGCTTTCTTTGGTGGTGCAACTTCCCGTCTCCGGTCCCTGTTTCATAA		MHHCFLWWCNFPSPVPVS*		MHHCFLWWCNFPSPVPVS*		GCGTCGTTTG	TCCCATTTCA	0	L	0	0	0	0	0
1388	960	an	AN5694.1	65.m07419	AO070309000110	0	-187	-68					ATGGCGGGGAAATCGCGTTGTCTACCATTCACCGCCTTTCCAAAGTCAATTTTCTGCCGCAAAAATAGCAAAAACTGGCAGTCGCGATTTCTCCCACATGAGATTCCATCCACTCCGTGA	ATGGCGGGGAAATCGCGTTGTCTACCATTCACCGCCTTTCCAAAGTCAATTTTCTGCCGCAAAAATAGCAAAAACTGGCAGTCGCGATTTCTCCCACATGAGATTCCATCCACTCCGTGA			MAGKSRCLPFTAFPKSIFCRKNSKNWQSRFLPHEIPSTP*	MAGKSRCLPFTAFPKSIFCRKNSKNWQSRFLPHEIPSTP*			TGAAGGGAAT	CACATTCATA	0	L	0	0	0	0	0
1389	960	an	AN5694.1	65.m07419	AO070309000110	0	-90	-43					ATGAGATTCCATCCACTCCGTGACACATTCATATCTATGCTTCCGTGA	ATGAGATTCCATCCACTCCGTGACACATTCATATCTATGCTTCCGTGA			MRFHPLRDTFISMLP*	MRFHPLRDTFISMLP*			TTTCTCCCAC	TCCTTCTGGT	0	L	0	0	0	0	0
1394	961	af	AN2258.1	71.m15899	AO070326000105	0			-146	-60			ATGGTACCGTCACGTCCCGAGGCTTCATGTGGCCCAAGCTTTTTTTTCGGGCTGCCACAAAATTTGTATCTCCCTCTTTTTTTTTGA		ATGGTACCGTCACGTCCCGAGGCTTCATGTGGCCCAAGCTTTTTTTTCGGGCTGCCACAAAATTTGTATCTCCCTCTTTTTTTTTGA		MVPSRPEASCGPSFFFGLPQNLYLPLFF*		MVPSRPEASCGPSFFFGLPQNLYLPLFF*		TTACAGGTGT	TAAGACGACA	0		FG06661.1	0	0	0	0
1395	961	af	AN2258.1	71.m15899	AO070326000105	0			-120	-46			ATGTGGCCCAAGCTTTTTTTTCGGGCTGCCACAAAATTTGTATCTCCCTCTTTTTTTTTGATAAGACGACATTGA		ATGTGGCCCAAGCTTTTTTTTCGGGCTGCCACAAAATTTGTATCTCCCTCTTTTTTTTTGATAAGACGACATTGA		MWPKLFFRAATKFVSPSFFLIRRH*		MWPKLFFRAATKFVSPSFFLIRRH*		CCGAGGCTTC	AGCTTTAAGG	0		FG06661.1	0	0	0	0
1393	961	an	AN2258.1	71.m15899	AO070326000105	0	-140	-72					ATGTGGTGGTCCGAGCTTTGTTATCTCAACCGTATCAAATTTATTTTTCAGCGACTTTTCGCGGGTTAG	ATGTGGTGGTCCGAGCTTTGTTATCTCAACCGTATCAAATTTATTTTTCAGCGACTTTTCGCGGGTTAG			MWWSELCYLNRIKFIFQRLFAG*	MWWSELCYLNRIKFIFQRLFAG*			CCGAGGCTTC	GTTAAGAGCT	0		FG06661.1	0	0	0	0
1396	961	ao	AN2258.1	71.m15899	AO070326000105	0					-195	-163	ATGTGTAATTATTGGTCGGTGGGTAACGGTTAG			ATGTGTAATTATTGGTCGGTGGGTAACGGTTAG	MCNYWSVGNG*			MCNYWSVGNG*	GGGGTTACGC	TACCACTTTT	0		FG06661.1	0	0	0	0
1397	961	ao	AN2258.1	71.m15899	AO070326000105	0					-126	-25	ATGGTACGGTACCTCCGAGGCTTCATGTGGTCAAAGCTTTTCCGCTCCTCCCAAAAAAAAAAAAGTCTCCAAGTTCACCCGGAAGTTCATCAGTTATCTGA			ATGGTACGGTACCTCCGAGGCTTCATGTGGTCAAAGCTTTTCCGCTCCTCCCAAAAAAAAAAAAAAGTCTCCAAGTTCACCCGGAAGTTCATCAGTTATCTGA	MVRYLRGFMWSKLFRSSQKKKKSPSSPGSSSVI*			MVRYLRGFMWSKLFRSSQKKKKSPSSPGSSSVI*	TCTGAAGCGT	CAACGGCACG	0		FG06661.1	0	0	0	0
1398	961	ao	AN2258.1	71.m15899	AO070326000105	0					-102	-25	ATGTGGTCAAAGCTTTTCCGCTCCTCCCAAAAAAAAAAAAAGTCTCCAAGTTCACCCGGAAGTTCATCAGTTATCTGA			ATGTGGTCAAAGCTTTTCCGCTCCTCCCAAAAAAAAAAAAAGTCTCCAAGTTCACCCGGAAGTTCATCAGTTATCTGA	MWSKLFRSSQKKKKSPSSPGSSSVI*			MWSKLFRSSQKKKKSPSSPGSSSVI*	CCGAGGCTTC	CAACGGCACG	0		FG06661.1	0	0	0	0
1399	964	af	AN2888.1	59.m08735	AO070338000126	0			-144	-133			ATGGCCTCCTGA		ATGGCCTCCTGA		MAS*		MAS*		GTGCCAGCGC	TGCTCGGCAC	0		FG06347.1	0	0	0	0
1400	964	af	AN2888.1	59.m08735	AO070338000126	0			-107	-81			ATGCCAGCTAACAGGGGAAATATCTGA		ATGCCAGCTAACAGGGGAAATATCTGA		MPANRGNI*		MPANRGNI*		ACACGAATAT	CACATCTTGC	0		FG06347.1	0	0	0	0
1401	964	ao	AN2888.1	59.m08735	AO070338000126	0					-258	-202	ATGTCTCTTTACCCGTCGTCATCTGCAAGTGGATGTGATGAACAACAGCTTTACTGA			ATGTCTCTTTACCCGTCGTCATCTGCAAGTGGATGTGATGAACAACAGCTTTACTGA	MSLYPSSSASGCDEQQLY*			MSLYPSSSASGCDEQQLY*	GGTACGAGTC	CCCGACATGT	0		FG06347.1	0	0	0	0
1402	964	ao	AN2888.1	59.m08735	AO070338000126	0					-221	-120	ATGAACAACAGCTTTACTGACCCGACATGTGACCAGATCAGATGTATTGGTCGTCCCCCCGCGCATAGCTCAATGATCTTCGAATATACGAAAACCAGTTGA			ATGAACAACAGCTTTACTGACCCGACATGTGACCAGATCAGATGTATTGGTCGTCCCCCCGCGCATAGCTCAATGATCTTCGAATATACGAAAACCAGTTGA	MNNSFTDPTCDQIRCIGRPPAHSSMIFEYTKTS*			MNNSFTDPTCDQIRCIGRPPAHSSMIFEYTKTS*	AGTGGATGTG	ATTTAAACTC	0		FG06347.1	0	0	0	0
1403	964	ao	AN2888.1	59.m08735	AO070338000126	0					-180	-154	ATGTATTGGTCGTCCCCCCGCGCATAG			ATGTATTGGTCGTCCCCCCGCGCATAG	MYWSSPRA*			MYWSSPRA*	ACCAGATCAG	CTCAATGATC	0		FG06347.1	0	0	0	0
1404	964	ao	AN2888.1	59.m08735	AO070338000126	0					-149	-120	ATGATCTTCGAATATACGAAAACCAGTTGA			ATGATCTTCGAATATACGAAAACCAGTTGA	MIFEYTKTS*			MIFEYTKTS*	GCATAGCTCA	ATTTAAACTC	0		FG06347.1	0	0	0	0
1407	965	af	AN8604.1	66.m04790	AO070340000151	0			-168	-97			ATGCTGTCCTGCGACATCATTCGTGTACTGCCATTTCACCATCCACTAATTGGGACTACTAAATGGGACTAG		ATGCTGTCCTGCGACATCATTCGTGTACTGCCATTTCACCATCCACTAATTGGGACTACTAAATGGGACTAG		MLSCDIIRVLPFHHPLIGTTKWD*		MLSCDIIRVLPFHHPLIGTTKWD*		TACATATATA	TATAGTAAGC	0	J	0	0	0	YIR042C	0
1408	965	af	AN8604.1	66.m04790	AO070340000151	0			-106	-92			ATGGGACTAGTATAG		ATGGGACTAGTATAG		MGLV*		MGLV*		GGACTACTAA	TAAGCGTCTG	0	J	0	0	0	YIR042C	0
1409	965	af	AN8604.1	66.m04790	AO070340000151	0			-80	-42			ATGACTCATAAATTCTGTCAGAGTGAATTGCCAAATTGA		ATGACTCATAAATTCTGTCAGAGTGAATTGCCAAATTGA		MTHKFCQSELPN*		MTHKFCQSELPN*		AAGCGTCTGC	TAACCCAGAA	0	J	0	0	0	YIR042C	0
1405	965	an	AN8604.1	66.m04790	AO070340000151	0	-99	-73					ATGTCAAAGTGCGGGGGCCTACGATGA	ATGTCAAAGTGCGGGGGCCTACGATGA			MSKCGGLR*	MSKCGGLR*			TTGCCCGAGT	GTCAGACCAT	0	J	0	0	0	YIR042C	0
1410	965	ao	AN8604.1	66.m04790	AO070340000151	0					-179	-132	ATGACGCACCTCGGCGATTCCACTAGTTTACTTTATTTACATAACTAA			ATGACGCACCTCGGCGATTCCACTAGTTTACTTTATTTACATAACTAA	MTHLGDSTSLLYLHN*			MTHLGDSTSLLYLHN*	AGGTACGGGA	ACAATGACTC	0	J	0	0	0	YIR042C	0
1411	965	ao	AN8604.1	66.m04790	AO070340000151	0					-128	-6	ATGACTCAGATACAAGATACAATAGCATATATTGAACCACCACTCCAACAGATCTACCTCACTCACACACTTTACAACCTCCCACATCAACACACCTACAACCATAACCACTACTACAACTAA			ATGACTCAGATACAAGATACAATAGCATATATTGAACCACCACTCCAACAGATCTACCTCACTCACACACTTTACAACCTCCCACATCAACACACCTACAACCATAACCACTACTACAACTAA	MTQIQDTIAYIEPPLQQIYLTHTLYNLPHQHTYNHNHYYN*			MTQIQDTIAYIEPPLQQIYLTHTLYNLPHQHTYNHNHYYN*	TAACTAAACA	ACAAAATGAC	0	J	0	0	0	YIR042C	0
1412	966	an	AN1955.1	58.m07338	AO070342000226	0	-190	-74					ATGATTGTATCATTCACTCTGTCCTTAAATCTCCCTCTTACCCTTTTCCATTGCCCCTCTTCCCTCCTCGTCGCCACGCTCCAGGCATTTATACCGGTCAAATCCCCCACTTACTGA	ATGATTGTATCATTCACTCTGTCCTTAAATCTCCCTCTTACCCTTTTCCATTGCCCCTCTTCCCTCCTCGTCGCCACGCTCCAGGCATTTATACCGGTCAAATCCCCCACTTACTGA			MIVSFTLSLNLPLTLFHCPSSLLVATLQAFIPVKSPTY*	MIVSFTLSLNLPLTLFHCPSSLLVATLQAFIPVKSPTY*			ATTTCGCTTC	CCAACACCAA	0		0	0	0	0	0
1413	966	ao	AN1955.1	58.m07338	AO070342000226	0					-119	-90	ATGACGGTATACTCCAGCGTCGCGCCATAG			ATGACGGTATACTCCAGCGTCGCGCCATAG	MTVYSSVAP*			MTVYSSVAP*	CTTCCCTTCC	ATCACTTTAT	0		0	0	0	0	0
1416	974	af	AN7760.1	71.m15792	AO070286000007	0			-217	-197			ATGTTTCTTTCTACCAATTAG		ATGTTTCTTTCTACCAATTAG		MFLSTN*		MFLSTN*		TATTCTTGCT	TCTGCTTAGG	0	U	0	0	0	0	0
1417	974	af	AN7760.1	71.m15792	AO070286000007	0			-130	-98			ATGGATTTCTTCGCAGTTGTCAATCTAATCTAA		ATGGATTTCTTCGCAGTTGTCAATCTAATCTAA		MDFFAVVNLI*		MDFFAVVNLI*		CTCTTTATCC	GCTCGCTGTT	0	U	0	0	0	0	0
1414	974	an	AN7760.1	71.m15792	AO070286000007	0	-126	-61					ATGAGCGTTCATCTCGTCGCCATGAGGCCGTTCTTTCCCCTCCTCCTTGCAACACCACTTCATTGA	ATGAGCGTTCATCTCGTCGCCATGAGGCCGTTCTTTCCCCTCCTCCTTGCAACACCACTTCATTGA			MSVHLVAMRPFFPLLLATPLH*	MSVHLVAMRPFFPLLLATPLH*			GCGTCATCAA	ATTCTTGCCC	0	U	0	0	0	0	0
1415	974	an	AN7760.1	71.m15792	AO070286000007	0	-105	-61					ATGAGGCCGTTCTTTCCCCTCCTCCTTGCAACACCACTTCATTGA	ATGAGGCCGTTCTTTCCCCTCCTCCTTGCAACACCACTTCATTGA			MRPFFPLLLATPLH*	MRPFFPLLLATPLH*			TCTCGTCGCC	ATTCTTGCCC	0	U	0	0	0	0	0
1418	974	ao	AN7760.1	71.m15792	AO070286000007	0					-112	-92	ATGATACATACATTGATCTGA			ATGATACATACATTGATCTGA	MIHTLI*			MIHTLI*	CCCTGCATAC	TCTCTCTCCC	0	U	0	0	0	0	0
1419	976	ao	AN1698.1	58.m07774	AO070305000022	0					-169	-149	ATGCTTGAAAGCTCAAAGTGA			ATGCTTGAAAGCTCAAAGTGA	MLESSK*			MLESSK*	CCAGAACCAT	TCTAATTGTG	0	K	0	0	0	0	0
1424	979	af	AN4017.1	54.m06577	AO070328000141	0			-259	-233			ATGAAAATGTGCGAGTATGTACAATAA		ATGAAAATGTGCGAGTATGTACAATAA		MKMCEYVQ*		MKMCEYVQ*		CCTCAATACT	TTCTGCCTGA	0	S	FG01957.1	MG06045.1	0	0	0
1425	979	af	AN4017.1	54.m06577	AO070328000141	0			-253	-233			ATGTGCGAGTATGTACAATAA		ATGTGCGAGTATGTACAATAA		MCEYVQ*		MCEYVQ*		TACTATGAAA	TTCTGCCTGA	0	S	FG01957.1	MG06045.1	0	0	0
1426	979	af	AN4017.1	54.m06577	AO070328000141	0			-243	-223			ATGTACAATAATTCTGCCTGA		ATGTACAATAATTCTGCCTGA		MYNNSA*		MYNNSA*		ATGTGCGAGT	ATTCAATCTT	0	S	FG01957.1	MG06045.1	0	0	0
1427	979	af	AN4017.1	54.m06577	AO070328000141	0			-172	-152			ATGCAGAGTGTCGGAGTTTAG		ATGCAGAGTGTCGGAGTTTAG		MQSVGV*		MQSVGV*		AGAGACTAGG	CAAACTTCGA	0	S	FG01957.1	MG06045.1	0	0	0
1420	979	an	AN4017.1	54.m06577	AO070328000141	0	-181	-155					ATGAACGAATCTAACGCCATTCATTGA	ATGAACGAATCTAACGCCATTCATTGA			MNESNAIH*	MNESNAIH*			CAGTAGAGTT	CATACTTGAT	0	S	FG01957.1	MG06045.1	0	0	0
1421	979	an	AN4017.1	54.m06577	AO070328000141	0	-126	-82					ATGACGCGCGGCATTAAATGTGTGGCTGGTGCAATATGTGGCTAG	ATGACGCGCGGCATTAAATGTGTGGCTGGTGCAATATGTGGCTAG			MTRGIKCVAGAICG*	MTRGIKCVAGAICG*			AAACCGCTCA	TGCCGTGTAC	0	S	FG01957.1	MG06045.1	0	0	0
1422	979	an	AN4017.1	54.m06577	AO070328000141	0	-109	-68					ATGTGTGGCTGGTGCAATATGTGGCTAGTGCCGTGTACGTAG	ATGTGTGGCTGGTGCAATATGTGGCTAGTGCCGTGTACGTAG			MCGWCNMWLVPCT*	MCGWCNMWLVPCT*			GCGGCATTAA	GCTCTTCCCG	0	S	FG01957.1	MG06045.1	0	0	0
1423	979	an	AN4017.1	54.m06577	AO070328000141	0	-91	-68					ATGTGGCTAGTGCCGTGTACGTAG	ATGTGGCTAGTGCCGTGTACGTAG			MWLVPCT*	MWLVPCT*			CTGGTGCAAT	GCTCTTCCCG	0	S	FG01957.1	MG06045.1	0	0	0
1428	979	ao	AN4017.1	54.m06577	AO070328000141	0					-94	-20	ATGCCGCCAGCCGCTGATGTGTACTCTTCCGCAACTCTCTATCTCCATTGTCCCATACCAACAATAGCTCTCTAG			ATGCCGCCAGCCGCTGATGTGTACTCTTCCGCAACTCTCTATCTCCATTGTCCCATACCAACAATAGCTCTCTAG	MPPAADVYSSATLYLHCPIPTIAL*			MPPAADVYSSATLYLHCPIPTIAL*	GATTACGACC	ACATATCGAA	0	S	FG01957.1	MG06045.1	0	0	0
1429	979	ao	AN4017.1	54.m06577	AO070328000141	0					-78	-28	ATGTGTACTCTTCCGCAACTCTCTATCTCCATTGTCCCATACCAACAATAG			ATGTGTACTCTTCCGCAACTCTCTATCTCCATTGTCCCATACCAACAATAG	MCTLPQLSISIVPYQQ*			MCTLPQLSISIVPYQQ*	CCAGCCGCTG	CTCTCTAGAC	0	S	FG01957.1	MG06045.1	0	0	0
1435	984	an	AN8167.1	53.m03810	AO070266000001	0	-127	-113					ATGTTCTATGGTTGA	ATGTTCTATGGTTGA			MFYG*	MFYG*			TTATCTCGCT	AGACTAACAC	0		0	0	0	0	0
1436	984	an	AN8167.1	53.m03810	AO070266000001	0	-120	-106					ATGGTTGAAGACTAA	ATGGTTGAAGACTAA			MVED*	MVED*			GCTATGTTCT	CACCAAGCGA	0		0	0	0	0	0
1437	984	ao	AN8167.1	53.m03810	AO070266000001	0					-245	-195	ATGATGCATTTCTATACTCCCCACCATCGCACCGACTATACTACTGTGTAG			ATGATGCATTTCTATACTCCCCACCATCGCACCGACTATACTACTGTGTAG	MMHFYTPHHRTDYTTV*			MMHFYTPHHRTDYTTV*	GTTATTGTTC	TAGCCAGCGG	0		0	0	0	0	0
1438	984	ao	AN8167.1	53.m03810	AO070266000001	0					-242	-195	ATGCATTTCTATACTCCCCACCATCGCACCGACTATACTACTGTGTAG			ATGCATTTCTATACTCCCCACCATCGCACCGACTATACTACTGTGTAG	MHFYTPHHRTDYTTV*			MHFYTPHHRTDYTTV*	ATTGTTCATG	TAGCCAGCGG	0		0	0	0	0	0
1439	984	ao	AN8167.1	53.m03810	AO070266000001	0					-130	-113	ATGATTCCTGATCATTGA			ATGATTCCTGATCATTGA	MIPDH*			MIPDH*	ATTCTGTTAT	CCCTGGTGAC	0		0	0	0	0	0
1441	990	af	AN3721.1	69.m15426	AO070341000353	0			-167	-93			ATGCGAAACCTAGAAACCCTGGAGGTCACCTCTAGTTTATTCTGGATTGGAGGAAGAATACGGTCGAACTATTAA		ATGCGAAACCTAGAAACCCTGGAGGTCACCTCTAGTTTATTCTGGATTGGAGGAAGAATACGGTCGAACTATTAA		MRNLETLEVTSSLFWIGGRIRSNY*		MRNLETLEVTSSLFWIGGRIRSNY*		TCTCATTGCT	CTCAGATCTC	0	Z	0	0	0	0	0
1440	990	an	AN3721.1	69.m15426	AO070341000353	0	-112	-101					ATGCTACGGTAA	ATGCTACGGTAA			MLR*	MLR*			TTATTAGATA	ACCGTGAAGG	0	Z	0	0	0	0	0
1442	990	ao	AN3721.1	69.m15426	AO070341000353	0					-147	-118	ATGCATCTGCCTCCTATGCAGCAGGTATAG			ATGCATCTGCCTCCTATGCAGCAGGTATAG	MHLPPMQQV*			MHLPPMQQV*	TTTAGATTGC	TGCGACAGAA	0	Z	0	0	0	0	0
1443	990	ao	AN3721.1	69.m15426	AO070341000353	0					-132	-118	ATGCAGCAGGTATAG			ATGCAGCAGGTATAG	MQQV*			MQQV*	TCTGCCTCCT	TGCGACAGAA	0	Z	0	0	0	0	0
1444	991	an	AN3595.1	58.m07394	AO070342000147	0	-226	-182					ATGCGCTCCGAAGAAGTTGTTCGGGACGATGCTTATATAAGCTGA	ATGCGCTCCGAAGAAGTTGTTCGGGACGATGCTTATATAAGCTGA			MRSEEVVRDDAYIS*	MRSEEVVRDDAYIS*			CGGAGGTAGT	AATTCCAACC	0		0	0	0	0	0
1445	991	an	AN3595.1	58.m07394	AO070342000147	0	-198	-187					ATGCTTATATAA	ATGCTTATATAA			MLI*	MLI*			GTTCGGGACG	GCTGAAATTC	0		0	0	0	0	0
1446	991	ao	AN3595.1	58.m07394	AO070342000147	0					-194	-54	ATGCTCAGAATTCCCCGGAAAAGAAAAAGGCATCCCGTTGATGCTTACGTAACGGCGTCCGATCCGCCAAATTTCTTGAGGACCTCCGATAAACTGAATCCCGCCGAACAGCCAGTCCAGATTGATTGGAGCTCGACCTGA			ATGCTCAGAATTCCCCGGAAAAGAAAAAGGCATCCCGTTGATGCTTACGTAACGGCGTCCGATCCGCCAAATTTCTTGAGGACCTCCGATAAACTGAATCCCGCCGAACAGCCAGTCCAGATTGATTGGAGCTCGACCTGA	MLRIPRKRKRHPVDAYVTASDPPNFLRTSDKLNPAEQPVQIDWSST*			MLRIPRKRKRHPVDAYVTASDPPNFLRTSDKLNPAEQPVQIDWSST*	AGGGAGACAA	CCCCTATCCT	0		0	0	0	0	0
1447	991	ao	AN3595.1	58.m07394	AO070342000147	0					-154	-143	ATGCTTACGTAA			ATGCTTACGTAA	MLT*			MLT*	CATCCCGTTG	CGGCGTCCGA	0		0	0	0	0	0
1448	992	af	AN0731.1	70.m15325	AO070343000492	0			-281	-147			ATGCATGACAAATTAATCTTATTTCTTTCTCACATAGAGGATGTATTCTTTTCCTTCGCTTATTTCATATCATTCATCAGAATCTCATGGAGTCTCCATGCTATTGATTTGACCACTGATGACCTTCATTGGTGA		ATGCATGACAAATTAATCTTATTTCTTTCTCACATAGAGGATGTATTCTTTTCCTTCGCTTATTTCATATCATTCATCAGAATCTCATGGAGTCTCCATGCTATTGATTTGACCACTGATGACCTTCATTGGTGA		MHDKLILFLSHIEDVFFSFAYFISFIRISWSLHAIDLTTDDLHW*		MHDKLILFLSHIEDVFFSFAYFISFIRISWSLHAIDLTTDDLHW*		GTCAAATTCT	CCCGAAACAA	0	R	0	0	0	0	0
1449	992	af	AN0731.1	70.m15325	AO070343000492	0			-277	-266			ATGACAAATTAA		ATGACAAATTAA		MTN*		MTN*		AATTCTATGC	TCTTATTTCT	0	R	0	0	0	0	0
1450	992	af	AN0731.1	70.m15325	AO070343000492	0			-241	-170			ATGTATTCTTTTCCTTCGCTTATTTCATATCATTCATCAGAATCTCATGGAGTCTCCATGCTATTGATTTGA		ATGTATTCTTTTCCTTCGCTTATTTCATATCATTCATCAGAATCTCATGGAGTCTCCATGCTATTGATTTGA		MYSFPSLISYHSSESHGVSMLLI*		MYSFPSLISYHSSESHGVSMLLI*		CACATAGAGG	CCACTGATGA	0	R	0	0	0	0	0
1451	992	af	AN0731.1	70.m15325	AO070343000492	0			-195	-175			ATGGAGTCTCCATGCTATTGA		ATGGAGTCTCCATGCTATTGA		MESPCY*		MESPCY*		TCAGAATCTC	TTTGACCACT	0	R	0	0	0	0	0
1452	992	af	AN0731.1	70.m15325	AO070343000492	0			-184	-170			ATGCTATTGATTTGA		ATGCTATTGATTTGA		MLLI*		MLLI*		TGGAGTCTCC	CCACTGATGA	0	R	0	0	0	0	0
1453	992	af	AN0731.1	70.m15325	AO070343000492	0			-163	-71			ATGACCTTCATTGGTGACCCGAAACAAAACAGTGTTGCGCCTTATCGTCGGTCTTTTGCGCAACTTCTCTTATCGCCCGAGTCAAAATCGTGA		ATGACCTTCATTGGTGACCCGAAACAAAACAGTGTTGCGCCTTATCGTCGGTCTTTTGCGCAACTTCTCTTATCGCCCGAGTCAAAATCGTGA		MTFIGDPKQNSVAPYRRSFAQLLLSPESKS*		MTFIGDPKQNSVAPYRRSFAQLLLSPESKS*		TTGACCACTG	ATCGATTTAC	0	R	0	0	0	0	0
1454	992	ao	AN0731.1	70.m15325	AO070343000492	0					-163	-140	ATGATGTGCCTTATTTTCTGCTGA			ATGATGTGCCTTATTTTCTGCTGA	MMCLIFC*			MMCLIFC*	TTGACTCAAC	CTGTGCTGCT	0	R	0	0	0	0	0
1455	992	ao	AN0731.1	70.m15325	AO070343000492	0					-160	-140	ATGTGCCTTATTTTCTGCTGA			ATGTGCCTTATTTTCTGCTGA	MCLIFC*			MCLIFC*	ACTCAACATG	CTGTGCTGCT	0	R	0	0	0	0	0

1456	995	af	AN1350.1	70.m14882	AO070237000010	0			-255	-100			ATGTGGCTAGTGAAAATTTGTGGCGCACCACTGCCGATAAATCGTATGGATGTTATCAACACCACAGAAAGCGATCGGGTAGTACCTCACTACTTGTACCAAAAACTCAGAGACCTTTTTTTTGGTCGCAAAGTCGCGCCTTGGGGGCAATACTAA		ATGTGGCTAGTGAAAATTTGTGGCGCACCACTGCCGATAAATCGTATGGATGTTATCAACACCACAGAAAGCGATCGGGTAGTACCTCACTACTTGTACCAAAAACTCAGAGACCTTTTTTTTGGTCGCAAAGTCGCGCCTTGGGGGCAATACTAA		MWLVKICGAPLPINRMDVINTTESDRVVPHYLYQKLRDLFFGRKVAPWGQY*		MWLVKICGAPLPINRMDVINTTESDRVVPHYLYQKLRDLFFGRKVAPWGQY*		TCCGACGCGG	GCGAACTTGT	0	S	0	0	0	0	0
1457	995	af	AN1350.1	70.m14882	AO070237000010	0			-210	-100			ATGGATGTTATCAACACCACAGAAAGCGATCGGGTAGTACCTCACTACTTGTACCAAAAACTCAGAGACCTTTTTTTTGGTCGCAAAGTCGCGCCTTGGGGGCAATACTAA		ATGGATGTTATCAACACCACAGAAAGCGATCGGGTAGTACCTCACTACTTGTACCAAAAACTCAGAGACCTTTTTTTTGGTCGCAAAGTCGCGCCTTGGGGGCAATACTAA		MDVINTTESDRVVPHYLYQKLRDLFFGRKVAPWGQY*		MDVINTTESDRVVPHYLYQKLRDLFFGRKVAPWGQY*		GATAAATCGT	GCGAACTTGT	0	S	0	0	0	0	0
1458	995	af	AN1350.1	70.m14882	AO070237000010	0			-206	-174			ATGTTATCAACACCACAGAAAGCGATCGGGTAG		ATGTTATCAACACCACAGAAAGCGATCGGGTAG		MLSTPQKAIG*		MLSTPQKAIG*		AATCGTATGG	TACCTCACTA	0	S	0	0	0	0	0
1459	995	ao	AN1350.1	70.m14882	AO070237000010	0					-178	-125	ATGCTCCCGCAGTGTGGCGCACCATTCCCGATAACATTGTCAAGAAATACTTAG			ATGCTCCCGCAGTGTGGCGCACCATTCCCGATAACATTGTCAAGAAATACTTAG	MLPQCGAPFPITLSRNT*			MLPQCGAPFPITLSRNT*	AGTGTGGCTA	TCCGCGAGCG	0	S	0	0	0	0	0
1462	1007	an	AN4060.1	54.m06703	AO070342000045	0	-225	-184					ATGAATATGGTTTGTGCTGCTACAGGCAAAAAGCCAGCTTAG	ATGAATATGGTTTGTGCTGCTACAGGCAAAAAGCCAGCTTAG			MNMVCAATGKKPA*	MNMVCAATGKKPA*			CTTAGTAATT	GGTTCGGCTA	0	J	0	0	0	YNL302C	0
1463	1007	an	AN4060.1	54.m06703	AO070342000045	0	-219	-184					ATGGTTTGTGCTGCTACAGGCAAAAAGCCAGCTTAG	ATGGTTTGTGCTGCTACAGGCAAAAAGCCAGCTTAG			MVCAATGKKPA*	MVCAATGKKPA*			AATTATGAAT	GGTTCGGCTA	0	J	0	0	0	YNL302C	0
1464	1009	an	AN7488.1	57.m05869	AO070287000050	0	-301	-287					ATGCGAACCTCTTAG	ATGCGAACCTCTTAG			MRTS*	MRTS*			CGATGCCTCG	CTGGGTGATA	0	E	0	MG10533.1	0	0	0
1465	1010	an	AN6887.1	71.m16033	AO070314000038	0	-77	-18					ATGCCTTGCTCACCTATCGATTTAGATATCTCTTCGTTAGTCGATGCTGCGCCGCCATAG	ATGCCTTGCTCACCTATCGATTTAGATATCTCTTCGTTAGTCGATGCTGCGCCGCCATAG			MPCSPIDLDISSLVDAAPP*	MPCSPIDLDISSLVDAAPP*			TCGAATTTCG	TTGCTCGGCG	0		0	0	0	0	0
1466	1010	ao	AN6887.1	71.m16033	AO070314000038	0					-94	-38	ATGCCTTACGCTGTACAACGCAGTGCACTCGCCCTCCTAATCCAACTCACTCGCTAG			ATGCCTTACGCTGTACAACGCAGTGCACTCGCCCTCCTAATCCAACTCACTCGCTAG	MPYAVQRSALALLIQLTR*			MPYAVQRSALALLIQLTR*	TCATCGATCG	TCGATGCAGC	0		0	0	0	0	0
1469	1011	af	AN0990.1	70.m15631	AO070318000147	0			-215	-186			ATGATCATTTTATCTTCTTTGCAATTCTGA		ATGATCATTTTATCTTCTTTGCAATTCTGA		MIILSSLQF*		MIILSSLQF*		GCATTGATTC	AAGTCTTGTC	0	A	0	0	0	0	0
1470	1011	af	AN0990.1	70.m15631	AO070318000147	0			-160	-134			ATGGCCGGTTTATCTCGCGCTGTTTGA		ATGGCCGGTTTATCTCGCGCTGTTTGA		MAGLSRAV*		MAGLSRAV*		ACGATACTCG	GATACAAAGC	0	A	0	0	0	0	0
1467	1011	an	AN0990.1	70.m15631	AO070318000147	0	-171	-100					ATGAGATTTATTCCGCATTTGCAGCGCATCAATGGCTGGCGAACACAGCGCGAACTGAGTCGCTTCATTTAA	ATGAGATTTATTCCGCATTTGCAGCGCATCAATGGCTGGCGAACACAGCGCGAACTGAGTCGCTTCATTTAA			MRFIPHLQRINGWRTQRELSRFI*	MRFIPHLQRINGWRTQRELSRFI*			ACTCTATCGT	GCTTTGTCTA	0	A	0	0	0	0	0
1468	1011	an	AN0990.1	70.m15631	AO070318000147	0	-140	-114					ATGGCTGGCGAACACAGCGCGAACTGA	ATGGCTGGCGAACACAGCGCGAACTGA			MAGEHSAN*	MAGEHSAN*			CAGCGCATCA	GTCGCTTCAT	0	A	0	0	0	0	0
1472	1011	ao	AN0990.1	70.m15631	AO070318000147	0					-155	-129	ATGGCTGATCTACTCCCGACAAATTAA			ATGGCTGATCTACTCCCGACAAATTAA	MADLLPTN*			MADLLPTN*	CACGCCTGCC	GTGTTACATG	0	A	0	0	0	0	0
1473	1011	ao	AN0990.1	70.m15631	AO070318000147	0					-121	-26	ATGAGAGGGATAGCTCCTAGTCCAGTCTTTGCGCTAACATTGCGCTTTATCCTCGGAAGGGCCACTGTGACGCAAAAGATAGATGAATTGTCTTAA			ATGAGAGGGATAGCTCCTAGTCCAGTCTTTGCGCTAACATTGCGCTTTATCCTCGGAAGGGCCACTGTGACGCAAAAGATAGATGAATTGTCTTAA	MRGIAPSPVFALTLRFILGRATVTQKIDELS*			MRGIAPSPVFALTLRFILGRATVTQKIDELS*	TAAGTGTTAC	CAAAACTTGC	0	A	0	0	0	0	0
1475	1012	af	AN7701.1	71.m15727	AO070325000108	0			-195	-127			ATGTCTGTCAGCTGCATTGCATCATTGCGATGTTTGTTCTCCACTACCCACACTAGTCCTTTTCAGTAA		ATGTCTGTCAGCTGCATTGCATCATTGCGATGTTTGTTCTCCACTACCCACACTAGTCCTTTTCAGTAA		MSVSCIASLRCLFSTTHTSPFQ*		MSVSCIASLRCLFSTTHTSPFQ*		AGATAACTAC	GTTCCGGAAT	0	J	FG09438.1	MG02598.1	NCU08071.1	0	0
1476	1012	af	AN7701.1	71.m15727	AO070325000108	0			-166	-140			ATGTTTGTTCTCCACTACCCACACTAG		ATGTTTGTTCTCCACTACCCACACTAG		MFVLHYPH*		MFVLHYPH*		CATCATTGCG	TCCTTTTCAG	0	J	FG09438.1	MG02598.1	NCU08071.1	0	0
1479	1018	af	AN6102.1	69.m15115	AO070280000068	0			-94	-59			ATGGATGACCTCGAATTCATCTCTTGCGTTGCTTGA		ATGGATGACCTCGAATTCATCTCTTGCGTTGCTTGA		MDDLEFISCVA*		MDDLEFISCVA*		AAATACCACG	GACAGTCTGT	0		0	0	0	0	0
1477	1018	an	AN6102.1	69.m15115	AO070280000068	0	-166	-134					ATGGATAGATTTCGTAGTCTCACCCAAAGATAG	ATGGATAGATTTCGTAGTCTCACCCAAAGATAG			MDRFRSLTQR*	MDRFRSLTQR*			TCGCATTCGT	AGACCTTGTG	0		0	0	0	0	0
1478	1018	an	AN6102.1	69.m15115	AO070280000068	0	-69	-46					ATGTCGCCCTCATTGGGGGTTTGA	ATGTCGCCCTCATTGGGGGTTTGA			MSPSLGV*	MSPSLGV*			AAGTAGACCG	GCAAATTTCA	0		0	0	0	0	0
1481	1022	af	AN4124.1	70.m14854	AO070335000032	0			-194	-111			ATGCGTCTTATCAGTTGTGTTACCCCCCGGGAAAGAAGTATCCATGCATGCTGGAATTGCGAGCAACCAGCTAGCTCTGGGTAA		ATGCGTCTTATCAGTTGTGTTACCCCCCGGGAAAGAAGTATCCATGCATGCTGGAATTGCGAGCAACCAGCTAGCTCTGGGTAA		MRLISCVTPRERSIHACWNCEQPASSG*		MRLISCVTPRERSIHACWNCEQPASSG*		TGATGATTCG	TAAATTACAC	0	E	0	MG01385.1	0	0	0
1482	1022	af	AN4124.1	70.m14854	AO070335000032	0			-151	-89			ATGCATGCTGGAATTGCGAGCAACCAGCTAGCTCTGGGTAATAAATTACACCTGCCTTGGTGA		ATGCATGCTGGAATTGCGAGCAACCAGCTAGCTCTGGGTAATAAATTACACCTGCCTTGGTGA		MHAGIASNQLALGNKLHLPW*		MHAGIASNQLALGNKLHLPW*		AGAAGTATCC	CTTGATTATC	0	E	0	MG01385.1	0	0	0
1483	1022	af	AN4124.1	70.m14854	AO070335000032	0			-147	-121			ATGCTGGAATTGCGAGCAACCAGCTAG		ATGCTGGAATTGCGAGCAACCAGCTAG		MLELRATS*		MLELRATS*		GTATCCATGC	CTCTGGGTAA	0	E	0	MG01385.1	0	0	0
1480	1022	an	AN4124.1	70.m14854	AO070335000032	0	-292	-224					ATGGAGACCGGTTTATCTCTCGTCACGGCCAGCCTCGAACTCCACTGGCCCATATACTTACCGGATTGA	ATGGAGACCGGTTTATCTCTCGTCACGGCCAGCCTCGAACTCCACTGGCCCATATACTTACCGGATTGA			METGLSLVTASLELHWPIYLPD*	METGLSLVTASLELHWPIYLPD*			CAAGACCCGT	GATCTAGACC	0	E	0	MG01385.1	0	0	0
1484	1022	ao	AN4124.1	70.m14854	AO070335000032	0					-183	-145	ATGTATTGGTATCTGGCCCGGATGAGCCAATTACATTGA			ATGTATTGGTATCTGGCCCGGATGAGCCAATTACATTGA	MYWYLARMSQLH*			MYWYLARMSQLH*	CTTCTGGACT	CAGCGGGTTT	0	E	0	MG01385.1	0	0	0
1485	1022	ao	AN4124.1	70.m14854	AO070335000032	0					-162	-145	ATGAGCCAATTACATTGA			ATGAGCCAATTACATTGA	MSQLH*			MSQLH*	TCTGGCCCGG	CAGCGGGTTT	0	E	0	MG01385.1	0	0	0
1486	1022	ao	AN4124.1	70.m14854	AO070335000032	0					-91	-44	ATGCTACTTACTATATGTATACGATCTGTATTGCTCTGGAGTGTGTGA			ATGCTACTTACTATATGTATACGATCTGTATTGCTCTGGAGTGTGTGA	MLLTICIRSVLLWSV*			MLLTICIRSVLLWSV*	AACCTAGTCT	AGATGATGCT	0	E	0	MG01385.1	0	0	0
1491	1026	af	AN5761.1	69.m14837	AO070193000007	0			-149	-78			ATGGATCTAAGACATTGGAGGAAAAATGTGGCAGCTACAAAAGTCAAGAACATGTATGACAGCATCGACTGA		ATGGATCTAAGACATTGGAGGAAAAATGTGGCAGCTACAAAAGTCAAGAACATGTATGACAGCATCGACTGA		MDLRHWRKNVAATKVKNMYDSID*		MDLRHWRKNVAATKVKNMYDSID*		ACCCCACAAG	GATCAGATTT	0		0	0	0	0	0
1492	1026	af	AN5761.1	69.m14837	AO070193000007	0			-124	-20			ATGTGGCAGCTACAAAAGTCAAGAACATGTATGACAGCATCGACTGAGATCAGATTTATTCGCAGCTGCCAGTGTGATTTGTATATAGAATATTATTCTTTTTAA		ATGTGGCAGCTACAAAAGTCAAGAACATGTATGACAGCATCGACTGAGATCAGATTTATTCGCAGCTGCCAGTGTGATTTGTATATAGAATATTATTCTTTTTAA		MWQLQKSRTCMTASTEIRFIRSCQCDLYIEYYSF*		MWQLQKSRTCMTASTEIRFIRSCQCDLYIEYYSF*		TGGAGGAAAA	TCTCTAACCT	0		0	0	0	0	0
1493	1026	af	AN5761.1	69.m14837	AO070193000007	0			-98	-78			ATGTATGACAGCATCGACTGA		ATGTATGACAGCATCGACTGA		MYDSID*		MYDSID*		AGTCAAGAAC	GATCAGATTT	0		0	0	0	0	0
1494	1026	af	AN5761.1	69.m14837	AO070193000007	0			-94	-20			ATGACAGCATCGACTGAGATCAGATTTATTCGCAGCTGCCAGTGTGATTTGTATATAGAATATTATTCTTTTTAA		ATGACAGCATCGACTGAGATCAGATTTATTCGCAGCTGCCAGTGTGATTTGTATATAGAATATTATTCTTTTTAA		MTASTEIRFIRSCQCDLYIEYYSF*		MTASTEIRFIRSCQCDLYIEYYSF*		AAGAACATGT	TCTCTAACCT	0		0	0	0	0	0
1488	1026	an	AN5761.1	69.m14837	AO070193000007	0	-203	-168					ATGACTCTCTTGCTTTTCTTGGTGGAGGAAGAATAA	ATGACTCTCTTGCTTTTCTTGGTGGAGGAAGAATAA			MTLLLFLVEEE*	MTLLLFLVEEE*			AAGAACTTTC	TGATGATCCA	0		0	0	0	0	0
1489	1026	an	AN5761.1	69.m14837	AO070193000007	0	-168	-130					ATGATGATCCATGTAGGTAGCTCGACCCCACACCTCTAA	ATGATGATCCATGTAGGTAGCTCGACCCCACACCTCTAA			MMIHVGSSTPHL*	MMIHVGSSTPHL*			AGGAAGAATA	GGGGAGCAAA	0		0	0	0	0	0
1490	1026	an	AN5761.1	69.m14837	AO070193000007	0	-165	-130					ATGATCCATGTAGGTAGCTCGACCCCACACCTCTAA	ATGATCCATGTAGGTAGCTCGACCCCACACCTCTAA			MIHVGSSTPHL*	MIHVGSSTPHL*			AAGAATAATG	GGGGAGCAAA	0		0	0	0	0	0
1495	1026	ao	AN5761.1	69.m14837	AO070193000007	0					-135	-109	ATGGGTCTCGACTTGACCTCACCTTGA			ATGGGTCTCGACTTGACCTCACCTTGA	MGLDLTSP*			MGLDLTSP*	TAGCAGCTTT	ATATCACTGA	0		0	0	0	0	0
1496	1026	ao	AN5761.1	69.m14837	AO070193000007	0					-96	-85	ATGCGGAGGTAA			ATGCGGAGGTAA	MRR*			MRR*	ATCACTGAAC	CATTCAGACA	0		0	0	0	0	0
1499	1029	af	AN4359.1	58.m07960	AO070261000002	0			-155	-6			ATGGATGTGATTATGTCAGCGTTCCAGGTCGCGTCTGCTCAAAACAAATCTATCAACTTATCCAACGCCACCCCAGGTCAGTTCAGTCTACCAACGTCTACCCCATTTTCCCCCCAATTGAGTCGCTGTGTACATGGCTCCTGCTGCTAG		ATGGATGTGATTATGTCAGCGTTCCAGGTCGCGTCTGCTCAAAACAAATCTATCAACTTATCCAACGCCACCCCAGGTCAGTTCAGTCTACCAACGTCTACCCCATTTTCCCCCCAATTGAGTCGCTGTGTACATGGCTCCTGCTGCTAG		MDVIMSAFQVASAQNKSINLSNATPGQFSLPTSTPFSPQLSRCVHGSCC*		MDVIMSAFQVASAQNKSINLSNATPGQFSLPTSTPFSPQLSRCVHGSCC*		TCGCCGACTG	TCAATATGGG	0		0	0	0	0	0
1500	1029	af	AN4359.1	58.m07960	AO070261000002	0			-143	-6			ATGTCAGCGTTCCAGGTCGCGTCTGCTCAAAACAAATCTATCAACTTATCCAACGCCACCCCAGGTCAGTTCAGTCTACCAACGTCTACCCCATTTTCCCCCCAATTGAGTCGCTGTGTACATGGCTCCTGCTGCTAG		ATGTCAGCGTTCCAGGTCGCGTCTGCTCAAAACAAATCTATCAACTTATCCAACGCCACCCCAGGTCAGTTCAGTCTACCAACGTCTACCCCATTTTCCCCCCAATTGAGTCGCTGTGTACATGGCTCCTGCTGCTAG		MSAFQVASAQNKSINLSNATPGQFSLPTSTPFSPQLSRCVHGSCC*		MSAFQVASAQNKSINLSNATPGQFSLPTSTPFSPQLSRCVHGSCC*		GGATGTGATT	TCAATATGGG	0		0	0	0	0	0
1497	1029	an	AN4359.1	58.m07960	AO070261000002	0	-146	-81					ATGAGGTTAGTCATCTCCATGTGGGGAGCTGGAGGAGGAGCGGAATTTAGAGCTTTGCGCCACTAA	ATGAGGTTAGTCATCTCCATGTGGGGAGCTGGAGGAGGAGCGGAATTTAGAGCTTTGCGCCACTAA			MRLVISMWGAGGGAEFRALRH*	MRLVISMWGAGGGAEFRALRH*			CGGGCTGGTG	TACTGCTTCC	0		0	0	0	0	0
1498	1029	an	AN4359.1	58.m07960	AO070261000002	0	-128	-81					ATGTGGGGAGCTGGAGGAGGAGCGGAATTTAGAGCTTTGCGCCACTAA	ATGTGGGGAGCTGGAGGAGGAGCGGAATTTAGAGCTTTGCGCCACTAA			MWGAGGGAEFRALRH*	MWGAGGGAEFRALRH*			AGTCATCTCC	TACTGCTTCC	0		0	0	0	0	0
1501	1029	ao	AN4359.1	58.m07960	AO070261000002	0					-148	-134	ATGTCAACCTCTTGA			ATGTCAACCTCTTGA	MSTS*			MSTS*	GCGCGAGATT	ACGGAAAGGC	0		0	0	0	0	0
1503	1030	af	AN8825.1	71.m15957	AO070271000056	0			-214	-200			ATGGATAGCTTTTGA		ATGGATAGCTTTTGA		MDSF*		MDSF*		CGCGGAAAAC	TTGATTGCTC	0	U	0	0	0	0	0
1502	1030	an	AN8825.1	71.m15957	AO070271000056	0	-241	-125					ATGGACGGGAAGACGCTCGAAGTGGACGTTGATTCTTTCTCCTCTCACAATTCAAAACTTCTCCTCCTTGCACCCTTTCTCTTTCGCGCGGCGCACTACGACCCTCCCAGCCCTTAA	ATGGACGGGAAGACGCTCGAAGTGGACGTTGATTCTTTCTCCTCTCACAATTCAAAACTTCTCCTCCTTGCACCCTTTCTCTTTCGCGCGGCGCACTACGACCCTCCCAGCCCTTAA			MDGKTLEVDVDSFSSHNSKLLLLAPFLFRAAHYDPPSP*	MDGKTLEVDVDSFSSHNSKLLLLAPFLFRAAHYDPPSP*			CACGTGGACC	CATTTGCTCC	0	U	0	0	0	0	0
1505	1033	af	AN1721.1	58.m07788	AO070305000036	0			-118	-83			ATGAATGCACCATTCCGTCCCGATGGTTGTTGCTGA		ATGAATGCACCATTCCGTCCCGATGGTTGTTGCTGA		MNAPFRPDGCC*		MNAPFRPDGCC*		AACCGCAGGA	TCTTTTGGAA	0	R	0	0	NCU08363.1	0	0
1504	1033	an	AN1721.1	58.m07788	AO070305000036	0	-119	-57					ATGGTCATCGTACCACTCTTTCTCTTGCCCGTCAGCTTCCCCTCAGTTCCTCCAGACTTCTAA	ATGGTCATCGTACCACTCTTTCTCTTGCCCGTCAGCTTCCCCTCAGTTCCTCCAGACTTCTAA			MVIVPLFLLPVSFPSVPPDF*	MVIVPLFLLPVSFPSVPPDF*			GAGCCCTGGG	GGCTAGCTCC	0	R	0	0	NCU08363.1	0	0
1506	1033	ao	AN1721.1	58.m07788	AO070305000036	0					-189	-145	ATGAGCCCTATCGCGACGGAGAATAATTCCTTCGCCCGGCGGTAG			ATGAGCCCTATCGCGACGGAGAATAATTCCTTCGCCCGGCGGTAG	MSPIATENNSFARR*			MSPIATENNSFARR*	CAGAATTCCG	GGACCATAAC	0	R	0	0	NCU08363.1	0	0
1507	1035	an	AN3747.1	65.m07387	AO070309000075	0	-162	-142					ATGCCAACGATGTCATGCTAA	ATGCCAACGATGTCATGCTAA			MPTMSC*	MPTMSC*			CTCTTTTTAA	CCTGAAATAC	0	O	0	0	0	0	0
1508	1035	an	AN3747.1	65.m07387	AO070309000075	0	-153	-142					ATGTCATGCTAA	ATGTCATGCTAA			MSC*	MSC*			AATGCCAACG	CCTGAAATAC	0	O	0	0	0	0	0
1509	1035	an	AN3747.1	65.m07387	AO070309000075	0	-148	-137					ATGCTAACCTGA	ATGCTAACCTGA			MLT*	MLT*			CAACGATGTC	AATACTTGCC	0	O	0	0	0	0	0
1511	1035	ao	AN3747.1	65.m07387	AO070309000075	0					-205	-182	ATGCGTGGCTTACTTTTGGCATAG			ATGCGTGGCTTACTTTTGGCATAG	MRGLLLA*			MRGLLLA*	TCCAAAGACC	CCTGTGAAGT	0	O	0	0	0	0	0
1514	1038	af	AN1266.1	70.m14945	AO070332000014	0			-227	-213			ATGGACCTGGGTTGA		ATGGACCTGGGTTGA		MDLG*		MDLG*		GTGTTGCGGC	CACTACGGAG	0	A	0	0	0	0	0
1515	1038	af	AN1266.1	70.m14945	AO070332000014	0			-195	-79			ATGAAAGAACCGCAGCCCCAGCGAAAACCAATCACTCACATCGCCACCAACTCACTACTACCAGTGCCGATTATTGATTGCCCGTCAACAACAGTTCAACAGCTGATGGAAGGGTAA		ATGAAAGAACCGCAGCCCCAGCGAAAACCAATCACTCACATCGCCACCAACTCACTACTACCAGTGCCGATTATTGATTGCCCGTCAACAACAGTTCAACAGCTGATGGAAGGGTAA		MKEPQPQRKPITHIATNSLLPVPIIDCPSTTVQQLMEG*		MKEPQPQRKPITHIATNSLLPVPIIDCPSTTVQQLMEG*		GAGTACTTTA	TAAATTGCTT	0	A	0	0	0	0	0
1513	1038	an	AN1266.1	70.m14945	AO070332000014	0	-191	-180					ATGGGCGACTGA	ATGGGCGACTGA			MGD*	MGD*			TGGCCTAAAA	AGGTCATTGA	0	A	0	0	0	0	0
1516	1038	ao	AN1266.1	70.m14945	AO070332000014	0					-261	-232	ATGGAGCTATCAACGTCACGTGATAGATAG			ATGGAGCTATCAACGTCACGTGATAGATAG	MELSTSRDR*			MELSTSRDR*	GAAGCTTGCC	GGCCCTTTGG	0	A	0	0	0	0	0
1517	1038	ao	AN1266.1	70.m14945	AO070332000014	0					-192	-133	ATGGATGGAGAACCGTATCTCCGCGCTTCGGAAGCCGCCAATCCTCGCCACCGTGCTTAA			ATGGATGGAGAACCGTATCTCCGCGCTTCGGAAGCCGCCAATCCTCGCCACCGTGCTTAA	MDGEPYLRASEAANPRHRA*			MDGEPYLRASEAANPRHRA*	TGAAAAAAGA	TCCGACCTTT	0	A	0	0	0	0	0

1518	1038	ao	AN1266.1	70.m14945	AO070332000014	0					-188	-90	ATGGAGAACCGTATCTCCGCGCTTCGGAAGCCGCCAATCCTCGCCACCGTGCTTAATCCGACCTTTACTGATTCTATAACAACAGAGCCTTGCTTTTAA			ATGGAGAACCGTATCTCCGCGCTTCGGAAGCCGCCAATCCTCGCCACCGTGCTTAATCCGACCTTTACTGATTCTATAACAACAGAGCCTTGCTTTTAA	MENRISALRKPPILATVLNPTFTDSITTEPCF*			MENRISALRKPPILATVLNPTFTDSITTEPCF*	AAAAGAATGG	TGGAAGGGTA	0	A	0	0	0	0	0
1512	1038	conserved	AN1266.1	70.m14945	AO070332000014	0	-105	-94	-90	-79	-90	-79	ATGGAAsGkTAA	ATGGAACGTTAA	ATGGAAGGGTAA	ATGGAAGGGTAA	MEr*	MER*	MEG*	MEG*	yydrCwkywr	TAwwkkvhyT	0	A	0	0	0	0	0
1521	1042	af	AN4556.1	57.m05568	AO070321000172	0			-232	-209			ATGCCTGAGAGCCTTAACGCCTGA		ATGCCTGAGAGCCTTAACGCCTGA		MPESLNA*		MPESLNA*		GTCTGCCAGT	GGCAGCCATA	0	R	0	0	NCU00080.1	0	0
1522	1042	af	AN4556.1	57.m05568	AO070321000172	0			-152	-36			ATGAGAGCGCTCGTCCGCGTTGTCATGATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		ATGAGAGCGCTCGTCCGCGTTGTCATGATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		MRALVRVVMMASISLFCLDVLIHLDRQEKHTESQWGVQ*		MRALVRVVMMASISLFCLDVLIHLDRQEKHTESQWGVQ*		ATTCTGTCCA	CTTCAAACTG	0	R	0	0	NCU00080.1	0	0
1523	1042	af	AN4556.1	57.m05568	AO070321000172	0			-128	-36			ATGATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		ATGATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		MMASISLFCLDVLIHLDRQEKHTESQWGVQ*		MMASISLFCLDVLIHLDRQEKHTESQWGVQ*		CCGCGTTGTC	CTTCAAACTG	0	R	0	0	NCU00080.1	0	0
1524	1042	af	AN4556.1	57.m05568	AO070321000172	0			-125	-36			ATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		ATGGCATCCATCTCTTTGTTTTGCCTCGATGTTTTGATTCACCTTGATCGACAAGAAAAACATACAGAATCACAGTGGGGTGTCCAATAA		MASISLFCLDVLIHLDRQEKHTESQWGVQ*		MASISLFCLDVLIHLDRQEKHTESQWGVQ*		CGTTGTCATG	CTTCAAACTG	0	R	0	0	NCU00080.1	0	0
1519	1042	an	AN4556.1	57.m05568	AO070321000172	0	-220	-182					ATGCGGATTAGCGCACCCCGCTTAAGCTCTTTAGTGTGA	ATGCGGATTAGCGCACCCCGCTTAAGCTCTTTAGTGTGA			MRISAPRLSSLV*	MRISAPRLSSLV*			TTACTACCTA	CTCGGCCTTG	0	R	0	0	NCU00080.1	0	0
1520	1042	an	AN4556.1	57.m05568	AO070321000172	0	-157	-116					ATGAACGTATTCCACCCTTTATCTGCGTCTATATCCTTATAA	ATGAACGTATTCCACCCTTTATCTGCGTCTATATCCTTATAA			MNVFHPLSASISL*	MNVFHPLSASISL*			TTGTGATTTC	TCGATTAACC	0	R	0	0	NCU00080.1	0	0
1525	1042	ao	AN4556.1	57.m05568	AO070321000172	0					-179	-153	ATGCCTTTATGCCTGAGGCATCAATAG			ATGCCTTTATGCCTGAGGCATCAATAG	MPLCLRHQ*			MPLCLRHQ*	CCGTTGATAC	CCAGTTGGCC	0	R	0	0	NCU00080.1	0	0
1526	1042	ao	AN4556.1	57.m05568	AO070321000172	0					-171	-118	ATGCCTGAGGCATCAATAGCCAGTTGGCCCAAGCTCCCTGTCCCGATGCGGTAA			ATGCCTGAGGCATCAATAGCCAGTTGGCCCAAGCTCCCTGTCCCGATGCGGTAA	MPEASIASWPKLPVPMR*			MPEASIASWPKLPVPMR*	ACATGCCTTT	GCGTGAGCTC	0	R	0	0	NCU00080.1	0	0
1527	1045	an	AN1181.1	70.m15760	AO070331000179	0	-247	-176					ATGCGCAATTTTCCTCTTTTCTTTTTCACCTACTTTCTTTTTTCACATTGCCTTACTGACATTGCGGCTTGA	ATGCGCAATTTTCCTCTTTTCTTTTTCACCTACTTTCTTTTTTCACATTGCCTTACTGACATTGCGGCTTGA			MRNFPLFFFTYFLFSHCLTDIAA*	MRNFPLFFFTYFLFSHCLTDIAA*			TCCCCGCCTC	CTGGGGCTCT	0	P	0	MG05526.1	0	0	0
1529	1046	af	AN1494.1	55.m03004	AO070334000211	0			-82	-68			ATGGTTGCTCATTGA		ATGGTTGCTCATTGA		MVAH*		MVAH*		TACGAGAGGA	GCTGGACATG	0	K	0	0	NCU02052.1	0	0
1530	1046	ao	AN1494.1	55.m03004	AO070334000211	0					-265	-251	ATGACTTCTGAATAA			ATGACTTCTGAATAA	MTSE*			MTSE*	TCTAGGTGCC	ACTTCTTTTT	0	K	0	0	NCU02052.1	0	0
1533	1051	af	AN9467.1	53.m03848	AO070322000047	0			-273	-247			ATGGTTCGAAATCCTGCAATTTCTTGA		ATGGTTCGAAATCCTGCAATTTCTTGA		MVRNPAIS*		MVRNPAIS*		TTCGACTTGA	TTGATAATTA	0	T	0	0	0	0	0
1534	1051	af	AN9467.1	53.m03848	AO070322000047	0			-206	-123			ATGCTCATGTGGTCATTCCAGGCCGAACATAATAAACAAATCACGCCGTGGCTCCTTGAACTGCGTTCGCGCTGCCCGACTTAA		ATGCTCATGTGGTCATTCCAGGCCGAACATAATAAACAAATCACGCCGTGGCTCCTTGAACTGCGTTCGCGCTGCCCGACTTAA		MLMWSFQAEHNKQITPWLLELRSRCPT*		MLMWSFQAEHNKQITPWLLELRSRCPT*		TGGCTGGGAC	CACCTCCTGC	0	T	0	0	0	0	0
1535	1051	af	AN9467.1	53.m03848	AO070322000047	0			-200	-123			ATGTGGTCATTCCAGGCCGAACATAATAAACAAATCACGCCGTGGCTCCTTGAACTGCGTTCGCGCTGCCCGACTTAA		ATGTGGTCATTCCAGGCCGAACATAATAAACAAATCACGCCGTGGCTCCTTGAACTGCGTTCGCGCTGCCCGACTTAA		MWSFQAEHNKQITPWLLELRSRCPT*		MWSFQAEHNKQITPWLLELRSRCPT*		GGACATGCTC	CACCTCCTGC	0	T	0	0	0	0	0
1536	1051	af	AN9467.1	53.m03848	AO070322000047	0			-63	-46			ATGTGGCTGGTTACATAG		ATGTGGCTGGTTACATAG		MWLVT*		MWLVT*		GACCGAGTAC	TCTTGACAAT	0	T	0	0	0	0	0
1531	1051	an	AN9467.1	53.m03848	AO070322000047	0	-186	-127					ATGCTATCTCCTGTCCGCAAATGCTCATGTGTCCAGGCCGACAGAAACAAACACTCCTAA	ATGCTATCTCCTGTCCGCAAATGCTCATGTGTCCAGGCCGACAGAAACAAACACTCCTAA			MLSPVRKCSCVQADRNKHS*	MLSPVRKCSCVQADRNKHS*			CTTTTTACCA	GAGTTGTCCC	0	T	0	0	0	0	0
1539	1054	af	AN9031.1	67.m02877	AO070339000005	0			-187	-155			ATGGAATTCTCTCCAGCCGGGGTTCCGAAGTAG		ATGGAATTCTCTCCAGCCGGGGTTCCGAAGTAG		MEFSPAGVPK*		MEFSPAGVPK*		GCATGGACTG	GAGTACTAAC	0	Q	0	0	0	0	0
1540	1054	af	AN9031.1	67.m02877	AO070339000005	0			-92	-42			ATGGAGATGGGTATAGTTAATACACTCTGCAGGCTTCCCGTCATCCTTTAG		ATGGAGATGGGTATAGTTAATACACTCTGCAGGCTTCCCGTCATCCTTTAG		MEMGIVNTLCRLPVIL*		MEMGIVNTLCRLPVIL*		AGCTATCAGT	TGACTGGTAA	0	Q	0	0	0	0	0
1541	1054	af	AN9031.1	67.m02877	AO070339000005	0			-86	-42			ATGGGTATAGTTAATACACTCTGCAGGCTTCCCGTCATCCTTTAG		ATGGGTATAGTTAATACACTCTGCAGGCTTCCCGTCATCCTTTAG		MGIVNTLCRLPVIL*		MGIVNTLCRLPVIL*		CAGTATGGAG	TGACTGGTAA	0	Q	0	0	0	0	0
1537	1054	an	AN9031.1	67.m02877	AO070339000005	0	-129	-109					ATGTCGGGGTGGTTCGGATGA	ATGTCGGGGTGGTTCGGATGA			MSGWFG*	MSGWFG*			TCTGGTCCCG	TGTGGTTTTG	0	Q	0	0	0	0	0
1538	1054	an	AN9031.1	67.m02877	AO070339000005	0	-74	-6					ATGTCACTCGCGCGCAGAAAAACCTGGAATTACCCGTTTGAAACATTGCGCCTCTTCTCTCACGAATGA	ATGTCACTCGCGCGCAGAAAAACCTGGAATTACCCGTTTGAAACATTGCGCCTCTTCTCTCACGAATGA			MSLARRKTWNYPFETLRLFSHE*	MSLARRKTWNYPFETLRLFSHE*			GGTACAAATC	TGAAAATGTG	0	Q	0	0	0	0	0
1542	1054	ao	AN9031.1	67.m02877	AO070339000005	0					-69	-31	ATGCGTTGGAGCAGGTATACATTCTCAAGCTGTCGGTGA			ATGCGTTGGAGCAGGTATACATTCTCAAGCTGTCGGTGA	MRWSRYTFSSCR*			MRWSRYTFSSCR*	GATAAGTTCA	TAGTTCTTCT	0	Q	0	0	0	0	0
1545	1056	af	AN7424.1	57.m05921	AO070197000004	0			-274	-143			ATGACCAATTTTGAATATGCTAGAGATATCGGCGGTGTTGATTGGCAGAATAAAAATATGACATTTTTGTTCTTCCTTGCTCTCCCGGATATTTTTCCCACTTTTTTTTTTCACACACACAGCATCTCTTGA		ATGACCAATTTTGAATATGCTAGAGATATCGGCGGTGTTGATTGGCAGAATAAAAATATGACATTTTTGTTCTTCCTTGCTCTCCCGGATATTTTTCCCACTTTTTTTTTTCACACACACAGCATCTCTTGA		MTNFEYARDIGGVDWQNKNMTFLFFLALPDIFPTFFFHTHSIS*		MTNFEYARDIGGVDWQNKNMTFLFFLALPDIFPTFFFHTHSIS*		ACATCGAGAA	TATTTTATTT	0	A	0	0	0	0	0
1546	1056	af	AN7424.1	57.m05921	AO070197000004	0			-258	-214			ATGCTAGAGATATCGGCGGTGTTGATTGGCAGAATAAAAATATGA		ATGCTAGAGATATCGGCGGTGTTGATTGGCAGAATAAAAATATGA		MLEISAVLIGRIKI*		MLEISAVLIGRIKI*		AATTTTGAAT	CATTTTTGTT	0	A	0	0	0	0	0
1547	1056	af	AN7424.1	57.m05921	AO070197000004	0			-217	-143			ATGACATTTTTGTTCTTCCTTGCTCTCCCGGATATTTTTCCCACTTTTTTTTTTCACACACACAGCATCTCTTGA		ATGACATTTTTGTTCTTCCTTGCTCTCCCGGATATTTTTCCCACTTTTTTTTTTCACACACACAGCATCTCTTGA		MTFLFFLALPDIFPTFFFHTHSIS*		MTFLFFLALPDIFPTFFFHTHSIS*		GAATAAAAAT	TATTTTATTT	0	A	0	0	0	0	0
1543	1056	an	AN7424.1	57.m05921	AO070197000004	0	-167	-153					ATGCCAAGCCGCTAA	ATGCCAAGCCGCTAA			MPSR*	MPSR*			AGACTAGTCC	CTACTAATAT	0	A	0	0	0	0	0
1544	1056	an	AN7424.1	57.m05921	AO070197000004	0	-144	-103					ATGGCTTACTGCAATATCTTCGGTACTCGCCACATGGATTAG	ATGGCTTACTGCAATATCTTCGGTACTCGCCACATGGATTAG			MAYCNIFGTRHMD*	MAYCNIFGTRHMD*			AACTACTAAT	TTTACAAAAT	0	A	0	0	0	0	0
1548	1056	ao	AN7424.1	57.m05921	AO070197000004	0					-177	-61	ATGGCAAAATCGCGGAAGATAAAAAAAAAAAGAGGAAAAACTATTCCAATCGTATATAGAGACAAAAGTCGTTTCAGGCAATACAAACTCAATTTGTTCCAAACACCAATTGCCTAA			ATGGCAAAATCGCGGAAGATAAAAAAAAAAAGAGGAAAAACTATTCCAATCGTATATAGAGACAAAAGTCGTTTCAGGCAATACAAACTCAATTTGTTCCAAACACCAATTGCCTAA	MAKSRKIKKKRGKTIPIVYRDKSRFRQYKLNLFQTPIA*			MAKSRKIKKKRGKTIPIVYRDKSRFRQYKLNLFQTPIA*	GCGGTGAGAC	TTTTTTCTCT	0	A	0	0	0	0	0
1550	1057	af	AN3463.1	59.m09324	AO070265000041	0			-214	-149			ATGCCTCACTATGTAACTCGCCTAGCGACCTCTGTCAAGGTCCTATTGCTATGTTGCTGTGATTGA		ATGCCTCACTATGTAACTCGCCTAGCGACCTCTGTCAAGGTCCTATTGCTATGTTGCTGTGATTGA		MPHYVTRLATSVKVLLLCCD*		MPHYVTRLATSVKVLLLCCD*		TTTATAAAGA	GATTTTCCAT	0	V	0	0	0	0	0
1551	1057	af	AN3463.1	59.m09324	AO070265000041	0			-164	-153			ATGTTGCTGTGA		ATGTTGCTGTGA		MLL*		MLL*		TCCTATTGCT	TTGAGATTTT	0	V	0	0	0	0	0
1552	1057	af	AN3463.1	59.m09324	AO070265000041	0			-87	-43			ATGAGTGAATTTCTATTATGCTCTTTTTGTCTGAGACTCGTGTGA		ATGAGTGAATTTCTATTATGCTCTTTTTGTCTGAGACTCGTGTGA		MSEFLLCSFCLRLV*		MSEFLLCSFCLRLV*		AGTGCTGCTG	TACCATAGGG	0	V	0	0	0	0	0
1553	1057	af	AN3463.1	59.m09324	AO070265000041	0			-70	-35			ATGCTCTTTTTGTCTGAGACTCGTGTGATACCATAG		ATGCTCTTTTTGTCTGAGACTCGTGTGATACCATAG		MLFLSETRVIP*		MLFLSETRVIP*		AATTTCTATT	GGCTCAACGA	0	V	0	0	0	0	0
1549	1057	an	AN3463.1	59.m09324	AO070265000041	0	-170	-141					ATGTTTTTTCTACCAACTCCGATCATGTAA	ATGTTTTTTCTACCAACTCCGATCATGTAA			MFFLPTPIM*	MFFLPTPIM*			CCCTGGACGA	GATACTCTGA	0	V	0	0	0	0	0
1555	1063	af	AN7279.1	54.m06323	AO070290000001	0			-244	-41			ATGATGACGCGGGGCCGTTTCTCCTCCCCCTGTCTTCCTCTTCGGGAGTATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		ATGATGACGCGGGGCCGTTTCTCCTCCCCCTGTCTTCCTCTTCGGGAGTATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		MMTRGRFSSPCLPLREYVANDRMDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		MMTRGRFSSPCLPLREYVANDRMDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		AATAATCTTC	ACGACTACTA	0		0	0	0	0	0
1556	1063	af	AN7279.1	54.m06323	AO070290000001	0			-241	-41			ATGACGCGGGGCCGTTTCTCCTCCCCCTGTCTTCCTCTTCGGGAGTATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		ATGACGCGGGGCCGTTTCTCCTCCCCCTGTCTTCCTCTTCGGGAGTATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		MTRGRFSSPCLPLREYVANDRMDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		MTRGRFSSPCLPLREYVANDRMDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		AATCTTCATG	ACGACTACTA	0		0	0	0	0	0
1557	1063	af	AN7279.1	54.m06323	AO070290000001	0			-195	-142			ATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAA		ATGTGGCTAATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAA		MWLMTGWICISQTEEPV*		MWLMTGWICISQTEEPV*		CTTCGGGAGT	GAACCGGAAT	0		0	0	0	0	0
1558	1063	af	AN7279.1	54.m06323	AO070290000001	0			-186	-142			ATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAA		ATGACAGGATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAA		MTGWICISQTEEPV*		MTGWICISQTEEPV*		TATGTGGCTA	GAACCGGAAT	0		0	0	0	0	0
1559	1063	af	AN7279.1	54.m06323	AO070290000001	0			-178	-41			ATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		ATGGATATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		MDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		MDMYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		TAATGACAGG	ACGACTACTA	0		0	0	0	0	0
1560	1063	af	AN7279.1	54.m06323	AO070290000001	0			-172	-41			ATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		ATGTATATCTCAAACAGAAGAGCCGGTGTAAGAACCGGAATCGACCCGTGGAGTATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		MYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		MYISNRRAGVRTGIDPWSMKVDVRVWDGRGYGGQLYNTLTRHS*		CAGGATGGAT	ACGACTACTA	0		0	0	0	0	0
1561	1063	af	AN7279.1	54.m06323	AO070290000001	0			-118	-41			ATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		ATGAAGGTGGACGTAAGAGTATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAACAAGGCACAGCTGA		MKVDVRVWDGRGYGGQLYNTLTRHS*		MKVDVRVWDGRGYGGQLYNTLTRHS*		CCCGTGGAGT	ACGACTACTA	0		0	0	0	0	0
1562	1063	af	AN7279.1	54.m06323	AO070290000001	0			-98	-63			ATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAA		ATGGGATGGAAGAGGGTATGGCGGCCAGCTATATAA		MGWKRVWRPAI*		MGWKRVWRPAI*		ACGTAAGAGT	CACGTTAACA	0		0	0	0	0	0
1563	1063	af	AN7279.1	54.m06323	AO070290000001	0			-93	-55			ATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAA		ATGGAAGAGGGTATGGCGGCCAGCTATATAACACGTTAA		MEEGMAASYITR*		MEEGMAASYITR*		AGAGTATGGG	CAAGGCACAG	0		0	0	0	0	0
1564	1063	af	AN7279.1	54.m06323	AO070290000001	0			-81	-55			ATGGCGGCCAGCTATATAACACGTTAA		ATGGCGGCCAGCTATATAACACGTTAA		MAASYITR*		MAASYITR*		GGAAGAGGGT	CAAGGCACAG	0		0	0	0	0	0
1554	1063	an	AN7279.1	54.m06323	AO070290000001	0	-205	-158					ATGCTCCATTTTACTTTCCCGCCGGAAGAAGTCGCGGGCAGCGTGTAG	ATGCTCCATTTTACTTTCCCGCCGGAAGAAGTCGCGGGCAGCGTGTAG			MLHFTFPPEEVAGSV*	MLHFTFPPEEVAGSV*			TGACCGGTCA	AATACCTCTT	0		0	0	0	0	0
1565	1063	ao	AN7279.1	54.m06323	AO070290000001	0					-252	-145	ATGCTGATGATCTTCTTCAGGAGGATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA			ATGCTGATGATCTTCTTCAGGAGGATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA	MLMIFFRRMSGHSSRTGILFPANVHVRTETRMRTG*			MLMIFFRRMSGHSSRTGILFPANVHVRTETRMRTG*	TCTTCCATAT	TCTTCCGGAC	0		0	0	0	0	0

1566	1063	ao	AN7279.1	54.m06323	AO070290000001	0					-246	-145	ATGATCTTCTTCAGGAGGATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA			ATGATCTTCTTCAGGAGGATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA	MIFFRRMSGHSSRTGILFPANVHVRTETRMRTG*			MIFFRRMSGHSSRTGILFPANVHVRTETRMRTG*	ATATATGCTG	TCTTCCGGAC	0		0	0	0	0	0
1567	1063	ao	AN7279.1	54.m06323	AO070290000001	0					-228	-145	ATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA			ATGTCCGGCCATTCCTCCAGGACAGGGATATTGTTCCCTGCTAATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGA	MSGHSSRTGILFPANVHVRTETRMRTG*			MSGHSSRTGILFPANVHVRTETRMRTG*	CTTCAGGAGG	TCTTCCGGAC	0		0	0	0	0	0
1568	1063	ao	AN7279.1	54.m06323	AO070290000001	0					-185	-123	ATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGATCTTCCGGACTGGCTCCGTTGA			ATGTACACGTTCGAACAGAGACGCGCATGCGCACCGGTTGATCTTCCGGACTGGCTCCGTTGA	MYTFEQRRACAPVDLPDWLR*			MYTFEQRRACAPVDLPDWLR*	TTCCCTGCTA	ACACTTTTGT	0		0	0	0	0	0
1569	1063	ao	AN7279.1	54.m06323	AO070290000001	0					-159	-145	ATGCGCACCGGTTGA			ATGCGCACCGGTTGA	MRTG*			MRTG*	AGAGACGCGC	TCTTCCGGAC	0		0	0	0	0	0
1571	1070	an	AN0894.1	70.m15505	AO070320000067	0	-209	-48					ATGGCCGTATCGCCTCTCTCCGCCTTCAAGCTAGCAACTTTTCTGCCGGGAGTTGATATTTTCCAAAAGATAAGGGCCGGTTTTTTTTCTCCTTTCGCCGCCATCAGTTACTCTTCACCTTTGAATTTTTTTTTTTCGGTTGCTTCGTGACTTTTTACATTGA	ATGGCCGTATCGCCTCTCTCCGCCTTCAAGCTAGCAACTTTTCTGCCGGGAGTTGATATTTTCCAAAAGATAAGGGCCGGTTTTTTTTCTCCTTTCGCCGCCATCAGTTACTCTTCACCTTTGAATTTTTTTTTTTCGGTTGCTTCGTGACTTTTTACATTGA			MAVSPLSAFKLATFLPGVDIFQKIRAGFFSPFAAISYSSPLNFFFRLLRDFLH*	MAVSPLSAFKLATFLPGVDIFQKIRAGFFSPFAAISYSSPLNFFFRLLRDFLH*			GCAGCCAATC	TAATTCTGGT	0	A	0	0	0	0	0
1572	1074	af	AN1066.1	70.m15166	AO070218000011	0			-207	-19			ATGCTGCTCGGTCTTTGTCTTCACTCTGACCTCATTTTGCCCTCATCCGAAATTTTCCCTATTTTGAGTGGTGGCTCATCTATAATTATCTTCTCTCACTCCATCCTCGCCTCAACTCTGCATTTGATACATATAATCCTCCTGTGGTTTCGATCTGCTCAGTACATACATACCTATCATCCGCACTAA		ATGCTGCTCGGTCTTTGTCTTCACTCTGACCTCATTTTGCCCTCATCCGAAATTTTCCCTATTTTGAGTGGTGGCTCATCTATAATTATCTTCTCTCACTCCATCCTCGCCTCAACTCTGCATTTGATACATATAATCCTCCTGTGGTTTCGATCTGCTCAGTACATACATACCTATCATCCGCACTAA		MLLGLCLHSDLILPSSEIFPILSGGSSIIIFSHSILASTLHLIHIILLWFRSAQYIHTYHPH*		MLLGLCLHSDLILPSSEIFPILSGGSSIIIFSHSILASTLHLIHIILLWFRSAQYIHTYHPH*		CACCCGGCCT	AACCCAAATC	0		0	0	0	0	0
1575	1079	af	AN0867.1	70.m15460	AO070320000018	0			-263	-240			ATGGGTCCAGGCAACTATAATTGA		ATGGGTCCAGGCAACTATAATTGA		MGPGNYN*		MGPGNYN*		CTGTTGCTCC	GACCTTTGCC	0		0	0	0	0	0
1576	1079	af	AN0867.1	70.m15460	AO070320000018	0			-225	-148			ATGGAGAGCGGAGTCAACCGATGTCTCGTTGCCCGTGGTGCCCTGTCGAATCCGTCCTGGATGTGTAGATTACATTGA		ATGGAGAGCGGAGTCAACCGATGTCTCGTTGCCCGTGGTGCCCTGTCGAATCCGTCCTGGATGTGTAGATTACATTGA		MESGVNRCLVARGALNPSWMCRLH*		MESGVNRCLVARGALNPSWMCRLH*		TTTGCCCTCC	AAGTCTTTTT	0		0	0	0	0	0
1577	1079	af	AN0867.1	70.m15460	AO070320000018	0			-205	-158			ATGTCTCGTTGCCCGTGGTGCCCTGTCGAATCCGTCCTGGATGTGTAG		ATGTCTCGTTGCCCGTGGTGCCCTGTCGAATCCGTCCTGGATGTGTAG		MSRCPWCPVESVLDV*		MSRCPWCPVESVLDV*		GAGTCAACCG	ATTACATTGA	0		0	0	0	0	0
1578	1079	af	AN0867.1	70.m15460	AO070320000018	0			-165	-148			ATGTGTAGATTACATTGA		ATGTGTAGATTACATTGA		MCRLH*		MCRLH*		TCCGTCCTGG	AAGTCTTTTT	0		0	0	0	0	0
1573	1079	an	AN0867.1	70.m15460	AO070320000018	0	-235	-98					ATGATCTTTGCCCAAGGCCGGGGGTTCGATTATAATTGGAGCCATTGCCCTCATCGGAGGAGAGAAAGTTTCGCCATGTTGAGCAGTTTCTTTTTTTTGTCTGCCAGGTCTGAGTTGTGGAGTTTTGAAGAAGTGTGA	ATGATCTTTGCCCAAGGCCGGGGGTTCGATTATAATTGGAGCCATTGCCCTCATCGGAGGAGAGAAAGTTTCGCCATGTTGAGCAGTTTCTTTTTTTTGTCTGCCAGGTCTGAGTTGTGGAGTTTTGAAGAAGTGTGA			MIFAQGRGFDYNWSHCPHRRRESFAMLSSFFFLSARSELWSFEEV*	MIFAQGRGFDYNWSHCPHRRRESFAMLSSFFFLSARSELWSFEEV*			GACCCAAGTG	GAGAGCTTGG	0		0	0	0	0	0
1574	1079	an	AN0867.1	70.m15460	AO070320000018	0	-160	-98					ATGTTGAGCAGTTTCTTTTTTTTGTCTGCCAGGTCTGAGTTGTGGAGTTTTGAAGAAGTGTGA	ATGTTGAGCAGTTTCTTTTTTTTGTCTGCCAGGTCTGAGTTGTGGAGTTTTGAAGAAGTGTGA			MLSSFFFLSARSELWSFEEV*	MLSSFFFLSARSELWSFEEV*			AAGTTTCGCC	GAGAGCTTGG	0		0	0	0	0	0
1579	1079	ao	AN0867.1	70.m15460	AO070320000018	0					-194	-102	ATGGACCAGATAAATTTCGAGCCATTGCCCTCTTCCGAAGAAGGTTTTGCCATGTTGACGTTAACAGTGATTCCTGGTCGTGGCGTCCGATGA			ATGGACCAGATAAATTTCGAGCCATTGCCCTCTTCCGAAGAAGGTTTTGCCATGTTGACGTTAACAGTGATTCCTGGTCGTGGCGTCCGATGA	MDQINFEPLPSSEEGFAMLTLTVIPGRGVR*			MDQINFEPLPSSEEGFAMLTLTVIPGRGVR*	CCTAGGGTCC	GTGAGAGATA	0		0	0	0	0	0
1580	1079	ao	AN0867.1	70.m15460	AO070320000018	0					-143	-102	ATGTTGACGTTAACAGTGATTCCTGGTCGTGGCGTCCGATGA			ATGTTGACGTTAACAGTGATTCCTGGTCGTGGCGTCCGATGA	MLTLTVIPGRGVR*			MLTLTVIPGRGVR*	AGGTTTTGCC	GTGAGAGATA	0		0	0	0	0	0
1581	1079	ao	AN0867.1	70.m15460	AO070320000018	0					-105	-91	ATGAGTGAGAGATAA			ATGAGTGAGAGATAA	MSER*			MSER*	GTGGCGTCCG	CTAAAAGTTC	0		0	0	0	0	0
1582	1081	af	AN6628.1	62.m03224	AO070326000079	0			-222	-193			ATGGTGGGGAACCGTGGGCGGAAAAGGTGA		ATGGTGGGGAACCGTGGGCGGAAAAGGTGA		MVGNRGRKR*		MVGNRGRKR*		AGTGGCCACT	GAGCTCTCCG	0	S	0	0	0	0	0
1584	1083	af	AN2143.1	72.m19698	AO070343000190	0			-72	-40			ATGCTGGGTCAGCTTATGCAGCTTACTGACTGA		ATGCTGGGTCAGCTTATGCAGCTTACTGACTGA		MLGQLMQLTD*		MLGQLMQLTD*		TCGCTTGTCA	TAATTTATTC	0	D	FG07139.1	MG07070.1	0	0	0
1583	1083	an	AN2143.1	72.m19698	AO070343000190	0	-72	-58					ATGTGTGTGGCATAA	ATGTGTGTGGCATAA			MCVA*	MCVA*			CCATCCGTCA	ACCGTCGGGA	0	D	FG07139.1	MG07070.1	0	0	0
1588	1084	af	AN4580.1	57.m05500	AO070316000165	0			-212	-201			ATGACAGCGTAG		ATGACAGCGTAG		MTA*		MTA*		TCTCCCCACC	GCTGTGTAGC	0	U	0	0	0	0	0
1589	1084	ao	AN4580.1	57.m05500	AO070316000165	0					-201	-124	ATGTCAAGATGCTGTTTAGTGTCCAGTTCGAAACTGCAGAACAGAGGGGTCTTTGAGAGTTGTCGATCTTTCAATTAG			ATGTCAAGATGCTGTTTAGTGTCCAGTTCGAAACTGCAGAACAGAGGGGTCTTTGAGAGTTGTCGATCTTTCAATTAG	MSRCCLVSSSKLQNRGVFESCRSFN*			MSRCCLVSSSKLQNRGVFESCRSFN*	CGACCGCCCG	CTTGGAATAA	0	U	0	0	0	0	0
1590	1084	ao	AN4580.1	57.m05500	AO070316000165	0					-193	-146	ATGCTGTTTAGTGTCCAGTTCGAAACTGCAGAACAGAGGGGTCTTTGA			ATGCTGTTTAGTGTCCAGTTCGAAACTGCAGAACAGAGGGGTCTTTGA	MLFSVQFETAEQRGL*			MLFSVQFETAEQRGL*	CGATGTCAAG	GAGTTGTCGA	0	U	0	0	0	0	0
1591	1086	ao	AN2854.1	59.m08698	AO070338000167	0					-162	-151	ATGGGTTCGTGA			ATGGGTTCGTGA	MGS*			MGS*	CGTGAATTAT	ATCGCGCACA	0	K	0	0	0	0	0
1593	1087	af	AN5484.1	69.m15469	AO070341000401	0			-224	-126			ATGCTTATGGGGATCCCCGACCGCCCCAGCGGGATTCACATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		ATGCTTATGGGGATCCCCGACCGCCCCAGCGGGATTCACATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		MLMGIPDRPSGIHMPAPNSPGKAGRNPSQITT*		MLMGIPDRPSGIHMPAPNSPGKAGRNPSQITT*		TGACAGCACC	TAAGAAGAAC	0	I	0	0	0	0	0
1594	1087	af	AN5484.1	69.m15469	AO070341000401	0			-218	-126			ATGGGGATCCCCGACCGCCCCAGCGGGATTCACATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		ATGGGGATCCCCGACCGCCCCAGCGGGATTCACATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		MGIPDRPSGIHMPAPNSPGKAGRNPSQITT*		MGIPDRPSGIHMPAPNSPGKAGRNPSQITT*		CACCATGCTT	TAAGAAGAAC	0	I	0	0	0	0	0
1595	1087	af	AN5484.1	69.m15469	AO070341000401	0			-185	-126			ATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		ATGCCTGCACCGAACTCTCCGGGGAAAGCTGGTCGTAATCCCAGCCAAATAACGACCTAA		MPAPNSPGKAGRNPSQITT*		MPAPNSPGKAGRNPSQITT*		CGGGATTCAC	TAAGAAGAAC	0	I	0	0	0	0	0
1592	1087	an	AN5484.1	69.m15469	AO070341000401	0	-225	-190					ATGCAGAGACCCAAAGGAGCATTGAGAGCGAGGTAA	ATGCAGAGACCCAAAGGAGCATTGAGAGCGAGGTAA			MQRPKGALRAR*	MQRPKGALRAR*			CAAGAGTCTA	ACGAGCCTCG	0	I	0	0	0	0	0
1596	1087	ao	AN5484.1	69.m15469	AO070341000401	0					-213	-157	ATGAAATCCCGCGACCGCCCTCCATTCACATGCCCCGAACACTCCGGGGAAGCTTGA			ATGAAATCCCGCGACCGCCCTCCATTCACATGCCCCGAACACTCCGGGGAAGCTTGA	MKSRDRPPFTCPEHSGEA*			MKSRDRPPFTCPEHSGEA*	ATGACGAGGC	CGTTCCTGGT	0	I	0	0	0	0	0
1597	1092	af	AN4821.1	56.m02445	AO070327000162	0			-183	-19			ATGACACACGAGACTGACAGGAGTTGGCTGGCGGACTTGAAAAGCTCCGGTGAGCCACGTGACATCCCCGCAAACCATACGATTAGTCATCCCTCTCTACCCCCACAAGCTCGGGGTGCGTTGGGTGTCTTCGCAAATGTCTGGCAAACAATTGTCAGGCTATGA		ATGACACACGAGACTGACAGGAGTTGGCTGGCGGACTTGAAAAGCTCCGGTGAGCCACGTGACATCCCCGCAAACCATACGATTAGTCATCCCTCTCTACCCCCACAAGCTCGGGGTGCGTTGGGTGTCTTCGCAAATGTCTGGCAAACAATTGTCAGGCTATGA		MTHETDRSWLADLKSSGEPRDIPANHTISHPSLPPQARGALGVFANVWQTIVRL*		MTHETDRSWLADLKSSGEPRDIPANHTISHPSLPPQARGALGVFANVWQTIVRL*		TTATACAACA	TCATGGATAC	0		0	0	0	0	0
1598	1092	ao	AN4821.1	56.m02445	AO070327000162	0					-193	-134	ATGCGAGTGGAACGAAGAACATACCCACACACTCTTTACGGGGACATGCACTTGGCTTGA			ATGCGAGTGGAACGAAGAACATACCCACACACTCTTTACGGGGACATGCACTTGGCTTGA	MRVERRTYPHTLYGDMHLA*			MRVERRTYPHTLYGDMHLA*	TCTGTGTATC	AACGCTGTAC	0		0	0	0	0	0
1599	1092	ao	AN4821.1	56.m02445	AO070327000162	0					-148	-134	ATGCACTTGGCTTGA			ATGCACTTGGCTTGA	MHLA*			MHLA*	TTACGGGGAC	AACGCTGTAC	0		0	0	0	0	0
1600	1092	ao	AN4821.1	56.m02445	AO070327000162	0					-106	-26	ATGCTGCACTTGGCAACCTGTCTCCACCCCCACACAACTCTATCAAGCTCTTCCGGCTACTATCACTTCCCAATCCAATAA			ATGCTGCACTTGGCAACCTGTCTCCACCCCCACACAACTCTATCAAGCTCTTCCGGCTACTATCACTTCCCAATCCAATAA	MLHLATCLHPHTTLSSSSGYYHFPIQ*			MLHLATCLHPHTTLSSSSGYYHFPIQ*	GGTGATTATC	GAATCTTGTC	0		0	0	0	0	0
1601	1096	conserved	AN5958.1	72.m19176	AO070340000315	0	-73	-35	-74	-36	-70	-32	ATGCGGyyCTyyryyCyTydTyyCmTkmGyGAyAGGTGA	ATGCGGCTCTTTACTCCTCATCCCCTTCGCGACAGGTGA	ATGCGGTCCTTCATCCTTTGTTTCCTGCGTGATAGGTGA	ATGCGGCCCTCCGCCCCTCTTCTCATTAGCGACAGGTGA	MRlftphplrDR*	MRLFTPHPLRDR*	MRSFILCFLRDR*	MRPSAPLLISDR*	bkyGwrCTCA	TwsrsAydCy	0	D	0	0	0	0	0
1606	1098	af	AN3390.1	55.m03190	AO070290000088	0			-219	-124			ATGAAACCATACCACTGCCAAATCGGGCAAGCCGGGTATATAATTCAATATATTCCAGGTCACCTTATATCAGTTACTGCAACATTTCATTTATAA		ATGAAACCATACCACTGCCAAATCGGGCAAGCCGGGTATATAATTCAATATATTCCAGGTCACCTTATATCAGTTACTGCAACATTTCATTTATAA		MKPYHCQIGQAGYIIQYIPGHLISVTATFHL*		MKPYHCQIGQAGYIIQYIPGHLISVTATFHL*		GCAGTGCCGA	GACGACTATC	0	G	0	0	0	0	0
1607	1098	af	AN3390.1	55.m03190	AO070290000088	0			-74	-15			ATGAACAGTCATTTGTCAGGACATCCAGAAGACCGGAACAGCCACACTGTCGACTCCTGA		ATGAACAGTCATTTGTCAGGACATCCAGAAGACCGGAACAGCCACACTGTCGACTCCTGA		MNSHLSGHPEDRNSHTVDS*		MNSHLSGHPEDRNSHTVDS*		CTCTTGGAGG	CTTCAGGCAC	0	G	0	0	0	0	0
1602	1098	an	AN3390.1	55.m03190	AO070290000088	0	-296	-276					ATGATAACAATCCCATGTTAA	ATGATAACAATCCCATGTTAA			MITIPC*	MITIPC*			GGATTGTTTC	TAGAAATGGG	0	G	0	0	0	0	0
1603	1098	an	AN3390.1	55.m03190	AO070290000088	0	-282	-184					ATGTTAATAGAAATGGGTCACTGTCAATCACCGATTGCTCTTTGCTGTATTAATTTTCCTAAATTTAGTATACAGTGTCTCATTCTTAGGGTGGCATGA	ATGTTAATAGAAATGGGTCACTGTCAATCACCGATTGCTCTTTGCTGTATTAATTTTCCTAAATTTAGTATACAGTGTCTCATTCTTAGGGTGGCATGA			MLIEMGHCQSPIALCCINFPKFSIQCLILRVA*	MLIEMGHCQSPIALCCINFPKFSIQCLILRVA*			TAACAATCCC	CGCTGTTTCG	0	G	0	0	0	0	0
1604	1098	an	AN3390.1	55.m03190	AO070290000088	0	-270	-184					ATGGGTCACTGTCAATCACCGATTGCTCTTTGCTGTATTAATTTTCCTAAATTTAGTATACAGTGTCTCATTCTTAGGGTGGCATGA	ATGGGTCACTGTCAATCACCGATTGCTCTTTGCTGTATTAATTTTCCTAAATTTAGTATACAGTGTCTCATTCTTAGGGTGGCATGA			MGHCQSPIALCCINFPKFSIQCLILRVA*	MGHCQSPIALCCINFPKFSIQCLILRVA*			GTTAATAGAA	CGCTGTTTCG	0	G	0	0	0	0	0
1605	1098	an	AN3390.1	55.m03190	AO070290000088	0	-187	-83					ATGACGCTGTTTCGTTCTGTATCAGACATATTTCAGCTGGATATATTATCTCCTAGTCCCGGAGAAACTCTGCAGCATTTAATCCAGAAAAGAGCCGGTGGCTAA	ATGACGCTGTTTCGTTCTGTATCAGACATATTTCAGCTGGATATATTATCTCCTAGTCCCGGAGAAACTCTGCAGCATTTAATCCAGAAAAGAGCCGGTGGCTAA			MTLFRSVSDIFQLDILSPSPGETLQHLIQKRAGG*	MTLFRSVSDIFQLDILSPSPGETLQHLIQKRAGG*			TTAGGGTGGC	GAGACGGGCT	0	G	0	0	0	0	0
1608	1098	ao	AN3390.1	55.m03190	AO070290000088	0					-81	-7	ATGCCCATGAACATCATTACCAGTTGGGTACAGCATTGCTTATATCCCGATCTACCTATCTCCTTTGTACGCTGA			ATGCCCATGAACATCATTACCAGTTGGGTACAGCATTGCTTATATCCCGATCTACCTATCTCCTTTGTACGCTGA	MPMNIITSWVQHCLYPDLPISFVR*			MPMNIITSWVQHCLYPDLPISFVR*	GTTTATAATC	CCTAACATGC	0	G	0	0	0	0	0
1609	1098	ao	AN3390.1	55.m03190	AO070290000088	0					-75	-7	ATGAACATCATTACCAGTTGGGTACAGCATTGCTTATATCCCGATCTACCTATCTCCTTTGTACGCTGA			ATGAACATCATTACCAGTTGGGTACAGCATTGCTTATATCCCGATCTACCTATCTCCTTTGTACGCTGA	MNIITSWVQHCLYPDLPISFVR*			MNIITSWVQHCLYPDLPISFVR*	AATCATGCCC	CCTAACATGC	0	G	0	0	0	0	0
1610	1099	af	AN3841.1	58.m07817	AO070305000076	0			-274	-236			ATGGACGGAGCACACGGTACCTTACTTTATCAACCATAG		ATGGACGGAGCACACGGTACCTTACTTTATCAACCATAG		MDGAHGTLLYQP*		MDGAHGTLLYQP*		ATCATTTGGG	TGCTGAATGA	0	I	0	0	NCU00896.1	0	0
1611	1099	af	AN3841.1	58.m07817	AO070305000076	0			-229	-158			ATGATTGTTCCCTTTCTCGCTGGGAAAATCATCTCCAGCCTTCTTCTTTCAGTCTCTCTTTCTCTTGGTTGA		ATGATTGTTCCCTTTCTCGCTGGGAAAATCATCTCCAGCCTTCTTCTTTCAGTCTCTCTTTCTCTTGGTTGA		MIVPFLAGKIISSLLLSVSLSLG*		MIVPFLAGKIISSLLLSVSLSLG*		ATAGTGCTGA	TTACTATTTT	0	I	0	0	NCU00896.1	0	0
1615	1104	af	AN5328.1	52.m03790	AO070339000247	0			-134	-51			ATGATGACGCGGCTAGGGCCATCATGTTCAGGGCGCCAGCAATCAAAGGGGTATAAAAGGCTGGCCATTGTTATGCCAGTATGA		ATGATGACGCGGCTAGGGCCATCATGTTCAGGGCGCCAGCAATCAAAGGGGTATAAAAGGCTGGCCATTGTTATGCCAGTATGA		MMTRLGPSCSGRQQSKGYKRLAIVMPV*		MMTRLGPSCSGRQQSKGYKRLAIVMPV*		GAGGCTGGAG	GAGGACACAC	0	Q	0	0	0	0	0
1616	1104	af	AN5328.1	52.m03790	AO070339000247	0			-131	-51			ATGACGCGGCTAGGGCCATCATGTTCAGGGCGCCAGCAATCAAAGGGGTATAAAAGGCTGGCCATTGTTATGCCAGTATGA		ATGACGCGGCTAGGGCCATCATGTTCAGGGCGCCAGCAATCAAAGGGGTATAAAAGGCTGGCCATTGTTATGCCAGTATGA		MTRLGPSCSGRQQSKGYKRLAIVMPV*		MTRLGPSCSGRQQSKGYKRLAIVMPV*		GCTGGAGATG	GAGGACACAC	0	Q	0	0	0	0	0
1617	1104	af	AN5328.1	52.m03790	AO070339000247	0			-111	-79			ATGTTCAGGGCGCCAGCAATCAAAGGGGTATAA		ATGTTCAGGGCGCCAGCAATCAAAGGGGTATAA		MFRAPAIKGV*		MFRAPAIKGV*		TAGGGCCATC	AAGGCTGGCC	0	Q	0	0	0	0	0
1618	1104	af	AN5328.1	52.m03790	AO070339000247	0			-62	-51			ATGCCAGTATGA		ATGCCAGTATGA		MPV*		MPV*		GGCCATTGTT	GAGGACACAC	0	Q	0	0	0	0	0

1612	1104	an	AN5328.1	52.m03790	AO070339000247	0	-188	-3					ATGGCTTGTCTCGAATTACGCACCCTCTTATACAACCTCCTTTTTATGAAACGTCACTGAACGACGTTTACGCGGCGCGATCCGGAAGCCCCTGGACCATGTCTATAAGAAGAAGAGGTTTCTCTGGGGAAATTCGATCATCATCAAGTCAGACATCAGACATCCTCTCCTCTCAATCAGCTTAA	ATGGCTTGTCTCGAATTACGCACCCTCTTATACAACCTCCTTTTTATGAAACGTCACTGAACGACGTTTACGCGGCGCGATCCGGAAGCCCCTGGACCATGTCTATAAGAAGAAGAGGTTTCTCTGGGGAAATTCGATCATCATCAAGTCAGACATCAGACATCCTCTCCTCTCAATCAGCTTAA			MACLELRTLLYNLLFYETSLNDVYAARSGSPWTMSIRRRGFSGEIRSSSSQTSDILSSQSA*	MACLELRTLLYNLLFYETSLNDVYAARSGSPWTMSIRRRGFSGEIRSSSSQTSDILSSQSA*			GCTACAGCCT	CAATGCGCTT	0	Q	0	0	0	0	0
1613	1104	an	AN5328.1	52.m03790	AO070339000247	0	-142	-128					ATGAAACGTCACTGA	ATGAAACGTCACTGA			MKRH*	MKRH*			CTCCTTTTTT	ACGACGTTTA	0	Q	0	0	0	0	0
1614	1104	an	AN5328.1	52.m03790	AO070339000247	0	-89	-3					ATGTCTATAAGAAGAAGAGGTTTCTCTGGGGAAATTCGATCATCATCAAGTCAGACATCAGACATCCTCTCCTCTCAATCAGCTTAA	ATGTCTATAAGAAGAAGAGGTTTCTCTGGGGAAATTCGATCATCATCAAGTCAGACATCAGACATCCTCTCCTCTCAATCAGCTTAA			MSIRRRGFSGEIRSSSSQTSDILSSQSA*	MSIRRRGFSGEIRSSSSQTSDILSSQSA*			CCCCTGGACC	CAATGCGCTT	0	Q	0	0	0	0	0
1620	1104	ao	AN5328.1	52.m03790	AO070339000247	0					-225	-193	ATGACAGGCACTAGAATAACGTCTCCTGCATAA			ATGACAGGCACTAGAATAACGTCTCCTGCATAA	MTGTRITSPA*			MTGTRITSPA*	TCCTTACGGG	AGGTTCCATA	0	Q	0	0	0	0	0
1621	1104	ao	AN5328.1	52.m03790	AO070339000247	0					-147	-121	ATGACGTGGATTTTCCGAAGCCGTTGA			ATGACGTGGATTTTCCGAAGCCGTTGA	MTWIFRSR*			MTWIFRSR*	CTTTGCTCCG	CAGGCTTGGA	0	Q	0	0	0	0	0
1625	1107	af	AN7313.1	56.m03103	AO070319000136	0			-139	-125			ATGCTCCGCAATTAG		ATGCTCCGCAATTAG		MLRN*		MLRN*		TATAGGCTGG	GCCCGGCTCC	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1626	1107	af	AN7313.1	56.m03103	AO070319000136	0			-114	-103			ATGCTCTGTTGA		ATGCTCTGTTGA		MLC*		MLC*		GCCCGGCTCC	CCCCGCTTGG	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1622	1107	an	AN7313.1	56.m03103	AO070319000136	0	-156	-28					ATGTGTCGGTTCCGATATCCCCACTGGAACACCTCGCTATGCATGGGTGAAACACGTATAAAAGGGCGCAGAAAGTGCCCTAACCAGCTGTTTTGCTCGTACCTATTCAAATCCTCAATCCATATGTAG	ATGTGTCGGTTCCGATATCCCCACTGGAACACCTCGCTATGCATGGGTGAAACACGTATAAAAGGGCGCAGAAAGTGCCCTAACCAGCTGTTTTGCTCGTACCTATTCAAATCCTCAATCCATATGTAG			MCRFRYPHWNTSLCMGETRIKGRRKCPNQLFCSYLFKSSIHM*	MCRFRYPHWNTSLCMGETRIKGRRKCPNQLFCSYLFKSSIHM*			ACTTGGCATT	CTGGGGTTGC	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1623	1107	an	AN7313.1	56.m03103	AO070319000136	0	-118	-107					ATGCATGGGTGA	ATGCATGGGTGA			MHG*	MHG*			ACACCTCGCT	AACACGTATA	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1624	1107	an	AN7313.1	56.m03103	AO070319000136	0	-114	-28					ATGGGTGAAACACGTATAAAAGGGCGCAGAAAGTGCCCTAACCAGCTGTTTTGCTCGTACCTATTCAAATCCTCAATCCATATGTAG	ATGGGTGAAACACGTATAAAAGGGCGCAGAAAGTGCCCTAACCAGCTGTTTTGCTCGTACCTATTCAAATCCTCAATCCATATGTAG			MGETRIKGRRKCPNQLFCSYLFKSSIHM*	MGETRIKGRRKCPNQLFCSYLFKSSIHM*			CTCGCTATGC	CTGGGGTTGC	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1627	1107	ao	AN7313.1	56.m03103	AO070319000136	0					-181	-83	ATGGACCGTGATGCATCAGTTAGACCATGCATGATAGATTGCAGCACAACCCCTCAGTCATGTCTCGACCTTTATCTTATCTGGACACATCACGCTTAA			ATGGACCGTGATGCATCAGTTAGACCATGCATGATAGATTGCAGCACAACCCCTCAGTCATGTCTCGACCTTTATCTTATCTGGACACATCACGCTTAA	MDRDASVRPCMIDCSTTPQSCLDLYLIWTHHA*			MDRDASVRPCMIDCSTTPQSCLDLYLIWTHHA*	TCCGATATTG	ATAGTTCATT	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1628	1107	ao	AN7313.1	56.m03103	AO070319000136	0					-171	-148	ATGCATCAGTTAGACCATGCATGA			ATGCATCAGTTAGACCATGCATGA	MHQLDHA*			MHQLDHA*	ATGGACCGTG	TAGATTGCAG	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1629	1107	ao	AN7313.1	56.m03103	AO070319000136	0					-151	-83	ATGATAGATTGCAGCACAACCCCTCAGTCATGTCTCGACCTTTATCTTATCTGGACACATCACGCTTAA			ATGATAGATTGCAGCACAACCCCTCAGTCATGTCTCGACCTTTATCTTATCTGGACACATCACGCTTAA	MIDCSTTPQSCLDLYLIWTHHA*			MIDCSTTPQSCLDLYLIWTHHA*	TAGACCATGC	ATAGTTCATT	0		FG11366.1	MG03844.1	NCU06861.1	0	0
1633	1110	af	AN9383.1	72.m19553	AO070336000233	0			-256	-227			ATGACGGATGACTATTGTGAAGAAACTTGA		ATGACGGATGACTATTGTGAAGAAACTTGA		MTDDYCEET*		MTDDYCEET*		ATCAGATATT	TATTTCTCCA	0	R	0	0	0	0	0
1634	1110	af	AN9383.1	72.m19553	AO070336000233	0			-249	-178			ATGACTATTGTGAAGAAACTTGATATTTCTCCACCACTCTGGTGGATGCTCCATGCCAAGATGGCTAGGTAA		ATGACTATTGTGAAGAAACTTGATATTTCTCCACCACTCTGGTGGATGCTCCATGCCAAGATGGCTAGGTAA		MTIVKKLDISPPLWWMLHAKMAR*		MTIVKKLDISPPLWWMLHAKMAR*		ATTATGACGG	TTCTCCGTTT	0	R	0	0	0	0	0
1635	1110	af	AN9383.1	72.m19553	AO070336000233	0			-204	-178			ATGCTCCATGCCAAGATGGCTAGGTAA		ATGCTCCATGCCAAGATGGCTAGGTAA		MLHAKMAR*		MLHAKMAR*		ACTCTGGTGG	TTCTCCGTTT	0	R	0	0	0	0	0
1636	1110	af	AN9383.1	72.m19553	AO070336000233	0			-189	-178			ATGGCTAGGTAA		ATGGCTAGGTAA		MAR*		MAR*		CCATGCCAAG	TTCTCCGTTT	0	R	0	0	0	0	0
1630	1110	an	AN9383.1	72.m19553	AO070336000233	0	-253	-212					ATGATTATGAATAATGACTGCTCCTCTCCACAATTTTCCTGA	ATGATTATGAATAATGACTGCTCCTCTCCACAATTTTCCTGA			MIMNNDCSSPQFS*	MIMNNDCSSPQFS*			TATAAATTGT	AGATGCCAAG	0	R	0	0	0	0	0
1631	1110	an	AN9383.1	72.m19553	AO070336000233	0	-247	-212					ATGAATAATGACTGCTCCTCTCCACAATTTTCCTGA	ATGAATAATGACTGCTCCTCTCCACAATTTTCCTGA			MNNDCSSPQFS*	MNNDCSSPQFS*			TTGTATGATT	AGATGCCAAG	0	R	0	0	0	0	0
1632	1110	an	AN9383.1	72.m19553	AO070336000233	0	-240	-58					ATGACTGCTCCTCTCCACAATTTTCCTGAAGATGCCAAGTTTGCCAAGCTGTCTGAAGGTCTTAATTTTTCCGGTGCGGAGAAGCTCAGTGTTAATTTCTCCGTCGGCCAGGGCCTTGGGATCGTCAGGCCTATCGTCAAGCATAGCTCCCCATGCAATGAGACCAGCCCCAACAAATTATAA	ATGACTGCTCCTCTCCACAATTTTCCTGAAGATGCCAAGTTTGCCAAGCTGTCTGAAGGTCTTAATTTTTCCGGTGCGGAGAAGCTCAGTGTTAATTTCTCCGTCGGCCAGGGCCTTGGGATCGTCAGGCCTATCGTCAAGCATAGCTCCCCATGCAATGAGACCAGCCCCAACAAATTATAA			MTAPLHNFPEDAKFAKLSEGLNFSGAEKLSVNFSVGQGLGIVRPIVKHSSPCNETSPNKL*	MTAPLHNFPEDAKFAKLSEGLNFSGAEKLSVNFSVGQGLGIVRPIVKHSSPCNETSPNKL*			ATTATGAATA	AAGGGGCCAG	0	R	0	0	0	0	0
1637	1110	ao	AN9383.1	72.m19553	AO070336000233	0					-230	-204	ATGCTATCGTGGCTTATCTGCAGCTAA			ATGCTATCGTGGCTTATCTGCAGCTAA	MLSWLICS*			MLSWLICS*	ATTTACCATC	ATTTAAAGTT	0	R	0	0	0	0	0
1645	1117	an	AN4672.1	71.m15660	AO070284000034	0	-279	-268					ATGAGGCAGTAA	ATGAGGCAGTAA			MRQ*	MRQ*			CTAGATACTA	GAGTAGTAAT	0	S	0	0	0	0	0
1646	1117	an	AN4672.1	71.m15660	AO070284000034	0	-247	-227					ATGCAGAAGCAGATCCGATGA	ATGCAGAAGCAGATCCGATGA			MQKQIR*	MQKQIR*			AATACTTGAG	AAGTGGGTTG	0	S	0	0	0	0	0
1647	1117	an	AN4672.1	71.m15660	AO070284000034	0	-230	-216					ATGAAAGTGGGTTGA	ATGAAAGTGGGTTGA			MKVG*	MKVG*			AGCAGATCCG	TCAAACAAAA	0	S	0	0	0	0	0
1648	1117	an	AN4672.1	71.m15660	AO070284000034	0	-206	-117					ATGCAGGTTCACCTATACAGGACTCGAGGACGTGTAAGAGAGTCCGTGTTGACGGCGGCTGTTGTCAGTACGACTATCGATAAGGCTTAG	ATGCAGGTTCACCTATACAGGACTCGAGGACGTGTAAGAGAGTCCGTGTTGACGGCGGCTGTTGTCAGTACGACTATCGATAAGGCTTAG			MQVHLYRTRGRVRESVLTAAVVSTTIDKA*	MQVHLYRTRGRVRESVLTAAVVSTTIDKA*			ATCAAACAAA	GCTTGGCACG	0	S	0	0	0	0	0
1649	1117	ao	AN4672.1	71.m15660	AO070284000034	0					-208	-131	ATGAAGATCAATCGATCACTGAACCCTGTTTCATCTCGTGTTTACAGTCAGCCCGGTTGGCGGTGCGACTATCGATAA			ATGAAGATCAATCGATCACTGAACCCTGTTTCATCTCGTGTTTACAGTCAGCCCGGTTGGCGGTGCGACTATCGATAA	MKINRSLNPVSSRVYSQPGWRCDYR*			MKINRSLNPVSSRVYSQPGWRCDYR*	AATCCGGAAG	GCGCCCTGTC	0	S	0	0	0	0	0
1651	1123	af	AN4842.1	59.m09137	AO070327000130	0			-97	-59			ATGTGGCACCATCCGGACTGGGCGTGCATCAGACAGTAA		ATGTGGCACCATCCGGACTGGGCGTGCATCAGACAGTAA		MWHHPDWACIRQ*		MWHHPDWACIRQ*		ACTAAACCAC	CCGTTCCGAA	0	C	FG09542.1	MG03006.1	0	0	0
1650	1123	an	AN4842.1	59.m09137	AO070327000130	0	-109	-86					ATGTTTCTGCCTCAGGCCACATAG	ATGTTTCTGCCTCAGGCCACATAG			MFLPQAT*	MFLPQAT*			TCACGTGCGT	TCAGCGCATC	0	C	FG09542.1	MG03006.1	0	0	0
1657	1127	af	AN0847.1	70.m15446	AO070216000006	0			-242	-201			ATGGTCAATTCCTATAGTTCACAACAAGCTCCACTACCGTGA		ATGGTCAATTCCTATAGTTCACAACAAGCTCCACTACCGTGA		MVNSYSSQQAPLP*		MVNSYSSQQAPLP*		GCACTGACGT	TTCGTGATAC	0	O	0	MG06648.1	NCU09485.1	0	0
1658	1127	af	AN0847.1	70.m15446	AO070216000006	0			-186	-142			ATGTACAGCCCGTTTTACACGGATCCTTCTTTCGACAATTACTAG		ATGTACAGCCCGTTTTACACGGATCCTTCTTTCGACAATTACTAG		MYSPFYTDPSFDNY*		MYSPFYTDPSFDNY*		TGATACCTGA	GGAAGGTCTT	0	O	0	MG06648.1	NCU09485.1	0	0
1659	1127	af	AN0847.1	70.m15446	AO070216000006	0			-73	-32			ATGCTCCTAGACTCTTCCTCCATGGTGCTCAGCTTTGTCTGA		ATGCTCCTAGACTCTTCCTCCATGGTGCTCAGCTTTGTCTGA		MLLDSSSMVLSFV*		MLLDSSSMVLSFV*		ATTTTGAGGT	CCTCTATTAT	0	O	0	MG06648.1	NCU09485.1	0	0
1656	1127	an	AN0847.1	70.m15446	AO070216000006	0	-81	-52					ATGCTACCAGGACCAGTCTCATCATTTTGA	ATGCTACCAGGACCAGTCTCATCATTTTGA			MLPGPVSSF*	MLPGPVSSF*			CTCCAAAGGT	GACACTCTGC	0	O	0	MG06648.1	NCU09485.1	0	0
1665	1131	af	AN0362.1	63.m00629	AO070318000042	0			-196	-41			ATGCTTGTCTCACTTAGGTTACATCGACTAAAGGGCATCAGTATTCTGGAGGCCCTCGTACTGAATCTCTGTCATAGTATAAAGACAGCATCCCCCCATCCAAACCTCCCGTTTCTCATCCTCATCCCAACATCTCTATTCTTTCTACGTCCCTAA		ATGCTTGTCTCACTTAGGTTACATCGACTAAAGGGCATCAGTATTCTGGAGGCCCTCGTACTGAATCTCTGTCATAGTATAAAGACAGCATCCCCCCATCCAAACCTCCCGTTTCTCATCCTCATCCCAACATCTCTATTCTTTCTACGTCCCTAA		MLVSLRLHRLKGISILEALVLNLCHSIKTASPHPNLPFLILIPTSLFFLRP*		MLVSLRLHRLKGISILEALVLNLCHSIKTASPHPNLPFLILIPTSLFFLRP*		AAACCAGCAG	AACTCCAGGG	0		0	0	0	0	0
1661	1131	an	AN0362.1	63.m00629	AO070318000042	0	-215	-189					ATGGATATATCGGCTTCGGCTACATGA	ATGGATATATCGGCTTCGGCTACATGA			MDISASAT*	MDISASAT*			TGTGGTCTGC	ACTATGCTGT	0		0	0	0	0	0
1662	1131	an	AN0362.1	63.m00629	AO070318000042	0	-192	-130					ATGAACTATGCTGTCATCGACGTATACGGAGCTGATCGTCTTGATCGTCAGGTTCGACTATAA	ATGAACTATGCTGTCATCGACGTATACGGAGCTGATCGTCTTGATCGTCAGGTTCGACTATAA			MNYAVIDVYGADRLDRQVRL*	MNYAVIDVYGADRLDRQVRL*			CTTCGGCTAC	ATCTTCCGGT	0		0	0	0	0	0
1663	1131	an	AN0362.1	63.m00629	AO070318000042	0	-185	-54					ATGCTGTCATCGACGTATACGGAGCTGATCGTCTTGATCGTCAGGTTCGACTATAAATCTTCCGGTGATTCCTCCGGGCATGGCTATCGTCGTAAAGCAACAAACCTTTTTATCTCTAGCTCTCTACCTTGA	ATGCTGTCATCGACGTATACGGAGCTGATCGTCTTGATCGTCAGGTTCGACTATAAATCTTCCGGTGATTCCTCCGGGCATGGCTATCGTCGTAAAGCAACAAACCTTTTTATCTCTAGCTCTCTACCTTGA			MLSSTYTELIVLIVRFDYKSSGDSSGHGYRRKATNLFISSSLP*	MLSSTYTELIVLIVRFDYKSSGDSSGHGYRRKATNLFISSSLP*			TACATGAACT	TCTCTACCTT	0		0	0	0	0	0
1664	1131	an	AN0362.1	63.m00629	AO070318000042	0	-106	-29					ATGGCTATCGTCGTAAAGCAACAAACCTTTTTATCTCTAGCTCTCTACCTTGATCTCTACCTTGATCTTTACCTCTAG	ATGGCTATCGTCGTAAAGCAACAAACCTTTTTATCTCTAGCTCTCTACCTTGATCTCTACCTTGATCTTTACCTCTAG			MAIVKQQTFLSLALYLDLYLDLYL*	MAIVKQQTFLSLALYLDLYLDLYL*			TCCTCCGGGC	AAAGTCAACT	0		0	0	0	0	0
1666	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-253	-233	ATGATCCAGATTTCGATATGA			ATGATCCAGATTTCGATATGA	MIQISI*			MIQISI*	CTGATAGGTT	TTATGCAGCG	0		0	0	0	0	0
1667	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-236	-201	ATGATTATGCAGCGGTTGGCGCCGACTGCAATGTAA			ATGATTATGCAGCGGTTGGCGCCGACTGCAATGTAA	MIMQRLAPTAM*			MIMQRLAPTAM*	AGATTTCGAT	CGTCTCTCTC	0		0	0	0	0	0
1668	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-230	-201	ATGCAGCGGTTGGCGCCGACTGCAATGTAA			ATGCAGCGGTTGGCGCCGACTGCAATGTAA	MQRLAPTAM*			MQRLAPTAM*	CGATATGATT	CGTCTCTCTC	0		0	0	0	0	0
1669	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-190	-50	ATGGCTCCACGAGATGCAGAATGTTGTATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGAAAACATTATAA			ATGGCTCCACGAGATGCAGAATGTTGTATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGAAAACATTATAA	MAPRDAECCMTLAIHGYLSASSSSGYKYEVDISTTCLSKQLSLKTL*			MAPRDAECCMTLAIHGYLSASSSSGYKYEVDISTTCLSKQLSLKTL*	CGTCTCTCTC	CCGTCTTCCA	0		0	0	0	0	0
1670	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-177	-160	ATGCAGAATGTTGTATGA			ATGCAGAATGTTGTATGA	MQNVV*			MQNVV*	GCTCCACGAG	CTCTCGCTAT	0		0	0	0	0	0
1671	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-170	-111	ATGTTGTATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAA			ATGTTGTATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAA	MLYDSRYPWISLSLLVLRI*			MLYDSRYPWISLSLLVLRI*	GAGATGCAGA	ATACGAGGTC	0		0	0	0	0	0
1672	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-163	-50	ATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGAAAACATTATAA			ATGACTCTCGCTATCCATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGAAAACATTATAA	MTLAIHGYLSASSSSGYKYEVDISTTCLSKQLSLKTL*			MTLAIHGYLSASSSSGYKYEVDISTTCLSKQLSLKTL*	AGAATGTTGT	CCGTCTTCCA	0		0	0	0	0	0
1673	1131	ao	AN0362.1	63.m00629	AO070318000042	0					-147	-61	ATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGA			ATGGATATCTCTCAGCCTCCTCGTCCTCCGGATATAAATACGAGGTCGATATCTCGACAACATGTCTCTCCAAACAGCTCAGTCTGA	MDISQPPRPPDINTRSISRQHVSPNSSV*			MDISQPPRPPDINTRSISRQHVSPNSSV*	CTCGCTATCC	AAACATTATA	0		0	0	0	0	0
1683	1136	af	AN1486.1	55.m02992	AO070334000193	0			-247	-203			ATGAGAATGGAGAGGGCCGTTTACTCCGCCTTCCAAAGCACGTGA		ATGAGAATGGAGAGGGCCGTTTACTCCGCCTTCCAAAGCACGTGA		MRMERAVYSAFQST*		MRMERAVYSAFQST*		TTGGGTGGTG	TGAGACTTTG	0	J	0	0	0	0	0
1684	1136	af	AN1486.1	55.m02992	AO070334000193	0			-241	-203			ATGGAGAGGGCCGTTTACTCCGCCTTCCAAAGCACGTGA		ATGGAGAGGGCCGTTTACTCCGCCTTCCAAAGCACGTGA		MERAVYSAFQST*		MERAVYSAFQST*		GGTGATGAGA	TGAGACTTTG	0	J	0	0	0	0	0
1685	1136	af	AN1486.1	55.m02992	AO070334000193	0			-203	-168			ATGAGACTTTGGGGGAGCAGTCCGAATCAATACTAG		ATGAGACTTTGGGGGAGCAGTCCGAATCAATACTAG		MRLWGSSPNQY*		MRLWGSSPNQY*		AAAGCACGTG	CGCCCTTCTC	0	J	0	0	0	0	0
1686	1136	af	AN1486.1	55.m02992	AO070334000193	0			-139	-80			ATGCGGAATAGTTTCTTGATTTCCTTTTGTAGACAAGTTTCGACAGCTTCGATAGCTTAA		ATGCGGAATAGTTTCTTGATTTCCTTTTGTAGACAAGTTTCGACAGCTTCGATAGCTTAA		MRNSFLISFCRQVSTASIA*		MRNSFLISFCRQVSTASIA*		GCAACAGTTG	TGAACAAGCA	0	J	0	0	0	0	0
1680	1136	an	AN1486.1	55.m02992	AO070334000193	0	-151	-119					ATGAACGATGCGGCTATCACGGAACAACATTGA	ATGAACGATGCGGCTATCACGGAACAACATTGA			MNDAAITEQH*	MNDAAITEQH*			GTCTGCTGTC	TGCGGGTACT	0	J	0	0	0	0	0

1681	1136	an	AN1486.1	55.m02992	AO070334000193	0	-144	-61					ATGCGGCTATCACGGAACAACATTGATGCGGGTACTGTGGCTTACCTTTCTGGGACAGTTCTGAGCTTGTTCTTTCTTTGCTGA	ATGCGGCTATCACGGAACAACATTGATGCGGGTACTGTGGCTTACCTTTCTGGGACAGTTCTGAGCTTGTTCTTTCTTTGCTGA			MRLSRNNIDAGTVAYLSGTVLSLFFLC*	MRLSRNNIDAGTVAYLSGTVLSLFFLC*			GTCATGAACG	GGAGCAGAGG	0	J	0	0	0	0	0
1682	1136	an	AN1486.1	55.m02992	AO070334000193	0	-119	-81					ATGCGGGTACTGTGGCTTACCTTTCTGGGACAGTTCTGA	ATGCGGGTACTGTGGCTTACCTTTCTGGGACAGTTCTGA			MRVLWLTFLGQF*	MRVLWLTFLGQF*			AACAACATTG	GCTTGTTCTT	0	J	0	0	0	0	0
1688	1140	af	AN1554.1	55.m03071	AO070339000300	0			-134	-117			ATGCCGTCAGATCTCTAA		ATGCCGTCAGATCTCTAA		MPSDL*		MPSDL*		CCAAGTCTCG	GGCCTCTCCA	0	MOT	0	0	0	0	0
1687	1140	an	AN1554.1	55.m03071	AO070339000300	0	-131	-117					ATGTCCGAATCATAG	ATGTCCGAATCATAG			MSES*	MSES*			GCCTCCCTCC	GCACCTCTCG	0	MOT	0	0	0	0	0
1689	1140	ao	AN1554.1	55.m03071	AO070339000300	0					-152	-126	ATGAGAGCCTATATGCGCCGTACTTAG			ATGAGAGCCTATATGCGCCGTACTTAG	MRAYMRRT*			MRAYMRRT*	CTTCTCCCCC	ATCTCCGCTT	0	MOT	0	0	0	0	0
1690	1140	ao	AN1554.1	55.m03071	AO070339000300	0					-140	-126	ATGCGCCGTACTTAG			ATGCGCCGTACTTAG	MRRT*			MRRT*	GAGAGCCTAT	ATCTCCGCTT	0	MOT	0	0	0	0	0
1692	1144	ao	AN6528.1	62.m03116	AO070270000028	0					-202	-164	ATGCACTTTGCTACATTACGTGGTCAAACTCTTGTATAA			ATGCACTTTGCTACATTACGTGGTCAAACTCTTGTATAA	MHFATLRGQTLV*			MHFATLRGQTLV*	AACACCCCTG	CAAATCGATA	0	O	0	0	0	0	0
1693	1145	af	AN7298.1	72.m19768	AO070297000040	0			-201	-55			ATGCCCAAACAATGCCTTGCGTGGAGGCATCCAAATGAGGAGCAATACATCTCTTTGGCCAATCATAGCCTCCTGTGTCAAGATTCTCCTCATCAGCTTCCATCCCACCCTCATCCAGTTTCGGACTATTCCTCTAACTGCTTATAG		ATGCCCAAACAATGCCTTGCGTGGAGGCATCCAAATGAGGAGCAATACATCTCTTTGGCCAATCATAGCCTCCTGTGTCAAGATTCTCCTCATCAGCTTCCATCCCACCCTCATCCAGTTTCGGACTATTCCTCTAACTGCTTATAG		MPKQCLAWRHPNEEQYISLANHSLLCQDSPHQLPSHPHPVSDYSSNCL*		MPKQCLAWRHPNEEQYISLANHSLLCQDSPHQLPSHPHPVSDYSSNCL*		GCGTGTCTAA	GGATCATCAG	0	R	0	0	0	0	0
1694	1145	af	AN7298.1	72.m19768	AO070297000040	0			-190	-164			ATGCCTTGCGTGGAGGCATCCAAATGA		ATGCCTTGCGTGGAGGCATCCAAATGA		MPCVEASK*		MPCVEASK*		TGCCCAAACA	GGAGCAATAC	0	R	0	0	0	0	0
1695	1145	ao	AN7298.1	72.m19768	AO070297000040	0					-242	-177	ATGAATGAGGGGAGCTGCTGCCCAGAAGAGGAGAAAGACCTCTCCTCCAATCACAACACCGGTTGA			ATGAATGAGGGGAGCTGCTGCCCAGAAGAGGAGAAAGACCTCTCCTCCAATCACAACACCGGTTGA	MNEGSCCPEEEKDLSSNHNTG*			MNEGSCCPEEEKDLSSNHNTG*	CACAGGATCA	CCCAACCTTC	0	R	0	0	0	0	0
1696	1145	ao	AN7298.1	72.m19768	AO070297000040	0					-238	-71	ATGAGGGGAGCTGCTGCCCAGAAGAGGAGAAAGACCTCTCCTCCAATCACAACACCGGTTGACCCAACCTTCTCCTCATTCCATCAGTCCTATAACATCGCTACTCCCTATATCTCACCCAGATATTGTACTTCTAACAAGCGCGGGCAACAAGGTTCTCGGTTCTAG			ATGAGGGGAGCTGCTGCCCAGAAGAGGAGAAAGACCTCTCCTCCAATCACAACACCGGTTGACCCAACCTTCTCCTCATTCCATCAGTCCTATAACATCGCTACTCCCTATATCTCACCCAGATATTGTACTTCTAACAAGCGCGGGCAACAAGGTTCTCGGTTCTAG	MRGAAAQKRRKTSPPITTPVDPTFSSFHQSYNIATPYISPRYCTSNKRGQQGSRF*			MRGAAAQKRRKTSPPITTPVDPTFSSFHQSYNIATPYISPRYCTSNKRGQQGSRF*	GGATCAATGA	TGGAGATAGC	0	R	0	0	0	0	0
1706	1154	af	AN5960.1	72.m19174	AO070340000311	0			-119	-105			ATGCAGCATTTGTAG		ATGCAGCATTTGTAG		MQHL*		MQHL*		ATCAGCACGA	GGCACACACA	0	J	0	0	NCU07830.1	0	0
1705	1154	an	AN5960.1	72.m19174	AO070340000311	0	-160	-146					ATGCCTCTCGCTTGA	ATGCCTCTCGCTTGA			MPLA*	MPLA*			CAGGCTATAG	TCTTGCAATC	0	J	0	0	NCU07830.1	0	0
1707	1154	ao	AN5960.1	72.m19174	AO070340000311	0					-191	-168	ATGCTAAGAACATTTAGTGCCTGA			ATGCTAAGAACATTTAGTGCCTGA	MLRTFSA*			MLRTFSA*	GTCAAGTAAG	GGCCTCGACT	0	J	0	0	NCU07830.1	0	0
1708	1159	ao	AN8845.1	71.m15979	AO070271000031	0					-225	-16	ATGCCTGATATTATTGTCTTTATCCACGACCGGCGTTATCGTGATCAGAACAGACTGCTGGGCAGTGCTGCAGCCTATTCGACCCTATTTATATATTCTGTGCTGTCAATTATTATCATTAACTTCTTCGTCTTTTCTTTTTCTCTTTTTGAGGATACATCATTTCTTTCCCTCTTCCAAGCTTCTCTTCCCAAGGCCACCTATTTTTAA			ATGCCTGATATTATTGTCTTTATCCACGACCGGCGTTATCGTGATCAGAACAGACTGCTGGGCAGTGCTGCAGCCTATTCGACCCTATTTATATATTCTGTGCTGTCAATTATTATCATTAACTTCTTCGTCTTTTCTTTTTCTCTTTTTGAGGATACATCATTTCTTTCCCTCTTCCAAGCTTCTCTTCCCAAGGCCACCTATTTTTAA	MPDIIVFIHDRRYRDQNRLLGSAAAYSTLFIYSVLSIIIINFFVFSFSLFEDTSFLSLFQASLPKATYF*			MPDIIVFIHDRRYRDQNRLLGSAAAYSTLFIYSVLSIIIINFFVFSFSLFEDTSFLSLFQASLPKATYF*	TCAGCGCTCC	GGCAACCAAG	0		0	0	NCU06223.1	0	0
1709	1160	af	AN9403.1	52.m04030	AO070274000014	0			-259	-236			ATGATAGCCATGGATAAACAATAA		ATGATAGCCATGGATAAACAATAA		MIAMDKQ*		MIAMDKQ*		ATATACTTGT	TACGGAAGAA	0	C	0	MG10569.1	0	0	0
1710	1160	af	AN9403.1	52.m04030	AO070274000014	0			-250	-236			ATGGATAAACAATAA		ATGGATAAACAATAA		MDKQ*		MDKQ*		TATGATAGCC	TACGGAAGAA	0	C	0	MG10569.1	0	0	0
1711	1160	ao	AN9403.1	52.m04030	AO070274000014	0					-252	-238	ATGAGCCGCCGGTGA			ATGAGCCGCCGGTGA	MSRR*			MSRR*	CTCCTACGGA	GGACCGCCCT	0	C	0	MG10569.1	0	0	0
1712	1160	ao	AN9403.1	52.m04030	AO070274000014	0					-192	-175	ATGCTCACCAAAAACTAA			ATGCTCACCAAAAACTAA	MLTKN*			MLTKN*	GTCTCTCGAA	AATCCCCATT	0	C	0	MG10569.1	0	0	0
1713	1164	an	AN9148.1	66.m04587	AO070332000144	0	-288	-49					ATGCCCGTTGTCTGCTTGAGACCTGTGCTTGTGCTTGTGTCGCACTGTTGCCGTCATCCCTCCTTGCCCGCGATCGACACCAGCAATAACACCGTCTGTGTTGTGGCAACGTGGATCAAGGCAGCCTGCCACTGCCCGGCTCAGTCGACTCAAGAACCAGCCAGAGTCTTATTTATTGCTGGTCTCGGTCACTTTCATCTGTCCTTTGACACTAACTGCTGTTTCTTATCAGTAGACTAA	ATGCCCGTTGTCTGCTTGAGACCTGTGCTTGTGCTTGTGTCGCACTGTTGCCGTCATCCCTCCTTGCCCGCGATCGACACCAGCAATAACACCGTCTGTGTTGTGGCAACGTGGATCAAGGCAGCCTGCCACTGCCCGGCTCAGTCGACTCAAGAACCAGCCAGAGTCTTATTTATTGCTGGTCTCGGTCACTTTCATCTGTCCTTTGACACTAACTGCTGTTTCTTATCAGTAGACTAA			MPVVCLRPVLVLVSHCCRHPSLPAIDTSNNTVCVVATWIKAACHCPAQSTQEPARVLFIAGLGHFHLSFDTNCCFLSVD*	MPVVCLRPVLVLVSHCCRHPSLPAIDTSNNTVCVVATWIKAACHCPAQSTQEPARVLFIAGLGHFHLSFDTNCCFLSVD*			TTGTTCTTTC	ATATCTGCTT	0	G	FG00524.1	MG01631.1	0	0	0
1714	1164	ao	AN9148.1	66.m04587	AO070332000144	0					-233	-147	ATGGTCCGCTTAAATCAAGTGTCGTGTCCTCTTGGCTCATCCTTCCCTTTGTGTTCATTCTTGCTTGCTCCTCACGCCCACTCTTAA			ATGGTCCGCTTAAATCAAGTGTCGTGTCCTCTTGGCTCATCCTTCCCTTTGTGTTCATTCTTGCTTGCTCCTCACGCCCACTCTTAA	MVRLNQVSCPLGSSFPLCSFLLAPHAHS*			MVRLNQVSCPLGSSFPLCSFLLAPHAHS*	GGGGTCCCCA	GCTTTCTGAA	0	G	FG00524.1	MG01631.1	0	0	0
1716	1165	af	AN0414.1	54.m06661	AO070338000256	0			-218	-189			ATGACCGGCAATTTGTTATCGGGGTCTTAA		ATGACCGGCAATTTGTTATCGGGGTCTTAA		MTGNLLSGS*		MTGNLLSGS*		TCTATTCCTT	ATTATTGAGT	0	Z	0	0	0	0	0
1717	1165	ao	AN0414.1	54.m06661	AO070338000256	0					-75	-64	ATGTTATTATAA			ATGTTATTATAA	MLL*			MLL*	AACTAGAAAC	GGTCTTATGC	0	Z	0	0	0	0	0
1720	1166	af	AN5516.1	69.m15443	AO070341000378	0			-153	-127			ATGACCTTGATCTCAGGTCAACTCTAA		ATGACCTTGATCTCAGGTCAACTCTAA		MTLISGQL*		MTLISGQL*		TCGCGTCACA	CTATCTTATC	0	B	0	0	0	0	0
1719	1166	an	AN5516.1	69.m15443	AO070341000378	0	-241	-95					ATGGCAGATCTGCTTGTACCCCAGAGATCAGGAAAGGCGGAAGTCAAACAGACATCATTCACTGCGGTCGCGTTCGCGGAATCGAGACACGACAGCATTTTCAACTCCCGTGACCGGATCTTCCGTCAGTCCACCCTCAGACTTTGA	ATGGCAGATCTGCTTGTACCCCAGAGATCAGGAAAGGCGGAAGTCAAACAGACATCATTCACTGCGGTCGCGTTCGCGGAATCGAGACACGACAGCATTTTCAACTCCCGTGACCGGATCTTCCGTCAGTCCACCCTCAGACTTTGA			MADLLVPQRSGKAEVKQTSFTAVAFAESRHDSIFNSRDRIFRQSTLRL*	MADLLVPQRSGKAEVKQTSFTAVAFAESRHDSIFNSRDRIFRQSTLRL*			ATACCAGGAG	CTTCTGACGC	0	B	0	0	0	0	0
1721	1166	ao	AN5516.1	69.m15443	AO070341000378	0					-180	-151	ATGACAGGAAACAACCCGAGCCTCCCGTGA			ATGACAGGAAACAACCCGAGCCTCCCGTGA	MTGNNPSLP*			MTGNNPSLP*	GAAACAGCTC	CCTTGACCTG	0	B	0	0	0	0	0
1722	1166	ao	AN5516.1	69.m15443	AO070341000378	0					-130	-116	ATGTCGTCAACTTGA			ATGTCGTCAACTTGA	MSST*			MSST*	TGTTCACCTC	CTCTGGATCT	0	B	0	0	0	0	0
1723	1166	ao	AN5516.1	69.m15443	AO070341000378	0					-105	-10	ATGATAGACAGTCCGCTAGCCGAGTGCGCAGTTCAACCAATCATCTCGCAACAGTCATCGCTCCTTGCCCCTAGCTTCATTCTCTTCTATGCATGA			ATGATAGACAGTCCGCTAGCCGAGTGCGCAGTTCAACCAATCATCTCGCAACAGTCATCGCTCCTTGCCCCTAGCTTCATTCTCTTCTATGCATGA	MIDSPLAECAVQPIISQQSSLLAPSFILFYA*			MIDSPLAECAVQPIISQQSSLLAPSFILFYA*	CTCTGGATCT	TTGTCCATCA	0	B	0	0	0	0	0
1726	1170	af	AN8213.1	53.m03760	AO070310000099	0			-187	-161			ATGAGACTAGTAAATGCTAGCAATTGA		ATGAGACTAGTAAATGCTAGCAATTGA		MRLVNASN*		MRLVNASN*		TAAACGATCG	TAAATCCACT	0	F	0	0	0	YJR057W	0
1727	1170	af	AN8213.1	53.m03760	AO070310000099	0			-174	-136			ATGCTAGCAATTGATAAATCCACTAGACTTACTCTGTAG		ATGCTAGCAATTGATAAATCCACTAGACTTACTCTGTAG		MLAIDKSTRLTL*		MLAIDKSTRLTL*		AGACTAGTAA	ACACCACAGT	0	F	0	0	0	YJR057W	0
1724	1170	an	AN8213.1	53.m03760	AO070310000099	0	-252	-241					ATGTGCAGCTGA	ATGTGCAGCTGA			MCS*	MCS*			AGGAGTGAGT	AAGAAAATGT	0	F	0	0	0	YJR057W	0
1725	1170	an	AN8213.1	53.m03760	AO070310000099	0	-234	-154					ATGTCAAGTTGTTGGCAGAGGCTGTTATCGATAAGTACTTGTTTCGCGACTCCAATTCCTCCAGATCACGGTGGACCTTAA	ATGTCAAGTTGTTGGCAGAGGCTGTTATCGATAAGTACTTGTTTCGCGACTCCAATTCCTCCAGATCACGGTGGACCTTAA			MSSCWQRLLSISTCFATPIPPDHGGP*	MSSCWQRLLSISTCFATPIPPDHGGP*			CTGAAAGAAA	TAACGAGACC	0	F	0	0	0	YJR057W	0
1728	1170	ao	AN8213.1	53.m03760	AO070310000099	0					-210	-187	ATGCCTGAAAATACAGACGGATAA			ATGCCTGAAAATACAGACGGATAA	MPENTDG*			MPENTDG*	GGGAAGTTGG	ATGAAATAAA	0	F	0	0	0	YJR057W	0
1729	1170	ao	AN8213.1	53.m03760	AO070310000099	0					-116	-81	ATGATCGGACAGGAAGATTGTATTTTATTTTTTTGA			ATGATCGGACAGGAAGATTGTATTTTATTTTTTTGA	MIGQEDCILFF*			MIGQEDCILFF*	CTCGTTGCAT	AGGGATACTT	0	F	0	0	0	YJR057W	0
1730	1173	an	AN9065.1	66.m04528	AO070332000209	0	-254	-228					ATGGAGGGGTTCTCGTGCGGTTTATAG	ATGGAGGGGTTCTCGTGCGGTTTATAG			MEGFSCGL*	MEGFSCGL*			AAGTCGTACC	ACTCTCCGCC	0		0	0	0	0	0
1731	1173	an	AN9065.1	66.m04528	AO070332000209	0	-126	-115					ATGCGGGTATAG	ATGCGGGTATAG			MRV*	MRV*			CTGCGGGCTT	TATGCGGAGC	0		0	0	0	0	0
1732	1173	an	AN9065.1	66.m04528	AO070332000209	0	-113	-102					ATGCGGAGCTAG	ATGCGGAGCTAG			MRS*	MRS*			CGGGTATAGT	CTTCAATCAC	0		0	0	0	0	0
1734	1175	an	AN5671.1	69.m15375	AO070342000266	0	-104	-60					ATGTTGACGCGCAATTTGGTTTGCACCGCCCTCTTTGCCTTTTAA	ATGTTGACGCGCAATTTGGTTTGCACCGCCCTCTTTGCCTTTTAA			MLTRNLVCTALFAF*	MLTRNLVCTALFAF*			CGGTTCATTC	GGTACCGCTA	0		0	0	0	0	0
1739	1176	af	AN2336.1	65.m07340	AO070343000082	0			-228	-199			ATGTCAGATATGACCTCAGTGCTAACATAA		ATGTCAGATATGACCTCAGTGCTAACATAA		MSDMTSVLT*		MSDMTSVLT*		ACCGGTAGGC	TGCTGCGAAA	0	M	0	0	0	0	0
1740	1176	af	AN2336.1	65.m07340	AO070343000082	0			-219	-199			ATGACCTCAGTGCTAACATAA		ATGACCTCAGTGCTAACATAA		MTSVLT*		MTSVLT*		CATGTCAGAT	TGCTGCGAAA	0	M	0	0	0	0	0
1741	1176	af	AN2336.1	65.m07340	AO070343000082	0			-199	-176			ATGCTGCGAAATGCCTGCCTATAA		ATGCTGCGAAATGCCTGCCTATAA		MLRNACL*		MLRNACL*		TGCTAACATA	GATTTGTCGA	0	M	0	0	0	0	0
1742	1176	af	AN2336.1	65.m07340	AO070343000082	0			-189	-55			ATGCCTGCCTATAAGATTTGTCGATCAGCGCATGTGCTGGCGAATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGATAGCAGGACGTTGTGGTATCAGTGGGGTTACAAGACTACCTGCCTTAGTATAA		ATGCCTGCCTATAAGATTTGTCGATCAGCGCATGTGCTGGCGAATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGATAGCAGGACGTTGTGGTATCAGTGGGGTTACAAGACTACCTGCCTTAGTATAA		MPAYKICRSAHVLANVTLHLFIQHIILIAGRCGISGVTRLPALV*		MPAYKICRSAHVLANVTLHLFIQHIILIAGRCGISGVTRLPALV*		ATGCTGCGAA	AAGATGGCCA	0	M	0	0	0	0	0
1743	1176	af	AN2336.1	65.m07340	AO070343000082	0			-158	-108			ATGTGCTGGCGAATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGA		ATGTGCTGGCGAATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGA		MCWRMSPFICSSSISY*		MCWRMSPFICSSSISY*		CGATCAGCGC	TAGCAGGACG	0	M	0	0	0	0	0
1744	1176	af	AN2336.1	65.m07340	AO070343000082	0			-146	-108			ATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGA		ATGTCACCCTTCATTTGTTCATCCAGCATATCATATTGA		MSPFICSSSISY*		MSPFICSSSISY*		GTGCTGGCGA	TAGCAGGACG	0	M	0	0	0	0	0
1735	1176	an	AN2336.1	65.m07340	AO070343000082	0	-252	-241					ATGATATCTTGA	ATGATATCTTGA			MIS*	MIS*			TGGGATAGGC	TAAGCAGCTG	0	M	0	0	0	0	0
1736	1176	an	AN2336.1	65.m07340	AO070343000082	0	-210	-97					ATGGGTCTGGCGGCTATCACGGAATTCAGAGCGCCTGTGAGGTTGGCTTGTCGGTGCATGTGCGCGAAATCATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGA	ATGGGTCTGGCGGCTATCACGGAATTCAGAGCGCCTGTGAGGTTGGCTTGTCGGTGCATGTGCGCGAAATCATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGA			MGLAAITEFRAPVRLACRCMCAKSWPSICPREFRADM*	MGLAAITEFRAPVRLACRCMCAKSWPSICPREFRADM*			CTCCACAGTC	CTTGAGCCAT	0	M	0	0	0	0	0
1737	1176	an	AN2336.1	65.m07340	AO070343000082	0	-153	-97					ATGTGCGCGAAATCATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGA	ATGTGCGCGAAATCATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGA			MCAKSWPSICPREFRADM*	MCAKSWPSICPREFRADM*			TTGTCGGTGC	CTTGAGCCAT	0	M	0	0	0	0	0
1738	1176	an	AN2336.1	65.m07340	AO070343000082	0	-139	-92					ATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGACTTGA	ATGGCCTTCCATTTGCCCGCGGGAATTTCGGGCAGATATGTGACTTGA			MAFHLPAGISGRYVT*	MAFHLPAGISGRYVT*			GCGCGAAATC	GCCATAGCAT	0	M	0	0	0	0	0
1746	1176	ao	AN2336.1	65.m07340	AO070343000082	0					-158	-45	ATGGATATGCGCTTCAACCCGACGCACAGCGCACGTGGTATCCGAATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG			ATGGATATGCGCTTCAACCCGACGCACAGCGCACGTGGTATCCGAATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG	MDMRFNPTHSARGIRMGRKGSSSSGLYKPFPGRAQTP*			MDMRFNPTHSARGIRMGRKGSSSSGLYKPFPGRAQTP*	TCGTGCCTCG	CAAGCAGCAT	0	M	0	0	0	0	0
1747	1176	ao	AN2336.1	65.m07340	AO070343000082	0					-152	-45	ATGCGCTTCAACCCGACGCACAGCGCACGTGGTATCCGAATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG			ATGCGCTTCAACCCGACGCACAGCGCACGTGGTATCCGAATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG	MRFNPTHSARGIRMGRKGSSSSGLYKPFPGRAQTP*			MRFNPTHSARGIRMGRKGSSSSGLYKPFPGRAQTP*	CTCGATGGAT	CAAGCAGCAT	0	M	0	0	0	0	0
1748	1176	ao	AN2336.1	65.m07340	AO070343000082	0					-113	-45	ATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG			ATGGGACGGAAAGGTAGCTCCTCCAGTGGGCTATATAAGCCTTTCCCTGGCCGGGCTCAGACTCCCTAG	MGRKGSSSSGLYKPFPGRAQTP*			MGRKGSSSSGLYKPFPGRAQTP*	TGGTATCCGA	CAAGCAGCAT	0	M	0	0	0	0	0
1749	1177	ao	AN7587.1	72.m19609	AO070343000300	0					-85	-65	ATGACGACCAGATATGGCTGA			ATGACGACCAGATATGGCTGA	MTTRYG*			MTTRYG*	GGGATGATAA	CGATGTTGGA	0	S	0	0	0	0	0
1750	1177	ao	AN7587.1	72.m19609	AO070343000300	0					-62	-3	ATGTTGGAACGCTACAGGACCTGGAAGAGATTGAAGAATGGAACGAGTATGGCGAGCTGA			ATGTTGGAACGCTACAGGACCTGGAAGAGATTGAAGAATGGAACGAGTATGGCGAGCTGA	MLERYRTWKRLKNGTSMAS*			MLERYRTWKRLKNGTSMAS*	ATGGCTGACG	GAATGCAGGT	0	S	0	0	0	0	0
1757	1180	af	AN4446.1	58.m09017	AO070273000007	0			-218	-189			ATGAAATCAACGACGAGATGCCGACCGTGA		ATGAAATCAACGACGAGATGCCGACCGTGA		MKSTTRCRP*		MKSTTRCRP*		AAATTAAAAG	TGGCTGAAAG	0	U	FG10067.1	MG08096.1	0	0	0

1758	1180	af	AN4446.1	58.m09017	AO070273000007	0			-201	-22			ATGCCGACCGTGATGGCTGAAAGAGGGAAACCGGTACGCAGAAAACGGCCGGTCTCCTCCATTCCATTCCGCCCATCGAATCGCGCCAAGACCGTCCCGTCGTTGGTGCCAGATCTTCATTCAGTCAACATCAACGACCGACAACGCCAGCTTCTCTTCCAGCATCGATTATCGCCCTGA		ATGCCGACCGTGATGGCTGAAAGAGGGAAACCGGTACGCAGAAAACGGCCGGTCTCCTCCATTCCATTCCGCCCATCGAATCGCGCCAAGACCGTCCCGTCGTTGGTGCCAGATCTTCATTCAGTCAACATCAACGACCGACAACGCCAGCTTCTCTTCCAGCATCGATTATCGCCCTGA		MPTVMAERGKPVRRKRPVSSIPFRPSNRAKTVPSLVPDLHSVNINDRQRQLLFQHRLSP*		MPTVMAERGKPVRRKRPVSSIPFRPSNRAKTVPSLVPDLHSVNINDRQRQLLFQHRLSP*		CAACGACGAG	CTTCAATTGG	0	U	FG10067.1	MG08096.1	0	0	0
1759	1180	af	AN4446.1	58.m09017	AO070273000007	0			-189	-22			ATGGCTGAAAGAGGGAAACCGGTACGCAGAAAACGGCCGGTCTCCTCCATTCCATTCCGCCCATCGAATCGCGCCAAGACCGTCCCGTCGTTGGTGCCAGATCTTCATTCAGTCAACATCAACGACCGACAACGCCAGCTTCTCTTCCAGCATCGATTATCGCCCTGA		ATGGCTGAAAGAGGGAAACCGGTACGCAGAAAACGGCCGGTCTCCTCCATTCCATTCCGCCCATCGAATCGCGCCAAGACCGTCCCGTCGTTGGTGCCAGATCTTCATTCAGTCAACATCAACGACCGACAACGCCAGCTTCTCTTCCAGCATCGATTATCGCCCTGA		MAERGKPVRRKRPVSSIPFRPSNRAKTVPSLVPDLHSVNINDRQRQLLFQHRLSP*		MAERGKPVRRKRPVSSIPFRPSNRAKTVPSLVPDLHSVNINDRQRQLLFQHRLSP*		GCCGACCGTG	CTTCAATTGG	0	U	FG10067.1	MG08096.1	0	0	0
1753	1180	an	AN4446.1	58.m09017	AO070273000007	0	-181	-119					ATGGATGTATACAGCGTTGACAGTGAGATGGAGGAGTGGTTGTTAATCGAGACGGGGGAATGA	ATGGATGTATACAGCGTTGACAGTGAGATGGAGGAGTGGTTGTTAATCGAGACGGGGGAATGA			MDVYSVDSEMEEWLLIETGE*	MDVYSVDSEMEEWLLIETGE*			TCAGTTTGAT	GAATTCGCGC	0	U	FG10067.1	MG08096.1	0	0	0
1754	1180	an	AN4446.1	58.m09017	AO070273000007	0	-177	-136					ATGTATACAGCGTTGACAGTGAGATGGAGGAGTGGTTGTTAA	ATGTATACAGCGTTGACAGTGAGATGGAGGAGTGGTTGTTAA			MYTALTVRWRSGC*	MYTALTVRWRSGC*			TTTGATATGG	TCGAGACGGG	0	U	FG10067.1	MG08096.1	0	0	0
1755	1180	an	AN4446.1	58.m09017	AO070273000007	0	-154	-119					ATGGAGGAGTGGTTGTTAATCGAGACGGGGGAATGA	ATGGAGGAGTGGTTGTTAATCGAGACGGGGGAATGA			MEEWLLIETGE*	MEEWLLIETGE*			TGACAGTGAG	GAATTCGCGC	0	U	FG10067.1	MG08096.1	0	0	0
1756	1180	an	AN4446.1	58.m09017	AO070273000007	0	-91	-62					ATGGCCTGGATCTGGATCTGGACAGCATAA	ATGGCCTGGATCTGGATCTGGACAGCATAA			MAWIWIWTA*	MAWIWIWTA*			ACTCCCGCCC	CATTAACGTG	0	U	FG10067.1	MG08096.1	0	0	0
1760	1180	ao	AN4446.1	58.m09017	AO070273000007	0					-258	-199	ATGAGAACAAGGAGGGTGAGGAACAGAAATACAGGAGATGAAGAACAAGAGGGGATATGA			ATGAGAACAAGGAGGGTGAGGAACAGAAATACAGGAGATGAAGAACAAGAGGGGATATGA	MRTRRVRNRNTGDEEQEGI*			MRTRRVRNRNTGDEEQEGI*	TAGTAGATAA	AAGGAGTGAA	0	U	FG10067.1	MG08096.1	0	0	0
1761	1180	ao	AN4446.1	58.m09017	AO070273000007	0					-202	-176	ATGAAAGGAGTGAAGAGTATGAGGTGA			ATGAAAGGAGTGAAGAGTATGAGGTGA	MKGVKSMR*			MKGVKSMR*	AAGAGGGGAT	AGGGGAGTTG	0	U	FG10067.1	MG08096.1	0	0	0
1762	1180	ao	AN4446.1	58.m09017	AO070273000007	0					-157	-98	ATGATCGAATGGAGAATTCAATTCGCGCCAAGACTCTTCCGTCCGTTGCTGCCACATTGA			ATGATCGAATGGAGAATTCAATTCGCGCCAAGACTCTTCCGTCCGTTGCTGCCACATTGA	MIEWRIQFAPRLFRPLLPH*			MIEWRIQFAPRLFRPLLPH*	TGTAAAGTGA	GCATCAACAT	0	U	FG10067.1	MG08096.1	0	0	0
1764	1184	af	AN5119.1	54.m06906	AO070291000062	0			-162	-100			ATGCACCGATGTACCTCAATTGATGATACTCTGTATTCTCTTACAATCACTGTGTACCCCTGA		ATGCACCGATGTACCTCAATTGATGATACTCTGTATTCTCTTACAATCACTGTGTACCCCTGA		MHRCTSIDDTLYSLTITVYP*		MHRCTSIDDTLYSLTITVYP*		CAATCTGCAG	CTGCAAACGA	0	R	0	0	0	YML014W	0
1765	1184	af	AN5119.1	54.m06906	AO070291000062	0			-154	-140			ATGTACCTCAATTGA		ATGTACCTCAATTGA		MYLN*		MYLN*		AGATGCACCG	TGATACTCTG	0	R	0	0	0	YML014W	0
1766	1184	af	AN5119.1	54.m06906	AO070291000062	0			-140	-48			ATGATACTCTGTATTCTCTTACAATCACTGTGTACCCCTGACTGCAAACGACACAGCTTAAGAAAATCCGGAACCCTCCGATTTTGCATGTGA		ATGATACTCTGTATTCTCTTACAATCACTGTGTACCCCTGACTGCAAACGACACAGCTTAAGAAAATCCGGAACCCTCCGATTTTGCATGTGA		MILCILLQSLCTPDCKRHSLRKSGTLRFCM*		MILCILLQSLCTPDCKRHSLRKSGTLRFCM*		ACCTCAATTG	GGGATTTTAA	0	R	0	0	0	YML014W	0
1763	1184	an	AN5119.1	54.m06906	AO070291000062	0	-159	-34					ATGATACGGTACCCACTTGCTCAAAGTTCCCAAAGTCATCCCACCGAGTGCAATAAGTGTCATAGTGGGCAATCGATCGCTTACCACTCCGATAAAGCTTTGAAGGATCCAGTGGGCTGCCGCTGA	ATGATACGGTACCCACTTGCTCAAAGTTCCCAAAGTCATCCCACCGAGTGCAATAAGTGTCATAGTGGGCAATCGATCGCTTACCACTCCGATAAAGCTTTGAAGGATCCAGTGGGCTGCCGCTGA			MIRYPLAQSSQSHPTECNKCHSGQSIAYHSDKALKDPVGCR*	MIRYPLAQSSQSHPTECNKCHSGQSIAYHSDKALKDPVGCR*			TACGCACTGT	GTCAAGTCGA	0	R	0	0	0	YML014W	0
1767	1184	ao	AN5119.1	54.m06906	AO070291000062	0					-168	-139	ATGGTATTGTATCATGTTTCTCGATGGTGA			ATGGTATTGTATCATGTTTCTCGATGGTGA	MVLYHVSRW*			MVLYHVSRW*	TACGGTGCGT	ATTCACTTCT	0	R	0	0	0	YML014W	0
1768	1184	ao	AN5119.1	54.m06906	AO070291000062	0					-155	-123	ATGTTTCTCGATGGTGAATTCACTTCTGATTGA			ATGTTTCTCGATGGTGAATTCACTTCTGATTGA	MFLDGEFTSD*			MFLDGEFTSD*	GTATTGTATC	CGTCTGTTAG	0	R	0	0	0	YML014W	0
1769	1184	ao	AN5119.1	54.m06906	AO070291000062	0					-145	-113	ATGGTGAATTCACTTCTGATTGACGTCTGTTAG			ATGGTGAATTCACTTCTGATTGACGTCTGTTAG	MVNSLLIDVC*			MVNSLLIDVC*	ATGTTTCTCG	ATTTCTCCTT	0	R	0	0	0	YML014W	0
1772	1186	af	AN1722.1	58.m07789	AO070305000037	0			-150	-34			ATGGTGCATTCATTCCTGCGGTTGTGGTCTCTGTGCCTCGCCGGGGAATTTCTGCCCTGTCAATCGCGACTCTTCCGAGACTCACTATCTCATGATCTAGATATCGTCCTATCGTGA		ATGGTGCATTCATTCCTGCGGTTGTGGTCTCTGTGCCTCGCCGGGGAATTTCTGCCCTGTCAATCGCGACTCTTCCGAGACTCACTATCTCATGATCTAGATATCGTCCTATCGTGA		MVHSFLRLWSLCLAGEFLPCQSRLFRDSLSHDLDIVLS*		MVHSFLRLWSLCLAGEFLPCQSRLFRDSLSHDLDIVLS*		TCGGGACGGA	TTTCAATATC	0	H	0	0	0	0	0
1770	1186	an	AN1722.1	58.m07789	AO070305000037	0	-163	-122					ATGACCATCCCAGGGCTCTTAGTGGCTCTTTCCAAAAAATGA	ATGACCATCCCAGGGCTCTTAGTGGCTCTTTCCAAAAAATGA			MTIPGLLVALSKK*	MTIPGLLVALSKK*			GAGTGGTACG	CTGCGCTTTT	0	H	0	0	0	0	0
1771	1186	an	AN1722.1	58.m07789	AO070305000037	0	-125	-96					ATGACTGCGCTTTTGGTCTTTATCGTCTGA	ATGACTGCGCTTTTGGTCTTTATCGTCTGA			MTALLVFIV*	MTALLVFIV*			TTTCCAAAAA	CCTACGATTT	0	H	0	0	0	0	0
1773	1186	ao	AN1722.1	58.m07789	AO070305000037	0					-168	-133	ATGGACCGATTGATTGATAGCTGTCAGAACAACTGA			ATGGACCGATTGATTGATAGCTGTCAGAACAACTGA	MDRLIDSCQNN*			MDRLIDSCQNN*	TTTTTTAAGA	ACTGCGGTTA	0	H	0	0	0	0	0
1774	1186	ao	AN1722.1	58.m07789	AO070305000037	0					-123	-79	ATGGTCCCTACCGCCGGGCGAAGGAATTATTCTCCGTCGCGATAG			ATGGTCCCTACCGCCGGGCGAAGGAATTATTCTCCGTCGCGATAG	MVPTAGRRNYSPSR*			MVPTAGRRNYSPSR*	AACTGCGGTT	GGCTCATCGG	0	H	0	0	0	0	0
1778	1189	af	AN0772.1	70.m15377	AO070316000067	0			-119	-75			ATGGACGCGTTCGAATACCCAGTTTCGCCAGCACCACGTCAATGA		ATGGACGCGTTCGAATACCCAGTTTCGCCAGCACCACGTCAATGA		MDAFEYPVSPAPRQ*		MDAFEYPVSPAPRQ*		TACCTCACTA	TGAGAAAAAT	0	IQR	0	0	0	0	0
1779	1189	af	AN0772.1	70.m15377	AO070316000067	0			-78	-25			ATGATGAGAAAAATATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGA		ATGATGAGAAAAATATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGA		MMRKIWPMCYCYQNLAL*		MMRKIWPMCYCYQNLAL*		CACCACGTCA	GTTGAATCTG	0	IQR	0	0	0	0	0
1780	1189	af	AN0772.1	70.m15377	AO070316000067	0			-75	-25			ATGAGAAAAATATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGA		ATGAGAAAAATATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGA		MRKIWPMCYCYQNLAL*		MRKIWPMCYCYQNLAL*		CACGTCAATG	GTTGAATCTG	0	IQR	0	0	0	0	0
1781	1189	af	AN0772.1	70.m15377	AO070316000067	0			-64	-20			ATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGAGTTGA		ATGGCCCATGTGCTACTGTTACCAAAATTTAGCACTCTGAGTTGA		MAHVLLLPKFSTLS*		MAHVLLLPKFSTLS*		TGAGAAAAAT	ATCTGTGGCC	0	IQR	0	0	0	0	0
1783	1189	ao	AN0772.1	70.m15377	AO070316000067	0					-184	-107	ATGAGTCTGGACGCGTTGTCAAAACCTGCCTCCAACACGGCGTCCATGAAAATGTCACTTCTGACGTGTTACCTCTAA			ATGAGTCTGGACGCGTTGTCAAAACCTGCCTCCAACACGGCGTCCATGAAAATGTCACTTCTGACGTGTTACCTCTAA	MSLDALSKPASNTASMKMSLLTCYL*			MSLDALSKPASNTASMKMSLLTCYL*	GGTTCTATAG	TTTTGTGTCG	0	IQR	0	0	0	0	0
1784	1189	ao	AN0772.1	70.m15377	AO070316000067	0					-139	-107	ATGAAAATGTCACTTCTGACGTGTTACCTCTAA			ATGAAAATGTCACTTCTGACGTGTTACCTCTAA	MKMSLLTCYL*			MKMSLLTCYL*	CACGGCGTCC	TTTTGTGTCG	0	IQR	0	0	0	0	0
1785	1189	ao	AN0772.1	70.m15377	AO070316000067	0					-133	-107	ATGTCACTTCTGACGTGTTACCTCTAA			ATGTCACTTCTGACGTGTTACCTCTAA	MSLLTCYL*			MSLLTCYL*	GTCCATGAAA	TTTTGTGTCG	0	IQR	0	0	0	0	0
1789	1197	af	AN2569.1	57.m05384	AO070317000049	0			-222	-181			ATGATTATTTCCCGGTCCACCAATCGGAGCGACTTTCCCTAG		ATGATTATTTCCCGGTCCACCAATCGGAGCGACTTTCCCTAG		MIISRSTNRSDFP*		MIISRSTNRSDFP*		ACTGCCCTTG	ATTCTTGTAT	0	G	0	0	0	0	0
1790	1197	af	AN2569.1	57.m05384	AO070317000049	0			-160	-149			ATGAAGGCATAG		ATGAAGGCATAG		MKA*		MKA*		TGCTTTCTTC	CTTTAATATG	0	G	0	0	0	0	0
1791	1197	af	AN2569.1	57.m05384	AO070317000049	0			-141	-115			ATGACTGTGGCTGATATGGCTGCGTAA		ATGACTGTGGCTGATATGGCTGCGTAA		MTVADMAA*		MTVADMAA*		TAGCTTTAAT	TTCTGTGGGG	0	G	0	0	0	0	0
1792	1197	af	AN2569.1	57.m05384	AO070317000049	0			-126	-115			ATGGCTGCGTAA		ATGGCTGCGTAA		MAA*		MAA*		TGTGGCTGAT	TTCTGTGGGG	0	G	0	0	0	0	0
1793	1197	af	AN2569.1	57.m05384	AO070317000049	0			-83	-54			ATGGCTTGGCAACACGACTCCAGCATATAA		ATGGCTTGGCAACACGACTCCAGCATATAA		MAWQHDSSI*		MAWQHDSSI*		CACCCGAACA	ACAGGTTGAG	0	G	0	0	0	0	0
1786	1197	an	AN2569.1	57.m05384	AO070317000049	0	-178	-86					ATGCACTGTCACTTTGCAATAACGCCGGGACGCCACCGGAAGGACAAAAGCGGGCATTTACCCTTATTAGATGCGGATGAGGCGGCGGTTTGA	ATGCACTGTCACTTTGCAATAACGCCGGGACGCCACCGGAAGGACAAAAGCGGGCATTTACCCTTATTAGATGCGGATGAGGCGGCGGTTTGA			MHCHFAITPGRHRKDKSGHLPLLDADEAAV*	MHCHFAITPGRHRKDKSGHLPLLDADEAAV*			CGCCTAATAT	AAACGCTTAT	0	G	0	0	0	0	0
1787	1197	an	AN2569.1	57.m05384	AO070317000049	0	-108	-55					ATGCGGATGAGGCGGCGGTTTGAAAACGCTTATAAGACGTTGTTGTGTCTGTAA	ATGCGGATGAGGCGGCGGTTTGAAAACGCTTATAAGACGTTGTTGTGTCTGTAA			MRMRRRFENAYKTLLCL*	MRMRRRFENAYKTLLCL*			CCCTTATTAG	CCCACGAAAC	0	G	0	0	0	0	0
1788	1197	an	AN2569.1	57.m05384	AO070317000049	0	-102	-55					ATGAGGCGGCGGTTTGAAAACGCTTATAAGACGTTGTTGTGTCTGTAA	ATGAGGCGGCGGTTTGAAAACGCTTATAAGACGTTGTTGTGTCTGTAA			MRRRFENAYKTLLCL*	MRRRFENAYKTLLCL*			TTAGATGCGG	CCCACGAAAC	0	G	0	0	0	0	0
1794	1197	ao	AN2569.1	57.m05384	AO070317000049	0					-116	-81	ATGGTTCATACACTGCCCGACAAGGCTTGTCGATGA			ATGGTTCATACACTGCCCGACAAGGCTTGTCGATGA	MVHTLPDKACR*			MVHTLPDKACR*	ACCTCCCCCC	ATGCCGTAAA	0	G	0	0	0	0	0
1795	1197	ao	AN2569.1	57.m05384	AO070317000049	0					-84	-64	ATGAATGCCGTAAATGGATAA			ATGAATGCCGTAAATGGATAA	MNAVNG*			MNAVNG*	AGGCTTGTCG	ATATCAGCAG	0	G	0	0	0	0	0
1799	1198	af	AN8601.1	58.m07263	AO070317000112	0			-173	-114			ATGAGCATCGTCCCGTTGTCGGCGCCGAGCTCACCGACTACCGAGCCCGGTCCTCGATAG		ATGAGCATCGTCCCGTTGTCGGCGCCGAGCTCACCGACTACCGAGCCCGGTCCTCGATAG		MSIVPLSAPSSPTTEPGPR*		MSIVPLSAPSSPTTEPGPR*		ACAATAGATA	GCTTCTCGAG	0		0	0	0	0	0
1800	1198	af	AN8601.1	58.m07263	AO070317000112	0			-101	-66			ATGGATATATTATGGGTGGATAGGGACACTGCCTGA		ATGGATATATTATGGGTGGATAGGGACACTGCCTGA		MDILWVDRDTA*		MDILWVDRDTA*		TTCTCGAGCC	GCATAAGGAC	0		0	0	0	0	0
1801	1198	af	AN8601.1	58.m07263	AO070317000112	0			-90	-79			ATGGGTGGATAG		ATGGGTGGATAG		MGG*		MGG*		TGGATATATT	GGACACTGCC	0		0	0	0	0	0
1796	1198	an	AN8601.1	58.m07263	AO070317000112	0	-257	-105					ATGACTCGAAGTTTCCTTGTTGGAAGCCGCGATGTCGCTGCCTTCAGGCCTCAATTTCTTCCATGCCGTCGAATTTATAAAGACGGACGTTCCTCAATTCCGCCGTTCACACATTTAACACTTTCCTCCATAACACATATATTCCTCTGCTAG	ATGACTCGAAGTTTCCTTGTTGGAAGCCGCGATGTCGCTGCCTTCAGGCCTCAATTTCTTCCATGCCGTCGAATTTATAAAGACGGACGTTCCTCAATTCCGCCGTTCACACATTTAACACTTTCCTCCATAACACATATATTCCTCTGCTAG			MTRSFLVGSRDVAAFRPQFLPCRRIYKDGRSSIPPFTHLTLSSITHIFLC*	MTRSFLVGSRDVAAFRPQFLPCRRIYKDGRSSIPPFTHLTLSSITHIFLC*			AATTAGCCTT	TCGGTCCAAA	0		0	0	0	0	0
1797	1198	an	AN8601.1	58.m07263	AO070317000112	0	-226	-140					ATGTCGCTGCCTTCAGGCCTCAATTTCTTCCATGCCGTCGAATTTATAAAGACGGACGTTCCTCAATTCCGCCGTTCACACATTTAA	ATGTCGCTGCCTTCAGGCCTCAATTTCTTCCATGCCGTCGAATTTATAAAGACGGACGTTCCTCAATTCCGCCGTTCACACATTTAA			MSLPSGLNFFHAVEFIKTDVPQFRRSHI*	MSLPSGLNFFHAVEFIKTDVPQFRRSHI*			GGAAGCCGCG	CACTTTCCTC	0		0	0	0	0	0
1798	1198	an	AN8601.1	58.m07263	AO070317000112	0	-195	-178					ATGCCGTCGAATTTATAA	ATGCCGTCGAATTTATAA			MPSNL*	MPSNL*			AATTTCTTCC	AGACGGACGT	0		0	0	0	0	0
1802	1200	af	AN6631.1	62.m03227	AO070326000083	0			-167	-3			ATGGTTTGCGGCTGTTGGTGGATGGGTGTTCGGAACACGGGAACGAAAGACTCACGTGACTATATCCCCATCCAAACCTTGCCGAAACAACCCTCATCTCGGAATGTCCAGGTTTGCACGTTGAAGTTCCCCTCTTCTCCTAATCCTCCACCATTCCACATATAA		ATGGTTTGCGGCTGTTGGTGGATGGGTGTTCGGAACACGGGAACGAAAGACTCACGTGACTATATCCCCATCCAAACCTTGCCGAAACAACCCTCATCTCGGAATGTCCAGGTTTGCACGTTGAAGTTCCCCTCTTCTCCTAATCCTCCACCATTCCACATATAA		MVCGCWWMGVRNTGTKDSRDYIPIQTLPKQPSSRNVQVCTLKFPSSPNPPPFHI*		MVCGCWWMGVRNTGTKDSRDYIPIQTLPKQPSSRNVQVCTLKFPSSPNPPPFHI*		AGTCTGCTTG	AAATGGCTGC	0	C	0	0	0	0	0
1803	1200	af	AN6631.1	62.m03227	AO070326000083	0			-146	-3			ATGGGTGTTCGGAACACGGGAACGAAAGACTCACGTGACTATATCCCCATCCAAACCTTGCCGAAACAACCCTCATCTCGGAATGTCCAGGTTTGCACGTTGAAGTTCCCCTCTTCTCCTAATCCTCCACCATTCCACATATAA		ATGGGTGTTCGGAACACGGGAACGAAAGACTCACGTGACTATATCCCCATCCAAACCTTGCCGAAACAACCCTCATCTCGGAATGTCCAGGTTTGCACGTTGAAGTTCCCCTCTTCTCCTAATCCTCCACCATTCCACATATAA		MGVRNTGTKDSRDYIPIQTLPKQPSSRNVQVCTLKFPSSPNPPPFHI*		MGVRNTGTKDSRDYIPIQTLPKQPSSRNVQVCTLKFPSSPNPPPFHI*		CTGTTGGTGG	AAATGGCTGC	0	C	0	0	0	0	0
1804	1200	af	AN6631.1	62.m03227	AO070326000083	0			-64	-44			ATGTCCAGGTTTGCACGTTGA		ATGTCCAGGTTTGCACGTTGA		MSRFAR*		MSRFAR*		TCATCTCGGA	AGTTCCCCTC	0	C	0	0	0	0	0
1805	1200	ao	AN6631.1	62.m03227	AO070326000083	0					-189	-112	ATGCATACATACACCGTACTCCTGTGTCTTGGCTGTATTCGTTTGTGTTCGGAACACGGGAACCCATCGGTCACGTGA			ATGCATACATACACCGTACTCCTGTGTCTTGGCTGTATTCGTTTGTGTTCGGAACACGGGAACCCATCGGTCACGTGA	MHTYTVLLCLGCIRLCSEHGNPSVT*			MHTYTVLLCLGCIRLCSEHGNPSVT*	CTAGGGCCCT	GGGACATCCC	0	C	0	0	0	0	0
1809	1208	af	AN4565.1	57.m05487	AO070250000008	0			-176	-135			ATGCAGCCTGTGGGATGGCATCTCTCCTCCAGTACCCCATAG		ATGCAGCCTGTGGGATGGCATCTCTCCTCCAGTACCCCATAG		MQPVGWHLSSSTP*		MQPVGWHLSSSTP*		TTGTAGATAG	TCCCTTATCT	0	X	0	0	0	0	0
1810	1208	af	AN4565.1	57.m05487	AO070250000008	0			-162	-7			ATGGCATCTCTCCTCCAGTACCCCATAGTCCCTTATCTTATCAGATCCCTCCCAAAGCGGTGCATTTCGGTCTACAGTATATCCGCCGCACCCCTGACAGCTGTCACCCACCTATTATCTACCCATCATCAGCTCAATCTCAACAAAGAAACCTAG		ATGGCATCTCTCCTCCAGTACCCCATAGTCCCTTATCTTATCAGATCCCTCCCAAAGCGGTGCATTTCGGTCTACAGTATATCCGCCGCACCCCTGACAGCTGTCACCCACCTATTATCTACCCATCATCAGCTCAATCTCAACAAAGAAACCTAG		MASLLQYPIVPYLIRSLPKRCISVYSISAAPLTAVTHLLSTHHQLNLNKET*		MASLLQYPIVPYLIRSLPKRCISVYSISAAPLTAVTHLLSTHHQLNLNKET*		AGCCTGTGGG	GTGAAAATGG	0	X	0	0	0	0	0

1806	1208	an	AN4565.1	57.m05487	AO070250000008	0	-162	-46					ATGCTTTTAGGAACGGAAAGGTCGCTACGCCACCCGTGCCCATATGTACTTGGACTACACAGTAATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGA	ATGCTTTTAGGAACGGAAAGGTCGCTACGCCACCCGTGCCCATATGTACTTGGACTACACAGTAATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGA			MLLGTERSLRHPCPYVLGLHSNGRSRARCGEPASTPQD*	MLLGTERSLRHPCPYVLGLHSNGRSRARCGEPASTPQD*			ACCTGCAAGG	GCTGGAGGGC	0	X	0	0	0	0	0
1807	1208	an	AN4565.1	57.m05487	AO070250000008	0	-119	-27					ATGTACTTGGACTACACAGTAATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGAGCTGGAGGGCAAGTATTAA	ATGTACTTGGACTACACAGTAATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGAGCTGGAGGGCAAGTATTAA			MYLDYTVMGDHVQDAENPLQLRRTELEGKY*	MYLDYTVMGDHVQDAENPLQLRRTELEGKY*			CCGTGCCCAT	CATTGGAATC	0	X	0	0	0	0	0
1808	1208	an	AN4565.1	57.m05487	AO070250000008	0	-98	-27					ATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGAGCTGGAGGGCAAGTATTAA	ATGGGCGATCACGTGCAAGATGCGGAGAACCCGCTTCAACTCCGCAGGACTGAGCTGGAGGGCAAGTATTAA			MGDHVQDAENPLQLRRTELEGKY*	MGDHVQDAENPLQLRRTELEGKY*			CTACACAGTA	CATTGGAATC	0	X	0	0	0	0	0
1811	1208	ao	AN4565.1	57.m05487	AO070250000008	0					-130	-89	ATGCAGCCAAGACCTTATCGCCGAAGTCTATCTTATCAGTAA			ATGCAGCCAAGACCTTATCGCCGAAGTCTATCTTATCAGTAA	MQPRPYRRSLSYQ*			MQPRPYRRSLSYQ*	TAGGTAACAA	TCAGTCTAAA	0	X	0	0	0	0	0
1813	1209	af	AN5003.1	59.m08907	AO070255000039	0			-168	-133			ATGCGAAACGTGTTTAGTCGCCATTTCGCGCTATAG		ATGCGAAACGTGTTTAGTCGCCATTTCGCGCTATAG		MRNVFSRHFAL*		MRNVFSRHFAL*		TGACATTTGT	TTACCGCGCT	0	R	0	0	0	0	0
1812	1209	an	AN5003.1	59.m08907	AO070255000039	0	-187	-149					ATGGCCACCTGCTTACTGGATTCGCGCAACGGTCTCTAG	ATGGCCACCTGCTTACTGGATTCGCGCAACGGTCTCTAG			MATCLLDSRNGL*	MATCLLDSRNGL*			CGATCATATT	TAGTCAGCAT	0	R	0	0	0	0	0
1814	1209	ao	AN5003.1	59.m08907	AO070255000039	0					-184	-92	ATGCTGACAGGAGTTGCGCAAATCGCTTCAGCAGTCAGCTTCGTGGGATCGACACCGCGTTTTCTCAACTCCCGGGAATCCCAACCAATTTAG			ATGCTGACAGGAGTTGCGCAAATCGCTTCAGCAGTCAGCTTCGTGGGATCGACACCGCGTTTTCTCAACTCCCGGGAATCCCAACCAATTTAG	MLTGVAQIASAVSFVGSTPRFLNSRESQPI*			MLTGVAQIASAVSFVGSTPRFLNSRESQPI*	TACGGCCCAC	CTGAAACATA	0	R	0	0	0	0	0
1815	1209	ao	AN5003.1	59.m08907	AO070255000039	0					-72	-49	ATGGGCCGAGGGTCACCTGAATAA			ATGGGCCGAGGGTCACCTGAATAA	MGRGSPE*			MGRGSPE*	ATCGTATTTA	CCCCTTGTCG	0	R	0	0	0	0	0
1816	1212	an	AN0075.1	71.m15353	AO070311000141	0	-139	-122					ATGCTCCCCGACTACTGA	ATGCTCCCCGACTACTGA			MLPDY*	MLPDY*			TCCATTATTA	ACCTCCACTT	0	O	0	0	0	0	0
1817	1212	ao	AN0075.1	71.m15353	AO070311000141	0					-128	-87	ATGCTCCATTTATCAGTCAACTTTCATTGCTCCGGAAATTGA			ATGCTCCATTTATCAGTCAACTTTCATTGCTCCGGAAATTGA	MLHLSVNFHCSGN*			MLHLSVNFHCSGN*	CTCCGCGCCG	TCATTTGCAG	0	O	0	0	0	0	0
1822	1215	af	AN6725.1	65.m07245	AO070339000169	0			-209	-39			ATGTCTCGAAGCTCCACTTCGCTTCTTTTAAGCTGGTTGAAGGCTTTTTTCTTCCTATTTCTCTTCCTTTCTGTCGCCCACACAAATTTATACACCACGACACCCTTGTATTTCTATCATCTGAGCTATCGCTGGATGCTCTCGCGCCATATCTCTGGTAGATTTGGTTAA		ATGTCTCGAAGCTCCACTTCGCTTCTTTTAAGCTGGTTGAAGGCTTTTTTCTTCCTATTTCTCTTCCTTTCTGTCGCCCACACAAATTTATACACCACGACACCCTTGTATTTCTATCATCTGAGCTATCGCTGGATGCTCTCGCGCCATATCTCTGGTAGATTTGGTTAA		MSRSSTSLLLSWLKAFFFLFLFLSVAHTNLYTTTPLYFYHLSYRWMLSRHISGRFG*		MSRSSTSLLLSWLKAFFFLFLFLSVAHTNLYTTTPLYFYHLSYRWMLSRHISGRFG*		GAGGTTCCTC	TATGTTGTGA	0	A	0	MG07164.1	NCU06763.1	0	0
1823	1215	af	AN6725.1	65.m07245	AO070339000169	0			-74	-39			ATGCTCTCGCGCCATATCTCTGGTAGATTTGGTTAA		ATGCTCTCGCGCCATATCTCTGGTAGATTTGGTTAA		MLSRHISGRFG*		MLSRHISGRFG*		CTATCGCTGG	TATGTTGTGA	0	A	0	MG07164.1	NCU06763.1	0	0
1818	1215	an	AN6725.1	65.m07245	AO070339000169	0	-123	-88					ATGGACTGGATGGCTATGGATGACGACTGCACATAA	ATGGACTGGATGGCTATGGATGACGACTGCACATAA			MDWMAMDDDCT*	MDWMAMDDDCT*			TGCTCATCAT	GCGTTCTTCC	0	A	0	MG07164.1	NCU06763.1	0	0
1819	1215	an	AN6725.1	65.m07245	AO070339000169	0	-114	-88					ATGGCTATGGATGACGACTGCACATAA	ATGGCTATGGATGACGACTGCACATAA			MAMDDDCT*	MAMDDDCT*			TATGGACTGG	GCGTTCTTCC	0	A	0	MG07164.1	NCU06763.1	0	0
1820	1215	an	AN6725.1	65.m07245	AO070339000169	0	-108	-88					ATGGATGACGACTGCACATAA	ATGGATGACGACTGCACATAA			MDDDCT*	MDDDCT*			CTGGATGGCT	GCGTTCTTCC	0	A	0	MG07164.1	NCU06763.1	0	0
1824	1215	ao	AN6725.1	65.m07245	AO070339000169	0					-195	-37	ATGCTCTTTTCTTTTTTTTTTTTTTGTTTTACCCTTCTCGCCCTCCCCATTGTTTCCCCTCTTCTATGCCTATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGA			ATGCTCTTTTCTTTTTTTTTTTTTTGTTTTACCCTTCTCGCCCTCCCCATTGTTTCCCCTCTTCTATGCCTATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGA	MLFSFFFFCFTLLALPIVSPLLCLCPNPSIDTLLDSRLYIFTRSLVDLVTVT*			MLFSFFFFCFTLLALPIVSPLLCLCPNPSIDTLLDSRLYIFTRSLVDLVTVT*	CGCGGTAGTC	CCGCATAATC	0	A	0	MG07164.1	NCU06763.1	0	0
1825	1215	ao	AN6725.1	65.m07245	AO070339000169	0					-130	-29	ATGCCTATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGACCGCATAA			ATGCCTATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGACCGCATAA	MPMPQPINRHSSRQSIVHFHQVAGRSGHCDMTA*			MPMPQPINRHSSRQSIVHFHQVAGRSGHCDMTA*	CCCCTCTTCT	TCGCGAGAGA	0	A	0	MG07164.1	NCU06763.1	0	0
1826	1215	ao	AN6725.1	65.m07245	AO070339000169	0					-124	-29	ATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGACCGCATAA			ATGCCCCAACCCATCAATCGACACTCTTCTAGACAGTCGATTGTACATTTTCACCAGGTCGCTGGTAGATCTGGTCACTGTGACATGACCGCATAA	MPQPINRHSSRQSIVHFHQVAGRSGHCDMTA*			MPQPINRHSSRQSIVHFHQVAGRSGHCDMTA*	TTCTATGCCT	TCGCGAGAGA	0	A	0	MG07164.1	NCU06763.1	0	0
1829	1216	af	AN5745.1	69.m15631	AO070341000002	0			-244	-206			ATGGTCGAATGGCACGTGATCATTTACATGCCCCACTAA		ATGGTCGAATGGCACGTGATCATTTACATGCCCCACTAA		MVEWHVIIYMPH*		MVEWHVIIYMPH*		TCGGGCATCA	CAAGATTCCA	0	J	0	0	0	0	0
1830	1216	af	AN5745.1	69.m15631	AO070341000002	0			-236	-81			ATGGCACGTGATCATTTACATGCCCCACTAACAAGATTCCATTGTGAAGTTGTTGCGGCAGCAGCGAGATTCTGTCTCTGCCATTCAGCAGAAAAAAACCATCGTCGGTCTTCGCCACGACAGTCTATCTCGTCCGAACACGGTAGATCCCGCTGA		ATGGCACGTGATCATTTACATGCCCCACTAACAAGATTCCATTGTGAAGTTGTTGCGGCAGCAGCGAGATTCTGTCTCTGCCATTCAGCAGAAAAAAACCATCGTCGGTCTTCGCCACGACAGTCTATCTCGTCCGAACACGGTAGATCCCGCTGA		MARDHLHAPLTRFHCEVVAAAARFCLCHSAEKNHRRSSPRQSISSEHGRSR*		MARDHLHAPLTRFHCEVVAAAARFCLCHSAEKNHRRSSPRQSISSEHGRSR*		CAATGGTCGA	ATCACCTCCT	0	J	0	0	0	0	0
1831	1216	af	AN5745.1	69.m15631	AO070341000002	0			-217	-206			ATGCCCCACTAA		ATGCCCCACTAA		MPH*		MPH*		GATCATTTAC	CAAGATTCCA	0	J	0	0	0	0	0
1828	1216	an	AN5745.1	69.m15631	AO070341000002	0	-149	-90					ATGCGGGCAAAAGAAAGGACTTTTGCCCACTTCAGACGAGTGTCTTGTGTCCGCCACTGA	ATGCGGGCAAAAGAAAGGACTTTTGCCCACTTCAGACGAGTGTCTTGTGTCCGCCACTGA			MRAKERTFAHFRRVSCVRH*	MRAKERTFAHFRRVSCVRH*			TTCATTAGGG	TCTTCCCTGC	0	J	0	0	0	0	0
1832	1216	ao	AN5745.1	69.m15631	AO070341000002	0					-227	-207	ATGAATGGGCGTGAATGGTAA			ATGAATGGGCGTGAATGGTAA	MNGREW*			MNGREW*	TTGACTCCTA	GGGTACACGT	0	J	0	0	0	0	0
1833	1216	ao	AN5745.1	69.m15631	AO070341000002	0					-223	-50	ATGGGCGTGAATGGTAAGGGTACACGTGACCCCGCTAGCCCCACCACCAGATCGTTTTATCGTGAAGTTATTGAGGGACGGCTCACTCGCCCACATCAAATTCGCCTTCTGGTTATTGATTCACCCACGACGACCCTCTTGTTGGGATACACGGCTTACTCACTCTGTTATTGA			ATGGGCGTGAATGGTAAGGGTACACGTGACCCCGCTAGCCCCACCACCAGATCGTTTTATCGTGAAGTTATTGAGGGACGGCTCACTCGCCCACATCAAATTCGCCTTCTGGTTATTGATTCACCCACGACGACCCTCTTGTTGGGATACACGGCTTACTCACTCTGTTATTGA	MGVNGKGTRDPASPTTRSFYREVIEGRLTRPHQIRLLVIDSPTTTLLLGYTAYSLCY*			MGVNGKGTRDPASPTTRSFYREVIEGRLTRPHQIRLLVIDSPTTTLLLGYTAYSLCY*	CTCCTAATGA	GTCATTAGAA	0	J	0	0	0	0	0
1834	1216	ao	AN5745.1	69.m15631	AO070341000002	0					-213	-34	ATGGTAAGGGTACACGTGACCCCGCTAGCCCCACCACCAGATCGTTTTATCGTGAAGTTATTGAGGGACGGCTCACTCGCCCACATCAAATTCGCCTTCTGGTTATTGATTCACCCACGACGACCCTCTTGTTGGGATACACGGCTTACTCACTCTGTTATTGAGTCATTAGAAGCTTGA			ATGGTAAGGGTACACGTGACCCCGCTAGCCCCACCACCAGATCGTTTTATCGTGAAGTTATTGAGGGACGGCTCACTCGCCCACATCAAATTCGCCTTCTGGTTATTGATTCACCCACGACGACCCTCTTGTTGGGATACACGGCTTACTCACTCTGTTATTGAGTCATTAGAAGCTTGA	MVRVHVTPLAPPPDRFIVKLLRDGSLAHIKFAFWLLIHPRRPSCWDTRLTHSVIESLEA*			MVRVHVTPLAPPPDRFIVKLLRDGSLAHIKFAFWLLIHPRRPSCWDTRLTHSVIESLEA*	ATGGGCGTGA	AGCTTTTACC	0	J	0	0	0	0	0
1835	1218	af	AN7450.1	57.m05893	AO070229000023	0			-123	-100			ATGATGCAAATTGGCACCCTTTGA		ATGATGCAAATTGGCACCCTTTGA		MMQIGTL*		MMQIGTL*		ACATTTTTCA	CTTTGTTGTA	0		0	0	0	0	0
1836	1218	af	AN7450.1	57.m05893	AO070229000023	0			-120	-100			ATGCAAATTGGCACCCTTTGA		ATGCAAATTGGCACCCTTTGA		MQIGTL*		MQIGTL*		TTTTTCAATG	CTTTGTTGTA	0		0	0	0	0	0
1837	1218	ao	AN7450.1	57.m05893	AO070229000023	0					-178	-125	ATGCTCCCCCTGTTACCCATTGTATGTCAATTTTCGACACTTCGGCACTCCTGA			ATGCTCCCCCTGTTACCCATTGTATGTCAATTTTCGACACTTCGGCACTCCTGA	MLPLLPIVCQFSTLRHS*			MLPLLPIVCQFSTLRHS*	ATACTTTCTA	AGCATGCTGC	0		0	0	0	0	0
1838	1218	ao	AN7450.1	57.m05893	AO070229000023	0					-155	-108	ATGTCAATTTTCGACACTTCGGCACTCCTGAAGCATGCTGCATATTAG			ATGTCAATTTTCGACACTTCGGCACTCCTGAAGCATGCTGCATATTAG	MSIFDTSALLKHAAY*			MSIFDTSALLKHAAY*	TACCCATTGT	ATTGATCAAT	0		0	0	0	0	0
1839	1218	ao	AN7450.1	57.m05893	AO070229000023	0					-121	-89	ATGCTGCATATTAGATTGATCAATTTCGCCTAG			ATGCTGCATATTAGATTGATCAATTTCGCCTAG	MLHIRLINFA*			MLHIRLINFA*	CTCCTGAAGC	TATCCAGTGA	0		0	0	0	0	0
1842	1219	af	AN1442.1	55.m02942	AO070232000005	0			-222	-196			ATGGACTCACAGACACTTCACCAGTGA		ATGGACTCACAGACACTTCACCAGTGA		MDSQTLHQ*		MDSQTLHQ*		TCGCCATTTT	ATATTATATA	0	U	0	MG04412.1	0	0	0
1843	1219	af	AN1442.1	55.m02942	AO070232000005	0			-101	-87			ATGACCCAAGTCTAA		ATGACCCAAGTCTAA		MTQV*		MTQV*		TGACGATACT	TCTGTACTAC	0	U	0	MG04412.1	0	0	0
1840	1219	an	AN1442.1	55.m02942	AO070232000005	0	-183	-142					ATGTACCTTCTTTTAGCCCAAACCTTTTGTCGATCCTTTTAA	ATGTACCTTCTTTTAGCCCAAACCTTTTGTCGATCCTTTTAA			MYLLLAQTFCRSF*	MYLLLAQTFCRSF*			CGTTCTCCTC	CGTACACAGC	0	U	0	MG04412.1	0	0	0
1841	1219	an	AN1442.1	55.m02942	AO070232000005	0	-115	-104					ATGACCAACTAA	ATGACCAACTAA			MTN*	MTN*			ACCTCGTACT	AACTCAGCCA	0	U	0	MG04412.1	0	0	0
1844	1219	ao	AN1442.1	55.m02942	AO070232000005	0					-87	-73	ATGACCCCAGCCTGA			ATGACCCCAGCCTGA	MTPA*			MTPA*	CAACGATATT	ATACTCCCCG	0	U	0	MG04412.1	0	0	0
1845	1221	an	AN9311.1	71.m15099	AO070298000046	0	-283	-212					ATGTCAGTAGTGGCAAGCAGTTTGGCATTCTGTCTCTCCGGAGAGAGGTTGTGTAAGCTGGGGATACCCTGA	ATGTCAGTAGTGGCAAGCAGTTTGGCATTCTGTCTCTCCGGAGAGAGGTTGTGTAAGCTGGGGATACCCTGA			MSVVASSLAFCLSGERLCKLGIP*	MSVVASSLAFCLSGERLCKLGIP*			AAACCCATGC	TCACAGGGAA	0		0	0	0	0	0
1846	1221	an	AN9311.1	71.m15099	AO070298000046	0	-165	-55					ATGCAGATCTGGGTGGGCACTGCACTCTCGCAGAGGGAATCTGGCTCACAATACGAGAGCCTTTTTAAATTCATTGTGTTCTCTATACAGGGTCTATCTCCTCATTCATAG	ATGCAGATCTGGGTGGGCACTGCACTCTCGCAGAGGGAATCTGGCTCACAATACGAGAGCCTTTTTAAATTCATTGTGTTCTCTATACAGGGTCTATCTCCTCATTCATAG			MQIWVGTALSQRESGSQYESLFKFIVFSIQGLSPHS*	MQIWVGTALSQRESGSQYESLFKFIVFSIQGLSPHS*			TGACAACTCA	ATCATCTCTC	0		0	0	0	0	0
1847	1221	ao	AN9311.1	71.m15099	AO070298000046	0					-75	-25	ATGACCATGGAAAGCTGTCCAACATTGCCTGTGATTTCTGGACAAAACTGA			ATGACCATGGAAAGCTGTCCAACATTGCCTGTGATTTCTGGACAAAACTGA	MTMESCPTLPVISGQN*			MTMESCPTLPVISGQN*	TGAATTTAAA	TCATCACCGA	0		0	0	0	0	0
1848	1221	ao	AN9311.1	71.m15099	AO070298000046	0					-69	-25	ATGGAAAGCTGTCCAACATTGCCTGTGATTTCTGGACAAAACTGA			ATGGAAAGCTGTCCAACATTGCCTGTGATTTCTGGACAAAACTGA	MESCPTLPVISGQN*			MESCPTLPVISGQN*	TAAAATGACC	TCATCACCGA	0		0	0	0	0	0
1851	1223	af	AN5681.1	65.m07407	AO070309000096	0			-234	-196			ATGGATTCTTCTGCCCCACGTGAGCTGGAGATAACGTGA		ATGGATTCTTCTGCCCCACGTGAGCTGGAGATAACGTGA		MDSSAPRELEIT*		MDSSAPRELEIT*		GGAATCCAAA	TAAAGGTCAC	0	O	FG07078.1	MG00145.1	0	0	0
1852	1223	af	AN5681.1	65.m07407	AO070309000096	0			-107	-60			ATGAAGCACAAGTTCCAGGAAATATCACGATGTTACTTGCCTGATTGA		ATGAAGCACAAGTTCCAGGAAATATCACGATGTTACTTGCCTGATTGA		MKHKFQEISRCYLPD*		MKHKFQEISRCYLPD*		TGGGGAAGAT	TTCCTTAACC	0	O	FG07078.1	MG00145.1	0	0	0
1853	1223	af	AN5681.1	65.m07407	AO070309000096	0			-78	-64			ATGTTACTTGCCTGA		ATGTTACTTGCCTGA		MLLA*		MLLA*		AAATATCACG	TTGATTCCTT	0	O	FG07078.1	MG00145.1	0	0	0
1849	1223	an	AN5681.1	65.m07407	AO070309000096	0	-212	-90					ATGCGCATATCATCACGTGGCTTTCCACGTGATTACAGCCGAGGCATAGGCCCGGCGTCTTATCTACATATCCGGGGAAACATCCCAGGCTTCTTCCCACCCATGATCTGTCTGCGGATGTGA	ATGCGCATATCATCACGTGGCTTTCCACGTGATTACAGCCGAGGCATAGGCCCGGCGTCTTATCTACATATCCGGGGAAACATCCCAGGCTTCTTCCCACCCATGATCTGTCTGCGGATGTGA			MRISSRGFPRDYSRGIGPASYLHIRGNIPGFFPPMICLRM*	MRISSRGFPRDYSRGIGPASYLHIRGNIPGFFPPMICLRM*			CCGCAATTAG	CTGTGGAGTA	0	O	FG07078.1	MG00145.1	0	0	0
1850	1223	an	AN5681.1	65.m07407	AO070309000096	0	-110	-90					ATGATCTGTCTGCGGATGTGA	ATGATCTGTCTGCGGATGTGA			MICLRM*	MICLRM*			CTTCCCACCC	CTGTGGAGTA	0	O	FG07078.1	MG00145.1	0	0	0
1854	1223	ao	AN5681.1	65.m07407	AO070309000096	0					-202	-110	ATGGCATTCGGGTCACGTGAATCACTCCCTCACGTGTGGACTGCCGAGGTATACCGTATCGCCGCTGCAGAGGCTCATTCTCCGGGGAAATGA			ATGGCATTCGGGTCACGTGAATCACTCCCTCACGTGTGGACTGCCGAGGTATACCGTATCGCCGCTGCAGAGGCTCATTCTCCGGGGAAATGA	MAFGSRESLPHVWTAEVYRIAAAEAHSPGK*			MAFGSRESLPHVWTAEVYRIAAAEAHSPGK*	AATTTCCCTG	TAACCACGTC	0	O	FG07078.1	MG00145.1	0	0	0
1855	1223	ao	AN5681.1	65.m07407	AO070309000096	0					-91	-77	ATGATGAGACGGTAG			ATGATGAGACGGTAG	MMRR*			MMRR*	TCAGTTAACA	AGCGAGCTTT	0	O	FG07078.1	MG00145.1	0	0	0
1856	1223	ao	AN5681.1	65.m07407	AO070309000096	0					-88	-77	ATGAGACGGTAG			ATGAGACGGTAG	MRR*			MRR*	GTTAACAATG	AGCGAGCTTT	0	O	FG07078.1	MG00145.1	0	0	0
1860	1224	af	AN8565.1	71.m15702	AO070311000007	0			-212	-114			ATGACGCCATTCGTCTCAGCGGTCTGTGGGGATCTGAGGCAGCTCTCCGCCTGCGCAATACGGAAAGTAAATGAAAGCCGCGGGCTCATGAACATTTGA		ATGACGCCATTCGTCTCAGCGGTCTGTGGGGATCTGAGGCAGCTCTCCGCCTGCGCAATACGGAAAGTAAATGAAAGCCGCGGGCTCATGAACATTTGA		MTPFVSAVCGDLRQLSACAIRKVNESRGLMNI*		MTPFVSAVCGDLRQLSACAIRKVNESRGLMNI*		TATTCAGCAA	ACTCCGGAGG	0	E	0	0	0	0	0
1861	1224	af	AN8565.1	71.m15702	AO070311000007	0			-142	-122			ATGAAAGCCGCGGGCTCATGA		ATGAAAGCCGCGGGCTCATGA		MKAAGS*		MKAAGS*		CGGAAAGTAA	ACATTTGAAC	0	E	0	0	0	0	0

1862	1224	af	AN8565.1	71.m15702	AO070311000007	0			-125	-114			ATGAACATTTGA		ATGAACATTTGA		MNI*		MNI*		CCGCGGGCTC	ACTCCGGAGG	0	E	0	0	0	0	0
1863	1224	af	AN8565.1	71.m15702	AO070311000007	0			-95	-30			ATGACTTCTCCACACCCGTTCATTTGGATTCAATTTCGCCTCGAGCATTCAGCTATTGCTCGATAG		ATGACTTCTCCACACCCGTTCATTTGGATTCAATTTCGCCTCGAGCATTCAGCTATTGCTCGATAG		MTSPHPFIWIQFRLEHSAIAR*		MTSPHPFIWIQFRLEHSAIAR*		GGTCAGAACA	TTGTCTTGCT	0	E	0	0	0	0	0
1857	1224	an	AN8565.1	71.m15702	AO070311000007	0	-165	-31					ATGGTCGTCGTGCAGTACTCTGTACCCCGTTCTACTCTAGTGTCGCGGCGGACACGGAAGCTAGTAATTCCGTTCCGAAGGCGATCTCGGAGCCCGGTCAGCGAGTCACCTGCAAATGCAATGCGGCGGCCATGA	ATGGTCGTCGTGCAGTACTCTGTACCCCGTTCTACTCTAGTGTCGCGGCGGACACGGAAGCTAGTAATTCCGTTCCGAAGGCGATCTCGGAGCCCGGTCAGCGAGTCACCTGCAAATGCAATGCGGCGGCCATGA			MVVVQYSVPRSTLVSRRTRKLVIPFRRRSRSPVSESPANAMRRP*	MVVVQYSVPRSTLVSRRTRKLVIPFRRRSRSPVSESPANAMRRP*			TTGTGTGCGG	TCCGTTCACA	0	E	0	0	0	0	0
1864	1224	ao	AN8565.1	71.m15702	AO070311000007	0					-186	-175	ATGACGCCATGA			ATGACGCCATGA	MTP*			MTP*	ACACGAGTAG	GCTTTCCCGC	0	E	0	0	0	0	0
1865	1229	ao	AN4090.1	54.m06735	AO070342000093	0					-135	-100	ATGTACAACATAATCTCGATAAAGAATCGCCGATAA			ATGTACAACATAATCTCGATAAAGAATCGCCGATAA	MYNIISIKNRR*			MYNIISIKNRR*	GTGATCACAA	CCAACCCAAC	0	S	0	0	0	0	0
1867	1234	af	AN1690.1	58.m07765	AO070305000010	0			-112	-47			ATGTATGCTCTATTTTTGCATCTTGTTTTGATTATTTCTTTCCCATCATCCCGTGAACATCCTTGA		ATGTATGCTCTATTTTTGCATCTTGTTTTGATTATTTCTTTCCCATCATCCCGTGAACATCCTTGA		MYALFLHLVLIISFPSSREHP*		MYALFLHLVLIISFPSSREHP*		TTACTGGCTG	GCACAGTTCT	0	S	0	0	0	0	0
1868	1234	af	AN1690.1	58.m07765	AO070305000010	0			-108	-82			ATGCTCTATTTTTGCATCTTGTTTTGA		ATGCTCTATTTTTGCATCTTGTTTTGA		MLYFCILF*		MLYFCILF*		TGGCTGATGT	TTATTTCTTT	0	S	0	0	0	0	0
1872	1235	af	AN4471.1	58.m07861	AO070305000130	0			-190	-47			ATGAAGCGCTCCGTAGCGGTGACTGCGCCACAGGCATGTAGGGCCGCCTCCTCAAACTGTCACCGCCTAGGATGCGATATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAGAGCGTTGAACTGTTGGTATTAG		ATGAAGCGCTCCGTAGCGGTGACTGCGCCACAGGCATGTAGGGCCGCCTCCTCAAACTGTCACCGCCTAGGATGCGATATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAGAGCGTTGAACTGTTGGTATTAG		MKRSVAVTAPQACRAASSNCHRLGCDMSGRKKKLSVLQHYRALNCWY*		MKRSVAVTAPQACRAASSNCHRLGCDMSGRKKKLSVLQHYRALNCWY*		TCTGTGCAGT	ATCCCTTAAG	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1873	1235	af	AN4471.1	58.m07861	AO070305000130	0			-119	-69			ATGCGATATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAG		ATGCGATATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAG		MRYVWQKKKVIRPPTL*		MRYVWQKKKVIRPPTL*		ACCGCCTAGG	AGCGTTGAAC	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1874	1235	af	AN4471.1	58.m07861	AO070305000130	0			-112	-47			ATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAGAGCGTTGAACTGTTGGTATTAG		ATGTCTGGCAGAAAAAAAAAGTTATCCGTCCTCCAACATTATAGAGCGTTGAACTGTTGGTATTAG		MSGRKKKLSVLQHYRALNCWY*		MSGRKKKLSVLQHYRALNCWY*		AGGATGCGAT	ATCCCTTAAG	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1869	1235	an	AN4471.1	58.m07861	AO070305000130	0	-179	-156					ATGGAGATTGAGCTACTGGCTTGA	ATGGAGATTGAGCTACTGGCTTGA			MEIELLA*	MEIELLA*			GGTTAACGTG	GCATGAACGC	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1870	1235	an	AN4471.1	58.m07861	AO070305000130	0	-100	-65					ATGTCTGGCAGAAAAAAAAGTTGCCCGCGTTTCTGA	ATGTCTGGCAGAAAAAAAAGTTGCCCGCGTTTCTGA			MSGRKKSCPRF*	MSGRKKSCPRF*			CAGAGCAGGA	TGCTCAGCCG	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1871	1235	an	AN4471.1	58.m07861	AO070305000130	0	-65	-51					ATGCTCAGCCGCTGA	ATGCTCAGCCGCTGA			MLSR*	MLSR*			CGCGTTTCTG	CCAGCAAGAG	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1875	1235	ao	AN4471.1	58.m07861	AO070305000130	0					-161	-12	ATGATCCTGCTAGTTCCACCCTCACCGCCTAATGCATTCGATAATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGAAAAAATCATTTGTCATTGGTGAAACATCAACCAACATTATCATTTAA			ATGATCCTGCTAGTTCCACCCTCACCGCCTAATGCATTCGATAATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGAAAAAATCATTTGTCATTGGTGAAACATCAACCAACATTATCATTTAA	MILLVPPSPPNAFDNVWQKKSCPLFLYGFHIYSLKKSFVIGETSTNIII*			MILLVPPSPPNAFDNVWQKKSCPLFLYGFHIYSLKKSFVIGETSTNIII*	CACCTCAGGC	GATTTTAGAT	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1876	1235	ao	AN4471.1	58.m07861	AO070305000130	0					-130	-59	ATGCATTCGATAATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGA			ATGCATTCGATAATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGA	MHSIMSGRKKVARFFCTAFISTA*			MHSIMSGRKKVARFFCTAFISTA*	TCACCGCCTA	AAAAATCATT	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1877	1235	ao	AN4471.1	58.m07861	AO070305000130	0					-118	-59	ATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGA			ATGTCTGGCAGAAAAAAAGTTGCCCGCTTTTTTTGTACGGCTTTCATATCTACAGCTTGA	MSGRKKVARFFCTAFISTA*			MSGRKKVARFFCTAFISTA*	GCATTCGATA	AAAAATCATT	0	S	FG05585.1	MG06429.1	NCU07864.1	YKL021C	0
1878	1236	an	AN0138.1	71.m15421	AO070321000114	0	-123	-100					ATGATGTTCGTCTCTCTCAATTGA	ATGATGTTCGTCTCTCTCAATTGA			MMFVSLN*	MMFVSLN*			GCAACCGTCC	AACAACAACC	0	KL	FG10862.1	0	0	0	0
1879	1236	an	AN0138.1	71.m15421	AO070321000114	0	-120	-100					ATGTTCGTCTCTCTCAATTGA	ATGTTCGTCTCTCTCAATTGA			MFVSLN*	MFVSLN*			ACCGTCCATG	AACAACAACC	0	KL	FG10862.1	0	0	0	0
1880	1236	ao	AN0138.1	71.m15421	AO070321000114	0					-137	-126	ATGATGTTATGA			ATGATGTTATGA	MML*			MML*	CGCAAGTCTA	CTTGACTGAT	0	KL	FG10862.1	0	0	0	0
1881	1237	af	AN6793.1	66.m04794	AO070326000029	0			-276	-262			ATGGTATTTGAATGA		ATGGTATTTGAATGA		MVFE*		MVFE*		TCAGTATACC	TTCGTCCTAA	0	R	0	0	0	0	0
1882	1237	af	AN6793.1	66.m04794	AO070326000029	0			-265	-209			ATGATTCGTCCTAATTCAGTCTACCACAGCTGCTGCGGGCCGAGGTTTTCCCGGTAG		ATGATTCGTCCTAATTCAGTCTACCACAGCTGCTGCGGGCCGAGGTTTTCCCGGTAG		MIRPNSVYHSCCGPRFSR*		MIRPNSVYHSCCGPRFSR*		TGGTATTTGA	GGCTGGTGAA	0	R	0	0	0	0	0
1883	1237	ao	AN6793.1	66.m04794	AO070326000029	0					-217	-191	ATGTTGAGGCTTAGTCACTGGTGTTGA			ATGTTGAGGCTTAGTCACTGGTGTTGA	MLRLSHWC*			MLRLSHWC*	AAGTAGTTTG	CCGGATATTT	0	R	0	0	0	0	0
1884	1239	ao	AN4019.1	54.m06552	AO070328000118	0					-211	-158	ATGATTGCGCGATCAAGTGCTAAAATGATCTGTTCCCGTCCACAGTTGTTTTGA			ATGATTGCGCGATCAAGTGCTAAAATGATCTGTTCCCGTCCACAGTTGTTTTGA	MIARSSAKMICSRPQLF*			MIARSSAKMICSRPQLF*	AGATCGGTCA	CTTCTGTTTT	0	R	0	0	0	0	0
1885	1239	ao	AN4019.1	54.m06552	AO070328000118	0					-187	-158	ATGATCTGTTCCCGTCCACAGTTGTTTTGA			ATGATCTGTTCCCGTCCACAGTTGTTTTGA	MICSRPQLF*			MICSRPQLF*	AAGTGCTAAA	CTTCTGTTTT	0	R	0	0	0	0	0
1886	1239	ao	AN4019.1	54.m06552	AO070328000118	0					-135	-109	ATGCGCCGCCCTTTTTTTTCCAGATAA			ATGCGCCGCCCTTTTTTTTCCAGATAA	MRRPFFSR*			MRRPFFSR*	CGTATCTTGT	TATCTTCCCC	0	R	0	0	0	0	0
1893	1240	af	AN4861.1	59.m09110	AO070329000146	0			-341	-288			ATGCATGCCACTCGCTCAAGTGATGAGAGCATTTGCAGCTCCAACTGTCTTTAA		ATGCATGCCACTCGCTCAAGTGATGAGAGCATTTGCAGCTCCAACTGTCTTTAA		MHATRSSDESICSSNCL*		MHATRSSDESICSSNCL*		GAGGCATTAC	TGCACATGCT	0	K	0	0	0	0	0
1894	1240	af	AN4861.1	59.m09110	AO070329000146	0			-337	-185			ATGCCACTCGCTCAAGTGATGAGAGCATTTGCAGCTCCAACTGTCTTTAATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		ATGCCACTCGCTCAAGTGATGAGAGCATTTGCAGCTCCAACTGTCTTTAATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		MPLAQVMRAFAAPTVFNAHAAGCGCAATVMANACCRGILSHQVMATCDIF*		MPLAQVMRAFAAPTVFNAHAAGCGCAATVMANACCRGILSHQVMATCDIF*		CATTACATGC	GGACCTTGCC	0	K	0	0	0	0	0
1895	1240	af	AN4861.1	59.m09110	AO070329000146	0			-319	-185			ATGAGAGCATTTGCAGCTCCAACTGTCTTTAATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		ATGAGAGCATTTGCAGCTCCAACTGTCTTTAATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		MRAFAAPTVFNAHAAGCGCAATVMANACCRGILSHQVMATCDIF*		MRAFAAPTVFNAHAAGCGCAATVMANACCRGILSHQVMATCDIF*		CGCTCAAGTG	GGACCTTGCC	0	K	0	0	0	0	0
1896	1240	af	AN4861.1	59.m09110	AO070329000146	0			-288	-250			ATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGA		ATGCACATGCTGCCGGATGTGGATGTGCCGCGACAGTGA		MHMLPDVDVPRQ*		MHMLPDVDVPRQ*		ACTGTCTTTA	TGGCAAACGC	0	K	0	0	0	0	0
1897	1240	af	AN4861.1	59.m09110	AO070329000146	0			-282	-250			ATGCTGCCGGATGTGGATGTGCCGCGACAGTGA		ATGCTGCCGGATGTGGATGTGCCGCGACAGTGA		MLPDVDVPRQ*		MLPDVDVPRQ*		TTTAATGCAC	TGGCAAACGC	0	K	0	0	0	0	0
1898	1240	af	AN4861.1	59.m09110	AO070329000146	0			-272	-195			ATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGA		ATGTGGATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGA		MWMCRDSDGKRLLQRNFVASGYGYL*		MWMCRDSDGKRLLQRNFVASGYGYL*		ATGCTGCCGG	CATTTTCTAA	0	K	0	0	0	0	0
1899	1240	af	AN4861.1	59.m09110	AO070329000146	0			-266	-195			ATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGA		ATGTGCCGCGACAGTGATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGA		MCRDSDGKRLLQRNFVASGYGYL*		MCRDSDGKRLLQRNFVASGYGYL*		CCGGATGTGG	CATTTTCTAA	0	K	0	0	0	0	0
1900	1240	af	AN4861.1	59.m09110	AO070329000146	0			-250	-185			ATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		ATGGCAAACGCTTGTTGCAGAGGAATTTTGTCGCATCAGGTTATGGCTACTTGTGACATTTTCTAA		MANACCRGILSHQVMATCDIF*		MANACCRGILSHQVMATCDIF*		CGCGACAGTG	GGACCTTGCC	0	K	0	0	0	0	0
1901	1240	af	AN4861.1	59.m09110	AO070329000146	0			-208	-185			ATGGCTACTTGTGACATTTTCTAA		ATGGCTACTTGTGACATTTTCTAA		MATCDIF*		MATCDIF*		GCATCAGGTT	GGACCTTGCC	0	K	0	0	0	0	0
1887	1240	an	AN4861.1	59.m09110	AO070329000146	0	-403	-347					ATGTGGTTTTATGTTACCGCCGTACCCTCAGCGCATGTCCTTTATGATTGTTTCTAG	ATGTGGTTTTATGTTACCGCCGTACCCTCAGCGCATGTCCTTTATGATTGTTTCTAG			MWFYVTAVPSAHVLYDCF*	MWFYVTAVPSAHVLYDCF*			AAGAGTGAGT	AGCCTGTGGT	0	K	0	0	0	0	0
1888	1240	an	AN4861.1	59.m09110	AO070329000146	0	-393	-331					ATGTTACCGCCGTACCCTCAGCGCATGTCCTTTATGATTGTTTCTAGAGCCTGTGGTCCTTGA	ATGTTACCGCCGTACCCTCAGCGCATGTCCTTTATGATTGTTTCTAGAGCCTGTGGTCCTTGA			MLPPYPQRMSFMIVSRACGP*	MLPPYPQRMSFMIVSRACGP*			ATGTGGTTTT	ATCTCAGCCT	0	K	0	0	0	0	0
1889	1240	an	AN4861.1	59.m09110	AO070329000146	0	-369	-331					ATGTCCTTTATGATTGTTTCTAGAGCCTGTGGTCCTTGA	ATGTCCTTTATGATTGTTTCTAGAGCCTGTGGTCCTTGA			MSFMIVSRACGP*	MSFMIVSRACGP*			CCCTCAGCGC	ATCTCAGCCT	0	K	0	0	0	0	0
1890	1240	an	AN4861.1	59.m09110	AO070329000146	0	-360	-331					ATGATTGTTTCTAGAGCCTGTGGTCCTTGA	ATGATTGTTTCTAGAGCCTGTGGTCCTTGA			MIVSRACGP*	MIVSRACGP*			CATGTCCTTT	ATCTCAGCCT	0	K	0	0	0	0	0
1891	1240	an	AN4861.1	59.m09110	AO070329000146	0	-276	-193					ATGTTAACAAGCACGTGCTACTGTCTCGTGCGGGCTAGGAACTGCCGGGCTCTCGCAGCCATCGTGGGGAAACCACAGATATGA	ATGTTAACAAGCACGTGCTACTGTCTCGTGCGGGCTAGGAACTGCCGGGCTCTCGCAGCCATCGTGGGGAAACCACAGATATGA			MLTSTCYCLVRARNCRALAAIVGKPQI*	MLTSTCYCLVRARNCRALAAIVGKPQI*			ATTGCAGAGA	TAAACGAGTC	0	K	0	0	0	0	0
1902	1240	ao	AN4861.1	59.m09110	AO070329000146	0					-307	-293	ATGATTTCGCAATAA			ATGATTTCGCAATAA	MISQ*			MISQ*	GAGAAGTTTC	TGGAGTTTCC	0	K	0	0	0	0	0
1903	1240	ao	AN4861.1	59.m09110	AO070329000146	0					-293	-210	ATGGAGTTTCCTAAAGAGGCACGTGCGCATGGGTTGTCCCGCCATACTCCAGCGCCCAGCGACGTCAGCCTTTTCTCTGAATGA			ATGGAGTTTCCTAAAGAGGCACGTGCGCATGGGTTGTCCCGCCATACTCCAGCGCCCAGCGACGTCAGCCTTTTCTCTGAATGA	MEFPKEARAHGLSRHTPAPSDVSLFSE*			MEFPKEARAHGLSRHTPAPSDVSLFSE*	TTTCGCAATA	TGGGTAGCTC	0	K	0	0	0	0	0
1904	1240	ao	AN4861.1	59.m09110	AO070329000146	0					-265	-203	ATGGGTTGTCCCGCCATACTCCAGCGCCCAGCGACGTCAGCCTTTTCTCTGAATGATGGGTAG			ATGGGTTGTCCCGCCATACTCCAGCGCCCAGCGACGTCAGCCTTTTCTCTGAATGATGGGTAG	MGCPAILQRPATSAFSLNDG*			MGCPAILQRPATSAFSLNDG*	GCACGTGCGC	CTCGGGAAGC	0	K	0	0	0	0	0
1906	1243	ao	AN2884.1	59.m08731	AO070338000130	0					-264	-247	ATGAGCAGGCTTATTTAG			ATGAGCAGGCTTATTTAG	MSRLI*			MSRLI*	ACTTACCCTT	CTTTAACCTT	0		0	0	0	0	0
1909	1245	af	AN0727.1	70.m15330	AO070343000486	0			-246	-229			ATGCTGCAAAAAAGTTGA		ATGCTGCAAAAAAGTTGA		MLQKS*		MLQKS*		TTCGGTGGTG	CCCTAGAACT	0	A	0	0	0	0	0
1908	1245	an	AN0727.1	70.m15330	AO070343000486	0	-214	-164					ATGTCCCAGCATTTTTTCTGCCGCTTGAAACCGCCTTCGCGGCCACGTTAG	ATGTCCCAGCATTTTTTCTGCCGCTTGAAACCGCCTTCGCGGCCACGTTAG			MSQHFFCRLKPPSRPR*	MSQHFFCRLKPPSRPR*			GAAGAAAAAA	CTGCCGCGAG	0	A	0	0	0	0	0
1910	1245	ao	AN0727.1	70.m15330	AO070343000486	0					-147	-103	ATGCCCGTGTCACTGCTAAGTATCCGCGCTGTTTTCTCACTTTAG			ATGCCCGTGTCACTGCTAAGTATCCGCGCTGTTTTCTCACTTTAG	MPVSLLSIRAVFSL*			MPVSLLSIRAVFSL*	CCCGTGATTT	TTCTCGGATT	0	A	0	0	0	0	0
1913	1248	af	AN5771.1	69.m14827	AO070249000009	0			-203	-135			ATGCATCTGCATCAATTGACTGCGTATCCACTTTCGATCCATCTGAATCGCGCACAGAAAGACGCCTGA		ATGCATCTGCATCAATTGACTGCGTATCCACTTTCGATCCATCTGAATCGCGCACAGAAAGACGCCTGA		MHLHQLTAYPLSIHLNRAQKDA*		MHLHQLTAYPLSIHLNRAQKDA*		CTGGAATTTC	GGGACAAATA	0		0	0	0	0	0
1911	1248	an	AN5771.1	69.m14827	AO070249000009	0	-245	-228					ATGCAGAACGGAGCCTAA	ATGCAGAACGGAGCCTAA			MQNGA*	MQNGA*			ACAATAACCT	GACTGTGTTG	0		0	0	0	0	0
1912	1248	an	AN5771.1	69.m14827	AO070249000009	0	-191	-180					ATGATTGCTTGA	ATGATTGCTTGA			MIA*	MIA*			CAACTGCTCT	GCAAGTCGTC	0		0	0	0	0	0
1915	1249	af	AN5821.1	72.m18948	AO070260000024	0			-238	-212			ATGTTGACAGCCATTTACTTTGCTTGA		ATGTTGACAGCCATTTACTTTGCTTGA		MLTAIYFA*		MLTAIYFA*		GATTCAACCT	AGCGCCCAAT	0	P	0	0	0	0	0
1914	1249	an	AN5821.1	72.m18948	AO070260000024	0	-163	-125					ATGCTCTACTGCACGAGTGTTTATAGCAAGGACCGATAA	ATGCTCTACTGCACGAGTGTTTATAGCAAGGACCGATAA			MLYCTSVYSKDR*	MLYCTSVYSKDR*			GGGCTTGACA	CTGTTTGTCT	0	P	0	0	0	0	0
1916	1252	af	AN1328.1	70.m14903	AO070303000092	0			-269	-231			ATGGATCTGTTGATACATATCCACTGGCTGATCGAATAG		ATGGATCTGTTGATACATATCCACTGGCTGATCGAATAG		MDLLIHIHWLIE*		MDLLIHIHWLIE*		AATTGTTGAA	GGTTTAGCGC	0	R	0	0	0	0	0
1917	1252	af	AN1328.1	70.m14903	AO070303000092	0			-209	-78			ATGATTTCTGGTTCTCAGTCATCATTATCAGTCGTCCATTGTTCGAGCTCCGCACCTGTTCAAGCCCATTTTCCATTCCGTCAGTGGCCAGGCAGTCCCAACTGGCATCTATATAACTGCCAGATCGCTTGA		ATGATTTCTGGTTCTCAGTCATCATTATCAGTCGTCCATTGTTCGAGCTCCGCACCTGTTCAAGCCCATTTTCCATTCCGTCAGTGGCCAGGCAGTCCCAACTGGCATCTATATAACTGCCAGATCGCTTGA		MISGSQSSLSVVHCSSSAPVQAHFPFRQWPGSPNWHLYNCQIA*		MISGSQSSLSVVHCSSSAPVQAHFPFRQWPGSPNWHLYNCQIA*		TTCAACCCAC	AAATCGGCCA	0	R	0	0	0	0	0
1918	1252	ao	AN1328.1	70.m14903	AO070303000092	0					-210	-49	ATGATACCGAAGATAGGGCACACCCCAACCGGGTTAGCGCAGCACCTGATCCGCATCACCTCCACCGCCCGCGGAGACAAATTAATCATACCAACATCAAAAACATATACTCAATCCCCTCTCAAACCGACGAACTCCCCTCAACCCCACCACCTCAATTAA			ATGATACCGAAGATAGGGCACACCCCAACCGGGTTAGCGCAGCACCTGATCCGCATCACCTCCACCGCCCGCGGAGACAAATTAATCATACCAACATCAAAAACATATACTCAATCCCCTCTCAAACCGACGAACTCCCCTCAACCCCACCACCTCAATTAA	MIPKIGHTPTGLAQHLIRITSTARGDKLIIPTSKTYTQSPLKPTNSPQPHHLN*			MIPKIGHTPTGLAQHLIRITSTARGDKLIIPTSKTYTQSPLKPTNSPQPHHLN*	TGCCAAAGGA	CCTCCTCTAC	0	R	0	0	0	0	0

1919	1254	af	AN5713.1	54.m06828	AO070324000145	0			-166	-95			ATGAGGAGCTTTGGGAAATTTTGGTCGAGAGCACCCCGGAGCTGTCAATCTTGGGATCGCTCAGGACACTGA		ATGAGGAGCTTTGGGAAATTTTGGTCGAGAGCACCCCGGAGCTGTCAATCTTGGGATCGCTCAGGACACTGA		MRSFGKFWSRAPRSCQSWDRSGH*		MRSFGKFWSRAPRSCQSWDRSGH*		GGGGGTTTCG	CTACTGATCT	0	O	FG06306.1	MG03310.1	NCU09700.1	YJL111W	0
1920	1254	ao	AN5713.1	54.m06828	AO070324000145	0					-187	-11	ATGATTGGTCACCGCCTCAGTGCTTTGGCGACATCGAGAAGCTCGGGGAAATTTTGGTCAAGAGCATTATTGAACCCCCCCGAGCTGGTAACTTTCAGGGCCACTTTCCATCTCCCGTGCGTCTCTTATTCTCTACCGGTCTTTACCAGCCCTATTTGTCGGTTCTTTTCGAAATAA			ATGATTGGTCACCGCCTCAGTGCTTTGGCGACATCGAGAAGCTCGGGGAAATTTTGGTCAAGAGCATTATTGAACCCCCCCGAGCTGGTAACTTTCAGGGCCACTTTCCATCTCCCGTGCGTCTCTTATTCTCTACCGGTCTTTACCAGCCCTATTTGTCGGTTCTTTTCGAAATAA	MIGHRLSALATSRSSGKFWSRALLNPPELVTFRATFHLPCVSYSLPVFTSPICRFFSK*			MIGHRLSALATSRSSGKFWSRALLNPPELVTFRATFHLPCVSYSLPVFTSPICRFFSK*	GAGACGCGGT	ATTAATCAAA	0	O	FG06306.1	MG03310.1	NCU09700.1	YJL111W	0
1923	1255	af	AN0292.1	54.m06490	AO070334000050	0			-265	-245			ATGAAGTCAAAGCAAGAGTAA		ATGAAGTCAAAGCAAGAGTAA		MKSKQE*		MKSKQE*		CCACTTGATG	CTGGAGCTAT	0	K	0	0	0	0	0
1924	1255	af	AN0292.1	54.m06490	AO070334000050	0			-236	-135			ATGTCATCACGTGCAGTGATGCCAGGCAGCGATGGATCTGATTATATAAGCCAGCTCACAGCGCTAACCCAAGTCAGTCCTAGCTCGATATCAGAAACGTGA		ATGTCATCACGTGCAGTGATGCCAGGCAGCGATGGATCTGATTATATAAGCCAGCTCACAGCGCTAACCCAAGTCAGTCCTAGCTCGATATCAGAAACGTGA		MSSRAVMPGSDGSDYISQLTALTQVSPSSISET*		MSSRAVMPGSDGSDYISQLTALTQVSPSSISET*		AACTGGAGCT	CTTTGCAAGC	0	K	0	0	0	0	0
1925	1255	af	AN0292.1	54.m06490	AO070334000050	0			-218	-135			ATGCCAGGCAGCGATGGATCTGATTATATAAGCCAGCTCACAGCGCTAACCCAAGTCAGTCCTAGCTCGATATCAGAAACGTGA		ATGCCAGGCAGCGATGGATCTGATTATATAAGCCAGCTCACAGCGCTAACCCAAGTCAGTCCTAGCTCGATATCAGAAACGTGA		MPGSDGSDYISQLTALTQVSPSSISET*		MPGSDGSDYISQLTALTQVSPSSISET*		ACGTGCAGTG	CTTTGCAAGC	0	K	0	0	0	0	0
1926	1255	af	AN0292.1	54.m06490	AO070334000050	0			-205	-188			ATGGATCTGATTATATAA		ATGGATCTGATTATATAA		MDLII*		MDLII*		CCAGGCAGCG	GCCAGCTCAC	0	K	0	0	0	0	0
1921	1255	an	AN0292.1	54.m06490	AO070334000050	0	-226	-182					ATGACAGGCAGCCTGTCACGTGCGAAGTTGGGGAAGATTTGCTGA	ATGACAGGCAGCCTGTCACGTGCGAAGTTGGGGAAGATTTGCTGA			MTGSLSRAKLGKIC*	MTGSLSRAKLGKIC*			GCCTTATCAA	CATAAGCACA	0	K	0	0	0	0	0
1922	1255	an	AN0292.1	54.m06490	AO070334000050	0	-135	-58					ATGTCGGAAGGGACATTTGATTCCCTCACATCCCAGTCACTGTGCATCAGCAACCCAGTTGCCTCAGTCTCCAATTAG	ATGTCGGAAGGGACATTTGATTCCCTCACATCCCAGTCACTGTGCATCAGCAACCCAGTTGCCTCAGTCTCCAATTAG			MSEGTFDSLTSQSLCISNPVASVSN*	MSEGTFDSLTSQSLCISNPVASVSN*			AATCAAAAAG	AGTTCTCTTG	0	K	0	0	0	0	0
1927	1255	ao	AN0292.1	54.m06490	AO070334000050	0					-230	-180	ATGCGAAGGCAGCTAAGCTTGCATCACGTGCGCGGGCCTGGGGAACACTAG			ATGCGAAGGCAGCTAAGCTTGCATCACGTGCGCGGGCCTGGGGAACACTAG	MRRQLSLHHVRGPGEH*			MRRQLSLHHVRGPGEH*	GAATATGAAG	AATCGGATTA	0	K	0	0	0	0	0
1928	1258	af	AN1340.1	70.m15734	AO070247000024	0			-170	-159			ATGTGCTTCTAA		ATGTGCTTCTAA		MCF*		MCF*		CAGGACTCTC	ATTCTTTCGT	0	A	0	0	0	0	0
1931	1260	af	AN1694.1	58.m07769	AO070305000018	0			-226	-185			ATGAACATAACCGACGGCCATACTTCTCCTGGTCGGATGTAA		ATGAACATAACCGACGGCCATACTTCTCCTGGTCGGATGTAA		MNITDGHTSPGRM*		MNITDGHTSPGRM*		ACTCTCTCAA	CATAGGATTT	0	R	0	0	NCU06029.1	0	0
1932	1260	af	AN1694.1	58.m07769	AO070305000018	0			-119	-108			ATGCTCAGTTGA		ATGCTCAGTTGA		MLS*		MLS*		CTATTCCAAA	ACTTCTCAGC	0	R	0	0	NCU06029.1	0	0
1929	1260	an	AN1694.1	58.m07769	AO070305000018	0	-190	-176					ATGCTATCTGGTTAA	ATGCTATCTGGTTAA			MLSG*	MLSG*			TCGTGCTCGG	TTCTGATTCC	0	R	0	0	NCU06029.1	0	0
1930	1260	an	AN1694.1	58.m07769	AO070305000018	0	-76	-62					ATGACCTCATTTTAA	ATGACCTCATTTTAA			MTSF*	MTSF*			CCGTCATTCC	TACATCCGTA	0	R	0	0	NCU06029.1	0	0
1936	1261	af	AN3344.1	53.m04025	AO070307000126	0			-229	-116			ATGCGAGTGGGCATGACTCGGGCCAGAGTAAGACAGATTGACAACGGAATATCACTAGATGAACTATTCCAGGATGGCGTGATAGGCAGTGATATGCTGTCCGATGTAACGTGA		ATGCGAGTGGGCATGACTCGGGCCAGAGTAAGACAGATTGACAACGGAATATCACTAGATGAACTATTCCAGGATGGCGTGATAGGCAGTGATATGCTGTCCGATGTAACGTGA		MRVGMTRARVRQIDNGISLDELFQDGVIGSDMLSDVT*		MRVGMTRARVRQIDNGISLDELFQDGVIGSDMLSDVT*		CGTAAGCCAC	AGCAATAATA	0		0	0	0	0	0
1937	1261	af	AN3344.1	53.m04025	AO070307000126	0			-217	-116			ATGACTCGGGCCAGAGTAAGACAGATTGACAACGGAATATCACTAGATGAACTATTCCAGGATGGCGTGATAGGCAGTGATATGCTGTCCGATGTAACGTGA		ATGACTCGGGCCAGAGTAAGACAGATTGACAACGGAATATCACTAGATGAACTATTCCAGGATGGCGTGATAGGCAGTGATATGCTGTCCGATGTAACGTGA		MTRARVRQIDNGISLDELFQDGVIGSDMLSDVT*		MTRARVRQIDNGISLDELFQDGVIGSDMLSDVT*		GCGAGTGGGC	AGCAATAATA	0		0	0	0	0	0
1938	1261	af	AN3344.1	53.m04025	AO070307000126	0			-171	-148			ATGAACTATTCCAGGATGGCGTGA		ATGAACTATTCCAGGATGGCGTGA		MNYSRMA*		MNYSRMA*		ATATCACTAG	TAGGCAGTGA	0		0	0	0	0	0
1939	1261	af	AN3344.1	53.m04025	AO070307000126	0			-136	-116			ATGCTGTCCGATGTAACGTGA		ATGCTGTCCGATGTAACGTGA		MLSDVT*		MLSDVT*		AGGCAGTGAT	AGCAATAATA	0		0	0	0	0	0
1933	1261	an	AN3344.1	53.m04025	AO070307000126	0	-190	-179					ATGAGAAAATAG	ATGAGAAAATAG			MRK*	MRK*			CTTCCAGACG	ACTGGGGCTG	0		0	0	0	0	0
1934	1261	an	AN3344.1	53.m04025	AO070307000126	0	-132	-112					ATGATACAAGCAGGTCATTAG	ATGATACAAGCAGGTCATTAG			MIQAGH*	MIQAGH*			CGTAGGATCC	TAATATATGT	0		0	0	0	0	0
1935	1261	an	AN3344.1	53.m04025	AO070307000126	0	-105	-55					ATGTGGAGAAATGAACACCATATTAAAGATGCATGCTTGGCCTCTCCCTAG	ATGTGGAGAAATGAACACCATATTAAAGATGCATGCTTGGCCTCTCCCTAG			MWRNEHHIKDACLASP*	MWRNEHHIKDACLASP*			TTAGTAATAT	AACACCGCCA	0		0	0	0	0	0
1940	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-292	-116	ATGCGAATAAGTCTAGCTCGGTCGTTATCCAGGAGCCGAGGACGATGGTGTAGTGACACGGCCTTGTTCGGGGAGTTTGGGAAATGGGTTTTTTTTTGTTTTATTGGTGCGTTTGCTATACATGTGTTACGACTTGCTTTAGATGCCTCGTATATCTTTGCTCGTACCCCGGATTAA			ATGCGAATAAGTCTAGCTCGGTCGTTATCCAGGAGCCGAGGACGATGGTGTAGTGACACGGCCTTGTTCGGGGAGTTTGGGAAATGGGTTTTTTTTTGTTTTATTGGTGCGTTTGCTATACATGTGTTACGACTTGCTTTAGATGCCTCGTATATCTTTGCTCGTACCCCGGATTAA	MRISLARSLSRSRGRWCSDTALFGEFGKWVFFCFIGAFAIHVLRLALDASYIFARTPD*			MRISLARSLSRSRGRWCSDTALFGEFGKWVFFCFIGAFAIHVLRLALDASYIFARTPD*	TCGTCGGTGG	TTGTTAGAAA	0		0	0	0	0	0
1941	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-209	-48	ATGGGTTTTTTTTTGTTTTATTGGTGCGTTTGCTATACATGTGTTACGACTTGCTTTAGATGCCTCGTATATCTTTGCTCGTACCCCGGATTAATTGTTAGAAATGTGACATGCCCCTCTTCTTTGACCATGACCATGACTGTCGTTTCCTCTGAAGGATAG			ATGGGTTTTTTTTTGTTTTATTGGTGCGTTTGCTATACATGTGTTACGACTTGCTTTAGATGCCTCGTATATCTTTGCTCGTACCCCGGATTAATTGTTAGAAATGTGACATGCCCCTCTTCTTTGACCATGACCATGACTGTCGTTTCCTCTGAAGGATAG	MGFFLFYWCVCYTCVTTCFRCLVYLCSYPGLIVRNVTCPSSLTMTMTVVSSEG*			MGFFLFYWCVCYTCVTTCFRCLVYLCSYPGLIVRNVTCPSSLTMTMTVVSSEG*	AGTTTGGGAA	AATACCAACT	0		0	0	0	0	0
1942	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-171	-151	ATGTGTTACGACTTGCTTTAG			ATGTGTTACGACTTGCTTTAG	MCYDLL*			MCYDLL*	TTTGCTATAC	ATGCCTCGTA	0		0	0	0	0	0
1943	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-150	-109	ATGCCTCGTATATCTTTGCTCGTACCCCGGATTAATTGTTAG			ATGCCTCGTATATCTTTGCTCGTACCCCGGATTAATTGTTAG	MPRISLLVPRINC*			MPRISLLVPRINC*	CTTGCTTTAG	AAATGTGACA	0		0	0	0	0	0
1944	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-99	-55	ATGCCCCTCTTCTTTGACCATGACCATGACTGTCGTTTCCTCTGA			ATGCCCCTCTTCTTTGACCATGACCATGACTGTCGTTTCCTCTGA	MPLFFDHDHDCRFL*			MPLFFDHDHDCRFL*	GAAATGTGAC	AGGATAGAAT	0		0	0	0	0	0
1945	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-80	-48	ATGACCATGACTGTCGTTTCCTCTGAAGGATAG			ATGACCATGACTGTCGTTTCCTCTGAAGGATAG	MTMTVVSSEG*			MTMTVVSSEG*	TTCTTTGACC	AATACCAACT	0		0	0	0	0	0
1946	1261	ao	AN3344.1	53.m04025	AO070307000126	0					-74	-48	ATGACTGTCGTTTCCTCTGAAGGATAG			ATGACTGTCGTTTCCTCTGAAGGATAG	MTVVSSEG*			MTVVSSEG*	GACCATGACC	AATACCAACT	0		0	0	0	0	0
1950	1270	af	AN3963.1	69.m15136	AO070252000013	0			-166	-89			ATGACCATTGGCCCATTCCGCGGAAACATTTTTTCGGATGCCGAGAAGAAAGTGTCCGAACCCATGCGCCGTATATAA		ATGACCATTGGCCCATTCCGCGGAAACATTTTTTCGGATGCCGAGAAGAAAGTGTCCGAACCCATGCGCCGTATATAA		MTIGPFRGNIFSDAEKKVSEPMRRI*		MTIGPFRGNIFSDAEKKVSEPMRRI*		GATCAATTGC	ATACCACCCC	0	O	0	0	0	0	0
1951	1270	af	AN3963.1	69.m15136	AO070252000013	0			-103	-89			ATGCGCCGTATATAA		ATGCGCCGTATATAA		MRRI*		MRRI*		GTCCGAACCC	ATACCACCCC	0	O	0	0	0	0	0
1949	1270	an	AN3963.1	69.m15136	AO070252000013	0	-219	-115					ATGCGGCAGGCAGTTAAAAATCCCACAGAGAATGTGTTCTATTGGGTGCGTTCCCTGCATCGGAGACATAGTCGGAGACTTCCCATCTATTTTAGTGCGGCCTGA	ATGCGGCAGGCAGTTAAAAATCCCACAGAGAATGTGTTCTATTGGGTGCGTTCCCTGCATCGGAGACATAGTCGGAGACTTCCCATCTATTTTAGTGCGGCCTGA			MRQAVKNPTENVFYWVRSLHRRHSRRLPIYFSAA*	MRQAVKNPTENVFYWVRSLHRRHSRRLPIYFSAA*			TTTCTAGTAG	ACCCTCTTCC	0	O	0	0	0	0	0
1952	1270	ao	AN3963.1	69.m15136	AO070252000013	0					-215	-180	ATGGCCATTGCTTCTATTCTAGGAGAAGGGGCGTGA			ATGGCCATTGCTTCTATTCTAGGAGAAGGGGCGTGA	MAIASILGEGA*			MAIASILGEGA*	GACTCACAAT	AGTCTAGATT	0	O	0	0	0	0	0
1953	1270	ao	AN3963.1	69.m15136	AO070252000013	0					-146	-120	ATGGAGCCTATTCGGAGACATTCTTAG			ATGGAGCCTATTCGGAGACATTCTTAG	MEPIRRHS*			MEPIRRHS*	CAAGACAACG	GGCTAAGTCT	0	O	0	0	0	0	0
1954	1273	af	AN4372.1	56.m03102	AO070275000045	0			-176	-36			ATGGCCTATATAAAGCTTCAGATTCCCTCACAGTGTATGCTTCCTTTCTCTCCTCATCCGCGCTCCTTTCGTCTTTCATATCCCATTGTATCTATCACGTTTAGGGTATCTGTTGACCAGAACCCTGTCCCATCTTTCTAA		ATGGCCTATATAAAGCTTCAGATTCCCTCACAGTGTATGCTTCCTTTCTCTCCTCATCCGCGCTCCTTTCGTCTTTCATATCCCATTGTATCTATCACGTTTAGGGTATCTGTTGACCAGAACCCTGTCCCATCTTTCTAA		MAYIKLQIPSQCMLPFSPHPRSFRLSYPIVSITFRVSVDQNPVPSF*		MAYIKLQIPSQCMLPFSPHPRSFRLSYPIVSITFRVSVDQNPVPSF*		CGCTCCCGTC	ACCGAGTCCC	0	M	0	0	0	0	0
1955	1273	af	AN4372.1	56.m03102	AO070275000045	0			-140	-36			ATGCTTCCTTTCTCTCCTCATCCGCGCTCCTTTCGTCTTTCATATCCCATTGTATCTATCACGTTTAGGGTATCTGTTGACCAGAACCCTGTCCCATCTTTCTAA		ATGCTTCCTTTCTCTCCTCATCCGCGCTCCTTTCGTCTTTCATATCCCATTGTATCTATCACGTTTAGGGTATCTGTTGACCAGAACCCTGTCCCATCTTTCTAA		MLPFSPHPRSFRLSYPIVSITFRVSVDQNPVPSF*		MLPFSPHPRSFRLSYPIVSITFRVSVDQNPVPSF*		CTCACAGTGT	ACCGAGTCCC	0	M	0	0	0	0	0
1956	1273	ao	AN4372.1	56.m03102	AO070275000045	0					-139	-29	ATGAAAAGAGTCTTGGACCCCTACGATGTCTTCCTTTCTCTCAGCATCGTCTCCATCAACCCTCCATTCCTTAGTCTTTCTTTCAGTCCATATTTGAAGGCGTCTTGTTGA			ATGAAAAGAGTCTTGGACCCCTACGATGTCTTCCTTTCTCTCAGCATCGTCTCCATCAACCCTCCATTCCTTAGTCTTTCTTTCAGTCCATATTTGAAGGCGTCTTGTTGA	MKRVLDPYDVFLSLSIVSINPPFLSLSFSPYLKASC*			MKRVLDPYDVFLSLSIVSINPPFLSLSFSPYLKASC*	GAAAGGGGAT	CCAAGTCCCT	0	M	0	0	0	0	0
1957	1273	ao	AN4372.1	56.m03102	AO070275000045	0					-114	-43	ATGTCTTCCTTTCTCTCAGCATCGTCTCCATCAACCCTCCATTCCTTAGTCTTTCTTTCAGTCCATATTTGA			ATGTCTTCCTTTCTCTCAGCATCGTCTCCATCAACCCTCCATTCCTTAGTCTTTCTTTCAGTCCATATTTGA	MSSFLSASSPSTLHSLVFLSVHI*			MSSFLSASSPSTLHSLVFLSVHI*	GACCCCTACG	AGGCGTCTTG	0	M	0	0	0	0	0
1959	1276	af	AN7470.1	57.m05874	AO070287000056	0			-286	-188			ATGCAAGCAAACCAGTTACCAGTAATGGCGGTTCTGACAGCCCAAGAGTCTTATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAG		ATGCAAGCAAACCAGTTACCAGTAATGGCGGTTCTGACAGCCCAAGAGTCTTATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAG		MQANQLPVMAVLTAQESYVIRHIRVGFKCIDL*		MQANQLPVMAVLTAQESYVIRHIRVGFKCIDL*		GGCAGGTGGA	TTAAAGAGAT	0		0	0	0	0	0
1960	1276	af	AN7470.1	57.m05874	AO070287000056	0			-262	-188			ATGGCGGTTCTGACAGCCCAAGAGTCTTATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAG		ATGGCGGTTCTGACAGCCCAAGAGTCTTATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAG		MAVLTAQESYVIRHIRVGFKCIDL*		MAVLTAQESYVIRHIRVGFKCIDL*		GTTACCAGTA	TTAAAGAGAT	0		0	0	0	0	0
1961	1276	af	AN7470.1	57.m05874	AO070287000056	0			-234	-184			ATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAGTTAA		ATGTCATTCGGCATATCCGTGTGGGTTTCAAATGCATTGATTTGTAGTTAA		MSFGISVWVSNALICS*		MSFGISVWVSNALICS*		CAAGAGTCTT	AGAGATGGCA	0		0	0	0	0	0
1962	1276	af	AN7470.1	57.m05874	AO070287000056	0			-179	-66			ATGGCAAGACTATTATATATAAATGCCAGCAGTATTTGCCAGTGAGGATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAATTATCAGCATTGA		ATGGCAAGACTATTATATATAAATGCCAGCAGTATTTGCCAGTGAGGATGTCGAGTCGTTCAGCGAGTACACTGCTAATCTACAAAGGTCAAAAATACTATAATTATCAGCATTGA		MARLLYKCQQYLPVRMSSRSASTLLIYKGQKYYNYQH*		MARLLYKCQQYLPVRMSSRSASTLLIYKGQKYYNYQH*		AGTTAAAGAG	GATTTCCCAA	0		0	0	0	0	0
1965	1276	ao	AN7470.1	57.m05874	AO070287000056	0					-101	-72	ATGTTGCGATCGCAATTGCTATTGTCCTGA			ATGTTGCGATCGCAATTGCTATTGTCCTGA	MLRSQLLLS*			MLRSQLLLS*	ACTTGGAAAA	CCCTGTAGTA	0		0	0	0	0	0
1966	1277	af	AN3763.1	65.m07359	AO070309000041	0			-253	-212			ATGGCTACGGTGTCTGGGGCGTCCTTTGGACTAGACCAGTAG		ATGGCTACGGTGTCTGGGGCGTCCTTTGGACTAGACCAGTAG		MATVSGASFGLDQ*		MATVSGASFGLDQ*		GGAGGAACTC	GTAAATGAGC	0	R	0	0	0	0	0
1967	1277	af	AN3763.1	65.m07359	AO070309000041	0			-207	-115			ATGAGCCCATTCCATGACTCCGCGCCATATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGACCCGACTTTAG		ATGAGCCCATTCCATGACTCCGCGCCATATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGACCCGACTTTAG		MSPFHDSAPYEYSALPFLPGSCLSISLTRL*		MSPFHDSAPYEYSALPFLPGSCLSISLTRL*		CAGTAGGTAA	CCTTTATTCA	0	R	0	0	0	0	0
1968	1277	af	AN3763.1	65.m07359	AO070309000041	0			-194	-126			ATGACTCCGCGCCATATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGA		ATGACTCCGCGCCATATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGA		MTPRHMNTRPSPFFQGLVFQSL*		MTPRHMNTRPSPFFQGLVFQSL*		AGCCCATTCC	CCCGACTTTA	0	R	0	0	0	0	0
1969	1277	af	AN3763.1	65.m07359	AO070309000041	0			-179	-126			ATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGA		ATGAATACTCGGCCCTCCCCTTTCTTCCAGGGTCTTGTCTTTCAATCTCTTTGA		MNTRPSPFFQGLVFQSL*		MNTRPSPFFQGLVFQSL*		TCCGCGCCAT	CCCGACTTTA	0	R	0	0	0	0	0
1971	1279	af	AN0905.1	70.m15514	AO070320000080	0			-240	-217			ATGACCATGCTTGCTTCAGTCTGA		ATGACCATGCTTGCTTCAGTCTGA		MTMLASV*		MTMLASV*		TCTGAGCTAA	TGAGATGAAG	0	DO	0	0	0	0	0

1972	1279	af	AN0905.1	70.m15514	AO070320000080	0			-234	-217			ATGCTTGCTTCAGTCTGA		ATGCTTGCTTCAGTCTGA		MLASV*		MLASV*		CTAAATGACC	TGAGATGAAG	0	DO	0	0	0	0	0
1973	1279	af	AN0905.1	70.m15514	AO070320000080	0			-212	-3			ATGAAGAGGTGTATGTTGAGCTATCAGTTTTCCCTGGGTGAAGTGCAAAGCAACGCGGCAAACGCGTGCCAAGCATCGTCGGTAAAATACCCACTCCAGCATCCATCAAACAACTACAGGAACAACCTTGACATCGTTACTAAGAACCTACTTATTCCACCGAACTCAATCGTTCTGTGTTACAGAGGATGGATTAAAATAAACTTATAA		ATGAAGAGGTGTATGTTGAGCTATCAGTTTTCCCTGGGTGAAGTGCAAAGCAACGCGGCAAACGCGTGCCAAGCATCGTCGGTAAAATACCCACTCCAGCATCCATCAAACAACTACAGGAACAACCTTGACATCGTTACTAAGAACCTACTTATTCCACCGAACTCAATCGTTCTGTGTTACAGAGGATGGATTAAAATAAACTTATAA		MKRCMLSYQFSLGEVQSNAANACQASSVKYPLQHPSNNYRNNLDIVTKNLLIPPNSIVLCYRGWIKINL*		MKRCMLSYQFSLGEVQSNAANACQASSVKYPLQHPSNNYRNNLDIVTKNLLIPPNSIVLCYRGWIKINL*		GTCTGATGAG	CTATGGCTGA	0	DO	0	0	0	0	0
1974	1279	af	AN0905.1	70.m15514	AO070320000080	0			-200	-3			ATGTTGAGCTATCAGTTTTCCCTGGGTGAAGTGCAAAGCAACGCGGCAAACGCGTGCCAAGCATCGTCGGTAAAATACCCACTCCAGCATCCATCAAACAACTACAGGAACAACCTTGACATCGTTACTAAGAACCTACTTATTCCACCGAACTCAATCGTTCTGTGTTACAGAGGATGGATTAAAATAAACTTATAA		ATGTTGAGCTATCAGTTTTCCCTGGGTGAAGTGCAAAGCAACGCGGCAAACGCGTGCCAAGCATCGTCGGTAAAATACCCACTCCAGCATCCATCAAACAACTACAGGAACAACCTTGACATCGTTACTAAGAACCTACTTATTCCACCGAACTCAATCGTTCTGTGTTACAGAGGATGGATTAAAATAAACTTATAA		MLSYQFSLGEVQSNAANACQASSVKYPLQHPSNNYRNNLDIVTKNLLIPPNSIVLCYRGWIKINL*		MLSYQFSLGEVQSNAANACQASSVKYPLQHPSNNYRNNLDIVTKNLLIPPNSIVLCYRGWIKINL*		GAAGAGGTGT	CTATGGCTGA	0	DO	0	0	0	0	0
1977	1282	af	AN4870.1	59.m08765	AO070338000090	0			-234	-223			ATGCGATTCTGA		ATGCGATTCTGA		MRF*		MRF*		GTCTCCAGCT	GCTGGTATAT	0		0	0	0	0	0
1978	1282	af	AN4870.1	59.m08765	AO070338000090	0			-198	-181			ATGGAGGATCAACCTTAA		ATGGAGGATCAACCTTAA		MEDQP*		MEDQP*		CGATTGATCA	AAGGAAAACC	0		0	0	0	0	0
1975	1282	an	AN4870.1	59.m08765	AO070338000090	0	-181	-32					ATGTGCCAGATTCGAACGAAGTATGTACTCATTCAACTGTGCCTGATTGTCTATATTCATTCTCTTCTCTCATTAACTATTGCATTGCACTTTACTTCTGCTATTGTCTACTATTGTTCGTTATTGATCCAGCAGCAGTTTTTCTCTTGA	ATGTGCCAGATTCGAACGAAGTATGTACTCATTCAACTGTGCCTGATTGTCTATATTCATTCTCTTCTCTCATTAACTATTGCATTGCACTTTACTTCTGCTATTGTCTACTATTGTTCGTTATTGATCCAGCAGCAGTTTTTCTCTTGA			MCQIRTKYVLIQLCLIVYIHSLLSLTIALHFTSAIVYYCSLLIQQQFFS*	MCQIRTKYVLIQLCLIVYIHSLLSLTIALHFTSAIVYYCSLLIQQQFFS*			GCCCTCAACA	GGCACAATCG	0		0	0	0	0	0
1976	1282	an	AN4870.1	59.m08765	AO070338000090	0	-159	-136					ATGTACTCATTCAACTGTGCCTGA	ATGTACTCATTCAACTGTGCCTGA			MYSFNCA*	MYSFNCA*			CGAACGAAGT	TTGTCTATAT	0		0	0	0	0	0
1979	1282	ao	AN4870.1	59.m08765	AO070338000090	0					-244	-200	ATGGACTGGAAAGCTGTCATCGGTGGTCCTGGGGATCAAGTTTAA			ATGGACTGGAAAGCTGTCATCGGTGGTCCTGGGGATCAAGTTTAA	MDWKAVIGGPGDQV*			MDWKAVIGGPGDQV*	GCCTACGGGG	AAGGCATATC	0		0	0	0	0	0
1980	1282	ao	AN4870.1	59.m08765	AO070338000090	0					-180	-130	ATGATGGAACGCTATTGTAGAGCAGCCACTCTTTCACAGAGTCTTACTTAG			ATGATGGAACGCTATTGTAGAGCAGCCACTCTTTCACAGAGTCTTACTTAG	MMERYCRAATLSQSLT*			MMERYCRAATLSQSLT*	CTCGCCCTCA	CTTGGTGTCG	0		0	0	0	0	0
1981	1282	ao	AN4870.1	59.m08765	AO070338000090	0					-177	-130	ATGGAACGCTATTGTAGAGCAGCCACTCTTTCACAGAGTCTTACTTAG			ATGGAACGCTATTGTAGAGCAGCCACTCTTTCACAGAGTCTTACTTAG	MERYCRAATLSQSLT*			MERYCRAATLSQSLT*	GCCCTCAATG	CTTGGTGTCG	0		0	0	0	0	0
1985	1287	af	AN6642.1	62.m03239	AO070295000022	0			-228	-199			ATGGAGGGGGGTTTCCGGCACGCCGGTTAG		ATGGAGGGGGGTTTCCGGCACGCCGGTTAG		MEGGFRHAG*		MEGGFRHAG*		TGTTCACGTC	GAGTGAGACA	0	P	0	0	0	0	0
1986	1287	af	AN6642.1	62.m03239	AO070295000022	0			-175	-122			ATGTCGCGATACCCCCGCAACGACGGGAGAAGAAAATCTGGTTCTACAACCTAG		ATGTCGCGATACCCCCGCAACGACGGGAGAAGAAAATCTGGTTCTACAACCTAG		MSRYPRNDGRRKSGSTT*		MSRYPRNDGRRKSGSTT*		TGACTTAAAT	GCTTTAATTT	0	P	0	0	0	0	0
1987	1287	ao	AN6642.1	62.m03239	AO070295000022	0					-285	-214	ATGATCCAAGAGCAACATATAAACCCGAGATCTCCCCGCCTCCTCCCGGATGGAAAAGAAAGAAAAGGTTAA			ATGATCCAAGAGCAACATATAAACCCGAGATCTCCCCGCCTCCTCCCGGATGGAAAAGAAAGAAAAGGTTAA	MIQEQHINPRSPRLLPDGKERKG*			MIQEQHINPRSPRLLPDGKERKG*	TGTTCGCGTC	ATCTCCTCCC	0	P	0	0	0	0	0
1988	1287	ao	AN6642.1	62.m03239	AO070295000022	0					-236	-144	ATGGAAAAGAAAGAAAAGGTTAAATCTCCTCCCTCAATTCCTCCCCGATCCATAGCTACTCCAATTCCAAGGTGTATTCTCTACCGGGTGTAG			ATGGAAAAGAAAGAAAAGGTTAAATCTCCTCCCTCAATTCCTCCCCGATCCATAGCTACTCCAATTCCAAGGTGTATTCTCTACCGGGTGTAG	MEKKEKVKSPPSIPPRSIATPIPRCILYRV*			MEKKEKVKSPPSIPPRSIATPIPRCILYRV*	CTCCTCCCGG	GTGTATGGAC	0	P	0	0	0	0	0
1989	1291	af	AN3987.1	53.m04057	AO070333000108	0			-191	-177			ATGGACCATAGTTAG		ATGGACCATAGTTAG		MDHS*		MDHS*		GTCTTACCTC	TTACATTAAT	0		0	0	0	0	0
1990	1291	af	AN3987.1	53.m04057	AO070333000108	0			-143	-99			ATGGTCGTGATGTGGATCCAGACTTCCAGATTGCGAACTATATAA		ATGGTCGTGATGTGGATCCAGACTTCCAGATTGCGAACTATATAA		MVVMWIQTSRLRTI*		MVVMWIQTSRLRTI*		AGTATCCCTC	TCTTCCAATT	0		0	0	0	0	0
1991	1291	af	AN3987.1	53.m04057	AO070333000108	0			-134	-99			ATGTGGATCCAGACTTCCAGATTGCGAACTATATAA		ATGTGGATCCAGACTTCCAGATTGCGAACTATATAA		MWIQTSRLRTI*		MWIQTSRLRTI*		CATGGTCGTG	TCTTCCAATT	0		0	0	0	0	0
2003	1296	af	AN5105.1	54.m06917	AO070291000074	0			-208	-197			ATGCGAGTTTGA		ATGCGAGTTTGA		MRV*		MRV*		ACCTCTTCAA	TATGCCTGTG	0	O	0	0	0	0	0
2004	1296	af	AN5105.1	54.m06917	AO070291000074	0			-195	-175			ATGCCTGTGTACCGCCCCTGA		ATGCCTGTGTACCGCCCCTGA		MPVYRP*		MPVYRP*		CGAGTTTGAT	GGATCATCTA	0	O	0	0	0	0	0
2005	1296	af	AN5105.1	54.m06917	AO070291000074	0			-165	-142			ATGCCAATTCATCTCTTTCTCTAA		ATGCCAATTCATCTCTTTCTCTAA		MPIHLFL*		MPIHLFL*		AGGATCATCT	ACTCAGTATT	0	O	0	0	0	0	0
2006	1296	af	AN5105.1	54.m06917	AO070291000074	0			-116	-54			ATGCGTTTCAATTTCCACTGGTGCCCTTGCAACGTGAACGCTGACTTCTCTGCATCGATCTAG		ATGCGTTTCAATTTCCACTGGTGCCCTTGCAACGTGAACGCTGACTTCTCTGCATCGATCTAG		MRFNFHWCPCNVNADFSASI*		MRFNFHWCPCNVNADFSASI*		ATCATTTTGT	AATGAGACCA	0	O	0	0	0	0	0
2001	1296	an	AN5105.1	54.m06917	AO070291000074	0	-157	-137					ATGAGTGTACCGTACTATTAG	ATGAGTGTACCGTACTATTAG			MSVPYY*	MSVPYY*			CCCGCCAGAT	TCGTTTATGT	0	O	0	0	0	0	0
2002	1296	an	AN5105.1	54.m06917	AO070291000074	0	-130	-74					ATGTTTGCTCTCTCTTCCTCGATCATTTCTATCTTTACATTGCCTGCTTGCATCTGA	ATGTTTGCTCTCTCTTCCTCGATCATTTCTATCTTTACATTGCCTGCTTGCATCTGA			MFALSSSIISIFTLPACI*	MFALSSSIISIFTLPACI*			TTAGTCGTTT	AGACCGGCCA	0	O	0	0	0	0	0
2007	1296	ao	AN5105.1	54.m06917	AO070291000074	0					-212	-180	ATGCTATCGGATATGAAACTGTCTTATTGTTGA			ATGCTATCGGATATGAAACTGTCTTATTGTTGA	MLSDMKLSYC*			MLSDMKLSYC*	ACTCCATATT	ACTCAATTGT	0	O	0	0	0	0	0
2008	1296	ao	AN5105.1	54.m06917	AO070291000074	0					-200	-180	ATGAAACTGTCTTATTGTTGA			ATGAAACTGTCTTATTGTTGA	MKLSYC*			MKLSYC*	GCTATCGGAT	ACTCAATTGT	0	O	0	0	0	0	0
2010	1300	af	AN3123.1	59.m08613	AO070303000024	0			-173	-156			ATGCGTGCCGCCAATTAA		ATGCGTGCCGCCAATTAA		MRAAN*		MRAAN*		TAAACGCGTG	ACTACTTCTT	0	PT	FG04030.1	0	NCU04512.1	0	0
2011	1300	af	AN3123.1	59.m08613	AO070303000024	0			-68	-9			ATGGTGTCCATCATAGCCAATTTATCGCAGGTGTCAGGGACCTTTTTGCGGGCCGCGTAG		ATGGTGTCCATCATAGCCAATTTATCGCAGGTGTCAGGGACCTTTTTGCGGGCCGCGTAG		MVSIIANLSQVSGTFLRAA*		MVSIIANLSQVSGTFLRAA*		TCAGTCTGAG	ACGCCGTCAT	0	PT	FG04030.1	0	NCU04512.1	0	0
2009	1300	an	AN3123.1	59.m08613	AO070303000024	0	-71	-15					ATGTTGTCAGCGACCGCGACTCCATTGCCACGGCCAGCACATCCTTCTGCGGCCTGA	ATGTTGTCAGCGACCGCGACTCCATTGCCACGGCCAGCACATCCTTCTGCGGCCTGA			MLSATATPLPRPAHPSAA*	MLSATATPLPRPAHPSAA*			TCTCCCTGAG	TAATCCCGCG	0	PT	FG04030.1	0	NCU04512.1	0	0
2012	1300	ao	AN3123.1	59.m08613	AO070303000024	0					-200	-159	ATGTCGGAACGCGTGAAATGCGTGTCCCCAGTCACGGGCTAG			ATGTCGGAACGCGTGAAATGCGTGTCCCCAGTCACGGGCTAG	MSERVKCVSPVTG*			MSERVKCVSPVTG*	TGGTAATTCA	ACCCTGACAG	0	PT	FG04030.1	0	NCU04512.1	0	0
2013	1300	ao	AN3123.1	59.m08613	AO070303000024	0					-183	-85	ATGCGTGTCCCCAGTCACGGGCTAGACCCTGACAGCTTGGATTCTGTTCTGCTTTACCTTTCCTCACCACGGCTTAGCCTCATCAACTATAGGGACTAG			ATGCGTGTCCCCAGTCACGGGCTAGACCCTGACAGCTTGGATTCTGTTCTGCTTTACCTTTCCTCACCACGGCTTAGCCTCATCAACTATAGGGACTAG	MRVPSHGLDPDSLDSVLLYLSSPRLSLINYRD*			MRVPSHGLDPDSLDSVLLYLSSPRLSLINYRD*	AACGCGTGAA	CTTCCCTTTT	0	PT	FG04030.1	0	NCU04512.1	0	0
2014	1300	ao	AN3123.1	59.m08613	AO070303000024	0					-68	-9	ATGCTGTCTGTCACGTCGATCTTGTTACCGATGTCTGGAATCTTCCTGCAGCCTGAATAA			ATGCTGTCTGTCACGTCGATCTTGTTACCGATGTCTGGAATCTTCCTGCAGCCTGAATAA	MLSVTSILLPMSGIFLQPE*			MLSVTSILLPMSGIFLQPE*	TTTTCGGGAG	ACTGCAACAT	0	PT	FG04030.1	0	NCU04512.1	0	0
2018	1301	af	AN8251.1	53.m03716	AO070310000057	0			-184	-125			ATGCGCGCGCACTTCCGCTCTCCCGCCCGAACCACCCCCAGTGACACCACCAAAAGTTAG		ATGCGCGCGCACTTCCGCTCTCCCGCCCGAACCACCCCCAGTGACACCACCAAAAGTTAG		MRAHFRSPARTTPSDTTKS*		MRAHFRSPARTTPSDTTKS*		TCCAGCTCTG	TCTCTTCCTT	0		0	0	0	0	0
2016	1301	an	AN8251.1	53.m03716	AO070310000057	0	-229	-158					ATGCTGAACATTTCATACACAACATCACTTCTTTCAGCACTCTTGAGTCCTCCGCCCGCTCGCTTCTGCTGA	ATGCTGAACATTTCATACACAACATCACTTCTTTCAGCACTCTTGAGTCCTCCGCCCGCTCGCTTCTGCTGA			MLNISYTTSLLSALLSPPPARFC*	MLNISYTTSLLSALLSPPPARFC*			TTCTCTTTCG	AGGCCACACT	0		0	0	0	0	0
2017	1301	an	AN8251.1	53.m03716	AO070310000057	0	-81	-16					ATGACTTCACAGCCAGCTAACCTCGGATCAGTTTATTTTGAGGAAGCTATAGAAAATTATATATAG	ATGACTTCACAGCCAGCTAACCTCGGATCAGTTTATTTTGAGGAAGCTATAGAAAATTATATATAG			MTSQPANLGSVYFEEAIENYI*	MTSQPANLGSVYFEEAIENYI*			GTCCCACCAT	CTGTCTGTCC	0		0	0	0	0	0
2019	1301	ao	AN8251.1	53.m03716	AO070310000057	0					-266	-48	ATGCTCTGGGAAAGTGAACCTAGGGAGAATTGCTTCCAGATTACACATCTTATAGCTCATCCATCCTTCGCCTCGCTTACTGGCTGCAGGGGCGCACTTCCGCTCTTCCGGCCGCAGCGATCAAGTGACACCACCTGTTGGTCCGTGGACTCTCTTTCCCTACACTTTCCAACCTTCACCTTATCTTCTACACCCGCACCCGGGGACATGACCCGCTGA			ATGCTCTGGGAAAGTGAACCTAGGGAGAATTGCTTCCAGATTACACATCTTATAGCTCATCCATCCTTCGCCTCGCTTACTGGCTGCAGGGGCGCACTTCCGCTCTTCCGGCCGCAGCGATCAAGTGACACCACCTGTTGGTCCGTGGACTCTCTTTCCCTACACTTTCCAACCTTCACCTTATCTTCTACACCCGCACCCGGGGACATGACCCGCTGA	MLWESEPRENCFQITHLIAHPSFASLTGCRGALPLFRPQRSSDTTCWSVDSLSLHFPTFTLSSTPAPGDMTR*			MLWESEPRENCFQITHLIAHPSFASLTGCRGALPLFRPQRSSDTTCWSVDSLSLHFPTFTLSSTPAPGDMTR*	CAGAGATTCT	CTTCTACCCA	0		0	0	0	0	0
2021	1302	af	AN2490.1	59.m08499	AO070312000130	0			-200	-180			ATGCCGTCCGCGAAATCCTGA		ATGCCGTCCGCGAAATCCTGA		MPSAKS*		MPSAKS*		CAAGGAGTCA	ACTTCTGAAC	0	R	0	0	0	0	0
2022	1302	af	AN2490.1	59.m08499	AO070312000130	0			-127	-101			ATGCACCCGCGTCGCGTCGAATCTTGA		ATGCACCCGCGTCGCGTCGAATCTTGA		MHPRRVES*		MHPRRVES*		CAAACATCTT	TAGGACTTGG	0	R	0	0	0	0	0
2023	1302	af	AN2490.1	59.m08499	AO070312000130	0			-62	-21			ATGATATATCTTGTGTCCTGTTTCAGTGACCTGTTGGCCTAA		ATGATATATCTTGTGTCCTGTTTCAGTGACCTGTTGGCCTAA		MIYLVSCFSDLLA*		MIYLVSCFSDLLA*		GAGACTTTGC	TAACAAGAGC	0	R	0	0	0	0	0
2024	1302	ao	AN2490.1	59.m08499	AO070312000130	0					-241	-209	ATGTATACTCTCATCATTACTCTAAAAGAATAA			ATGTATACTCTCATCATTACTCTAAAAGAATAA	MYTLIITLKE*			MYTLIITLKE*	AGTGACCTCA	ACATTTAATA	0	R	0	0	0	0	0
2025	1302	ao	AN2490.1	59.m08499	AO070312000130	0					-199	-188	ATGTCGTTATGA			ATGTCGTTATGA	MSL*			MSL*	AACATTTAAT	CATAAAATGT	0	R	0	0	0	0	0
2026	1302	ao	AN2490.1	59.m08499	AO070312000130	0					-170	-117	ATGAATCATGTTTGGTTCCTAACTAACTGCAAACAAAACAAACACTTAAAGTAA			ATGAATCATGTTTGGTTCCTAACTAACTGCAAACAAAACAAACACTTAAAGTAA	MNHVWFLTNCKQNKHLK*			MNHVWFLTNCKQNKHLK*	TGTGAAGCAG	TCTCGCGCCG	0	R	0	0	0	0	0
2027	1302	ao	AN2490.1	59.m08499	AO070312000130	0					-163	-149	ATGTTTGGTTCCTAA			ATGTTTGGTTCCTAA	MFGS*			MFGS*	CAGATGAATC	CTAACTGCAA	0	R	0	0	0	0	0
2035	1303	af	AN6869.1	71.m15260	AO070314000053	0			-113	-66			ATGTGCATGCGACTGTGCGGTCATAAATATATCCATCCTCCTTCGTAG		ATGTGCATGCGACTGTGCGGTCATAAATATATCCATCCTCCTTCGTAG		MCMRLCGHKYIHPPS*		MCMRLCGHKYIHPPS*		TGGACAGGCA	CCTATGGTAT	0	E	0	MG10533.1	0	0	0
2036	1303	af	AN6869.1	71.m15260	AO070314000053	0			-107	-66			ATGCGACTGTGCGGTCATAAATATATCCATCCTCCTTCGTAG		ATGCGACTGTGCGGTCATAAATATATCCATCCTCCTTCGTAG		MRLCGHKYIHPPS*		MRLCGHKYIHPPS*		GGCAATGTGC	CCTATGGTAT	0	E	0	MG10533.1	0	0	0
2028	1303	an	AN6869.1	71.m15260	AO070314000053	0	-191	-180					ATGCATCCGTGA	ATGCATCCGTGA			MHP*	MHP*			TACTGTGGGT	GGGTTGATGA	0	E	0	MG10533.1	0	0	0
2029	1303	an	AN6869.1	71.m15260	AO070314000053	0	-173	-162					ATGATGAGATGA	ATGATGAGATGA			MMR*	MMR*			GTGAGGGTTG	GACCAATCGT	0	E	0	MG10533.1	0	0	0
2030	1303	an	AN6869.1	71.m15260	AO070314000053	0	-165	-127					ATGAGACCAATCGTCTATCCCAAGTCCATGTATCGTTAG	ATGAGACCAATCGTCTATCCCAAGTCCATGTATCGTTAG			MRPIVYPKSMYR*	MRPIVYPKSMYR*			TGATGATGAG	AAGAGATAGC	0	E	0	MG10533.1	0	0	0
2031	1303	an	AN6869.1	71.m15260	AO070314000053	0	-138	-127					ATGTATCGTTAG	ATGTATCGTTAG			MYR*	MYR*			TCCCAAGTCC	AAGAGATAGC	0	E	0	MG10533.1	0	0	0
2032	1303	an	AN6869.1	71.m15260	AO070314000053	0	-95	-63					ATGGGGAGCCCCAATGTATGGGTGCATACATAA	ATGGGGAGCCCCAATGTATGGGTGCATACATAA			MGSPNVWVHT*	MGSPNVWVHT*			CGGCTTTGGA	ATAGCCATCC	0	E	0	MG10533.1	0	0	0
2033	1303	an	AN6869.1	71.m15260	AO070314000053	0	-82	-59					ATGTATGGGTGCATACATAAATAG	ATGTATGGGTGCATACATAAATAG			MYGCIHK*	MYGCIHK*			GGGAGCCCCA	CCATCCCCTC	0	E	0	MG10533.1	0	0	0
2034	1303	an	AN6869.1	71.m15260	AO070314000053	0	-78	-13					ATGGGTGCATACATAAATAGCCATCCCCTCATTTCAAGCTATCCCGTAACCCACCCTCATCCTTAG	ATGGGTGCATACATAAATAGCCATCCCCTCATTTCAAGCTATCCCGTAACCCACCCTCATCCTTAG			MGAYINSHPLISSYPVTHPHP*	MGAYINSHPLISSYPVTHPHP*			GCCCCAATGT	GAAGCACTCA	0	E	0	MG10533.1	0	0	0
2037	1303	ao	AN6869.1	71.m15260	AO070314000053	0					-147	-109	ATGAAGATTATGATTGCCGTGAAAGGGTCACATAAATAG			ATGAAGATTATGATTGCCGTGAAAGGGTCACATAAATAG	MKIMIAVKGSHK*			MKIMIAVKGSHK*	ATTTGAGGGG	CAGATTTGTT	0	E	0	MG10533.1	0	0	0
2038	1303	ao	AN6869.1	71.m15260	AO070314000053	0					-138	-109	ATGATTGCCGTGAAAGGGTCACATAAATAG			ATGATTGCCGTGAAAGGGTCACATAAATAG	MIAVKGSHK*			MIAVKGSHK*	GATGAAGATT	CAGATTTGTT	0	E	0	MG10533.1	0	0	0
2041	1311	ao	AN8363.1	52.m04104	AO070274000030	0					-193	-143	ATGCGGGATATTCGGGGCATATCTATTGATCGGCAAAGGTGCCCTGTATGA			ATGCGGGATATTCGGGGCATATCTATTGATCGGCAAAGGTGCCCTGTATGA	MRDIRGISIDRQRCPV*			MRDIRGISIDRQRCPV*	GGAGACCAGA	AAGAATATCC	0	R	0	0	0	0	0
2045	1322	af	AN4829.1	59.m08969	AO070305000061	0			-175	-149			ATGATAGTGCAGCGTCATGTATGTTAA		ATGATAGTGCAGCGTCATGTATGTTAA		MIVQRHVC*		MIVQRHVC*		GTACCTTAGA	TCCTCCTAAT	0	R	0	0	0	0	0
2046	1322	af	AN4829.1	59.m08969	AO070305000061	0			-159	-127			ATGTATGTTAATCCTCCTAATGTTAATCCATGA		ATGTATGTTAATCCTCCTAATGTTAATCCATGA		MYVNPPNVNP*		MYVNPPNVNP*		GTGCAGCGTC	GAATCCGGCC	0	R	0	0	0	0	0

2047	1322	af	AN4829.1	59.m08969	AO070305000061	0			-155	-54			ATGTTAATCCTCCTAATGTTAATCCATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAA		ATGTTAATCCTCCTAATGTTAATCCATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAA		MLILLMLIHENPAGNPSDFTPEKHHLHRILPTI*		MLILLMLIHENPAGNPSDFTPEKHHLHRILPTI*		AGCGTCATGT	TCCCCTCCCA	0	R	0	0	0	0	0
2048	1322	af	AN4829.1	59.m08969	AO070305000061	0			-140	-54			ATGTTAATCCATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAA		ATGTTAATCCATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAA		MLIHENPAGNPSDFTPEKHHLHRILPTI*		MLIHENPAGNPSDFTPEKHHLHRILPTI*		AATCCTCCTA	TCCCCTCCCA	0	R	0	0	0	0	0
2049	1322	af	AN4829.1	59.m08969	AO070305000061	0			-130	-2			ATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAATCCCCTCCCATCGCCTCAAAGCCACCCTTTTGTGAGTCGTGGAAAAAAGTAA		ATGAGAATCCGGCCGGAAACCCCTCGGATTTCACTCCGGAAAAGCACCATCTCCATCGGATATTACCTACTATATAATCCCCTCCCATCGCCTCAAAGCCACCCTTTTGTGAGTCGTGGAAAAAAGTAA		MRIRPETPRISLRKSTISIGYYLLYNPLPSPQSHPFVSRGKK*		MRIRPETPRISLRKSTISIGYYLLYNPLPSPQSHPFVSRGKK*		ATGTTAATCC	AATGGCCCTA	0	R	0	0	0	0	0
2050	1322	ao	AN4829.1	59.m08969	AO070305000061	0					-213	-193	ATGGATAATTATCCGCCATAG			ATGGATAATTATCCGCCATAG	MDNYPP*			MDNYPP*	TGTAAAATCA	TATGGGAAGA	0	R	0	0	0	0	0
2051	1322	ao	AN4829.1	59.m08969	AO070305000061	0					-191	-171	ATGGGAAGAGATGAGGGGTAA			ATGGGAAGAGATGAGGGGTAA	MGRDEG*			MGRDEG*	CCGCCATAGT	ATCTATCACC	0	R	0	0	0	0	0
2056	1323	af	AN4495.1	57.m05636	AO070311000047	0			-283	-206			ATGGCAAAGCGCGGCGTGTGTAGACCTTGGAATGATCCTGTCATGGTGACTCGGTTTATTTTTATTCGCTGTGTTTAA		ATGGCAAAGCGCGGCGTGTGTAGACCTTGGAATGATCCTGTCATGGTGACTCGGTTTATTTTTATTCGCTGTGTTTAA		MAKRGVCRPWNDPVMVTRFIFIRCV*		MAKRGVCRPWNDPVMVTRFIFIRCV*		CTTACTATTA	TGATTTTGTC	0	L	0	0	0	0	0
2057	1323	af	AN4495.1	57.m05636	AO070311000047	0			-252	-235			ATGATCCTGTCATGGTGA		ATGATCCTGTCATGGTGA		MILSW*		MILSW*		AGACCTTGGA	CTCGGTTTAT	0	L	0	0	0	0	0
2058	1323	af	AN4495.1	57.m05636	AO070311000047	0			-241	-206			ATGGTGACTCGGTTTATTTTTATTCGCTGTGTTTAA		ATGGTGACTCGGTTTATTTTTATTCGCTGTGTTTAA		MVTRFIFIRCV*		MVTRFIFIRCV*		TGATCCTGTC	TGATTTTGTC	0	L	0	0	0	0	0
2059	1323	af	AN4495.1	57.m05636	AO070311000047	0			-206	-174			ATGATTTTGTCTGAACTACACGGATTTTCTTAA		ATGATTTTGTCTGAACTACACGGATTTTCTTAA		MILSELHGFS*		MILSELHGFS*		GCTGTGTTTA	ATTGAATCTC	0	L	0	0	0	0	0
2060	1323	af	AN4495.1	57.m05636	AO070311000047	0			-81	-64			ATGCTTATGATCTCATGA		ATGCTTATGATCTCATGA		MLMIS*		MLMIS*		AATTATTTGC	CTTTATAGCC	0	L	0	0	0	0	0
2061	1323	af	AN4495.1	57.m05636	AO070311000047	0			-75	-64			ATGATCTCATGA		ATGATCTCATGA		MIS*		MIS*		TTGCATGCTT	CTTTATAGCC	0	L	0	0	0	0	0
2062	1323	af	AN4495.1	57.m05636	AO070311000047	0			-67	-56			ATGACTTTATAG		ATGACTTTATAG		MTL*		MTL*		TTATGATCTC	CCCGTATAAA	0	L	0	0	0	0	0
2052	1323	an	AN4495.1	57.m05636	AO070311000047	0	-191	-159					ATGTTTTATTATTTCACTAATGTCACCTGTTAA	ATGTTTTATTATTTCACTAATGTCACCTGTTAA			MFYYFTNVTC*	MFYYFTNVTC*			TAATCCTGTA	GTGTTAAGAC	0	L	0	0	0	0	0
2053	1323	an	AN4495.1	57.m05636	AO070311000047	0	-172	-152					ATGTCACCTGTTAAGTGTTAA	ATGTCACCTGTTAAGTGTTAA			MSPVKC*	MSPVKC*			TATTTCACTA	GACTGAATGT	0	L	0	0	0	0	0
2054	1323	an	AN4495.1	57.m05636	AO070311000047	0	-145	-50					ATGTGTACTGCCGCCGAGCCGCCAACGGCACTAAACCTCCGAAGCAAGCTTGTTTATATCTTCTTCCCTGTACATTCTGCAGCGGTCGAACATTGA	ATGTGTACTGCCGCCGAGCCGCCAACGGCACTAAACCTCCGAAGCAAGCTTGTTTATATCTTCTTCCCTGTACATTCTGCAGCGGTCGAACATTGA			MCTAAEPPTALNLRSKLVYIFFPVHSAAVEH*	MCTAAEPPTALNLRSKLVYIFFPVHSAAVEH*			TTAAGACTGA	ACATGATATT	0	L	0	0	0	0	0
2063	1323	ao	AN4495.1	57.m05636	AO070311000047	0					-185	-90	ATGACCCGTCGTTTTAAGGTTTTTTTTTCTTTTACTTTTCTTGCTTTTATTACACCTCATATCAGAGAAGCGCAAGATGAGATTATACTTATTTGA			ATGACCCGTCGTTTTAAGGTTTTTTTTTCTTTTACTTTTCTTGCTTTTATTACACCTCATATCAGAGAAGCGCAAGATGAGATTATACTTATTTGA	MTRRFKVFFSFTFLAFITPHIREAQDEIILI*			MTRRFKVFFSFTFLAFITPHIREAQDEIILI*	CCCTCCTTTC	CATGGCTTCC	0	L	0	0	0	0	0
2064	1323	ao	AN4495.1	57.m05636	AO070311000047	0					-109	-74	ATGAGATTATACTTATTTGACATGGCTTCCCTCTGA			ATGAGATTATACTTATTTGACATGGCTTCCCTCTGA	MRLYLFDMASL*			MRLYLFDMASL*	GAAGCGCAAG	AACAAACAAG	0	L	0	0	0	0	0
2065	1323	ao	AN4495.1	57.m05636	AO070311000047	0					-88	-74	ATGGCTTCCCTCTGA			ATGGCTTCCCTCTGA	MASL*			MASL*	CTTATTTGAC	AACAAACAAG	0	L	0	0	0	0	0
2068	1329	af	AN8989.1	71.m15101	AO070336000110	0			-226	-164			ATGTACGGATTTCTTATACATTCCTTCTGGGTTTCTACAGTCTTCTGGAATAGCCCACTTTAA		ATGTACGGATTTCTTATACATTCCTTCTGGGTTTCTACAGTCTTCTGGAATAGCCCACTTTAA		MYGFLIHSFWVSTVFWNSPL*		MYGFLIHSFWVSTVFWNSPL*		CCAACTTAAG	AATAACTCTT	0	E	0	0	0	0	0
2069	1329	af	AN8989.1	71.m15101	AO070336000110	0			-140	-108			ATGGCTTGTCTTGGGGCCAACTCTACTCAGTGA		ATGGCTTGTCTTGGGGCCAACTCTACTCAGTGA		MACLGANSTQ*		MACLGANSTQ*		TGCTGGCTAA	CGTCACACCA	0	E	0	0	0	0	0
2070	1329	af	AN8989.1	71.m15101	AO070336000110	0			-83	-33			ATGGGACGAGTGTCTTATCTACCAATTTTCCCCAAGCAATCGCAATCGTAA		ATGGGACGAGTGTCTTATCTACCAATTTTCCCCAAGCAATCGCAATCGTAA		MGRVSYLPIFPKQSQS*		MGRVSYLPIFPKQSQS*		ACCAAGCGTC	TCAACTACAG	0	E	0	0	0	0	0
2066	1329	an	AN8989.1	71.m15101	AO070336000110	0	-192	-169					ATGATGAGGGGGACCGTTGAGTAG	ATGATGAGGGGGACCGTTGAGTAG			MMRGTVE*	MMRGTVE*			GCCACGACCG	ACCTCGTATC	0	E	0	0	0	0	0
2067	1329	an	AN8989.1	71.m15101	AO070336000110	0	-189	-169					ATGAGGGGGACCGTTGAGTAG	ATGAGGGGGACCGTTGAGTAG			MRGTVE*	MRGTVE*			ACGACCGATG	ACCTCGTATC	0	E	0	0	0	0	0
2071	1329	ao	AN8989.1	71.m15101	AO070336000110	0					-290	-261	ATGAACGACGCCCATGAAACATTAAAGTAG			ATGAACGACGCCCATGAAACATTAAAGTAG	MNDAHETLK*			MNDAHETLK*	TAATTAGGGC	GTATTATTGA	0	E	0	0	0	0	0
2072	1329	ao	AN8989.1	71.m15101	AO070336000110	0					-277	-266	ATGAAACATTAA			ATGAAACATTAA	MKH*			MKH*	AACGACGCCC	AGTAGGTATT	0	E	0	0	0	0	0
2073	1329	ao	AN8989.1	71.m15101	AO070336000110	0					-209	-195	ATGGGTGATTGCTAG			ATGGGTGATTGCTAG	MGDC*			MGDC*	TGGTAGGGAT	GCAGATCTTT	0	E	0	0	0	0	0
2076	1331	ao	AN4270.1	65.m07444	AO070277000018	0					-259	-242	ATGTTGGTGCTTAGGTAA			ATGTTGGTGCTTAGGTAA	MLVLR*			MLVLR*	CCTGATATCC	CTGCGGAGTA	0	TU	0	0	0	0	0
2077	1331	ao	AN4270.1	65.m07444	AO070277000018	0					-200	-138	ATGGGATTAGCGCAGGCGCTCCGCGTCCCTGACTGCGGCCGTCGTCACCGGCAGCGCTCCTGA			ATGGGATTAGCGCAGGCGCTCCGCGTCCCTGACTGCGGCCGTCGTCACCGGCAGCGCTCCTGA	MGLAQALRVPDCGRRHRQRS*			MGLAQALRVPDCGRRHRQRS*	CACTATCTAA	CCTTTCATCG	0	TU	0	0	0	0	0
2082	1333	af	AN7481.1	57.m05862	AO070287000038	0			-212	-114			ATGTTTTTAGTTGCGAGACATCAACTCAACGATTTGGTATATCACGTGATATCAACTCCGCCTGGCTCGACGCTAGTCCATATCTGGCACGATCCATGA		ATGTTTTTAGTTGCGAGACATCAACTCAACGATTTGGTATATCACGTGATATCAACTCCGCCTGGCTCGACGCTAGTCCATATCTGGCACGATCCATGA		MFLVARHQLNDLVYHVISTPPGSTLVHIWHDP*		MFLVARHQLNDLVYHVISTPPGSTLVHIWHDP*		TAGATCCAAC	AGCTCAACCT	0	D	0	0	0	0	0
2080	1333	an	AN7481.1	57.m05862	AO070287000038	0	-192	-154					ATGCTATGGAAGTATTCCAGACTGCAAGCAGGTGTTTAA	ATGCTATGGAAGTATTCCAGACTGCAAGCAGGTGTTTAA			MLWKYSRLQAGV*	MLWKYSRLQAGV*			TGTGAGCAAT	GCCCATTGAA	0	D	0	0	0	0	0
2083	1333	ao	AN7481.1	57.m05862	AO070287000038	0					-204	-121	ATGTTGCCCATCCGAATCGAGGAAAGAGTCAACATCGGATCACGTGATCTTATACATGGTGGTGGCACGCTAAGCCCCTTCTAG			ATGTTGCCCATCCGAATCGAGGAAAGAGTCAACATCGGATCACGTGATCTTATACATGGTGGTGGCACGCTAAGCCCCTTCTAG	MLPIRIEERVNIGSRDLIHGGGTLSPF*			MLPIRIEERVNIGSRDLIHGGGTLSPF*	TGGTAGTCGA	TCCAACCATG	0	D	0	0	0	0	0
2084	1333	ao	AN7481.1	57.m05862	AO070287000038	0					-149	-132	ATGGTGGTGGCACGCTAA			ATGGTGGTGGCACGCTAA	MVVAR*			MVVAR*	GATCTTATAC	GCCCCTTCTA	0	D	0	0	0	0	0
2085	1333	ao	AN7481.1	57.m05862	AO070287000038	0					-113		ATGGAATTTGAAGAAATGTTGGAGATCATCCCAAACTGTCGTTGTCGCCATTCCTCCTTCGCCATCAATCTTAATTATACCAAGCAAAGCTCAGTTTCCTATAAATCCCCATAA			ATGGAATTTGAAGAAATGTTGGAGATCATCCCAAACTGTCGTTGTCGCCATTCCTCCTTCGCCATCAATCTTAATTATACCAAGCAAAGCTCAGTTTCCTATAAATCCCCATAA	MEFEEMLEIIPNCRCRHSSFAINLNYTKQSSVSYKSP*			MEFEEMLEIIPNCRCRHSSFAINLNYTKQSSVSYKSP*	TAGTCCAACC	TGTCTCTGCC	0	D	0	0	0	0	0
2086	1333	ao	AN7481.1	57.m05862	AO070287000038	0					-98		ATGTTGGAGATCATCCCAAACTGTCGTTGTCGCCATTCCTCCTTCGCCATCAATCTTAATTATACCAAGCAAAGCTCAGTTTCCTATAAATCCCCATAA			ATGTTGGAGATCATCCCAAACTGTCGTTGTCGCCATTCCTCCTTCGCCATCAATCTTAATTATACCAAGCAAAGCTCAGTTTCCTATAAATCCCCATAA	MLEIIPNCRCRHSSFAINLNYTKQSSVSYKSP*			MLEIIPNCRCRHSSFAINLNYTKQSSVSYKSP*	ATTTGAAGAA	TGTCTCTGCC	0	D	0	0	0	0	0
2087	1340	af	AN9186.1	53.m03966	AO070333000111	0			-287	-246			ATGGTGATCGCTATCCGTCGGCATACGCTAGCCCAAGCTTAA		ATGGTGATCGCTATCCGTCGGCATACGCTAGCCCAAGCTTAA		MVIAIRRHTLAQA*		MVIAIRRHTLAQA*		TTATCAGCCA	CCGAAGCTTT	0	G	0	0	0	0	0
2088	1340	af	AN9186.1	53.m03966	AO070333000111	0			-227	-90			ATGAATCGTGTAAACGAGCTCGCTAAGTCGCTAGTACTTCTCTATTTGTCTTGGCCAATTGCTGATCTCGGCATATACACGTGTGACGCGTTTGTTGACAACGGTCTTCCGACGGAGATAGCAGTCTCCAACAGCTAG		ATGAATCGTGTAAACGAGCTCGCTAAGTCGCTAGTACTTCTCTATTTGTCTTGGCCAATTGCTGATCTCGGCATATACACGTGTGACGCGTTTGTTGACAACGGTCTTCCGACGGAGATAGCAGTCTCCAACAGCTAG		MNRVNELAKSLVLLYLSWPIADLGIYTCDAFVDNGLPTEIAVSNS*		MNRVNELAKSLVLLYLSWPIADLGIYTCDAFVDNGLPTEIAVSNS*		TTGCCAAGTT	ATAAGCAGCT	0	G	0	0	0	0	0
2095	1343	af	AN5486.1	69.m15721	AO070341000397	0			-202	-149			ATGGTTTGCTGGAGAAAGCCCCAGCGACAGTCGGACGGACAGAGGAAAGCCTGA		ATGGTTTGCTGGAGAAAGCCCCAGCGACAGTCGGACGGACAGAGGAAAGCCTGA		MVCWRKPQRQSDGQRKA*		MVCWRKPQRQSDGQRKA*		GTAGATCACG	AGTCGGTAAG	0	E	0	MG06196.1	0	YLR351C	YLR351C
2092	1343	an	AN5486.1	69.m15721	AO070341000397	0	-196	-131					ATGTCTCTGCAATTGTACTTATTGCTGATCCTTATTGGCGAGCAGAACATCGCCGGCAATGACTAA	ATGTCTCTGCAATTGTACTTATTGCTGATCCTTATTGGCGAGCAGAACATCGCCGGCAATGACTAA			MSLQLYLLLILIGEQNIAGND*	MSLQLYLLLILIGEQNIAGND*			CCTGCACTTG	GCTGACAAGA	0	E	0	MG06196.1	0	YLR351C	YLR351C
2093	1343	an	AN5486.1	69.m15721	AO070341000397	0	-138	-118					ATGACTAAGCTGACAAGATGA	ATGACTAAGCTGACAAGATGA			MTKLTR*	MTKLTR*			ATCGCCGGCA	CATCAAGCCC	0	E	0	MG06196.1	0	YLR351C	YLR351C
2094	1343	an	AN5486.1	69.m15721	AO070341000397	0	-121	-41					ATGACATCAAGCCCAAAAGGACGAAGATCGGCAGTATCATCATCTCCAACTCCCGGCTTTCTCCCCGCATTGCTTCAATGA	ATGACATCAAGCCCAAAAGGACGAAGATCGGCAGTATCATCATCTCCAACTCCCGGCTTTCTCCCCGCATTGCTTCAATGA			MTSSPKGRRSAVSSSPTPGFLPALLQ*	MTSSPKGRRSAVSSSPTPGFLPALLQ*			AGCTGACAAG	CAACATTCAT	0	E	0	MG06196.1	0	YLR351C	YLR351C
2096	1343	ao	AN5486.1	69.m15721	AO070341000397	0					-248	-225	ATGGTACTCCAACGACTCGGTTAG			ATGGTACTCCAACGACTCGGTTAG	MVLQRLG*			MVLQRLG*	AATGAATGAA	TGTCCCCGGG	0	E	0	MG06196.1	0	YLR351C	YLR351C
2099	1345	af	AN7563.1	72.m19998	AO070343000404	0			-237	-211			ATGCGAGACGAAGTGCCAGGCTTCTAA		ATGCGAGACGAAGTGCCAGGCTTCTAA		MRDEVPGF*		MRDEVPGF*		CCTGTAAGGA	CAACAGCAGA	0	D	0	0	0	0	0
2100	1345	af	AN7563.1	72.m19998	AO070343000404	0			-192	-178			ATGAACTTGTATTGA		ATGAACTTGTATTGA		MNLY*		MNLY*		GAAGTGTTTT	TTATTGAGTT	0	D	0	0	0	0	0
2101	1345	af	AN7563.1	72.m19998	AO070343000404	0			-163	-152			ATGCAGACATAG		ATGCAGACATAG		MQT*		MQT*		TGAGTTGGTT	TTCCCTACAC	0	D	0	0	0	0	0
2097	1345	an	AN7563.1	72.m19998	AO070343000404	0	-144	-109					ATGCGTGGTCAGATATTCGATATGGACCACCTCTGA	ATGCGTGGTCAGATATTCGATATGGACCACCTCTGA			MRGQIFDMDHL*	MRGQIFDMDHL*			CCCAGGACTG	AGCAGCAACA	0	D	0	0	0	0	0
2098	1345	an	AN7563.1	72.m19998	AO070343000404	0	-123	-109					ATGGACCACCTCTGA	ATGGACCACCTCTGA			MDHL*	MDHL*			GATATTCGAT	AGCAGCAACA	0	D	0	0	0	0	0
2102	1345	ao	AN7563.1	72.m19998	AO070343000404	0					-209	-171	ATGAAACATATTCCGAGGCCTGATGAACTGACCCTCTAA			ATGAAACATATTCCGAGGCCTGATGAACTGACCCTCTAA	MKHIPRPDELTL*			MKHIPRPDELTL*	AGACAGTCTC	TAGGTTCATG	0	D	0	0	0	0	0
2103	1345	ao	AN7563.1	72.m19998	AO070343000404	0					-158	-144	ATGGAGCCGTGTTAA			ATGGAGCCGTGTTAA	MEPC*			MEPC*	GGTTCATGGT	TGATTGTATC	0	D	0	0	0	0	0
2104	1345	ao	AN7563.1	72.m19998	AO070343000404	0					-144	-85	ATGATTGTATCGGTTTTGCGAACTTCTCTTCATATTCACACATCAACACATATACCCTAA			ATGATTGTATCGGTTTTGCGAACTTCTCTTCATATTCACACATCAACACATATACCCTAA	MIVSVLRTSLHIHTSTHIP*			MIVSVLRTSLHIHTSTHIP*	AGCCGTGTTA	TTTATCCACT	0	D	0	0	0	0	0
2107	1347	af	AN1381.1	70.m14842	AO070243000011	0			-250	-206			ATGATTCATCGCTCGGAGCCCGAATGGTTCCAATCTGGTATCTAA		ATGATTCATCGCTCGGAGCCCGAATGGTTCCAATCTGGTATCTAA		MIHRSEPEWFQSGI*		MIHRSEPEWFQSGI*		CAAGGTGCGG	CTAGGCTTCC	0	S	0	0	0	0	0
2105	1347	an	AN1381.1	70.m14842	AO070243000011	0	-194	-147					ATGAATCATCGGCCTTCGGCAGACGCTTTCGACTTGAGCAACGAATAA	ATGAATCATCGGCCTTCGGCAGACGCTTTCGACTTGAGCAACGAATAA			MNHRPSADAFDLSNE*	MNHRPSADAFDLSNE*			TCAGTGTTGG	CCCCACAACT	0	S	0	0	0	0	0
2106	1347	an	AN1381.1	70.m14842	AO070243000011	0	-130	-95					ATGTCCTCCTTCTGCCTCGTTGACTACTCTTTTTAA	ATGTCCTCCTTCTGCCTCGTTGACTACTCTTTTTAA			MSSFCLVDYSF*	MSSFCLVDYSF*			AACTCTGATA	AGGACTTTGT	0	S	0	0	0	0	0
2108	1347	ao	AN1381.1	70.m14842	AO070243000011	0					-242	-39	ATGTCAAAAGTGGGGTGGATTACTTCTGATCGGAGAAGGTGGGAAGAAAGTAGGAATTGTGGCAGAAAAAGAAACAACAATTCTATATGCTTCAGGTCACAAAACACTTCCACAATTCAGTATAAGTCCGGAACTCTTTTCTTGACTACTGATCGGTTCCGAAATCCATTCCTTCTCGCTTTTTCCCTTCTTTGCTATCGTTAA			ATGTCAAAAGTGGGGTGGATTACTTCTGATCGGAGAAGGTGGGAAGAAAGTAGGAATTGTGGCAGAAAAAGAAACAACAATTCTATATGCTTCAGGTCACAAAACACTTCCACAATTCAGTATAAGTCCGGAACTCTTTTCTTGACTACTGATCGGTTCCGAAATCCATTCCTTCTCGCTTTTTCCCTTCTTTGCTATCGTTAA	MSKVGWITSDRRRWEESRNCGRKRNNNSICFRSQNTSTIQYKSGTLFLTTDRFRNPFLLAFSLLCYR*			MSKVGWITSDRRRWEESRNCGRKRNNNSICFRSQNTSTIQYKSGTLFLTTDRFRNPFLLAFSLLCYR*	TGGATGAGAG	ACACCCATTC	0	S	0	0	0	0	0
2109	1347	ao	AN1381.1	70.m14842	AO070243000011	0					-156	-118	ATGCTTCAGGTCACAAAACACTTCCACAATTCAGTATAA			ATGCTTCAGGTCACAAAACACTTCCACAATTCAGTATAA	MLQVTKHFHNSV*			MLQVTKHFHNSV*	ACAATTCTAT	GTCCGGAACT	0	S	0	0	0	0	0
2110	1350	an	AN6262.1	72.m19395	AO070304000027	0	-233	-165					ATGCATCATGAACTTTTCTCGTCGAACAAAGAAAACAACCATTGCCATTGCCAACTACCATCAGCTTGA	ATGCATCATGAACTTTTCTCGTCGAACAAAGAAAACAACCATTGCCATTGCCAACTACCATCAGCTTGA			MHHELFSSNKENNHCHCQLPSA*	MHHELFSSNKENNHCHCQLPSA*			AATCGTCTTT	TATGTAAAGC	0		0	0	0	0	0
2111	1350	an	AN6262.1	72.m19395	AO070304000027	0	-226	-158					ATGAACTTTTCTCGTCGAACAAAGAAAACAACCATTGCCATTGCCAACTACCATCAGCTTGATATGTAA	ATGAACTTTTCTCGTCGAACAAAGAAAACAACCATTGCCATTGCCAACTACCATCAGCTTGATATGTAA			MNFSRRTKKTTIAIANYHQLDM*	MNFSRRTKKTTIAIANYHQLDM*			TTTATGCATC	AGCGCAGCTG	0		0	0	0	0	0
2112	1351	af	AN4491.1	57.m05640	AO070311000043	0			-161	-117			ATGTATACTCCCTTCAGGAGCTCTTGTTTCTCAAGAAGTGACTAA		ATGTATACTCCCTTCAGGAGCTCTTGTTTCTCAAGAAGTGACTAA		MYTPFRSSCFSRSD*		MYTPFRSSCFSRSD*		CTGGCCTCTG	TCCTCAGTTA	0		0	MG04220.1	0	0	0

2113	1351	af	AN4491.1	57.m05640	AO070311000043	0			-92	-51			ATGAACACAGAATTTGATTCAAGGCCATTCACCTTCCCTTAA		ATGAACACAGAATTTGATTCAAGGCCATTCACCTTCCCTTAA		MNTEFDSRPFTFP*		MNTEFDSRPFTFP*		CAAAAATGGC	ATATCCACAA	0		0	MG04220.1	0	0	0
2114	1351	ao	AN4491.1	57.m05640	AO070311000043	0					-187	-176	ATGGTGGTTTGA			ATGGTGGTTTGA	MVV*			MVV*	CTCTATATAA	TGTTCGCTAC	0		0	MG04220.1	0	0	0
2115	1351	ao	AN4491.1	57.m05640	AO070311000043	0					-176	-108	ATGTTCGCTACCCACCTTGCAAAAAAAAAAGTGTACTCCGTTAATTCGCAAGATCAGTTAACTGTTTAA			ATGTTCGCTACCCACCTTGCAAAAAAAAAAGTGTACTCCGTTAATTCGCAAGATCAGTTAACTGTTTAA	MFATHLAKKKVYSVNSQDQLTV*			MFATHLAKKKVYSVNSQDQLTV*	TGGTGGTTTG	CTGCAACAAT	0		0	MG04220.1	0	0	0
2116	1351	ao	AN4491.1	57.m05640	AO070311000043	0					-94	-71	ATGACAAAGAACCTTATGAAATAA			ATGACAAAGAACCTTATGAAATAA	MTKNLMK*			MTKNLMK*	CAACAATGGC	AAGACCTTTT	0		0	MG04220.1	0	0	0
2134	1372	af	AN8032.1	53.m03880	AO070322000129	0			-264	-253			ATGCTCAGGTAG		ATGCTCAGGTAG		MLR*		MLR*		GAGCAACCAG	ACGCATAATC	0	IE	FG06786.1	MG08631.1	0	0	0
2135	1372	af	AN8032.1	53.m03880	AO070322000129	0			-134	-108			ATGAGGGTCGTTACGTCATGTGGATAG		ATGAGGGTCGTTACGTCATGTGGATAG		MRVVTSCG*		MRVVTSCG*		ACAGGACATA	ATGCAGCAGA	0	IE	FG06786.1	MG08631.1	0	0	0
2136	1372	af	AN8032.1	53.m03880	AO070322000129	0			-117	-91			ATGTGGATAGATGCAGCAGACTGGTAA		ATGTGGATAGATGCAGCAGACTGGTAA		MWIDAADW*		MWIDAADW*		TCGTTACGTC	CGGCAGAGGG	0	IE	FG06786.1	MG08631.1	0	0	0
2137	1372	af	AN8032.1	53.m03880	AO070322000129	0			-107	-57			ATGCAGCAGACTGGTAACGGCAGAGGGGCACTGGAATTGCTATTTCAGTAA		ATGCAGCAGACTGGTAACGGCAGAGGGGCACTGGAATTGCTATTTCAGTAA		MQQTGNGRGALELLFQ*		MQQTGNGRGALELLFQ*		ATGTGGATAG	GCGTCCAGCA	0	IE	FG06786.1	MG08631.1	0	0	0
2138	1372	ao	AN8032.1	53.m03880	AO070322000129	0					-248	-189	ATGACACCTGATCCAGAAAGTACTAAAGAACTCAGCTGTACAAACTACGTGATAACATAA			ATGACACCTGATCCAGAAAGTACTAAAGAACTCAGCTGTACAAACTACGTGATAACATAA	MTPDPESTKELSCTNYVIT*			MTPDPESTKELSCTNYVIT*	TAATGGGATG	CCCCTCCTAG	0	IE	FG06786.1	MG08631.1	0	0	0
2141	1373	af	AN1728.1	69.m15042	AO070324000059	0			-141	-124			ATGTCAGCCTGCACGTGA		ATGTCAGCCTGCACGTGA		MSACT*		MSACT*		TCAGTGGTTT	CTGCCTGGTT	0	C	0	0	0	0	0
2142	1373	af	AN1728.1	69.m15042	AO070324000059	0			-73	-56			ATGTCTCCGGTTGCTTGA		ATGTCTCCGGTTGCTTGA		MSPVA*		MSPVA*		CTCCCTGTGG	ACCGCCCCTC	0	C	0	0	0	0	0
2139	1373	an	AN1728.1	69.m15042	AO070324000059	0	-212	-3					ATGCGTGGAGGCAAAGAGACAAGAATCAAAGTTGAAGCTTTGATGTGTTGGGTTGCGTTTGCATATTTTGCATTCTTTGTCATCCAATCACGTGTTGCGGTCACGTGTACTACGCGAAAGCTCCCTTTGGGACGAGGCCGACGTCTATCCTCCCGCCGTCCGATCCGCCCTCCAATTGCCTCACCACTTGTGTTGGGATTGCTGCAATAA	ATGCGTGGAGGCAAAGAGACAAGAATCAAAGTTGAAGCTTTGATGTGTTGGGTTGCGTTTGCATATTTTGCATTCTTTGTCATCCAATCACGTGTTGCGGTCACGTGTACTACGCGAAAGCTCCCTTTGGGACGAGGCCGACGTCTATCCTCCCGCCGTCCGATCCGCCCTCCAATTGCCTCACCACTTGTGTTGGGATTGCTGCAATAA			MRGGKETRIKVEALMCWVAFAYFAFFVIQSRVAVTCTTRKLPLGRGRRLSSRRPIRPPIASPLVLGLLQ*	MRGGKETRIKVEALMCWVAFAYFAFFVIQSRVAVTCTTRKLPLGRGRRLSSRRPIRPPIASPLVLGLLQ*			TGACGGAGAA	ATATGGCCGC	0	C	0	0	0	0	0
2140	1373	an	AN1728.1	69.m15042	AO070324000059	0	-170	-3					ATGTGTTGGGTTGCGTTTGCATATTTTGCATTCTTTGTCATCCAATCACGTGTTGCGGTCACGTGTACTACGCGAAAGCTCCCTTTGGGACGAGGCCGACGTCTATCCTCCCGCCGTCCGATCCGCCCTCCAATTGCCTCACCACTTGTGTTGGGATTGCTGCAATAA	ATGTGTTGGGTTGCGTTTGCATATTTTGCATTCTTTGTCATCCAATCACGTGTTGCGGTCACGTGTACTACGCGAAAGCTCCCTTTGGGACGAGGCCGACGTCTATCCTCCCGCCGTCCGATCCGCCCTCCAATTGCCTCACCACTTGTGTTGGGATTGCTGCAATAA			MCWVAFAYFAFFVIQSRVAVTCTTRKLPLGRGRRLSSRRPIRPPIASPLVLGLLQ*	MCWVAFAYFAFFVIQSRVAVTCTTRKLPLGRGRRLSSRRPIRPPIASPLVLGLLQ*			TGAAGCTTTG	ATATGGCCGC	0	C	0	0	0	0	0
2143	1373	ao	AN1728.1	69.m15042	AO070324000059	0					-126	-109	ATGTCAGCGTGCACGTGA			ATGTCAGCGTGCACGTGA	MSACT*			MSACT*	TGCGTGGCTT	TGTCTCACGT	0	C	0	0	0	0	0
2144	1374	af	AN3028.1	59.m08999	AO070337000070	0			-215	-198			ATGATCATTGATCTTTAG		ATGATCATTGATCTTTAG		MIIDL*		MIIDL*		CCGTGCATAG	GTGCGCTCAA	0	L	0	0	0	0	0
2146	1380	af	AN3167.1	59.m09511	AO070256000023	0			-159	-121			ATGCAAAAATTCCCGCCAACAGCCAGAAAAATTAACTAA		ATGCAAAAATTCCCGCCAACAGCCAGAAAAATTAACTAA		MQKFPPTARKIN*		MQKFPPTARKIN*		TTAGTTTTCG	CCTCCAGCTC	0	AJ	0	0	0	YOR310C	0
2145	1380	an	AN3167.1	59.m09511	AO070256000023	0	-186	-139					ATGCGGGCCACAAGCCACAGCAGGCGCTTTTTCTGCACTTTTTACTGA	ATGCGGGCCACAAGCCACAGCAGGCGCTTTTTCTGCACTTTTTACTGA			MRATSHSRRFFCTFY*	MRATSHSRRFFCTFY*			CTAGCCACAA	CAGCCAAAAA	0	AJ	0	0	0	YOR310C	0
2147	1381	af	AN4390.1	58.m07933	AO070261000036	0			-99	-73			ATGGATTGTCGTCGGACCCTTACTTGA		ATGGATTGTCGTCGGACCCTTACTTGA		MDCRRTLT*		MDCRRTLT*		GCTCGTGAAG	TGCCAACCTG	0		0	0	0	0	0
2148	1381	af	AN4390.1	58.m07933	AO070261000036	0			-73	-50			ATGCCAACCTGCGAAGCCTGCTAA		ATGCCAACCTGCGAAGCCTGCTAA		MPTCEAC*		MPTCEAC*		CCCTTACTTG	TGACATTACT	0		0	0	0	0	0
2150	1381	ao	AN4390.1	58.m07933	AO070261000036	0					-132	-85	ATGTGTTCCCTTGTGTACACCAATATATGGCATTCCGCCCACCATTAA			ATGTGTTCCCTTGTGTACACCAATATATGGCATTCCGCCCACCATTAA	MCSLVYTNIWHSAHH*			MCSLVYTNIWHSAHH*	CATTCATTGA	GCCCTGGTTG	0		0	0	0	0	0
2151	1381	ao	AN4390.1	58.m07933	AO070261000036	0					-106	-50	ATGGCATTCCGCCCACCATTAAGCCCTGGTTGCCTCTCATTTGAAGAAAGACCTTGA			ATGGCATTCCGCCCACCATTAAGCCCTGGTTGCCTCTCATTTGAAGAAAGACCTTGA	MAFRPPLSPGCLSFEERP*			MAFRPPLSPGCLSFEERP*	ACACCAATAT	TCATGTCCAA	0		0	0	0	0	0
2154	1384	af	AN5367.1	72.m19826	AO070296000095	0			-223	-203			ATGTCGAATCCAAATGGTTGA		ATGTCGAATCCAAATGGTTGA		MSNPNG*		MSNPNG*		GCGTCTTGAA	TAATTTGGGA	0		0	0	0	0	0
2155	1384	af	AN5367.1	72.m19826	AO070296000095	0			-210	-160			ATGGTTGATAATTTGGGATGGCGGAGAAACCCGGTGTATGGAGTCTGTTGA		ATGGTTGATAATTTGGGATGGCGGAGAAACCCGGTGTATGGAGTCTGTTGA		MVDNLGWRRNPVYGVC*		MVDNLGWRRNPVYGVC*		TCGAATCCAA	GTATCCACCC	0		0	0	0	0	0
2156	1384	af	AN5367.1	72.m19826	AO070296000095	0			-193	-92			ATGGCGGAGAAACCCGGTGTATGGAGTCTGTTGAGTATCCACCCGCAAAAACTTCTGCCTTCAGGGGCAAAACGTTTCGTGTCAAAGTCGACCACAGACTAG		ATGGCGGAGAAACCCGGTGTATGGAGTCTGTTGAGTATCCACCCGCAAAAACTTCTGCCTTCAGGGGCAAAACGTTTCGTGTCAAAGTCGACCACAGACTAG		MAEKPGVWSLLSIHPQKLLPSGAKRFVSKSTTD*		MAEKPGVWSLLSIHPQKLLPSGAKRFVSKSTTD*		ATAATTTGGG	GTAGAGCTCA	0		0	0	0	0	0
2157	1384	af	AN5367.1	72.m19826	AO070296000095	0			-63	-46			ATGCACGATCATGCATGA		ATGCACGATCATGCATGA		MHDHA*		MHDHA*		ACGAAAGATC	TCAGTCTCTC	0		0	0	0	0	0
2153	1384	an	AN5367.1	72.m19826	AO070296000095	0	-103	-68					ATGGCAAAAGCCACAAACTTGCTTCCATACAAGTGA	ATGGCAAAAGCCACAAACTTGCTTCCATACAAGTGA			MAKATNLLPYK*	MAKATNLLPYK*			TTCAGCACGC	CAAAATCGGC	0		0	0	0	0	0
2160	1386	af	AN8194.1	53.m03779	AO070310000126	0			-188	-90			ATGATGGGGACTAGTCCTATTGTGGTATACTGCAAACACAACAAACGGCGGCAGAACGCAAAGCTGTCCAGAACTCCCACTCCTCCTGAGCTCCGTTGA		ATGATGGGGACTAGTCCTATTGTGGTATACTGCAAACACAACAAACGGCGGCAGAACGCAAAGCTGTCCAGAACTCCCACTCCTCCTGAGCTCCGTTGA		MMGTSPIVVYCKHNKRRQNAKLSRTPTPPELR*		MMGTSPIVVYCKHNKRRQNAKLSRTPTPPELR*		TACCTACTGA	CGTCGCGTGT	0	U	FG06115.1	0	NCU03800.1	0	0
2161	1386	af	AN8194.1	53.m03779	AO070310000126	0			-185	-90			ATGGGGACTAGTCCTATTGTGGTATACTGCAAACACAACAAACGGCGGCAGAACGCAAAGCTGTCCAGAACTCCCACTCCTCCTGAGCTCCGTTGA		ATGGGGACTAGTCCTATTGTGGTATACTGCAAACACAACAAACGGCGGCAGAACGCAAAGCTGTCCAGAACTCCCACTCCTCCTGAGCTCCGTTGA		MGTSPIVVYCKHNKRRQNAKLSRTPTPPELR*		MGTSPIVVYCKHNKRRQNAKLSRTPTPPELR*		CTACTGAATG	CGTCGCGTGT	0	U	FG06115.1	0	NCU03800.1	0	0
2158	1386	an	AN8194.1	53.m03779	AO070310000126	0	-216	-169					ATGAAGCTCTTTACAATTTGCAGGGAAACCATATGTTCAATATTCTAG	ATGAAGCTCTTTACAATTTGCAGGGAAACCATATGTTCAATATTCTAG			MKLFTICRETICSIF*	MKLFTICRETICSIF*			TTACCTACCA	TAGAGGTAAA	0	U	FG06115.1	0	NCU03800.1	0	0
2159	1386	an	AN8194.1	53.m03779	AO070310000126	0	-113	-69					ATGCAAACAAGCCAAACAACACAACAACAGCTGGCCAGAACTTGA	ATGCAAACAAGCCAAACAACACAACAACAGCTGGCCAGAACTTGA			MQTSQTTQQQLART*	MQTSQTTQQQLART*			GCGGAGGCGG	CCCAACTCCA	0	U	FG06115.1	0	NCU03800.1	0	0
2162	1386	ao	AN8194.1	53.m03779	AO070310000126	0					-126	-61	ATGCAAACATGGCAAACACGGCGGAACACACAGCTGGCCAGAACTTCGACTCGCGCCTTGTGCTAA			ATGCAAACATGGCAAACACGGCGGAACACACAGCTGGCCAGAACTTCGACTCGCGCCTTGTGCTAA	MQTWQTRRNTQLARTSTRALC*			MQTWQTRRNTQLARTSTRALC*	GGCATGTATC	ATCAAGACAT	0	U	FG06115.1	0	NCU03800.1	0	0
2167	1387	af	AN1832.1	58.m07674	AO070318000085	0			-203	-177			ATGCATCTTGATGGCTTGCGGCCGTGA		ATGCATCTTGATGGCTTGCGGCCGTGA		MHLDGLRP*		MHLDGLRP*		CAAACGAACC	CCTACTGTTG	0		0	0	0	0	0
2168	1387	af	AN1832.1	58.m07674	AO070318000085	0			-193	-119			ATGGCTTGCGGCCGTGACCTACTGTTGGGGTGGGCCGGTGGCGTGTCTACCCTGATGGCCCAAATCCAACAATGA		ATGGCTTGCGGCCGTGACCTACTGTTGGGGTGGGCCGGTGGCGTGTCTACCCTGATGGCCCAAATCCAACAATGA		MACGRDLLLGWAGGVSTLMAQIQQ*		MACGRDLLLGWAGGVSTLMAQIQQ*		ATGCATCTTG	GTACCTCTCT	0		0	0	0	0	0
2169	1387	af	AN1832.1	58.m07674	AO070318000085	0			-139	-119			ATGGCCCAAATCCAACAATGA		ATGGCCCAAATCCAACAATGA		MAQIQQ*		MAQIQQ*		GTCTACCCTG	GTACCTCTCT	0		0	0	0	0	0
2170	1387	af	AN1832.1	58.m07674	AO070318000085	0			-122	-21			ATGAGTACCTCTCTGGCACCGCGAAAGGAGGCCATCCTCGAGGTATATAAGGATGTTCTACCTCTGGCTACAATGCAAGAGTCACGCACCATCCAACCTTGA		ATGAGTACCTCTCTGGCACCGCGAAAGGAGGCCATCCTCGAGGTATATAAGGATGTTCTACCTCTGGCTACAATGCAAGAGTCACGCACCATCCAACCTTGA		MSTSLAPRKEAILEVYKDVLPLATMQESRTIQP*		MSTSLAPRKEAILEVYKDVLPLATMQESRTIQP*		AAATCCAACA	AAAAGAAAAT	0		0	0	0	0	0
2163	1387	an	AN1832.1	58.m07674	AO070318000085	0	-198	-49					ATGCAAAGTGATGCCATACGCAAGGCATCAGAAGATACGAGGGACCCAAGGAGTTCCATCTCTTGGGGATCCAAGGGTACTCGAGAGTTGAGGAAGAGGAAAGGCATAAATACCGTCAGCATGGCGGCCCTGCATGTCCCTGCAGATTGA	ATGCAAAGTGATGCCATACGCAAGGCATCAGAAGATACGAGGGACCCAAGGAGTTCCATCTCTTGGGGATCCAAGGGTACTCGAGAGTTGAGGAAGAGGAAAGGCATAAATACCGTCAGCATGGCGGCCCTGCATGTCCCTGCAGATTGA			MQSDAIRKASEDTRDPRSSISWGSKGTRELRKRKGINTVSMAALHVPAD*	MQSDAIRKASEDTRDPRSSISWGSKGTRELRKRKGINTVSMAALHVPAD*			AAGACGTGGG	CAGCGGTCGA	0		0	0	0	0	0
2164	1387	an	AN1832.1	58.m07674	AO070318000085	0	-188	-108					ATGCCATACGCAAGGCATCAGAAGATACGAGGGACCCAAGGAGTTCCATCTCTTGGGGATCCAAGGGTACTCGAGAGTTGA	ATGCCATACGCAAGGCATCAGAAGATACGAGGGACCCAAGGAGTTCCATCTCTTGGGGATCCAAGGGTACTCGAGAGTTGA			MPYARHQKIRGTQGVPSLGDPRVLES*	MPYARHQKIRGTQGVPSLGDPRVLES*			ATGCAAAGTG	GGAAGAGGAA	0		0	0	0	0	0
2165	1387	an	AN1832.1	58.m07674	AO070318000085	0	-78	-49					ATGGCGGCCCTGCATGTCCCTGCAGATTGA	ATGGCGGCCCTGCATGTCCCTGCAGATTGA			MAALHVPAD*	MAALHVPAD*			TACCGTCAGC	CAGCGGTCGA	0		0	0	0	0	0
2166	1387	an	AN1832.1	58.m07674	AO070318000085	0	-65	-33					ATGTCCCTGCAGATTGACAGCGGTCGAGCTTGA	ATGTCCCTGCAGATTGACAGCGGTCGAGCTTGA			MSLQIDSGRA*	MSLQIDSGRA*			GCGGCCCTGC	AACCCAGAGC	0		0	0	0	0	0
2172	1387	ao	AN1832.1	58.m07674	AO070318000085	0					-205	-158	ATGAAGATACTCCCGTACGATCGCCCGCAGCTATACCGAAATCTCTGA			ATGAAGATACTCCCGTACGATCGCCCGCAGCTATACCGAAATCTCTGA	MKILPYDRPQLYRNL*			MKILPYDRPQLYRNL*	AGTTATCGAA	ATACGATCCG	0		0	0	0	0	0
2173	1391	af	AN1232.1	70.m14987	AO070331000244	0			-133	-77			ATGCTTTGTGATGGATTTTGGCTTTTGATACTAATCAGCTATTTAGTTGAAGTTTAA		ATGCTTTGTGATGGATTTTGGCTTTTGATACTAATCAGCTATTTAGTTGAAGTTTAA		MLCDGFWLLILISYLVEV*		MLCDGFWLLILISYLVEV*		GTTTTCTGTG	TACTACAGGA	0		0	0	0	0	0
2174	1391	af	AN1232.1	70.m14987	AO070331000244	0			-123	-106			ATGGATTTTGGCTTTTGA		ATGGATTTTGGCTTTTGA		MDFGF*		MDFGF*		ATGCTTTGTG	TACTAATCAG	0		0	0	0	0	0
2175	1392	af	AN3299.1	57.m05363	AO070333000258	0			-293	-273			ATGCGAATAGGGTCGTTGTGA		ATGCGAATAGGGTCGTTGTGA		MRIGSL*		MRIGSL*		ATGTCAGAAC	CTATCTTGTC	0	O	0	0	0	0	0
2176	1392	af	AN3299.1	57.m05363	AO070333000258	0			-229	-113			ATGAATATGCCGGCAATAAGTTTAAGCGGGGCCATTATTGATAAGCAATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAA		ATGAATATGCCGGCAATAAGTTTAAGCGGGGCCATTATTGATAAGCAATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAA		MNMPAISLSGAIIDKQWHYSPQFSRVPLASIVIPPHCC*		MNMPAISLSGAIIDKQWHYSPQFSRVPLASIVIPPHCC*		GCTTATTGTG	CTCCCGTAAG	0	O	0	0	0	0	0
2177	1392	af	AN3299.1	57.m05363	AO070333000258	0			-223	-113			ATGCCGGCAATAAGTTTAAGCGGGGCCATTATTGATAAGCAATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAA		ATGCCGGCAATAAGTTTAAGCGGGGCCATTATTGATAAGCAATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAA		MPAISLSGAIIDKQWHYSPQFSRVPLASIVIPPHCC*		MPAISLSGAIIDKQWHYSPQFSRVPLASIVIPPHCC*		TGTGATGAAT	CTCCCGTAAG	0	O	0	0	0	0	0
2178	1392	af	AN3299.1	57.m05363	AO070333000258	0			-182	-96			ATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAACTCCCGTAAGCTTATAA		ATGGCATTATTCTCCACAATTCTCACGCGTTCCGCTGGCATCTATCGTCATTCCCCCTCACTGTTGCTAACTCCCGTAAGCTTATAA		MALFSTILTRSAGIYRHSPSLLLTPVSL*		MALFSTILTRSAGIYRHSPSLLLTPVSL*		TTGATAAGCA	ATCAACAATC	0	O	0	0	0	0	0
2180	1396	ao	AN5452.1	69.m15743	AO070239000031	0					-272	-261	ATGTCAAACTAG			ATGTCAAACTAG	MSN*			MSN*	TAGAACAAAC	TGTAGCTTCA	0	A	0	MG06457.1	0	0	0
2186	1399	af	AN6524.1	62.m03113	AO070270000023	0			-232	-170			ATGCACGACACAGAGCAGGCTGTAAGAATAATCGTCAGCAGGTGTGGGCTACTGGGCGCCTGA		ATGCACGACACAGAGCAGGCTGTAAGAATAATCGTCAGCAGGTGTGGGCTACTGGGCGCCTGA		MHDTEQAVRIIVSRCGLLGA*		MHDTEQAVRIIVSRCGLLGA*		AGTCTGTAGC	AGGGAATTTA	0		0	0	0	0	0
2187	1399	af	AN6524.1	62.m03113	AO070270000023	0			-116	-99			ATGATGGCTTCTTGTTGA		ATGATGGCTTCTTGTTGA		MMASC*		MMASC*		TGACGCGTGC	TCAGAGACCC	0		0	0	0	0	0
2188	1399	af	AN6524.1	62.m03113	AO070270000023	0			-113	-99			ATGGCTTCTTGTTGA		ATGGCTTCTTGTTGA		MASC*		MASC*		CGCGTGCATG	TCAGAGACCC	0		0	0	0	0	0
2182	1399	an	AN6524.1	62.m03113	AO070270000023	0	-140	-99					ATGGAGACTGGGCCTGACCATGATCGGGCCATTTGTCGATAG	ATGGAGACTGGGCCTGACCATGATCGGGCCATTTGTCGATAG			METGPDHDRAICR*	METGPDHDRAICR*			AGCATTGGAT	TGAAGTCGTA	0		0	0	0	0	0
2183	1399	an	AN6524.1	62.m03113	AO070270000023	0	-121	-59					ATGATCGGGCCATTTGTCGATAGTGAAGTCGTAGTAGCTATGAAGACGAACGGAGGTCGGTAG	ATGATCGGGCCATTTGTCGATAGTGAAGTCGTAGTAGCTATGAAGACGAACGGAGGTCGGTAG			MIGPFVDSEVVVAMKTNGGR*	MIGPFVDSEVVVAMKTNGGR*			GGGCCTGACC	ATGGGCTCTA	0		0	0	0	0	0
2184	1399	an	AN6524.1	62.m03113	AO070270000023	0	-82	-59					ATGAAGACGAACGGAGGTCGGTAG	ATGAAGACGAACGGAGGTCGGTAG			MKTNGGR*	MKTNGGR*			CGTAGTAGCT	ATGGGCTCTA	0		0	0	0	0	0
2189	1399	ao	AN6524.1	62.m03113	AO070270000023	0					-259	-185	ATGTACGGAGTATTCCGTACGCTATCCAGATCCTTATTTCCATATAGCAGGCTGTATCGATGGTTCCAATCGTAA			ATGTACGGAGTATTCCGTACGCTATCCAGATCCTTATTTCCATATAGCAGGCTGTATCGATGGTTCCAATCGTAA	MYGVFRTLSRSLFPYSRLYRWFQS*			MYGVFRTLSRSLFPYSRLYRWFQS*	GGGACACCAT	GTCAATCTAC	0		0	0	0	0	0
2190	1399	ao	AN6524.1	62.m03113	AO070270000023	0					-200	-126	ATGGTTCCAATCGTAAGTCAATCTACGAGATCTATTACCAATATTTGGAGATCTATCCTGTTATGCAGACCTTGA			ATGGTTCCAATCGTAAGTCAATCTACGAGATCTATTACCAATATTTGGAGATCTATCCTGTTATGCAGACCTTGA	MVPIVSQSTRSITNIWRSILLCRP*			MVPIVSQSTRSITNIWRSILLCRP*	GGCTGTATCG	TTATGAAGTC	0		0	0	0	0	0
2191	1399	ao	AN6524.1	62.m03113	AO070270000023	0					-138	-106	ATGCAGACCTTGATTATGAAGTCCCCATATTAA			ATGCAGACCTTGATTATGAAGTCCCCATATTAA	MQTLIMKSPY*			MQTLIMKSPY*	CTATCCTGTT	TCATATCTCT	0		0	0	0	0	0

2192	1399	ao	AN6524.1	62.m03113	AO070270000023	0					-123	-106	ATGAAGTCCCCATATTAA			ATGAAGTCCCCATATTAA	MKSPY*			MKSPY*	GACCTTGATT	TCATATCTCT	0		0	0	0	0	0
2193	1400	an	AN4674.1	71.m15664	AO070284000032	0	-320	-240					ATGGAACACAAGGTTCGACATGAACTGAACAAAAGCGAAGGTCTTTCAGTGCCGGACACTACATACCTAAGTCGGCTGTGA	ATGGAACACAAGGTTCGACATGAACTGAACAAAAGCGAAGGTCTTTCAGTGCCGGACACTACATACCTAAGTCGGCTGTGA			MEHKVRHELNKSEGLSVPDTTYLSRL*	MEHKVRHELNKSEGLSVPDTTYLSRL*			CACTGACTTC	TACAAGAGCC	0	GO	0	0	0	0	0
2195	1400	ao	AN4674.1	71.m15664	AO070284000032	0					-418	-341	ATGTCGCGGGATCGCATGATAGTTGCAAGCCCATTTCCATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAATTAA			ATGTCGCGGGATCGCATGATAGTTGCAAGCCCATTTCCATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAATTAA	MSRDRMIVASPFPCVRGLWLIDVSN*			MSRDRMIVASPFPCVRGLWLIDVSN*	GTTCACAGGT	CTGCCACACT	0	GO	0	0	0	0	0
2196	1400	ao	AN4674.1	71.m15664	AO070284000032	0					-403	-341	ATGATAGTTGCAAGCCCATTTCCATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAATTAA			ATGATAGTTGCAAGCCCATTTCCATGTGTTCGTGGTCTGTGGCTGATCGACGTCAGTAATTAA	MIVASPFPCVRGLWLIDVSN*			MIVASPFPCVRGLWLIDVSN*	GCGGGATCGC	CTGCCACACT	0	GO	0	0	0	0	0
2198	1407	af	AN5983.1	72.m19943	AO070340000297	0			-199	-38			ATGAGTGGCACTTGCATGAGCATCCACTCACAAGCCGAGGTCGCCAGCGGTCAGCTTCATCTAAGAAGCGGAGCGATTCTGGGCAATTCATTTCGTTTCGTTCTGCATCCTTACATCTCCTCCGTCTCGTCCCTCTGTTCGCGATTCTATTCCAAGCGGTGA		ATGAGTGGCACTTGCATGAGCATCCACTCACAAGCCGAGGTCGCCAGCGGTCAGCTTCATCTAAGAAGCGGAGCGATTCTGGGCAATTCATTTCGTTTCGTTCTGCATCCTTACATCTCCTCCGTCTCGTCCCTCTGTTCGCGATTCTATTCCAAGCGGTGA		MSGTCMSIHSQAEVASGQLHLRSGAILGNSFRFVLHPYISSVSSLCSRFYSKR*		MSGTCMSIHSQAEVASGQLHLRSGAILGNSFRFVLHPYISSVSSLCSRFYSKR*		TGATTGTTCT	AACGTCTATT	0	S	0	0	0	0	0
2199	1407	af	AN5983.1	72.m19943	AO070340000297	0			-184	-38			ATGAGCATCCACTCACAAGCCGAGGTCGCCAGCGGTCAGCTTCATCTAAGAAGCGGAGCGATTCTGGGCAATTCATTTCGTTTCGTTCTGCATCCTTACATCTCCTCCGTCTCGTCCCTCTGTTCGCGATTCTATTCCAAGCGGTGA		ATGAGCATCCACTCACAAGCCGAGGTCGCCAGCGGTCAGCTTCATCTAAGAAGCGGAGCGATTCTGGGCAATTCATTTCGTTTCGTTCTGCATCCTTACATCTCCTCCGTCTCGTCCCTCTGTTCGCGATTCTATTCCAAGCGGTGA		MSIHSQAEVASGQLHLRSGAILGNSFRFVLHPYISSVSSLCSRFYSKR*		MSIHSQAEVASGQLHLRSGAILGNSFRFVLHPYISSVSSLCSRFYSKR*		TGGCACTTGC	AACGTCTATT	0	S	0	0	0	0	0
2204	1411	af	AN1013.1	70.m15230	AO070312000015	0			-287	-216			ATGTTTCGAACTAACAAGAATAGTGTAATGATATTCATAGTATTTCTCAAATGTTCTACCGACGCTGCGTAG		ATGTTTCGAACTAACAAGAATAGTGTAATGATATTCATAGTATTTCTCAAATGTTCTACCGACGCTGCGTAG		MFRTNKNSVMIFIVFLKCSTDAA*		MFRTNKNSVMIFIVFLKCSTDAA*		CCCTTGTGCA	CGTTGTCTAT	0	J	0	0	NCU04331.1	0	0
2205	1411	af	AN1013.1	70.m15230	AO070312000015	0			-260	-216			ATGATATTCATAGTATTTCTCAAATGTTCTACCGACGCTGCGTAG		ATGATATTCATAGTATTTCTCAAATGTTCTACCGACGCTGCGTAG		MIFIVFLKCSTDAA*		MIFIVFLKCSTDAA*		GAATAGTGTA	CGTTGTCTAT	0	J	0	0	NCU04331.1	0	0
2206	1411	af	AN1013.1	70.m15230	AO070312000015	0			-237	-133			ATGTTCTACCGACGCTGCGTAGCGTTGTCTATACGGGGTACTTCGTTGTGGTTGTCCCCCCGCTCGTGGCCAACCTCAATTTGCGCTGGGATGCAGCCACGCTAA		ATGTTCTACCGACGCTGCGTAGCGTTGTCTATACGGGGTACTTCGTTGTGGTTGTCCCCCCGCTCGTGGCCAACCTCAATTTGCGCTGGGATGCAGCCACGCTAA		MFYRRCVALSIRGTSLWLSPRSWPTSICAGMQPR*		MFYRRCVALSIRGTSLWLSPRSWPTSICAGMQPR*		TATTTCTCAA	GCGAAACCAT	0	J	0	0	NCU04331.1	0	0
2207	1411	af	AN1013.1	70.m15230	AO070312000015	0			-147	-133			ATGCAGCCACGCTAA		ATGCAGCCACGCTAA		MQPR*		MQPR*		TTGCGCTGGG	GCGAAACCAT	0	J	0	0	NCU04331.1	0	0
2208	1411	ao	AN1013.1	70.m15230	AO070312000015	0					-203	-189	ATGGGTGTAGAATAG			ATGGGTGTAGAATAG	MGVE*			MGVE*	AACCCCGAAG	TCAGCCATCA	0	J	0	0	NCU04331.1	0	0
2209	1421	an	AN6730.1	65.m07240	AO070339000174	0	-107	-84					ATGGCCATCCCGTCCACTGTCTGA	ATGGCCATCCCGTCCACTGTCTGA			MAIPSTV*	MAIPSTV*			TTCATATAGG	TGTTTGACTC	0	F	0	0	0	0	0
2210	1421	an	AN6730.1	65.m07240	AO070339000174	0	-84	-43					ATGTTTGACTCAGGAAACCGTCAATCCCCGCCCATCTTCTAG	ATGTTTGACTCAGGAAACCGTCAATCCCCGCCCATCTTCTAG			MFDSGNRQSPPIF*	MFDSGNRQSPPIF*			CCACTGTCTG	GCTCCCGCAT	0	F	0	0	0	0	0
2212	1433	af	AN5725.1	54.m06845	AO070324000126	0			-113	-72			ATGATCAGTCGGCAGTCGTCAGCCGGACATCCCACCCATTGA		ATGATCAGTCGGCAGTCGTCAGCCGGACATCCCACCCATTGA		MISRQSSAGHPTH*		MISRQSSAGHPTH*		TGAGCCGAAT	CTATTTTCTG	0	M	0	0	NCU06779.1	YNL048W	YNL048W
2214	1433	ao	AN5725.1	54.m06845	AO070324000126	0					-200	-159	ATGAAAGTCATACCATACAATACCATACCGAACTGTTTCTGA			ATGAAAGTCATACCATACAATACCATACCGAACTGTTTCTGA	MKVIPYNTIPNCF*			MKVIPYNTIPNCF*	GTGGGCTTTG	TCGGCACGGA	0	M	0	0	NCU06779.1	YNL048W	YNL048W
2223	1437	af	AN6362.1	69.m15744	AO070337000045	0			-181	-158			ATGAATGTAGCTCGCGCACGCTGA		ATGAATGTAGCTCGCGCACGCTGA		MNVARAR*		MNVARAR*		CGCAAAATAG	TTGGCTGCTG	0		0	0	0	0	0
2224	1437	af	AN6362.1	69.m15744	AO070337000045	0			-129	-118			ATGCTTTTCTAG		ATGCTTTTCTAG		MLF*		MLF*		ACTCTCTTCA	GTATCATTCT	0		0	0	0	0	0
2222	1437	an	AN6362.1	69.m15744	AO070337000045	0	-137	-120					ATGACAACCCCGCAGTGA	ATGACAACCCCGCAGTGA			MTTPQ*	MTTPQ*			TACACTGCCA	CATTTCAACA	0		0	0	0	0	0
2225	1437	ao	AN6362.1	69.m15744	AO070337000045	0					-149	-123	ATGCAGCCAGTCAAAGGAAGCGAGTGA			ATGCAGCCAGTCAAAGGAAGCGAGTGA	MQPVKGSE*			MQPVKGSE*	ATAAAAGTCA	CATACCCCGC	0		0	0	0	0	0
2231	1440	af	AN1870.1	57.m05747	AO070341000187	0			-177	-106			ATGACCTGTCAGTGTCGATCTGTCCCCCGCATTATGCATAGCATTCACGGTCTAGTCCATACATACCAGTAG		ATGACCTGTCAGTGTCGATCTGTCCCCCGCATTATGCATAGCATTCACGGTCTAGTCCATACATACCAGTAG		MTCQCRSVPRIMHSIHGLVHTYQ*		MTCQCRSVPRIMHSIHGLVHTYQ*		ATTGTGGCAG	CCAGGGTACA	0		0	0	0	0	0
2232	1440	af	AN1870.1	57.m05747	AO070341000187	0			-144	-106			ATGCATAGCATTCACGGTCTAGTCCATACATACCAGTAG		ATGCATAGCATTCACGGTCTAGTCCATACATACCAGTAG		MHSIHGLVHTYQ*		MHSIHGLVHTYQ*		CCCCCGCATT	CCAGGGTACA	0		0	0	0	0	0
2226	1440	an	AN1870.1	57.m05747	AO070341000187	0	-259	-212					ATGCTCAGTATCCAAGAAAAGAAAGAAAACATCATGAAGGTGTTGTGA	ATGCTCAGTATCCAAGAAAAGAAAGAAAACATCATGAAGGTGTTGTGA			MLSIQEKKENIMKVL*	MLSIQEKKENIMKVL*			GCACAACCAA	CGGGGACTTC	0		0	0	0	0	0
2227	1440	an	AN1870.1	57.m05747	AO070341000187	0	-226	-212					ATGAAGGTGTTGTGA	ATGAAGGTGTTGTGA			MKVL*	MKVL*			AGAAAACATC	CGGGGACTTC	0		0	0	0	0	0
2228	1440	an	AN1870.1	57.m05747	AO070341000187	0	-192	-160					ATGCAAGCAGCAAGGGAGGATAGAGGAGAATGA	ATGCAAGCAGCAAGGGAGGATAGAGGAGAATGA			MQAAREDRGE*	MQAAREDRGE*			CTGCACGAGA	ATGGATGTTG	0		0	0	0	0	0
2229	1440	an	AN1870.1	57.m05747	AO070341000187	0	-163	-143					ATGAATGGATGTTGGTGTTGA	ATGAATGGATGTTGGTGTTGA			MNGCWC*	MNGCWC*			ATAGAGGAGA	TCGACGTCCA	0		0	0	0	0	0
2230	1440	an	AN1870.1	57.m05747	AO070341000187	0	-155	-111					ATGTTGGTGTTGATCGACGTCCAAGCGTTGCAACCCCAGCTTTGA	ATGTTGGTGTTGATCGACGTCCAAGCGTTGCAACCCCAGCTTTGA			MLVLIDVQALQPQL*	MLVLIDVQALQPQL*			GAATGAATGG	CCCCTCCCAC	0		0	0	0	0	0
2233	1440	ao	AN1870.1	57.m05747	AO070341000187	0					-209	-162	ATGACCGCAACTGACCAAAACACCGCCGATCATGTGCGCAATATCTGA			ATGACCGCAACTGACCAAAACACCGCCGATCATGTGCGCAATATCTGA	MTATDQNTADHVRNI*			MTATDQNTADHVRNI*	ACCCGATACC	TCACCCGCAT	0		0	0	0	0	0
2236	1441	af	AN8445.1	52.m03678	AO070341000302	0			-231	-211			ATGCAACTCCAGCCGGGTTGA		ATGCAACTCCAGCCGGGTTGA		MQLQPG*		MQLQPG*		TCCTGCTTGA	GGTGCCATTC	0	R	0	0	0	0	0
2237	1441	af	AN8445.1	52.m03678	AO070341000302	0			-183	-127			ATGGCGACGCGGGGAATTATTGGCAGTGGCGGGCTTACGGCCCCGATTGGGAAGTAG		ATGGCGACGCGGGGAATTATTGGCAGTGGCGGGCTTACGGCCCCGATTGGGAAGTAG		MATRGIIGSGGLTAPIGK*		MATRGIIGSGGLTAPIGK*		AATTGCTGCG	TGAGGGCCGT	0	R	0	0	0	0	0
2234	1441	an	AN8445.1	52.m03678	AO070341000302	0	-131	-48					ATGAGTATTGCCAGCATTCATCTGGCAAACAGCGGTGCGGTGGCTGGAGTGCAGGACTATAAAAGGACTGCCCTTCCTGCATGA	ATGAGTATTGCCAGCATTCATCTGGCAAACAGCGGTGCGGTGGCTGGAGTGCAGGACTATAAAAGGACTGCCCTTCCTGCATGA			MSIASIHLANSGAVAGVQDYKRTALPA*	MSIASIHLANSGAVAGVQDYKRTALPA*			ACCGATCTGC	AACAAGGGCG	0	R	0	0	0	0	0
2238	1441	ao	AN8445.1	52.m03678	AO070341000302	0					-272	-132	ATGAGGCGTGCTTTTGTTGGCGGATGGCGTTGGAATTTGAAGCACATCGAGGGCGGCGGAGAGGTTGGGAAGAGGGGAAGTGGGAAATTGGGAAATGAGATATGGGAAAAAAGGGTAGTCGCGATTCGGGGGTGGTGCTAA			ATGAGGCGTGCTTTTGTTGGCGGATGGCGTTGGAATTTGAAGCACATCGAGGGCGGCGGAGAGGTTGGGAAGAGGGGAAGTGGGAAATTGGGAAATGAGATATGGGAAAAAAGGGTAGTCGCGATTCGGGGGTGGTGCTAA	MRRAFVGGWRWNLKHIEGGGEVGKRGSGKLGNEIWEKRVVAIRGWC*			MRRAFVGGWRWNLKHIEGGGEVGKRGSGKLGNEIWEKRVVAIRGWC*	CCCTCACGAT	TTTAAGGTAT	0	R	0	0	0	0	0
2239	1441	ao	AN8445.1	52.m03678	AO070341000302	0					-249	-175	ATGGCGTTGGAATTTGAAGCACATCGAGGGCGGCGGAGAGGTTGGGAAGAGGGGAAGTGGGAAATTGGGAAATGA			ATGGCGTTGGAATTTGAAGCACATCGAGGGCGGCGGAGAGGTTGGGAAGAGGGGAAGTGGGAAATTGGGAAATGA	MALEFEAHRGRRRGWEEGKWEIGK*			MALEFEAHRGRRRGWEEGKWEIGK*	TTGTTGGCGG	GATATGGGAA	0	R	0	0	0	0	0
2240	1441	ao	AN8445.1	52.m03678	AO070341000302	0					-178	-155	ATGAGATATGGGAAAAAAGGGTAG			ATGAGATATGGGAAAAAAGGGTAG	MRYGKKG*			MRYGKKG*	AAATTGGGAA	TCGCGATTCG	0	R	0	0	0	0	0
2241	1441	ao	AN8445.1	52.m03678	AO070341000302	0					-171	-127	ATGGGAAAAAAGGGTAGTCGCGATTCGGGGGTGGTGCTAATTTAA			ATGGGAAAAAAGGGTAGTCGCGATTCGGGGGTGGTGCTAATTTAA	MGKKGSRDSGVVLI*			MGKKGSRDSGVVLI*	GAAATGAGAT	GGTATTTAAA	0	R	0	0	0	0	0
2242	1442	ao	AN5512.1	69.m15451	AO070341000384	0					-155	-132	ATGTCCTCTCAACACTGCACGTGA			ATGTCCTCTCAACACTGCACGTGA	MSSQHCT*			MSSQHCT*	ATGCCTCAGG	CCCTTGGGTC	0	R	FG04986.1	0	0	0	0
2248	1448	af	AN3429.1	69.m15368	AO070265000003	0			-133	-101			ATGATGGCAATTGCTTTTCTACCTGAGTCATGA		ATGATGGCAATTGCTTTTCTACCTGAGTCATGA		MMAIAFLPES*		MMAIAFLPES*		TTCGCTGCTG	GATAGTTCTC	0	Q	0	0	0	0	0
2249	1448	af	AN3429.1	69.m15368	AO070265000003	0			-130	-101			ATGGCAATTGCTTTTCTACCTGAGTCATGA		ATGGCAATTGCTTTTCTACCTGAGTCATGA		MAIAFLPES*		MAIAFLPES*		GCTGCTGATG	GATAGTTCTC	0	Q	0	0	0	0	0
2243	1448	an	AN3429.1	69.m15368	AO070265000003	0	-244	-227					ATGATGCCTGACTCCTGA	ATGATGCCTGACTCCTGA			MMPDS*	MMPDS*			ACAAAGTGAT	GGCAGAAACA	0	Q	0	0	0	0	0
2244	1448	an	AN3429.1	69.m15368	AO070265000003	0	-241	-227					ATGCCTGACTCCTGA	ATGCCTGACTCCTGA			MPDS*	MPDS*			AAGTGATATG	GGCAGAAACA	0	Q	0	0	0	0	0
2245	1448	an	AN3429.1	69.m15368	AO070265000003	0	-215	-168					ATGTTAACTAACTACCTAGTTAATTATAAGGGATATCACCCAGATTAA	ATGTTAACTAACTACCTAGTTAATTATAAGGGATATCACCCAGATTAA			MLTNYLVNYKGYHPD*	MLTNYLVNYKGYHPD*			GCAGAAACAA	ACCATCAATT	0	Q	0	0	0	0	0
2246	1448	an	AN3429.1	69.m15368	AO070265000003	0	-150	-85					ATGTCAATCAATAGTGATTTAAAAACTGTACTGATACGCCAACTAGCCTTTCTAGGGCTAGAGTAA	ATGTCAATCAATAGTGATTTAAAAACTGTACTGATACGCCAACTAGCCTTTCTAGGGCTAGAGTAA			MSINSDLKTVLIRQLAFLGLE*	MSINSDLKTVLIRQLAFLGLE*			ATTCTATAAA	CTCTGATGCT	0	Q	0	0	0	0	0
2247	1448	an	AN3429.1	69.m15368	AO070265000003	0	-74	-60					ATGACTCATCGCTAA	ATGACTCATCGCTAA			MTHR*	MTHR*			CTCTGATGCT	ACAGAATATA	0	Q	0	0	0	0	0
2250	1448	ao	AN3429.1	69.m15368	AO070265000003	0					-162	-94	ATGTTACTTACTATTTTGGTCACGAACGGAACCATGCTTCATTCCCTTGGGCATTCGATGCAATCGTGA			ATGTTACTTACTATTTTGGTCACGAACGGAACCATGCTTCATTCCCTTGGGCATTCGATGCAATCGTGA	MLLTILVTNGTMLHSLGHSMQS*			MLLTILVTNGTMLHSLGHSMQS*	GCAGGGAGTC	CATTAGTCAA	0	Q	0	0	0	0	0
2251	1448	ao	AN3429.1	69.m15368	AO070265000003	0					-129	-94	ATGCTTCATTCCCTTGGGCATTCGATGCAATCGTGA			ATGCTTCATTCCCTTGGGCATTCGATGCAATCGTGA	MLHSLGHSMQS*			MLHSLGHSMQS*	GAACGGAACC	CATTAGTCAA	0	Q	0	0	0	0	0
2252	1448	ao	AN3429.1	69.m15368	AO070265000003	0					-105	-94	ATGCAATCGTGA			ATGCAATCGTGA	MQS*			MQS*	TGGGCATTCG	CATTAGTCAA	0	Q	0	0	0	0	0
2253	1448	ao	AN3429.1	69.m15368	AO070265000003	0					-78	-52	ATGACTCACCTATATAATTGTGGTTGA			ATGACTCACCTATATAATTGTGGTTGA	MTHLYNCG*			MTHLYNCG*	GTCAACAGCA	TTATTTATAT	0	Q	0	0	0	0	0
2254	1449	af	AN4425.1	58.m09002	AO070273000062	0			-219	-166			ATGTCTAGACGGTTAAAGTCAAACCCACAGCGGAAGGGAGTGCTCCTCTGCTGA		ATGTCTAGACGGTTAAAGTCAAACCCACAGCGGAAGGGAGTGCTCCTCTGCTGA		MSRRLKSNPQRKGVLLC*		MSRRLKSNPQRKGVLLC*		TTACCCAGGT	GTTAAATGGA	0	L	0	0	0	0	0
2255	1449	af	AN4425.1	58.m09002	AO070273000062	0			-160	-143			ATGGATTGGAAACGGTAG		ATGGATTGGAAACGGTAG		MDWKR*		MDWKR*		GCTGAGTTAA	TATTGCACAC	0	L	0	0	0	0	0
2256	1449	ao	AN4425.1	58.m09002	AO070273000062	0					-195	-118	ATGTTTCACACTGCCCAATATCTACAAGTGTTCTGCCTCAGTCAGGGCTGGGTAGATTGTCGGTTTCTGTACCTATAA			ATGTTTCACACTGCCCAATATCTACAAGTGTTCTGCCTCAGTCAGGGCTGGGTAGATTGTCGGTTTCTGTACCTATAA	MFHTAQYLQVFCLSQGWVDCRFLYL*			MFHTAQYLQVFCLSQGWVDCRFLYL*	TAGTGGAGGT	CTCACCTGAG	0	L	0	0	0	0	0
2259	1452	af	AN4977.1	59.m09403	AO070288000044	0			-82	-62			ATGTCTGCTCACTGTCTGTAG		ATGTCTGCTCACTGTCTGTAG		MSAHCL*		MSAHCL*		CTAAATTGCC	ACTTCAGAGC	0	C	0	0	0	0	0
2257	1452	an	AN4977.1	59.m09403	AO070288000044	0	-178	-125					ATGGTTTTTTCTCGACGGGTCTCTCGCCAGTTGAACCCCATTAGCCCAAAGTGA	ATGGTTTTTTCTCGACGGGTCTCTCGCCAGTTGAACCCCATTAGCCCAAAGTGA			MVFSRRVSRQLNPISPK*	MVFSRRVSRQLNPISPK*			GCGGGCGGCT	TCATTCGCCT	0	C	0	0	0	0	0
2258	1452	an	AN4977.1	59.m09403	AO070288000044	0	-81	-61					ATGTCTCACTGTGCTCTGTAG	ATGTCTCACTGTGCTCTGTAG			MSHCAL*	MSHCAL*			AGCAAGAGTT	ACTCAGCAAG	0	C	0	0	0	0	0
2260	1452	ao	AN4977.1	59.m09403	AO070288000044	0					-71	-51	ATGCATCTGTTCCGCTTATAG			ATGCATCTGTTCCGCTTATAG	MHLFRL*			MHLFRL*	ACCCCTTGTC	GACATCTAAA	0	C	0	0	0	0	0
2264	1454	af	AN5940.1	54.m06971	AO070313000131	0			-187	-98			ATGTTGGGGTCAACGATGCCGGCGATTACAGTCATACTATTGGGTCGCTCGGGTAAGAGTCCAAGTACAGCTTACGCTCCCAGTAGATAA		ATGTTGGGGTCAACGATGCCGGCGATTACAGTCATACTATTGGGTCGCTCGGGTAAGAGTCCAAGTACAGCTTACGCTCCCAGTAGATAA		MLGSTMPAITVILLGRSGKSPSTAYAPSR*		MLGSTMPAITVILLGRSGKSPSTAYAPSR*		CAACAATCAC	ATGTTCGCTC	0	S	0	0	0	0	0
2265	1454	af	AN5940.1	54.m06971	AO070313000131	0			-172	-98			ATGCCGGCGATTACAGTCATACTATTGGGTCGCTCGGGTAAGAGTCCAAGTACAGCTTACGCTCCCAGTAGATAA		ATGCCGGCGATTACAGTCATACTATTGGGTCGCTCGGGTAAGAGTCCAAGTACAGCTTACGCTCCCAGTAGATAA		MPAITVILLGRSGKSPSTAYAPSR*		MPAITVILLGRSGKSPSTAYAPSR*		GGGGTCAACG	ATGTTCGCTC	0	S	0	0	0	0	0
2266	1454	af	AN5940.1	54.m06971	AO070313000131	0			-97	-77			ATGTTCGCTCAGGCTGAGTAG		ATGTTCGCTCAGGCTGAGTAG		MFAQAE*		MFAQAE*		CAGTAGATAA	TAGAAAAGTG	0	S	0	0	0	0	0
2261	1454	an	AN5940.1	54.m06971	AO070313000131	0	-196	-140					ATGACTCATGTTCCAGCCTCAACCGAACTGTGGCCGTATAGAGTAGTATCGACTTAG	ATGACTCATGTTCCAGCCTCAACCGAACTGTGGCCGTATAGAGTAGTATCGACTTAG			MTHVPASTELWPYRVVST*	MTHVPASTELWPYRVVST*			TTTGCAGACA	ATTCTCATCA	0	S	0	0	0	0	0
2262	1454	an	AN5940.1	54.m06971	AO070313000131	0	-189	-151					ATGTTCCAGCCTCAACCGAACTGTGGCCGTATAGAGTAG	ATGTTCCAGCCTCAACCGAACTGTGGCCGTATAGAGTAG			MFQPQPNCGRIE*	MFQPQPNCGRIE*			ACAATGACTC	TATCGACTTA	0	S	0	0	0	0	0
2263	1454	an	AN5940.1	54.m06971	AO070313000131	0	-63	-25					ATGCCACCCAGAGCTACTCTTCTCTTACAATTTCAATAA	ATGCCACCCAGAGCTACTCTTCTCTTACAATTTCAATAA			MPPRATLLLQFQ*	MPPRATLLLQFQ*			TATAGATCCC	AACTCAATGA	0	S	0	0	0	0	0

2267	1454	ao	AN5940.1	54.m06971	AO070313000131	0					-220	-149	ATGATATCTCGTGTGTGGTTGGGGTTCACTGAGGACGAATTACGGACACGGGAAGTGTTGGGATTTAAATAA			ATGATATCTCGTGTGTGGTTGGGGTTCACTGAGGACGAATTACGGACACGGGAAGTGTTGGGATTTAAATAA	MISRVWLGFTEDELRTREVLGFK*			MISRVWLGFTEDELRTREVLGFK*	AACGAATATC	TTCTCAACAC	0	S	0	0	0	0	0
2270	1455	af	AN8682.1	62.m03389	AO070315000102	0			-194	-96			ATGGAGTACTTGGTAGTTGGAGTGATATACTCTTATATCACGTGTCGTGGATCAAGGTCTCTCACCGCTTTCGCAGGTGGAGGCGATTCTGCCGCATAA		ATGGAGTACTTGGTAGTTGGAGTGATATACTCTTATATCACGTGTCGTGGATCAAGGTCTCTCACCGCTTTCGCAGGTGGAGGCGATTCTGCCGCATAA		MEYLVVGVIYSYITCRGSRSLTAFAGGGDSAA*		MEYLVVGVIYSYITCRGSRSLTAFAGGGDSAA*		GAAAGTACCT	AACTAGGGAA	0	J	FG08578.1	0	NCU03159.1	0	0
2271	1455	af	AN8682.1	62.m03389	AO070315000102	0			-81	-55			ATGCTGCATTATTTTTTCGCAGAATAA		ATGCTGCATTATTTTTTCGCAGAATAA		MLHYFFAE*		MLHYFFAE*		AGGGAATTAA	GCGACGAGTC	0	J	FG08578.1	0	NCU03159.1	0	0
2268	1455	an	AN8682.1	62.m03389	AO070315000102	0	-161	-45					ATGGATAAGTGGCGTTGGCGGACCGCAGTGGTCTCTTGCGGCAACTATATGCTATTCACCGCCTCCATACATTCTGCCGCAGAAAATCCGATTTTCTTCACAGCATTTCAACCGTGA	ATGGATAAGTGGCGTTGGCGGACCGCAGTGGTCTCTTGCGGCAACTATATGCTATTCACCGCCTCCATACATTCTGCCGCAGAAAATCCGATTTTCTTCACAGCATTTCAACCGTGA			MDKWRWRTAVVSCGNYMLFTASIHSAAENPIFFTAFQP*	MDKWRWRTAVVSCGNYMLFTASIHSAAENPIFFTAFQP*			AAATGTAGAT	ACTCCAATCG	0	J	FG08578.1	0	NCU03159.1	0	0
2269	1455	an	AN8682.1	62.m03389	AO070315000102	0	-113	-45					ATGCTATTCACCGCCTCCATACATTCTGCCGCAGAAAATCCGATTTTCTTCACAGCATTTCAACCGTGA	ATGCTATTCACCGCCTCCATACATTCTGCCGCAGAAAATCCGATTTTCTTCACAGCATTTCAACCGTGA			MLFTASIHSAAENPIFFTAFQP*	MLFTASIHSAAENPIFFTAFQP*			CGGCAACTAT	ACTCCAATCG	0	J	FG08578.1	0	NCU03159.1	0	0
2272	1455	ao	AN8682.1	62.m03389	AO070315000102	0					-248	-231	ATGCTAGTATGCTACTAG			ATGCTAGTATGCTACTAG	MLVCY*			MLVCY*	GTAGTAGGCT	TAGTAGCGTG	0	J	FG08578.1	0	NCU03159.1	0	0
2277	1456	af	AN0936.1	70.m15567	AO070320000127	0			-123	-94			ATGCCCTTGTGTCGATCGGAACTGTTGTGA		ATGCCCTTGTGTCGATCGGAACTGTTGTGA		MPLCRSELL*		MPLCRSELL*		TTGCGAAGGG	TAGTGGGGAA	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2273	1456	an	AN0936.1	70.m15567	AO070320000127	0	-243	-217					ATGTATCTTATTAGCAGTAGTAAATAA	ATGTATCTTATTAGCAGTAGTAAATAA			MYLISSSK*	MYLISSSK*			ATGAGCTGAC	TGTAGCTGTT	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2274	1456	an	AN0936.1	70.m15567	AO070320000127	0	-181	-164					ATGTACTACTCAGAGTAA	ATGTACTACTCAGAGTAA			MYYSE*	MYYSE*			GGGCTGTAGT	CCGGACATAG	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2275	1456	an	AN0936.1	70.m15567	AO070320000127	0	-153	-136					ATGCCTCTTGGGCGCTAG	ATGCCTCTTGGGCGCTAG			MPLGR*	MPLGR*			CCGGACATAG	TAAACATTGG	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2276	1456	an	AN0936.1	70.m15567	AO070320000127	0	-121	-44					ATGGTGGTCCAGACTAGGCCATCACGGGATCCGTCCACCACTGGCTTTCGGCGACTCGCCGATCGGTCAGTCGACTAA	ATGGTGGTCCAGACTAGGCCATCACGGGATCCGTCCACCACTGGCTTTCGGCGACTCGCCGATCGGTCAGTCGACTAA			MVVQTRPSRDPSTTGFRLADRSVD*	MVVQTRPSRDPSTTGFRRLADRSVD*			CATTGGAACA	TCCGCGGTCG	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2278	1456	ao	AN0936.1	70.m15567	AO070320000127	0					-198	-157	ATGAGCAGGAAGGACTGCAAAGACCCTTATTTTCGACGATAA			ATGAGCAGGAAGGACTGCAAAGACCCTTATTTTCGACGATAA	MSRKDCKDPYFRR*			MSRKDCKDPYFRR*	TAACTTTCGG	GGTTTGTGTA	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2279	1456	ao	AN0936.1	70.m15567	AO070320000127	0					-109	-20	ATGAATCACGAGAGCTTTATTAAAGATCGGGCCGATCGGCAATCGCGTCGTGTTTCACGGGCCAGCTTCGAAAAATTCCTGGTACGATAA			ATGAATCACGAGAGCTTTATTAAAGATCGGGCCGATCGGCAATCGCGTCGTGTTTCACGGGCCAGCTTCGAAAAATTCCTGGTACGATAA	MNHESFIKDRADRQSRRVSRASFEKFLVR*			MNHESFIKDRADRQSRRVSRASFEKFLVR*	AGAAGTGGGG	TATCAACCCC	0	J	FG00749.1	MG01322.1	0	YKL194C	0
2280	1457	af	AN7418.1	57.m05460	AO070323000154	0			-102	-34			ATGGCTGTCCGTTGTAGAACGTGGCTCCTACGAAAGGATTGCAAGCACATGCCTACTCTTCTTTATTGA		ATGGCTGTCCGTTGTAGAACGTGGCTCCTACGAAAGGATTGCAAGCACATGCCTACTCTTCTTTATTGA		MAVRCRTWLLRKDCKHMPTLLY*		MAVRCRTWLLRKDCKHMPTLLY*		AAGTGAAGCT	TATGCAAACT	0	HC	0	0	0	0	0
2282	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-282	-217	ATGAGAGATCTGATAATGCTCCAAAACATTGTCTTTATACGCGTCTCGGTCCCAGGAAAAGCATGA			ATGAGAGATCTGATAATGCTCCAAAACATTGTCTTTATACGCGTCTCGGTCCCAGGAAAAGCATGA	MRDLIMLQNIVFIRVSVPGKA*			MRDLIMLQNIVFIRVSVPGKA*	TTTACTTCTG	TGACGATCTC	0	HC	0	0	0	0	0
2283	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-267	-217	ATGCTCCAAAACATTGTCTTTATACGCGTCTCGGTCCCAGGAAAAGCATGA			ATGCTCCAAAACATTGTCTTTATACGCGTCTCGGTCCCAGGAAAAGCATGA	MLQNIVFIRVSVPGKA*			MLQNIVFIRVSVPGKA*	AGATCTGATA	TGACGATCTC	0	HC	0	0	0	0	0
2284	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-220	-155	ATGATGACGATCTCCATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG			ATGATGACGATCTCCATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG	MMTISMRSKTLAKATSAYSAG*			MMTISMRSKTLAKATSAYSAG*	CAGGAAAAGC	ACAAGGTTGT	0	HC	0	0	0	0	0
2285	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-217	-155	ATGACGATCTCCATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG			ATGACGATCTCCATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG	MTISMRSKTLAKATSAYSAG*			MTISMRSKTLAKATSAYSAG*	GAAAAGCATG	ACAAGGTTGT	0	HC	0	0	0	0	0
2286	1457	ao	AN7418.1	57.m05460	AO070323000154	0					-205	-155	ATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG			ATGAGGTCTAAGACCCTTGCCAAGGCCACGTCTGCATATTCGGCGGGGTAG	MRSKTLAKATSAYSAG*			MRSKTLAKATSAYSAG*	GACGATCTCC	ACAAGGTTGT	0	HC	0	0	0	0	0
2289	1458	af	AN5702.1	54.m06817	AO070324000158	0			-265	-116			ATGGTAATCCTCATACATCTCAATGTGGATAGTGAATACACTGTGCGGGCGGTGAACCAACCATTCCAATCAGTCCAGCCGAGCGGAGAAACTGGATGCCAAGATTTCAACACCCACCTAAATTTTTCGAGGTATCGCAGCTTTCGTTGA		ATGGTAATCCTCATACATCTCAATGTGGATAGTGAATACACTGTGCGGGCGGTGAACCAACCATTCCAATCAGTCCAGCCGAGCGGAGAAACTGGATGCCAAGATTTCAACACCCACCTAAATTTTTCGAGGTATCGCAGCTTTCGTTGA		MVILIHLNVDSEYTVRAVNQPFQSVQPSGETGCQDFNTHLNFSRYRSFR*		MVILIHLNVDSEYTVRAVNQPFQSVQPSGETGCQDFNTHLNFSRYRSFR*		TCCTCCAATT	CGACTTTGAC	0	S	0	0	0	0	0
2290	1458	af	AN5702.1	54.m06817	AO070324000158	0			-243	-211			ATGTGGATAGTGAATACACTGTGCGGGCGGTGA		ATGTGGATAGTGAATACACTGTGCGGGCGGTGA		MWIVNTLCGR*		MWIVNTLCGR*		ATACATCTCA	ACCAACCATT	0	S	0	0	0	0	0
2291	1458	af	AN5702.1	54.m06817	AO070324000158	0			-170	-27			ATGCCAAGATTTCAACACCCACCTAAATTTTTCGAGGTATCGCAGCTTTCGTTGACGACTTTGACTGACCGCTTCTGGACGACCAGCAGGACAAAGCAACGTCCGAATATTGCAACGAGATCGCTCGTGTCTATAATTGGATAG		ATGCCAAGATTTCAACACCCACCTAAATTTTTCGAGGTATCGCAGCTTTCGTTGACGACTTTGACTGACCGCTTCTGGACGACCAGCAGGACAAAGCAACGTCCGAATATTGCAACGAGATCGCTCGTGTCTATAATTGGATAG		MPRFQHPPKFFEVSQLSLTTLTDRFWTTSRTKQRPNIATRSLVSIIG*		MPRFQHPPKFFEVSQLSLTTLTDRFWTTSRTKQRPNIATRSLVSIIG*		GAGAAACTGG	TCTGCGGTCT	0	S	0	0	0	0	0
2288	1458	an	AN5702.1	54.m06817	AO070324000158	0	-191	-39					ATGAAATCCACTATTCGGCCCTGGGCGGTGAAGAACCTCGCAGCCGAGTGGAGAAGCAAATGCCAAGATTTCAAGCCCACCCAGTTTTTTTCAAGCGGGCATATCGCGTTTTCGCTCCTTCGACCGACCGACTCGATACAGAGTACAGACTAG	ATGAAATCCACTATTCGGCCCTGGGCGGTGAAGAACCTCGCAGCCGAGTGGAGAAGCAAATGCCAAGATTTCAAGCCCACCCAGTTTTTTTCAAGCGGGCATATCGCGTTTTCGCTCCTTCGACCGACCGACTCGATACAGAGTACAGACTAG			MKSTIRPWAVKNLAAEWRSKCQDFKPTQFFSSGHIAFSLLRPTDSIQSTD*	MKSTIRPWAVKNLAAEWRSKCQDFKPTQFFSSGHIAFSLLRPTDSIQSTD*			GAAGAATACA	TTCAACGTCC	0	S	0	0	0	0	0
2292	1458	ao	AN5702.1	54.m06817	AO070324000158	0					-221	-6	ATGATAAGTCAGCAAGCCCACGATGTGGCAGGCGGTGAACCACTAGCAAAAAGCAAGCGGAGAAAAAGAATGCCAAGATTTCGAACCGCCCACCCAATTTTTTCGAGAGTTATCGCGTCCATACTACAAAAAAACCCCCCTCAACGTCCAGGTGACAATCACCCAATCCTACATAATACCCGGAACGGAGCTACTGTGAATCTCCGATTCAAGTAG			ATGATAAGTCAGCAAGCCCACGATGTGGCAGGCGGTGAACCACTAGCAAAAAGCAAGCGGAGAAAAAGAATGCCAAGATTTCGAACCGCCCACCCAATTTTTTCGAGAGTTATCGCGTCCATACTACAAAAAAACCCCCCTCAACGTCCAGGTGACAATCACCCAATCCTACATAATACCCGGAACGGAGCTACTGTGAATCTCCGATTCAAGTAG	MISQQAHDVAGGEPLAKSKRRKRMPRFRTAHPIFSRVIASILQKNPPQRPGDNHPILHNTRNGATVNLRFK*			MISQQAHDVAGGEPLAKSKRRKRMPRFRTAHPIFSRVIASILQKNPPQRPGDNHPILHNTRNGATVNLRFK*	ATTAGTCGAC	GAAAAATGGA	0	S	0	0	0	0	0
2293	1458	ao	AN5702.1	54.m06817	AO070324000158	0					-199	-176	ATGTGGCAGGCGGTGAACCACTAG			ATGTGGCAGGCGGTGAACCACTAG	MWQAVNH*			MWQAVNH*	CAAGCCCACG	CAAAAAGCAA	0	S	0	0	0	0	0
2294	1458	ao	AN5702.1	54.m06817	AO070324000158	0					-152	-6	ATGCCAAGATTTCGAACCGCCCACCCAATTTTTTCGAGAGTTATCGCGTCCATACTACAAAAAAACCCCCCTCAACGTCCAGGTGACAATCACCCAATCCTACATAATACCCGGAACGGAGCTACTGTGAATCTCCGATTCAAGTAG			ATGCCAAGATTTCGAACCGCCCACCCAATTTTTTCGAGAGTTATCGCGTCCATACTACAAAAAAACCCCCCTCAACGTCCAGGTGACAATCACCCAATCCTACATAATACCCGGAACGGAGCTACTGTGAATCTCCGATTCAAGTAG	MPRFRTAHPIFSRVIASILQKNPPQRPGDNHPILHNTRNGATVNLRFK*			MPRFRTAHPIFSRVIASILQKNPPQRPGDNHPILHNTRNGATVNLRFK*	GAGAAAAAGA	GAAAAATGGA	0	S	0	0	0	0	0
2295	1465	af	AN4331.1	58.m07989	AO070240000009	0			-123	-91			ATGTTCCTAGCAGAAAGTGGGTCCGGGCGGTGA		ATGTTCCTAGCAGAAAGTGGGTCCGGGCGGTGA		MFLAESGSGR*		MFLAESGSGR*		CCCAGCGCCA	GCACAGCTGG	0	L	0	0	0	0	0
2296	1465	ao	AN4331.1	58.m07989	AO070240000009	0					-137	-48	ATGGTTTTGAAGATAAAAGTGGGTCTAGGCGGTGAAGAGAGCTCGGCTCAACTGCGATTAGATAGTGATTGGGTTGATGACTACGACTAG			ATGGTTTTGAAGATAAAAGTGGGTCTAGGCGGTGAAGAGAGCTCGGCTCAACTGCGATTAGATAGTGATTGGGTTGATGACTACGACTAG	MVLKIKVGLGGEESSAQLRLDSDWVDDYD*			MVLKIKVGLGGEESSAQLRLDSDWVDDYD*	ATTCCCAGTG	TAGTACCTAC	0	L	0	0	0	0	0
2297	1465	ao	AN4331.1	58.m07989	AO070240000009	0					-61	-29	ATGACTACGACTAGTAGTACCTACCGCTTTTGA			ATGACTACGACTAGTAGTACCTACCGCTTTTGA	MTTTSSTYRF*			MTTTSSTYRF*	GATTGGGTTG	AGTCCCGCCT	0	L	0	0	0	0	0
2301	1471	af	AN0042.1	71.m15317	AO070314000121	0			-70	-50			ATGCGGCATAGGATGTTCTGA		ATGCGGCATAGGATGTTCTGA		MRHRMF*		MRHRMF*		TGCTGGCTTC	GTCTGGACGC	0	P	0	0	0	0	0
2298	1471	an	AN0042.1	71.m15317	AO070314000121	0	-110	-72					ATGAGAGTCCATCTGCCTCAATGCCAAGGGTGGAAGTAA	ATGAGAGTCCATCTGCCTCAATGCCAAGGGTGGAAGTAA			MRVHLPQCQGWK*	MRVHLPQCQGWK*			CATTACTCGA	CCTTCACTGC	0	P	0	0	0	0	0
2299	1471	an	AN0042.1	71.m15317	AO070314000121	0	-90	-52					ATGCCAAGGGTGGAAGTAACCTTCACTGCATGTGCCTGA	ATGCCAAGGGTGGAAGTAACCTTCACTGCATGTGCCTGA			MPRVEVTFTACA*	MPRVEVTFTACA*			ATCTGCCTCA	ATTAGTTTCT	0	P	0	0	0	0	0
2300	1471	an	AN0042.1	71.m15317	AO070314000121	0	-61	-47					ATGTGCCTGAATTAG	ATGTGCCTGAATTAG			MCLN*	MCLN*			CCTTCACTGC	TTTCTTGCTT	0	P	0	0	0	0	0
2302	1472	an	AN8709.1	62.m03360	AO070315000136	0	-163	-95					ATGCAATGCAGATATAGAGTGCATAGTTTTCAACTTGACTCATTATTACTACGGGACGATCTCGCCTAG	ATGCAATGCAGATATAGAGTGCATAGTTTTCAACTTGACTCATTATTACTACGGGACGATCTCGCCTAG			MQCRYRVHSFQLDSLLLRDDLA*	MQCRYRVHSFQLDSLLLRDDLA*			TTTGGTACAA	TATAAGACCG	0	E	0	MG04156.1	0	0	0
2303	1472	an	AN8709.1	62.m03360	AO070315000136	0	-158	-147					ATGCAGATATAG	ATGCAGATATAG			MQI*	MQI*			TACAAATGCA	AGTGCATAGT	0	E	0	MG04156.1	0	0	0
2304	1472	ao	AN8709.1	62.m03360	AO070315000136	0					-237	-205	ATGCCACTACTAATATATCACACTAGCCATTGA			ATGCCACTACTAATATATCACACTAGCCATTGA	MPLLIYHTSH*			MPLLIYHTSH*	TATCGGGCCA	GTCATGCAGA	0	E	0	MG04156.1	0	0	0
2305	1472	ao	AN8709.1	62.m03360	AO070315000136	0					-201	-175	ATGCAGAAAACCAATTCTGTAATCTGA			ATGCAGAAAACCAATTCTGTAATCTGA	MQKTNSVI*			MQKTNSVI*	CCATTGAGTC	TTACTTATTT	0	E	0	MG04156.1	0	0	0
2313	1473	af	AN5307.1	70.m15393	AO070316000053	0			-262	-242			ATGTCTGTCTATTCTTCTTGA		ATGTCTGTCTATTCTTCTTGA		MSVYSS*		MSVYSS*		GAGGAAAACA	TTTTCACGAG	0	C	0	0	0	0	0
2314	1473	af	AN5307.1	70.m15393	AO070316000053	0			-180	-148			ATGTATTTGGCACTATTTGGCACGGGCAAGTGA		ATGTATTTGGCACTATTTGGCACGGGCAAGTGA		MYLALFGTGK*		MYLALFGTGK*		TCCACGTTCC	GGTCATCATG	0	C	0	0	0	0	0
2315	1473	af	AN5307.1	70.m15393	AO070316000053	0			-140	-66			ATGAGTTCAGGCCCGGGTTTCACCGTGGGAAGGACTGCGCAAAAAAGCTTACTTTCACAGATAAAAATAAAATGA		ATGAGTTCAGGCCCGGGTTTCACCGTGGGAAGGACTGCGCAAAAAAGCTTACTTTCACAGATAAAAATAAAATGA		MSSGPGFTVGRTAQKSLLSQIKIK*		MSSGPGFTVGRTAQKSLLSQIKIK*		TGAGGTCATC	TAACAGATCC	0	C	0	0	0	0	0
2316	1473	af	AN5307.1	70.m15393	AO070316000053	0			-69	-43			ATGATAACAGATCCAAGGCAGTCATAA		ATGATAACAGATCCAAGGCAGTCATAA		MITDPRQS*		MITDPRQS*		TAAAAATAAA	AATAGTGCTA	0	C	0	0	0	0	0
2306	1473	an	AN5307.1	70.m15393	AO070316000053	0	-214	-122					ATGAGGGCGATGCAAATCGCAGACTGCTTCAGTTGTATTTATTCTTTTCTATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAG	ATGAGGGCGATGCAAATCGCAGACTGCTTCAGTTGTATTTATTCTTTTCTATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAG			MRAMQIADCFSCIYSFLWRWAPLSMVAVPG*	MRAMQIADCFSCIYSFLWRWAPLSMVAVPG*			CTGGAATGTT	TTTGAGGGTA	0	C	0	0	0	0	0
2307	1473	an	AN5307.1	70.m15393	AO070316000053	0	-205	-122					ATGCAAATCGCAGACTGCTTCAGTTGTATTTATTCTTTTCTATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAG	ATGCAAATCGCAGACTGCTTCAGTTGTATTTATTCTTTTCTATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAG			MQIADCFSCIYSFLWRWAPLSMVAVPG*	MQIADCFSCIYSFLWRWAPLSMVAVPG*			TATGAGGGCG	TTTGAGGGTA	0	C	0	0	0	0	0
2308	1473	an	AN5307.1	70.m15393	AO070316000053	0	-164	-117					ATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAGTTTGA	ATGGAGATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAGTTTGA			MEMGSTVYGCRARLV*	MEMGSTVYGCRARLV*			ATTCTTTTCT	GGGTAATGAG	0	C	0	0	0	0	0
2309	1473	an	AN5307.1	70.m15393	AO070316000053	0	-158	-117					ATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAGTTTGA	ATGGGCTCCACTGTCTATGGTTGCCGTGCCCGGTTAGTTTGA			MGSTVYGCRARLV*	MGSTVYGCRARLV*			TTCTATGGAG	GGGTAATGAG	0	C	0	0	0	0	0
2310	1473	an	AN5307.1	70.m15393	AO070316000053	0	-142	-122					ATGGTTGCCGTGCCCGGTTAG	ATGGTTGCCGTGCCCGGTTAG			MVAVPG*	MVAVPG*			TCCACTGTCT	TTTGAGGGTA	0	C	0	0	0	0	0
2311	1473	an	AN5307.1	70.m15393	AO070316000053	0	-111	-100					ATGAGGTCATAA	ATGAGGTCATAA			MRS*	MRS*			TTTGAGGGTA	GTATGTATTT	0	C	0	0	0	0	0
2317	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-275	-261	ATGGAAGCAGGATAG			ATGGAAGCAGGATAG	MEAG*			MEAG*	CTTCGGTGAG	AAGCCTCGAA	0	C	0	0	0	0	0
2318	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-207	-178	ATGTGCTTCCGATTCCTTCCACCGCCCTAA			ATGTGCTTCCGATTCCTTCCACCGCCCTAA	MCFRFLPPP*			MCFRFLPPP*	GTGGACATTG	CTTTTTGTTT	0	C	0	0	0	0	0

2319	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-165	-16	ATGCACCGAGGAGATGAGGTCATCATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAAACAACTACATAAAAAGCTCTTCGATCAATATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA			ATGCACCGAGGAGATGAGGTCATCATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAAACAACTACATAAAAAGCTCTTCGATCAATATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA	MHRGDEVIMCSEPKTHCGFAFDRRTLNNYIKSSSINMSVSATPPGEAGS*			MHRGDEVIMCSEPKTHCGFAFDRRTLNNYIKSSSINMSVSATPPGEAGS*	TTTTGTTTCC	AATAATATAC	0	C	0	0	0	0	0
2320	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-152	-87	ATGAGGTCATCATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAA			ATGAGGTCATCATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAA	MRSSCVQNQRLIVVLLSIVEP*			MRSSCVQNQRLIVVLLSIVEP*	CACCGAGGAG	ACAACTACAT	0	C	0	0	0	0	0
2321	1473	ao	AN5307.1	70.m15393	AO070316000053	0					-141	-16	ATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAAACAACTACATAAAAAGCTCTTCGATCAATATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA			ATGTGTTCAGAACCAAAGACTCATTGTGGTTTTGCTTTCGATCGTCGAACCTTAAACAACTACATAAAAAGCTCTTCGATCAATATGTCAGTGTCTGCAACTCCACCCGGAGAGGCTGGTTCCTAA	MCSEPKTHCGFAFDRRTLNNYIKSSSINMSVSATPPGEAGS*			MCSEPKTHCGFAFDRRTLNNYIKSSSINMSVSATPPGEAGS*	TGAGGTCATC	AATAATATAC	0	C	0	0	0	0	0
2323	1474	an	AN0931.1	70.m15539	AO070320000122	0	-110	-93					ATGTTCCCGAGCCGCTGA	ATGTTCCCGAGCCGCTGA			MFPSR*	MFPSR*			TTTCCAATTC	GCATTGTCAG	0	T	0	0	0	0	0
2324	1474	ao	AN0931.1	70.m15539	AO070320000122	0					-111	-76	ATGACTGACATTGCCTGGATTTGCGACATCGCTTGA			ATGACTGACATTGCCTGGATTTGCGACATCGCTTGA	MTDIAWICDIA*			MTDIAWICDIA*	ACGTCCTTTC	AGCCATTGGG	0	T	0	0	0	0	0
2325	1484	af	AN5638.1	58.m07325	AO070342000239	0			-212	-117			ATGCTGTTTGATGATTATTCTTCGAGCGCTGCAATTGTTCTACAGTTGTATGGCGTTGGTCCCATAGATGGCATTACCGATCTCAGCATCTCTTAA		ATGCTGTTTGATGATTATTCTTCGAGCGCTGCAATTGTTCTACAGTTGTATGGCGTTGGTCCCATAGATGGCATTACCGATCTCAGCATCTCTTAA		MLFDDYSSSAAIVLQLYGVGPIDGITDLSIS*		MLFDDYSSSAAIVLQLYGVGPIDGITDLSIS*		GGAGGGGCGA	TTGATAACAT	0	TO	0	0	0	0	0
2326	1484	af	AN5638.1	58.m07325	AO070342000239	0			-202	-146			ATGATTATTCTTCGAGCGCTGCAATTGTTCTACAGTTGTATGGCGTTGGTCCCATAG		ATGATTATTCTTCGAGCGCTGCAATTGTTCTACAGTTGTATGGCGTTGGTCCCATAG		MIILRALQLFYSCMALVP*		MIILRALQLFYSCMALVP*		ATGCTGTTTG	ATGGCATTAC	0	TO	0	0	0	0	0
2327	1484	af	AN5638.1	58.m07325	AO070342000239	0			-163	-146			ATGGCGTTGGTCCCATAG		ATGGCGTTGGTCCCATAG		MALVP*		MALVP*		CTACAGTTGT	ATGGCATTAC	0	TO	0	0	0	0	0
2328	1484	af	AN5638.1	58.m07325	AO070342000239	0			-145	-113			ATGGCATTACCGATCTCAGCATCTCTTAATTGA		ATGGCATTACCGATCTCAGCATCTCTTAATTGA		MALPISASLN*		MALPISASLN*		GGTCCCATAG	TAACATTTAT	0	TO	0	0	0	0	0
2329	1484	ao	AN5638.1	58.m07325	AO070342000239	0					-130	-50	ATGGCATACCAACAGCAACATTTTCCACAGTTTCATAGCTTGCGTTCTTTTCATAATTCTTTTCTCTTTTCCTTATCTTGA			ATGGCATACCAACAGCAACATTTTCCACAGTTTCATAGCTTGCGTTCTTTTCATAATTCTTTTCTCTTTTCCTTATCTTGA	MAYQQQHFPQFHSLRSFHNSFLFSLS*			MAYQQQHFPQFHSLRSFHNSFLFSLS*	AGATCTTGAG	TTTATAATTA	0	TO	0	0	0	0	0
2330	1485	af	AN6339.1	72.m19459	AO070236000015	0			-192	-73			ATGGGAGGGATCTCAGACCTGACTGTGATTGAACATCAATATTTGCAGTTTATGCCTTCGCCAGAGGCATTGAGAAGCTCACAGGCTAGCTTACCAGCCAACGCCTCGAGGACGTTTTGA		ATGGGAGGGATCTCAGACCTGACTGTGATTGAACATCAATATTTGCAGTTTATGCCTTCGCCAGAGGCATTGAGAAGCTCACAGGCTAGCTTACCAGCCAACGCCTCGAGGACGTTTTGA		MGGISDLTVIEHQYLQFMPSPEALRSSQASLPANASRTF*		MGGISDLTVIEHQYLQFMPSPEALRSSQASLPANASRTF*		CCCGTCTGCA	GTCCGCTCTG	0	T	0	0	0	0	0
2331	1485	af	AN6339.1	72.m19459	AO070236000015	0			-141	-73			ATGCCTTCGCCAGAGGCATTGAGAAGCTCACAGGCTAGCTTACCAGCCAACGCCTCGAGGACGTTTTGA		ATGCCTTCGCCAGAGGCATTGAGAAGCTCACAGGCTAGCTTACCAGCCAACGCCTCGAGGACGTTTTGA		MPSPEALRSSQASLPANASRTF*		MPSPEALRSSQASLPANASRTF*		TTTGCAGTTT	GTCCGCTCTG	0	T	0	0	0	0	0
2334	1491	af	AN6244.1	72.m19413	AO070304000098	0			-224	-192			ATGGACCTTTTTTTATTGATATCCTTTGCATAG		ATGGACCTTTTTTTATTGATATCCTTTGCATAG		MDLFLLISFA*		MDLFLLISFA*		TAGTTCTCCT	CCCACAATTG	0	J	0	0	0	0	0
2336	1497	af	AN5721.1	54.m07020	AO070324000129	0			-250	-227			ATGATAACGTCATGTGATAGATAA		ATGATAACGTCATGTGATAGATAA		MITSCDR*		MITSCDR*		GGCATGGGAA	CGTATCGTAT	0	S	0	0	0	0	0
2337	1497	af	AN5721.1	54.m07020	AO070324000129	0			-218	-201			ATGGTAATATGGAACTAA		ATGGTAATATGGAACTAA		MVIWN*		MVIWN*		AACGTATCGT	GTTGGTAAGG	0	S	0	0	0	0	0
2338	1497	af	AN5721.1	54.m07020	AO070324000129	0			-210	-193			ATGGAACTAAGTTGGTAA		ATGGAACTAAGTTGGTAA		MELSW*		MELSW*		GTATGGTAAT	GGTACCGTAC	0	S	0	0	0	0	0
2339	1497	af	AN5721.1	54.m07020	AO070324000129	0			-133	-32			ATGTCTGTGGTCTTCGTTCTCCTCTCCAGATATCTGCCAGAAACAGATCATTTAAGGATTGATCGCCTTCAAGTAATTTGGTGTGGAGTATTACTGACATAG		ATGTCTGTGGTCTTCGTTCTCCTCTCCAGATATCTGCCAGAAACAGATCATTTAAGGATTGATCGCCTTCAAGTAATTTGGTGTGGAGTATTACTGACATAG		MSVVFVLLSRYLPETDHLRIDRLQVIWCGVLLT*		MSVVFVLLSRYLPETDHLRIDRLQVIWCGVLLT*		TTGTGTCGTC	AGTCTCATCG	0	S	0	0	0	0	0
2335	1497	an	AN5721.1	54.m07020	AO070324000129	0	-211	-53					ATGGTATTTGTAGTGGGATACTCCGCACTAAGCCGGTTTCGGATCCCGCCATTAAGTCCATTGTCGTCATCCCCGCAGTCACAAAATCTCTATTCTACTATACTCCAACATCTAATACTATCTGGAGGGGCTATTGCAAGAGGCAACACATGGTCATAA	ATGGTATTTGTAGTGGGATACTCCGCACTAAGCCGGTTTCGGATCCCGCCATTAAGTCCATTGTCGTCATCCCCGCAGTCACAAAATCTCTATTCTACTATACTCCAACATCTAATACTATCTGGAGGGGCTATTGCAAGAGGCAACACATGGTCATAA			MVFVVGYSALSRFRIPPLSPLSSSPQSQNLYSTILQHLILSGGAIARGNTWS*	MVFVVGYSALSRFRIPPLSPLSSSPQSQNLYSTILQHLILSGGAIARGNTWS*			CGGTACCAGA	CGCATTTTCA	0	S	0	0	0	0	0
2340	1497	ao	AN5721.1	54.m07020	AO070324000129	0					-231	-184	ATGACGGCTTATCATGTGATACCGTATTGTTTTGTCTTCGTATCGTAA			ATGACGGCTTATCATGTGATACCGTATTGTTTTGTCTTCGTATCGTAA	MTAYHVIPYCFVFVS*			MTAYHVIPYCFVFVS*	GACCCCAGCC	CGTCGTACCG	0	S	0	0	0	0	0
2341	1497	ao	AN5721.1	54.m07020	AO070324000129	0					-173	-27	ATGTCCCGCGCTAATCCCAAGCAGGCTGTGTCGTCATTCCCCGCGGTTGTAAATGAACAAAAAAGCACTTTTTACTGCTTATACATCAAAAAAACCAAATCACCAATTCCCCGCGCGGGCCTCAATAATCACACTACGCTTGGCTGA			ATGTCCCGCGCTAATCCCAAGCAGGCTGTGTCGTCATTCCCCGCGGTTGTAAATGAACAAAAAAGCACTTTTTACTGCTTATACATCAAAAAAACCAAATCACCAATTCCCCGCGCGGGCCTCAATAATCACACTACGCTTGGCTGA	MSRANPKQAVSSFPAVVNEQKSTFYCLYIKKTKSPIPRAGLNNHTTLG*			MSRANPKQAVSSFPAVVNEQKSTFYCLYIKKTKSPIPRAGLNNHTTLG*	CGTCGTACCG	TTTTTTAAAC	0	S	0	0	0	0	0
2344	1500	af	AN2848.1	59.m09356	AO070334000119	0			-273	-211			ATGGTTTTCATATGGACGTGGACGGTTGGTCTGTCCCTGATCATTATGATATCACACATGTAG		ATGGTTTTCATATGGACGTGGACGGTTGGTCTGTCCCTGATCATTATGATATCACACATGTAG		MVFIWTWTVGLSLIIMISHM*		MVFIWTWTVGLSLIIMISHM*		GGTTCTTCAG	TCTTAATGGA	0	AD	0	0	0	0	0
2345	1500	af	AN2848.1	59.m09356	AO070334000119	0			-262	-134			ATGGACGTGGACGGTTGGTCTGTCCCTGATCATTATGATATCACACATGTAGTCTTAATGGAAGAAATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		ATGGACGTGGACGGTTGGTCTGTCCCTGATCATTATGATATCACACATGTAGTCTTAATGGAAGAAATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		MDVDGWSVPDHYDITHVVLMEEMRVKLRENSRSFVCQSLSAY*		MDVDGWSVPDHYDITHVVLMEEMRVKLRENSRSFVCQSLSAY*		TGGTTTTCAT	GGAGCATCCA	0	AD	0	0	0	0	0
2346	1500	af	AN2848.1	59.m09356	AO070334000119	0			-228	-211			ATGATATCACACATGTAG		ATGATATCACACATGTAG		MISHM*		MISHM*		CCTGATCATT	TCTTAATGGA	0	AD	0	0	0	0	0
2347	1500	af	AN2848.1	59.m09356	AO070334000119	0			-205	-134			ATGGAAGAAATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		ATGGAAGAAATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		MEEMRVKLRENSRSFVCQSLSAY*		MEEMRVKLRENSRSFVCQSLSAY*		TGTAGTCTTA	GGAGCATCCA	0	AD	0	0	0	0	0
2348	1500	af	AN2848.1	59.m09356	AO070334000119	0			-196	-134			ATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		ATGAGAGTTAAGCTGCGCGAAAATTCTAGAAGCTTTGTCTGCCAGTCTCTTTCAGCGTATTAA		MRVKLRENSRSFVCQSLSAY*		MRVKLRENSRSFVCQSLSAY*		AATGGAAGAA	GGAGCATCCA	0	AD	0	0	0	0	0
2342	1500	an	AN2848.1	59.m09356	AO070334000119	0	-143	-132					ATGATAATCTGA	ATGATAATCTGA			MII*	MII*			TAGACCTTCA	CCGCCCACAG	0	AD	0	0	0	0	0
2343	1500	an	AN2848.1	59.m09356	AO070334000119	0	-66	-22					ATGATTCTTCCAACAATCAATAGGCACCCGATTTCGTTTCCTTGA	ATGATTCTTCCAACAATCAATAGGCACCCGATTTCGTTTCCTTGA			MILPTINRHPISFP*	MILPTINRHPISFP*			AAGAACAACG	GTTATTGCTT	0	AD	0	0	0	0	0
2349	1500	ao	AN2848.1	59.m09356	AO070334000119	0					-174	-145	ATGGAACTGCACCCTGTATATAGCTTCTAA			ATGGAACTGCACCCTGTATATAGCTTCTAA	MELHPVYSF*			MELHPVYSF*	CTTTTTGAAG	TTCGATAAAT	0	AD	0	0	0	0	0
2350	1504	af	AN4109.1	52.m04073	AO070342000385	0			-98	-75			ATGGTGCCCGTTAAAATGCGCTGA		ATGGTGCCCGTTAAAATGCGCTGA		MVPVKMR*		MVPVKMR*		CTGTTTAGTG	TTCCTCAAAC	0	G	0	0	0	0	0
2351	1504	ao	AN4109.1	52.m04073	AO070342000385	0					-275	-168	ATGCAAGAATTGCGCAAACACCACTATTATGAGCAATTGGGACTCTTATCCAGTAGCCAAGTCCCTGACACTAGATCTGTGGAGCCACTCTTATCTATCCTTTCTTGA			ATGCAAGAATTGCGCAAACACCACTATTATGAGCAATTGGGACTCTTATCCAGTAGCCAAGTCCCTGACACTAGATCTGTGGAGCCACTCTTATCTATCCTTTCTTGA	MQELRKHHYYEQLGLLSSSQVPDTRSVEPLLSILS*			MQELRKHHYYEQLGLLSSSQVPDTRSVEPLLSILS*	CCAACTGCCG	AAATAATACA	0	G	0	0	0	0	0
2352	1504	ao	AN4109.1	52.m04073	AO070342000385	0					-247	-152	ATGAGCAATTGGGACTCTTATCCAGTAGCCAAGTCCCTGACACTAGATCTGTGGAGCCACTCTTATCTATCCTTTCTTGAAAATAATACACATTAG			ATGAGCAATTGGGACTCTTATCCAGTAGCCAAGTCCCTGACACTAGATCTGTGGAGCCACTCTTATCTATCCTTTCTTGAAAATAATACACATTAG	MSNWDSYPVAKSLTLDLWSHSYLSFLENNTH*			MSNWDSYPVAKSLTLDLWSHSYLSFLENNTH*	CACCACTATT	TCGAACAACA	0	G	0	0	0	0	0
2353	1504	ao	AN4109.1	52.m04073	AO070342000385	0					-142	-125	ATGTTGGGGGATTTTTAG			ATGTTGGGGGATTTTTAG	MLGDF*			MLGDF*	GTCGAACAAC	CGTAGCTGCT	0	G	0	0	0	0	0
2355	1506	af	AN2154.1	72.m20002	AO070343000203	0			-98	-78			ATGCTTCTCTTGCACCTTTGA		ATGCTTCTCTTGCACCTTTGA		MLLLHL*		MLLLHL*		TTCCTGTCAC	CTTTCCGATC	0		0	0	0	0	0
2354	1506	an	AN2154.1	72.m20002	AO070343000203	0	-156	-145					ATGACGCTATAG	ATGACGCTATAG			MTL*	MTL*			TCCTGCTGCA	CTCGGCTCAA	0		0	0	0	0	0
2356	1506	ao	AN2154.1	72.m20002	AO070343000203	0					-196	-170	ATGCTTCAGCATTTTGCGCTGTTTTAA			ATGCTTCAGCATTTTGCGCTGTTTTAA	MLQHFALF*			MLQHFALF*	AACCGACCCA	CCACAGCAAC	0		0	0	0	0	0
2357	1506	ao	AN2154.1	72.m20002	AO070343000203	0					-122	-96	ATGACGCAGGCCAATCATAGAACATAA			ATGACGCAGGCCAATCATAGAACATAA	MTQANHRT*			MTQANHRT*	TCCGCTTCAC	AATAAAACCC	0		0	0	0	0	0
2358	1506	ao	AN2154.1	72.m20002	AO070343000203	0					-66	-10	ATGCCTCTGCCCCTACCCTTGATCCCTCGCCGCTTTTTCAACATTTTGCTCTGCTGA			ATGCCTCTGCCCCTACCCTTGATCCCTCGCCGCTTTTTCAACATTTTGCTCTGCTGA	MPLPLPLIPRRFFNILLC*			MPLPLPLIPRRFFNILLC*	CCCCTCTCAC	GTCTCAATCA	0		0	0	0	0	0
2361	1510	ao	AN7759.1	71.m15791	AO070286000006	0					-238	-218	ATGATCGATACCAAAGTCTAG			ATGATCGATACCAAAGTCTAG	MIDTKV*			MIDTKV*	CCATACGCGT	ACTCCCCGCG	0	WV	0	0	0	0	0
2366	1512	af	AN0400.1	58.m07671	AO070292000069	0			-235	-149			ATGGCTGTGGCTAAGCGATCCGACTGGGTTGACATGCTTCTGATATCATCGTCCCATCATTCCCGAATCGAGGATGATCGAGGATGA		ATGGCTGTGGCTAAGCGATCCGACTGGGTTGACATGCTTCTGATATCATCGTCCCATCATTCCCGAATCGAGGATGATCGAGGATGA		MAVAKRSDWVDMLLISSSHHSRIEDDRG*		MAVAKRSDWVDMLLISSSHHSRIEDDRG*		TCATACGGCT	ACGGTGACAT	0		0	0	0	0	0
2367	1512	af	AN0400.1	58.m07671	AO070292000069	0			-202	-149			ATGCTTCTGATATCATCGTCCCATCATTCCCGAATCGAGGATGATCGAGGATGA		ATGCTTCTGATATCATCGTCCCATCATTCCCGAATCGAGGATGATCGAGGATGA		MLLISSSHHSRIEDDRG*		MLLISSSHHSRIEDDRG*		CTGGGTTGAC	ACGGTGACAT	0		0	0	0	0	0
2368	1512	af	AN0400.1	58.m07671	AO070292000069	0			-162	-142			ATGATCGAGGATGAACGGTGA		ATGATCGAGGATGAACGGTGA		MIEDER*		MIEDER*		CGAATCGAGG	CATCAACTGC	0		0	0	0	0	0
2369	1512	af	AN0400.1	58.m07671	AO070292000069	0			-152	-108			ATGAACGGTGACATCAACTGCCGTCTGCGAGGAGTGGGTTTATAA		ATGAACGGTGACATCAACTGCCGTCTGCGAGGAGTGGGTTTATAA		MNGDINCRLRGVGL*		MNGDINCRLRGVGL*		ATGATCGAGG	AGCCTTATCT	0		0	0	0	0	0
2362	1512	an	AN0400.1	58.m07671	AO070292000069	0	-176	-57					ATGATGTTTTTGTCTCTTGATATCATATCTCGGTCATTCATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA	ATGATGTTTTTGTCTCTTGATATCATATCTCGGTCATTCATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA			MMFLSLDIISRSFMTSYDYQVHTSIHINHHPASMEYIKS*	MMFLSLDIISRSFMTSYDYQVHTSIHINHHPASMEYIKS*			TCTCGCCTTC	TTTCTATTAA	0		0	0	0	0	0
2363	1512	an	AN0400.1	58.m07671	AO070292000069	0	-173	-57					ATGTTTTTGTCTCTTGATATCATATCTCGGTCATTCATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA	ATGTTTTTGTCTCTTGATATCATATCTCGGTCATTCATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA			MFLSLDIISRSFMTSYDYQVHTSIHINHHPASMEYIKS*	MFLSLDIISRSFMTSYDYQVHTSIHINHHPASMEYIKS*			CGCCTTCATG	TTTCTATTAA	0		0	0	0	0	0
2364	1512	an	AN0400.1	58.m07671	AO070292000069	0	-137	-57					ATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA	ATGACATCATACGACTATCAGGTACACACCTCTATACATATAAATCACCATCCTGCCTCAATGGAATACATTAAATCATAA			MTSYDYQVHTSIHINHHPASMEYIKS*	MTSYDYQVHTSIHINHHPASMEYIKS*			TCGGTCATTC	TTTCTATTAA	0		0	0	0	0	0
2365	1512	an	AN0400.1	58.m07671	AO070292000069	0	-77	-57					ATGGAATACATTAAATCATAA	ATGGAATACATTAAATCATAA			MEYIKS*	MEYIKS*			TCCTGCCTCA	TTTCTATTAA	0		0	0	0	0	0
2370	1512	ao	AN0400.1	58.m07671	AO070292000069	0					-262	-200	ATGTCCCCAAACACTGATATCATAACCCCATCATACATCCACACCAGAACAGGGAACAAGTGA			ATGTCCCCAAACACTGATATCATAACCCCATCATACATCCACACCAGAACAGGGAACAAGTGA	MSPNTDIITPSYIHTRTGNK*			MSPNTDIITPSYIHTRTGNK*	ATAACCACCC	CATCACATAC	0		0	0	0	0	0
2371	1513	af	AN7285.1	72.m19779	AO070297000027	0			-243	-217			ATGGCCGAGCCGAGGGAAAGCAGTTAA		ATGGCCGAGCCGAGGGAAAGCAGTTAA		MAEPRESS*		MAEPRESS*		GACTCAGGCA	CCCCAACTCT	0		0	0	0	0	0
2372	1513	af	AN7285.1	72.m19779	AO070297000027	0			-130	-26			ATGATACCTCTCCAACTTTGTCACTATCACTTGTGCCGCCATTGTTGCAATTTCTCACAATTACTATCCATTCCTCCTGCCCTCATCTCGATTCTTTCTCGCTGA		ATGATACCTCTCCAACTTTGTCACTATCACTTGTGCCGCCATTGTTGCAATTTCTCACAATTACTATCCATTCCTCCTGCCCTCATCTCGATTCTTTCTCGCTGA		MIPLQLCHYHLCRHCCNFSQLLSIPPALISILSR*		MIPLQLCHYHLCRHCCNFSQLLSIPPALISILSR*		GCTTCAATTT	TCGCATTCTC	0		0	0	0	0	0
2373	1513	ao	AN7285.1	72.m19779	AO070297000027	0					-152	-138	ATGTCCTCCTGTTAG			ATGTCCTCCTGTTAG	MSSC*			MSSC*	GTTAAGTGTC	CTGCATCCCA	0		0	0	0	0	0
2375	1515	af	AN1996.1	58.m07605	AO070301000091	0			-254	-162			ATGAGTGAAGAGTATGATCGGACATTGGTTGCCTGCTCTGAGATTGCCGAGATTGTGGATATGTTGATTTCAGATTACCTGACTTTCGATTAG		ATGAGTGAAGAGTATGATCGGACATTGGTTGCCTGCTCTGAGATTGCCGAGATTGTGGATATGTTGATTTCAGATTACCTGACTTTCGATTAG		MSEEYDRTLVACSEIAEIVDMLISDYLTFD*		MSEEYDRTLVACSEIAEIVDMLISDYLTFD*		TTGTCGCTAT	TCTCAGAGAA	0	S	FG01498.1	0	0	0	0

2376	1515	af	AN1996.1	58.m07605	AO070301000091	0			-241	-188			ATGATCGGACATTGGTTGCCTGCTCTGAGATTGCCGAGATTGTGGATATGTTGA		ATGATCGGACATTGGTTGCCTGCTCTGAGATTGCCGAGATTGTGGATATGTTGA		MIGHWLPALRLPRLWIC*		MIGHWLPALRLPRLWIC*		AGTGAAGAGT	TTTCAGATTA	0	S	FG01498.1	0	0	0	0
2377	1515	af	AN1996.1	58.m07605	AO070301000091	0			-194	-162			ATGTTGATTTCAGATTACCTGACTTTCGATTAG		ATGTTGATTTCAGATTACCTGACTTTCGATTAG		MLISDYLTFD*		MLISDYLTFD*		GATTGTGGAT	TCTCAGAGAA	0	S	FG01498.1	0	0	0	0
2374	1515	an	AN1996.1	58.m07605	AO070301000091	0	-171	-142					ATGCCTTACAGGCATTTTTTGAGGGATTGA	ATGCCTTACAGGCATTTTTTGAGGGATTGA			MPYRHFLRD*	MPYRHFLRD*			TTTCCTCGGC	ACAGAAACGC	0	S	FG01498.1	0	0	0	0
2378	1515	ao	AN1996.1	58.m07605	AO070301000091	0					-228	-202	ATGGCTGCGTTGGTCTTGTTGCTTTGA			ATGGCTGCGTTGGTCTTGTTGCTTTGA	MAALVLLL*			MAALVLLL*	CAGCAATAGC	AACGGAAGAC	0	S	FG01498.1	0	0	0	0
2379	1515	ao	AN1996.1	58.m07605	AO070301000091	0					-179	-156	ATGCCATTGCGCATTCAAAATTGA			ATGCCATTGCGCATTCAAAATTGA	MPLRIQN*			MPLRIQN*	GATCTGGGCG	TTGTTATCAA	0	S	FG01498.1	0	0	0	0
2381	1523	af	AN3015.1	59.m09005	AO070337000100	0			-239	-210			ATGTACGAGTATACGCAAATTGTGTCATGA		ATGTACGAGTATACGCAAATTGTGTCATGA		MYEYTQIVS*		MYEYTQIVS*		CAATCGGAAA	GCATATTGAT	0	S	0	0	0	0	0
2382	1523	af	AN3015.1	59.m09005	AO070337000100	0			-213	-163			ATGAGCATATTGATTGCACATATTGCAAGCCAACTAATATCTGAAAGGTGA		ATGAGCATATTGATTGCACATATTGCAAGCCAACTAATATCTGAAAGGTGA		MSILIAHIASQLISER*		MSILIAHIASQLISER*		AAATTGTGTC	AACTATTCTC	0	S	0	0	0	0	0
2380	1523	an	AN3015.1	59.m09005	AO070337000100	0	-196	-173					ATGGTACTGGAGGTTATTGAGTAG	ATGGTACTGGAGGTTATTGAGTAG			MVLEVIE*	MVLEVIE*			GGTTGTGTTA	ATGTGGTAAC	0	S	0	0	0	0	0
2383	1523	ao	AN3015.1	59.m09005	AO070337000100	0					-218	-192	ATGAAGTGGGTTATGTATTGTATGTAG			ATGAAGTGGGTTATGTATTGTATGTAG	MKWVMYCM*			MKWVMYCM*	GGACCTAGGA	TTAATGAAAT	0	S	0	0	0	0	0
2384	1523	ao	AN3015.1	59.m09005	AO070337000100	0					-206	-192	ATGTATTGTATGTAG			ATGTATTGTATGTAG	MYCM*			MYCM*	GAAGTGGGTT	TTAATGAAAT	0	S	0	0	0	0	0
2385	1523	ao	AN3015.1	59.m09005	AO070337000100	0					-188	-174	ATGAAATTAAATTGA			ATGAAATTAAATTGA	MKLN*			MKLN*	TATGTAGTTA	TTTTCATTCC	0	S	0	0	0	0	0
2387	1529	an	AN9384.1	54.m06360	AO070253000015	0	-265	-242					ATGATGCTTGGGGCAACTCTTTAG	ATGATGCTTGGGGCAACTCTTTAG			MMLGATL*	MMLGATL*			GCCAGTAAGA	CTCTTCGCCT	0	QI	0	0	0	0	0
2388	1529	an	AN9384.1	54.m06360	AO070253000015	0	-262	-242					ATGCTTGGGGCAACTCTTTAG	ATGCTTGGGGCAACTCTTTAG			MLGATL*	MLGATL*			AGTAAGAATG	CTCTTCGCCT	0	QI	0	0	0	0	0
2389	1529	an	AN9384.1	54.m06360	AO070253000015	0	-86	-30					ATGCTCTCAACAGCTAAATTCGCCAGGATGCCCAGGACCAACGGACTGACTGACTGA	ATGCTCTCAACAGCTAAATTCGCCAGGATGCCCAGGACCAACGGACTGACTGACTGA			MLSTAKFARMPRTNGLTD*	MLSTAKFARMPRTNGLTD*			TAAAGCCTTC	CTGACGAACT	0	QI	0	0	0	0	0
2391	1529	ao	AN9384.1	54.m06360	AO070253000015	0					-157	-62	ATGGTTGAAATTCGGCAAATGCTCCTGCGAAGGTTACACTTGCTGGTGCGGGTCCTTGCCCTGAACTCTTTGTCTACTTACATCGAAGGTATATAA			ATGGTTGAAATTCGGCAAATGCTCCTGCGAAGGTTACACTTGCTGGTGCGGGTCCTTGCCCTGAACTCTTTGTCTACTTACATCGAAGGTATATAA	MVEIRQMLLRRLHLLVRVLALNSLSTYIEGI*			MVEIRQMLLRRLHLLVRVLALNSLSTYIEGI*	GAAGAGTTCT	AAGCTTCCCC	0	QI	0	0	0	0	0
2392	1529	ao	AN9384.1	54.m06360	AO070253000015	0					-139	-62	ATGCTCCTGCGAAGGTTACACTTGCTGGTGCGGGTCCTTGCCCTGAACTCTTTGTCTACTTACATCGAAGGTATATAA			ATGCTCCTGCGAAGGTTACACTTGCTGGTGCGGGTCCTTGCCCTGAACTCTTTGTCTACTTACATCGAAGGTATATAA	MLLRRLHLLVRVLALNSLSTYIEGI*			MLLRRLHLLVRVLALNSLSTYIEGI*	AATTCGGCAA	AAGCTTCCCC	0	QI	0	0	0	0	0
2393	1531	an	AN0901.1	70.m15510	AO070283000043	0	-267	-25					ATGGATCGGGCTCTATCTTGCGGTGTTTGGACTAGAGCTACGATGAGCTCCTCAAATCAAATCAGAAGAATCCCAAAGGATCTTACATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAACTTTCGAGGTGATTAG	ATGGATCGGGCTCTATCTTGCGGTGTTTGGACTAGAGCTACGATGAGCTCCTCAAATCAAATCAGAAGAATCCCAAAGGATCTTACATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAACTTTCGAGGTGATTAG			MDRALSCGVWTRATMSSSNQIRRIPKDLTCQRSCPTRLEGFKFGAKSGKASFICLAFTVEKGLYIQRYRPFAHDYNFRGD*	MDRALSCGVWTRATMSSSNQIRRIPKDLTCQRSCPTRLEGFKFGAKSGKASFICLAFTVEKGLYIQRYRPFAHDYNFRGD*			TCTACATCCA	GTGGCTCTCG	0	Q	0	0	0	0	0
2394	1531	an	AN0901.1	70.m15510	AO070283000043	0	-225	-25					ATGAGCTCCTCAAATCAAATCAGAAGAATCCCAAAGGATCTTACATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAACTTTCGAGGTGATTAG	ATGAGCTCCTCAAATCAAATCAGAAGAATCCCAAAGGATCTTACATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAACTTTCGAGGTGATTAG			MSSSNQIRRIPKDLTCQRSCPTRLEGFKFGAKSGKASFICLAFTVEKGLYIQRYRPFAHDYNFRGD*	MSSSNQIRRIPKDLTCQRSCPTRLEGFKFGAKSGKASFICLAFTVEKGLYIQRYRPFAHDYNFRGD*			TAGAGCTACG	GTGGCTCTCG	0	Q	0	0	0	0	0
2395	1531	an	AN0901.1	70.m15510	AO070283000043	0	-181	-41					ATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAA	ATGCCAGCGCAGCTGTCCTACTCGGCTGGAGGGATTCAAGTTCGGAGCAAAGAGCGGCAAAGCGTCATTCATTTGCCTAGCGTTCACCGTGGAAAAGGGCTTATATATTCAGAGGTATCGCCCATTCGCGCACGATTATAA			MPAQLSYSAGGIQVRSKERQSVIHLPSVHRGKGLIYSEVSPIRARL*	MPAQLSYSAGGIQVRSKERQSVIHLPSVHRGKGLIYSEVSPIRARL*			AGGATCTTAC	CTTTCGAGGT	0	Q	0	0	0	0	0
2397	1533	af	AN2053.1	58.m07641	AO070292000020	0			-224	-195			ATGTGCAACCGTAAAGAAGGCAACACATGA		ATGTGCAACCGTAAAGAAGGCAACACATGA		MCNRKEGNT*		MCNRKEGNT*		GGCTATCTAT	TGACATCGCA	0	F	0	0	NCU00356.1	0	0
2398	1533	af	AN2053.1	58.m07641	AO070292000020	0			-198	-67			ATGATGACATCGCAGGTCACAAGTCTTGGCACTATTCCTCCTGACAGCACCTTTGACTTATCACTGTTCAGCACCTTGGCTTCATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGA		ATGATGACATCGCAGGTCACAAGTCTTGGCACTATTCCTCCTGACAGCACCTTTGACTTATCACTGTTCAGCACCTTGGCTTCATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGA		MMTSQVTSLGTIPPDSTFDLSLFSTLASWWAVVRASHEMLTMT*		MMTSQVTSLGTIPPDSTFDLSLFSTLASWWAVVRASHEMLTMT*		AAGGCAACAC	TTGCCGCCGT	0	F	0	0	NCU00356.1	0	0
2399	1533	af	AN2053.1	58.m07641	AO070292000020	0			-195	-67			ATGACATCGCAGGTCACAAGTCTTGGCACTATTCCTCCTGACAGCACCTTTGACTTATCACTGTTCAGCACCTTGGCTTCATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGA		ATGACATCGCAGGTCACAAGTCTTGGCACTATTCCTCCTGACAGCACCTTTGACTTATCACTGTTCAGCACCTTGGCTTCATGGTGGGCAGTGGTTCGTGCAAGCCACGAAATGTTAACCATGACTTGA		MTSQVTSLGTIPPDSTFDLSLFSTLASWWAVVRASHEMLTMT*		MTSQVTSLGTIPPDSTFDLSLFSTLASWWAVVRASHEMLTMT*		GCAACACATG	TTGCCGCCGT	0	F	0	0	NCU00356.1	0	0
2402	1533	ao	AN2053.1	58.m07641	AO070292000020	0					-204	-79	ATGATCGGCTTAGTGGGCCAACGTGACCTGGCTCGGCAGGTGACCTGCTTATCGCCGATAAATCACCCCGGTCGTAGATCCAGCTCGCTTCCAACGTTCTCCTTTTATACAGGTCGTCCAGGTTGA			ATGATCGGCTTAGTGGGCCAACGTGACCTGGCTCGGCAGGTGACCTGCTTATCGCCGATAAATCACCCCGGTCGTAGATCCAGCTCGCTTCCAACGTTCTCCTTTTATACAGGTCGTCCAGGTTGA	MIGLVGQRDLARQVTCLSPINHPGRRSSSLPTFSFYTGRPG*			MIGLVGQRDLARQVTCLSPINHPGRRSSSLPTFSFYTGRPG*	GACGCATCAA	TCATGGATTG	0	F	0	0	NCU00356.1	0	0
2408	1534	af	AN2534.1	59.m08439	AO070300000048	0			-152	-90			ATGTTTTGCACAAATAGTTCATTGTACTCTGGGAACCCGTCAGCTATACTATCGGTTAAATGA		ATGTTTTGCACAAATAGTTCATTGTACTCTGGGAACCCGTCAGCTATACTATCGGTTAAATGA		MFCTNSSLYSGNPSAILSVK*		MFCTNSSLYSGNPSAILSVK*		AAACGGGCAA	ATGGCACGCA	0	G	0	0	0	0	0
2409	1534	af	AN2534.1	59.m08439	AO070300000048	0			-89	-27			ATGGCACGCATATATATATAGAAAATTTGTTCCCTCCTACCATGCCTCTTTTCTCACCATTGTGA		ATGGCACGCATATATATATAGAAAATTTGTTCCCTCCTACCATGCCTCTTTTCTCACCATTGTGA		MARIYIENLFPPTMPLFSPL*		MARIYIENLFPPTMPLFSPL*		GGTTAAATGA	AATTGACTGG	0	G	0	0	0	0	0
2404	1534	an	AN2534.1	59.m08439	AO070300000048	0	-216	-94					ATGGAGCGGAGATCCGCTTCGCCATTATCTTCAAGCTGTTATTGTTTGACTACGCAAGAAATGATCCTGTGGGGGCTTCTTCCACAAATAGCTTCACCCCTGGGCTTGCTGGGTTGCGTATAA	ATGGAGCGGAGATCCGCTTCGCCATTATCTTCAAGCTGTTATTGTTTGACTACGCAAGAAATGATCCTGTGGGGGCTTCTTCCACAAATAGCTTCACCCCTGGGCTTGCTGGGTTGCGTATAA			MERRSASPLSSSCYCLTTQEMILWGLLPQIASPLGLLGCV*	MERRSASPLSSSCYCLTTQEMILWGLLPQIASPLGLLGCV*			TGTTCTCGGT	AACCAGTGTT	0	G	0	0	0	0	0
2405	1534	an	AN2534.1	59.m08439	AO070300000048	0	-156	-94					ATGATCCTGTGGGGGCTTCTTCCACAAATAGCTTCACCCCTGGGCTTGCTGGGTTGCGTATAA	ATGATCCTGTGGGGGCTTCTTCCACAAATAGCTTCACCCCTGGGCTTGCTGGGTTGCGTATAA			MILWGLLPQIASPLGLLGCV*	MILWGLLPQIASPLGLLGCV*			TACGCAAGAA	AACCAGTGTT	0	G	0	0	0	0	0
2406	1534	an	AN2534.1	59.m08439	AO070300000048	0	-72	-58					ATGGGGATTGTATGA	ATGGGGATTGTATGA			MGIV*	MGIV*			TGCTGCGAGA	CCCTTATCTA	0	G	0	0	0	0	0
2407	1534	an	AN2534.1	59.m08439	AO070300000048	0	-61	-47					ATGACCCTTATCTAA	ATGACCCTTATCTAA			MTLI*	MTLI*			TGGGGATTGT	GTCGCAGTGA	0	G	0	0	0	0	0
2411	1536	af	AN7710.1	71.m15734	AO070325000117	0			-250	-233			ATGCGCGCAGCCCGTTGA		ATGCGCGCAGCCCGTTGA		MRAAR*		MRAAR*		TACTTAAGGA	TGTTTGCCAC	0	R	FG05132.1	MG08166.1	0	0	0
2413	1537	af	AN1135.1	70.m15102	AO070331000126	0			-181	-158			ATGGCAATAAGCTCTATGGTGTAG		ATGGCAATAAGCTCTATGGTGTAG		MAISSMV*		MAISSMV*		CCCCGCATTA	TCCCTGGATA	0	E	0	0	0	0	0
2414	1537	af	AN1135.1	70.m15102	AO070331000126	0			-64	-47			ATGCCCTGCTACCGCTAG		ATGCCCTGCTACCGCTAG		MPCYR*		MPCYR*		CAGTTCCCCC	CTTTCAGACT	0	E	0	0	0	0	0
2415	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-218	-171	ATGCTTAGTAAATTTAAATGCAGATGTTTTACCCATGCGATAAGATGA			ATGCTTAGTAAATTTAAATGCAGATGTTTTACCCATGCGATAAGATGA	MLSKFKCRCFTHAIR*			MLSKFKCRCFTHAIR*	CTACTCCGTA	GTATGAGAAT	0	E	0	0	0	0	0
2416	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-201	-157	ATGCAGATGTTTTACCCATGCGATAAGATGAGTATGAGAATATAA			ATGCAGATGTTTTACCCATGCGATAAGATGAGTATGAGAATATAA	MQMFYPCDKMSMRI*			MQMFYPCDKMSMRI*	GTAAATTTAA	TAGTGAAACT	0	E	0	0	0	0	0
2417	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-195	-157	ATGTTTTACCCATGCGATAAGATGAGTATGAGAATATAA			ATGTTTTACCCATGCGATAAGATGAGTATGAGAATATAA	MFYPCDKMSMRI*			MFYPCDKMSMRI*	TTAAATGCAG	TAGTGAAACT	0	E	0	0	0	0	0
2418	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-174	-157	ATGAGTATGAGAATATAA			ATGAGTATGAGAATATAA	MSMRI*			MSMRI*	ATGCGATAAG	TAGTGAAACT	0	E	0	0	0	0	0
2419	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-168	-157	ATGAGAATATAA			ATGAGAATATAA	MRI*			MRI*	TAAGATGAGT	TAGTGAAACT	0	E	0	0	0	0	0
2420	1537	ao	AN1135.1	70.m15102	AO070331000126	0					-104	-84	ATGCTTTACTCCACATCCTAG			ATGCTTTACTCCACATCCTAG	MLYSTS*			MLYSTS*	TATTTCTATT	ATACACACTT	0	E	0	0	0	0	0
2427	1543	af	AN3580.1	58.m07378	AO070342000169	0			-171	-100			ATGGAAATCCTGGCATCTAATATCTCCATATTCGTCTTAGAAAGGGAAGGGGTGCTGGTTTTCAGCACCTAA		ATGGAAATCCTGGCATCTAATATCTCCATATTCGTCTTAGAAAGGGAAGGGGTGCTGGTTTTCAGCACCTAA		MEILASNISIFVLEREGVLVFST*		MEILASNISIFVLEREGVLVFST*		CCCACCATGG	CAACAATCGG	0	Q	0	0	0	0	0
2422	1543	an	AN3580.1	58.m07378	AO070342000169	0	-180	-55					ATGAAAAGTGGACCCACATGGATGGATATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG	ATGAAAAGTGGACCCACATGGATGGATATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG			MKSGPTWMDMFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*	MKSGPTWMDMFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*			CAATTTTCGT	CTCGAGGCTG	0	Q	0	0	0	0	0
2423	1543	an	AN3580.1	58.m07378	AO070342000169	0	-159	-55					ATGGATATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG	ATGGATATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG			MDMFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*	MDMFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*			ACCCACATGG	CTCGAGGCTG	0	Q	0	0	0	0	0
2424	1543	an	AN3580.1	58.m07378	AO070342000169	0	-153	-55					ATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG	ATGTTCACACTTGATATCTTCACAAAGAGCCGGCGTAATAATGGATCGAGATCACATTCTAGGCTCTTACTCATAGCTGGAATGTTCTCAATACTTTAG			MFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*	MFTLDIFTKSRRNNGSRSHSRLLLIAGMFSIL*			ATGGATGGAT	CTCGAGGCTG	0	Q	0	0	0	0	0
2425	1543	an	AN3580.1	58.m07378	AO070342000169	0	-113	-78					ATGGATCGAGATCACATTCTAGGCTCTTACTCATAG	ATGGATCGAGATCACATTCTAGGCTCTTACTCATAG			MDRDHILGSYS*	MDRDHILGSYS*			CGGCGTAATA	CTGGAATGTT	0	Q	0	0	0	0	0
2426	1543	an	AN3580.1	58.m07378	AO070342000169	0	-72	-55					ATGTTCTCAATACTTTAG	ATGTTCTCAATACTTTAG			MFSIL*	MFSIL*			CATAGCTGGA	CTCGAGGCTG	0	Q	0	0	0	0	0
2428	1543	ao	AN3580.1	58.m07378	AO070342000169	0					-160	-122	ATGAGTGGACCCACAATGGATAGAAACGCTGAGATCTGA			ATGAGTGGACCCACAATGGATAGAAACGCTGAGATCTGA	MSGPTMDRNAEI*			MSGPTMDRNAEI*	ACGGCTCCGG	GATTACTGTA	0	Q	0	0	0	0	0
2429	1543	ao	AN3580.1	58.m07378	AO070342000169	0					-101	-66	ATGGAAGTGCTATGTCTATTGGCAGACTCAGTATAG			ATGGAAGTGCTATGTCTATTGGCAGACTCAGTATAG	MEVLCLLADSV*			MEVLCLLADSV*	TTTTCAAACG	TATAATTACC	0	Q	0	0	0	0	0
2430	1543	ao	AN3580.1	58.m07378	AO070342000169	0					-90	-61	ATGTCTATTGGCAGACTCAGTATAGTATAA			ATGTCTATTGGCAGACTCAGTATAGTATAA	MSIGRLSIV*			MSIGRLSIV*	TGGAAGTGCT	TTACCTTCTA	0	Q	0	0	0	0	0
2421	1543	conserved	AN3580.1	58.m07378	AO070342000169	0	-163	-140	-175	-152	-145	-122	ATGGATrGAwAysyTsrsAyyTrA	ATGGATGGATATGTTCACACTTGA	ATGGATGGAAATCCTGGCATCTAA	ATGGATAGAAACGCTGAGATCTGA	MDgyvht*	MDGYVHT*	MDGNPGI*	MDRNAEI*	kkGrmCCmmm	kATywyyryA	0	Q	0	0	0	0	0
2431	1553	af	AN4259.1	65.m07433	AO070277000032	0			-294	-256			ATGCAAATCGATATTAATCATGAATTCAATCCAAGGTAA		ATGCAAATCGATATTAATCATGAATTCAATCCAAGGTAA		MQIDINHEFNPR*		MQIDINHEFNPR*		CAAGAACCAT	TATACGTCTG	0	R	0	0	NCU02813.1	0	0
2432	1553	af	AN4259.1	65.m07433	AO070277000032	0			-275	-234			ATGAATTCAATCCAAGGTAATATACGTCTGTTGTTGTACTGA		ATGAATTCAATCCAAGGTAATATACGTCTGTTGTTGTACTGA		MNSIQGNIRLLLY*		MNSIQGNIRLLLY*		GATATTAATC	AATAGTTTCT	0	R	0	0	NCU02813.1	0	0
2433	1556	an	AN9471.1	72.m19419	AO070304000088	0	-152	-102					ATGGATGTACTCTCACAGATCGCGAGCAAGGGAGCAAGGGATCGCCGCTAA	ATGGATGTACTCTCACAGATCGCGAGCAAGGGAGCAAGGGATCGCCGCTAA			MDVLSQIASKGARDRR*	MDVLSQIASKGARDRR*			GATCTCTTCA	GCTTGACTAC	0	F	0	0	0	0	0
2434	1556	an	AN9471.1	72.m19419	AO070304000088	0	-148	-89					ATGTACTCTCACAGATCGCGAGCAAGGGAGCAAGGGATCGCCGCTAAGCTTGACTACTGA	ATGTACTCTCACAGATCGCGAGCAAGGGAGCAAGGGATCGCCGCTAAGCTTGACTACTGA			MYSHRSRAREQGIAAKLDY*	MYSHRSRAREQGIAAKLDY*			TCTTCAATGG	CATCAGTTCC	0	F	0	0	0	0	0
2435	1556	ao	AN9471.1	72.m19419	AO070304000088	0					-166	-113	ATGGAGCTCTCCCCGCCTTCGATGTCATTGATCTTGAATCTTATTTCCGTTTAG			ATGGAGCTCTCCCCGCCTTCGATGTCATTGATCTTGAATCTTATTTCCGTTTAG	MELSPPSMSLILNLISV*			MELSPPSMSLILNLISV*	AGAGCTGCCA	TGTTTCGCAC	0	F	0	0	0	0	0
2436	1556	ao	AN9471.1	72.m19419	AO070304000088	0					-145	-113	ATGTCATTGATCTTGAATCTTATTTCCGTTTAG			ATGTCATTGATCTTGAATCTTATTTCCGTTTAG	MSLILNLISV*			MSLILNLISV*	CCCGCCTTCG	TGTTTCGCAC	0	F	0	0	0	0	0

2437	1556	ao	AN9471.1	72.m19419	AO070304000088	0					-76	-59	ATGTATATACGAGTTTGA			ATGTATATACGAGTTTGA	MYIRV*			MYIRV*	CGGTCTTCTG	TCTCTTAAAT	0	F	0	0	0	0	0
2441	1569	af	AN5629.1	58.m07554	AO070301000028	0			-216	-187			ATGCTTGGAACATTATATATTCATGACTAA		ATGCTTGGAACATTATATATTCATGACTAA		MLGTLYIHD*		MLGTLYIHD*		AAAATCAAGA	GCGCATGGCA	0	C	FG09250.1	0	0	0	0
2442	1569	af	AN5629.1	58.m07554	AO070301000028	0			-194	-168			ATGACTAAGCGCATGGCACGTGACTGA		ATGACTAAGCGCATGGCACGTGACTGA		MTKRMARD*		MTKRMARD*		TTATATATTC	TACGGACCAA	0	C	FG09250.1	0	0	0	0
2443	1569	af	AN5629.1	58.m07554	AO070301000028	0			-182	-168			ATGGCACGTGACTGA		ATGGCACGTGACTGA		MARD*		MARD*		GACTAAGCGC	TACGGACCAA	0	C	FG09250.1	0	0	0	0
2439	1569	an	AN5629.1	58.m07554	AO070301000028	0	-256	-83					ATGCCTGGTACTGACAAATCTATATCCTTTGAGTCTTGTCACGTTTATAGTTATGCTGAGTTCCCGTTTTGGCGTGATGTAAGATCACGTGTACATGCTGACCAAGCGTCACGTGATTTATTCCGTCCAATCACTGACCGGACAAAGCCGGATATTCAGCAACCGCAGAATTGA	ATGCCTGGTACTGACAAATCTATATCCTTTGAGTCTTGTCACGTTTATAGTTATGCTGAGTTCCCGTTTTGGCGTGATGTAAGATCACGTGTACATGCTGACCAAGCGTCACGTGATTTATTCCGTCCAATCACTGACCGGACAAAGCCGGATATTCAGCAACCGCAGAATTGA			MPGTDKSISFESCHVYSYAEFPFWRDVRSRVHADQASRDLFRPITDRTKPDIQQPQN*	MPGTDKSISFESCHVYSYAEFPFWRDVRSRVHADQASRDLFRPITDRTKPDIQQPQN*			TTCGGTGACC	AGCTGGAACG	0	C	FG09250.1	0	0	0	0
2440	1569	an	AN5629.1	58.m07554	AO070301000028	0	-204	-175					ATGCTGAGTTCCCGTTTTGGCGTGATGTAA	ATGCTGAGTTCCCGTTTTGGCGTGATGTAA			MLSSRFGVM*	MLSSRFGVM*			GTTTATAGTT	GATCACGTGT	0	C	FG09250.1	0	0	0	0
2444	1569	ao	AN5629.1	58.m07554	AO070301000028	0					-212	-162	ATGATTAGTAATACATATCGATGGATATCTGACTCAGCACATACCACGTGA			ATGATTAGTAATACATATCGATGGATATCTGACTCAGCACATACCACGTGA	MISNTYRWISDSAHTT*			MISNTYRWISDSAHTT*	TAAAACAATA	CTTAATCGGG	0	C	FG09250.1	0	0	0	0
2445	1569	ao	AN5629.1	58.m07554	AO070301000028	0					-192	-181	ATGGATATCTGA			ATGGATATCTGA	MDI*			MDI*	ATACATATCG	CTCAGCACAT	0	C	FG09250.1	0	0	0	0
2446	1578	an	AN6501.1	62.m03089	AO070222000017	0	-201	-106					ATGACGGTCGATCAAGCTTCTCTCCATTTCTTCCGCTACCACACTACCTATTTCTCACATTTCCTAAGCTCATCTTGGATCACACATACAAAGTAA	ATGACGGTCGATCAAGCTTCTCTCCATTTCTTCCGCTACCACACTACCTATTTCTCACATTTCCTAAGCTCATCTTGGATCACACATACAAAGTAA			MTVDQASLHFFRYHTTYFSHFLSSSWITHTK*	MTVDQASLHFFRYHTTYFSHFLSSSWITHTK*			GTAGGGAGCC	TCTTACTAAT	0	A	0	0	0	YOR319W	0
2447	1578	ao	AN6501.1	62.m03089	AO070222000017	0					-97	-44	ATGTACCATACTACCAACAATTTTACGTACTATCTTCTAGCTACTTTCTGCTAA			ATGTACCATACTACCAACAATTTTACGTACTATCTTCTAGCTACTTTCTGCTAA	MYHTTNNFTYYLLATFC*			MYHTTNNFTYYLLATFC*	CCGATAATTC	GTCGTGTACC	0	A	0	0	0	YOR319W	0
2450	1582	af	AN3366.1	66.m04634	AO070281000026	0			-219	-157			ATGTCTGTCAAGAGCATCATCACGTCGGACCTCATCACGTTCTTCTTCATCCCCAATTATTAG		ATGTCTGTCAAGAGCATCATCACGTCGGACCTCATCACGTTCTTCTTCATCCCCAATTATTAG		MSVKSIITSDLITFFFIPNY*		MSVKSIITSDLITFFFIPNY*		CCTACCATTC	CCTGGTATCT	0		0	0	0	0	0
2448	1582	an	AN3366.1	66.m04634	AO070281000026	0	-193	-170					ATGGCCGCGACAACCATGCCGTGA	ATGGCCGCGACAACCATGCCGTGA			MAATTMP*	MAATTMP*			GCTTCCCCTC	CGATGAGACT	0		0	0	0	0	0
2449	1582	an	AN3366.1	66.m04634	AO070281000026	0	-167	-153					ATGAGACTGCACTAG	ATGAGACTGCACTAG			MRLH*	MRLH*			TGCCGTGACG	ATCGTACCTT	0		0	0	0	0	0
2452	1595	af	AN0707.1	70.m15314	AO070343000502	0			-175	-161			ATGCGACATCATTAA		ATGCGACATCATTAA		MRHH*		MRHH*		CCTGATCTTG	ACGAGGATAA	0	LA	0	0	0	YOR048C	0
2453	1595	af	AN0707.1	70.m15314	AO070343000502	0			-86	-66			ATGGAGCGCATCAGGAACTGA		ATGGAGCGCATCAGGAACTGA		MERIRN*		MERIRN*		GAGAAAGCTG	TTGGATCTCA	0	LA	0	0	0	YOR048C	0
2451	1595	an	AN0707.1	70.m15314	AO070343000502	0	-120	-94					ATGGAGCATCGCGTTGGGCGTGGCTAA	ATGGAGCATCGCGTTGGGCGTGGCTAA			MEHRVGRG*	MEHRVGRG*			TGAGTCGCTG	AATTTCTAGT	0	LA	0	0	0	YOR048C	0
2454	1595	ao	AN0707.1	70.m15314	AO070343000502	0					-115	-89	ATGGAGTCTGCTACGAAGTTTATCTGA			ATGGAGTCTGCTACGAAGTTTATCTGA	MESATKFI*			MESATKFI*	GCGACAGCCC	ATCGCGATAA	0	LA	0	0	0	YOR048C	0
2456	1598	af	AN8858.1	71.m15996	AO070271000015	0			-196	-167			ATGCGCAAGCCACTGCCCTTGAATTCCTAG		ATGCGCAAGCCACTGCCCTTGAATTCCTAG		MRKPLPLNS*		MRKPLPLNS*		GTTTGATTTC	TTGACAAGGT	0	K	0	0	0	0	0
2455	1598	an	AN8858.1	71.m15996	AO070271000015	0	-191	-120					ATGCTATCTGGCCATCACCATACTGTGATCTTCCCTTGCAACTTACACAGTGTGTATAACGCAACCGTCTGA	ATGCTATCTGGCCATCACCATACTGTGATCTTCCCTTGCAACTTACACAGTGTGTATAACGCAACCGTCTGA			MLSGHHHTVIFPCNLHSVYNATV*	MLSGHHHTVIFPCNLHSVYNATV*			TGTGTATTGA	CACCCTACAT	0	K	0	0	0	0	0
2458	1601	af	AN8605.1	59.m09455	AO070314000022	0			-246	-196			ATGGCCTATGCAGATAAACAGACGCATGGCAGAGATCATGGCGTGCGTTGA		ATGGCCTATGCAGATAAACAGACGCATGGCAGAGATCATGGCGTGCGTTGA		MAYADKQTHGRDHGVR*		MAYADKQTHGRDHGVR*		CTGATATTTC	ATGCGGAGAC	0	O	0	0	0	0	0
2459	1601	af	AN8605.1	59.m09455	AO070314000022	0			-239	-180			ATGCAGATAAACAGACGCATGGCAGAGATCATGGCGTGCGTTGAATGCGGAGACCTATGA		ATGCAGATAAACAGACGCATGGCAGAGATCATGGCGTGCGTTGAATGCGGAGACCTATGA		MQINRRMAEIMACVECGDL*		MQINRRMAEIMACVECGDL*		TTCATGGCCT	CGTGGCACGA	0	O	0	0	0	0	0
2460	1601	af	AN8605.1	59.m09455	AO070314000022	0			-221	-180			ATGGCAGAGATCATGGCGTGCGTTGAATGCGGAGACCTATGA		ATGGCAGAGATCATGGCGTGCGTTGAATGCGGAGACCTATGA		MAEIMACVECGDL*		MAEIMACVECGDL*		AAACAGACGC	CGTGGCACGA	0	O	0	0	0	0	0
2461	1601	af	AN8605.1	59.m09455	AO070314000022	0			-209	-180			ATGGCGTGCGTTGAATGCGGAGACCTATGA		ATGGCGTGCGTTGAATGCGGAGACCTATGA		MACVECGDL*		MACVECGDL*		GGCAGAGATC	CGTGGCACGA	0	O	0	0	0	0	0
2457	1601	an	AN8605.1	59.m09455	AO070314000022	0	-187	-176					ATGGTTGGCTAG	ATGGTTGGCTAG			MVG*	MVG*			CAACGACAAG	TTGGGCTGGA	0	O	0	0	0	0	0
2462	1601	ao	AN8605.1	59.m09455	AO070314000022	0					-187	-161	ATGTTGAAAATAAAAACTGCCCAATGA			ATGTTGAAAATAAAAACTGCCCAATGA	MLKIKTAQ*			MLKIKTAQ*	TAAGAAGTGG	TAAGGGTTTT	0	O	0	0	0	0	0
2463	1601	ao	AN8605.1	59.m09455	AO070314000022	0					-164	-99	ATGATAAGGGTTTTGGCGTACGCGAAAATTTTATCAACAGGCATGTACGTCACTACCCCGCGATAA			ATGATAAGGGTTTTGGCGTACGCGAAAATTTTATCAACAGGCATGTACGTCACTACCCCGCGATAA	MIRVLAYAKILSTGMYVTTPR*			MIRVLAYAKILSTGMYVTTPR*	AAACTGCCCA	AATCTCGTAT	0	O	0	0	0	0	0
2464	1601	ao	AN8605.1	59.m09455	AO070314000022	0					-122	-99	ATGTACGTCACTACCCCGCGATAA			ATGTACGTCACTACCCCGCGATAA	MYVTTPR*			MYVTTPR*	ATCAACAGGC	AATCTCGTAT	0	O	0	0	0	0	0
2474	1606	an	AN4034.1	54.m06562	AO070328000126	0	-302	-285					ATGCTCCTCGGCGAATGA	ATGCTCCTCGGCGAATGA			MLLGE*	MLLGE*			CGCAATTTCT	GAGCCTCCCC	0	K	0	0	0	0	0
2475	1606	an	AN4034.1	54.m06562	AO070328000126	0	-288	-208					ATGAGAGCCTCCCCGCATCTCATCTACGCCGCTAGAGCAGAGTTGTCATGGACGCGCTGCCAATCCTCCCAACAGCCCTGA	ATGAGAGCCTCCCCGCATCTCATCTACGCCGCTAGAGCAGAGTTGTCATGGACGCGCTGCCAATCCTCCCAACAGCCCTGA			MRASPHLIYAARAELSWTRCQSSQQP*	MRASPHLIYAARAELSWTRCQSSQQP*			TCCTCGGCGA	TCTGCTTTTT	0	K	0	0	0	0	0
2476	1606	an	AN4034.1	54.m06562	AO070328000126	0	-241	-80					ATGGACGCGCTGCCAATCCTCCCAACAGCCCTGATCTGCTTTTTTGTCCCTGCTCAGGCTGTTGTGAAGCAGCTCGATGCCAGCCTAATCCCGCTTCCTTCCCTTGGTCCATGCGCCTTGAACCTGATCCTGAAAGCCAGTTGCGTGGTGTGCACTCTCTGA	ATGGACGCGCTGCCAATCCTCCCAACAGCCCTGATCTGCTTTTTTGTCCCTGCTCAGGCTGTTGTGAAGCAGCTCGATGCCAGCCTAATCCCGCTTCCTTCCCTTGGTCCATGCGCCTTGAACCTGATCCTGAAAGCCAGTTGCGTGGTGTGCACTCTCTGA			MDALPILPTALICFFVPAQAVVKQLDASLIPLPSLGPCALNLILKASCVVCTL*	MDALPILPTALICFFVPAQAVVKQLDASLIPLPSLGPCALNLILKASCVVCTL*			CAGAGTTGTC	CGTGGATGCC	0	K	0	0	0	0	0
2477	1606	an	AN4034.1	54.m06562	AO070328000126	0	-165	-154					ATGCCAGCCTAA	ATGCCAGCCTAA			MPA*	MPA*			AAGCAGCTCG	TCCCGCTTCC	0	K	0	0	0	0	0
2478	1606	ao	AN4034.1	54.m06562	AO070328000126	0					-319	-302	ATGATCATCGTCGAATAA			ATGATCATCGTCGAATAA	MIIVE*			MIIVE*	CGCTTCTCAT	CCATCCCGGT	0	K	0	0	0	0	0
2496	1616	ao	AN5701.1	65.m07424	AO070309000122	0					-181	-164	ATGCAATTGACCTTCTAA			ATGCAATTGACCTTCTAA	MQLTF*			MQLTF*	CAACTTCTGC	CTATCACTCG	0	E	0	0	0	0	0
2501	1619	af	AN3794.1	57.m05968	AO070337000233	0			-190	-107			ATGTCAGAAACGATTAACACCACGAACAACACTATTCCCCAACACCACCGGAATGATCGTTTAGCGGCTGGCTCTAATTCTTGA		ATGTCAGAAACGATTAACACCACGAACAACACTATTCCCCAACACCACCGGAATGATCGTTTAGCGGCTGGCTCTAATTCTTGA		MSETINTTNNTIPQHHRNDRLAAGSNS*		MSETINTTNNTIPQHHRNDRLAAGSNS*		CAGAAAAAGA	GCCAAGGTAG	0	R	0	0	0	0	0
2500	1619	conserved	AN3794.1	57.m05968	AO070337000233	0	-148	-137	-138	-127	-152	-141	ATGwyyrTwTAG	ATGTCTGTATAG	ATGATCGTTTAG	ATGATTATATAG	Msv*	MSV*	MIV*	MII*	yAmywmCGGA	CGGyhGGCTC	0	R	0	0	0	0	0
2505	1622	af	AN1572.1	55.m03104	AO070339000262	0			-114	-88			ATGATTAGTAAACATCAAACACTTTAA		ATGATTAGTAAACATCAAACACTTTAA		MISKHQTL*		MISKHQTL*		AAGCAACGAT	TATGCGGCTG	0		0	0	0	0	0
2502	1622	an	AN1572.1	55.m03104	AO070339000262	0	-218	-183					ATGCAGGGAAATATCCTTATGTGGAATAGCCTTTAG	ATGCAGGGAAATATCCTTATGTGGAATAGCCTTTAG			MQGNILMWNSL*	MQGNILMWNSL*			ATCCACTAGG	AACTCCACCA	0		0	0	0	0	0
2503	1622	an	AN1572.1	55.m03104	AO070339000262	0	-200	-183					ATGTGGAATAGCCTTTAG	ATGTGGAATAGCCTTTAG			MWNSL*	MWNSL*			AAATATCCTT	AACTCCACCA	0		0	0	0	0	0
2504	1622	an	AN1572.1	55.m03104	AO070339000262	0	-150	-112					ATGAGACCCGCTCAGTTACGAGATTTCAGCCGCAGATAG	ATGAGACCCGCTCAGTTACGAGATTTCAGCCGCAGATAG			MRPAQLRDFSRR*	MRPAQLRDFSRR*			ATTTCATGGT	GAGCCCAAAC	0		0	0	0	0	0
2506	1622	ao	AN1572.1	55.m03104	AO070339000262	0					-140	-105	ATGGATGCTGATCACCAACCACATCGTAAGCCCTAA			ATGGATGCTGATCACCAACCACATCGTAAGCCCTAA	MDADHQPHRKP*			MDADHQPHRKP*	TTTCCCGCAA	TGCAAACTGA	0		0	0	0	0	0
2507	1622	ao	AN1572.1	55.m03104	AO070339000262	0					-136	-95	ATGCTGATCACCAACCACATCGTAAGCCCTAATGCAAACTGA			ATGCTGATCACCAACCACATCGTAAGCCCTAATGCAAACTGA	MLITNHIVSPNAN*			MLITNHIVSPNAN*	CCGCAAATGG	AAAATTAGTC	0		0	0	0	0	0
2508	1622	ao	AN1572.1	55.m03104	AO070339000262	0					-105	-79	ATGCAAACTGAAAAATTAGTCGCTTAG			ATGCAAACTGAAAAATTAGTCGCTTAG	MQTEKLVA*			MQTEKLVA*	GTAAGCCCTA	CCTAACTCAA	0		0	0	0	0	0
2509	1623	af	AN7541.1	58.m07272	AO070340000242	0			-115	-77			ATGAGTCTCTATCAATCCAAGAACCGTAGATATAAATAA		ATGAGTCTCTATCAATCCAAGAACCGTAGATATAAATAA		MSLYQSKNRRYK*		MSLYQSKNRRYK*		AGTGCCGAGG	GACCCCTGCC	0		0	0	0	0	0
2510	1623	ao	AN7541.1	58.m07272	AO070340000242	0					-188	-147	ATGATGACCCTGGCCATTGAGCGACAAATGGTTTCGAGTTGA			ATGATGACCCTGGCCATTGAGCGACAAATGGTTTCGAGTTGA	MMTLAIERQMVSS*			MMTLAIERQMVSS*	TTTCGATAGA	TATGGCACTG	0		0	0	0	0	0
2511	1623	ao	AN7541.1	58.m07272	AO070340000242	0					-185	-147	ATGACCCTGGCCATTGAGCGACAAATGGTTTCGAGTTGA			ATGACCCTGGCCATTGAGCGACAAATGGTTTCGAGTTGA	MTLAIERQMVSS*			MTLAIERQMVSS*	CGATAGAATG	TATGGCACTG	0		0	0	0	0	0
2512	1623	ao	AN7541.1	58.m07272	AO070340000242	0					-161	-147	ATGGTTTCGAGTTGA			ATGGTTTCGAGTTGA	MVSS*			MVSS*	TGAGCGACAA	TATGGCACTG	0		0	0	0	0	0
2513	1623	ao	AN7541.1	58.m07272	AO070340000242	0					-145	-110	ATGGCACTGAATGCCGAAGTATACCCTGTTGGCTAG			ATGGCACTGAATGCCGAAGTATACCCTGTTGGCTAG	MALNAEVYPVG*			MALNAEVYPVG*	TCGAGTTGAT	CATCGGTAGT	0		0	0	0	0	0
2514	1623	ao	AN7541.1	58.m07272	AO070340000242	0					-64	-11	ATGTTGTATACCAGGGTACTACTCCAGACTCGAATACAGTCATTCACACACTAA			ATGTTGTATACCAGGGTACTACTCCAGACTCGAATACAGTCATTCACACACTAA	MLYTRVLLQTRIQSFTH*			MLYTRVLLQTRIQSFTH*	TCTTCCCAAG	ACCAGCCACC	0		0	0	0	0	0
2516	1624	af	AN3576.1	58.m07374	AO070342000173	0			-148	-104			ATGCCGCCTTGCGTACGTATGCAGGAGACACGCAGCATCATGTAG		ATGCCGCCTTGCGTACGTATGCAGGAGACACGCAGCATCATGTAG		MPPCVRMQETRSIM*		MPPCVRMQETRSIM*		CTGCCATCAT	ACACATCACG	0	R	0	MG04806.1	0	0	0
2517	1624	af	AN3576.1	58.m07374	AO070342000173	0			-130	-104			ATGCAGGAGACACGCAGCATCATGTAG		ATGCAGGAGACACGCAGCATCATGTAG		MQETRSIM*		MQETRSIM*		TTGCGTACGT	ACACATCACG	0	R	0	MG04806.1	0	0	0
2515	1624	an	AN3576.1	58.m07374	AO070342000173	0	-205	-29					ATGACGCGGCGCACGCTATTCTGCCGACCATCGATTCTCACCGCCCTAGGTAAAGACACGCAACGCAACAGCATCGTCTCAAACCTCTCACTCTCGATAGCGAGGGCAGCGGCTGTTGCCACGAACGGGAAAAAGCACGAAATTGACACACGACCTTATCTGATATCTTGTCACTAA	ATGACGCGGCGCACGCTATTCTGCCGACCATCGATTCTCACCGCCCTAGGTAAAGACACGCAACGCAACAGCATCGTCTCAAACCTCTCACTCTCGATAGCGAGGGCAGCGGCTGTTGCCACGAACGGGAAAAAGCACGAAATTGACACACGACCTTATCTGATATCTTGTCACTAA			MTRRTLFCRPSILTALGKDTQRNSIVSNLSLSIARAAVATNGKKHEIDTRPYLISCH*	MTRRTLFCRPSILTALGKDTQRNSIVSNLSLSIARAAVATNGKKHEIDTRPYLISCH*			CGCTTCGACC	GCGGGCTCTT	0	R	0	MG04806.1	0	0	0
2518	1624	ao	AN3576.1	58.m07374	AO070342000173	0					-146	-78	ATGGAGACACGCAACATCATCGCATTCATTCCGCCCTGTCGACTATTCTTCCTGAGAAGAGCCAAGTAA			ATGGAGACACGCAACATCATCGCATTCATTCCGCCCTGTCGACTATTCTTCCTGAGAAGAGCCAAGTAA	METRNIIAFIPPCRLFFLRRAK*			METRNIIAFIPPCRLFFLRRAK*	CCGCCCTGTC	GCGTATATGC	0	R	0	MG04806.1	0	0	0
2519	1624	ao	AN3576.1	58.m07374	AO070342000173	0					-71	-27	ATGCTCCTGTCTTTGTCGCTAGCTTTCTTGCTTGCCCTGTATTAG			ATGCTCCTGTCTTTGTCGCTAGCTTTCTTGCTTGCCCTGTATTAG	MLLSLSLAFLLALY*			MLLSLSLAFLLALY*	GTAAGCGTAT	ATACTAAGGT	0	R	0	MG04806.1	0	0	0
2520	1627	an	AN9498.1	69.m15234	AO070188000007	0	-167	-144					ATGGTGGGATACTGGTCGGAATAG	ATGGTGGGATACTGGTCGGAATAG			MVGYWSE*	MVGYWSE*			TTTCCCCTCA	ATAGCTTATC	0	R	0	0	0	0	0
2521	1627	ao	AN9498.1	69.m15234	AO070188000007	0					-208	-182	ATGGCGGGGCAAGGATGGAGGGGATAA			ATGGCGGGGCAAGGATGGAGGGGATAA	MAGQGWRG*			MAGQGWRG*	ATTCTTGACA	CAATGGAATG	0	R	0	0	0	0	0
2522	1627	ao	AN9498.1	69.m15234	AO070188000007	0					-194	-162	ATGGAGGGGATAACAATGGAATGTGATGCCTGA			ATGGAGGGGATAACAATGGAATGTGATGCCTGA	MEGITMECDA*			MEGITMECDA*	CGGGGCAAGG	GGCTAAAGAC	0	R	0	0	0	0	0
2523	1627	ao	AN9498.1	69.m15234	AO070188000007	0					-179	-162	ATGGAATGTGATGCCTGA			ATGGAATGTGATGCCTGA	MECDA*			MECDA*	GGGGATAACA	GGCTAAAGAC	0	R	0	0	0	0	0
2524	1627	ao	AN9498.1	69.m15234	AO070188000007	0					-169	-149	ATGCCTGAGGCTAAAGACTGA			ATGCCTGAGGCTAAAGACTGA	MPEAKD*			MPEAKD*	ATGGAATGTG	TATGACCGAG	0	R	0	0	0	0	0
2525	1627	ao	AN9498.1	69.m15234	AO070188000007	0					-147	-61	ATGACCGAGCCAATCGGTGAACGGGTTATCGTCCCGCTCCGAAGCCTATCTCATTATAAGCTGCGGGAACGGCAGCGGTGTAGTTGA			ATGACCGAGCCAATCGGTGAACGGGTTATCGTCCCGCTCCGAAGCCTATCTCATTATAAGCTGCGGGAACGGCAGCGGTGTAGTTGA	MTEPIGERVIVPLRSLSHYKLRERQRCS*			MTEPIGERVIVPLRSLSHYKLRERQRCS*	AAAGACTGAT	TCTACTAACA	0	R	0	0	0	0	0
2526	1628	an	AN1394.1	70.m14828	AO070233000008	0	-248	-237					ATGCCGAATTAG	ATGCCGAATTAG			MPN*	MPN*			GAGAGGCGCT	GATTAGAATC	0	DTZ	0	0	0	0	0
2527	1628	an	AN1394.1	70.m14828	AO070233000008	0	-186	-133					ATGGCTGCTCTCTCCCTCTCGATCGATACCAGACCAGCTCGATTTTTTGGGTGA	ATGGCTGCTCTCTCCCTCTCGATCGATACCAGACCAGCTCGATTTTTTGGGTGA			MAALSLSIDTRPARFFG*	MAALSLSIDTRPARFFG*			GGGGTCTATC	AGTCTCGATC	0	DTZ	0	0	0	0	0
2528	1628	ao	AN1394.1	70.m14828	AO070233000008	0					-179	-141	ATGGTCTGCATCTCTCCATCTCTAGCAACTTGGGGATAG			ATGGTCTGCATCTCTCCATCTCTAGCAACTTGGGGATAG	MVCISPSLATWG*			MVCISPSLATWG*	CATACCAGTG	CAAACTTATC	0	DTZ	0	0	0	0	0
2530	1629	af	AN5770.1	69.m14828	AO070249000008	0			-195	-163			ATGTATCATAGGTGGATTGTGGACAGATCATAG		ATGTATCATAGGTGGATTGTGGACAGATCATAG		MYHRWIVDRS*		MYHRWIVDRS*		CCGCCTTTCG	TTTACCAAAA	0	O	0	0	0	0	0
2531	1629	af	AN5770.1	69.m14828	AO070249000008	0			-136	-23			ATGTGTGACGCTCATTCCACCATTTCTCAAACTTTTTGTGCAGGACTTGTTATCCTGAGGAGAGTCAAGTCTAGACTTCTATTTGATTCTTTGTTCGGGCCATTGCGGCATTGA		ATGTGTGACGCTCATTCCACCATTTCTCAAACTTTTTGTGCAGGACTTGTTATCCTGAGGAGAGTCAAGTCTAGACTTCTATTTGATTCTTTGTTCGGGCCATTGCGGCATTGA		MCDAHSTISQTFCAGLVILRRVKSRLLFDSLFGPLRH*		MCDAHSTISQTFCAGLVILRRVKSRLLFDSLFGPLRH*		ACTCTAATTC	CCGCTTCCCC	0	O	0	0	0	0	0
2529	1629	an	AN5770.1	69.m14828	AO070249000008	0	-117	-106					ATGATGGAATAA	ATGATGGAATAA			MME*	MME*			GTCAGCGCTG	TACTCTTGGG	0	O	0	0	0	0	0
2532	1629	ao	AN5770.1	69.m14828	AO070249000008	0					-204	-154	ATGACAGATCATAGCTTAGGTTATTTGCCTGAGAATGATAGGGTAACATAG			ATGACAGATCATAGCTTAGGTTATTTGCCTGAGAATGATAGGGTAACATAG	MTDHSLGYLPENDRVT*			MTDHSLGYLPENDRVT*	TTGGTGCCTG	TCGAATAGGA	0	O	0	0	0	0	0
2533	1629	ao	AN5770.1	69.m14828	AO070249000008	0					-170	-159	ATGATAGGGTAA			ATGATAGGGTAA	MIG*			MIG*	TTGCCTGAGA	CATAGTCGAA	0	O	0	0	0	0	0

2534	1631	af	AN0410.1	54.m06664	AO070294000082	0			-185	-165			ATGATATTCAAGCAGGTCTAA		ATGATATTCAAGCAGGTCTAA		MIFKQV*		MIFKQV*		CGGACGATTC	TCTCTTTTCC	0	TR	0	0	0	0	0
2535	1632	ao	AN1991.1	58.m07600	AO070301000081	0					-214	-89	ATGTCTATCGTGGCCCGTTTCACTCTTCCACAACTCAGGTGCCTGTCTTCCTCGCTGCCTGCTGTCCGTACTTTGGCCTTTCTAATCGTTCATCTTACACCCAAAGTGCGTTTGTCTTTTCAATAG			ATGTCTATCGTGGCCCGTTTCACTCTTCCACAACTCAGGTGCCTGTCTTCCTCGCTGCCTGCTGTCCGTACTTTGGCCTTTCTAATCGTTCATCTTACACCCAAAGTGCGTTTGTCTTTTCAATAG	MSIVARFTLPQLRCLSSSLPAVRTLAFLIVHLTPKVRLSFQ*			MSIVARFTLPQLRCLSSSLPAVRTLAFLIVHLTPKVRLSFQ*	ACTTACATTT	CCAACCCAGG	0	S	0	0	0	0	0
2540	1634	af	AN3759.1	65.m07497	AO070309000045	0			-226	-203			ATGCAAGCGAGATGTGTCGAATGA		ATGCAAGCGAGATGTGTCGAATGA		MQARCVE*		MQARCVE*		CAAAGGAATC	TGCTCCTCGA	0	O	0	0	0	0	0
2541	1634	af	AN3759.1	65.m07497	AO070309000045	0			-215	-144			ATGTGTCGAATGATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		ATGTGTCGAATGATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		MCRMMLLDFSVFNPQFDLRLSRI*		MCRMMLLDFSVFNPQFDLRLSRI*		TGCAAGCGAG	CTCTTCGATA	0	O	0	0	0	0	0
2542	1634	af	AN3759.1	65.m07497	AO070309000045	0			-206	-144			ATGATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		ATGATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		MMLLDFSVFNPQFDLRLSRI*		MMLLDFSVFNPQFDLRLSRI*		GATGTGTCGA	CTCTTCGATA	0	O	0	0	0	0	0
2543	1634	af	AN3759.1	65.m07497	AO070309000045	0			-203	-144			ATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		ATGCTCCTCGACTTCTCCGTCTTTAACCCTCAGTTTGATTTACGTCTCTCTAGAATATAA		MLLDFSVFNPQFDLRLSRI*		MLLDFSVFNPQFDLRLSRI*		GTGTCGAATG	CTCTTCGATA	0	O	0	0	0	0	0
2536	1634	an	AN3759.1	65.m07497	AO070309000045	0	-203	-189					ATGCAAGGAAGATGA	ATGCAAGGAAGATGA			MQGR*	MQGR*			CACCTTGCTC	ACCGTGCCGT	0	O	0	0	0	0	0
2537	1634	an	AN3759.1	65.m07497	AO070309000045	0	-192	-136					ATGAACCGTGCCGTCTTGCTCAGCACAACTTCTTTGTCGCTCATTGAACACTATTAA	ATGAACCGTGCCGTCTTGCTCAGCACAACTTCTTTGTCGCTCATTGAACACTATTAA			MNRAVLLSTTSLSLIEHY*	MNRAVLLSTTSLSLIEHY*			TGCAAGGAAG	CTCTGGTTCC	0	O	0	0	0	0	0
2538	1634	an	AN3759.1	65.m07497	AO070309000045	0	-105	-85					ATGTATATCGTATCGCTCTAA	ATGTATATCGTATCGCTCTAA			MYIVSL*	MYIVSL*			TTAACCTTCT	TAGCACTCGC	0	O	0	0	0	0	0
2545	1635	af	AN6894.1	71.m16019	AO070314000028	0			-299	-261			ATGCCGGGTACAGCTGTTCGACAAAAGGCAAATACATAA		ATGCCGGGTACAGCTGTTCGACAAAAGGCAAATACATAA		MPGTAVRQKANT*		MPGTAVRQKANT*		TCCAAATTCC	TAGCAGCGCG	0	O	FG05403.1	0	NCU00181.1	0	0
2546	1635	af	AN6894.1	71.m16019	AO070314000028	0			-178	-161			ATGGAGATGATCTCCTAA		ATGGAGATGATCTCCTAA		MEMIS*		MEMIS*		CTTAGTTAAA	ATACTCCGTA	0	O	FG05403.1	0	NCU00181.1	0	0
2547	1635	af	AN6894.1	71.m16019	AO070314000028	0			-172	-161			ATGATCTCCTAA		ATGATCTCCTAA		MIS*		MIS*		TAAAATGGAG	ATACTCCGTA	0	O	FG05403.1	0	NCU00181.1	0	0
2544	1635	an	AN6894.1	71.m16019	AO070314000028	0	-127	-107					ATGTGCCTGAGGCATAAATAA	ATGTGCCTGAGGCATAAATAA			MCLRHK*	MCLRHK*			TAGTGCCTTT	CTAATCCGTA	0	O	FG05403.1	0	NCU00181.1	0	0
2549	1635	ao	AN6894.1	71.m16019	AO070314000028	0					-188	-129	ATGCCCATGTCAGTCCGTATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA			ATGCCCATGTCAGTCCGTATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA	MPMSVRMFNKVDHSILQMD*			MPMSVRMFNKVDHSILQMD*	CTAGCAGCCG	TTCTAGTCTA	0	O	FG05403.1	0	NCU00181.1	0	0
2550	1635	ao	AN6894.1	71.m16019	AO070314000028	0					-182	-129	ATGTCAGTCCGTATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA			ATGTCAGTCCGTATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA	MSVRMFNKVDHSILQMD*			MSVRMFNKVDHSILQMD*	GCCGATGCCC	TTCTAGTCTA	0	O	FG05403.1	0	NCU00181.1	0	0
2551	1635	ao	AN6894.1	71.m16019	AO070314000028	0					-170	-129	ATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA			ATGTTCAATAAGGTAGATCATTCTATCCTCCAGATGGATTAA	MFNKVDHSILQMD*			MFNKVDHSILQMD*	GTCAGTCCGT	TTCTAGTCTA	0	O	FG05403.1	0	NCU00181.1	0	0
2552	1635	ao	AN6894.1	71.m16019	AO070314000028	0					-93	-16	ATGCCGGAGCAATACATCATGTCTTGCGGCGCGGCCAGCGGTCGCATTTACGAAGATTCGGTCAGAATATCAACATAA			ATGCCGGAGCAATACATCATGTCTTGCGGCGCGGCCAGCGGTCGCATTTACGAAGATTCGGTCAGAATATCAACATAA	MPEQYIMSCGAASGRIYEDSVRIST*			MPEQYIMSCGAASGRIYEDSVRIST*	CTTCGCATCT	AACTTCATCG	0	O	FG05403.1	0	NCU00181.1	0	0
2553	1635	ao	AN6894.1	71.m16019	AO070314000028	0					-75	-16	ATGTCTTGCGGCGCGGCCAGCGGTCGCATTTACGAAGATTCGGTCAGAATATCAACATAA			ATGTCTTGCGGCGCGGCCAGCGGTCGCATTTACGAAGATTCGGTCAGAATATCAACATAA	MSCGAASGRIYEDSVRIST*			MSCGAASGRIYEDSVRIST*	GCAATACATC	AACTTCATCG	0	O	FG05403.1	0	NCU00181.1	0	0
2554	1636	ao	AN0902.1	70.m15511	AO070320000074	0					-270	-220	ATGGGCATGACCTGTCATACTGTCAACTCAAGAAGATCCCTGCACTATTAA			ATGGGCATGACCTGTCATACTGTCAACTCAAGAAGATCCCTGCACTATTAA	MGMTCHTVNSRRSLHY*			MGMTCHTVNSRRSLHY*	AACTTGGACA	CCTTGTCATA	0		0	0	0	0	0
2555	1636	ao	AN0902.1	70.m15511	AO070320000074	0					-264	-220	ATGACCTGTCATACTGTCAACTCAAGAAGATCCCTGCACTATTAA			ATGACCTGTCATACTGTCAACTCAAGAAGATCCCTGCACTATTAA	MTCHTVNSRRSLHY*			MTCHTVNSRRSLHY*	GACAATGGGC	CCTTGTCATA	0		0	0	0	0	0
2556	1636	ao	AN0902.1	70.m15511	AO070320000074	0					-139	-44	ATGTACTCTCGGCATCTCGCATGGGTTACCGATTCGAGCCGAACATCCACACCCCTTACTTTAAGACCATACCATATCATCCACACAACTGTGTAA			ATGTACTCTCGGCATCTCGCATGGGTTACCGATTCGAGCCGAACATCCACACCCCTTACTTTAAGACCATACCATATCATCCACACAACTGTGTAA	MYSRHLAWVTDSSRTSTPLTLRPYHIIHTTV*			MYSRHLAWVTDSSRTSTPLTLRPYHIIHTTV*	AGACACACTA	CTTGCCCCGT	0		0	0	0	0	0
2558	1639	af	AN4702.1	71.m15684	AO070329000178	0			-175	-125			ATGATCAGTTTTCTGCGGTTCGGACGGTTGAACTGTTCGCCAACAGCTTGA		ATGATCAGTTTTCTGCGGTTCGGACGGTTGAACTGTTCGCCAACAGCTTGA		MISFLRFGRLNCSPTA*		MISFLRFGRLNCSPTA*		CTCTTCGGTG	CTTGACTTGC	0		FG02810.1	0	0	0	0
2557	1639	an	AN4702.1	71.m15684	AO070329000178	0	-145	-119					ATGATCTGTATCGCTCGCATCGAGTGA	ATGATCTGTATCGCTCGCATCGAGTGA			MICIARIE*	MICIARIE*			CGGGTCGAGG	GCTCTTTCTC	0		FG02810.1	0	0	0	0
2559	1639	ao	AN4702.1	71.m15684	AO070329000178	0					-193	-170	ATGATGATCCTGTTAAACGATTAA			ATGATGATCCTGTTAAACGATTAA	MMILLND*			MMILLND*	GCTTGTTTCG	ACTGCTCGCA	0		FG02810.1	0	0	0	0
2560	1639	ao	AN4702.1	71.m15684	AO070329000178	0					-190	-170	ATGATCCTGTTAAACGATTAA			ATGATCCTGTTAAACGATTAA	MILLND*			MILLND*	TGTTTCGATG	ACTGCTCGCA	0		FG02810.1	0	0	0	0
2561	1639	ao	AN4702.1	71.m15684	AO070329000178	0					-125	-114	ATGTGTTTCTAA			ATGTGTTTCTAA	MCF*			MCF*	GAATCTCTGG	GCCGAGAGAG	0		FG02810.1	0	0	0	0
2566	1640	af	AN7401.1	69.m15499	AO070333000099	0			-75	-40			ATGGAATTTTTTTTTGCGATTGACTGGACTAGATAA		ATGGAATTTTTTTTTGCGATTGACTGGACTAGATAA		MEFFFAIDWTR*		MEFFFAIDWTR*		GACCTAAGCA	CTATTCTTCT	0	G	FG06445.1	0	NCU04997.1	0	0
2562	1640	an	AN7401.1	69.m15499	AO070333000099	0	-226	-134					ATGTGCTTGTCCCTTGTCATTCCAAGAGATGCGAGACCCTCCCGTGCAGAACCACGGAGGATGGCTCCGGGCCGGATACAGACCTCAGATTGA	ATGTGCTTGTCCCTTGTCATTCCAAGAGATGCGAGACCCTCCCGTGCAGAACCACGGAGGATGGCTCCGGGCCGGATACAGACCTCAGATTGA			MCLSLVIPRDARPSRAEPRRMAPGRIQTSD*	MCLSLVIPRDARPSRAEPRRMAPGRIQTSD*			TCCCCTAGCA	ATCATTTATC	0	G	FG06445.1	0	NCU04997.1	0	0
2563	1640	an	AN7401.1	69.m15499	AO070333000099	0	-198	-73					ATGCGAGACCCTCCCGTGCAGAACCACGGAGGATGGCTCCGGGCCGGATACAGACCTCAGATTGAATCATTTATCCGAATTGCCGTAATATGTTGGGGGGTTGAAGTGGTATATGAGCAGCTCTGA	ATGCGAGACCCTCCCGTGCAGAACCACGGAGGATGGCTCCGGGCCGGATACAGACCTCAGATTGAATCATTTATCCGAATTGCCGTAATATGTTGGGGGGTTGAAGTGGTATATGAGCAGCTCTGA			MRDPPVQNHGGWLRAGYRPQIESFIRIAVICWGVEVVYEQL*	MRDPPVQNHGGWLRAGYRPQIESFIRIAVICWGVEVVYEQL*			ATTCCAAGAG	TCTCCCTCAA	0	G	FG06445.1	0	NCU04997.1	0	0
2564	1640	an	AN7401.1	69.m15499	AO070333000099	0	-166	-134					ATGGCTCCGGGCCGGATACAGACCTCAGATTGA	ATGGCTCCGGGCCGGATACAGACCTCAGATTGA			MAPGRIQTSD*	MAPGRIQTSD*			ACCACGGAGG	ATCATTTATC	0	G	FG06445.1	0	NCU04997.1	0	0
2565	1640	an	AN7401.1	69.m15499	AO070333000099	0	-109	-95					ATGTTGGGGGGTTGA	ATGTTGGGGGGTTGA			MLGG*	MLGG*			TTGCCGTAAT	AGTGGTATAT	0	G	FG06445.1	0	NCU04997.1	0	0
2567	1643	an	AN3065.1	59.m08933	AO070337000007	0	-273	-121					ATGGACTGCAGCTTTGAGCCTCTGCTAGTGTTCGCGTTTGTTGGCTTGTTATCGTCGAAGCCCAATTTATTCTCTATTCAGCTTTTATATATTGTCGCCTACTGTTCCTTTGTATTCTTTGCTTCGTCTCCTTCTGACCCACCTGAAAGATAG	ATGGACTGCAGCTTTGAGCCTCTGCTAGTGTTCGCGTTTGTTGGCTTGTTATCGTCGAAGCCCAATTTATTCTCTATTCAGCTTTTATATATTGTCGCCTACTGTTCCTTTGTATTCTTTGCTTCGTCTCCTTCTGACCCACCTGAAAGATAG			MDCSFEPLLVFAFVGLLSSKPNLFSIQLLYIVAYCSFVFFASSPSDPPER*	MDCSFEPLLVFAFVGLLSSKPNLFSIQLLYIVAYCSFVFFASSPSDPPER*			CCCTGTGCCT	GATAGTGCGA	0	T	0	0	0	0	0
2571	1648	af	AN1433.1	55.m02939	AO070232000013	0			-253	-221			ATGGCTATTATGTGGCTTAGCTTACCAACTTGA		ATGGCTATTATGTGGCTTAGCTTACCAACTTGA		MAIMWLSLPT*		MAIMWLSLPT*		AACGCCGAGA	GATTACTCCC	0	R	FG03601.1	MG10414.1	0	0	0
2572	1648	af	AN1433.1	55.m02939	AO070232000013	0			-244	-221			ATGTGGCTTAGCTTACCAACTTGA		ATGTGGCTTAGCTTACCAACTTGA		MWLSLPT*		MWLSLPT*		AATGGCTATT	GATTACTCCC	0	R	FG03601.1	MG10414.1	0	0	0
2573	1648	af	AN1433.1	55.m02939	AO070232000013	0			-193	-83			ATGTTGGTTCCGGATCGTCTGTTGGACTCCTGTTGGAGGAGGTCCCTGAACCTGAGCCCGGAGTCTCGTGCTCGCGACAGTTGTCCTCGGTGTAGGGTATCACTTAAATAG		ATGTTGGTTCCGGATCGTCTGTTGGACTCCTGTTGGAGGAGGTCCCTGAACCTGAGCCCGGAGTCTCGTGCTCGCGACAGTTGTCCTCGGTGTAGGGTATCACTTAAATAG		MLVPDRLLDSCWRRSLNLSPESRARDSCPRCRVSLK*		MLVPDRLLDSCWRRSLNLSPESRARDSCPRCRVSLK*		ACTGGGAAAG	TGTTTGATCA	0	R	FG03601.1	MG10414.1	0	0	0
2568	1648	an	AN1433.1	55.m02939	AO070232000013	0	-252	-229					ATGCCAATATGCGGCCTGAGCTAG	ATGCCAATATGCGGCCTGAGCTAG			MPICGLS*	MPICGLS*			GTTGGTCTAC	GGATGGGGCT	0	R	FG03601.1	MG10414.1	0	0	0
2569	1648	an	AN1433.1	55.m02939	AO070232000013	0	-159	-94					ATGCTGAAGTATTGGGGCATAAGCTGCCGAACTCCGCGGCAGGCTTGTTGCATGCTTTTCTTCTAG	ATGCTGAAGTATTGGGGCATAAGCTGCCGAACTCCGCGGCAGGCTTGTTGCATGCTTTTCTTCTAG			MLKYWGISCRTPRQACCMLFF*	MLKYWGISCRTPRQACCMLFF*			CGAACAATGC	ACTCTTTTAA	0	R	FG03601.1	MG10414.1	0	0	0
2570	1648	an	AN1433.1	55.m02939	AO070232000013	0	-108	-94					ATGCTTTTCTTCTAG	ATGCTTTTCTTCTAG			MLFF*	MLFF*			GGCTTGTTGC	ACTCTTTTAA	0	R	FG03601.1	MG10414.1	0	0	0
2574	1648	ao	AN1433.1	55.m02939	AO070232000013	0					-107	-57	ATGTTAAAAAGACAGGCAGAGCCTACCAGTAACTGTGTTTCCTGGATTTAG			ATGTTAAAAAGACAGGCAGAGCCTACCAGTAACTGTGTTTCCTGGATTTAG	MLKRQAEPTSNCVSWI*			MLKRQAEPTSNCVSWI*	TGCAGCGGGA	GCTCCCTATT	0	R	FG03601.1	MG10414.1	0	0	0
2578	1651	af	AN1827.1	58.m07672	AO070292000070	0			-212	-147			ATGCTTCGAGTCAAAATTGGTAGGAAAGAGACTCATAAAAGGCATGGACCTTGCCGATGGGAGTAA		ATGCTTCGAGTCAAAATTGGTAGGAAAGAGACTCATAAAAGGCATGGACCTTGCCGATGGGAGTAA		MLRVKIGRKETHKRHGPCRWE*		MLRVKIGRKETHKRHGPCRWE*		GATGATCTAC	GTACTTCATA	0	G	0	0	0	0	0
2579	1651	af	AN1827.1	58.m07672	AO070292000070	0			-169	-29			ATGGACCTTGCCGATGGGAGTAAGTACTTCATATCAAACTTCCCAACGACTAATACAGGTCCCGGCAATTCGTTCCTTTCTGTTTACTTCTTCATTTGTCTTTCCTTCCATTGGGCTTGTAGTCCCAGATTCACTCGTTAA		ATGGACCTTGCCGATGGGAGTAAGTACTTCATATCAAACTTCCCAACGACTAATACAGGTCCCGGCAATTCGTTCCTTTCTGTTTACTTCTTCATTTGTCTTTCCTTCCATTGGGCTTGTAGTCCCAGATTCACTCGTTAA		MDLADGSKYFISNFPTTNTGPGNSFLSVYFFICLSFHWACSPRFTR*		MDLADGSKYFISNFPTTNTGPGNSFLSVYFFICLSFHWACSPRFTR*		CATAAAAGGC	TCTGCTTAAT	0	G	0	0	0	0	0
2580	1651	af	AN1827.1	58.m07672	AO070292000070	0			-156	-10			ATGGGAGTAAGTACTTCATATCAAACTTCCCAACGACTAATACAGGTCCCGGCAATTCGTTCCTTTCTGTTTACTTCTTCATTTGTCTTTCCTTCCATTGGGCTTGTAGTCCCAGATTCACTCGTTAATCTGCTTAATTCTCAATAA		ATGGGAGTAAGTACTTCATATCAAACTTCCCAACGACTAATACAGGTCCCGGCAATTCGTTCCTTTCTGTTTACTTCTTCATTTGTCTTTCCTTCCATTGGGCTTGTAGTCCCAGATTCACTCGTTAATCTGCTTAATTCTCAATAA		MGVSTSYQTSQRLIQVPAIRSFLFTSSFVFPSIGLVVPDSLVNLLNSQ*		MGVSTSYQTSQRLIQVPAIRSFLFTSSFVFPSIGLVVPDSLVNLLNSQ*		GACCTTGCCG	CGAGATATCA	0	G	0	0	0	0	0
2575	1651	an	AN1827.1	58.m07672	AO070292000070	0	-242	-150					ATGCTGGTAACATGCCTCCCTGAATGCCTGGGCCCATACCCTAAAGCGCCTGATAAAAGGTGCAACAGAGCCGCTGTTAACGGAGGAACTTGA	ATGCTGGTAACATGCCTCCCTGAATGCCTGGGCCCATACCCTAAAGCGCCTGATAAAAGGTGCAACAGAGCCGCTGTTAACGGAGGAACTTGA			MLVTCLPECLGPYPKAPDKRCNRAAVNGGT*	MLVTCLPECLGPYPKAPDKRCNRAAVNGGT*			CCCCTGAGGC	GCAGAGGCGA	0	G	0	0	0	0	0
2576	1651	an	AN1827.1	58.m07672	AO070292000070	0	-231	-220					ATGCCTCCCTGA	ATGCCTCCCTGA			MPP*	MPP*			TGCTGGTAAC	ATGCCTGGGC	0	G	0	0	0	0	0
2577	1651	an	AN1827.1	58.m07672	AO070292000070	0	-219	-199					ATGCCTGGGCCCATACCCTAA	ATGCCTGGGCCCATACCCTAA			MPGPIP*	MPGPIP*			GCCTCCCTGA	AGCGCCTGAT	0	G	0	0	0	0	0
2581	1651	ao	AN1827.1	58.m07672	AO070292000070	0					-231	-217	ATGTCATCCGGATGA			ATGTCATCCGGATGA	MSSG*			MSSG*	CGATGGGTTA	TAAAAAGGTC	0	G	0	0	0	0	0
2582	1651	ao	AN1827.1	58.m07672	AO070292000070	0					-220	-119	ATGATAAAAAGGTCAACCATGTCCAACCGTCTCGTGGTGGAGGAAACGAGAAGTCGCAAGGCCAGATTAGAAGTCTTTCTTTCAGATACTTTCCTTAATTGA			ATGATAAAAAGGTCAACCATGTCCAACCGTCTCGTGGTGGAGGAAACGAGAAGTCGCAAGGCCAGATTAGAAGTCTTTCTTTCAGATACTTTCCTTAATTGA	MIKRSTMSNRLVVEETRSRKARLEVFLSDTFLN*			MIKRSTMSNRLVVEETRSRKARLEVFLSDTFLN*	TGTCATCCGG	TATTTATTGC	0	G	0	0	0	0	0
2583	1651	ao	AN1827.1	58.m07672	AO070292000070	0					-202	-119	ATGTCCAACCGTCTCGTGGTGGAGGAAACGAGAAGTCGCAAGGCCAGATTAGAAGTCTTTCTTTCAGATACTTTCCTTAATTGA			ATGTCCAACCGTCTCGTGGTGGAGGAAACGAGAAGTCGCAAGGCCAGATTAGAAGTCTTTCTTTCAGATACTTTCCTTAATTGA	MSNRLVVEETRSRKARLEVFLSDTFLN*			MSNRLVVEETRSRKARLEVFLSDTFLN*	AAGGTCAACC	TATTTATTGC	0	G	0	0	0	0	0
2585	1652	af	AN2272.1	71.m15917	AO070295000048	0			-210	-160			ATGGGGCAACTGGCCGCCGGCCGCCGATCTTACTCGATGGGCTCGGAGTAA		ATGGGGCAACTGGCCGCCGGCCGCCGATCTTACTCGATGGGCTCGGAGTAA		MGQLAAGRRSYSMGSE*		MGQLAAGRRSYSMGSE*		GACCGCCTGG	ACTGAACCTT	0	G	FG06932.1	MG06270.1	NCU00414.1	0	0
2586	1652	af	AN2272.1	71.m15917	AO070295000048	0			-174	-160			ATGGGCTCGGAGTAA		ATGGGCTCGGAGTAA		MGSE*		MGSE*		ATCTTACTCG	ACTGAACCTT	0	G	FG06932.1	MG06270.1	NCU00414.1	0	0
2584	1652	an	AN2272.1	71.m15917	AO070295000048	0	-207	-145					ATGAAATATTGCGGCCTGGAGTTTCAGGTGTTCATCTGCTGCCCCTCCATAGTAATTCTTTAG	ATGAAATATTGCGGCCTGGAGTTTCAGGTGTTCATCTGCTGCCCCTCCATAGTAATTCTTTAG			MKYCGLEFQVFICCPSIVIL*	MKYCGLEFQVFICCPSIVIL*			GCTGCACCGG	GCCGGGCGAC	0	G	FG06932.1	MG06270.1	NCU00414.1	0	0

2587	1652	ao	AN2272.1	71.m15917	AO070295000048	0					-200	-12	ATGATCCGGATCTTCTTTCTGTTGCTGCCCCTCCGGACCATCATCCCTCCCCCACCTTTTCTTGCATTCTCACCCTCACCTTCTCCTCTTCTTCCTCCTCTCAGAGATTTTCTTTTCTTGACATTTTCCCTTCCTCTCCACACGTCCCTTCTCGCTCGTCCTTTCTTTACAGGCACTTTCTCTAGTTGA			ATGATCCGGATCTTCTTTCTGTTGCTGCCCCTCCGGACCATCATCCCTCCCCCACCTTTTCTTGCATTCTCACCCTCACCTTCTCCTCTTCTTCCTCCTCTCAGAGATTTTCTTTTCTTGACATTTTCCCTTCCTCTCCACACGTCCCTTCTCGCTCGTCCTTTCTTTACAGGCACTTTCTCTAGTTGA	MIRIFFLLLPLRTIIPPPPFLAFSPSPSPLLPPLRDFLFLTFSLPLHTSLLARPFFTGTFSS*			MIRIFFLLLPLRTIIPPPPFLAFSPSPSPLLPPLRDFLFLTFSLPLHTSLLARPFFTGTFSS*	GGTACGGCAT	AATAAACGAC	0	G	FG06932.1	MG06270.1	NCU00414.1	0	0
2588	1659	af	AN3620.1	58.m07407	AO070342000132	0			-167	-144			ATGTACTGTAAATCGGAAAGTTGA		ATGTACTGTAAATCGGAAAGTTGA		MYCKSES*		MYCKSES*		CCGTCTTTCT	AAGCCAAAAG	0	DL	FG00281.1	MG03676.1	0	0	0
2590	1659	ao	AN3620.1	58.m07407	AO070342000132	0					-145	-125	ATGTACCATATACCCAGTTAA			ATGTACCATATACCCAGTTAA	MYHIPS*			MYHIPS*	GATCTTTTCA	GAGAGAAGCA	0	DL	FG00281.1	MG03676.1	0	0	0
2592	1663	af	AN3408.1	66.m04620	AO070281000045	0			-185	-171			ATGGATCAGAGATAA		ATGGATCAGAGATAA		MDQR*		MDQR*		GCCTGATTGA	GACCGGGCCC	0	E	0	0	0	0	0
2591	1663	an	AN3408.1	66.m04620	AO070281000045	0	-98	-3					ATGGTGCGACTCGCCTCCGTCGCGGCTGCCTTTTTTACCTTCTGCGACAAGTCAAGCCCATTCTGTCCGACGAGGATTTCCCTTGCCGTCCTCTAA	ATGGTGCGACTCGCCTCCGTCGCGGCTGCCTTTTTTACCTTCTGCGACAAGTCAAGCCCATTCTGTCCGACGAGGATTTCCCTTGCCGTCCTCTAA			MVRLASVAAAFFTFCDKSSPFCPTRISLAVL*	MVRLASVAAAFFTFCDKSSPFCPTRISLAVL*			TGAGTATAAT	TCATGGCTGC	0	E	0	0	0	0	0
2593	1663	ao	AN3408.1	66.m04620	AO070281000045	0					-185	-123	ATGATAAGACCGGTCCCGCATCGGATCCCAGACCAGGCTTTCCCACTAGGAACGGGAATATAA			ATGATAAGACCGGTCCCGCATCGGATCCCAGACCAGGCTTTCCCACTAGGAACGGGAATATAA	MIRPVPHRIPDQAFPLGTGI*			MIRPVPHRIPDQAFPLGTGI*	GTCGCTTCGA	GGTGGCTCTC	0	E	0	0	0	0	0
2594	1664	af	AN4687.1	71.m15670	AO070284000042	0			-218	-117			ATGAAGCTGGAGTCCGGGGACTTCATCGTCATGCCCTTCTTTTTCTTCCCCATCATCAACCTGCGGTCTTTCCCTTCTCAAAATTACTTCCCACCTTTTTGA		ATGAAGCTGGAGTCCGGGGACTTCATCGTCATGCCCTTCTTTTTCTTCCCCATCATCAACCTGCGGTCTTTCCCTTCTCAAAATTACTTCCCACCTTTTTGA		MKLESGDFIVMPFFFFPIINLRSFPSQNYFPPF*		MKLESGDFIVMPFFFFPIINLRSFPSQNYFPPF*		TCCGCAGCCG	GGACATTGTC	0	EI	0	MG02541.1	0	0	0
2595	1664	af	AN4687.1	71.m15670	AO070284000042	0			-188	-117			ATGCCCTTCTTTTTCTTCCCCATCATCAACCTGCGGTCTTTCCCTTCTCAAAATTACTTCCCACCTTTTTGA		ATGCCCTTCTTTTTCTTCCCCATCATCAACCTGCGGTCTTTCCCTTCTCAAAATTACTTCCCACCTTTTTGA		MPFFFFPIINLRSFPSQNYFPPF*		MPFFFFPIINLRSFPSQNYFPPF*		CTTCATCGTC	GGACATTGTC	0	EI	0	MG02541.1	0	0	0
2604	1669	af	AN1986.1	58.m07593	AO070301000073	0			-256	-233			ATGAGTAAAAATAAACCTGGATGA		ATGAGTAAAAATAAACCTGGATGA		MSKNKPG*		MSKNKPG*		TGCTACCACA	GAGTCATCAG	0	P	0	0	0	0	0
2605	1669	af	AN1986.1	58.m07593	AO070301000073	0			-236	-183			ATGAGAGTCATCAGCTGCTTGAAGAACATGGAGGTACGGAGGAAAGAGAATTGA		ATGAGAGTCATCAGCTGCTTGAAGAACATGGAGGTACGGAGGAAAGAGAATTGA		MRVISCLKNMEVRRKEN*		MRVISCLKNMEVRRKEN*		ATAAACCTGG	AGTACGGAGT	0	P	0	0	0	0	0
2606	1669	af	AN1986.1	58.m07593	AO070301000073	0			-209	-183			ATGGAGGTACGGAGGAAAGAGAATTGA		ATGGAGGTACGGAGGAAAGAGAATTGA		MEVRRKEN*		MEVRRKEN*		CTTGAAGAAC	AGTACGGAGT	0	P	0	0	0	0	0
2607	1669	af	AN1986.1	58.m07593	AO070301000073	0			-135	-88			ATGACATATGACGCGCATCTTCGTTTCTCCTCCGCATTTCATCCGTAA		ATGACATATGACGCGCATCTTCGTTTCTCCTCCGCATTTCATCCGTAA		MTYDAHLRFSSAFHP*		MTYDAHLRFSSAFHP*		AGGAAAGACT	CCTTCTCCAT	0	P	0	0	0	0	0
2608	1669	af	AN1986.1	58.m07593	AO070301000073	0			-128	-33			ATGACGCGCATCTTCGTTTCTCCTCCGCATTTCATCCGTAACCTTCTCCATCCTTCATCTGTTCGGCACTCACGCATCCCCTTTATAGTCGATTGA		ATGACGCGCATCTTCGTTTCTCCTCCGCATTTCATCCGTAACCTTCTCCATCCTTCATCTGTTCGGCACTCACGCATCCCCTTTATAGTCGATTGA		MTRIFVSPPHFIRNLLHPSSVRHSRIPFIVD*		MTRIFVSPPHFIRNLLHPSSVRHSRIPFIVD*		ACTATGACAT	AGGTCAGCTG	0	P	0	0	0	0	0
2601	1669	an	AN1986.1	58.m07593	AO070301000073	0	-196	-134					ATGAGTAGAACAAAAAGGCTTGGCGCGATCGACGATGATTTCATGCTCTTTTTAGTGCCGTGA	ATGAGTAGAACAAAAAGGCTTGGCGCGATCGACGATGATTTCATGCTCTTTTTAGTGCCGTGA			MSRTKRLGAIDDDFMLFLVP*	MSRTKRLGAIDDDFMLFLVP*			CACTATACCT	TGCCATCGAT	0	P	0	0	0	0	0
2602	1669	an	AN1986.1	58.m07593	AO070301000073	0	-162	-142					ATGATTTCATGCTCTTTTTAG	ATGATTTCATGCTCTTTTTAG			MISCSF*	MISCSF*			GCGATCGACG	TGCCGTGATG	0	P	0	0	0	0	0
2603	1669	an	AN1986.1	58.m07593	AO070301000073	0	-154	-134					ATGCTCTTTTTAGTGCCGTGA	ATGCTCTTTTTAGTGCCGTGA			MLFLVP*	MLFLVP*			CGATGATTTC	TGCCATCGAT	0	P	0	0	0	0	0
2609	1669	ao	AN1986.1	58.m07593	AO070301000073	0					-197	-186	ATGCCGTTGTAA			ATGCCGTTGTAA	MPL*			MPL*	TTGTCTAATA	TTGGTGATGG	0	P	0	0	0	0	0
2610	1669	ao	AN1986.1	58.m07593	AO070301000073	0					-179	-54	ATGGAATTAAATGCGGAGAAAGTCACGCCGAATGGAGTTAAGCTCCAAATAAGCTATGATGCCATCCATTTCCTTTACCTCCACTTTTCTCTGCTCTTGCACCTCCCAGCGTCCCTCTTCGAATGA			ATGGAATTAAATGCGGAGAAAGTCACGCCGAATGGAGTTAAGCTCCAAATAAGCTATGATGCCATCCATTTCCTTTACCTCCACTTTTCTCTGCTCTTGCACCTCCCAGCGTCCCTCTTCGAATGA	MELNAEKVTPNGVKLQISYDAIHFLYLHFSLLLHLPASLFE*			MELNAEKVTPNGVKLQISYDAIHFLYLHFSLLLHLPASLFE*	GTAATTGGTG	TATCCATCTC	0	P	0	0	0	0	0
2611	1669	ao	AN1986.1	58.m07593	AO070301000073	0					-169	-128	ATGCGGAGAAAGTCACGCCGAATGGAGTTAAGCTCCAAATAA			ATGCGGAGAAAGTCACGCCGAATGGAGTTAAGCTCCAAATAA	MRRKSRRMELSSK*			MRRKSRRMELSSK*	ATGGAATTAA	GCTATGATGC	0	P	0	0	0	0	0
2612	1669	ao	AN1986.1	58.m07593	AO070301000073	0					-148	-128	ATGGAGTTAAGCTCCAAATAA			ATGGAGTTAAGCTCCAAATAA	MELSSK*			MELSSK*	GTCACGCCGA	GCTATGATGC	0	P	0	0	0	0	0
2614	1671	af	AN6626.1	62.m03217	AO070315000108	0			-103	-92			ATGCAAAAATAG		ATGCAAAAATAG		MQK*		MQK*		GTGCTGACCT	AGCCAAGCCT	0	R	0	0	0	0	0
2615	1671	ao	AN6626.1	62.m03217	AO070315000108	0					-189	-172	ATGAAGCAAAACCCTTGA			ATGAAGCAAAACCCTTGA	MKQNP*			MKQNP*	AAATCAGTAA	AACAAAAAAC	0	R	0	0	0	0	0
2617	1674	an	AN2598.1	70.m15706	AO070330000106	0	-203	-150					ATGAGCTCTGATCCTGTACCCCTCACCCCGAAGGCCATGATCAGTCTCATTTAA	ATGAGCTCTGATCCTGTACCCCTCACCCCGAAGGCCATGATCAGTCTCATTTAA			MSSDPVPLTPKAMISLI*	MSSDPVPLTPKAMISLI*			TATCTTGCTC	GCATACATTA	0	E	0	0	0	0	0
2618	1674	an	AN2598.1	70.m15706	AO070330000106	0	-167	-150					ATGATCAGTCTCATTTAA	ATGATCAGTCTCATTTAA			MISLI*	MISLI*			CCCGAAGGCC	GCATACATTA	0	E	0	0	0	0	0
2619	1675	an	AN3308.1	52.m03702	AO070330000181	0	-166	-152					ATGTTCCCTTCGTAA	ATGTTCCCTTCGTAA			MFPS*	MFPS*			TTTCTCTGGG	CTTAGCATTG	0	G	0	0	0	0	0
2621	1677	ao	AN2869.1	59.m08714	AO070338000153	0					-228	-109	ATGACACCTTCCCCTTTTAGATCGCATGACACTGTTCTTTTTTCATGTCGTCTGCTTCTCCCCCGCACTTTTTCCTTCTTAAACCCTTTCTCTCCCCCTATTCCCATCTCCTCCCTTTGA			ATGACACCTTCCCCTTTTAGATCGCATGACACTGTTCTTTTTTCATGTCGTCTGCTTCTCCCCCGCACTTTTTCCTTCTTAAACCCTTTCTCTCCCCCTATTCCCATCTCCTCCCTTTGA	MTPSPFRSHDTVLFSCRLLLPRTFSFLNPFSPPIPISSL*			MTPSPFRSHDTVLFSCRLLLPRTFSFLNPFSPPIPISSL*	CAGGTCTTCC	AAAGTACTGC	0	R	0	0	0	0	0
2622	1677	ao	AN2869.1	59.m08714	AO070338000153	0					-203	-147	ATGACACTGTTCTTTTTTCATGTCGTCTGCTTCTCCCCCGCACTTTTTCCTTCTTAA			ATGACACTGTTCTTTTTTCATGTCGTCTGCTTCTCCCCCGCACTTTTTCCTTCTTAA	MTLFFFHVVCFSPALFPS*			MTLFFFHVVCFSPALFPS*	TTTAGATCGC	ACCCTTTCTC	0	R	0	0	0	0	0
2629	1679	af	AN1923.1	69.m14941	AO070341000112	0			-448	-215			ATGACCTGGCAGCTTAGGCTCGCATCTCGCATGCGGCCATCTCCGTTGGTGTTGGGACGTTCAGTTTCCCGGCCGACTATTCGGTCACCGCGCCATCAGGCTTTCTGCTGGGCGGTAGGGCTACCCGCGGGGGTCTCTAGCCCCAGGACCTCTCCAGGTATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		ATGACCTGGCAGCTTAGGCTCGCATCTCGCATGCGGCCATCTCCGTTGGTGTTGGGACGTTCAGTTTCCCGGCCGACTATTCGGTCACCGCGCCATCAGGCTTTCTGCTGGGCGGTAGGGCTACCCGCGGGGGTCTCTAGCCCCAGGACCTCTCCAGGTATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		MTWQLRLASRMRPSPLVLGRSVSRPTIRSPRHQAFCWAVGLPAGVSSPRTSPGMFRFAFGRLSLAPFGPENRPISQP*		MTWQLRLASRMRPSPLVLGRSVSRPTIRSPRHQAFCWAVGLPAGVSSPRTSPGMFRFAFGRLSLAPFGPENRPISQP*		GAAGCGCAGT	ACCATCATTG	0	E	0	0	0	0	0
2630	1679	af	AN1923.1	69.m14941	AO070341000112	0			-418	-215			ATGCGGCCATCTCCGTTGGTGTTGGGACGTTCAGTTTCCCGGCCGACTATTCGGTCACCGCGCCATCAGGCTTTCTGCTGGGCGGTAGGGCTACCCGCGGGGGTCTCTAGCCCCAGGACCTCTCCAGGTATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		ATGCGGCCATCTCCGTTGGTGTTGGGACGTTCAGTTTCCCGGCCGACTATTCGGTCACCGCGCCATCAGGCTTTCTGCTGGGCGGTAGGGCTACCCGCGGGGGTCTCTAGCCCCAGGACCTCTCCAGGTATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		MRPSPLVLGRSVSRPTIRSPRHQAFCWAVGLPAGVSSPRTSPGMFRFAFGRLSLAPFGPENRPISQP*		MRPSPLVLGRSVSRPTIRSPRHQAFCWAVGLPAGVSSPRTSPGMFRFAFGRLSLAPFGPENRPISQP*		CGCATCTCGC	ACCATCATTG	0	E	0	0	0	0	0
2631	1679	af	AN1923.1	69.m14941	AO070341000112	0			-289	-215			ATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		ATGTTCCGGTTTGCTTTCGGGAGACTCTCCCTAGCTCCGTTTGGCCCCGAAAATCGTCCGATCAGCCAACCATGA		MFRFAFGRLSLAPFGPENRPISQP*		MFRFAFGRLSLAPFGPENRPISQP*		CTCTCCAGGT	ACCATCATTG	0	E	0	0	0	0	0
2632	1679	af	AN1923.1	69.m14941	AO070341000112	0			-218	-180			ATGAACCATCATTGGATGCTGTTCTTTATGAGGCAATAA		ATGAACCATCATTGGATGCTGTTCTTTATGAGGCAATAA		MNHHWMLFFMRQ*		MNHHWMLFFMRQ*		TCAGCCAACC	ATGTATGGTC	0	E	0	0	0	0	0
2633	1679	af	AN1923.1	69.m14941	AO070341000112	0			-203	-180			ATGCTGTTCTTTATGAGGCAATAA		ATGCTGTTCTTTATGAGGCAATAA		MLFFMRQ*		MLFFMRQ*		CCATCATTGG	ATGTATGGTC	0	E	0	0	0	0	0
2634	1679	af	AN1923.1	69.m14941	AO070341000112	0			-191	-180			ATGAGGCAATAA		ATGAGGCAATAA		MRQ*		MRQ*		GCTGTTCTTT	ATGTATGGTC	0	E	0	0	0	0	0
2635	1679	af	AN1923.1	69.m14941	AO070341000112	0			-179	-87			ATGTATGGTCTGGCACTTGGCATACGGCCACGTCCTTTCCCCTCATCTCGTGACAAATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGA		ATGTATGGTCTGGCACTTGGCATACGGCCACGTCCTTTCCCCTCATCTCGTGACAAATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGA		MYGLALGIRPRPFPSSRDKCVSFTPYPPHL*		MYGLALGIRPRPFPSSRDKCVSFTPYPPHL*		GAGGCAATAA	GTCAATCGTT	0	E	0	0	0	0	0
2636	1679	af	AN1923.1	69.m14941	AO070341000112	0			-175	-59			ATGGTCTGGCACTTGGCATACGGCCACGTCCTTTCCCCTCATCTCGTGACAAATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGAGTCAATCGTTCGGTTCTCAGGTACATAA		ATGGTCTGGCACTTGGCATACGGCCACGTCCTTTCCCCTCATCTCGTGACAAATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGAGTCAATCGTTCGGTTCTCAGGTACATAA		MVWHLAYGHVLSPHLVTNASLLLRTHPTFESIVRFSGT*		MVWHLAYGHVLSPHLVTNASLLLRTHPTFESIVRFSGT*		CAATAAATGT	TGCATGACTT	0	E	0	0	0	0	0
2637	1679	af	AN1923.1	69.m14941	AO070341000112	0			-123	-52			ATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGAGTCAATCGTTCGGTTCTCAGGTACATAATGCATGA		ATGCGTCTCTTTTACTCCGTACCCACCCCACCTTTGAGTCAATCGTTCGGTTCTCAGGTACATAATGCATGA		MRLFYSVPTPPLSQSFGSQVHNA*		MRLFYSVPTPPLSQSFGSQVHNA*		CTCGTGACAA	CTTGATCTCG	0	E	0	0	0	0	0
2623	1679	an	AN1923.1	69.m14941	AO070341000112	0	-469	-158					ATGACCTGGCAAGGGATCGCAACCCATGTGCGGACACCGCTGCGGCGGGCAGTGACTTTCCAGCCGAATAATGCTCGGCTCGCGCGACAGAGCCAGATTTATCAGTCTCGTTCGTTCTCTCGAGCAGCGTTAGCCGCGGGAAGATCGAGTGTGTTGTCGGGTAAGTGGCCTCGGGAACCCCCGAGAGAGCCTGCGAGTCTCCAAGTCCGCCTTCCTGATGGCTCCGATCTCCATCTGCATTATTGCCAGATCGGTGCCAGCCGGCCTGGGCAGAGTCCACACCTCGTGACATCCCTGATGAGTGATTTATAA	ATGACCTGGCAAGGGATCGCAACCCATGTGCGGACACCGCTGCGGCGGGCAGTGACTTTCCAGCCGAATAATGCTCGGCTCGCGCGACAGAGCCAGATTTATCAGTCTCGTTCGTTCTCTCGAGCAGCGTTAGCCGCGGGAAGATCGAGTGTGTTGTCGGGTAAGTGGCCTCGGGAACCCCCGAGAGAGCCTGCGAGTCTCCAAGTCCGCCTTCCTGATGGCTCCGATCTCCATCTGCATTATTGCCAGATCGGTGCCAGCCGGCCTGGGCAGAGTCCACACCTCGTGACATCCCTGATGAGTGATTTATAA			MTWQGIATHVRTPLRRAVTFQPNNARLARQSQIYQSRSFSRAALAAGRSSVLSGKWPREPPREPASLQVRLPDGSDLHLHYCQIGASRPGQSPHLVTSLMSDL*	MTWQGIATHVRTPLRRAVTFQPNNARLARQSQIYQSRSFSRAALAAGRSSVLSGKWPREPPREPASLQVRLPDGSDLHLHYCQIGASRPGQSPHLVTSLMSDL*			AGTCGACAGA	AATCAAAAGC	0	E	0	0	0	0	0
2626	1679	an	AN1923.1	69.m14941	AO070341000112	0	-252	-181					ATGGCTCCGATCTCCATCTGCATTATTGCCAGATCGGTGCCAGCCGGCCTGGGCAGAGTCCACACCTCGTGA	ATGGCTCCGATCTCCATCTGCATTATTGCCAGATCGGTGCCAGCCGGCCTGGGCAGAGTCCACACCTCGTGA			MAPISICIIARSVPAGLGRVHTS*	MAPISICIIARSVPAGLGRVHTS*			CGCCTTCCTG	CATCCCTGAT	0	E	0	0	0	0	0
2627	1679	an	AN1923.1	69.m14941	AO070341000112	0	-172	-158					ATGAGTGATTTATAA	ATGAGTGATTTATAA			MSDL*	MSDL*			GACATCCCTG	AATCAAAAGC	0	E	0	0	0	0	0
2628	1679	an	AN1923.1	69.m14941	AO070341000112	0	-103	-68					ATGGGACCATTTGCCCGACTACATGGCCTGACCTGA	ATGGGACCATTTGCCCGACTACATGGCCTGACCTGA			MGPFARLHGLT*	MGPFARLHGLT*			CGGTCTACCA	GATTTATACC	0	E	0	0	0	0	0
2638	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-416	-30	ATGACCTGGCAGTTAAGACTCGTGCGGGCATCTCCGCTACGATGCTCACTTTCCCGGCCGAATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAGGCCTTCTTCAGGTATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA			ATGACCTGGCAGTTAAGACTCGTGCGGGCATCTCCGCTACGATGCTCACTTTCCCGGCCGAATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAGGCCTTCTTCAGGTATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA	MTWQLRLVRASPLRCSLSRPNGPWHIPRASSSSTRFPAGAFRPSSGMCFGNLSFGPMGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*			MTWQLRLVRASPLRCSLSRPNGPWHIPRASSSSTRFPAGAFRPSSGMCFGNLSFGPMGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*	CCTCAGCATC	CCCCTCTCGA	0	E	0	0	0	0	0

2640	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-355	-200	ATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAGGCCTTCTTCAGGTATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAG			ATGGTCCGTGGCATATCCCGCGGGCGTCTTCCAGCAGCACAAGGTTCCCCGCCGGGGCTTTTAGGCCTTCTTCAGGTATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAG	MVRGISRGRLPAAQGSPPGLLGLLQVCVSEISRSVPWGRSFYTCSLDATSV*			MVRGISRGRLPAAQGSPPGLLGLLQVCVSEISRSVPWGRSFYTCSLDATSV*	TCCCGGCCGA	TCACTTTCCT	0	E	0	0	0	0	0
2641	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-278	-30	ATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA			ATGTGTTTCGGAAATCTCTCGTTCGGTCCCATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA	MCFGNLSFGPMGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*			MCFGNLSFGPMGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*	TTCTTCAGGT	CCCCTCTCGA	0	E	0	0	0	0	0
2642	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-248	-30	ATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA			ATGGGGCCGATCCTTCTACACCTGTTCATTGGATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGAACTGTCACCCGCTCAAAAGCAAAGATATCCCCCTCACCCCGTGACATGCATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA	MGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*			MGPILLHLFIGCHICLVTFLVCIFELSPAQKQRYPPHPVTCMVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*	GTTCGGTCCC	CCCCTCTCGA	0	E	0	0	0	0	0
2643	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-216	-175	ATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGA			ATGCCACATCTGTTTAGTCACTTTCCTGGTCTGTATTTTTGA	MPHLFSHFPGLYF*			MPHLFSHFPGLYF*	TGTTCATTGG	ACTGTCACCC	0	E	0	0	0	0	0
2644	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-125	-30	ATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA			ATGGTCATTCCTTCCCCTCATGGGGGTCGCCATTTAAATATCCAATGGATGCTCCATCCGGGCGAGCGCTCGACTCCATCAAAGCAAGACAACTGA	MVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*			MVIPSPHGGRHLNIQWMLHPGERSTPSKQDN*	CGTGACATGC	CCCCTCTCGA	0	E	0	0	0	0	0
2645	1679	ao	AN1923.1	69.m14941	AO070341000112	0					-106	-89	ATGGGGGTCGCCATTTAA			ATGGGGGTCGCCATTTAA	MGVAI*			MGVAI*	CCTTCCCCTC	ATATCCAATG	0	E	0	0	0	0	0
2648	1680	af	AN3720.1	69.m15726	AO070341000352	0			-239	-141			ATGATACCTTGGATTCGTTTTCACATTTGTCTGAAGCGTAACCCTGCTTGTTGGTACGCGGATTGCCCTGAGTCATTGATCCCCCCGCCCCTCGCTTGA		ATGATACCTTGGATTCGTTTTCACATTTGTCTGAAGCGTAACCCTGCTTGTTGGTACGCGGATTGCCCTGAGTCATTGATCCCCCCGCCCCTCGCTTGA		MIPWIRFHICLKRNPACWYADCPESLIPPPLA*		MIPWIRFHICLKRNPACWYADCPESLIPPPLA*		GCATCTGCCT	ACAGGTGCTG	0	U	0	0	0	0	0
2647	1680	an	AN3720.1	69.m15726	AO070341000352	0	-159	-139					ATGCCTTCCCTCTTATCGTGA	ATGCCTTCCCTCTTATCGTGA			MPSLLS*	MPSLLS*			TTAGTTGCAG	CCGAAGCATT	0	U	0	0	0	0	0
2649	1680	ao	AN3720.1	69.m15726	AO070341000352	0					-211	-179	ATGGTTGGACCGTTAACGAATTTTGGCTGTTAG			ATGGTTGGACCGTTAACGAATTTTGGCTGTTAG	MVGPLTNFGC*			MVGPLTNFGC*	CTCAATTTAT	TACGCAGATT	0	U	0	0	0	0	0
2652	1683	af	AN6912.1	71.m15220	AO070219000017	0			-219	-202			ATGAGAAGAGAAGGTTGA		ATGAGAAGAGAAGGTTGA		MRREG*		MRREG*		GGAGGATCAA	AGAAGATCTG	0		0	0	0	0	0
2653	1683	af	AN6912.1	71.m15220	AO070219000017	0			-180	-76			ATGGGACAAGGAGTCTTACGCCAGCTCGCGTCAGCCTCTGTAAAAGAAACCGCGGGCTGCGGTTGCGGTCTCTGTTGGCCACCGGAGCTTTTCTTCTATCGATAA		ATGGGACAAGGAGTCTTACGCCAGCTCGCGTCAGCCTCTGTAAAAGAAACCGCGGGCTGCGGTTGCGGTCTCTGTTGGCCACCGGAGCTTTTCTTCTATCGATAA		MGQGVLRQLASASVKETAGCGCGLCWPPELFFYR*		MGQGVLRQLASASVKETAGCGCGLCWPPELFFYR*		TGCATCTGCT	GCGGCTTCTC	0		0	0	0	0	0
2650	1683	an	AN6912.1	71.m15220	AO070219000017	0	-216	-112					ATGAAGAGTTATAAGACGACGCATAGAGACAGCGATGCTGGAGCACAGGCAACTACAGAAAACGTTGTATGGAGGAGGAAGCACCTGCAGATCGCCTGCATGTAA	ATGAAGAGTTATAAGACGACGCATAGAGACAGCGATGCTGGAGCACAGGCAACTACAGAAAACGTTGTATGGAGGAGGAAGCACCTGCAGATCGCCTGCATGTAA			MKSYKTTHRDSDAGAQATTENVVWRRKHLQIACM*	MKSYKTTHRDSDAGAQATTENVVWRRKHLQIACM*			TTCATGGCTG	GCGCCCCAGT	0		0	0	0	0	0
2651	1683	an	AN6912.1	71.m15220	AO070219000017	0	-182	-72					ATGCTGGAGCACAGGCAACTACAGAAAACGTTGTATGGAGGAGGAAGCACCTGCAGATCGCCTGCATGTAAGCGCCCCAGTTGCGCTTCTGGCCGGTGTAGTCTCCCGTAA	ATGCTGGAGCACAGGCAACTACAGAAAACGTTGTATGGAGGAGGAAGCACCTGCAGATCGCCTGCATGTAAGCGCCCCAGTTGCGCTTCTGGCCGGTGTAGTCTCCCGTAA			MLEHRQLQKTLYGGGSTCRSPACKRPSCASGRCSLP*	MLEHRQLQKTLYGGGSTCRSPACKRPSCASGRCSLP*			AGAGACAGCG	CCGTGTTTTA	0		0	0	0	0	0
2654	1683	ao	AN6912.1	71.m15220	AO070219000017	0					-210	-199	ATGGACGGGTAA			ATGGACGGGTAA	MDG*			MDG*	TCGAATACTC	AAGAATGAAA	0		0	0	0	0	0
2655	1683	ao	AN6912.1	71.m15220	AO070219000017	0					-194	-159	ATGAAAATGAGTTTGTATATCTTAAGTATAGATTGA			ATGAAAATGAGTTTGTATATCTTAAGTATAGATTGA	MKMSLYILSID*			MKMSLYILSID*	GGGTAAAAGA	TGATATTTGG	0		0	0	0	0	0
2656	1683	ao	AN6912.1	71.m15220	AO070219000017	0					-188	-159	ATGAGTTTGTATATCTTAAGTATAGATTGA			ATGAGTTTGTATATCTTAAGTATAGATTGA	MSLYILSID*			MSLYILSID*	AAGAATGAAA	TGATATTTGG	0		0	0	0	0	0
2657	1683	ao	AN6912.1	71.m15220	AO070219000017	0					-159	-31	ATGATATTTGGACTGTTTGCCTGTCGGAGTTTAATAAGCGTCTCGGGCTTCACTTTTGGTTTCTGTGGCTACCCGGACTCGTTATCGATAGCGACTATTGTCTCCACTGAAAATATTCTACGGCTGTGA			ATGATATTTGGACTGTTTGCCTGTCGGAGTTTAATAAGCGTCTCGGGCTTCACTTTTGGTTTCTGTGGCTACCCGGACTCGTTATCGATAGCGACTATTGTCTCCACTGAAAATATTCTACGGCTGTGA	MIFGLFACRSLISVSGFTFGFCGYPDSLSIATIVSTENILRL*			MIFGLFACRSLISVSGFTFGFCGYPDSLSIATIVSTENILRL*	GTATAGATTG	TAAAACACAA	0		0	0	0	0	0
2658	1685	af	AN8755.1	62.m03322	AO070250000017	0			-233	-210			ATGCGGAAAGAGGAAGACAAATAG		ATGCGGAAAGAGGAAGACAAATAG		MRKEEDK*		MRKEEDK*		AACCTGCGAA	GCGACATCGG	0	C	0	MG02616.1	0	0	0
2659	1685	af	AN8755.1	62.m03322	AO070250000017	0			-142	-104			ATGGCGAGGGACGCTGGCAATCTCTCCCAAAAGGCTTAA		ATGGCGAGGGACGCTGGCAATCTCTCCCAAAAGGCTTAA		MARDAGNLSQKA*		MARDAGNLSQKA*		GATCGGTCCA	GCTCCCCAGG	0	C	0	MG02616.1	0	0	0
2661	1685	ao	AN8755.1	62.m03322	AO070250000017	0					-208	-143	ATGGGACGGCGGGGAAACGGGAACCCCAGACCGACCGAGGTTGGCGGGTCGGCCCATTTAATTTAG			ATGGGACGGCGGGGAAACGGGAACCCCAGACCGACCGAGGTTGGCGGGTCGGCCCATTTAATTTAG	MGRRGNGNPRPTEVGGSAHLI*			MGRRGNGNPRPTEVGGSAHLI*	CTTCAATTGG	TCATTAACGC	0	C	0	MG02616.1	0	0	0
2662	1688	an	AN2531.1	59.m08446	AO070300000119	0	-218	-18					ATGAATCCAAGGAATGAACCCAACTACGGTTGCTTAGAAATCCCAATCGGCCAGCGAGTCAGCCAAGAACACAGACTGTTGCTTACAGTCTTAAGTGCCAGCTCAGACCTCCTTTCCTTCTCAATCCTTCAAAAGAAAAAATCTCCGGCGTCAACGTCCATTCGTCCAATGGGCGATTTCTCCAGATTATTGAATATTTGA	ATGAATCCAAGGAATGAACCCAACTACGGTTGCTTAGAAATCCCAATCGGCCAGCGAGTCAGCCAAGAACACAGACTGTTGCTTACAGTCTTAAGTGCCAGCTCAGACCTCCTTTCCTTCTCAATCCTTCAAAAGAAAAAATCTCCGGCGTCAACGTCCATTCGTCCAATGGGCGATTTCTCCAGATTATTGAATATTTGA			MNPRNEPNYGCLEIPIGQRVSQEHRLLLTVLSASSDLLSFSILQKKKSPASTSIRPMGDFSRLLNI*	MNPRNEPNYGCLEIPIGQRVSQEHRLLLTVLSASSDLLSFSILQKKKSPASTSIRPMGDFSRLLNI*			GGCTTATCTG	AAATTCATAC	0	R	0	MG07444.1	0	0	0
2663	1688	an	AN2531.1	59.m08446	AO070300000119	0	-205	-182					ATGAACCCAACTACGGTTGCTTAG	ATGAACCCAACTACGGTTGCTTAG			MNPTTVA*	MNPTTVA*			AATCCAAGGA	AAATCCCAAT	0	R	0	MG07444.1	0	0	0
2665	1688	ao	AN2531.1	59.m08446	AO070300000119	0					-154	-116	ATGGGTATTTATGTAAGTGTGCATATTTCCCCAGAGTAG			ATGGGTATTTATGTAAGTGTGCATATTTCCCCAGAGTAG	MGIYVSVHISPE*			MGIYVSVHISPE*	CCATCCAGTC	CACGTTTGAA	0	R	0	MG07444.1	0	0	0
2667	1692	af	AN1056.1	70.m15179	AO070336000055	0			-74	-27			ATGGTACCTCCGGCTACACTGAACAAGAAAATACTCTATAATTTTTAG		ATGGTACCTCCGGCTACACTGAACAAGAAAATACTCTATAATTTTTAG		MVPPATLNKKILYNF*		MVPPATLNKKILYNF*		CCCACCGCCA	ATATCTGGCT	0	T	0	0	0	0	0
2666	1692	an	AN1056.1	70.m15179	AO070336000055	0	-75	-46					ATGATATTCGATCCTATTCTCTTATTATAA	ATGATATTCGATCCTATTCTCTTATTATAA			MIFDPILLL*	MIFDPILLL*			CAGTGCATGC	CAGATCTCAT	0	T	0	0	0	0	0
2668	1692	ao	AN1056.1	70.m15179	AO070336000055	0					-76	-59	ATGCGACAATTAATCTAG			ATGCGACAATTAATCTAG	MRQLI*			MRQLI*	CCACTTCTGC	TCCACGTGAA	0	T	0	0	0	0	0
2671	1694	af	AN6075.1	72.m19066	AO070340000119	0			-258	-184			ATGGTACTTTTGCAAGCCGATCCTCTGCCCCAATATTCAATACGGCGATCTTGGTCCTCCCTGGGAGGCGGATAG		ATGGTACTTTTGCAAGCCGATCCTCTGCCCCAATATTCAATACGGCGATCTTGGTCCTCCCTGGGAGGCGGATAG		MVLLQADPLPQYSIRRSWSSLGGG*		MVLLQADPLPQYSIRRSWSSLGGG*		ATTCGCGGCA	CTGAGCCATT	0	Q	0	0	0	0	0
2669	1694	an	AN6075.1	72.m19066	AO070340000119	0	-219	-142					ATGGCAACGAGAATTGGTGCGGTGGATCCTGCTAGAAAGATCACGAGAGAGTTGGAGAGATGTGGTGAGTATAAATAA	ATGGCAACGAGAATTGGTGCGGTGGATCCTGCTAGAAAGATCACGAGAGAGTTGGAGAGATGTGGTGAGTATAAATAA			MATRIGAVDPARKITRELERCGEYK*	MATRIGAVDPARKITRELERCGEYK*			ATTCCAAAAC	GAATACCGAG	0	Q	0	0	0	0	0
2670	1694	an	AN6075.1	72.m19066	AO070340000119	0	-122	-111					ATGGTACGCTAG	ATGGTACGCTAG			MVR*	MVR*			GGCCATTCAG	CTGCTACCCT	0	Q	0	0	0	0	0
2672	1694	ao	AN6075.1	72.m19066	AO070340000119	0					-204	-124	ATGCGACAAGGAAATAGTCTCACCTTAGCTCACGATCGACCCGTGTCATTAGCACGCTCTGAGACCGTCTTCCATGGTTAG			ATGCGACAAGGAAATAGTCTCACCTTAGCTCACGATCGACCCGTGTCATTAGCACGCTCTGAGACCGTCTTCCATGGTTAG	MRQGNSLTLAHDRPVSLARSETVFHG*			MRQGNSLTLAHDRPVSLARSETVFHG*	GGTCGATCCG	TGGCTGCGTT	0	Q	0	0	0	0	0
2673	1694	ao	AN6075.1	72.m19066	AO070340000119	0					-131	-81	ATGGTTAGTGGCTGCGTTACATCGGATTGCACTCCCGGCGAGATACTGTGA			ATGGTTAGTGGCTGCGTTACATCGGATTGCACTCCCGGCGAGATACTGTGA	MVSGCVTSDCTPGEIL*			MVSGCVTSDCTPGEIL*	ACCGTCTTCC	CAAACAACTA	0	Q	0	0	0	0	0
2680	1700	af	AN7447.1	57.m05898	AO070229000019	0			-226	-137			ATGTCTCATTCTGCCCTCCCTCGTTGGTTGTATGCCTGTGCTCTGTTGTTGATCTTTAGTAGTGAATGCCTCAAAATGCGGAGATCCTGA		ATGTCTCATTCTGCCCTCCCTCGTTGGTTGTATGCCTGTGCTCTGTTGTTGATCTTTAGTAGTGAATGCCTCAAAATGCGGAGATCCTGA		MSHSALPRWLYACALLLIFSSECLKMRRS*		MSHSALPRWLYACALLLIFSSECLKMRRS*		ATTTATTTTC	TAAGATAAGC	0	A	0	0	0	0	0
2681	1700	af	AN7447.1	57.m05898	AO070229000019	0			-195	-175			ATGCCTGTGCTCTGTTGTTGA		ATGCCTGTGCTCTGTTGTTGA		MPVLCC*		MPVLCC*		CGTTGGTTGT	TCTTTAGTAG	0	A	0	0	0	0	0
2682	1700	af	AN7447.1	57.m05898	AO070229000019	0			-161	-129			ATGCCTCAAAATGCGGAGATCCTGATAAGATAA		ATGCCTCAAAATGCGGAGATCCTGATAAGATAA		MPQNAEILIR*		MPQNAEILIR*		TTAGTAGTGA	GCGGGTCGGA	0	A	0	0	0	0	0
2683	1700	af	AN7447.1	57.m05898	AO070229000019	0			-151	-137			ATGCGGAGATCCTGA		ATGCGGAGATCCTGA		MRRS*		MRRS*		ATGCCTCAAA	TAAGATAAGC	0	A	0	0	0	0	0
2676	1700	an	AN7447.1	57.m05898	AO070229000019	0	-228	-190					ATGGCAATACCAATACGTCTATACTCCATCGTACTGTAA	ATGGCAATACCAATACGTCTATACTCCATCGTACTGTAA			MAIPIRLYSIVL*	MAIPIRLYSIVL*			TTATCAACAA	CCGTGATAGT	0	A	0	0	0	0	0
2677	1700	an	AN7447.1	57.m05898	AO070229000019	0	-161	-129					ATGGGCTGGATGATGGCCTGGTTGATAAGATAA	ATGGGCTGGATGATGGCCTGGTTGATAAGATAA			MGWMMAWLIR*	MGWMMAWLIR*			CGTATAAGAG	CGGAGCGGAA	0	A	0	0	0	0	0
2678	1700	an	AN7447.1	57.m05898	AO070229000019	0	-152	-129					ATGATGGCCTGGTTGATAAGATAA	ATGATGGCCTGGTTGATAAGATAA			MMAWLIR*	MMAWLIR*			GATGGGCTGG	CGGAGCGGAA	0	A	0	0	0	0	0
2679	1700	an	AN7447.1	57.m05898	AO070229000019	0	-149	-129					ATGGCCTGGTTGATAAGATAA	ATGGCCTGGTTGATAAGATAA			MAWLIR*	MAWLIR*			GGGCTGGATG	CGGAGCGGAA	0	A	0	0	0	0	0
2684	1700	ao	AN7447.1	57.m05898	AO070229000019	0					-236	-201	ATGAATTCCACTAGTGTTCGAGGATCCATAGAGTAG			ATGAATTCCACTAGTGTTCGAGGATCCATAGAGTAG	MNSTSVRGSIE*			MNSTSVRGSIE*	CCTACGACCT	TACGCAGTGG	0	A	0	0	0	0	0
2685	1700	ao	AN7447.1	57.m05898	AO070229000019	0					-176	-165	ATGATACTGTAA			ATGATACTGTAA	MIL*			MIL*	TCTTAGATAT	CTACGTTTGG	0	A	0	0	0	0	0
2686	1700	ao	AN7447.1	57.m05898	AO070229000019	0					-116	-45	ATGTTCTTGCGCTCATTGCCTCTTGAAAGCATGAAACAACTTCCTGCTACCTCAGAATCTTGGTACACTTAA			ATGTTCTTGCGCTCATTGCCTCTTGAAAGCATGAAACAACTTCCTGCTACCTCAGAATCTTGGTACACTTAA	MFLRSLPLESMKQLPATSESWYT*			MFLRSLPLESMKQLPATSESWYT*	GAGCGGGACA	GCTTACTTAA	0	A	0	0	0	0	0
2687	1700	ao	AN7447.1	57.m05898	AO070229000019	0					-86	-45	ATGAAACAACTTCCTGCTACCTCAGAATCTTGGTACACTTAA			ATGAAACAACTTCCTGCTACCTCAGAATCTTGGTACACTTAA	MKQLPATSESWYT*			MKQLPATSESWYT*	TCTTGAAAGC	GCTTACTTAA	0	A	0	0	0	0	0
2691	1704	af	AN1087.1	52.m04007	AO070293000079	0			-236	-156			ATGACTTGGCAAATAACTTTAACCAGACGTAAGTTTAGCAATCGAGCCTCGTGTCGATGGCGTGTACATGATATGCAGTGA		ATGACTTGGCAAATAACTTTAACCAGACGTAAGTTTAGCAATCGAGCCTCGTGTCGATGGCGTGTACATGATATGCAGTGA		MTWQITLTRRKFSNRASCRWRVHDMQ*		MTWQITLTRRKFSNRASCRWRVHDMQ*		CAGAGGGCGA	TACCACGCTA	0	Q	0	0	0	0	0
2692	1704	af	AN1087.1	52.m04007	AO070293000079	0			-180	-166			ATGGCGTGTACATGA		ATGGCGTGTACATGA		MACT*		MACT*		CCTCGTGTCG	TATGCAGTGA	0	Q	0	0	0	0	0
2693	1704	af	AN1087.1	52.m04007	AO070293000079	0			-169	-47			ATGATATGCAGTGATACCACGCTAACAATCCCTTGCTTCCCAGTCTCACCGATGATCGGCATATCAAGAGTTACACAATGGAGGGGACGGGCTATTCCTAAATATGCGCTGATCCCTTGCTAG		ATGATATGCAGTGATACCACGCTAACAATCCCTTGCTTCCCAGTCTCACCGATGATCGGCATATCAAGAGTTACACAATGGAGGGGACGGGCTATTCCTAAATATGCGCTGATCCCTTGCTAG		MICSDTTLTIPCFPVSPMIGISRVTQWRGRAIPKYALIPC*		MICSDTTLTIPCFPVSPMIGISRVTQWRGRAIPKYALIPC*		TGGCGTGTAC	ACTGAAATCC	0	Q	0	0	0	0	0

2694	1704	af	AN1087.1	52.m04007	AO070293000079	0			-118	-47			ATGATCGGCATATCAAGAGTTACACAATGGAGGGGACGGGCTATTCCTAAATATGCGCTGATCCCTTGCTAG		ATGATCGGCATATCAAGAGTTACACAATGGAGGGGACGGGCTATTCCTAAATATGCGCTGATCCCTTGCTAG		MIGISRVTQWRGRAIPKYALIPC*		MIGISRVTQWRGRAIPKYALIPC*		AGTCTCACCG	ACTGAAATCC	0	Q	0	0	0	0	0
2695	1704	af	AN1087.1	52.m04007	AO070293000079	0			-92	-69			ATGGAGGGGACGGGCTATTCCTAA		ATGGAGGGGACGGGCTATTCCTAA		MEGTGYS*		MEGTGYS*		GAGTTACACA	ATATGCGCTG	0	Q	0	0	0	0	0
2688	1704	an	AN1087.1	52.m04007	AO070293000079	0	-252	-235					ATGTTGCAGTATACTTAA	ATGTTGCAGTATACTTAA			MLQYT*	MLQYT*			GGTCAAGCTA	TCCGGACAGA	0	Q	0	0	0	0	0
2689	1704	an	AN1087.1	52.m04007	AO070293000079	0	-159	-121					ATGAGAGTTCATGTTGTACAGCGCAGTTCTCGATCCTAA	ATGAGAGTTCATGTTGTACAGCGCAGTTCTCGATCCTAA			MRVHVVQRSSRS*	MRVHVVQRSSRS*			AAGCTGTATA	TTTAAGGTTC	0	Q	0	0	0	0	0
2690	1704	an	AN1087.1	52.m04007	AO070293000079	0	-149	-12					ATGTTGTACAGCGCAGTTCTCGATCCTAATTTAAGGTTCAAGGTTGCATCCCTTGACTGCCCAGTCCATTCTCACTACCACCTGGGCAACCACTTCCACATCACCTACCTCACGATCGATCCATGGTTCAATTACTGA	ATGTTGTACAGCGCAGTTCTCGATCCTAATTTAAGGTTCAAGGTTGCATCCCTTGACTGCCCAGTCCATTCTCACTACCACCTGGGCAACCACTTCCACATCACCTACCTCACGATCGATCCATGGTTCAATTACTGA			MLYSAVLDPNLRFKVASLDCPVHSHYHLGNHFHITYLTIDPWFNY*	MLYSAVLDPNLRFKVASLDCPVHSHYHLGNHFHITYLTIDPWFNY*			ATGAGAGTTC	CTGATTCCAC	0	Q	0	0	0	0	0
2696	1704	ao	AN1087.1	52.m04007	AO070293000079	0					-176	-138	ATGTCGCCGATGATTGGCTGCTCGTCAGTGCTGGCCTGA			ATGTCGCCGATGATTGGCTGCTCGTCAGTGCTGGCCTGA	MSPMIGCSSVLA*			MSPMIGCSSVLA*	TGCTTTAGTA	TTCTGGAGAA	0	Q	0	0	0	0	0
2697	1704	ao	AN1087.1	52.m04007	AO070293000079	0					-167	-138	ATGATTGGCTGCTCGTCAGTGCTGGCCTGA			ATGATTGGCTGCTCGTCAGTGCTGGCCTGA	MIGCSSVLA*			MIGCSSVLA*	AATGTCGCCG	TTCTGGAGAA	0	Q	0	0	0	0	0
2698	1704	ao	AN1087.1	52.m04007	AO070293000079	0					-123	-37	ATGCTCTGGACTTGCATCTCGTTGTCTGCACTCATGGACGAGGTAGGGCTTCATAAGTCACGACTGATGGATCTTCACAAAGCCTAA			ATGCTCTGGACTTGCATCTCGTTGTCTGCACTCATGGACGAGGTAGGGCTTCATAAGTCACGACTGATGGATCTTCACAAAGCCTAA	MLWTCISLSALMDEVGLHKSRLMDLHKA*			MLWTCISLSALMDEVGLHKSRLMDLHKA*	GGAGAACTTG	GACTTCAACA	0	Q	0	0	0	0	0
2699	1704	ao	AN1087.1	52.m04007	AO070293000079	0					-90	-37	ATGGACGAGGTAGGGCTTCATAAGTCACGACTGATGGATCTTCACAAAGCCTAA			ATGGACGAGGTAGGGCTTCATAAGTCACGACTGATGGATCTTCACAAAGCCTAA	MDEVGLHKSRLMDLHKA*			MDEVGLHKSRLMDLHKA*	GTCTGCACTC	GACTTCAACA	0	Q	0	0	0	0	0
2701	1710	an	AN6639.1	62.m03234	AO070326000091	0	-202	-182					ATGCCCGGCCCAGAGGCGTAA	ATGCCCGGCCCAGAGGCGTAA			MPGPEA*	MPGPEA*			GTGCGGGTAA	AAGCCACGGC	0	R	0	MG02836.1	0	0	YPR002W
2705	1717	af	AN4613.1	57.m05530	AO070267000029	0			-232	-167			ATGAAGAGTACCAACCACGCTCGCGGCTGTCTGGACAAATCTTTCCTAGATAAGTGTATTATGTAA		ATGAAGAGTACCAACCACGCTCGCGGCTGTCTGGACAAATCTTTCCTAGATAAGTGTATTATGTAA		MKSTNHARGCLDKSFLDKCIM*		MKSTNHARGCLDKSFLDKCIM*		CTGCTTTTGA	TCGTAGATAT	0	J	0	0	0	0	0
2706	1717	af	AN4613.1	57.m05530	AO070267000029	0			-144	-37			ATGAGAGCTGTGAAATTTCACCAGGAACACTGCGTCTTGGCGAAAGTTTCCCCATGCAAAGCTCCCTGGGTGGCGTTACAATTTCTGCCTTCACTCACGGCTCACTAG		ATGAGAGCTGTGAAATTTCACCAGGAACACTGCGTCTTGGCGAAAGTTTCCCCATGCAAAGCTCCCTGGGTGGCGTTACAATTTCTGCCTTCACTCACGGCTCACTAG		MRAVKFHQEHCVLAKVSPCKAPWVALQFLPSLTAH*		MRAVKFHQEHCVLAKVSPCKAPWVALQFLPSLTAH*		TGAGTGACCA	AATCCTGGCT	0	J	0	0	0	0	0
2707	1717	af	AN4613.1	57.m05530	AO070267000029	0			-91	-2			ATGCAAAGCTCCCTGGGTGGCGTTACAATTTCTGCCTTCACTCACGGCTCACTAGAATCCTGGCTCGGTGCGCGTGGGAGAAGCTGTTAG		ATGCAAAGCTCCCTGGGTGGCGTTACAATTTCTGCCTTCACTCACGGCTCACTAGAATCCTGGCTCGGTGCGCGTGGGAGAAGCTGTTAG		MQSSLGGVTISAFTHGSLESWLGARGRSC*		MQSSLGGVTISAFTHGSLESWLGARGRSC*		AAGTTTCCCC	GATGCTGTCA	0	J	0	0	0	0	0
2702	1717	an	AN4613.1	57.m05530	AO070267000029	0	-186	-139					ATGCGGATTTATGAAGCGCACGGACCGTTTATGTCAATACTTATGTAA	ATGCGGATTTATGAAGCGCACGGACCGTTTATGTCAATACTTATGTAA			MRIYEAHGPFMSILM*	MRIYEAHGPFMSILM*			TAAGCTCTCT	CTAGCGTAAA	0	J	0	0	0	0	0
2703	1717	an	AN4613.1	57.m05530	AO070267000029	0	-176	-135					ATGAAGCGCACGGACCGTTTATGTCAATACTTATGTAACTAG	ATGAAGCGCACGGACCGTTTATGTCAATACTTATGTAACTAG			MKRTDRLCQYLCN*	MKRTDRLCQYLCN*			ATGCGGATTT	CGTAAACCTA	0	J	0	0	0	0	0
2704	1717	an	AN4613.1	57.m05530	AO070267000029	0	-156	-139					ATGTCAATACTTATGTAA	ATGTCAATACTTATGTAA			MSILM*	MSILM*			CGGACCGTTT	CTAGCGTAAA	0	J	0	0	0	0	0
2708	1717	ao	AN4613.1	57.m05530	AO070267000029	0					-205	-176	ATGTCCTTTAAGATAATGCACATACTATGA			ATGTCCTTTAAGATAATGCACATACTATGA	MSFKIMHIL*			MSFKIMHIL*	GCATAATCTC	GAATTACATA	0	J	0	0	0	0	0
2709	1717	ao	AN4613.1	57.m05530	AO070267000029	0					-190	-176	ATGCACATACTATGA			ATGCACATACTATGA	MHIL*			MHIL*	CTTTAAGATA	GAATTACATA	0	J	0	0	0	0	0
2710	1717	ao	AN4613.1	57.m05530	AO070267000029	0					-179	-165	ATGAGAATTACATAA			ATGAGAATTACATAA	MRIT*			MRIT*	TGCACATACT	TTGGACTACC	0	J	0	0	0	0	0
2711	1717	ao	AN4613.1	57.m05530	AO070267000029	0					-118	-35	ATGGCCGCATTTCTTGGCAAAGATTTTCCTAACAGAGCTCTCACGAGTGGCGTTTTTCCTCCATCCCCAGACTCAGGTCGCTGA			ATGGCCGCATTTCTTGGCAAAGATTTTCCTAACAGAGCTCTCACGAGTGGCGTTTTTCCTCCATCCCCAGACTCAGGTCGCTGA	MAAFLGKDFPNRALTSGVFPPSPDSGR*			MAAFLGKDFPNRALTSGVFPPSPDSGR*	GGAATTTCTG	TTATCGCTTC	0	J	0	0	0	0	0
2713	1723	af	AN4479.1	57.m05654	AO070311000025	0			-263	-159			ATGTCTTACTCGAGCCTTTATCCTTTTCATTCGTCATCTGCATTCTTCCTCTCCTTCCCTGCCTCGATGCCCTCGCGACTTATGCTCTCGTCTTCGACATCTTAG		ATGTCTTACTCGAGCCTTTATCCTTTTCATTCGTCATCTGCATTCTTCCTCTCCTTCCCTGCCTCGATGCCCTCGCGACTTATGCTCTCGTCTTCGACATCTTAG		MSYSSLYPFHSSSAFFLSFPASMPSRLMLSSSTS*		MSYSSLYPFHSSSAFFLSFPASMPSRLMLSSSTS*		TCTCTGTTTG	CACCTATTTA	0	T	0	0	0	0	0
2714	1723	af	AN4479.1	57.m05654	AO070311000025	0			-197	-159			ATGCCCTCGCGACTTATGCTCTCGTCTTCGACATCTTAG		ATGCCCTCGCGACTTATGCTCTCGTCTTCGACATCTTAG		MPSRLMLSSSTS*		MPSRLMLSSSTS*		CCCTGCCTCG	CACCTATTTA	0	T	0	0	0	0	0
2715	1723	af	AN4479.1	57.m05654	AO070311000025	0			-182	-159			ATGCTCTCGTCTTCGACATCTTAG		ATGCTCTCGTCTTCGACATCTTAG		MLSSSTS*		MLSSSTS*		CTCGCGACTT	CACCTATTTA	0	T	0	0	0	0	0
2717	1723	ao	AN4479.1	57.m05654	AO070311000025	0					-184	-167	ATGTTGCCCTCCCTTTAA			ATGTTGCCCTCCCTTTAA	MLPSL*			MLPSL*	GATTTCTTTC	AACTGTTAAC	0	T	0	0	0	0	0
2720	1726	af	AN7741.1	71.m16099	AO070325000162	0			-197	-159			ATGAACCCGATTGATACCTTAGTACACCGTGTCTGCTGA		ATGAACCCGATTGATACCTTAGTACACCGTGTCTGCTGA		MNPIDTLVHRVC*		MNPIDTLVHRVC*		TACGAATGGG	GTAGAAATGT	0	U	0	MG05484.1	NCU09673.1	YOL062C	0
2721	1726	af	AN7741.1	71.m16099	AO070325000162	0			-152	-99			ATGTTCTGGACTAAACTGACCGACTTCCCCACCTACGGCCCCCATTTATCCTGA		ATGTTCTGGACTAAACTGACCGACTTCCCCACCTACGGCCCCCATTTATCCTGA		MFWTKLTDFPTYGPHLS*		MFWTKLTDFPTYGPHLS*		CTGAGTAGAA	GAGCTTCTCC	0	U	0	MG05484.1	NCU09673.1	YOL062C	0
2730	1728	af	AN8078.1	53.m03931	AO070330000044	0			-264	-184			ATGGCGATGCAGACGGACTACGGCGACTGGACGATTCTGCAGATCCTTGCTGGGGGGAGGACAATAGCAGACACGGAATAG		ATGGCGATGCAGACGGACTACGGCGACTGGACGATTCTGCAGATCCTTGCTGGGGGGAGGACAATAGCAGACACGGAATAG		MAMQTDYGDWTILQILAGGRTIADTE*		MAMQTDYGDWTILQILAGGRTIADTE*		CCTCCATCTA	GCGCACCGCA	0	Q	0	0	0	0	0
2731	1728	af	AN8078.1	53.m03931	AO070330000044	0			-258	-184			ATGCAGACGGACTACGGCGACTGGACGATTCTGCAGATCCTTGCTGGGGGGAGGACAATAGCAGACACGGAATAG		ATGCAGACGGACTACGGCGACTGGACGATTCTGCAGATCCTTGCTGGGGGGAGGACAATAGCAGACACGGAATAG		MQTDYGDWTILQILAGGRTIADTE*		MQTDYGDWTILQILAGGRTIADTE*		TCTAATGGCG	GCGCACCGCA	0	Q	0	0	0	0	0
2732	1728	af	AN8078.1	53.m03931	AO070330000044	0			-170	-141			ATGATATGTGCACCACGGCGGAGGGAATGA		ATGATATGTGCACCACGGCGGAGGGAATGA		MICAPRRRE*		MICAPRRRE*		CACCGCAGGG	GGGGTGGCCT	0	Q	0	0	0	0	0
2733	1728	af	AN8078.1	53.m03931	AO070330000044	0			-165	-112			ATGTGCACCACGGCGGAGGGAATGAGGGGTGGCCTCGAACGGCTCTCCCAGTGA		ATGTGCACCACGGCGGAGGGAATGAGGGGTGGCCTCGAACGGCTCTCCCAGTGA		MCTTAEGMRGGLERLSQ*		MCTTAEGMRGGLERLSQ*		CAGGGATGAT	CCGAGTCTCT	0	Q	0	0	0	0	0
2734	1728	af	AN8078.1	53.m03931	AO070330000044	0			-144	-112			ATGAGGGGTGGCCTCGAACGGCTCTCCCAGTGA		ATGAGGGGTGGCCTCGAACGGCTCTCCCAGTGA		MRGGLERLSQ*		MRGGLERLSQ*		GGCGGAGGGA	CCGAGTCTCT	0	Q	0	0	0	0	0
2728	1728	an	AN8078.1	53.m03931	AO070330000044	0	-168	-55					ATGACGCGGACGACACACCCCCGACCCCGGAAATGTACCGTGCACCGCAAGCAGCATCAGACGTCGATTAACGTCGGTCGTGGCCGACCAGCCAGATATAAAGGCCGTCCTTAG	ATGACGCGGACGACACACCCCCGACCCCGGAAATGTACCGTGCACCGCAAGCAGCATCAGACGTCGATTAACGTCGGTCGTGGCCGACCAGCCAGATATAAAGGCCGTCCTTAG			MTRTTHPRPRKCTVHRKQHQTSINVGRGRPARYKGRP*	MTRTTHPRPRKCTVHRKQHQTSINVGRGRPARYKGRP*			GCAAGCGCGG	ACGACTTGAT	0	Q	0	0	0	0	0
2729	1728	an	AN8078.1	53.m03931	AO070330000044	0	-136	-98					ATGTACCGTGCACCGCAAGCAGCATCAGACGTCGATTAA	ATGTACCGTGCACCGCAAGCAGCATCAGACGTCGATTAA			MYRAPQAASDVD*	MYRAPQAASDVD*			GACCCCGGAA	CGTCGGTCGT	0	Q	0	0	0	0	0
2735	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-244	-179	ATGATGGCTGCCCTCTTCAGCTGCATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA			ATGATGGCTGCCCTCTTCAGCTGCATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA	MMAALFSCMVGDRLIFYHQVP*			MMAALFSCMVGDRLIFYHQVP*	TGTACCAGTA	CGTTGAACCA	0	Q	0	0	0	0	0
2736	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-241	-179	ATGGCTGCCCTCTTCAGCTGCATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA			ATGGCTGCCCTCTTCAGCTGCATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA	MAALFSCMVGDRLIFYHQVP*			MAALFSCMVGDRLIFYHQVP*	ACCAGTAATG	CGTTGAACCA	0	Q	0	0	0	0	0
2737	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-220	-179	ATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA			ATGGTTGGCGACAGGCTCATATTCTACCACCAAGTACCGTGA	MVGDRLIFYHQVP*			MVGDRLIFYHQVP*	CTTCAGCTGC	CGTTGAACCA	0	Q	0	0	0	0	0
2738	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-169	-11	ATGGTCGGAAAGGTCCCGTGCAACAGACGTAATAACCCCTGCGGAGACTTGATGCTTAAACCAAAGATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG			ATGGTCGGAAAGGTCCCGTGCAACAGACGTAATAACCCCTGCGGAGACTTGATGCTTAAACCAAAGATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG	MVGKVPCNRRNNPCGDLMLKPKMFGIKPRRVACHFSCNEIFPSITIFSPSP*			MVGKVPCNRRNNPCGDLMLKPKMFGIKPRRVACHFSCNEIFPSITIFSPSP*	ACGTTGAACC	ACGTTCAGAG	0	Q	0	0	0	0	0
2739	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-118	-11	ATGCTTAAACCAAAGATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG			ATGCTTAAACCAAAGATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG	MLKPKMFGIKPRRVACHFSCNEIFPSITIFSPSP*			MLKPKMFGIKPRRVACHFSCNEIFPSITIFSPSP*	CGGAGACTTG	ACGTTCAGAG	0	Q	0	0	0	0	0
2740	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-103	-11	ATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG			ATGTTTGGTATAAAACCCCGGCGCGTCGCATGCCACTTTAGCTGCAATGAGATTTTCCCTTCGATAACGACCATCTTCTCCCCTTCTCCTTAG	MFGIKPRRVACHFSCNEIFPSITIFSPSP*			MFGIKPRRVACHFSCNEIFPSITIFSPSP*	TAAACCAAAG	ACGTTCAGAG	0	Q	0	0	0	0	0
2741	1728	ao	AN8078.1	53.m03931	AO070330000044	0					-74	-63	ATGCCACTTTAG			ATGCCACTTTAG	MPL*			MPL*	GGCGCGTCGC	CTGCAATGAG	0	Q	0	0	0	0	0
2744	1732	af	AN8583.1	70.m15077	AO070339000078	0			-260	-216			ATGACCGCCACTAGAACGCGGTTGCTGAGGGTATGCGCTGGTTGA		ATGACCGCCACTAGAACGCGGTTGCTGAGGGTATGCGCTGGTTGA		MTATRTRLLRVCAG*		MTATRTRLLRVCAG*		AGGAGCAGCC	ACTTGTATTT	0	V	0	0	0	0	0
2745	1732	af	AN8583.1	70.m15077	AO070339000078	0			-228	-184			ATGCGCTGGTTGAACTTGTATTTTTTGTATTCCTCTGGCAAATAG		ATGCGCTGGTTGAACTTGTATTTTTTGTATTCCTCTGGCAAATAG		MRWLNLYFLYSSGK*		MRWLNLYFLYSSGK*		TGCTGAGGGT	ACGGTTACAG	0	V	0	0	0	0	0
2746	1732	af	AN8583.1	70.m15077	AO070339000078	0			-160	-11			ATGCCACTACCAGACATCATACACCTATATCAAGGCACGTCTCGTCGGTTTTGGCAGACCAGAGTCAAGATTGGAATACCGGACACTCCACAGTACATCGTGCCAGTCGCTTCATTTCTCCATTCTGAGGAACAAAAGAAAAACATCTGA		ATGCCACTACCAGACATCATACACCTATATCAAGGCACGTCTCGTCGGTTTTGGCAGACCAGAGTCAAGATTGGAATACCGGACACTCCACAGTACATCGTGCCAGTCGCTTCATTTCTCCATTCTGAGGAACAAAAGAAAAACATCTGA		MPLPDIIHLYQGTSRRFWQTRVKIGIPDTPQYIVPVASFLHSEEQKKNI*		MPLPDIIHLYQGTSRRFWQTRVKIGIPDTPQYIVPVASFLHSEEQKKNI*		TCATCCAGAA	AATCTCCATC	0	V	0	0	0	0	0
2743	1732	an	AN8583.1	70.m15077	AO070339000078	0	-170	-114					ATGGACGTGTTCTGCGACTTTCAGAAAAGAGTAGCTATTTTAAAAGGTCCTCAATAG	ATGGACGTGTTCTGCGACTTTCAGAAAAGAGTAGCTATTTTAAAAGGTCCTCAATAG			MDVFCDFQKRVAILKGPQ*	MDVFCDFQKRVAILKGPQ*			CCTGCAGGAA	ATAGGTTTAC	0	V	0	0	0	0	0
2747	1732	ao	AN8583.1	70.m15077	AO070339000078	0					-194	-132	ATGACATCTTACGTACTCAATGACATGTTTCGACATTGTTCCTTGATGACAAAAGCCAGATAA			ATGACATCTTACGTACTCAATGACATGTTTCGACATTGTTCCTTGATGACAAAAGCCAGATAA	MTSYVLNDMFRHCSLMTKAR*			MTSYVLNDMFRHCSLMTKAR*	GTATAATAGC	GTGATACGCT	0	V	0	0	0	0	0
2748	1732	ao	AN8583.1	70.m15077	AO070339000078	0					-175	-149	ATGACATGTTTCGACATTGTTCCTTGA			ATGACATGTTTCGACATTGTTCCTTGA	MTCFDIVP*			MTCFDIVP*	TACGTACTCA	TGACAAAAGC	0	V	0	0	0	0	0
2749	1732	ao	AN8583.1	70.m15077	AO070339000078	0					-170	-132	ATGTTTCGACATTGTTCCTTGATGACAAAAGCCAGATAA			ATGTTTCGACATTGTTCCTTGATGACAAAAGCCAGATAA	MFRHCSLMTKAR*			MFRHCSLMTKAR*	ACTCAATGAC	GTGATACGCT	0	V	0	0	0	0	0
2750	1732	ao	AN8583.1	70.m15077	AO070339000078	0					-149	-132	ATGACAAAAGCCAGATAA			ATGACAAAAGCCAGATAA	MTKAR*			MTKAR*	TTGTTCCTTG	GTGATACGCT	0	V	0	0	0	0	0
2754	1736	af	AN5918.1	72.m19885	AO070340000367	0			-235	-152			ATGCCACTTTGGCGTGGCGATACTCTGAGAGGCGTGTGTGCTGCAAGGAGAAGTAAATGCATCCGGCTGGTCAGGTGTCAATGA		ATGCCACTTTGGCGTGGCGATACTCTGAGAGGCGTGTGTGCTGCAAGGAGAAGTAAATGCATCCGGCTGGTCAGGTGTCAATGA		MPLWRGDTLRGVCAARRSKCIRLVRCQ*		MPLWRGDTLRGVCAARRSKCIRLVRCQ*		GTCTTTGGTC	TAGAGAGCTT	0	P	0	MG06442.1	0	YDR256C	0
2755	1736	af	AN5918.1	72.m19885	AO070340000367	0			-179	-138			ATGCATCCGGCTGGTCAGGTGTCAATGATAGAGAGCTTGTGA		ATGCATCCGGCTGGTCAGGTGTCAATGATAGAGAGCTTGTGA		MHPAGQVSMIESL*		MHPAGQVSMIESL*		GGAGAAGTAA	TGCAAGGGCT	0	P	0	MG06442.1	0	YDR256C	0
2756	1736	af	AN5918.1	72.m19885	AO070340000367	0			-155	-138			ATGATAGAGAGCTTGTGA		ATGATAGAGAGCTTGTGA		MIESL*		MIESL*		TCAGGTGTCA	TGCAAGGGCT	0	P	0	MG06442.1	0	YDR256C	0
2757	1736	af	AN5918.1	72.m19885	AO070340000367	0			-138	-76			ATGCAAGGGCTGAAAAGACCCAGTCCAGAGAGGCGCATGTATTCGAATTTTAGCGGTGAATGA		ATGCAAGGGCTGAAAAGACCCAGTCCAGAGAGGCGCATGTATTCGAATTTTAGCGGTGAATGA		MQGLKRPSPERRMYSNFSGE*		MQGLKRPSPERRMYSNFSGE*		AGAGCTTGTG	GAACCACTTG	0	P	0	MG06442.1	0	YDR256C	0

2758	1736	af	AN5918.1	72.m19885	AO070340000367	0			-102	-76			ATGTATTCGAATTTTAGCGGTGAATGA		ATGTATTCGAATTTTAGCGGTGAATGA		MYSNFSGE*		MYSNFSGE*		AGAGAGGCGC	GAACCACTTG	0	P	0	MG06442.1	0	YDR256C	0
2751	1736	an	AN5918.1	72.m19885	AO070340000367	0	-182	-117					ATGAAGCAGTTTCAACTCGAAAGGTTTATATTTGGCATTAGCTTACTTATTACTGTCCCCTCATGA	ATGAAGCAGTTTCAACTCGAAAGGTTTATATTTGGCATTAGCTTACTTATTACTGTCCCCTCATGA			MKQFQLERFIFGISLLITVPS*	MKQFQLERFIFGISLLITVPS*			TCTTAGCGCG	GGAGCACTCT	0	P	0	MG06442.1	0	YDR256C	0
2752	1736	an	AN5918.1	72.m19885	AO070340000367	0	-120	-94					ATGAGGAGCACTCTGGACTGCATATAA	ATGAGGAGCACTCTGGACTGCATATAA			MRSTLDCI*	MRSTLDCI*			CTGTCCCCTC	CCCCCGCATG	0	P	0	MG06442.1	0	YDR256C	0
2753	1736	an	AN5918.1	72.m19885	AO070340000367	0	-86	-39					ATGTCCTCTGGCCAACCTGTCTTCAATTCTTTTTTCGACTTCAATTAG	ATGTCCTCTGGCCAACCTGTCTTCAATTCTTTTTTCGACTTCAATTAG			MSSGQPVFNSFFDFN*	MSSGQPVFNSFFDFN*			TAACCCCCGC	CGATCAATTA	0	P	0	MG06442.1	0	YDR256C	0
2759	1736	ao	AN5918.1	72.m19885	AO070340000367	0					-262	-242	ATGGATTTGAGGAACCGCTAG			ATGGATTTGAGGAACCGCTAG	MDLRNR*			MDLRNR*	TGAAGCTGGA	TACCTACCGT	0	P	0	MG06442.1	0	YDR256C	0
2760	1736	ao	AN5918.1	72.m19885	AO070340000367	0					-184	-107	ATGTCTTTGTCCAACTCGACCACTTTTATACACTACTTGCTTTCCCCTCCCTTCCTGTCGGCTCCATTCACGATTTGA			ATGTCTTTGTCCAACTCGACCACTTTTATACACTACTTGCTTTCCCCTCCCTTCCTGTCGGCTCCATTCACGATTTGA	MSLSNSTTFIHYLLSPPFLSAPFTI*			MSLSNSTTFIHYLLSPPFLSAPFTI*	TTAAATTACC	ACTCCGGGTA	0	P	0	MG06442.1	0	YDR256C	0
2761	1739	an	AN1396.1	70.m14826	AO070233000012	0	-253	-236					ATGGGCAACCCCAACTAA	ATGGGCAACCCCAACTAA			MGNPN*	MGNPN*			CGTGATAGGT	ATCCTTCGTC	0	C	FG03249.1	0	0	0	0
2762	1739	ao	AN1396.1	70.m14826	AO070233000012	0					-193	-107	ATGCCGTTTCCGAGTCATTGTCATGAAAACCTTCTGTTCACACCCGGAATTTCGAACCTTGTCAAACCATTAATCGGCTCACGTTAA			ATGCCGTTTCCGAGTCATTGTCATGAAAACCTTCTGTTCACACCCGGAATTTCGAACCTTGTCAAACCATTAATCGGCTCACGTTAA	MPFPSHCHENLLFTPGISNLVKPLIGSR*			MPFPSHCHENLLFTPGISNLVKPLIGSR*	AGGTACGTAA	AACAGAAAAA	0	C	FG03249.1	0	0	0	0
2763	1739	ao	AN1396.1	70.m14826	AO070233000012	0					-171	-121	ATGAAAACCTTCTGTTCACACCCGGAATTTCGAACCTTGTCAAACCATTAA			ATGAAAACCTTCTGTTCACACCCGGAATTTCGAACCTTGTCAAACCATTAA	MKTFCSHPEFRTLSNH*			MKTFCSHPEFRTLSNH*	AGTCATTGTC	TCGGCTCACG	0	C	FG03249.1	0	0	0	0
2766	1740	af	AN5197.1	69.m14896	AO070237000027	0			-90	-61			ATGCTCCCCTGTTCTTTTTTTGATGACTAG		ATGCTCCCCTGTTCTTTTTTTGATGACTAG		MLPCSFFDD*		MLPCSFFDD*		ACGCGGTTTC	TGATGATAAT	0	S	0	0	0	0	0
2764	1740	an	AN5197.1	69.m14896	AO070237000027	0	-119	-54					ATGTTCTTTGACCACCAACACTACTCGTGCTTTCTCAGCGATTCTTCCTGGCTTGTTTTCTTCTGA	ATGTTCTTTGACCACCAACACTACTCGTGCTTTCTCAGCGATTCTTCCTGGCTTGTTTTCTTCTGA			MFFDHQHYSCFLSDSSWLVFF*	MFFDHQHYSCFLSDSSWLVFF*			CGCCGATTCG	CAAGTTGTAA	0	S	0	0	0	0	0
2771	1741	af	AN6529.1	62.m03117	AO070270000029	0			-117	-61			ATGGCCGGCTCAATTACCTTCTGTTCTTCACACTCATTTCGTTATCGCTACTTTTGA		ATGGCCGGCTCAATTACCTTCTGTTCTTCACACTCATTTCGTTATCGCTACTTTTGA		MAGSITFCSSHSFRYRYF*		MAGSITFCSSHSFRYRYF*		GGTCAACCGC	CTAATTAATT	0	M	0	0	0	0	0
2772	1741	ao	AN6529.1	62.m03117	AO070270000029	0					-85	-74	ATGTTTTTGTGA			ATGTTTTTGTGA	MFL*			MFL*	ATAGAAACAT	CCCCCTTCTT	0	M	0	0	0	0	0
2780	1743	af	AN8594.1	70.m15668	AO070280000033	0			-217	-161			ATGCGGGGAATGGAATCAAACCGAGTCAAGAGTCAGAAAGTGAGCTTGCTGTCGTGA		ATGCGGGGAATGGAATCAAACCGAGTCAAGAGTCAGAAAGTGAGCTTGCTGTCGTGA		MRGMESNRVKSQKVSLLS*		MRGMESNRVKSQKVSLLS*		CCCCTCTCCA	ATGGTGGTCT	0	Q	0	0	0	0	0
2781	1743	af	AN8594.1	70.m15668	AO070280000033	0			-208	-161			ATGGAATCAAACCGAGTCAAGAGTCAGAAAGTGAGCTTGCTGTCGTGA		ATGGAATCAAACCGAGTCAAGAGTCAGAAAGTGAGCTTGCTGTCGTGA		MESNRVKSQKVSLLS*		MESNRVKSQKVSLLS*		AATGCGGGGA	ATGGTGGTCT	0	Q	0	0	0	0	0
2782	1743	af	AN8594.1	70.m15668	AO070280000033	0			-160	-149			ATGGTGGTCTGA		ATGGTGGTCTGA		MVV*		MVV*		GCTGTCGTGA	TAGCCTGAGA	0	Q	0	0	0	0	0
2783	1743	af	AN8594.1	70.m15668	AO070280000033	0			-122	-72			ATGGTGTCATTTGATCATTGTCGGGGATTGCCTATCGTAGGTGATATATAG		ATGGTGTCATTTGATCATTGTCGGGGATTGCCTATCGTAGGTGATATATAG		MVSFDHCRGLPIVGDI*		MVSFDHCRGLPIVGDI*		CAGTGGAGTG	AGTCAATATC	0	Q	0	0	0	0	0
2773	1743	an	AN8594.1	70.m15668	AO070280000033	0	-163	-125					ATGGTTCCTTCATGTTCCAGGATGCTGCGAATGGTCTAA	ATGGTTCCTTCATGTTCCAGGATGCTGCGAATGGTCTAA			MVPSCSRMLRMV*	MVPSCSRMLRMV*			TGGCTCCCAC	GCATGGGGAA	0	Q	0	0	0	0	0
2774	1743	an	AN8594.1	70.m15668	AO070280000033	0	-152	-69					ATGTTCCAGGATGCTGCGAATGGTCTAAGCATGGGGAAGCTGGACCGTATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA	ATGTTCCAGGATGCTGCGAATGGTCTAAGCATGGGGAAGCTGGACCGTATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA			MFQDAANGLSMGKLDRMTAGAGGGGCI*	MFQDAANGLSMGKLDRMTAGAGGGGCI*			TGGTTCCTTC	ATGTCGCCAT	0	Q	0	0	0	0	0
2775	1743	an	AN8594.1	70.m15668	AO070280000033	0	-142	-125					ATGCTGCGAATGGTCTAA	ATGCTGCGAATGGTCTAA			MLRMV*	MLRMV*			ATGTTCCAGG	GCATGGGGAA	0	Q	0	0	0	0	0
2776	1743	an	AN8594.1	70.m15668	AO070280000033	0	-122	-69					ATGGGGAAGCTGGACCGTATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA	ATGGGGAAGCTGGACCGTATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA			MGKLDRMTAGAGGGGCI*	MGKLDRMTAGAGGGGCI*			TGGTCTAAGC	ATGTCGCCAT	0	Q	0	0	0	0	0
2777	1743	an	AN8594.1	70.m15668	AO070280000033	0	-104	-69					ATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA	ATGACAGCCGGTGCAGGTGGGGGAGGTTGTATATGA			MTAGAGGGGCI*	MTAGAGGGGCI*			GCTGGACCGT	ATGTCGCCAT	0	Q	0	0	0	0	0
2778	1743	an	AN8594.1	70.m15668	AO070280000033	0	-72	-46					ATGAATGTCGCCATCGCGGATTCTTAA	ATGAATGTCGCCATCGCGGATTCTTAA			MNVAIADS*	MNVAIADS*			GAGGTTGTAT	TCCCATCCTC	0	Q	0	0	0	0	0
2779	1743	an	AN8594.1	70.m15668	AO070280000033	0	-68	-6					ATGTCGCCATCGCGGATTCTTAATCCCATCCTCGCCGTCGCTGAAGAGCCACGCACACATTAA	ATGTCGCCATCGCGGATTCTTAATCCCATCCTCGCCGTCGCTGAAGAGCCACGCACACATTAA			MSPSRILNPILAVAEEPRTH*	MSPSRILNPILAVAEEPRTH*			TTGTATATGA	CCACCATGCC	0	Q	0	0	0	0	0
2784	1743	ao	AN8594.1	70.m15668	AO070280000033	0					-213	-190	ATGCACGAGGTGATGTGGAGATAA			ATGCACGAGGTGATGTGGAGATAA	MHEVMWR*			MHEVMWR*	ACTGAAACGT	TAGTGTCTTT	0	Q	0	0	0	0	0
2785	1743	ao	AN8594.1	70.m15668	AO070280000033	0					-201	-190	ATGTGGAGATAA			ATGTGGAGATAA	MWR*			MWR*	GCACGAGGTG	TAGTGTCTTT	0	Q	0	0	0	0	0
2786	1743	ao	AN8594.1	70.m15668	AO070280000033	0					-175	-146	ATGTCTTATCGTGGAAGGGAAGATATATAG			ATGTCTTATCGTGGAAGGGAAGATATATAG	MSYRGREDI*			MSYRGREDI*	GTCTTTTGCG	AAATGGTGTG	0	Q	0	0	0	0	0
2788	1745	af	AN4957.1	59.m08862	AO070288000019	0			-240	-184			ATGTGGTGTGTCTCTGCCCCCCAGCCCCTCAGACCCTCCCCATGTTTCCCCTTATGA		ATGTGGTGTGTCTCTGCCCCCCAGCCCCTCAGACCCTCCCCATGTTTCCCCTTATGA		MWCVSAPQPLRPSPCFPL*		MWCVSAPQPLRPSPCFPL*		TGAAGCATCG	CATAGAGATT	0	G	FG04085.1	0	0	0	0
2789	1745	af	AN4957.1	59.m08862	AO070288000019	0			-199	-179			ATGTTTCCCCTTATGACATAG		ATGTTTCCCCTTATGACATAG		MFPLMT*		MFPLMT*		GACCCTCCCC	AGATTAGTTT	0	G	FG04085.1	0	0	0	0
2787	1745	an	AN4957.1	59.m08862	AO070288000019	0	-152	-69					ATGAGATCACAGGCACATTTTCTTCTACTATTCTCACTTTCATCGCAGTCTCTTTTCTTTATTTCTTCTCTGTATTATTTCTAG	ATGAGATCACAGGCACATTTTCTTCTACTATTCTCACTTTCATCGCAGTCTCTTTTCTTTATTTCTTCTCTGTATTATTTCTAG			MRSQAHFLLLFSLSSQSLFFISSLYYF*	MRSQAHFLLLFSLSSQSLFFISSLYYF*			GAACCCCTCT	GATTCACTTG	0	G	FG04085.1	0	0	0	0
2790	1745	ao	AN4957.1	59.m08862	AO070288000019	0					-128	-90	ATGATCGCAGTTTTCTCTTATATTAGCACCTTGGTTTAA			ATGATCGCAGTTTTCTCTTATATTAGCACCTTGGTTTAA	MIAVFSYISTLV*			MIAVFSYISTLV*	CACCCCTCTT	TTAAATACCC	0	G	FG04085.1	0	0	0	0
2792	1751	af	AN6223.1	72.m19432	AO070304000071	0			-186	-82			ATGGTTGGTTGTGAAGCTAGAGGAAACTATCTCTGTTCTACTTCTGACCGCATCACCGCTTTGGCTTCTCCGCATTCACACTCATTTCTCCAACTATCTTTCTAA		ATGGTTGGTTGTGAAGCTAGAGGAAACTATCTCTGTTCTACTTCTGACCGCATCACCGCTTTGGCTTCTCCGCATTCACACTCATTTCTCCAACTATCTTTCTAA		MVGCEARGNYLCSTSDRITALASPHSHSFLQLSF*		MVGCEARGNYLCSTSDRITALASPHSHSFLQLSF*		AAGCCATCCG	TCTCGCCCTA	0	K	0	0	0	0	0
2791	1751	an	AN6223.1	72.m19432	AO070304000071	0	-111	-58					ATGTCAATTTTAGCTCCTCTTTCCAAGCTCAACTCCACCTCCCGATCCATATGA	ATGTCAATTTTAGCTCCTCTTTCCAAGCTCAACTCCACCTCCCGATCCATATGA			MSILAPLSKLNSTSRSI*	MSILAPLSKLNSTSRSI*			TCGATAAGCA	TACTCGCCTA	0	K	0	0	0	0	0
2793	1751	ao	AN6223.1	72.m19432	AO070304000071	0					-225	-199	ATGTTTGCTTATGCGGGTTGCCATTAA			ATGTTTGCTTATGCGGGTTGCCATTAA	MFAYAGCH*			MFAYAGCH*	GGAGTAATTA	ATTGACAGTT	0	K	0	0	0	0	0
2794	1751	ao	AN6223.1	72.m19432	AO070304000071	0					-215	-171	ATGCGGGTTGCCATTAAATTGACAGTTGGAGAAAGTTGGAGTTGA			ATGCGGGTTGCCATTAAATTGACAGTTGGAGAAAGTTGGAGTTGA	MRVAIKLTVGESWS*			MRVAIKLTVGESWS*	ATGTTTGCTT	GTCTAAATTA	0	K	0	0	0	0	0
2795	1751	ao	AN6223.1	72.m19432	AO070304000071	0					-161	-78	ATGCGACATGAAAGGAAATCTTATCGCCGGCGATCTACAATTTATCGCCGATCAACCTCAGGCAAAGCTACAGGACCTCTTTGA			ATGCGACATGAAAGGAAATCTTATCGCCGGCGATCTACAATTTATCGCCGATCAACCTCAGGCAAAGCTACAGGACCTCTTTGA	MRHERKSYRRRSTIYRRSTSGKATGPL*			MRHERKSYRRRSTIYRRSTSGKATGPL*	AGTCTAAATT	TTCAATTGTC	0	K	0	0	0	0	0
2797	1752	af	AN6288.1	72.m19347	AO070308000004	0			-188	-159			ATGGCTAACCCCTCTGGCATTGGAATGTAG		ATGGCTAACCCCTCTGGCATTGGAATGTAG		MANPSGIGM*		MANPSGIGM*		ATACGGGTGG	GCGCATTTTC	0	D	0	0	NCU01605.1	YIL106W	0
2796	1752	an	AN6288.1	72.m19347	AO070308000004	0	-166	-155					ATGCACTACTAA	ATGCACTACTAA			MHY*	MHY*			AAACTACTAC	CCTGAGTGTC	0	D	0	0	NCU01605.1	YIL106W	0
2798	1758	af	AN7736.1	71.m15766	AO070325000157	0			-235	-209			ATGACTGTCTCGTATGTGAGTCAGTAA		ATGACTGTCTCGTATGTGAGTCAGTAA		MTVSYVSQ*		MTVSYVSQ*		CCTAGCCACT	GCAAAGCAAA	0	R	FG08845.1	MG03061.1	NCU02147.1	0	0
2799	1758	af	AN7736.1	71.m15766	AO070325000157	0			-196	-59			ATGACAGAGCGCACAATTCTAGAACACTTCCATCAAGGATTAAGATCATTATCCTGGAGCCTGCGTTCTCCTAATACAGCGGTAGCCCCACACGAAGGCGGTACCTTTACTGATCACTTTGAAGGGACATTTCACTGA		ATGACAGAGCGCACAATTCTAGAACACTTCCATCAAGGATTAAGATCATTATCCTGGAGCCTGCGTTCTCCTAATACAGCGGTAGCCCCACACGAAGGCGGTACCTTTACTGATCACTTTGAAGGGACATTTCACTGA		MTERTILEHFHQGLRSLSWSLRSPNTAVAPHEGGTFTDHFEGTFH*		MTERTILEHFHQGLRSLSWSLRSPNTAVAPHEGGTFTDHFEGTFH*		AAAGCAAAAT	AATAAATTTG	0	R	FG08845.1	MG03061.1	NCU02147.1	0	0
2800	1758	ao	AN7736.1	71.m15766	AO070325000157	0					-161	-102	ATGGTCGCAGATTTAATACTAAGACAGAGTACATTAAATATTCTGTATTCGGTGCCTTAA			ATGGTCGCAGATTTAATACTAAGACAGAGTACATTAAATATTCTGTATTCGGTGCCTTAA	MVADLILRQSTLNILYSVP*			MVADLILRQSTLNILYSVP*	ACACCTTTTA	AGGCGGTAAA	0	R	FG08845.1	MG03061.1	NCU02147.1	0	0
2803	1763	af	AN0802.1	70.m15403	AO070239000016	0			-216	-166			ATGTCGCAGCTGGAGCACTCTCTCGGGCATTGTCACATGGGCCATATGTAG		ATGTCGCAGCTGGAGCACTCTCTCGGGCATTGTCACATGGGCCATATGTAG		MSQLEHSLGHCHMGHM*		MSQLEHSLGHCHMGHM*		CCAGCTGGGC	GCGGCAATTC	0	NI	0	MG01311.1	0	0	0
2804	1763	af	AN0802.1	70.m15403	AO070239000016	0			-180	-166			ATGGGCCATATGTAG		ATGGGCCATATGTAG		MGHM*		MGHM*		GCATTGTCAC	GCGGCAATTC	0	NI	0	MG01311.1	0	0	0
2801	1763	an	AN0802.1	70.m15403	AO070239000016	0	-155	-108					ATGTCTCTCGGCTGTCACATGTGTTGGATAGGCGGCAATTCCTTGTGA	ATGTCTCTCGGCTGTCACATGTGTTGGATAGGCGGCAATTCCTTGTGA			MSLGCHMCWIGGNSL*	MSLGCHMCWIGGNSL*			CCACCTGGGG	CTTCCCACGT	0	NI	0	MG01311.1	0	0	0
2802	1763	an	AN0802.1	70.m15403	AO070239000016	0	-137	-108					ATGTGTTGGATAGGCGGCAATTCCTTGTGA	ATGTGTTGGATAGGCGGCAATTCCTTGTGA			MCWIGGNSL*	MCWIGGNSL*			CGGCTGTCAC	CTTCCCACGT	0	NI	0	MG01311.1	0	0	0
2805	1763	ao	AN0802.1	70.m15403	AO070239000016	0					-188	-153	ATGCCTTGGGGGCTTTGTCACATGGGCCGTATGTAG			ATGCCTTGGGGGCTTTGTCACATGGGCCGTATGTAG	MPWGLCHMGRM*			MPWGLCHMGRM*	ACATTCGTTC	GCGGCAATTC	0	NI	0	MG01311.1	0	0	0
2806	1763	ao	AN0802.1	70.m15403	AO070239000016	0					-167	-153	ATGGGCCGTATGTAG			ATGGGCCGTATGTAG	MGRM*			MGRM*	GCTTTGTCAC	GCGGCAATTC	0	NI	0	MG01311.1	0	0	0
2808	1769	af	AN4958.1	59.m08863	AO070288000020	0			-245	-234			ATGAGAAGTTGA		ATGAGAAGTTGA		MRS*		MRS*		AAGGCACAAG	ATCTTCCGCT	0	S	0	0	0	0	0
2809	1769	af	AN4958.1	59.m08863	AO070288000020	0			-170	-120			ATGGAAATTAAACCTGACCTGAAGTCCCGACGCGTTGAGAGCATCCCTTAG		ATGGAAATTAAACCTGACCTGAAGTCCCGACGCGTTGAGAGCATCCCTTAG		MEIKPDLKSRRVESIP*		MEIKPDLKSRRVESIP*		GCGTCCACAG	AGCTACGATC	0	S	0	0	0	0	0
2807	1769	an	AN4958.1	59.m08863	AO070288000020	0	-118	-107					ATGGAGCCATAG	ATGGAGCCATAG			MEP*	MEP*			GTTTGAAACG	GACGCGTCTT	0	S	0	0	0	0	0
2810	1769	ao	AN4958.1	59.m08863	AO070288000020	0					-94	-71	ATGAATCTCAGGCACGCGTTTTAG			ATGAATCTCAGGCACGCGTTTTAG	MNLRHAF*			MNLRHAF*	CGGAGTTAAA	AGTAGTGAGC	0	S	0	0	0	0	0
2813	1771	af	AN1683.1	58.m08994	AO070305000002	0			-261	-211			ATGAGGTGTTTGGCCGACAGCCAGAACTGCAGGAATCCGGGAAATAATTAG		ATGAGGTGTTTGGCCGACAGCCAGAACTGCAGGAATCCGGGAAATAATTAG		MRCLADSQNCRNPGNN*		MRCLADSQNCRNPGNN*		CGAGGAGAGA	GGCTTGCGTG	0	O	0	0	0	YMR149W	0
2814	1771	af	AN1683.1	58.m08994	AO070305000002	0			-184	-170			ATGCCCCAACTCTGA		ATGCCCCAACTCTGA		MPQL*		MPQL*		GTGGACGCCG	CTATCAGGGA	0	O	0	0	0	YMR149W	0
2812	1771	an	AN1683.1	58.m08994	AO070305000002	0	-173	-135					ATGGGAGACAGCCCGAAGGAGAGAAGGGCAGGCAATTAG	ATGGGAGACAGCCCGAAGGAGAGAAGGGCAGGCAATTAG			MGDSPKERRAGN*	MGDSPKERRAGN*			GGCGTTGAGG	GGCTCAAGGC	0	O	0	0	0	YMR149W	0
2816	1775	an	AN9083.1	66.m04541	AO070332000196	0	-214	-173					ATGAATAGTGACACCAGACGGAGATGTAATCGCGTTGTGTAA	ATGAATAGTGACACCAGACGGAGATGTAATCGCGTTGTGTAA			MNSDTRRRCNRVV*	MNSDTRRRCNRVV*			GCAGAGGAAA	TAGTCTGTAA	0	F	0	0	0	YML022W	0
2818	1776	ao	AN3010.1	59.m09008	AO070337000106	0					-134	-63	ATGCCGCTCATTGGTTGCTGGGGACTTTTTGGTGCTTGCTCCCGGAGCGTCGGAGCTTGGCTTTCTCTCTAA			ATGCCGCTCATTGGTTGCTGGGGACTTTTTGGTGCTTGCTCCCGGAGCGTCGGAGCTTGGCTTTCTCTCTAA	MPLIGCWGLFGACSRSVGAWLSL*			MPLIGCWGLFGACSRSVGAWLSL*	GCGGGCTGCG	TTTTGAGAAA	0	S	0	0	0	YOL093W	YOL093W
2819	1777	af	AN4929.1	59.m08831	AO070338000014	0			-234	-70			ATGGCTGTAAAGGGACAGATAATTCATGACCACTCACTCAATCCTATTCCTCCAGCCCAAGGTGCGGGGAAGTTCTTTAGCTACGCACAGCTGCCCGCTGTCATCTGCCCTCCTGAAGCTCAACGTGTCTCAATTTTCCAACCCCAGCACTTGATCAAACCTTAG		ATGGCTGTAAAGGGACAGATAATTCATGACCACTCACTCAATCCTATTCCTCCAGCCCAAGGTGCGGGGAAGTTCTTTAGCTACGCACAGCTGCCCGCTGTCATCTGCCCTCCTGAAGCTCAACGTGTCTCAATTTTCCAACCCCAGCACTTGATCAAACCTTAG		MAVKGQIIHDHSLNPIPPAQGAGKFFSYAQLPAVICPPEAQRVSIFQPQHLIKP*		MAVKGQIIHDHSLNPIPPAQGAGKFFSYAQLPAVICPPEAQRVSIFQPQHLIKP*		AACTGTCTCA	CTAACACCAT	0	Z	0	0	0	0	0
2820	1777	af	AN4929.1	59.m08831	AO070338000014	0			-209	-81			ATGACCACTCACTCAATCCTATTCCTCCAGCCCAAGGTGCGGGGAAGTTCTTTAGCTACGCACAGCTGCCCGCTGTCATCTGCCCTCCTGAAGCTCAACGTGTCTCAATTTTCCAACCCCAGCACTTGA		ATGACCACTCACTCAATCCTATTCCTCCAGCCCAAGGTGCGGGGAAGTTCTTTAGCTACGCACAGCTGCCCGCTGTCATCTGCCCTCCTGAAGCTCAACGTGTCTCAATTTTCCAACCCCAGCACTTGA		MTTHSILFLQPKVRGSSLATHSCPLSSALLKLNVSQFSNPST*		MTTHSILFLQPKVRGSSLATHSCPLSSALLKLNVSQFSNPST*		CAGATAATTC	TCAAACCTTA	0	Z	0	0	0	0	0
2821	1777	ao	AN4929.1	59.m08831	AO070338000014	0					-195	-97	ATGACCTTGACCCTGTGTACAGCACAAGCTATCCTACTAGCTGTAGCTTCACTTGCGCCGCATTGCCCCTCTCTTCCCCCCCCGAATCTGCCCATGTGA			ATGACCTTGACCCTGTGTACAGCACAAGCTATCCTACTAGCTGTAGCTTCACTTGCGCCGCATTGCCCCTCTCTTCCCCCCCCGAATCTGCCCATGTGA	MTLTLCTAQAILLAVASLAPHCPSLPPPNLPM*			MTLTLCTAQAILLAVASLAPHCPSLPPPNLPM*	CCCCCTTCAA	CCGAGGAGCC	0	Z	0	0	0	0	0
2823	1779	af	AN6057.1	72.m19101	AO070340000195	0			-253	-212			ATGCGCAGTGACCTCATCCAAGATCTTGTCAAGCATACATAG		ATGCGCAGTGACCTCATCCAAGATCTTGTCAAGCATACATAG		MRSDLIQDLVKHT*		MRSDLIQDLVKHT*		CCAGAATCCC	CATAAGAATC	0	QI	0	0	0	0	0

2824	1779	af	AN6057.1	72.m19101	AO070340000195	0			-189	-112			ATGGTTGCATTGTTCGTCGTGCCCATTGTTCTTGTGTCCCCTTTCCCCACCTTGCGTCTGTTAAAGGGCCTCGGTTAG		ATGGTTGCATTGTTCGTCGTGCCCATTGTTCTTGTGTCCCCTTTCCCCACCTTGCGTCTGTTAAAGGGCCTCGGTTAG		MVALFVVPIVLVSPFPTLRLLKGLG*		MVALFVVPIVLVSPFPTLRLLKGLG*		TGTGAAGAAA	AGTCACGTTT	0	QI	0	0	0	0	0
2825	1779	af	AN6057.1	72.m19101	AO070340000195	0			-69	-46			ATGCCAGAGAAATATGGAATTTGA		ATGCCAGAGAAATATGGAATTTGA		MPEKYGI*		MPEKYGI*		GCGAGGATCC	GCTACCAGAG	0	QI	0	0	0	0	0
2822	1779	an	AN6057.1	72.m19101	AO070340000195	0	-239	-189					ATGTCTACCAGACTGGGGAAGCCGAAGCCAAACTCCAGGGCTATGCCATAA	ATGTCTACCAGACTGGGGAAGCCGAAGCCAAACTCCAGGGCTATGCCATAA			MSTRLGKPKPNSRAMP*	MSTRLGKPKPNSRAMP*			ATAGCCCTAG	CCACTATAGC	0	QI	0	0	0	0	0
2826	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-258	-238	ATGGCTGCGGCATTAATATGA			ATGGCTGCGGCATTAATATGA	MAAALI*			MAAALI*	GCCTAAGCCA	AGTCATCTAT	0	QI	0	0	0	0	0
2827	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-241	-77	ATGAAGTCATCTATATGGGGTATAACTAGATGGGGATTAATTCATTTCAGCCATGTCACTCGTCTCCTTTGCAGCACTAGACCAGGATGCTTCTCCACTTCTGTGCCTGTATCCTCGGTGATGATTTTATCGCCCGAGGTAGAACCGATCAATCTGGAGGGCTAA			ATGAAGTCATCTATATGGGGTATAACTAGATGGGGATTAATTCATTTCAGCCATGTCACTCGTCTCCTTTGCAGCACTAGACCAGGATGCTTCTCCACTTCTGTGCCTGTATCCTCGGTGATGATTTTATCGCCCGAGGTAGAACCGATCAATCTGGAGGGCTAA	MKSSIWGITRWGLIHFSHVTRLLCSTRPGCFSTSVPVSSVMILSPEVEPINLEG*			MKSSIWGITRWGLIHFSHVTRLLCSTRPGCFSTSVPVSSVMILSPEVEPINLEG*	CGGCATTAAT	ATATCGCTGT	0	QI	0	0	0	0	0
2828	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-227	-213	ATGGGGTATAACTAG			ATGGGGTATAACTAG	MGYN*			MGYN*	AGTCATCTAT	ATGGGGATTA	0	QI	0	0	0	0	0
2829	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-212	-162	ATGGGGATTAATTCATTTCAGCCATGTCACTCGTCTCCTTTGCAGCACTAG			ATGGGGATTAATTCATTTCAGCCATGTCACTCGTCTCCTTTGCAGCACTAG	MGINSFQPCHSSPLQH*			MGINSFQPCHSSPLQH*	GTATAACTAG	ACCAGGATGC	0	QI	0	0	0	0	0
2830	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-189	-121	ATGTCACTCGTCTCCTTTGCAGCACTAGACCAGGATGCTTCTCCACTTCTGTGCCTGTATCCTCGGTGA			ATGTCACTCGTCTCCTTTGCAGCACTAGACCAGGATGCTTCTCCACTTCTGTGCCTGTATCCTCGGTGA	MSLVSFAALDQDASPLLCLYPR*			MSLVSFAALDQDASPLLCLYPR*	CATTTCAGCC	TGATTTTATC	0	QI	0	0	0	0	0
2831	1779	ao	AN6057.1	72.m19101	AO070340000195	0					-121	-77	ATGATTTTATCGCCCGAGGTAGAACCGATCAATCTGGAGGGCTAA			ATGATTTTATCGCCCGAGGTAGAACCGATCAATCTGGAGGGCTAA	MILSPEVEPINLEG*			MILSPEVEPINLEG*	ATCCTCGGTG	ATATCGCTGT	0	QI	0	0	0	0	0
2833	1781	af	AN7651.1	57.m05410	AO070268000008	0			-202	-161			ATGCTCTCAGTCGATATCTTCTCGCACACTCTCTTCGAATAA		ATGCTCTCAGTCGATATCTTCTCGCACACTCTCTTCGAATAA		MLSVDIFSHTLFE*		MLSVDIFSHTLFE*		GATACCCCAT	ACTTTAATCT	0		0	0	0	0	0
2832	1781	an	AN7651.1	57.m05410	AO070268000008	0	-152	-87					ATGCGTATTCATTTCTTTGTTGATGCTCCAAAAGATATTGCTGTCGGCTCTCGGCTCTCCTACTGA	ATGCGTATTCATTTCTTTGTTGATGCTCCAAAAGATATTGCTGTCGGCTCTCGGCTCTCCTACTGA			MRIHFFVDAPKDIAVGSRLSY*	MRIHFFVDAPKDIAVGSRLSY*			CACCTCTTTG	TACATTCTTT	0		0	0	0	0	0
2834	1782	af	AN7352.1	72.m20006	AO070278000048	0			-241	-227			ATGAATTATTGTTAG		ATGAATTATTGTTAG		MNYC*		MNYC*		TCTTCCAGTA	CCTCATGAGC	0	O	0	0	0	0	0
2835	1782	af	AN7352.1	72.m20006	AO070278000048	0			-222	-49			ATGAGCCATCTTTCCTGTGCCACTTCTCTTCTTCGTGCATTGGACACTTCACCAATCTGCCCCCCGCTATTTAAAGGCCCGGACTGGACGACTGGACGACCTGCGACGCCGAGCCTCCATCCTTTCATTTCCGCGACCCCAGGTTCAGCTTCGTTTCAGGCCTCAATGCGTTAA		ATGAGCCATCTTTCCTGTGCCACTTCTCTTCTTCGTGCATTGGACACTTCACCAATCTGCCCCCCGCTATTTAAAGGCCCGGACTGGACGACTGGACGACCTGCGACGCCGAGCCTCCATCCTTTCATTTCCGCGACCCCAGGTTCAGCTTCGTTTCAGGCCTCAATGCGTTAA		MSHLSCATSLLRALDTSPICPPLFKGPDWTTGRPATPSLHPFISATPGSASFQASMR*		MSHLSCATSLLRALDTSPICPPLFKGPDWTTGRPATPSLHPFISATPGSASFQASMR*		TGTTAGCCTC	GTTCGACCTA	0	O	0	0	0	0	0
2836	1782	ao	AN7352.1	72.m20006	AO070278000048	0					-192	-175	ATGCGTGTGTGTCACTAA			ATGCGTGTGTGTCACTAA	MRVCH*			MRVCH*	TTTGGAAGCG	CGTTTAACCT	0	O	0	0	0	0	0
2839	1783	af	AN7474.1	57.m05855	AO070287000028	0			-143	-114			ATGGTTTCTTCGGCTCGGATCTTCAACTGA		ATGGTTTCTTCGGCTCGGATCTTCAACTGA		MVSSARIFN*		MVSSARIFN*		GTCGTGCCCC	ACATCACTTT	0	R	0	0	0	0	0
2837	1783	an	AN7474.1	57.m05855	AO070287000028	0	-204	-187					ATGCCATACGCACTCTGA	ATGCCATACGCACTCTGA			MPYAL*	MPYAL*			CTTACACCTA	GCTAATCTTC	0	R	0	0	0	0	0
2838	1783	an	AN7474.1	57.m05855	AO070287000028	0	-126	-109					ATGGTTGTTCTGGGGTGA	ATGGTTGTTCTGGGGTGA			MVVLG*	MVVLG*			CTCTAAACAT	GCTTTTGACC	0	R	0	0	0	0	0
2840	1783	ao	AN7474.1	57.m05855	AO070287000028	0					-131	-102	ATGGTTCTTTTCGAGAACGTCTCCGACTGA			ATGGTTCTTTTCGAGAACGTCTCCGACTGA	MVLFENVSD*			MVLFENVSD*	CGATCAACAC	ACCGGATTTC	0	R	0	0	0	0	0
2841	1786	an	AN8491.1	72.m19790	AO070297000017	0	-181	-149					ATGGGTATAGATGGGGCAGCAAAACTGCGCTAA	ATGGGTATAGATGGGGCAGCAAAACTGCGCTAA			MGIDGAAKLR*	MGIDGAAKLR*			GGAGCGGTCC	ACCTGACCCA	0	J	0	MG00482.1	0	YPL211W	0
2842	1786	an	AN8491.1	72.m19790	AO070297000017	0	-171	-112					ATGGGGCAGCAAAACTGCGCTAAACCTGACCCAGCAGAGCTAGCCCAAATAATACGCTAA	ATGGGGCAGCAAAACTGCGCTAAACCTGACCCAGCAGAGCTAGCCCAAATAATACGCTAA			MGQQNCAKPDPAELAQIIR*	MGQQNCAKPDPAELAQIIR*			ATGGGTATAG	CCGTATTTGT	0	J	0	MG00482.1	0	YPL211W	0
2843	1786	ao	AN8491.1	72.m19790	AO070297000017	0					-154	-71	ATGGTTGGTTTTGAGCGGTTCCCGTCCGAAACTTTTTTTTCTTTGCGGTGCCAAGACTTTTATGCCAAAAGCTCTCCACCTTAG			ATGGTTGGTTTTGAGCGGTTCCCGTCCGAAACTTTTTTTTCTTTGCGGTGCCAAGACTTTTATGCCAAAAGCTCTCCACCTTAG	MVGFERFPSETFFSLRCQDFYAKSSPP*			MVGFERFPSETFFSLRCQDFYAKSSPP*	GTGAGGGTCG	ACTTTTTTTG	0	J	0	MG00482.1	0	YPL211W	0
2844	1788	ao	AN1963.1	58.m07568	AO070301000044	0					-121	-20	ATGGGACTGGTAGGATACGGCGAAATAGACTGCCGACCGCCGACATCTACACACGGACAGGCTTCGGACGCCTTTGTCACACGTTCCATTCCTTTGTACTAG			ATGGGACTGGTAGGATACGGCGAAATAGACTGCCGACCGCCGACATCTACACACGGACAGGCTTCGGACGCCTTTGTCACACGTTCCATTCCTTTGTACTAG	MGLVGYGEIDCRPPTSTHGQASDAFVTRSIPLY*			MGLVGYGEIDCRPPTSTHGQASDAFVTRSIPLY*	GATTTGTTGG	CTCTTTGTCT	0		0	0	0	0	0
2845	1791	an	AN6892.1	71.m15247	AO070314000029	0	-239	-213					ATGTCATTGCATAATTCTAGTTGCTGA	ATGTCATTGCATAATTCTAGTTGCTGA			MSLHNSSC*	MSLHNSSC*			GTTTCAACAG	CCGTATACCT	0	T	0	MG05207.1	0	0	0
2847	1792	an	AN8723.1	62.m03343	AO070315000151	0	-426	-316					ATGTTTTACTCTTTTCTTACAGCTGACGATCCAATCCATTCGCTTCCGCATCAACCCATCCCTCCATCCTTCGTCTTCCTCCCTTCCCTGATTCCGAGGATGCCAAATTAA	ATGTTTTACTCTTTTCTTACAGCTGACGATCCAATCCATTCGCTTCCGCATCAACCCATCCCTCCATCCTTCGTCTTCCTCCCTTCCCTGATTCCGAGGATGCCAAATTAA			MFYSFLTADDPIHSLPHQPIPPSFVFLPSLIPRMPN*	MFYSFLTADDPIHSLPHQPIPPSFVFLPSLIPRMPN*			ATCTTTCTGT	TGTCCGCAGT	0		0	0	0	0	0
2848	1792	an	AN8723.1	62.m03343	AO070315000151	0	-327	-316					ATGCCAAATTAA	ATGCCAAATTAA			MPN*	MPN*			GATTCCGAGG	TGTCCGCAGT	0		0	0	0	0	0
2849	1792	an	AN8723.1	62.m03343	AO070315000151	0	-316	-284					ATGTCCGCAGTGGATTACTTGTCCATTTTTTGA	ATGTCCGCAGTGGATTACTTGTCCATTTTTTGA			MSAVDYLSIF*	MSAVDYLSIF*			TGCCAAATTA	GGAGATAATC	0		0	0	0	0	0
2852	1792	ao	AN8723.1	62.m03343	AO070315000151	0					-278	-267	ATGACACCTTAG			ATGACACCTTAG	MTP*			MTP*	ATTTCCCCCA	GCCTGTCGGT	0		0	0	0	0	0
2853	1797	af	AN6577.1	62.m03163	AO070326000023	0			-113	-51			ATGGGAATAAGAAATATCGGCCACGTGATCCGGATATCCGCCAGTATTTTTCCATGGCAATAA		ATGGGAATAAGAAATATCGGCCACGTGATCCGGATATCCGCCAGTATTTTTCCATGGCAATAA		MGIRNIGHVIRISASIFPWQ*		MGIRNIGHVIRISASIFPWQ*		TCGGACATAA	TGCAGTTTCA	0	J	0	0	0	0	0
2856	1797	ao	AN6577.1	62.m03163	AO070326000023	0					-86	-72	ATGCGTATTAGCTAG			ATGCGTATTAGCTAG	MRIS*			MRIS*	CCTGCACGTG	ATTTTCTGTT	0	J	0	0	0	0	0
2857	1809	af	AN7661.1	57.m05428	AO070268000032	0			-115	-53			ATGCAGTCTTATCAAGATATCCATCTAAAGCTATCATTGTTAACAATCTTGTCTTTAATATAG		ATGCAGTCTTATCAAGATATCCATCTAAAGCTATCATTGTTAACAATCTTGTCTTTAATATAG		MQSYQDIHLKLSLLTILSLI*		MQSYQDIHLKLSLLTILSLI*		CTTGACAGGT	TACAAGACTA	0	K	0	0	0	0	0
2859	1809	ao	AN7661.1	57.m05428	AO070268000032	0					-189	-97	ATGCACACCCTAGGTTACACTACCTGGTACTTTTGTCCAGAGGAACCATTCACCCTTCTGCTCCCATCTTCGTTGTCAATATCCGATGGTTAA			ATGCACACCCTAGGTTACACTACCTGGTACTTTTGTCCAGAGGAACCATTCACCCTTCTGCTCCCATCTTCGTTGTCAATATCCGATGGTTAA	MHTLGYTTWYFCPEEPFTLLLPSSLSISDG*			MHTLGYTTWYFCPEEPFTLLLPSSLSISDG*	TGCCTGAGGT	TAGGAGCAAA	0	K	0	0	0	0	0
2860	1809	ao	AN7661.1	57.m05428	AO070268000032	0					-104	-42	ATGGTTAATAGGAGCAAAGGCTTGTTTCGCGATAACACATTTACACCGCAAACGGACTCATAG			ATGGTTAATAGGAGCAAAGGCTTGTTTCGCGATAACACATTTACACCGCAAACGGACTCATAG	MVNRSKGLFRDNTFTPQTDS*			MVNRSKGLFRDNTFTPQTDS*	TCAATATCCG	CCATAGTGGC	0	K	0	0	0	0	0
2863	1810	af	AN4445.1	58.m07880	AO070273000008	0			-258	-244			ATGTTGACTGAATGA		ATGTTGACTGAATGA		MLTE*		MLTE*		TCGGTCGTTG	AGATCTGGCA	0	BK	0	0	0	YGR002C	0
2864	1810	af	AN4445.1	58.m07880	AO070273000008	0			-247	-104			ATGAAGATCTGGCACCAACGACGGGACGGTCTTGGCGCGATTCGATGGGCGGAATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGATTTCATCTTTTAA		ATGAAGATCTGGCACCAACGACGGGACGGTCTTGGCGCGATTCGATGGGCGGAATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGATTTCATCTTTTAA		MKIWHQRRDGLGAIRWAEWNGGDRPFSAYRFPSFSHHGRHLVVDFIF*		MKIWHQRRDGLGAIRWAEWNGGDRPFSAYRFPSFSHHGRHLVVDFIF*		TGTTGACTGA	TTTCTAATTT	0	BK	0	0	0	YGR002C	0
2865	1810	af	AN4445.1	58.m07880	AO070273000008	0			-203	-117			ATGGGCGGAATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGA		ATGGGCGGAATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGA		MGGMEWRRPAVFCVPVSLFQPSRSASRR*		MGGMEWRRPAVFCVPVSLFQPSRSASRR*		GCGCGATTCG	TTTCATCTTT	0	BK	0	0	0	YGR002C	0
2866	1810	af	AN4445.1	58.m07880	AO070273000008	0			-194	-117			ATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGA		ATGGAATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGA		MEWRRPAVFCVPVSLFQPSRSASRR*		MEWRRPAVFCVPVSLFQPSRSASRR*		GATGGGCGGA	TTTCATCTTT	0	BK	0	0	0	YGR002C	0
2867	1810	af	AN4445.1	58.m07880	AO070273000008	0			-189	-97			ATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGATTTCATCTTTTAATTTCTAA		ATGGAGGAGACCGGCCGTTTTCTGCGTACCGGTTTCCCTCTTTCAGCCATCACGGTCGGCATCTCGTCGTTGATTTCATCTTTTAATTTCTAA		MEETGRFLRTGFPLSAITVGISSLISSFNF*		MEETGRFLRTGFPLSAITVGISSLISSFNF*		GCGGAATGGA	TTTTCTCTTA	0	BK	0	0	0	YGR002C	0
2861	1810	an	AN4445.1	58.m07880	AO070273000008	0	-209	-129					ATGTTATGCTGTCCAGATCCAGATCCAGGCCATGGGCGGGAGTGGGCTTGGCGCGAATTCTCATTCCCCCGTCTCGATTAA	ATGTTATGCTGTCCAGATCCAGATCCAGGCCATGGGCGGGAGTGGGCTTGGCGCGAATTCTCATTCCCCCGTCTCGATTAA			MLCCPDPDPGHGREWAWREFSFPRLD*	MLCCPDPDPGHGREWAWREFSFPRLD*			GAACACGTTA	CAACCACTCC	0	BK	0	0	0	YGR002C	0
2862	1810	an	AN4445.1	58.m07880	AO070273000008	0	-178	-77					ATGGGCGGGAGTGGGCTTGGCGCGAATTCTCATTCCCCCGTCTCGATTAACAACCACTCCTCCATCTCACTGTCAACGCTGTATACATCCATATCAAACTGA	ATGGGCGGGAGTGGGCTTGGCGCGAATTCTCATTCCCCCGTCTCGATTAACAACCACTCCTCCATCTCACTGTCAACGCTGTATACATCCATATCAAACTGA			MGGSGLGANSHSPVSINNHSSISLSTLYTSISN*	MGGSGLGANSHSPVSINNHSSISLSTLYTSISN*			GATCCAGGCC	TTCAACGAAA	0	BK	0	0	0	YGR002C	0
2868	1810	ao	AN4445.1	58.m07880	AO070273000008	0					-240	-7	ATGTTGATGCTCAATGTGGCAGCAACGGACGGAAGAGTCTTGGCGCGAATTGAATTCTCCATTCGATCATTCACTTTACAACTCCCCTTCACCTCATACTCTTCACTCCTTTCATATCCCCTCTTGTTCTTCATCTCCTGTATTTCTGTTCCTCACCCTCCTTGTTCTCATTTATCTACTAATAACCAACAAATCTTTATCCGTGATCTTCAAGAACTCCAACAGTGGTGGTAG			ATGTTGATGCTCAATGTGGCAGCAACGGACGGAAGAGTCTTGGCGCGAATTGAATTCTCCATTCGATCATTCACTTTACAACTCCCCTTCACCTCATACTCTTCACTCCTTTCATATCCCCTCTTGTTCTTCATCTCCTGTATTTCTGTTCCTCACCCTCCTTGTTCTCATTTATCTACTAATAACCAACAAATCTTTATCCGTGATCTTCAAGAACTCCAACAGTGGTGGTAG	MLMLNVAATDGRVLARIEFSIRSFTLQLPFTSYSSLLSYPLLFFISCISVPHPPCSHLSTNNQQIFIRDLQELQQWW*			MLMLNVAATDGRVLARIEFSIRSFTLQLPFTSYSSLLSYPLLFFISCISVPHPPCSHLSTNNQQIFIRDLQELQQWW*	AGGTGGCCGA	CCCGCCATGG	0	BK	0	0	0	YGR002C	0
2869	1810	ao	AN4445.1	58.m07880	AO070273000008	0					-234	-7	ATGCTCAATGTGGCAGCAACGGACGGAAGAGTCTTGGCGCGAATTGAATTCTCCATTCGATCATTCACTTTACAACTCCCCTTCACCTCATACTCTTCACTCCTTTCATATCCCCTCTTGTTCTTCATCTCCTGTATTTCTGTTCCTCACCCTCCTTGTTCTCATTTATCTACTAATAACCAACAAATCTTTATCCGTGATCTTCAAGAACTCCAACAGTGGTGGTAG			ATGCTCAATGTGGCAGCAACGGACGGAAGAGTCTTGGCGCGAATTGAATTCTCCATTCGATCATTCACTTTACAACTCCCCTTCACCTCATACTCTTCACTCCTTTCATATCCCCTCTTGTTCTTCATCTCCTGTATTTCTGTTCCTCACCCTCCTTGTTCTCATTTATCTACTAATAACCAACAAATCTTTATCCGTGATCTTCAAGAACTCCAACAGTGGTGGTAG	MLNVAATDGRVLARIEFSIRSFTLQLPFTSYSSLLSYPLLFFISCISVPHPPCSHLSTNNQQIFIRDLQELQQWW*			MLNVAATDGRVLARIEFSIRSFTLQLPFTSYSSLLSYPLLFFISCISVPHPPCSHLSTNNQQIFIRDLQELQQWW*	CCGAATGTTG	CCCGCCATGG	0	BK	0	0	0	YGR002C	0
2871	1811	af	AN7540.1	72.m19557	AO070277000037	0			-163	-101			ATGGAGCCAAGGCCACCAGCCACAGGGACACACAACTCGCAACACAAAAATTCGGGATCGTGA		ATGGAGCCAAGGCCACCAGCCACAGGGACACACAACTCGCAACACAAAAATTCGGGATCGTGA		MEPRPPATGTHNSQHKNSGS*		MEPRPPATGTHNSQHKNSGS*		AGTGTGGCTG	GAATCGTCCC	0	J	FG01314.1	MG00341.1	NCU07380.1	0	0
2870	1811	an	AN7540.1	72.m19557	AO070277000037	0	-210	-85					ATGTACTGCTCCATAGGGCGGTGCCAAGTCCACCAGCCACAGTACCACTCGCGACACAAAAAATCGCCTTTCTCTGGGTTCCCAATATCCCGCCGCCTGCAAGCTTACCGTCCCCAGATCTCATAA	ATGTACTGCTCCATAGGGCGGTGCCAAGTCCACCAGCCACAGTACCACTCGCGACACAAAAAATCGCCTTTCTCTGGGTTCCCAATATCCCGCCGCCTGCAAGCTTACCGTCCCCAGATCTCATAA			MYCSIGRCQVHQPQYHSRHKKSPFSGFPISRRLQAYRPQIS*	MYCSIGRCQVHQPQYHSRHKKSPFSGFPISRRLQAYRPQIS*			GTGGCTAGGC	GGCTACCTCG	0	J	FG01314.1	MG00341.1	NCU07380.1	0	0
2875	1812	af	AN9304.1	70.m15663	AO070280000073	0			-131	-66			ATGCCCGCTGTAAGAGAAGTATATGAGAGACAAACAATGCCTGCGAGCAGTCTATCTATCAATTGA		ATGCCCGCTGTAAGAGAAGTATATGAGAGACAAACAATGCCTGCGAGCAGTCTATCTATCAATTGA		MPAVREVYERQTMPASSLSIN*		MPAVREVYERQTMPASSLSIN*		ATCATTGGAA	CAACACTGTA	0	O	0	0	0	0	0
2876	1812	af	AN9304.1	70.m15663	AO070280000073	0			-109	-29			ATGAGAGACAAACAATGCCTGCGAGCAGTCTATCTATCAATTGACAACACTGTAAGAGCAATCTACCTCCTAACCTCCTAA		ATGAGAGACAAACAATGCCTGCGAGCAGTCTATCTATCAATTGACAACACTGTAAGAGCAATCTACCTCCTAACCTCCTAA		MRDKQCLRAVYLSIDNTVRAIYLLTS*		MRDKQCLRAVYLSIDNTVRAIYLLTS*		AGAGAAGTAT	CAAAATCAAC	0	O	0	0	0	0	0
2877	1812	af	AN9304.1	70.m15663	AO070280000073	0			-95	-66			ATGCCTGCGAGCAGTCTATCTATCAATTGA		ATGCCTGCGAGCAGTCTATCTATCAATTGA		MPASSLSIN*		MPASSLSIN*		GAGACAAACA	CAACACTGTA	0	O	0	0	0	0	0
2872	1812	an	AN9304.1	70.m15663	AO070280000073	0	-207	-181					ATGGATCCAAATCCCCACCTGGCCTGA	ATGGATCCAAATCCCCACCTGGCCTGA			MDPNPHLA*	MDPNPHLA*			TGCTTTCCCC	GCTCCGACAA	0	O	0	0	0	0	0

2873	1812	an	AN9304.1	70.m15663	AO070280000073	0	-135	-124					ATGCGGTGCTGA	ATGCGGTGCTGA			MRC*	MRC*			CGCCGGTGGG	GAAATGTGCC	0	O	0	0	0	0	0
2874	1812	an	AN9304.1	70.m15663	AO070280000073	0	-120	-97					ATGTGCCGACCAGATTATCTTTAG	ATGTGCCGACCAGATTATCTTTAG			MCRPDYL*	MCRPDYL*			GTGCTGAGAA	CGGTATTTAT	0	O	0	0	0	0	0
2881	1814	af	AN7492.1	57.m05852	AO070287000025	0			-248	-162			ATGCGACTGCCGGTATCTGCTAGGGATACAGTCATCAACACTTCTTCATTTTCAGCCTGGCCCCTTTCTACAGCATTTTCTATATAG		ATGCGACTGCCGGTATCTGCTAGGGATACAGTCATCAACACTTCTTCATTTTCAGCCTGGCCCCTTTCTACAGCATTTTCTATATAG		MRLPVSARDTVINTSSFSAWPLSTAFSI*		MRLPVSARDTVINTSSFSAWPLSTAFSI*		TGGAAAGGTG	AAATTTTACG	0	S	FG09810.1	MG01422.1	0	0	0
2882	1814	af	AN7492.1	57.m05852	AO070287000025	0			-147	-121			ATGCTGGCTACGTTATTGATAAGATAA		ATGCTGGCTACGTTATTGATAAGATAA		MLATLLIR*		MLATLLIR*		TTTACGATTC	GCTCTTGACC	0	S	FG09810.1	MG01422.1	0	0	0
2878	1814	an	AN7492.1	57.m05852	AO070287000025	0	-184	-143					ATGGCTTCGAAACCAAGTAAGGTACAATTCATGCTCGATTAA	ATGGCTTCGAAACCAAGTAAGGTACAATTCATGCTCGATTAA			MASKPSKVQFMLD*	MASKPSKVQFMLD*			TGTATTGAAC	CTCGGTCCAT	0	S	FG09810.1	MG01422.1	0	0	0
2879	1814	an	AN7492.1	57.m05852	AO070287000025	0	-154	-143					ATGCTCGATTAA	ATGCTCGATTAA			MLD*	MLD*			GGTACAATTC	CTCGGTCCAT	0	S	FG09810.1	MG01422.1	0	0	0
2880	1814	an	AN7492.1	57.m05852	AO070287000025	0	-121	-89					ATGCAGGTCGTGGCCAATATAAATAAGGCTTGA	ATGCAGGTCGTGGCCAATATAAATAAGGCTTGA			MQVVANINKA*	MQVVANINKA*			TTCGTTTTTG	CCGCCCTGGA	0	S	FG09810.1	MG01422.1	0	0	0
2883	1814	ao	AN7492.1	57.m05852	AO070287000025	0					-207	-91	ATGTATGCTTTCGAAGGCCAAAGCTTGCATTATCTGGTTGGATCTCGACTATTCGCCTTTCTGGTGAAGAACTATATCGAAGTTGATCACAGTATCGATAATATTGATAAGTATTGA			ATGTATGCTTTCGAAGGCCAAAGCTTGCATTATCTGGTTGGATCTCGACTATTCGCCTTTCTGGTGAAGAACTATATCGAAGTTGATCACAGTATCGATAATATTGATAAGTATTGA	MYAFEGQSLHYLVGSRLFAFLVKNYIEVDHSIDNIDKY*			MYAFEGQSLHYLVGSRLFAFLVKNYIEVDHSIDNIDKY*	TAAGTCATAT	CCGCCCAACT	0	S	FG09810.1	MG01422.1	0	0	0
2884	1814	ao	AN7492.1	57.m05852	AO070287000025	0					-203	-141	ATGCTTTCGAAGGCCAAAGCTTGCATTATCTGGTTGGATCTCGACTATTCGCCTTTCTGGTGA			ATGCTTTCGAAGGCCAAAGCTTGCATTATCTGGTTGGATCTCGACTATTCGCCTTTCTGGTGA	MLSKAKACIIWLDLDYSPFW*			MLSKAKACIIWLDLDYSPFW*	TCATATATGT	AGAACTATAT	0	S	FG09810.1	MG01422.1	0	0	0
2888	1816	af	AN8539.1	52.m03979	AO070294000060	0			-190	-131			ATGCGGCGTCAGACATGCCCATTAGAATGCTCCCCTAAAGCCAAACGGCAGAGTATATAG		ATGCGGCGTCAGACATGCCCATTAGAATGCTCCCCTAAAGCCAAACGGCAGAGTATATAG		MRRQTCPLECSPKAKRQSI*		MRRQTCPLECSPKAKRQSI*		AGCATTATCA	GGAAGCAAGA	0	J	0	0	0	0	0
2889	1816	af	AN8539.1	52.m03979	AO070294000060	0			-176	-153			ATGCCCATTAGAATGCTCCCCTAA		ATGCCCATTAGAATGCTCCCCTAA		MPIRMLP*		MPIRMLP*		GGCGTCAGAC	AGCCAAACGG	0	J	0	0	0	0	0
2890	1816	af	AN8539.1	52.m03979	AO070294000060	0			-164	-153			ATGCTCCCCTAA		ATGCTCCCCTAA		MLP*		MLP*		GCCCATTAGA	AGCCAAACGG	0	J	0	0	0	0	0
2891	1816	af	AN8539.1	52.m03979	AO070294000060	0			-113	-60			ATGGAGAAACACCGTAGAAGCACTCTAGAGGAGAAACCAAAGAAAACGAACTAG		ATGGAGAAACACCGTAGAAGCACTCTAGAGGAGAAACCAAAGAAAACGAACTAG		MEKHRRSTLEEKPKKTN*		MEKHRRSTLEEKPKKTN*		AGAGGTACAC	ACTCATCAAC	0	J	0	0	0	0	0
2885	1816	an	AN8539.1	52.m03979	AO070294000060	0	-242	-180					ATGTCTAGGCGCCCTGGGCTTAGCCGCCAACCCCTGTATGCCGAGTCGGACTATCGAGTCTGA	ATGTCTAGGCGCCCTGGGCTTAGCCGCCAACCCCTGTATGCCGAGTCGGACTATCGAGTCTGA			MSRRPGLSRQPLYAESDYRV*	MSRRPGLSRQPLYAESDYRV*			GACGTGAGAG	ACATATAAGG	0	J	0	0	0	0	0
2886	1816	an	AN8539.1	52.m03979	AO070294000060	0	-205	-134					ATGCCGAGTCGGACTATCGAGTCTGAACATATAAGGCAGAGGGTGCGGGATACTCGCGCTCAAGAGTTCTGA	ATGCCGAGTCGGACTATCGAGTCTGAACATATAAGGCAGAGGGTGCGGGATACTCGCGCTCAAGAGTTCTGA			MPSRTIESEHIRQRVRDTRAQEF*	MPSRTIESEHIRQRVRDTRAQEF*			CAACCCCTGT	TCTTGAAGTG	0	J	0	0	0	0	0
2887	1816	an	AN8539.1	52.m03979	AO070294000060	0	-112	-92					ATGTACAATATCCCATACTGA	ATGTACAATATCCCATACTGA			MYNIPY*	MYNIPY*			TGGGCGTTGG	TAAACTCGCG	0	J	0	0	0	0	0
2892	1816	ao	AN8539.1	52.m03979	AO070294000060	0					-98	-30	ATGGCGGAAAAGCTTGAGCTGTACAACCATACCTGCAAGAAGAAGATCAAGACCTTTGCACATTGCTAG			ATGGCGGAAAAGCTTGAGCTGTACAACCATACCTGCAAGAAGAAGATCAAGACCTTTGCACATTGCTAG	MAEKLELYNHTCKKKIKTFAHC*			MAEKLELYNHTCKKKIKTFAHC*	AACACTGAGC	CTCTTACTTT	0	J	0	0	0	0	0
2896	1817	af	AN2723.1	70.m15716	AO070309000061	0			-241	-194			ATGACCCGAGGGCGCTCTCCCGGCACTCCCCGCCGAGAGCTCTGTTAG		ATGACCCGAGGGCGCTCTCCCGGCACTCCCCGCCGAGAGCTCTGTTAG		MTRGRSPGTPRRELC*		MTRGRSPGTPRRELC*		TTAGTTAGAA	TTCTCCAGGT	0	E	0	0	0	0	0
2897	1817	af	AN2723.1	70.m15716	AO070309000061	0			-148	-83			ATGCGGGCTGGGGTGGAGCCGAAGGGAGCTAATGGCAGTGCTCATCTAGAGGTATATGTACTATAA		ATGCGGGCTGGGGTGGAGCCGAAGGGAGCTAATGGCAGTGCTCATCTAGAGGTATATGTACTATAA		MRAGVEPKGANGSAHLEVYVL*		MRAGVEPKGANGSAHLEVYVL*		CTTGTGACCG	CATGGCCAGC	0	E	0	0	0	0	0
2898	1817	af	AN2723.1	70.m15716	AO070309000061	0			-117	-100			ATGGCAGTGCTCATCTAG		ATGGCAGTGCTCATCTAG		MAVLI*		MAVLI*		AAGGGAGCTA	AGGTATATGT	0	E	0	0	0	0	0
2899	1817	af	AN2723.1	70.m15716	AO070309000061	0			-93	-46			ATGTACTATAACATGGCCAGCTGGATCAATGAAATGCGCAAATTCTAA		ATGTACTATAACATGGCCAGCTGGATCAATGAAATGCGCAAATTCTAA		MYYNMASWINEMRKF*		MYYNMASWINEMRKF*		CTAGAGGTAT	GTGCAATCTT	0	E	0	0	0	0	0
2900	1817	af	AN2723.1	70.m15716	AO070309000061	0			-81	-46			ATGGCCAGCTGGATCAATGAAATGCGCAAATTCTAA		ATGGCCAGCTGGATCAATGAAATGCGCAAATTCTAA		MASWINEMRKF*		MASWINEMRKF*		GTACTATAAC	GTGCAATCTT	0	E	0	0	0	0	0
2893	1817	an	AN2723.1	70.m15716	AO070309000061	0	-123	-109					ATGCGGAGAAAGTAG	ATGCGGAGAAAGTAG			MRRK*	MRRK*			TGAGGGGTCG	TCATGGTCAT	0	E	0	0	0	0	0
2894	1817	an	AN2723.1	70.m15716	AO070309000061	0	-106	-47					ATGGTCATCATTGTGCAGACATATAAGCGGGCAGGTAGATGGAAGTCCAGAGTTGATTAA	ATGGTCATCATTGTGCAGACATATAAGCGGGCAGGTAGATGGAAGTCCAGAGTTGATTAA			MVIIVQTYKRAGRWKSRVD*	MVIIVQTYKRAGRWKSRVD*			GAAAGTAGTC	CAGTAGGTAT	0	E	0	0	0	0	0
2895	1817	an	AN2723.1	70.m15716	AO070309000061	0	-68	-51					ATGGAAGTCCAGAGTTGA	ATGGAAGTCCAGAGTTGA			MEVQS*	MEVQS*			GGGCAGGTAG	TTAACAGTAG	0	E	0	0	0	0	0
2902	1817	ao	AN2723.1	70.m15716	AO070309000061	0					-234	-220	ATGACATCGCTCTGA			ATGACATCGCTCTGA	MTSL*			MTSL*	ATTGATTCTA	ATTCCGGGTC	0	E	0	0	0	0	0
2903	1817	ao	AN2723.1	70.m15716	AO070309000061	0					-132	-91	ATGCAAGACGAACATTATGTCTCGCCCATAAGAAACAAATAA			ATGCAAGACGAACATTATGTCTCGCCCATAAGAAACAAATAA	MQDEHYVSPIRNK*			MQDEHYVSPIRNK*	GGAGTATCTA	AATCCACATT	0	E	0	0	0	0	0
2904	1817	ao	AN2723.1	70.m15716	AO070309000061	0					-116	-102	ATGTCTCGCCCATAA			ATGTCTCGCCCATAA	MSRP*			MSRP*	GACGAACATT	GAAACAAATA	0	E	0	0	0	0	0
2905	1819	af	AN6922.1	71.m15188	AO070313000063	0			-162	-103			ATGGGCCCTCTTCTTCTCTGTCGTTATAAATATCCAGTCGATTTAGCCCTTCAGCCTTGA		ATGGGCCCTCTTCTTCTCTGTCGTTATAAATATCCAGTCGATTTAGCCCTTCAGCCTTGA		MGPLLLCRYKYPVDLALQP*		MGPLLLCRYKYPVDLALQP*		GGACATTTGG	TTGACCGCGA	0	R	0	0	0	0	0
2910	1821	af	AN8018.1	53.m04191	AO070322000067	0			-223	-125			ATGGCAGTGACAGTAAGACCAAGCTGTTTAGTTTGGAACTTTTCGCATGAGGTAGGAGACCAGGTCCACTGTGCTCCTGTGTTCGTTTCGCCACGATGA		ATGGCAGTGACAGTAAGACCAAGCTGTTTAGTTTGGAACTTTTCGCATGAGGTAGGAGACCAGGTCCACTGTGCTCCTGTGTTCGTTTCGCCACGATGA		MAVTVRPSCLVWNFSHEVGDQVHCAPVFVSPR*		MAVTVRPSCLVWNFSHEVGDQVHCAPVFVSPR*		AAGCCTATCC	CGACATCCAT	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2911	1821	af	AN8018.1	53.m04191	AO070322000067	0			-128	-96			ATGACGACATCCATCACGACCAGTGAGAATTAA		ATGACGACATCCATCACGACCAGTGAGAATTAA		MTTSITTSEN*		MTTSITTSEN*		TTTCGCCACG	ATAAGTTAAT	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2912	1821	af	AN8018.1	53.m04191	AO070322000067	0			-77	-45			ATGCAATGGCATATCAACACGCCATTGGGATGA		ATGCAATGGCATATCAACACGCCATTGGGATGA		MQWHINTPLG*		MQWHINTPLG*		ATATAGAACC	GCCAAAATTG	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2913	1821	af	AN8018.1	53.m04191	AO070322000067	0			-72	-34			ATGGCATATCAACACGCCATTGGGATGAGCCAAAATTGA		ATGGCATATCAACACGCCATTGGGATGAGCCAAAATTGA		MAYQHAIGMSQN*		MAYQHAIGMSQN*		GAACCATGCA	TTTCAGCGCT	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2906	1821	an	AN8018.1	53.m04191	AO070322000067	0	-176	-159					ATGCAAATGTGCAGTTGA	ATGCAAATGTGCAGTTGA			MQMCS*	MQMCS*			TGAAGTCACT	AGTCGGGTGG	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2907	1821	an	AN8018.1	53.m04191	AO070322000067	0	-170	-159					ATGTGCAGTTGA	ATGTGCAGTTGA			MCS*	MCS*			CACTATGCAA	AGTCGGGTGG	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2908	1821	an	AN8018.1	53.m04191	AO070322000067	0	-117	-34					ATGACGACATACAACAAGATGCCACCCAGTAACAGGCGTTTGTTTAAATCGAGCTCGCGTGCTCCGTTACCTTGCGTCGTCTAA	ATGACGACATACAACAAGATGCCACCCAGTAACAGGCGTTTGTTTAAATCGAGCTCGCGTGCTCCGTTACCTTGCGTCGTCTAA			MTTYNKMPPSNRRLFKSSSRAPLPCVV*	MTTYNKMPPSNRRLFKSSSRAPLPCVV*			CCTCGCCATC	CCGCATATAC	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2909	1821	an	AN8018.1	53.m04191	AO070322000067	0	-99	-34					ATGCCACCCAGTAACAGGCGTTTGTTTAAATCGAGCTCGCGTGCTCCGTTACCTTGCGTCGTCTAA	ATGCCACCCAGTAACAGGCGTTTGTTTAAATCGAGCTCGCGTGCTCCGTTACCTTGCGTCGTCTAA			MPPSNRRLFKSSSRAPLPCVV*	MPPSNRRLFKSSSRAPLPCVV*			ATACAACAAG	CCGCATATAC	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2915	1821	ao	AN8018.1	53.m04191	AO070322000067	0					-114	-103	ATGACGCCATAG			ATGACGCCATAG	MTP*			MTP*	TTACGCCACG	AGGAAAGAAA	0	S	FG03429.1	MG03349.1	NCU09799.1	0	0
2919	1840	af	AN0989.1	70.m15630	AO070318000148	0			-163	-152			ATGTCGACCTAA		ATGTCGACCTAA		MST*		MST*		CTGCGATTTC	GCGTCCTGAG	0	B	0	0	0	0	0
2920	1840	af	AN0989.1	70.m15630	AO070318000148	0			-141	-67			ATGGTTACGGCTGGCGGCGGCGGCGGTTCGAGCAGTCCGCTCACGTTTTCAACTCACGCGCGGACATCTTTATAG		ATGGTTACGGCTGGCGGCGGCGGCGGTTCGAGCAGTCCGCTCACGTTTTCAACTCACGCGCGGACATCTTTATAG		MVTAGGGGGSSSPLTFSTHARTSL*		MVTAGGGGGSSSPLTFSTHARTSL*		GCGTCCTGAG	TCGCGACATT	0	B	0	0	0	0	0
2917	1840	an	AN0989.1	70.m15630	AO070318000148	0	-160	-59					ATGGTCACAGGTGGCGGCGGCGGCGGTTTTCAGCAGTCCGCTTCACGATTCGATTCACGCGCAAAGTATTCACTCTGTTCGCGGATGCAGGGCAAACTTTGA	ATGGTCACAGGTGGCGGCGGCGGCGGTTTTCAGCAGTCCGCTTCACGATTCGATTCACGCGCAAAGTATTCACTCTGTTCGCGGATGCAGGGCAAACTTTGA			MVTGGGGGGFQQSASRFDSRAKYSLCSRMQGKL*	MVTGGGGGGFQQSASRFDSRAKYSLCSRMQGKL*			ATGTCTTGAG	TCGAAAACCA	0	B	0	0	0	0	0
2918	1840	an	AN0989.1	70.m15630	AO070318000148	0	-76	-59					ATGCAGGGCAAACTTTGA	ATGCAGGGCAAACTTTGA			MQGKL*	MQGKL*			CTGTTCGCGG	TCGAAAACCA	0	B	0	0	0	0	0
2921	1840	ao	AN0989.1	70.m15630	AO070318000148	0					-175	-155	ATGTTGGACGCTATTTCCTGA			ATGTTGGACGCTATTTCCTGA	MLDAIS*			MLDAIS*	TGACGACTCT	GATGGTTACA	0	B	0	0	0	0	0
2922	1840	ao	AN0989.1	70.m15630	AO070318000148	0					-153	-70	ATGGTTACAGTTGGTGGTGGTGGCGGTTCGAGCAATCCGCTCAGTTTCGACTTTCGCGCGGCCGTGGCCTTTGCATCTCGATAG			ATGGTTACAGTTGGTGGTGGTGGCGGTTCGAGCAATCCGCTCAGTTTCGACTTTCGCGCGGCCGTGGCCTTTGCATCTCGATAG	MVTVGGGGGSSNPLSFDFRAAVAFASR*			MVTVGGGGGSSNPLSFDFRAAVAFASR*	ATTTCCTGAG	ACGTGACCGA	0	B	0	0	0	0	0
2924	1844	an	AN4864.1	59.m09108	AO070329000150	0	-165	-16					ATGGTTCTTTCGACCAACAACAGTCCGCCCTGTCAAAACTCCAGTTTGCTCACATACTCCGTTATAGGCTGTCCCTACCCTGGCCTCGTTTCTTCTCCAATTGCTGTTCCTCTTTATATAGCAGGTTTGCGGTCAATGGAAGACCACTGA	ATGGTTCTTTCGACCAACAACAGTCCGCCCTGTCAAAACTCCAGTTTGCTCACATACTCCGTTATAGGCTGTCCCTACCCTGGCCTCGTTTCTTCTCCAATTGCTGTTCCTCTTTATATAGCAGGTTTGCGGTCAATGGAAGACCACTGA			MVLSTNNSPPCQNSSLLTYSVIGCPYPGLVSSPIAVPLYIAGLRSMEDH*	MVLSTNNSPPCQNSSLLTYSVIGCPYPGLVSSPIAVPLYIAGLRSMEDH*			GACCTCCAAA	ATATTATCAC	0	GE	0	MG09310.1	0	YOR002W	0
2925	1844	ao	AN4864.1	59.m09108	AO070329000150	0					-189	-82	ATGTCATTCTCCGGAACCAACAATTGCATTGAGCTGGCCGCATCCATCTATTCGACTCCGTACCCCGACTCTTTCTTCTCTATCCGATTCACCAGATTTTGTCCTTAG			ATGTCATTCTCCGGAACCAACAATTGCATTGAGCTGGCCGCATCCATCTATTCGACTCCGTACCCCGACTCTTTCTTCTCTATCCGATTCACCAGATTTTGTCCTTAG	MSFSGTNNCIELAASIYSTPYPDSFFSIRFTRFCP*			MSFSGTNNCIELAASIYSTPYPDSFFSIRFTRFCP*	TTCCCACTGT	TCTCATCTAT	0	GE	0	MG09310.1	0	YOR002W	0
2929	1846	af	AN5748.1	69.m14846	AO070341000005	0			-426	-175			ATGAAGTGGCCACACCTACCATTTCCGCTGTACAACTACCTTGCTGAGAGACACTCCTCAAGAGGCTTGGTAGAAGGGACGCCGGACGACCTGGTACGTACTTCAGCTTCTCTTAAAAGCAGCATTGATTATTCCGTGGGCAATCTTGTCTGGACAACGTACATTGATATGTTTGTTTGTGTCTGCGGGACGGAGAATTTAGCGAGCTCAATCACCAAGCTCAAGACTGGTGTCGAATTCCAAGGTTGCTAA		ATGAAGTGGCCACACCTACCATTTCCGCTGTACAACTACCTTGCTGAGAGACACTCCTCAAGAGGCTTGGTAGAAGGGACGCCGGACGACCTGGTACGTACTTCAGCTTCTCTTAAAAGCAGCATTGATTATTCCGTGGGCAATCTTGTCTGGACAACGTACATTGATATGTTTGTTTGTGTCTGCGGGACGGAGAATTTAGCGAGCTCAATCACCAAGCTCAAGACTGGTGTCGAATTCCAAGGTTGCTAA		MKWPHLPFPLYNYLAERHSSRGLVEGTPDDLVRTSASLKSSIDYSVGNLVWTTYIDMFVCVCGTENLASSITKLKTGVEFQGC*		MKWPHLPFPLYNYLAERHSSRGLVEGTPDDLVRTSASLKSSIDYSVGNLVWTTYIDMFVCVCGTENLASSITKLKTGVEFQGC*		AAGTCGCAAC	CGTTTCGTCT	0	G	0	0	0	YJR131W	0
2926	1846	an	AN5748.1	69.m14846	AO070341000005	0	-199	-116					ATGCTAACATCCTTCAGGATCTATCCATGCCGGCTTAAGCTGCAGTTATTATCCTCCGAACGTGACAACGAAGAGCGACGATAG	ATGCTAACATCCTTCAGGATCTATCCATGCCGGCTTAAGCTGCAGTTATTATCCTCCGAACGTGACAACGAAGAGCGACGATAG			MLTSFRIYPCRLKLQLLSSERDNEERR*	MLTSFRIYPCRLKLQLLSSERDNEERR*			GTCGTAGCAG	CACACCGACC	0	G	0	0	0	YJR131W	0
2933	1846	ao	AN5748.1	69.m14846	AO070341000005	0					-430	-398	ATGAATCTATTTATCTTTTGTCCTTTCTCATGA			ATGAATCTATTTATCTTTTGTCCTTTCTCATGA	MNLFIFCPFS*			MNLFIFCPFS*	TGCGCACCTC	GTAACGCATT	0	G	0	0	0	YJR131W	0
2934	1846	ao	AN5748.1	69.m14846	AO070341000005	0					-401	-384	ATGAGTAACGCATTGTAA			ATGAGTAACGCATTGTAA	MSNAL*			MSNAL*	GTCCTTTCTC	AGCTCCACAA	0	G	0	0	0	YJR131W	0
2935	1846	ao	AN5748.1	69.m14846	AO070341000005	0					-351	-322	ATGCACGCTTGGTTAGTTGTTGACACCTAG			ATGCACGCTTGGTTAGTTGTTGACACCTAG	MHAWLVVDT*			MHAWLVVDT*	TAGGCAATCA	CTTCAACCTG	0	G	0	0	0	YJR131W	0
2940	1851	af	AN7521.1	59.m08965	AO070280000062	0			-197	-27			ATGCCTTTCTTCACACATCTATCATGCAATCAAGGTCGAGTGGCTCATTGGACCTTCGGAGTGGAGTCTTCTGATGTGCCATATTATGCTACCAGCAGGTGTATTTATATTGAAGAAGTTCCCGCCAGAACTTCTCTCTCGCATTGCCTTTACCATCACTCCTCATTCTGA		ATGCCTTTCTTCACACATCTATCATGCAATCAAGGTCGAGTGGCTCATTGGACCTTCGGAGTGGAGTCTTCTGATGTGCCATATTATGCTACCAGCAGGTGTATTTATATTGAAGAAGTTCCCGCCAGAACTTCTCTCTCGCATTGCCTTTACCATCACTCCTCATTCTGA		MPFFTHLSCNQGRVAHWTFGVESSDVPYYATSRCIYIEEVPARTSLSHCLYHHSSF*		MPFFTHLSCNQGRVAHWTFGVESSDVPYYATSRCIYIEEVPARTSLSHCLYHHSSF*		TCGGGCGAAG	GCCGCAAGTG	0	I	0	0	0	0	0
2941	1851	af	AN7521.1	59.m08965	AO070280000062	0			-174	-124			ATGCAATCAAGGTCGAGTGGCTCATTGGACCTTCGGAGTGGAGTCTTCTGA		ATGCAATCAAGGTCGAGTGGCTCATTGGACCTTCGGAGTGGAGTCTTCTGA		MQSRSSGSLDLRSGVF*		MQSRSSGSLDLRSGVF*		CACATCTATC	TGTGCCATAT	0	I	0	0	0	0	0

2938	1851	an	AN7521.1	59.m08965	AO070280000062	0	-185	-108					ATGACGCTGCAAACTGGAACAAGCAATAGACGGTCCACGGCCGTGTTACGTGTACACGGCTGTGCGGCACTCACCTAA	ATGACGCTGCAAACTGGAACAAGCAATAGACGGTCCACGGCCGTGTTACGTGTACACGGCTGTGCGGCACTCACCTAA			MTLQTGTSNRRSTAVLRVHGCAALT*	MTLQTGTSNRRSTAVLRVHGCAALT*			GGAGAGACAG	TCAGGCCGTA	0	I	0	0	0	0	0
2939	1851	an	AN7521.1	59.m08965	AO070280000062	0	-98	-75					ATGCGACGCCCGAGGACTATATAA	ATGCGACGCCCGAGGACTATATAA			MRRPRTI*	MRRPRTI*			ATCAGGCCGT	ACACTCAAAC	0	I	0	0	0	0	0
2942	1855	af	AN8312.1	72.m19891	AO070307000026	0			-232	-41			ATGGTAACCAAACACAAGGAAACAGTCAGGGTTGTATCTGTCAGGGATAAACTAGCAGGTAACTTTAACATGATATATAAGATTGACATCTGTTGTCTGGTAAATACCCTTCTTTTTGACTATTTCTTTCTATTATGTATACTCTCAATTAGATTACATCCTTGTCACTGTCAATCCTTACTCATTATTTAA		ATGGTAACCAAACACAAGGAAACAGTCAGGGTTGTATCTGTCAGGGATAAACTAGCAGGTAACTTTAACATGATATATAAGATTGACATCTGTTGTCTGGTAAATACCCTTCTTTTTGACTATTTCTTTCTATTATGTATACTCTCAATTAGATTACATCCTTGTCACTGTCAATCCTTACTCATTATTTAA		MVTKHKETVRVVSVRDKLAGNFNMIYKIDICCLVNTLLFDYFFLLCILSIRLHPCHCQSLLII*		MVTKHKETVRVVSVRDKLAGNFNMIYKIDICCLVNTLLFDYFFLLCILSIRLHPCHCQSLLII*		ATCCTGAGGC	TCATTCAGCA	0		0	0	0	0	0
2943	1855	af	AN8312.1	72.m19891	AO070307000026	0			-163	-41			ATGATATATAAGATTGACATCTGTTGTCTGGTAAATACCCTTCTTTTTGACTATTTCTTTCTATTATGTATACTCTCAATTAGATTACATCCTTGTCACTGTCAATCCTTACTCATTATTTAA		ATGATATATAAGATTGACATCTGTTGTCTGGTAAATACCCTTCTTTTTGACTATTTCTTTCTATTATGTATACTCTCAATTAGATTACATCCTTGTCACTGTCAATCCTTACTCATTATTTAA		MIYKIDICCLVNTLLFDYFFLLCILSIRLHPCHCQSLLII*		MIYKIDICCLVNTLLFDYFFLLCILSIRLHPCHCQSLLII*		TAACTTTAAC	TCATTCAGCA	0		0	0	0	0	0
2944	1855	af	AN8312.1	72.m19891	AO070307000026	0			-98	-81			ATGTATACTCTCAATTAG		ATGTATACTCTCAATTAG		MYTLN*		MYTLN*		TCTTTCTATT	ATTACATCCT	0		0	0	0	0	0
2945	1855	ao	AN8312.1	72.m19891	AO070307000026	0					-288	-241	ATGGTGAAACATGGGACGACAACCTACAGACAGATCAATGGAACATAA			ATGGTGAAACATGGGACGACAACCTACAGACAGATCAATGGAACATAA	MVKHGTTTYRQINGT*			MVKHGTTTYRQINGT*	CGGCACTACA	TGAAACGGCT	0		0	0	0	0	0
2946	1855	ao	AN8312.1	72.m19891	AO070307000026	0					-278	-180	ATGGGACGACAACCTACAGACAGATCAATGGAACATAATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGATATAA			ATGGGACGACAACCTACAGACAGATCAATGGAACATAATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGATATAA	MGRQPTDRSMEHNETAGAGSVRNSLAGRSGLI*			MGRQPTDRSMEHNETAGAGSVRNSLAGRSGLI*	ATGGTGAAAC	AAGATCGACT	0		0	0	0	0	0
2947	1855	ao	AN8312.1	72.m19891	AO070307000026	0					-251	-180	ATGGAACATAATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGATATAA			ATGGAACATAATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGATATAA	MEHNETAGAGSVRNSLAGRSGLI*			MEHNETAGAGSVRNSLAGRSGLI*	AGACAGATCA	AAGATCGACT	0		0	0	0	0	0
2948	1855	ao	AN8312.1	72.m19891	AO070307000026	0					-241	-185	ATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGA			ATGAAACGGCTGGAGCTGGGTCCGTCCGGAACAGCCTGGCGGGCCGTTCAGGATTGA	MKRLELGPSGTAWRAVQD*			MKRLELGPSGTAWRAVQD*	ATGGAACATA	TATAAAAGAT	0		0	0	0	0	0
2953	1857	af	AN0998.1	70.m15216	AO070312000041	0			-274	-257			ATGATGAGATGCTCCTGA		ATGATGAGATGCTCCTGA		MMRCS*		MMRCS*		AGTCCAGACG	CCCGTTTCTT	0		0	0	0	0	0
2954	1857	af	AN0998.1	70.m15216	AO070312000041	0			-271	-257			ATGAGATGCTCCTGA		ATGAGATGCTCCTGA		MRCS*		MRCS*		CCAGACGATG	CCCGTTTCTT	0		0	0	0	0	0
2955	1857	af	AN0998.1	70.m15216	AO070312000041	0			-266	-66			ATGCTCCTGACCCGTTTCTTCCTGAGGCCGCAAGCTCCACTCGGTGGGTCTTACAGTACAGTACACGTAAGATTAAGGTGTTGCACATTTAAACATGAGGTTGTGTGTTTAGTTTTGTATCATATTACCGAACCTCAAGGTATGTTATCCTTATCACTGAGCTCTCCTAATTCCCTACCTGAGGATGAGCGACATACCTAG		ATGCTCCTGACCCGTTTCTTCCTGAGGCCGCAAGCTCCACTCGGTGGGTCTTACAGTACAGTACACGTAAGATTAAGGTGTTGCACATTTAAACATGAGGTTGTGTGTTTAGTTTTGTATCATATTACCGAACCTCAAGGTATGTTATCCTTATCACTGAGCTCTCCTAATTCCCTACCTGAGGATGAGCGACATACCTAG		MLLTRFFLRPQAPLGGSYSTVHVRLRCCTFKHEVVCLVLYHITEPQGMLSLSLSSPNSLPEDERHT*		MLLTRFFLRPQAPLGGSYSTVHVRLRCCTFKHEVVCLVLYHITEPQGMLSLSLSSPNSLPEDERHT*		CGATGATGAG	TACAGTTCGA	0		0	0	0	0	0
2956	1857	af	AN0998.1	70.m15216	AO070312000041	0			-172	-155			ATGAGGTTGTGTGTTTAG		ATGAGGTTGTGTGTTTAG		MRLCV*		MRLCV*		ACATTTAAAC	TTTTGTATCA	0		0	0	0	0	0
2957	1857	af	AN0998.1	70.m15216	AO070312000041	0			-125	-66			ATGTTATCCTTATCACTGAGCTCTCCTAATTCCCTACCTGAGGATGAGCGACATACCTAG		ATGTTATCCTTATCACTGAGCTCTCCTAATTCCCTACCTGAGGATGAGCGACATACCTAG		MLSLSLSSPNSLPEDERHT*		MLSLSLSSPNSLPEDERHT*		ACCTCAAGGT	TACAGTTCGA	0		0	0	0	0	0
2949	1857	an	AN0998.1	70.m15216	AO070312000041	0	-127	-29					ATGACGTTGTATGTATCATACAGTAATTATGTTCCTGCATGTTTCGCGATAAGAGTCGAAGATAAAACATCGCCAAAAGCTAGCTTCCGCTACGTTTAA	ATGACGTTGTATGTATCATACAGTAATTATGTTCCTGCATGTTTCGCGATAAGAGTCGAAGATAAAACATCGCCAAAAGCTAGCTTCCGCTACGTTTAA			MTLYVSYSNYVPACFAIRVEDKTSPKASFRYV*	MTLYVSYSNYVPACFAIRVEDKTSPKASFRYV*			GCCAGCTCCG	TCAGTGATTG	0		0	0	0	0	0
2950	1857	an	AN0998.1	70.m15216	AO070312000041	0	-117	-76					ATGTATCATACAGTAATTATGTTCCTGCATGTTTCGCGATAA	ATGTATCATACAGTAATTATGTTCCTGCATGTTTCGCGATAA			MYHTVIMFLHVSR*	MYHTVIMFLHVSR*			ATGACGTTGT	GAGTCGAAGA	0		0	0	0	0	0
2951	1857	an	AN0998.1	70.m15216	AO070312000041	0	-99	-76					ATGTTCCTGCATGTTTCGCGATAA	ATGTTCCTGCATGTTTCGCGATAA			MFLHVSR*	MFLHVSR*			TACAGTAATT	GAGTCGAAGA	0		0	0	0	0	0
2952	1857	an	AN0998.1	70.m15216	AO070312000041	0	-89	-63					ATGTTTCGCGATAAGAGTCGAAGATAA	ATGTTTCGCGATAAGAGTCGAAGATAA			MFRDKSRR*	MFRDKSRR*			ATGTTCCTGC	AACATCGCCA	0		0	0	0	0	0
2959	1857	ao	AN0998.1	70.m15216	AO070312000041	0					-233	-165	ATGATGCTCCTTATCCCGTGCCTGAGGCCTGGAGCTCCACGAGTGGGTCTTACGGTACAATACATTTGA			ATGATGCTCCTTATCCCGTGCCTGAGGCCTGGAGCTCCACGAGTGGGTCTTACGGTACAATACATTTGA	MMLLIPCLRPGAPRVGLTVQYI*			MMLLIPCLRPGAPRVGLTVQYI*	TTCCCAAAAG	ATGGCCGTTT	0		0	0	0	0	0
2960	1857	ao	AN0998.1	70.m15216	AO070312000041	0					-230	-165	ATGCTCCTTATCCCGTGCCTGAGGCCTGGAGCTCCACGAGTGGGTCTTACGGTACAATACATTTGA			ATGCTCCTTATCCCGTGCCTGAGGCCTGGAGCTCCACGAGTGGGTCTTACGGTACAATACATTTGA	MLLIPCLRPGAPRVGLTVQYI*			MLLIPCLRPGAPRVGLTVQYI*	CCAAAAGATG	ATGGCCGTTT	0		0	0	0	0	0
2961	1857	ao	AN0998.1	70.m15216	AO070312000041	0					-164	-114	ATGGCCGTTTCGCATATTGTACGCTATGACGTTGGCGGTAAATTTTGGTAA			ATGGCCGTTTCGCATATTGTACGCTATGACGTTGGCGGTAAATTTTGGTAA	MAVSHIVRYDVGGKFW*			MAVSHIVRYDVGGKFW*	ATACATTTGA	TTCTACCACA	0		0	0	0	0	0
2962	1857	ao	AN0998.1	70.m15216	AO070312000041	0					-139	-92	ATGACGTTGGCGGTAAATTTTGGTAATTCTACCACATGTACGGAGTAG			ATGACGTTGGCGGTAAATTTTGGTAATTCTACCACATGTACGGAGTAG	MTLAVNFGNSTTCTE*			MTLAVNFGNSTTCTE*	ATTGTACGCT	GATGGTATTC	0		0	0	0	0	0
2963	1857	ao	AN0998.1	70.m15216	AO070312000041	0					-90	-46	ATGGTATTCTGTAGATGCGATAAGAACTTCTACTACGGATACTGA			ATGGTATTCTGTAGATGCGATAAGAACTTCTACTACGGATACTGA	MVFCRCDKNFYYGY*			MVFCRCDKNFYYGY*	ACGGAGTAGG	ACCCCGCCAA	0		0	0	0	0	0
2967	1863	af	AN5048.1	59.m08678	AO070338000188	0			-205	-173			ATGAAGCGCTTTTTTTTCCCACCGCACCCCTAA		ATGAAGCGCTTTTTTTTCCCACCGCACCCCTAA		MKRFFFPPHP*		MKRFFFPPHP*		ACGCGATTAG	GAGATCTTGT	0	R	0	0	0	0	0
2970	1863	ao	AN5048.1	59.m08678	AO070338000188	0					-175	-95	ATGAAGCGCTTTTTTCCCACTCACCTTGGGGTCGCTTTTTCGCTCCAGATCACTAGCCCCCAGAACGTCCAACGGGACTAG			ATGAAGCGCTTTTTTCCCACTCACCTTGGGGTCGCTTTTTCGCTCCAGATCACTAGCCCCCAGAACGTCCAACGGGACTAG	MKRFFPTHLGVAFSLQITSPQNVQRD*			MKRFFPTHLGVAFSLQITSPQNVQRD*	ACGCGATTAG	TGCTGGCTTT	0	R	0	0	0	0	0
2972	1865	af	AN1547.1	55.m03067	AO070339000307	0			-270	-235			ATGACTATTGCTATTCCTACTACTCTTATTGCATAG		ATGACTATTGCTATTCCTACTACTCTTATTGCATAG		MTIAIPTTLIA*		MTIAIPTTLIA*		TAGAAGGGAC	ACTTACCTCT	0	C	FG08266.1	MG06609.1	0	0	0
2973	1865	ao	AN1547.1	55.m03067	AO070339000307	0					-244	-152	ATGGATTCAACGGGGAAAGAATTCAATACCTGTCATCCCTTGTCCCGGGGTTCATCGCTCTCCACTTTGGGGTTTTTGTGGCGGGGGGGTTGA			ATGGATTCAACGGGGAAAGAATTCAATACCTGTCATCCCTTGTCCCGGGGTTCATCGCTCTCCACTTTGGGGTTTTTGTGGCGGGGGGGTTGA	MDSTGKEFNTCHPLSRGSSLSTLGFLWRGG*			MDSTGKEFNTCHPLSRGSSLSTLGFLWRGG*	GCAGTAATTA	GTTCCTGTAC	0	C	FG08266.1	MG06609.1	0	0	0
2975	1870	af	AN9434.1	58.m07857	AO070305000126	0			-203	-66			ATGCCAGTCATGGAATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		ATGCCAGTCATGGAATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		MPVMEWVVLPFLSLNQSFLHCFPMTDLAHILNCPSNTDSVLDCLN*		MPVMEWVVLPFLSLNQSFLHCFPMTDLAHILNCPSNTDSVLDCLN*		TGTTACCTGG	CTTTGTTTAG	0	O	0	0	0	0	0
2976	1870	af	AN9434.1	58.m07857	AO070305000126	0			-194	-66			ATGGAATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		ATGGAATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		MEWVVLPFLSLNQSFLHCFPMTDLAHILNCPSNTDSVLDCLN*		MEWVVLPFLSLNQSFLHCFPMTDLAHILNCPSNTDSVLDCLN*		GATGCCAGTC	CTTTGTTTAG	0	O	0	0	0	0	0
2977	1870	af	AN9434.1	58.m07857	AO070305000126	0			-189	-91			ATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGA		ATGGGTGGTGCTCCCGTTTCTTTCATTGAACCAGTCATTCCTCCACTGTTTTCCGATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGA		MGGAPVSFIEPVIPPLFSDDRPCSYFKLSFKY*		MGGAPVSFIEPVIPPLFSDDRPCSYFKLSFKY*		CAGTCATGGA	CTCTGTACTA	0	O	0	0	0	0	0
2978	1870	af	AN9434.1	58.m07857	AO070305000126	0			-134	-66			ATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		ATGACAGACCTTGCTCATATTTTAAACTGTCCTTCAAATACTGACTCTGTACTAGATTGTCTCAACTAG		MTDLAHILNCPSNTDSVLDCLN*		MTDLAHILNCPSNTDSVLDCLN*		CTGTTTTCCG	CTTTGTTTAG	0	O	0	0	0	0	0
2974	1870	an	AN9434.1	58.m07857	AO070305000126	0	-162	-94					ATGTTTGCTAGAGTAGTTCGAATTCCACTGCGGCGTATAGCCTTAAGGCCAAACCCTAAATTCAACTAG	ATGTTTGCTAGAGTAGTTCGAATTCCACTGCGGCGTATAGCCTTAAGGCCAAACCCTAAATTCAACTAG			MFARVVRIPLRRIALRPNPKFN*	MFARVVRIPLRRIALRPNPKFN*			AGCACTTCCA	CTAATCATCT	0	O	0	0	0	0	0
2979	1870	ao	AN9434.1	58.m07857	AO070305000126	0					-242	-126	ATGTTCACCAATTTTGTCTCAGCATGTTTTTGGGATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAGTTTACTTTGATTTAGTAGTGAAATCCGTGCTTTAG			ATGTTCACCAATTTTGTCTCAGCATGTTTTTGGGATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAGTTTACTTTGATTTAGTAGTGAAATCCGTGCTTTAG	MFTNFVSACFWDAVHLSLLLQYSICILVYFDLVVKSVL*			MFTNFVSACFWDAVHLSLLLQYSICILVYFDLVVKSVL*	TGGGCGTATT	CTTGTGGTTT	0	O	0	0	0	0	0
2980	1870	ao	AN9434.1	58.m07857	AO070305000126	0					-219	-151	ATGTTTTTGGGATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAGTTTACTTTGA			ATGTTTTTGGGATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAGTTTACTTTGA	MFLGCCSPQSASSIFYLYLSLL*			MFLGCCSPQSASSIFYLYLSLL*	TTGTCTCAGC	TTTAGTAGTG	0	O	0	0	0	0	0
2981	1870	ao	AN9434.1	58.m07857	AO070305000126	0					-208	-161	ATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAG			ATGCTGTTCACCTCAGTCTGCTTCTTCAATATTCTATTTGTATCTTAG	MLFTSVCFFNILFVS*			MLFTSVCFFNILFVS*	TGTTTTTGGG	TTTACTTTGA	0	O	0	0	0	0	0
2982	1871	af	AN6290.1	72.m19345	AO070308000002	0			-254	-225			ATGTTTACTCCTACTTTTCAAATGCTCTAG		ATGTTTACTCCTACTTTTCAAATGCTCTAG		MFTPTFQML*		MFTPTFQML*		AATTATTATC	AGCTGGCCTG	0		0	0	0	0	0
2983	1871	af	AN6290.1	72.m19345	AO070308000002	0			-213	-151			ATGAGACTTCACTGTCTATTCTGTGTAGGCATACACGCGCTGGACAGTCACATGATGAAATAG		ATGAGACTTCACTGTCTATTCTGTGTAGGCATACACGCGCTGGACAGTCACATGATGAAATAG		MRLHCLFCVGIHALDSHMMK*		MRLHCLFCVGIHALDSHMMK*		GCTGGCCTGC	TTGCCTCAGG	0		0	0	0	0	0
2984	1871	af	AN6290.1	72.m19345	AO070308000002	0			-162	-151			ATGATGAAATAG		ATGATGAAATAG		MMK*		MMK*		GGACAGTCAC	TTGCCTCAGG	0		0	0	0	0	0
2985	1871	af	AN6290.1	72.m19345	AO070308000002	0			-135	-97			ATGAAATTTGCTTCTTGGCCGGATCTGAGTTTCAATTGA		ATGAAATTTGCTTCTTGGCCGGATCTGAGTTTCAATTGA		MKFASWPDLSFN*		MKFASWPDLSFN*		TCAGGCCATA	TCAAAGTTGT	0		0	0	0	0	0
2986	1871	ao	AN6290.1	72.m19345	AO070308000002	0					-218	-141	ATGGATCCCTTTGTATCTACTAGTATACTCTGTGTTCTCTCCCCAAAATCCAACGTCATTCTTATCGCTTTCCGATAA			ATGGATCCCTTTGTATCTACTAGTATACTCTGTGTTCTCTCCCCAAAATCCAACGTCATTCTTATCGCTTTCCGATAA	MDPFVSTSILCVLSPKSNVILIAFR*			MDPFVSTSILCVLSPKSNVILIAFR*	AGAATCATTA	GATCACGTGA	0		0	0	0	0	0
2988	1874	an	AN0874.1	70.m15477	AO070320000033	0	-201	-163					ATGCGCTCATCGACCAATTCACTCGATACCTTCCCTTGA	ATGCGCTCATCGACCAATTCACTCGATACCTTCCCTTGA			MRSSTNSLDTFP*	MRSSTNSLDTFP*			TTCTTCACTT	ATCTCATTTC	0	A	0	MG06313.1	0	0	0
2990	1881	an	AN5230.1	57.m05701	AO070337000247	0	-102	-34					ATGTCCAGCTCGGTGTCCACCCCTCACGATCGCTCTACGACATACTATCCCTCAACGCACCTTGAATAA	ATGTCCAGCTCGGTGTCCACCCCTCACGATCGCTCTACGACATACTATCCCTCAACGCACCTTGAATAA			MSSSVSTPHDRSTTYYPSTHLE*	MSSSVSTPHDRSTTYYPSTHLE*			TTCTGTTCCA	CGACCAGTCG	0		FG00670.1	0	NCU03211.1	0	0
2991	1884	an	AN3440.1	59.m09302	AO070265000015	0	-74	-39					ATGCAGCCCACTGTTCGCTTCACACCCTTATCATAG	ATGCAGCCCACTGTTCGCTTCACACCCTTATCATAG			MQPTVRFTPLS*	MQPTVRFTPLS*			CCGACGCCGC	AACGTTCTTG	0	G	0	0	0	0	0
2992	1884	ao	AN3440.1	59.m09302	AO070265000015	0					-218	-6	ATGGCTTCGGCGAACAAGCCGTGCATGACAACACGACCCTTTTCCGTCAATTTTCTCACAAAATTCCTCTGGGTTGTCGGTAGATCTGCTTTCAAACCCTATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGAATCACCAGCTCAATTACTCGACAGCCCGGAAACGTATCTCTGCCGAATAG			ATGGCTTCGGCGAACAAGCCGTGCATGACAACACGACCCTTTTCCGTCAATTTTCTCACAAAATTCCTCTGGGTTGTCGGTAGATCTGCTTTCAAACCCTATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGAATCACCAGCTCAATTACTCGACAGCCCGGAAACGTATCTCTGCCGAATAG	MASANKPCMTTRPFSVNFLTKFLWVVGRSAFKPYVHNIGYWSVQNSINGKVSLVNHQLNYSTARKRISAE*			MASANKPCMTTRPFSVNFLTKFLWVVGRSAFKPYVHNIGYWSVQNSINGKVSLVNHQLNYSTARKRISAE*	TGTGGTCCTA	CAAATATGCT	0	G	0	0	0	0	0

2993	1884	ao	AN3440.1	59.m09302	AO070265000015	0					-194	-6	ATGACAACACGACCCTTTTCCGTCAATTTTCTCACAAAATTCCTCTGGGTTGTCGGTAGATCTGCTTTCAAACCCTATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGAATCACCAGCTCAATTACTCGACAGCCCGGAAACGTATCTCTGCCGAATAG			ATGACAACACGACCCTTTTCCGTCAATTTTCTCACAAAATTCCTCTGGGTTGTCGGTAGATCTGCTTTCAAACCCTATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGAATCACCAGCTCAATTACTCGACAGCCCGGAAACGTATCTCTGCCGAATAG	MTTRPFSVNFLTKFLWVVGRSAFKPYVHNIGYWSVQNSINGKVSLVNHQLNYSTARKRISAE*			MTTRPFSVNFLTKFLWVVGRSAFKPYVHNIGYWSVQNSINGKVSLVNHQLNYSTARKRISAE*	CAAGCCGTGC	CAAATATGCT	0	G	0	0	0	0	0
2994	1884	ao	AN3440.1	59.m09302	AO070265000015	0					-118	-56	ATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGA			ATGTACACAACATTGGGTATTGGTCTGTACAAAACTCGATCAATGGCAAGGTCTCCCTTGTGA	MYTTLGIGLYKTRSMARSPL*			MYTTLGIGLYKTRSMARSPL*	TTCAAACCCT	ATCACCAGCT	0	G	0	0	0	0	0
2995	1884	ao	AN3440.1	59.m09302	AO070265000015	0					-76	-56	ATGGCAAGGTCTCCCTTGTGA			ATGGCAAGGTCTCCCTTGTGA	MARSPL*			MARSPL*	AACTCGATCA	ATCACCAGCT	0	G	0	0	0	0	0
2998	1888	af	AN8639.1	71.m15152	AO070297000062	0			-161	-144			ATGAACCTGCTTGGCTGA		ATGAACCTGCTTGGCTGA		MNLLG*		MNLLG*		GGTCCAGCTC	CGGCTCATCC	0	G	FG06051.1	MG03860.1	0	0	0
2996	1888	an	AN8639.1	71.m15152	AO070297000062	0	-268	-242					ATGGTGAAGAATAATCTGAGTCCCTGA	ATGGTGAAGAATAATCTGAGTCCCTGA			MVKNNLSP*	MVKNNLSP*			AGATACGATA	CATCAATCAG	0	G	FG06051.1	MG03860.1	0	0	0
2997	1888	an	AN8639.1	71.m15152	AO070297000062	0	-206	-183					ATGACCTGGCAACAACCGGCGTAA	ATGACCTGGCAACAACCGGCGTAA			MTWQQPA*	MTWQQPA*			ACATTATTAT	GGAGATCTTC	0	G	FG06051.1	MG03860.1	0	0	0
2999	1888	ao	AN8639.1	71.m15152	AO070297000062	0					-142	-125	ATGATGATCCTCTTATAG			ATGATGATCCTCTTATAG	MMILL*			MMILL*	CAAGGATATC	TAGTGCTACT	0	G	FG06051.1	MG03860.1	0	0	0
3000	1888	ao	AN8639.1	71.m15152	AO070297000062	0					-139	-125	ATGATCCTCTTATAG			ATGATCCTCTTATAG	MILL*			MILL*	GGATATCATG	TAGTGCTACT	0	G	FG06051.1	MG03860.1	0	0	0
3007	1889	af	AN6438.1	58.m07697	AO070299000087	0			-163	-104			ATGGAATGGGAGATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAG		ATGGAATGGGAGATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAG		MEWEMIEPKSYLLRILRRD*		MEWEMIEPKSYLLRILRRD*		AAACAGACGA	AATGATACAA	0	O	0	0	NCU02515.1	0	0
3008	1889	af	AN6438.1	58.m07697	AO070299000087	0			-158	-99			ATGGGAGATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAGAATGA		ATGGGAGATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAGAATGA		MGDDRAQELSPAHSPSGLE*		MGDDRAQELSPAHSPSGLE*		GACGAATGGA	TACAATCGTC	0	O	0	0	NCU02515.1	0	0
3009	1889	af	AN6438.1	58.m07697	AO070299000087	0			-151	-104			ATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAG		ATGATCGAGCCCAAGAGCTATCTCCTGCGCATTCTCCGTCGGGATTAG		MIEPKSYLLRILRRD*		MIEPKSYLLRILRRD*		GGAATGGGAG	AATGATACAA	0	O	0	0	NCU02515.1	0	0
3010	1889	af	AN6438.1	58.m07697	AO070299000087	0			-102	-52			ATGATACAATCGTCTTCGCTCTGGTATGCGGGGTTATTCCCCCATATTTAA		ATGATACAATCGTCTTCGCTCTGGTATGCGGGGTTATTCCCCCATATTTAA		MIQSSSLWYAGLFPHI*		MIQSSSLWYAGLFPHI*		CGGGATTAGA	GGTCAGGGAG	0	O	0	0	NCU02515.1	0	0
3011	1889	af	AN6438.1	58.m07697	AO070299000087	0			-77	-12			ATGCGGGGTTATTCCCCCATATTTAAGGTCAGGGAGGCGATGCAAGTACCTCGCTGTGGCTGCTAG		ATGCGGGGTTATTCCCCCATATTTAAGGTCAGGGAGGCGATGCAAGTACCTCGCTGTGGCTGCTAG		MRGYSPIFKVREAMQVPRCGC*		MRGYSPIFKVREAMQVPRCGC*		TCGCTCTGGT	CCGCAGTCAA	0	O	0	0	NCU02515.1	0	0
3001	1889	an	AN6438.1	58.m07697	AO070299000087	0	-263	-186					ATGCCGCTAATCGCGCCTTCTCTCTCTACGGTTATCGGCGGTTGGCCATGCAGCCATGGCTTGGCGCATTGTTCCTGA	ATGCCGCTAATCGCGCCTTCTCTCTCTACGGTTATCGGCGGTTGGCCATGCAGCCATGGCTTGGCGCATTGTTCCTGA			MPLIAPSLSTVIGGWPCSHGLAHCS*	MPLIAPSLSTVIGGWPCSHGLAHCS*			TAAGCCTGCG	CTGACGGACA	0	O	0	0	NCU02515.1	0	0
3002	1889	an	AN6438.1	58.m07697	AO070299000087	0	-216	-91					ATGCAGCCATGGCTTGGCGCATTGTTCCTGACTGACGGACATGGAGATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGA	ATGCAGCCATGGCTTGGCGCATTGTTCCTGACTGACGGACATGGAGATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGA			MQPWLGALFLTDGHGDEPILGQCRRRFESLGCVCAAGAALA*	MQPWLGALFLTDGHGDEPILGQCRRRFESLGCVCAAGAALA*			GCGGTTGGCC	GCATACCGGG	0	O	0	0	NCU02515.1	0	0
3003	1889	an	AN6438.1	58.m07697	AO070299000087	0	-208	-182					ATGGCTTGGCGCATTGTTCCTGACTGA	ATGGCTTGGCGCATTGTTCCTGACTGA			MAWRIVPD*	MAWRIVPD*			CCATGCAGCC	CGGACATGGA	0	O	0	0	NCU02515.1	0	0
3004	1889	an	AN6438.1	58.m07697	AO070299000087	0	-176	-72					ATGGAGATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAA	ATGGAGATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAA			MEMNPFWANADAASKVWGVFALRGLLWREHTGCL*	MEMNPFWANADAASKVWGVFALRGLLWREHTGCL*			ACTGACGGAC	ATTGCGCCCA	0	O	0	0	NCU02515.1	0	0
3005	1889	an	AN6438.1	58.m07697	AO070299000087	0	-170	-72					ATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAA	ATGAACCCATTTTGGGCCAATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAA			MNPFWANADAASKVWGVFALRGLLWREHTGCL*	MNPFWANADAASKVWGVFALRGLLWREHTGCL*			GGACATGGAG	ATTGCGCCCA	0	O	0	0	NCU02515.1	0	0
3006	1889	an	AN6438.1	58.m07697	AO070299000087	0	-151	-50					ATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAAATTGCGCCCATCCCTCCCATGA	ATGCCGACGCCGCTTCGAAAGTTTGGGGTGTGTTTGCGCTGCGGGGGCTGCTCTGGCGTGAGCATACCGGGTGTCTTTAAATTGCGCCCATCCCTCCCATGA			MPTPLRKFGVCLRCGGCSGVSIPGVFKLRPSLP*	MPTPLRKFGVCLRCGGCSGVSIPGVFKLRPSLP*			TTTTGGGCCA	TTTCGAAAGC	0	O	0	0	NCU02515.1	0	0
3013	1889	ao	AN6438.1	58.m07697	AO070299000087	0					-241	-230	ATGAAGCTGTAG			ATGAAGCTGTAG	MKL*			MKL*	TTTGCCACCA	CTTGTCCAAC	0	O	0	0	NCU02515.1	0	0
3014	1889	ao	AN6438.1	58.m07697	AO070299000087	0					-199	-179	ATGAGAATCTTGGCAGGATAG			ATGAGAATCTTGGCAGGATAG	MRILAG*			MRILAG*	GGTTTTTTTT	GAAAAGTTGG	0	O	0	0	NCU02515.1	0	0
3015	1889	ao	AN6438.1	58.m07697	AO070299000087	0					-151	-134	ATGCAGGAGGTGGAGTGA			ATGCAGGAGGTGGAGTGA	MQEVE*			MQEVE*	GAAGGAGCTA	CTGATAAGAC	0	O	0	0	NCU02515.1	0	0
3016	1889	ao	AN6438.1	58.m07697	AO070299000087	0					-87	-70	ATGGGACTATTTATTTAA			ATGGGACTATTTATTTAA	MGLFI*			MGLFI*	GGACCAATTT	ACGGGAAGTC	0	O	0	0	NCU02515.1	0	0
3017	1894	an	AN0359.1	54.m06392	AO070318000037	0	-218	-189					ATGTACCCTTATCCCAGGTATGAACTATAA	ATGTACCCTTATCCCAGGTATGAACTATAA			MYPYPRYEL*	MYPYPRYEL*			AATTGTATTC	ATGTATGTAT	0	J	0	0	0	0	0
3018	1894	an	AN0359.1	54.m06392	AO070318000037	0	-199	-143					ATGAACTATAAATGTATGTATGAATTAATATATCACAAGATGCTGTATAAGAGGTAG	ATGAACTATAAATGTATGTATGAATTAATATATCACAAGATGCTGTATAAGAGGTAG			MNYKCMYELIYHKMLYKR*	MNYKCMYELIYHKMLYKR*			TATCCCAGGT	TCTGAAAGTT	0	J	0	0	0	0	0
3019	1894	an	AN0359.1	54.m06392	AO070318000037	0	-188	-177					ATGTATGTATGA	ATGTATGTATGA			MYV*	MYV*			TGAACTATAA	ATTAATATAT	0	J	0	0	0	0	0
3020	1894	an	AN0359.1	54.m06392	AO070318000037	0	-184	-143					ATGTATGAATTAATATATCACAAGATGCTGTATAAGAGGTAG	ATGTATGAATTAATATATCACAAGATGCTGTATAAGAGGTAG			MYELIYHKMLYKR*	MYELIYHKMLYKR*			CTATAAATGT	TCTGAAAGTT	0	J	0	0	0	0	0
3021	1894	an	AN0359.1	54.m06392	AO070318000037	0	-160	-143					ATGCTGTATAAGAGGTAG	ATGCTGTATAAGAGGTAG			MLYKR*	MLYKR*			ATATCACAAG	TCTGAAAGTT	0	J	0	0	0	0	0
3022	1894	an	AN0359.1	54.m06392	AO070318000037	0	-95	-6					ATGTCGGCACAGAGGTCGGGCCGCACACACAAAGATTTCGATCCCTCCACCAAGAACCGGCTGCCCCCTTCACATCGCCATCAGCGCTAA	ATGTCGGCACAGAGGTCGGGCCGCACACACAAAGATTTCGATCCCTCCACCAAGAACCGGCTGCCCCCTTCACATCGCCATCAGCGCTAA			MSAQRSGRTHKDFDPSTKNRLPPSHRHQR*	MSAQRSGRTHKDFDPSTKNRLPPSHRHQR*			CCGTTGCGAT	CAACCATGGC	0	J	0	0	0	0	0
3026	1899	af	AN5330.1	62.m03273	AO070333000250	0			-194	-63			ATGGTTTCGATCTACAATCTGCCCCCTGGTTTCAAATACGAGTCGGAAATATATCTGCCAAGCCGGCCATTCCCTCCAATCAGCGACTATGAGTCACTATCACCAATAATCACAACAGTCTCGCATCTATAA		ATGGTTTCGATCTACAATCTGCCCCCTGGTTTCAAATACGAGTCGGAAATATATCTGCCAAGCCGGCCATTCCCTCCAATCAGCGACTATGAGTCACTATCACCAATAATCACAACAGTCTCGCATCTATAA		MVSIYNLPPGFKYESEIYLPSRPFPPISDYESLSPIITTVSHL*		MVSIYNLPPGFKYESEIYLPSRPFPPISDYESLSPIITTVSHL*		AGACATCAAC	GCAGCTGGAT	0	KR	0	0	0	0	0
3027	1899	af	AN5330.1	62.m03273	AO070333000250	0			-106	-86			ATGAGTCACTATCACCAATAA		ATGAGTCACTATCACCAATAA		MSHYHQ*		MSHYHQ*		ATCAGCGACT	TCACAACAGT	0	KR	0	0	0	0	0
3023	1899	an	AN5330.1	62.m03273	AO070333000250	0	-213	-145					ATGTTTGTAAACAGGCCATCACCTAAATCTCCTTGGGAATTCACACTGTCGATGACGGTTGAAGTATGA	ATGTTTGTAAACAGGCCATCACCTAAATCTCCTTGGGAATTCACACTGTCGATGACGGTTGAAGTATGA			MFVNRPSPKSPWEFTLSMTVEV*	MFVNRPSPKSPWEFTLSMTVEV*			CGACATCATT	CTCACACTTA	0	KR	0	0	0	0	0
3024	1899	an	AN5330.1	62.m03273	AO070333000250	0	-162	-145					ATGACGGTTGAAGTATGA	ATGACGGTTGAAGTATGA			MTVEV*	MTVEV*			CACACTGTCG	CTCACACTTA	0	KR	0	0	0	0	0
3025	1899	an	AN5330.1	62.m03273	AO070333000250	0	-148	-134					ATGACTCACACTTAG	ATGACTCACACTTAG			MTHT*	MTHT*			CGGTTGAAGT	TATCATCCTG	0	KR	0	0	0	0	0
3028	1899	ao	AN5330.1	62.m03273	AO070333000250	0					-289	-101	ATGAATATTTACCATTCGATGCATGTCTTAGATTCGCAATCGACTGCCAAGAGTTGCCGTGACTCATCTCGTACTTCAACCCACAAGGATATAACAAGAGTGTCTTCCTCGCATATCCCAGGCTTTAGCACATCCTCATATTCTGCATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGA			ATGAATATTTACCATTCGATGCATGTCTTAGATTCGCAATCGACTGCCAAGAGTTGCCGTGACTCATCTCGTACTTCAACCCACAAGGATATAACAAGAGTGTCTTCCTCGCATATCCCAGGCTTTAGCACATCCTCATATTCTGCATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGA	MNIYHSMHVLDSQSTAKSCRDSSRTSTHKDITRVSSSHIPGFSTSSYSACLCQFKTINSLNS*			MNIYHSMHVLDSQSTAKSCRDSSRTSTHKDITRVSSSHIPGFSTSSYSACLCQFKTINSLNS*	GTTTCTACAT	GTGTCTAGAT	0	KR	0	0	0	0	0
3029	1899	ao	AN5330.1	62.m03273	AO070333000250	0					-271	-101	ATGCATGTCTTAGATTCGCAATCGACTGCCAAGAGTTGCCGTGACTCATCTCGTACTTCAACCCACAAGGATATAACAAGAGTGTCTTCCTCGCATATCCCAGGCTTTAGCACATCCTCATATTCTGCATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGA			ATGCATGTCTTAGATTCGCAATCGACTGCCAAGAGTTGCCGTGACTCATCTCGTACTTCAACCCACAAGGATATAACAAGAGTGTCTTCCTCGCATATCCCAGGCTTTAGCACATCCTCATATTCTGCATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGA	MHVLDSQSTAKSCRDSSRTSTHKDITRVSSSHIPGFSTSSYSACLCQFKTINSLNS*			MHVLDSQSTAKSCRDSSRTSTHKDITRVSSSHIPGFSTSSYSACLCQFKTINSLNS*	TTACCATTCG	GTGTCTAGAT	0	KR	0	0	0	0	0
3030	1899	ao	AN5330.1	62.m03273	AO070333000250	0					-143	-93	ATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGAGTGTCTAG			ATGTCTTTGTCAGTTCAAGACGATAAACTCACTGAACAGTTGAGTGTCTAG	MSLSVQDDKLTEQLSV*			MSLSVQDDKLTEQLSV*	CATATTCTGC	ATTATACACA	0	KR	0	0	0	0	0
3034	1902	af	AN2061.1	57.m05757	AO070341000209	0			-278	-168			ATGGTTGTCATCACTCGGAGAATTGCAATGCAGCCTTTGCTGTGGAGGTTGCACAACCCATCGACTGTGACGAAGACAAGACTGGCCTCCTTTCAAGTTGACTCTCGTTGA		ATGGTTGTCATCACTCGGAGAATTGCAATGCAGCCTTTGCTGTGGAGGTTGCACAACCCATCGACTGTGACGAAGACAAGACTGGCCTCCTTTCAAGTTGACTCTCGTTGA		MVVITRRIAMQPLLWRLHNPSTVTKTRLASFQVDSR*		MVVITRRIAMQPLLWRLHNPSTVTKTRLASFQVDSR*		TGAAGACTTG	GGCAGGACAA	0	Q	0	MG03880.1	0	0	0
3035	1902	af	AN2061.1	57.m05757	AO070341000209	0			-251	-168			ATGCAGCCTTTGCTGTGGAGGTTGCACAACCCATCGACTGTGACGAAGACAAGACTGGCCTCCTTTCAAGTTGACTCTCGTTGA		ATGCAGCCTTTGCTGTGGAGGTTGCACAACCCATCGACTGTGACGAAGACAAGACTGGCCTCCTTTCAAGTTGACTCTCGTTGA		MQPLLWRLHNPSTVTKTRLASFQVDSR*		MQPLLWRLHNPSTVTKTRLASFQVDSR*		GAGAATTGCA	GGCAGGACAA	0	Q	0	MG03880.1	0	0	0
3036	1902	af	AN2061.1	57.m05757	AO070341000209	0			-139	-113			ATGGCGTACAACAATATCAACAAGTGA		ATGGCGTACAACAATATCAACAAGTGA		MAYNNINK*		MAYNNINK*		TTGGAGAAAT	TCATGGTTGC	0	Q	0	MG03880.1	0	0	0
3031	1902	an	AN2061.1	57.m05757	AO070341000209	0	-155	-72					ATGCGGGACGGCGGGCCGTTATCTCCATCTCATCACATGCGCCTTTGGAGAGGGGCAACATATATGAACACATTGCCCTTTTGA	ATGCGGGACGGCGGGCCGTTATCTCCATCTCATCACATGCGCCTTTGGAGAGGGGCAACATATATGAACACATTGCCCTTTTGA			MRDGGPLSPSHHMRLWRGATYMNTLPF*	MRDGGPLSPSHHMRLWRGATYMNTLPF*			GAAGACAGAG	CTCTAAACTC	0	Q	0	MG03880.1	0	0	0
3032	1902	an	AN2061.1	57.m05757	AO070341000209	0	-119	-72					ATGCGCCTTTGGAGAGGGGCAACATATATGAACACATTGCCCTTTTGA	ATGCGCCTTTGGAGAGGGGCAACATATATGAACACATTGCCCTTTTGA			MRLWRGATYMNTLPF*	MRLWRGATYMNTLPF*			ATCTCATCAC	CTCTAAACTC	0	Q	0	MG03880.1	0	0	0
3033	1902	an	AN2061.1	57.m05757	AO070341000209	0	-92	-72					ATGAACACATTGCCCTTTTGA	ATGAACACATTGCCCTTTTGA			MNTLPF*	MNTLPF*			GGCAACATAT	CTCTAAACTC	0	Q	0	MG03880.1	0	0	0
3037	1902	ao	AN2061.1	57.m05757	AO070341000209	0					-215	-141	ATGGCAAAAGCAACCAATTGGAGAATTGCCATCCAGCAAGCTCCATCCTATAATAGGAAGGAGCGATGCGTATGA			ATGGCAAAAGCAACCAATTGGAGAATTGCCATCCAGCAAGCTCCATCCTATAATAGGAAGGAGCGATGCGTATGA	MAKATNWRIAIQQAPSYNRKERCV*			MAKATNWRIAIQQAPSYNRKERCV*	CCACGTCCCC	CCATTCACCC	0	Q	0	MG03880.1	0	0	0
3038	1902	ao	AN2061.1	57.m05757	AO070341000209	0					-70	-35	ATGGCTTTCCACTCTCGTCCTCCATCGAGTGGTTGA			ATGGCTTTCCACTCTCGTCCTCCATCGAGTGGTTGA	MAFHSRPPSSG*			MAFHSRPPSSG*	TATTTATACT	AGAGACAACT	0	Q	0	MG03880.1	0	0	0
3039	1903	ao	AN3708.1	69.m15413	AO070341000333	0					-224	-141	ATGCCAAGACACCACTGGTTCGAATCCCTCCACTGCCACCCTACCTTCGTTTTTCCTGTTCCATTCTTCCCTTCCATACGATAA			ATGCCAAGACACCACTGGTTCGAATCCCTCCACTGCCACCCTACCTTCGTTTTTCCTGTTCCATTCTTCCCTTCCATACGATAA	MPRHHWFESLHCHPTFVFPVPFFPSIR*			MPRHHWFESLHCHPTFVFPVPFFPSIR*	CCTTATATTA	TATTCCCCCC	0	T	0	0	0	0	0
3042	1904	af	AN3729.1	69.m15386	AO070342000283	0			-114	-100			ATGGGTAGTCCTTGA		ATGGGTAGTCCTTGA		MGSP*		MGSP*		TAATCATTTA	TGTAAGGTTC	0	M	0	0	0	0	0
3040	1904	an	AN3729.1	69.m15386	AO070342000283	0	-185	-159					ATGATCTTTAGATTCGCTCGTCTATAA	ATGATCTTTAGATTCGCTCGTCTATAA			MIFRFARL*	MIFRFARL*			CGCCTAGTGC	CCGCTGATTT	0	M	0	0	0	0	0
3041	1904	an	AN3729.1	69.m15386	AO070342000283	0	-101	-39					ATGGGCCTTTGTTTCTGTGAGTTTGGTTGTCTTGTTACTTGCATTTTTTGGGTTCAGAACTAA	ATGGGCCTTTGTTTCTGTGAGTTTGGTTGTCTTGTTACTTGCATTTTTTGGGTTCAGAACTAA			MGLCFCEFGCLVTCIFWVQN*	MGLCFCEFGCLVTCIFWVQN*			CTAATATTTA	CAGCAACAAG	0	M	0	0	0	0	0
3043	1904	ao	AN3729.1	69.m15386	AO070342000283	0					-157	-143	ATGCAAAAATATTGA			ATGCAAAAATATTGA	MQKY*			MQKY*	AGTCCCGTTG	GAATCGATCA	0	M	0	0	0	0	0
3044	1904	ao	AN3729.1	69.m15386	AO070342000283	0					-119	-105	ATGGGTCACTGTTAA			ATGGGTCACTGTTAA	MGHC*			MGHC*	TGAAATTTGG	GGTGAGTCGA	0	M	0	0	0	0	0
3045	1904	ao	AN3729.1	69.m15386	AO070342000283	0					-73	-47	ATGGATTTGCTTGCGTGCCAGGGCTAA			ATGGATTTGCTTGCGTGCCAGGGCTAA	MDLLACQG*			MDLLACQG*	CTTCGAATTT	GCTTGTATTA	0	M	0	0	0	0	0
3048	1907	af	AN4597.1	57.m05519	AO070267000013	0			-162	-100			ATGTTGTTATGGCAGAAAATCACGCCTTTCCCCTTCAGGTCAAAAGGTAAACAACCCACCTAA		ATGTTGTTATGGCAGAAAATCACGCCTTTCCCCTTCAGGTCAAAAGGTAAACAACCCACCTAA		MLLWQKITPFPFRSKGKQPT*		MLLWQKITPFPFRSKGKQPT*		GCTTTGTTTC	TCCACTACCA	0	BD	0	0	0	0	0

3049	1907	af	AN4597.1	57.m05519	AO070267000013	0			-154	-113			ATGGCAGAAAATCACGCCTTTCCCCTTCAGGTCAAAAGGTAA		ATGGCAGAAAATCACGCCTTTCCCCTTCAGGTCAAAAGGTAA		MAENHAFPLQVKR*		MAENHAFPLQVKR*		TCATGTTGTT	ACAACCCACC	0	BD	0	0	0	0	0
3047	1907	an	AN4597.1	57.m05519	AO070267000013	0	-231	-202					ATGCTCATCGATCTTTGCGATAACAGCTGA	ATGCTCATCGATCTTTGCGATAACAGCTGA			MLIDLCDNS*	MLIDLCDNS*			GTAGCTGTTG	TAGTTCGGTT	0	BD	0	0	0	0	0
3050	1907	ao	AN4597.1	57.m05519	AO070267000013	0					-248	-117	ATGCCAAAGATTACTCTTATCATGTTGACCTGTACCATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA			ATGCCAAAGATTACTCTTATCATGTTGACCTGTACCATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA	MPKITLIMLTCTMVTVHTDDIIRAVAARLLWQKNKAFPLWATM*			MPKITLIMLTCTMVTVHTDDIIRAVAARLLWQKNKAFPLWATM*	TTTGATATAA	ACAACCCACT	0	BD	0	0	0	0	0
3051	1907	ao	AN4597.1	57.m05519	AO070267000013	0					-227	-117	ATGTTGACCTGTACCATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA			ATGTTGACCTGTACCATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA	MLTCTMVTVHTDDIIRAVAARLLWQKNKAFPLWATM*			MLTCTMVTVHTDDIIRAVAARLLWQKNKAFPLWATM*	TACTCTTATC	ACAACCCACT	0	BD	0	0	0	0	0
3052	1907	ao	AN4597.1	57.m05519	AO070267000013	0					-212	-117	ATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA			ATGGTTACAGTACATACGGATGACATAATACGGGCGGTGGCTGCCAGACTGTTGTGGCAGAAAAACAAGGCTTTTCCTCTTTGGGCGACAATGTAA	MVTVHTDDIIRAVAARLLWQKNKAFPLWATM*			MVTVHTDDIIRAVAARLLWQKNKAFPLWATM*	GACCTGTACC	ACAACCCACT	0	BD	0	0	0	0	0
3056	1908	af	AN2320.1	62.m03412	AO070269000057	0			-214	-95			ATGACGAATCATGTCGTGGAAATACCTCGTAATGGCCCTTCTTCGCGTGCATCTTGCGTGATGATAACACGCAATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		ATGACGAATCATGTCGTGGAAATACCTCGTAATGGCCCTTCTTCGCGTGCATCTTGCGTGATGATAACACGCAATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		MTNHVVEIPRNGPSSRASCVMITRNGEWMRGHGKLRPSP*		MTNHVVEIPRNGPSSRASCVMITRNGEWMRGHGKLRPSP*		AGTGGAGATA	AGAGGTTGAG	0	C	0	0	0	0	0
3057	1908	af	AN2320.1	62.m03412	AO070269000057	0			-204	-154			ATGTCGTGGAAATACCTCGTAATGGCCCTTCTTCGCGTGCATCTTGCGTGA		ATGTCGTGGAAATACCTCGTAATGGCCCTTCTTCGCGTGCATCTTGCGTGA		MSWKYLVMALLRVHLA*		MSWKYLVMALLRVHLA*		ATGACGAATC	TGATAACACG	0	C	0	0	0	0	0
3058	1908	af	AN2320.1	62.m03412	AO070269000057	0			-183	-154			ATGGCCCTTCTTCGCGTGCATCTTGCGTGA		ATGGCCCTTCTTCGCGTGCATCTTGCGTGA		MALLRVHLA*		MALLRVHLA*		ATACCTCGTA	TGATAACACG	0	C	0	0	0	0	0
3059	1908	af	AN2320.1	62.m03412	AO070269000057	0			-154	-95			ATGATAACACGCAATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		ATGATAACACGCAATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		MITRNGEWMRGHGKLRPSP*		MITRNGEWMRGHGKLRPSP*		ATCTTGCGTG	AGAGGTTGAG	0	C	0	0	0	0	0
3060	1908	af	AN2320.1	62.m03412	AO070269000057	0			-141	-28			ATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGAAGAGGTTGAGCGAGAGAGGGAGTATAACTACTCTTCACCGAGTTGGATCAGCGAGCTCAAGAGTTGA		ATGGCGAATGGATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGAAGAGGTTGAGCGAGAGAGGGAGTATAACTACTCTTCACCGAGTTGGATCAGCGAGCTCAAGAGTTGA		MANGCGVMASYDLPLEEVEREREYNYSSPSWISELKS*		MANGCGVMASYDLPLEEVEREREYNYSSPSWISELKS*		ATAACACGCA	CAGGAACGCT	0	C	0	0	0	0	0
3061	1908	af	AN2320.1	62.m03412	AO070269000057	0			-130	-95			ATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		ATGCGGGGTCATGGCAAGCTACGACCTTCCCCTTGA		MRGHGKLRPSP*		MRGHGKLRPSP*		TGGCGAATGG	AGAGGTTGAG	0	C	0	0	0	0	0
3062	1908	af	AN2320.1	62.m03412	AO070269000057	0			-120	-28			ATGGCAAGCTACGACCTTCCCCTTGAAGAGGTTGAGCGAGAGAGGGAGTATAACTACTCTTCACCGAGTTGGATCAGCGAGCTCAAGAGTTGA		ATGGCAAGCTACGACCTTCCCCTTGAAGAGGTTGAGCGAGAGAGGGAGTATAACTACTCTTCACCGAGTTGGATCAGCGAGCTCAAGAGTTGA		MASYDLPLEEVEREREYNYSSPSWISELKS*		MASYDLPLEEVEREREYNYSSPSWISELKS*		ATGCGGGGTC	CAGGAACGCT	0	C	0	0	0	0	0
3053	1908	an	AN2320.1	62.m03412	AO070269000057	0	-178	-101					ATGGATATGAATGCTGGGTTCGATCCGTGCAACGCTTGCGCGATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA	ATGGATATGAATGCTGGGTTCGATCCGTGCAACGCTTGCGCGATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA			MDMNAGFDPCNACAMGGGYGDILRG*	MDMNAGFDPCNACAMGGGYGDILRG*			TCTTTGTACA	GAGCATGAGT	0	C	0	0	0	0	0
3054	1908	an	AN2320.1	62.m03412	AO070269000057	0	-172	-101					ATGAATGCTGGGTTCGATCCGTGCAACGCTTGCGCGATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA	ATGAATGCTGGGTTCGATCCGTGCAACGCTTGCGCGATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA			MNAGFDPCNACAMGGGYGDILRG*	MNAGFDPCNACAMGGGYGDILRG*			TACAATGGAT	GAGCATGAGT	0	C	0	0	0	0	0
3055	1908	an	AN2320.1	62.m03412	AO070269000057	0	-136	-101					ATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA	ATGGGGGGAGGCTATGGCGATATTCTGCGGGGCTAA			MGGGYGDILRG*	MGGGYGDILRG*			CGCTTGCGCG	GAGCATGAGT	0	C	0	0	0	0	0
3063	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-241	-218	ATGACGAATCGCACCCCTGCATAA			ATGACGAATCGCACCCCTGCATAA	MTNRTPA*			MTNRTPA*	AGCGGACCCA	TCAAAGACTT	0	C	0	0	0	0	0
3064	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-170	-108	ATGACGCTTGCTGATGGCGAGAGTGCGGGGTTAATGAAATTTTCATTTTCATTCTTCTCTTAA			ATGACGCTTGCTGATGGCGAGAGTGCGGGGTTAATGAAATTTTCATTTTCATTCTTCTCTTAA	MTLADGESAGLMKFSFSFFS*			MTLADGESAGLMKFSFSFFS*	CGGTTACGCG	GTAGATATAT	0	C	0	0	0	0	0
3065	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-157	-137	ATGGCGAGAGTGCGGGGTTAA			ATGGCGAGAGTGCGGGGTTAA	MARVRG*			MARVRG*	ACGCTTGCTG	TGAAATTTTC	0	C	0	0	0	0	0
3066	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-137	-108	ATGAAATTTTCATTTTCATTCTTCTCTTAA			ATGAAATTTTCATTTTCATTCTTCTCTTAA	MKFSFSFFS*			MKFSFSFFS*	TGCGGGGTTA	GTAGATATAT	0	C	0	0	0	0	0
3067	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-95	-72	ATGGGTATTTATGTAGATAGATGA			ATGGGTATTTATGTAGATAGATGA	MGIYVDR*			MGIYVDR*	AGATATATAG	ATGGATAATA	0	C	0	0	0	0	0
3068	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-75	-64	ATGAATGGATAA			ATGAATGGATAA	MNG*			MNG*	ATGTAGATAG	TATACATATA	0	C	0	0	0	0	0
3069	1908	ao	AN2320.1	62.m03412	AO070269000057	0					-71	-24	ATGGATAATATACATATATCTAAGGTGTCAAATTCCAATATCACCTAA			ATGGATAATATACATATATCTAAGGTGTCAAATTCCAATATCACCTAA	MDNIHISKVSNSNIT*			MDNIHISKVSNSNIT*	AGATAGATGA	CTTACACACA	0	C	0	0	0	0	0
3071	1913	af	AN5113.1	54.m07051	AO070291000066	0			-263	-249			ATGTGTTGGTCATAA		ATGTGTTGGTCATAA		MCWS*		MCWS*		GGATTAAGGT	TGTGCAGAGT	0	U	0	0	0	0	0
3072	1913	af	AN5113.1	54.m07051	AO070291000066	0			-249	-193			ATGTGCAGAGTCCCCCTTTTATGGAATCTTACCTCGGCATCGTCTTGTCTTGGGTAA		ATGTGCAGAGTCCCCCTTTTATGGAATCTTACCTCGGCATCGTCTTGTCTTGGGTAA		MCRVPLLWNLTSASSCLG*		MCRVPLLWNLTSASSCLG*		GTTGGTCATA	GAGCCGGACA	0	U	0	0	0	0	0
3073	1913	af	AN5113.1	54.m07051	AO070291000066	0			-229	-47			ATGGAATCTTACCTCGGCATCGTCTTGTCTTGGGTAAGAGCCGGACACGTGCCGCTGTACTCCGTACTCCGTACCCCAGACTCGACTCCTGCGACCATCCAGCGAGGCCATCTCGATCTCGATCTCAGCCTGATGGCTCTCTTTCGCAGCCTCGAAACCTTCAATTGCTTTTGCAAAAAGTGA		ATGGAATCTTACCTCGGCATCGTCTTGTCTTGGGTAAGAGCCGGACACGTGCCGCTGTACTCCGTACTCCGTACCCCAGACTCGACTCCTGCGACCATCCAGCGAGGCCATCTCGATCTCGATCTCAGCCTGATGGCTCTCTTTCGCAGCCTCGAAACCTTCAATTGCTTTTGCAAAAAGTGA		MESYLGIVLSWVRAGHVPLYSVLRTPDSTPATIQRGHLDLDLSLMALFRSLETFNCFCKK*		MESYLGIVLSWVRAGHVPLYSVLRTPDSTPATIQRGHLDLDLSLMALFRSLETFNCFCKK*		TCCCCCTTTT	TATTCTTGTA	0	U	0	0	0	0	0
3074	1913	af	AN5113.1	54.m07051	AO070291000066	0			-97	-47			ATGGCTCTCTTTCGCAGCCTCGAAACCTTCAATTGCTTTTGCAAAAAGTGA		ATGGCTCTCTTTCGCAGCCTCGAAACCTTCAATTGCTTTTGCAAAAAGTGA		MALFRSLETFNCFCKK*		MALFRSLETFNCFCKK*		TCTCAGCCTG	TATTCTTGTA	0	U	0	0	0	0	0
3070	1913	an	AN5113.1	54.m07051	AO070291000066	0	-136	-38					ATGACACGTGCTGTCGCTCCCATCCACATCTCATCTCCTGTTGGCAACATCCTACCAAGTGACCGAAACATTTGTCCATCGCTTTCATTTCTACTCTAA	ATGACACGTGCTGTCGCTCCCATCCACATCTCATCTCCTGTTGGCAACATCCTACCAAGTGACCGAAACATTTGTCCATCGCTTTCATTTCTACTCTAA			MTRAVAPIHISSPVGNILPSDRNICPSLSFLL*	MTRAVAPIHISSPVGNILPSDRNICPSLSFLL*			TCCTTGGCGT	GCTCAGCTGC	0	U	0	0	0	0	0
3075	1913	ao	AN5113.1	54.m07051	AO070291000066	0					-127	-62	ATGCGGAGAGCACGTGTTGAACATATCCCCTGTCACTTGTTGCTTGACTTCAGCCACATACTTTAG			ATGCGGAGAGCACGTGTTGAACATATCCCCTGTCACTTGTTGCTTGACTTCAGCCACATACTTTAG	MRRARVEHIPCHLLLDFSHIL*			MRRARVEHIPCHLLLDFSHIL*	ATTCCTTGGC	TTGTTACGTT	0	U	0	0	0	0	0
3082	1914	af	AN5557.1	57.m05387	AO070294000076	0			-159	-73			ATGGTTCTGAAGATCATCTGCCACGGTCCAAGGGCAACGAGGCTAACTCCGTTATTTCCGTGGATGACGATGCGGGGTGCAGGATGA		ATGGTTCTGAAGATCATCTGCCACGGTCCAAGGGCAACGAGGCTAACTCCGTTATTTCCGTGGATGACGATGCGGGGTGCAGGATGA		MVLKIICHGPRATRLTPLFPWMTMRGAG*		MVLKIICHGPRATRLTPLFPWMTMRGAG*		AGACTCGGAT	GCACATATAA	0	IQR	0	0	0	0	0
3083	1914	af	AN5557.1	57.m05387	AO070294000076	0			-96	-73			ATGACGATGCGGGGTGCAGGATGA		ATGACGATGCGGGGTGCAGGATGA		MTMRGAG*		MTMRGAG*		ATTTCCGTGG	GCACATATAA	0	IQR	0	0	0	0	0
3084	1914	af	AN5557.1	57.m05387	AO070294000076	0			-90	-73			ATGCGGGGTGCAGGATGA		ATGCGGGGTGCAGGATGA		MRGAG*		MRGAG*		GTGGATGACG	GCACATATAA	0	IQR	0	0	0	0	0
3085	1914	af	AN5557.1	57.m05387	AO070294000076	0			-76	-35			ATGAGCACATATAACCGCACATCAGGAACCTTCTGTCCCTGA		ATGAGCACATATAACCGCACATCAGGAACCTTCTGTCCCTGA		MSTYNRTSGTFCP*		MSTYNRTSGTFCP*		GGGGTGCAGG	TGTCTTCTGC	0	IQR	0	0	0	0	0
3076	1914	an	AN5557.1	57.m05387	AO070294000076	0	-212	-6					ATGTATTTTTATGTTCAGTTCAGTCTATCATGTCGAAGATTAGTCTGTGTCTCCCTAAATATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGAAAACTCCGCTATCTCCGAATGCATTCCCCGCACTACAAATTCCCGCGTCAACAGCGCAGACGATGCTACAAGTTCCCAACAGCAGCTATAA	ATGTATTTTTATGTTCAGTTCAGTCTATCATGTCGAAGATTAGTCTGTGTCTCCCTAAATATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGAAAACTCCGCTATCTCCGAATGCATTCCCCGCACTACAAATTCCCGCGTCAACAGCGCAGACGATGCTACAAGTTCCCAACAGCAGCTATAA			MYFYVQFSLSCRRLVCVSLNMVYYYGYLCSSIAYTYASENSAISECIPRTTNSRVNSADDATSSQQQL*	MYFYVQFSLSCRRLVCVSLNMVYYYGYLCSSIAYTYASENSAISECIPRTTNSRVNSADDATSSQQQL*			GCTGACGAAC	CTACAATGGC	0	IQR	0	0	0	0	0
3077	1914	an	AN5557.1	57.m05387	AO070294000076	0	-202	-170					ATGTTCAGTTCAGTCTATCATGTCGAAGATTAG	ATGTTCAGTTCAGTCTATCATGTCGAAGATTAG			MFSSVYHVED*	MFSSVYHVED*			ATGTATTTTT	TCTGTGTCTC	0	IQR	0	0	0	0	0
3078	1914	an	AN5557.1	57.m05387	AO070294000076	0	-183	-97					ATGTCGAAGATTAGTCTGTGTCTCCCTAAATATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGA	ATGTCGAAGATTAGTCTGTGTCTCCCTAAATATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGA			MSKISLCLPKYGLLLWLSMLQYSLHLRQ*	MSKISLCLPKYGLLLWLSMLQYSLHLRQ*			TCAGTCTATC	AAACTCCGCT	0	IQR	0	0	0	0	0
3079	1914	an	AN5557.1	57.m05387	AO070294000076	0	-152	-6					ATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGAAAACTCCGCTATCTCCGAATGCATTCCCCGCACTACAAATTCCCGCGTCAACAGCGCAGACGATGCTACAAGTTCCCAACAGCAGCTATAA	ATGGTTTACTACTATGGTTATCTATGCTCCAGTATAGCTTACACCTACGCCAGTGAAAACTCCGCTATCTCCGAATGCATTCCCCGCACTACAAATTCCCGCGTCAACAGCGCAGACGATGCTACAAGTTCCCAACAGCAGCTATAA			MVYYYGYLCSSIAYTYASENSAISECIPRTTNSRVNSADDATSSQQQL*	MVYYYGYLCSSIAYTYASENSAISECIPRTTNSRVNSADDATSSQQQL*			CTCCCTAAAT	CTACAATGGC	0	IQR	0	0	0	0	0
3080	1914	an	AN5557.1	57.m05387	AO070294000076	0	-139	-116					ATGGTTATCTATGCTCCAGTATAG	ATGGTTATCTATGCTCCAGTATAG			MVIYAPV*	MVIYAPV*			GTTTACTACT	CTTACACCTA	0	IQR	0	0	0	0	0
3081	1914	an	AN5557.1	57.m05387	AO070294000076	0	-129	-97					ATGCTCCAGTATAGCTTACACCTACGCCAGTGA	ATGCTCCAGTATAGCTTACACCTACGCCAGTGA			MLQYSLHLRQ*	MLQYSLHLRQ*			ATGGTTATCT	AAACTCCGCT	0	IQR	0	0	0	0	0
3086	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-201	-97	ATGTTTACTAGATGGAAGATCCATAGGTATAAAGATGTTTCTATAATGCATTACTTTATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA			ATGTTTACTAGATGGAAGATCCATAGGTATAAAGATGTTTCTATAATGCATTACTTTATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA	MFTRWKIHRYKDVSIMHYFMTAYAGPQLSPQTPG*			MFTRWKIHRYKDVSIMHYFMTAYAGPQLSPQTPG*	ATATTATAGC	AGCGGGGAAC	0	IQR	0	0	0	0	0
3087	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-190	-176	ATGGAAGATCCATAG			ATGGAAGATCCATAG	MEDP*			MEDP*	TGTTTACTAG	GTATAAAGAT	0	IQR	0	0	0	0	0
3088	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-167	-156	ATGTTTCTATAA			ATGTTTCTATAA	MFL*			MFL*	AGGTATAAAG	TGCATTACTT	0	IQR	0	0	0	0	0
3089	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-156	-97	ATGCATTACTTTATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA			ATGCATTACTTTATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA	MHYFMTAYAGPQLSPQTPG*			MHYFMTAYAGPQLSPQTPG*	TGTTTCTATA	AGCGGGGAAC	0	IQR	0	0	0	0	0
3090	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-144	-97	ATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA			ATGACTGCTTATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGA	MTAYAGPQLSPQTPG*			MTAYAGPQLSPQTPG*	GCATTACTTT	AGCGGGGAAC	0	IQR	0	0	0	0	0
3091	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-134	-15	ATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGAAGCGGGGAACAATCAGAGGATATATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGAGTGTTAGTCAGTAA			ATGCTGGTCCACAGTTATCTCCGCAAACTCCGGGATGAAGCGGGGAACAATCAGAGGATATATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGAGTGTTAGTCAGTAA	MLVHSYLRKLRDEAGNNQRIYASSSPSHQVPSAALSVSQ*			MLVHSYLRKLRDEAGNNQRIYASSSPSHQVPSAALSVSQ*	ATGACTGCTT	AGACAAAAGT	0	IQR	0	0	0	0	0
3092	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-100	-29	ATGAAGCGGGGAACAATCAGAGGATATATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGA			ATGAAGCGGGGAACAATCAGAGGATATATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGA	MKRGTIRGYMPPHLPATKFRLPH*			MKRGTIRGYMPPHLPATKFRLPH*	AAACTCCGGG	GTGTTAGTCA	0	IQR	0	0	0	0	0
3093	1914	ao	AN5557.1	57.m05387	AO070294000076	0					-73	-29	ATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGA			ATGCCTCCTCATCTCCCAGCCACCAAGTTCCGTCTGCCGCATTGA	MPPHLPATKFRLPH*			MPPHLPATKFRLPH*	CAGAGGATAT	GTGTTAGTCA	0	IQR	0	0	0	0	0
3096	1916	af	AN3419.1	59.m08742	AO070303000071	0			-177	-127			ATGTACAACAGCACTTCATCAAAATCGATGCTGAACTCGATCTCTAAATAA		ATGTACAACAGCACTTCATCAAAATCGATGCTGAACTCGATCTCTAAATAA		MYNSTSSKSMLNSISK*		MYNSTSSKSMLNSISK*		ACCATTCACA	GCAGGTTGCC	0	E	0	0	0	0	0
3097	1916	af	AN3419.1	59.m08742	AO070303000071	0			-150	-127			ATGCTGAACTCGATCTCTAAATAA		ATGCTGAACTCGATCTCTAAATAA		MLNSISK*		MLNSISK*		ATCAAAATCG	GCAGGTTGCC	0	E	0	0	0	0	0

3094	1916	an	AN3419.1	59.m08742	AO070303000071	0	-188	-123					ATGACATTCAACCTCGCCTTGATATTACGCGAGTCAATTCCAGACATCAAGACCTTCCTATCTTAA	ATGACATTCAACCTCGCCTTGATATTACGCGAGTCAATTCCAGACATCAAGACCTTCCTATCTTAA			MTFNLALILRESIPDIKTFLS*	MTFNLALILRESIPDIKTFLS*			ATCTTCAACA	GTCTTTGTAA	0	E	0	0	0	0	0
3095	1916	an	AN3419.1	59.m08742	AO070303000071	0	-92	-69					ATGACTGAGCGAACTAAATACTGA	ATGACTGAGCGAACTAAATACTGA			MTERTKY*	MTERTKY*			TTAGATACCC	CTCCGATTCA	0	E	0	0	0	0	0
3098	1922	af	AN0385.1	54.m06359	AO070318000082	0			-206	-183			ATGAACATATCCATAAGGTGGTAA		ATGAACATATCCATAAGGTGGTAA		MNISIRW*		MNISIRW*		TGGAGTTGAC	GGATAAGGTA	0	EH	FG05696.1	MG02125.1	0	0	0
3099	1922	af	AN0385.1	54.m06359	AO070318000082	0			-165	-97			ATGCCAACGTGGATGCGTAGTGTTGTTCCCCGCCTGGCCCAATTCATCAACAGTCGGCGGAATAAATAA		ATGCCAACGTGGATGCGTAGTGTTGTTCCCCGCCTGGCCCAATTCATCAACAGTCGGCGGAATAAATAA		MPTWMRSVVPRLAQFINSRRNK*		MPTWMRSVVPRLAQFINSRRNK*		GTACTCTTGC	ATCACCCCTC	0	EH	FG05696.1	MG02125.1	0	0	0
3100	1922	af	AN0385.1	54.m06359	AO070318000082	0			-153	-97			ATGCGTAGTGTTGTTCCCCGCCTGGCCCAATTCATCAACAGTCGGCGGAATAAATAA		ATGCGTAGTGTTGTTCCCCGCCTGGCCCAATTCATCAACAGTCGGCGGAATAAATAA		MRSVVPRLAQFINSRRNK*		MRSVVPRLAQFINSRRNK*		GCCAACGTGG	ATCACCCCTC	0	EH	FG05696.1	MG02125.1	0	0	0
3101	1922	ao	AN0385.1	54.m06359	AO070318000082	0					-226	-194	ATGGTCGTATTCGTGCAATGTGTTGATACCTGA			ATGGTCGTATTCGTGCAATGTGTTGATACCTGA	MVVFVQCVDT*			MVVFVQCVDT*	CGGGGTAGCG	AGAGTAATGG	0	EH	FG05696.1	MG02125.1	0	0	0
3102	1922	ao	AN0385.1	54.m06359	AO070318000082	0					-187	-38	ATGGAATATGTACACCTGATACCCGCGCTAGACTGTTTTCGGCGGTCATCCCACCTTTACCCAAGCATGAATCATCAGCTTATTTTTGTCTACATCTACTTCTACCTCTTCCTCTTCCTCTTCTTCCCCCCTCTTTCACTTTCTCAATAA			ATGGAATATGTACACCTGATACCCGCGCTAGACTGTTTTCGGCGGTCATCCCACCTTTACCCAAGCATGAATCATCAGCTTATTTTTGTCTACATCTACTTCTACCTCTTCCTCTTCCTCTTCTTCCCCCCTCTTTCACTTTCTCAATAA	MEYVHLIPALDCFRRSSHLYPSMNHQLIFVYIYFYLFLFLFFPPLSLSQ*			MEYVHLIPALDCFRRSSHLYPSMNHQLIFVYIYFYLFLFLFFPPLSLSQ*	CTGAAGAGTA	ACCCAATTTT	0	EH	FG05696.1	MG02125.1	0	0	0
3103	1922	ao	AN0385.1	54.m06359	AO070318000082	0					-180	-169	ATGTACACCTGA			ATGTACACCTGA	MYT*			MYT*	GTAATGGAAT	TACCCGCGCT	0	EH	FG05696.1	MG02125.1	0	0	0
3104	1922	ao	AN0385.1	54.m06359	AO070318000082	0					-121	-38	ATGAATCATCAGCTTATTTTTGTCTACATCTACTTCTACCTCTTCCTCTTCCTCTTCTTCCCCCCTCTTTCACTTTCTCAATAA			ATGAATCATCAGCTTATTTTTGTCTACATCTACTTCTACCTCTTCCTCTTCCTCTTCTTCCCCCCTCTTTCACTTTCTCAATAA	MNHQLIFVYIYFYLFLFLFFPPLSLSQ*			MNHQLIFVYIYFYLFLFLFFPPLSLSQ*	TTACCCAAGC	ACCCAATTTT	0	EH	FG05696.1	MG02125.1	0	0	0
3105	1927	af	AN1199.1	70.m15020	AO070331000204	0			-121	-110			ATGACTGTATAG		ATGACTGTATAG		MTV*		MTV*		ACTAATCTCT	ACCCGCCCAA	0	E	FG10375.1	0	0	0	0
3113	1928	af	AN1487.1	55.m02993	AO070334000194	0			-755	-738			ATGTGGGTCGGATCTTGA		ATGTGGGTCGGATCTTGA		MWVGS*		MWVGS*		ATGATTGTCG	GTTGTCGAAT	0		0	0	0	0	0
3109	1928	an	AN1487.1	55.m02993	AO070334000194	0	-244	-113					ATGCCTCTCGCTCCGTTTAACTTGCTGGTACGTAGTCGGCCCCCGGCCCCATCGCAAAACTTCCCCTACCACACAATCGTTCTGTCAGCGCGCATTGGTTTCCATAATGGTCTTACTCTGCGCCTTAGATGA	ATGCCTCTCGCTCCGTTTAACTTGCTGGTACGTAGTCGGCCCCCGGCCCCATCGCAAAACTTCCCCTACCACACAATCGTTCTGTCAGCGCGCATTGGTTTCCATAATGGTCTTACTCTGCGCCTTAGATGA			MPLAPFNLLVRSRPPAPSQNFPYHTIVLSARIGFHNGLTLRLR*	MPLAPFNLLVRSRPPAPSQNFPYHTIVLSARIGFHNGLTLRLR*			ATTCTAATGC	CCGTCAAAGG	0		0	0	0	0	0
3110	1928	an	AN1487.1	55.m02993	AO070334000194	0	-138	-73					ATGGTCTTACTCTGCGCCTTAGATGACCGTCAAAGGTCATCAGCTCCCTATATAATGGACTGCTAA	ATGGTCTTACTCTGCGCCTTAGATGACCGTCAAAGGTCATCAGCTCCCTATATAATGGACTGCTAA			MVLLCALDDRQRSSAPYIMDC*	MVLLCALDDRQRSSAPYIMDC*			GGTTTCCATA	CGGTGCTCAT	0		0	0	0	0	0
3111	1928	an	AN1487.1	55.m02993	AO070334000194	0	-116	-84					ATGACCGTCAAAGGTCATCAGCTCCCTATATAA	ATGACCGTCAAAGGTCATCAGCTCCCTATATAA			MTVKGHQLPI*	MTVKGHQLPI*			TGCGCCTTAG	TGGACTGCTA	0		0	0	0	0	0
3112	1928	an	AN1487.1	55.m02993	AO070334000194	0	-84	-73					ATGGACTGCTAA	ATGGACTGCTAA			MDC*	MDC*			TCCCTATATA	CGGTGCTCAT	0		0	0	0	0	0
3114	1928	ao	AN1487.1	55.m02993	AO070334000194	0					-876	-823	ATGCTGTTTAGTTCTATCCTTCTTCTTCCGAACTACTTGGGATTAAACACTTGA			ATGCTGTTTAGTTCTATCCTTCTTCTTCCGAACTACTTGGGATTAAACACTTGA	MLFSSILLLPNYLGLNT*			MLFSSILLLPNYLGLNT*	GTGACTCTCG	TTGGTTGAGG	0		0	0	0	0	0
3119	1931	af	AN2960.1	59.m09082	AO070337000210	0			-78	-43			ATGGGTATATCTGGAGAAGTATCTCAGCTTGTATGA		ATGGGTATATCTGGAGAAGTATCTCAGCTTGTATGA		MGISGEVSQLV*		MGISGEVSQLV*		GGGAGTCCAT	CTTGTTCTAA	0	Q	0	0	0	0	0
3115	1931	an	AN2960.1	59.m09082	AO070337000210	0	-154	-113					ATGAATCATATCCCGCAGACATTGCGCCAGAATGCCAGTTAA	ATGAATCATATCCCGCAGACATTGCGCCAGAATGCCAGTTAA			MNHIPQTLRQNAS*	MNHIPQTLRQNAS*			TGTGAAGGAG	CCGGGTAATC	0	Q	0	0	0	0	0
3116	1931	an	AN2960.1	59.m09082	AO070337000210	0	-123	-91					ATGCCAGTTAACCGGGTAATCGGATCAAAATGA	ATGCCAGTTAACCGGGTAATCGGATCAAAATGA			MPVNRVIGSK*	MPVNRVIGSK*			TTGCGCCAGA	ACGGTCTATA	0	Q	0	0	0	0	0
3117	1931	an	AN2960.1	59.m09082	AO070337000210	0	-94	-47					ATGAACGGTCTATATAACACGTCGATGGTCCGCAGGCCTCGTCGGTAG	ATGAACGGTCTATATAACACGTCGATGGTCCGCAGGCCTCGTCGGTAG			MNGLYNTSMVRRPRR*	MNGLYNTSMVRRPRR*			TCGGATCAAA	CTGTTGAGAA	0	Q	0	0	0	0	0
3118	1931	an	AN2960.1	59.m09082	AO070337000210	0	-70	-47					ATGGTCCGCAGGCCTCGTCGGTAG	ATGGTCCGCAGGCCTCGTCGGTAG			MVRRPRR*	MVRRPRR*			TAACACGTCG	CTGTTGAGAA	0	Q	0	0	0	0	0
3120	1931	ao	AN2960.1	59.m09082	AO070337000210	0					-104	-84	ATGGGTATATCTAGGAGTTAG			ATGGGTATATCTAGGAGTTAG	MGISRS*			MGISRS*	ATGTGATGCG	CCCCCTGGCG	0	Q	0	0	0	0	0
3121	1934	conserved	AN2086.1	57.m05787	AO070341000244	0	-71	-45	-71	-45	-71	-45	ATGCwCCAAAGwbCAGwsyAymhTTAG	ATGCTCCAAAGTCCAGAGTACACTTAG	ATGCACCAAAGTTCAGTCTATCTTTAG	ATGCTCCAAAGAGCAGAGCATCATTAG	MlQspeyt*	MLQSPEYT*	MHQSSVYL*	MLQRAEHH*	CCTTCyCCyC	GCGACCGTCC	0	YU	0	0	0	0	0
3122	1939	an	AN4230.1	54.m06786	AO070234000016	0	-146	-135					ATGCTTAGCTAG	ATGCTTAGCTAG			MLS*	MLS*			ATGAGTCGAA	CGGAACAGGC	0	I	0	MG09516.1	0	0	0
3123	1939	an	AN4230.1	54.m06786	AO070234000016	0	-97	-62					ATGGGCCCGATTCGGAGAACTACTTCATACTTATAG	ATGGGCCCGATTCGGAGAACTACTTCATACTTATAG			MGPIRRTTSYL*	MGPIRRTTSYL*			GGGGCCGGCG	CTTTTCCTCT	0	I	0	MG09516.1	0	0	0
3125	1939	ao	AN4230.1	54.m06786	AO070234000016	0					-219	-208	ATGCATGCTTAA			ATGCATGCTTAA	MHA*			MHA*	AAAGGCGGAA	TCGACCTCGG	0	I	0	MG09516.1	0	0	0
3126	1939	ao	AN4230.1	54.m06786	AO070234000016	0					-215	-54	ATGCTTAATCGACCTCGGCTTTTGGCGTTCAAACAAGTTAAGCTATCGGCGAAGTACCCGAATGAAATGACAGGAACATCTCCAATCGAGCTCCGGTCCCGACCCCGGAAAGTACATGATATACATGCGTTACTACCCCAACTTTACACGACTTGGATCTGA			ATGCTTAATCGACCTCGGCTTTTGGCGTTCAAACAAGTTAAGCTATCGGCGAAGTACCCGAATGAAATGACAGGAACATCTCCAATCGAGCTCCGGTCCCGACCCCGGAAAGTACATGATATACATGCGTTACTACCCCAACTTTACACGACTTGGATCTGA	MLNRPRLLAFKQVKLSAKYPNEMTGTSPIELRSRPRKVHDIHALLPQLYTTWI*			MLNRPRLLAFKQVKLSAKYPNEMTGTSPIELRSRPRKVHDIHALLPQLYTTWI*	GCGGAAATGC	TTCAATCTAC	0	I	0	MG09516.1	0	0	0
3127	1939	ao	AN4230.1	54.m06786	AO070234000016	0					-149	-54	ATGACAGGAACATCTCCAATCGAGCTCCGGTCCCGACCCCGGAAAGTACATGATATACATGCGTTACTACCCCAACTTTACACGACTTGGATCTGA			ATGACAGGAACATCTCCAATCGAGCTCCGGTCCCGACCCCGGAAAGTACATGATATACATGCGTTACTACCCCAACTTTACACGACTTGGATCTGA	MTGTSPIELRSRPRKVHDIHALLPQLYTTWI*			MTGTSPIELRSRPRKVHDIHALLPQLYTTWI*	CCCGAATGAA	TTCAATCTAC	0	I	0	MG09516.1	0	0	0
3129	1942	an	AN6553.1	62.m03449	AO070270000058	0	-97	-23					ATGAGGGACGTGTACAGACATCCGCAACGACTCGAGAGCCCAAGGGTATCAAGCAAATTTCGCTGCCTTGAATGA	ATGAGGGACGTGTACAGACATCCGCAACGACTCGAGAGCCCAAGGGTATCAAGCAAATTTCGCTGCCTTGAATGA			MRDVYRHPQRLESPRVSSKFRCLE*	MRDVYRHPQRLESPRVSSKFRCLE*			GACCTGCTGG	GCGTCATTCC	0	T	0	0	0	0	0
3130	1942	ao	AN6553.1	62.m03449	AO070270000058	0					-252	-205	ATGTATGTATATACTACGTACTCAGTCCGAGAGACTACTAGTAGATAG			ATGTATGTATATACTACGTACTCAGTCCGAGAGACTACTAGTAGATAG	MYVYTTYSVRETTSR*			MYVYTTYSVRETTSR*	AGGACAACGG	GGCTTCAGTC	0	T	0	0	0	0	0
3131	1942	ao	AN6553.1	62.m03449	AO070270000058	0					-248	-75	ATGTATATACTACGTACTCAGTCCGAGAGACTACTAGTAGATAGGGCTTCAGTCTTTGTCTCTAAACTGACCGCCTTGGTGGAGGTTTCTCCGAAGCCGACCTCAAAAGGGAAAAGCGGATTTAATATCGCGATCAAACACCCCCAAATGGTGATAATCAACTTCTACTTCTAA			ATGTATATACTACGTACTCAGTCCGAGAGACTACTAGTAGATAGGGCTTCAGTCTTTGTCTCTAAACTGACCGCCTTGGTGGAGGTTTCTCCGAAGCCGACCTCAAAAGGGAAAAGCGGATTTAATATCGCGATCAAACACCCCCAAATGGTGATAATCAACTTCTACTTCTAA	MYILRTQSERLLVDRASVFVSKLTALVEVSPKPTSKGKSGFNIAIKHPQMVIINFYF*			MYILRTQSERLLVDRASVFVSKLTALVEVSPKPTSKGKSGFNIAIKHPQMVIINFYF*	CAACGGATGT	ATGAACGAAA	0	T	0	0	0	0	0
3132	1942	ao	AN6553.1	62.m03449	AO070270000058	0					-101	-75	ATGGTGATAATCAACTTCTACTTCTAA			ATGGTGATAATCAACTTCTACTTCTAA	MVIINFYF*			MVIINFYF*	ACACCCCCAA	ATGAACGAAA	0	T	0	0	0	0	0
3134	1946	af	AN7192.1	69.m15187	AO070306000133	0			-198	-127			ATGCTGGCTCGTGTTTGTTCCTGCGAGGCAAGGATGACTATGGCGATGATACCTCGCATAAGCGCTAGTTGA		ATGCTGGCTCGTGTTTGTTCCTGCGAGGCAAGGATGACTATGGCGATGATACCTCGCATAAGCGCTAGTTGA		MLARVCSCEARMTMAMIPRISAS*		MLARVCSCEARMTMAMIPRISAS*		GAGGACGAAA	CCAGCCTTTC	0		0	0	0	0	0
3135	1946	af	AN7192.1	69.m15187	AO070306000133	0			-165	-127			ATGACTATGGCGATGATACCTCGCATAAGCGCTAGTTGA		ATGACTATGGCGATGATACCTCGCATAAGCGCTAGTTGA		MTMAMIPRISAS*		MTMAMIPRISAS*		CGAGGCAAGG	CCAGCCTTTC	0		0	0	0	0	0
3136	1946	af	AN7192.1	69.m15187	AO070306000133	0			-159	-127			ATGGCGATGATACCTCGCATAAGCGCTAGTTGA		ATGGCGATGATACCTCGCATAAGCGCTAGTTGA		MAMIPRISAS*		MAMIPRISAS*		AAGGATGACT	CCAGCCTTTC	0		0	0	0	0	0
3137	1946	af	AN7192.1	69.m15187	AO070306000133	0			-153	-127			ATGATACCTCGCATAAGCGCTAGTTGA		ATGATACCTCGCATAAGCGCTAGTTGA		MIPRISAS*		MIPRISAS*		GACTATGGCG	CCAGCCTTTC	0		0	0	0	0	0
3133	1946	an	AN7192.1	69.m15187	AO070306000133	0	-118	-98					ATGTATCATTTATTCTCGTAA	ATGTATCATTTATTCTCGTAA			MYHLFS*	MYHLFS*			TCCTCCCTCC	GGTCTTCTTC	0		0	0	0	0	0
3138	1946	ao	AN7192.1	69.m15187	AO070306000133	0					-151	-119	ATGGTCCATCGACTCCAACAAAATGGCCGATAA			ATGGTCCATCGACTCCAACAAAATGGCCGATAA	MVHRLQQNGR*			MVHRLQQNGR*	CTCGGTCGTA	CACCTAGTTC	0		0	0	0	0	0
3139	1946	ao	AN7192.1	69.m15187	AO070306000133	0					-129	-112	ATGGCCGATAACACCTAG			ATGGCCGATAACACCTAG	MADNT*			MADNT*	CTCCAACAAA	TTCAATGCAT	0		0	0	0	0	0
3140	1946	ao	AN7192.1	69.m15187	AO070306000133	0					-107		ATGCATCGACCACTCTTGACACGCTTCATCCTCCCATTCCCATCCTCCATTCCCTTGCTTCTCACTCGTTTCAGCCTCTCACCTGTGAGAGCGCTCGTACTTCCATGA			ATGCATCGACCACTCTTGACACGCTTCATCCTCCCATTCCCATCCTCCATTCCCTTGCTTCTCACTCGTTTCAGCCTCTCACCTGTGAGAGCGCTCGTACTTCCATGA	MHRPLLTRFILPFPSSIPLLLTRFSLSPVRALVLP*			MHRPLLTRFILPFPSSIPLLLTRFSLSPVRALVLP*	ACCTAGTTCA	TGTCCAAGAG	0		0	0	0	0	0
3143	1951	af	AN0868.1	70.m15459	AO070320000019	0			-242	-114			ATGATCCGTACAGCCGAATCTACTCTCAACGGACCGATTAGTGATGCCAATCGTCATCTAAAGTCGGCACATCCAAGCGATGGAGATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGA		ATGATCCGTACAGCCGAATCTACTCTCAACGGACCGATTAGTGATGCCAATCGTCATCTAAAGTCGGCACATCCAAGCGATGGAGATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGA		MIRTAESTLNGPISDANRHLKSAHPSDGDASAFTNSGVSCSA*		MIRTAESTLNGPISDANRHLKSAHPSDGDASAFTNSGVSCSA*		CAATAATACG	AGATTTGAGG	0	I	0	MG02999.1	NCU00580.1	0	0
3144	1951	af	AN0868.1	70.m15459	AO070320000019	0			-199	-182			ATGCCAATCGTCATCTAA		ATGCCAATCGTCATCTAA		MPIVI*		MPIVI*		CCGATTAGTG	AGTCGGCACA	0	I	0	MG02999.1	NCU00580.1	0	0
3145	1951	af	AN0868.1	70.m15459	AO070320000019	0			-163	-77			ATGGAGATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGAAGATTTGAGGACGCTGCCATCATCCGCCTTCGAATAA		ATGGAGATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGAAGATTTGAGGACGCTGCCATCATCCGCCTTCGAATAA		MEMPRHLPIRESRAAREDLRTLPSSAFE*		MEMPRHLPIRESRAAREDLRTLPSSAFE*		CATCCAAGCG	TAATTCCTCT	0	I	0	MG02999.1	NCU00580.1	0	0
3146	1951	af	AN0868.1	70.m15459	AO070320000019	0			-157	-77			ATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGAAGATTTGAGGACGCTGCCATCATCCGCCTTCGAATAA		ATGCCTCGGCATTTACCAATTCGGGAGTCTCGTGCAGCGCGTGAAGATTTGAGGACGCTGCCATCATCCGCCTTCGAATAA		MPRHLPIRESRAAREDLRTLPSSAFE*		MPRHLPIRESRAAREDLRTLPSSAFE*		AGCGATGGAG	TAATTCCTCT	0	I	0	MG02999.1	NCU00580.1	0	0
3141	1951	an	AN0868.1	70.m15459	AO070320000019	0	-168	-94					ATGGGGCTAGCCGTGGGTCAAGTAGCGCGTGAAGGCACCTTCGGTATCTCTGAGAATCTCAGGATTACTCTCTAA	ATGGGGCTAGCCGTGGGTCAAGTAGCGCGTGAAGGCACCTTCGGTATCTCTGAGAATCTCAGGATTACTCTCTAA			MGLAVGQVAREGTFGISENLRITL*	MGLAVGQVAREGTFGISENLRITL*			TATTACCGTA	ATTCACTCTC	0	I	0	MG02999.1	NCU00580.1	0	0
3147	1951	ao	AN0868.1	70.m15459	AO070320000019	0					-177	-145	ATGGAAGTTGAAACAGGTGGAACGCCTCGGTAA			ATGGAAGTTGAAACAGGTGGAACGCCTCGGTAA	MEVETGGTPR*			MEVETGGTPR*	GCACGAAACC	TTACCTGATT	0	I	0	MG02999.1	NCU00580.1	0	0
3150	1953	af	AN4535.1	57.m05586	AO070321000149	0			-211	-188			ATGGTTTGCATCACCTCACTATGA		ATGGTTTGCATCACCTCACTATGA		MVCITSL*		MVCITSL*		TCGTTGCGGA	GTTTCTAGGC	0	R	0	0	0	0	0
3151	1953	af	AN4535.1	57.m05586	AO070321000149	0			-191	-180			ATGAGTTTCTAG		ATGAGTTTCTAG		MSF*		MSF*		TCACCTCACT	GCCAATTTCA	0	R	0	0	0	0	0
3148	1953	an	AN4535.1	57.m05586	AO070321000149	0	-209	-171					ATGTTGGTGGCCGGGGTTTGGCGCCATATCAGCTGCTGA	ATGTTGGTGGCCGGGGTTTGGCGCCATATCAGCTGCTGA			MLVAGVWRHISC*	MLVAGVWRHISC*			GTTTCAATCA	TTGCGGATAT	0	R	0	0	0	0	0
3149	1953	an	AN4535.1	57.m05586	AO070321000149	0	-155	-141					ATGACCACTTTCTGA	ATGACCACTTTCTGA			MTTF*	MTTF*			GATATCGAGG	AGACTGTGTG	0	R	0	0	0	0	0
3152	1953	ao	AN4535.1	57.m05586	AO070321000149	0					-194	-180	ATGACCACGATCTAA			ATGACCACGATCTAA	MTTI*			MTTI*	AACCGTCACT	AACCCAAATC	0	R	0	0	0	0	0
3155	1956	af	AN1586.1	70.m15285	AO070333000174	0			-227	-99			ATGTGGTACTCCCGCATCAACCTACCTCTAAAGGTTCAGCGTATCCTGAGTTCCTTAGATGGTGCTTTTGCGGTGGAATGGTGTGGTTTTGCTCTAACCAGACTGCTAGTTTGTACCCATGGACATTAA		ATGTGGTACTCCCGCATCAACCTACCTCTAAAGGTTCAGCGTATCCTGAGTTCCTTAGATGGTGCTTTTGCGGTGGAATGGTGTGGTTTTGCTCTAACCAGACTGCTAGTTTGTACCCATGGACATTAA		MWYSRINLPLKVQRILSSLDGAFAVEWCGFALTRLLVCTHGH*		MWYSRINLPLKVQRILSSLDGAFAVEWCGFALTRLLVCTHGH*		GTCACCATCA	AAAGCCATGT	0	Q	0	0	0	0	0
3156	1956	af	AN1586.1	70.m15285	AO070333000174	0			-169	-131			ATGGTGCTTTTGCGGTGGAATGGTGTGGTTTTGCTCTAA		ATGGTGCTTTTGCGGTGGAATGGTGTGGTTTTGCTCTAA		MVLLRWNGVVLL*		MVLLRWNGVVLL*		AGTTCCTTAG	CCAGACTGCT	0	Q	0	0	0	0	0

3157	1956	af	AN1586.1	70.m15285	AO070333000174	0			-150	-22			ATGGTGTGGTTTTGCTCTAACCAGACTGCTAGTTTGTACCCATGGACATTAAAAAGCCATGTCTCCCCTCAGTATAGTTCGGTGTTCCAGCTTCGGCTTTCCATCTACGATTGCGTCAATACAGATTGA		ATGGTGTGGTTTTGCTCTAACCAGACTGCTAGTTTGTACCCATGGACATTAAAAAGCCATGTCTCCCCTCAGTATAGTTCGGTGTTCCAGCTTCGGCTTTCCATCTACGATTGCGTCAATACAGATTGA		MVWFCSNQTASLYPWTLKSHVSPQYSSVFQLRLSIYDCVNTD*		MVWFCSNQTASLYPWTLKSHVSPQYSSVFQLRLSIYDCVNTD*		TTGCGGTGGA	TAGACACTTC	0	Q	0	0	0	0	0
3158	1956	af	AN1586.1	70.m15285	AO070333000174	0			-109	-74			ATGGACATTAAAAAGCCATGTCTCCCCTCAGTATAG		ATGGACATTAAAAAGCCATGTCTCCCCTCAGTATAG		MDIKKPCLPSV*		MDIKKPCLPSV*		GTTTGTACCC	TTCGGTGTTC	0	Q	0	0	0	0	0
3153	1956	an	AN1586.1	70.m15285	AO070333000174	0	-277	-260					ATGTTAACTCCCGGCTAG	ATGTTAACTCCCGGCTAG			MLTPG*	MLTPG*			CCTTTAGGGG	CCCTAACCTT	0	Q	0	0	0	0	0
3154	1956	an	AN1586.1	70.m15285	AO070333000174	0	-235	-146					ATGGCTGGCCCGGTTATACTTAACGTTAGCGATCAGGAGGCGCCTTTCGATAACATCCTCGTATCTGCGTGGCCAACAGGCCCGACCTAG	ATGGCTGGCCCGGTTATACTTAACGTTAGCGATCAGGAGGCGCCTTTCGATAACATCCTCGTATCTGCGTGGCCAACAGGCCCGACCTAG			MAGPVILNVSDQEAPFDNILVSAWPTGPT*	MAGPVILNVSDQEAPFDNILVSAWPTGPT*			GTCAGGCCCC	TCGGTCAGCC	0	Q	0	0	0	0	0
3159	1956	ao	AN1586.1	70.m15285	AO070333000174	0					-165	-139	ATGACAAAGAGGTTTCAACCTATTTGA			ATGACAAAGAGGTTTCAACCTATTTGA	MTKRFQPI*			MTKRFQPI*	AGTTGATACG	ACACCTTCGT	0	Q	0	0	0	0	0
3160	1960	an	AN5990.1	72.m19150	AO070340000287	0	-235	-152					ATGGAGGATAGACGATCGTATAGCCGGAGCCTTGGGTGCTGTTTAGTAATCTATCTCTCCAATATTCAGGATTTATTCGCCTAG	ATGGAGGATAGACGATCGTATAGCCGGAGCCTTGGGTGCTGTTTAGTAATCTATCTCTCCAATATTCAGGATTTATTCGCCTAG			MEDRRSYSRSLGCCLVIYLSNIQDLFA*	MEDRRSYSRSLGCCLVIYLSNIQDLFA*			AGCACTGCGG	ACAATCCGTA	0	I	0	0	0	0	0
3166	1961	af	AN3927.1	69.m15001	AO070341000039	0			-250	-164			ATGGCAGAGACTTGTGATAACAACGCCGCGATAATGAAAATCACGCGGGCCAATGACGCCTTGCGGCCTGAGGCGGTGAAGACGTGA		ATGGCAGAGACTTGTGATAACAACGCCGCGATAATGAAAATCACGCGGGCCAATGACGCCTTGCGGCCTGAGGCGGTGAAGACGTGA		MAETCDNNAAIMKITRANDALRPEAVKT*		MAETCDNNAAIMKITRANDALRPEAVKT*		TGAATCTTCA	CTTCATTGTT	0	T	0	0	0	0	0
3167	1961	af	AN3927.1	69.m15001	AO070341000039	0			-217	-164			ATGAAAATCACGCGGGCCAATGACGCCTTGCGGCCTGAGGCGGTGAAGACGTGA		ATGAAAATCACGCGGGCCAATGACGCCTTGCGGCCTGAGGCGGTGAAGACGTGA		MKITRANDALRPEAVKT*		MKITRANDALRPEAVKT*		CGCCGCGATA	CTTCATTGTT	0	T	0	0	0	0	0
3168	1961	af	AN3927.1	69.m15001	AO070341000039	0			-198	-172			ATGACGCCTTGCGGCCTGAGGCGGTGA		ATGACGCCTTGCGGCCTGAGGCGGTGA		MTPCGLRR*		MTPCGLRR*		ACGCGGGCCA	AGACGTGACT	0	T	0	0	0	0	0
3169	1961	af	AN3927.1	69.m15001	AO070341000039	0			-127	-62			ATGTCGACGTTGGCAAGAAGGACGGCGCTCTGCATCTATCTACTGCGTTCAGAATTTCTCCAATAG		ATGTCGACGTTGGCAAGAAGGACGGCGCTCTGCATCTATCTACTGCGTTCAGAATTTCTCCAATAG		MSTLARRTALCIYLLRSEFLQ*		MSTLARRTALCIYLLRSEFLQ*		CATACAAATA	ATCAATCTGA	0	T	0	0	0	0	0
3161	1961	an	AN3927.1	69.m15001	AO070341000039	0	-156	-76					ATGAATTCTGAATGTTGCTGCTTTGATAATGAGAAACCAGCGAAAGATTCCGCGTATGCCATCCTAAACAGAAGGCGGTAA	ATGAATTCTGAATGTTGCTGCTTTGATAATGAGAAACCAGCGAAAGATTCCGCGTATGCCATCCTAAACAGAAGGCGGTAA			MNSECCCFDNEKPAKDSAYAILNRRR*	MNSECCCFDNEKPAKDSAYAILNRRR*			AACCTCTTGA	GAGCTTTACT	0	T	0	0	0	0	0
3162	1961	an	AN3927.1	69.m15001	AO070341000039	0	-145	-131					ATGTTGCTGCTTTGA	ATGTTGCTGCTTTGA			MLLL*	MLLL*			TGAATTCTGA	TAATGAGAAA	0	T	0	0	0	0	0
3163	1961	an	AN3927.1	69.m15001	AO070341000039	0	-128	-90					ATGAGAAACCAGCGAAAGATTCCGCGTATGCCATCCTAA	ATGAGAAACCAGCGAAAGATTCCGCGTATGCCATCCTAA			MRNQRKIPRMPS*	MRNQRKIPRMPS*			TGCTTTGATA	ACAGAAGGCG	0	T	0	0	0	0	0
3164	1961	an	AN3927.1	69.m15001	AO070341000039	0	-101	-90					ATGCCATCCTAA	ATGCCATCCTAA			MPS*	MPS*			GATTCCGCGT	ACAGAAGGCG	0	T	0	0	0	0	0
3171	1961	ao	AN3927.1	69.m15001	AO070341000039	0					-247	-200	ATGAATCTATCGCGAAGATCCAGAAGAATAATAATCCCCAGCCAATGA			ATGAATCTATCGCGAAGATCCAGAAGAATAATAATCCCCAGCCAATGA	MNLSRRSRRIIIPSQ*			MNLSRRSRRIIIPSQ*	ATCGGCCTGA	GGGGTGTCGC	0	T	0	0	0	0	0
3172	1961	ao	AN3927.1	69.m15001	AO070341000039	0					-203	-114	ATGAGGGGTGTCGCTGACAGGGCGGTGAGGGTCCCCGATTGCGCTTGTCGGCGTCATCCAACAAAAGTTATTCGATGTTCAAGCTCATGA			ATGAGGGGTGTCGCTGACAGGGCGGTGAGGGTCCCCGATTGCGCTTGTCGGCGTCATCCAACAAAAGTTATTCGATGTTCAAGCTCATGA	MRGVADRAVRVPDCACRRHPTKVIRCSSS*			MRGVADRAVRVPDCACRRHPTKVIRCSSS*	TCCCCAGCCA	AAGCACTTCG	0	T	0	0	0	0	0
3173	1961	ao	AN3927.1	69.m15001	AO070341000039	0					-129	-67	ATGTTCAAGCTCATGAAAGCACTTCGATTATATCGCTCAGGAACCGAATATGACCTATCTTGA			ATGTTCAAGCTCATGAAAGCACTTCGATTATATCGCTCAGGAACCGAATATGACCTATCTTGA	MFKLMKALRLYRSGTEYDLS*			MFKLMKALRLYRSGTEYDLS*	AAGTTATTCG	CTTGTCTAAA	0	T	0	0	0	0	0
3174	1961	ao	AN3927.1	69.m15001	AO070341000039	0					-117	-67	ATGAAAGCACTTCGATTATATCGCTCAGGAACCGAATATGACCTATCTTGA			ATGAAAGCACTTCGATTATATCGCTCAGGAACCGAATATGACCTATCTTGA	MKALRLYRSGTEYDLS*			MKALRLYRSGTEYDLS*	GTTCAAGCTC	CTTGTCTAAA	0	T	0	0	0	0	0
3175	1961	ao	AN3927.1	69.m15001	AO070341000039	0					-80	-33	ATGACCTATCTTGACTTGTCTAAACTACCTAATTTTAATAATTCATAG			ATGACCTATCTTGACTTGTCTAAACTACCTAATTTTAATAATTCATAG	MTYLDLSKLPNFNNS*			MTYLDLSKLPNFNNS*	GGAACCGAAT	ATATCATTTC	0	T	0	0	0	0	0
3178	1962	af	AN3719.1	69.m15727	AO070341000350	0			-189	-172			ATGCCAAAGTATACTTGA		ATGCCAAAGTATACTTGA		MPKYT*		MPKYT*		ATTGAGTTCA	TAAGCCCTCA	0	T	0	0	0	0	0
3179	1962	af	AN3719.1	69.m15727	AO070341000350	0			-112	-29			ATGATTGATGCACTGTTGTGGGGGGTGACCTTGACTATGATCAGATCTGCAACTCACATTTGCAATCAAAGAGCTCTTGACTAA		ATGATTGATGCACTGTTGTGGGGGGTGACCTTGACTATGATCAGATCTGCAACTCACATTTGCAATCAAAGAGCTCTTGACTAA		MIDALLWGVTLTMIRSATHICNQRALD*		MIDALLWGVTLTMIRSATHICNQRALD*		AATTTGAACA	CCTTCTTTGA	0	T	0	0	0	0	0
3180	1962	af	AN3719.1	69.m15727	AO070341000350	0			-105	-85			ATGCACTGTTGTGGGGGGTGA		ATGCACTGTTGTGGGGGGTGA		MHCCGG*		MHCCGG*		ACAATGATTG	CCTTGACTAT	0	T	0	0	0	0	0
3181	1962	af	AN3719.1	69.m15727	AO070341000350	0			-76	-29			ATGATCAGATCTGCAACTCACATTTGCAATCAAAGAGCTCTTGACTAA		ATGATCAGATCTGCAACTCACATTTGCAATCAAAGAGCTCTTGACTAA		MIRSATHICNQRALD*		MIRSATHICNQRALD*		GACCTTGACT	CCTTCTTTGA	0	T	0	0	0	0	0
3176	1962	an	AN3719.1	69.m15727	AO070341000350	0	-183	-133					ATGCGAGACGTACGCGCGGCCTGCAGTGTGTACCTGCATGAAACACACTAA	ATGCGAGACGTACGCGCGGCCTGCAGTGTGTACCTGCATGAAACACACTAA			MRDVRAACSVYLHETH*	MRDVRAACSVYLHETH*			TTCAAGTATT	GACTGCTGCT	0	T	0	0	0	0	0
3177	1962	an	AN3719.1	69.m15727	AO070341000350	0	-146	-27					ATGAAACACACTAAGACTGCTGCTTGGGTGCCATATCTCTGCACATATCTTATTGCCCCTGTTAAGCTGATTAGCATTCATTACTTGTTAATCTCACATTTTACCTCGCATAAGTGCTGA	ATGAAACACACTAAGACTGCTGCTTGGGTGCCATATCTCTGCACATATCTTATTGCCCCTGTTAAGCTGATTAGCATTCATTACTTGTTAATCTCACATTTTACCTCGCATAAGTGCTGA			MKHTKTAAWVPYLCTYLIAPVKLISIHYLLISHFTSHKC*	MKHTKTAAWVPYLCTYLIAPVKLISIHYLLISHFTSHKC*			GTGTACCTGC	CACCTTTCAG	0	T	0	0	0	0	0
3182	1962	ao	AN3719.1	69.m15727	AO070341000350	0					-216	-169	ATGTTTACTGCTATGTTGTCCGCCGATGATCTATCGGATAGTTTGTGA			ATGTTTACTGCTATGTTGTCCGCCGATGATCTATCGGATAGTTTGTGA	MFTAMLSADDLSDSL*			MFTAMLSADDLSDSL*	TGAACCTGCC	CACAACTACA	0	T	0	0	0	0	0
3183	1962	ao	AN3719.1	69.m15727	AO070341000350	0					-204	-169	ATGTTGTCCGCCGATGATCTATCGGATAGTTTGTGA			ATGTTGTCCGCCGATGATCTATCGGATAGTTTGTGA	MLSADDLSDSL*			MLSADDLSDSL*	GTTTACTGCT	CACAACTACA	0	T	0	0	0	0	0
3184	1962	ao	AN3719.1	69.m15727	AO070341000350	0					-156	-70	ATGCCTTGCCTTGTTGCTGGGAGTCGCGGTCAAGTTGACTGCCTCACTCACGGTAGTCAATGCGGAAGTGAAGCGCAGTGCATTTAG			ATGCCTTGCCTTGTTGCTGGGAGTCGCGGTCAAGTTGACTGCCTCACTCACGGTAGTCAATGCGGAAGTGAAGCGCAGTGCATTTAG	MPCLVAGSRGQVDCLTHGSQCGSEAQCI*			MPCLVAGSRGQVDCLTHGSQCGSEAQCI*	CAACTACACA	CAACCAACCA	0	T	0	0	0	0	0
3185	1962	ao	AN3719.1	69.m15727	AO070341000350	0					-97	-86	ATGCGGAAGTGA			ATGCGGAAGTGA	MRK*			MRK*	ACGGTAGTCA	AGCGCAGTGC	0	T	0	0	0	0	0
3191	1964	af	AN7558.1	72.m19578	AO070343000397	0			-156	-106			ATGCATCCATCAAACTGCGTATCTCCCGCGAGGACGCCAGACATTCCATGA		ATGCATCCATCAAACTGCGTATCTCCCGCGAGGACGCCAGACATTCCATGA		MHPSNCVSPARTPDIP*		MHPSNCVSPARTPDIP*		CACTGACGTC	ATGAAGCAAT	0		0	0	0	0	0
3192	1964	af	AN7558.1	72.m19578	AO070343000397	0			-105	-25			ATGAAGCAATCTATTGTACAATCACAGGAAGACGAAGTCATTGTATTGCCCCTTCTATTGATCTTTTTTTCTTATCGCTAA		ATGAAGCAATCTATTGTACAATCACAGGAAGACGAAGTCATTGTATTGCCCCTTCTATTGATCTTTTTTTCTTATCGCTAA		MKQSIVQSQEDEVIVLPLLLIFFSYR*		MKQSIVQSQEDEVIVLPLLLIFFSYR*		CATTCCATGA	GCTGCGTTTG	0		0	0	0	0	0
3186	1964	an	AN7558.1	72.m19578	AO070343000397	0	-240	-229					ATGAAGCGATAA	ATGAAGCGATAA			MKR*	MKR*			ATCACTTATT	CAACCAGTAT	0		0	0	0	0	0
3187	1964	an	AN7558.1	72.m19578	AO070343000397	0	-220	-158					ATGACTTCATGCCAGAAATCGGGGAAACCCCCAGGCCATGGCGCAGTGATCTTCGGATTCTAG	ATGACTTCATGCCAGAAATCGGGGAAACCCCCAGGCCATGGCGCAGTGATCTTCGGATTCTAG			MTSCQKSGKPPGHGAVIFGF*	MTSCQKSGKPPGHGAVIFGF*			AACAACCAGT	ACTGAGTATC	0		0	0	0	0	0
3188	1964	an	AN7558.1	72.m19578	AO070343000397	0	-212	-153					ATGCCAGAAATCGGGGAAACCCCCAGGCCATGGCGCAGTGATCTTCGGATTCTAGACTGA	ATGCCAGAAATCGGGGAAACCCCCAGGCCATGGCGCAGTGATCTTCGGATTCTAGACTGA			MPEIGETPRPWRSDLRILD*	MPEIGETPRPWRSDLRILD*			GTATGACTTC	GTATCTTGAC	0		0	0	0	0	0
3189	1964	an	AN7558.1	72.m19578	AO070343000397	0	-183	-172					ATGGCGCAGTGA	ATGGCGCAGTGA			MAQ*	MAQ*			CCCCCAGGCC	TCTTCGGATT	0		0	0	0	0	0
3190	1964	an	AN7558.1	72.m19578	AO070343000397	0	-139	-104					ATGCCCTTATCAGCATATAAACCATCAGCAGCATAA	ATGCCCTTATCAGCATATAAACCATCAGCAGCATAA			MPLSAYKPSAA*	MPLSAYKPSAA*			TCTTGACGTC	AACATTGACT	0		0	0	0	0	0
3193	1964	ao	AN7558.1	72.m19578	AO070343000397	0					-144	-112	ATGACGTCACATCCACATCAAGCATCAATATAA			ATGACGTCACATCCACATCAAGCATCAATATAA	MTSHPHQASI*			MTSHPHQASI*	CTATCTACCC	CCACTTCAAC	0		0	0	0	0	0
3199	1965	af	AN9405.1	52.m04032	AO070274000012	0			-196	-74			ATGATAATGCAGAAAAAAAGCAAGCACAGGACATTTGTAGGAGTTCCAACAACCCAAGGACGGACACTCTCCCAATGCTACCTAAGGCTTGATCATGATGATGACGATGCGATGAACTTATGA		ATGATAATGCAGAAAAAAAGCAAGCACAGGACATTTGTAGGAGTTCCAACAACCCAAGGACGGACACTCTCCCAATGCTACCTAAGGCTTGATCATGATGATGACGATGCGATGAACTTATGA		MIMQKKSKHRTFVGVPTTQGRTLSQCYLRLDHDDDDAMNL*		MIMQKKSKHRTFVGVPTTQGRTLSQCYLRLDHDDDDAMNL*		CGACAAGCCA	GTCGTTTAAT	0		0	0	0	0	0
3200	1965	af	AN9405.1	52.m04032	AO070274000012	0			-190	-74			ATGCAGAAAAAAAGCAAGCACAGGACATTTGTAGGAGTTCCAACAACCCAAGGACGGACACTCTCCCAATGCTACCTAAGGCTTGATCATGATGATGACGATGCGATGAACTTATGA		ATGCAGAAAAAAAGCAAGCACAGGACATTTGTAGGAGTTCCAACAACCCAAGGACGGACACTCTCCCAATGCTACCTAAGGCTTGATCATGATGATGACGATGCGATGAACTTATGA		MQKKSKHRTFVGVPTTQGRTLSQCYLRLDHDDDDAMNL*		MQKKSKHRTFVGVPTTQGRTLSQCYLRLDHDDDDAMNL*		GCCAATGATA	GTCGTTTAAT	0		0	0	0	0	0
3201	1965	af	AN9405.1	52.m04032	AO070274000012	0			-122	-105			ATGCTACCTAAGGCTTGA		ATGCTACCTAAGGCTTGA		MLPKA*		MLPKA*		CACTCTCCCA	TCATGATGAT	0		0	0	0	0	0
3194	1965	an	AN9405.1	52.m04032	AO070274000012	0	-261	-244					ATGTTGAATGGGATGTGA	ATGTTGAATGGGATGTGA			MLNGM*	MLNGM*			AGGACCAATA	TGATGATCAA	0		0	0	0	0	0
3195	1965	an	AN9405.1	52.m04032	AO070274000012	0	-254	-123					ATGGGATGTGATGATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAGAAGGAATCGAGAACCAGATCTCCACAGCTCCAAACCTGGATTTGGCGAGTCTCGTCCTCCAACCATAG	ATGGGATGTGATGATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAGAAGGAATCGAGAACCAGATCTCCACAGCTCCAAACCTGGATTTGGCGAGTCTCGTCCTCCAACCATAG			MGCDDDQRGPERLGRANSATVEGIENQISTAPNLDLASLVLQP*	MGCDDDQRGPERLGRANSATVEGIENQISTAPNLDLASLVLQP*			ATAATGTTGA	ACCCATATCC	0		0	0	0	0	0
3196	1965	an	AN9405.1	52.m04032	AO070274000012	0	-244	-191					ATGATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAG	ATGATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAG			MMINGVLKGWGGRTQRQ*	MMINGVLKGWGGRTQRQ*			ATGGGATGTG	AAGGAATCGA	0		0	0	0	0	0
3197	1965	an	AN9405.1	52.m04032	AO070274000012	0	-241	-191					ATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAG	ATGATCAACGGGGTCCTGAAAGGTTGGGGCGGGCGAACTCAGCGACAGTAG			MINGVLKGWGGRTQRQ*	MINGVLKGWGGRTQRQ*			GGATGTGATG	AAGGAATCGA	0		0	0	0	0	0
3207	1965	ao	AN9405.1	52.m04032	AO070274000012	0					-166	-89	ATGAAATACTGTAAGAATATTAAATCCCATTTCATGCCTGGTGATATTGATGAGACCTCCATTGCAATGATTAAATAG			ATGAAATACTGTAAGAATATTAAATCCCATTTCATGCCTGGTGATATTGATGAGACCTCCATTGCAATGATTAAATAG	MKYCKNIKSHFMPGDIDETSIAMIK*			MKYCKNIKSHFMPGDIDETSIAMIK*	AGCATTAGTG	AGGTAAAACA	0		0	0	0	0	0
3208	1965	ao	AN9405.1	52.m04032	AO070274000012	0					-133	-89	ATGCCTGGTGATATTGATGAGACCTCCATTGCAATGATTAAATAG			ATGCCTGGTGATATTGATGAGACCTCCATTGCAATGATTAAATAG	MPGDIDETSIAMIK*			MPGDIDETSIAMIK*	ATCCCATTTC	AGGTAAAACA	0		0	0	0	0	0
3209	1965	ao	AN9405.1	52.m04032	AO070274000012	0					-117	-97	ATGAGACCTCCATTGCAATGA			ATGAGACCTCCATTGCAATGA	MRPPLQ*			MRPPLQ*	GGTGATATTG	TTAAATAGAG	0		0	0	0	0	0
3210	1965	ao	AN9405.1	52.m04032	AO070274000012	0					-100	-89	ATGATTAAATAG			ATGATTAAATAG	MIK*			MIK*	CTCCATTGCA	AGGTAAAACA	0		0	0	0	0	0
3217	1966	af	AN8796.1	71.m15603	AO070276000064	0			-252	-235			ATGACGCCGACGCAATGA		ATGACGCCGACGCAATGA		MTPTQ*		MTPTQ*		CCCAAACGAA	CGGAGGCCTG	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3218	1966	af	AN8796.1	71.m15603	AO070276000064	0			-238	-134			ATGACGGAGGCCTGGCTGTCCCCCCATCTCCATCAGCCGATAATCCGAAGACCCATTTGTCTCGTTCATCCCGTACACAAAGTCCAGTTGCACATATGTATATGA		ATGACGGAGGCCTGGCTGTCCCCCCATCTCCATCAGCCGATAATCCGAAGACCCATTTGTCTCGTTCATCCCGTACACAAAGTCCAGTTGCACATATGTATATGA		MTEAWLSPHLHQPIIRRPICLVHPVHKVQLHICI*		MTEAWLSPHLHQPIIRRPICLVHPVHKVQLHICI*		CGCCGACGCA	GGAGCCTACA	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3211	1966	an	AN8796.1	71.m15603	AO070276000064	0	-219	-199					ATGACGAGGCTGGTCCTGTGA	ATGACGAGGCTGGTCCTGTGA			MTRLVL*	MTRLVL*			GCGCGATGAT	TCCTCCTCCA	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3212	1966	an	AN8796.1	71.m15603	AO070276000064	0	-184	-173					ATGCAAAGCTGA	ATGCAAAGCTGA			MQS*	MQS*			CCTCCAACTT	CCTGCGCTTC	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3221	1966	ao	AN8796.1	71.m15603	AO070276000064	0					-225	-214	ATGCAACGATGA			ATGCAACGATGA	MQR*			MQR*	TCCCCTCATC	GGCTGGTCAA	0	T	FG05865.1	0	NCU01099.1	YML121W	0
3222	1966	ao	AN8796.1	71.m15603	AO070276000064	0					-217	-185	ATGAGGCTGGTCAAGTGCTCATCCATGCACTAG			ATGAGGCTGGTCAAGTGCTCATCCATGCACTAG	MRLVKCSSMH*			MRLVKCSSMH*	TCATGCAACG	ACCAAAGTGC	0	T	FG05865.1	0	NCU01099.1	YML121W	0

3224	1969	af	AN1334.1	70.m14897	AO070303000099	0			-120	-7			ATGCGTATTGTCAACCATTATCATTTTTCCTGGTCGAATCCTTCCTCGGTAGCTCTCCTGGCACCCCCATCTGCCTTTATTCTCCCATTTTTTAGCTATTTTTTTTCACATTGA		ATGCGTATTGTCAACCATTATCATTTTTCCTGGTCGAATCCTTCCTCGGTAGCTCTCCTGGCACCCCCATCTGCCTTTATTCTCCCATTTTTTAGCTATTTTTTTTCACATTGA		MRIVNHYHFSWSNPSSVALLAPPSAFILPFFSYFFSH*		MRIVNHYHFSWSNPSSVALLAPPSAFILPFFSYFFSH*		GATCACGTAC	CCGATCATGT	0	UO	0	MG01006.1	0	0	0
3227	1971	af	AN8217.1	53.m03756	AO070310000095	0			-242	-204			ATGTCTAACCTTAGGTTGCCTAGGTCATATTCGTACTAG		ATGTCTAACCTTAGGTTGCCTAGGTCATATTCGTACTAG		MSNLRLPRSYSY*		MSNLRLPRSYSY*		ATATAATAAG	TGCCACGCTA	0	GMO	0	0	0	0	0
3228	1971	af	AN8217.1	53.m03756	AO070310000095	0			-113	-81			ATGATTGTTCGTGTTGGCCTCCAGCTCTGGTAG		ATGATTGTTCGTGTTGGCCTCCAGCTCTGGTAG		MIVRVGLQLW*		MIVRVGLQLW*		TTATCTGTTC	ATGCAGGTCA	0	GMO	0	0	0	0	0
3229	1971	af	AN8217.1	53.m03756	AO070310000095	0			-80	-27			ATGCAGGTCAGCGCTGAAAGTTCTGTACTTACAATACTTTCAGAGGTTGAGTGA		ATGCAGGTCAGCGCTGAAAGTTCTGTACTTACAATACTTTCAGAGGTTGAGTGA		MQVSAESSVLTILSEVE*		MQVSAESSVLTILSEVE*		GCTCTGGTAG	CTCTGATTGC	0	GMO	0	0	0	0	0
3225	1971	an	AN8217.1	53.m03756	AO070310000095	0	-210	-34					ATGAGGTGTCTCACCCCGGCTTGCTCGAAGAGGACTAGTGCTGGAGCTCTCCGCTCTCCAGAGGCCAGCCTGGAAGCACTGGTTAACAGCACTGGTCAACAGCACTGTGTGGACCTTAACTCTGGTAGATGCAGGTCAGAGCACCTTGTGGCAAGCGTTGATTCACTCGGAGATTGA	ATGAGGTGTCTCACCCCGGCTTGCTCGAAGAGGACTAGTGCTGGAGCTCTCCGCTCTCCAGAGGCCAGCCTGGAAGCACTGGTTAACAGCACTGGTCAACAGCACTGTGTGGACCTTAACTCTGGTAGATGCAGGTCAGAGCACCTTGTGGCAAGCGTTGATTCACTCGGAGATTGA			MRCLTPACSKRTSAGALRSPEASLEALVNSTGQQHCVDLNSGRCRSEHLVASVDSLGD*	MRCLTPACSKRTSAGALRSPEASLEALVNSTGQQHCVDLNSGRCRSEHLVASVDSLGD*			GGTCTGAATT	GTGTCTCTGG	0	GMO	0	0	0	0	0
3226	1971	an	AN8217.1	53.m03756	AO070310000095	0	-82	-50					ATGCAGGTCAGAGCACCTTGTGGCAAGCGTTGA	ATGCAGGTCAGAGCACCTTGTGGCAAGCGTTGA			MQVRAPCGKR*	MQVRAPCGKR*			ACTCTGGTAG	TTCACTCGGA	0	GMO	0	0	0	0	0
3230	1971	ao	AN8217.1	53.m03756	AO070310000095	0					-277	-254	ATGCCTGATTGCCTTACAGCCTGA			ATGCCTGATTGCCTTACAGCCTGA	MPDCLTA*			MPDCLTA*	GGCCAGAGCT	GGTTTTCGAC	0	GMO	0	0	0	0	0
3231	1971	ao	AN8217.1	53.m03756	AO070310000095	0					-80	-63	ATGCAGGCCAGCACATAG			ATGCAGGCCAGCACATAG	MQAST*			MQAST*	GCTCAGGTAG	TGGCCGACAA	0	GMO	0	0	0	0	0
3232	1972	an	AN6900.1	71.m15236	AO070314000015	0	-151	-137					ATGGTTTACCGGTAG	ATGGTTTACCGGTAG			MVYR*	MVYR*			AAGCCCCTCC	TGCACTACTC	0	G	FG06702.1	MG08905.1	NCU07550.1	0	0
3233	1972	ao	AN6900.1	71.m15236	AO070314000015	0					-126	-100	ATGTCATCGCTCTTCCCTGTCGTCTGA			ATGTCATCGCTCTTCCCTGTCGTCTGA	MSSLFPVV*			MSSLFPVV*	TCCACCTTTT	TCTTCTTCTA	0	G	FG06702.1	MG08905.1	NCU07550.1	0	0
3239	1974	ao	AN2335.1	71.m16079	AO070323000004	0					-126	-88	ATGAAAGCAACACCCGATTGGATTGTGCCTCTTTATTAA			ATGAAAGCAACACCCGATTGGATTGTGCCTCTTTATTAA	MKATPDWIVPLY*			MKATPDWIVPLY*	GCCGTCGGCC	CCGCTGGAAG	0	R	FG05284.1	0	0	0	0
3240	1974	ao	AN2335.1	71.m16079	AO070323000004	0					-73	-35	ATGCGATATACGAGTATTCTCACAAAGACCGTTGAATAA			ATGCGATATACGAGTATTCTCACAAAGACCGTTGAATAA	MRYTSILTKTVE*			MRYTSILTKTVE*	TGGAAGTCCC	TTCAGGACTA	0	R	FG05284.1	0	0	0	0
3244	1977	af	AN0262.1	54.m06966	AO070334000096	0			-267	-202			ATGGTATCGACAAGGATATCTACATACAGCATCTGGAAAGATCGCGATTGCATGAACACCTTATAA		ATGGTATCGACAAGGATATCTACATACAGCATCTGGAAAGATCGCGATTGCATGAACACCTTATAA		MVSTRISTYSIWKDRDCMNTL*		MVSTRISTYSIWKDRDCMNTL*		ATAGCAATAG	GTAATGGTAG	0	J	0	0	0	0	0
3245	1977	af	AN0262.1	54.m06966	AO070334000096	0			-216	-202			ATGAACACCTTATAA		ATGAACACCTTATAA		MNTL*		MNTL*		TCGCGATTGC	GTAATGGTAG	0	J	0	0	0	0	0
3246	1977	af	AN0262.1	54.m06966	AO070334000096	0			-198	-181			ATGGTAGAAGTCATGTGA		ATGGTAGAAGTCATGTGA		MVEVM*		MVEVM*		CTTATAAGTA	TTACGGTGGG	0	J	0	0	0	0	0
3247	1977	af	AN0262.1	54.m06966	AO070334000096	0			-107	-90			ATGTCCTCAACTTCTTAA		ATGTCCTCAACTTCTTAA		MSSTS*		MSSTS*		CCAAGCTAAA	GGAAATTTTG	0	J	0	0	0	0	0
3241	1977	an	AN0262.1	54.m06966	AO070334000096	0	-260	-249					ATGAACAACTAA	ATGAACAACTAA			MNN*	MNN*			ATACAAATCC	ATTCATGACG	0	J	0	0	0	0	0
3242	1977	an	AN0262.1	54.m06966	AO070334000096	0	-244	-200					ATGACGGCTTTCAAGCTTTTAATTGTCGTTGTTGCTCCTATGTGA	ATGACGGCTTTCAAGCTTTTAATTGTCGTTGTTGCTCCTATGTGA			MTAFKLLIVVVAPM*	MTAFKLLIVVVAPM*			AACTAAATTC	TAAACCTGTA	0	J	0	0	0	0	0
3243	1977	an	AN0262.1	54.m06966	AO070334000096	0	-172	-161					ATGTTCGGTTGA	ATGTTCGGTTGA			MFG*	MFG*			GTATCACGTG	GCCCTACTAG	0	J	0	0	0	0	0
3248	1977	ao	AN0262.1	54.m06966	AO070334000096	0					-210	-193	ATGGTATGGAGCTCATGA			ATGGTATGGAGCTCATGA	MVWSS*			MVWSS*	CTCTGGAACT	TATGCATCAC	0	J	0	0	0	0	0
3249	1977	ao	AN0262.1	54.m06966	AO070334000096	0					-205	-179	ATGGAGCTCATGATATGCATCACGTGA			ATGGAGCTCATGATATGCATCACGTGA	MELMICIT*			MELMICIT*	GAACTATGGT	CACTGGGCGG	0	J	0	0	0	0	0
3250	1977	ao	AN0262.1	54.m06966	AO070334000096	0					-196	-179	ATGATATGCATCACGTGA			ATGATATGCATCACGTGA	MICIT*			MICIT*	TATGGAGCTC	CACTGGGCGG	0	J	0	0	0	0	0
3251	1977	ao	AN0262.1	54.m06966	AO070334000096	0					-191	-144	ATGCATCACGTGACACTGGGCGGGTTGAGCCCTGGGCACTTTACCTGA			ATGCATCACGTGACACTGGGCGGGTTGAGCCCTGGGCACTTTACCTGA	MHHVTLGGLSPGHFT*			MHHVTLGGLSPGHFT*	AGCTCATGAT	TTGGGCGTCT	0	J	0	0	0	0	0
3252	1979	conserved	AN2736.1	54.m07003	AO070338000218	0	-58	-5	-61	-5	-94	-41	ATGskydmbwrwysmmmmyrCAGmATGwrCCyTGsGTbwAhhmysvmkrrswrmTAA	ATGCGTTCCAGTCGAACCTGCAGCATGAGCCTTGCGTCAATTCCCGAGAACTAA	ATGGTCACTTGTCGCAACTGCAGCATGTGCCCTGCGTTTACCACCCCTGAGAGCTAA	ATGGTTGAGAAATCCCAACACAGAATGTACCTTGGGTGTAAACTGAAGAGCTAA	MrssrtcsMslasipen*	MRSSRTCSMSLASIPEN*	MVTCRNCSMCPAFTTPES*	MVEKSQHRMYLGCKLKS*	vAryyGryrs	TGGAATGyCy	0	U	0	MG01331.1	NCU03024.1	0	0
3253	1979	conserved	AN2736.1	54.m07003	AO070338000218	0	-34	-5	-37	-5	-70	-41	ATGwrCCyTGsGTbwAhhmysvmkrrswrmTAA	ATGAGCCTTGCGTCAATTCCCGAGAACTAA	ATGTGCCCTGCGTTTACCACCCCTGAGAGCTAA	ATGTACCTTGGGTGTAAACTGAAGAGCTAA	Mslasipen*	MSLASIPEN*	MCPAFTTPES*	MYLGCKLKS*	mmmmyrCAGm	TGGAATGyCy	0	U	0	MG01331.1	NCU03024.1	0	0
3277	1986	af	AN5830.1	72.m18958	AO070260000016	0			-155	-93			ATGACGCCTTTGCGGGGTTCATGTCTTCTCTCTCAAATCAACAAGAAATATCAACCATGTTGA		ATGACGCCTTTGCGGGGTTCATGTCTTCTCTCTCAAATCAACAAGAAATATCAACCATGTTGA		MTPLRGSCLLSQINKKYQPC*		MTPLRGSCLLSQINKKYQPC*		GTAGGGCAAG	TCTTTCATAA	0	R	0	0	NCU03617.1	0	0
3278	1986	af	AN5830.1	72.m18958	AO070260000016	0			-135	-19			ATGTCTTCTCTCTCAAATCAACAAGAAATATCAACCATGTTGATCTTTCATAATATTTCCATACCGTATGGGATTCGATTGTCCCTGAATAACTGCCATAACCATCGAAATTCATGA		ATGTCTTCTCTCTCAAATCAACAAGAAATATCAACCATGTTGATCTTTCATAATATTTCCATACCGTATGGGATTCGATTGTCCCTGAATAACTGCCATAACCATCGAAATTCATGA		MSSLSNQQEISTMLIFHNISIPYGIRLSLNNCHNHRNS*		MSSLSNQQEISTMLIFHNISIPYGIRLSLNNCHNHRNS*		TGCGGGGTTC	ACTACCAAGT	0	R	0	0	NCU03617.1	0	0
3279	1986	af	AN5830.1	72.m18958	AO070260000016	0			-99	-19			ATGTTGATCTTTCATAATATTTCCATACCGTATGGGATTCGATTGTCCCTGAATAACTGCCATAACCATCGAAATTCATGA		ATGTTGATCTTTCATAATATTTCCATACCGTATGGGATTCGATTGTCCCTGAATAACTGCCATAACCATCGAAATTCATGA		MLIFHNISIPYGIRLSLNNCHNHRNS*		MLIFHNISIPYGIRLSLNNCHNHRNS*		AATATCAACC	ACTACCAAGT	0	R	0	0	NCU03617.1	0	0
3280	1986	af	AN5830.1	72.m18958	AO070260000016	0			-68	-48			ATGGGATTCGATTGTCCCTGA		ATGGGATTCGATTGTCCCTGA		MGFDCP*		MGFDCP*		TCCATACCGT	ATAACTGCCA	0	R	0	0	NCU03617.1	0	0
3273	1986	an	AN5830.1	72.m18958	AO070260000016	0	-189	-133					ATGAGCCGGACTCCTATTCGCAACCAGACCCGTCAGAACCGTTCCCCGCATGACTAA	ATGAGCCGGACTCCTATTCGCAACCAGACCCGTCAGAACCGTTCCCCGCATGACTAA			MSRTPIRNQTRQNRSPHD*	MSRTPIRNQTRQNRSPHD*			GTACTCCGAA	GCCCGCGATG	0	R	0	0	NCU03617.1	0	0
3274	1986	an	AN5830.1	72.m18958	AO070260000016	0	-140	-111					ATGACTAAGCCCGCGATGGCGTTAAGATAA	ATGACTAAGCCCGCGATGGCGTTAAGATAA			MTKPAMALR*	MTKPAMALR*			CGTTCCCCGC	CAGACTCCTC	0	R	0	0	NCU03617.1	0	0
3275	1986	an	AN5830.1	72.m18958	AO070260000016	0	-125	-111					ATGGCGTTAAGATAA	ATGGCGTTAAGATAA			MALR*	MALR*			TAAGCCCGCG	CAGACTCCTC	0	R	0	0	NCU03617.1	0	0
3276	1986	an	AN5830.1	72.m18958	AO070260000016	0	-66	-43					ATGTTTATTGAAGTACCACGGTGA	ATGTTTATTGAAGTACCACGGTGA			MFIEVPR*	MFIEVPR*			TTGATATCTT	ACTAAGATTT	0	R	0	0	NCU03617.1	0	0
3281	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-225	-211	ATGGTGTTCTCATGA			ATGGTGTTCTCATGA	MVFS*			MVFS*	AGTTGAAGTC	TCCTGACTAA	0	R	0	0	NCU03617.1	0	0
3282	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-214	-161	ATGATCCTGACTAAGCAACGACGAGTCGTTGGAAGGGCGAGGGCGATGACGTGA			ATGATCCTGACTAAGCAACGACGAGTCGTTGGAAGGGCGAGGGCGATGACGTGA	MILTKQRRVVGRARAMT*			MILTKQRRVVGRARAMT*	TGGTGTTCTC	ACATTAACAG	0	R	0	0	NCU03617.1	0	0
3283	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-141	-49	ATGATGGTATGTATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG			ATGATGGTATGTATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG	MMVCMYIYVHNYYPCIPDLTLPLNNLASMP*			MMVCMYIYVHNYYPCIPDLTLPLNNLASMP*	GTGAACCCGC	AATTAGGTCA	0	R	0	0	NCU03617.1	0	0
3284	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-138	-49	ATGGTATGTATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG			ATGGTATGTATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG	MVCMYIYVHNYYPCIPDLTLPLNNLASMP*			MVCMYIYVHNYYPCIPDLTLPLNNLASMP*	AACCCGCATG	AATTAGGTCA	0	R	0	0	NCU03617.1	0	0
3285	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-133	-110	ATGTATGTACATATATGTACATAA			ATGTATGTACATATATGTACATAA	MYVHICT*			MYVHICT*	GCATGATGGT	TTACTACCCT	0	R	0	0	NCU03617.1	0	0
3286	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-129	-49	ATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG			ATGTACATATATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAGCGTCAATGCCCTAG	MYIYVHNYYPCIPDLTLPLNNLASMP*			MYIYVHNYYPCIPDLTLPLNNLASMP*	GATGGTATGT	AATTAGGTCA	0	R	0	0	NCU03617.1	0	0
3287	1986	ao	AN5830.1	72.m18958	AO070260000016	0					-119	-63	ATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAG			ATGTACATAATTACTACCCTTGCATTCCAGACCTTACACTCCCTCTCAATAACTTAG	MYIITTLAFQTLHSLSIT*			MYIITTLAFQTLHSLSIT*	ATGTACATAT	CGTCAATGCC	0	R	0	0	NCU03617.1	0	0
3288	1988	an	AN7348.1	72.m19729	AO070278000051	0	-151	-137					ATGTTCTCGAAGTGA	ATGTTCTCGAAGTGA			MFSK*	MFSK*			ACTCTTCGGG	CGTCGAGTAC	0	S	0	MG05262.1	0	0	0
3289	1988	ao	AN7348.1	72.m19729	AO070278000051	0					-189	-136	ATGCTTCGGAGGTGCTCCCCCACCGTGAAAGAAAAAATAAAAATCCTTGAATGA			ATGCTTCGGAGGTGCTCCCCCACCGTGAAAGAAAAAATAAAAATCCTTGAATGA	MLRRCSPTVKEKIKILE*			MLRRCSPTVKEKIKILE*	TGAAGATTGA	ACACCGAATT	0	S	0	MG05262.1	0	0	0
3290	1988	ao	AN7348.1	72.m19729	AO070278000051	0					-139	-89	ATGAACACCGAATTTGACGGCCTTCTCGATCATATCCCGCGGATTTACTAA			ATGAACACCGAATTTGACGGCCTTCTCGATCATATCCCGCGGATTTACTAA	MNTEFDGLLDHIPRIY*			MNTEFDGLLDHIPRIY*	AAATCCTTGA	CGGCCTCCCA	0	S	0	MG05262.1	0	0	0
3292	1989	af	AN8928.1	53.m03878	AO070281000035	0			-234	-67			ATGTCCGTTGGAACTGCCGGAAGGATAGCTTCCGGACGAAGAGAGGCGAACGGCCGTGAAAATTATAATAATAATAAAAGTCAACTACACCCACCGCTCAAGGGTCCGGGCAGACTGATATTCGCCAAGGAATTGAAACAGATATACCGGCTAGTTGATCTGTTCTGA		ATGTCCGTTGGAACTGCCGGAAGGATAGCTTCCGGACGAAGAGAGGCGAACGGCCGTGAAAATTATAATAATAATAAAAGTCAACTACACCCACCGCTCAAGGGTCCGGGCAGACTGATATTCGCCAAGGAATTGAAACAGATATACCGGCTAGTTGATCTGTTCTGA		MSVGTAGRIASGRREANGRENYNNNKSQLHPPLKGPGRLIFAKELKQIYRLVDLF*		MSVGTAGRIASGRREANGRENYNNNKSQLHPPLKGPGRLIFAKELKQIYRLVDLF*		AAAGGTGAAA	TTGCAACAAA	0	Q	0	0	0	0	0
3291	1989	an	AN8928.1	53.m03878	AO070281000035	0	-89	-57					ATGAGTATAACTGTCTATTATCTGGCCCTGTAG	ATGAGTATAACTGTCTATTATCTGGCCCTGTAG			MSITVYYLAL*	MSITVYYLAL*			GTAAAGAACC	CTTGCTCAGA	0	Q	0	0	0	0	0
3293	1989	ao	AN8928.1	53.m03878	AO070281000035	0					-289	-227	ATGGAGGTTTTTGCTCCCGAGCACTACCCTATTGTGGGGGGCCTCAAAACTATGAAACCGTAA			ATGGAGGTTTTTGCTCCCGAGCACTACCCTATTGTGGGGGGCCTCAAAACTATGAAACCGTAA	MEVFAPEHYPIVGGLKTMKP*			MEVFAPEHYPIVGGLKTMKP*	CTACTCGGGT	ATAATGAATA	0	Q	0	0	0	0	0
3294	1989	ao	AN8928.1	53.m03878	AO070281000035	0					-238	-227	ATGAAACCGTAA			ATGAAACCGTAA	MKP*			MKP*	CCTCAAAACT	ATAATGAATA	0	Q	0	0	0	0	0
3295	1991	af	AN1990.1	58.m07598	AO070301000078	0			-185	-147			ATGACTCTTACCTCTTGGTACTACACATATAAACCCTGA		ATGACTCTTACCTCTTGGTACTACACATATAAACCCTGA		MTLTSWYYTYKP*		MTLTSWYYTYKP*		TCTTCCAGTT	AATTCTTTGA	0	E	0	0	0	0	0
3296	1991	ao	AN1990.1	58.m07598	AO070301000078	0					-257	-228	ATGGACTCCACCCACTTTTCCTGTCTATGA			ATGGACTCCACCCACTTTTCCTGTCTATGA	MDSTHFSCL*			MDSTHFSCL*	CGCCTTTTAA	CTCTTTTCCT	0	E	0	0	0	0	0
3297	1991	ao	AN1990.1	58.m07598	AO070301000078	0					-231	-175	ATGACTCTTTTCCTGCTTTCCTTTTTTTACCTCCCGGGTATTCATATAAACATTTGA			ATGACTCTTTTCCTGCTTTCCTTTTTTTACCTCCCGGGTATTCATATAAACATTTGA	MTLFLLSFFYLPGIHINI*			MTLFLLSFFYLPGIHINI*	TTTCCTGTCT	TCGTTTAGCC	0	E	0	0	0	0	0
3300	1993	af	AN3916.1	69.m15661	AO070324000103	0			-230	-207			ATGCCAGACGGAAAAAATTGTGTGA		ATGCCAGACGGAAAAAATTGTGTGA		MPDGKIV*		MPDGKIV*		CGCAGATCAA	CCAGAGAAAT	0	G	0	0	0	0	0
3301	1993	af	AN3916.1	69.m15661	AO070324000103	0			-198	-160			ATGGCGTGGGATAGCTTGCTCGAGGATTATTTAAGATAG		ATGGCGTGGGATAGCTTGCTCGAGGATTATTTAAGATAG		MAWDSLLEDYLR*		MAWDSLLEDYLR*		GACCAGAGAA	AATGGGTGCT	0	G	0	0	0	0	0
3302	1993	af	AN3916.1	69.m15661	AO070324000103	0			-111	-19			ATGTCTCCCCAGTGTCTCTGTGGGGTTCACCATCCACTTTGCTGTCTATCCCAAAGCCTTCCCACGGAGTTCACTGTTGTTCCAGAGTCCTGA		ATGTCTCCCCAGTGTCTCTGTGGGGTTCACCATCCACTTTGCTGTCTATCCCAAAGCCTTCCCACGGAGTTCACTGTTGTTCCAGAGTCCTGA		MSPQCLCGVHHPLCCLSQSLPTEFTVVPES*		MSPQCLCGVHHPLCCLSQSLPTEFTVVPES*		TCTTTTTCGA	ACATAAGACC	0	G	0	0	0	0	0
3298	1993	an	AN3916.1	69.m15661	AO070324000103	0	-247	-62					ATGGCGAGACGGAAAAAATTGTGAAACCACTCGTCGTACTCATGCTTTGTCAAAGAAGTATTTAAACAAAGCTGGAGACGCACTTACTCCCTCCGGTATCTCATCCAGAGGAGTGCAATTTCACCTCTTACGCATCCTCACTTTTTCTCCCCCTTCTGCCTGTTTACCTCAACCAGTCGGCAGGTGA	ATGGCGAGACGGAAAAAATTGTGAAACCACTCGTCGTACTCATGCTTTGTCAAAGAAGTATTTAAACAAAGCTGGAGACGCACTTACTCCCTCCGGTATCTCATCCAGAGGAGTGCAATTTCACCTCTTACGCATCCTCACTTTTTCTCCCCCTTCTGCCTGTTTACCTCAACCAGTCGGCAGGTGA			MARRKNCETTRRTHALSKKYLNKAGDALTPSGISSRGVQFHLLRILTFSPPSACLPQPVGR*	MARRKNCETTRRTHALSKKYLNKAGDALTPSGISSRGVQFHLLRILTFSPPSACLPQPVGR*			CAGATATTGG	AATCAGAATA	0	G	0	0	0	0	0
3299	1993	an	AN3916.1	69.m15661	AO070324000103	0	-207	-184					ATGCTTTGTCAAAGAAGTATTTAA	ATGCTTTGTCAAAGAAGTATTTAA			MLCQRSI*	MLCQRSI*			CGTCGTACTC	ACAAAGCTGG	0	G	0	0	0	0	0
3304	1997	af	AN3084.1	59.m08663	AO070334000122	0			-116	-99			ATGACAATTTGCAAATGA		ATGACAATTTGCAAATGA		MTICK*		MTICK*		AGGCAGAAAG	CCTGAGATTC	0	R	0	0	0	0	0

3303	1997	an	AN3084.1	59.m08663	AO070334000122	0	-213	-115					ATGCTGCCTAAATCCACGCGCTTCTCTGGACCAGAACCATCGATTCGGGACAACAGGGAAGCTGGGGCATTACATCTATCTCAACTGGCCCGTCTTTAG	ATGCTGCCTAAATCCACGCGCTTCTCTGGACCAGAACCATCGATTCGGGACAACAGGGAAGCTGGGGCATTACATCTATCTCAACTGGCCCGTCTTTAG			MLPKSTRFSGPEPSIRDNREAGALHLSQLARL*	MLPKSTRFSGPEPSIRDNREAGALHLSQLARL*			CTGTGCTGTC	TGCCTGCTCA	0	R	0	0	0	0	0
3306	1999	af	AN2748.1	54.m06683	AO070338000223	0			-266	-204			ATGAAGATTTCGATATCGCGACCCTCCAAAATAGCGGCGGAAAAAGTTCCTTGGCCCCATTAA		ATGAAGATTTCGATATCGCGACCCTCCAAAATAGCGGCGGAAAAAGTTCCTTGGCCCCATTAA		MKISISRPSKIAAEKVPWPH*		MKISISRPSKIAAEKVPWPH*		CTTGGTGAAG	CACTAAGCCT	0	R	0	0	0	YPR186C	0
3307	1999	af	AN2748.1	54.m06683	AO070338000223	0			-139	-98			ATGATACATTTTTCAACAGTTAATGTGTGCTTGATACGTTGA		ATGATACATTTTTCAACAGTTAATGTGTGCTTGATACGTTGA		MIHFSTVNVCLIR*		MIHFSTVNVCLIR*		AAAATTTTGT	CCGTTATCCA	0	R	0	0	0	YPR186C	0
3308	1999	af	AN2748.1	54.m06683	AO070338000223	0			-117	-106			ATGTGTGCTTGA		ATGTGTGCTTGA		MCA*		MCA*		TCAACAGTTA	TACGTTGACC	0	R	0	0	0	YPR186C	0
3309	1999	af	AN2748.1	54.m06683	AO070338000223	0			-83	-57			ATGCTCTTAATGGTCGTCTTCCCGTGA		ATGCTCTTAATGGTCGTCTTCCCGTGA		MLLMVVFP*		MLLMVVFP*		TATCCAGTCA	AGCCTAATAT	0	R	0	0	0	YPR186C	0
3310	1999	af	AN2748.1	54.m06683	AO070338000223	0			-74	-57			ATGGTCGTCTTCCCGTGA		ATGGTCGTCTTCCCGTGA		MVVFP*		MVVFP*		AATGCTCTTA	AGCCTAATAT	0	R	0	0	0	YPR186C	0
3305	1999	an	AN2748.1	54.m06683	AO070338000223	0	-168	-142					ATGCCGCTAGCCCATTTTGGTATGTAA	ATGCCGCTAGCCCATTTTGGTATGTAA			MPLAHFGM*	MPLAHFGM*			AAAGTTCCTG	CACTCACCGC	0	R	0	0	0	YPR186C	0
3311	1999	ao	AN2748.1	54.m06683	AO070338000223	0					-249	-202	ATGTTGCGACGGAGCTTCCGAGTGAAGAATTCGATATCGCGACTCTAG			ATGTTGCGACGGAGCTTCCGAGTGAAGAATTCGATATCGCGACTCTAG	MLRRSFRVKNSISRL*			MLRRSFRVKNSISRL*	GAAGCGATTG	AAGGCGGCGG	0	R	0	0	0	YPR186C	0
3316	2003	af	AN2161.1	72.m19680	AO070343000216	0			-265	-119			ATGACAAATGGAAACAACATCCATGGGAATGTAGGACAATGGCTGCTCATTATATCACCCCCAGACCGGCCCGGTGCGGAGATTCCGCCCTCCTTGGCATTGTCTTCCAAACTATTTATGGTGTCTGGTCGTCTATCTTATCAGTAA		ATGACAAATGGAAACAACATCCATGGGAATGTAGGACAATGGCTGCTCATTATATCACCCCCAGACCGGCCCGGTGCGGAGATTCCGCCCTCCTTGGCATTGTCTTCCAAACTATTTATGGTGTCTGGTCGTCTATCTTATCAGTAA		MTNGNNIHGNVGQWLLIISPPDRPGAEIPPSLALSSKLFMVSGRLSYQ*		MTNGNNIHGNVGQWLLIISPPDRPGAEIPPSLALSSKLFMVSGRLSYQ*		ATCGGAAATC	CTAGTGCATC	0		0	MG10359.1	0	0	0
3317	2003	af	AN2161.1	72.m19680	AO070343000216	0			-258	-232			ATGGAAACAACATCCATGGGAATGTAG		ATGGAAACAACATCCATGGGAATGTAG		METTSMGM*		METTSMGM*		ATCATGACAA	GACAATGGCT	0		0	MG10359.1	0	0	0
3318	2003	af	AN2161.1	72.m19680	AO070343000216	0			-243	-232			ATGGGAATGTAG		ATGGGAATGTAG		MGM*		MGM*		AACAACATCC	GACAATGGCT	0		0	MG10359.1	0	0	0
3319	2003	af	AN2161.1	72.m19680	AO070343000216	0			-227	-90			ATGGCTGCTCATTATATCACCCCCAGACCGGCCCGGTGCGGAGATTCCGCCCTCCTTGGCATTGTCTTCCAAACTATTTATGGTGTCTGGTCGTCTATCTTATCAGTAACTAGTGCATCGCCTTATGATACGGACTGA		ATGGCTGCTCATTATATCACCCCCAGACCGGCCCGGTGCGGAGATTCCGCCCTCCTTGGCATTGTCTTCCAAACTATTTATGGTGTCTGGTCGTCTATCTTATCAGTAACTAGTGCATCGCCTTATGATACGGACTGA		MAAHYITPRPARCGDSALLGIVFQTIYGVWSSILSVTSASPYDTD*		MAAHYITPRPARCGDSALLGIVFQTIYGVWSSILSVTSASPYDTD*		ATGTAGGACA	ATGAGTCATT	0		0	MG10359.1	0	0	0
3320	2003	af	AN2161.1	72.m19680	AO070343000216	0			-148	-119			ATGGTGTCTGGTCGTCTATCTTATCAGTAA		ATGGTGTCTGGTCGTCTATCTTATCAGTAA		MVSGRLSYQ*		MVSGRLSYQ*		CAAACTATTT	CTAGTGCATC	0		0	MG10359.1	0	0	0
3321	2003	af	AN2161.1	72.m19680	AO070343000216	0			-103	-86			ATGATACGGACTGAATGA		ATGATACGGACTGAATGA		MIRTE*		MIRTE*		GCATCGCCTT	GTCATTATCT	0		0	MG10359.1	0	0	0
3322	2003	af	AN2161.1	72.m19680	AO070343000216	0			-89	-72			ATGAGTCATTATCTATAG		ATGAGTCATTATCTATAG		MSHYL*		MSHYL*		TACGGACTGA	AACTGATAGT	0		0	MG10359.1	0	0	0
3313	2003	an	AN2161.1	72.m19680	AO070343000216	0	-215	-24					ATGATGGGCAAGCTCCATTGTTTCTTCTTACACCGTACAGTTCGCCCACAAATATCAATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA	ATGATGGGCAAGCTCCATTGTTTCTTCTTACACCGTACAGTTCGCCCACAAATATCAATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA			MMGKLHCFFLHRTVRPQISMAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*	MMGKLHCFFLHRTVRPQISMAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*			TACTCCAAGA	GACACAACAG	0		0	MG10359.1	0	0	0
3314	2003	an	AN2161.1	72.m19680	AO070343000216	0	-212	-24					ATGGGCAAGCTCCATTGTTTCTTCTTACACCGTACAGTTCGCCCACAAATATCAATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA	ATGGGCAAGCTCCATTGTTTCTTCTTACACCGTACAGTTCGCCCACAAATATCAATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA			MGKLHCFFLHRTVRPQISMAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*	MGKLHCFFLHRTVRPQISMAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*			TCCAAGAATG	GACACAACAG	0		0	MG10359.1	0	0	0
3315	2003	an	AN2161.1	72.m19680	AO070343000216	0	-158	-24					ATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA	ATGGCTTGGGCCCCACGGTACTGTAGCACAACTCTTCCGGTTGCTATTGACAAACAACACTATAACAACACTATCATTCCCCTTAAATCTCTTCGTTATCTTTGCCGCCGGCCTCCGCACGGAAAAGTCTGGTGA			MAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*	MAWAPRYCSTTLPVAIDKQHYNNTIIPLKSLRYLCRRPPHGKVW*			ACAAATATCA	GACACAACAG	0		0	MG10359.1	0	0	0
3324	2005	af	AN6512.1	62.m03099	AO070270000007	0			-217	-173			ATGACTTCACATGACATACATTGGAGTGAGGGCACCATAGATTAG		ATGACTTCACATGACATACATTGGAGTGAGGGCACCATAGATTAG		MTSHDIHWSEGTID*		MTSHDIHWSEGTID*		GAGTAGTCAC	CGGCAATCGA	0	RK	FG07165.1	0	0	YFL028C	0
3325	2005	af	AN6512.1	62.m03099	AO070270000007	0			-207	-178			ATGACATACATTGGAGTGAGGGCACCATAG		ATGACATACATTGGAGTGAGGGCACCATAG		MTYIGVRAP*		MTYIGVRAP*		ATGACTTCAC	ATTAGCGGCA	0	RK	FG07165.1	0	0	YFL028C	0
3326	2005	af	AN6512.1	62.m03099	AO070270000007	0			-90	-58			ATGAACCCCTTGCCATTTAGAAGTAGTAAGTGA		ATGAACCCCTTGCCATTTAGAAGTAGTAAGTGA		MNPLPFRSSK*		MNPLPFRSSK*		AAATAGTCTT	TTTTCACACT	0	RK	FG07165.1	0	0	YFL028C	0
3332	2007	af	AN7483.1	57.m05865	AO070287000044	0			-137	-99			ATGCCTAGATCCGAGACGACGAGGAGAGTGGGTATCTAA		ATGCCTAGATCCGAGACGACGAGGAGAGTGGGTATCTAA		MPRSETTRRVGI*		MPRSETTRRVGI*		GGAGAAAGTC	TTCTTGCGCA	0		0	0	0	0	0
3333	2007	af	AN7483.1	57.m05865	AO070287000044	0			-89	-78			ATGTCCCATTGA		ATGTCCCATTGA		MSH*		MSH*		ATTCTTGCGC	TGCTAGGGCA	0		0	0	0	0	0
3334	2007	af	AN7483.1	57.m05865	AO070287000044	0			-78	-16			ATGCTAGGGCAGCTGATACGGACCATTCGAGGAATGTGTCGGCAAATCACTTCCAGCAGCTGA		ATGCTAGGGCAGCTGATACGGACCATTCGAGGAATGTGTCGGCAAATCACTTCCAGCAGCTGA		MLGQLIRTIRGMCRQITSSS*		MLGQLIRTIRGMCRQITSSS*		TGTCCCATTG	TGACGATTCT	0		0	0	0	0	0
3327	2007	an	AN7483.1	57.m05865	AO070287000044	0	-280	-212					ATGGCAACTCTACGAATGTACACACGGGCGCCAGTGCCCGCCGTTTCTGGGGCTATCTGGCTGACATAA	ATGGCAACTCTACGAATGTACACACGGGCGCCAGTGCCCGCCGTTTCTGGGGCTATCTGGCTGACATAA			MATLRMYTRAPVPAVSGAIWLT*	MATLRMYTRAPVPAVSGAIWLT*			TAGGTCTTTA	TCCAAGTCGT	0		0	0	0	0	0
3328	2007	an	AN7483.1	57.m05865	AO070287000044	0	-265	-212					ATGTACACACGGGCGCCAGTGCCCGCCGTTTCTGGGGCTATCTGGCTGACATAA	ATGTACACACGGGCGCCAGTGCCCGCCGTTTCTGGGGCTATCTGGCTGACATAA			MYTRAPVPAVSGAIWLT*	MYTRAPVPAVSGAIWLT*			AACTCTACGA	TCCAAGTCGT	0		0	0	0	0	0
3329	2007	an	AN7483.1	57.m05865	AO070287000044	0	-154	-80					ATGTTGGCAGTCTTATCTCAAACTTTGTTGCTTGGATTTGACTACTTAAAGCACATATTGTTATCTGTGCAATGA	ATGTTGGCAGTCTTATCTCAAACTTTGTTGCTTGGATTTGACTACTTAAAGCACATATTGTTATCTGTGCAATGA			MLAVLSQTLLLGFDYLKHILLSVQ*	MLAVLSQTLLLGFDYLKHILLSVQ*			TTGCGTGTTA	CTTGCCATGC	0		0	0	0	0	0
3336	2007	ao	AN7483.1	57.m05865	AO070287000044	0					-100	-38	ATGCCTGGCGATGGAAGCGTGATTCTGTTCTTGTTCGGACTAACCACCTCAGATATGGGCTAG			ATGCCTGGCGATGGAAGCGTGATTCTGTTCTTGTTCGGACTAACCACCTCAGATATGGGCTAG	MPGDGSVILFLFGLTTSDMG*			MPGDGSVILFLFGLTTSDMG*	CTTTTCTTTG	GCGGATGTTT	0		0	0	0	0	0
3337	2007	ao	AN7483.1	57.m05865	AO070287000044	0					-90	-79	ATGGAAGCGTGA			ATGGAAGCGTGA	MEA*			MEA*	ATGCCTGGCG	TTCTGTTCTT	0		0	0	0	0	0
3339	2011	an	AN4465.1	58.m07850	AO070305000119	0	-233	-210					ATGAGATACTGTAGCTACTATTAG	ATGAGATACTGTAGCTACTATTAG			MRYCSYY*	MRYCSYY*			AGCAAACCTT	ACGTTGAGTC	0	T	0	0	0	0	0
3341	2012	af	AN8185.1	53.m03793	AO070310000139	0			-144	-67			ATGGTTTGCCTCCGAACTTGGGTTCTTCTTCGAGTTTTAACGACCAGTCACGACGGCGACGACTACAACAGTCTGTGA		ATGGTTTGCCTCCGAACTTGGGTTCTTCTTCGAGTTTTAACGACCAGTCACGACGGCGACGACTACAACAGTCTGTGA		MVCLRTWVLLRVLTTSHDGDDYNSL*		MVCLRTWVLLRVLTTSHDGDDYNSL*		CATTCAGTGA	CGCTGCCGCA	0	LD	0	0	0	0	0
3340	2012	an	AN8185.1	53.m03793	AO070310000139	0	-175	-116					ATGATCATATCCCGTGGTCCTTATATCTCAACGAATAGTTTGCGCTTGAAGCTAGCTTAG	ATGATCATATCCCGTGGTCCTTATATCTCAACGAATAGTTTGCGCTTGAAGCTAGCTTAG			MIISRGPYISTNSLRLKLA*	MIISRGPYISTNSLRLKLA*			CTTGAGTATT	TTTCTTCAAT	0	LD	0	0	0	0	0
3342	2012	ao	AN8185.1	53.m03793	AO070310000139	0					-246	-184	ATGTTTCTTTCCGTTTGGAACGTCGTTTTATTTCGTTTTAGTTTGGAGCCCCACGTTCTCTGA			ATGTTTCTTTCCGTTTGGAACGTCGTTTTATTTCGTTTTAGTTTGGAGCCCCACGTTCTCTGA	MFLSVWNVVLFRFSLEPHVL*			MFLSVWNVVLFRFSLEPHVL*	CCTCCTTTTA	GAATTCGGAG	0	LD	0	0	0	0	0
3343	2012	ao	AN8185.1	53.m03793	AO070310000139	0					-131	-93	ATGATTTGCCTCCGAATTCGAATACTTCTTCGCTTTTGA			ATGATTTGCCTCCGAATTCGAATACTTCTTCGCTTTTGA	MICLRIRILLRF*			MICLRIRILLRF*	CATTTATTGA	CGACTACGAC	0	LD	0	0	0	0	0
3350	2013	af	AN6870.1	71.m15261	AO070314000052	0			-248	-210			ATGGGCTTTTTGTGGCTGCTTAGCATGGCGAGACCATGA		ATGGGCTTTTTGTGGCTGCTTAGCATGGCGAGACCATGA		MGFLWLLSMARP*		MGFLWLLSMARP*		GATAGCGCAG	AGCACCTGTC	0	R	FG02207.1	MG10534.1	0	0	0
3351	2013	af	AN6870.1	71.m15261	AO070314000052	0			-224	-210			ATGGCGAGACCATGA		ATGGCGAGACCATGA		MARP*		MARP*		GCTGCTTAGC	AGCACCTGTC	0	R	FG02207.1	MG10534.1	0	0	0
3352	2013	af	AN6870.1	71.m15261	AO070314000052	0			-213	-196			ATGAAGCACCTGTCTTGA		ATGAAGCACCTGTCTTGA		MKHLS*		MKHLS*		TGGCGAGACC	AAATTTGAGA	0	R	FG02207.1	MG10534.1	0	0	0
3353	2013	af	AN6870.1	71.m15261	AO070314000052	0			-185	-168			ATGACGATAGGAGACTGA		ATGACGATAGGAGACTGA		MTIGD*		MTIGD*		AAATTTGAGA	TCTAACGGGA	0	R	FG02207.1	MG10534.1	0	0	0
3354	2013	af	AN6870.1	71.m15261	AO070314000052	0			-89	-60			ATGGTGTATGATGTGATATATACGGAGTAG		ATGGTGTATGATGTGATATATACGGAGTAG		MVYDVIYTE*		MVYDVIYTE*		TCTAGACATA	TTGCTTCTCG	0	R	FG02207.1	MG10534.1	0	0	0
3344	2013	an	AN6870.1	71.m15261	AO070314000052	0	-155	-129					ATGTACCAATGTATGAAGAGTGGATGA	ATGTACCAATGTATGAAGAGTGGATGA			MYQCMKSG*	MYQCMKSG*			AGGTCTTGGG	CCGGCTTGGA	0	R	FG02207.1	MG10534.1	0	0	0
3345	2013	an	AN6870.1	71.m15261	AO070314000052	0	-147	-112					ATGTATGAAGAGTGGATGACCGGCTTGGAATTATGA	ATGTATGAAGAGTGGATGACCGGCTTGGAATTATGA			MYEEWMTGLEL*	MYEEWMTGLEL*			GGATGTACCA	AAACATGCAT	0	R	FG02207.1	MG10534.1	0	0	0
3346	2013	an	AN6870.1	71.m15261	AO070314000052	0	-143	-129					ATGAAGAGTGGATGA	ATGAAGAGTGGATGA			MKSG*	MKSG*			GTACCAATGT	CCGGCTTGGA	0	R	FG02207.1	MG10534.1	0	0	0
3347	2013	an	AN6870.1	71.m15261	AO070314000052	0	-132	-112					ATGACCGGCTTGGAATTATGA	ATGACCGGCTTGGAATTATGA			MTGLEL*	MTGLEL*			TGAAGAGTGG	AAACATGCAT	0	R	FG02207.1	MG10534.1	0	0	0
3348	2013	an	AN6870.1	71.m15261	AO070314000052	0	-115	-89					ATGAAAACATGCATGTACGACGAATGA	ATGAAAACATGCATGTACGACGAATGA			MKTCMYDE*	MKTCMYDE*			GCTTGGAATT	GTAACCTTGG	0	R	FG02207.1	MG10534.1	0	0	0
3349	2013	an	AN6870.1	71.m15261	AO070314000052	0	-103	-89					ATGTACGACGAATGA	ATGTACGACGAATGA			MYDE*	MYDE*			GAAAACATGC	GTAACCTTGG	0	R	FG02207.1	MG10534.1	0	0	0
3355	2013	ao	AN6870.1	71.m15261	AO070314000052	0					-106	-89	ATGCAGCAAGTAATATAG			ATGCAGCAAGTAATATAG	MQQVI*			MQQVI*	CAAGGTGTCT	GGTCGTGGCT	0	R	FG02207.1	MG10534.1	0	0	0
3364	2017	af	AN2243.1	71.m15877	AO070326000130	0			-236				ATGGTTCTGGCACCCACCGTCTTCACTTCTCAGGTATGTCCTGTCCTTGCCGATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAGTACCCTTCAGGACTACATCTCGGATCACCTCTGGAAAGCTTCCGGAAACTATTGAGACCACCCACACATTACTACACGCTTCCACATTTCTTCTCATCCTACCCAACAAATAA		ATGGTTCTGGCACCCACCGTCTTCACTTCTCAGGTATGTCCTGTCCTTGCCGATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAGTACCCTTCAGGACTACATCTCGGATCACCTCTGGAAAGCTTCCGGAAACTATTGAGACCACCCACACATTACTACACGCTTCCACATTTCTTCTCATCCTACCCAACAAATAA		MVLAPTVFTSQVCPVLADGHMDVIPATAIRPHHIRKNRADIVPFRTTSRITSGKLPETIETTHTLLHASTFLLILPNK*		MVLAPTVFTSQVCPVLADGHMDVIPATAIRPHHIRKNRADIVPFRTTSRITSGKLPETIETTHTLLHASTFLLILPNK*		AGTCGCGCTT	TGTTCGCTCG	0	R	0	MG01743.1	0	0	0
3365	2017	af	AN2243.1	71.m15877	AO070326000130	0			-201	-133			ATGTCCTGTCCTTGCCGATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAG		ATGTCCTGTCCTTGCCGATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAG		MSCPCRWPHGCHTRHRHTSTPH*		MSCPCRWPHGCHTRHRHTSTPH*		CTTCTCAGGT	AAAGAACAGA	0	R	0	MG01743.1	0	0	0
3366	2017	af	AN2243.1	71.m15877	AO070326000130	0			-184	-113			ATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAG		ATGGCCACATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAG		MATWMSYPPPPYVHTTLERTELT*		MATWMSYPPPPYVHTTLERTELT*		GTCCTTGCCG	TACCCTTCAG	0	R	0	MG01743.1	0	0	0
3367	2017	af	AN2243.1	71.m15877	AO070326000130	0			-176				ATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAGTACCCTTCAGGACTACATCTCGGATCACCTCTGGAAAGCTTCCGGAAACTATTGAGACCACCCACACATTACTACACGCTTCCACATTTCTTCTCATCCTACCCAACAAATAA		ATGGATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAGTACCCTTCAGGACTACATCTCGGATCACCTCTGGAAAGCTTCCGGAAACTATTGAGACCACCCACACATTACTACACGCTTCCACATTTCTTCTCATCCTACCCAACAAATAA		MDVIPATAIRPHHIRKNRADIVPFRTTSRITSGKLPETIETTHTLLHASTFLLILPNK*		MDVIPATAIRPHHIRKNRADIVPFRTTSRITSGKLPETIETTHTLLHASTFLLILPNK*		CGATGGCCAC	TGTTCGCTCG	0	R	0	MG01743.1	0	0	0
3368	2017	af	AN2243.1	71.m15877	AO070326000130	0			-172	-113			ATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAG		ATGTCATACCCGCCACCGCCATACGTCCACACCACATTAGAAAGAACAGAGCTGACATAG		MSYPPPPYVHTTLERTELT*		MSYPPPPYVHTTLERTELT*		GGCCACATGG	TACCCTTCAG	0	R	0	MG01743.1	0	0	0
3359	2017	an	AN2243.1	71.m15877	AO070326000130	0	-219	-40					ATGCCAGCGGCACCTTCCACCTTCACTTCTCAGGTATGCTCGCTCTCTTCTCTTTCCTATGATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAACGGTTACCAGGATTACATCTCGGACCACCTCTGGAAAGCTTCCGGAAACTATTGAAGCGTCCCTCGAATAA	ATGCCAGCGGCACCTTCCACCTTCACTTCTCAGGTATGCTCGCTCTCTTCTCTTTCCTATGATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAACGGTTACCAGGATTACATCTCGGACCACCTCTGGAAAGCTTCCGGAAACTATTGAAGCGTCCCTCGAATAA			MPAAPSTFTSQVCSLSSLSYDDSSIVHKLYGKSTVLTVTRITSRTTSGKLPETIEASLE*	MPAAPSTFTSQVCSLSSLSYDDSSIVHKLYGKSTVLTVTRITSRTTSGKLPETIEASLE*			AATCGCGTTC	ATTTCGATCC	0	R	0	MG01743.1	0	0	0
3360	2017	an	AN2243.1	71.m15877	AO070326000130	0	-184	-158					ATGCTCGCTCTCTTCTCTTTCCTATGA	ATGCTCGCTCTCTTCTCTTTCCTATGA			MLALFSFL*	MLALFSFL*			CTTCTCAGGT	TGACTCTTCC	0	R	0	MG01743.1	0	0	0

3361	2017	an	AN2243.1	71.m15877	AO070326000130	0	-161	-111					ATGATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAA	ATGATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAA			MMTLPSSTNCTGSPLC*	MMTLPSSTNCTGSPLC*			TCTCTTTCCT	CGGTTACCAG	0	R	0	MG01743.1	0	0	0
3362	2017	an	AN2243.1	71.m15877	AO070326000130	0	-158	-111					ATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAA	ATGACTCTTCCATCGTCCACAAATTGTACGGGAAGTCCACTGTGCTAA			MTLPSSTNCTGSPLC*	MTLPSSTNCTGSPLC*			CTTTCCTATG	CGGTTACCAG	0	R	0	MG01743.1	0	0	0
3370	2017	ao	AN2243.1	71.m15877	AO070326000130	0					-261	-202	ATGCGTTTTTTCTCGACCTTCACTTCTCAGGTATGTAGACCCCCGTTCAGGTCCACGTGA			ATGCGTTTTTTCTCGACCTTCACTTCTCAGGTATGTAGACCCCCGTTCAGGTCCACGTGA	MRFFSTFTSQVCRPPFRST*			MRFFSTFTSQVCRPPFRST*	CGTCGCGCTT	CACTCCCGTG	0	R	0	MG01743.1	0	0	0
3371	2017	ao	AN2243.1	71.m15877	AO070326000130	0					-191	-156	ATGGACAAGCCCTTGTCTGTTTCCGGGTCGTGTTGA			ATGGACAAGCCCTTGTCTGTTTCCGGGTCGTGTTGA	MDKPLSVSGSC*			MDKPLSVSGSC*	CACTCCCGTG	ACGACCTTTA	0	R	0	MG01743.1	0	0	0
3373	2021	af	AN9087.1	66.m04545	AO070332000190	0			-85	-47			ATGCGCACTGAAACAGATTCTCACCGACGGCTTTCATAA		ATGCGCACTGAAACAGATTCTCACCGACGGCTTTCATAA		MRTETDSHRRLS*		MRTETDSHRRLS*		GAGACTGTGG	GGGACGAACA	0	K	0	0	0	0	0
3372	2021	an	AN9087.1	66.m04545	AO070332000190	0	-78	-58					ATGTGCGTATCAGCTATCTAA	ATGTGCGTATCAGCTATCTAA			MCVSAI*	MCVSAI*			CAGCCTGTGG	ATCGCTCCCG	0	K	0	0	0	0	0
3374	2021	ao	AN9087.1	66.m04545	AO070332000190	0					-85	-50	ATGCGCGTTAAACTCATCTATCGCCGACATCTTTGA			ATGCGCGTTAAACTCATCTATCGCCGACATCTTTGA	MRVKLIYRRHL*			MRVKLIYRRHL*	GAGACGGTGG	TCGACGACAA	0	K	0	0	0	0	0
3375	2022	af	AN2793.1	69.m15497	AO070333000101	0			-261	-250			ATGATTTCTTAG		ATGATTTCTTAG		MIS*		MIS*		TAGACCTTAA	AACAATGTTG	0	E	0	0	0	0	0
3376	2022	af	AN2793.1	69.m15497	AO070333000101	0			-245	-120			ATGTTGTGCAGCTCAGCCGTATCTACTCGAATGAATTGCATCGGACGAACCCCGCGGTCTCGTCAACCCCGCAGCATCGGTTGGAGACCGATCGCCGATACAGGAGCTACGACTATGCTTATATAG		ATGTTGTGCAGCTCAGCCGTATCTACTCGAATGAATTGCATCGGACGAACCCCGCGGTCTCGTCAACCCCGCAGCATCGGTTGGAGACCGATCGCCGATACAGGAGCTACGACTATGCTTATATAG		MLCSSAVSTRMNCIGRTPRSRQPRSIGWRPIADTGATTMLI*		MLCSSAVSTRMNCIGRTPRSRQPRSIGWRPIADTGATTMLI*		TCTTAGAACA	TTCTTTGTCA	0	E	0	0	0	0	0
3377	2022	af	AN2793.1	69.m15497	AO070333000101	0			-215	-120			ATGAATTGCATCGGACGAACCCCGCGGTCTCGTCAACCCCGCAGCATCGGTTGGAGACCGATCGCCGATACAGGAGCTACGACTATGCTTATATAG		ATGAATTGCATCGGACGAACCCCGCGGTCTCGTCAACCCCGCAGCATCGGTTGGAGACCGATCGCCGATACAGGAGCTACGACTATGCTTATATAG		MNCIGRTPRSRQPRSIGWRPIADTGATTMLI*		MNCIGRTPRSRQPRSIGWRPIADTGATTMLI*		ATCTACTCGA	TTCTTTGTCA	0	E	0	0	0	0	0
3378	2022	af	AN2793.1	69.m15497	AO070333000101	0			-131	-120			ATGCTTATATAG		ATGCTTATATAG		MLI*		MLI*		AGCTACGACT	TTCTTTGTCA	0	E	0	0	0	0	0
3379	2022	af	AN2793.1	69.m15497	AO070333000101	0			-91	-41			ATGGTCACATCAGGCTTTGAATCAAGTCTGTGGTATTGCGTTGGATACTGA		ATGGTCACATCAGGCTTTGAATCAAGTCTGTGGTATTGCGTTGGATACTGA		MVTSGFESSLWYCVGY*		MVTSGFESSLWYCVGY*		TAGTCTTTCC	TCACCTTCTC	0	E	0	0	0	0	0
3380	2022	ao	AN2793.1	69.m15497	AO070333000101	0					-130	-29	ATGGGGCGAACGGAAGAGTCATTGAAATATATACACTATAGTAATCTACTTGTTCATCTAGTAACTTCCTCAAACCTATCACGCACGACCAACCCATTCTAG			ATGGGGCGAACGGAAGAGTCATTGAAATATATACACTATAGTAATCTACTTGTTCATCTAGTAACTTCCTCAAACCTATCACGCACGACCAACCCATTCTAG	MGRTEESLKYIHYSNLLVHLVTSSNLSRTTNPF*			MGRTEESLKYIHYSNLLVHLVTSSNLSRTTNPF*	AAAGAGCAAT	TATAATCAAA	0	E	0	0	0	0	0
3381	2023	an	AN4908.1	59.m08812	AO070338000038	0	-231	-199					ATGCATTTGCTTGGATACAGGGTGGTTGCTTGA	ATGCATTTGCTTGGATACAGGGTGGTTGCTTGA			MHLLGYRVVA*	MHLLGYRVVA*			GGTTTGTTTG	TTCAATTGCC	0	R	0	0	0	0	0
3382	2029	an	AN7570.1	72.m19589	AO070343000416	0	-194	-165					ATGATTGGCGGTGCAGTCACTGCTCTTTGA	ATGATTGGCGGTGCAGTCACTGCTCTTTGA			MIGGAVTAL*	MIGGAVTAL*			CAGTAGTGTG	GGCTAGTGAC	0	Z	0	0	0	0	0
3383	2029	an	AN7570.1	72.m19589	AO070343000416	0	-140	-63					ATGATCCGGGCGCTTTCTCCTCCTTCCCATCTCCCCATTAACGCTTTTTCTTCCAACCGTCATCTGTTGTCTAATTGA	ATGATCCGGGCGCTTTCTCCTCCTTCCCATCTCCCCATTAACGCTTTTTCTTCCAACCGTCATCTGTTGTCTAATTGA			MIRALSPPSHLPINAFSSNRHLLSN*	MIRALSPPSHLPINAFSSNRHLLSN*			GCCTTCTTAG	AGACTTTCAG	0	Z	0	0	0	0	0
3388	2033	af	AN0573.1	69.m15273	AO070272000052	0			-252	-208			ATGAGATTACCGTCCCTCCTGGCTTCGCCAATCCCGATTTACTAA		ATGAGATTACCGTCCCTCCTGGCTTCGCCAATCCCGATTTACTAA		MRLPSLLASPIPIY*		MRLPSLLASPIPIY*		GTCTGCCGGA	CCCCAAAAAA	0	U	FG01644.1	0	0	0	0
3389	2033	af	AN0573.1	69.m15273	AO070272000052	0			-182	-162			ATGGGGAGGGCCAACGTCTAA		ATGGGGAGGGCCAACGTCTAA		MGRANV*		MGRANV*		CGGACCACAC	AGAAAGGTTT	0	U	FG01644.1	0	0	0	0
3387	2033	an	AN0573.1	69.m15273	AO070272000052	0	-93	-58					ATGCAAGAAAGATCCCGCCGACCGAAGCATTCATGA	ATGCAAGAAAGATCCCGCCGACCGAAGCATTCATGA			MQERSRRPKHS*	MQERSRRPKHS*			TCCCTCATTT	AGCCCGTGGC	0	U	FG01644.1	0	0	0	0
3390	2033	ao	AN0573.1	69.m15273	AO070272000052	0					-205	-134	ATGATCTGCAGATTTCTACCCATCCATGAGAGGCAATCACGACATCCCACTAGCGAGAGTACCAAGGGCTAA			ATGATCTGCAGATTTCTACCCATCCATGAGAGGCAATCACGACATCCCACTAGCGAGAGTACCAAGGGCTAA	MICRFLPIHERQSRHPTSESTKG*			MICRFLPIHERQSRHPTSESTKG*	GCTTTGTGGG	TTAGATGAGA	0	U	FG01644.1	0	0	0	0
3391	2033	ao	AN0573.1	69.m15273	AO070272000052	0					-180	-130	ATGAGAGGCAATCACGACATCCCACTAGCGAGAGTACCAAGGGCTAATTAG			ATGAGAGGCAATCACGACATCCCACTAGCGAGAGTACCAAGGGCTAATTAG	MRGNHDIPLARVPRAN*			MRGNHDIPLARVPRAN*	CTACCCATCC	ATGAGACGAT	0	U	FG01644.1	0	0	0	0
3392	2033	ao	AN0573.1	69.m15273	AO070272000052	0					-129	-88	ATGAGACGATTACCGGGCTTCCATATCGAACTTATTTTCTAA			ATGAGACGATTACCGGGCTTCCATATCGAACTTATTTTCTAA	MRRLPGFHIELIF*			MRRLPGFHIELIF*	GGCTAATTAG	CAGTCTTTTG	0	U	FG01644.1	0	0	0	0
3397	2036	af	AN8767.1	52.m03894	AO070299000022	0			-288	-235			ATGCAGTCCAGAGAACCTGAAGGCCCAAAAAAGCAGCCGACAACCAACGTATGA		ATGCAGTCCAGAGAACCTGAAGGCCCAAAAAAGCAGCCGACAACCAACGTATGA		MQSREPEGPKKQPTTNV*		MQSREPEGPKKQPTTNV*		TCCTCAAACC	CAACTTGCCA	0	M	0	0	0	0	0
3398	2036	af	AN8767.1	52.m03894	AO070299000022	0			-238	-62			ATGACAACTTGCCAATTCAGGAACCGTTGTCGCCTTACCTGGAATCCTGCCGGCTTCTCATCTCTGCGACCAGTGAAAGCCCCCCACGTGGCGACGGAGAGATGCGGGTCTGCTCAGGACAACGATTTATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAA		ATGACAACTTGCCAATTCAGGAACCGTTGTCGCCTTACCTGGAATCCTGCCGGCTTCTCATCTCTGCGACCAGTGAAAGCCCCCCACGTGGCGACGGAGAGATGCGGGTCTGCTCAGGACAACGATTTATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAA		MTTCQFRNRCRLTWNPAGFSSLRPVKAPHVATERCGSAQDNDLCCYCLPLCVVFSPIY*		MTTCQFRNRCRLTWNPAGFSSLRPVKAPHVATERCGSAQDNDLCCYCLPLCVVFSPIY*		CAACCAACGT	TTCAGCCGAC	0	M	0	0	0	0	0
3399	2036	af	AN8767.1	52.m03894	AO070299000022	0			-137	-42			ATGCGGGTCTGCTCAGGACAACGATTTATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAATTCAGCCGACAACAAAGTGA		ATGCGGGTCTGCTCAGGACAACGATTTATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAATTCAGCCGACAACAAAGTGA		MRVCSGQRFMLLLLATLRGFLPYLLIQPTTK*		MRVCSGQRFMLLLLATLRGFLPYLLIQPTTK*		CGACGGAGAG	ATACTCACTT	0	M	0	0	0	0	0
3400	2036	af	AN8767.1	52.m03894	AO070299000022	0			-110	-42			ATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAATTCAGCCGACAACAAAGTGA		ATGTTGTTACTGCTTGCCACTCTGCGTGGTTTTCTCCCCTATCTATTAATTCAGCCGACAACAAAGTGA		MLLLLATLRGFLPYLLIQPTTK*		MLLLLATLRGFLPYLLIQPTTK*		ACAACGATTT	ATACTCACTT	0	M	0	0	0	0	0
3395	2036	an	AN8767.1	52.m03894	AO070299000022	0	-87	-37					ATGTCGGCGTGTATGCATATCGAGTCAAACACTCCTAGAGACGACCCTTAA	ATGTCGGCGTGTATGCATATCGAGTCAAACACTCCTAGAGACGACCCTTAA			MSACMHIESNTPRDDP*	MSACMHIESNTPRDDP*			TGGATATCGA	TTTTCCATCA	0	M	0	0	0	0	0
3396	2036	an	AN8767.1	52.m03894	AO070299000022	0	-75	-37					ATGCATATCGAGTCAAACACTCCTAGAGACGACCCTTAA	ATGCATATCGAGTCAAACACTCCTAGAGACGACCCTTAA			MHIESNTPRDDP*	MHIESNTPRDDP*			GTCGGCGTGT	TTTTCCATCA	0	M	0	0	0	0	0
3402	2036	ao	AN8767.1	52.m03894	AO070299000022	0					-165	-100	ATGTTATCGAAGAAAAAAAGTGCCCGATATTTGATCCACAGCACATCCCGTGGGTTGCAAAAATGA			ATGTTATCGAAGAAAAAAAGTGCCCGATATTTGATCCACAGCACATCCCGTGGGTTGCAAAAATGA	MLSKKKSARYLIHSTSRGLQK*			MLSKKKSARYLIHSTSRGLQK*	CTCACAAAGA	CATAGCCTTC	0	M	0	0	0	0	0
3404	2037	af	AN1632.1	58.m07722	AO070299000042	0			-83	-39			ATGGGCCCCCATCATCCGTCGACGTTACTGCTGCTGCTGAGGTAG		ATGGGCCCCCATCATCCGTCGACGTTACTGCTGCTGCTGAGGTAG		MGPHHPSTLLLLLR*		MGPHHPSTLLLLLR*		TACTCCCCTG	TCGTGTAGTT	0	OUT	0	0	0	0	0
3403	2037	an	AN1632.1	58.m07722	AO070299000042	0	-111	-67					ATGGGCCTCTATTCTCCGTCATTACCGTTGTTGTCTGTGAGGTAG	ATGGGCCTCTATTCTCCGTCATTACCGTTGTTGTCTGTGAGGTAG			MGLYSPSLPLLSVR*	MGLYSPSLPLLSVR*			ACCCTACCCT	CTGTTGGCTG	0	OUT	0	0	0	0	0
3405	2037	ao	AN1632.1	58.m07722	AO070299000042	0					-121	-74	ATGGGCCACTTCCATCAGCAATCGTTGTTGCTGCCGTTGCTGAGGTAG			ATGGGCCACTTCCATCAGCAATCGTTGTTGCTGCCGTTGCTGAGGTAG	MGHFHQQSLLLPLLR*			MGHFHQQSLLLPLLR*	CCTTCCCCTG	TTGTGGCCGC	0	OUT	0	0	0	0	0
3409	2040	af	AN3233.1	58.m07220	AO070307000047	0			-118	-29			ATGGTTATAAAGCCATGTTCCCCTCAGCCGGTCGATCATCACCTGTGTTCAAGGCAACTTCAACTCTTTGCACGCAATAATCCCCTCTGA		ATGGTTATAAAGCCATGTTCCCCTCAGCCGGTCGATCATCACCTGTGTTCAAGGCAACTTCAACTCTTTGCACGCAATAATCCCCTCTGA		MVIKPCSPQPVDHHLCSRQLQLFARNNPL*		MVIKPCSPQPVDHHLCSRQLQLFARNNPL*		AGAAGGAAAA	ATTTTGGGCT	0	R	0	0	0	0	0
3410	2040	af	AN3233.1	58.m07220	AO070307000047	0			-104	-39			ATGTTCCCCTCAGCCGGTCGATCATCACCTGTGTTCAAGGCAACTTCAACTCTTTGCACGCAATAA		ATGTTCCCCTCAGCCGGTCGATCATCACCTGTGTTCAAGGCAACTTCAACTCTTTGCACGCAATAA		MFPSAGRSSPVFKATSTLCTQ*		MFPSAGRSSPVFKATSTLCTQ*		TTATAAAGCC	TCCCCTCTGA	0	R	0	0	0	0	0
3406	2040	an	AN3233.1	58.m07220	AO070307000047	0	-165	-28					ATGAACTGGTCATGCGAGATAGATAACATGGAAGATATTGCAATCGACCTAGAGCTATTTTACGAGGAGTATTCCCCCCAGACTGTTCTTCTCCACGGGGTATTGAAAATTCTTTCAGCTCCGGAGTGGCACTCTTGA	ATGAACTGGTCATGCGAGATAGATAACATGGAAGATATTGCAATCGACCTAGAGCTATTTTACGAGGAGTATTCCCCCCAGACTGTTCTTCTCCACGGGGTATTGAAAATTCTTTCAGCTCCGGAGTGGCACTCTTGA			MNWSCEIDNMEDIAIDLELFYEEYSPQTVLLHGVLKILSAPEWHS*	MNWSCEIDNMEDIAIDLELFYEEYSPQTVLLHGVLKILSAPEWHS*			AACAGCCATT	GTCCTTCTGT	0	R	0	0	0	0	0
3407	2040	an	AN3233.1	58.m07220	AO070307000047	0	-154	-140					ATGCGAGATAGATAA	ATGCGAGATAGATAA			MRDR*	MRDR*			TGAACTGGTC	CATGGAAGAT	0	R	0	0	0	0	0
3408	2040	an	AN3233.1	58.m07220	AO070307000047	0	-138	-28					ATGGAAGATATTGCAATCGACCTAGAGCTATTTTACGAGGAGTATTCCCCCCAGACTGTTCTTCTCCACGGGGTATTGAAAATTCTTTCAGCTCCGGAGTGGCACTCTTGA	ATGGAAGATATTGCAATCGACCTAGAGCTATTTTACGAGGAGTATTCCCCCCAGACTGTTCTTCTCCACGGGGTATTGAAAATTCTTTCAGCTCCGGAGTGGCACTCTTGA			MEDIAIDLELFYEEYSPQTVLLHGVLKILSAPEWHS*	MEDIAIDLELFYEEYSPQTVLLHGVLKILSAPEWHS*			GATAGATAAC	GTCCTTCTGT	0	R	0	0	0	0	0
3411	2040	ao	AN3233.1	58.m07220	AO070307000047	0					-127	-104	ATGGGTCACTCCAAGAGTGGATAG			ATGGGTCACTCCAAGAGTGGATAG	MGHSKSG*			MGHSKSG*	TTCGGCCATT	GCCCGATAGG	0	R	0	0	0	0	0
3415	2041	af	AN2957.1	58.m07219	AO070307000048	0			-143	-96			ATGTCTGGGTGTTGCAAGGTTCTCGGTTATGAAATGGAATTTACCTGA		ATGTCTGGGTGTTGCAAGGTTCTCGGTTATGAAATGGAATTTACCTGA		MSGCCKVLGYEMEFT*		MSGCCKVLGYEMEFT*		GAAACAACTT	AGCCAGGCCT	0		0	0	0	0	0
3416	2041	af	AN2957.1	58.m07219	AO070307000048	0			-110	-96			ATGGAATTTACCTGA		ATGGAATTTACCTGA		MEFT*		MEFT*		CGGTTATGAA	AGCCAGGCCT	0		0	0	0	0	0
3413	2041	an	AN2957.1	58.m07219	AO070307000048	0	-106	-65					ATGTCCCGTGCCACGAGTCCCTTAATGCCACTCACAGGCTGA	ATGTCCCGTGCCACGAGTCCCTTAATGCCACTCACAGGCTGA			MSRATSPLMPLTG*	MSRATSPLMPLTG*			GACTTTTCAC	TTGACGATCA	0		0	0	0	0	0
3414	2041	an	AN2957.1	58.m07219	AO070307000048	0	-82	-65					ATGCCACTCACAGGCTGA	ATGCCACTCACAGGCTGA			MPLTG*	MPLTG*			GAGTCCCTTA	TTGACGATCA	0		0	0	0	0	0
3417	2041	ao	AN2957.1	58.m07219	AO070307000048	0					-194	-180	ATGGTGACAGAATGA			ATGGTGACAGAATGA	MVTE*			MVTE*	GAGCGTAGAC	AGGCGGTGAA	0		0	0	0	0	0
3418	2041	ao	AN2957.1	58.m07219	AO070307000048	0					-183	-52	ATGAAGGCGGTGAAACTGATCAATCAGAGTCCCATAATGTGTTGGGATGCCTACTATGGAGCTAGATCGGGATTAGTGTTTGCACGCCTGACCGCCTACCACGCTGGGGACGCGTGTTGTTTCCTCCGGTGA			ATGAAGGCGGTGAAACTGATCAATCAGAGTCCCATAATGTGTTGGGATGCCTACTATGGAGCTAGATCGGGATTAGTGTTTGCACGCCTGACCGCCTACCACGCTGGGGACGCGTGTTGTTTCCTCCGGTGA	MKAVKLINQSPIMCWDAYYGARSGLVFARLTAYHAGDACCFLR*			MKAVKLINQSPIMCWDAYYGARSGLVFARLTAYHAGDACCFLR*	TGGTGACAGA	TTCGCAGGAA	0		0	0	0	0	0
3419	2041	ao	AN2957.1	58.m07219	AO070307000048	0					-147	-52	ATGTGTTGGGATGCCTACTATGGAGCTAGATCGGGATTAGTGTTTGCACGCCTGACCGCCTACCACGCTGGGGACGCGTGTTGTTTCCTCCGGTGA			ATGTGTTGGGATGCCTACTATGGAGCTAGATCGGGATTAGTGTTTGCACGCCTGACCGCCTACCACGCTGGGGACGCGTGTTGTTTCCTCCGGTGA	MCWDAYYGARSGLVFARLTAYHAGDACCFLR*			MCWDAYYGARSGLVFARLTAYHAGDACCFLR*	GAGTCCCATA	TTCGCAGGAA	0		0	0	0	0	0
3420	2041	ao	AN2957.1	58.m07219	AO070307000048	0					-137	-108	ATGCCTACTATGGAGCTAGATCGGGATTAG			ATGCCTACTATGGAGCTAGATCGGGATTAG	MPTMELDRD*			MPTMELDRD*	ATGTGTTGGG	TGTTTGCACG	0		0	0	0	0	0
3421	2041	ao	AN2957.1	58.m07219	AO070307000048	0					-128	-108	ATGGAGCTAGATCGGGATTAG			ATGGAGCTAGATCGGGATTAG	MELDRD*			MELDRD*	GATGCCTACT	TGTTTGCACG	0		0	0	0	0	0
3422	2042	af	AN3758.1	65.m07366	AO070309000048	0			-154	-131			ATGCATTGTGTTAGGGCTCAGTAA		ATGCATTGTGTTAGGGCTCAGTAA		MHCVRAQ*		MHCVRAQ*		AGAGACCTTG	CTGCTCGGCG	0	O	0	0	0	0	YNL315C
3423	2042	af	AN3758.1	65.m07366	AO070309000048	0			-105	-85			ATGATTGCGATGATTATATAA		ATGATTGCGATGATTATATAA		MIAMII*		MIAMII*		TCGGTGACTG	TCAAATCTCG	0	O	0	0	0	0	YNL315C
3424	2042	af	AN3758.1	65.m07366	AO070309000048	0			-96	-85			ATGATTATATAA		ATGATTATATAA		MII*		MII*		GATGATTGCG	TCAAATCTCG	0	O	0	0	0	0	YNL315C
3425	2042	ao	AN3758.1	65.m07366	AO070309000048	0					-208	-161	ATGAGAGCTTTAGAAAAATTAAGAATTGGTGAAGTTATAGGCATTTAG			ATGAGAGCTTTAGAAAAATTAAGAATTGGTGAAGTTATAGGCATTTAG	MRALEKLRIGEVIGI*			MRALEKLRIGEVIGI*	TAAAATTTTA	AAACTGGCCA	0	O	0	0	0	0	YNL315C
3426	2042	ao	AN3758.1	65.m07366	AO070309000048	0					-143	-123	ATGTGTCGCTCGCCAAAGTAG			ATGTGTCGCTCGCCAAAGTAG	MCRSPK*			MCRSPK*	CCATGTTTTG	AAAAATATGC	0	O	0	0	0	0	YNL315C
3427	2042	ao	AN3758.1	65.m07366	AO070309000048	0					-116	-12	ATGCCAAGAACTGAAGATTTGATACTTTTGCATACTCCGTCACTAAATCCGTTACGGTTTCCGCAACTTTTCCATCCTCCGCTCGCGGGTCCCAAGATATACTGA			ATGCCAAGAACTGAAGATTTGATACTTTTGCATACTCCGTCACTAAATCCGTTACGGTTTCCGCAACTTTTCCATCCTCCGCTCGCGGGTCCCAAGATATACTGA	MPRTEDLILLHTPSLNPLRFPQLFHPPLAGPKIY*			MPRTEDLILLHTPSLNPLRFPQLFHPPLAGPKIY*	GTAGAAAAAT	AAGACTGGAA	0	O	0	0	0	0	YNL315C
3429	2045	af	AN0770.1	70.m15373	AO070316000074	0			-115	-77			ATGCAACATAGCCGTCGCCCGCCATTTGGAACCCCGTGA		ATGCAACATAGCCGTCGCCCGCCATTTGGAACCCCGTGA		MQHSRRPPFGTP*		MQHSRRPPFGTP*		TTGAGAGTTC	TAGCATACAA	0	T	0	0	NCU01928.1	0	0

3438	2047	af	AN9511.1	69.m15659	AO070324000090	0			-174	-58			ATGATGCTGGTGTGGAGAGCTGTCTTGTCTGGCGGTCTGCAAACAAAGCAAACACGGTCCAATCAGGCACGCCTTAATCGGTTATCGATAGATCGACAAGTTATCACCGTTTCATGA		ATGATGCTGGTGTGGAGAGCTGTCTTGTCTGGCGGTCTGCAAACAAAGCAAACACGGTCCAATCAGGCACGCCTTAATCGGTTATCGATAGATCGACAAGTTATCACCGTTTCATGA		MMLVWRAVLSGGLQTKQTRSNQARLNRLSIDRQVITVS*		MMLVWRAVLSGGLQTKQTRSNQARLNRLSIDRQVITVS*		CTTGCCCAAG	TGGACGAGCA	0	R	0	0	0	0	0
3439	2047	af	AN9511.1	69.m15659	AO070324000090	0			-171	-58			ATGCTGGTGTGGAGAGCTGTCTTGTCTGGCGGTCTGCAAACAAAGCAAACACGGTCCAATCAGGCACGCCTTAATCGGTTATCGATAGATCGACAAGTTATCACCGTTTCATGA		ATGCTGGTGTGGAGAGCTGTCTTGTCTGGCGGTCTGCAAACAAAGCAAACACGGTCCAATCAGGCACGCCTTAATCGGTTATCGATAGATCGACAAGTTATCACCGTTTCATGA		MLVWRAVLSGGLQTKQTRSNQARLNRLSIDRQVITVS*		MLVWRAVLSGGLQTKQTRSNQARLNRLSIDRQVITVS*		GCCCAAGATG	TGGACGAGCA	0	R	0	0	0	0	0
3440	2047	af	AN9511.1	69.m15659	AO070324000090	0			-61	-2			ATGATGGACGAGCATTGGAACATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		ATGATGGACGAGCATTGGAACATGGGACTTGACGCACTGTCGCTCATTTGGTCTACCTAA		MMDEHWNMGLDALSLIWST*		MMDEHWNMGLDALSLIWST*		TCACCGTTTC	CATGGCGAGC	0	R	0	0	0	0	0
3434	2047	an	AN9511.1	69.m15659	AO070324000090	0	-184	-113					ATGACGGGTGACCACTTCCGTGATGAAGCTGTCCTCAAACGTGGGGATGCAAACAAAACAAACCCACGTTAA	ATGACGGGTGACCACTTCCGTGATGAAGCTGTCCTCAAACGTGGGGATGCAAACAAAACAAACCCACGTTAA			MTGDHFRDEAVLKRGDANKTNPR*	MTGDHFRDEAVLKRGDANKTNPR*			CGCAATAAGT	TCAGTAGATT	0	R	0	0	0	0	0
3435	2047	an	AN9511.1	69.m15659	AO070324000090	0	-162	-106					ATGAAGCTGTCCTCAAACGTGGGGATGCAAACAAAACAAACCCACGTTAATCAGTAG	ATGAAGCTGTCCTCAAACGTGGGGATGCAAACAAAACAAACCCACGTTAATCAGTAG			MKLSSNVGMQTKQTHVNQ*	MKLSSNVGMQTKQTHVNQ*			CACTTCCGTG	ATTATGGATA	0	R	0	0	0	0	0
3436	2047	an	AN9511.1	69.m15659	AO070324000090	0	-138	-106					ATGCAAACAAAACAAACCCACGTTAATCAGTAG	ATGCAAACAAAACAAACCCACGTTAATCAGTAG			MQTKQTHVNQ*	MQTKQTHVNQ*			AAACGTGGGG	ATTATGGATA	0	R	0	0	0	0	0
3443	2047	ao	AN9511.1	69.m15659	AO070324000090	0					-127	-104	ATGATTATTTATCGCGCTTTCTAG			ATGATTATTTATCGCGCTTTCTAG	MIIYRAF*			MIIYRAF*	TATCGGCATC	ATTTCTGTAC	0	R	0	0	0	0	0
3444	2047	ao	AN9511.1	69.m15659	AO070324000090	0					-72	-52	ATGATGGCATGTGATAGATAA			ATGATGGCATGTGATAGATAA	MMACDR*			MMACDR*	AGGACTTCAA	AGGCGTAAAC	0	R	0	0	0	0	0
3445	2047	ao	AN9511.1	69.m15659	AO070324000090	0					-69	-52	ATGGCATGTGATAGATAA			ATGGCATGTGATAGATAA	MACDR*			MACDR*	ACTTCAAATG	AGGCGTAAAC	0	R	0	0	0	0	0
3447	2049	af	AN8329.1	67.m02964	AO070330000092	0			-262	-182			ATGGTGGGGATCTTGATGGATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		ATGGTGGGGATCTTGATGGATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		MVGILMDGDWKRPRMGPSLVFWDEEG*		MVGILMDGDWKRPRMGPSLVFWDEEG*		GCCGGCGCGG	ACGAAATGAC	0	E	0	0	0	0	0
3448	2049	af	AN8329.1	67.m02964	AO070330000092	0			-247	-182			ATGGATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		ATGGATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		MDGDWKRPRMGPSLVFWDEEG*		MDGDWKRPRMGPSLVFWDEEG*		GGGGATCTTG	ACGAAATGAC	0	E	0	0	0	0	0
3449	2049	af	AN8329.1	67.m02964	AO070330000092	0			-243	-205			ATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAG		ATGGCGATTGGAAGAGACCGCGAATGGGGCCATCATTAG		MAIGRDREWGHH*		MAIGRDREWGHH*		ATCTTGATGG	TTTTCTGGGA	0	E	0	0	0	0	0
3450	2049	af	AN8329.1	67.m02964	AO070330000092	0			-220	-182			ATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		ATGGGGCCATCATTAGTTTTCTGGGATGAAGAGGGGTAG		MGPSLVFWDEEG*		MGPSLVFWDEEG*		GAGACCGCGA	ACGAAATGAC	0	E	0	0	0	0	0
3451	2049	af	AN8329.1	67.m02964	AO070330000092	0			-195	-148			ATGAAGAGGGGTAGACGAAATGACTGTGAACGAGGTTCGAGGCTTTGA		ATGAAGAGGGGTAGACGAAATGACTGTGAACGAGGTTCGAGGCTTTGA		MKRGRRNDCERGSRL*		MKRGRRNDCERGSRL*		GTTTTCTGGG	CATGTAATTT	0	E	0	0	0	0	0
3452	2049	af	AN8329.1	67.m02964	AO070330000092	0			-176	-141			ATGACTGTGAACGAGGTTCGAGGCTTTGACATGTAA		ATGACTGTGAACGAGGTTCGAGGCTTTGACATGTAA		MTVNEVRGFDM*		MTVNEVRGFDM*		GGTAGACGAA	TTTGGCCCCG	0	E	0	0	0	0	0
3446	2049	an	AN8329.1	67.m02964	AO070330000092	0	-182	-165					ATGATCGTGGCCTGGTAA	ATGATCGTGGCCTGGTAA			MIVAW*	MIVAW*			GGGTGGAACA	CAGGGGGCAA	0	E	0	0	0	0	0
3453	2049	ao	AN8329.1	67.m02964	AO070330000092	0					-254	-213	ATGAAATGCCGCCGATGGAACGAATCTGCCGTGAGTCGCTGA			ATGAAATGCCGCCGATGGAACGAATCTGCCGTGAGTCGCTGA	MKCRRWNESAVSR*			MKCRRWNESAVSR*	AGACGGAATC	TGGGGGCCAA	0	E	0	0	0	0	0
3454	2049	ao	AN8329.1	67.m02964	AO070330000092	0					-249	-163	ATGCCGCCGATGGAACGAATCTGCCGTGAGTCGCTGATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA			ATGCCGCCGATGGAACGAATCTGCCGTGAGTCGCTGATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA	MPPMERICRESLMGANFSQRKNDVVPFI*			MPPMERICRESLMGANFSQRKNDVVPFI*	GAATCATGAA	TTGGCCCCTT	0	E	0	0	0	0	0
3455	2049	ao	AN8329.1	67.m02964	AO070330000092	0					-240	-163	ATGGAACGAATCTGCCGTGAGTCGCTGATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA			ATGGAACGAATCTGCCGTGAGTCGCTGATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA	MERICRESLMGANFSQRKNDVVPFI*			MERICRESLMGANFSQRKNDVVPFI*	AATGCCGCCG	TTGGCCCCTT	0	E	0	0	0	0	0
3456	2049	ao	AN8329.1	67.m02964	AO070330000092	0					-213	-163	ATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA			ATGGGGGCCAACTTCTCCCAACGCAAAAACGACGTGGTCCCGTTCATCTGA	MGANFSQRKNDVVPFI*			MGANFSQRKNDVVPFI*	TGAGTCGCTG	TTGGCCCCTT	0	E	0	0	0	0	0
3457	2049	ao	AN8329.1	67.m02964	AO070330000092	0					-104	-81	ATGTTTCGTGCGGTTATAAAATAG			ATGTTTCGTGCGGTTATAAAATAG	MFRAVIK*			MFRAVIK*	AGTTTCGCGC	CCCATATTGC	0	E	0	0	0	0	0
3458	2052	af	AN3499.1	58.m07226	AO070333000037	0			-240	-166			ATGGAAAGCCAGAGCCTCTTGAAGTCCAGACCAATGATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		ATGGAAAGCCAGAGCCTCTTGAAGTCCAGACCAATGATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		MESQSLLKSRPMMSVACLSGLVGN*		MESQSLLKSRPMMSVACLSGLVGN*		CGTCTAGCCA	CATGAAGGCA	0	O	0	0	0	0	0
3459	2052	af	AN3499.1	58.m07226	AO070333000037	0			-207	-166			ATGATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		ATGATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		MMSVACLSGLVGN*		MMSVACLSGLVGN*		GTCCAGACCA	CATGAAGGCA	0	O	0	0	0	0	0
3460	2052	af	AN3499.1	58.m07226	AO070333000037	0			-204	-166			ATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		ATGTCCGTGGCTTGCCTTTCAGGGCTGGTAGGTAACTAA		MSVACLSGLVGN*		MSVACLSGLVGN*		CAGACCAATG	CATGAAGGCA	0	O	0	0	0	0	0
3461	2052	af	AN3499.1	58.m07226	AO070333000037	0			-164	-42			ATGAAGGCAATTAAGACGGACGCTGGCCCAGATCACAAGGGCGACCTGACATGTAGTGACAAGCCGAGCTGCCTAATCTATTTAATCCCTCGTCCGTCCACTGCCGAAGAAACGCAGGGTTGA		ATGAAGGCAATTAAGACGGACGCTGGCCCAGATCACAAGGGCGACCTGACATGTAGTGACAAGCCGAGCTGCCTAATCTATTTAATCCCTCGTCCGTCCACTGCCGAAGAAACGCAGGGTTGA		MKAIKTDAGPDHKGDLTCSDKPSCLIYLIPRPSTAEETQG*		MKAIKTDAGPDHKGDLTCSDKPSCLIYLIPRPSTAEETQG*		GGTAACTAAC	GTCGTTATCG	0	O	0	0	0	0	0
3462	2052	ao	AN3499.1	58.m07226	AO070333000037	0					-174	-145	ATGACTCTCCATAGCCGTGTAGCCGTCTAA			ATGACTCTCCATAGCCGTGTAGCCGTCTAA	MTLHSRVAV*			MTLHSRVAV*	TTCTACCAGC	GCGTCGGCTT	0	O	0	0	0	0	0
3463	2052	ao	AN3499.1	58.m07226	AO070333000037	0					-97	-50	ATGGACTGCAGCCGCGACTCATGTATTTATTTCCACCCTTCCTCTTAG			ATGGACTGCAGCCGCGACTCATGTATTTATTTCCACCCTTCCTCTTAG	MDCSRDSCIYFHPSS*			MDCSRDSCIYFHPSS*	CGGACAAGGT	AGGGGTTTTG	0	O	0	0	0	0	0
3464	2052	ao	AN3499.1	58.m07226	AO070333000037	0					-77	-36	ATGTATTTATTTCCACCCTTCCTCTTAGAGGGGTTTGGTAG			ATGTATTTATTTCCACCCTTCCTCTTAGAGGGGTTTGGTAG	MYLFPPFLLEGFW*			MYLFPPFLLEGFW*	GCCGCGACTC	TCACTGTCTC	0	O	0	0	0	0	0
3465	2059	af	AN6815.1	69.m15180	AO070252000017	0			-148	-8			ATGCTTTTGTCAAGAAAGTCGGTATCACTGCACACTGATATCTGCGTCATCTGCAGCTTCCCCGCACTGATAAGCATGCATCCTCAACCCTCTTCCTTCATACTATCATCACCTCAAAGCTACCTAACTCGTAGACCATAG		ATGCTTTTGTCAAGAAAGTCGGTATCACTGCACACTGATATCTGCGTCATCTGCAGCTTCCCCGCACTGATAAGCATGCATCCTCAACCCTCTTCCTTCATACTATCATCACCTCAAAGCTACCTAACTCGTAGACCATAG		MLLSRKSVSLHTDICVICSFPALISMHPQPSSFILSSPQSYLTRRP*		MLLSRKSVSLHTDICVICSFPALISMHPQPSSFILSSPQSYLTRRP*		AGAATACTAG	GAATACAATG	0	FQ	0	0	0	0	0
3466	2059	af	AN6815.1	69.m15180	AO070252000017	0			-73	-8			ATGCATCCTCAACCCTCTTCCTTCATACTATCATCACCTCAAAGCTACCTAACTCGTAGACCATAG		ATGCATCCTCAACCCTCTTCCTTCATACTATCATCACCTCAAAGCTACCTAACTCGTAGACCATAG		MHPQPSSFILSSPQSYLTRRP*		MHPQPSSFILSSPQSYLTRRP*		ACTGATAAGC	GAATACAATG	0	FQ	0	0	0	0	0
3467	2059	ao	AN6815.1	69.m15180	AO070252000017	0					-186	-100	ATGTACATAATTTATTCGGATACAATCGAGTTGAGATACCATTACTATTCGTCCGCTTATCACTGTTTACTATTACCCCACCTCTAA			ATGTACATAATTTATTCGGATACAATCGAGTTGAGATACCATTACTATTCGTCCGCTTATCACTGTTTACTATTACCCCACCTCTAA	MYIIYSDTIELRYHYYSSAYHCLLLPHL*			MYIIYSDTIELRYHYYSSAYHCLLLPHL*	CCCTGTGAAG	TCAAATACTA	0	FQ	0	0	0	0	0
3469	2060	af	AN5824.1	72.m18951	AO070260000022	0			-181	-155			ATGAAGTTTTATGGAAATACTTTATAA		ATGAAGTTTTATGGAAATACTTTATAA		MKFYGNTL*		MKFYGNTL*		GAGATCATTG	ATATCGCGAT	0	R	0	0	0	0	0
3470	2060	af	AN5824.1	72.m18951	AO070260000022	0			-171	-43			ATGGAAATACTTTATAAATATCGCGATGTACCTATAGCCCAAAGTCTGCGGTTGTCATCTCCGAACGCTTCACGGTGTACCATCCTCGCTACCAGCGTCCTTTCGTTCCTCGAAGTCGGATCGAGTTAG		ATGGAAATACTTTATAAATATCGCGATGTACCTATAGCCCAAAGTCTGCGGTTGTCATCTCCGAACGCTTCACGGTGTACCATCCTCGCTACCAGCGTCCTTTCGTTCCTCGAAGTCGGATCGAGTTAG		MEILYKYRDVPIAQSLRLSSPNASRCTILATSVLSFLEVGSS*		MEILYKYRDVPIAQSLRLSSPNASRCTILATSVLSFLEVGSS*		ATGAAGTTTT	ATTTCCCTCA	0	R	0	0	0	0	0
3471	2060	af	AN5824.1	72.m18951	AO070260000022	0			-146	-135			ATGTACCTATAG		ATGTACCTATAG		MYL*		MYL*		AAATATCGCG	CCCAAAGTCT	0	R	0	0	0	0	0
3468	2060	an	AN5824.1	72.m18951	AO070260000022	0	-223	-68					ATGATACAACATTCCCTTCAATCTCCTCACTTTTTAGACTTCAGGGTGAGAAAGGAGCATTGTTTTTTTTTTTTTTGTTTACAACCTCCGCATTGCGCTTTGAGCCGTAGCGCCTCCCCGAATCTCTATCGTGTCACCTCCGCCTCACTCTTTTGA	ATGATACAACATTCCCTTCAATCTCCTCACTTTTTAGACTTCAGGGTGAGAAAGGAGCATTGTTTTTTTTTTTTTGTTTACAACCTCCGCATTGCGCTTTGAGCCGTAGCGCCTCCCCGAATCTCTATCGTGTCACCTCCGCCTCACTCTTTTGA			MIQHSLQSPHFLDFRVRKEHCFFFFCLQPPHCALSRSASPNLYRVTSASLF*	MIQHSLQSPHFLDFRVRKEHCFFFFCLQPPHCALSRSASPNLYRVTSASLF*			TTTTCCCTTC	TCCTAGTAAT	0	R	0	0	0	0	0
3472	2060	ao	AN5824.1	72.m18951	AO070260000022	0					-151	-140	ATGCTTCTTTAG			ATGCTTCTTTAG	MLL*			MLL*	TGATTCAGCA	ATCGTGTGGA	0	R	0	0	0	0	0
3476	2066	af	AN1474.1	55.m02975	AO070306000096	0			-266	-234			ATGCCAGTCAGACTTTTAATCGACAACCTGTGA		ATGCCAGTCAGACTTTTAATCGACAACCTGTGA		MPVRLLIDNL*		MPVRLLIDNL*		GGCCTTTCTG	GATCTGATTC	0	A	0	0	0	0	0
3477	2066	af	AN1474.1	55.m02975	AO070306000096	0			-178	-152			ATGCATCATCCGATCAGGCGGAGATAG		ATGCATCATCCGATCAGGCGGAGATAG		MHHPIRRR*		MHHPIRRR*		ACCGAAGTCA	CCGGAGATAG	0	A	0	0	0	0	0
3473	2066	an	AN1474.1	55.m02975	AO070306000096	0	-200	-165					ATGTTGTTGCTACCGGTTGAGCTTTGTGATAACTGA	ATGTTGTTGCTACCGGTTGAGCTTTGTGATAACTGA			MLLLPVELCDN*	MLLLPVELCDN*			AATTGAAGTT	TCAGCAGATC	0	A	0	0	0	0	0
3474	2066	an	AN1474.1	55.m02975	AO070306000096	0	-127	-80					ATGTCCATGCTCGGAACGGATCAACAAGGCTCCGGAAGATTTTCTTGA	ATGTCCATGCTCGGAACGGATCAACAAGGCTCCGGAAGATTTTCTTGA			MSMLGTDQQGSGRFS*	MSMLGTDQQGSGRFS*			AGCCAAGCTT	GTTTCATTTT	0	A	0	0	0	0	0
3475	2066	an	AN1474.1	55.m02975	AO070306000096	0	-121	-80					ATGCTCGGAACGGATCAACAAGGCTCCGGAAGATTTTCTTGA	ATGCTCGGAACGGATCAACAAGGCTCCGGAAGATTTTCTTGA			MLGTDQQGSGRFS*	MLGTDQQGSGRFS*			GCTTATGTCC	GTTTCATTTT	0	A	0	0	0	0	0
3478	2066	ao	AN1474.1	55.m02975	AO070306000096	0					-187	-176	ATGCGACATTGA			ATGCGACATTGA	MRH*			MRH*	CATAGTTATC	TAATCACGCT	0	A	0	0	0	0	0
3479	2066	ao	AN1474.1	55.m02975	AO070306000096	0					-132	-55	ATGGCGGAACATCATTTCCCCGGCAGATTTTCTCCATCCAACTTTTTTTTTTGTCGGTCAAATGTATACAGCTTCTGA			ATGGCGGAACATCATTTCCCCGGCAGATTTTCTCCATCCAACTTTTTTTTTTGTCGGTCAAATGTATACAGCTTCTGA	MAEHHFPGRFSPSNFFFCRSNVYSF*			MAEHHFPGRFSPSNFFFCRSNVYSF*	CCCGGACACC	TTGCGACATT	0	A	0	0	0	0	0
3480	2066	ao	AN1474.1	55.m02975	AO070306000096	0					-71	-3	ATGTATACAGCTTCTGATTGCGACATTGCTGGCCCACGACGGAGATACAGCGATTCTCCAATCAAGTAA			ATGTATACAGCTTCTGATTGCGACATTGCTGGCCCACGACGGAGATACAGCGATTCTCCAATCAAGTAA	MYTASDCDIAGPRRRYSDSPIK*			MYTASDCDIAGPRRRYSDSPIK*	TGTCGGTCAA	TCATGGCAAC	0	A	0	0	0	0	0
3481	2068	an	AN6204.1	72.m19303	AO070308000089	0	-69	-49					ATGGAAAATATTGCTGGATAG	ATGGAAAATATTGCTGGATAG			MENIAG*	MENIAG*			TAATTGACAC	AAGAAGAGGC	0		0	0	0	0	0
3482	2068	ao	AN6204.1	72.m19303	AO070308000089	0					-240	-214	ATGGAATCCTGGATGGTAGCTTTTTGA			ATGGAATCCTGGATGGTAGCTTTTTGA	MESWMVAF*			MESWMVAF*	ACACATCTGG	TCGGTTGTAT	0		0	0	0	0	0
3483	2068	ao	AN6204.1	72.m19303	AO070308000089	0					-228	-214	ATGGTAGCTTTTTGA			ATGGTAGCTTTTTGA	MVAF*			MVAF*	GGAATCCTGG	TCGGTTGTAT	0		0	0	0	0	0
3484	2074	af	AN5501.1	56.m02455	AO070328000018	0			-245	-123			ATGTTCGGCTACATTTCTTTACTTTACGGACAAACTGTCATCCAGAGATTTGTAACAAGCAGAAGAAAATGTCGCCGTATCCGGAGACAACCAGATCAGGCTTCGCGGGCAGCTATCATATAA		ATGTTCGGCTACATTTCTTTACTTTACGGACAAACTGTCATCCAGAGATTTGTAACAAGCAGAAGAAAATGTCGCCGTATCCGGAGACAACCAGATCAGGCTTCGCGGGCAGCTATCATATAA		MFGYISLLYGQTVIQRFVTSRRKCRRIRRQPDQASRAII*		MFGYISLLYGQTVIQRFVTSRRKCRRIRRQPDQASRAII*		ATTATCCCGA	AGACCACCAC	0	I	0	0	0	0	0
3485	2074	af	AN5501.1	56.m02455	AO070328000018	0			-177	-79			ATGTCGCCGTATCCGGAGACAACCAGATCAGGCTTCGCGGGCAGCTATCATATAAAGACCACCACAATGGTGAGTCTGCTATTCGATAACATTTCCTGA		ATGTCGCCGTATCCGGAGACAACCAGATCAGGCTTCGCGGGCAGCTATCATATAAAGACCACCACAATGGTGAGTCTGCTATTCGATAACATTTCCTGA		MSPYPETTRSGFAGSYHIKTTTMVSLLFDNIS*		MSPYPETTRSGFAGSYHIKTTTMVSLLFDNIS*		GCAGAAGAAA	TCATACTGCG	0	I	0	0	0	0	0
3486	2074	af	AN5501.1	56.m02455	AO070328000018	0			-111	-79			ATGGTGAGTCTGCTATTCGATAACATTTCCTGA		ATGGTGAGTCTGCTATTCGATAACATTTCCTGA		MVSLLFDNIS*		MVSLLFDNIS*		GACCACCACA	TCATACTGCG	0	I	0	0	0	0	0
3487	2074	ao	AN5501.1	56.m02455	AO070328000018	0					-197	-153	ATGGAATCTCTGTTGAATCAGTCACCATGGATTGTTCCGACATAA			ATGGAATCTCTGTTGAATCAGTCACCATGGATTGTTCCGACATAA	MESLLNQSPWIVPT*			MESLLNQSPWIVPT*	CGGAGTATCT	AGCCTGGGGG	0	I	0	0	0	0	0
3488	2074	ao	AN5501.1	56.m02455	AO070328000018	0					-171	-55	ATGGATTGTTCCGACATAAAGCCTGGGGGAGGATGGAATACACGGACGGAGCTTCAAGTCACCACATCGTATACATCACCAAAACAACCATTACTATTCGATTCCCAGTTCAATTAA			ATGGATTGTTCCGACATAAAGCCTGGGGGAGGATGGAATACACGGACGGAGCTTCAAGTCACCACATCGTATACATCACCAAAACAACCATTACTATTCGATTCCCAGTTCAATTAA	MDCSDIKPGGGWNTRTELQVTTSYTSPKQPLLFDSQFN*			MDCSDIKPGGGWNTRTELQVTTSYTSPKQPLLFDSQFN*	ATCAGTCACC	GCTCCTTCCA	0	I	0	0	0	0	0

3489	2074	ao	AN5501.1	56.m02455	AO070328000018	0					-139	-32	ATGGAATACACGGACGGAGCTTCAAGTCACCACATCGTATACATCACCAAAACAACCATTACTATTCGATTCCCAGTTCAATTAAGCTCCTTCCATCTTGCCGCATAA			ATGGAATACACGGACGGAGCTTCAAGTCACCACATCGTATACATCACCAAAACAACCATTACTATTCGATTCCCAGTTCAATTAAGCTCCTTCCATCTTGCCGCATAA	MEYTDGASSHHIVYITKTTITIRFPVQLSSFHLAA*			MEYTDGASSHHIVYITKTTITIRFPVQLSSFHLAA*	CTGGGGGAGG	AGAATTCTTG	0	I	0	0	0	0	0
3490	2075	af	AN4774.1	59.m09209	AO070329000078	0			-211	-113			ATGAATAAGCTTCGTCCTGGGTTAGGTATTTCCGCGGAAATTCAAAAAGCCATTCGAAACCTTTTGCTCAAGGCTGAGGATCGAAGGCGGTTGGGCTAG		ATGAATAAGCTTCGTCCTGGGTTAGGTATTTCCGCGGAAATTCAAAAAGCCATTCGAAACCTTTTGCTCAAGGCTGAGGATCGAAGGCGGTTGGGCTAG		MNKLRPGLGISAEIQKAIRNLLLKAEDRRRLG*		MNKLRPGLGISAEIQKAIRNLLLKAEDRRRLG*		TCTCCAGCGT	ATATAGGAGT	0	H	0	MG10321.1	0	0	0
3492	2080	af	AN6123.1	72.m19036	AO070340000074	0			-167	-120			ATGGTTCGTTTGTTTGGTGATGATCGAGTCACGTGGTTGATAAGATAA		ATGGTTCGTTTGTTTGGTGATGATCGAGTCACGTGGTTGATAAGATAA		MVRLFGDDRVTWLIR*		MVRLFGDDRVTWLIR*		AACAGGGGAC	CCATCTGATG	0	S	0	0	0	0	0
3493	2080	af	AN6123.1	72.m19036	AO070340000074	0			-148	-128			ATGATCGAGTCACGTGGTTGA		ATGATCGAGTCACGTGGTTGA		MIESRG*		MIESRG*		TTGTTTGGTG	TAAGATAACC	0	S	0	0	0	0	0
3494	2080	af	AN6123.1	72.m19036	AO070340000074	0			-112	-80			ATGAACTCATCTCCAACTACTGTAACTAACTGA		ATGAACTCATCTCCAACTACTGTAACTAACTGA		MNSSPTTVTN*		MNSSPTTVTN*		TAACCATCTG	TCTTCAACTT	0	S	0	0	0	0	0
3491	2080	an	AN6123.1	72.m19036	AO070340000074	0	-136	-122					ATGATCACGTGCTGA	ATGATCACGTGCTGA			MITC*	MITC*			ATAGTGATAA	TATGATAACG	0	S	0	0	0	0	0
3497	2082	af	AN5742.1	69.m14840	AO070193000003	0			-218	-174			ATGCGCTACTGCCAGGAGGAGCAACTATCTTCGCTTCTGGGGTAG		ATGCGCTACTGCCAGGAGGAGCAACTATCTTCGCTTCTGGGGTAG		MRYCQEEQLSSLLG*		MRYCQEEQLSSLLG*		GACCTTGATA	CACGGCTGAT	0	G	FG01593.1	0	0	0	0
3498	2082	af	AN5742.1	69.m14840	AO070193000003	0			-165	-142			ATGGCGTCGTGTAGGAGTACATAA		ATGGCGTCGTGTAGGAGTACATAA		MASCRST*		MASCRST*		AGCACGGCTG	AGGGCCTGTT	0	G	FG01593.1	0	0	0	0
3495	2082	an	AN5742.1	69.m14840	AO070193000003	0	-223	-194					ATGCGCTTCCTTAGTACGCTACAACGTTGA	ATGCGCTTCCTTAGTACGCTACAACGTTGA			MRFLSTLQR*	MRFLSTLQR*			CTACCCAAAA	GCAGCTTCAT	0	G	FG01593.1	0	0	0	0
3496	2082	an	AN5742.1	69.m14840	AO070193000003	0	-145	-38					ATGGTGAGCAGCTGCTTTTGGCCCGTACATCTTTCTCTGAGCGCCTGGTTTTGCACGTCTTTATGTGCCGCTTTTTGGCGCCATTTATACCATCAGTTCCCAGTGTGA	ATGGTGAGCAGCTGCTTTTGGCCCGTACATCTTTCTCTGAGCGCCTGGTTTTGCACGTCTTTATGTGCCGCTTTTTGGCGCCATTTATACCATCAGTTCCCAGTGTGA			MVSSCFWPVHLSLSAWFCTSLCAAFWRHLYHQFPV*	MVSSCFWPVHLSLSAWFCTSLCAAFWRHLYHQFPV*			CTACATAAGG	ATTATAAAGT	0	G	FG01593.1	0	0	0	0
3500	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-240	-166	ATGGATCACCTTATCACTACCCCCAATGAGGGCTACCACATTCCCCCCTCTTCGCGGCCTTTTTACCAGGAATGA			ATGGATCACCTTATCACTACCCCCAATGAGGGCTACCACATTCCCCCCTCTTCGCGGCCTTTTTACCAGGAATGA	MDHLITTPNEGYHIPPSSRPFYQE*			MDHLITTPNEGYHIPPSSRPFYQE*	AGGTCTGGGG	CTCGAGCTAC	0	G	FG01593.1	0	0	0	0
3501	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-215	-27	ATGAGGGCTACCACATTCCCCCCTCTTCGCGGCCTTTTTACCAGGAATGACTCGAGCTACGACCTTAGCGAGGTTGAATATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGAACTATTCTACACCCTGA			ATGAGGGCTACCACATTCCCCCCTCTTCGCGGCCTTTTTACCAGGAATGACTCGAGCTACGACCTTAGCGAGGTTGAATATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGAACTATTCTACACCCTGA	MRATTFPPLRGLFTRNDSSYDLSEVEYVEMVPLDEVCACDPGLHVQGVFTTILYLGLNYSTP*			MRATTFPPLRGLFTRNDSSYDLSEVEYVEMVPLDEVCACDPGLHVQGVFTTILYLGLNYSTP*	ACTACCCCCA	AGAGTACCGC	0	G	FG01593.1	0	0	0	0
3502	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-169	-44	ATGACTCGAGCTACGACCTTAGCGAGGTTGAATATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA			ATGACTCGAGCTACGACCTTAGCGAGGTTGAATATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA	MTRATTLARLNMSRWYHWMRSVPATPDCTSRVSSPLSYILG*			MTRATTLARLNMSRWYHWMRSVPATPDCTSRVSSPLSYILG*	TTTACCAGGA	ACTATTCTAC	0	G	FG01593.1	0	0	0	0
3503	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-136	-44	ATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA			ATGTCGAGATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA	MSRWYHWMRSVPATPDCTSRVSSPLSYILG*			MSRWYHWMRSVPATPDCTSRVSSPLSYILG*	GAGGTTGAAT	ACTATTCTAC	0	G	FG01593.1	0	0	0	0
3504	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-128	-27	ATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGAACTATTCTACACCCTGA			ATGGTACCATTGGATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGAACTATTCTACACCCTGA	MVPLDEVCACDPGLHVQGVFTTILYLGLNYSTP*			MVPLDEVCACDPGLHVQGVFTTILYLGLNYSTP*	ATATGTCGAG	AGAGTACCGC	0	G	FG01593.1	0	0	0	0
3505	2082	ao	AN5742.1	69.m14840	AO070193000003	0					-115	-44	ATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA			ATGAGGTCTGTGCCTGCGACCCCGGACTGCACGTCCAGGGTGTCTTCACCACTATCCTATATCTTGGGTTGA	MRSVPATPDCTSRVSSPLSYILG*			MRSVPATPDCTSRVSSPLSYILG*	GTACCATTGG	ACTATTCTAC	0	G	FG01593.1	0	0	0	0
3508	2083	af	AN1397.1	70.m14825	AO070233000013	0			-238	-128			ATGCTACTCCCGGCTTCCGTCTGGCTAGAAAATGCGGGGTGCGATTCAACGTCTTTGACGGCTACATCCATTAGAGAGGGCGGAAATGTTCCTCTCTCAGGAAGGGTATGA		ATGCTACTCCCGGCTTCCGTCTGGCTAGAAAATGCGGGGTGCGATTCAACGTCTTTGACGGCTACATCCATTAGAGAGGGCGGAAATGTTCCTCTCTCAGGAAGGGTATGA		MLLPASVWLENAGCDSTSLTATSIREGGNVPLSGRV*		MLLPASVWLENAGCDSTSLTATSIREGGNVPLSGRV*		AAACTTGGGC	GACACCAAAC	0	Q	0	0	0	0	0
3509	2083	af	AN1397.1	70.m14825	AO070233000013	0			-207	-181			ATGCGGGGTGCGATTCAACGTCTTTGA		ATGCGGGGTGCGATTCAACGTCTTTGA		MRGAIQRL*		MRGAIQRL*		TGGCTAGAAA	CGGCTACATC	0	Q	0	0	0	0	0
3510	2083	af	AN1397.1	70.m14825	AO070233000013	0			-153	-67			ATGTTCCTCTCTCAGGAAGGGTATGAGACACCAAACAGTTCAGTTGCAGGAGTCACAGACGTCTGCCCTATATTACATCTGGGGTGA		ATGTTCCTCTCTCAGGAAGGGTATGAGACACCAAACAGTTCAGTTGCAGGAGTCACAGACGTCTGCCCTATATTACATCTGGGGTGA		MFLSQEGYETPNSSVAGVTDVCPILHLG*		MFLSQEGYETPNSSVAGVTDVCPILHLG*		GAGGGCGGAA	GACGGACATT	0	Q	0	0	0	0	0
3511	2083	af	AN1397.1	70.m14825	AO070233000013	0			-131	-45			ATGAGACACCAAACAGTTCAGTTGCAGGAGTCACAGACGTCTGCCCTATATTACATCTGGGGTGAGACGGACATTCACCTCCATTAA		ATGAGACACCAAACAGTTCAGTTGCAGGAGTCACAGACGTCTGCCCTATATTACATCTGGGGTGAGACGGACATTCACCTCCATTAA		MRHQTVQLQESQTSALYYIWGETDIHLH*		MRHQTVQLQESQTSALYYIWGETDIHLH*		CAGGAAGGGT	CATTGACCAT	0	Q	0	0	0	0	0
3506	2083	an	AN1397.1	70.m14825	AO070233000013	0	-228	-181					ATGCGGGGTGGATCTAAGCGCCTGAACCTTGCTTATAGCGCTCTGTGA	ATGCGGGGTGGATCTAAGCGCCTGAACCTTGCTTATAGCGCTCTGTGA			MRGGSKRLNLAYSAL*	MRGGSKRLNLAYSAL*			CGTTCAGAAA	GACGGAAAAG	0	Q	0	0	0	0	0
3507	2083	an	AN1397.1	70.m14825	AO070233000013	0	-109	-2					ATGAGAGCCCAGGTTACACTATTGAATCTCAGGAATCTAACAACTTCGAGCCACACCAGATACAAACGAGACATTTCAGGTACAAACAACAGAAGCTACTTGCGCTAG	ATGAGAGCCCAGGTTACACTATTGAATCTCAGGAATCTAACAACTTCGAGCCACACCAGATACAAACGAGACATTTCAGGTACAAACAACAGAAGCTACTTGCGCTAG			MRAQVTLLNLRNLTTSSHTRYKRDISGTNNRSYLR*	MRAQVTLLNLRNLTTSSHTRYKRDISGTNNRSYLR*			GCCATACTAT	TATGGCCATC	0	Q	0	0	0	0	0
3513	2083	ao	AN1397.1	70.m14825	AO070233000013	0					-132	-25	ATGTCTAACAGAACGGAAAGCTTCCTCCTTTGCGGCATGCGAAGACTATTACATTTAAAGCCTCATGGACGTGTGGCATCCTCTGTCCGCGACAAACCACGACAGTAG			ATGTCTAACAGAACGGAAAGCTTCCTCCTTTGCGGCATGCGAAGACTATTACATTTAAAGCCTCATGGACGTGTGGCATCCTCTGTCCGCGACAAACCACGACAGTAG	MSNRTESFLLCGMRRLLHLKPHGRVASSVRDKPRQ*			MSNRTESFLLCGMRRLLHLKPHGRVASSVRDKPRQ*	CTACTTTCCT	AAGCAAAACT	0	Q	0	0	0	0	0
3514	2083	ao	AN1397.1	70.m14825	AO070233000013	0					-96	-25	ATGCGAAGACTATTACATTTAAAGCCTCATGGACGTGTGGCATCCTCTGTCCGCGACAAACCACGACAGTAG			ATGCGAAGACTATTACATTTAAAGCCTCATGGACGTGTGGCATCCTCTGTCCGCGACAAACCACGACAGTAG	MRRLLHLKPHGRVASSVRDKPRQ*			MRRLLHLKPHGRVASSVRDKPRQ*	CCTTTGCGGC	AAGCAAAACT	0	Q	0	0	0	0	0
3522	2086	af	AN3147.1	59.m08516	AO070256000043	0			-255	-151			ATGATGTCACTGATCACGTGCTGTCACGCCAGTCTGCACTATTTGTTTAGTTTGTTATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAA		ATGATGTCACTGATCACGTGCTGTCACGCCAGTCTGCACTATTTGTTTAGTTTGTTATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAA		MMSLITCCHASLHYLFSLLCFYCLSLCSGVARPR*		MMSLITCCHASLHYLFSLLCFYCLSLCSGVARPR*		TCAAGGGGCG	TTGTGGCTTG	0	G	FG01974.1	0	NCU07947.1	0	0
3523	2086	af	AN3147.1	59.m08516	AO070256000043	0			-252	-151			ATGTCACTGATCACGTGCTGTCACGCCAGTCTGCACTATTTGTTTAGTTTGTTATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAA		ATGTCACTGATCACGTGCTGTCACGCCAGTCTGCACTATTTGTTTAGTTTGTTATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAA		MSLITCCHASLHYLFSLLCFYCLSLCSGVARPR*		MSLITCCHASLHYLFSLLCFYCLSLCSGVARPR*		AGGGGCGATG	TTGTGGCTTG	0	G	FG01974.1	0	NCU07947.1	0	0
3524	2086	af	AN3147.1	59.m08516	AO070256000043	0			-199	-119			ATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAATTGTGGCTTGCGTGGACTGTTACTGGCGGTGA		ATGTTTTTACTGTTTGTCACTATGCTCAGGGGTCGCCCGGCCCCGCTAATTGTGGCTTGCGTGGACTGTTACTGGCGGTGA		MFLLFVTMLRGRPAPLIVACVDCYWR*		MFLLFVTMLRGRPAPLIVACVDCYWR*		TTAGTTTGTT	GTGACAGCTC	0	G	FG01974.1	0	NCU07947.1	0	0
3525	2086	af	AN3147.1	59.m08516	AO070256000043	0			-178	-119			ATGCTCAGGGGTCGCCCGGCCCCGCTAATTGTGGCTTGCGTGGACTGTTACTGGCGGTGA		ATGCTCAGGGGTCGCCCGGCCCCGCTAATTGTGGCTTGCGTGGACTGTTACTGGCGGTGA		MLRGRPAPLIVACVDCYWR*		MLRGRPAPLIVACVDCYWR*		GTTTGTCACT	GTGACAGCTC	0	G	FG01974.1	0	NCU07947.1	0	0
3515	2086	an	AN3147.1	59.m08516	AO070256000043	0	-221	-108					ATGACGTCGTTGTATGTCGGTGGGAGATCCTGTTTGCGCTGTTTGCGTATGCTAGTGTGTTTGCGTTGTTTGCGCGGCGGCCCCGCCATGCTTCATGGTTGCGTGGCCTACTAG	ATGACGTCGTTGTATGTCGGTGGGAGATCCTGTTTGCGCTGTTTGCGTATGCTAGTGTGTTTGCGTTGTTTGCGCGGCGGCCCCGCCATGCTTCATGGTTGCGTGGCCTACTAG			MTSLYVGGRSCLRCLRMLVCLRCLRGGPAMLHGCVAY*	MTSLYVGGRSCLRCLRMLVCLRCLRGGPAMLHGCVAY*			ACTTGAAGCT	TGGCGGTGAA	0	G	FG01974.1	0	NCU07947.1	0	0
3516	2086	an	AN3147.1	59.m08516	AO070256000043	0	-208	-167					ATGTCGGTGGGAGATCCTGTTTGCGCTGTTTGCGTATGCTAG	ATGTCGGTGGGAGATCCTGTTTGCGCTGTTTGCGTATGCTAG			MSVGDPVCAVCVC*	MSVGDPVCAVCVC*			ACGTCGTTGT	TGTGTTTGCG	0	G	FG01974.1	0	NCU07947.1	0	0
3517	2086	an	AN3147.1	59.m08516	AO070256000043	0	-173	-108					ATGCTAGTGTGTTTGCGTTGTTTGCGCGGCGGCCCCGCCATGCTTCATGGTTGCGTGGCCTACTAG	ATGCTAGTGTGTTTGCGTTGTTTGCGCGGCGGCCCCGCCATGCTTCATGGTTGCGTGGCCTACTAG			MLVCLRCLRGGPAMLHGCVAY*	MLVCLRCLRGGPAMLHGCVAY*			CTGTTTGCGT	TGGCGGTGAA	0	G	FG01974.1	0	NCU07947.1	0	0
3518	2086	an	AN3147.1	59.m08516	AO070256000043	0	-134	-108					ATGCTTCATGGTTGCGTGGCCTACTAG	ATGCTTCATGGTTGCGTGGCCTACTAG			MLHGCVAY*	MLHGCVAY*			CGGCCCCGCC	TGGCGGTGAA	0	G	FG01974.1	0	NCU07947.1	0	0
3519	2086	an	AN3147.1	59.m08516	AO070256000043	0	-127	-83					ATGGTTGCGTGGCCTACTAGTGGCGGTGAAGCTGTTGATGAATGA	ATGGTTGCGTGGCCTACTAGTGGCGGTGAAGCTGTTGATGAATGA			MVAWPTSGGEAVDE*	MVAWPTSGGEAVDE*			GCCATGCTTC	CACCAAACAG	0	G	FG01974.1	0	NCU07947.1	0	0
3520	2086	an	AN3147.1	59.m08516	AO070256000043	0	-90	-37					ATGAATGACACCAAACAGCTCATACCCCTTACTTTTCTCCTATACACAATTTGA	ATGAATGACACCAAACAGCTCATACCCCTTACTTTTCTCCTATACACAATTTGA			MNDTKQLIPLTFLLYTI*	MNDTKQLIPLTFLLYTI*			GAAGCTGTTG	TTCTTTCAAG	0	G	FG01974.1	0	NCU07947.1	0	0
3521	2086	an	AN3147.1	59.m08516	AO070256000043	0	-86	-12					ATGACACCAAACAGCTCATACCCCTTACTTTTCTCCTATACACAATTTGATTCTTTCAAGCGCTGCAGTTTATAG	ATGACACCAAACAGCTCATACCCCTTACTTTTCTCCTATACACAATTTGATTCTTTCAAGCGCTGCAGTTTATAG			MTPNSSYPLLFSYTQFDSFKRCSL*	MTPNSSYPLLFSYTQFDSFKRCSL*			CTGTTGATGA	AACGATTCAT	0	G	FG01974.1	0	NCU07947.1	0	0
3526	2086	ao	AN3147.1	59.m08516	AO070256000043	0					-267	-121	ATGACGTCGTTGTTCTTCAGCTCTGGTCACACCGTTGCTTTGTTTGTGCTGTTTGATTCGTTTGCAGATGTAAATCAGGGGCCGTGGTCTGGACCCGCTGATTGGCCTGGCCGCTTGCGTGGCATTGTCCCGCTAACGGCGGTGTGA			ATGACGTCGTTGTTCTTCAGCTCTGGTCACACCGTTGCTTTGTTTGTGCTGTTTGATTCGTTTGCAGATGTAAATCAGGGGCCGTGGTCTGGACCCGCTGATTGGCCTGGCCGCTTGCGTGGCATTGTCCCGCTAACGGCGGTGTGA	MTSLFFSSGHTVALFVLFDSFADVNQGPWSGPADWPGRLRGIVPLTAV*			MTSLFFSSGHTVALFVLFDSFADVNQGPWSGPADWPGRLRGIVPLTAV*	ACTTCAGGCG	CAGTTAAACA	0	G	FG01974.1	0	NCU07947.1	0	0
3527	2089	an	AN6651.1	62.m03251	AO070269000002	0	-89	-42					ATGAGCCTTGAGCGGTGCGTCAGTTGGAGGCTAACAAGACGAAGATAG	ATGAGCCTTGAGCGGTGCGTCAGTTGGAGGCTAACAAGACGAAGATAG			MSLERCVSWRLTRRR*	MSLERCVSWRLTRRR*			AGTTCAGTCG	AGAATTTCAA	0	EJ	0	MG02572.1	0	YPL226W	0
3528	2091	af	AN5157.1	54.m07060	AO070291000010	0			-142	-116			ATGAGCAAGATATCGATCAAACATTGA		ATGAGCAAGATATCGATCAAACATTGA		MSKISIKH*		MSKISIKH*		TGTACTCCGC	TTTTCGGATA	0	R	0	0	0	0	0
3533	2094	af	AN3119.1	59.m08617	AO070303000028	0			-238	-35			ATGGTGACTCATATCACTGCAGGTTCAAGCTCTCCCTTAATCAGTCTCAATGGCATCACCGGCTCAAGTCCGGCTGCGGAGAAAGAAGAAAATCGCCTCGGACTTGATGCGAATGCGGAGACCCCGCTAACACATCCAAATAAGTTGATGCGACAGCTCTTCACACAGAGACCATGTTTCCTCCATTTTTTATTTCGCAAATAA		ATGGTGACTCATATCACTGCAGGTTCAAGCTCTCCCTTAATCAGTCTCAATGGCATCACCGGCTCAAGTCCGGCTGCGGAGAAAGAAGAAAATCGCCTCGGACTTGATGCGAATGCGGAGACCCCGCTAACACATCCAAATAAGTTGATGCGACAGCTCTTCACACAGAGACCATGTTTCCTCCATTTTTTATTTCGCAAATAA		MVTHITAGSSSPLISLNGITGSSPAAEKEENRLGLDANAETPLTHPNKLMRQLFTQRPCFLHFLFRK*		MVTHITAGSSSPLISLNGITGSSPAAEKEENRLGLDANAETPLTHPNKLMRQLFTQRPCFLHFLFRK*		TTTACAAGTG	CTCGCCTTGA	0	MG	0	0	0	0	0
3534	2094	af	AN3119.1	59.m08617	AO070303000028	0			-189	-109			ATGGCATCACCGGCTCAAGTCCGGCTGCGGAGAAAGAAGAAAATCGCCTCGGACTTGATGCGAATGCGGAGACCCCGCTAA		ATGGCATCACCGGCTCAAGTCCGGCTGCGGAGAAAGAAGAAAATCGCCTCGGACTTGATGCGAATGCGGAGACCCCGCTAA		MASPAQVRLRRKKKIASDLMRMRRPR*		MASPAQVRLRRKKKIASDLMRMRRPR*		ATCAGTCTCA	CACATCCAAA	0	MG	0	0	0	0	0
3535	2094	af	AN3119.1	59.m08617	AO070303000028	0			-132	-109			ATGCGAATGCGGAGACCCCGCTAA		ATGCGAATGCGGAGACCCCGCTAA		MRMRRPR*		MRMRRPR*		CTCGGACTTG	CACATCCAAA	0	MG	0	0	0	0	0
3536	2094	af	AN3119.1	59.m08617	AO070303000028	0			-126	-109			ATGCGGAGACCCCGCTAA		ATGCGGAGACCCCGCTAA		MRRPR*		MRRPR*		CTTGATGCGA	CACATCCAAA	0	MG	0	0	0	0	0

3537	2094	af	AN3119.1	59.m08617	AO070303000028	0			-91	-35			ATGCGACAGCTCTTCACACAGAGACCATGTTTCCTCCATTTTTTATTTCGCAAATAA		ATGCGACAGCTCTTCACACAGAGACCATGTTTCCTCCATTTTTTATTTCGCAAATAA		MRQLFTQRPCFLHFLFRK*		MRQLFTQRPCFLHFLFRK*		AAATAAGTTG	CTCGCCTTGA	0	MG	0	0	0	0	0
3529	2094	an	AN3119.1	59.m08617	AO070303000028	0	-145	-116					ATGCGAATGTGGAGGCAATCCCCACTATAG	ATGCGAATGTGGAGGCAATCCCCACTATAG			MRMWRQSPL*	MRMWRQSPL*			TTCGGACTTG	ACAGGACCAT	0	MG	0	0	0	0	0
3530	2094	an	AN3119.1	59.m08617	AO070303000028	0	-139	-116					ATGTGGAGGCAATCCCCACTATAG	ATGTGGAGGCAATCCCCACTATAG			MWRQSPL*	MWRQSPL*			CTTGATGCGA	ACAGGACCAT	0	MG	0	0	0	0	0
3531	2094	an	AN3119.1	59.m08617	AO070303000028	0	-103	-53					ATGGGCATGTCAACCAGATTCTTTTTTAAGACCAAGACCCCCAAGACCTGA	ATGGGCATGTCAACCAGATTCTTTTTTAAGACCAAGACCCCCAAGACCTGA			MGMSTRFFFKTKTPKT*	MGMSTRFFFKTKTPKT*			AGGACCATAG	GAAAGGCTGG	0	MG	0	0	0	0	0
3532	2094	an	AN3119.1	59.m08617	AO070303000028	0	-97	-53					ATGTCAACCAGATTCTTTTTTAAGACCAAGACCCCCAAGACCTGA	ATGTCAACCAGATTCTTTTTTAAGACCAAGACCCCCAAGACCTGA			MSTRFFFKTKTPKT*	MSTRFFFKTKTPKT*			ATAGATGGGC	GAAAGGCTGG	0	MG	0	0	0	0	0
3538	2094	ao	AN3119.1	59.m08617	AO070303000028	0					-94	-53	ATGATGATATTGCCCTATATGAACCAATTCGCTCGAACCTGA			ATGATGATATTGCCCTATATGAACCAATTCGCTCGAACCTGA	MMILPYMNQFART*			MMILPYMNQFART*	CCGAAGGCGA	GTAAATACAT	0	MG	0	0	0	0	0
3539	2094	ao	AN3119.1	59.m08617	AO070303000028	0					-91	-53	ATGATATTGCCCTATATGAACCAATTCGCTCGAACCTGA			ATGATATTGCCCTATATGAACCAATTCGCTCGAACCTGA	MILPYMNQFART*			MILPYMNQFART*	AAGGCGAATG	GTAAATACAT	0	MG	0	0	0	0	0
3540	2094	ao	AN3119.1	59.m08617	AO070303000028	0					-76	-53	ATGAACCAATTCGCTCGAACCTGA			ATGAACCAATTCGCTCGAACCTGA	MNQFART*			MNQFART*	ATTGCCCTAT	GTAAATACAT	0	MG	0	0	0	0	0
3543	2098	af	AN6669.1	62.m03302	AO070321000010	0			-274	-239			ATGGGGCCGACTGATCAGAGGGAAAGAGAAACGTGA		ATGGGGCCGACTGATCAGAGGGAAAGAGAAACGTGA		MGPTDQRERET*		MGPTDQRERET*		CCGGACCGGC	GAGAAAGAGC	0	R	0	0	0	0	0
3541	2098	an	AN6669.1	62.m03302	AO070321000010	0	-197	-144					ATGCAGGCCGCCGTCAGCTATAAATTGCGGTGCCCTCCCGTCGTCTCCCTCTGA	ATGCAGGCCGCCGTCAGCTATAAATTGCGGTGCCCTCCCGTCGTCTCCCTCTGA			MQAAVSYKLRCPPVVSL*	MQAAVSYKLRCPPVVSL*			TTTCAACCCC	TGCTCACCTG	0	R	0	0	0	0	0
3542	2098	an	AN6669.1	62.m03302	AO070321000010	0	-144	-73					ATGCTCACCTGCTCTCCATCCTCTCTCTCCGTCTCGAGTCTCCTCCGCGCCTCTCCGCACCCCCGGCCTTGA	ATGCTCACCTGCTCTCCATCCTCTCTCTCCGTCTCGAGTCTCCTCCGCGCCTCTCCGCACCCCCGGCCTTGA			MLTCSPSSLSVSSLLRASPHPRP*	MLTCSPSSLSVSSLLRASPHPRP*			TCTCCCTCTG	GCCCCACCGC	0	R	0	0	0	0	0
3544	2098	ao	AN6669.1	62.m03302	AO070321000010	0					-219	-19	ATGCCGATTTGCAACTTTTGTAACACCGCCAGAGTTATAAAAGCACATCCATTCCCCTGCTTCGCTTCGGTTCATTTCTCCCGTTCGCCGTGTTCTCATTCACCCTCCTGTTCTTCCTTGTCGATCGCTGGACAGAGCATCTCTTTTCTCCTTTTCTCTTTCCCACACCCGTATATACCTACGAGCCCTGTGCTAGGTTGA			ATGCCGATTTGCAACTTTTGTAACACCGCCAGAGTTATAAAAGCACATCCATTCCCCTGCTTCGCTTCGGTTCATTTCTCCCGTTCGCCGTGTTCTCATTCACCCTCCTGTTCTTCCTTGTCGATCGCTGGACAGAGCATCTCTTTTCTCCTTTTCTCTTTCCCACACCCGTATATACCTACGAGCCCTGTGCTAGGTTGA	MPICNFCNTARVIKAHPFPCFASVHFSRSPCSHSPSCSSLSIAGQSISFLLFSFPHPYIPTSPVLG*			MPICNFCNTARVIKAHPFPCFASVHFSRSPCSHSPSCSSLSIAGQSISFLLFSFPHPYIPTSPVLG*	GTCCGGCTTT	CGCAGCAGCT	0	R	0	0	0	0	0
3547	2101	af	AN9446.1	59.m09152	AO070327000156	0			-89	-36			ATGGGTCACCAGTGTTCTTTTAAGCTTCTGCGGATAAGGACACTGAACTTGTAA		ATGGGTCACCAGTGTTCTTTTAAGCTTCTGCGGATAAGGACACTGAACTTGTAA		MGHQCSFKLLRIRTLNL*		MGHQCSFKLLRIRTLNL*		TTACTCCGAG	TCACTCCCCT	0	H	0	0	0	YDR531W	0
3545	2101	an	AN9446.1	59.m09152	AO070327000156	0	-237	-220					ATGTTGTCCACTGACTAG	ATGTTGTCCACTGACTAG			MLSTD*	MLSTD*			TGTTCATTGA	AGAGCAACAT	0	H	0	0	0	YDR531W	0
3546	2101	an	AN9446.1	59.m09152	AO070327000156	0	-99	-67					ATGGTAAAAGAACATCAGCTCCTTCTCTTATAA	ATGGTAAAAGAACATCAGCTCCTTCTCTTATAA			MVKEHQLLLL*	MVKEHQLLLL*			CGATATCGAT	CCTCCTTCTT	0	H	0	0	0	YDR531W	0
3548	2101	ao	AN9446.1	59.m09152	AO070327000156	0					-115	-104	ATGTCACCCTGA			ATGTCACCCTGA	MSP*			MSP*	TTACTCCGAG	ACCACCGCGG	0	H	0	0	0	YDR531W	0
3549	2102	af	AN3101.1	59.m08643	AO070334000142	0			-82	-32			ATGAGTGCCACATTATCTTCCTGTGGAGTCGGATTTGCCCAGGACAACTGA		ATGAGTGCCACATTATCTTCCTGTGGAGTCGGATTTGCCCAGGACAACTGA		MSATLSSCGVGFAQDN*		MSATLSSCGVGFAQDN*		CGTCCGAGAG	GTATCTGTCC	0	T	0	0	0	0	0
3550	2102	ao	AN3101.1	59.m08643	AO070334000142	0					-99	-49	ATGAGTGCCTCATTTGGCTCCTGTGGAGTTGGATTCGCCCAGGAGAATTGA			ATGAGTGCCTCATTTGGCTCCTGTGGAGTTGGATTCGCCCAGGAGAATTGA	MSASFGSCGVGFAQEN*			MSASFGSCGVGFAQEN*	CGTCCGAGAG	TTATCTGACC	0	T	0	0	0	0	0
3551	2104	af	AN1491.1	55.m02999	AO070334000203	0			-282	-265			ATGGAATTGTTGGTTTAA		ATGGAATTGTTGGTTTAA		MELLV*		MELLV*		CGTCTATAGA	GACTACTTGT	0	OT	FG02532.1	MG05682.1	NCU00157.1	0	0
3553	2107	af	AN6697.1	65.m07286	AO070339000128	0			-301	-245			ATGTGCAATCGACCCTCTCCCATCCTTGTCTGCTTTCTAGATTTGCACCACATTTGA		ATGTGCAATCGACCCTCTCCCATCCTTGTCTGCTTTCTAGATTTGCACCACATTTGA		MCNRPSPILVCFLDLHHI*		MCNRPSPILVCFLDLHHI*		ACGTTGAGGT	ATTGTGGCAC	0		FG01351.1	0	NCU02668.1	0	0
3554	2107	af	AN6697.1	65.m07286	AO070339000128	0			-182	-132			ATGAACTCTTGTGTATCTGTGCCAATGGCGCTTGTTGCATTGAGTGGATGA		ATGAACTCTTGTGTATCTGTGCCAATGGCGCTTGTTGCATTGAGTGGATGA		MNSCVSVPMALVALSG*		MNSCVSVPMALVALSG*		AGAGAGAGCA	CAATCTCAAT	0		FG01351.1	0	NCU02668.1	0	0
3555	2107	af	AN6697.1	65.m07286	AO070339000128	0			-158	-132			ATGGCGCTTGTTGCATTGAGTGGATGA		ATGGCGCTTGTTGCATTGAGTGGATGA		MALVALSG*		MALVALSG*		ATCTGTGCCA	CAATCTCAAT	0		FG01351.1	0	NCU02668.1	0	0
3556	2107	af	AN6697.1	65.m07286	AO070339000128	0			-135	-58			ATGACAATCTCAATATGCAATGGATTGGATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAA		ATGACAATCTCAATATGCAATGGATTGGATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAA		MTISICNGLDALQYSPELIFSRSVR*		MTISICNGLDALQYSPELIFSRSVR*		CATTGAGTGG	TTGGCATGAA	0		FG01351.1	0	NCU02668.1	0	0
3557	2107	af	AN6697.1	65.m07286	AO070339000128	0			-121	-86			ATGCAATGGATTGGATGCCTTACAATACAGTCCTGA		ATGCAATGGATTGGATGCCTTACAATACAGTCCTGA		MQWIGCLTIQS*		MQWIGCLTIQS*		CAATCTCAAT	ACTCATTTTC	0		FG01351.1	0	NCU02668.1	0	0
3558	2107	af	AN6697.1	65.m07286	AO070339000128	0			-116	-6			ATGGATTGGATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAATTGGCATGAATATAAGATTACCGACATTGTGAGCGCAGTATTAGGGACGTGA		ATGGATTGGATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAATTGGCATGAATATAAGATTACCGACATTGTGAGCGCAGTATTAGGGACGTGA		MDWMPYNTVLNSFSLGAYANWHEYKITDIVSAVLGT*		MDWMPYNTVLNSFSLGAYANWHEYKITDIVSAVLGT*		TCAATATGCA	ACACAATGAA	0		FG01351.1	0	NCU02668.1	0	0
3559	2107	af	AN6697.1	65.m07286	AO070339000128	0			-107	-6			ATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAATTGGCATGAATATAAGATTACCGACATTGTGAGCGCAGTATTAGGGACGTGA		ATGCCTTACAATACAGTCCTGAACTCATTTTCTCTCGGAGCGTACGCTAATTGGCATGAATATAAGATTACCGACATTGTGAGCGCAGTATTAGGGACGTGA		MPYNTVLNSFSLGAYANWHEYKITDIVSAVLGT*		MPYNTVLNSFSLGAYANWHEYKITDIVSAVLGT*		AATGGATTGG	ACACAATGAA	0		FG01351.1	0	NCU02668.1	0	0
3552	2107	an	AN6697.1	65.m07286	AO070339000128	0	-236	-99					ATGTACGTCAATCTTTTCCAGATTCCAGTAATATATCCTCGTGCATTTTTGTCCACTGAGTCGCTGGTTCTAGCGGCTGCCGACACTCGACTCCACACCCATTTGTGTTCCCCCCCTGGACCATCGCAAGCACATTGA	ATGTACGTCAATCTTTTCCAGATTCCAGTAATATATCCTCGTGCATTTTTGTCCACTGAGTCGCTGGTTCTAGCGGCTGCCGACACTCGACTCCACACCCATTTGTGTTCCCCCCCTGGACCATCGCAAGCACATTGA			MYVNLFQIPVIYPRAFLSTESLVLAAADTRLHTHLCSPPGPSQAH*	MYVNLFQIPVIYPRAFLSTESLVLAAADTRLHTHLCSPPGPSQAH*			CCGTCAATCG	CCTGCGGGTG	0		FG01351.1	0	NCU02668.1	0	0
3561	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-326	-192	ATGTATGTATCCTCGTTCCGAGAAAATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGACCATCGGCTATGCTACCCATGTCGCATGTTGA			ATGTATGTATCCTCGTTCCGAGAAAATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGACCATCGGCTATGCTACCCATGTCGCATGTTGA	MYVSSFRENDGHSLQIAPRLDSSHSSPRCSERWVTIGYATHVAC*			MYVSSFRENDGHSLQIAPRLDSSHSSPRCSERWVTIGYATHVAC*	TGCGACGTCG	ACTGTTGCCG	0		FG01351.1	0	NCU02668.1	0	0
3562	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-322	-224	ATGTATCCTCGTTCCGAGAAAATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA			ATGTATCCTCGTTCCGAGAAAATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA	MYPRSEKMMDTPSKLHLAWTPVIVHRGVRSVG*			MYPRSEKMMDTPSKLHLAWTPVIVHRGVRSVG*	ACGTCGATGT	CCATCGGCTA	0		FG01351.1	0	NCU02668.1	0	0
3563	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-301	-224	ATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA			ATGATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA	MMDTPSKLHLAWTPVIVHRGVRSVG*			MMDTPSKLHLAWTPVIVHRGVRSVG*	TTCCGAGAAA	CCATCGGCTA	0		FG01351.1	0	NCU02668.1	0	0
3564	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-298	-224	ATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA			ATGGACACTCCCTCCAAATTGCACCTCGCCTGGACTCCAGTCATAGTTCACCGAGGTGTTCGGAGCGTTGGGTGA	MDTPSKLHLAWTPVIVHRGVRSVG*			MDTPSKLHLAWTPVIVHRGVRSVG*	CGAGAAAATG	CCATCGGCTA	0		FG01351.1	0	NCU02668.1	0	0
3565	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-214	-137	ATGCTACCCATGTCGCATGTTGAACTGTTGCCGCCAGTAACGTTTCCATATTGTGCCGCAGCATGCGTGGATCAGTAA			ATGCTACCCATGTCGCATGTTGAACTGTTGCCGCCAGTAACGTTTCCATATTGTGCCGCAGCATGCGTGGATCAGTAA	MLPMSHVELLPPVTFPYCAAACVDQ*			MLPMSHVELLPPVTFPYCAAACVDQ*	ACCATCGGCT	CATGGCGCGC	0		FG01351.1	0	NCU02668.1	0	0
3566	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-205	-137	ATGTCGCATGTTGAACTGTTGCCGCCAGTAACGTTTCCATATTGTGCCGCAGCATGCGTGGATCAGTAA			ATGTCGCATGTTGAACTGTTGCCGCCAGTAACGTTTCCATATTGTGCCGCAGCATGCGTGGATCAGTAA	MSHVELLPPVTFPYCAAACVDQ*			MSHVELLPPVTFPYCAAACVDQ*	TATGCTACCC	CATGGCGCGC	0		FG01351.1	0	NCU02668.1	0	0
3567	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-198	-175	ATGTTGAACTGTTGCCGCCAGTAA			ATGTTGAACTGTTGCCGCCAGTAA	MLNCCRQ*			MLNCCRQ*	CCCATGTCGC	CGTTTCCATA	0		FG01351.1	0	NCU02668.1	0	0
3568	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-152	-102	ATGCGTGGATCAGTAACATGGCGCGCAATCTGTTCACATGTGACTCCATAG			ATGCGTGGATCAGTAACATGGCGCGCAATCTGTTCACATGTGACTCCATAG	MRGSVTWRAICSHVTP*			MRGSVTWRAICSHVTP*	GTGCCGCAGC	CCATATCCTC	0		FG01351.1	0	NCU02668.1	0	0
3569	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-135	-73	ATGGCGCGCAATCTGTTCACATGTGACTCCATAGCCATATCCTCATGGATATACGCAAGCTAA			ATGGCGCGCAATCTGTTCACATGTGACTCCATAGCCATATCCTCATGGATATACGCAAGCTAA	MARNLFTCDSIAISSWIYAS*			MARNLFTCDSIAISSWIYAS*	GATCAGTAAC	CTGGTATTTT	0		FG01351.1	0	NCU02668.1	0	0
3570	2107	ao	AN6697.1	65.m07286	AO070339000128	0					-91	-56	ATGGATATACGCAAGCTAACTGGTATTTTGCATTGA			ATGGATATACGCAAGCTAACTGGTATTTTGCATTGA	MDIRKLTGILH*			MDIRKLTGILH*	CCATATCCTC	TATAGCCATA	0		FG01351.1	0	NCU02668.1	0	0
3571	2108	ao	AN6010.1	72.m19133	AO070340000269	0					-185	-156	ATGTTTCCTTCTCCCCCGGAAAAGACTTGA			ATGTTTCCTTCTCCCCCGGAAAAGACTTGA	MFPSPPEKT*			MFPSPPEKT*	CCTTCTTTTT	AAACCATCAT	0	O	0	MG04191.1	NCU08693.1	0	0
3573	2110	af	AN2153.1	72.m19688	AO070343000202	0			-259	-158			ATGAGGGAAGAGCATGAGGAGAAAAACAGAAAAAAAAATAGTCGAGTGGGAAAAAGTGCGATCCACCAGCGGACGAAGACAAACAGTGCAAACATCCTATGA		ATGAGGGAAGAGCATGAGGAGAAAAACAGAAAAAAAAATAGTCGAGTGGGAAAAAGTGCGATCCACCAGCGGACGAAGACAAACAGTGCAAACATCCTATGA		MREEHEEKNRKKNSRVGKSAIHQRTKTNSANIL*		MREEHEEKNRKKNSRVGKSAIHQRTKTNSANIL*		CAGGGAGAAG	AATCGCAGAT	0	J	0	MG07084.1	NCU08026.1	0	0
3574	2110	af	AN2153.1	72.m19688	AO070343000202	0			-246	-88			ATGAGGAGAAAAACAGAAAAAAAAATAGTCGAGTGGGAAAAAGTGCGATCCACCAGCGGACGAAGACAAACAGTGCAAACATCCTATGAAATCGCAGATTTCCGTTTCTGGACTGGGAAAGAAAGTCGCTGGGAGGTTACTTGTCTGGATTTGTGTTAA		ATGAGGAGAAAAACAGAAAAAAAAATAGTCGAGTGGGAAAAAGTGCGATCCACCAGCGGACGAAGACAAACAGTGCAAACATCCTATGAAATCGCAGATTTCCGTTTCTGGACTGGGAAAGAAAGTCGCTGGGAGGTTACTTGTCTGGATTTGTGTTAA		MRRKTEKKIVEWEKVRSTSGRRQTVQTSYEIADFRFWTGKESRWEVTCLDLC*		MRRKTEKKIVEWEKVRSTSGRRQTVQTSYEIADFRFWTGKESRWEVTCLDLC*		AGGGAAGAGC	AGAAGCATTG	0	J	0	MG07084.1	NCU08026.1	0	0
3572	2110	an	AN2153.1	72.m19688	AO070343000202	0	-136	-11					ATGGCAAACGGTGCAAACAGCCTCAAAATTGGAGATTCCGCTTCGAGTGGACTGCTTCGACAGCTCGGTCAACTTAATTATTCTCATACGATCGCTATCGGTCGCTCAAGGAACTGCGGGTGCTGA	ATGGCAAACGGTGCAAACAGCCTCAAAATTGGAGATTCCGCTTCGAGTGGACTGCTTCGACAGCTCGGTCAACTTAATTATTCTCATACGATCGCTATCGGTCGCTCAAGGAACTGCGGGTGCTGA			MANGANSLKIGDSASSGLLRQLGQLNYSHTIAIGRSRNCGC*	MANGANSLKIGDSASSGLLRQLGQLNYSHTIAIGRSRNCGC*			GACTCCACAC	GACATGTGTA	0	J	0	MG07084.1	NCU08026.1	0	0
3576	2111	an	AN7437.1	57.m05908	AO070229000007	0	-217	-68					ATGGGTATCTCCTCTCGTATATTCAAGTTAAAAGCTTGCAGAAGCATGTCTTGTCAAGTGATTTTCATCAGTATTCACGATCCTCCCGTGTCATACACTAATATCATCTTCTACTTACAGCGAATATGCATTGAGAGTAGACTGGAATAA	ATGGGTATCTCCTCTCGTATATTCAAGTTAAAAGCTTGCAGAAGCATGTCTTGTCAAGTGATTTTCATCAGTATTCACGATCCTCCCGTGTCATACACTAATATCATCTTCTACTTACAGCGAATATGCATTGAGAGTAGACTGGAATAA			MGISSRIFKLKACRSMSCQVIFISIHDPPVSYTNIIFYLQRICIESRLE*	MGISSRIFKLKACRSMSCQVIFISIHDPPVSYTNIIFYLQRICIESRLE*			CCATATTGAT	GAAAAGCGCC	0	R	0	0	NCU07504.1	0	0
3577	2111	an	AN7437.1	57.m05908	AO070229000007	0	-172	-68					ATGTCTTGTCAAGTGATTTTCATCAGTATTCACGATCCTCCCGTGTCATACACTAATATCATCTTCTACTTACAGCGAATATGCATTGAGAGTAGACTGGAATAA	ATGTCTTGTCAAGTGATTTTCATCAGTATTCACGATCCTCCCGTGTCATACACTAATATCATCTTCTACTTACAGCGAATATGCATTGAGAGTAGACTGGAATAA			MSCQVIFISIHDPPVSYTNIIFYLQRICIESRLE*	MSCQVIFISIHDPPVSYTNIIFYLQRICIESRLE*			TTGCAGAAGC	GAAAAGCGCC	0	R	0	0	NCU07504.1	0	0

3579	2111	ao	AN7437.1	57.m05908	AO070229000007	0					-222	-103	ATGTCTCATCAAGGCATACCTCCTCGTCCATGGCTTTTTCTCACCCTCTCAGTCTGCCTTCTGCTTATTGTACTATATCGCTTCACCCCCCCCCCCCCCCCCCCCCTCCCTCCCCGGGTGA			ATGTCTCATCAAGGCATACCTCCTCGTCCATGGCTTTTTCTCACCCTCTCAGTCTGCCTTCTGCTTATTGTACTATATCGCTTCACCCCCCCCCCCCCCCCCCCCTCCCTCCCCGGGTGA	MSHQGIPPRPWLFLTLSVCLLLIVLYRFTPPPPPPSLPG*			MSHQGIPPRPWLFLTLSVCLLLIVLYRFTPPPPPPSLPG*	ACTTCAAGGT	TTGGAAAGGT	0	R	0	0	NCU07504.1	0	0
3580	2111	ao	AN7437.1	57.m05908	AO070229000007	0					-193	-77	ATGGCTTTTTCTCACCCTCTCAGTCTGCCTTCTGCTTATTGTACTATATCGCTTCACCCCCCCCCCCCCCCCCCCCCCTCCCTCCCCGGGTGATTGGAAAGGTGCAGAAGAGCGATTAA			ATGGCTTTTTCTCACCCTCTCAGTCTGCCTTCTGCTTATTGTACTATATCGCTTCACCCCCCCCCCCCCCCCCCCCCTCCCTCCCCGGGTGATTGGAAAGGTGCAGAAGAGCGATTAA	MAFSHPLSLPSAYCTISLHPPPPPPLPPRVIGKVQKSD*			MAFSHPLSLPSAYCTISLHPPPPPPLPPRVIGKVQKSD*	CTCCTCGTCC	CCGGAAACCA	0	R	0	0	NCU07504.1	0	0
3581	2112	an	AN5820.1	72.m18947	AO070260000026	0	-213	-133					ATGGCGACAAAATGGCGAGACTTAAGCGGGCGGCTATCCTCGGCGAGGGGCATTCTGCTGGTTGCGTACATTGAGTTTTGA	ATGGCGACAAAATGGCGAGACTTAAGCGGGCGGCTATCCTCGGCGAGGGGCATTCTGCTGGTTGCGTACATTGAGTTTTGA			MATKWRDLSGRLSSARGILLVAYIEF*	MATKWRDLSGRLSSARGILLVAYIEF*			GCAACATCAG	ACTTTTGTCT	0	E	0	0	0	0	0
3582	2112	an	AN5820.1	72.m18947	AO070260000026	0	-202	-140					ATGGCGAGACTTAAGCGGGCGGCTATCCTCGGCGAGGGGCATTCTGCTGGTTGCGTACATTGA	ATGGCGAGACTTAAGCGGGCGGCTATCCTCGGCGAGGGGCATTCTGCTGGTTGCGTACATTGA			MARLKRAAILGEGHSAGCVH*	MARLKRAAILGEGHSAGCVH*			TGGCGACAAA	GTTTTGAACT	0	E	0	0	0	0	0
3583	2112	ao	AN5820.1	72.m18947	AO070260000026	0					-228	-37	ATGAGAAGAACCACTACGTTCTTCAAATGTGGCGGCAACGGTTACCTTCGGGTGGGGTGTGTAACATCTTACGAGATTTTTTTCCTTTTCCTTGTTGAACCTTTCCCTCATTTTAACGCTTCTTTCCCTTTCCCTTTTTACCCTCCTTTACTTTCTTTTCCTTCTTGTTTTCTCCCTTTCTCTCTGGCTTGA			ATGAGAAGAACCACTACGTTCTTCAAATGTGGCGGCAACGGTTACCTTCGGGTGGGGTGTGTAACATCTTACGAGATTTTTTTCCTTTTCCTTGTTGAACCTTTCCCTCATTTTAACGCTTCTTTCCCTTTCCCTTTTTACCCTCCTTTACTTTCTTTTCCTTCTTGTTTTCTCCCTTTCTCTCTGGCTTGA	MRRTTTFFKCGGNGYLRVGCVTSYEIFFLFVEPFPHFNASFPFPFYPPLLSFPSCFLPFSLA*			MRRTTTFFKCGGNGYLRVGCVTSYEIFFLFVEPFPHFNASFPFPFYPPLLSFPSCFLPFSLA*	AGCATATCAT	ATTCGTTTGC	0	E	0	0	0	0	0
3584	2112	ao	AN5820.1	72.m18947	AO070260000026	0					-202	-131	ATGTGGCGGCAACGGTTACCTTCGGGTGGGGTGTGTAACATCTTACGAGATTTTTTTCCTTTTCCTTGTTGA			ATGTGGCGGCAACGGTTACCTTCGGGTGGGGTGTGTAACATCTTACGAGATTTTTTTCCTTTTCCTTGTTGA	MWRQRLPSGGVCNILRDFFPFPC*			MWRQRLPSGGVCNILRDFFPFPC*	CGTTCTTCAA	ACCTTTCCCT	0	E	0	0	0	0	0
3585	2113	af	AN6655.1	62.m03451	AO070269000011	0			-240	-97			ATGCCCCGCGCCGGAGCTGTGTCACAGTATCGTGTCTCTTCTTGGGGAGCTCGTCGACTCCTGACCGTCTTTTCCTCCGTACATTCTCGAGTGCTCAGTTGCCTCATAGATTGCCTGTCTTTTCTTGGACTTTTAATCTCATAG		ATGCCCCGCGCCGGAGCTGTGTCACAGTATCGTGTCTCTTCTTGGGGAGCTCGTCGACTCCTGACCGTCTTTTCCTCCGTACATTCTCGAGTGCTCAGTTGCCTCATAGATTGCCTGTCTTTTCTTGGACTTTTAATCTCATAG		MPRAGAVSQYRVSSWGARRLLTVFSSVHSRVLSCLIDCLSFLGLLIS*		MPRAGAVSQYRVSSWGARRLLTVFSSVHSRVLSCLIDCLSFLGLLIS*		TTCGATCCAC	GAAGCCGTTT	0	IQR	FG00177.1	0	0	0	0
3586	2113	ao	AN6655.1	62.m03451	AO070269000011	0					-80	-30	ATGACATCATCCAGAAGTCCGATGTCCCCGCCGAGGATAACTACTCACTGA			ATGACATCATCCAGAAGTCCGATGTCCCCGCCGAGGATAACTACTCACTGA	MTSSRSPMSPPRITTH*			MTSSRSPMSPPRITTH*	CAGTCTGCTT	GAATCGCTTG	0	IQR	FG00177.1	0	0	0	0
3588	2115	af	AN5110.1	54.m07050	AO070291000069	0			-225	-157			ATGCTGCTTGTCATTTCCACTGAACATTTTAGCATTAGCTTTTTTCAGACATCGAAGATTTTAAAGTGA		ATGCTGCTTGTCATTTCCACTGAACATTTTAGCATTAGCTTTTTTCAGACATCGAAGATTTTAAAGTGA		MLLVISTEHFSISFFQTSKILK*		MLLVISTEHFSISFFQTSKILK*		TGCAGTAATC	TCGCATCATA	0	S	FG05197.1	0	NCU01758.1	0	0
3592	2116	af	AN2045.1	58.m07633	AO070292000012	0			-194	-87			ATGTTGCTCTTTTTCACTGATTTCAAACATTCAACATCTGTCAAGCAACTTTGCCTTGGCCATGCTGCATCACGACCGCCTGATGCTGCCTTGTCGTTTCGTTATTGA		ATGTTGCTCTTTTTCACTGATTTCAAACATTCAACATCTGTCAAGCAACTTTGCCTTGGCCATGCTGCATCACGACCGCCTGATGCTGCCTTGTCGTTTCGTTATTGA		MLLFFTDFKHSTSVKQLCLGHAASRPPDAALSFRY*		MLLFFTDFKHSTSVKQLCLGHAASRPPDAALSFRY*		TAACATCCGA	CTAAACTCCA	0	G	0	0	0	0	0
3593	2116	af	AN2045.1	58.m07633	AO070292000012	0			-133	-83			ATGCTGCATCACGACCGCCTGATGCTGCCTTGTCGTTTCGTTATTGACTAA		ATGCTGCATCACGACCGCCTGATGCTGCCTTGTCGTTTCGTTATTGACTAA		MLHHDRLMLPCRFVID*		MLHHDRLMLPCRFVID*		TGCCTTGGCC	ACTCCAGCTT	0	G	0	0	0	0	0
3594	2116	af	AN2045.1	58.m07633	AO070292000012	0			-112	-83			ATGCTGCCTTGTCGTTTCGTTATTGACTAA		ATGCTGCCTTGTCGTTTCGTTATTGACTAA		MLPCRFVID*		MLPCRFVID*		CGACCGCCTG	ACTCCAGCTT	0	G	0	0	0	0	0
3589	2116	an	AN2045.1	58.m07633	AO070292000012	0	-209	-93					ATGAAGTTTCACTTGCAACCTGGGAATTCTTTCTTCTCACAAATTTCCAACCGAACCAAGGTTGAAACTGCGCTGGCATTAGCATGCCGCAGTACGCTCGTTCATGTTGCTGATTGA	ATGAAGTTTCACTTGCAACCTGGGAATTCTTTCTTCTCACAAATTTCCAACCGAACCAAGGTTGAAACTGCGCTGGCATTAGCATGCCGCAGTACGCTCGTTCATGTTGCTGATTGA			MKFHLQPGNSFFSQISNRTKVETALALACRSTLVHVAD*	MKFHLQPGNSFFSQISNRTKVETALALACRSTLVHVAD*			GACTTCCCAG	TCAAGAATTG	0	G	0	0	0	0	0
3590	2116	an	AN2045.1	58.m07633	AO070292000012	0	-126	-97					ATGCCGCAGTACGCTCGTTCATGTTGCTGA	ATGCCGCAGTACGCTCGTTCATGTTGCTGA			MPQYARSCC*	MPQYARSCC*			TGGCATTAGC	TTGATCAAGA	0	G	0	0	0	0	0
3591	2116	an	AN2045.1	58.m07633	AO070292000012	0	-106	-35					ATGTTGCTGATTGATCAAGAATTGATCTGGCTCAAGCTGTACACAGCTATCCCTTCCTTTCAATGCAATTGA	ATGTTGCTGATTGATCAAGAATTGATCTGGCTCAAGCTGTACACAGCTATCCCTTCCTTTCAATGCAATTGA			MLLIDQELIWLKLYTAIPSFQCN*	MLLIDQELIWLKLYTAIPSFQCN*			ACGCTCGTTC	CGTCTATAAT	0	G	0	0	0	0	0
3595	2116	ao	AN2045.1	58.m07633	AO070292000012	0					-241	-41	ATGGATGCTCCAGGCTTTTCTCTTCCTGACTTGGATAATTTGGATCTCTTCTTTCCTCTCCACAGCATTAGATGTGCTATTCTAACCTCTGAGCATGTTGTATTTACATTCCTTAATGTTGTTTCTTTCTTTTTCGACCTAATCTTGAGCTCCAAAGAGCTCATTAGCATTCCTTCGTCCACTGTCCTTCCAGTTTTCTAA			ATGGATGCTCCAGGCTTTTCTCTTCCTGACTTGGATAATTTGGATCTCTTCTTTCCTCTCCACAGCATTAGATGTGCTATTCTAACCTCTGAGCATGTTGTATTTACATTCCTTAATGTTGTTTCTTTCTTTTTCGACCTAATCTTGAGCTCCAAAGAGCTCATTAGCATTCCTTCGTCCACTGTCCTTCCAGTTTTCTAA	MDAPGFSLPDLDNLDLFFPLHSIRCAILTSEHVVFTFLNVVSFFFDLILSSKELISIPSSTVLPVF*			MDAPGFSLPDLDNLDLFFPLHSIRCAILTSEHVVFTFLNVVSFFFDLILSSKELISIPSSTVLPVF*	TCCCCCCTTG	TCAAGACCAC	0	G	0	0	0	0	0
3596	2116	ao	AN2045.1	58.m07633	AO070292000012	0					-237	-157	ATGCTCCAGGCTTTTCTCTTCCTGACTTGGATAATTTGGATCTCTTCTTTCCTCTCCACAGCATTAGATGTGCTATTCTAA			ATGCTCCAGGCTTTTCTCTTCCTGACTTGGATAATTTGGATCTCTTCTTTCCTCTCCACAGCATTAGATGTGCTATTCTAA	MLQAFLFLTWIIWISSFLSTALDVLF*			MLQAFLFLTWIIWISSFLSTALDVLF*	CCCTTGATGG	CCTCTGAGCA	0	G	0	0	0	0	0
3597	2116	ao	AN2045.1	58.m07633	AO070292000012	0					-170	-150	ATGTGCTATTCTAACCTCTGA			ATGTGCTATTCTAACCTCTGA	MCYSNL*			MCYSNL*	ACAGCATTAG	GCATGTTGTA	0	G	0	0	0	0	0
3598	2116	ao	AN2045.1	58.m07633	AO070292000012	0					-147	-100	ATGTTGTATTTACATTCCTTAATGTTGTTTCTTTCTTTTTCGACCTAA			ATGTTGTATTTACATTCCTTAATGTTGTTTCTTTCTTTTTCGACCTAA	MLYLHSLMLFLSFST*			MLYLHSLMLFLSFST*	ACCTCTGAGC	TCTTGAGCTC	0	G	0	0	0	0	0
3599	2116	ao	AN2045.1	58.m07633	AO070292000012	0					-126	-100	ATGTTGTTTCTTTCTTTTTCGACCTAA			ATGTTGTTTCTTTCTTTTTCGACCTAA	MLFLSFST*			MLFLSFST*	ACATTCCTTA	TCTTGAGCTC	0	G	0	0	0	0	0
3601	2118	af	AN2529.1	59.m08450	AO070300000122	0			-247	-122			ATGATTCAAATTTGTATATATTTGTATCCATCGTGCCAGAGGCCTTGCCGTGCTCTACGAACTCTCAAGACTCATCATTGTTCTTTATCATCCCAGTGCTCTGCTAGCTATATAGGAAGGTCGTAA		ATGATTCAAATTTGTATATATTTGTATCCATCGTGCCAGAGGCCTTGCCGTGCTCTACGAACTCTCAAGACTCATCATTGTTCTTTATCATCCCAGTGCTCTGCTAGCTATATAGGAAGGTCGTAA		MIQICIYLYPSCQRPCRALRTLKTHHCSLSSQCSASYIGRS*		MIQICIYLYPSCQRPCRALRTLKTHHCSLSSQCSASYIGRS*		TCCATTTTCT	AAGTTGCCGA	0	I	FG09979.1	MG07309.1	0	0	0
3600	2118	an	AN2529.1	59.m08450	AO070300000122	0	-241	-179					ATGCGATCAAATATTATTCTCGTGCTATATTTAGGGTTCTATTGCGAGCGAGATATAGTCTAA	ATGCGATCAAATATTATTCTCGTGCTATATTTAGGGTTCTATTGCGAGCGAGATATAGTCTAA			MRSNIILVLYLGFYCERDIV*	MRSNIILVLYLGFYCERDIV*			CTGGCTGTTA	CCCATTTCCT	0	I	FG09979.1	MG07309.1	0	0	0
3605	2119	af	AN9339.1	52.m03838	AO070315000069	0			-125	-114			ATGGATATATAA		ATGGATATATAA		MDI*		MDI*		AGTGGGTTTG	ACCAGCCTCT	0	P	FG06733.1	MG06442.1	0	0	0
3606	2119	af	AN9339.1	52.m03838	AO070315000069	0			-73	-17			ATGATCAAGCACAAGCCCAAATTGGACGCGCTTCCTTTCCAATCTGTCACCGCATAA		ATGATCAAGCACAAGCCCAAATTGGACGCGCTTCCTTTCCAATCTGTCACCGCATAA		MIKHKPKLDALPFQSVTA*		MIKHKPKLDALPFQSVTA*		GATCCCCTTG	CGGAGACTTA	0	P	FG06733.1	MG06442.1	0	0	0
3602	2119	an	AN9339.1	52.m03838	AO070315000069	0	-201	-106					ATGGAAAGATGGGAGGCCGTATTGTGTTCCTGCAGAGACGATCGTCCTGTTGCCTCGCTTGGTATAAATACACCCGTGTGGCCTGTCCTACGCTAG	ATGGAAAGATGGGAGGCCGTATTGTGTTCCTGCAGAGACGATCGTCCTGTTGCCTCGCTTGGTATAAATACACCCGTGTGGCCTGTCCTACGCTAG			MERWEAVLCSCRDDRPVASLGINTPVWPVLR*	MERWEAVLCSCRDDRPVASLGINTPVWPVLR*			CATCAATGTG	GAATGCAGCG	0	P	FG06733.1	MG06442.1	0	0	0
3603	2119	an	AN9339.1	52.m03838	AO070315000069	0	-193	-41					ATGGGAGGCCGTATTGTGTTCCTGCAGAGACGATCGTCCTGTTGCCTCGCTTGGTATAAATACACCCGTGTGGCCTGTCCTACGCTAGGAATGCAGCGCCCTTTACCCGACCTCAAGCCCGACCTCCTCTGCATTCCTATCCCTCTTTCCTAA	ATGGGAGGCCGTATTGTGTTCCTGCAGAGACGATCGTCCTGTTGCCTCGCTTGGTATAAATACACCCGTGTGGCCTGTCCTACGCTAGGAATGCAGCGCCCTTTACCCGACCTCAAGCCCGACCTCCTCTGCATTCCTATCCCTCTTTCCTAA			MGGRIVFLQRRSSCCLAWYKYTRVACPTLGMQRPLPDLKPDLLCIPIPLS*	MGGRIVFLQRRSSCCLAWYKYTRVACPTLGMQRPLPDLKPDLLCIPIPLS*			TGATGGAAAG	AAACCACCAA	0	P	FG06733.1	MG06442.1	0	0	0
3604	2119	an	AN9339.1	52.m03838	AO070315000069	0	-103	-41					ATGCAGCGCCCTTTACCCGACCTCAAGCCCGACCTCCTCTGCATTCCTATCCCTCTTTCCTAA	ATGCAGCGCCCTTTACCCGACCTCAAGCCCGACCTCCTCTGCATTCCTATCCCTCTTTCCTAA			MQRPLPDLKPDLLCIPIPLS*	MQRPLPDLKPDLLCIPIPLS*			TACGCTAGGA	AAACCACCAA	0	P	FG06733.1	MG06442.1	0	0	0
3607	2119	ao	AN9339.1	52.m03838	AO070315000069	0					-238	-218	ATGAATTCCTTGGCTGCTTAA			ATGAATTCCTTGGCTGCTTAA	MNSLAA*			MNSLAA*	TGGGATGCGA	TTAAACGATC	0	P	FG06733.1	MG06442.1	0	0	0
3616	2126	af	AN1177.1	70.m15040	AO070331000173	0			-209	-180			ATGAATGCAAGGCAGGTGAGGGGAGCTTAA		ATGAATGCAAGGCAGGTGAGGGGAGCTTAA		MNARQVRGA*		MNARQVRGA*		AATTGCACCG	TTGAGTCAAA	0	U	0	MG06860.1	0	0	0
3617	2126	af	AN1177.1	70.m15040	AO070331000173	0			-205	-191			ATGCAAGGCAGGTGA		ATGCAAGGCAGGTGA		MQGR*		MQGR*		GCACCGATGA	GGGGAGCTTA	0	U	0	MG06860.1	0	0	0
3618	2126	af	AN1177.1	70.m15040	AO070331000173	0			-102	-79			ATGCTAAACAACAACTTGTACTAA		ATGCTAAACAACAACTTGTACTAA		MLNNNLY*		MLNNNLY*		TCCCTCTCGA	TCAACTCCCA	0	U	0	MG06860.1	0	0	0
3615	2126	an	AN1177.1	70.m15040	AO070331000173	0	-225	-211					ATGATTCCCAGGTAG	ATGATTCCCAGGTAG			MIPR*	MIPR*			ATTTGCGCTG	GCGAGGGGGG	0	U	0	MG06860.1	0	0	0
3619	2126	ao	AN1177.1	70.m15040	AO070331000173	0					-228	-214	ATGCAAGGCTGGTGA			ATGCAAGGCTGGTGA	MQGW*			MQGW*	CATGCTGTGA	GGGGAGTCGA	0	U	0	MG06860.1	0	0	0
3621	2128	af	AN1477.1	55.m02982	AO070334000159	0			-198	-181			ATGGGAGTGGTGGGGTAA		ATGGGAGTGGTGGGGTAA		MGVVG*		MGVVG*		GTTTAGCCTG	TTTCTTGGGG	0		FG08946.1	0	NCU01900.1	0	0
3622	2128	af	AN1477.1	55.m02982	AO070334000159	0			-127	-47			ATGTATAAGAGGAACGTTACGTTCAATATCAGGATGCTCATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		ATGTATAAGAGGAACGTTACGTTCAATATCAGGATGCTCATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		MYKRNVTFNIRMLMRPLQHFSPFSLD*		MYKRNVTFNIRMLMRPLQHFSPFSLD*		GGCGCTCAAG	ACTAGACTAG	0		FG08946.1	0	NCU01900.1	0	0
3623	2128	af	AN1477.1	55.m02982	AO070334000159	0			-94	-47			ATGCTCATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		ATGCTCATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		MLMRPLQHFSPFSLD*		MLMRPLQHFSPFSLD*		CAATATCAGG	ACTAGACTAG	0		FG08946.1	0	NCU01900.1	0	0
3624	2128	af	AN1477.1	55.m02982	AO070334000159	0			-88	-47			ATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		ATGCGGCCACTTCAGCACTTCAGTCCCTTCTCGCTCGACTAG		MRPLQHFSPFSLD*		MRPLQHFSPFSLD*		CAGGATGCTC	ACTAGACTAG	0		FG08946.1	0	NCU01900.1	0	0
3620	2128	an	AN1477.1	55.m02982	AO070334000159	0	-200	-138					ATGCCCAGCACCTTGTACTTTAGCCGGCGGATAAATAGGCGGCCATTGCCATCAATATTCTAA	ATGCCCAGCACCTTGTACTTTAGCCGGCGGATAAATAGGCGGCCATTGCCATCAATATTCTAA			MPSTLYFSRRINRRPLPSIF*	MPSTLYFSRRINRRPLPSIF*			GAAATTGGAA	GTCAAGATCA	0		FG08946.1	0	NCU01900.1	0	0
3625	2128	ao	AN1477.1	55.m02982	AO070334000159	0					-146	-126	ATGTTTAGGCTATACGGCTAA			ATGTTTAGGCTATACGGCTAA	MFRLYG*			MFRLYG*	GTATCCATTT	ACTAGATTAT	0		FG08946.1	0	NCU01900.1	0	0
3628	2129	af	AN2925.1	59.m09078	AO070337000214	0			-110	-99			ATGGCTTGTTGA		ATGGCTTGTTGA		MAC*		MAC*		GACAGTTAGC	TTTGATAATT	0	O	0	0	0	0	0
3626	2129	an	AN2925.1	59.m09078	AO070337000214	0	-138	-118					ATGTGGTTGTCTACTTGCTGA	ATGTGGTTGTCTACTTGCTGA			MWLSTC*	MWLSTC*			TGAATTGCTG	GCCAATGTTC	0	O	0	0	0	0	0
3627	2129	an	AN2925.1	59.m09078	AO070337000214	0	-113	-102					ATGTTCTGCTGA	ATGTTCTGCTGA			MFC*	MFC*			TGCTGAGCCA	TCGATACCCC	0	O	0	0	0	0	0
3629	2129	ao	AN2925.1	59.m09078	AO070337000214	0					-147	-118	ATGCGATTCTTGCCGAGGATAACTGGCTGA			ATGCGATTCTTGCCGAGGATAACTGGCTGA	MRFLPRITG*			MRFLPRITG*	ACGTTTGTTA	TGGCTATGAC	0	O	0	0	0	0	0
3630	2129	ao	AN2925.1	59.m09078	AO070337000214	0					-118	-101	ATGGCTATGACAGGTTGA			ATGGCTATGACAGGTTGA	MAMTG*			MAMTG*	TAACTGGCTG	TTTGACTTAC	0	O	0	0	0	0	0
3631	2129	ao	AN2925.1	59.m09078	AO070337000214	0					-112	-101	ATGACAGGTTGA			ATGACAGGTTGA	MTG*			MTG*	GCTGATGGCT	TTTGACTTAC	0	O	0	0	0	0	0
3640	2136	af	AN4329.1	58.m07991	AO070240000007	0			-237	-58			ATGAGCTCCAAAGGGGTCTTGATGCTGCTCAATGAGCCAATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		ATGAGCTCCAAAGGGGTCTTGATGCTGCTCAATGAGCCAATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		MSSKGVLMLLNEPMKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		MSSKGVLMLLNEPMKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		TTGCCTAGCT	TCACTTCTTT	0	R	0	0	0	0	0
3641	2136	af	AN4329.1	58.m07991	AO070240000007	0			-216	-58			ATGCTGCTCAATGAGCCAATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		ATGCTGCTCAATGAGCCAATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		MLLNEPMKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		MLLNEPMKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		AGGGGTCTTG	TCACTTCTTT	0	R	0	0	0	0	0
3642	2136	af	AN4329.1	58.m07991	AO070240000007	0			-206	-195			ATGAGCCAATGA		ATGAGCCAATGA		MSQ*		MSQ*		ATGCTGCTCA	AGAAGATGCA	0	R	0	0	0	0	0

3643	2136	af	AN4329.1	58.m07991	AO070240000007	0			-198	-58			ATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		ATGAAGAAGATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		MKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		MKKMQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		CAATGAGCCA	TCACTTCTTT	0	R	0	0	0	0	0
3644	2136	af	AN4329.1	58.m07991	AO070240000007	0			-189	-58			ATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		ATGCAAAGAAGAATTGCAGACCATCACGCCAGTTGTCGGCAAGTTCCACGGTTAAGCCGACCTCCGAGCTCCCCCGCCCTGCCCCGCGTCCAAGGAAGCTCTCATGGGCTAAACTTCATTTTCTTGCTTTGA		MQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		MQRRIADHHASCRQVPRLSRPPSSPALPRVQGSSHGLNFIFLL*		AATGAAGAAG	TCACTTCTTT	0	R	0	0	0	0	0
3638	2136	an	AN4329.1	58.m07991	AO070240000007	0	-259	-215					ATGCAGAATTGTAGTCCGATCCCACTCCAATTGCCCGGTAGATGA	ATGCAGAATTGTAGTCCGATCCCACTCCAATTGCCCGGTAGATGA			MQNCSPIPLQLPGR*	MQNCSPIPLQLPGR*			AGTCTTTGAA	GATTGGCTAA	0	R	0	0	0	0	0
3639	2136	an	AN4329.1	58.m07991	AO070240000007	0	-218	-153					ATGAGATTGGCTAACAAGGGAACTCCCGGCTCTCCATTCCTTCGGCCCCCGAGGCTGAACCGGTGA	ATGAGATTGGCTAACAAGGGAACTCCCGGCTCTCCATTCCTTCGGCCCCCGAGGCTGAACCGGTGA			MRLANKGTPGSPFLRPPRLNR*	MRLANKGTPGSPFLRPPRLNR*			TGCCCGGTAG	ATTGGTGAAT	0	R	0	0	0	0	0
3645	2138	an	AN5005.1	59.m08905	AO070255000035	0	-254	-156					ATGAATCCGGGCCTTGCAAGTAATTTAACCCAACTGAGACGAGCCGCGTCGCGACGCGTTTCCACTAAAAAAAGCGCGTGGAGAACTCTCCAATTTTAA	ATGAATCCGGGCCTTGCAAGTAATTTAACCCAACTGAGACGAGCCGCGTCGCGACGCGTTTCCACTAAAAAAAGCGCGTGGAGAACTCTCCAATTTTAA			MNPGLASNLTQLRRAASRRVSTKKSAWRTLQF*	MNPGLASNLTQLRRAASRRVSTKKSAWRTLQF*			ATTTGTCGCG	CCGCCCCATC	0		0	0	0	0	0
3646	2138	an	AN5005.1	59.m08905	AO070255000035	0	-67	-50					ATGTTTATACTTCACTGA	ATGTTTATACTTCACTGA			MFILH*	MFILH*			AATTACTTTC	ATAGCCGAAC	0		0	0	0	0	0
3648	2138	ao	AN5005.1	59.m08905	AO070255000035	0					-119	-45	ATGCGAACCATTCCCCAATTGCATTTGTATTTTACGCATCAAACCTTCCTAATTGTCTATATGTTCCTTCCATAA			ATGCGAACCATTCCCCAATTGCATTTGTATTTTACGCATCAAACCTTCCTAATTGTCTATATGTTCCTTCCATAA	MRTIPQLHLYFTHQTFLIVYMFLP*			MRTIPQLHLYFTHQTFLIVYMFLP*	CACTCCTTCC	TCTATATCTC	0		0	0	0	0	0
3661	2144	af	AN8406.1	52.m04077	AO070302000057	0			-158	-90			ATGGCGCCACATCAAGCGGCAACTGTAAGCCGAGGTATCCCAGCCCTCAACGCGGGGTATGTGGATTGA		ATGGCGCCACATCAAGCGGCAACTGTAAGCCGAGGTATCCCAGCCCTCAACGCGGGGTATGTGGATTGA		MAPHQAATVSRGIPALNAGYVD*		MAPHQAATVSRGIPALNAGYVD*		TCAACTCCAA	TCACCTGGAG	0	ER	0	0	0	0	0
3662	2144	af	AN8406.1	52.m04077	AO070302000057	0			-100	-20			ATGTGGATTGATCACCTGGAGGCTTCGAATAGAAATACTCGACGGGCAGCTATACACCTCAAAACACCAACCACCAACTAA		ATGTGGATTGATCACCTGGAGGCTTCGAATAGAAATACTCGACGGGCAGCTATACACCTCAAAACACCAACCACCAACTAA		MWIDHLEASNRNTRRAAIHLKTPTTN*		MWIDHLEASNRNTRRAAIHLKTPTTN*		AACGCGGGGT	GAACAGGGAA	0	ER	0	0	0	0	0
3658	2144	an	AN8406.1	52.m04077	AO070302000057	0	-254	-117					ATGCCGCTAAAAAGGCTTTTTGAAGACCACTCGGCGACTCTGGCCGAATTGATCTTCCGCAAATTCGACTTCAAACCCCGCAACGAATTACTCTCCGCATCGCCGAACACCAAATGCCGCGCCTGGGAACGAGGCTGA	ATGCCGCTAAAAAGGCTTTTTGAAGACCACTCGGCGACTCTGGCCGAATTGATCTTCCGCAAATTCGACTTCAAACCCCGCAACGAATTACTCTCCGCATCGCCGAACACCAAATGCCGCGCCTGGGAACGAGGCTGA			MPLKRLFEDHSATLAELIFRKFDFKPRNELLSASPNTKCRAWERG*	MPLKRLFEDHSATLAELIFRKFDFKPRNELLSASPNTKCRAWERG*			ATCCCGGGTC	CCAACCGAGG	0	ER	0	0	0	0	0
3659	2144	an	AN8406.1	52.m04077	AO070302000057	0	-141	-43					ATGCCGCGCCTGGGAACGAGGCTGACCAACCGAGGTCAAGTAACCGGGCGCCATATAAATCACCCCTCACATCATGCCACCGTGCCAATCCTGGATTGA	ATGCCGCGCCTGGGAACGAGGCTGACCAACCGAGGTCAAGTAACCGGGCGCCATATAAATCACCCCTCACATCATGCCACCGTGCCAATCCTGGATTGA			MPRLGTRLTNRGQVTGRHINHPSHHATVPILD*	MPRLGTRLTNRGQVTGRHINHPSHHATVPILD*			CGAACACCAA	TCCACGATCC	0	ER	0	0	0	0	0
3660	2144	an	AN8406.1	52.m04077	AO070302000057	0	-68	-24					ATGCCACCGTGCCAATCCTGGATTGATCCACGATCCAACGTCTAA	ATGCCACCGTGCCAATCCTGGATTGATCCACGATCCAACGTCTAA			MPPCQSWIDPRSNV*	MPPCQSWIDPRSNV*			CCCTCACATC	AGCAGATAAA	0	ER	0	0	0	0	0
3663	2144	ao	AN8406.1	52.m04077	AO070302000057	0					-135	-70	ATGCGGACGTCACAGCCGAGGCTGTTGTGCCCCTCAGGCGGGGTGATCGAGACTCGAGAGGAGTAA			ATGCGGACGTCACAGCCGAGGCTGTTGTGCCCCTCAGGCGGGGTGATCGAGACTCGAGAGGAGTAA	MRTSQPRLLCPSGGVIETREE*			MRTSQPRLLCPSGGVIETREE*	CAGAGTGAAC	GTAGTTCTTC	0	ER	0	0	0	0	0
3667	2147	af	AN6856.1	71.m15269	AO070314000073	0			-179	-81			ATGATCTCAGCGACTCGACCATATGACATCACACCGTCCAGCATCTGGTATAAAGCCCTATCAATCTCTGACCATGACCACACATTCATACTTCAATGA		ATGATCTCAGCGACTCGACCATATGACATCACACCGTCCAGCATCTGGTATAAAGCCCTATCAATCTCTGACCATGACCACACATTCATACTTCAATGA		MISATRPYDITPSSIWYKALSISDHDHTFILQ*		MISATRPYDITPSSIWYKALSISDHDHTFILQ*		CCCACAAAAT	GCTCAAATAC	0		FG08562.1	0	NCU02596.1	0	0
3668	2147	af	AN6856.1	71.m15269	AO070314000073	0			-84	-61			ATGAGCTCAAATACAATCCACTAA		ATGAGCTCAAATACAATCCACTAA		MSSNTIH*		MSSNTIH*		TCATACTTCA	TTGACCTCAC	0		FG08562.1	0	NCU02596.1	0	0
3664	2147	an	AN6856.1	71.m15269	AO070314000073	0	-212	-195					ATGATCTCAGTGCTTTAG	ATGATCTCAGTGCTTTAG			MISVL*	MISVL*			GGCCCCACGT	ACTCCGAATA	0		FG08562.1	0	NCU02596.1	0	0
3665	2147	an	AN6856.1	71.m15269	AO070314000073	0	-180	-55					ATGATGACATCACTCTTCGAACCTTTATACCTATATAGACCTGCTCTGCAAGCGTATTGTAGCTTTTCATCAATTACACTCACACTCATCGCCCAGCCATATAATAATCCGAATAGCCACATATAG	ATGATGACATCACTCTTCGAACCTTTATACCTATATAGACCTGCTCTGCAAGCGTATTGTAGCTTTTCATCAATTACACTCACACTCATCGCCCAGCCATATAATAATCCGAATAGCCACATATAG			MMTSLFEPLYLYRPALQAYCSFSSITLTLIAQPYNNPNSHI*	MMTSLFEPLYLYRPALQAYCSFSSITLTLIAQPYNNPNSHI*			CGAATATGGT	TCTCACAGCC	0		FG08562.1	0	NCU02596.1	0	0
3666	2147	an	AN6856.1	71.m15269	AO070314000073	0	-177	-55					ATGACATCACTCTTCGAACCTTTATACCTATATAGACCTGCTCTGCAAGCGTATTGTAGCTTTTCATCAATTACACTCACACTCATCGCCCAGCCATATAATAATCCGAATAGCCACATATAG	ATGACATCACTCTTCGAACCTTTATACCTATATAGACCTGCTCTGCAAGCGTATTGTAGCTTTTCATCAATTACACTCACACTCATCGCCCAGCCATATAATAATCCGAATAGCCACATATAG			MTSLFEPLYLYRPALQAYCSFSSITLTLIAQPYNNPNSHI*	MTSLFEPLYLYRPALQAYCSFSSITLTLIAQPYNNPNSHI*			ATATGGTATG	TCTCACAGCC	0		FG08562.1	0	NCU02596.1	0	0
3669	2147	ao	AN6856.1	71.m15269	AO070314000073	0					-199	-149	ATGTGCCCCACCTATGATCTCAGCGACCTCAACCATGACATCACAATATAG			ATGTGCCCCACCTATGATCTCAGCGACCTCAACCATGACATCACAATATAG	MCPTYDLSDLNHDITI*			MCPTYDLSDLNHDITI*	TATTGTTGTA	CAATACAAGA	0		FG08562.1	0	NCU02596.1	0	0
3670	2147	ao	AN6856.1	71.m15269	AO070314000073	0					-186	-118	ATGATCTCAGCGACCTCAACCATGACATCACAATATAGCAATACAAGACAGTATAAAGCATCGTCCTGA			ATGATCTCAGCGACCTCAACCATGACATCACAATATAGCAATACAAGACAGTATAAAGCATCGTCCTGA	MISATSTMTSQYSNTRQYKASS*			MISATSTMTSQYSNTRQYKASS*	TGCCCCACCT	CCTCAATTCC	0		FG08562.1	0	NCU02596.1	0	0
3671	2147	ao	AN6856.1	71.m15269	AO070314000073	0					-165	-118	ATGACATCACAATATAGCAATACAAGACAGTATAAAGCATCGTCCTGA			ATGACATCACAATATAGCAATACAAGACAGTATAAAGCATCGTCCTGA	MTSQYSNTRQYKASS*			MTSQYSNTRQYKASS*	GACCTCAACC	CCTCAATTCC	0		FG08562.1	0	NCU02596.1	0	0
3673	2148	af	AN9159.1	56.m02469	AO070317000031	0			-213	-142			ATGGCGATCATTCTCGATATGCAATCTGCGCCGAGGCTTAGCCACAGGACCAGTCAAAGCCTCGGTGAGTAG		ATGGCGATCATTCTCGATATGCAATCTGCGCCGAGGCTTAGCCACAGGACCAGTCAAAGCCTCGGTGAGTAG		MAIILDMQSAPRLSHRTSQSLGE*		MAIILDMQSAPRLSHRTSQSLGE*		TCTTCACCCA	TCCGAAAGGA	0		0	0	0	0	0
3674	2148	af	AN9159.1	56.m02469	AO070317000031	0			-195	-142			ATGCAATCTGCGCCGAGGCTTAGCCACAGGACCAGTCAAAGCCTCGGTGAGTAG		ATGCAATCTGCGCCGAGGCTTAGCCACAGGACCAGTCAAAGCCTCGGTGAGTAG		MQSAPRLSHRTSQSLGE*		MQSAPRLSHRTSQSLGE*		CATTCTCGAT	TCCGAAAGGA	0		0	0	0	0	0
3672	2148	an	AN9159.1	56.m02469	AO070317000031	0	-240	-208					ATGCATAATTGCGCTAAATATAAGCTGCACTAA	ATGCATAATTGCGCTAAATATAAGCTGCACTAA			MHNCAKYKLH*	MHNCAKYKLH*			TGCACTATTC	ACGCTCACCT	0		0	0	0	0	0
3675	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-220	-185	ATGAATGGCTGCCCTGAATGCAACCTGCTAAGATAA			ATGAATGGCTGCCCTGAATGCAACCTGCTAAGATAA	MNGCPECNLLR*			MNGCPECNLLR*	AAGAAGAGGA	TCAATCATGC	0		0	0	0	0	0
3676	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-216	-190	ATGGCTGCCCTGAATGCAACCTGCTAA			ATGGCTGCCCTGAATGCAACCTGCTAA	MAALNATC*			MAALNATC*	AGAGGAATGA	GATAATCAAT	0		0	0	0	0	0
3677	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-203	-144	ATGCAACCTGCTAAGATAATCAATCATGCATGCATGATCCTGGAATTCCACTCCATCTGA			ATGCAACCTGCTAAGATAATCAATCATGCATGCATGATCCTGGAATTCCACTCCATCTGA	MQPAKIINHACMILEFHSI*			MQPAKIINHACMILEFHSI*	GCTGCCCTGA	TCTCACATGA	0		0	0	0	0	0
3678	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-178	-167	ATGCATGCATGA			ATGCATGCATGA	MHA*			MHA*	ATAATCAATC	TCCTGGAATT	0		0	0	0	0	0
3679	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-170	-144	ATGATCCTGGAATTCCACTCCATCTGA			ATGATCCTGGAATTCCACTCCATCTGA	MILEFHSI*			MILEFHSI*	TCATGCATGC	TCTCACATGA	0		0	0	0	0	0
3680	2148	ao	AN9159.1	56.m02469	AO070317000031	0					-137	-54	ATGACCCCGCCAACCCCTTCACCGACTTGCTTCTTATTTATAAAATCCCCCCACCACAAACAAGATCACCGCTCACTCGCATAA			ATGACCCCGCCAACCCCTTCACCGACTTGCTTCTTATTTATAAAATCCCCCCACCACAAACAAGATCACCGCTCACTCGCATAA	MTPPTPSPTCFLFIKSPHHKQDHRSLA*			MTPPTPSPTCFLFIKSPHHKQDHRSLA*	CTGATCTCAC	ACTCCACCCT	0		0	0	0	0	0
3684	2155	af	AN4771.1	59.m09211	AO070329000081	0			-222	-109			ATGGGCTTGATCGGCATATCTAGCAGCAGATACAGAATACTTTGTACAGAGTATCTCATCTTCCCCATAAGCAAACAAGACAAACTGATCGTTTATCACCCGCTTTATCAGTGA		ATGGGCTTGATCGGCATATCTAGCAGCAGATACAGAATACTTTGTACAGAGTATCTCATCTTCCCCATAAGCAAACAAGACAAACTGATCGTTTATCACCCGCTTTATCAGTGA		MGLIGISSSRYRILCTEYLIFPISKQDKLIVYHPLYQ*		MGLIGISSSRYRILCTEYLIFPISKQDKLIVYHPLYQ*		GTCTTCGTTG	TCCGCCAAAA	0	R	0	0	0	0	0
3682	2155	an	AN4771.1	59.m09211	AO070329000081	0	-168	-139					ATGTTGCCTCAAAGCGTAACAATCACGTGA	ATGTTGCCTCAAAGCGTAACAATCACGTGA			MLPQSVTIT*	MLPQSVTIT*			AATTGCCCAG	TATACAGATG	0	R	0	0	0	0	0
3683	2155	an	AN4771.1	59.m09211	AO070329000081	0	-131						ATGGGCGGGTGCAAACCGTGCAAACTCTTATCGCCAAAGCAGCCGAAGCAAAAAAAAAGATATCCTGATACTGGCTGGCACGGTTGGGTTTTGCGAGACACACCCAACTCGAGGGTCTTCTACCGCTCCTAA	ATGGGCGGGTGCAAACCGTGCAAACTCTTATCGCCAAAGCAGCCGAAGCAAAAAAAAAGATATCCTGATACTGGCTGGCACGGTTGGGTTTTGCGAGACACACCCAACTCGAGGGTCTTCTACCGCTCCTAA			MGGCKPCKLLSPKQPKQKKRYPDTGWHGWVLRDTPNSRVFYRS*	MGGCKPCKLLSPKQPKQKKRYPDTGWHGWVLRDTPNSRVFYRS*			TGATATACAG	TGCTCTCAGA	0	R	0	0	0	0	0
3688	2156	af	AN2830.1	71.m15507	AO070330000102	0			-174	-136			ATGAACCCCATTATTCACATGCGTGAGCATCAACAATGA		ATGAACCCCATTATTCACATGCGTGAGCATCAACAATGA		MNPIIHMREHQQ*		MNPIIHMREHQQ*		GGGGTTTTTC	TCTTCTGGTC	0	I	0	0	0	0	0
3689	2156	af	AN2830.1	71.m15507	AO070330000102	0			-156	-136			ATGCGTGAGCATCAACAATGA		ATGCGTGAGCATCAACAATGA		MREHQQ*		MREHQQ*		CATTATTCAC	TCTTCTGGTC	0	I	0	0	0	0	0
3690	2156	af	AN2830.1	71.m15507	AO070330000102	0			-139	-92			ATGATCTTCTGGTCTTCAAACCATGATGCCACAGAAGTTGAAGCATAA		ATGATCTTCTGGTCTTCAAACCATGATGCCACAGAAGTTGAAGCATAA		MIFWSSNHDATEVEA*		MIFWSSNHDATEVEA*		AGCATCAACA	AATAGAGGCC	0	I	0	0	0	0	0
3691	2156	af	AN2830.1	71.m15507	AO070330000102	0			-117	-28			ATGATGCCACAGAAGTTGAAGCATAAAATAGAGGCCATTCCCCGGCCAACTCCCTCCCTCTTGGATGGAGTATTATTTGCAGGCAGATAA		ATGATGCCACAGAAGTTGAAGCATAAAATAGAGGCCATTCCCCGGCCAACTCCCTCCCTCTTGGATGGAGTATTATTTGCAGGCAGATAA		MMPQKLKHKIEAIPRPTPSLLDGVLFAGR*		MMPQKLKHKIEAIPRPTPSLLDGVLFAGR*		TCTTCAAACC	TAGAGGGGCC	0	I	0	0	0	0	0
3692	2156	af	AN2830.1	71.m15507	AO070330000102	0			-114	-28			ATGCCACAGAAGTTGAAGCATAAAATAGAGGCCATTCCCCGGCCAACTCCCTCCCTCTTGGATGGAGTATTATTTGCAGGCAGATAA		ATGCCACAGAAGTTGAAGCATAAAATAGAGGCCATTCCCCGGCCAACTCCCTCCCTCTTGGATGGAGTATTATTTGCAGGCAGATAA		MPQKLKHKIEAIPRPTPSLLDGVLFAGR*		MPQKLKHKIEAIPRPTPSLLDGVLFAGR*		TCAAACCATG	TAGAGGGGCC	0	I	0	0	0	0	0
3685	2156	an	AN2830.1	71.m15507	AO070330000102	0	-154	-143					ATGAACGCTTGA	ATGAACGCTTGA			MNA*	MNA*			CCACGAACGC	ACGCATGAAA	0	I	0	0	0	0	0
3686	2156	an	AN2830.1	71.m15507	AO070330000102	0	-138	-82					ATGAAAATCACATGCGGCCAATTTGAGCCGAAATGGGGCTCTGTGGGAATCGATTAG	ATGAAAATCACATGCGGCCAATTTGAGCCGAAATGGGGCTCTGTGGGAATCGATTAG			MKITCGQFEPKWGSVGID*	MKITCGQFEPKWGSVGID*			GCTTGAACGC	ATATAAGAAT	0	I	0	0	0	0	0
3687	2156	an	AN2830.1	71.m15507	AO070330000102	0	-127	-113					ATGCGGCCAATTTGA	ATGCGGCCAATTTGA			MRPI*	MRPI*			TGAAAATCAC	GCCGAAATGG	0	I	0	0	0	0	0
3693	2156	ao	AN2830.1	71.m15507	AO070330000102	0					-153	-106	ATGCCACGGCAGTCTAAAAGTTTGCCGTTTCGTGGCCAAAGGTTGTAG			ATGCCACGGCAGTCTAAAAGTTTGCCGTTTCGTGGCCAAAGGTTGTAG	MPRQSKSLPFRGQRL*			MPRQSKSLPFRGQRL*	TTAGAAATAC	TGGCCATGGC	0	I	0	0	0	0	0
3694	2156	ao	AN2830.1	71.m15507	AO070330000102	0					-100	-83	ATGGCAGAAGCTTCCTGA			ATGGCAGAAGCTTCCTGA	MAEAS*			MAEAS*	TGTAGTGGCC	TATTAAATAG	0	I	0	0	0	0	0
3696	2157	an	AN6721.1	53.m03953	AO070335000072	0	-171	-139					ATGAACTACAGGCAGATATCAGAGGTATCATGA	ATGAACTACAGGCAGATATCAGAGGTATCATGA			MNYRQISEVS*	MNYRQISEVS*			AGCAGATCGA	CGGAGTTGGA	0	R	0	0	0	0	0
3697	2157	an	AN6721.1	53.m03953	AO070335000072	0	-142	-95					ATGACGGAGTTGGAAGCAACCGCAACCTCTACGCTACATCATGATTAG	ATGACGGAGTTGGAAGCAACCGCAACCTCTACGCTACATCATGATTAG			MTELEATATSTLHHD*	MTELEATATSTLHHD*			CAGAGGTATC	TTGACGCGCT	0	R	0	0	0	0	0
3698	2157	an	AN6721.1	53.m03953	AO070335000072	0	-102	-91					ATGATTAGTTGA	ATGATTAGTTGA			MIS*	MIS*			ACGCTACATC	CGCGCTGAGA	0	R	0	0	0	0	0
3700	2157	ao	AN6721.1	53.m03953	AO070335000072	0					-127	-104	ATGCGACGCTGGCAAGGCATATAA			ATGCGACGCTGGCAAGGCATATAA	MRRWQGI*			MRRWQGI*	CATTCTCGAG	ATCGCCATTC	0	R	0	0	0	0	0
3701	2158	af	AN0446.1	54.m06638	AO070338000308	0			-265	-218			ATGTATTTCACTCAACCCCTTGGTTTGGACTTCCTTATTTGTATCTGA		ATGTATTTCACTCAACCCCTTGGTTTGGACTTCCTTATTTGTATCTGA		MYFTQPLGLDFLICI*		MYFTQPLGLDFLICI*		GCCTCGGTGC	TGTTGCTGTC	0	R	0	0	0	0	0
3702	2158	af	AN0446.1	54.m06638	AO070338000308	0			-218	-132			ATGTTGCTGTCCGGCCCGAAGTGTTTGGTTAGGGCTTCGTTCTGGATAACTGACCTTGGGCTCCTACTCATCTCGTCTACTTGCTAG		ATGTTGCTGTCCGGCCCGAAGTGTTTGGTTAGGGCTTCGTTCTGGATAACTGACCTTGGGCTCCTACTCATCTCGTCTACTTGCTAG		MLLSGPKCLVRASFWITDLGLLLISSTC*		MLLSGPKCLVRASFWITDLGLLLISSTC*		TTTGTATCTG	CTTTTTTTAG	0	R	0	0	0	0	0

3704	2161	af	AN6143.1	72.m19021	AO070340000060	0			-226	-167			ATGAGCTCTCAAGGGCGGAGCTTTCACCTCGTCTTGGCGCGCTTTTCTTCCTGCAACTAA		ATGAGCTCTCAAGGGCGGAGCTTTCACCTCGTCTTGGCGCGCTTTTCTTCCTGCAACTAA		MSSQGRSFHLVLARFSSCN*		MSSQGRSFHLVLARFSSCN*		GCTAGACATC	AAATCCCCAG	0		FG05487.1	0	0	0	0
3703	2161	an	AN6143.1	72.m19021	AO070340000060	0	-182	-87					ATGAGCGCAGGAGAGCTTAGTTTGGGTTTGTCTTGGCGCCTCAGCTTTTGCTTCGTCCGGCCATTCTTCAACAAGTCTACCGAAAATTTCTTGTGA	ATGAGCGCAGGAGAGCTTAGTTTGGGTTTGTCTTGGCGCCTCAGCTTTTGCTTCGTCCGGCCATTCTTCAACAAGTCTACCGAAAATTTCTTGTGA			MSAGELSLGLSWRLSFCFVRPFFNKSTENFL*	MSAGELSLGLSWRLSFCFVRPFFNKSTENFL*			AAGCGGAGGG	AGCTCAACGG	0		FG05487.1	0	0	0	0
3705	2161	ao	AN6143.1	72.m19021	AO070340000060	0					-234	-55	ATGCAGTCAAGGAAAGCTCACCAATGGAGCTTGTTCACGGAAACTTACGCTGCTCTTGGCGCGCGCCCGTTGTCCAGTGCTTCCACCAAAATTTCCCCAGACACTGTTCTGTTACCGGCGCATTCTCCCGCCAGGATTCCCAGCACTGTCACTTTCATTTCGCAACATTATCGCTGGTAG			ATGCAGTCAAGGAAAGCTCACCAATGGAGCTTGTTCACGGAAACTTACGCTGCTCTTGGCGCGCGCCCGTTGTCCAGTGCTTCCACCAAAATTTCCCCAGACACTGTTCTGTTACCGGCGCATTCTCCCGCCAGGATTCCCAGCACTGTCACTTTCATTTCGCAACATTATCGCTGGTAG	MQSRKAHQWSLFTETYAALGARPLSSASTKISPDTVLLPAHSPARIPSTVTFISQHYRW*			MQSRKAHQWSLFTETYAALGARPLSSASTKISPDTVLLPAHSPARIPSTVTFISQHYRW*	GTTGTGGCAG	GGGTGGGAAG	0		FG05487.1	0	0	0	0
3707	2162	af	AN6067.1	72.m19056	AO070340000108	0			-187	-170			ATGAAATCGTTTAGTTGA		ATGAAATCGTTTAGTTGA		MKSFS*		MKSFS*		TACCTGCTGT	AACGATCCCA	0	J	0	MG08866.1	NCU00366.1	0	0
3708	2162	af	AN6067.1	72.m19056	AO070340000108	0			-108	-31			ATGTCTTGTCTTTTCAAGATATCACTGGTCCATAATCCCTCCCGCTTCGTTTTCAAGCAGCTCGTCACCGTTTTGTGA		ATGTCTTGTCTTTTCAAGATATCACTGGTCCATAATCCCTCCCGCTTCGTTTTCAAGCAGCTCGTCACCGTTTTGTGA		MSCLFKISLVHNPSRFVFKQLVTVL*		MSCLFKISLVHNPSRFVFKQLVTVL*		CTCGCTACGC	AAATAATAAT	0	J	0	MG08866.1	NCU00366.1	0	0
3706	2162	an	AN6067.1	72.m19056	AO070340000108	0	-123	-49					ATGTCTTGTCTCTTGAAGAATTCTTTCATCCAGGTTCCCTCCCGCTTCTTCAATCGCCTCTCGTCGCCTCTTTGA	ATGTCTTGTCTCTTGAAGAATTCTTTCATCCAGGTTCCCTCCCGCTTCTTCAATCGCCTCTCGTCGCCTCTTTGA			MSCLLKNSFIQVPSRFFNRLSSPL*	MSCLLKNSFIQVPSRFFNRLSSPL*			CTCGCGGCGT	ATCCTCTGAA	0	J	0	MG08866.1	NCU00366.1	0	0
3709	2162	ao	AN6067.1	72.m19056	AO070340000108	0					-94	-26	ATGTCTTGTACTTCCAAGGCATCCTTAGTCCGGAATCCCTCCCGCTTCGTTTTCAGACACCTTAAGTAA			ATGTCTTGTACTTCCAAGGCATCCTTAGTCCGGAATCCCTCCCGCTTCGTTTTCAGACACCTTAAGTAA	MSCTSKASLVRNPSRFVFRHLK*			MSCTSKASLVRNPSRFVFRHLK*	CTCAATACGC	ACAAAGATTT	0	J	0	MG08866.1	NCU00366.1	0	0
3711	2164	af	AN3579.1	58.m07377	AO070342000170	0			-152	-141			ATGCGCAGTTGA		ATGCGCAGTTGA		MRS*		MRS*		TCCCATCTTT	TCGTGATCTT	0	S	0	0	0	0	0
3712	2164	af	AN3579.1	58.m07377	AO070342000170	0			-91	-74			ATGATCCTACACCTGTAA		ATGATCCTACACCTGTAA		MILHL*		MILHL*		GCTCGTGTCC	GCGCTGATCA	0	S	0	0	0	0	0
3710	2164	an	AN3579.1	58.m07377	AO070342000170	0	-231	-190					ATGTTCTTTCTCTCGCTGGGGGTCACATCTCGCCCGCTCTAA	ATGTTCTTTCTCTCGCTGGGGGTCACATCTCGCCCGCTCTAA			MFFLSLGVTSRPL*	MFFLSLGVTSRPL*			CCGCTCACTC	CTGATAAACG	0	S	0	0	0	0	0
3713	2164	ao	AN3579.1	58.m07377	AO070342000170	0					-239	-213	ATGTATCAGCTCACGCTGGGGGCATAG			ATGTATCAGCTCACGCTGGGGGCATAG	MYQLTLGA*			MYQLTLGA*	CCAACTTCCC	ATACGCCCTC	0	S	0	0	0	0	0
3718	2167	af	AN5200.1	69.m14899	AO070237000030	0			-125	-75			ATGCGACATATCATTCCACACGTGAGAAGACATAAGGCGTCGGTCGTGTGA		ATGCGACATATCATTCCACACGTGAGAAGACATAAGGCGTCGGTCGTGTGA		MRHIIPHVRRHKASVV*		MRHIIPHVRRHKASVV*		CCGACATCGC	GCTTGCAGAG	0	CR	FG01395.1	0	0	0	0
3714	2167	an	AN5200.1	69.m14899	AO070237000030	0	-193	-173					ATGGACAAAATGGTCTCGTGA	ATGGACAAAATGGTCTCGTGA			MDKMVS*	MDKMVS*			TAAACCAACA	CCGTGACACC	0	CR	FG01395.1	0	0	0	0
3715	2167	an	AN5200.1	69.m14899	AO070237000030	0	-184	-173					ATGGTCTCGTGA	ATGGTCTCGTGA			MVS*	MVS*			AATGGACAAA	CCGTGACACC	0	CR	FG01395.1	0	0	0	0
3716	2167	an	AN5200.1	69.m14899	AO070237000030	0	-160	-125					ATGGCGTGCGTCACGAGCGAGATCGCCGCCAACTAA	ATGGCGTGCGTCACGAGCGAGATCGCCGCCAACTAA			MACVTSEIAAN*	MACVTSEIAAN*			GTGACACCGC	CCAGGAACCA	0	CR	FG01395.1	0	0	0	0
3717	2167	an	AN5200.1	69.m14899	AO070237000030	0	-90	-25					ATGCCAATCTTGGTTGGAGGTGATACAGCGTCATTGGAGACCAATCGATTCGTCGCACCTGCGTGA	ATGCCAATCTTGGTTGGAGGTGATACAGCGTCATTGGAGACCAATCGATTCGTCGCACCTGCGTGA			MPILVGGDTASLETNRFVAPA*	MPILVGGDTASLETNRFVAPA*			CTGCATCTGC	CCGATTCGTC	0	CR	FG01395.1	0	0	0	0
3719	2167	ao	AN5200.1	69.m14899	AO070237000030	0					-220	-203	ATGAGAACGAAAATTTAA			ATGAGAACGAAAATTTAA	MRTKI*			MRTKI*	TGTGATACTT	GCGTAGAAAG	0	CR	FG01395.1	0	0	0	0
3720	2167	ao	AN5200.1	69.m14899	AO070237000030	0					-191	-93	ATGGATGGCGCAACCAACGCTGGTTGTCATTGGGGAGAAATCGTCCGATGCCACTCACGTGGAAATCACGTGAGGCAAAGTTCTATCCATGAGCCATAG			ATGGATGGCGCAACCAACGCTGGTTGTCATTGGGGAGAAATCGTCCGATGCCACTCACGTGGAAATCACGTGAGGCAAAGTTCTATCCATGAGCCATAG	MDGATNAGCHWGEIVRCHSRGNHVRQSSIHEP*			MDGATNAGCHWGEIVRCHSRGNHVRQSSIHEP*	CGTAGAAAGT	TGATTGATAA	0	CR	FG01395.1	0	0	0	0
3721	2167	ao	AN5200.1	69.m14899	AO070237000030	0					-187	-119	ATGGCGCAACCAACGCTGGTTGTCATTGGGGAGAAATCGTCCGATGCCACTCACGTGGAAATCACGTGA			ATGGCGCAACCAACGCTGGTTGTCATTGGGGAGAAATCGTCCGATGCCACTCACGTGGAAATCACGTGA	MAQPTLVVIGEKSSDATHVEIT*			MAQPTLVVIGEKSSDATHVEIT*	GAAAGTATGG	GGCAAAGTTC	0	CR	FG01395.1	0	0	0	0
3722	2167	ao	AN5200.1	69.m14899	AO070237000030	0					-144	-100	ATGCCACTCACGTGGAAATCACGTGAGGCAAAGTTCTATCCATGA			ATGCCACTCACGTGGAAATCACGTGAGGCAAAGTTCTATCCATGA	MPLTWKSREAKFYP*			MPLTWKSREAKFYP*	AAATCGTCCG	GCCATAGTGA	0	CR	FG01395.1	0	0	0	0
3723	2167	ao	AN5200.1	69.m14899	AO070237000030	0					-103	-86	ATGAGCCATAGTGATTGA			ATGAGCCATAGTGATTGA	MSHSD*			MSHSD*	AGTTCTATCC	TAATATAAGG	0	CR	FG01395.1	0	0	0	0
3725	2170	af	AN8853.1	71.m15988	AO070271000021	0			-254	-210			ATGAAATTTGCTCCAACACCCCGCTGGACCTGGACGGCAAACTGA		ATGAAATTTGCTCCAACACCCCGCTGGACCTGGACGGCAAACTGA		MKFAPTPRWTWTAN*		MKFAPTPRWTWTAN*		ACGGAGCCTG	CCAGCTTTAA	0	J	0	0	0	0	0
3724	2170	an	AN8853.1	71.m15988	AO070271000021	0	-154	-47					ATGGCCCGAAATTTTACATCTCCTTCCCTTTTCGATCACGGGGATTCCTTACTACGTCAACTCGCGATATTGACAATTTGTCTCAAGAACCAGGTGGCCAACCCTTAA	ATGGCCCGAAATTTTACATCTCCTTCCCTTTTCGATCACGGGGATTCCTTACTACGTCAACTCGCGATATTGACAATTTGTCTCAAGAACCAGGTGGCCAACCCTTAA			MARNFTSPSLFDHGDSLLRQLAILTICLKNQVANP*	MARNFTSPSLFDHGDSLLRQLAILTICLKNQVANP*			AGCTCCTTAC	TCGTCTCTAA	0	J	0	0	0	0	0
3726	2170	ao	AN8853.1	71.m15988	AO070271000021	0					-267	-142	ATGAAATTTGCTGAAAACACCCCCGCTGCTGCATTTGGACGGCACATTGAACTAGCCTCAAGGTATGCAAATTGTCTCTCTCAAGTCCTGGCTCTATTGATTGTTTGTTCTCCCTCCCTATCTTAA			ATGAAATTTGCTGAAAACACCCCCGCTGCTGCATTTGGACGGCACATTGAACTAGCCTCAAGGTATGCAAATTGTCTCTCTCAAGTCCTGGCTCTATTGATTGTTTGTTCTCCCTCCCTATCTTAA	MKFAENTPAAAFGRHIELASRYANCLSQVLALLIVCSPSLS*			MKFAENTPAAAFGRHIELASRYANCLSQVLALLIVCSPSLS*	ACGGTGCCTG	ATACGTCGCA	0	J	0	0	0	0	0
3727	2170	ao	AN8853.1	71.m15988	AO070271000021	0					-203	-168	ATGCAAATTGTCTCTCTCAAGTCCTGGCTCTATTGA			ATGCAAATTGTCTCTCTCAAGTCCTGGCTCTATTGA	MQIVSLKSWLY*			MQIVSLKSWLY*	GCCTCAAGGT	TTGTTTGTTC	0	J	0	0	0	0	0
3730	2171	af	AN6351.1	72.m19504	AO070275000048	0			-105	-34			ATGCTATTGTCTTCTCTGAACTGGTCTCACCCGCTGTATGCTCTAGATTCTTTCTTTTTCCAAGTGTGTTGA		ATGCTATTGTCTTCTCTGAACTGGTCTCACCCGCTGTATGCTCTAGATTCTTTCTTTTTCCAAGTGTGTTGA		MLLSSLNWSHPLYALDSFFFQVC*		MLLSSLNWSHPLYALDSFFFQVC*		GATTTATCCG	GCTCGGCTGC	0	U	0	0	0	0	0
3728	2171	an	AN6351.1	72.m19504	AO070275000048	0	-213	-82					ATGCCGCTCCCAATTTCAGGTCGAGCTTCAAGCAAATCTTCCCCCGCTTCTTCATTCTGTCAACTAGCTGGCAATTTTCATCGTGCCTTGCACACACACATAATACAAGACTCTTTATATTGCTCAAGTTGA	ATGCCGCTCCCAATTTCAGGTCGAGCTTCAAGCAAATCTTCCCCCGCTTCTTCATTCTGTCAACTAGCTGGCAATTTTCATCGTGCCTTGCACACACACATAATACAAGACTCTTTATATTGCTCAAGTTGA			MPLPISGRASSKSSPASSFCQLAGNFHRALHTHIIQDSLYCSS*	MPLPISGRASSKSSPASSFCQLAGNFHRALHTHIIQDSLYCSS*			GCAGGTGACG	TCTCGGATTA	0	U	0	0	0	0	0
3729	2171	an	AN6351.1	72.m19504	AO070275000048	0	-64	-32					ATGCGAACTTCCGACCAGCGCTCCGGATCCTGA	ATGCGAACTTCCGACCAGCGCTCCGGATCCTGA			MRTSDQRSGS*	MRTSDQRSGS*			TTACCCGCGT	TCGAGGCTGC	0	U	0	0	0	0	0
3731	2171	ao	AN6351.1	72.m19504	AO070275000048	0					-72	-43	ATGAGTTGCTCGTTTGTCTCGGATTCTTAG			ATGAGTTGCTCGTTTGTCTCGGATTCTTAG	MSCSFVSDS*			MSCSFVSDS*	GTTATTGTTT	ATTGCCAGGG	0	U	0	0	0	0	0
3735	2176	af	AN6421.1	70.m15032	AO070302000085	0			-180	-157			ATGAAATGCCCTCAGTTTGTGTAG		ATGAAATGCCCTCAGTTTGTGTAG		MKCPQFV*		MKCPQFV*		CACCAAGATA	ATGAGGTAGG	0		0	0	0	0	0
3732	2176	an	AN6421.1	70.m15032	AO070302000085	0	-197	-99					ATGCGAATTCGTGCTGAAAGAGGACGAATTAGTAATGAGGAAGCATGGCTGGATCGTGCCCATACAGCTGACGAGAGGGGTAGCGTTTTAAGTCTATAA	ATGCGAATTCGTGCTGAAAGAGGACGAATTAGTAATGAGGAAGCATGGCTGGATCGTGCCCATACAGCTGACGAGAGGGGTAGCGTTTTAAGTCTATAA			MRIRAERGRISNEEAWLDRAHTADERGSVLSL*	MRIRAERGRISNEEAWLDRAHTADERGSVLSL*			CTGGCTGCTT	AAGCATCCTA	0		0	0	0	0	0
3733	2176	an	AN6421.1	70.m15032	AO070302000085	0	-163	-107					ATGAGGAAGCATGGCTGGATCGTGCCCATACAGCTGACGAGAGGGGTAGCGTTTTAA	ATGAGGAAGCATGGCTGGATCGTGCCCATACAGCTGACGAGAGGGGTAGCGTTTTAA			MRKHGWIVPIQLTRGVAF*	MRKHGWIVPIQLTRGVAF*			CGAATTAGTA	GTCTATAAAA	0		0	0	0	0	0
3734	2176	an	AN6421.1	70.m15032	AO070302000085	0	-153	-127					ATGGCTGGATCGTGCCCATACAGCTGA	ATGGCTGGATCGTGCCCATACAGCTGA			MAGSCPYS*	MAGSCPYS*			ATGAGGAAGC	CGAGAGGGGT	0		0	0	0	0	0
3736	2176	ao	AN6421.1	70.m15032	AO070302000085	0					-223	-95	ATGCTGTTGGCAAGCTATCATCAACACGGAAAAGATACTTTAGGCGCCGTTTCTGTGAGTCACATAAGTGCAATTTGTCAGCTGGAAAAGCATCAAGGACATATAAGGATGCGACATCGCCCCTGTTAA			ATGCTGTTGGCAAGCTATCATCAACACGGAAAAGATACTTTAGGCGCCGTTTCTGTGAGTCACATAAGTGCAATTTGTCAGCTGGAAAAGCATCAAGGACATATAAGGATGCGACATCGCCCCTGTTAA	MLLASYHQHGKDTLGAVSVSHISAICQLEKHQGHIRMRHRPC*			MLLASYHQHGKDTLGAVSVSHISAICQLEKHQGHIRMRHRPC*	ATCCACATCA	TGGAGCCATT	0		0	0	0	0	0
3737	2176	ao	AN6421.1	70.m15032	AO070302000085	0					-115	-95	ATGCGACATCGCCCCTGTTAA			ATGCGACATCGCCCCTGTTAA	MRHRPC*			MRHRPC*	ACATATAAGG	TGGAGCCATT	0		0	0	0	0	0
3738	2176	ao	AN6421.1	70.m15032	AO070302000085	0					-95	-60	ATGGAGCCATTCATGAATCAGAGAGAATCTCATTGA			ATGGAGCCATTCATGAATCAGAGAGAATCTCATTGA	MEPFMNQRESH*			MEPFMNQRESH*	GCCCCTGTTA	GCATCGGCCC	0		0	0	0	0	0
3739	2176	ao	AN6421.1	70.m15032	AO070302000085	0					-83	-60	ATGAATCAGAGAGAATCTCATTGA			ATGAATCAGAGAGAATCTCATTGA	MNQRESH*			MNQRESH*	GGAGCCATTC	GCATCGGCCC	0		0	0	0	0	0
3741	2179	af	AN0764.1	70.m15368	AO070316000081	0			-116	-99			ATGGGTCGAGTCTATTAA		ATGGGTCGAGTCTATTAA		MGRVY*		MGRVY*		ACAAGAGCTG	ACCTGGTGGT	0	Q	0	MG02619.1	0	0	0
3740	2179	an	AN0764.1	70.m15368	AO070316000081	0	-137	-120					ATGCGGGGGGTTGCGTAG	ATGCGGGGGGTTGCGTAG			MRGVA*	MRGVA*			ATACATCCCC	TTTTGCTCGA	0	Q	0	MG02619.1	0	0	0
3742	2179	ao	AN0764.1	70.m15368	AO070316000081	0					-203	-9	ATGAAGGAACCAATTCCGCTGCAACCATGCTTATTCAACTCTTATGCATCATCCGATCTGCCCAATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGACTTTTTCCCTTTACTTTTGTCTTCTTCCACCCATTCTTAGTGATACGTACTCTTCAATAGTGAGGAATTGA			ATGAAGGAACCAATTCCGCTGCAACCATGCTTATTCAACTCTTATGCATCATCCGATCTGCCCAATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGACTTTTTCCCTTTACTTTTGTCTTCTTCCACCCATTCTTAGTGATACGTACTCTTCAATAGTGAGGAATTGA	MKEPIPLQPCLFNSYASSDLPNAGGDDPLFLAVYRNHNSQLTFSLYFCLLPPILSDTYSSIVRN*			MKEPIPLQPCLFNSYASSDLPNAGGDDPLFLAVYRNHNSQLTFSLYFCLLPPILSDTYSSIVRN*	CACATTCCCC	AACACAAAAT	0	Q	0	MG02619.1	0	0	0
3743	2179	ao	AN0764.1	70.m15368	AO070316000081	0					-177	-127	ATGCTTATTCAACTCTTATGCATCATCCGATCTGCCCAATGCGGGGGGTGA			ATGCTTATTCAACTCTTATGCATCATCCGATCTGCCCAATGCGGGGGGTGA	MLIQLLCIIRSAQCGG*			MLIQLLCIIRSAQCGG*	CGCTGCAACC	TGATCCACTC	0	Q	0	MG02619.1	0	0	0
3744	2179	ao	AN0764.1	70.m15368	AO070316000081	0					-160	-80	ATGCATCATCCGATCTGCCCAATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA			ATGCATCATCCGATCTGCCCAATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA	MHHPICPMRGVMIHSSLQYIGTTTRN*			MHHPICPMRGVMIHSSLQYIGTTTRN*	TTCAACTCTT	CTTTTTCCCT	0	Q	0	MG02619.1	0	0	0
3745	2179	ao	AN0764.1	70.m15368	AO070316000081	0					-139	-80	ATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA			ATGCGGGGGGTGATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA	MRGVMIHSSLQYIGTTTRN*			MRGVMIHSSLQYIGTTTRN*	GATCTGCCCA	CTTTTTCCCT	0	Q	0	MG02619.1	0	0	0
3746	2179	ao	AN0764.1	70.m15368	AO070316000081	0					-127	-80	ATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA			ATGATCCACTCTTCCTTGCAGTATATAGGAACCACAACTCGCAATTGA	MIHSSLQYIGTTTRN*			MIHSSLQYIGTTTRN*	GCGGGGGGTG	CTTTTTCCCT	0	Q	0	MG02619.1	0	0	0
3748	2183	af	AN1775.1	69.m15062	AO070324000034	0			-258	-238			ATGATAATATTATATATATAA		ATGATAATATTATATATATAA		MIILYI*		MIILYI*		TATGATGCTC	TTATCCTCAG	0	MO	FG02191.1	0	NCU05644.1	0	0
3749	2183	af	AN1775.1	69.m15062	AO070324000034	0			-201	-190			ATGTATGAATAG		ATGTATGAATAG		MYE*		MYE*		GACATCATTC	GTTGTGCTCA	0	MO	FG02191.1	0	NCU05644.1	0	0
3750	2183	af	AN1775.1	69.m15062	AO070324000034	0			-197	-153			ATGAATAGGTTGTGCTCACCTTGTCATATAGAATCCAGAGACTAA		ATGAATAGGTTGTGCTCACCTTGTCATATAGAATCCAGAGACTAA		MNRLCSPCHIESRD*		MNRLCSPCHIESRD*		TCATTCATGT	ACTCAATTGG	0	MO	FG02191.1	0	NCU05644.1	0	0
3751	2183	af	AN1775.1	69.m15062	AO070324000034	0			-102	-61			ATGCACCACAATCCCCACTTAATGGTTTCCCTGAAAAGTTAG		ATGCACCACAATCCCCACTTAATGGTTTCCCTGAAAAGTTAG		MHHNPHLMVSLKS*		MHHNPHLMVSLKS*		AGCATCTTTG	GAAAGGTCAA	0	MO	FG02191.1	0	NCU05644.1	0	0
3752	2183	af	AN1775.1	69.m15062	AO070324000034	0			-81	-61			ATGGTTTCCCTGAAAAGTTAG		ATGGTTTCCCTGAAAAGTTAG		MVSLKS*		MVSLKS*		TCCCCACTTA	GAAAGGTCAA	0	MO	FG02191.1	0	NCU05644.1	0	0
3747	2183	an	AN1775.1	69.m15062	AO070324000034	0	-68	-51					ATGGCTTCTAGCCCCTGA	ATGGCTTCTAGCCCCTGA			MASSP*	MASSP*			GACCTTTTAC	CCGAAAGACA	0	MO	FG02191.1	0	NCU05644.1	0	0

3754	2184	af	AN7725.1	71.m15752	AO070325000141	0			-266	-234			ATGGAACGAAGACATAATTCGGCGGGGACATGA		ATGGAACGAAGACATAATTCGGCGGGGACATGA		MERRHNSAGT*		MERRHNSAGT*		CCGCGGCCGG	AAATGTGGGT	0	H	0	0	0	0	0
3755	2184	af	AN7725.1	71.m15752	AO070325000141	0			-237	-118			ATGAAAATGTGGGTGATCGATACGGAATTTTTGGTTCTTCGGAGGCGACAAAGGGCGCAACGGTCGAGGTTAGTAGTTATCTTGACTCACACTTACAGGGCCCGTCTTCGGTCTTCTTAA		ATGAAAATGTGGGTGATCGATACGGAATTTTTGGTTCTTCGGAGGCGACAAAGGGCGCAACGGTCGAGGTTAGTAGTTATCTTGACTCACACTTACAGGGCCCGTCTTCGGTCTTCTTAA		MKMWVIDTEFLVLRRRQRAQRSRLVVILTHTYRARLRSS*		MKMWVIDTEFLVLRRRQRAQRSRLVVILTHTYRARLRSS*		CGGCGGGGAC	GAACTGGGTT	0	H	0	0	0	0	0
3756	2184	af	AN7725.1	71.m15752	AO070325000141	0			-231	-118			ATGTGGGTGATCGATACGGAATTTTTGGTTCTTCGGAGGCGACAAAGGGCGCAACGGTCGAGGTTAGTAGTTATCTTGACTCACACTTACAGGGCCCGTCTTCGGTCTTCTTAA		ATGTGGGTGATCGATACGGAATTTTTGGTTCTTCGGAGGCGACAAAGGGCGCAACGGTCGAGGTTAGTAGTTATCTTGACTCACACTTACAGGGCCCGTCTTCGGTCTTCTTAA		MWVIDTEFLVLRRRQRAQRSRLVVILTHTYRARLRSS*		MWVIDTEFLVLRRRQRAQRSRLVVILTHTYRARLRSS*		GGACATGAAA	GAACTGGGTT	0	H	0	0	0	0	0
3753	2184	an	AN7725.1	71.m15752	AO070325000141	0	-245	-225					ATGGCGGTTTTTGGCGGGTAA	ATGGCGGTTTTTGGCGGGTAA			MAVFGG*	MAVFGG*			TGATTGGCGA	GTCAGATAAT	0	H	0	0	0	0	0
3757	2184	ao	AN7725.1	71.m15752	AO070325000141	0					-186	-67	ATGGACACCGCGCCCTATGTTGACAGTGGTTGTCTTCTGCGGCGATTGCCTTTGAGTCACCATTCTTTCACTTTAAATATCCCAGCTCGGCTTCCTTCTTCTTTTCTCCCCTGTTCTTAG			ATGGACACCGCGCCCTATGTTGACAGTGGTTGTCTTCTGCGGCGATTGCCTTTGAGTCACCATTCTTTCACTTTAAATATCCCAGCTCGGCTTCCTTCTTCTTTTCTCCCCTGTTCTTAG	MDTAPYVDSGCLLRRLPLSHHSFTLNIPARLPSSFLPCS*			MDTAPYVDSGCLLRRLPLSHHSFTLNIPARLPSSFLPCS*	GGTGGGTTCC	ACCATCCTTC	0	H	0	0	0	0	0
3758	2184	ao	AN7725.1	71.m15752	AO070325000141	0					-170	-132	ATGTTGACAGTGGTTGTCTTCTGCGGCGATTGCCTTTGA			ATGTTGACAGTGGTTGTCTTCTGCGGCGATTGCCTTTGA	MLTVVVFCGDCL*			MLTVVVFCGDCL*	ACCGCGCCCT	GTCACCATTC	0	H	0	0	0	0	0
3761	2185	af	AN6571.1	62.m03162	AO070326000014	0			-196	-173			ATGTCTCTTGCACTGCGCTCGTAA		ATGTCTCTTGCACTGCGCTCGTAA		MSLALRS*		MSLALRS*		TTGCTCTTGA	AATCTTTCTG	0		0	0	0	0	0
3759	2185	an	AN6571.1	62.m03162	AO070326000014	0	-151	-56					ATGTCTGCCATTAAGAATTCAAGGCCAATTGTCAAGTACTTATATATGCGCGCCTGTGTCACATATAACGCTGATCAATTGCAGCTTGCGTGTTGA	ATGTCTGCCATTAAGAATTCAAGGCCAATTGTCAAGTACTTATATATGCGCGCCTGTGTCACATATAACGCTGATCAATTGCAGCTTGCGTGTTGA			MSAIKNSRPIVKYLYMRACVTYNADQLQLAC*	MSAIKNSRPIVKYLYMRACVTYNADQLQLAC*			CCTGTGGCCG	ACACGTCCCA	0		0	0	0	0	0
3760	2185	an	AN6571.1	62.m03162	AO070326000014	0	-106	-56					ATGCGCGCCTGTGTCACATATAACGCTGATCAATTGCAGCTTGCGTGTTGA	ATGCGCGCCTGTGTCACATATAACGCTGATCAATTGCAGCTTGCGTGTTGA			MRACVTYNADQLQLAC*	MRACVTYNADQLQLAC*			GTACTTATAT	ACACGTCCCA	0		0	0	0	0	0
3762	2186	af	AN2236.1	71.m15828	AO070326000140	0			-147	-97			ATGTTTACTGTTCCCGTCGCGATTCGACGGTTTGGGGTTTTTCCAATCTGA		ATGTTTACTGTTCCCGTCGCGATTCGACGGTTTGGGGTTTTTCCAATCTGA		MFTVPVAIRRFGVFPI*		MFTVPVAIRRFGVFPI*		TCCGTCGCGC	TAACATAGAG	0	S	0	0	0	0	0
3763	2186	ao	AN2236.1	71.m15828	AO070326000140	0					-169	-134	ATGTCGAGCTGCTTTCGACGCATTGAGTTCCCCTAA			ATGTCGAGCTGCTTTCGACGCATTGAGTTCCCCTAA	MSSCFRRIEFP*			MSSCFRRIEFP*	ATCGCATTAC	GATATCCGCA	0	S	0	0	0	0	0
3766	2188	af	AN1503.1	55.m03013	AO070334000220	0			-190	-83			ATGGCAGGCGTCCCACCATCTCTGTTCTCTTTAACAAACCCTTTCCTCCCTTTTTCTGCTCTTCTCTATCCCGATAAATCCTCCAAATTGAGCTCCTCTACCTGGTAA		ATGGCAGGCGTCCCACCATCTCTGTTCTCTTTAACAAACCCTTTCCTCCCTTTTTCTGCTCTTCTCTATCCCGATAAATCCTCCAAATTGAGCTCCTCTACCTGGTAA		MAGVPPSLFSLTNPFLPFSALLYPDKSSKLSSSTW*		MAGVPPSLFSLTNPFLPFSALLYPDKSSKLSSSTW*		TTTCTTAATC	CTCTTGTTCC	0	EM	0	0	NCU05977.1	0	0
3767	2188	af	AN1503.1	55.m03013	AO070334000220	0			-72	-55			ATGCAGGCCTACACTTGA		ATGCAGGCCTACACTTGA		MQAYT*		MQAYT*		CTCTTGTTCC	AATCATCTTC	0	EM	0	0	NCU05977.1	0	0
3765	2188	an	AN1503.1	55.m03013	AO070334000220	0	-182	-117					ATGACTTCCTCCACTTTTAAACCCTCCTCCTCCCCGGGGATTTCCCTCCAGCTGTCCATTTTCTAA	ATGACTTCCTCCACTTTTAAACCCTCCTCCTCCCCGGGGATTTCCCTCCAGCTGTCCATTTTCTAA			MTSSTFKPSSSPGISLQLSIF*	MTSSTFKPSSSPGISLQLSIF*			AGCAGACTCC	TCCGTCGCAT	0	EM	0	0	NCU05977.1	0	0
3769	2191	af	AN3793.1	57.m05691	AO070337000236	0			-358	-302			ATGCCATTCTTGTCTCGGTCGGCTTCTGCAAATTCCCCTCGTCCTTCATCGACTTGA		ATGCCATTCTTGTCTCGGTCGGCTTCTGCAAATTCCCCTCGTCCTTCATCGACTTGA		MPFLSRSASANSPRPSST*		MPFLSRSASANSPRPSST*		CTGTACTGTG	ACGGTCGGTA	0	TR	0	0	0	0	0
3768	2191	an	AN3793.1	57.m05691	AO070337000236	0	-333	-322					ATGTCACGCTAA	ATGTCACGCTAA			MSR*	MSR*			CGGCCGCTTC	TAATCCCAGT	0	TR	0	0	0	0	0
3773	2192	af	AN5992.1	72.m19148	AO070340000285	0			-216	-145			ATGGAAACGCGTCTCTTTCGCGTCGCGACGTGTTTTGCACCAAAAAGTTACGGGCGCCAAAAGATCCACTAA		ATGGAAACGCGTCTCTTTCGCGTCGCGACGTGTTTTGCACCAAAAAGTTACGGGCGCCAAAAGATCCACTAA		METRLFRVATCFAPKSYGRQKIH*		METRLFRVATCFAPKSYGRQKIH*		AATCTGAGGA	TGAAGTACAC	0	L	0	0	0	0	0
3772	2192	an	AN5992.1	72.m19148	AO070340000285	0	-205	-53					ATGGCTGCATTACCCAAGACGCGTCTTTCGCGACGCGAACGTGCTTTACGCCTCAGGCTGCAAACTCCTTTGGTGGAGGAACGCAGAAAACTGCCTGGCGCCCAGTCTTGTCAAGTTACAACTTCCGCAGCACCTGCGCCCTCTTCTTGCTGA	ATGGCTGCATTACCCAAGACGCGTCTTTCGCGACGCGAACGTGCTTTACGCCTCAGGCTGCAAACTCCTTTGGTGGAGGAACGCAGAAAACTGCCTGGCGCCCAGTCTTGTCAAGTTACAACTTCCGCAGCACCTGCGCCCTCTTCTTGCTGA			MAALPKTRLSRRERALRLRLQTPLVEERRKLPGAQSCQVTTSAAPAPSSC*	MAALPKTRLSRRERALRLRLQTPLVEERRKLPGAQSCQVTTSAAPAPSSC*			CCTTGGGAAA	GCTTCTGGAC	0	L	0	0	0	0	0
3774	2192	ao	AN5992.1	72.m19148	AO070340000285	0					-231	-148	ATGGAAACGCGTCGGTTTTCGTGTCGCGACGTGTTTTTGCGCCTCAGGTTTCTGGGCCTAAGGTTGCTGGGGTTCCGAAATTGA			ATGGAAACGCGTCGGTTTTCGTGTCGCGACGTGTTTTTGCGCCTCAGGTTTCTGGGCCTAAGGTTGCTGGGGTTCCGAAATTGA	METRRFSCRDVFLRLRFLGLRLLGFRN*			METRRFSCRDVFLRLRFLGLRLLGFRN*	AATATAAGGA	TCCACTACCA	0	L	0	0	0	0	0
3778	2193	af	AN2114.1	57.m05820	AO070341000297	0			-134	-114			ATGATCGGTTTTATGGTTTGA		ATGATCGGTTTTATGGTTTGA		MIGFMV*		MIGFMV*		TCAGCGCTGA	AATGTATGCT	0	HC	0	0	NCU08315.1	0	0
3779	2193	af	AN2114.1	57.m05820	AO070341000297	0			-112	-41			ATGTATGCTATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAA		ATGTATGCTATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAA		MYAMPVVNPLLRTTFSTNSRHFT*		MYAMPVVNPLLRTTFSTNSRHFT*		ATGGTTTGAA	TCAATTCATC	0	HC	0	0	NCU08315.1	0	0
3780	2193	af	AN2114.1	57.m05820	AO070341000297	0			-108	-10			ATGCTATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAATCAATTCATCAGCAGCTCGCGATCCGGGTAA		ATGCTATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAATCAATTCATCAGCAGCTCGCGATCCGGGTAA		MLCLWSIPFSERHFRPTPAISHNQFISSSRSG*		MLCLWSIPFSERHFRPTPAISHNQFISSSRSG*		TTTGAAATGT	GAGACAGAAA	0	HC	0	0	NCU08315.1	0	0
3781	2193	af	AN2114.1	57.m05820	AO070341000297	0			-103	-41			ATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAA		ATGCCTGTGGTCAATCCCCTTCTCAGAACGACATTTTCGACCAACTCCCGCCATTTCACATAA		MPVVNPLLRTTFSTNSRHFT*		MPVVNPLLRTTFSTNSRHFT*		AATGTATGCT	TCAATTCATC	0	HC	0	0	NCU08315.1	0	0
3776	2193	an	AN2114.1	57.m05820	AO070341000297	0	-184	-158					ATGATGTGCCCCATTCACTGCCGTTGA	ATGATGTGCCCCATTCACTGCCGTTGA			MMCPIHCR*	MMCPIHCR*			ATGAATTCAA	TCATAGATAA	0	HC	0	0	NCU08315.1	0	0
3777	2193	an	AN2114.1	57.m05820	AO070341000297	0	-181	-158					ATGTGCCCCATTCACTGCCGTTGA	ATGTGCCCCATTCACTGCCGTTGA			MCPIHCR*	MCPIHCR*			AATTCAAATG	TCATAGATAA	0	HC	0	0	NCU08315.1	0	0
3782	2193	ao	AN2114.1	57.m05820	AO070341000297	0					-165	-64	ATGTTTATTCGACATGAGGTGCGGTGTGTGCGATGGATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGA			ATGTTTATTCGACATGAGGTGCGGTGTGTGCGATGGATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGA	MFIRHEVRCVRWMVEKGKPRVFAISWLNIPSSA*			MFIRHEVRCVRWMVEKGKPRVFAISWLNIPSSA*	AAGTTCCGAT	GTTCTTGAAA	0	HC	0	0	NCU08315.1	0	0
3783	2193	ao	AN2114.1	57.m05820	AO070341000297	0					-152	-123	ATGAGGTGCGGTGTGTGCGATGGATGGTAG			ATGAGGTGCGGTGTGTGCGATGGATGGTAG	MRCGVCDGW*			MRCGVCDGW*	TTTATTCGAC	AAAAGGGGAA	0	HC	0	0	NCU08315.1	0	0
3784	2193	ao	AN2114.1	57.m05820	AO070341000297	0					-133	-56	ATGGATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGAGTTCTTGA			ATGGATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGAGTTCTTGA	MDGRKGEASRLCNLLAQHSLECLSS*			MDGRKGEASRLCNLLAQHSLECLSS*	GGTGTGTGCG	AATACACCCT	0	HC	0	0	NCU08315.1	0	0
3785	2193	ao	AN2114.1	57.m05820	AO070341000297	0					-129	-64	ATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGA			ATGGTAGAAAAGGGGAAGCCTCGCGTCTTTGCAATCTCTTGGCTCAACATTCCCTCGAGTGCTTGA	MVEKGKPRVFAISWLNIPSSA*			MVEKGKPRVFAISWLNIPSSA*	TGTGCGATGG	GTTCTTGAAA	0	HC	0	0	NCU08315.1	0	0
3787	2201	af	AN3371.1	66.m04639	AO070281000010	0			-281	-258			ATGCCATACATTGGCTGTTCTTGA		ATGCCATACATTGGCTGTTCTTGA		MPYIGCS*		MPYIGCS*		TATTGCTGCC	TGCTGCTTGA	0		0	0	NCU06056.1	0	0
3788	2201	af	AN3371.1	66.m04639	AO070281000010	0			-258	-124			ATGCTGCTTGAGTTTATCACTTGGTATTCCCTTCTTCTGGTCCATTCCTATCTAGTTGTTGCTTCCTTTGAAGCCTTCTATCTTCTCCGCACAACCTCATGTTTGACAACACGGTACATTGTCGACGTCCGCTGA		ATGCTGCTTGAGTTTATCACTTGGTATTCCCTTCTTCTGGTCCATTCCTATCTAGTTGTTGCTTCCTTTGAAGCCTTCTATCTTCTCCGCACAACCTCATGTTTGACAACACGGTACATTGTCGACGTCCGCTGA		MLLEFITWYSLLLVHSYLVVASFEAFYLLRTTSCLTTRYIVDVR*		MLLEFITWYSLLLVHSYLVVASFEAFYLLRTTSCLTTRYIVDVR*		GCTGTTCTTG	CAGATCTACT	0		0	0	NCU06056.1	0	0
3786	2201	an	AN3371.1	66.m04639	AO070281000010	0	-178	-80					ATGTTCTCGATTCTTTTCTTCTTCTGCATTTGTTTTTACGGCTTCTTTCTCCTCGTCTTCTCGCTCGTTTCCGGCTTGCTAACTTGGGTTTCCCCATAG	ATGTTCTCGATTCTTTTCTTCTTCTGCATTTGTTTTTACGGCTTCTTTCTCCTCGTCTTCTCGCTCGTTTCCGGCTTGCTAACTTGGGTTTCCCCATAG			MFSILFFFCICFYGFFLLVFSLVSGLLTWVSP*	MFSILFFFCICFYGFFLLVFSLVSGLLTWVSP*			GTTTAGCGTC	CCATTTCCCT	0		0	0	NCU06056.1	0	0
3789	2201	ao	AN3371.1	66.m04639	AO070281000010	0					-238	-134	ATGTCTCAGCCTCTCTTTTTTTCTGCGTGCTTTTTCCTTGCCATAAATTTTTCTCCTCCCTTCTTTCTTTACATTTTGTACAACCCAAAATTGATCCCAAAATAA			ATGTCTCAGCCTCTCTTTTTTTCTGCGTGCTTTTTCCTTGCCATAAATTTTTCTCCTCCCTTCTTTCTTTACATTTTGTACAACCCAAAATTGATCCCAAAATAA	MSQPLFFSACFFLAINFSPPFFLYILYNPKLIPK*			MSQPLFFSACFFLAINFSPPFFLYILYNPKLIPK*	GACCTGCAGT	AGTCTATGCT	0		0	0	NCU06056.1	0	0
3790	2201	ao	AN3371.1	66.m04639	AO070281000010	0					-128	-57	ATGCTGACACTGAGGTCATTTTTCTTTTTTTTTTTTTTGTTTTTTTTAGTAACCCTTACATTCACGATCTGA			ATGCTGACACTGAGGTCATTTTTCTTTTTTTTTTTTTTGTTTTTTTTAGTAACCCTTACATTCACGATCTGA	MLTLRSFFFFFFLFFLVTLTFTI*			MLTLRSFFFFFFLFFLVTLTFTI*	AATAAAGTCT	CGATCATCTG	0		0	0	NCU06056.1	0	0
3792	2202	af	AN4976.1	59.m08879	AO070288000043	0			-161	-108			ATGAATCCTTGTCATCATCAATCTCTGTGGCTTTTGACTGACTCGGTATTCTGA		ATGAATCCTTGTCATCATCAATCTCTGTGGCTTTTGACTGACTCGGTATTCTGA		MNPCHHQSLWLLTDSVF*		MNPCHHQSLWLLTDSVF*		TTATTGTGAC	GAGGTTAGAC	0	K	0	0	0	0	0
3791	2202	an	AN4976.1	59.m08879	AO070288000043	0	-332	-318					ATGCCTCCCCCATAA	ATGCCTCCCCCATAA			MPPP*	MPPP*			CCAATCGCAT	TTTCCCATCT	0	K	0	0	0	0	0
3793	2202	ao	AN4976.1	59.m08879	AO070288000043	0					-292	-245	ATGTTTTCTTGCTTTCCCTCTTGCAAAAATTTTTTCTGCCTTCTTTGA			ATGTTTTCTTGCTTTCCCTCTTGCAAAAATTTTTTCTGCCTTCTTTGA	MFSCFPSCKNFFCLL*			MFSCFPSCKNFFCLL*	CACAAAGGGT	CCGCATCTTG	0	K	0	0	0	0	0
3794	2202	ao	AN4976.1	59.m08879	AO070288000043	0					-219	-202	ATGTGGTGTTGTTGCTAG			ATGTGGTGTTGTTGCTAG	MWCCC*			MWCCC*	CTTTGCGGTC	ACCGACTTGT	0	K	0	0	0	0	0
3795	2203	ao	AN4997.1	59.m09454	AO070288000080	0					-259	-218	ATGAAACGAGTAACGATCTGTAGAGAAAAAGGAATTCAATAA			ATGAAACGAGTAACGATCTGTAGAGAAAAAGGAATTCAATAA	MKRVTICREKGIQ*			MKRVTICREKGIQ*	AAGTAAAAAT	TTGTAAACTG	0	I	FG10779.1	0	0	0	0
3801	2210	af	AN8033.1	53.m03881	AO070322000128	0			-153	-88			ATGTCAGTTGTTCCAAGCGTCAGAGCGGATAAGTCTCCGATCGTCACCGCCTTGGCCATGATGTAG		ATGTCAGTTGTTCCAAGCGTCAGAGCGGATAAGTCTCCGATCGTCACCGCCTTGGCCATGATGTAG		MSVVPSVRADKSPIVTALAMM*		MSVVPSVRADKSPIVTALAMM*		GATATATCTA	GCAGTACGCC	0	C	0	0	0	0	0
3797	2210	an	AN8033.1	53.m03881	AO070322000128	0	-248	-60					ATGGAAGCTCCCGAGCAAGGTTCCGCCATAGCGGATATCTTAGTACTAAGCGATTCAGAGATGTGCCGTGTTAACGTGTTCTTATTCGTTGGATTTGCGCATCTCTGTATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA	ATGGAAGCTCCCGAGCAAGGTTCCGCCATAGCGGATATCTTAGTACTAAGCGATTCAGAGATGTGCCGTGTTAACGTGTTCTTATTCGTTGGATTTGCGCATCTCTGTATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA			MEAPEQGSAIADILVLSDSEMCRVNVFLFVGFAHLCMLLIHADTGEERALNKRAFRSGLRTD*	MEAPEQGSAIADILVLSDSEMCRVNVFLFVGFAHLCMLLIHADTGEERALNKRAFRSGLRTD*			GCCACAGAAT	ATCTTTTGAC	0	C	0	0	0	0	0
3798	2210	an	AN8033.1	53.m03881	AO070322000128	0	-188	-60					ATGTGCCGTGTTAACGTGTTCTTATTCGTTGGATTTGCGCATCTCTGTATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA	ATGTGCCGTGTTAACGTGTTCTTATTCGTTGGATTTGCGCATCTCTGTATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA			MCRVNVFLFVGFAHLCMLLIHADTGEERALNKRAFRSGLRTD*	MCRVNVFLFVGFAHLCMLLIHADTGEERALNKRAFRSGLRTD*			CGATTCAGAG	ATCTTTTGAC	0	C	0	0	0	0	0
3799	2210	an	AN8033.1	53.m03881	AO070322000128	0	-140	-60					ATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA	ATGCTGCTCATACATGCCGATACCGGGGAAGAGCGGGCGCTGAATAAGCGAGCTTTTCGGAGCGGACTCCGAACGGACTGA			MLLIHADTGEERALNKRAFRSGLRTD*	MLLIHADTGEERALNKRAFRSGLRTD*			GCATCTCTGT	ATCTTTTGAC	0	C	0	0	0	0	0
3800	2210	an	AN8033.1	53.m03881	AO070322000128	0	-127	-98					ATGCCGATACCGGGGAAGAGCGGGCGCTGA	ATGCCGATACCGGGGAAGAGCGGGCGCTGA			MPIPGKSGR*	MPIPGKSGR*			CTGCTCATAC	ATAAGCGAGC	0	C	0	0	0	0	0
3802	2210	ao	AN8033.1	53.m03881	AO070322000128	0					-232	-158	ATGGATGATTTAATGAATAAGAATAGATCAGGTACACCTGATATACATTATTCTTCGATTTTATCTGTTTGCTAA			ATGGATGATTTAATGAATAAGAATAGATCAGGTACACCTGATATACATTATTCTTCGATTTTATCTGTTTGCTAA	MDDLMNKNRSGTPDIHYSSILSVC*			MDDLMNKNRSGTPDIHYSSILSVC*	CACCAGTAGA	CCATTGAACC	0	C	0	0	0	0	0

3803	2210	ao	AN8033.1	53.m03881	AO070322000128	0					-220	-158	ATGAATAAGAATAGATCAGGTACACCTGATATACATTATTCTTCGATTTTATCTGTTTGCTAA			ATGAATAAGAATAGATCAGGTACACCTGATATACATTATTCTTCGATTTTATCTGTTTGCTAA	MNKNRSGTPDIHYSSILSVC*			MNKNRSGTPDIHYSSILSVC*	GGATGATTTA	CCATTGAACC	0	C	0	0	0	0	0
3804	2210	ao	AN8033.1	53.m03881	AO070322000128	0					-117	-52	ATGTTCGGTCGGGATGTCGTGAGCACTCCGGAGTCGGCGCCAACTCCGGCTCGGCCAGCTTTTTAG			ATGTTCGGTCGGGATGTCGTGAGCACTCCGGAGTCGGCGCCAACTCCGGCTCGGCCAGCTTTTTAG	MFGRDVVSTPESAPTPARPAF*			MFGRDVVSTPESAPTPARPAF*	AAATTTTTCC	TTCTGCCGTT	0	C	0	0	0	0	0
3805	2211	af	AN2314.1	71.m15520	AO070323000036	0			-237	-148			ATGCTCCTCCCCCGCAATGGGCTTGGGCTTGCTGAGGGACAAAAGCAGGTTTCCCTCCTCCCGGTCCCTTGCAATCGTTACATTTTGTAG		ATGCTCCTCCCCCGCAATGGGCTTGGGCTTGCTGAGGGACAAAAGCAGGTTTCCCTCCTCCCGGTCCCTTGCAATCGTTACATTTTGTAG		MLLPRNGLGLAEGQKQVSLLPVPCNRYIL*		MLLPRNGLGLAEGQKQVSLLPVPCNRYIL*		GCCTATCTAG	AAAGAAAAAT	0	G	0	0	0	0	0
3806	2214	an	AN6560.1	62.m03147	AO070326000001	0	-121	-80					ATGATACCAAAGGGATTATTGCGGCCATCGTCGACCGGATAG	ATGATACCAAAGGGATTATTGCGGCCATCGTCGACCGGATAG			MIPKGLLRPSSTG*	MIPKGLLRPSSTG*			AAGAGGGTTT	CGAATCGTTC	0	Z	0	0	0	0	0
3807	2214	ao	AN6560.1	62.m03147	AO070326000001	0					-99	-88	ATGCAGTGTTAA			ATGCAGTGTTAA	MQC*			MQC*	CGTGACTTGA	GAAGTGGAGA	0	Z	0	0	0	0	0
3808	2215	an	AN4763.1	59.m09489	AO070327000053	0	-286	-173					ATGTGGCTGATCACCCAAAGGGGTGAGACAGGGGCAGAAACAGATGCGCCTGTCTCCTTATCTAGGAATGCGCGGCTGGTAGAATTTACTATGCAAATGCTAACTATATTTTGA	ATGTGGCTGATCACCCAAAGGGGTGAGACAGGGGCAGAAACAGATGCGCCTGTCTCCTTATCTAGGAATGCGCGGCTGGTAGAATTTACTATGCAAATGCTAACTATATTTTGA			MWLITQRGETGAETDAPVSLSRNARLVEFTMQMLTIF*	MWLITQRGETGAETDAPVSLSRNARLVEFTMQMLTIF*			TTTGCAAGGT	TGGGCTCTAG	0	R	0	0	0	0	0
3809	2215	an	AN4763.1	59.m09489	AO070327000053	0	-243	-205					ATGCGCCTGTCTCCTTATCTAGGAATGCGCGGCTGGTAG	ATGCGCCTGTCTCCTTATCTAGGAATGCGCGGCTGGTAG			MRLSPYLGMRGW*	MRLSPYLGMRGW*			GCAGAAACAG	AATTTACTAT	0	R	0	0	0	0	0
3810	2215	an	AN4763.1	59.m09489	AO070327000053	0	-219	-205					ATGCGCGGCTGGTAG	ATGCGCGGCTGGTAG			MRGW*	MRGW*			TTATCTAGGA	AATTTACTAT	0	R	0	0	0	0	0
3811	2215	an	AN4763.1	59.m09489	AO070327000053	0	-196	-173					ATGCAAATGCTAACTATATTTTGA	ATGCAAATGCTAACTATATTTTGA			MQMLTIF*	MQMLTIF*			AGAATTTACT	TGGGCTCTAG	0	R	0	0	0	0	0
3812	2215	an	AN4763.1	59.m09489	AO070327000053	0	-190	-173					ATGCTAACTATATTTTGA	ATGCTAACTATATTTTGA			MLTIF*	MLTIF*			TACTATGCAA	TGGGCTCTAG	0	R	0	0	0	0	0
3813	2215	an	AN4763.1	59.m09489	AO070327000053	0	-173	-132					ATGGGCTCTAGGTCACTTACACTCTTTTTTGTCCATTGCTAG	ATGGGCTCTAGGTCACTTACACTCTTTTTTGTCCATTGCTAG			MGSRSLTLFFVHC*	MGSRSLTLFFVHC*			CTATATTTTG	TGGATTGCTT	0	R	0	0	0	0	0
3815	2216	af	AN4042.1	54.m06570	AO070328000135	0			-81	-61			ATGAGAACTACGTCTCCCTGA		ATGAGAACTACGTCTCCCTGA		MRTTSP*		MRTTSP*		CTCCGTATTT	ATTTTTGAGT	0	QI	0	0	0	0	0
3816	2216	ao	AN4042.1	54.m06570	AO070328000135	0					-210	-199	ATGTATCCGTAA			ATGTATCCGTAA	MYP*			MYP*	CTTGACAGTA	CCGTCCGCCG	0	QI	0	0	0	0	0
3819	2217	af	AN1163.1	70.m15058	AO070331000153	0			-238	-89			ATGGGCCCTACACGTGATCTGGGAGGTGACGGAGCTTGGTCGGTTCTGATAGAGAGCTTCAGCCACTCACAGCGCTCCCAAAGGTGGAGCGTTCGAGAAGCATCAGGATGCTTGGATCACCTTGGGACCGCTGAGGACTCGGGTATATAA		ATGGGCCCTACACGTGATCTGGGAGGTGACGGAGCTTGGTCGGTTCTGATAGAGAGCTTCAGCCACTCACAGCGCTCCCAAAGGTGGAGCGTTCGAGAAGCATCAGGATGCTTGGATCACCTTGGGACCGCTGAGGACTCGGGTATATAA		MGPTRDLGGDGAWSVLIESFSHSQRSQRWSVREASGCLDHLGTAEDSGI*		MGPTRDLGGDGAWSVLIESFSHSQRSQRWSVREASGCLDHLGTAEDSGI*		AAGCCCCTCG	CACTTGCCTT	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3820	2217	af	AN1163.1	70.m15058	AO070331000153	0			-131	-105			ATGCTTGGATCACCTTGGGACCGCTGA		ATGCTTGGATCACCTTGGGACCGCTGA		MLGSPWDR*		MLGSPWDR*		AAGCATCAGG	GGACTCGGGT	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3817	2217	an	AN1163.1	70.m15058	AO070331000153	0	-225	-103					ATGGAGCTTGGCTGCCCAGCGGCCCAGCAGATTCCCTGGATTCGAGCTTCCGCCACTCATCTTTTCGCCCTTCGCGGCCGAGGTGGAGCTTTCGAGAAGGCTCGCGTTGATTTCAATGGCTGA	ATGGAGCTTGGCTGCCCAGCGGCCCAGCAGATTCCCTGGATTCGAGCTTCCGCCACTCATCTTTTCGCCCTTCGCGGCCGAGGTGGAGCTTTCGAGAAGGCTCGCGTTGATTTCAATGGCTGA			MELGCPAAQQIPWIRASATHLFALRGRGGAFEKARVDFNG*	MELGCPAAQQIPWIRASATHLFALRGRGGAFEKARVDFNG*			TCAGTAGCTA	GTAGATAAAG	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3818	2217	an	AN1163.1	70.m15058	AO070331000153	0	-110	-99					ATGGCTGAGTAG	ATGGCTGAGTAG			MAE*	MAE*			GTTGATTTCA	ATAAAGGCTT	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3821	2217	ao	AN1163.1	70.m15058	AO070331000153	0					-214	-14	ATGGGGCCTCACGTGATTGTTAACGGAGCTGTCGGCCGTTTAGGAGAGCTTCCGCCACTCACCGTTGCCGCCGCGGTGGAGCTTTCGAGAAGCGTCACGATGCTTGGGGTTGCTGGGGTATATAGCCATCCCATAGTCTCTCGCATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG			ATGGGGCCTCACGTGATTGTTAACGGAGCTGTCGGCCGTTTAGGAGAGCTTCCGCCACTCACCGTTGCCGCCGCGGTGGAGCTTTCGAGAAGCGTCACGATGCTTGGGGTTGCTGGGGTATATAGCCATCCCATAGTCTCTCGCATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG	MGPHVIVNGAVGRLGELPPLTVAAAVELSRSVTMLGVAGVYSHPIVSRMEDLDWYLNQTSQSRINC*			MGPHVIVNGAVGRLGELPPLTVAAAVELSRSVTMLGVAGVYSHPIVSRMEDLDWYLNQTSQSRINC*	AAGCCCCTCG	ATTTTAGCTA	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3822	2217	ao	AN1163.1	70.m15058	AO070331000153	0					-115	-14	ATGCTTGGGGTTGCTGGGGTATATAGCCATCCCATAGTCTCTCGCATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG			ATGCTTGGGGTTGCTGGGGTATATAGCCATCCCATAGTCTCTCGCATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG	MLGVAGVYSHPIVSRMEDLDWYLNQTSQSRINC*			MLGVAGVYSHPIVSRMEDLDWYLNQTSQSRINC*	AAGCGTCACG	ATTTTAGCTA	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3823	2217	ao	AN1163.1	70.m15058	AO070331000153	0					-70	-14	ATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG			ATGGAAGACCTCGATTGGTACTTGAATCAAACTTCCCAATCTCGAATCAATTGCTAG	MEDLDWYLNQTSQSRINC*			MEDLDWYLNQTSQSRINC*	AGTCTCTCGC	ATTTTAGCTA	0	O	FG01015.1	0	NCU02630.1	YDR258C	0
3825	2218	af	AN9144.1	66.m04609	AO070332000114	0			-126	-91			ATGTGGTGGGGAATGGTATACTCACGGACTTCATAG		ATGTGGTGGGGAATGGTATACTCACGGACTTCATAG		MWWGMVYSRTS*		MWWGMVYSRTS*		CTAGAAACGG	CTTCTGTTGT	0	E	0	0	0	0	0
3826	2218	af	AN9144.1	66.m04609	AO070332000114	0			-114	-91			ATGGTATACTCACGGACTTCATAG		ATGGTATACTCACGGACTTCATAG		MVYSRTS*		MVYSRTS*		GTGGTGGGGA	CTTCTGTTGT	0	E	0	0	0	0	0
3831	2222	af	AN1555.1	55.m03072	AO070339000298	0			-122	-105			ATGCTCGGCAGTCCCTAA		ATGCTCGGCAGTCCCTAA		MLGSP*		MLGSP*		AAGTGCATTC	ATGTGAGTGC	0	M	0	0	0	0	0
3829	2222	an	AN1555.1	55.m03072	AO070339000298	0	-169	-158					ATGCTAATCTAA	ATGCTAATCTAA			MLI*	MLI*			GCTATCGCCT	GGTCAGTCGG	0	M	0	0	0	0	0
3830	2222	an	AN1555.1	55.m03072	AO070339000298	0	-131	-90					ATGAGAAAGCTCGCTTCGGAACTCCAGTTAGTGGTGGGATAA	ATGAGAAAGCTCGCTTCGGAACTCCAGTTAGTGGTGGGATAA			MRKLASELQLVVG*	MRKLASELQLVVG*			TCTGGCGGTC	AGGAAGGCTT	0	M	0	0	0	0	0
3835	2222	ao	AN1555.1	55.m03072	AO070339000298	0					-165	-133	ATGCGAAGATCCAGTCAGTCAACATCGCTTTGA			ATGCGAAGATCCAGTCAGTCAACATCGCTTTGA	MRRSSQSTSL*			MRRSSQSTSL*	CTACTTGTCT	TAAAAAACTA	0	M	0	0	0	0	0
3836	2222	ao	AN1555.1	55.m03072	AO070339000298	0					-113	-96	ATGCGCGCCTCAATTTAA			ATGCGCGCCTCAATTTAA	MRASI*			MRASI*	ATCGCCGTCT	CGGTGAGTGT	0	M	0	0	0	0	0
3837	2222	ao	AN1555.1	55.m03072	AO070339000298	0					-79	-8	ATGCGTATTCCACCATCTGTGTGGATCCTACAATTGCTTGCATCTCGCCATGCTCACACTCTAGTTCCTTAG			ATGCGTATTCCACCATCTGTGTGGATCCTACAATTGCTTGCATCTCGCCATGCTCACACTCTAGTTCCTTAG	MRIPPSVWILQLLASRHAHTLVP*			MRIPPSVWILQLLASRHAHTLVP*	GTGTGTCCTG	AAGCGTCATG	0	M	0	0	0	0	0
3839	2224	an	AN2069.1	57.m05769	AO070341000218	0	-79	-35					ATGGTAACTAACGCAATCGCTTCTTTCCTCATCCAGATTACTTGA	ATGGTAACTAACGCAATCGCTTCTTTCCTCATCCAGATTACTTGA			MVTNAIASFLIQIT*	MVTNAIASFLIQIT*			GTTAGCAGAA	AACTTCTCGC	0	C	0	0	0	0	0
3840	2224	ao	AN2069.1	57.m05769	AO070341000218	0					-236	-123	ATGATGAGGAGAACCTCTTCTTCCCTGTTCATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA			ATGATGAGGAGAACCTCTTCTTCCCTGTTCATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA	MMRRTSSSLFMPPSIPCAVIHPGQVLGTSLVNATTPG*			MMRRTSSSLFMPPSIPCAVIHPGQVLGTSLVNATTPG*	ACGGGGGCGC	TATCTTTTAA	0	C	0	0	0	0	0
3841	2224	ao	AN2069.1	57.m05769	AO070341000218	0					-233	-123	ATGAGGAGAACCTCTTCTTCCCTGTTCATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA			ATGAGGAGAACCTCTTCTTCCCTGTTCATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA	MRRTSSSLFMPPSIPCAVIHPGQVLGTSLVNATTPG*			MRRTSSSLFMPPSIPCAVIHPGQVLGTSLVNATTPG*	GGGGCGCATG	TATCTTTTAA	0	C	0	0	0	0	0
3842	2224	ao	AN2069.1	57.m05769	AO070341000218	0					-206	-123	ATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA			ATGCCGCCATCGATTCCCTGCGCAGTAATTCACCCGGGGCAGGTTCTCGGTACTTCGTTGGTGAACGCTACCACCCCTGGATGA	MPPSIPCAVIHPGQVLGTSLVNATTPG*			MPPSIPCAVIHPGQVLGTSLVNATTPG*	TTCCCTGTTC	TATCTTTTAA	0	C	0	0	0	0	0
3844	2226	af	AN5494.1	69.m15722	AO070341000390	0			-162	-58			ATGGTGTTTCGACTCATTGACCCTTGCTTGTCGTGCCCAAAACACCACAAAGGACAATGGTATTGCGCCGAATCTCGCCGGAAGAAATTACTTTACCGACCGTGA		ATGGTGTTTCGACTCATTGACCCTTGCTTGTCGTGCCCAAAACACCACAAAGGACAATGGTATTGCGCCGAATCTCGCCGGAAGAAATTACTTTACCGACCGTGA		MVFRLIDPCLSCPKHHKGQWYCAESRRKKLLYRP*		MVFRLIDPCLSCPKHHKGQWYCAESRRKKLLYRP*		TATTACGCCC	ATCAATAGTG	0	D	FG01506.1	MG03729.1	0	0	0
3845	2226	af	AN5494.1	69.m15722	AO070341000390	0			-106	-50			ATGGTATTGCGCCGAATCTCGCCGGAAGAAATTACTTTACCGACCGTGAATCAATAG		ATGGTATTGCGCCGAATCTCGCCGGAAGAAATTACTTTACCGACCGTGAATCAATAG		MVLRRISPEEITLPTVNQ*		MVLRRISPEEITLPTVNQ*		ACAAAGGACA	TGTTCGATTT	0	D	FG01506.1	MG03729.1	0	0	0
3843	2226	an	AN5494.1	69.m15722	AO070341000390	0	-81	-67					ATGAAGAACGAGTAA	ATGAAGAACGAGTAA			MKNE*	MKNE*			CCCAAGAAGA	TACTCGAAAC	0	D	FG01506.1	MG03729.1	0	0	0
3846	2226	ao	AN5494.1	69.m15722	AO070341000390	0					-224	-210	ATGTCCTCATCATGA			ATGTCCTCATCATGA	MSSS*			MSSS*	TCTCGTGTTT	ATGTTGCGGC	0	D	FG01506.1	MG03729.1	0	0	0
3847	2226	ao	AN5494.1	69.m15722	AO070341000390	0					-213	-100	ATGAATGTTGCGGCCGGCGGATCAACATATTACCCAAAGAGGATAAAGTGGCAACTCGCGTGCCGCGTTTCTCAGCCATCTGGACCCTTGCCTATCTTCATCATTCCAGGATAA			ATGAATGTTGCGGCCGGCGGATCAACATATTACCCAAAGAGGATAAAGTGGCAACTCGCGTGCCGCGTTTCTCAGCCATCTGGACCCTTGCCTATCTTCATCATTCCAGGATAA	MNVAAGGSTYYPKRIKWQLACRVSQPSGPLPIFIIPG*			MNVAAGGSTYYPKRIKWQLACRVSQPSGPLPIFIIPG*	TGTCCTCATC	TGGATCTAAA	0	D	FG01506.1	MG03729.1	0	0	0
3848	2226	ao	AN5494.1	69.m15722	AO070341000390	0					-209	-168	ATGTTGCGGCCGGCGGATCAACATATTACCCAAAGAGGATAA			ATGTTGCGGCCGGCGGATCAACATATTACCCAAAGAGGATAA	MLRPADQHITQRG*			MLRPADQHITQRG*	CTCATCATGA	AGTGGCAACT	0	D	FG01506.1	MG03729.1	0	0	0
3849	2226	ao	AN5494.1	69.m15722	AO070341000390	0					-100	-74	ATGGATCTAAACCTAGCTTCTGTATGA			ATGGATCTAAACCTAGCTTCTGTATGA	MDLNLASV*			MDLNLASV*	TTCCAGGATA	CAAGGATCTT	0	D	FG01506.1	MG03729.1	0	0	0
3850	2226	ao	AN5494.1	69.m15722	AO070341000390	0					-77	-15	ATGACAAGGATCTTTCTGTCTTTCTACTCAGCCCGACTGGTTCTACTACAGCCAGGCTCATAG			ATGACAAGGATCTTTCTGTCTTTCTACTCAGCCCGACTGGTTCTACTACAGCCAGGCTCATAG	MTRIFLSFYSARLVLLQPGS*			MTRIFLSFYSARLVLLQPGS*	TAGCTTCTGT	AGCGCCATCT	0	D	FG01506.1	MG03729.1	0	0	0
3853	2228	af	AN5657.1	58.m07322	AO070342000247	0			-156	-136			ATGGCTGCTATACAAGAGTGA		ATGGCTGCTATACAAGAGTGA		MAAIQE*		MAAIQE*		CTCTGCACGG	CAGCCCTTCC	0		0	0	0	0	0
3854	2228	af	AN5657.1	58.m07322	AO070342000247	0			-83				ATGGTTCTCCTCCAGACTGAATTTATCATCGATAGGGCTCCCTCGAGCCGAGCGCGTCCTCCTCCCTTCTCTTTGATGACATAA		ATGGTTCTCCTCCAGACTGAATTTATCATCGATAGGGCTCCCTCGAGCCGAGCGCGTCCTCCTCCCTTCTCTTTGATGACATAA		MVLLQTEFIIDRAPSSRARPPPFSLMT*		MVLLQTEFIIDRAPSSRARPPPFSLMT*		TTTGATTTCA	TGGTGGTGTT	0		0	0	0	0	0
3851	2228	an	AN5657.1	58.m07322	AO070342000247	0	-66	-46					ATGGAACAGCCTGGCTCATGA	ATGGAACAGCCTGGCTCATGA			MEQPGS*	MEQPGS*			TTATAAAGCT	TCAGGGCTCT	0		0	0	0	0	0
3860	2229	af	AN4111.1	52.m03714	AO070342000382	0			-170	-93			ATGGGTGATGGTGATGATGTGATCGCATACACAGAATTTCCCGAACATGTACTTGCTAATCGACTAAAGCGGGGATGA		ATGGGTGATGGTGATGATGTGATCGCATACACAGAATTTCCCGAACATGTACTTGCTAATCGACTAAAGCGGGGATGA		MGDGDDVIAYTEFPEHVLANRLKRG*		MGDGDDVIAYTEFPEHVLANRLKRG*		AGAAGACGTA	TTCCATGCCG	0	Q	0	0	0	0	0
3861	2229	af	AN4111.1	52.m03714	AO070342000382	0			-163	-149			ATGGTGATGATGTGA		ATGGTGATGATGTGA		MVMM*		MVMM*		GTAATGGGTG	TCGCATACAC	0	Q	0	0	0	0	0
3862	2229	af	AN4111.1	52.m03714	AO070342000382	0			-124	-104			ATGTACTTGCTAATCGACTAA		ATGTACTTGCTAATCGACTAA		MYLLID*		MYLLID*		TTTCCCGAAC	AGCGGGGATG	0	Q	0	0	0	0	0
3863	2229	af	AN4111.1	52.m03714	AO070342000382	0			-88	-74			ATGCCGTATAATTAA		ATGCCGTATAATTAA		MPYN*		MPYN*		GGATGATTCC	CCTGGAATCG	0	Q	0	0	0	0	0
3855	2229	an	AN4111.1	52.m03714	AO070342000382	0	-176	-99					ATGCGCAATGATATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGA	ATGCGCAATGATATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGA			MRNDMQRWCDSVLSRLGMHITNIHP*	MRNDMQRWCDSVLSRLGMHITNIHP*			GCTCGTGGCA	ACAGATAAGT	0	Q	0	0	0	0	0
3856	2229	an	AN4111.1	52.m03714	AO070342000382	0	-169	-35					ATGATATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGAACAGATAAGTTCGCTGCTCTCCCGATCCACTTTGAAATGTGTTGATATTATCGAACAACGATAG	ATGATATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGAACAGATAAGTTCGCTGCTCTCCCGATCCACTTTGAAATGTGTTGATATTATCGAACAACGATAG			MICNDGAIASFQDWVCTSRTSIPEQISSLLSRSTLKCVDIIEQR*	MICNDGAIASFQDWVCTSRTSIPEQISSLLSRSTLKCVDIIEQR*			GCAATGCGCA	TGATATTATA	0	Q	0	0	0	0	0
3857	2229	an	AN4111.1	52.m03714	AO070342000382	0	-164	-99					ATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGA	ATGCAACGATGGTGCGATAGCGTCCTTTCAAGATTGGGTATGCACATCACGAACATCCATCCCTGA			MQRWCDSVLSRLGMHITNIHP*	MQRWCDSVLSRLGMHITNIHP*			GCGCAATGAT	ACAGATAAGT	0	Q	0	0	0	0	0
3858	2229	an	AN4111.1	52.m03714	AO070342000382	0	-156	-145					ATGGTGCGATAG	ATGGTGCGATAG			MVR*	MVR*			ATATGCAACG	CGTCCTTTCA	0	Q	0	0	0	0	0
3859	2229	an	AN4111.1	52.m03714	AO070342000382	0	-125	-99					ATGCACATCACGAACATCCATCCCTGA	ATGCACATCACGAACATCCATCCCTGA			MHITNIHP*	MHITNIHP*			AAGATTGGGT	ACAGATAAGT	0	Q	0	0	0	0	0

3865	2229	ao	AN4111.1	52.m03714	AO070342000382	0					-240	-184	ATGAGGGGTTGCAACTGTGGGAATATGTACGGGATCCTTCACATATGTGACGAATGA			ATGAGGGGTTGCAACTGTGGGAATATGTACGGGATCCTTCACATATGTGACGAATGA	MRGCNCGNMYGILHICDE*			MRGCNCGNMYGILHICDE*	TTGCGGAGAG	GATGTAGAAG	0	Q	0	0	0	0	0
3866	2229	ao	AN4111.1	52.m03714	AO070342000382	0					-216	-184	ATGTACGGGATCCTTCACATATGTGACGAATGA			ATGTACGGGATCCTTCACATATGTGACGAATGA	MYGILHICDE*			MYGILHICDE*	CTGTGGGAAT	GATGTAGAAG	0	Q	0	0	0	0	0
3867	2229	ao	AN4111.1	52.m03714	AO070342000382	0					-187	-161	ATGAGATGTAGAAGGCGTAATGGTTAA			ATGAGATGTAGAAGGCGTAATGGTTAA	MRCRRRNG*			MRCRRRNG*	TATGTGACGA	TGGCGATGAT	0	Q	0	0	0	0	0
3868	2229	ao	AN4111.1	52.m03714	AO070342000382	0					-168	-124	ATGGTTAATGGCGATGATGTGATCCCGTCGCCGCGGGTGACTTAA			ATGGTTAATGGCGATGATGTGATCCCGTCGCCGCGGGTGACTTAA	MVNGDDVIPSPRVT*			MVNGDDVIPSPRVT*	AGAAGGCGTA	TCAAGATTAT	0	Q	0	0	0	0	0
3869	2229	ao	AN4111.1	52.m03714	AO070342000382	0					-161	-147	ATGGCGATGATGTGA			ATGGCGATGATGTGA	MAMM*			MAMM*	GTAATGGTTA	TCCCGTCGCC	0	Q	0	0	0	0	0
3874	2230	af	AN3418.1	66.m04615	AO070203000002	0			-238	-80			ATGAGCAGCATGCGAATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		ATGAGCAGCATGCGAATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		MSSMRMMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		MSSMRMMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		TGAGAATAAC	CCTGCGGGCT	0		0	0	0	0	0
3875	2230	af	AN3418.1	66.m04615	AO070203000002	0			-229	-80			ATGCGAATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		ATGCGAATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		MRMMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		MRMMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		CATGAGCAGC	CCTGCGGGCT	0		0	0	0	0	0
3876	2230	af	AN3418.1	66.m04615	AO070203000002	0			-223	-80			ATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		ATGATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		MMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		MMQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		CAGCATGCGA	CCTGCGGGCT	0		0	0	0	0	0
3877	2230	af	AN3418.1	66.m04615	AO070203000002	0			-220	-80			ATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		ATGCAATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAA		MQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		MQCLHTSDLYPAAVCQAPSGPKGDIPKSNRGSKRLWCATFPRSTGI*		CATGCGAATG	CCTGCGGGCT	0		0	0	0	0	0
3878	2230	af	AN3418.1	66.m04615	AO070203000002	0			-215	-33			ATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		ATGCCTTCATACTTCGGATCTCTATCCCGCAGCAGTATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		MPSYFGSLSRSSMPGTFRTQRGYPKIKPWVQTPMVRYVSSKHRYITCGLFLWAEKDLSTD*		MPSYFGSLSRSSMPGTFRTQRGYPKIKPWVQTPMVRYVSSKHRYITCGLFLWAEKDLSTD*		GAATGATGCA	GCACCTCATC	0		0	0	0	0	0
3879	2230	af	AN3418.1	66.m04615	AO070203000002	0			-179	-33			ATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		ATGCCAGGCACCTTCCGGACCCAAAGGGGATATCCCAAAATCAAACCGTGGGTCCAAACGCCTATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		MPGTFRTQRGYPKIKPWVQTPMVRYVSSKHRYITCGLFLWAEKDLSTD*		MPGTFRTQRGYPKIKPWVQTPMVRYVSSKHRYITCGLFLWAEKDLSTD*		CCGCAGCAGT	GCACCTCATC	0		0	0	0	0	0
3880	2230	af	AN3418.1	66.m04615	AO070203000002	0			-116	-33			ATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		ATGGTGCGCTACGTTTCCTCGAAGCACCGGTATATAACCTGCGGGCTGTTCCTATGGGCAGAGAAAGATTTGTCCACTGACTGA		MVRYVSSKHRYITCGLFLWAEKDLSTD*		MVRYVSSKHRYITCGLFLWAEKDLSTD*		CCAAACGCCT	GCACCTCATC	0		0	0	0	0	0
3881	2230	af	AN3418.1	66.m04615	AO070203000002	0			-63	-37			ATGGGCAGAGAAAGATTTGTCCACTGA		ATGGGCAGAGAAAGATTTGTCCACTGA		MGRERFVH*		MGRERFVH*		GGCTGTTCCT	CTGAGCACCT	0		0	0	0	0	0
3870	2230	an	AN3418.1	66.m04615	AO070203000002	0	-155	-144					ATGAAGCACTAG	ATGAAGCACTAG			MKH*	MKH*			AAGAATACTC	CCATGCTCTT	0		0	0	0	0	0
3871	2230	an	AN3418.1	66.m04615	AO070203000002	0	-141	-58					ATGCTCTTTGGAGACGGCCACCGGGCCGGTCCATGTATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAA	ATGCTCTTTGGAGACGGCCACCGGGCCGGTCCATGTATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAA			MLFGDGHRAGPCMERHTSWRLNVPGGV*	MLFGDGHRAGPCMERHTSWRLNVPGGV*			AGCACTAGCC	GTTGAGTCAA	0		0	0	0	0	0
3872	2230	an	AN3418.1	66.m04615	AO070203000002	0	-109	-53					ATGTATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAAGTTGA	ATGTATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAAGTTGA			MYGTAYFVETQRPWRSIS*	MYGTAYFVETQRPWRSIS*			GGGCCGGTCC	GTCAATTCTT	0		0	0	0	0	0
3873	2230	an	AN3418.1	66.m04615	AO070203000002	0	-105	-58					ATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAA	ATGGAACGGCATACTTCGTGGAGACTCAACGTCCCTGGAGGAGTATAA			MERHTSWRLNVPGGV*	MERHTSWRLNVPGGV*			CGGTCCATGT	GTTGAGTCAA	0		0	0	0	0	0
3882	2230	ao	AN3418.1	66.m04615	AO070203000002	0					-200	-72	ATGAAACGTCCGGGAAAAAAGTGCGTGAATCAGATCGGACTGTCGGGCCGGAATGTTTGCAGTCCCATATCTGGCACTCTGAAGATTCCACAAGCCTTGATCCGCTGTCTGTACGTGATGCATAAATAA			ATGAAACGTCCGGGAAAAAAGTGCGTGAATCAGATCGGACTGTCGGGCCGGAATGTTTGCAGTCCCATATCTGGCACTCTGAAGATTCCACAAGCCTTGATCCGCTGTCTGTACGTGATGCATAAATAA	MKRPGKKCVNQIGLSGRNVCSPISGTLKIPQALIRCLYVMHK*			MKRPGKKCVNQIGLSGRNVCSPISGTLKIPQALIRCLYVMHK*	CATATTGGAG	CAGCTACTTC	0		0	0	0	0	0
3883	2230	ao	AN3418.1	66.m04615	AO070203000002	0					-148	-119	ATGTTTGCAGTCCCATATCTGGCACTCTGA			ATGTTTGCAGTCCCATATCTGGCACTCTGA	MFAVPYLAL*			MFAVPYLAL*	TCGGGCCGGA	AGATTCCACA	0		0	0	0	0	0
3884	2230	ao	AN3418.1	66.m04615	AO070203000002	0					-83	-72	ATGCATAAATAA			ATGCATAAATAA	MHK*			MHK*	TCTGTACGTG	CAGCTACTTC	0		0	0	0	0	0
3885	2233	an	AN8050.1	53.m03894	AO070292000100	0	-149	-126					ATGACACTTGATACGTATCCCTAA	ATGACACTTGATACGTATCCCTAA			MTLDTYP*	MTLDTYP*			TCTACTCAAA	TTGTTCCCCC	0	S	0	MG01675.1	0	0	0
3887	2234	af	AN3873.1	58.m08992	AO070305000057	0			-251	-234			ATGCCTCGGCACCGTTAA		ATGCCTCGGCACCGTTAA		MPRHR*		MPRHR*		TATCTCGGAT	AGATGGCCCG	0	CR	0	0	0	0	0
3888	2234	af	AN3873.1	58.m08992	AO070305000057	0			-231	-88			ATGGCCCGATTCGGAGAGTTATCAGTGTGCCGTCATAGCAGGTGGAGCTCTGCCTTACGTCAAGGACTAAAGGTCGAGAGCTTTCGAGAGCTTGGGTTAGAGTTATATATCTGCTTCAGGCCTCCCTGGTCAGTACATTTCTAG		ATGGCCCGATTCGGAGAGTTATCAGTGTGCCGTCATAGCAGGTGGAGCTCTGCCTTACGTCAAGGACTAAAGGTCGAGAGCTTTCGAGAGCTTGGGTTAGAGTTATATATCTGCTTCAGGCCTCCCTGGTCAGTACATTTCTAG		MARFGELSVCRHSRWSSALRQGLKVESFRELGLELYICFRPPWSVHF*		MARFGELSVCRHSRWSSALRQGLKVESFRELGLELYICFRPPWSVHF*		ACCGTTAAAG	CTAAAAGCCT	0	CR	0	0	0	0	0
3886	2234	an	AN3873.1	58.m08992	AO070305000057	0	-107	-72					ATGGAGCTTATAAATACAGCATCCCGTTCCCTTTAG	ATGGAGCTTATAAATACAGCATCCCGTTCCCTTTAG			MELINTASRSL*	MELINTASRSL*			GTTACGTCAA	CTGTCCCACT	0	CR	0	0	0	0	0
3889	2234	ao	AN3873.1	58.m08992	AO070305000057	0					-198	-7	ATGGCTCCCAGTTACTCATCTACCGAATCCTTATTCGAGGATCGTCATAGATGTGGGGATCTGCCCACTTACGTCAAGAATACAGGCTTCCAGAAGCTTTATAACTACATAAACCCCCTCCACCAAGGAGCTAAGCGTCGAATTTTTTGCATACCAAATCACAATTATTTCATCCCTTATTGTCCCCAGTAA			ATGGCTCCCAGTTACTCATCTACCGAATCCTTATTCGAGGATCGTCATAGATGTGGGGATCTGCCCACTTACGTCAAGAATACAGGCTTCCAGAAGCTTTATAACTACATAAACCCCCTCCACCAAGGAGCTAAGCGTCGAATTTTTTGCATACCAAATCACAATTATTTCATCCCTTATTGTCCCCAGTAA	MAPSYSSTESLFEDRHRCGDLPTYVKNTGFQKLYNYINPLHQGAKRRIFCIPNHNYFIPYCPQ*			MAPSYSSTESLFEDRHRCGDLPTYVKNTGFQKLYNYINPLHQGAKRRIFCIPNHNYFIPYCPQ*	TTCGGAGAGA	TTCATCATGG	0	CR	0	0	0	0	0
3890	2234	ao	AN3873.1	58.m08992	AO070305000057	0					-148	-95	ATGTGGGGATCTGCCCACTTACGTCAAGAATACAGGCTTCCAGAAGCTTTATAA			ATGTGGGGATCTGCCCACTTACGTCAAGAATACAGGCTTCCAGAAGCTTTATAA	MWGSAHLRQEYRLPEAL*			MWGSAHLRQEYRLPEAL*	ATCGTCATAG	CTACATAAAC	0	CR	0	0	0	0	0
3891	2236	an	AN5098.1	53.m04123	AO070310000002	0	-195	-172					ATGCAATGGCTGATTGGAAGGTAG	ATGCAATGGCTGATTGGAAGGTAG			MQWLIGR*	MQWLIGR*			ACGTGAGAGT	CCGCAGATCC	0	A	FG04320.1	0	0	0	0
3892	2236	an	AN5098.1	53.m04123	AO070310000002	0	-190	-149					ATGGCTGATTGGAAGGTAGCCGCAGATCCGCGCCGACCATGA	ATGGCTGATTGGAAGGTAGCCGCAGATCCGCGCCGACCATGA			MADWKVAADPRRP*	MADWKVAADPRRP*			AGAGTATGCA	AAGCATCAGT	0	A	FG04320.1	0	0	0	0
3893	2236	an	AN5098.1	53.m04123	AO070310000002	0	-152	-126					ATGAAAGCATCAGTCATACTGATTTGA	ATGAAAGCATCAGTCATACTGATTTGA			MKASVILI*	MKASVILI*			CGCGCCGACC	GAGCGCATTA	0	A	FG04320.1	0	0	0	0
3894	2236	ao	AN5098.1	53.m04123	AO070310000002	0					-215	-156	ATGCCGGCTGGTAATGTCACAGAATGTCATTCCGGAAACCACGACTCATTTTACACTTGA			ATGCCGGCTGGTAATGTCACAGAATGTCATTCCGGAAACCACGACTCATTTTACACTTGA	MPAGNVTECHSGNHDSFYT*			MPAGNVTECHSGNHDSFYT*	GGCACGTGAT	ACTCAAAATT	0	A	FG04320.1	0	0	0	0
3895	2236	ao	AN5098.1	53.m04123	AO070310000002	0					-202	-113	ATGTCACAGAATGTCATTCCGGAAACCACGACTCATTTTACACTTGAACTCAAAATTAAATACTTTGATCAAAGAATCACAGTACATTGA			ATGTCACAGAATGTCATTCCGGAAACCACGACTCATTTTACACTTGAACTCAAAATTAAATACTTTGATCAAAGAATCACAGTACATTGA	MSQNVIPETTTHFTLELKIKYFDQRITVH*			MSQNVIPETTTHFTLELKIKYFDQRITVH*	CCGGCTGGTA	CTTTCACTCT	0	A	FG04320.1	0	0	0	0
3896	2236	ao	AN5098.1	53.m04123	AO070310000002	0					-192	-85	ATGTCATTCCGGAAACCACGACTCATTTTACACTTGAACTCAAAATTAAATACTTTGATCAAAGAATCACAGTACATTGACTTTCACTCTCACTCCCTACTTGTTTAG			ATGTCATTCCGGAAACCACGACTCATTTTACACTTGAACTCAAAATTAAATACTTTGATCAAAGAATCACAGTACATTGACTTTCACTCTCACTCCCTACTTGTTTAG	MSFRKPRLILHLNSKLNTLIKESQYIDFHSHSLLV*			MSFRKPRLILHLNSKLNTLIKESQYIDFHSHSLLV*	ATGTCACAGA	GTGTTTCTAT	0	A	FG04320.1	0	0	0	0
3897	2238	an	AN0092.1	71.m15367	AO070311000123	0	-159	-55					ATGTGGGCCAGGACTGAACTAGCGTCGATTCGGTCGATAAGTCCTTGGATTTTTTTCTCGCCGATAAACTGGATTCTTCAAGAACAAGCCTCATATCCAGGTTAG	ATGTGGGCCAGGACTGAACTAGCGTCGATTCGGTCGATAAGTCCTTGGATTTTTTTCTCGCCGATAAACTGGATTCTTCAAGAACAAGCCTCATATCCAGGTTAG			MWARTELASIRSISPWIFFSPINWILQEQASYPG*	MWARTELASIRSISPWIFFSPINWILQEQASYPG*			GGTGTCAATT	CTCTGTCGTC	0	AR	0	0	0	0	0
3898	2238	ao	AN0092.1	71.m15367	AO070311000123	0					-216	-184	ATGTGGCTAGTGATCAGCCACCGCCACAGTTGA			ATGTGGCTAGTGATCAGCCACCGCCACAGTTGA	MWLVISHRHS*			MWLVISHRHS*	GTATTTGGCT	CAGAAAAGAG	0	AR	0	0	0	0	0
3899	2243	an	AN2334.1	71.m16080	AO070323000005	0	-284	-204					ATGAAAGGCCATGTTGCACTCGGCATCCACCACGGCAAGTCCACTGAGTCCCCCACGATCGTCTGTCGTCGGTCGGACTAA	ATGAAAGGCCATGTTGCACTCGGCATCCACCACGGCAAGTCCACTGAGTCCCCCACGATCGTCTGTCGTCGGTCGGACTAA			MKGHVALGIHHGKSTESPTIVCRRSD*	MKGHVALGIHHGKSTESPTIVCRRSD*			GGAGCTCCAC	CTCCGTGCGA	0	G	0	0	0	0	0
3900	2243	an	AN2334.1	71.m16080	AO070323000005	0	-274	-119					ATGTTGCACTCGGCATCCACCACGGCAAGTCCACTGAGTCCCCCACGATCGTCTGTCGTCGGTCGGACTAACTCCGTGCGACGGCCTGCCCAGGTGGGTATACTCTGCCTGCACAGCGCGGGGTGTTATAAAACACCCTTGTCGCCTCTACCTTAA	ATGTTGCACTCGGCATCCACCACGGCAAGTCCACTGAGTCCCCCACGATCGTCTGTCGTCGGTCGGACTAACTCCGTGCGACGGCCTGCCCAGGTGGGTATACTCTGCCTGCACAGCGCGGGGTGTTATAAAACACCCTTGTCGCCTCTACCTTAA			MLHSASTTASPLSPPRSSVVGRTNSVRRPAQVGILCLHSAGCYKTPLSPLP*	MLHSASTTASPLSPPRSSVVGRTNSVRRPAQVGILCLHSAGCYKTPLSPLP*			ATGAAAGGCC	CAGCACTATT	0	G	0	0	0	0	0
3901	2243	ao	AN2334.1	71.m16080	AO070323000005	0					-117	-61	ATGCTTTGCGACAATACATATAATAAACCCATTGTTCCGTTGTCTGGCCTTTCGTAA			ATGCTTTGCGACAATACATATAATAAACCCATTGTTCCGTTGTCTGGCCTTTCGTAA	MLCDNTYNKPIVPLSGLS*			MLCDNTYNKPIVPLSGLS*	CGACTTTCGT	TCACTTGTCT	0	G	0	0	0	0	0
3904	2244	af	AN6151.1	71.m15834	AO070326000149	0			-267	-208			ATGTCGACCAAGGCCAGAAACATCATAGACAACATCCGTTCCTCTGACTGGTCAGTTTGA		ATGTCGACCAAGGCCAGAAACATCATAGACAACATCCGTTCCTCTGACTGGTCAGTTTGA		MSTKARNIIDNIRSSDWSV*		MSTKARNIIDNIRSSDWSV*		GCCTGATAAT	GAGCAATAGC	0	G	0	0	0	0	0
3902	2244	an	AN6151.1	71.m15834	AO070326000149	0	-195	-154					ATGTACGCCTCTCGAATGCTTGATTCTGAGTGGTCAATTTGA	ATGTACGCCTCTCGAATGCTTGATTCTGAGTGGTCAATTTGA			MYASRMLDSEWSI*	MYASRMLDSEWSI*			CCACTACTAA	GAGCAACGTC	0	G	0	0	0	0	0
3903	2244	an	AN6151.1	71.m15834	AO070326000149	0	-180	-154					ATGCTTGATTCTGAGTGGTCAATTTGA	ATGCTTGATTCTGAGTGGTCAATTTGA			MLDSEWSI*	MLDSEWSI*			CGCCTCTCGA	GAGCAACGTC	0	G	0	0	0	0	0
3905	2244	ao	AN6151.1	71.m15834	AO070326000149	0					-195	-76	ATGTACTGCTTCTTCGTGATTGGTCACTTCGAGAGCAACGATCATGTATACACCTACTCAATTACAAATAGAGTGACTCAAGTCTCCTATAATAAATTTGCCCATCATCTTGAAGCCTGA			ATGTACTGCTTCTTCGTGATTGGTCACTTCGAGAGCAACGATCATGTATACACCTACTCAATTACAAATAGAGTGACTCAAGTCTCCTATAATAAATTTGCCCATCATCTTGAAGCCTGA	MYCFFVIGHFESNDHVYTYSITNRVTQVSYNKFAHHLEA*			MYCFFVIGHFESNDHVYTYSITNRVTQVSYNKFAHHLEA*	GAGAAGTCCG	CTTTCTTCTC	0	G	0	0	0	0	0
3906	2244	ao	AN6151.1	71.m15834	AO070326000149	0					-152	-120	ATGTATACACCTACTCAATTACAAATAGAGTGA			ATGTATACACCTACTCAATTACAAATAGAGTGA	MYTPTQLQIE*			MYTPTQLQIE*	AGCAACGATC	CTCAAGTCTC	0	G	0	0	0	0	0

3908	2247	af	AN5338.1	69.m15570	AO070333000229	0			-258	-232			ATGCTTGAACCATACCACCTTCCTTAG		ATGCTTGAACCATACCACCTTCCTTAG		MLEPYHLP*		MLEPYHLP*		CGCCTACGTC	AACATACCAG	0	P	FG06539.1	0	NCU07332.1	0	0
3907	2247	an	AN5338.1	69.m15570	AO070333000229	0	-228	-211					ATGGAGACTGTACCTTGA	ATGGAGACTGTACCTTGA			METVP*	METVP*			TTGAAACACT	ACTAGGTCAA	0	P	FG06539.1	0	NCU07332.1	0	0
3909	2247	ao	AN5338.1	69.m15570	AO070333000229	0					-265	-212	ATGATGAAACCATTGGTCCTTCTTGCGTGGCCTTCTCCTTTTCACATGCATTGA			ATGATGAAACCATTGGTCCTTCTTGCGTGGCCTTCTCCTTTTCACATGCATTGA	MMKPLVLLAWPSPFHMH*			MMKPLVLLAWPSPFHMH*	TCTCTCCCGC	AAAGAAAACG	0	P	FG06539.1	0	NCU07332.1	0	0
3910	2247	ao	AN5338.1	69.m15570	AO070333000229	0					-262	-212	ATGAAACCATTGGTCCTTCTTGCGTGGCCTTCTCCTTTTCACATGCATTGA			ATGAAACCATTGGTCCTTCTTGCGTGGCCTTCTCCTTTTCACATGCATTGA	MKPLVLLAWPSPFHMH*			MKPLVLLAWPSPFHMH*	CTCCCGCATG	AAAGAAAACG	0	P	FG06539.1	0	NCU07332.1	0	0
3911	2247	ao	AN5338.1	69.m15570	AO070333000229	0					-170	-105	ATGGTTTTGCATCTTGCTGCCATTGAAAAAGCGCCTCGATTCTCTCCTCTCGTCGTCTTTCTTTGA			ATGGTTTTGCATCTTGCTGCCATTGAAAAAGCGCCTCGATTCTCTCCTCTCGTCGTCTTTCTTTGA	MVLHLAAIEKAPRFSPLVVFL*			MVLHLAAIEKAPRFSPLVVFL*	CCACTACGTC	CACACACAAA	0	P	FG06539.1	0	NCU07332.1	0	0
3913	2249	af	AN2730.1	54.m06671	AO070338000210	0			-202	-188			ATGGAGTCTGCTTGA		ATGGAGTCTGCTTGA		MESA*		MESA*		CATCAACGCC	ATACAGTCGT	0	P	0	0	0	0	0
3912	2249	an	AN2730.1	54.m06671	AO070338000210	0	-168	-148					ATGGCTAGCCAGTTCGCTTAA	ATGGCTAGCCAGTTCGCTTAA			MASQFA*	MASQFA*			ACCGTCCGAC	ATCAACTGAA	0	P	0	0	0	0	0
3914	2249	ao	AN2730.1	54.m06671	AO070338000210	0					-226	-212	ATGGACCTTGTTTGA			ATGGACCTTGTTTGA	MDLV*			MDLV*	GGTTCTGGCT	ACACGGCTTT	0	P	0	0	0	0	0
3917	2251	af	AN6753.1	65.m07189	AO070339000200	0			-112	-101			ATGTTCTACTGA		ATGTTCTACTGA		MFY*		MFY*		TGGAAGTCGT	TTTCTGTGCC	0	CR	0	0	0	0	0
3915	2251	an	AN6753.1	65.m07189	AO070339000200	0	-183	-172					ATGTGGCGATGA	ATGTGGCGATGA			MWR*	MWR*			TGGCGTACGT	CTAATGTATA	0	CR	0	0	0	0	0
3916	2251	an	AN6753.1	65.m07189	AO070339000200	0	-168	-82					ATGTATACAAGACAGGCGCTAAAAAAACATCCCCACCACGATTTCAAAGCAAGTGGACCTCAACTGTCCTTCCACTCGATTCTGTAG	ATGTATACAAGACAGGCGCTAAAAAAACATCCCCACCACGATTTCAAAGCAAGTGGACCTCAACTGTCCTTCCACTCGATTCTGTAG			MYTRQALKKHPHHDFKASGPQLSFHSIL*	MYTRQALKKHPHHDFKASGPQLSFHSIL*			GCGATGACTA	ACCATATCTG	0	CR	0	0	0	0	0
3918	2251	ao	AN6753.1	65.m07189	AO070339000200	0					-264	-163	ATGCACGGCCTATCGAGGGGCAAAAAAAAGTCTGAAACGGAGCAACATTCGGTATCATATTGTCCTAAAACTCGGTATATCGCCGTGACAAGTCGCCTCTAA			ATGCACGGCCTATCGAGGGGCAAAAAAAAGTCTGAAACGGAGCAACATTCGGTATCATATTGTCCTAAAACTCGGTATATCGCCGTGACAAGTCGCCTCTAA	MHGLSRGKKKSETEQHSVSYCPKTRYIAVTSRL*			MHGLSRGKKKSETEQHSVSYCPKTRYIAVTSRL*	AATCGGAGCA	AGATATCCAC	0	CR	0	0	0	0	0
3919	2251	ao	AN6753.1	65.m07189	AO070339000200	0					-124	-80	ATGGAGCAACACTTCGGAGGTTTTCTGTCGGGGGACAGAGTGTAG			ATGGAGCAACACTTCGGAGGTTTTCTGTCGGGGGACAGAGTGTAG	MEQHFGGFLSGDRV*			MEQHFGGFLSGDRV*	ATCAAGGGCT	TATTTAAAGT	0	CR	0	0	0	0	0
3920	2252	af	AN5917.1	72.m19214	AO070340000369	0			-124	-113			ATGTCACCTTGA		ATGTCACCTTGA		MSP*		MSP*		TTTCTACTAC	CTCGGAACAT	0	R	0	MG07546.1	0	YGR289C	0
3921	2252	ao	AN5917.1	72.m19214	AO070340000369	0					-220	-152	ATGTTCCTGGGTAGAAGCGGAAGTGGGGACTCAAGAGGCCCCGCCGAGCCAGAGGCCATAAATTTCTAG			ATGTTCCTGGGTAGAAGCGGAAGTGGGGACTCAAGAGGCCCCGCCGAGCCAGAGGCCATAAATTTCTAG	MFLGRSGSGDSRGPAEPEAINF*			MFLGRSGSGDSRGPAEPEAINF*	GCGTTCTGCG	CGACGTCGTC	0	R	0	MG07546.1	0	YGR289C	0
3922	2254	an	AN4493.1	57.m05638	AO070343000131	0	-197	-183					ATGTATTCTCATTAA	ATGTATTCTCATTAA			MYSH*	MYSH*			ATTTTCTCCA	TATCTCTTCC	0	B	0	0	0	0	0
3923	2254	ao	AN4493.1	57.m05638	AO070343000131	0					-144	-82	ATGCCTCGTCTGCTTCCTTATCTTCTTCTCTTTGACTTGTATACCATCTCGATGACCGAATGA			ATGCCTCGTCTGCTTCCTTATCTTCTTCTCTTTGACTTGTATACCATCTCGATGACCGAATGA	MPRLLPYLLLFDLYTISMTE*			MPRLLPYLLLFDLYTISMTE*	CTATTTATAT	TCACGGCGGA	0	B	0	0	0	0	0
3924	2254	ao	AN4493.1	57.m05638	AO070343000131	0					-93	-82	ATGACCGAATGA			ATGACCGAATGA	MTE*			MTE*	TACCATCTCG	TCACGGCGGA	0	B	0	0	0	0	0
3925	2256	an	AN0691.1	70.m15294	AO070343000521	0	-172	-155					ATGTCGACGTCACGTTGA	ATGTCGACGTCACGTTGA			MSTSR*	MSTSR*			GACAAGCATC	ATCCAACCCA	0		0	0	0	0	0
3926	2256	ao	AN0691.1	70.m15294	AO070343000521	0					-240	-196	ATGCGGAGCCCTAAGCCCTGGTTTTCTGAAGTAGGTGGGCAATAG			ATGCGGAGCCCTAAGCCCTGGTTTTCTGAAGTAGGTGGGCAATAG	MRSPKPWFSEVGGQ*			MRSPKPWFSEVGGQ*	AGCGGTATCC	TACGATTGCA	0		0	0	0	0	0
3927	2256	ao	AN0691.1	70.m15294	AO070343000521	0					-155	-120	ATGATGCGCTCTAAAACCAGGCTTTACAGAATGTAG			ATGATGCGCTCTAAAACCAGGCTTTACAGAATGTAG	MMRSKTRLYRM*			MMRSKTRLYRM*	CGGGGTCTAG	ACTCTCCATT	0		0	0	0	0	0
3928	2256	ao	AN0691.1	70.m15294	AO070343000521	0					-152	-120	ATGCGCTCTAAAACCAGGCTTTACAGAATGTAG			ATGCGCTCTAAAACCAGGCTTTACAGAATGTAG	MRSKTRLYRM*			MRSKTRLYRM*	GGTCTAGATG	ACTCTCCATT	0		0	0	0	0	0
3929	2256	ao	AN0691.1	70.m15294	AO070343000521	0					-81	-67	ATGTGCTGTGTGTAA			ATGTGCTGTGTGTAA	MCCV*			MCCV*	TCGCAAATAT	AGAAAGCTGC	0		0	0	0	0	0
3930	2257	an	AN7428.1	57.m05916	AO070197000009	0	-225	-160					ATGCTGCAGCAGGTACATAGTACGGACTTGAAATACCACGCTGTGTCGTCCTTCGGTTTTTCTTAA	ATGCTGCAGCAGGTACATAGTACGGACTTGAAATACCACGCTGTGTCGTCCTTCGGTTTTTCTTAA			MLQQVHSTDLKYHAVSSFGFS*	MLQQVHSTDLKYHAVSSFGFS*			CTTTCCCCAA	AGATCCAGCC	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3931	2257	ao	AN7428.1	57.m05916	AO070197000009	0					-229	-167	ATGATACTATGTCTTACTATCAATACCTACCTTACTCCATCCCCATGCCACCTTGACATGTAG			ATGATACTATGTCTTACTATCAATACCTACCTTACTCCATCCCCATGCCACCTTGACATGTAG	MILCLTINTYLTPSPCHLDM*			MILCLTINTYLTPSPCHLDM*	CTGCCCCACC	TCAGATGAAC	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3932	2257	ao	AN7428.1	57.m05916	AO070197000009	0					-221	-174	ATGTCTTACTATCAATACCTACCTTACTCCATCCCCATGCCACCTTGA			ATGTCTTACTATCAATACCTACCTTACTCCATCCCCATGCCACCTTGA	MSYYQYLPYSIPMPP*			MSYYQYLPYSIPMPP*	CCATGATACT	CATGTAGTCA	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3933	2257	ao	AN7428.1	57.m05916	AO070197000009	0					-185	-174	ATGCCACCTTGA			ATGCCACCTTGA	MPP*			MPP*	CTCCATCCCC	CATGTAGTCA	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3934	2257	ao	AN7428.1	57.m05916	AO070197000009	0					-162	-151	ATGAACAATTAG			ATGAACAATTAG	MNN*			MNN*	ATGTAGTCAG	GTACCAGACA	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3935	2257	ao	AN7428.1	57.m05916	AO070197000009	0					-86	-63	ATGATTACCGTCTTTCTCCTTTAA			ATGATTACCGTCTTTCTCCTTTAA	MITVFLL*			MITVFLL*	CTGGTCCTGC	GGGCTACTAC	0	H	FG10226.1	0	NCU06672.1	YHR171W	YHR171W
3939	2259	af	AN4593.1	57.m05516	AO070267000009	0			-93	-37			ATGCGACGGCCGGTGATGATTGTGATGATTAGATTTGGTATCTTCTTCTTTATCTGA		ATGCGACGGCCGGTGATGATTGTGATGATTAGATTTGGTATCTTCTTCTTTATCTGA		MRRPVMIVMIRFGIFFFI*		MRRPVMIVMIRFGIFFFI*		ACGACAGGTT	GCTCCCTTCT	0	K	0	0	0	0	0
3940	2259	af	AN4593.1	57.m05516	AO070267000009	0			-78	-37			ATGATTGTGATGATTAGATTTGGTATCTTCTTCTTTATCTGA		ATGATTGTGATGATTAGATTTGGTATCTTCTTCTTTATCTGA		MIVMIRFGIFFFI*		MIVMIRFGIFFFI*		ACGGCCGGTG	GCTCCCTTCT	0	K	0	0	0	0	0
3941	2259	af	AN4593.1	57.m05516	AO070267000009	0			-69	-37			ATGATTAGATTTGGTATCTTCTTCTTTATCTGA		ATGATTAGATTTGGTATCTTCTTCTTTATCTGA		MIRFGIFFFI*		MIRFGIFFFI*		GATGATTGTG	GCTCCCTTCT	0	K	0	0	0	0	0
3936	2259	an	AN4593.1	57.m05516	AO070267000009	0	-114	-13					ATGAATCATTATGACTGTGAAGGGAGATCGGATATGAAAGTGACGGCCTCATCCTCCATTTTCACAATTCTTGATACGCAATCTTACAGCTCCTCACCTTGA	ATGAATCATTATGACTGTGAAGGGAGATCGGATATGAAAGTGACGGCCTCATCCTCCATTTTCACAATTCTTGATACGCAATCTTACAGCTCCTCACCTTGA			MNHYDCEGRSDMKVTASSIFTILDTQSYSSSP*	MNHYDCEGRSDMKVTASSIFTILDTQSYSSSP*			TACAACGAAG	ACCGTGTTCA	0	K	0	0	0	0	0
3937	2259	an	AN4593.1	57.m05516	AO070267000009	0	-104	-78					ATGACTGTGAAGGGAGATCGGATATGA	ATGACTGTGAAGGGAGATCGGATATGA			MTVKGDRI*	MTVKGDRI*			ATGAATCATT	AAGTGACGGC	0	K	0	0	0	0	0
3938	2259	an	AN4593.1	57.m05516	AO070267000009	0	-81	-13					ATGAAAGTGACGGCCTCATCCTCCATTTTCACAATTCTTGATACGCAATCTTACAGCTCCTCACCTTGA	ATGAAAGTGACGGCCTCATCCTCCATTTTCACAATTCTTGATACGCAATCTTACAGCTCCTCACCTTGA			MKVTASSSIFTILDTQSYSSSP*	MKVTASSSIFTILDTQSYSSSP*			GAGATCGGAT	ACCGTGTTCA	0	K	0	0	0	0	0
3942	2259	ao	AN4593.1	57.m05516	AO070267000009	0					-183	-109	ATGAGTCAGCAGATCACCAATGACATGCCATCTGATAAATGCGATAAAGAATATGGGGCTGATTGTCAAGCTTAA			ATGAGTCAGCAGATCACCAATGACATGCCATCTGATAAATGCGATAAAGAATATGGGGCTGATTGTCAAGCTTAA	MSQQITNDMPSDKCDKEYGADCQA*			MSQQITNDMPSDKCDKEYGADCQA*	CCCGGGGTGG	TGATGACGAT	0	K	0	0	0	0	0
3943	2259	ao	AN4593.1	57.m05516	AO070267000009	0					-159	-109	ATGCCATCTGATAAATGCGATAAAGAATATGGGGCTGATTGTCAAGCTTAA			ATGCCATCTGATAAATGCGATAAAGAATATGGGGCTGATTGTCAAGCTTAA	MPSDKCDKEYGADCQA*			MPSDKCDKEYGADCQA*	CACCAATGAC	TGATGACGAT	0	K	0	0	0	0	0
3944	2259	ao	AN4593.1	57.m05516	AO070267000009	0					-109	-89	ATGATGACGATATATTTCTGA			ATGATGACGATATATTTCTGA	MMTIYF*			MMTIYF*	GTCAAGCTTA	CTTCTTTTTT	0	K	0	0	0	0	0
3945	2259	ao	AN4593.1	57.m05516	AO070267000009	0					-106	-89	ATGACGATATATTTCTGA			ATGACGATATATTTCTGA	MTIYF*			MTIYF*	AAGCTTAATG	CTTCTTTTTT	0	K	0	0	0	0	0
3948	2269	af	AN9012.1	56.m02340	AO070321000044	0			-258	-241			ATGGTCTTCTTTGATTAG		ATGGTCTTCTTTGATTAG		MVFFD*		MVFFD*		TTCACTGGTA	TTGCAATCTC	0	EM	0	0	NCU05977.1	0	0
3946	2269	an	AN9012.1	56.m02340	AO070321000044	0	-212	-123					ATGTATTTCTGTATGGAGCCAGCCACCAGGGTAGGAAGGCGTTTCCGTCGAGCCCTAGCTTATATCTACCTAGGTTTACCAGACGATTAA	ATGTATTTCTGTATGGAGCCAGCCACCAGGGTAGGAAGGCGTTTCCGTCGAGCCCTAGCTTATATCTACCTAGGTTTACCAGACGATTAA			MYFCMEPATRVGRRFRRALAYIYLGLPDD*	MYFCMEPATRVGRRFRRALAYIYLGLPDD*			AGTGGTTCCT	TTTACCCTAT	0	EM	0	0	NCU05977.1	0	0
3947	2269	an	AN9012.1	56.m02340	AO070321000044	0	-200	-123					ATGGAGCCAGCCACCAGGGTAGGAAGGCGTTTCCGTCGAGCCCTAGCTTATATCTACCTAGGTTTACCAGACGATTAA	ATGGAGCCAGCCACCAGGGTAGGAAGGCGTTTCCGTCGAGCCCTAGCTTATATCTACCTAGGTTTACCAGACGATTAA			MEPATRVGRRFRRALAYIYLGLPDD*	MEPATRVGRRFRRALAYIYLGLPDD*			GTATTTCTGT	TTTACCCTAT	0	EM	0	0	NCU05977.1	0	0
3949	2269	ao	AN9012.1	56.m02340	AO070321000044	0					-100	-14	ATGCCAGCAACCGACGAGCTTACAGCATACAATCTGTTCAAGATACTCATACCACTACATTCGAAGAGCCTCATTCCAATCACATAA			ATGCCAGCAACCGACGAGCTTACAGCATACAATCTGTTCAAGATACTCATACCACTACATTCGAAGAGCCTCATTCCAATCACATAA	MPATDELTAYNLFKILIPLHSKSLIPIT*			MPATDELTAYNLFKILIPLHSKSLIPIT*	AGGAATAACA	CCAAACCACC	0	EM	0	0	NCU05977.1	0	0
3952	2272	af	AN5585.1	58.m07512	AO070328000019	0			-234	-139			ATGAAACAGAAGGTGAAGGTTAGAGGTGAAGACCAAGTAGTTTCCCGAATGGATCTCAATCACATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		ATGAAACAGAAGGTGAAGGTTAGAGGTGAAGACCAAGTAGTTTCCCGAATGGATCTCAATCACATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		MKQKVKVRGEDQVVSRMDLNHMITWSGQVGR*		MKQKVKVRGEDQVVSRMDLNHMITWSGQVGR*		TGCTATAGCT	ACAATTTTCT	0	I	0	0	0	YLR100W	0
3953	2272	af	AN5585.1	58.m07512	AO070328000019	0			-186	-139			ATGGATCTCAATCACATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		ATGGATCTCAATCACATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		MDLNHMITWSGQVGR*		MDLNHMITWSGQVGR*		AGTTTCCCGA	ACAATTTTCT	0	I	0	0	0	YLR100W	0
3954	2272	af	AN5585.1	58.m07512	AO070328000019	0			-171	-139			ATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		ATGATCACCTGGAGCGGGCAGGTCGGGCGATAA		MITWSGQVGR*		MITWSGQVGR*		TCTCAATCAC	ACAATTTTCT	0	I	0	0	0	YLR100W	0
3950	2272	an	AN5585.1	58.m07512	AO070328000019	0	-169	-128					ATGTGCCTTCTAAACGATAAACGTACAGAGAGGAGAGTTTGA	ATGTGCCTTCTAAACGATAAACGTACAGAGAGGAGAGTTTGA			MCLLNDKRTERRV*	MCLLNDKRTERRV*			CTGGGTTGAC	ACCTGTGGTA	0	I	0	0	0	YLR100W	0
3951	2272	an	AN5585.1	58.m07512	AO070328000019	0	-115	-53					ATGCTTACATCATCCACCACTTCAAGATGCACCAATCACCCCGAGAGGTCCCAGTCGGGATAG	ATGCTTACATCATCCACCACTTCAAGATGCACCAATCACCCCGAGAGGTCCCAGTCGGGATAG			MLTSSTTSRCTNHPERSQSG*	MLTSSTTSRCTNHPERSQSG*			CTGTGGTAGG	TTGCTGGATC	0	I	0	0	0	YLR100W	0
3955	2272	ao	AN5585.1	58.m07512	AO070328000019	0					-142	-59	ATGAATCCAGGCACACATAAGGTTAGGAAACTATTCCCGGTCAGGCCTAGCGCACAGGAACACATCCCCGTGAATCTCAATTAG			ATGAATCCAGGCACACATAAGGTTAGGAAACTATTCCCGGTCAGGCCTAGCGCACAGGAACACATCCCCGTGAATCTCAATTAG	MNPGTHKVRKLFPVRPSAQEHIPVNLN*			MNPGTHKVRKLFPVRPSAQEHIPVNLN*	GGATTAGCCA	TTTCCATCCT	0	I	0	0	0	YLR100W	0
3956	2274	af	AN3220.1	67.m02928	AO070330000070	0			-170	-90			ATGTCGGAGATTTCGACCCCACGCTTCTACTCCGCGTTTTCTCCGCAGTGTTCATGCACGGGGTATAAAGCTGGGAAGTGA		ATGTCGGAGATTTCGACCCCACGCTTCTACTCCGCGTTTTCTCCGCAGTGTTCATGCACGGGGTATAAAGCTGGGAAGTGA		MSEISTPRFYSAFSPQCSCTGYKAGK*		MSEISTPRFYSAFSPQCSCTGYKAGK*		CGTGGTCCTG	TCGTCTGTCC	0	GEPR	FG10483.1	MG05600.1	0	0	0
3959	2279	af	AN2103.1	57.m05804	AO070341000261	0			-267	-238			ATGTATATGGTGCCAGATCAATTGAGATAG		ATGTATATGGTGCCAGATCAATTGAGATAG		MYMVPDQLR*		MYMVPDQLR*		CAACGCGTAC	CGACTTGACA	0	S	0	0	0	0	0
3960	2279	af	AN2103.1	57.m05804	AO070341000261	0			-261	-238			ATGGTGCCAGATCAATTGAGATAG		ATGGTGCCAGATCAATTGAGATAG		MVPDQLR*		MVPDQLR*		GTACATGTAT	CGACTTGACA	0	S	0	0	0	0	0
3961	2279	af	AN2103.1	57.m05804	AO070341000261	0			-162	-130			ATGTTCAACCGCTGTGGAATGCCGACCCTATGA		ATGTTCAACCGCTGTGGAATGCCGACCCTATGA		MFNRCGMPTL*		MFNRCGMPTL*		ACAATGGAAA	TTCGCCATCT	0	S	0	0	0	0	0
3962	2279	af	AN2103.1	57.m05804	AO070341000261	0			-144	-130			ATGCCGACCCTATGA		ATGCCGACCCTATGA		MPTL*		MPTL*		CCGCTGTGGA	TTCGCCATCT	0	S	0	0	0	0	0
3958	2279	an	AN2103.1	57.m05804	AO070341000261	0	-136	-65					ATGCGGAGACAAATTTCTCCGCTTGATGAGCTCCAGTCCGACCGCGGCTCCGTCATCCATCTCCAAGTCTAA	ATGCGGAGACAAATTTCTCCGCTTGATGAGCTCCAGTCCGACCGCGGCTCCGTCATCCATCTCCAAGTCTAA			MRRQISPLDELQSDRGSVIHLQV*	MRRQISPLDELQSDRGSVIHLQV*			GGATTAATTA	GCCTAAAAGT	0	S	0	0	0	0	0
3963	2280	af	AN7589.1	72.m19611	AO070343000303	0			-263	-249			ATGTTCTGCACCTAG		ATGTTCTGCACCTAG		MFCT*		MFCT*		CTACAACCTC	TCCTCAACCG	0	L	0	0	0	0	0
3964	2280	ao	AN7589.1	72.m19611	AO070343000303	0					-281	-225	ATGCGCCACGGATCGATCGTGATCTTCACCTACTTCTTTGTGGTCATTTTACCTTAA			ATGCGCCACGGATCGATCGTGATCTTCACCTACTTCTTTGTGGTCATTTTACCTTAA	MRHGSIVIFTYFFVVILP*			MRHGSIVIFTYFFVVILP*	TATCAGAGCC	TTTTCTTTTT	0	L	0	0	0	0	0
3965	2284	ao	AN5833.1	72.m18961	AO070260000012	0					-134	-102	ATGCCTGCTTTTGGGCTTTATGATTACTACTAG			ATGCCTGCTTTTGGGCTTTATGATTACTACTAG	MPAFGLYDYY*			MPAFGLYDYY*	ATTTTATTGA	TAACTAGTTA	0	I	0	0	0	0	0
3966	2284	ao	AN5833.1	72.m18961	AO070260000012	0					-115	-95	ATGATTACTACTAGTAACTAG			ATGATTACTACTAGTAACTAG	MITTSN*			MITTSN*	TTTGGGCTTT	TTAGTTGTCT	0	I	0	0	0	0	0
3968	2286	af	AN4387.1	58.m07937	AO070261000033	0			-73	-47			ATGCTCGGTTCCGGGAGCCCTCGTTGA		ATGCTCGGTTCCGGGAGCCCTCGTTGA		MLGSGSPR*		MLGSGSPR*		GAGCACCGAC	TTGCAAAGAC	0	C	0	0	0	YIL006W	0
3967	2286	an	AN4387.1	58.m07937	AO070261000033	0	-78	-49					ATGCTCGGGTCCGGGATCCCTTATCGGTAA	ATGCTCGGGTCCGGGATCCCTTATCGGTAA			MLGSGIPYR*	MLGSGIPYR*			GGGCACCGAC	AGCATCAAAA	0	C	0	0	0	YIL006W	0

3969	2286	ao	AN4387.1	58.m07937	AO070261000033	0					-70	-38	ATGCTCGGGTCCGGGAACCCTCGTGACAATTAA			ATGCTCGGGTCCGGGAACCCTCGTGACAATTAA	MLGSGNPRDN*			MLGSGNPRDN*	GAGCACCGCT	GACGGATAGA	0	C	0	0	0	YIL006W	0
3974	2288	af	AN9286.1	71.m15143	AO070279000041	0			-129	-91			ATGAGCAAAAGTAGCGGCAGCTGGATGACGACTGTCTAA		ATGAGCAAAAGTAGCGGCAGCTGGATGACGACTGTCTAA		MSKSSGSWMTTV*		MSKSSGSWMTTV*		GTTGGCTTCA	CGCCACGATA	0	G	0	0	0	0	0
3975	2288	af	AN9286.1	71.m15143	AO070279000041	0			-105	-91			ATGACGACTGTCTAA		ATGACGACTGTCTAA		MTTV*		MTTV*		CGGCAGCTGG	CGCCACGATA	0	G	0	0	0	0	0
3976	2288	af	AN9286.1	71.m15143	AO070279000041	0			-78	-58			ATGGGTACGAGGAGCCTTTAA		ATGGGTACGAGGAGCCTTTAA		MGTRSL*		MGTRSL*		CCACGATACT	AGGCAGCGCT	0	G	0	0	0	0	0
3970	2288	an	AN9286.1	71.m15143	AO070279000041	0	-223	-194					ATGCGAGAACGAGGTCTGCCCGGCATATAG	ATGCGAGAACGAGGTCTGCCCGGCATATAG			MRERGLPGI*	MRERGLPGI*			CCCCGCCAAA	CCTGAAATGA	0	G	0	0	0	0	0
3971	2288	an	AN9286.1	71.m15143	AO070279000041	0	-187	-77					ATGATGCATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAG	ATGATGCATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAG			MMHGRTSGVEKHRRIGPFPATAKELPVPSAGLCVCA*	MMHGRTSGVEKHRRIGPFPATAKELPVPSAGLCVCA*			ATAGCCTGAA	ATTTAAAAGC	0	G	0	0	0	0	0
3972	2288	an	AN9286.1	71.m15143	AO070279000041	0	-184	-77					ATGCATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAG	ATGCATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAG			MHGRTSGVEKHRRIGPFPATAKELPVPSAGLCVCA*	MHGRTSGVEKHRRIGPFPATAKELPVPSAGLCVCA*			GCCTGAAATG	ATTTAAAAGC	0	G	0	0	0	0	0
3973	2288	an	AN9286.1	71.m15143	AO070279000041	0	-180	-4					ATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAGATTTAAAAGCCCAGCGGCGGACGCAACTAAATCAGGACAGACACCTACAGCTCAAGTAGCAGCTTTAACATAG	ATGGCCGAACATCAGGGGTGGAAAAACATCGACGCATCGGACCTTTTCCGGCGACCGCAAAAGAGCTTCCCGTACCTAGTGCAGGGCTCTGCGTCTGTGCATAGATTTAAAAGCCCAGCGGCGGACGCAACTAAATCAGGACAGACACCTACAGCTCAAGTAGCAGCTTTAACATAG			MAEHQGWKNIDASDLFRRPQKSFPYLVQGSASVHRFKSPAADATKSGQTPTAQVAALT*	MAEHQGWKNIDASDLFRRPQKSFPYLVQGSASVHRFKSPAADATKSGQTPTAQVAALT*			GAAATGATGC	AAGATGCGGA	0	G	0	0	0	0	0
3977	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-176	-150	ATGGGTGCATATGGCGGTCTGTCATGA			ATGGGTGCATATGGCGGTCTGTCATGA	MGAYGGLS*			MGAYGGLS*	AGAGTAAAAT	CCCCACGTTT	0	G	0	0	0	0	0
3978	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-166	-128	ATGGCGGTCTGTCATGACCCCACGTTTACCCCGGATTAA			ATGGCGGTCTGTCATGACCCCACGTTTACCCCGGATTAA	MAVCHDPTFTPD*			MAVCHDPTFTPD*	ATGGGTGCAT	TATAGCCTGA	0	G	0	0	0	0	0
3979	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-153	-118	ATGACCCCACGTTTACCCCGGATTAATATAGCCTGA			ATGACCCCACGTTTACCCCGGATTAATATAGCCTGA	MTPRLPRINIA*			MTPRLPRINIA*	GCGGTCTGTC	ATTCATGGGT	0	G	0	0	0	0	0
3980	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-113	-75	ATGGGTATTGTTAGCGTGGGGATCCGTATCGGGAAATGA			ATGGGTATTGTTAGCGTGGGGATCCGTATCGGGAAATGA	MGIVSVGIRIGK*			MGIVSVGIRIGK*	GCCTGAATTC	GCAAGATGCA	0	G	0	0	0	0	0
3981	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-78	-13	ATGAGCAAGATGCAGATCTCGGTATTTAAATCACCCCAATTGCTCTACGAGAAGAGCCAACTCTAG			ATGAGCAAGATGCAGATCTCGGTATTTAAATCACCCCAATTGCTCTACGAGAAGAGCCAACTCTAG	MSKMQISVFKSPQLLYEKSQL*			MSKMQISVFKSPQLLYEKSQL*	GTATCGGGAA	AACGTCAACA	0	G	0	0	0	0	0
3982	2288	ao	AN9286.1	71.m15143	AO070279000041	0					-69	-13	ATGCAGATCTCGGTATTTAAATCACCCCAATTGCTCTACGAGAAGAGCCAACTCTAG			ATGCAGATCTCGGTATTTAAATCACCCCAATTGCTCTACGAGAAGAGCCAACTCTAG	MQISVFKSPQLLYEKSQL*			MQISVFKSPQLLYEKSQL*	AATGAGCAAG	AACGTCAACA	0	G	0	0	0	0	0
3984	2289	af	AN1074.1	70.m15148	AO070285000074	0			-263	-249			ATGAATGGCGTTTAG		ATGAATGGCGTTTAG		MNGV*		MNGV*		GCTTCGGAGA	CGGAGGAGAT	0	E	0	0	0	0	0
3985	2289	af	AN1074.1	70.m15148	AO070285000074	0			-259	-110			ATGGCGTTTAGCGGAGGAGATTTTTGGGAGCGGTCACCAGCTAGACAACTATTTTCCCTTCCGGCGTTGCGGACAACAGGCGGCAGTTCCTTATCAGCGGGTCTTGGCATCGTCTATCAGTTCGGAAAGCTAGTGCGCAGCTCCATTTAA		ATGGCGTTTAGCGGAGGAGATTTTTGGGAGCGGTCACCAGCTAGACAACTATTTTCCCTTCCGGCGTTGCGGACAACAGGCGGCAGTTCCTTATCAGCGGGTCTTGGCATCGTCTATCAGTTCGGAAAGCTAGTGCGCAGCTCCATTTAA		MAFSGGDFWERSPARQLFSLPALRTTGGSSLSAGLGIVYQFGKLVRSSI*		MAFSGGDFWERSPARQLFSLPALRTTGGSSLSAGLGIVYQFGKLVRSSI*		CGGAGAATGA	TCACGATTTC	0	E	0	0	0	0	0
3983	2289	an	AN1074.1	70.m15148	AO070285000074	0	-144	-16					ATGACGCGCTTATCAGTTGGTCTTGGCGCTTTATCTACTCTCCGTCGACATCATCTCGACCGTTTCCTTCTTCCACCTCTCTCAGACCTCTCCTCTCTGCTCAATTTCTTCGTTCTCAGCATATCTTGA	ATGACGCGCTTATCAGTTGGTCTTGGCGCTTTATCTACTCTCCGTCGACATCATCTCGACCGTTTCCTTCTTCCACCTCTCTCAGACCTCTCCTCTCTGCTCAATTTCTTCGTTCTCAGCATATCTTGA			MTRLSVGLGALSTLRRHHLDRFLLPPLSDLSSLLNFFVLSIS*	MTRLSVGLGALSTLRRHHLDRFLLPPLSDLSSLLNFFVLSIS*			CAACTGCAGC	TCATAAATCT	0	E	0	0	0	0	0
3986	2289	ao	AN1074.1	70.m15148	AO070285000074	0					-221	-177	ATGGGGACGATGAGATTTTCCCGACTTGCGGCCAACGGATTGTAA			ATGGGGACGATGAGATTTTCCCGACTTGCGGCCAACGGATTGTAA	MGTMRFSRLAANGL*			MGTMRFSRLAANGL*	GAACAACGGG	AGGCGCTTAT	0	E	0	0	0	0	0
3987	2289	ao	AN1074.1	70.m15148	AO070285000074	0					-212	-177	ATGAGATTTTCCCGACTTGCGGCCAACGGATTGTAA			ATGAGATTTTCCCGACTTGCGGCCAACGGATTGTAA	MRFSRLAANGL*			MRFSRLAANGL*	GATGGGGACG	AGGCGCTTAT	0	E	0	0	0	0	0
3988	2290	an	AN4987.1	59.m08890	AO070288000055	0	-151	-116					ATGACCTCCTTTTCCGATCATCCTACTCGCTGTTGA	ATGACCTCCTTTTCCGATCATCCTACTCGCTGTTGA			MTSFSDHPTRC*	MTSFSDHPTRC*			TCCTCAACTC	TCTACGCAAC	0	T	FG09908.1	MG07335.1	0	0	0
3991	2291	af	AN5333.1	69.m15580	AO070290000026	0			-249	-202			ATGAGACTGCCTAAGTTGTCGCGTTCTCCATCCTTGTCTTCTGATTGA		ATGAGACTGCCTAAGTTGTCGCGTTCTCCATCCTTGTCTTCTGATTGA		MRLPKLSRSPSLSSD*		MRLPKLSRSPSLSSD*		GTGGTGTATT	CCGGAATATC	0		0	0	0	0	0
3989	2291	an	AN5333.1	69.m15580	AO070290000026	0	-132	-76					ATGCTCTGCTGCAGCGGCTTCGTATTGATCATATCAAAAAATACGGGTACGACCTGA	ATGCTCTGCTGCAGCGGCTTCGTATTGATCATATCAAAAAATACGGGTACGACCTGA			MLCCSGFVLIISKNTGTT*	MLCCSGFVLIISKNTGTT*			ACATCTGGAA	CTCGACGTAT	0		0	0	0	0	0
3992	2291	ao	AN5333.1	69.m15580	AO070290000026	0					-181	-98	ATGGGAACTGCCAAAACACCCGATTCATGCATTAATCAATGGCCTCCTTGGCGGCTAATCTGTATGCGACACGGTGCTGAATAG			ATGGGAACTGCCAAAACACCCGATTCATGCATTAATCAATGGCCTCCTTGGCGGCTAATCTGTATGCGACACGGTGCTGAATAG	MGTAKTPDSCINQWPPWRLICMRHGAE*			MGTAKTPDSCINQWPPWRLICMRHGAE*	TCTTAATCTA	TGGTAGGTAC	0		0	0	0	0	0
3993	2291	ao	AN5333.1	69.m15580	AO070290000026	0					-143	-102	ATGGCCTCCTTGGCGGCTAATCTGTATGCGACACGGTGCTGA			ATGGCCTCCTTGGCGGCTAATCTGTATGCGACACGGTGCTGA	MASLAANLYATRC*			MASLAANLYATRC*	GCATTAATCA	ATAGTGGTAG	0		0	0	0	0	0
3994	2291	ao	AN5333.1	69.m15580	AO070290000026	0					-118	-98	ATGCGACACGGTGCTGAATAG			ATGCGACACGGTGCTGAATAG	MRHGAE*			MRHGAE*	GCTAATCTGT	TGGTAGGTAC	0		0	0	0	0	0
3996	2292	af	AN6640.1	62.m03237	AO070295000024	0			-166	-149			ATGGCAATCTCCATTTAG		ATGGCAATCTCCATTTAG		MAISI*		MAISI*		TTTTGGAGTC	CAAGTCAAGA	0	R	0	0	0	0	0
3995	2292	an	AN6640.1	62.m03237	AO070295000024	0	-212	-99					ATGTGCGGGGTCCCGAGTTTTGACCGGATCAGGCTACCCAAGAGCACGCTCGCCTGGCCTGGACTTCTTTTAAAAGACCAGCATCCTCAGCACGGGTCTTCATCTGCTTGGTGA	ATGTGCGGGGTCCCGAGTTTTGACCGGATCAGGCTACCCAAGAGCACGCTCGCCTGGCCTGGACTTCTTTTAAAAGACCAGCATCCTCAGCACGGGTCTTCATCTGCTTGGTGA			MCGVPSFDRIRLPKSTLAWPGLLLKDQHPQHGSSSAW*	MCGVPSFDRIRLPKSTLAWPGLLLKDQHPQHGSSSAW*			TTCTCCAACC	ACTGAGGATA	0	R	0	0	0	0	0
3997	2292	ao	AN6640.1	62.m03237	AO070295000024	0					-216	-136	ATGGATTCAGTCCGCGATAAGAAATCCAGTAACGACATGATTGGTCTCAACAAGCGAAGCATTGCCGAGCAGTCGAATTAG			ATGGATTCAGTCCGCGATAAGAAATCCAGTAACGACATGATTGGTCTCAACAAGCGAAGCATTGCCGAGCAGTCGAATTAG	MDSVRDKKSSNDMIGLNKRSIAEQSN*			MDSVRDKKSSNDMIGLNKRSIAEQSN*	GAGATAATCG	AAATGTCCTC	0	R	0	0	0	0	0
3998	2292	ao	AN6640.1	62.m03237	AO070295000024	0					-180	-136	ATGATTGGTCTCAACAAGCGAAGCATTGCCGAGCAGTCGAATTAG			ATGATTGGTCTCAACAAGCGAAGCATTGCCGAGCAGTCGAATTAG	MIGLNKRSIAEQSN*			MIGLNKRSIAEQSN*	CAGTAACGAC	AAATGTCCTC	0	R	0	0	0	0	0
3999	2292	ao	AN6640.1	62.m03237	AO070295000024	0					-133	-35	ATGTCCTCATCTCATCATCCAAGTGGAGACGAAGCATGTCTGGGAACATATAAAAGATACCTGACGACACACCTCGTGTGGACCAAACCAAGCAATTGA			ATGTCCTCATCTCATCATCCAAGTGGAGACGAAGCATGTCTGGGAACATATAAAAGATACCTGACGACACACCTCGTGTGGACCAAACCAAGCAATTGA	MSSSHHPSGDEACLGTYKRYLTTHLVWTKPSN*			MSSSHHPSGDEACLGTYKRYLTTHLVWTKPSN*	CGAATTAGAA	TTGATCTAAC	0	R	0	0	0	0	0
4000	2292	ao	AN6640.1	62.m03237	AO070295000024	0					-98	-81	ATGTCTGGGAACATATAA			ATGTCTGGGAACATATAA	MSGNI*			MSGNI*	GAGACGAAGC	AAGATACCTG	0	R	0	0	0	0	0
4003	2300	an	AN8689.1	62.m03383	AO070315000110	0	-274	-98					ATGAATTATTATAATCGTCCGTTCGCCTCATCTTATCTTATTTTTATTACTGCCATCTCCGCTGTTTCCCTCCCATTCCCCAGAACGACCTCCTACATTTCCCCTCCTTACTCCAGTCCATATTCTCTTCTTAAGGTCCTTCCGCCTGCTTTGACGCTTTCTGATATCCTCAGGTAA	ATGAATTATTATAATCGTCCGTTCGCCTCATCTTATCTTATTTTTATTACTGCCATCTCCGCTGTTTCCCTCCCATTCCCCAGAACGACCTCCTACATTTCCCCTCCTTACTCCAGTCCATATTCTCTTCTTAAGGTCCTTCCGCCTGCTTTGACGCTTTCTGATATCCTCAGGTAA			MNYYNRPFASSYLIFITAISAVSLPFPRTTSYISPPYSSPYSLLKVLPPALTLSDILR*	MNYYNRPFASSYLIFITAISAVSLPFPRTTSYISPPYSSPYSLLKVLPPALTLSDILR*			TTACCTCTTT	GTCCCAGTAA	0	G	0	0	0	0	0
4004	2300	an	AN8689.1	62.m03383	AO070315000110	0	-79	-44					ATGCCTACAATTGCTGCAAAGTCCGCTTTGATTTGA	ATGCCTACAATTGCTGCAAAGTCCGCTTTGATTTGA			MPTIAAKSALI*	MPTIAAKSALI*			AAACTCCAGA	CCTTGCTTAT	0	G	0	0	0	0	0
4007	2306	an	AN6601.1	62.m03196	AO070326000052	0	-188	-162					ATGAATGCGGATGGCATTCAGATCTAG	ATGAATGCGGATGGCATTCAGATCTAG			MNADGIQI*	MNADGIQI*			TTGTATTCGA	CCTAGAACTG	0	R	0	0	0	0	0
4008	2306	an	AN6601.1	62.m03196	AO070326000052	0	-184	-119					ATGCGGATGGCATTCAGATCTAGCCTAGAACTGCCGGACTTCTGGACCGCCGTTGGCCGGGGCTAG	ATGCGGATGGCATTCAGATCTAGCCTAGAACTGCCGGACTTCTGGACCGCCGTTGGCCGGGGCTAG			MRMAFRSSLELPDFWTAVGRG*	MRMAFRSSLELPDFWTAVGRG*			ATTCGAATGA	TCCGCCCTTA	0	R	0	0	0	0	0
4009	2306	an	AN6601.1	62.m03196	AO070326000052	0	-178	-119					ATGGCATTCAGATCTAGCCTAGAACTGCCGGACTTCTGGACCGCCGTTGGCCGGGGCTAG	ATGGCATTCAGATCTAGCCTAGAACTGCCGGACTTCTGGACCGCCGTTGGCCGGGGCTAG			MAFRSSLELPDFWTAVGRG*	MAFRSSLELPDFWTAVGRG*			ATGAATGCGG	TCCGCCCTTA	0	R	0	0	0	0	0
4010	2306	ao	AN6601.1	62.m03196	AO070326000052	0					-241	-38	ATGTGGAGAAATGAGTACAGAAGGAACAATCGCGTTATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAGTTCAACGGATTACTAGCAAGTCCGCGTTCGTGGCCTTTTCCTTTTTCTCTTCTCCCTTCCCCTGCTTTTACCCTCCCTCTCTTGTCGACTAG			ATGTGGAGAAATGAGTACAGAAGGAACAATCGCGTTATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAGTTCAACGGATTACTAGCAAGTCCGCGTTCGTGGCCTTTTCCTTTTTCTCTTCTCCCTTCCCCTGCTTTTACCCTCCCTCTCTTGTCGACTAG	MWRNEYRRNNRVMSCADKNNLSTRQDKTTRVLDQSGVVQRITSKSAFVAFSFFSSPFPCFYPPSLVD*			MWRNEYRRNNRVMSCADKNNLSTRQDKTTRVLDQSGVVQRITSKSAFVAFSFFSSPFPCFYPPSLVD*	AGGGTGTGAA	GCCACTGCAG	0	R	0	0	0	0	0
4011	2306	ao	AN6601.1	62.m03196	AO070326000052	0					-231	-130	ATGAGTACAGAAGGAACAATCGCGTTATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAG			ATGAGTACAGAAGGAACAATCGCGTTATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAG	MSTEGTIALCHAPIRTIYRPAKIKRPEFWTKAA*			MSTEGTIALCHAPIRTIYRPAKIKRPEFWTKAA*	ATGTGGAGAA	TTCAACGGAT	0	R	0	0	0	0	0
4012	2306	ao	AN6601.1	62.m03196	AO070326000052	0					-205	-38	ATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAGTTCAACGGATTACTAGCAAGTCCGCGTTCGTGGCCTTTTCCTTTTTCTCTTCTCCCTTCCCCTGCTTTTACCCTCCCTCTCTTGTCGACTAG			ATGTCATGCGCCGATAAGAACAATTTATCGACCCGCCAAGATAAAACGACCCGAGTTCTGGACCAAAGCGGCGTAGTTCAACGGATTACTAGCAAGTCCGCGTTCGTGGCCTTTTCCTTTTTCTCTTCTCCCTTCCCCTGCTTTTACCCTCCCTCTCTTGTCGACTAG	MSCADKNNLSTRQDKTTRVLDQSGVVQRITSKSAFVAFSFFSSPFPCFYPPSLVD*			MSCADKNNLSTRQDKTTRVLDQSGVVQRITSKSAFVAFSFFSSPFPCFYPPSLVD*	CAATCGCGTT	GCCACTGCAG	0	R	0	0	0	0	0
4013	2306	ao	AN6601.1	62.m03196	AO070326000052	0					-200	-189	ATGCGCCGATAA			ATGCGCCGATAA	MRR*			MRR*	GCGTTATGTC	GAACAATTTA	0	R	0	0	0	0	0
4014	2307	af	AN5578.1	58.m07505	AO070328000026	0			-298	-56			ATGGCAGAAGAATCGGCTCGAAGGAGGAACGGGGAACAAACGTCATTGTTTCTCTACCTCGGAGCTCGCGTTTCCCCGTCCCGTCACCGCCCGAGTGATTACGAAAGAAATCAGATATGGCTGATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTTCATAGATCTGATCAACCCCACTTTGCACGCCCTCAGTTATACTGA		ATGGCAGAAGAATCGGCTCGAAGGAGGAACGGGGAACAAACGTCATTGTTTCTCTACCTCGGAGCTCGCGTTTCCCCGTCCCGTCACCGCCCGAGTGATTACGAAAGAAATCAGATATGGCTGATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTTCATAGATCTGATCAACCCCACTTTGCACGCCCTCAGTTATACTGA		MAEESARRRNGEQTSLFLYLGARVSPSRHRPSDYERNQIWLMIIFKFQVLEADHTASLPAHFSWIFHRSDQPHFARPQLY*		MAEESARRRNGEQTSLFLYLGARVSPSRHRPSDYERNQIWLMIIFKFQVLEADHTASLPAHFSWIFHRSDQPHFARPQLY*		GAAGGGTAGA	AAAGGCTGTG	0	A	0	MG00288.1	NCU06950.1	0	0
4015	2307	af	AN5578.1	58.m07505	AO070328000026	0			-182	-96			ATGGCTGATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTTCATAG		ATGGCTGATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTTCATAG		MADDYLQVSSSGSRSHGVVASSFFMDFS*		MADDYLQVSSSGSRSHGVVASSFFMDFS*		GAAATCAGAT	ATCTGATCAA	0	A	0	MG00288.1	NCU06950.1	0	0

4016	2307	af	AN5578.1	58.m07505	AO070328000026	0			-175	-56			ATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTCATAGATCTGATCAACCCCACTTTGCACGCCCTCAGTTATACTGA		ATGATTATCTTCAAGTTTCAAGTTCTGGAAGCCGATCACACGGCGTCGTTGCCAGCTCATTTTTCATGGATTTTCATAGATCTGATCAACCCCACTTTGCACGCCCTCAGTTATACTGA		MIIFKFQVLEADHTASLPAHFSWIFHRSDQPHFARPQLY*		MIIFKFQVLEADHTASLPAHFSWIFHRSDQPHFARPQLY*		GATATGGCTG	AAAGGCTGTG	0	A	0	MG00288.1	NCU06950.1	0	0
4017	2307	af	AN5578.1	58.m07505	AO070328000026	0			-110	-96			ATGGATTTTTCATAG		ATGGATTTTTCATAG		MDFS*		MDFS*		CTCATTTTTC	ATCTGATCAA	0	A	0	MG00288.1	NCU06950.1	0	0
4018	2307	ao	AN5578.1	58.m07505	AO070328000026	0					-218	-78	ATGCAACGAACGTCATTGTTGCTCGGCCCCTCGGACTTGAATTTTCCCCGCGCCGAAATGTCCGATAATCAACTTTCCTTTCTCGTTATCGTGCGTATCTCAACCCACAGCTCCTTCGTGGCTCTCAAACGTGTCGTTTGA			ATGCAACGAACGTCATTGTTGCTCGGCCCCTCGGACTTGAATTTTCCCCGCGCCGAAATGTCCGATAATCAACTTTCCTTTCTCGTTATCGTGCGTATCTCAACCCACAGCTCCTTCGTGGCTCTCAAACGTGTCGTTTGA	MQRTSLLLGPSDLNFPRAEMSDNQLSFLVIVRISTHSSFVALKRVV*			MQRTSLLLGPSDLNFPRAEMSDNQLSFLVIVRISTHSSFVALKRVV*	GGGAGATTCG	CCGTTTCATT	0	A	0	MG00288.1	NCU06950.1	0	0
4019	2307	ao	AN5578.1	58.m07505	AO070328000026	0					-161	-78	ATGTCCGATAATCAACTTTCCTTTCTCGTTATCGTGCGTATCTCAACCCACAGCTCCTTCGTGGCTCTCAAACGTGTCGTTTGA			ATGTCCGATAATCAACTTTCCTTTCTCGTTATCGTGCGTATCTCAACCCACAGCTCCTTCGTGGCTCTCAAACGTGTCGTTTGA	MSDNQLSFLVIVRISTHSSFVALKRVV*			MSDNQLSFLVIVRISTHSSFVALKRVV*	CCGCGCCGAA	CCGTTTCATT	0	A	0	MG00288.1	NCU06950.1	0	0
4023	2308	af	AN5559.1	58.m07485	AO070328000052	0			-212	-183			ATGCGCATCGAGGGAGCGCTTACCTCATGA		ATGCGCATCGAGGGAGCGCTTACCTCATGA		MRIEGALTS*		MRIEGALTS*		AGGCGCAGGA	CAAAGGTGTC	0	R	0	0	0	0	0
4024	2308	af	AN5559.1	58.m07485	AO070328000052	0			-186	-91			ATGACAAAGGTGTCGCATACCTCCCTAGAAGCCTGCTCTGAAGATAGCAACATCCTGCCCGTACATCGTATCCCTGGCTCCGGTGCTCTGATCTGA		ATGACAAAGGTGTCGCATACCTCCCTAGAAGCCTGCTCTGAAGATAGCAACATCCTGCCCGTACATCGTATCCCTGGCTCCGGTGCTCTGATCTGA		MTKVSHTSLEACSEDSNILPVHRIPGSGALI*		MTKVSHTSLEACSEDSNILPVHRIPGSGALI*		CGCTTACCTC	AGCCCTTCAA	0	R	0	0	0	0	0
4025	2308	af	AN5559.1	58.m07485	AO070328000052	0			-80				ATGCGTCTCGCCCTCGTGGATGTATCTCGTCCACGAGATCTTCTAACGATTGGATATTCCTATGACTTGAGCTCTTCCTGA		ATGCGTCTCGCCCTCGTGGATGTATCTCGTCCACGAGATCTTCTAACGATTGGATATTCCTATGACTTGAGCTCTTCCTGA		MRLALVDVSRPRDLLTIGYSYDLSSS*		MRLALVDVSRPRDLLTIGYSYDLSSS*		AGCCCTTCAA	TGCAGACCAA	0	R	0	0	0	0	0
4026	2308	af	AN5559.1	58.m07485	AO070328000052	0			-61	-35			ATGTATCTCGTCCACGAGATCTTCTAA		ATGTATCTCGTCCACGAGATCTTCTAA		MYLVHEIF*		MYLVHEIF*		GCCCTCGTGG	CGATTGGATA	0	R	0	0	0	0	0
4020	2308	an	AN5559.1	58.m07485	AO070328000052	0	-248	-156					ATGCATTCATTCATTCGATTATCTCGGTCTCCCTCTCCTCGTTTACCCCCTTGTCTTGCGGAGCGGATGCTAACTCTGCTAGAGTACTTTTAG	ATGCATTCATTCATTCGATTATCTCGGTCTCCCTCTCCTCGTTTACCCCCTTGTCTTGCGGAGCGGATGCTAACTCTGCTAGAGTACTTTTAG			MHSFIRLSRSPSPRLPPCLAERMLTLLEYF*	MHSFIRLSRSPSPRLPPCLAERMLTLLEYF*			CATCCCTTGC	GCACTATCAA	0	R	0	0	0	0	0
4021	2308	an	AN5559.1	58.m07485	AO070328000052	0	-182	-156					ATGCTAACTCTGCTAGAGTACTTTTAG	ATGCTAACTCTGCTAGAGTACTTTTAG			MLTLLEYF*	MLTLLEYF*			TGCGGAGCGG	GCACTATCAA	0	R	0	0	0	0	0
4022	2308	an	AN5559.1	58.m07485	AO070328000052	0	-130	-56					ATGGCTGGCTATCTATGCGCTTACTTTCCTCTCGTTATCCCCAGTCTACTTGCATTCAAGACCCGCCTAATCTAG	ATGGCTGGCTATCTATGCGCTTACTTTCCTCTCGTTATCCCCAGTCTACTTGCATTCAAGACCCGCCTAATCTAG			MAGYLCAYFPLVIPSLLAFKTRLI*	MAGYLCAYFPLVIPSLLAFKTRLI*			TACGGAGGCA	TATATAAAGT	0	R	0	0	0	0	0
4027	2308	ao	AN5559.1	58.m07485	AO070328000052	0					-161	-150	ATGTCTGTTTGA			ATGTCTGTTTGA	MSV*			MSV*	GCAGCTACGT	TATCTGTTTG	0	R	0	0	0	0	0
4029	2309	af	AN4792.1	59.m09189	AO070329000054	0			-177	-103			ATGGTGTCGATGCTCAAAAGATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAA		ATGGTGTCGATGCTCAAAAGATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAA		MVSMLKRCGCKHDYRRTATNILAL*		MVSMLKRCGCKHDYRRTATNILAL*		CCTCCGTTAA	CCATCCTTTT	0	C	0	0	0	0	0
4030	2309	af	AN4792.1	59.m09189	AO070329000054	0			-168	-103			ATGCTCAAAAGATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAA		ATGCTCAAAAGATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAA		MLKRCGCKHDYRRTATNILAL*		MLKRCGCKHDYRRTATNILAL*		AATGGTGTCG	CCATCCTTTT	0	C	0	0	0	0	0
4031	2309	af	AN4792.1	59.m09189	AO070329000054	0			-157	-59			ATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAACCATCCTTTTCCCACCTTGTTCGGTGTACATCTTCACCAGTTAA		ATGCGGCTGCAAGCACGATTACCGAAGAACCGCAACGAACATTTTGGCCTTATAACCATCCTTTTCCCACCTTGTTCGGTGTACATCTTCACCAGTTAA		MRLQARLPKNRNEHFGLITILFPPCSVYIFTS*		MRLQARLPKNRNEHFGLITILFPPCSVYIFTS*		TGCTCAAAAG	TTATTCTTCC	0	C	0	0	0	0	0
4028	2309	an	AN4792.1	59.m09189	AO070329000054	0	-157	-104					ATGGAGTTTCTCCTCGTGCCGGCGCTTGACCATATTATTATTCCCCAGGATTGA	ATGGAGTTTCTCCTCGTGCCGGCGCTTGACCATATTATTATTCCCCAGGATTGA			MEFLLVPALDHIIIPQD*	MEFLLVPALDHIIIPQD*			TTGGCGGCCG	TTGAAAAAGT	0	C	0	0	0	0	0
4032	2309	ao	AN4792.1	59.m09189	AO070329000054	0					-238	-146	ATGACAAGTTTTTTTGCTTACTACCCCAACTCGGCCGATATCCGATGCTACTCCTCATTATTAGTGTCGATGGCGTATGAGCTTACCGCATGA			ATGACAAGTTTTTTTGCTTACTACCCCAACTCGGCCGATATCCGATGCTACTCCTCATTATTAGTGTCGATGGCGTATGAGCTTACCGCATGA	MTSFFAYYPNSADIRCYSSLLVSMAYELTA*			MTSFFAYYPNSADIRCYSSLLVSMAYELTA*	CTCAATTTAA	AGAGCGGGCA	0	C	0	0	0	0	0
4033	2309	ao	AN4792.1	59.m09189	AO070329000054	0					-194	-159	ATGCTACTCCTCATTATTAGTGTCGATGGCGTATGA			ATGCTACTCCTCATTATTAGTGTCGATGGCGTATGA	MLLLIISVDGV*			MLLLIISVDGV*	CCGATATCCG	GCTTACCGCA	0	C	0	0	0	0	0
4034	2309	ao	AN4792.1	59.m09189	AO070329000054	0					-169	-146	ATGGCGTATGAGCTTACCGCATGA			ATGGCGTATGAGCTTACCGCATGA	MAYELTA*			MAYELTA*	ATTAGTGTCG	AGAGCGGGCA	0	C	0	0	0	0	0
4035	2309	ao	AN4792.1	59.m09189	AO070329000054	0					-162	-118	ATGAGCTTACCGCATGAAGAGCGGGCAGTCAGGTGCGGCGTATAA			ATGAGCTTACCGCATGAAGAGCGGGCAGTCAGGTGCGGCGTATAA	MSLPHEERAVRCGV*			MSLPHEERAVRCGV*	TCGATGGCGT	AGCTGTCGCA	0	C	0	0	0	0	0
4036	2309	ao	AN4792.1	59.m09189	AO070329000054	0					-149	-93	ATGAAGAGCGGGCAGTCAGGTGCGGCGTATAAAGCTGTCGCAGTCCCCGAGACATAG			ATGAAGAGCGGGCAGTCAGGTGCGGCGTATAAAGCTGTCGCAGTCCCCGAGACATAG	MKSGQSGAAYKAVAVPET*			MKSGQSGAAYKAVAVPET*	AGCTTACCGC	CAAGAGAAAT	0	C	0	0	0	0	0
4037	2310	an	AN1176.1	70.m15041	AO070331000171	0	-216	-163					ATGTTCGGTTGGAAATCAACCGCTAAAACCGGGAATTTTTTTGTCTCTGGTTGA	ATGTTCGGTTGGAAATCAACCGCTAAAACCGGGAATTTTTTTGTCTCTGGTTGA			MFGWKSTAKTGNFFVSG*	MFGWKSTAKTGNFFVSG*			TTTCTAATTC	CTTTACCTAG	0	IT	0	0	0	0	0
4046	2311	af	AN1198.1	70.m15021	AO070331000203	0			-241	-158			ATGCGTTTTTTTTTTTATCTTCTCATATATGCTTCTCTCCCTTCATCATCATCATCGGATCTCGTCTCCATCACATCAAGTTGA		ATGCGTTTTTTTTTTTATCTTCTCATATATGCTTCTCTCCCTTCATCATCATCATCGGATCTCGTCTCCATCACATCAAGTTGA		MRFFFYLLIYASLPSSSSSDLVSITSS*		MRFFFYLLIYASLPSSSSSDLVSITSS*		ATATTTAGGC	GATCATTCCG	0	E	0	MG04826.1	NCU02727.1	0	0
4047	2311	af	AN1198.1	70.m15021	AO070331000203	0			-213	-106			ATGCTTCTCTCCCTTCATCATCATCATCGGATCTCGTCTCCATCACATCAAGTTGAGATCATTCCGGATTGCACCGAGTGTCCGCGGAATTGTCCTATCTCCACGTGA		ATGCTTCTCTCCCTTCATCATCATCATCGGATCTCGTCTCCATCACATCAAGTTGAGATCATTCCGGATTGCACCGAGTGTCCGCGGAATTGTCCTATCTCCACGTGA		MLLSLHHHHRISSPSHQVEIIPDCTECPRNCPIST*		MLLSLHHHHRISSPSHQVEIIPDCTECPRNCPIST*		CTTCTCATAT	CTTTTCCGTT	0	E	0	MG04826.1	NCU02727.1	0	0
4043	2311	an	AN1198.1	70.m15021	AO070331000203	0	-141	-70					ATGCATATCTTATCACTCCGCGGGATTCTCCTATCACACGTGACTTTACCGGTAACTATGACGCTTTTCTGA	ATGCATATCTTATCACTCCGCGGGATTCTCCTATCACACGTGACTTTACCGGTAACTATGACGCTTTTCTGA			MHILSLRGILLSHVTLPVTMTLF*	MHILSLRGILLSHVTLPVTMTLF*			CGGCCAAGTC	ACTCCATTTC	0	E	0	MG04826.1	NCU02727.1	0	0
4044	2311	an	AN1198.1	70.m15021	AO070331000203	0	-84	-70					ATGACGCTTTTCTGA	ATGACGCTTTTCTGA			MTLF*	MTLF*			ACCGGTAACT	ACTCCATTTC	0	E	0	MG04826.1	NCU02727.1	0	0
4048	2311	ao	AN1198.1	70.m15021	AO070331000203	0					-229	-164	ATGTCAATCTGGCCTATCGATTCACACCATCGTAGATGCTTTATCTTGCGTAAATCCAGTAAGTAA			ATGTCAATCTGGCCTATCGATTCACACCATCGTAGATGCTTTATCTTGCGTAAATCCAGTAAGTAA	MSIWPIDSHHRRCFILRKSSK*			MSIWPIDSHHRRCFILRKSSK*	TTCGCTGAAG	TCCTCCCGAC	0	E	0	MG04826.1	NCU02727.1	0	0
4049	2311	ao	AN1198.1	70.m15021	AO070331000203	0					-194	-177	ATGCTTTATCTTGCGTAA			ATGCTTTATCTTGCGTAA	MLYLA*			MLYLA*	ACCATCGTAG	ATCCAGTAAG	0	E	0	MG04826.1	NCU02727.1	0	0
4050	2312	an	AN4905.1	59.m08809	AO070338000040	0	-230	-156					ATGCCGGATCTCCGGCCAGGCAAAATGACTTGCACCACCTTCATTAATAATAGAGTATTGGATTTGTGTAGATAA	ATGCCGGATCTCCGGCCAGGCAAAATGACTTGCACCACCTTCATTAATAATAGAGTATTGGATTTGTGTAGATAA			MPDLRPGKMTCTTFINNRVLDLCR*	MPDLRPGKMTCTTFINNRVLDLCR*			CAGAGTACAA	TGAGCGGGGT	0	O	FG02000.1	MG06747.1	NCU04109.1	0	0
4051	2312	an	AN4905.1	59.m08809	AO070338000040	0	-206	-156					ATGACTTGCACCACCTTCATTAATAATAGAGTATTGGATTTGTGTAGATAA	ATGACTTGCACCACCTTCATTAATAATAGAGTATTGGATTTGTGTAGATAA			MTCTTFINNRVLDLCR*	MTCTTFINNRVLDLCR*			GCCAGGCAAA	TGAGCGGGGT	0	O	FG02000.1	MG06747.1	NCU04109.1	0	0
4055	2314	af	AN0247.1	54.m06700	AO070338000240	0			-147	-127			ATGGGTTTCATTTTTGTTTAG		ATGGGTTTCATTTTTGTTTAG		MGFIFV*		MGFIFV*		CCCTCTCTTT	TCTGCCCCTA	0	R	FG00732.1	0	0	0	0
4052	2314	an	AN0247.1	54.m06700	AO070338000240	0	-185	-150					ATGACGGGCCCAAGCCTTAATCTACTGGTTGTATAA	ATGACGGGCCCAAGCCTTAATCTACTGGTTGTATAA			MTGPSLNLLVV*	MTGPSLNLLVV*			AATCAGTTCA	TGACCTGCCA	0	R	FG00732.1	0	0	0	0
4053	2314	an	AN0247.1	54.m06700	AO070338000240	0	-150	-130					ATGACCTGCCAGTACACGTGA	ATGACCTGCCAGTACACGTGA			MTCQYT*	MTCQYT*			TGGTTGTATA	CCTTTAGGCG	0	R	FG00732.1	0	0	0	0
4057	2315	af	AN6776.1	54.m06380	AO070339000063	0			-164	-12			ATGCAATACACGATGAGGCGGCCAGTTTCTTACAATGGCCACTTTACTCGCTTATTGATTACATTTAGCCCCCACCTAAGCTGCTTACCCATCCTATTCTTGCACAATAGGCCAACTCAACTTGTATGCTTCCCCCAAACCGAACAAAAGTGA		ATGCAATACACGATGAGGCGGCCAGTTTCTTACAATGGCCACTTTACTCGCTTATTGATTACATTTAGCCCCCACCTAAGCTGCTTACCCATCCTATTCTTGCACAATAGGCCAACTCAACTTGTATGCTTCCCCCAAACCGAACAAAAGTGA		MQYTMRRPVSYNGHFTRLLITFSPHLSCLPILFLHNRPTQLVCFPQTEQK*		MQYTMRRPVSYNGHFTRLLITFSPHLSCLPILFLHNRPTQLVCFPQTEQK*		GCTATTTTAT	TATCAGAAGG	0	R	0	0	0	0	0
4058	2315	af	AN6776.1	54.m06380	AO070339000063	0			-152	-12			ATGAGGCGGCCAGTTTCTTACAATGGCCACTTTACTCGCTTATTGATTACATTTAGCCCCCACCTAAGCTGCTTACCCATCCTATTCTTGCACAATAGGCCAACTCAACTTGTATGCTTCCCCCAAACCGAACAAAAGTGA		ATGAGGCGGCCAGTTTCTTACAATGGCCACTTTACTCGCTTATTGATTACATTTAGCCCCCACCTAAGCTGCTTACCCATCCTATTCTTGCACAATAGGCCAACTCAACTTGTATGCTTCCCCCAAACCGAACAAAAGTGA		MRRPVSYNGHFTRLLITFSPHLSCLPILFLHNRPTQLVCFPQTEQK*		MRRPVSYNGHFTRLLITFSPHLSCLPILFLHNRPTQLVCFPQTEQK*		GCAATACACG	TATCAGAAGG	0	R	0	0	0	0	0
4059	2315	af	AN6776.1	54.m06380	AO070339000063	0			-130	-107			ATGGCCACTTTACTCGCTTATTGA		ATGGCCACTTTACTCGCTTATTGA		MATLLAY*		MATLLAY*		GTTTCTTACA	TTACATTTAG	0	R	0	0	0	0	0
4056	2315	an	AN6776.1	54.m06380	AO070339000063	0	-164	-105					ATGGTTCCTAAAATACTACGGCTGACTATCAGTTCAAAAAACGCACTGTCTGACTATTAA	ATGGTTCCTAAAATACTACGGCTGACTATCAGTTCAAAAAACGCACTGTCTGACTATTAA			MVPKILRLTISSKNALSDY*	MVPKILRLTISSKNALSDY*			AGAGCTGCTT	GGACTCTAGC	0	R	0	0	0	0	0
4061	2317	af	AN6165.1	72.m19014	AO070340000051	0			-251	-207			ATGTCCGACGTCAGATCGCAGCCGAAAAAGGTCAAAAAAAGCTAA		ATGTCCGACGTCAGATCGCAGCCGAAAAAGGTCAAAAAAAGCTAA		MSDVRSQPKKVKKS*		MSDVRSQPKKVKKS*		GGTGTAGCGC	TGTTAGCCAT	0	J	0	0	0	0	0
4062	2317	af	AN6165.1	72.m19014	AO070340000051	0			-207	-193			ATGTTAGCCATCTAA		ATGTTAGCCATCTAA		MLAI*		MLAI*		AAAAAAGCTA	ATGCAACAGA	0	J	0	0	0	0	0
4063	2317	af	AN6165.1	72.m19014	AO070340000051	0			-192	-130			ATGCAACAGAAGTCTCTTCATGCGCGCCTACGTTTCCCTGCGTCAGTGCTTGTCTGGGATTAA		ATGCAACAGAAGTCTCTTCATGCGCGCCTACGTTTCCCTGCGTCAGTGCTTGTCTGGGATTAA		MQQKSLHARLRFPASVLVWD*		MQQKSLHARLRFPASVLVWD*		AGCCATCTAA	TCTATCCCCC	0	J	0	0	0	0	0
4060	2317	an	AN6165.1	72.m19014	AO070340000051	0	-223	-14					ATGCGAAAAAACCCCCGGCAAGAAAAAGAAGGCCGACCATCATTCCAGATAATTCGTTCTCCATGCGCTCCCACCTCCTTCTACGGCAGTGGTCGACTCCTAATCACCTGTGTACACGAATACCTTCACAAGTCCTTCGCTCAACCTTTCCGAACCGTCTTCTCCTTTCTACCGACTGCCGCGGAGCCCGTCTACGATGGTGGCAGGTGA	ATGCGAAAAAACCCCCGGCAAGAAAAAGAAGGCCGACCATCATTCCAGATAATTCGTTCTCCATGCGCTCCCACCTCCTTCTACGGCAGTGGTCGACTCCTAATCACCTGTGTACACGAATACCTTCACAAGTCCTTCGCTCAACCTTTCCGAACCGTCTTCTCCTTTCTACCGACTGCCGCGGAGCCCGTCTACGATGGTGGCAGGTGA			MRKNPRQEKEGRPSFQIIRSPCAPTSFYGSGRLLITCVHEYLHKSFAQPFRTVFSFLPTAAEPVYDGGR*	MRKNPRQEKEGRPSFQIIRSPCAPTSFYGSGRLLITCVHEYLHKSFAQPFRTVFSFLPTAAEPVYDGGR*			AGCGACCGAA	AACGCAACGA	0	J	0	0	0	0	0
4065	2318	af	AN8968.1	70.m15193	AO070342000435	0			-243	-229			ATGTCAACATCATGA		ATGTCAACATCATGA		MSTS*		MSTS*		GAACCGCAAA	CAGAGTCGTA	0		0	0	0	0	0
4066	2318	af	AN8968.1	70.m15193	AO070342000435	0			-232	-110			ATGACAGAGTCGTATGGCCATATATTATGGCGATTGAGACACAACCCATCTAGTCCTAATAATACCGCTTTGGGGGTAAGCTGGCTGCTGGCGCCCCCGCACGCAAAACACCATCTGGAGTAG		ATGACAGAGTCGTATGGCCATATATTATGGCGATTGAGACACAACCCATCTAGTCCTAATAATACCGCTTTGGGGGTAAGCTGGCTGCTGGCGCCCCCGCACGCAAAACACCATCTGGAGTAG		MTESYGHILWRLRHNPSSPNNTALGVSWLLAPPHAKHHLE*		MTESYGHILWRLRHNPSSPNNTALGVSWLLAPPHAKHHLE*		TGTCAACATC	ACCCGATATC	0		0	0	0	0	0
4067	2318	af	AN8968.1	70.m15193	AO070342000435	0			-219	-196			ATGGCCATATATTATGGCGATTGA		ATGGCCATATATTATGGCGATTGA		MAIYYGD*		MAIYYGD*		ACAGAGTCGT	GACACAACCC	0		0	0	0	0	0
4068	2318	af	AN8968.1	70.m15193	AO070342000435	0			-206	-180			ATGGCGATTGAGACACAACCCATCTAG		ATGGCGATTGAGACACAACCCATCTAG		MAIETQPI*		MAIETQPI*		GCCATATATT	TCCTAATAAT	0		0	0	0	0	0
4064	2318	an	AN8968.1	70.m15193	AO070342000435	0	-106	-50					ATGCGGGGTTCCAATGCTTATAAAGCTCACTCTCTACTTACTCCTCTCCCACATTGA	ATGCGGGGTTCCAATGCTTATAAAGCTCACTCTCTACTTACTCCTCTCCCACATTGA			MRGSNAYKAHSLLTPLPH*	MRGSNAYKAHSLLTPLPH*			ACGTTACCTG	CACAAACGCT	0		0	0	0	0	0
4069	2318	ao	AN8968.1	70.m15193	AO070342000435	0					-116	-93	ATGAGATCCACTGGGAGGTCGTGA			ATGAGATCCACTGGGAGGTCGTGA	MRSTGRS*			MRSTGRS*	CTGCAGGTGG	GGATTAATAA	0		0	0	0	0	0
4070	2318	ao	AN8968.1	70.m15193	AO070342000435	0					-67	-5	ATGGAAGGCGGAGAATTTATAAAAAAGCATCTACATGCATGTATGATCTCAAGAAACAGATGA			ATGGAAGGCGGAGAATTTATAAAAAAGCATCTACATGCATGTATGATCTCAAGAAACAGATGA	MEGGEFIKKHLHACMISRNR*			MEGGEFIKKHLHACMISRNR*	TTTCATTGTC	CAAAATGGCT	0		0	0	0	0	0
4073	2319	af	AN2155.1	72.m19686	AO070343000207	0			-238	-185			ATGATTGATCTATCTTATCGCGGGGCGCTCCGACACCGCAGTGACTGTTCCTGA		ATGATTGATCTATCTTATCGCGGGGCGCTCCGACACCGCAGTGACTGTTCCTGA		MIDLSYRGALRHRSDCS*		MIDLSYRGALRHRSDCS*		TGTAGGATCT	GAACATCACC	0	D	0	MG06151.1	0	YGL091C	0

4074	2319	ao	AN2155.1	72.m19686	AO070343000207	0					-215	-141	ATGAGATCGCTCTTATCGAAGACTCCGACACCGCACGTAGGATATCCAATCGCTACTAGAATGTTTGTAAGCTAG			ATGAGATCGCTCTTATCGAAGACTCCGACACCGCACGTAGGATATCCAATCGCTACTAGAATGTTTGTAAGCTAG	MRSLLSKTPTPHVGYPIATRMFVS*			MRSLLSKTPTPHVGYPIATRMFVS*	TTAAGGGTTT	TAACCTTATC	0	D	0	MG06151.1	0	YGL091C	0
4075	2319	ao	AN2155.1	72.m19686	AO070343000207	0					-155	-141	ATGTTTGTAAGCTAG			ATGTTTGTAAGCTAG	MFVS*			MFVS*	CGCTACTAGA	TAACCTTATC	0	D	0	MG06151.1	0	YGL091C	0
4076	2319	ao	AN2155.1	72.m19686	AO070343000207	0					-73	-29	ATGTTGCGTTTGTACAAGTTCTTTTTATCCTCCTTTCTATATTAG			ATGTTGCGTTTGTACAAGTTCTTTTTATCCTCCTTTCTATATTAG	MLRLYKFFLSSFLY*			MLRLYKFFLSSFLY*	TTTCTATCAA	AGCAATAGCT	0	D	0	MG06151.1	0	YGL091C	0
4079	2321	af	AN2449.1	69.m15211	AO070264000029	0			-191	-174			ATGCATATGAATCTCTGA		ATGCATATGAATCTCTGA		MHMNL*		MHMNL*		TCTAAGGGGA	GAAATGTTAT	0	J	0	0	0	0	0
4080	2321	af	AN2449.1	69.m15211	AO070264000029	0			-185	-174			ATGAATCTCTGA		ATGAATCTCTGA		MNL*		MNL*		GGGAATGCAT	GAAATGTTAT	0	J	0	0	0	0	0
4081	2321	af	AN2449.1	69.m15211	AO070264000029	0			-170	-69			ATGTTATCAGTCGACAGCTTCCCCGCGATTTGTTCGGAGCCGTCACAAGCGGAACTGATAAGCTTGGACCATCGAGTTTTACTTTTTTTTATCGGAGATTGA		ATGTTATCAGTCGACAGCTTCCCCGCGATTTGTTCGGAGCCGTCACAAGCGGAACTGATAAGCTTGGACCATCGAGTTTTACTTTTTTTTATCGGAGATTGA		MLSVDSFPAICSEPSQAELISLDHRVLLFFIGD*		MLSVDSFPAICSEPSQAELISLDHRVLLFFIGD*		TCTCTGAGAA	TATCGGCTCT	0	J	0	0	0	0	0
4077	2321	an	AN2449.1	69.m15211	AO070264000029	0	-160	-140					ATGATGTGGACTGGACTCTGA	ATGATGTGGACTGGACTCTGA			MMWTGL*	MMWTGL*			TGGGGATGTG	GTCGATCGGG	0	J	0	0	0	0	0
4078	2321	an	AN2449.1	69.m15211	AO070264000029	0	-157	-140					ATGTGGACTGGACTCTGA	ATGTGGACTGGACTCTGA			MWTGL*	MWTGL*			GGATGTGATG	GTCGATCGGG	0	J	0	0	0	0	0
4082	2321	ao	AN2449.1	69.m15211	AO070264000029	0					-281	-267	ATGGACAGAGGATAA			ATGGACAGAGGATAA	MDRG*			MDRG*	CCATGTGCCC	GAGTGAGTGT	0	J	0	0	0	0	0
4083	2321	ao	AN2449.1	69.m15211	AO070264000029	0					-76	-62	ATGCAGGGTCCCTGA			ATGCAGGGTCCCTGA	MQGP*			MQGP*	GCTCCACCTG	AGCTTTTTTC	0	J	0	0	0	0	0
4087	2323	af	AN7660.1	57.m05936	AO070268000029	0			-221	-189			ATGGAAAAGAGGGGTATCTGCCGGGATGCCTGA		ATGGAAAAGAGGGGTATCTGCCGGGATGCCTGA		MEKRGICRDA*		MEKRGICRDA*		CTGGAAAAGA	TGATAAGGTG	0	H	0	0	0	0	0
4088	2323	af	AN7660.1	57.m05936	AO070268000029	0			-196	-92			ATGCCTGATGATAAGGTGCGGAGAGAACCTGATGAGATAACAGGTCACATGCAGATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		ATGCCTGATGATAAGGTGCGGAGAGAACCTGATGAGATAACAGGTCACATGCAGATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		MPDDKVRREPDEITGHMQMQGDNTRPIPSSLAIS*		MPDDKVRREPDEITGHMQMQGDNTRPIPSSLAIS*		ATCTGCCGGG	CTCTGCTCTT	0	H	0	0	0	0	0
4089	2323	af	AN7660.1	57.m05936	AO070268000029	0			-189	-157			ATGATAAGGTGCGGAGAGAACCTGATGAGATAA		ATGATAAGGTGCGGAGAGAACCTGATGAGATAA		MIRCGENLMR*		MIRCGENLMR*		GGGATGCCTG	CAGGTCACAT	0	H	0	0	0	0	0
4090	2323	af	AN7660.1	57.m05936	AO070268000029	0			-148	-92			ATGCAGATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		ATGCAGATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		MQMQGDNTRPIPSSLAIS*		MQMQGDNTRPIPSSLAIS*		AACAGGTCAC	CTCTGCTCTT	0	H	0	0	0	0	0
4091	2323	af	AN7660.1	57.m05936	AO070268000029	0			-142	-92			ATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		ATGCAGGGGGACAACACTCGCCCAATCCCTTCTTCTCTCGCCATCTCTTGA		MQGDNTRPIPSSLAIS*		MQGDNTRPIPSSLAIS*		TCACATGCAG	CTCTGCTCTT	0	H	0	0	0	0	0
4084	2323	an	AN7660.1	57.m05936	AO070268000029	0	-196	-92					ATGCCATGTACGGAGTCCCGACGTAAGGCAGCTCAGCAGATAAGGTGCGGAGAAACGGGTCACATGCAGTGTAGGGTGCCTTCCCAGTTCTCGCTTTGCTTTTGA	ATGCCATGTACGGAGTCCCGACGTAAGGCAGCTCAGCAGATAAGGTGCGGAGAAACGGGTCACATGCAGTGTAGGGTGCCTTCCCAGTTCTCGCTTTGCTTTTGA			MPCTESRRKAAQQIRCGETGHMQCRVPSQFSLCF*	MPCTESRRKAAQQIRCGETGHMQCRVPSQFSLCF*			GCGAGGTAAG	CCTTCCCTTT	0	H	0	0	0	0	0
4085	2323	an	AN7660.1	57.m05936	AO070268000029	0	-191	-171					ATGTACGGAGTCCCGACGTAA	ATGTACGGAGTCCCGACGTAA			MYGVPT*	MYGVPT*			GTAAGATGCC	GGCAGCTCAG	0	H	0	0	0	0	0
4086	2323	an	AN7660.1	57.m05936	AO070268000029	0	-133	-92					ATGCAGTGTAGGGTGCCTTCCCAGTTCTCGCTTTGCTTTTGA	ATGCAGTGTAGGGTGCCTTCCCAGTTCTCGCTTTGCTTTTGA			MQCRVPSQFSLCF*	MQCRVPSQFSLCF*			AACGGGTCAC	CCTTCCCTTT	0	H	0	0	0	0	0
4092	2323	ao	AN7660.1	57.m05936	AO070268000029	0					-253	-188	ATGATAAGGCGATACGATACGATAAGGTGCGGAGAGACCAGAATGAAAGAAAGTTCAAGTCAATGA			ATGATAAGGCGATACGATACGATAAGGTGCGGAGAGACCAGAATGAAAGAAAGTTCAAGTCAATGA	MIRRYDTIRCGETRMKESSSQ*			MIRRYDTIRCGETRMKESSSQ*	AGGGGAAACA	TTACAGTACC	0	H	0	0	0	0	0
4093	2323	ao	AN7660.1	57.m05936	AO070268000029	0					-211	-188	ATGAAAGAAAGTTCAAGTCAATGA			ATGAAAGAAAGTTCAAGTCAATGA	MKESSSQ*			MKESSSQ*	AGAGACCAGA	TTACAGTACC	0	H	0	0	0	0	0
4094	2323	ao	AN7660.1	57.m05936	AO070268000029	0					-191	-135	ATGATTACAGTACCAATTCACAGGTCACATGCAGTAAGGAGGGAATGCAAGCTGTAA			ATGATTACAGTACCAATTCACAGGTCACATGCAGTAAGGAGGGAATGCAAGCTGTAA	MITVPIHRSHAVRRECKL*			MITVPIHRSHAVRRECKL*	GTTCAAGTCA	AATGAGACGT	0	H	0	0	0	0	0
4095	2323	ao	AN7660.1	57.m05936	AO070268000029	0					-147	-130	ATGCAAGCTGTAAAATGA			ATGCAAGCTGTAAAATGA	MQAVK*			MQAVK*	TAAGGAGGGA	GACGTTCTGC	0	H	0	0	0	0	0
4100	2325	af	AN8822.1	71.m15633	AO070276000020	0			-218	-201			ATGAACCACCGACAATGA		ATGAACCACCGACAATGA		MNHRQ*		MNHRQ*		GACTTACTGC	GCCTCTTATT	0	I	FG07372.1	MG03998.1	0	0	0
4101	2325	af	AN8822.1	71.m15633	AO070276000020	0			-204	-187			ATGAGCCTCTTATTCTGA		ATGAGCCTCTTATTCTGA		MSLLF*		MSLLF*		ACCACCGACA	TGTTCAAGAA	0	I	FG07372.1	MG03998.1	0	0	0
4102	2325	af	AN8822.1	71.m15633	AO070276000020	0			-187	-131			ATGTTCAAGAACCTCTGCCATGCTATCCATCACCTTTTCGCCCAATCGAGGATATAG		ATGTTCAAGAACCTCTGCCATGCTATCCATCACCTTTTCGCCCAATCGAGGATATAG		MFKNLCHAIHHLFAQSRI*		MFKNLCHAIHHLFAQSRI*		TCTTATTCTG	CCCCAACTCC	0	I	FG07372.1	MG03998.1	0	0	0
4103	2325	af	AN8822.1	71.m15633	AO070276000020	0			-168	-94			ATGCTATCCATCACCTTTTCGCCCAATCGAGGATATAGCCCCAACTCCTCCTGCACACAACCCCCACACCGATAA		ATGCTATCCATCACCTTTTCGCCCAATCGAGGATATAGCCCCAACTCCTCCTGCACACAACCCCCACACCGATAA		MLSITFSPNRGYSPNSSCTQPPHR*		MLSITFSPNRGYSPNSSCTQPPHR*		AACCTCTGCC	AGCTGCCTTA	0	I	FG07372.1	MG03998.1	0	0	0
4096	2325	an	AN8822.1	71.m15633	AO070276000020	0	-199	-155					ATGTATATTCTGGTACGGTGGTGTGATATATGTATACTTTGGTAA	ATGTATATTCTGGTACGGTGGTGTGATATATGTATACTTTGGTAA			MYILVRWCDICILW*	MYILVRWCDICILW*			TTGGCCAGCA	TAATTATGTA	0	I	FG07372.1	MG03998.1	0	0	0
4097	2325	an	AN8822.1	71.m15633	AO070276000020	0	-170	-117					ATGTATACTTTGGTAATAATTATGTACGGTAATTACCAGTACATTCAACCTTAA	ATGTATACTTTGGTAATAATTATGTACGGTAATTACCAGTACATTCAACCTTAA			MYTLVIIMYGNYQYIQP*	MYTLVIIMYGNYQYIQP*			GGTGTGATAT	TTCTATGCCT	0	I	FG07372.1	MG03998.1	0	0	0
4098	2325	an	AN8822.1	71.m15633	AO070276000020	0	-149	-117					ATGTACGGTAATTACCAGTACATTCAACCTTAA	ATGTACGGTAATTACCAGTACATTCAACCTTAA			MYGNYQYIQP*	MYGNYQYIQP*			GGTAATAATT	TTCTATGCCT	0	I	FG07372.1	MG03998.1	0	0	0
4099	2325	an	AN8822.1	71.m15633	AO070276000020	0	-112	-68					ATGCCTCTCCACCATAGAGTTGACCTTAGCTCCATCCACCTGTGA	ATGCCTCTCCACCATAGAGTTGACCTTAGCTCCATCCACCTGTGA			MPLHHRVDLSSIHL*	MPLHHRVDLSSIHL*			CCTTAATTCT	ACTAATCGAC	0	I	FG07372.1	MG03998.1	0	0	0
4104	2325	ao	AN8822.1	71.m15633	AO070276000020	0					-267	-244	ATGTCAATGAACCGGTATACTTAG			ATGTCAATGAACCGGTATACTTAG	MSMNRYT*			MSMNRYT*	ACGGAAAGCA	GGTTTACAAT	0	I	FG07372.1	MG03998.1	0	0	0
4105	2325	ao	AN8822.1	71.m15633	AO070276000020	0					-261	-244	ATGAACCGGTATACTTAG			ATGAACCGGTATACTTAG	MNRYT*			MNRYT*	AGCAATGTCA	GGTTTACAAT	0	I	FG07372.1	MG03998.1	0	0	0
4106	2325	ao	AN8822.1	71.m15633	AO070276000020	0					-224	-123	ATGTATATGCATAGCTTATGTAAGGAGTACTACACTAATGCACGATATCAATATCCATATCAAGATCTATCAATTTCTATATACGACAGCTTCCGCCCATAA			ATGTATATGCATAGCTTATGTAAGGAGTACTACACTAATGCACGATATCAATATCCATATCAAGATCTATCAATTTCTATATACGACAGCTTCCGCCCATAA	MYMHSLCKEYYTNARYQYPYQDLSISIYDSFRP*			MYMHSLCKEYYTNARYQYPYQDLSISIYDSFRP*	TGGGGTATTT	ATTACAAATC	0	I	FG07372.1	MG03998.1	0	0	0
4107	2325	ao	AN8822.1	71.m15633	AO070276000020	0					-218	-123	ATGCATAGCTTATGTAAGGAGTACTACACTAATGCACGATATCAATATCCATATCAAGATCTATCAATTTCTATATACGACAGCTTCCGCCCATAA			ATGCATAGCTTATGTAAGGAGTACTACACTAATGCACGATATCAATATCCATATCAAGATCTATCAATTTCTATATACGACAGCTTCCGCCCATAA	MHSLCKEYYTNARYQYPYQDLSISIYDSFRP*			MHSLCKEYYTNARYQYPYQDLSISIYDSFRP*	ATTTATGTAT	ATTACAAATC	0	I	FG07372.1	MG03998.1	0	0	0
4112	2326	af	AN3363.1	66.m04629	AO070281000032	0			-213	-151			ATGCGGGTTTGTTTACATTTTCCTTTTTCAGTCTCCGTCGAGCCACACAACAAACGTTGGCCTAA		ATGCGGGTTTGTTTACATTTTCCTTTTTCAGTCTCCGTCGAGCCACACAACAAACGTTGGCCTAA		MRVCLHFPFSVSVEPQQTLA*		MRVCLHFPFSVSVEPQQTLA*		TGTGCGCAAC	TTACTTTGAT	0	Z	FG00697.1	0	0	0	0
4108	2326	an	AN3363.1	66.m04629	AO070281000032	0	-178	-59					ATGATGGTCCAAGCGCTGGGGTTTGTTTATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGA	ATGATGGTCCAAGCGCTGGGGTTTGTTTATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGA			MMVQALGFVYVFLFWPTEQQPTTTTFCDTAPQRDSLLIY*	MMVQALGFVYVFLFWPTEQQPTTTTFCDTAPQRDSLLIY*			CCAGAGTCAC	GTTTGGTCTT	0	Z	FG00697.1	0	0	0	0
4109	2326	an	AN3363.1	66.m04629	AO070281000032	0	-175	-59					ATGGTCCAAGCGCTGGGGTTTGTTTATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGA	ATGGTCCAAGCGCTGGGGTTTGTTTATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGA			MVQALGFVYVFLFWPTEQQPTTTTFCDTAPQRDSLLIY*	MVQALGFVYVFLFWPTEQQPTTTTFCDTAPQRDSLLIY*			GAGTCACATG	GTTTGGTCTT	0	Z	FG00697.1	0	0	0	0
4110	2326	an	AN3363.1	66.m04629	AO070281000032	0	-150	-22					ATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGAGTTTGGTCTTATGTCCAATTATTGTTTCTGTACCTAA	ATGTTTTCCTTTTCTGGCCAACGGAACAACAGCCGACAACCACGACATTTTGCGACACCGCCCCTCAGCGAGACTCATTGCTTATTTACTGAGTTTGGTCTTATGTCCAATTATTGTTTCTGTACCTAA			MFSFSGQRNNSRQPRHFATPPLSETHCLFTEFGLMSNYCFCT*	MFSFSGQRNNSRQPRHFATPPLSETHCLFTEFGLMSNYCFCT*			GGGTTTGTTT	TTCCTACCGT	0	Z	FG00697.1	0	0	0	0
4113	2326	ao	AN3363.1	66.m04629	AO070281000032	0					-210	-28	ATGACTCCTGAGCACAGACCACCATTGGGCACGTGCGTCAATGTTGTTAGTTTGTTTACATTTTCCTTTCTGGGCCTTCCCGGGAAGTCACTGACTTCTCCTGGACATATCAAAGTGGCGCGACATCACTTCCAGTCGCACACGACAAATTACATATACATCCTCTTTACCTTATTGTGGTAG			ATGACTCCTGAGCACAGACCACCATTGGGCACGTGCGTCAATGTTGTTAGTTTGTTTACATTTTCCTTTCTGGGCCTTCCCGGGAAGTCACTGACTTCTCCTGGACATATCAAAGTGGCGCGACATCACTTCCAGTCGCACACGACAAATTACATATACATCCTCTTTACCTTATTGTGGTAG	MTPEHRPPLGTCVNVVSLFTFSFLGLPGKSLTSPGHIKVARHHFQSHTTNYIYILFTLLW*			MTPEHRPPLGTCVNVVSLFTFSFLGLPGKSLTSPGHIKVARHHFQSHTTNYIYILFTLLW*	AAATGCCGGC	TGAGCTTGTG	0	Z	FG00697.1	0	0	0	0
4114	2326	ao	AN3363.1	66.m04629	AO070281000032	0					-170	-117	ATGTTGTTAGTTTGTTTACATTTTCCTTTCTGGGCCTTCCCGGGAAGTCACTGA			ATGTTGTTAGTTTGTTTACATTTTCCTTTCTGGGCCTTCCCGGGAAGTCACTGA	MLLVCLHFPFWAFPGSH*			MLLVCLHFPFWAFPGSH*	ACGTGCGTCA	CTTCTCCTGG	0	Z	FG00697.1	0	0	0	0
4116	2330	af	AN1696.1	58.m07772	AO070305000020	0			-253	-242			ATGGACTTTTGA		ATGGACTTTTGA		MDF*		MDF*		TTGTCGGTTG	AAGAACACGT	0	I	0	0	0	0	0
4115	2330	an	AN1696.1	58.m07772	AO070305000020	0	-171	-94					ATGACGAATCCCGGACCCATAAGTATCAGCACCTGCTGCAAAGAACCCAGACTCCACTATCGCAACAATTGCATATAA	ATGACGAATCCCGGACCCATAAGTATCAGCACCTGCTGCAAAGAACCCAGACTCCACTATCGCAACAATTGCATATAA			MTNPGPISISTCCKEPRLHYRNNCI*	MTNPGPISISTCCKEPRLHYRNNCI*			ACAATCGCCG	GACCGCGCAC	0	I	0	0	0	0	0
4117	2330	ao	AN1696.1	58.m07772	AO070305000020	0					-189	-97	ATGTCGATCCCTCGCAAGGCCACGTTGGACGGAAAGGAACTCGCATGCCGCTTGCGGTCCACTGGTGGTTACGCAATCACCTTCCGCATTTAA			ATGTCGATCCCTCGCAAGGCCACGTTGGACGGAAAGGAACTCGCATGCCGCTTGCGGTCCACTGGTGGTTACGCAATCACCTTCCGCATTTAA	MSIPRKATLDGKELACRLRSTGGYAITFRI*			MSIPRKATLDGKELACRLRSTGGYAITFRI*	GATTGGGTGG	TCGGGAATCA	0	I	0	0	0	0	0
4118	2330	ao	AN1696.1	58.m07772	AO070305000020	0					-145	-17	ATGCCGCTTGCGGTCCACTGGTGGTTACGCAATCACCTTCCGCATTTAATCGGGAATCATTTAATATCGAGAACTCCTCTCCTGAGAATCCTCGTGGGGAGGGAATTGCGCCTCGACCACATTCCTTAA			ATGCCGCTTGCGGTCCACTGGTGGTTACGCAATCACCTTCCGCATTTAATCGGGAATCATTTAATATCGAGAACTCCTCTCCTGAGAATCCTCGTGGGGAGGGAATTGCGCCTCGACCACATTCCTTAA	MPLAVHWWLRNHLPHLIGNHLISRTPLLRILVGRELRLDHIP*			MPLAVHWWLRNHLPHLIGNHLISRTPLLRILVGRELRLDHIP*	AGGAACTCGC	CCCACCTGTC	0	I	0	0	0	0	0
4121	2333	af	AN6890.1	71.m15249	AO070314000031	0			-233	-18			ATGGGCGAATCGTCGCCAGCAACGGGACCTCCGCAGATTCACTTTAAGCTCGGCCAGCTCGGGGAAAGCATCATCATCACTACCTTCATTCTTCGAGTCGAGAATCAGCGCAAAAATCGTTGTAACATATATTTTTCAATTTTCGTTGACGAAACCATTATCCAGGTGCTCACTAGAATGATCGGACGAATACAACACTCGCACTGCTATTGCTGA		ATGGGCGAATCGTCGCCAGCAACGGGACCTCCGCAGATTCACTTTAAGCTCGGCCAGCTCGGGGAAAGCATCATCATCACTACCTTCATTCTTCGAGTCGAGAATCAGCGCAAAAATCGTTGTAACATATATTTTTCAATTTTCGTTGACGAAACCATTATCCAGGTGCTCACTAGAATGATCGGACGAATACAACACTCGCACTGCTATTGCTGA		MGESSPATGPPQIHFKLGQLGESIIITTFILRVENQRKNRCNIYFSIFVDETIIQVLTRMIGRIQHSHCYC*		MGESSPATGPPQIHFKLGQLGESIIITTFILRVENQRKNRCNIYFSIFVDETIIQVLTRMIGRIQHSHCYC*		TTGGAACAGA	GTCCTTAACC	0	R	0	0	0	0	0
4119	2333	an	AN6890.1	71.m15249	AO070314000031	0	-153	-58					ATGGGAGGTCCCGACCTCAACTCAACCTCCAGGCGGTCGCCCTTATCTTGTTACCACATAAACTCGGCGCGGTTGTTCTTGTATCACCGTGATTGA	ATGGGAGGTCCCGACCTCAACTCAACCTCCAGGCGGTCGCCCTTATCTTGTTACCACATAAACTCGGCGCGGTTGTTCTTGTATCACCGTGATTGA			MGGPDLNSTSRRSPLSCYHINSARLFLYHRD*	MGGPDLNSTSRRSPLSCYHINSARLFLYHRD*			CCAAGTGGAG	CTTGCATGAC	0	R	0	0	0	0	0
4123	2333	ao	AN6890.1	71.m15249	AO070314000031	0					-200	-150	ATGGGCAAACCCGCCGCAACCTCCGCAGAGCAATGGATGCTTTGTGTTTAA			ATGGGCAAACCCGCCGCAACCTCCGCAGAGCAATGGATGCTTTGTGTTTAA	MGKPAATSAEQWMLCV*			MGKPAATSAEQWMLCV*	ACCAAACCAA	GCTCCCATCA	0	R	0	0	0	0	0
4124	2333	ao	AN6890.1	71.m15249	AO070314000031	0					-168	-133	ATGGATGCTTTGTGTTTAAGCTCCCATCATTCTTAA			ATGGATGCTTTGTGTTTAAGCTCCCATCATTCTTAA	MDALCLSSHHS*			MDALCLSSHHS*	CCGCAGAGCA	TGAACCTTCG	0	R	0	0	0	0	0
4125	2333	ao	AN6890.1	71.m15249	AO070314000031	0					-164	-150	ATGCTTTGTGTTTAA			ATGCTTTGTGTTTAA	MLCV*			MLCV*	AGAGCAATGG	GCTCCCATCA	0	R	0	0	0	0	0
4126	2333	ao	AN6890.1	71.m15249	AO070314000031	0					-133	-116	ATGAACCTTCGAGTTTAG			ATGAACCTTCGAGTTTAG	MNLRV*			MNLRV*	ATCATTCTTA	CGCACATCTC	0	R	0	0	0	0	0
4128	2334	af	AN3889.1	70.m15376	AO070316000069	0			-289	-266			ATGTGGGGGGACAGGAATGAGTAA		ATGTGGGGGGACAGGAATGAGTAA		MWGDRNE*		MWGDRNE*		TGGCCTCCGC	CGCAACAGGG	0	IQR	0	0	0	0	0
4129	2334	af	AN3889.1	70.m15376	AO070316000069	0			-273	-253			ATGAGTAACGCAACAGGGTGA		ATGAGTAACGCAACAGGGTGA		MSNATG*		MSNATG*		GGGGACAGGA	TATTTATGGT	0	IQR	0	0	0	0	0

4130	2334	af	AN3889.1	70.m15376	AO070316000069	0			-247	-185			ATGGTCATGAAGTGTCATCAGGTCGCGATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		ATGGTCATGAAGTGTCATCAGGTCGCGATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		MVMKCHQVAMVKSHKDSFPK*		MVMKCHQVAMVKSHKDSFPK*		GGTGATATTT	GCGGTTGCTG	0	IQR	0	0	0	0	0
4131	2334	af	AN3889.1	70.m15376	AO070316000069	0			-241	-185			ATGAAGTGTCATCAGGTCGCGATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		ATGAAGTGTCATCAGGTCGCGATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		MKCHQVAMVKSHKDSFPK*		MKCHQVAMVKSHKDSFPK*		ATTTATGGTC	GCGGTTGCTG	0	IQR	0	0	0	0	0
4132	2334	af	AN3889.1	70.m15376	AO070316000069	0			-220	-185			ATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		ATGGTGAAGTCTCATAAGGATTCTTTTCCGAAATAA		MVKSHKDSFPK*		MVKSHKDSFPK*		TCAGGTCGCG	GCGGTTGCTG	0	IQR	0	0	0	0	0
4133	2334	ao	AN3889.1	70.m15376	AO070316000069	0					-166	-83	ATGAATGGAAGAAATCATCGCAAAGCAATACCAAGAGCAAAAGAAACTCTTTTATTATATCCCGGGGACTATCTTGGTTCATAG			ATGAATGGAAGAAATCATCGCAAAGCAATACCAAGAGCAAAAGAAACTCTTTTATTATATCCCGGGGACTATCTTGGTTCATAG	MNGRNHRKAIPRAKETLLLYPGDYLGS*			MNGRNHRKAIPRAKETLLLYPGDYLGS*	GACATTTATT	CACTTGAAGA	0	IQR	0	0	0	0	0
4134	2334	ao	AN3889.1	70.m15376	AO070316000069	0					-162	-76	ATGGAAGAAATCATCGCAAAGCAATACCAAGAGCAAAAGAAACTCTTTTATTATATCCCGGGGACTATCTTGGTTCATAGCACTTGA			ATGGAAGAAATCATCGCAAAGCAATACCAAGAGCAAAAGAAACTCTTTTATTATATCCCGGGGACTATCTTGGTTCATAGCACTTGA	MEEIIAKQYQEQKKLFYYIPGTILVHST*			MEEIIAKQYQEQKKLFYYIPGTILVHST*	TTTATTATGA	AGAGGAGCGA	0	IQR	0	0	0	0	0
4138	2335	af	AN0941.1	70.m15572	AO070320000131	0			-187	-68			ATGCGCCTGGTGTTGTCATACAGCCAGACGAACGCCTGCGCCACTGGCCGTGCTCCGGGAAAGTGTTGGATGCATCCGACAGAATGTTCTGCCGCTCAGGCGCACGTCAAACGCATATAA		ATGCGCCTGGTGTTGTCATACAGCCAGACGAACGCCTGCGCCACTGGCCGTGCTCCGGGAAAGTGTTGGATGCATCCGACAGAATGTTCTGCCGCTCAGGCGCACGTCAAACGCATATAA		MRLVLSYSQTNACATGRAPGKCWMHPTECSAAQAHVKRI*		MRLVLSYSQTNACATGRAPGKCWMHPTECSAAQAHVKRI*		GGTTGATCTG	ACCCTGGTGT	0	G	0	0	0	0	0
4139	2335	af	AN0941.1	70.m15572	AO070320000131	0			-118	-68			ATGCATCCGACAGAATGTTCTGCCGCTCAGGCGCACGTCAAACGCATATAA		ATGCATCCGACAGAATGTTCTGCCGCTCAGGCGCACGTCAAACGCATATAA		MHPTECSAAQAHVKRI*		MHPTECSAAQAHVKRI*		AAAGTGTTGG	ACCCTGGTGT	0	G	0	0	0	0	0
4135	2335	an	AN0941.1	70.m15572	AO070320000131	0	-176	-30					ATGCAAGCCTCTCTTCATTCCGGTCTCGCTCAAACATATGGCGCAGTCGATCCACTGCGCATGTTGACTGTGCTCTATTGTCACTCGTGCCATCTGGTTGCGGATATTTTAACTGCGGTGTTCACCCACTTTGTCGATTCCTCCTAA	ATGCAAGCCTCTCTTCATTCCGGTCTCGCTCAAACATATGGCGCAGTCGATCCACTGCGCATGTTGACTGTGCTCTATTGTCACTCGTGCCATCTGGTTGCGGATATTTTAACTGCGGTGTTCACCCACTTTGTCGATTCCTCCTAA			MQASLHSGLAQTYGAVDPLRMLTVLYCHSCHLVADILTAVFTHFVDSS*	MQASLHSGLAQTYGAVDPLRMLTVLYCHSCHLVADILTAVFTHFVDSS*			ATCCGGAACC	GGAACTCGAC	0	G	0	0	0	0	0
4136	2335	an	AN0941.1	70.m15572	AO070320000131	0	-139	-110					ATGGCGCAGTCGATCCACTGCGCATGTTGA	ATGGCGCAGTCGATCCACTGCGCATGTTGA			MAQSIHCAC*	MAQSIHCAC*			GCTCAAACAT	CTGTGCTCTA	0	G	0	0	0	0	0
4137	2335	an	AN0941.1	70.m15572	AO070320000131	0	-116	-30					ATGTTGACTGTGCTCTATTGTCACTCGTGCCATCTGGTTGCGGATATTTTAACTGCGGTGTTCACCCACTTTGTCGATTCCTCCTAA	ATGTTGACTGTGCTCTATTGTCACTCGTGCCATCTGGTTGCGGATATTTTAACTGCGGTGTTCACCCACTTTGTCGATTCCTCCTAA			MLTVLYCHSCHLVADILTAVFTHFVDSS*	MLTVLYCHSCHLVADILTAVFTHFVDSS*			TCCACTGCGC	GGAACTCGAC	0	G	0	0	0	0	0
4140	2335	ao	AN0941.1	70.m15572	AO070320000131	0					-198	-184	ATGCAGTTGATGTGA			ATGCAGTTGATGTGA	MQLM*			MQLM*	GTTGACCGTG	GCAGTCATAC	0	G	0	0	0	0	0
4142	2336	af	AN0947.1	70.m15586	AO070320000146	0			-227	-207			ATGTCAATATTAATATGTTAA		ATGTCAATATTAATATGTTAA		MSILIC*		MSILIC*		TGCGATAACT	TATTCATGGC	0	H	0	0	0	0	0
4143	2336	af	AN0947.1	70.m15586	AO070320000146	0			-213	-118			ATGTTAATATTCATGGCGGTGACTAATCTTGGTCCAGCGGGGGTCGCCGATTCCGCGGAGTTGGGAGTCATTGAGCACAATCCTTTGTTCCTTTGA		ATGTTAATATTCATGGCGGTGACTAATCTTGGTCCAGCGGGGGTCGCCGATTCCGCGGAGTTGGGAGTCATTGAGCACAATCCTTTGTTCCTTTGA		MLIFMAVTNLGPAGVADSAELGVIEHNPLFL*		MLIFMAVTNLGPAGVADSAELGVIEHNPLFL*		CAATATTAAT	TAAGAAACCC	0	H	0	0	0	0	0
4144	2336	af	AN0947.1	70.m15586	AO070320000146	0			-201	-118			ATGGCGGTGACTAATCTTGGTCCAGCGGGGGTCGCCGATTCCGCGGAGTTGGGAGTCATTGAGCACAATCCTTTGTTCCTTTGA		ATGGCGGTGACTAATCTTGGTCCAGCGGGGGTCGCCGATTCCGCGGAGTTGGGAGTCATTGAGCACAATCCTTTGTTCCTTTGA		MAVTNLGPAGVADSAELGVIEHNPLFL*		MAVTNLGPAGVADSAELGVIEHNPLFL*		GTTAATATTC	TAAGAAACCC	0	H	0	0	0	0	0
4145	2336	af	AN0947.1	70.m15586	AO070320000146	0			-104	-60			ATGCAACTTTGTTTGGGGCTTCTTCGAGGCTTTCCCCCTTCCTAA		ATGCAACTTTGTTTGGGGCTTCTTCGAGGCTTTCCCCCTTCCTAA		MQLCLGLLRGFPPS*		MQLCLGLLRGFPPS*		GAAACCCACA	ATGCAGGACA	0	H	0	0	0	0	0
4141	2336	an	AN0947.1	70.m15586	AO070320000146	0	-162	-79					ATGGAGGCGACCGAACCCGCGGAGAACAGCGACGATAAGAAATTCCTTATTATCCCATCCTTCCATCGTTTGCCTTGGTTTTAG	ATGGAGGCGACCGAACCCGCGGAGAACAGCGACGATAAGAAATTCCTTATTATCCCATCCTTCCATCGTTTGCCTTGGTTTTAG			MEATEPAENSDDKKFLIIPSFHRLPWF*	MEATEPAENSDDKKFLIIPSFHRLPWF*			AAGTCAGGTG	TTGTTAGTGC	0	H	0	0	0	0	0
4146	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-233	-222	ATGTCCGAATGA			ATGTCCGAATGA	MSE*			MSE*	CAAGGCGGGC	AGTTAGTTCT	0	H	0	0	0	0	0
4147	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-225	-112	ATGAAGTTAGTTCTGCGGAGAAGCAGCCTGCCAGCGAATGAAATGCCACGGGATGACTCGATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG			ATGAAGTTAGTTCTGCGGAGAAGCAGCCTGCCAGCGAATGAAATGCCACGGGATGACTCGATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG	MKLVLRRSSLPANEMPRDDSMMISKLSWDPFPSFPYP*			MKLVLRRSSLPANEMPRDDSMMISKLSWDPFPSFPYP*	GCATGTCCGA	ATTTTTGCCT	0	H	0	0	0	0	0
4148	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-188	-162	ATGAAATGCCACGGGATGACTCGATGA			ATGAAATGCCACGGGATGACTCGATGA	MKCHGMTR*			MKCHGMTR*	CTGCCAGCGA	TGATAAGCAA	0	H	0	0	0	0	0
4149	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-183	-112	ATGCCACGGGATGACTCGATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG			ATGCCACGGGATGACTCGATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG	MPRDDSMMISKLSWDPFPSFPYP*			MPRDDSMMISKLSWDPFPSFPYP*	AGCGAATGAA	ATTTTTGCCT	0	H	0	0	0	0	0
4150	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-173	-162	ATGACTCGATGA			ATGACTCGATGA	MTR*			MTR*	ATGCCACGGG	TGATAAGCAA	0	H	0	0	0	0	0
4151	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-165	-112	ATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG			ATGATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG	MMISKLSWDPFPSFPYP*			MMISKLSWDPFPSFPYP*	GGATGACTCG	ATTTTTGCCT	0	H	0	0	0	0	0
4152	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-162	-112	ATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG			ATGATAAGCAAGCTTTCTTGGGATCCATTCCCCTCCTTCCCTTACCCATAG	MISKLSWDPFPSFPYP*			MISKLSWDPFPSFPYP*	TGACTCGATG	ATTTTTGCCT	0	H	0	0	0	0	0
4153	2336	ao	AN0947.1	70.m15586	AO070320000146	0					-90	-55	ATGCCCACCACTCCCCCGTTCAAACTTATTTATTGA			ATGCCCACCACTCCCCCGTTCAAACTTATTTATTGA	MPTTPPFKLIY*			MPTTPPFKLIY*	TAAGACCCAA	TATGCCGGAA	0	H	0	0	0	0	0
4156	2337	af	AN0209.1	71.m15472	AO070321000035	0			-176	-120			ATGATGGAGCCTGCTTTAGTGGTTGCAAACCGCCAAGAGTTCGAGAAAGAAGAGTAG		ATGATGGAGCCTGCTTTAGTGGTTGCAAACCGCCAAGAGTTCGAGAAAGAAGAGTAG		MMEPALVVANRQEFEKEE*		MMEPALVVANRQEFEKEE*		TATCATTGCC	ATAAATGCGG	0	P	0	MG05526.1	0	0	0
4157	2337	af	AN0209.1	71.m15472	AO070321000035	0			-173	-120			ATGGAGCCTGCTTTAGTGGTTGCAAACCGCCAAGAGTTCGAGAAAGAAGAGTAG		ATGGAGCCTGCTTTAGTGGTTGCAAACCGCCAAGAGTTCGAGAAAGAAGAGTAG		MEPALVVANRQEFEKEE*		MEPALVVANRQEFEKEE*		CATTGCCATG	ATAAATGCGG	0	P	0	MG05526.1	0	0	0
4158	2337	af	AN0209.1	71.m15472	AO070321000035	0			-115	-56			ATGCGGGAGAGTCTTTTTGAAGGGCCGCTGATCCCTACGGATCACCGTATGGCTGTTTGA		ATGCGGGAGAGTCTTTTTGAAGGGCCGCTGATCCCTACGGATCACCGTATGGCTGTTTGA		MRESLFEGPLIPTDHRMAV*		MRESLFEGPLIPTDHRMAV*		GAGTAGATAA	TTGTGAGCCG	0	P	0	MG05526.1	0	0	0
4159	2337	af	AN0209.1	71.m15472	AO070321000035	0			-67	-56			ATGGCTGTTTGA		ATGGCTGTTTGA		MAV*		MAV*		GGATCACCGT	TTGTGAGCCG	0	P	0	MG05526.1	0	0	0
4155	2337	an	AN0209.1	71.m15472	AO070321000035	0	-154	-131					ATGGAGCCTTCAGGGCAAGGTTAA	ATGGAGCCTTCAGGGCAAGGTTAA			MEPSGQG*	MEPSGQG*			CTGAAGAACG	ATTGTGAGCA	0	P	0	MG05526.1	0	0	0
4160	2337	ao	AN0209.1	71.m15472	AO070321000035	0					-196	-146	ATGGTAGTCTGGGTCCAGCCAAGACATATTGCAAACCAAGAGAGAAGATGA			ATGGTAGTCTGGGTCCAGCCAAGACATATTGCAAACCAAGAGAGAAGATGA	MVVWVQPRHIANQERR*			MVVWVQPRHIANQERR*	TCCCGACCCT	GGATAAATTG	0	P	0	MG05526.1	0	0	0
4161	2337	ao	AN0209.1	71.m15472	AO070321000035	0					-149	-12	ATGAGGATAAATTGCGATGGAGACCGACAGCTTCTCCCGATTCTTGCTTGCCTCCCAAGATCGATCGTTGGTGAAACAAGAACGAGTGCTATAATACATATTTCTTGTCATCTTACCTCCTCACCAAATACAGAGTGA			ATGAGGATAAATTGCGATGGAGACCGACAGCTTCTCCCGATTCTTGCTTGCCTCCCAAGATCGATCGTTGGTGAAACAAGAACGAGTGCTATAATACATATTTCTTGTCATCTTACCTCCTCACCAAATACAGAGTGA	MRINCDGDRQLLPILACLPRSIVGETRTSAIIHISCHLTSSPNTE*			MRINCDGDRQLLPILACLPRSIVGETRTSAIIHISCHLTSSPNTE*	AAGAGAGAAG	GCCTGCTCGC	0	P	0	MG05526.1	0	0	0
4162	2337	ao	AN0209.1	71.m15472	AO070321000035	0					-133	-56	ATGGAGACCGACAGCTTCTCCCGATTCTTGCTTGCCTCCCAAGATCGATCGTTGGTGAAACAAGAACGAGTGCTATAA			ATGGAGACCGACAGCTTCTCCCGATTCTTGCTTGCCTCCCAAGATCGATCGTTGGTGAAACAAGAACGAGTGCTATAA	METDSFSRFLLASQDRSLVKQERVL*			METDSFSRFLLASQDRSLVKQERVL*	ATAAATTGCG	TACATATTTC	0	P	0	MG05526.1	0	0	0
4163	2344	af	AN6157.1	72.m19005	AO070340000038	0			-233	-132			ATGTGGCCTGTCTCCATCCAGATTGGCACGCAATTTTTACACGCGGAAAAGATCGAGATAGAGTACGACTTTAAATTTAGTCCCCGGCGGCTTCTATTTTAG		ATGTGGCCTGTCTCCATCCAGATTGGCACGCAATTTTTACACGCGGAAAAGATCGAGATAGAGTACGACTTTAAATTTAGTCCCCGGCGGCTTCTATTTTAG		MWPVSIQIGTQFLHAEKIEIEYDFKFSPRRLLF*		MWPVSIQIGTQFLHAEKIEIEYDFKFSPRRLLF*		TACAGCACCG	AATATTTGAG	0	F	0	0	0	0	0
4164	2344	ao	AN6157.1	72.m19005	AO070340000038	0					-273	-229	ATGAGGCATGTGGCTCACCCCACAGGCGGAGAAACGTGTGGCTAG			ATGAGGCATGTGGCTCACCCCACAGGCGGAGAAACGTGTGGCTAG	MRHVAHPTGGETCG*			MRHVAHPTGGETCG*	TTTGGTCAAA	TGCATGACAG	0	F	0	0	0	0	0
4165	2344	ao	AN6157.1	72.m19005	AO070340000038	0					-266	-222	ATGTGGCTCACCCCACAGGCGGAGAAACGTGTGGCTAGTGCATGA			ATGTGGCTCACCCCACAGGCGGAGAAACGTGTGGCTAGTGCATGA	MWLTPQAEKRVASA*			MWLTPQAEKRVASA*	AAAATGAGGC	CAGTCCCCTC	0	F	0	0	0	0	0
4166	2344	ao	AN6157.1	72.m19005	AO070340000038	0					-225	-196	ATGACAGTCCCCTCCATAGATTCAATTTAA			ATGACAGTCCCCTCCATAGATTCAATTTAA	MTVPSIDSI*			MTVPSIDSI*	TGGCTAGTGC	TTTTTCGCGG	0	F	0	0	0	0	0
4168	2345	af	AN6147.1	72.m19018	AO070340000055	0			-167	-156			ATGAATTGCTAA		ATGAATTGCTAA		MNC*		MNC*		CTGCGTTTCT	ATCTACGCTC	0	B	0	0	0	0	0
4170	2346	af	AN2585.1	57.m05814	AO070341000273	0			-244	-131			ATGGCTTGGGTAGTATCCGACACGACTCTACGAATCAGGGATCTTGCTCGGTCTTTGCACCTGTCCCAAGTCTCAAATCACAATGGACGGCCCTGGTTAGACCGACCTATATAA		ATGGCTTGGGTAGTATCCGACACGACTCTACGAATCAGGGATCTTGCTCGGTCTTTGCACCTGTCCCAAGTCTCAAATCACAATGGACGGCCCTGGTTAGACCGACCTATATAA		MAWVVSDTTLRIRDLARSLHLSQVSNHNGRPWLDRPI*		MAWVVSDTTLRIRDLARSLHLSQVSNHNGRPWLDRPI*		CCTCAGAATC	ATCATGCTTT	0	R	0	0	0	0	0
4171	2346	af	AN2585.1	57.m05814	AO070341000273	0			-162	-145			ATGGACGGCCCTGGTTAG		ATGGACGGCCCTGGTTAG		MDGPG*		MDGPG*		TCAAATCACA	ACCGACCTAT	0	R	0	0	0	0	0
4172	2346	ao	AN2585.1	57.m05814	AO070341000273	0					-283	-95	ATGGATCTGGAAGCTATCCGGCCGTCCTGCGAATCAGCACTGCAGCTCGGCCTTTGGCTTTTTCTAATCTTTGGTTGGCTCTTTGATTTTCAAGTAATTAGTATGGGTGGGCAACCCTACCATGTCATCTATATAAATCGTACGGTAGCTCCTGAATTTCCCGTCCTCTCTTGTGTTACAGTAGAGTGA			ATGGATCTGGAAGCTATCCGGCCGTCCTGCGAATCAGCACTGCAGCTCGGCCTTTGGCTTTTTCTAATCTTTGGTTGGCTCTTTGATTTTCAAGTAATTAGTATGGGTGGGCAACCCTACCATGTCATCTATATAAATCGTACGGTAGCTCCTGAATTTCCCGTCCTCTCTTGTGTTACAGTAGAGTGA	MDLEAIRPSCESALQLGLWLFLIFGWLFDFQVISMGGQPYHVIYINRTVAPEFPVLSCVTVE*			MDLEAIRPSCESALQLGLWLFLIFGWLFDFQVISMGGQPYHVIYINRTVAPEFPVLSCVTVE*	TTTCTGTCTC	ATTGTACACT	0	R	0	0	0	0	0
4173	2346	ao	AN2585.1	57.m05814	AO070341000273	0					-181	-95	ATGGGTGGGCAACCCTACCATGTCATCTATATAAATCGTACGGTAGCTCCTGAATTTCCCGTCCTCTCTTGTGTTACAGTAGAGTGA			ATGGGTGGGCAACCCTACCATGTCATCTATATAAATCGTACGGTAGCTCCTGAATTTCCCGTCCTCTCTTGTGTTACAGTAGAGTGA	MGGQPYHVIYINRTVAPEFPVLSCVTVE*			MGGQPYHVIYINRTVAPEFPVLSCVTVE*	AGTAATTAGT	ATTGTACACT	0	R	0	0	0	0	0
4174	2346	ao	AN2585.1	57.m05814	AO070341000273	0					-162	-148	ATGTCATCTATATAA			ATGTCATCTATATAA	MSSI*			MSSI*	CAACCCTACC	ATCGTACGGT	0	R	0	0	0	0	0
4177	2348	af	AN4160.1	58.m07365	AO070342000189	0			-234	-208			ATGCTTCTTTCAGGAATTTCCCCGTAG		ATGCTTCTTTCAGGAATTTCCCCGTAG		MLLSGISP*		MLLSGISP*		ATAATTGAAA	GATGCCGCTA	0		0	0	0	0	0
4178	2348	af	AN4160.1	58.m07365	AO070342000189	0			-206	-192			ATGCCGCTACTTTAG		ATGCCGCTACTTTAG		MPLL*		MPLL*		TCCCCGTAGG	TGATACGTGA	0		0	0	0	0	0
4179	2348	af	AN4160.1	58.m07365	AO070342000189	0			-113	-48			ATGGTGTCTCATACTTTGCATGATACCCCAATTGATTATAAAGCAGTCATCTCGAGTGGCTGCTAG		ATGGTGTCTCATACTTTGCATGATACCCCAATTGATTATAAAGCAGTCATCTCGAGTGGCTGCTAG		MVSHTLHDTPIDYKAVISSGC*		MVSHTLHDTPIDYKAVISSGC*		TTGGTTGTTG	TTGTTCCTTC	0		0	0	0	0	0
4180	2348	af	AN4160.1	58.m07365	AO070342000189	0			-94	-35			ATGATACCCCAATTGATTATAAAGCAGTCATCTCGAGTGGCTGCTAGTTGTTCCTTCTAA		ATGATACCCCAATTGATTATAAAGCAGTCATCTCGAGTGGCTGCTAGTTGTTCCTTCTAA		MIPQLIIKQSSRVAASCSF*		MIPQLIIKQSSRVAASCSF*		CATACTTTGC	TGTGATTTAT	0		0	0	0	0	0
4176	2348	an	AN4160.1	58.m07365	AO070342000189	0	-128	-102					ATGAACTCGCTTTGTTGCAGATCGTGA	ATGAACTCGCTTTGTTGCAGATCGTGA			MNSLCCRS*	MNSLCCRS*			GGTACCTGAG	AGCTCTTGTG	0		0	0	0	0	0
4181	2348	ao	AN4160.1	58.m07365	AO070342000189	0					-204	-187	ATGCTTTTAATAGTCTAG			ATGCTTTTAATAGTCTAG	MLLIV*			MLLIV*	AACTTTGGCG	TGAGTTTTCA	0		0	0	0	0	0
4182	2348	ao	AN4160.1	58.m07365	AO070342000189	0					-169	-140	ATGGTGTTGCCCGGTCAGCCCGTCAGATAG			ATGGTGTTGCCCGGTCAGCCCGTCAGATAG	MVLPGQPVR*			MVLPGQPVR*	TCACAATTGC	AAGATAATGA	0		0	0	0	0	0
4183	2348	ao	AN4160.1	58.m07365	AO070342000189	0					-133	-107	ATGAACTGCGCAGCGGTGCAGTATTGA			ATGAACTGCGCAGCGGTGCAGTATTGA	MNCAAVQY*			MNCAAVQY*	ATAGAAGATA	GAAGAGGCCC	0		0	0	0	0	0
4184	2348	ao	AN4160.1	58.m07365	AO070342000189	0					-72	-40	ATGCGTGATACCCAGCATTTGTCTAGTTATTGA			ATGCGTGATACCCAGCATTTGTCTAGTTATTGA	MRDTQHLSSY*			MRDTQHLSSY*	CTATCGTTTT	TCTGGTTACA	0		0	0	0	0	0
4190	2349	af	AN3535.1	57.m05320	AO070343000460	0			-249	-229			ATGTCGCATCAGGTTAAATAA		ATGTCGCATCAGGTTAAATAA		MSHQVK*		MSHQVK*		CCAGATTAGC	ATTTTCTTGG	0		0	0	0	0	0
4191	2349	af	AN3535.1	57.m05320	AO070343000460	0			-217	-200			ATGTACCAATTCCAATGA		ATGTACCAATTCCAATGA		MYQFQ*		MYQFQ*		TTTTCTTGGC	GCCCGCTGAG	0		0	0	0	0	0
4192	2349	af	AN3535.1	57.m05320	AO070343000460	0			-203	-135			ATGAGCCCGCTGAGTTTCTCTCATTTGAATCGGCTACATCGCAGGCAGTGGAGCGGTTGCATCATTTGA		ATGAGCCCGCTGAGTTTCTCTCATTTGAATCGGCTACATCGCAGGCAGTGGAGCGGTTGCATCATTTGA		MSPLSFSHLNRLHRRQWSGCII*		MSPLSFSHLNRLHRRQWSGCII*		ACCAATTCCA	GGCCAAGAAC	0		0	0	0	0	0

4193	2349	af	AN3535.1	57.m05320	AO070343000460	0			-105	-46			ATGCACCCTCCGAATGCAATCCGTAGAAATGTCAATCCCGACACCTTCTATTCTCTCTAG		ATGCACCCTCCGAATGCAATCCGTAGAAATGTCAATCCCGACACCTTCTATTCTCTCTAG		MHPPNAIRRNVNPDTFYSL*		MHPPNAIRRNVNPDTFYSL*		AGGCATCCGG	GTTCAATCTT	0		0	0	0	0	0
4185	2349	an	AN3535.1	57.m05320	AO070343000460	0	-263	-243					ATGCAAAATTCATCCAATTAG	ATGCAAAATTCATCCAATTAG			MQNSSN*	MQNSSN*			TTAGAATTCG	TTCAGCGAGC	0		0	0	0	0	0
4186	2349	an	AN3535.1	57.m05320	AO070343000460	0	-219	-196					ATGGTCTGTGATAAATGCGGGTAA	ATGGTCTGTGATAAATGCGGGTAA			MVCDKCG*	MVCDKCG*			TTTGTTATCA	TGGAACGTCG	0		0	0	0	0	0
4187	2349	an	AN3535.1	57.m05320	AO070343000460	0	-205	-80					ATGCGGGTAATGGAACGTCGCGAAGGGCCCGAAAACGGAAATTTAGGGCATCCCCCAGCGACCGGAATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA	ATGCGGGTAATGGAACGTCGCGAAGGGCCCGAAAACGGAAATTTAGGGCATCCCCCAGCGACCGGAATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA			MRVMERREGPENGNLGHPPATGMGIGRRPSISTLNFSLALK*	MRVMERREGPENGNLGHPPATGMGIGRRPSISTLNFSLALK*			TCTGTGATAA	ATTAGAGCTC	0		0	0	0	0	0
4188	2349	an	AN3535.1	57.m05320	AO070343000460	0	-196	-80					ATGGAACGTCGCGAAGGGCCCGAAAACGGAAATTTAGGGCATCCCCCAGCGACCGGAATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA	ATGGAACGTCGCGAAGGGCCCGAAAACGGAAATTTAGGGCATCCCCCAGCGACCGGAATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA			MERREGPENGNLGHPPATGMGIGRRPSISTLNFSLALK*	MERREGPENGNLGHPPATGMGIGRRPSISTLNFSLALK*			AATGCGGGTA	ATTAGAGCTC	0		0	0	0	0	0
4189	2349	an	AN3535.1	57.m05320	AO070343000460	0	-139	-80					ATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA	ATGGGAATAGGTAGAAGACCATCAATCTCCACGCTTAACTTCTCCCTAGCCTTGAAATAA			MGIGRRPSISTLNFSLALK*	MGIGRRPSISTLNFSLALK*			AGCGACCGGA	ATTAGAGCTC	0		0	0	0	0	0
4196	2350	af	AN0646.1	70.m15248	AO070343000583	0			-366	-337			ATGTATTGTCTATTCGGTATGCTGATCTAG		ATGTATTGTCTATTCGGTATGCTGATCTAG		MYCLFGMLI*		MYCLFGMLI*		ATCAACCGGT	GTTGACTTAC	0	A	0	0	0	0	0
4197	2350	af	AN0646.1	70.m15248	AO070343000583	0			-348	-337			ATGCTGATCTAG		ATGCTGATCTAG		MLI*		MLI*		TCTATTCGGT	GTTGACTTAC	0	A	0	0	0	0	0
4194	2350	an	AN0646.1	70.m15248	AO070343000583	0	-374	-330					ATGGTCGTGCTCAGATTGCCCATACTAAGATCTCGATGTATCTAG	ATGGTCGTGCTCAGATTGCCCATACTAAGATCTCGATGTATCTAG			MVVLRLPILRSRCI*	MVVLRLPILRSRCI*			AGTATTCTAA	TCTCATTCTT	0	A	0	0	0	0	0
4195	2350	an	AN0646.1	70.m15248	AO070343000583	0	-339	-208					ATGTATCTAGTCTCATTCTTGCCCCTCTGTTGTGCCACACTGGATTTCGTGGAAGAGACACAGGGGCTTTCATTCTTTTTGTTACAAGACGAAGCGCCTGTTCTTACGTCCATTGACGCCGACCGATTTTGA	ATGTATCTAGTCTCATTCTTGCCCCTCTGTTGTGCCACACTGGATTTCGTGGAAGAGACACAGGGGCTTTCATTCTTTTTGTTACAAGACGAAGCGCCTGTTCTTACGTCCATTGACGCCGACCGATTTTGA			MYLVSFLPLCCATLDFVETQGLSFFLLQDEAPVLTSIDADRF*	MYLVSFLPLCCATLDFVETQGLSFFLLQDEAPVLTSIDADRF*			TAAGATCTCG	CCAACTCCTT	0	A	0	0	0	0	0
4199	2351	af	AN4290.1	58.m08029	AO070158000001	0			-274	-206			ATGCCCTATAGAGATGCCCTAGAGATTAGCCCTAGCCCTAGTGCTTATACAGTTTTAGAGATTATATAA		ATGCCCTATAGAGATGCCCTAGAGATTAGCCCTAGCCCTAGTGCTTATACAGTTTTAGAGATTATATAA		MPYRDALEISPSPSAYTVLEII*		MPYRDALEISPSPSAYTVLEII*		TATAGTTATA	TATAGAGTCT	0	J	0	0	0	YPR118W	0
4200	2351	af	AN4290.1	58.m08029	AO070158000001	0			-117	-88			ATGGGGGGTGTGTTTCTATTAAGACCCTAG		ATGGGGGGTGTGTTTCTATTAAGACCCTAG		MGGVFLLRP*		MGGVFLLRP*		TGCCACTAAG	AATCAATCCC	0	J	0	0	0	YPR118W	0
4201	2351	ao	AN4290.1	58.m08029	AO070158000001	0					-205	-113	ATGTTACTCATTGATGAGGGGTGTGTTGCCCCACCTGAAGCGTTTTACGGAGTACTACTCCGTATGTATGTCAGTCAGTCAACCTTTAGGTGA			ATGTTACTCATTGATGAGGGGTGTGTTGCCCCACCTGAAGCGTTTTACGGAGTACTACTCCGTATGTATGTCAGTCAGTCAACCTTTAGGTGA	MLLIDEGCVAPPEAFYGVLLRMYVSQSTFR*			MLLIDEGCVAPPEAFYGVLLRMYVSQSTFR*	AGCCTAAGTT	AGCGCGAGCT	0	J	0	0	0	YPR118W	0
4202	2351	ao	AN4290.1	58.m08029	AO070158000001	0					-142	-113	ATGTATGTCAGTCAGTCAACCTTTAGGTGA			ATGTATGTCAGTCAGTCAACCTTTAGGTGA	MYVSQSTFR*			MYVSQSTFR*	ACTACTCCGT	AGCGCGAGCT	0	J	0	0	0	YPR118W	0
4205	2355	af	AN6409.1	67.m02948	AO070276000080	0			-186	-142			ATGTTCGTATTGGGGCACCACGGCGGATTTAAGCACATCGAATGA		ATGTTCGTATTGGGGCACCACGGCGGATTTAAGCACATCGAATGA		MFVLGHHGGFKHIE*		MFVLGHHGGFKHIE*		GGGGGCTGCG	TTAGCAAGCT	0		0	0	0	0	0
4206	2355	af	AN6409.1	67.m02948	AO070276000080	0			-145	-95			ATGATTAGCAAGCTGCGCCCCACGCTTGGCAAGGCTCAATGTGTCGACTGA		ATGATTAGCAAGCTGCGCCCCACGCTTGGCAAGGCTCAATGTGTCGACTGA		MISKLRPTLGKAQCVD*		MISKLRPTLGKAQCVD*		AGCACATCGA	CCGTTGATCG	0		0	0	0	0	0
4207	2355	ao	AN6409.1	67.m02948	AO070276000080	0					-247	-155	ATGCAAATTGCCAAGGAGTGGTTATTAAATCACGCGAGGGTGTCGTGCAGCCTTGCCGGATCTCCGCACTCGCCTCGTATTCGGGAGGGTTGA			ATGCAAATTGCCAAGGAGTGGTTATTAAATCACGCGAGGGTGTCGTGCAGCCTTGCCGGATCTCCGCACTCGCCTCGTATTCGGGAGGGTTGA	MQIAKEWLLNHARVSCSLAGSPHSPRIREG*			MQIAKEWLLNHARVSCSLAGSPHSPRIREG*	AGGACTGCTA	ACGCTAAGCA	0		0	0	0	0	0
4208	2355	ao	AN6409.1	67.m02948	AO070276000080	0					-104	-12	ATGGAGAAGATGGTACATCTAGAGTTTATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA			ATGGAGAAGATGGTACATCTAGAGTTTATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA	MEKMVHLEFMAPSSLFYVHYRLLNLLATHP*			MEKMVHLEFMAPSSLFYVHYRLLNLLATHP*	GGCGATATTT	TCATCACAGA	0		0	0	0	0	0
4209	2355	ao	AN6409.1	67.m02948	AO070276000080	0					-95	-12	ATGGTACATCTAGAGTTTATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA			ATGGTACATCTAGAGTTTATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA	MVHLEFMAPSSLFYVHYRLLNLLATHP*			MVHLEFMAPSSLFYVHYRLLNLLATHP*	TATGGAGAAG	TCATCACAGA	0		0	0	0	0	0
4210	2355	ao	AN6409.1	67.m02948	AO070276000080	0					-77	-12	ATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA			ATGGCGCCTAGTTCTTTATTTTATGTGCACTATCGTCTCCTCAATCTACTAGCAACCCATCCTTGA	MAPSSLFYVHYRLLNLLATHP*			MAPSSLFYVHYRLLNLLATHP*	TCTAGAGTTT	TCATCACAGA	0		0	0	0	0	0
4212	2359	af	AN8880.1	56.m02291	AO070293000010	0			-242	-156			ATGCAAGCGCGGCTCTGCACGCGTTGGTCACAAGAAGGCTCGATGCTTGACCACTCTTTTGCAATTCAACGTCTCAGATTGTTATAG		ATGCAAGCGCGGCTCTGCACGCGTTGGTCACAAGAAGGCTCGATGCTTGACCACTCTTTTGCAATTCAACGTCTCAGATTGTTATAG		MQARLCTRWSQEGSMLDHSFAIQRLRLL*		MQARLCTRWSQEGSMLDHSFAIQRLRLL*		AGATATCAGC	CAGGAATACT	0	R	FG00615.1	0	0	0	0
4213	2359	af	AN8880.1	56.m02291	AO070293000010	0			-200	-156			ATGCTTGACCACTCTTTTGCAATTCAACGTCTCAGATTGTTATAG		ATGCTTGACCACTCTTTTGCAATTCAACGTCTCAGATTGTTATAG		MLDHSFAIQRLRLL*		MLDHSFAIQRLRLL*		AGAAGGCTCG	CAGGAATACT	0	R	FG00615.1	0	0	0	0
4215	2361	af	AN2393.1	54.m06368	AO070296000121	0			-194	-72			ATGATGATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		ATGATGATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		MMMIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		MMMIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		TACTTGTAAG	GCTATCACTC	0	IQR	0	0	0	0	0
4216	2361	af	AN2393.1	54.m06368	AO070296000121	0			-191	-72			ATGATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		ATGATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		MMIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		MMIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		TTGTAAGATG	GCTATCACTC	0	IQR	0	0	0	0	0
4217	2361	af	AN2393.1	54.m06368	AO070296000121	0			-188	-72			ATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		ATGATTAAAGCCGGAGTTGACGGATTTTGCGACATCTTAGCCCCGTCAACGCTGACCGATTTGAGTCATCAGTCGCAACACCTTTTTTCCGGTACAAAGTATATATATCATAAATAA		MIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		MIKAGVDGFCDILAPSTLTDLSHQSQHLFSGTKYIYHK*		TAAGATGATG	GCTATCACTC	0	IQR	0	0	0	0	0
4218	2361	ao	AN2393.1	54.m06368	AO070296000121	0					-241	-131	ATGGAGTTAGGCCAGTATTGGAATGACGCCAATTACTCCTGCCTATCGTCTCATACAATAAGGGAGATCTTGTTTTCGGTCATAAAAGCAACGACTTTAACCCCGCCTTAG			ATGGAGTTAGGCCAGTATTGGAATGACGCCAATTACTCCTGCCTATCGTCTCATACAATAAGGGAGATCTTGTTTTCGGTCATAAAAGCAACGACTTTAACCCCGCCTTAG	MELGQYWNDANYSCLSSHTIREILFSVIKATTLTPP*			MELGQYWNDANYSCLSSHTIREILFSVIKATTLTPP*	CCCGGCCCCC	ACCCGTTATT	0	IQR	0	0	0	0	0
4219	2361	ao	AN2393.1	54.m06368	AO070296000121	0					-219	-181	ATGACGCCAATTACTCCTGCCTATCGTCTCATACAATAA			ATGACGCCAATTACTCCTGCCTATCGTCTCATACAATAA	MTPITPAYRLIQ*			MTPITPAYRLIQ*	CAGTATTGGA	GGGAGATCTT	0	IQR	0	0	0	0	0
4224	2364	af	AN3828.1	58.m07804	AO070305000065	0			-278	-183			ATGCAATCAAAACTCATAGGGCTCGAGATCTTTCCGCAGGAAAAGCCATGTTTCCAAGCCTGGTCCGCTAAAATTCTACTGAGGAACTTGCACTAA		ATGCAATCAAAACTCATAGGGCTCGAGATCTTTCCGCAGGAAAAGCCATGTTTCCAAGCCTGGTCCGCTAAAATTCTACTGAGGAACTTGCACTAA		MQSKLIGLEIFPQEKPCFQAWSAKILLRNLH*		MQSKLIGLEIFPQEKPCFQAWSAKILLRNLH*		CGATTCCTGC	ATTAGCAGCC	0		0	0	0	0	0
4225	2364	af	AN3828.1	58.m07804	AO070305000065	0			-231	-208			ATGTTTCCAAGCCTGGTCCGCTAA		ATGTTTCCAAGCCTGGTCCGCTAA		MFPSLVR*		MFPSLVR*		AGGAAAAGCC	AATTCTACTG	0		0	0	0	0	0
4226	2364	af	AN3828.1	58.m07804	AO070305000065	0			-153	-142			ATGAGGTCATGA		ATGAGGTCATGA		MRS*		MRS*		ACGCTTCTGA	TCCGTTCCAA	0		0	0	0	0	0
4227	2364	af	AN3828.1	58.m07804	AO070305000065	0			-145	-59			ATGATCCGTTCCAACGGTCAAGGCACACTTACTATGCCAAAAGACGGACAGTTTTCATCATACTACTTCAGCGCTACGTACAAGTGA		ATGATCCGTTCCAACGGTCAAGGCACACTTACTATGCCAAAAGACGGACAGTTTTCATCATACTACTTCAGCGCTACGTACAAGTGA		MIRSNGQGTLTMPKDGQFSSYYFSATYK*		MIRSNGQGTLTMPKDGQFSSYYFSATYK*		GAATGAGGTC	TTTATCAGTC	0		0	0	0	0	0
4228	2364	af	AN3828.1	58.m07804	AO070305000065	0			-112	-59			ATGCCAAAAGACGGACAGTTTTCATCATACTACTTCAGCGCTACGTACAAGTGA		ATGCCAAAAGACGGACAGTTTTCATCATACTACTTCAGCGCTACGTACAAGTGA		MPKDGQFSSYYFSATYK*		MPKDGQFSSYYFSATYK*		CACACTTACT	TTTATCAGTC	0		0	0	0	0	0
4220	2364	an	AN3828.1	58.m07804	AO070305000065	0	-218	-135					ATGCAAACTGAACAAACACATCTTTATCTTATCGTCAAGATTACAAAAAAATTACCGCGGATCATCTGCGAAGCAGGCATCTTAA	ATGCAAACTGAACAAACACATCTTTATCTTATCGTCAAGATTACAAAAAAATTACCGCGGATCATCTGCGAAGCAGGCATCTTAA			MQTEQTHLYLIVKITKNYRGSSAKQAS*	MQTEQTHLYLIVKITKNYRGSSAKQAS*			CAGTAATTAT	CCCAGCATCA	0		0	0	0	0	0
4221	2364	an	AN3828.1	58.m07804	AO070305000065	0	-103	-11					ATGGGTGCGGCTGCGAACTTATCCATGCTTCGCCAATTACCGTACATCCTAATACTATTTAGCCAGCGGCCGTTGATGTTCATACTCCCATGA	ATGGGTGCGGCTGCGAACTTATCCATGCTTCGCCAATTACCGTACATCCTAATACTATTTAGCCAGCGGCCGTTGATGTTCATACTCCCATGA			MGAAANLSMLRQLPYILILFSQRPLMFILP*	MGAAANLSMLRQLPYILILFSQRPLMFILP*			ACCTACCCAC	ATCTCGAGGC	0		0	0	0	0	0
4222	2364	an	AN3828.1	58.m07804	AO070305000065	0	-79	-11					ATGCTTCGCCAATTACCGTACATCCTAATACTATTTAGCCAGCGGCCGTTGATGTTCATACTCCCATGA	ATGCTTCGCCAATTACCGTACATCCTAATACTATTTAGCCAGCGGCCGTTGATGTTCATACTCCCATGA			MLRQLPYILILFSQRPLMFILP*	MLRQLPYILILFSQRPLMFILP*			GAACTTATCC	ATCTCGAGGC	0		0	0	0	0	0
4233	2367	af	AN8566.1	52.m03913	AO070307000099	0			-128	-72			ATGATTATAAGAGCAGTGATGTCTCTCTCTCATTTCTTTGTCAATCATCCTCCGTAG		ATGATTATAAGAGCAGTGATGTCTCTCTCTCATTTCTTTGTCAATCATCCTCCGTAG		MIIRAVMSLSHFFVNHPP*		MIIRAVMSLSHFFVNHPP*		ACATAGTGAA	ACAATTTACT	0	Q	0	0	NCU04072.1	0	0
4234	2367	af	AN8566.1	52.m03913	AO070307000099	0			-110	-72			ATGTCTCTCTCTCATTTCTTTGTCAATCATCCTCCGTAG		ATGTCTCTCTCTCATTTCTTTGTCAATCATCCTCCGTAG		MSLSHFFVNHPP*		MSLSHFFVNHPP*		AAGAGCAGTG	ACAATTTACT	0	Q	0	0	NCU04072.1	0	0
4230	2367	an	AN8566.1	52.m03913	AO070307000099	0	-144	-76					ATGTGGGCACGGTACTATGGCCCGTCCATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGA	ATGTGGGCACGGTACTATGGCCCGTCCATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGA			MWARYYGPSMGSRFICRHLQLP*	MWARYYGPSMGSRFICRHLQLP*			CTCAGTCGGC	ACGATATAAG	0	Q	0	0	NCU04072.1	0	0
4231	2367	an	AN8566.1	52.m03913	AO070307000099	0	-128	-9					ATGGCCCGTCCATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGAACGATATAAGGCCCGCCACTTCCCTCACGATGACCGTCCTTCTTCCATATCCTCACAGCTTCACTGA	ATGGCCCGTCCATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGAACGATATAAGGCCCGCCACTTCCCTCACGATGACCGTCCTTCTTCCATATCCTCACAGCTTCACTGA			MARPWVADSSAVTSSSLERYKARHFPHDDRPSSISSQLH*	MARPWVADSSAVTSSSLERYKARHFPHDDRPSSISSQLH*			GCACGGTACT	CCGCCAATAT	0	Q	0	0	NCU04072.1	0	0
4232	2367	an	AN8566.1	52.m03913	AO070307000099	0	-117	-76					ATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGA	ATGGGTAGCCGATTCATCTGCCGTCACCTCCAGCTCCCTTGA			MGSRFICRHLQLP*	MGSRFICRHLQLP*			TGGCCCGTCC	ACGATATAAG	0	Q	0	0	NCU04072.1	0	0
4235	2367	ao	AN8566.1	52.m03913	AO070307000099	0					-247	-173	ATGGACCAATCCAGTCGGCACCTCTCAACGGGATATTTTTGGTCCAACACGGTTGCCCACCCCCCACAAGGATGA			ATGGACCAATCCAGTCGGCACCTCTCAACGGGATATTTTTGGTCCAACACGGTTGCCCACCCCCCACAAGGATGA	MDQSSRHLSTGYFWSNTVAHPPQG*			MDQSSRHLSTGYFWSNTVAHPPQG*	ATAAAAAAAA	GGAGCCGAAA	0	Q	0	0	NCU04072.1	0	0
4236	2367	ao	AN8566.1	52.m03913	AO070307000099	0					-176	-108	ATGAGGAGCCGAAAAGATTTGCCGTCGGCATCCCTAACTATCCAGACTTGCCTGAGATCGTGTATATAG			ATGAGGAGCCGAAAAGATTTGCCGTCGGCATCCCTAACTATCCAGACTTGCCTGAGATCGTGTATATAG	MRSRKDLPSASLTIQTCLRSCI*			MRSRKDLPSASLTIQTCLRSCI*	CCCCACAAGG	ACCTTCGACG	0	Q	0	0	NCU04072.1	0	0
4238	2369	af	AN6307.1	72.m19327	AO070308000062	0			-168	-157			ATGTCCCGGTGA		ATGTCCCGGTGA		MSR*		MSR*		GAGCTCGCTG	CATTGAGCCC	0	U	FG07250.1	MG06367.1	0	0	0
4237	2369	an	AN6307.1	72.m19327	AO070308000062	0	-109	-92					ATGTCCCGGCGACATTGA	ATGTCCCGGCGACATTGA			MSRRH*	MSRRH*			AGTGCATTTA	TTGAGCGCTC	0	U	FG07250.1	MG06367.1	0	0	0
4239	2369	ao	AN6307.1	72.m19327	AO070308000062	0					-153	-142	ATGTCCCGGTGA			ATGTCCCGGTGA	MSR*			MSR*	GAGCTTGTGT	CATTCAACTA	0	U	FG07250.1	MG06367.1	0	0	0
4242	2370	af	AN6191.1	72.m19289	AO070308000110	0			-204	-160			ATGGCCGAGACCATTGCCCAGATCCTTAAGGCTCCAAGGCTCTAA		ATGGCCGAGACCATTGCCCAGATCCTTAAGGCTCCAAGGCTCTAA		MAETIAQILKAPRL*		MAETIAQILKAPRL*		GCGGAGATCG	GGCTACCGTA	0	H	0	0	0	YNR029C	0
4243	2370	af	AN6191.1	72.m19289	AO070308000110	0			-138	-64			ATGACCAGGGAAGCCCTGAGCCCTAAGTGCTGCCTCCGCTCTGAGAACAGACGTCATTCTTCCCCGCAGGATTAA		ATGACCAGGGAAGCCCTGAGCCCTAAGTGCTGCCTCCGCTCTGAGAACAGACGTCATTCTTCCCCGCAGGATTAA		MTREALSPKCCLRSENRRHSSPQD*		MTREALSPKCCLRSENRRHSSPQD*		CCAGAAGCCC	GGTACAGTGA	0	H	0	0	0	YNR029C	0
4240	2370	an	AN6191.1	72.m19289	AO070308000110	0	-225	-208					ATGGAGCTAGCTCCCTAG	ATGGAGCTAGCTCCCTAG			MELAP*	MELAP*			CTCCAACTGA	GTGAGTAAAG	0	H	0	0	0	YNR029C	0

4241	2370	an	AN6191.1	72.m19289	AO070308000110	0	-163	-92					ATGACCCTCACAGCCCTAGCCCTATCTCCTTCCCCTCTTGGTAACGTCATTGGTTTGCCCAGATCTAGGTGA	ATGACCCTCACAGCCCTAGCCCTATCTCCTTCCCCTCTTGGTAACGTCATTGGTTTGCCCAGATCTAGGTGA			MTLTALALSPSPLGNVIGLPRSR*	MTLTALALSPSPLGNVIGLPRSR*			TGAACGACCC	GGTCAAGAAC	0	H	0	0	0	YNR029C	0
4244	2370	ao	AN6191.1	72.m19289	AO070308000110	0					-167	-126	ATGACGGGACGGAGACGGAGATACCACCGGCGGAGCTCATGA			ATGACGGGACGGAGACGGAGATACCACCGGCGGAGCTCATGA	MTGRRRRYHRRSS*			MTGRRRRYHRRSS*	TCTGGAAGGA	CTAGTCAGTG	0	H	0	0	0	YNR029C	0
4245	2370	ao	AN6191.1	72.m19289	AO070308000110	0					-129	-103	ATGACTAGTCAGTGCCCTAAGCCCTAG			ATGACTAGTCAGTGCCCTAAGCCCTAG	MTSQCPKP*			MTSQCPKP*	GGCGGAGCTC	CTAATCCTCT	0	H	0	0	0	YNR029C	0
4247	2372	af	AN8002.1	53.m03844	AO070322000044	0			-269	-213			ATGCACAGAGATTGCTCCCGCAGCAGCACTGCACATTATTCTGCTGTCTCGCATTAG		ATGCACAGAGATTGCTCCCGCAGCAGCACTGCACATTATTCTGCTGTCTCGCATTAG		MHRDCSRSSTAHYSAVSH*		MHRDCSRSSTAHYSAVSH*		GCTGATGGTA	GGAATAATTA	0	DO	0	0	NCU01377.1	0	0
4248	2372	af	AN8002.1	53.m03844	AO070322000044	0			-186	-97			ATGTCACGAAAGCAGAAACCTGTCTGTGTCTTGCAAGCAAGTTGTCCGATTCCACAAGCGTTGGCCACTGTCTCCGCCGAATACAACTAA		ATGTCACGAAAGCAGAAACCTGTCTGTGTCTTGCAAGCAAGTTGTCCGATTCCACAAGCGTTGGCCACTGTCTCCGCCGAATACAACTAA		MSRKQKPVCVLQASCPIPQALATVSAEYN*		MSRKQKPVCVLQASCPIPQALATVSAEYN*		AAGGAGACAT	ACGCTTTTGC	0	DO	0	0	NCU01377.1	0	0
4249	2372	af	AN8002.1	53.m03844	AO070322000044	0			-77	-21			ATGCGCTTCTGCCCTCGCGGTGGTTCTCAGTACTCTCGTGCCTCGATTGACTCTTAG		ATGCGCTTCTGCCCTCGCGGTGGTTCTCAGTACTCTCGTGCCTCGATTGACTCTTAG		MRFCPRGGSQYSRASIDS*		MRFCPRGGSQYSRASIDS*		CTCACCCTCC	TCTACGGTCT	0	DO	0	0	NCU01377.1	0	0
4246	2372	an	AN8002.1	53.m03844	AO070322000044	0	-63	-46					ATGCCGCTCAGCCTCTAG	ATGCCGCTCAGCCTCTAG			MPLSL*	MPLSL*			GCGCTCGCCC	AACCTCGCCA	0	DO	0	0	NCU01377.1	0	0
4250	2372	ao	AN8002.1	53.m03844	AO070322000044	0					-290	-264	ATGCAATTCCGCGGATCGCATCCATAG			ATGCAATTCCGCGGATCGCATCCATAG	MQFRGSHP*			MQFRGSHP*	ACAGTCAAAC	ATTCCAATCT	0	DO	0	0	NCU01377.1	0	0
4251	2372	ao	AN8002.1	53.m03844	AO070322000044	0					-107	-42	ATGCGCCTAATCTTTATCGCCCCTCCGGACCCCATGCCTCACTGCAACAACTCCGAGCTTCCCTAA			ATGCGCCTAATCTTTATCGCCCCTCCGGACCCCATGCCTCACTGCAACAACTCCGAGCTTCCCTAA	MRLIFIAPPDPMPHCNNSELP*			MRLIFIAPPDPMPHCNNSELP*	GAACCAACGA	TCCCTTTTGC	0	DO	0	0	NCU01377.1	0	0
4252	2372	ao	AN8002.1	53.m03844	AO070322000044	0					-74	-42	ATGCCTCACTGCAACAACTCCGAGCTTCCCTAA			ATGCCTCACTGCAACAACTCCGAGCTTCCCTAA	MPHCNNSELP*			MPHCNNSELP*	TCCGGACCCC	TCCCTTTTGC	0	DO	0	0	NCU01377.1	0	0
4256	2373	af	AN1772.1	69.m15064	AO070324000030	0			-158	-126			ATGCTCCTACCAGTGAATTACCCCACGGGGTAG		ATGCTCCTACCAGTGAATTACCCCACGGGGTAG		MLLPVNYPTG*		MLLPVNYPTG*		CTTGGGGGAG	ATTTGTGGGG	0		0	0	0	0	0
4253	2373	an	AN1772.1	69.m15064	AO070324000030	0	-213	-184					ATGCTGGTGTCAAATATGGAGCGGGATTAA	ATGCTGGTGTCAAATATGGAGCGGGATTAA			MLVSNMERD*	MLVSNMERD*			ATGCTTCACA	TTTGCAAAAT	0		0	0	0	0	0
4254	2373	an	AN1772.1	69.m15064	AO070324000030	0	-198	-184					ATGGAGCGGGATTAA	ATGGAGCGGGATTAA			MERD*	MERD*			GGTGTCAAAT	TTTGCAAAAT	0		0	0	0	0	0
4255	2373	an	AN1772.1	69.m15064	AO070324000030	0	-161	-105					ATGATTAGGCTGATCTCTGGGTACGGCCGTTGGTTCTTCCCGAGGAGAACCGAGTGA	ATGATTAGGCTGATCTCTGGGTACGGCCGTTGGTTCTTCCCGAGGAGAACCGAGTGA			MIRLISGYGRWFFPRRTE*	MIRLISGYGRWFFPRRTE*			ATCACGAATC	TATAAGAACT	0		0	0	0	0	0
4257	2373	ao	AN1772.1	69.m15064	AO070324000030	0					-154	-122	ATGTACCGACGGATTGAAAGTTTGAAACGCTAA			ATGTACCGACGGATTGAAAGTTTGAAACGCTAA	MYRRIESLKR*			MYRRIESLKR*	TCCGATCTTC	ATGACATGTT	0		0	0	0	0	0
4258	2373	ao	AN1772.1	69.m15064	AO070324000030	0					-121	-23	ATGACATGTTCCTTAGTACTGTCAGCAGTCTCCGGTATCTCCGAGGCAGCTACATATATAAAGTCACCAAGCTCACGGCAGAGGAAAATGTCTCCGTGA			ATGACATGTTCCTTAGTACTGTCAGCAGTCTCCGGTATCTCCGAGGCAGCTACATATATAAAGTCACCAAGCTCACGGCAGAGGAAAATGTCTCCGTGA	MTCSLVLSAVSGISEAATYIKSPSSRQRKMSP*			MTCSLVLSAVSGISEAATYIKSPSSRQRKMSP*	GAAACGCTAA	ACAACAACCA	0		0	0	0	0	0
4260	2374	an	AN6618.1	62.m03214	AO070326000068	0	-177	-145					ATGGTTGGTGTTCGCGTTAGACCCCGCCATTGA	ATGGTTGGTGTTCGCGTTAGACCCCGCCATTGA			MVGVRVRPRH*	MVGVRVRPRH*			CGAAGATCAC	TCTAATCTAT	0	T	0	0	0	0	0
4263	2374	ao	AN6618.1	62.m03214	AO070326000068	0					-221	-195	ATGGGTGGAGATCACATGCAGCCGTGA			ATGGGTGGAGATCACATGCAGCCGTGA	MGGDHMQP*			MGGDHMQP*	TGGCAGTTTC	TCAGGTGGAT	0	T	0	0	0	0	0
4264	2374	ao	AN6618.1	62.m03214	AO070326000068	0					-206	-195	ATGCAGCCGTGA			ATGCAGCCGTGA	MQP*			MQP*	TGGAGATCAC	TCAGGTGGAT	0	T	0	0	0	0	0
4265	2374	ao	AN6618.1	62.m03214	AO070326000068	0					-77	-60	ATGAACTGTCTTTCCTGA			ATGAACTGTCTTTCCTGA	MNCLS*			MNCLS*	ACGGAGAACG	GTCATTTGAA	0	T	0	0	0	0	0
4267	2375	af	AN8064.1	53.m03915	AO070330000020	0			-232	-209			ATGTCATCACCAGATGAGGCCTAA		ATGTCATCACCAGATGAGGCCTAA		MSSPDEA*		MSSPDEA*		GTGCCCATTC	ACCCAACTAA	0	L	0	0	0	0	0
4268	2375	af	AN8064.1	53.m03915	AO070330000020	0			-219	-199			ATGAGGCCTAAACCCAACTAA		ATGAGGCCTAAACCCAACTAA		MRPKPN*		MRPKPN*		TCATCACCAG	GGCAAACCAT	0	L	0	0	0	0	0
4269	2375	af	AN8064.1	53.m03915	AO070330000020	0			-171	-37			ATGATTTTCCGGCTCCGAAACCCTTTACGCGCTGGCGGAGTTCGGACGCGTTTAAGCTTCATTTTTTTTTTTAAAAAAAAAGAGTACCATTTACAGAACATTAGAAAGCATTGTTTTAGCCTTTGTTCCTGTTGA		ATGATTTTCCGGCTCCGAAACCCTTTACGCGCTGGCGGAGTTCGGACGCGTTTAAGCTTCATTTTTTTTTTTTAAAAAAAAAGAGTACCATTTACAGAACATTAGAAAGCATTGTTTTAGCCTTTGTTCCTGTTGA		MIFRLRNPLRAGGVRTRLSFIFFFKKKEYHLQNIRKHCFSLCSC*		MIFRLRNPLRAGGVRTRLSFIFFFKKKEYHLQNIRKHCFSLCSC*		CTGCCTCCCC	GCCCACCGAC	0	L	0	0	0	0	0
4266	2375	an	AN8064.1	53.m03915	AO070330000020	0	-209	-108					ATGTCATCACCGCCGCAGCAACAACAGAGAGGCCTCAGGGCTTGGCACCCAGCTCCGCAGATTTTCCGACGCCGAACCTCTTTACGCGCTGCGGCATCCTGA	ATGTCATCACCGCCGCAGCAACAACAGAGAGGCCTCAGGGCTTGGCACCCAGCTCCGCAGATTTTCCGACGCCGAACCTCTTTACGCGCTGCGGCATCCTGA			MSSPPQQQRGLRAWHPAPQIFRRRTSLRAAAS*	MSSPPQQQRGLRAWHPAPQIFRRRTSLRAAAS*			AGGAGGCCGC	CGCGTCGAAA	0	L	0	0	0	0	0
4270	2375	ao	AN8064.1	53.m03915	AO070330000020	0					-203	-174	ATGTCATCACCTATAGGGCTGAGCTCCTGA			ATGTCATCACCTATAGGGCTGAGCTCCTGA	MSSPIGLSS*			MSSPIGLSS*	CGGGAGGTGC	AGCAATGAAA	0	L	0	0	0	0	0
4271	2375	ao	AN8064.1	53.m03915	AO070330000020	0					-164	-120	ATGATTTTCCGGCGCCGAACCTCTTTACGCGCGGGTGTGTTTTGA			ATGATTTTCCGGCGCCGAACCTCTTTACGCGCGGGTGTGTTTTGA	MIFRRRTSLRAGVF*			MIFRRRTSLRAGVF*	AAGCAATGAA	CGCGTCTTGC	0	L	0	0	0	0	0
4275	2377	af	AN0484.1	69.m15370	AO070336000183	0			-205	-122			ATGGTGGGCCTTATCAGTGGAAATTGCCGTGCAGGGGGGGGGGGGTTGGGTTTAGGTACTGCTGCCATGCGAACTGGGGAGTGA		ATGGTGGGCCTTATCAGTGGAAATTGCCGTGCAGGGGGGGGGGGTTGGGTTTAGGTACTGCTGCCATGCGAACTGGGGAGTGA		MVGLISGNCRAGGGGLGLGTAAMRTGE*		MVGLISGNCRAGGGGLGLGTAAMRTGE*		TGTGCACGGG	ACGGTTTTTC	0		0	0	0	0	0
4273	2377	an	AN0484.1	69.m15370	AO070336000183	0	-108	-88					ATGGAGATAAGTATGTGCTAG	ATGGAGATAAGTATGTGCTAG			MEISMC*	MEISMC*			AAGGCGGGCC	CTAGCCGGCA	0		0	0	0	0	0
4274	2377	an	AN0484.1	69.m15370	AO070336000183	0	-63	-46					ATGGCCCTCGATTTTTGA	ATGGCCCTCGATTTTTGA			MALDF*	MALDF*			TACCGCGACG	GTGAGCTCAG	0		0	0	0	0	0
4280	2379	af	AN0249.1	54.m06702	AO070338000242	0			-202	-125			ATGATGCAAACAATTCATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		ATGATGCAAACAATTCATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		MMQTIHERIFSFPHAMAYSATALFT*		MMQTIHERIFSFPHAMAYSATALFT*		CAGCTCCGCC	TCTCTTAATT	0		0	0	0	0	0
4281	2379	af	AN0249.1	54.m06702	AO070338000242	0			-199	-125			ATGCAAACAATTCATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		ATGCAAACAATTCATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		MQTIHERIFSFPHAMAYSATALFT*		MQTIHERIFSFPHAMAYSATALFT*		CTCCGCCATG	TCTCTTAATT	0		0	0	0	0	0
4282	2379	af	AN0249.1	54.m06702	AO070338000242	0			-186	-109			ATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAGTCTCTTAATTGACTAG		ATGAACGCATCTTCAGCTTCCCCCACGCTATGGCGTATTCGGCTACAGCTTTGTTTACTTAGTCTCTTAATTGACTAG		MNASSASPTLWRIRLQLCLLSLLID*		MNASSASPTLWRIRLQLCLLSLLID*		CAAACAATTC	CATGCTCGCA	0		0	0	0	0	0
4283	2379	af	AN0249.1	54.m06702	AO070338000242	0			-157	-125			ATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		ATGGCGTATTCGGCTACAGCTTTGTTTACTTAG		MAYSATALFT*		MAYSATALFT*		CCCCCACGCT	TCTCTTAATT	0		0	0	0	0	0
4284	2379	af	AN0249.1	54.m06702	AO070338000242	0			-107	-27			ATGCTCGCATTACCATCGGAGCCTACTAGCGACAATTTCTCGTCGTCTGTTCTTCTGGTGATGACCTTTAATTGCTGCTAG		ATGCTCGCATTACCATCGGAGCCTACTAGCGACAATTTCTCGTCGTCTGTTCTTCTGGTGATGACCTTTAATTGCTGCTAG		MLALPSEPTSDNFSSSVLLVMTFNCC*		MLALPSEPTSDNFSSSVLLVMTFNCC*		ATTGACTAGC	ATACTCTCCC	0		0	0	0	0	0
4279	2379	an	AN0249.1	54.m06702	AO070338000242	0	-157	-86					ATGTATTCACTTTTTATATTTCACTTTCTGGACCATCACTTCGTTGGGTTCACTGCCCACGGACTCGGATGA	ATGTATTCACTTTTTATATTTCACTTTCTGGACCATCACTTCGTTGGGTTCACTGCCCACGGACTCGGATGA			MYSLFIFHFLDHHFVGFTAHGLG*	MYSLFIFHFLDHHFVGFTAHGLG*			TATCTCCCGC	GTTGTCAACA	0		0	0	0	0	0
4287	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-203	-21	ATGATACAAAACTGCGACGTGGGGGTGCAGTCATGTCACCCCCATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGAGAAGTTACTAACTCAGGATTGTCTCGCTTATACGTATGAAAATGAACTTGCATTTTCTCTATGCTTGACTCTCCTCTGCGCTCGTGAACAGAAGCTCTAG			ATGATACAAAACTGCGACGTGGGGGTGCAGTCATGTCACCCCCATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGAGAAGTTACTAACTCAGGATTGTCTCGCTTATACGTATGAAAATGAACTTGCATTTTCTCTATGCTTGACTCTCCTCTGCGCTCGTGAACAGAAGCTCTAG	MIQNCDVGVQSCHPHALSETLRLSGELEKLLTQDCLAYTYENELAFSLCLTLLCAREQKL*			MIQNCDVGVQSCHPHALSETLRLSGELEKLLTQDCLAYTYENELAFSLCLTLLCAREQKL*	CCCTTACTTA	AGCCCACCCC	0		0	0	0	0	0
4288	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-171	-121	ATGTCACCCCCATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGA			ATGTCACCCCCATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGA	MSPPCPLRNPSPFRGT*			MSPPCPLRNPSPFRGT*	GGGTGCAGTC	GAAGTTACTA	0		0	0	0	0	0
4289	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-160	-110	ATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGAGAAGTTACTAA			ATGCCCTCTCAGAAACCCTTCGCCTTTCAGGGGAACTTGAGAAGTTACTAA	MPSQKPFAFQGNLRSY*			MPSQKPFAFQGNLRSY*	TGTCACCCCC	CTCAGGATTG	0		0	0	0	0	0
4290	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-85	-53	ATGAAAATGAACTTGCATTTTCTCTATGCTTGA			ATGAAAATGAACTTGCATTTTCTCTATGCTTGA	MKMNLHFLYA*			MKMNLHFLYA*	GCTTATACGT	CTCTCCTCTG	0		0	0	0	0	0
4291	2379	ao	AN0249.1	54.m06702	AO070338000242	0					-79	-53	ATGAACTTGCATTTTCTCTATGCTTGA			ATGAACTTGCATTTTCTCTATGCTTGA	MNLHFLYA*			MNLHFLYA*	ACGTATGAAA	CTCTCCTCTG	0		0	0	0	0	0
4293	2380	af	AN6703.1	65.m07276	AO070339000139	0			-219	-199			ATGATTCCCCAGATGGAATAA		ATGATTCCCCAGATGGAATAA		MIPQME*		MIPQME*		AGGTAGTATT	CCGGGGTGAG	0	GEPR	0	0	0	0	0
4294	2380	ao	AN6703.1	65.m07276	AO070339000139	0					-251	-219	ATGGAAAGGAAATTCTGCGGGGCCCCTCCTTAG			ATGGAAAGGAAATTCTGCGGGGCCCCTCCTTAG	MERKFCGAPP*			MERKFCGAPP*	GGTGACAAGG	CAGTATTTTG	0	GEPR	0	0	0	0	0
4295	2381	af	AN6170.1	72.m19001	AO070340000032	0			-119	-93			ATGAGCCATACCCCTGCTTTGGAATAA		ATGAGCCATACCCCTGCTTTGGAATAA		MSHTPALE*		MSHTPALE*		TTCTTACTTC	CAATACACCA	0	O	0	0	0	0	0
4296	2381	ao	AN6170.1	72.m19001	AO070340000032	0					-203	-177	ATGGACTGTTCGAATCTGCTGCTATAA			ATGGACTGTTCGAATCTGCTGCTATAA	MDCSNLLL*			MDCSNLLL*	CGTATATTTT	TTCAAAAAGC	0	O	0	0	0	0	0
4305	2383	af	AN3711.1	69.m15416	AO070341000337	0			-426	-325			ATGGCTAGCATTACTTCAGCATCCCTTCTCTCGGAGGCTGAGTTCGGTTGCGGTAAGCAGGCATCATCACGACGCGATCCTCGCTATAGATCTTCAAACTGA		ATGGCTAGCATTACTTCAGCATCCCTTCTCTCGGAGGCTGAGTTCGGTTGCGGTAAGCAGGCATCATCACGACGCGATCCTCGCTATAGATCTTCAAACTGA		MASITSASLLSEAEFGCGKQASSRRDPRYRSSN*		MASITSASLLSEAEFGCGKQASSRRDPRYRSSN*		CTTCGGCATC	CTCGTAGTAA	0	O	0	0	0	0	0
4297	2383	an	AN3711.1	69.m15416	AO070341000337	0	-372	-235					ATGGCGACCGTTGCTTCGGTTTCCCTCCTTTCGGAGGCCGAGTTCGGTTGCGGTATGGACACCATATGGGCATTACCATCTTCTTTTGGAGCTAACACAGACCAAAGAACACCTAGCATCTCAGCTCATGCACGATAG	ATGGCGACCGTTGCTTCGGTTTCCCTCCTTTCGGAGGCCGAGTTCGGTTGCGGTATGGACACCATATGGGCATTACCATCTTCTTTTGGAGCTAACACAGACCAAAGAACACCTAGCATCTCAGCTCATGCACGATAG			MATVASVSLLSEAEFGCGMDTIWALPSSFGANTDQRTPSISAHAR*	MATVASVSLLSEAEFGCGMDTIWALPSSFGANTDQRTPSISAHAR*			CGCTTCTACT	CGCCGCTAGC	0	O	0	0	0	0	0
4298	2383	an	AN3711.1	69.m15416	AO070341000337	0	-318	-235					ATGGACACCATATGGGCATTACCATCTTCTTTTGGAGCTAACACAGACCAAAGAACACCTAGCATCTCAGCTCATGCACGATAG	ATGGACACCATATGGGCATTACCATCTTCTTTTGGAGCTAACACAGACCAAAGAACACCTAGCATCTCAGCTCATGCACGATAG			MDTIWALPSSFGANTDQRTPSISAHAR*	MDTIWALPSSFGANTDQRTPSISAHAR*			CGGTTGCGGT	CGCCGCTAGC	0	O	0	0	0	0	0
4299	2383	an	AN3711.1	69.m15416	AO070341000337	0	-307	-278					ATGGGCATTACCATCTTCTTTTGGAGCTAA	ATGGGCATTACCATCTTCTTTTGGAGCTAA			MGITIFFWS*	MGITIFFWS*			TGGACACCAT	CACAGACCAA	0	O	0	0	0	0	0
4300	2383	an	AN3711.1	69.m15416	AO070341000337	0	-245	-45					ATGCACGATAGCGCCGCTAGCAACCAGTTCAAGGCATCCTTCATCAAGACGCACAATGCTCTCGGACGGCGCGATATATTCAATTCAAATCCGTCAAGTTATTTGAAGCCGAAGTATACATGTTTAACCTGCTCTGAGCCGTGTATGAATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGA	ATGCACGATAGCGCCGCTAGCAACCAGTTCAAGGCATCCTTCATCAAGACGCACAATGCTCTCGGACGGCGCGATATATTCAATTCAAATCCGTCAAGTTATTTGAAGCCGAAGTATACATGTTTAACCTGCTCTGAGCCGTGTATGAATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGA			MHDSAASNQFKASFIKTHNALGRRDIFNSNPSSYLKPKYTCLTCSEPCMNGDRKSHTENTGHQFCK*	MHDSAASNQFKASFIKTHNALGRRDIFNSNPSSYLKPKYTCLTCSEPCMNGDRKSHTENTGHQFCK*			ATCTCAGCTC	AAGGTATTGA	0	O	0	0	0	0	0
4303	2383	an	AN3711.1	69.m15416	AO070341000337	0	-101	-45					ATGAATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGA	ATGAATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGA			MNGDRKSHTENTGHQFCK*	MNGDRKSHTENTGHQFCK*			TGAGCCGTGT	AAGGTATTGA	0	O	0	0	0	0	0
4304	2383	an	AN3711.1	69.m15416	AO070341000337	0	-97	-35					ATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGAAAGGTATTGA	ATGGCGACCGGAAGTCACACACAGAAAACACTGGTCATCAATTCTGTAAGTGAAAGGTATTGA			MATGSHTQKTLVINSVSERY*	MATGSHTQKTLVINSVSERY*			CCGTGTATGA	TTTGGCACCG	0	O	0	0	0	0	0
4308	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-676	-608	ATGGCTAGTGTGGCTTGTGTGTCGCTCCTCTCCGAGGCTGAGTTTGGTTGCGGTATGCGGTCACCTTGA			ATGGCTAGTGTGGCTTGTGTGTCGCTCCTCTCCGAGGCTGAGTTTGGTTGCGGTATGCGGTCACCTTGA	MASVACVSLLSEAEFGCGMRSP*			MASVACVSLLSEAEFGCGMRSP*	CCACCTCGCA	AAGCTCCTAG	0	O	0	0	0	0	0
4309	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-622	-608	ATGCGGTCACCTTGA			ATGCGGTCACCTTGA	MRSP*			MRSP*	TGGTTGCGGT	AAGCTCCTAG	0	O	0	0	0	0	0

4310	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-585	-322	ATGCTAACTTGCCTGGAAGAGCATCTTACGGCGCAGCTTTCCCAGGACGGAGGCGCGGGTGACCAGTTTAAGGCATCTTTCATCAAGACACATAATGCTTTGGCTCCTCGCTCCAGATCCGGGGAATCGGCTACTACACAAAAAGGCCTACGTACAACTAGCTTTTTAAAACCAAAGTACATGTGCTTGACCTGCTCCGAGTCATTCATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG			ATGCTAACTTGCCTGGAAGAGCATCTTACGGCGCAGCTTTCCCAGGACGGAGGCGCGGGTGACCAGTTTAAGGCATCTTTCATCAAGACACATAATGCTTTGGCTCCTCGCTCCAGATCCGGGGAATCGGCTACTACACAAAAAGGCCTACGTACAACTAGCTTTTTAAAACCAAAGTACATGTGCTTGACCTGCTCCGAGTCATTCATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG	MLTCLEEHLTAQLSQDGGAGDQFKASFIKTHNALAPRSRSGESATTQKGLRTTSFLKPKYMCLTCSESFMNGDRKAHTGKTGHQFCE*			MLTCLEEHLTAQLSQDGGAGDQFKASFIKTHNALAPRSRSGESATTQKGLRTTSFLKPKYMCLTCSESFMNGDRKAHTGKTGHQFCE*	CTTGTCTTCA	GCCAAATTCG	0	O	0	0	0	0	0
4312	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-405	-322	ATGTGCTTGACCTGCTCCGAGTCATTCATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG			ATGTGCTTGACCTGCTCCGAGTCATTCATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG	MCLTCSESFMNGDRKAHTGKTGHQFCE*			MCLTCSESFMNGDRKAHTGKTGHQFCE*	ACCAAAGTAC	GCCAAATTCG	0	O	0	0	0	0	0
4313	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-378	-322	ATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG			ATGAATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAG	MNGDRKAHTGKTGHQFCE*			MNGDRKAHTGKTGHQFCE*	CGAGTCATTC	GCCAAATTCG	0	O	0	0	0	0	0
4314	2383	ao	AN3711.1	69.m15416	AO070341000337	0					-374	-309	ATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAGGCCAAATTCGTGA			ATGGCGACCGAAAGGCCCATACAGGAAAGACCGGTCATCAATTCTGTGAGTAGGCCAAATTCGTGA	MATERPIQERPVINSVSRPNS*			MATERPIQERPVINSVSRPNS*	TCATTCATGA	CCAAAGCCAT	0	O	0	0	0	0	0
4316	2384	af	AN5498.1	69.m15455	AO070341000387	0			-228	-88			ATGGCTTTCGAAAACTATCAGTCGCAATCACTTCCTCCCTTCCCCAACACACTGCATCTGTCCTCTGCGTCTTTACCGTATGACGACTCAAACTTAATTAGTGAAGTTACTGATCCATTTATATGCTCGAGAGCAGCTTAA		ATGGCTTTCGAAAACTATCAGTCGCAATCACTTCCTCCCTTCCCCAACACACTGCATCTGTCCTCTGCGTCTTTACCGTATGACGACTCAAACTTAATTAGTGAAGTTACTGATCCATTTATATGCTCGAGAGCAGCTTAA		MAFENYQSQSLPPFPNTLHLSSASLPYDDSNLISEVTDPFICSRAA*		MAFENYQSQSLPPFPNTLHLSSASLPYDDSNLISEVTDPFICSRAA*		GCTACTGATT	AATAAGATCT	0	K	FG08619.1	0	NCU03909.1	0	0
4317	2384	af	AN5498.1	69.m15455	AO070341000387	0			-149	-132			ATGACGACTCAAACTTAA		ATGACGACTCAAACTTAA		MTTQT*		MTTQT*		TCTTTACCGT	TTAGTGAAGT	0	K	FG08619.1	0	NCU03909.1	0	0
4318	2384	af	AN5498.1	69.m15455	AO070341000387	0			-106	-83			ATGCTCGAGAGCAGCTTAAAATAA		ATGCTCGAGAGCAGCTTAAAATAA		MLESSLK*		MLESSLK*		ATCCATTTAT	GATCTCCCTG	0	K	FG08619.1	0	NCU03909.1	0	0
4315	2384	an	AN5498.1	69.m15455	AO070341000387	0	-129	-106					ATGATAACCTCAGATCCCGCATAG	ATGATAACCTCAGATCCCGCATAG			MITSDPA*	MITSDPA*			CTAATATCAC	GGTCCGCACA	0	K	FG08619.1	0	NCU03909.1	0	0
4319	2384	ao	AN5498.1	69.m15455	AO070341000387	0					-280	-134	ATGAACAGGAGGCTATGGCTACAGCAGCAAAGAACAGCGCATTACCAAGCCCAACAAAGGCTGCTGACAGCCTACTCGGTGCGCCATACTCCAGGGAAGACTTGCATATCTCTAGGTGGCTGTATTTCTCTTTGGACTTTCGAATGA			ATGAACAGGAGGCTATGGCTACAGCAGCAAAGAACAGCGCATTACCAAGCCCAACAAAGGCTGCTGACAGCCTACTCGGTGCGCCATACTCCAGGGAAGACTTGCATATCTCTAGGTGGCTGTATTTCTCTTTGGACTTTCGAATGA	MNRRLWLQQQRTAHYQAQQRLLTAYSVRHTPGKTCISLGGCISLWTFE*			MNRRLWLQQQRTAHYQAQQRLLTAYSVRHTPGKTCISLGGCISLWTFE*	GTTACTCCGG	GCTTGTGCGA	0	K	FG08619.1	0	NCU03909.1	0	0
4320	2384	ao	AN5498.1	69.m15455	AO070341000387	0					-266	-93	ATGGCTACAGCAGCAAAGAACAGCGCATTACCAAGCCCAACAAAGGCTGCTGACAGCCTACTCGGTGCGCCATACTCCAGGGAAGACTTGCATATCTCTAGGTGGCTGTATTTCTCTTTGGACTTTCGAATGAGCTTGTGCGACCTCTACTTGAGCTCTGTTTGGCTCCGGTGA			ATGGCTACAGCAGCAAAGAACAGCGCATTACCAAGCCCAACAAAGGCTGCTGACAGCCTACTCGGTGCGCCATACTCCAGGGAAGACTTGCATATCTCTAGGTGGCTGTATTTCTCTTTGGACTTTCGAATGAGCTTGTGCGACCTCTACTTGAGCTCTGTTTGGCTCCGGTGA	MATAAKNSALPSPTKAADSLLGAPYSREDLHISRWLYFSLDFRMSLCDLYLSSVWLR*			MATAAKNSALPSPTKAADSLLGAPYSREDLHISRWLYFSLDFRMSLCDLYLSSVWLR*	ACAGGAGGCT	GCCAAGCCTT	0	K	FG08619.1	0	NCU03909.1	0	0
4321	2384	ao	AN5498.1	69.m15455	AO070341000387	0					-137	-93	ATGAGCTTGTGCGACCTCTACTTGAGCTCTGTTTGGCTCCGGTGA			ATGAGCTTGTGCGACCTCTACTTGAGCTCTGTTTGGCTCCGGTGA	MSLCDLYLSSVWLR*			MSLCDLYLSSVWLR*	GGACTTTCGA	GCCAAGCCTT	0	K	FG08619.1	0	NCU03909.1	0	0
4322	2387	af	AN2166.1	72.m19674	AO070343000226	0			-186	-160			ATGTACTCAAAACAAGGTAGTATTTGA		ATGTACTCAAAACAAGGTAGTATTTGA		MYSKQGSI*		MYSKQGSI*		GTAGGGTGGC	CATACTACAT	0		0	0	0	0	0
4323	2387	af	AN2166.1	72.m19674	AO070343000226	0			-140	-123			ATGGAAATCATACCATGA		ATGGAAATCATACCATGA		MEIIP*		MEIIP*		TTGTTTGATA	GCCTGCGCAT	0		0	0	0	0	0
4324	2387	af	AN2166.1	72.m19674	AO070343000226	0			-126	-85			ATGAGCCTGCGCATGCAGTCTCCAACAACACATATAAGCTGA		ATGAGCCTGCGCATGCAGTCTCCAACAACACATATAAGCTGA		MSLRMQSPTTHIS*		MSLRMQSPTTHIS*		AAATCATACC	TTGCTCAACC	0		0	0	0	0	0
4325	2387	af	AN2166.1	72.m19674	AO070343000226	0			-114	-85			ATGCAGTCTCCAACAACACATATAAGCTGA		ATGCAGTCTCCAACAACACATATAAGCTGA		MQSPTTHIS*		MQSPTTHIS*		GAGCCTGCGC	TTGCTCAACC	0		0	0	0	0	0
4326	2387	ao	AN2166.1	72.m19674	AO070343000226	0					-272	-216	ATGGGGCTTGTTCCCGACGTAGTATTCGGTATACGACATTGTTGGGTAATAGATTGA			ATGGGGCTTGTTCCCGACGTAGTATTCGGTATACGACATTGTTGGGTAATAGATTGA	MGLVPDVVFGIRHCWVID*			MGLVPDVVFGIRHCWVID*	CCTGGGTAGT	AGTTGTATGG	0		0	0	0	0	0
4327	2387	ao	AN2166.1	72.m19674	AO070343000226	0					-209	-93	ATGGATGCTACACAAATCCATTGTTGTTGTTCTGAATGGAGTATAAAAATTTGTTTCCTCTCTGGCTTTTCGCATGAACTTTTTTTTTCTCTTTCCCACTTCAACGTTCATCTTTAA			ATGGATGCTACACAAATCCATTGTTGTTGTTCTGAATGGAGTATAAAAATTTGTTTCCTCTCTGGCTTTTCGCATGAACTTTTTTTTTCTCTTTCCCACTTCAACGTTCATCTTTAA	MDATQIHCCCSEWSIKICFLSGFSHELFFSLSHFNVHL*			MDATQIHCCCSEWSIKICFLSGFSHELFFSLSHFNVHL*	TTGAAGTTGT	TTGAACTCAT	0		0	0	0	0	0
4328	2387	ao	AN2166.1	72.m19674	AO070343000226	0					-205	-164	ATGCTACACAAATCCATTGTTGTTGTTCTGAATGGAGTATAA			ATGCTACACAAATCCATTGTTGTTGTTCTGAATGGAGTATAA	MLHKSIVVVLNGV*			MLHKSIVVVLNGV*	AGTTGTATGG	AAATTTGTTT	0		0	0	0	0	0
4329	2387	ao	AN2166.1	72.m19674	AO070343000226	0					-174	-133	ATGGAGTATAAAAATTTGTTTCCTCTCTGGCTTTTCGCATGA			ATGGAGTATAAAAATTTGTTTCCTCTCTGGCTTTTCGCATGA	MEYKNLFPLWLFA*			MEYKNLFPLWLFA*	GTTGTTCTGA	ACTTTTTTTT	0		0	0	0	0	0
4330	2387	ao	AN2166.1	72.m19674	AO070343000226	0					-136	-89	ATGAACTTTTTTTTTCTCTTTCCCACTTCAACGTTCATCTTTAATTGA			ATGAACTTTTTTTTTCTCTTTCCCACTTCAACGTTCATCTTTAATTGA	MNFFFLFPTSTFIFN*			MNFFFLFPTSTFIFN*	GGCTTTTCGC	ACTCATTATT	0		0	0	0	0	0
4331	2390	af	AN7440.1	57.m05911	AO070229000004	0			-230	-195			ATGCATACGCGCCGTGAGTTCGCGACAAGTTCCTAG		ATGCATACGCGCCGTGAGTTCGCGACAAGTTCCTAG		MHTRREFATSS*		MHTRREFATSS*		TGGTCCACAT	AAAGCTTTGG	0	BD	0	0	0	0	0
4332	2390	af	AN7440.1	57.m05911	AO070229000004	0			-124	-86			ATGTCGGCTTCGCAACTCCAGTTTCCCATTCTCATTTAG		ATGTCGGCTTCGCAACTCCAGTTTCCCATTCTCATTTAG		MSASQLQFPILI*		MSASQLQFPILI*		CGCGAAGCGG	ATGTGCTTCA	0	BD	0	0	0	0	0
4333	2390	af	AN7440.1	57.m05911	AO070229000004	0			-85	-44			ATGTGCTTCATTTTTCATTACTGGAAAAGTGCCTGCTGGTAA		ATGTGCTTCATTTTTCATTACTGGAAAAGTGCCTGCTGGTAA		MCFIFHYWKSACW*		MCFIFHYWKSACW*		TCTCATTTAG	TTCGAGACTA	0	BD	0	0	0	0	0
4334	2390	ao	AN7440.1	57.m05911	AO070229000004	0					-226	-137	ATGCCAAGAGATAGAACAACTATTTCCTTCTTTATCTTTTCGCGCTTGCACAACCCCTGGACCATTGTTCTTTTCTCTATTGGATCTTAA			ATGCCAAGAGATAGAACAACTATTTCCTTCTTTATCTTTTCGCGCTTGCACAACCCCTGGACCATTGTTCTTTTCTCTATTGGATCTTAA	MPRDRTTISFFIFSRLHNPWTIVLFSIGS*			MPRDRTTISFFIFSRLHNPWTIVLFSIGS*	CCGTCATCGA	TTCTTGTTTC	0	BD	0	0	0	0	0
4338	2391	af	AN5888.1	72.m19242	AO070245000019	0			-199	-98			ATGTCAATCACTCACCGCCATGTGAGCGGTCTCAAACAACCGGCAGAACCGGCATGGGAGCGTCGAGGGTGCAATGATGCCAGATTGCAATCCTTTGCCTAG		ATGTCAATCACTCACCGCCATGTGAGCGGTCTCAAACAACCGGCAGAACCGGCATGGGAGCGTCGAGGGTGCAATGATGCCAGATTGCAATCCTTTGCCTAG		MSITHRHVSGLKQPAEPAWERRGCNDARLQSFA*		MSITHRHVSGLKQPAEPAWERRGCNDARLQSFA*		TCAGCTAAGT	ATGCAATAAT	0	G	0	0	0	0	0
4339	2391	af	AN5888.1	72.m19242	AO070245000019	0			-146	-123			ATGGGAGCGTCGAGGGTGCAATGA		ATGGGAGCGTCGAGGGTGCAATGA		MGASRVQ*		MGASRVQ*		CAGAACCGGC	TGCCAGATTG	0	G	0	0	0	0	0
4340	2391	af	AN5888.1	72.m19242	AO070245000019	0			-126	-76			ATGATGCCAGATTGCAATCCTTTGCCTAGATGCAATAATGCCAGAGATTGA		ATGATGCCAGATTGCAATCCTTTGCCTAGATGCAATAATGCCAGAGATTGA		MMPDCNPLPRCNNARD*		MMPDCNPLPRCNNARD*		CGAGGGTGCA	TCCATTTTTG	0	G	0	0	0	0	0
4341	2391	af	AN5888.1	72.m19242	AO070245000019	0			-123	-76			ATGCCAGATTGCAATCCTTTGCCTAGATGCAATAATGCCAGAGATTGA		ATGCCAGATTGCAATCCTTTGCCTAGATGCAATAATGCCAGAGATTGA		MPDCNPLPRCNNARD*		MPDCNPLPRCNNARD*		GGGTGCAATG	TCCATTTTTG	0	G	0	0	0	0	0
4335	2391	an	AN5888.1	72.m19242	AO070245000019	0	-195	-142					ATGCTCTCGATACCGCCTTTACATTGCTTTGTATCCACCGGCAGAATCCAATGA	ATGCTCTCGATACCGCCTTTACATTGCTTTGTATCCACCGGCAGAATCCAATGA			MLSIPPLHCFVSTGRIQ*	MLSIPPLHCFVSTGRIQ*			TAAGGCGTAC	CAACGTAAGC	0	G	0	0	0	0	0
4336	2391	an	AN5888.1	72.m19242	AO070245000019	0	-145	-134					ATGACAACGTAA	ATGACAACGTAA			MTT*	MTT*			GCAGAATCCA	GCTCCGCGTA	0	G	0	0	0	0	0
4337	2391	an	AN5888.1	72.m19242	AO070245000019	0	-124	-74					ATGTATTTTGCGTATTTTTGCGTATACTTCGTTGAAGCCAGATTGCAGTAA	ATGTATTTTGCGTATTTTTGCGTATACTTCGTTGAAGCCAGATTGCAGTAA			MYFAYFCVYFVEARLQ*	MYFAYFCVYFVEARLQ*			AGCTCCGCGT	TTGGATCTCA	0	G	0	0	0	0	0
4342	2391	ao	AN5888.1	72.m19242	AO070245000019	0					-188	-129	ATGATCTTTGACTTTGACCTACCGCCAGAGATAAGCGGTCAAATTTATTTGGCAGAATGA			ATGATCTTTGACTTTGACCTACCGCCAGAGATAAGCGGTCAAATTTATTTGGCAGAATGA	MIFDFDLPPEISGQIYLAE*			MIFDFDLPPEISGQIYLAE*	AAAGTTGCGG	TGCTCATTAT	0	G	0	0	0	0	0
4343	2391	ao	AN5888.1	72.m19242	AO070245000019	0					-132	-76	ATGATGCTCATTATCGCCTTGAAGCCAGATTGCTTCTACAAGTGGTTCTCTCTATAG			ATGATGCTCATTATCGCCTTGAAGCCAGATTGCTTCTACAAGTGGTTCTCTCTATAG	MMLIIALKPDCFYKWFSL*			MMLIIALKPDCFYKWFSL*	ATTTGGCAGA	TTCCTTAGAC	0	G	0	0	0	0	0
4344	2391	ao	AN5888.1	72.m19242	AO070245000019	0					-129	-76	ATGCTCATTATCGCCTTGAAGCCAGATTGCTTCTACAAGTGGTTCTCTCTATAG			ATGCTCATTATCGCCTTGAAGCCAGATTGCTTCTACAAGTGGTTCTCTCTATAG	MLIIALKPDCFYKWFSL*			MLIIALKPDCFYKWFSL*	TGGCAGAATG	TTCCTTAGAC	0	G	0	0	0	0	0
4346	2392	af	AN4663.1	71.m15712	AO070250000002	0			-289	-266			ATGGATATTCGGCATTCTATCTGA		ATGGATATTCGGCATTCTATCTGA		MDIRHSI*		MDIRHSI*		CGGCCAGGCG	AAACAGGTCA	0	E	FG09525.1	MG01296.1	NCU04698.1	0	0
4347	2392	af	AN4663.1	71.m15712	AO070250000002	0			-117	-97			ATGCTATCATATTTGAAATAG		ATGCTATCATATTTGAAATAG		MLSYLK*		MLSYLK*		GTCGAGCGCA	CCAGGGCCTT	0	E	FG09525.1	MG01296.1	NCU04698.1	0	0
4345	2392	an	AN4663.1	71.m15712	AO070250000002	0	-63	-16					ATGTCCACGGTCCAACTGACACCTGTTAGGAGCTCTGTCTGCGCCTGA	ATGTCCACGGTCCAACTGACACCTGTTAGGAGCTCTGTCTGCGCCTGA			MSTVQLTPVRSSVCA*	MSTVQLTPVRSSVCA*			TCTCTACCTA	TCACCAAATA	0	E	FG09525.1	MG01296.1	NCU04698.1	0	0
4348	2392	ao	AN4663.1	71.m15712	AO070250000002	0					-241	-218	ATGGACTTTGAGCTTTCTATCTGA			ATGGACTTTGAGCTTTCTATCTGA	MDFELSI*			MDFELSI*	TGGCCGGAGT	GAAGCATCGG	0	E	FG09525.1	MG01296.1	NCU04698.1	0	0
4349	2394	an	AN3432.1	59.m09292	AO070265000009	0	-165	-127					ATGATGTTCCAAGTTGCGCGACGGGTAATTGCGGGGTAG	ATGATGTTCCAAGTTGCGCGACGGGTAATTGCGGGGTAG			MMFQVARRVIAG*	MMFQVARRVIAG*			GGATAAATTG	AAGCCCCTCC	0	G	FG06059.1	MG03853.1	NCU09705.1	YNR071C	0
4350	2394	an	AN3432.1	59.m09292	AO070265000009	0	-162	-127					ATGTTCCAAGTTGCGCGACGGGTAATTGCGGGGTAG	ATGTTCCAAGTTGCGCGACGGGTAATTGCGGGGTAG			MFQVARRVIAG*	MFQVARRVIAG*			TAAATTGATG	AAGCCCCTCC	0	G	FG06059.1	MG03853.1	NCU09705.1	YNR071C	0
4353	2394	ao	AN3432.1	59.m09292	AO070265000009	0					-128	-111	ATGCGGGGTACGGAGTAG			ATGCGGGGTACGGAGTAG	MRGTE*			MRGTE*	GGGACAGTCT	TGCCCCTCGT	0	G	FG06059.1	MG03853.1	NCU09705.1	YNR071C	0
4355	2396	af	AN6367.1	72.m19493	AO070279000053	0			-101	-15			ATGTACCAGAGGTACAAAGAGCAATCTTCGCGACGCTTCAAACATGTCACTCATAAGGCCCTCCTGGCCGATTATGCGATTAAGTAA		ATGTACCAGAGGTACAAAGAGCAATCTTCGCGACGCTTCAAACATGTCACTCATAAGGCCCTCCTGGCCGATTATGCGATTAAGTAA		MYQRYKEQSSRRFKHVTHKALLADYAIK*		MYQRYKEQSSRRFKHVTHKALLADYAIK*		GTTCCCGACA	ACAGCATTTT	0	T	0	0	0	0	0
4354	2396	an	AN6367.1	72.m19493	AO070279000053	0	-226	-119					ATGACTCAAGCCGGCAGTTCTTTGCCTGCATCGCCGTCCTGGTTGGGCGGTGAAGGTCACCTTCCCGTGACATTGTCAGGCCCTAGCCCTCTTTTCCGGAAAGGGTGA	ATGACTCAAGCCGGCAGTTCTTTGCCTGCATCGCCGTCCTGGTTGGGCGGTGAAGGTCACCTTCCCGTGACATTGTCAGGCCCTAGCCCTCTTTTCCGGAAAGGGTGA			MTQAGSSLPASPSWLGGEGHLPVTLSGPSPLFRKG*	MTQAGSSLPASPSWLGGEGHLPVTLSGPSPLFRKG*			TTCTCGTCCG	GCATAGAGAT	0	T	0	0	0	0	0
4356	2396	ao	AN6367.1	72.m19493	AO070279000053	0					-250	-218	ATGCGGCAGTTCTGTTTGCGCCCAGGGCGGTGA			ATGCGGCAGTTCTGTTTGCGCCCAGGGCGGTGA	MRQFCLRPGR*			MRQFCLRPGR*	CGTTGACTCA	GTGAGTCACT	0	T	0	0	0	0	0
4357	2396	ao	AN6367.1	72.m19493	AO070279000053	0					-195	-184	ATGATCACCTGA			ATGATCACCTGA	MIT*			MIT*	CAGTTCACAG	TTCAGCTACA	0	T	0	0	0	0	0

4358	2397	an	AN1103.1	70.m15129	AO070285000035	0	-208	-17					ATGGACTCTGGGATGCTCAGGGATCAGCCCCTAGACGGAAAGGGAAAGGCGGGATCACTAACACCCGGTAACTATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAGATTGA	ATGGACTCTGGGATGCTCAGGGATCAGCCCCTAGACGGAAAGGGAAAGGCGGGATCACTAACACCCGGTAACTATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAGATTGA			MDSGMLRDQPLDGKGKAGSLTPGNYENELWSLHILRATLPSLPTTSESLSKISHFYLARSKVD*	MDSGMLRDQPLDGKGKAGSLTPGNYENELWSLHILRATLPSLPTTSESLSKISHFYLARSKVD*			AAGCATCTTG	TAGTTCTACC	0	I	FG04103.1	MG05196.1	0	0	0
4359	2397	an	AN1103.1	70.m15129	AO070285000035	0	-196	-17					ATGCTCAGGGATCAGCCCCTAGACGGAAAGGGAAAGGCGGGATCACTAACACCCGGTAACTATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAGATTGA	ATGCTCAGGGATCAGCCCCTAGACGGAAAGGGAAAGGCGGGATCACTAACACCCGGTAACTATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAGATTGA			MLRDQPLDGKGKAGSLTPGNYENELWSLHILRATLPSLPTTSESLSKISHFYLARSKVD*	MLRDQPLDGKGKAGSLTPGNYENELWSLHILRATLPSLPTTSESLSKISHFYLARSKVD*			GGACTCTGGG	TAGTTCTACC	0	I	FG04103.1	MG05196.1	0	0	0
4360	2397	an	AN1103.1	70.m15129	AO070285000035	0	-135	-22					ATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAG	ATGAGAATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAG			MRMSCGPSIFSELLSPPCQPLLSLYRRFLTFTSQDPR*	MRMSCGPSIFSELLSPPCQPLLSLYRRFLTFTSQDPR*			CCCGGTAACT	ATTGATAGTT	0	I	FG04103.1	MG05196.1	0	0	0
4361	2397	an	AN1103.1	70.m15129	AO070285000035	0	-129	-22					ATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAG	ATGAGCTGTGGTCCCTCCATATTCTCCGAGCTACTCTCCCCTCCTTGCCAACCACTTCTGAGTCTTTATCGAAGATTTCTCACTTTTACCTCGCAAGATCCAAGGTAG			MSCGPSIFSELLSPPCQPLLSLYRRFLTFTSQDPR*	MSCGPSIFSELLSPPCQPLLSLYRRFLTFTSQDPR*			AACTATGAGA	ATTGATAGTT	0	I	FG04103.1	MG05196.1	0	0	0
4362	2397	ao	AN1103.1	70.m15129	AO070285000035	0					-211	-194	ATGTCCGGAAGTCACTGA			ATGTCCGGAAGTCACTGA	MSGSH*			MSGSH*	TTTAGCTACT	TCAGCTCAAT	0	I	FG04103.1	MG05196.1	0	0	0
4365	2398	af	AN1086.1	70.m15160	AO070285000086	0			-283	-110			ATGATTGCATTCCCCTCAGAACGGAGTTGCTCCGATACTGTGCCAGCCTCACTACCACTTTTGCCAGGTTTGGCTTTTGTTCTTTCCTTGGTCTCGTTTCGAAGCGTCGAAACCATCCAGCAAGACTCGACCGATCTTTCTTTCAGCAGGCCCGTGTCCGAGTTGTCCGAGTGA		ATGATTGCATTCCCCTCAGAACGGAGTTGCTCCGATACTGTGCCAGCCTCACTACCACTTTTGCCAGGTTTGGCTTTTGTTCTTTCCTTGGTCTCGTTTCGAAGCGTCGAAACCATCCAGCAAGACTCGACCGATCTTTCTTTCAGCAGGCCCGTGTCCGAGTTGTCCGAGTGA		MIAFPSERSCSDTVPASLPLLPGLAFVLSLVSFRSVETIQQDSTDLSFSRPVSELSE*		MIAFPSERSCSDTVPASLPLLPGLAFVLSLVSFRSVETIQQDSTDLSFSRPVSELSE*		TTGGTGGGGT	ACAAAATCAT	0	R	0	0	0	0	0
4363	2398	an	AN1086.1	70.m15160	AO070285000086	0	-199	-53					ATGTACGTCTCCGCTTGCTGGCGGACTTGCTCCGAACCGGACGTCCCCCACCTGGCTCCGATTCTCATGCATTATTTAGTTGCGGGACATGTGGACGTGCTGCTGGAGGCTAATCGTGACAGCTCTACCGTGCTCCAGACTGCTTAA	ATGTACGTCTCCGCTTGCTGGCGGACTTGCTCCGAACCGGACGTCCCCCACCTGGCTCCGATTCTCATGCATTATTTAGTTGCGGGACATGTGGACGTGCTGCTGGAGGCTAATCGTGACAGCTCTACCGTGCTCCAGACTGCTTAA			MYVSACWRTCSEPDVPHLAPILMHYLVAGHVDVLLEANRDSSTVLQTA*	MYVSACWRTCSEPDVPHLAPILMHYLVAGHVDVLLEANRDSSTVLQTA*			TGGTTAATGT	GATTTTCATC	0	R	0	0	0	0	0
4364	2398	an	AN1086.1	70.m15160	AO070285000086	0	-133	-53					ATGCATTATTTAGTTGCGGGACATGTGGACGTGCTGCTGGAGGCTAATCGTGACAGCTCTACCGTGCTCCAGACTGCTTAA	ATGCATTATTTAGTTGCGGGACATGTGGACGTGCTGCTGGAGGCTAATCGTGACAGCTCTACCGTGCTCCAGACTGCTTAA			MHYLVAGHVDVLLEANRDSSTVLQTA*	MHYLVAGHVDVLLEANRDSSTVLQTA*			TCCGATTCTC	GATTTTCATC	0	R	0	0	0	0	0
4366	2398	ao	AN1086.1	70.m15160	AO070285000086	0					-238	-140	ATGAGCAAGGATGTATCCAGTGTACAGTACAGTACACATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAA			ATGAGCAAGGATGTATCCAGTGTACAGTACAGTACACATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAA	MSKDVSSVQYSTHVSERVGGLPVPNLGISLPV*			MSKDVSSVQYSTHVSERVGGLPVPNLGISLPV*	CCACTCTTCC	TTCATCGCTC	0	R	0	0	0	0	0
4367	2398	ao	AN1086.1	70.m15160	AO070285000086	0					-228	-40	ATGTATCCAGTGTACAGTACAGTACACATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAATTCATCGCTCTCGGACATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG			ATGTATCCAGTGTACAGTACAGTACACATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAATTCATCGCTCTCGGACATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG	MYPVYSTVHMYPNVSAGFLFQTWASLYLFNSSLSDMVRPIEFPHFCNAIKSRGAFARRAVDR*			MYPVYSTVHMYPNVSAGFLFQTWASLYLFNSSLSDMVRPIEFPHFCNAIKSRGAFARRAVDR*	ATGAGCAAGG	ATCGATACAC	0	R	0	0	0	0	0
4368	2398	ao	AN1086.1	70.m15160	AO070285000086	0					-201	-40	ATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAATTCATCGCTCTCGGACATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG			ATGTATCCGAACGTGTCGGCGGGCTTCCTGTTCCAAACTTGGGCATCTCTTTACCTGTTTAATTCATCGCTCTCGGACATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG	MYPNVSAGFLFQTWASLYLFNSSLSDMVRPIEFPHFCNAIKSRGAFARRAVDR*			MYPNVSAGFLFQTWASLYLFNSSLSDMVRPIEFPHFCNAIKSRGAFARRAVDR*	TACAGTACAC	ATCGATACAC	0	R	0	0	0	0	0
4369	2398	ao	AN1086.1	70.m15160	AO070285000086	0					-123	-40	ATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG			ATGGTCCGACCGATTGAGTTTCCCCACTTCTGCAATGCTATAAAGTCCAGAGGGGCATTCGCCCGCAGAGCGGTTGATCGTTAG	MVRPIEFPHFCNAIKSRGAFARRAVDR*			MVRPIEFPHFCNAIKSRGAFARRAVDR*	GCTCTCGGAC	ATCGATACAC	0	R	0	0	0	0	0
4378	2400	af	AN8899.1	57.m05984	AO070294000091	0			-166	-86			ATGCAGGCTGATAAGCATACCAGTTCCACCCAGCGCCGTCTCAGTGACATGAGGCACTTGAGATACCGGCCTGCAGTATAA		ATGCAGGCTGATAAGCATACCAGTTCCACCCAGCGCCGTCTCAGTGACATGAGGCACTTGAGATACCGGCCTGCAGTATAA		MQADKHTSSTQRRLSDMRHLRYRPAV*		MQADKHTSSTQRRLSDMRHLRYRPAV*		ACGACTGACG	AAGAGGGACA	0	E	0	0	0	0	0
4379	2400	af	AN8899.1	57.m05984	AO070294000091	0			-118	-86			ATGAGGCACTTGAGATACCGGCCTGCAGTATAA		ATGAGGCACTTGAGATACCGGCCTGCAGTATAA		MRHLRYRPAV*		MRHLRYRPAV*		TCTCAGTGAC	AAGAGGGACA	0	E	0	0	0	0	0
4371	2400	an	AN8899.1	57.m05984	AO070294000091	0	-280	-263					ATGACTCGAGGGCTCTGA	ATGACTCGAGGGCTCTGA			MTRGL*	MTRGL*			AAATAGCCTG	GCATGGAGTA	0	E	0	0	0	0	0
4372	2400	an	AN8899.1	57.m05984	AO070294000091	0	-260	-192					ATGGAGTATAGCAGACCCATGTTCTTCGATATTGTATACGACAATTACCCCGTCTATTCTTGTCAATGA	ATGGAGTATAGCAGACCCATGTTCTTCGATATTGTATACGACAATTACCCCGTCTATTCTTGTCAATGA			MEYSRPMFFDIVYDNYPVYSCQ*	MEYSRPMFFDIVYDNYPVYSCQ*			GGCTCTGAGC	CCGAGCTAGT	0	E	0	0	0	0	0
4373	2400	an	AN8899.1	57.m05984	AO070294000091	0	-242	-192					ATGTTCTTCGATATTGTATACGACAATTACCCCGTCTATTCTTGTCAATGA	ATGTTCTTCGATATTGTATACGACAATTACCCCGTCTATTCTTGTCAATGA			MFFDIVYDNYPVYSCQ*	MFFDIVYDNYPVYSCQ*			TAGCAGACCC	CCGAGCTAGT	0	E	0	0	0	0	0
4374	2400	an	AN8899.1	57.m05984	AO070294000091	0	-195	-175					ATGACCGAGCTAGTCTACTAA	ATGACCGAGCTAGTCTACTAA			MTELVY*	MTELVY*			ATTCTTGTCA	AGTAACTCAA	0	E	0	0	0	0	0
4375	2400	an	AN8899.1	57.m05984	AO070294000091	0	-155	-120					ATGTATCATTGGATGATTCTATTACCTTACATATGA	ATGTATCATTGGATGATTCTATTACCTTACATATGA			MYHWMILLPYI*	MYHWMILLPYI*			ACTGAATAGG	GTCAGATAAA	0	E	0	0	0	0	0
4376	2400	an	AN8899.1	57.m05984	AO070294000091	0	-143	-120					ATGATTCTATTACCTTACATATGA	ATGATTCTATTACCTTACATATGA			MILLPYI*	MILLPYI*			GTATCATTGG	GTCAGATAAA	0	E	0	0	0	0	0
4377	2400	an	AN8899.1	57.m05984	AO070294000091	0	-123	-100					ATGAGTCAGATAAACAGCTCCTAG	ATGAGTCAGATAAACAGCTCCTAG			MSQINSS*	MSQINSS*			TACCTTACAT	CTATATATAT	0	E	0	0	0	0	0
4380	2401	af	AN1331.1	70.m14901	AO070303000094	0			-192	-157			ATGTGTAACGTCATTCTTCCTACGTCCCTGGACTAG		ATGTGTAACGTCATTCTTCCTACGTCCCTGGACTAG		MCNVILPTSLD*		MCNVILPTSLD*		GTCTCTATCG	CTCTGTCATC	0		0	0	0	0	0
4381	2401	ao	AN1331.1	70.m14901	AO070303000094	0					-138	-127	ATGGTCTCTTGA			ATGGTCTCTTGA	MVS*			MVS*	CTCGTTGTGG	TACTGATATC	0		0	0	0	0	0
4382	2401	ao	AN1331.1	70.m14901	AO070303000094	0					-93	-49	ATGCAGTCGCAGTCACTGACCTTCTTTTTCTTCTTAAACCATTGA			ATGCAGTCGCAGTCACTGACCTTCTTTTTCTTCTTAAACCATTGA	MQSQSLTFFFFLNH*			MQSQSLTFFFFLNH*	GTCATCGTCG	AATCAAATCC	0		0	0	0	0	0
4384	2402	af	AN6266.1	72.m19391	AO070304000022	0			-236	-201			ATGCCAAGATTTCACGCTCGCTTGCCCACACCTTAA		ATGCCAAGATTTCACGCTCGCTTGCCCACACCTTAA		MPRFHARLPTP*		MPRFHARLPTP*		AGGAAAATTC	ACTAATAGAT	0	S	FG04403.1	0	0	0	0
4383	2402	an	AN6266.1	72.m19391	AO070304000022	0	-189	-91					ATGCTCGCTTGTTTTTTTCCTCCACCGCCTAATTTTTTCAACAGACTCCGATCTATATTGCTACTCACGCTCACTGAGAGCCTTACTTGTTTGTGCTGA	ATGCTCGCTTGTTTTTTTCCTCCACCGCCTAATTTTTTCAACAGACTCCGATCTATATTGCTACTCACGCTCACTGAGAGCCTTACTTGTTTGTGCTGA			MLACFFPPPPNFFNRLRSILLLTLTESLTCLC*	MLACFFPPPPNFFNRLRSILLLTLTESLTCLC*			GCCTTTCTGG	TTTAATCTCC	0	S	FG04403.1	0	0	0	0
4385	2402	ao	AN6266.1	72.m19391	AO070304000022	0					-237	-175	ATGCCAAGACTTTTTTTTCCCTTTCGCTTGTCCACCACAGCGGATTTTTTTTCTGCAAACTGA			ATGCCAAGACTTTTTTTTCCCTTTCGCTTGTCCACCACAGCGGATTTTTTTTCTGCAAACTGA	MPRLFFPFRLSTTADFFSAN*			MPRLFFPFRLSTTADFFSAN*	AGGAAAATTC	CCGCCAGGCG	0	S	FG04403.1	0	0	0	0
4389	2404	af	AN8982.1	57.m05505	AO070316000169	0			-162	-64			ATGATCCGACTCTCTGATTTGAATAGATATGGCATGATAGTGTGCCCCATTTCTGTCATTGAAATACAGCTTCACTCCCAATCGCAGTCTCGCAGATGA		ATGATCCGACTCTCTGATTTGAATAGATATGGCATGATAGTGTGCCCCATTTCTGTCATTGAAATACAGCTTCACTCCCAATCGCAGTCTCGCAGATGA		MIRLSDLNRYGMIVCPISVIEIQLHSQSQSRR*		MIRLSDLNRYGMIVCPISVIEIQLHSQSQSRR*		ACAGCTCGGA	GTATCTGGTT	0	R	0	0	0	0	0
4390	2404	af	AN8982.1	57.m05505	AO070316000169	0			-129	-64			ATGATAGTGTGCCCCATTTCTGTCATTGAAATACAGCTTCACTCCCAATCGCAGTCTCGCAGATGA		ATGATAGTGTGCCCCATTTCTGTCATTGAAATACAGCTTCACTCCCAATCGCAGTCTCGCAGATGA		MIVCPISVIEIQLHSQSQSRR*		MIVCPISVIEIQLHSQSQSRR*		TAGATATGGC	GTATCTGGTT	0	R	0	0	0	0	0
4391	2404	af	AN8982.1	57.m05505	AO070316000169	0			-67	-23			ATGAGTATCTGGTTCACATCCGTCCAATCCGCGTTGCCAGCGTAA		ATGAGTATCTGGTTCACATCCGTCCAATCCGCGTTGCCAGCGTAA		MSIWFTSVQSALPA*		MSIWFTSVQSALPA*		AGTCTCGCAG	AACACTGCCT	0	R	0	0	0	0	0
4386	2404	an	AN8982.1	57.m05505	AO070316000169	0	-225	-67					ATGCATGGCATCCGCGACATACCTCCAACATTGTCGCTTGGGGATACTGTGAGCTGCCCTGATAAGCCCTATCAAGTCTCGGCAGGACCTTCCTTTGGCCCACAGTGCCAGCCGATAGGCGCCCGCACAGATGGGCAGTGGACCTCTGCAAAGCGCTGA	ATGCATGGCATCCGCGACATACCTCCAACATTGTCGCTTGGGGATACTGTGAGCTGCCCTGATAAGCCCTATCAAGTCTCGGCAGGACCTTCCTTTGGCCCACAGTGCCAGCCGATAGGCGCCCGCACAGATGGGCAGTGGACCTCTGCAAAGCGCTGA			MHGIRDIPPTLSLGDTVSCPDKPYQVSAGPSFGPQCQPIGARTDGQWTSAKR*	MHGIRDIPPTLSLGDTVSCPDKPYQVSAGPSFGPQCQPIGARTDGQWTSAKR*			TCCGGTTTGG	GGGTTAAATA	0	R	0	0	0	0	0
4387	2404	an	AN8982.1	57.m05505	AO070316000169	0	-221	-174					ATGGCATCCGCGACATACCTCCAACATTGTCGCTTGGGGATACTGTGA	ATGGCATCCGCGACATACCTCCAACATTGTCGCTTGGGGATACTGTGA			MASATYLQHCRLGIL*	MASATYLQHCRLGIL*			GTTTGGATGC	GCTGCCCTGA	0	R	0	0	0	0	0
4388	2404	an	AN8982.1	57.m05505	AO070316000169	0	-95	-60					ATGGGCAGTGGACCTCTGCAAAGCGCTGAGGGTTAA	ATGGGCAGTGGACCTCTGCAAAGCGCTGAGGGTTAA			MGSGPLQSAEG*	MGSGPLQSAEG*			GCCCGCACAG	ATACCACCTC	0	R	0	0	0	0	0
4392	2404	ao	AN8982.1	57.m05505	AO070316000169	0					-265	-98	ATGCATCATGCTTCTTGTTTTCCCTTCCATATATTCCATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAGCGTCTCTGCTTATTGATGGCATGACCTATTCACATATATAA			ATGCATCATGCTTCTTGTTTTCCCTTCCATATATTCCATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAGCGTCTCTGCTTATTGATGGCATGACCTATTCACATATATAA	MHHASCFPFHIFHVGGDKATLPVFAPGNGQGFTCCSFRDNQLASLLIDGMTYSHI*			MHHASCFPFHIFHVGGDKATLPVFAPGNGQGFTCCSFRDNQLASLLIDGMTYSHI*	TCATTCATCC	AAACGCGGGA	0	R	0	0	0	0	0
4393	2404	ao	AN8982.1	57.m05505	AO070316000169	0					-258	-139	ATGCTTCTTGTTTTCCCTTCCATATATTCCATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG			ATGCTTCTTGTTTTCCCTTCCATATATTCCATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG	MLLVFPSIYSMSEVIRPPCRFLLQEMVKALPVAVFGITS*			MLLVFPSIYSMSEVIRPPCRFLLQEMVKALPVAVFGITS*	TCCATGCATC	CGTCTCTGCT	0	R	0	0	0	0	0
4394	2404	ao	AN8982.1	57.m05505	AO070316000169	0					-228	-139	ATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG			ATGTCGGAGGTGATAAGGCCACCTTGCCGGTTTTTGCTCCAGGAAATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG	MSEVIRPPCRFLLQEMVKALPVAVFGITS*			MSEVIRPPCRFLLQEMVKALPVAVFGITS*	CATATATTCC	CGTCTCTGCT	0	R	0	0	0	0	0
4395	2404	ao	AN8982.1	57.m05505	AO070316000169	0					-183	-139	ATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG			ATGGTCAAGGCTTTACCTGTTGCAGTTTTCGGGATAACCAGCTAG	MVKALPVAVFGITS*			MVKALPVAVFGITS*	GCTCCAGGAA	CGTCTCTGCT	0	R	0	0	0	0	0
4396	2404	ao	AN8982.1	57.m05505	AO070316000169	0					-118	-98	ATGACCTATTCACATATATAA			ATGACCTATTCACATATATAA	MTYSHI*			MTYSHI*	TATTGATGGC	AAACGCGGGA	0	R	0	0	0	0	0
4400	2406	af	AN8430.1	71.m15302	AO070317000096	0			-253	-239			ATGGGACAGTCATAG		ATGGGACAGTCATAG		MGQS*		MGQS*		TGGCCGTGGC	ATCGCATGTC	0	R	0	0	0	0	0
4401	2406	af	AN8430.1	71.m15302	AO070317000096	0			-233	-201			ATGTCTTTCCAAAACCGGGTGCTTGCTAATTAA		ATGTCTTTCCAAAACCGGGTGCTTGCTAATTAA		MSFQNRVLAN*		MSFQNRVLAN*		CATAGATCGC	GCTACTCTTT	0	R	0	0	0	0	0
4402	2406	af	AN8430.1	71.m15302	AO070317000096	0			-187	-170			ATGCAAAAACTAATGTAG		ATGCAAAAACTAATGTAG		MQKLM*		MQKLM*		ACTCTTTTAG	AATCCATTTA	0	R	0	0	0	0	0

4397	2406	an	AN8430.1	71.m15302	AO070317000096	0	-214	-53					ATGTGGATGAATTTTACGCCGTTTGTTCGGATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA	ATGTGGATGAATTTTACGCCGTTTGTTCGGATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA			MWMNFTPFVRMGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*	MWMNFTPFVRMGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*			GTCTAACCTA	AACTCTTTCC	0	R	0	0	0	0	0
4398	2406	an	AN8430.1	71.m15302	AO070317000096	0	-208	-53					ATGAATTTTACGCCGTTTGTTCGGATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA	ATGAATTTTACGCCGTTTGTTCGGATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA			MNFTPFVRMGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*	MNFTPFVRMGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*			CCTAATGTGG	AACTCTTTCC	0	R	0	0	0	0	0
4399	2406	an	AN8430.1	71.m15302	AO070317000096	0	-184	-53					ATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA	ATGGGGACCTTGGGGGTGGTATTTGTGGTATTTTGTGGTATCGATAAGTACAGTTTATCAGCGCATTGTAACTCAAACGGATATAAGAAACCCACGTTCGTCCGTTGCCACTGGGAAGTGTTAAGTCGTTGA			MGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*	MGTLGVVFVVFCGIDKYSLSAHCNSNGYKKPTFVRCHWEVLSR*			GTTTGTTCGG	AACTCTTTCC	0	R	0	0	0	0	0
4403	2406	ao	AN8430.1	71.m15302	AO070317000096	0					-192	-166	ATGTGGAACCGTCGGAGACAGGTCTAA			ATGTGGAACCGTCGGAGACAGGTCTAA	MWNRRRQV*			MWNRRRQV*	ATCCAGTAAG	CCTGTATTGG	0	R	0	0	0	0	0
4410	2407	af	AN6923.1	59.m08483	AO070318000108	0			-299	-222			ATGAATCAGACGACTCTGGGGACTGTGGTATGCACTAAACCGTCCATCAGAAACAGAAACAACGGGCCATGCCGCTAA		ATGAATCAGACGACTCTGGGGACTGTGGTATGCACTAAACCGTCCATCAGAAACAGAAACAACGGGCCATGCCGCTAA		MNQTTLGTVVCTKPSIRNRNNGPCR*		MNQTTLGTVVCTKPSIRNRNNGPCR*		CCCCAGGTTA	ATGGCCCGTT	0	R	0	0	NCU08152.1	0	0
4411	2407	af	AN6923.1	59.m08483	AO070318000108	0			-231	-133			ATGCCGCTAAATGGCCCGTTTGTTTCTCTCGGGTTATCTTCTGGAGCTGTGTCCGGTTTGGTGGTTGTCGTTTGCGAGAGCAGAGCACAGAGTATTTAA		ATGCCGCTAAATGGCCCGTTTGTTTCTCTCGGGTTATCTTCTGGAGCTGTGTCCGGTTTGGTGGTTGTCGTTTGCGAGAGCAGAGCACAGAGTATTTAA		MPLNGPFVSLGLSSGAVSGLVVVVCESRAQSI*		MPLNGPFVSLGLSSGAVSGLVVVVCESRAQSI*		ACAACGGGCC	CCACTGTGGG	0	R	0	0	NCU08152.1	0	0
4404	2407	an	AN6923.1	59.m08483	AO070318000108	0	-240	-199					ATGTTACGTTGCACTGCGGCCTGTTTTGGGAGCGAAACTTAA	ATGTTACGTTGCACTGCGGCCTGTTTTGGGAGCGAAACTTAA			MLRCTAACFGSET*	MLRCTAACFGSET*			ACACGGCTGG	CATCGCTGGT	0	R	0	0	NCU08152.1	0	0
4405	2407	an	AN6923.1	59.m08483	AO070318000108	0	-188	-126					ATGGGGGAGGTTGCCCTGCTATGTGGTTCGGGTGCGCAGCATGGCCTGGTCTTCCCCAGCTGA	ATGGGGGAGGTTGCCCTGCTATGTGGTTCGGGTGCGCAGCATGGCCTGGTCTTCCCCAGCTGA			MGEVALLCGSGAQHGLVFPS*	MGEVALLCGSGAQHGLVFPS*			CATCGCTGGT	GCTCGACAAG	0	R	0	0	NCU08152.1	0	0
4406	2407	an	AN6923.1	59.m08483	AO070318000108	0	-168	-82					ATGTGGTTCGGGTGCGCAGCATGGCCTGGTCTTCCCCAGCTGAGCTCGACAAGGGTGCATGTACGGGGAAATATAAAGCTCCATTAA	ATGTGGTTCGGGTGCGCAGCATGGCCTGGTCTTCCCCAGCTGAGCTCGACAAGGGTGCATGTACGGGGAAATATAAAGCTCCATTAA			MWFGCAAWPGLPQLSSTRVHVRGNIKLH*	MWFGCAAWPGLPQLSSTRVHVRGNIKLH*			TTGCCCTGCT	CCGCCTCCTT	0	R	0	0	NCU08152.1	0	0
4407	2407	an	AN6923.1	59.m08483	AO070318000108	0	-148	-32					ATGGCCTGGTCTTCCCCAGCTGAGCTCGACAAGGGTGCATGTACGGGGAAATATAAAGCTCCATTAACCGCCTCCTTGGTGTTTCTCTTCTTCCTGATGCTTTTCTTCATTGATTAG	ATGGCCTGGTCTTCCCCAGCTGAGCTCGACAAGGGTGCATGTACGGGGAAATATAAAGCTCCATTAACCGCCTCCTTGGTGTTTCTCTTCTTCCTGATGCTTTTCTTCATTGATTAG			MAWSSPAELDKGACTGKYKAPLTASLVFLFFLMLFFID*	MAWSSPAELDKGACTGKYKAPLTASLVFLFFLMLFFID*			GGTGCGCAGC	TGTGCTGTTG	0	R	0	0	NCU08152.1	0	0
4408	2407	an	AN6923.1	59.m08483	AO070318000108	0	-110	-93					ATGTACGGGGAAATATAA	ATGTACGGGGAAATATAA			MYGEI*	MYGEI*			ACAAGGGTGC	AGCTCCATTA	0	R	0	0	NCU08152.1	0	0
4414	2408	af	AN2342.1	71.m15578	AO070319000156	0			-179	-90			ATGTTGAAAGTTTCAGGACAAGCTCAGAAAAGACCCACTCGTACTCGTTCAAAAATTTCCCGAAAGGGTAATTTGATCCACCATCTATAG		ATGTTGAAAGTTTCAGGACAAGCTCAGAAAAGACCCACTCGTACTCGTTCAAAAATTTCCCGAAAGGGTAATTTGATCCACCATCTATAG		MLKVSGQAQKRPTRTRSKISRKGNLIHHL*		MLKVSGQAQKRPTRTRSKISRKGNLIHHL*		TTTGGGTCCC	AGACAGCAAT	0		0	0	0	0	0
4415	2408	af	AN2342.1	71.m15578	AO070319000156	0			-81	-49			ATGCAGTATATGAGGCCACCATGGTCGTCGTAG		ATGCAGTATATGAGGCCACCATGGTCGTCGTAG		MQYMRPPWSS*		MQYMRPPWSS*		AGAGACAGCA	CTCTTTTCTT	0		0	0	0	0	0
4416	2408	af	AN2342.1	71.m15578	AO070319000156	0			-72	-49			ATGAGGCCACCATGGTCGTCGTAG		ATGAGGCCACCATGGTCGTCGTAG		MRPPWSS*		MRPPWSS*		AATGCAGTAT	CTCTTTTCTT	0		0	0	0	0	0
4413	2408	an	AN2342.1	71.m15578	AO070319000156	0	-217	-203					ATGCATCTCCACTAA	ATGCATCTCCACTAA			MHLH*	MHLH*			TAAAAATAAC	AATCTCGAAG	0		0	0	0	0	0
4417	2408	ao	AN2342.1	71.m15578	AO070319000156	0					-279	-259	ATGAGAATCAACAGGAACTAA			ATGAGAATCAACAGGAACTAA	MRINRN*			MRINRN*	CAGAGTAACA	ACCTAAGCAT	0		0	0	0	0	0
4418	2408	ao	AN2342.1	71.m15578	AO070319000156	0					-123	-25	ATGGGTAGATCCGATATAAATCAGGGATGGGGGTACTGCTTCTCGTGGAATAAACATTTCCTTTTCATTAATGTCTCTGAGTACAGTTCAGTAAATTAG			ATGGGTAGATCCGATATAAATCAGGGATGGGGGTACTGCTTCTCGTGGAATAAACATTTCCTTTTCATTAATGTCTCTGAGTACAGTTCAGTAAATTAG	MGRSDINQGWGYCFSWNKHFLFINVSEYSSVN*			MGRSDINQGWGYCFSWNKHFLFINVSEYSSVN*	TCTAATACGT	CACATTGACC	0		0	0	0	0	0
4419	2408	ao	AN2342.1	71.m15578	AO070319000156	0					-97	-71	ATGGGGGTACTGCTTCTCGTGGAATAA			ATGGGGGTACTGCTTCTCGTGGAATAA	MGVLLLVE*			MGVLLLVE*	TAAATCAGGG	ACATTTCCTT	0		0	0	0	0	0
4423	2409	af	AN2343.1	71.m15577	AO070319000157	0			-264	-31			ATGCATGTGCATTCTAATTGGCCACTCATGACGGAATTCAGTGGACATTTTTCAGATCAACCGATTTTTAATCTATTCTCCTTTGATGCATACTGGGAATCTCCACAGGTAGAAGTTTGTAGAAATATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		ATGCATGTGCATTCTAATTGGCCACTCATGACGGAATTCAGTGGACATTTTTCAGATCAACCGATTTTTAATCTATTCTCCTTTGATGCATACTGGGAATCTCCACAGGTAGAAGTTTGTAGAAATATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		MHVHSNWPLMTEFSGHFSDQPIFNLFSFDAYWESPQVEVCRNMTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		MHVHSNWPLMTEFSGHFSDQPIFNLFSFDAYWESPQVEVCRNMTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		AGTCAAAACT	TTCAGATTCA	0	R	FG01866.1	0	0	0	0
4424	2409	af	AN2343.1	71.m15577	AO070319000157	0			-260	-234			ATGTGCATTCTAATTGGCCACTCATGA		ATGTGCATTCTAATTGGCCACTCATGA		MCILIGHS*		MCILIGHS*		AAAACTATGC	CGGAATTCAG	0	R	FG01866.1	0	0	0	0
4425	2409	af	AN2343.1	71.m15577	AO070319000157	0			-237	-31			ATGACGGAATTCAGTGGACATTTTTCAGATCAACCGATTTTTAATCTATTCTCCTTTGATGCATACTGGGAATCTCCACAGGTAGAAGTTTGTAGAAATATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		ATGACGGAATTCAGTGGACATTTTTCAGATCAACCGATTTTTAATCTATTCTCCTTTGATGCATACTGGGAATCTCCACAGGTAGAAGTTTGTAGAAATATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		MTEFSGHFSDQPIFNLFSFDAYWESPQVEVCRNMTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		MTEFSGHFSDQPIFNLFSFDAYWESPQVEVCRNMTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		TTGGCCACTC	TTCAGATTCA	0	R	FG01866.1	0	0	0	0
4426	2409	af	AN2343.1	71.m15577	AO070319000157	0			-179	-153			ATGCATACTGGGAATCTCCACAGGTAG		ATGCATACTGGGAATCTCCACAGGTAG		MHTGNLHR*		MHTGNLHR*		TTCTCCTTTG	AAGTTTGTAG	0	R	FG01866.1	0	0	0	0
4427	2409	af	AN2343.1	71.m15577	AO070319000157	0			-138	-31			ATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		ATGACGGTGCCTGTGCGTGCTGGGGAACATAAATACCCTCTTCCCTACTCCATACAGACAGAGGAGAAATCAATCACCATCGATCAAGTCATCAACATCTCCAGATAA		MTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		MTVPVRAGEHKYPLPYSIQTEEKSITIDQVINISR*		TTGTAGAAAT	TTCAGATTCA	0	R	FG01866.1	0	0	0	0
4421	2409	an	AN2343.1	71.m15577	AO070319000157	0	-224	-174					ATGATTGCGCGATGGCGTCCCGCCGAATTTCTAATCATCGCGTCTCGCTGA	ATGATTGCGCGATGGCGTCCCGCCGAATTTCTAATCATCGCGTCTCGCTGA			MIARWRPAEFLIIASR*	MIARWRPAEFLIIASR*			AAGCCCAGTT	CAAACCCCTC	0	R	FG01866.1	0	0	0	0
4422	2409	an	AN2343.1	71.m15577	AO070319000157	0	-213	-115					ATGGCGTCCCGCCGAATTTCTAATCATCGCGTCTCGCTGACAAACCCCTCGAGAGGGCCCCGTCGCCCGCCTCTCATTGGCTGGCTTGGGCGGAATTAA	ATGGCGTCCCGCCGAATTTCTAATCATCGCGTCTCGCTGACAAACCCCTCGAGAGGGCCCCGTCGCCCGCCTCTCATTGGCTGGCTTGGGCGGAATTAA			MASRRISNHRVSLTNPSRGPRRPPLIGWLGRN*	MASRRISNHRVSLTNPSRGPRRPPLIGWLGRN*			TGATTGCGCG	CAATCGCACA	0	R	FG01866.1	0	0	0	0
4428	2409	ao	AN2343.1	71.m15577	AO070319000157	0					-234	-211	ATGGATCTCAATGCGATAATGTGA			ATGGATCTCAATGCGATAATGTGA	MDLNAIM*			MDLNAIM*	GCCGATTCAA	TTGGCGATTG	0	R	FG01866.1	0	0	0	0
4429	2409	ao	AN2343.1	71.m15577	AO070319000157	0					-175	-155	ATGAAATTTTTATGGAAATGA			ATGAAATTTTTATGGAAATGA	MKFLWK*			MKFLWK*	AGAAATACTT	AACTAAATCG	0	R	FG01866.1	0	0	0	0
4430	2409	ao	AN2343.1	71.m15577	AO070319000157	0					-164	-72	ATGGAAATGAAACTAAATCGCGGGGCACCAAACATTCTGCGATGGCGAGATTGCATATATAAGATCTCAATTTCCTGTTCAATAGACTCTTAG			ATGGAAATGAAACTAAATCGCGGGGCACCAAACATTCTGCGATGGCGAGATTGCATATATAAGATCTCAATTTCCTGTTCAATAGACTCTTAG	MEMKLNRGAPNILRWRDCIYKISISCSIDS*			MEMKLNRGAPNILRWRDCIYKISISCSIDS*	TGAAATTTTT	ATCTCATCAG	0	R	FG01866.1	0	0	0	0
4431	2409	ao	AN2343.1	71.m15577	AO070319000157	0					-158	-72	ATGAAACTAAATCGCGGGGCACCAAACATTCTGCGATGGCGAGATTGCATATATAAGATCTCAATTTCCTGTTCAATAGACTCTTAG			ATGAAACTAAATCGCGGGGCACCAAACATTCTGCGATGGCGAGATTGCATATATAAGATCTCAATTTCCTGTTCAATAGACTCTTAG	MKLNRGAPNILRWRDCIYKISISCSIDS*			MKLNRGAPNILRWRDCIYKISISCSIDS*	TTTTATGGAA	ATCTCATCAG	0	R	FG01866.1	0	0	0	0
4432	2409	ao	AN2343.1	71.m15577	AO070319000157	0					-123	-103	ATGGCGAGATTGCATATATAA			ATGGCGAGATTGCATATATAA	MARLHI*			MARLHI*	ACATTCTGCG	GATCTCAATT	0	R	FG01866.1	0	0	0	0
4434	2410	af	AN0879.1	70.m15805	AO070320000039	0			-195	-172			ATGCGGGATAACTATCTTAGGTAG		ATGCGGGATAACTATCTTAGGTAG		MRDNYLR*		MRDNYLR*		TTTGGTAAGG	TTTAGCCCTA	0	S	0	0	0	0	0
4435	2410	af	AN0879.1	70.m15805	AO070320000039	0			-162	-100			ATGGACTGCTTAGTCATTAAGTCACCGCCGTCCGTCGGAACCGCAAAAGTATCCATAGGATGA		ATGGACTGCTTAGTCATTAAGTCACCGCCGTCCGTCGGAACCGCAAAAGTATCCATAGGATGA		MDCLVIKSPPSVGTAKVSIG*		MDCLVIKSPPSVGTAKVSIG*		GTTTAGCCCT	CTCGCCATCA	0	S	0	0	0	0	0
4436	2410	af	AN0879.1	70.m15805	AO070320000039	0			-103	-20			ATGACTCGCCATCACCACAACTCTATAGTCAAGCACAACTCTTTCCCTTTGTCTGCACTTCCATCAGAGAGCTTTCACACTTGA		ATGACTCGCCATCACCACAACTCTATAGTCAAGCACAACTCTTTCCCTTTGTCTGCACTTCCATCAGAGAGCTTTCACACTTGA		MTRHHHNSIVKHNSFPLSALPSESFHT*		MTRHHHNSIVKHNSFPLSALPSESFHT*		TATCCATAGG	CTTATAATAA	0	S	0	0	0	0	0
4433	2410	an	AN0879.1	70.m15805	AO070320000039	0	-218	-171					ATGCCAAGCAATACTACGAAGACAGCATACTCTTATACATCAGCTTAG	ATGCCAAGCAATACTACGAAGACAGCATACTCTTATACATCAGCTTAG			MPSNTTKTAYSYTSA*	MPSNTTKTAYSYTSA*			TCCCGATCAC	TCATACACCC	0	S	0	0	0	0	0
4437	2410	ao	AN0879.1	70.m15805	AO070320000039	0					-238	-167	ATGATGTCCAAACAAGATAAGTTCACAAATCTATACAGCAACAAAAAGACCAGGGCAATGTCAATCATGTGA			ATGATGTCCAAACAAGATAAGTTCACAAATCTATACAGCAACAAAAAGACCAGGGCAATGTCAATCATGTGA	MMSKQDKFTNLYSNKKTRAMSIM*			MMSKQDKFTNLYSNKKTRAMSIM*	GAAATCACAT	ACATGCATAA	0	S	0	0	0	0	0
4438	2410	ao	AN0879.1	70.m15805	AO070320000039	0					-235	-167	ATGTCCAAACAAGATAAGTTCACAAATCTATACAGCAACAAAAAGACCAGGGCAATGTCAATCATGTGA			ATGTCCAAACAAGATAAGTTCACAAATCTATACAGCAACAAAAAGACCAGGGCAATGTCAATCATGTGA	MSKQDKFTNLYSNKKTRAMSIM*			MSKQDKFTNLYSNKKTRAMSIM*	ATCACATATG	ACATGCATAA	0	S	0	0	0	0	0
4439	2410	ao	AN0879.1	70.m15805	AO070320000039	0					-181	-167	ATGTCAATCATGTGA			ATGTCAATCATGTGA	MSIM*			MSIM*	GACCAGGGCA	ACATGCATAA	0	S	0	0	0	0	0
4440	2410	ao	AN0879.1	70.m15805	AO070320000039	0					-164	-132	ATGCATAAAGTTTACATAAGTGAAATGTTTTAG			ATGCATAAAGTTTACATAAGTGAAATGTTTTAG	MHKVYISEMF*			MHKVYISEMF*	TCATGTGAAC	TCAGTCTCCA	0	S	0	0	0	0	0
4441	2412	af	AN8012.1	53.m03860	AO070322000060	0			-237	-160			ATGCACAGAGGAGTGATCATCATCATACTCGACCAAACAATTTCCCGATTGAGCTGGAGAGCAAACATAGCAAAATAA		ATGCACAGAGGAGTGATCATCATCATACTCGACCAAACAATTTCCCGATTGAGCTGGAGAGCAAACATAGCAAAATAA		MHRGVIIIILDQTISRLSWRANIAK*		MHRGVIIIILDQTISRLSWRANIAK*		GAATGTGACA	TGCAAACAAT	0	H	0	MG08649.1		0	0
4442	2412	af	AN8012.1	53.m03860	AO070322000060	0			-160	-113			ATGCAAACAATGCAAATTTCCATCTCCGAGGGGTTTCCGTTATCGTAG		ATGCAAACAATGCAAATTTCCATCTCCGAGGGGTTTCCGTTATCGTAG		MQTMQISISEGFPLS*		MQTMQISISEGFPLS*		TAGCAAAATA	ATGTTCTCGG	0	H	0	MG08649.1	0	0	0
4443	2412	af	AN8012.1	53.m03860	AO070322000060	0			-151	-113			ATGCAAATTTCCATCTCCGAGGGGTTTCCGTTATCGTAG		ATGCAAATTTCCATCTCCGAGGGGTTTCCGTTATCGTAG		MQISISEGFPLS*		MQISISEGFPLS*		AATGCAAACA	ATGTTCTCGG	0	H	0	MG08649.1	0	0	0
4444	2412	af	AN8012.1	53.m03860	AO070322000060	0			-112	-80			ATGTTCTCGGCCCCTCGTCGTTCTTGGTATTGA		ATGTTCTCGGCCCCTCGTCGTTCTTGGTATTGA		MFSAPRRSWY*		MFSAPRRSWY*		GTTATCGTAG	TCTTGTAGCA	0	H	0	MG08649.1	0	0	0
4445	2412	ao	AN8012.1	53.m03860	AO070322000060	0					-209	-126	ATGTTGAACCCGAGTACACAGTACGGGAAAGGCGGAACTTCTGATTGGTCAATGGACGGGCAAACAGGGCAAACAAAGCGCTGA			ATGTTGAACCCGAGTACACAGTACGGGAAAGGCGGAACTTCTGATTGGTCAATGGACGGGCAAACAGGGCAAACAAAGCGCTGA	MLNPSTQYGKGGTSDWSMDGQTGQTKR*			MLNPSTQYGKGGTSDWSMDGQTGQTKR*	CAACCTTAGA	GGGGCTTTAC	0	H	0	MG08649.1	0	0	0
4446	2412	ao	AN8012.1	53.m03860	AO070322000060	0					-158	-126	ATGGACGGGCAAACAGGGCAAACAAAGCGCTGA			ATGGACGGGCAAACAGGGCAAACAAAGCGCTGA	MDGQTGQTKR*			MDGQTGQTKR*	TGATTGGTCA	GGGGCTTTAC	0	H	0	MG08649.1	0	0	0
4449	2416	af	AN9076.1	66.m04773	AO070332000205	0			-172	-113			ATGTTCGACGATCGATACTTCCATCTACACCTGCGTTACTTTTGCCTACTTCCATCCTGA		ATGTTCGACGATCGATACTTCCATCTACACCTGCGTTACTTTTGCCTACTTCCATCCTGA		MFDDRYFHLHLRYFCLLPS*		MFDDRYFHLHLRYFCLLPS*		TTCCTATTAA	GTGATTTGTG	0		0	0	0	0	0
4447	2416	an	AN9076.1	66.m04773	AO070332000205	0	-201	-130					ATGTTGTTAATAGTTCTGTCCTTCTCCACTCGACTCAAGATACATATAGCTGACATGCTCGTCTTCTTCTGA	ATGTTGTTAATAGTTCTGTCCTTCTCCACTCGACTCAAGATACATATAGCTGACATGCTCGTCTTCTTCTGA			MLLIVLSFSTRLKIHIADMLVFF*	MLLIVLSFSTRLKIHIADMLVFF*			CTGCTCCCAA	TCTACATTTC	0		0	0	0	0	0

4448	2416	an	AN9076.1	66.m04773	AO070332000205	0	-147	-130					ATGCTCGTCTTCTTCTGA	ATGCTCGTCTTCTTCTGA			MLVFF*	MLVFF*			TATAGCTGAC	TCTACATTTC	0		0	0	0	0	0
4450	2417	af	AN5375.1	69.m15528	AO070333000155	0			-176	-153			ATGACAACCAGTCAATGCAGATAG		ATGACAACCAGTCAATGCAGATAG		MTTSQCR*		MTTSQCR*		CTCCCGTCGC	CTCTCCTGAT	0		0	0	0	0	0
4451	2417	af	AN5375.1	69.m15528	AO070333000155	0			-162	-121			ATGCAGATAGCTCTCCTGATTTACTCCTTTCTTCTAGCCTGA		ATGCAGATAGCTCTCCTGATTTACTCCTTTCTTCTAGCCTGA		MQIALLIYSFLLA*		MQIALLIYSFLLA*		CAACCAGTCA	TATTCAACGG	0		0	0	0	0	0
4452	2417	ao	AN5375.1	69.m15528	AO070333000155	0					-219	-37	ATGCACGTGACATGTTATCGGCATTGTTTGCGGGAACCGCCGACAGCTCCATCAGTCCTCAATCAACAAACCTCACTCGCGCAATATAGAGCAGCACATTCACGCTCACGACACCTCTACACGAATCCAACACCAATCAATTGCACTCACCACCCCTCTACAAACCCCTCACCAATGCTCTAA			ATGCACGTGACATGTTATCGGCATTGTTTGCGGGAACCGCCGACAGCTCCATCAGTCCTCAATCAACAAACCTCACTCGCGCAATATAGAGCAGCACATTCACGCTCACGACACCTCTACACGAATCCAACACCAATCAATTGCACTCACCACCCCTCTACAAACCCCTCACCAATGCTCTAA	MHVTCYRHCLREPPTAPSVLNQQTSLAQYRAAHSRSRHLYTNPTPINCTHHPSTNPSPML*			MHVTCYRHCLREPPTAPSVLNQQTSLAQYRAAHSRSRHLYTNPTPINCTHHPSTNPSPML*	AACAGCAAGC	CTCACACGCA	0		0	0	0	0	0
4453	2417	ao	AN5375.1	69.m15528	AO070333000155	0					-208	-131	ATGTTATCGGCATTGTTTGCGGGAACCGCCGACAGCTCCATCAGTCCTCAATCAACAAACCTCACTCGCGCAATATAG			ATGTTATCGGCATTGTTTGCGGGAACCGCCGACAGCTCCATCAGTCCTCAATCAACAAACCTCACTCGCGCAATATAG	MLSALFAGTADSSISPQSTNLTRAI*			MLSALFAGTADSSISPQSTNLTRAI*	TGCACGTGAC	AGCAGCACAT	0		0	0	0	0	0
4457	2418	af	AN4887.1	59.m08783	AO070338000071	0			-203	-192			ATGTCTGATTAA		ATGTCTGATTAA		MSD*		MSD*		TATACGTCTG	GTCCAAGGTC	0	T	0	0	0	0	0
4458	2418	af	AN4887.1	59.m08783	AO070338000071	0			-167	-144			ATGAGATTTCGAGGCTCGTTTTAG		ATGAGATTTCGAGGCTCGTTTTAG		MRFRGSF*		MRFRGSF*		CTGCGAAGGC	GACCACACAC	0	T	0	0	0	0	0
4454	2418	an	AN4887.1	59.m08783	AO070338000071	0	-155	-72					ATGAACAACCTCCAGCGGGACATGAATGACGAGCTGAAATCGCCGCTAGATTGCAAGGATAACCTGCTCAGAAAAGAGGCCTAG	ATGAACAACCTCCAGCGGGACATGAATGACGAGCTGAAATCGCCGCTAGATTGCAAGGATAACCTGCTCAGAAAAGAGGCCTAG			MNNLQRDMNDELKSPLDCKDNLLRKEA*	MNNLQRDMNDELKSPLDCKDNLLRKEA*			CTTCAAGGCA	GATCATCTGA	0	T	0	0	0	0	0
4455	2418	an	AN4887.1	59.m08783	AO070338000071	0	-134	-72					ATGAATGACGAGCTGAAATCGCCGCTAGATTGCAAGGATAACCTGCTCAGAAAAGAGGCCTAG	ATGAATGACGAGCTGAAATCGCCGCTAGATTGCAAGGATAACCTGCTCAGAAAAGAGGCCTAG			MNDELKSPLDCKDNLLRKEA*	MNDELKSPLDCKDNLLRKEA*			CCAGCGGGAC	GATCATCTGA	0	T	0	0	0	0	0
4456	2418	an	AN4887.1	59.m08783	AO070338000071	0	-130	-119					ATGACGAGCTGA	ATGACGAGCTGA			MTS*	MTS*			CGGGACATGA	AATCGCCGCT	0	T	0	0	0	0	0
4459	2418	ao	AN4887.1	59.m08783	AO070338000071	0					-163	-137	ATGATGAGTTTCACCTTCATGCCATAA			ATGATGAGTTTCACCTTCATGCCATAA	MMSFTFMP*			MMSFTFMP*	CTGAGCGCCG	AATTCTGGGA	0	T	0	0	0	0	0
4460	2418	ao	AN4887.1	59.m08783	AO070338000071	0					-160	-137	ATGAGTTTCACCTTCATGCCATAA			ATGAGTTTCACCTTCATGCCATAA	MSFTFMP*			MSFTFMP*	AGCGCCGATG	AATTCTGGGA	0	T	0	0	0	0	0
4464	2419	af	AN2829.1	67.m02989	AO070339000034	0			-77	-48			ATGGAGCCAAAGACATATCAACCTCGGTGA		ATGGAGCCAAAGACATATCAACCTCGGTGA		MEPKTYQPR*		MEPKTYQPR*		GCACAGGATA	GTTCTGGATT	0	JIT	0	0	0	0	0
4461	2419	an	AN2829.1	67.m02989	AO070339000034	0	-182	-138					ATGGGCAGTGACTGGCGCACCTATCCCTGTCGCCGATTGGCATGA	ATGGGCAGTGACTGGCGCACCTATCCCTGTCGCCGATTGGCATGA			MGSDWRTYPCRRLA*	MGSDWRTYPCRRLA*			AACTACCTGC	CACGTTTGAT	0	JIT	0	0	0	0	0
4462	2419	an	AN2829.1	67.m02989	AO070339000034	0	-141	-115					ATGACACGTTTGATTGGTGCTGAGTGA	ATGACACGTTTGATTGGTGCTGAGTGA			MTRLIGAE*	MTRLIGAE*			GCCGATTGGC	TGGGTACGAT	0	JIT	0	0	0	0	0
4463	2419	an	AN2829.1	67.m02989	AO070339000034	0	-115	-101					ATGGGTACGATTTGA	ATGGGTACGATTTGA			MGTI*	MGTI*			GTGCTGAGTG	TTCTCAGCGT	0	JIT	0	0	0	0	0
4466	2420	af	AN6083.1	72.m19924	AO070340000133	0			-234	-166			ATGTTAGAAAGCCTCCGATCTGACAAATGCGACATGGCGAGGACTGGATGTGATTGGCGGAGAGTGTAG		ATGTTAGAAAGCCTCCGATCTGACAAATGCGACATGGCGAGGACTGGATGTGATTGGCGGAGAGTGTAG		MLESLRSDKCDMARTGCDWRRV*		MLESLRSDKCDMARTGCDWRRV*		CAACATTACG	GGTTTAGGGC	0	J	0	0	0	YLR075W	0
4467	2420	af	AN6083.1	72.m19924	AO070340000133	0			-201	-166			ATGGCGAGGACTGGATGTGATTGGCGGAGAGTGTAG		ATGGCGAGGACTGGATGTGATTGGCGGAGAGTGTAG		MARTGCDWRRV*		MARTGCDWRRV*		CAAATGCGAC	GGTTTAGGGC	0	J	0	0	0	YLR075W	0
4468	2420	ao	AN6083.1	72.m19924	AO070340000133	0					-224	-162	ATGTCGCCGAAGTCTGACAAATGCGGTCTGGTCGCGGCAGCCGCTGATTGGTGGAGACGGTAG			ATGTCGCCGAAGTCTGACAAATGCGGTCTGGTCGCGGCAGCCGCTGATTGGTGGAGACGGTAG	MSPKSDKCGLVAAAADWWRR*			MSPKSDKCGLVAAAADWWRR*	CAAGTTTGAA	GGTTTAGGGT	0	J	0	0	0	YLR075W	0
4465	2420	conserved	AN6083.1	72.m19924	AO070340000133	0	-199	-173	-208	-182	-204	-178	ATGCGdymTrkysrbkrCdGsmksTGA	ATGCGTCATATCCGTTGCGGGCGGTGA	ATGCGACATGGCGAGGACTGGATGTGA	ATGCGGTCTGGTCGCGGCAGCCGCTGA	MRhircgr*	MRHIRCGR*	MRHGEDWM*	MRSGRGSR*	rrTCyGmyrr	TTGGyGGAkA	0	J	0	0	0	YLR075W	0
4480	2423	af	AN5884.1	72.m19247	AO070245000024	0			-134	-93			ATGGTTTCCGTCGAGCTGTACTCTGGTCTCTGCATTCGGTGA		ATGGTTTCCGTCGAGCTGTACTCTGGTCTCTGCATTCGGTGA		MVSVELYSGLCIR*		MVSVELYSGLCIR*		AAAGAATGTG	TCTAAGATAA	0	F	0	MG07135.1	0	YML106W	0
4479	2423	an	AN5884.1	72.m19247	AO070245000024	0	-126	-76					ATGAGGAAAACTCATCCAACTTTCTCCCTATACTTCCTAGCAATTGCATAG	ATGAGGAAAACTCATCCAACTTTCTCCCTATACTTCCTAGCAATTGCATAG			MRKTHPTFSLYFLAIA*	MRKTHPTFSLYFLAIA*			GCAAAAAAAG	ACGTTGACTT	0	F	0	MG07135.1	0	YML106W	0
4481	2424	an	AN5883.1	72.m19248	AO070245000025	0	-62	-30					ATGTTCTCTGCTGGCCCCAAAAAACAGTGCTGA	ATGTTCTCTGCTGGCCCCAAAAAACAGTGCTGA			MFSAGPKKQC*	MFSAGPKKQC*			CCAAACTGTC	TGGCTCGAGC	0	E	0	0	NCU07690.1	0	0
4485	2425	af	AN4636.1	57.m05549	AO070248000018	0			-145	-134			ATGACGTCATAG		ATGACGTCATAG		MTS*		MTS*		GCGATGCCGC	CTGCGTCCAT	0		0	0	0	0	0
4483	2425	an	AN4636.1	57.m05549	AO070248000018	0	-188	-153					ATGACGTGTACATTATTGAGTTCCTGCAAAGTGTAG	ATGACGTGTACATTATTGAGTTCCTGCAAAGTGTAG			MTCTLLSSCKV*	MTCTLLSSCKV*			ATCTATTGTT	AGTTCATAGT	0		0	0	0	0	0
4484	2425	an	AN4636.1	57.m05549	AO070248000018	0	-127	-113					ATGACGTCAGTGTAG	ATGACGTCAGTGTAG			MTSV*	MTSV*			TCAACCAGTA	CATAACCGCA	0		0	0	0	0	0
4486	2425	ao	AN4636.1	57.m05549	AO070248000018	0					-241	-221	ATGGTGAATAGCGTCTTCTGA			ATGGTGAATAGCGTCTTCTGA	MVNSVF*			MVNSVF*	CTTCCTAAAC	TTGTATTGCG	0		0	0	0	0	0
4487	2425	ao	AN4636.1	57.m05549	AO070248000018	0					-192	-160	ATGAACTCTATTGATGTATGTATATTAAACTAA			ATGAACTCTATTGATGTATGTATATTAAACTAA	MNSIDVCILN*			MNSIDVCILN*	CCTCTTGTGT	GTGGGCCGAG	0		0	0	0	0	0
4488	2425	ao	AN4636.1	57.m05549	AO070248000018	0					-179	-165	ATGTATGTATATTAA			ATGTATGTATATTAA	MYVY*			MYVY*	AACTCTATTG	ACTAAGTGGG	0		0	0	0	0	0
4489	2425	ao	AN4636.1	57.m05549	AO070248000018	0					-175	-125	ATGTATATTAAACTAAGTGGGCCGAGACACTCGATCTATCGGATCGGGTAA			ATGTATATTAAACTAAGTGGGCCGAGACACTCGATCTATCGGATCGGGTAA	MYIKLSGPRHSIYRIG*			MYIKLSGPRHSIYRIG*	CTATTGATGT	TATAAATAGA	0		0	0	0	0	0
4490	2425	ao	AN4636.1	57.m05549	AO070248000018	0					-90	-55	ATGTGCCCGCCGCTAAGCCTCCTGAGAAGAAAATAA			ATGTGCCCGCCGCTAAGCCTCCTGAGAAGAAAATAA	MCPPLSLLRRK*			MCPPLSLLRRK*	CCGTGACGTC	AAAACATTCA	0		0	0	0	0	0
4491	2426	ao	AN7511.1	57.m05828	AO070258000009	0					-223	-206	ATGGTGGTACTAATTTAA			ATGGTGGTACTAATTTAA	MVVLI*			MVVLI*	CAGTAATCAC	CCCTTCAGGT	0		0	0	0	0	0
4492	2426	ao	AN7511.1	57.m05828	AO070258000009	0					-189	-139	ATGTGCATACGTAGTTGCCCTGCATATGCTGTACTTCTTGGCAAGGTATGA			ATGTGCATACGTAGTTGCCCTGCATATGCTGTACTTCTTGGCAAGGTATGA	MCIRSCPAYAVLLGKV*			MCIRSCPAYAVLLGKV*	AGGTACTCCC	GAACCCATAA	0		0	0	0	0	0
4499	2428	an	AN3877.1	56.m02409	AO070263000010	0	-162	-85					ATGGCTTGGTTCCAGACTCATGTAGTGATCCACTCGCTTAGAATGTGTCTTCGCATAGCCGCATCTCTTAAAATCTGA	ATGGCTTGGTTCCAGACTCATGTAGTGATCCACTCGCTTAGAATGTGTCTTCGCATAGCCGCATCTCTTAAAATCTGA			MAWFQTHVVIHSLRMCLRIAASLKI*	MAWFQTHVVIHSLRMCLRIAASLKI*			TATTTCCCGA	AGCCGCTGCC	0		0	0	0	0	0
4500	2428	an	AN3877.1	56.m02409	AO070263000010	0	-120	-85					ATGTGTCTTCGCATAGCCGCATCTCTTAAAATCTGA	ATGTGTCTTCGCATAGCCGCATCTCTTAAAATCTGA			MCLRIAASLKI*	MCLRIAASLKI*			CTCGCTTAGA	AGCCGCTGCC	0		0	0	0	0	0
4501	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-197	-84	ATGCCGCTGCCATCAACGGCGTGTGAATGGTGGATTGCGAGCAATCATAGCCACAATGCCGGTGGCCAATGCCCCCTGGCTAATGGCTGTCGTCTGACATGGCTCGGAGAATAA			ATGCCGCTGCCATCAACGGCGTGTGAATGGTGGATTGCGAGCAATCATAGCCACAATGCCGGTGGCCAATGCCCCCTGGCTAATGGCTGTCGTCTGACATGGCTCGGAGAATAA	MPLPSTACEWWIASNHSHNAGGQCPLANGCRLTWLGE*			MPLPSTACEWWIASNHSHNAGGQCPLANGCRLTWLGE*	TTACCGAGGC	ATATGATGGC	0		0	0	0	0	0
4502	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-171	-148	ATGGTGGATTGCGAGCAATCATAG			ATGGTGGATTGCGAGCAATCATAG	MVDCEQS*			MVDCEQS*	CGGCGTGTGA	CCACAATGCC	0		0	0	0	0	0
4503	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-142	-101	ATGCCGGTGGCCAATGCCCCCTGGCTAATGGCTGTCGTCTGA			ATGCCGGTGGCCAATGCCCCCTGGCTAATGGCTGTCGTCTGA	MPVANAPWLMAVV*			MPVANAPWLMAVV*	CATAGCCACA	CATGGCTCGG	0		0	0	0	0	0
4504	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-129	-115	ATGCCCCCTGGCTAA			ATGCCCCCTGGCTAA	MPPG*			MPPG*	CCGGTGGCCA	TGGCTGTCGT	0		0	0	0	0	0
4505	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-115	-101	ATGGCTGTCGTCTGA			ATGGCTGTCGTCTGA	MAVV*			MAVV*	CCCCTGGCTA	CATGGCTCGG	0		0	0	0	0	0
4506	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-99	-34	ATGGCTCGGAGAATAAATATGATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA			ATGGCTCGGAGAATAAATATGATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA	MARRINMMAILPPTPTIHHLC*			MARRINMMAILPPTPTIHHLC*	GTCGTCTGAC	ACATACAGAA	0		0	0	0	0	0
4507	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-81	-34	ATGATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA			ATGATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA	MMAILPPTPTIHHLC*			MMAILPPTPTIHHLC*	GAGAATAAAT	ACATACAGAA	0		0	0	0	0	0
4508	2428	ao	AN3877.1	56.m02409	AO070263000010	0					-78	-34	ATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA			ATGGCCATTCTTCCTCCCACGCCCACAATTCATCACCTTTGTTGA	MAILPPTPTIHHLC*			MAILPPTPTIHHLC*	AATAAATATG	ACATACAGAA	0		0	0	0	0	0
4518	2431	af	AN8829.1	72.m19523	AO070271000051	0			-160	-137			ATGCTGGGACTTGCGGAAACCTAG		ATGCTGGGACTTGCGGAAACCTAG		MLGLAET*		MLGLAET*		CAGTACGGCG	AAACACATAT	0		0	0	0	0	0
4516	2431	an	AN8829.1	72.m19523	AO070271000051	0	-158	-87					ATGACAGCTATGACGAACATCTCTAGACCGGGAACATATATAAGGGTCTCTTCAACCCATAGTTCTTACTGA	ATGACAGCTATGACGAACATCTCTAGACCGGGAACATATATAAGGGTCTCTTCAACCCATAGTTCTTACTGA			MTAMTNISRPGTYIRVSSTHSSY*	MTAMTNISRPGTYIRVSSTHSSY*			GAGTTCCATA	GATAACAAGC	0		0	0	0	0	0
4517	2431	an	AN8829.1	72.m19523	AO070271000051	0	-149	-87					ATGACGAACATCTCTAGACCGGGAACATATATAAGGGTCTCTTCAACCCATAGTTCTTACTGA	ATGACGAACATCTCTAGACCGGGAACATATATAAGGGTCTCTTCAACCCATAGTTCTTACTGA			MTNISRPGTYIRVSSTHSSY*	MTNISRPGTYIRVSSTHSSY*			AATGACAGCT	GATAACAAGC	0		0	0	0	0	0
4519	2431	ao	AN8829.1	72.m19523	AO070271000051	0					-171	-157	ATGACGGCTATCTGA			ATGACGGCTATCTGA	MTAI*			MTAI*	ATACATAAGG	TGTCAGAAGT	0		0	0	0	0	0
4520	2431	ao	AN8829.1	72.m19523	AO070271000051	0					-138	-127	ATGGGGGACTGA			ATGGGGGACTGA	MGD*			MGD*	GTGCGTTGGG	AACGCTTATA	0		0	0	0	0	0
4522	2434	an	AN7337.1	72.m19735	AO070278000065	0	-119	-99					ATGAACTGCTTGAAGAAGTAA	ATGAACTGCTTGAAGAAGTAA			MNCLKK*	MNCLKK*			CGGGCGTCTG	TTCGGTCTTT	0	R	0	0	0	0	0
4527	2436	af	AN4684.1	71.m15668	AO070284000040	0			-245	-198			ATGCGGGCTAGCCATCTTTGGCTTCTTGCTAGTCCCCGGATTAGTTAA		ATGCGGGCTAGCCATCTTTGGCTTCTTGCTAGTCCCCGGATTAGTTAA		MRASHLWLLASPRIS*		MRASHLWLLASPRIS*		AGTGGTGAAA	GCATCACATG	0	I	FG08571.1	MG02622.1	0	0	0
4528	2436	af	AN4684.1	71.m15668	AO070284000040	0			-190	-89			ATGAAAATGAACGGCACGATCCCGCATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGATTGATCATGAAGTGTTCTGGTTTAATCCTTGA		ATGAAAATGAACGGCACGATCCCGCATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGATTGATCATGAAGTGTTCTGGTTTAATCCTTGA		MKMNGTIPHDVAVLVDLQKNEALIDHEVFWFNP*		MKMNGTIPHDVAVLVDLQKNEALIDHEVFWFNP*		TAAGCATCAC	TTCAGCGCAT	0	I	FG08571.1	MG02622.1	0	0	0
4529	2436	af	AN4684.1	71.m15668	AO070284000040	0			-184	-89			ATGAACGGCACGATCCCGCATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGATTGATCATGAAGTGTTCTGGTTTAATCCTTGA		ATGAACGGCACGATCCCGCATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGATTGATCATGAAGTGTTCTGGTTTAATCCTTGA		MNGTIPHDVAVLVDLQKNEALIDHEVFWFNP*		MNGTIPHDVAVLVDLQKNEALIDHEVFWFNP*		TCACATGAAA	TTCAGCGCAT	0	I	FG08571.1	MG02622.1	0	0	0
4530	2436	af	AN4684.1	71.m15668	AO070284000040	0			-165	-121			ATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGA		ATGACGTCGCGGTCTTGGTTGATCTCCAAAAGAACGAAGCATTGA		MTSRSWLISKRTKH*		MTSRSWLISKRTKH*		ACGATCCCGC	TTGATCATGA	0	I	FG08571.1	MG02622.1	0	0	0
4531	2436	af	AN4684.1	71.m15668	AO070284000040	0			-114	-37			ATGAAGTGTTCTGGTTTAATCCTTGATTCAGCGCATCATGTTAGTCGGTGGAGTGCCACTTCCAGCACCCTTCATTAA		ATGAAGTGTTCTGGTTTAATCCTTGATTCAGCGCATCATGTTAGTCGGTGGAGTGCCACTTCCAGCACCCTTCATTAA		MKCSGLILDSAHHVSRWSATSSTLH*		MKCSGLILDSAHHVSRWSATSSTLH*		TTGATTGATC	TCCATATCTG	0	I	FG08571.1	MG02622.1	0	0	0
4523	2436	an	AN4684.1	71.m15668	AO070284000040	0	-176	-84					ATGGAAACAGACGGTGGTCTCCCTATCTCCTGGATGACGTCGCGGTTAGTTTATTGCTCAGTTGGGGGTGCTGGGGGCTTGCGGAAAATATAA	ATGGAAACAGACGGTGGTCTCCCTATCTCCTGGATGACGTCGCGGTTAGTTTATTGCTCAGTTGGGGGTGCTGGGGGCTTGCGGAAAATATAA			METDGGLPISWMTSRLVYCSVGGAGGLRKI*	METDGGLPISWMTSRLVYCSVGGAGGLRKI*			GCATTATCAC	CTCCTCATCC	0	I	FG08571.1	MG02622.1	0	0	0
4524	2436	an	AN4684.1	71.m15668	AO070284000040	0	-143	-84					ATGACGTCGCGGTTAGTTTATTGCTCAGTTGGGGGTGCTGGGGGCTTGCGGAAAATATAA	ATGACGTCGCGGTTAGTTTATTGCTCAGTTGGGGGTGCTGGGGGCTTGCGGAAAATATAA			MTSRLVYCSVGGAGGLRKI*	MTSRLVYCSVGGAGGLRKI*			TATCTCCTGG	CTCCTCATCC	0	I	FG08571.1	MG02622.1	0	0	0
4525	2436	an	AN4684.1	71.m15668	AO070284000040	0	-63	-52					ATGAACTTCTAA	ATGAACTTCTAA			MNF*	MNF*			GTTGCACAAG	CCAAGTTATG	0	I	FG08571.1	MG02622.1	0	0	0
4532	2436	ao	AN4684.1	71.m15668	AO070284000040	0					-226	-206	ATGGGGCCATCCCCGGATTAG			ATGGGGCCATCCCCGGATTAG	MGPSPD*			MGPSPD*	GAAGGCAAAA	ATAAGCAGCT	0	I	FG08571.1	MG02622.1	0	0	0
4533	2436	ao	AN4684.1	71.m15668	AO070284000040	0					-83	-51	ATGATGGAGTTCAGGCCTCGGATTGCGCGATAG			ATGATGGAGTTCAGGCCTCGGATTGCGCGATAG	MMEFRPRIAR*			MMEFRPRIAR*	TTTCCCCCCC	ACTTGTCACC	0	I	FG08571.1	MG02622.1	0	0	0
4534	2436	ao	AN4684.1	71.m15668	AO070284000040	0					-80	-51	ATGGAGTTCAGGCCTCGGATTGCGCGATAG			ATGGAGTTCAGGCCTCGGATTGCGCGATAG	MEFRPRIAR*			MEFRPRIAR*	CCCCCCCATG	ACTTGTCACC	0	I	FG08571.1	MG02622.1	0	0	0
4536	2438	af	AN5143.1	54.m06878	AO070291000032	0			-141	-88			ATGTTCATGCGCTTTATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		ATGTTCATGCGCTTTATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		MFMRFMFCAVCRDASST*		MFMRFMFCAVCRDASST*		CATTGAGGGC	TCCCCAACAA	0	P	0	0	0	0	0
4537	2438	af	AN5143.1	54.m06878	AO070291000032	0			-135	-88			ATGCGCTTTATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		ATGCGCTTTATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		MRFMFCAVCRDASST*		MRFMFCAVCRDASST*		GGGCATGTTC	TCCCCAACAA	0	P	0	0	0	0	0

4538	2438	af	AN5143.1	54.m06878	AO070291000032	0			-126	-88			ATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		ATGTTTTGTGCTGTTTGTCGAGACGCTTCTTCAACATAA		MFCAVCRDASST*		MFCAVCRDASST*		CATGCGCTTT	TCCCCAACAA	0	P	0	0	0	0	0
4539	2438	af	AN5143.1	54.m06878	AO070291000032	0			-73	-53			ATGCAGTTGAACCGAGTATAG		ATGCAGTTGAACCGAGTATAG		MQLNRV*		MQLNRV*		CAACAAGCCC	CATTGCCACT	0	P	0	0	0	0	0
4535	2438	an	AN5143.1	54.m06878	AO070291000032	0	-201	-175					ATGTTTCCCCTCCATCGCGATAACTGA	ATGTTTCCCCTCCATCGCGATAACTGA			MFPLHRDN*	MFPLHRDN*			TATTTTTGCT	AGAATTTTCT	0	P	0	0	0	0	0
4540	2439	ao	AN5131.1	54.m06897	AO070291000050	0					-63	-19	ATGTACCTAGTACTCATAGTAAACCGACCTAGTTGTATCCATTAA			ATGTACCTAGTACTCATAGTAAACCGACCTAGTTGTATCCATTAA	MYLVLIVNRPSCIH*			MYLVLIVNRPSCIH*	TATCTCGTTG	CTGATTCGAT	0	Z	0	0	0	0	0
4543	2440	af	AN9158.1	67.m02923	AO070293000072	0			-105	-76			ATGGATAGGGAAGACGCATATAAGTTATGA		ATGGATAGGGAAGACGCATATAAGTTATGA		MDREDAYKL*		MDREDAYKL*		GTCAAATGAA	ACCATGCTCG	0	IQR	0	0	0	0	0
4541	2440	an	AN9158.1	67.m02923	AO070293000072	0	-228	-142					ATGAACCCGGCGGGCAGCATCAACAGGCCAAGTCGGCGCATTCAATTCGAGGTACTGATTAGAAATGCAAATAATGGACTGATTTGA	ATGAACCCGGCGGGCAGCATCAACAGGCCAAGTCGGCGCATTCAATTCGAGGTACTGATTAGAAATGCAAATAATGGACTGATTTGA			MNPAGSINRPSRRIQFEVLIRNANNGLI*	MNPAGSINRPSRRIQFEVLIRNANNGLI*			AACATCAAAC	AATCCAGCTT	0	IQR	0	0	0	0	0
4542	2440	an	AN9158.1	67.m02923	AO070293000072	0	-164	-147					ATGCAAATAATGGACTGA	ATGCAAATAATGGACTGA			MQIMD*	MQIMD*			CTGATTAGAA	TTTGAAATCC	0	IQR	0	0	0	0	0
4544	2440	ao	AN9158.1	67.m02923	AO070293000072	0					-213	-1	ATGTCGTTCATGTTGCGATTTTGCTGGAGACCATGTATAGGCAATAGGAGGCACCATCAAGCCACGAGGTATAAAGGTAGGGTTGAGGCCAGGGGTTGGAGGGAGCAACTCTACCGAGGAAGCCATCTCAGCAACTCTCCAGGTACTCTTGGCACGAACGAAATCTACTGTTTTTTGATCTCTTGGAATCCTTTCCCTACCAGGATAGAATAA			ATGTCGTTCATGTTGCGATTTTGCTGGAGACCATGTATAGGCAATAGGAGGCACCATCAAGCCACGAGGTATAAAGGTAGGGTTGAGGCCAGGGGTTGGAGGGAGCAACTCTACCGAGGAAGCCATCTCAGCAACTCTCCAGGTACTCTTGGCACGAACGAAATCTACTGTTTTTTGATCTCTTGGAATCCTTTCCCTACCAGGATAGAATAA	MSFMLRFCWRPCIGNRRHHQATRYKGRVEARGWREQLYRGSHLSNSPGTLGTNEIYCFLISWNPFPTRIE*			MSFMLRFCWRPCIGNRRHHQATRYKGRVEARGWREQLYRGSHLSNSPGTLGTNEIYCFLISWNPFPTRIE*	ACGAAGTACG	ATGGCATCCT	0	IQR	0	0	0	0	0
4545	2440	ao	AN9158.1	67.m02923	AO070293000072	0					-204	-1	ATGTTGCGATTTTGCTGGAGACCATGTATAGGCAATAGGAGGCACCATCAAGCCACGAGGTATAAAGGTAGGGTTGAGGCCAGGGGTTGGAGGGAGCAACTCTACCGAGGAAGCCATCTCAGCAACTCTCCAGGTACTCTTGGCACGAACGAAATCTACTGTTTTTTGATCTCTTGGAATCCTTTCCCTACCAGGATAGAATAA			ATGTTGCGATTTTGCTGGAGACCATGTATAGGCAATAGGAGGCACCATCAAGCCACGAGGTATAAAGGTAGGGTTGAGGCCAGGGGTTGGAGGGAGCAACTCTACCGAGGAAGCCATCTCAGCAACTCTCCAGGTACTCTTGGCACGAACGAAATCTACTGTTTTTTGATCTCTTGGAATCCTTTCCCTACCAGGATAGAATAA	MLRFCWRPCIGNRRHHQATRYKGRVEARGWREQLYRGSHLSNSPGTLGTNEIYCFLISWNPFPTRIE*			MLRFCWRPCIGNRRHHQATRYKGRVEARGWREQLYRGSHLSNSPGTLGTNEIYCFLISWNPFPTRIE*	GATGTCGTTC	ATGGCATCCT	0	IQR	0	0	0	0	0
4546	2440	ao	AN9158.1	67.m02923	AO070293000072	0					-181	-167	ATGTATAGGCAATAG			ATGTATAGGCAATAG	MYRQ*			MYRQ*	GCTGGAGACC	GAGGCACCAT	0	IQR	0	0	0	0	0
4547	2442	an	AN1571.1	69.m15602	AO070298000116	0	-181	-98					ATGGAGGCAATTATTGGAGGAAATACGTACTGCACTGACAAACCCCATCCTGCTCTCCGGAGGGGAGCATCTCAGGCAGGCTGA	ATGGAGGCAATTATTGGAGGAAATACGTACTGCACTGACAAACCCCATCCTGCTCTCCGGAGGGGAGCATCTCAGGCAGGCTGA			MEAIIGGNTYCTDKPHPALRRGASQAG*	MEAIIGGNTYCTDKPHPALRRGASQAG*			GTTGCCCGTG	ACAATGGGTA	0		FG03813.1	MG06009.1	NCU09775.1	0	0
4548	2442	an	AN1571.1	69.m15602	AO070298000116	0	-94	-83					ATGGGTATATAG	ATGGGTATATAG			MGI*	MGI*			AGGCTGAACA	AGGGCGAAGT	0		FG03813.1	MG06009.1	NCU09775.1	0	0
4549	2442	ao	AN1571.1	69.m15602	AO070298000116	0					-115	-29	ATGCACCAATGTCCCACGATTTACTTACTCTATCACACTGGCTCTTCGAGTATCTCCGCGCCGGCTTTGAAACACTCACAGGCGTGA			ATGCACCAATGTCCCACGATTTACTTACTCTATCACACTGGCTCTTCGAGTATCTCCGCGCCGGCTTTGAAACACTCACAGGCGTGA	MHQCPTIYLLYHTGSSSISAPALKHSQA*			MHQCPTIYLLYHTGSSSISAPALKHSQA*	GATACACAGG	CCGTCTCACC	0		FG03813.1	MG06009.1	NCU09775.1	0	0
4551	2443	af	AN7359.1	52.m03956	AO070302000084	0			-203	-159			ATGTGCAAATCATACCACCTATTAGCAGTGCTCAGGATTCCCTAA		ATGTGCAAATCATACCACCTATTAGCAGTGCTCAGGATTCCCTAA		MCKSYHLLAVLRIP*		MCKSYHLLAVLRIP*		TCTCGGAAAG	TAAGCAAGTC	0	QI	0	0	0	0	0
4550	2443	an	AN7359.1	52.m03956	AO070302000084	0	-155	-126					ATGATAGGAGTGGACCGATGGGTTGACTAG	ATGATAGGAGTGGACCGATGGGTTGACTAG			MIGVDRWVD*	MIGVDRWVD*			ACTGGCTAGA	GAATGCTTGG	0	QI	0	0	0	0	0
4552	2443	ao	AN7359.1	52.m03956	AO070302000084	0					-268	-257	ATGTATTTCTAG			ATGTATTTCTAG	MYF*			MYF*	TAGGTAGAGG	GCTTTCAATT	0	QI	0	0	0	0	0
4553	2443	ao	AN7359.1	52.m03956	AO070302000084	0					-169	-134	ATGCAAGGATGCGAAGGTATCACCTGTGCTATATAG			ATGCAAGGATGCGAAGGTATCACCTGTGCTATATAG	MQGCEGITCAI*			MQGCEGITCAI*	AGGTGGGGTT	GCACCTGCTA	0	QI	0	0	0	0	0
4554	2443	ao	AN7359.1	52.m03956	AO070302000084	0					-161	-123	ATGCGAAGGTATCACCTGTGCTATATAGGCACCTGCTAA			ATGCGAAGGTATCACCTGTGCTATATAGGCACCTGCTAA	MRRYHLCYIGTC*			MRRYHLCYIGTC*	TTATGCAAGG	GAGTGGGATA	0	QI	0	0	0	0	0
4556	2445	af	AN0681.1	71.m15200	AO070303000069	0			-85	-59			ATGCACTCAGTACCATACATCTTATAA		ATGCACTCAGTACCATACATCTTATAA		MHSVPYIL*		MHSVPYIL*		CTACTATCAA	ATCTGAGTAG	0	E	0	0	0	0	0
4555	2445	an	AN0681.1	71.m15200	AO070303000069	0	-94	-50					ATGCAGCCGTGGTCAACTGAACTTCGCAACAGCTCGTGTCCCTGA	ATGCAGCCGTGGTCAACTGAACTTCGCAACAGCTCGTGTCCCTGA			MQPWSTELRNSSCP*	MQPWSTELRNSSCP*			TGTAGTATAA	AAGGCTGGTC	0	E	0	0	0	0	0
4557	2445	ao	AN0681.1	71.m15200	AO070303000069	0					-235	-182	ATGGTAGTGGGGCGTTTAAACCACATTACACCCAATGGGACACCGATAATTTAA			ATGGTAGTGGGGCGTTTAAACCACATTACACCCAATGGGACACCGATAATTTAA	MVVGRLNHITPNGTPII*			MVVGRLNHITPNGTPII*	TGGGAAGTTG	GGACAAGCAT	0	E	0	0	0	0	0
4558	2445	ao	AN0681.1	71.m15200	AO070303000069	0					-201	-187	ATGGGACACCGATAA			ATGGGACACCGATAA	MGHR*			MGHR*	ATTACACCCA	TTTAAGGACA	0	E	0	0	0	0	0
4564	2448	af	AN2123.1	69.m15162	AO070306000102	0			-282	-250			ATGTCAAACTGCGCATTGAGGAAGGAGAAATAA		ATGTCAAACTGCGCATTGAGGAAGGAGAAATAA		MSNCALRKEK*		MSNCALRKEK*		CTCCCCGCGC	CAAGGAGATA	0	K	0	0	0	0	0
4562	2448	an	AN2123.1	69.m15162	AO070306000102	0	-245	-66					ATGCGCTGGACCAGGGATAGGAATAATAAAGGTGTAGGCGGTCTTGTCGGCCATAGCAGCTGCCCGAACGCACGGGCCATCACCAACCTCTGGATCTCCGCGATGATTGCGGGCGAAAACATCCCAACATTTGTAGCTTCTAACCTTCCATTTCCAGCGACTCCAGTGCGCTGGACCTAG	ATGCGCTGGACCAGGGATAGGAATAATAAAGGTGTAGGCGGTCTTGTCGGCCATAGCAGCTGCCCGAACGCACGGGCCATCACCAACCTCTGGATCTCCGCGATGATTGCGGGCGAAAACATCCCAACATTTGTAGCTTCTAACCTTCCATTTCCAGCGACTCCAGTGCGCTGGACCTAG			MRWTRDRNNKGVGGLVGHSSCPNARAITNLWISAMIAGENIPTFVASNLPFPATPVRWT*	MRWTRDRNNKGVGGLVGHSSCPNARAITNLWISAMIAGENIPTFVASNLPFPATPVRWT*			ACTGGAGAGC	CGACCGACTA	0	K	0	0	0	0	0
4563	2448	an	AN2123.1	69.m15162	AO070306000102	0	-143	-66					ATGATTGCGGGCGAAAACATCCCAACATTTGTAGCTTCTAACCTTCCATTTCCAGCGACTCCAGTGCGCTGGACCTAG	ATGATTGCGGGCGAAAACATCCCAACATTTGTAGCTTCTAACCTTCCATTTCCAGCGACTCCAGTGCGCTGGACCTAG			MIAGENIPTFVASNLPFPATPVRWT*	MIAGENIPTFVASNLPFPATPVRWT*			GATCTCCGCG	CGACCGACTA	0	K	0	0	0	0	0
4565	2448	ao	AN2123.1	69.m15162	AO070306000102	0					-189	-166	ATGCGAGACCACTGCCGCCTTTAG			ATGCGAGACCACTGCCGCCTTTAG	MRDHCRL*			MRDHCRL*	TGCGACAATC	ACGCACGGAC	0	K	0	0	0	0	0
4566	2456	af	AN9274.1	59.m08422	AO070333000200	0			-86	-69			ATGTCCTTAGCCGGATGA		ATGTCCTTAGCCGGATGA		MSLAG*		MSLAG*		TGACTCGGCA	CCCTCATAAT	0		0	0	0	0	0
4569	2461	af	AN1290.1	55.m03194	AO070339000255	0			-144	-43			ATGAGTATGTTTCTCTCATCTCAACCCCCGTTCCCTTTCATCATTCCTCTCTATTCTGTCGTCCATCCTTATTCCATCAAATTCCAGCCGGTTTGTGAGTAA		ATGAGTATGTTTCTCTCATCTCAACCCCCGTTCCCTTTCATCATTCCTCTCTATTCTGTCGTCCATCCTTATTCCATCAAATTCCAGCCGGTTTGTGAGTAA		MSMFLSSQPPFPFIIPLYSVVHPYSIKFQPVCE*		MSMFLSSQPPFPFIIPLYSVVHPYSIKFQPVCE*		ATCAAGTGAC	ATTTCTGAAA	0	P	0	0	0	YJL094C	0
4570	2461	af	AN1290.1	55.m03194	AO070339000255	0			-138	-43			ATGTTTCTCTCATCTCAACCCCCGTTCCCTTTCATCATTCCTCTCTATTCTGTCGTCCATCCTTATTCCATCAAATTCCAGCCGGTTTGTGAGTAA		ATGTTTCTCTCATCTCAACCCCCGTTCCCTTTCATCATTCCTCTCTATTCTGTCGTCCATCCTTATTCCATCAAATTCCAGCCGGTTTGTGAGTAA		MFLSSQPPFPFIIPLYSVVHPYSIKFQPVCE*		MFLSSQPPFPFIIPLYSVVHPYSIKFQPVCE*		TGACATGAGT	ATTTCTGAAA	0	P	0	0	0	YJL094C	0
4567	2461	an	AN1290.1	55.m03194	AO070339000255	0	-216	-190					ATGGCCAAGGATTCTATCCGCAGTTAA	ATGGCCAAGGATTCTATCCGCAGTTAA			MAKDSIRS*	MAKDSIRS*			TGACCGACAG	CCTTGAATAT	0	P	0	0	0	YJL094C	0
4568	2461	an	AN1290.1	55.m03194	AO070339000255	0	-181	-170					ATGATTCATTGA	ATGATTCATTGA			MIH*	MIH*			AACCTTGAAT	CTCCTCCCCA	0	P	0	0	0	YJL094C	0
4571	2462	af	AN5971.1	72.m19187	AO070340000329	0			-168	-94			ATGAGGCCCCGGAGTCATTGTTTCTCCGCTAACCGACAGAACCTCAACCTTCGTACAAATCACTCCGCAGGATAG		ATGAGGCCCCGGAGTCATTGTTTCTCCGCTAACCGACAGAACCTCAACCTTCGTACAAATCACTCCGCAGGATAG		MRPRSHCFSANRQNLNLRTNHSAG*		MRPRSHCFSANRQNLNLRTNHSAG*		TTACTGCATT	TCCGGCTATT	0	C	0	0	0	0	0
4572	2462	ao	AN5971.1	72.m19187	AO070340000329	0					-238	-89	ATGGGTAAACCCCCTAAGCGCGGAGAGATCGATAAGTTTAGTTCCCTTCAGATGAAAGTGGCCGGAACGTCCTGGTGGAATCTCTGTTTCTCCGCCTCCCGACGGAACCTCAACTTCGCTCCCGAAGTCAATGACAACCTGAGATACTAA			ATGGGTAAACCCCCTAAGCGCGGAGAGATCGATAAGTTTAGTTCCCTTCAGATGAAAGTGGCCGGAACGTCCTGGTGGAATCTCTGTTTCTCCGCCTCCCGACGGAACCTCAACTTCGCTCCCGAAGTCAATGACAACCTGAGATACTAA	MGKPPKRGEIDKFSSLQMKVAGTSWWNLCFSASRRNLNFAPEVNDNLRY*			MGKPPKRGEIDKFSSLQMKVAGTSWWNLCFSASRRNLNFAPEVNDNLRY*	CGGGTTGAGA	ATTACATGGT	0	C	0	0	0	0	0
4573	2462	ao	AN5971.1	72.m19187	AO070340000329	0					-187	-89	ATGAAAGTGGCCGGAACGTCCTGGTGGAATCTCTGTTTCTCCGCCTCCCGACGGAACCTCAACTTCGCTCCCGAAGTCAATGACAACCTGAGATACTAA			ATGAAAGTGGCCGGAACGTCCTGGTGGAATCTCTGTTTCTCCGCCTCCCGACGGAACCTCAACTTCGCTCCCGAAGTCAATGACAACCTGAGATACTAA	MKVAGTSWWNLCFSASRRNLNFAPEVNDNLRY*			MKVAGTSWWNLCFSASRRNLNFAPEVNDNLRY*	TTCCCTTCAG	ATTACATGGT	0	C	0	0	0	0	0
4574	2462	ao	AN5971.1	72.m19187	AO070340000329	0					-108	-97	ATGACAACCTGA			ATGACAACCTGA	MTT*			MTT*	CCCGAAGTCA	GATACTAAAT	0	C	0	0	0	0	0
4575	2463	ao	AN5975.1	72.m19192	AO070340000331	0					-261	-250	ATGTTTCTGTAG			ATGTTTCTGTAG	MFL*			MFL*	CCATCGTGAA	TACATTTAAT	0	G	0	0	0	0	0
4579	2465	af	AN8454.1	52.m03681	AO070341000304	0			-218	-99			ATGGCCAATAGGGGAGTGCACGTGACTTATCGCGGGGGGGTGGCTCGGCATTCGACCACCAATCAGAGCTCTTTGGCCCATACTGTACCACACGAGGCGTATCTTTTGCAGAATCAGTAG		ATGGCCAATAGGGGAGTGCACGTGACTTATCGCGGGGGGGTGGCTCGGCATTCGACCACCAATCAGAGCTCTTTGGCCCATACTGTACCACACGAGGCGTATCTTTTGCAGAATCAGTAG		MANRGVHVTYRGGVARHSTTNQSSLAHTVPHEAYLLQNQ*		MANRGVHVTYRGGVARHSTTNQSSLAHTVPHEAYLLQNQ*		GGAGTCGGAG	GTAGATATGC	0	Q	0	0	0	0	0
4576	2465	an	AN8454.1	52.m03681	AO070341000304	0	-164	-87					ATGCGAGGAGGATGCAGATCCATCAAGCCGAAAGGGCGGGGGACGGTACTGATAAAGATATGCCCAGTCAACATATAA	ATGCGAGGAGGATGCAGATCCATCAAGCCGAAAGGGCGGGGGACGGTACTGATAAAGATATGCCCAGTCAACATATAA			MRGGCRSIKPKGRGTVLIKICPVNI*	MRGGCRSIKPKGRGTVLIKICPVNI*			TCCAACTCCC	GACACCTCCA	0	Q	0	0	0	0	0
4577	2465	an	AN8454.1	52.m03681	AO070341000304	0	-153	-64					ATGCAGATCCATCAAGCCGAAAGGGCGGGGGACGGTACTGATAAAGATATGCCCAGTCAACATATAAGACACCTCCACCCTCTCCAATAG	ATGCAGATCCATCAAGCCGAAAGGGCGGGGGACGGTACTGATAAAGATATGCCCAGTCAACATATAAGACACCTCCACCCTCTCCAATAG			MQIHQAERAGDGTDKDMPSQHIRHLHPLQ*	MQIHQAERAGDGTDKDMPSQHIRHLHPLQ*			TGCGAGGAGG	TGGACTGTCT	0	Q	0	0	0	0	0
4578	2465	an	AN8454.1	52.m03681	AO070341000304	0	-105	-64					ATGCCCAGTCAACATATAAGACACCTCCACCCTCTCCAATAG	ATGCCCAGTCAACATATAAGACACCTCCACCCTCTCCAATAG			MPSQHIRHLHPLQ*	MPSQHIRHLHPLQ*			TGATAAAGAT	TGGACTGTCT	0	Q	0	0	0	0	0
4580	2465	ao	AN8454.1	52.m03681	AO070341000304	0					-216	-193	ATGAACCAATCAGCCACCGGTTAA			ATGAACCAATCAGCCACCGGTTAA	MNQSATG*			MNQSATG*	TGAGTCGGGT	CACAGATGTC	0	Q	0	0	0	0	0
4581	2465	ao	AN8454.1	52.m03681	AO070341000304	0					-187	-164	ATGTCAATTCCCAAAGGGGCTTAA			ATGTCAATTCCCAAAGGGGCTTAA	MSIPKGA*			MSIPKGA*	GTTAACACAG	AGCCAAATTA	0	Q	0	0	0	0	0
4582	2466	an	AN8502.1	52.m03748	AO070342000411	0	-148	-104					ATGAAACCTGATCGGGGAGGAAATGGTCATGCTGATGCTCCATGA	ATGAAACCTGATCGGGGAGGAAATGGTCATGCTGATGCTCCATGA			MKPDRGGNGHADAP*	MKPDRGGNGHADAP*			TAGCTCGACA	CCCGCTGATC	0	G	0	0	0	0	0
4583	2466	an	AN8502.1	52.m03748	AO070342000411	0	-126	-61					ATGGTCATGCTGATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA	ATGGTCATGCTGATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA			MVMLMLHDPLIVGIKSLRDPG*	MVMLMLHDPLIVGIKSLRDPG*			CGGGGAGGAA	GTCACGCAGG	0	G	0	0	0	0	0
4584	2466	an	AN8502.1	52.m03748	AO070342000411	0	-120	-61					ATGCTGATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA	ATGCTGATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA			MLMLHDPLIVGIKSLRDPG*	MLMLHDPLIVGIKSLRDPG*			GGAAATGGTC	GTCACGCAGG	0	G	0	0	0	0	0
4585	2466	an	AN8502.1	52.m03748	AO070342000411	0	-114	-61					ATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA	ATGCTCCATGACCCGCTGATCGTGGGTATAAAGTCGTTACGGGACCCTGGTTAA			MLHDPLIVGIKSLRDPG*	MLHDPLIVGIKSLRDPG*			GGTCATGCTG	GTCACGCAGG	0	G	0	0	0	0	0
4586	2466	an	AN8502.1	52.m03748	AO070342000411	0	-107	-96					ATGACCCGCTGA	ATGACCCGCTGA			MTR*	MTR*			CTGATGCTCC	TCGTGGGTAT	0	G	0	0	0	0	0
4587	2466	ao	AN8502.1	52.m03748	AO070342000411	0					-250	-152	ATGAGATCATCCTGCACATGGAGAGGCACCCCCACGTCGGCTTGTGCCGTTGCTTGGCTGGTCCTACCCCGGGATTTGGGTGGAGTGGGTTGGGCATGA			ATGAGATCATCCTGCACATGGAGAGGCACCCCCACGTCGGCTTGTGCCGTTGCTTGGCTGGTCCTACCCCGGGATTTGGGTGGAGTGGGTTGGGCATGA	MRSSCTWRGTPTSACAVAWLVLPRDLGGVGWA*			MRSSCTWRGTPTSACAVAWLVLPRDLGGVGWA*	TCGTCCCCGG	TGGTCGTTTG	0	G	0	0	0	0	0
4588	2466	ao	AN8502.1	52.m03748	AO070342000411	0					-233	-123	ATGGAGAGGCACCCCCACGTCGGCTTGTGCCGTTGCTTGGCTGGTCCTACCCCGGGATTTGGGTGGAGTGGGTTGGGCATGATGGTCGTTTGCGACCGTGTCATCCTATAA			ATGGAGAGGCACCCCCACGTCGGCTTGTGCCGTTGCTTGGCTGGTCCTACCCCGGGATTTGGGTGGAGTGGGTTGGGCATGATGGTCGTTTGCGACCGTGTCATCCTATAA	MERHPHVGLCRCLAGPTPGFGWSGLGMMVVCDRVIL*			MERHPHVGLCRCLAGPTPGFGWSGLGMMVVCDRVIL*	CATCCTGCAC	TAGTCTCTCC	0	G	0	0	0	0	0
4589	2466	ao	AN8502.1	52.m03748	AO070342000411	0					-155	-123	ATGATGGTCGTTTGCGACCGTGTCATCCTATAA			ATGATGGTCGTTTGCGACCGTGTCATCCTATAA	MMVVCDRVIL*			MMVVCDRVIL*	TGGGTTGGGC	TAGTCTCTCC	0	G	0	0	0	0	0

4590	2466	ao	AN8502.1	52.m03748	AO070342000411	0					-152	-123	ATGGTCGTTTGCGACCGTGTCATCCTATAA			ATGGTCGTTTGCGACCGTGTCATCCTATAA	MVVCDRVIL*			MVVCDRVIL*	GTTGGGCATG	TAGTCTCTCC	0	G	0	0	0	0	0
4594	2468	af	AN2173.1	72.m19667	AO070343000244	0			-223	-191			ATGGAGAGTTTGTGTTGGGCTTCATTTCATTAA		ATGGAGAGTTTGTGTTGGGCTTCATTTCATTAA		MESLCWASFH*		MESLCWASFH*		TGGATTTCTC	CAACTGCAAT	0	F	0	0	0	YNL083W	YNL083W
4591	2468	an	AN2173.1	72.m19667	AO070343000244	0	-199	-173					ATGGCCATTATCAGGCCTGAACGTTAA	ATGGCCATTATCAGGCCTGAACGTTAA			MAIIRPER*	MAIIRPER*			TTGATTTCTC	TCTGCGATAT	0	F	0	0	0	YNL083W	YNL083W
4605	2472	af	AN2016.1	58.m07624	AO070202000009	0			-270	-250			ATGATCTACTTTCCCTTCTGA		ATGATCTACTTTCCCTTCTGA		MIYFPF*		MIYFPF*		TTTTTTCTCC	ACAACTTATC	0		0	0	0	0	0
4606	2472	af	AN2016.1	58.m07624	AO070202000009	0			-189	-157			ATGGTTGTATTCATGGCTGAGTGCTACATGTAA		ATGGTTGTATTCATGGCTGAGTGCTACATGTAA		MVVFMAECYM*		MVVFMAECYM*		CGTGCTGGTC	CTATCAGCAT	0		0	0	0	0	0
4607	2472	af	AN2016.1	58.m07624	AO070202000009	0			-177	-157			ATGGCTGAGTGCTACATGTAA		ATGGCTGAGTGCTACATGTAA		MAECYM*		MAECYM*		GGTTGTATTC	CTATCAGCAT	0		0	0	0	0	0
4608	2472	af	AN2016.1	58.m07624	AO070202000009	0			-126	-109			ATGGCCTCAAGGCGTTGA		ATGGCCTCAAGGCGTTGA		MASRR*		MASRR*		GCGATTCACA	GATTATTTTG	0		0	0	0	0	0
4602	2472	an	AN2016.1	58.m07624	AO070202000009	0	-139	-98					ATGCGTACGTCTGCAAGGACTATAGCGATTTTATACTGTTGA	ATGCGTACGTCTGCAAGGACTATAGCGATTTTATACTGTTGA			MRTSARTIAILYC*	MRTSARTIAILYC*			ATTTTCACCC	CGAGCAATCC	0		0	0	0	0	0
4603	2472	an	AN2016.1	58.m07624	AO070202000009	0	-84	-58					ATGACCCGCATGCCTCTTCAAGACTAG	ATGACCCGCATGCCTCTTCAAGACTAG			MTRMPLQD*	MTRMPLQD*			GCAATCCGAC	CTTCTCATCT	0		0	0	0	0	0
4604	2472	an	AN2016.1	58.m07624	AO070202000009	0	-75	-58					ATGCCTCTTCAAGACTAG	ATGCCTCTTCAAGACTAG			MPLQD*	MPLQD*			CATGACCCGC	CTTCTCATCT	0		0	0	0	0	0
4609	2472	ao	AN2016.1	58.m07624	AO070202000009	0					-120	-37	ATGGCGACACAGCCCGCTTCGCTATCCCTCGCTTTTACGTCGGCCATTCTTCTAGTTGCTCTCGCGGGATGCCATGATTTCTAA			ATGGCGACACAGCCCGCTTCGCTATCCCTCGCTTTTACGTCGGCCATTCTTCTAGTTGCTCTCGCGGGATGCCATGATTTCTAA	MATQPASLSLAFTSAILLVALAGCHDF*			MATQPASLSLAFTSAILLVALAGCHDF*	CTCAACCGTG	AGGCTCCACA	0		0	0	0	0	0
4613	2474	af	AN0842.1	70.m15442	AO070216000002	0			-82	-41			ATGAACGACATCCCGCAACTTCTCATATGTGGACCCGAATGA		ATGAACGACATCCCGCAACTTCTCATATGTGGACCCGAATGA		MNDIPQLLICGPE*		MNDIPQLLICGPE*		TGAAGGAGGT	GAGACGTCGT	0	R	0	0	0	0	0
4611	2474	an	AN0842.1	70.m15442	AO070216000002	0	-211	-197					ATGCTGTGGCTTTAG	ATGCTGTGGCTTTAG			MLWL*	MLWL*			CGGCCAGGTG	GCGCGGAGAG	0	R	0	0	0	0	0
4612	2474	an	AN0842.1	70.m15442	AO070216000002	0	-70	-35					ATGAGGGTACCGCATCCTCGCGTTTACTCCTGCTAG	ATGAGGGTACCGCATCCTCGCGTTTACTCCTGCTAG			MRVPHPRVYSC*	MRVPHPRVYSC*			CAGACCTGCA	AACCGACAGC	0	R	0	0	0	0	0
4616	2474	ao	AN0842.1	70.m15442	AO070216000002	0					-84	-37	ATGAGGATCGTAGAACTCGTTTATCCTTTACAACGCGGATTCGCATGA			ATGAGGATCGTAGAACTCGTTTATCCTTTACAACGCGGATTCGCATGA	MRIVELVYPLQRGFA*			MRIVELVYPLQRGFA*	GGATCCTGAG	GAGCCCCTCA	0	R	0	0	0	0	0
4618	2475	an	AN1073.1	70.m15165	AO070218000012	0	-195	-175					ATGTGTGGGGAGGATAAGTAA	ATGTGTGGGGAGGATAAGTAA			MCGEDK*	MCGEDK*			AAGCAGGACC	CTATTTTGAG	0	E	0	0	0	0	0
4621	2478	af	AN5176.1	69.m14873	AO070247000007	0			-253	-131			ATGGCTAACCCCTATAATCTTAGACAAACATCGCTCTCCTATCTTGAAACAGGTAAATGCGACGGACTGACGGACCGTTGGACCGGACGTGTTGAGATGAAAATATGCAGCACTCCCAGCTAG		ATGGCTAACCCCTATAATCTTAGACAAACATCGCTCTCCTATCTTGAAACAGGTAAATGCGACGGACTGACGGACCGTTGGACCGGACGTGTTGAGATGAAAATATGCAGCACTCCCAGCTAG		MANPYNLRQTSLSYLETGKCDGLTDRWTGRVEMKICSTPS*		MANPYNLRQTSLSYLETGKCDGLTDRWTGRVEMKICSTPS*		CATTGCCTGC	CTAGCTTCCG	0		0	0	0	0	0
4622	2478	af	AN5176.1	69.m14873	AO070247000007	0			-197	-159			ATGCGACGGACTGACGGACCGTTGGACCGGACGTGTTGA		ATGCGACGGACTGACGGACCGTTGGACCGGACGTGTTGA		MRRTDGPLDRTC*		MRRTDGPLDRTC*		AAACAGGTAA	GATGAAAATA	0		0	0	0	0	0
4623	2478	af	AN5176.1	69.m14873	AO070247000007	0			-157	-131			ATGAAAATATGCAGCACTCCCAGCTAG		ATGAAAATATGCAGCACTCCCAGCTAG		MKICSTPS*		MKICSTPS*		ACGTGTTGAG	CTAGCTTCCG	0		0	0	0	0	0
4619	2478	an	AN5176.1	69.m14873	AO070247000007	0	-158	-126					ATGGTAGATAGATTATCCCTAGTGAGCATGTAA	ATGGTAGATAGATTATCCCTAGTGAGCATGTAA			MVDRLSLVSM*	MVDRLSLVSM*			TGGTTCAGGC	GCTATGAGAG	0		0	0	0	0	0
4620	2478	an	AN5176.1	69.m14873	AO070247000007	0	-122	-90					ATGAGAGAGTATCACCTTGAGATCAAGGTATAA	ATGAGAGAGTATCACCTTGAGATCAAGGTATAA			MREYHLEIKV*	MREYHLEIKV*			CATGTAAGCT	AGACCTCTAG	0		0	0	0	0	0
4624	2478	ao	AN5176.1	69.m14873	AO070247000007	0					-248	-147	ATGGCTTCCTCAATCTCTATGAAACGGTCATTTCAGCGGCTTCACGGTCCGTTGCACCGGCTGGTATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGA			ATGGCTTCCTCAATCTCTATGAAACGGTCATTTCAGCGGCTTCACGGTCCGTTGCACCGGCTGGTATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGA	MASSISMKRSFQRLHGPLHRLVWIGLRTGIFPK*			MASSISMKRSFQRLHGPLHRLVWIGLRTGIFPK*	CGGTTCCTGT	ACACCGGGGT	0		0	0	0	0	0
4625	2478	ao	AN5176.1	69.m14873	AO070247000007	0					-230	-147	ATGAAACGGTCATTTCAGCGGCTTCACGGTCCGTTGCACCGGCTGGTATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGA			ATGAAACGGTCATTTCAGCGGCTTCACGGTCCGTTGCACCGGCTGGTATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGA	MKRSFQRLHGPLHRLVWIGLRTGIFPK*			MKRSFQRLHGPLHRLVWIGLRTGIFPK*	CTCAATCTCT	ACACCGGGGT	0		0	0	0	0	0
4626	2478	ao	AN5176.1	69.m14873	AO070247000007	0					-183	-124	ATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGAACACCGGGGTGTTTCTCTCGTAA			ATGGATAGGGCTTCGTACAGGAATTTTTCCGAAATGAACACCGGGGTGTTTCTCTCGTAA	MDRASYRNFSEMNTGVFLS*			MDRASYRNFSEMNTGVFLS*	ACCGGCTGGT	TTCCGAAGGC	0		0	0	0	0	0
4627	2478	ao	AN5176.1	69.m14873	AO070247000007	0					-150	-124	ATGAACACCGGGGTGTTTCTCTCGTAA			ATGAACACCGGGGTGTTTCTCTCGTAA	MNTGVFLS*			MNTGVFLS*	TTTTTCCGAA	TTCCGAAGGC	0		0	0	0	0	0
4629	2481	af	AN2440.1	69.m15218	AO070264000039	0			-155	-138			ATGCCCTGTCAGCTCTGA		ATGCCCTGTCAGCTCTGA		MPCQL*		MPCQL*		CAACGGATGC	ATCTAACTTG	0	G	0	MG04113.1	0	0	0
4628	2481	an	AN2440.1	69.m15218	AO070264000039	0	-199	-53					ATGGAAAAAGTCGCTTCGGAGGGGTACCTTCTTACCCCCACCGGGCACCTCTCCCCCGGACTTTTCGCAGAATCCACAAGCATATTAATAGATGCGCAGTCTCCGGCTTCGGTCCAACTCCTGTCTTTCTCTTCCGTCCTATCTTAG	ATGGAAAAAGTCGCTTCGGAGGGGTACCTTCTTACCCCCACCGGGCACCTCTCCCCCGGACTTTTCGCAGAATCCACAAGCATATTAATAGATGCGCAGTCTCCGGCTTCGGTCCAACTCCTGTCTTTCTCTTCCGTCCTATCTTAG			MEKVASEGYLLTPTGHLSPGLFAESTSILIDAQSPASVQLLSFSSVLS*	MEKVASEGYLLTPTGHLSPGLFAESTSILIDAQSPASVQLLSFSSVLS*			TGAGTGGCCC	TCCTCGTGCT	0	G	0	MG04113.1	0	0	0
4630	2485	ao	AN0609.1	70.m15670	AO070280000031	0					-189	-172	ATGAAAAGAGGCGTTTGA			ATGAAAAGAGGCGTTTGA	MKRGV*			MKRGV*	GTGCCGAGAG	TGGAACGCCC	0	IQ	0	0	0	0	0
4631	2485	ao	AN0609.1	70.m15670	AO070280000031	0					-172	-119	ATGGAACGCCCGGAAGGATCCAGACAAAGACAACTAGATCCCGAGGTATATTGA			ATGGAACGCCCGGAAGGATCCAGACAAAGACAACTAGATCCCGAGGTATATTGA	MERPEGSRQRQLDPEVY*			MERPEGSRQRQLDPEVY*	GAGGCGTTTG	CGCCTAGAAT	0	IQ	0	0	0	0	0
4632	2489	af	AN5109.1	54.m06913	AO070296000005	0			-250	-218			ATGAAACTATTATCTGGAATCGCATCAATTTAG		ATGAAACTATTATCTGGAATCGCATCAATTTAG		MKLLSGIASI*		MKLLSGIASI*		TTAAACCTTG	CAAGAGTTGC	0	R	FG06240.1	MG03160.1	NCU01759.1	0	0
4633	2489	af	AN5109.1	54.m06913	AO070296000005	0			-205	-185			ATGATTGAGTACATTTTATAA		ATGATTGAGTACATTTTATAA		MIEYIL*		MIEYIL*		AGAGTTGCGA	TATAATATAT	0	R	FG06240.1	MG03160.1	NCU01759.1	0	0
4634	2489	ao	AN5109.1	54.m06913	AO070296000005	0					-195	-142	ATGAGGAATATTGGATCCACCTTACATCACACTTGCCGGCTGACAAATTTATGA			ATGAGGAATATTGGATCCACCTTACATCACACTTGCCGGCTGACAAATTTATGA	MRNIGSTLHHTCRLTNL*			MRNIGSTLHHTCRLTNL*	GATTGGTCGT	AGACGTGATT	0	R	FG06240.1	MG03160.1	NCU01759.1	0	0
4635	2489	ao	AN5109.1	54.m06913	AO070296000005	0					-145	-134	ATGAAGACGTGA			ATGAAGACGTGA	MKT*			MKT*	TGACAAATTT	TTGTATTGAT	0	R	FG06240.1	MG03160.1	NCU01759.1	0	0
4636	2492	an	AN8277.1	53.m04091	AO070310000023	0	-294	-259					ATGTCCTATCGTTCAGGGTCCTATTTGGACCGCTAG	ATGTCCTATCGTTCAGGGTCCTATTTGGACCGCTAG			MSYRSGSYLDR*	MSYRSGSYLDR*			CCTACCATTT	AAATAGACTC	0	E	FG01417.1	0	0	0	0
4637	2492	ao	AN8277.1	53.m04091	AO070310000023	0					-71	-54	ATGGAACATCATCCTTGA			ATGGAACATCATCCTTGA	MEHHP*			MEHHP*	GTAACTCTAC	TATACAATCC	0	E	FG01417.1	0	0	0	0
4640	2494	af	AN8344.1	53.m04018	AO070312000017	0			-217	-47			ATGCTCCGAAGCAGAGTCATAGCTTGGTGCCAAGTAATCTGGATCTTTCTGAATTTGGACAGCATCGCCTTCTGTTTCATTCAGGTGCTCCGCGGGACGCCGAGATGGATGGGTCGCATACTGACATTCCGGTTTAAATATTCCAGGAACCAGCGTTTCCTACATTCCTGA		ATGCTCCGAAGCAGAGTCATAGCTTGGTGCCAAGTAATCTGGATCTTTCTGAATTTGGACAGCATCGCCTTCTGTTTCATTCAGGTGCTCCGCGGGACGCCGAGATGGATGGGTCGCATACTGACATTCCGGTTTAAATATTCCAGGAACCAGCGTTTCCTACATTCCTGA		MLRSRVIAWCQVIWIFLNLDSIAFCFIQVLRGTPRWMGRILTFRFKYSRNQRFLHS*		MLRSRVIAWCQVIWIFLNLDSIAFCFIQVLRGTPRWMGRILTFRFKYSRNQRFLHS*		GCTGCTGCCA	TGCCGGAACA	0	Q	0	0	0	0	0
4641	2494	af	AN8344.1	53.m04018	AO070312000017	0			-113	-81			ATGGATGGGTCGCATACTGACATTCCGGTTTAA		ATGGATGGGTCGCATACTGACATTCCGGTTTAA		MDGSHTDIPV*		MDGSHTDIPV*		GGACGCCGAG	ATATTCCAGG	0	Q	0	0	0	0	0
4642	2494	af	AN8344.1	53.m04018	AO070312000017	0			-109	-47			ATGGGTCGCATACTGACATTCCGGTTTAAATATTCCAGGAACCAGCGTTTCCTACATTCCTGA		ATGGGTCGCATACTGACATTCCGGTTTAAATATTCCAGGAACCAGCGTTTCCTACATTCCTGA		MGRILTFRFKYSRNQRFLHS*		MGRILTFRFKYSRNQRFLHS*		GCCGAGATGG	TGCCGGAACA	0	Q	0	0	0	0	0
4639	2494	an	AN8344.1	53.m04018	AO070312000017	0	-110	-51					ATGTCGGGCCATTCGTCAACAACTCTCCGAGCTCTGGGCGGAGCTCGTATAAAATTCTGA	ATGTCGGGCCATTCGTCAACAACTCTCCGAGCTCTGGGCGGAGCTCGTATAAAATTCTGA			MSGHSSTTLRALGGARIKF*	MSGHSSTTLRALGGARIKF*			GGTGTTTGAG	GCCCCTTCCC	0	Q	0	0	0	0	0
4644	2494	ao	AN8344.1	53.m04018	AO070312000017	0					-255	-148	ATGGATTTCCTATGGCTCAGCTGGCCCCCCTATCTACGTATAAAGCAACCCTCTCGGCACATACCTGCCAGCTTTCCTCTGCAGTTCGACATGAACGATTTTTCATGA			ATGGATTTCCTATGGCTCAGCTGGCCCCCCTATCTACGTATAAAGCAACCCTCTCGGCACATACCTGCCAGCTTTCCTCTGCAGTTCGACATGAACGATTTTTCATGA	MDFLWLSWPPYLRIKQPSRHIPASFPLQFDMNDFS*			MDFLWLSWPPYLRIKQPSRHIPASFPLQFDMNDFS*	TTCGAACACT	GTTCAGAGGC	0	Q	0	0	0	0	0
4645	2494	ao	AN8344.1	53.m04018	AO070312000017	0					-165	-148	ATGAACGATTTTTCATGA			ATGAACGATTTTTCATGA	MNDFS*			MNDFS*	GCAGTTCGAC	GTTCAGAGGC	0	Q	0	0	0	0	0
4648	2495	af	AN0780.1	70.m15390	AO070316000056	0			-215	-81			ATGCGTATTCCTTGGTCACAGACAGACACTCGGTCATTTCAAATGGCGGCGGCCAACGTCACCAGACTGACGTGTCCCCTGTCCCTCCACGCTGAAATTTTCAACGACAACGCCAAAAAAAAGGTCATCGACTGA		ATGCGTATTCCTTGGTCACAGACAGACACTCGGTCATTTCAAATGGCGGCGGCCAACGTCACCAGACTGACGTGTCCCCTGTCCCTCCACGCTGAAATTTTCAACGACAACGCCAAAAAAAAGGTCATCGACTGA		MRIPWSQTDTRSFQMAAANVTRLTCPLSLHAEIFNDNAKKKVID*		MRIPWSQTDTRSFQMAAANVTRLTCPLSLHAEIFNDNAKKKVID*		AATAGAGTGC	GACCGAGCCA	0	E	0	0	NCU09116.1	0	0
4649	2495	af	AN0780.1	70.m15390	AO070316000056	0			-173	-81			ATGGCGGCGGCCAACGTCACCAGACTGACGTGTCCCCTGTCCCTCCACGCTGAAATTTTCAACGACAACGCCAAAAAAAAGGTCATCGACTGA		ATGGCGGCGGCCAACGTCACCAGACTGACGTGTCCCCTGTCCCTCCACGCTGAAATTTTCAACGACAACGCCAAAAAAAAGGTCATCGACTGA		MAAANVTRLTCPLSLHAEIFNDNAKKKVID*		MAAANVTRLTCPLSLHAEIFNDNAKKKVID*		GTCATTTCAA	GACCGAGCCA	0	E	0	0	NCU09116.1	0	0
4646	2495	an	AN0780.1	70.m15390	AO070316000056	0	-192	-124					ATGATCAGCTCAAGGATAAGAGTCAACCTTAGCCTAAACGGTGATGGCAGTTTGCGGCGCCGTAGATAA	ATGATCAGCTCAAGGATAAGAGTCAACCTTAGCCTAAACGGTGATGGCAGTTTGCGGCGCCGTAGATAA			MISSRIRVNLSLNGDGSLRRRR*	MISSRIRVNLSLNGDGSLRRRR*			GCCTTATCGC	GATAGAGAGA	0	E	0	0	NCU09116.1	0	0
4647	2495	an	AN0780.1	70.m15390	AO070316000056	0	-114	-76					ATGCCAAAATATATCTCCCGACAGAGAATATCAGTATAG	ATGCCAAAATATATCTCCCGACAGAGAATATCAGTATAG			MPKYISRQRISV*	MPKYISRQRISV*			AGATAGAGAG	AGTTTCTTAC	0	E	0	0	NCU09116.1	0	0
4650	2495	ao	AN0780.1	70.m15390	AO070316000056	0					-221	-186	ATGAGCCGCAATCTTCAACTCCAACAAACGGAATAA			ATGAGCCGCAATCTTCAACTCCAACAAACGGAATAA	MSRNLQLQQTE*			MSRNLQLQQTE*	AGCGAAGTGC	GGCAATGTTG	0	E	0	0	NCU09116.1	0	0
4651	2495	ao	AN0780.1	70.m15390	AO070316000056	0					-181	-134	ATGTTGCTGACGTGGTTGCCCGTGATATATAATTGTATGCAAAACTGA			ATGTTGCTGACGTGGTTGCCCGTGATATATAATTGTATGCAAAACTGA	MLLTWLPVIYNCMQN*			MLLTWLPVIYNCMQN*	GAATAAGGCA	GGAATCTCAC	0	E	0	0	NCU09116.1	0	0
4652	2495	ao	AN0780.1	70.m15390	AO070316000056	0					-145	-134	ATGCAAAACTGA			ATGCAAAACTGA	MQN*			MQN*	ATATAATTGT	GGAATCTCAC	0	E	0	0	NCU09116.1	0	0
4653	2495	ao	AN0780.1	70.m15390	AO070316000056	0					-86	-69	ATGCACGATTGTCATTGA			ATGCACGATTGTCATTGA	MHDCH*			MHDCH*	CCACCGGGTC	TAGGCCACAG	0	E	0	0	NCU09116.1	0	0
4657	2496	af	AN3359.1	66.m04660	AO070317000081	0			-173	-108			ATGATCGCATGTCTTGTGTCTCATGGTGGCCGTTGCACGGACTTATCAGCCATGAGAGCCAGATAG		ATGATCGCATGTCTTGTGTCTCATGGTGGCCGTTGCACGGACTTATCAGCCATGAGAGCCAGATAG		MIACLVSHGGRCTDLSAMRAR*		MIACLVSHGGRCTDLSAMRAR*		ATCTATCGGG	CCGACCTCGG	0	E	0	0	0	0	0
4658	2496	af	AN3359.1	66.m04660	AO070317000081	0			-165	-73			ATGTCTTGTGTCTCATGGTGGCCGTTGCACGGACTTATCAGCCATGAGAGCCAGATAGCCGACCTCGGGCCGCCAGAAAAAATCCCTACTTAA		ATGTCTTGTGTCTCATGGTGGCCGTTGCACGGACTTATCAGCCATGAGAGCCAGATAGCCGACCTCGGGCCGCCAGAAAAAATCCCTACTTAA		MSCVSWWPLHGLISHESQIADLGPPEKIPT*		MSCVSWWPLHGLISHESQIADLGPPEKIPT*		GGATGATCGC	CCTCCCGTCC	0	E	0	0	0	0	0
4659	2496	af	AN3359.1	66.m04660	AO070317000081	0			-151	-119			ATGGTGGCCGTTGCACGGACTTATCAGCCATGA		ATGGTGGCCGTTGCACGGACTTATCAGCCATGA		MVAVARTYQP*		MVAVARTYQP*		CTTGTGTCTC	GAGCCAGATA	0	E	0	0	0	0	0
4660	2496	af	AN3359.1	66.m04660	AO070317000081	0			-122	-108			ATGAGAGCCAGATAG		ATGAGAGCCAGATAG		MRAR*		MRAR*		CTTATCAGCC	CCGACCTCGG	0	E	0	0	0	0	0
4654	2496	an	AN3359.1	66.m04660	AO070317000081	0	-266	-201					ATGCATTCGCGACTAGAAGATAAGCCGAGCCCATCGGGCTTCTTGGCGCTGGCTGGCGCGGGTTAG	ATGCATTCGCGACTAGAAGATAAGCCGAGCCCATCGGGCTTCTTGGCGCTGGCTGGCGCGGGTTAG			MHSRLEDKPSPSGFLALAGAG*	MHSRLEDKPSPSGFLALAGAG*			CGGTACCCCA	ACTCGGGGCC	0	E	0	0	0	0	0
4655	2496	an	AN3359.1	66.m04660	AO070317000081	0	-139	-128					ATGCTACTCTGA	ATGCTACTCTGA			MLL*	MLL*			AATACGGTCG	AGGACAGCTG	0	E	0	0	0	0	0
4661	2496	ao	AN3359.1	66.m04660	AO070317000081	0					-258	-244	ATGAAGCTGAACTAA			ATGAAGCTGAACTAA	MKLN*			MKLN*	CTTCCCGTTA	GACGAATACG	0	E	0	0	0	0	0
4662	2496	ao	AN3359.1	66.m04660	AO070317000081	0					-181	-71	ATGTTACGCCCGAGGCTAGTGGCTTGTTCTTTTTTCTGCTTGGCCCGCAACGTCTGGCGACTTTATAACCGAGGGTGTCCCGCGCATAGCTTCTTCATCTCTCGCTCTTGA			ATGTTACGCCCGAGGCTAGTGGCTTGTTCTTTTTTCTGCTTGGCCCGCAACGTCTGGCGACTTTATAACCGAGGGTGTCCCGCGCATAGCTTCTTCATCTCTCGCTCTTGA	MLRPRLVACSFFCLARNVWRLYNRGCPAHSFFISRS*			MLRPRLVACSFFCLARNVWRLYNRGCPAHSFFISRS*	AAGGCAACAC	CCATTTCTAA	0	E	0	0	0	0	0
4665	2497	af	AN0862.1	70.m15466	AO070320000011	0			-246	-157			ATGGCAATACTCACCGAGTACGCTGTCTTTCCTCAACCGCTCCATGACAATAGACACCTCCGTGTACCATCTCATCTCGTCCCATCCTAA		ATGGCAATACTCACCGAGTACGCTGTCTTTCCTCAACCGCTCCATGACAATAGACACCTCCGTGTACCATCTCATCTCGTCCCATCCTAA		MAILTEYAVFPQPLHDNRHLRVPSHLVPS*		MAILTEYAVFPQPLHDNRHLRVPSHLVPS*		TATAGATCAT	CAGAACAGCC	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C

4666	2497	af	AN0862.1	70.m15466	AO070320000011	0			-203	-21			ATGACAATAGACACCTCCGTGTACCATCTCATCTCGTCCCATCCTAACAGAACAGCCATGCTGCTGTATCCTGCCCCGCACGGACCACCTCCCACCACAGTCAAATCAGTCTCCAAATCCACCAAGAATCAGATACTCAAGCCCATTAAGCCCATCGCCACAAAGCTCTCAACCCTCACTTAA		ATGACAATAGACACCTCCGTGTACCATCTCATCTCGTCCCATCCTAACAGAACAGCCATGCTGCTGTATCCTGCCCCGCACGGACCACCTCCCACCACAGTCAAATCAGTCTCCAAATCCACCAAGAATCAGATACTCAAGCCCATTAAGCCCATCGCCACAAAGCTCTCAACCCTCACTTAA		MTIDTSVYHLISSHPNRTAMLLYPAPHGPPPTTVKSVSKSTKNQILKPIKPIATKLSTLT*		MTIDTSVYHLISSHPNRTAMLLYPAPHGPPPTTVKSVSKSTKNQILKPIKPIATKLSTLT*		CAACCGCTCC	ACCCTAAAGC	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C
4667	2497	af	AN0862.1	70.m15466	AO070320000011	0			-146	-21			ATGCTGCTGTATCCTGCCCCGCACGGACCACCTCCCACCACAGTCAAATCAGTCTCCAAATCCACCAAGAATCAGATACTCAAGCCCATTAAGCCCATCGCCACAAAGCTCTCAACCCTCACTTAA		ATGCTGCTGTATCCTGCCCCGCACGGACCACCTCCCACCACAGTCAAATCAGTCTCCAAATCCACCAAGAATCAGATACTCAAGCCCATTAAGCCCATCGCCACAAAGCTCTCAACCCTCACTTAA		MLLYPAPHGPPPTTVKSVSKSTKNQILKPIKPIATKLSTLT*		MLLYPAPHGPPPTTVKSVSKSTKNQILKPIKPIATKLSTLT*		CAGAACAGCC	ACCCTAAAGC	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C
4663	2497	an	AN0862.1	70.m15466	AO070320000011	0	-187	-170					ATGATCAGATATACATAG	ATGATCAGATATACATAG			MIRYT*	MIRYT*			CTCAGAAGAT	AAATATAACT	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C
4664	2497	an	AN0862.1	70.m15466	AO070320000011	0	-138	-22					ATGATAGATCAGTTTGCAGGACTTCGTAATCGAGTCCATCAGTACATCAAAGAAGCCCCGCACAGACCACCTCCACTCAAATACCAAAATATCCTCATCCTTAACCCACCATCGTAG	ATGATAGATCAGTTTGCAGGACTTCGTAATCGAGTCCATCAGTACATCAAAGAAGCCCCGCACAGACCACCTCCACTCAAATACCAAAATATCCTCATCCTTAACCCACCATCGTAG			MIDQFAGLRNRVHQYIKEAPHRPPPLKYQNILILNPPS*	MIDQFAGLRNRVHQYIKEAPHRPPPLKYQNILILNPPS*			TAAGTACATT	TCAATAACCG	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C
4668	2497	ao	AN0862.1	70.m15466	AO070320000011	0					-162	-31	ATGAACCATCAGCCACAACATCCCCGCCAAGAACAAGCCGTGCACAGACCACCCACCGAAACCACATCAAACCAAATTAAACTTAAGATCTATCAAGAAACAAATCCCTCCAGCCCCTCCACAATACTATAA			ATGAACCATCAGCCACAACATCCCCGCCAAGAACAAGCCGTGCACAGACCACCCACCGAAACCACATCAAACCAAATTAAACTTAAGATCTATCAAGAAACAAATCCCTCCAGCCCCTCCACAATACTATAA	MNHQPQHPRQEQAVHRPPTETTSNQIKLKIYQETNPSSPSTIL*			MNHQPQHPRQEQAVHRPPTETTSNQIKLKIYQETNPSSPSTIL*	TAACAAGGCC	GATATAGACA	0	O	FG10822.1	MG06730.1	0	YNL153C	YNL153C
4669	2498	af	AN0490.1	65.m07309	AO070321000178	0			-256	-245			ATGCTATCTTGA		ATGCTATCTTGA		MLS*		MLS*		GAAATTGAGG	GTCATAATGC	0	F	0	0	0	0	0
4670	2498	af	AN0490.1	65.m07309	AO070321000178	0			-238	-182			ATGCCTCCTGTTGCCTGCAAGATCGTCGATGGATGCCTGGTGAGTTCCCCAGATTGA		ATGCCTCCTGTTGCCTGCAAGATCGTCGATGGATGCCTGGTGAGTTCCCCAGATTGA		MPPVACKIVDGCLVSSPD*		MPPVACKIVDGCLVSSPD*		TTGAGTCATA	TGATAAGATA	0	F	0	0	0	0	0
4671	2498	af	AN0490.1	65.m07309	AO070321000178	0			-210	-196			ATGGATGCCTGGTGA		ATGGATGCCTGGTGA		MDAW*		MDAW*		AAGATCGTCG	GTTCCCCAGA	0	F	0	0	0	0	0
4672	2498	af	AN0490.1	65.m07309	AO070321000178	0			-206	-171			ATGCCTGGTGAGTTCCCCAGATTGATGATAAGATAA		ATGCCTGGTGAGTTCCCCAGATTGATGATAAGATAA		MPGEFPRLMIR*		MPGEFPRLMIR*		TCGTCGATGG	GCTGCTGAGA	0	F	0	0	0	0	0
4673	2498	af	AN0490.1	65.m07309	AO070321000178	0			-182	-171			ATGATAAGATAA		ATGATAAGATAA		MIR*		MIR*		CCCCAGATTG	GCTGCTGAGA	0	F	0	0	0	0	0
4674	2498	ao	AN0490.1	65.m07309	AO070321000178	0					-133	-122	ATGATTGATTAG			ATGATTGATTAG	MID*			MID*	CACCGCCCAC	GTAAGTTATG	0	F	0	0	0	0	0
4675	2498	ao	AN0490.1	65.m07309	AO070321000178	0					-114	-94	ATGAATTTTTTTTTTCTATAG			ATGAATTTTTTTTTTCTATAG	MNFFFL*			MNFFFL*	TAGGTAAGTT	AGTCACCAAA	0	F	0	0	0	0	0
4676	2502	af	AN4711.1	71.m15699	AO070329000164	0			-267	-166			ATGTACCGACGTCATTGCTACCCCACCAAAAACTGTCAGCTCCAAACAGCTCATGTCATGCACCATTTGCTAGAATTCTCGTACTTCACCAGATTCAACTGA		ATGTACCGACGTCATTGCTACCCCACCAAAAACTGTCAGCTCCAAACAGCTCATGTCATGCACCATTTGCTAGAATTCTCGTACTTCACCAGATTCAACTGA		MYRRHCYPTKNCQLQTAHVMHHLLEFSYFTRFN*		MYRRHCYPTKNCQLQTAHVMHHLLEFSYFTRFN*		CCGATGGAAG	CGAGCTTCTG	0		0	0	0	0	0
4677	2502	af	AN4711.1	71.m15699	AO070329000164	0			-215	-195			ATGTCATGCACCATTTGCTAG		ATGTCATGCACCATTTGCTAG		MSCTIC*		MSCTIC*		CAAACAGCTC	AATTCTCGTA	0		0	0	0	0	0
4678	2502	af	AN4711.1	71.m15699	AO070329000164	0			-210	-166			ATGCACCATTTGCTAGAATTCTCGTACTTCACCAGATTCAACTGA		ATGCACCATTTGCTAGAATTCTCGTACTTCACCAGATTCAACTGA		MHHLLEFSYFTRFN*		MHHLLEFSYFTRFN*		AGCTCATGTC	CGAGCTTCTG	0		0	0	0	0	0
4679	2502	af	AN4711.1	71.m15699	AO070329000164	0			-133	-92			ATGATGGTGATATCTTGCTTCGAAGTTGAGCTACTACCTTGA		ATGATGGTGATATCTTGCTTCGAAGTTGAGCTACTACCTTGA		MMVISCFEVELLP*		MMVISCFEVELLP*		GCCGTTCTAG	CCTTGTGTGC	0		0	0	0	0	0
4680	2502	af	AN4711.1	71.m15699	AO070329000164	0			-130	-92			ATGGTGATATCTTGCTTCGAAGTTGAGCTACTACCTTGA		ATGGTGATATCTTGCTTCGAAGTTGAGCTACTACCTTGA		MVISCFEVELLP*		MVISCFEVELLP*		GTTCTAGATG	CCTTGTGTGC	0		0	0	0	0	0
4681	2502	ao	AN4711.1	71.m15699	AO070329000164	0					-244	-206	ATGCACAGCGTTCTAGACCGTAGGCCCGCGCTACGTTGA			ATGCACAGCGTTCTAGACCGTAGGCCCGCGCTACGTTGA	MHSVLDRRPALR*			MHSVLDRRPALR*	TGGCTTATAG	CGTCACACTC	0		0	0	0	0	0
4682	2504	an	AN3258.1	55.m03211	AO070336000226	0	-265	-191					ATGAGTTCCACTTATTGGTTCCTCGCAAAGGCCCAAGTCACTAGCCCAATTGATATCTGGAACGCGACCAATTAG	ATGAGTTCCACTTATTGGTTCCTCGCAAAGGCCCAAGTCACTAGCCCAATTGATATCTGGAACGCGACCAATTAG			MSSTYWFLAKAQVTSPIDIWNATN*	MSSTYWFLAKAQVTSPIDIWNATN*			GGCACAGCCA	CTGGTTCTTG	0		0	0	0	0	0
4683	2504	an	AN3258.1	55.m03211	AO070336000226	0	-154	-125					ATGTTGGGTGAACCCTTTATAATGTTATAA	ATGTTGGGTGAACCCTTTATAATGTTATAA			MLGEPFIML*	MLGEPFIML*			GGAGAAGTGA	ATTTACCGCA	0		0	0	0	0	0
4684	2504	an	AN3258.1	55.m03211	AO070336000226	0	-113	-96					ATGCACGGTGTGTGCTGA	ATGCACGGTGTGTGCTGA			MHGVC*	MHGVC*			TTTACCGCAC	TCTTGATCGG	0		0	0	0	0	0
4686	2507	af	AN6138.1	72.m19026	AO070340000064	0			-109	-68			ATGCTCGCCTATCGCTCGAGACTATCCCCTCACCGACTCTGA		ATGCTCGCCTATCGCTCGAGACTATCCCCTCACCGACTCTGA		MLAYRSRLSPHRL*		MLAYRSRLSPHRL*		GGCCGACCTC	CCCGCGTACC	0	D	0	0	0	0	0
4685	2507	an	AN6138.1	72.m19026	AO070340000064	0	-109	-92					ATGCTCCCTCTCGACTGA	ATGCTCCCTCTCGACTGA			MLPLD*	MLPLD*			ATCCTGCCTG	CGATTATTTC	0	D	0	0	0	0	0
4687	2507	ao	AN6138.1	72.m19026	AO070340000064	0					-147	-127	ATGCTTGCTCTTCTTGAGTGA			ATGCTTGCTCTTCTTGAGTGA	MLALLE*			MLALLE*	TGCCTACCAA	ACATCTCCCT	0	D	0	0	0	0	0
4689	2508	af	AN5455.1	69.m15477	AO070341000411	0			-174	-118			ATGGTTGGAGAAAAAAGACTCCAAAAAAAAGTTGCTCCGGCCATTAGTCGATCTTGA		ATGGTTGGAGAAAAAAGACTCCAAAAAAAAGTTGCTCCGGCCATTAGTCGATCTTGA		MVGEKRLQKKVAPAISRS*		MVGEKRLQKKVAPAISRS*		GCTGCCATTT	CGGAAAGAAA	0	S	FG07262.1	MG04995.1	0	0	0
4694	2510	af	AN0665.1	70.m15268	AO070343000555	0			-181	-137			ATGGAGAGTTGCATCTCATTGCGCGATCAAGATAACTTGCCATGA		ATGGAGAGTTGCATCTCATTGCGCGATCAAGATAACTTGCCATGA		MESCISLRDQDNLP*		MESCISLRDQDNLP*		AAGATAGAAT	ACGGCAGACC	0	U	0	0	0	0	0
4695	2510	af	AN0665.1	70.m15268	AO070343000555	0			-140	-48			ATGAACGGCAGACCTGCTCTCACCGCCTTACGATCCCAAGAAATGGGCCGTGTTTTGAGGCCAACGTATACTTGTCTACCTCTACAATATTAA		ATGAACGGCAGACCTGCTCTCACCGCCTTACGATCCCAAGAAATGGGCCGTGTTTTGAGGCCAACGTATACTTGTCTACCTCTACAATATTAA		MNGRPALTALRSQEMGRVLRPTYTCLPLQY*		MNGRPALTALRSQEMGRVLRPTYTCLPLQY*		ATAACTTGCC	TCCTATTTCA	0	U	0	0	0	0	0
4696	2510	af	AN0665.1	70.m15268	AO070343000555	0			-98	-48			ATGGGCCGTGTTTTGAGGCCAACGTATACTTGTCTACCTCTACAATATTAA		ATGGGCCGTGTTTTGAGGCCAACGTATACTTGTCTACCTCTACAATATTAA		MGRVLRPTYTCLPLQY*		MGRVLRPTYTCLPLQY*		ATCCCAAGAA	TCCTATTTCA	0	U	0	0	0	0	0
4692	2510	an	AN0665.1	70.m15268	AO070343000555	0	-174	-142					ATGCCTGAAACTCGGACTCGGTGTTCTGTATAG	ATGCCTGAAACTCGGACTCGGTGTTCTGTATAG			MPETRTRCSV*	MPETRTRCSV*			TATCAAATTA	ATGCTTCGGG	0	U	0	0	0	0	0
4693	2510	an	AN0665.1	70.m15268	AO070343000555	0	-141	-76					ATGCTTCGGGAGACCTGCCCTTCCAGCTCGGCCCACTTGCCACATGATCTGCGGAAGCCAACTTGA	ATGCTTCGGGAGACCTGCCCTTCCAGCTCGGCCCACTTGCCACATGATCTGCGGAAGCCAACTTGA			MLRETCPSSSAHLPHDLRKPT*	MLRETCPSSSAHLPHDLRKPT*			TTCTGTATAG	CTACTTTCCA	0	U	0	0	0	0	0
4697	2510	ao	AN0665.1	70.m15268	AO070343000555	0					-195	-169	ATGAGGCATTTACTCCGTACTAAGTAG			ATGAGGCATTTACTCCGTACTAAGTAG	MRHLLRTK*			MRHLLRTK*	CACAGGGTAG	GGCTGGACTG	0	U	0	0	0	0	0
4698	2510	ao	AN0665.1	70.m15268	AO070343000555	0					-152	-132	ATGATAAAGTTGATTGACTGA			ATGATAAAGTTGATTGACTGA	MIKLID*			MIKLID*	ACTGCGGTGA	TACCGTCACC	0	U	0	0	0	0	0
4699	2511	af	AN6500.1	62.m03439	AO070222000014	0			-239	-186			ATGATTGGAAGCTGCCTGGCCGGTGTGGGGAGGAGGGGCTGGCGCACTCTTAG		ATGATTGGAAGCTGCCTGGCCGGTGTGGGGAGGAGGGGCTGGCGCACTCTTAG		MIGSCLAGVGRRGLAHS*		MIGSCLAGVGRRGLAHS*		GCACCAAGAT	GGGCTCTTCC	0	J	0	0	0	0	0
4700	2511	af	AN6500.1	62.m03439	AO070222000014	0			-146	-3			ATGCCGAAAACGGCCGCCTTAGCGAGAGTGTGGGATTCTGTTCTTGGCACGATCGCACACAATAACGATCCCAGGCAATTAAAGTATACCAGCCTCGCGTCGAGTTCGATCTGTTCCCATTCAATCAGCTTGAAAGAGACATAA		ATGCCGAAAACGGCCGCCTTAGCGAGAGTGTGGGATTCTGTTCTTGGCACGATCGCACACAATAACGATCCCAGGCAATTAAAGTATACCAGCCTCGCGTCGAGTTCGATCTGTTCCCATTCAATCAGCTTGAAAGAGACATAA		MPKTAALARVWDSVLGTIAHNNDPRQLKYTSLASSSICSHSISLKET*		MPKTAALARVWDSVLGTIAHNNDPRQLKYTSLASSSICSHSISLKET*		AGGCCAGACT	CAATGGCCGC	0	J	0	0	0	0	0
4701	2512	af	AN5913.1	72.m19958	AO070248000033	0			-206	-165			ATGATACCACTATCAGATTATCCCCGCATTTATCAACGATAG		ATGATACCACTATCAGATTATCCCCGCATTTATCAACGATAG		MIPLSDYPRIYQR*		MIPLSDYPRIYQR*		CGATCTACTG	AATCATCTGA	0	Q	0	MG03880.1	NCU01754.1	0	0
4702	2512	af	AN5913.1	72.m19958	AO070248000033	0			-147	-136			ATGCGATCATAA		ATGCGATCATAA		MRS*		MRS*		TGATTAGTCG	TTCAGGCAAA	0	Q	0	MG03880.1	NCU01754.1	0	0
4703	2512	ao	AN5913.1	72.m19958	AO070248000033	0					-239	-189	ATGTATAAACCCCGCCTGTCAATCCGTTGCAATCATGCATTAACGCATTAA			ATGTATAAACCCCGCCTGTCAATCCGTTGCAATCATGCATTAACGCATTAA	MYKPRLSIRCNHALTH*			MYKPRLSIRCNHALTH*	CGGAGGACAG	CTAGCACCAT	0	Q	0	MG03880.1	NCU01754.1	0	0
4705	2513	af	AN0485.1	58.m08875	AO070252000019	0			-179	-156			ATGACATTATGTCTCCCACAATAA		ATGACATTATGTCTCCCACAATAA		MTLCLPQ*		MTLCLPQ*		AGCGCTTATC	TGGGCGTGTC	0	I	0	0	0	0	0
4706	2513	af	AN0485.1	58.m08875	AO070252000019	0			-171	-91			ATGTCTCCCACAATAATGGGCGTGTCGAAACCGAGGTATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAA		ATGTCTCCCACAATAATGGGCGTGTCGAAACCGAGGTATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAA		MSPTIMGVSKPRYADHAGDFHMPCAQ*		MSPTIMGVSKPRYADHAGDFHMPCAQ*		TCATGACATT	GGCTGGTCTG	0	I	0	0	0	0	0
4707	2513	af	AN0485.1	58.m08875	AO070252000019	0			-156	-91			ATGGGCGTGTCGAAACCGAGGTATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAA		ATGGGCGTGTCGAAACCGAGGTATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAA		MGVSKPRYADHAGDFHMPCAQ*		MGVSKPRYADHAGDFHMPCAQ*		TCCCACAATA	GGCTGGTCTG	0	I	0	0	0	0	0
4708	2513	af	AN0485.1	58.m08875	AO070252000019	0			-134	-75			ATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAAGGCTGGTCTGGATTAA		ATGCCGATCATGCGGGGGACTTTCATATGCCCTGTGCGCAATAAGGCTGGTCTGGATTAA		MPIMRGTFICPVRNKAGLD*		MPIMRGTFICPVRNKAGLD*		AAACCGAGGT	TATATAGGGC	0	I	0	0	0	0	0
4709	2513	af	AN0485.1	58.m08875	AO070252000019	0			-125	-75			ATGCGGGGGACTTTCATATGCCCTGTGCGCAATAAGGCTGGTCTGGATTAA		ATGCGGGGGACTTTCATATGCCCTGTGCGCAATAAGGCTGGTCTGGATTAA		MRGTFICPVRNKAGLD*		MRGTFICPVRNKAGLD*		TATGCCGATC	TATATAGGGC	0	I	0	0	0	0	0
4710	2513	af	AN0485.1	58.m08875	AO070252000019	0			-108	-91			ATGCCCTGTGCGCAATAA		ATGCCCTGTGCGCAATAA		MPCAQ*		MPCAQ*		GGACTTTCAT	GGCTGGTCTG	0	I	0	0	0	0	0
4704	2513	an	AN0485.1	58.m08875	AO070252000019	0	-140	-36					ATGCTTTGGACTCTTAGGAGGGTCAGCTTTCACCAGGCGAGGCGTGAGGTTAAATCGACCGGGTCGCCCTGGTCCTCACCCTCCCAACAACTCACTCCTTTCTAA	ATGCTTTGGACTCTTAGGAGGGTCAGCTTTCACCAGGCGAGGCGTGAGGTTAAATCGACCGGGTCGCCCTGGTCCTCACCCTCCCAACAACTCACTCCTTTCTAA			MLWTLRRVSFHQARREVKSTGSPWSSPSQQLTPF*	MLWTLRRVSFHQARREVKSTGSPWSSPSQQLTPF*			TTGATTTCAT	CATTTTCTCT	0	I	0	0	0	0	0
4711	2513	ao	AN0485.1	58.m08875	AO070252000019	0					-293	-228	ATGTACCTCTTACCCCTCACGCTTACATACCGAGGAAGAACCCCAGGCTCTTGGTCCCTTTATTAA			ATGTACCTCTTACCCCTCACGCTTACATACCGAGGAAGAACCCCAGGCTCTTGGTCCCTTTATTAA	MYLLPLTLTYRGRTPGSWSLY*			MYLLPLTLTYRGRTPGSWSLY*	ATCGTCCCTG	AGTAGCTGCG	0	I	0	0	0	0	0
4712	2513	ao	AN0485.1	58.m08875	AO070252000019	0					-208	-125	ATGTGGATCGGTGCTCAACTGTCGGTATACACTAAGCCAAGGGGTCTATTTAATATTTCAATTGGGACCACCCCGCGGTATTAA			ATGTGGATCGGTGCTCAACTGTCGGTATACACTAAGCCAAGGGGTCTATTTAATATTTCAATTGGGACCACCCCGCGGTATTAA	MWIGAQLSVYTKPRGLFNISIGTTPRY*			MWIGAQLSVYTKPRGLFNISIGTTPRY*	GAGATTTCAC	GGAAAGGTCG	0	I	0	0	0	0	0
4713	2516	af	AN3365.1	66.m04631	AO070281000028	0			-147	-70			ATGGAAAAGGCTCCCCCGCCATCCGTACACCTCTCCTCTACAGTCTACCCAGTTTGGAGGTTAACTGACCTAATTTGA		ATGGAAAAGGCTCCCCCGCCATCCGTACACCTCTCCTCTACAGTCTACCCAGTTTGGAGGTTAACTGACCTAATTTGA		MEKAPPPSVHLSSTVYPVWRLTDLI*		MEKAPPPSVHLSSTVYPVWRLTDLI*		AGATAAGTAG	TCACGATATT	0	V	0	0	0	0	0
4714	2516	ao	AN3365.1	66.m04631	AO070281000028	0					-268	-254	ATGATTAGTTACTAA			ATGATTAGTTACTAA	MISY*			MISY*	TTAGGTCCAA	CTTGCTACTA	0	V	0	0	0	0	0
4715	2516	ao	AN3365.1	66.m04631	AO070281000028	0					-97	-53	ATGACACCATCTGACGACATTGCCGATACGGTATGTAAAAGTTGA			ATGACACCATCTGACGACATTGCCGATACGGTATGTAAAAGTTGA	MTPSDDIADTVCKS*			MTPSDDIADTVCKS*	CCGCGATCAG	TTGTCCTCTT	0	V	0	0	0	0	0
4717	2517	af	AN2278.1	71.m15923	AO070295000054	0			-293	-258			ATGCTAAACATCACAAAATCTGTCGCAATCTATTAA		ATGCTAAACATCACAAAATCTGTCGCAATCTATTAA		MLNITKSVAIY*		MLNITKSVAIY*		ACCCCAATCC	ACAGAGGTCG	0	BK	0	0	0	0	0
4722	2521	af	AN1685.1	58.m07761	AO070305000004	0			-138	-115			ATGCGGAAGGGGAGTGCGATGTGA		ATGCGGAAGGGGAGTGCGATGTGA		MRKGSAM*		MRKGSAM*		CCCGTTTCGT	GTCGGGCGGG	0	R	0	0	0	0	0
4723	2521	af	AN1685.1	58.m07761	AO070305000004	0			-83	-12			ATGGCCGGCGTGTCCGGCGAGGGGAGGATGGTTTCCCGATCAGATTCAACGACGGAGGAATCGCAACCCTAA		ATGGCCGGCGTGTCCGGCGAGGGGAGGATGGTTTCCCGATCAGATTCAACGACGGAGGAATCGCAACCCTAA		MAGVSGEGRMVSRSDSTTEESQP*		MAGVSGEGRMVSRSDSTTEESQP*		AAGCTATATA	TTGTCGGTAT	0	R	0	0	0	0	0
4719	2521	an	AN1685.1	58.m07761	AO070305000004	0	-206	-123					ATGGGTCAAACCCCCCCCTTCTTCCCGTCTGCACGTCTGATGGCTCTTTCTGTAACCGATAGCGGACCGACTAGGCATCGTTGA	ATGGGTCAAACCCCCCCCTTCTTCCCGTCTGCACGTCTGATGGCTCTTTCTGTAACCGATAGCGGACCGACTAGGCATCGTTGA			MGQTPPFFPSARLMALSVTDSGPTRHR*	MGQTPPFFPSARLMALSVTDSGPTRHR*			CTCGCACTCA	TCCACAATAT	0	R	0	0	0	0	0
4720	2521	an	AN1685.1	58.m07761	AO070305000004	0	-167	-123					ATGGCTCTTTCTGTAACCGATAGCGGACCGACTAGGCATCGTTGA	ATGGCTCTTTCTGTAACCGATAGCGGACCGACTAGGCATCGTTGA			MALSVTDSGPTRHR*	MALSVTDSGPTRHR*			TGCACGTCTG	TCCACAATAT	0	R	0	0	0	0	0
4721	2521	an	AN1685.1	58.m07761	AO070305000004	0	-104	-84					ATGCAACTCAGTCGAATATGA	ATGCAACTCAGTCGAATATGA			MQLSRI*	MQLSRI*			ATCTCAGACA	AGGGGCTACA	0	R	0	0	0	0	0
4725	2521	ao	AN1685.1	58.m07761	AO070305000004	0					-236	-180	ATGTCTTACACTGCAGGCTTATCCTCTTTCACCCCCCACTACACTACCGCTTCACTAG			ATGTCTTACACTGCAGGCTTATCCTCTTTCACCCCCCACTACACTACCGCTTCACTAG	MSYTAGLSSFTPTTLPLH*			MSYTAGLSSFTPTTLPLH*	ATCGGACACC	CACCACGGCT	0	R	0	0	0	0	0

4726	2521	ao	AN1685.1	58.m07761	AO070305000004	0					-101	-87	ATGAGACGGAAATGA			ATGAGACGGAAATGA	MRRK*			MRRK*	TGGGATCAAC	AGGGCTTATA	0	R	0	0	0	0	0
4727	2521	ao	AN1685.1	58.m07761	AO070305000004	0					-77	-6	ATGAGGACCGTCCCGTCCGCGTGGAGGGGTTGTTCCGTCGTTTGTCTAACAGTAAAAGGGTTGCAATCGTGA			ATGAGGACCGTCCCGTCCGCGTGGAGGGGTTGTTCCGTCGTTTGTCTAACAGTAAAAGGGTTGCAATCGTGA	MRTVPSAWRGCSVVCLTVKGLQS*			MRTVPSAWRGCSVVCLTVKGLQS*	AAGGGCTTAT	GCATCATGGC	0	R	0	0	0	0	0
4728	2522	an	AN4040.1	53.m04000	AO070308000008	0	-223	-161					ATGCAGGCGCAATTGAAAAGTCCCGTCCCTAGTCCATCGTTCCTCCCTAGTTGGCGGCATTAA	ATGCAGGCGCAATTGAAAAGTCCCGTCCCTAGTCCATCGTTCCTCCCTAGTTGGCGGCATTAA			MQAQLKSPVPSPSFLPSWRH*	MQAQLKSPVPSPSFLPSWRH*			AACCACAATA	TCATGAATGG	0		0	0	0	0	0
4729	2522	an	AN4040.1	53.m04000	AO070308000008	0	-154	-86					ATGGATGGCTCAAGTGCTCACCTGCATTTCATCATAAAGTCACCGAGATTCCCCAGGGTCTCATACTGA	ATGGATGGCTCAAGTGCTCACCTGCATTTCATCATAAAGTCACCGAGATTCCCCAGGGTCTCATACTGA			MDGSSAHLHFIIKSPRFPRVSY*	MDGSSAHLHFIIKSPRFPRVSY*			TTAATCATGA	TCTCTTTTGT	0		0	0	0	0	0
4730	2522	an	AN4040.1	53.m04000	AO070308000008	0	-150	-118					ATGGCTCAAGTGCTCACCTGCATTTCATCATAA	ATGGCTCAAGTGCTCACCTGCATTTCATCATAA			MAQVLTCISS*	MAQVLTCISS*			TCATGAATGG	AGTCACCGAG	0		0	0	0	0	0
4731	2522	ao	AN4040.1	53.m04000	AO070308000008	0					-125	-108	ATGGTATCATACAAGTAG			ATGGTATCATACAAGTAG	MVSYK*			MVSYK*	ACTTGATGAG	TAGTCTTGAA	0		0	0	0	0	0
4732	2522	ao	AN4040.1	53.m04000	AO070308000008	0					-98	-78	ATGTTCAAGTCAAGTATATAA			ATGTTCAAGTCAAGTATATAA	MFKSSI*			MFKSSI*	GTAGTCTTGA	AGAGGAGGAG	0		0	0	0	0	0
4735	2524	af	AN8206.1	53.m03768	AO070310000111	0			-201	-151			ATGCTGGCTGGAGCCCTCTGTCGGACACTCCAAAGCCGAATCACGGTATAG		ATGCTGGCTGGAGCCCTCTGTCGGACACTCCAAAGCCGAATCACGGTATAG		MLAGALCRTLQSRITV*		MLAGALCRTLQSRITV*		TGTCCATAGT	CGGGGCTAAC	0	Q	0	0	0	0	0
4736	2524	af	AN8206.1	53.m03768	AO070310000111	0			-134	-15			ATGAGATTCGGGTGGTTTACTTTCAAGTCCTACTTAGCATTCTGGCCACTCTCGGCTAAGGAGCTCTATAGCAGTCCATCCAATGCACCTTGTAGCAGATCTGTCTTATACTCATCCTGA		ATGAGATTCGGGTGGTTTACTTTCAAGTCCTACTTAGCATTCTGGCCACTCTCGGCTAAGGAGCTCTATAGCAGTCCATCCAATGCACCTTGTAGCAGATCTGTCTTATACTCATCCTGA		MRFGWFTFKSYLAFWPLSAKELYSSPSNAPCSRSVLYSS*		MRFGWFTFKSYLAFWPLSAKELYSSPSNAPCSRSVLYSS*		TAACTTGCCG	CAAGGCCTCT	0	Q	0	0	0	0	0
4733	2524	an	AN8206.1	53.m03768	AO070310000111	0	-166	-20					ATGATCCCTGGCAGTCAACTATGCATATGGCGGGGCTTGATATCATCAGGTCCGACATCGGGAGATACGCGGCCCATTTTAGTGGCATCAGAGTCAGTGGAGGTCTCCAAAATGACAGAACACTTCTACCTCAATCATCTACGCTGA	ATGATCCCTGGCAGTCAACTATGCATATGGCGGGGCTTGATATCATCAGGTCCGACATCGGGAGATACGCGGCCCATTTTAGTGGCATCAGAGTCAGTGGAGGTCTCCAAAATGACAGAACACTTCTACCTCAATCATCTACGCTGA			MIPGSQLCIWRGLISSGPTSGDTRPILVASESVEVSKMTEHFYLNHLR*	MIPGSQLCIWRGLISSGPTSGDTRPILVASESVEVSKMTEHFYLNHLR*			ATTCGGTGGG	GAGGCGATGC	0	Q	0	0	0	0	0
4737	2524	ao	AN8206.1	53.m03768	AO070310000111	0					-253	-158	ATGAATCATTGTGAAGAAATCTTATTTCCTTCCATTCCAAACCCTGGTTTATACCAAAGTTTACGATGTTATCCGAGGCCCCATGCTGTACAGTAA			ATGAATCATTGTGAAGAAATCTTATTTCCTTCCATTCCAAACCCTGGTTTATACCAAAGTTTACGATGTTATCCGAGGCCCCATGCTGTACAGTAA	MNHCEEILFPSIPNPGLYQSLRCYPRPHAVQ*			MNHCEEILFPSIPNPGLYQSLRCYPRPHAVQ*	ATAAAAGTTT	CCTAAGGTGG	0	Q	0	0	0	0	0
4738	2524	ao	AN8206.1	53.m03768	AO070310000111	0					-188	-153	ATGTTATCCGAGGCCCCATGCTGTACAGTAACCTAA			ATGTTATCCGAGGCCCCATGCTGTACAGTAACCTAA	MLSEAPCCTVT*			MLSEAPCCTVT*	AAAGTTTACG	GGTGGTAAAT	0	Q	0	0	0	0	0
4739	2524	ao	AN8206.1	53.m03768	AO070310000111	0					-171	-145	ATGCTGTACAGTAACCTAAGGTGGTAA			ATGCTGTACAGTAACCTAAGGTGGTAA	MLYSNLRW*			MLYSNLRW*	CCGAGGCCCC	ATGTTACTAG	0	Q	0	0	0	0	0
4740	2524	ao	AN8206.1	53.m03768	AO070310000111	0					-144	-91	ATGTTACTAGTAGTAGATCACGACATTGCCCGGCGGGGTGATTTAACTCCATAA			ATGTTACTAGTAGTAGATCACGACATTGCCCGGCGGGGTGATTTAACTCCATAA	MLLVVDHDIARRGDLTP*			MLLVVDHDIARRGDLTP*	AAGGTGGTAA	CAGAAAACAG	0	Q	0	0	0	0	0
4741	2525	conserved	AN0056.1	71.m15325	AO070314000131	0	-196	-140	-195	-145	-221	-165	ATGykbksrryTkyCwdCywCrymTCwCArCTyvhwmmAmmybrmwyykdrTsCTGA	ATGCGTGCAACTTCCTACTACATCTCACAGCTCGATCAACACTGCATTGAGTGCTGA	ATGTTGTGGATTGCCATCCTCGCCTCTCAACTTCCAACAACTGAATCCTGA	ATGTTCTGGGTTGTCTGCCTCACATCTCAACTTATACAACACCGCACTGTATCCTGA	MratsyyiSQLdqhciec*	MRATSYYISQLDQHCIEC*	MLWIAILASQLPTTES*	MFWVVCLTSQLIQHRTVS*	ymAwAGkrTy	rrbbykwkwy	0		0	0	0	0	0
4746	2531	af	AN5602.1	58.m07526	AO070328000002	0			-260	-198			ATGATGAGATATCATAGCTGGCACCAGTCAGACGGGGTGGTTATAAACCATATCCACTGTTGA		ATGATGAGATATCATAGCTGGCACCAGTCAGACGGGGTGGTTATAAACCATATCCACTGTTGA		MMRYHSWHQSDGVVINHIHC*		MMRYHSWHQSDGVVINHIHC*		CTCGCTTCAT	TTAGCTCTGG	0	S	0	0	NCU04087.1	0	0
4747	2531	af	AN5602.1	58.m07526	AO070328000002	0			-130	-32			ATGACTCACATCGATTGCTTGAGATTGGTTACTAATGCCATTACTTTTGCAGAACCTAGTAACTCGGTTATCCACTGCGAGCAAGCCTTTCCGATATAA		ATGACTCACATCGATTGCTTGAGATTGGTTACTAATGCCATTACTTTTGCAGAACCTAGTAACTCGGTTATCCACTGCGAGCAAGCCTTTCCGATATAA		MTHIDCLRLVTNAITFAEPSNSVIHCEQAFPI*		MTHIDCLRLVTNAITFAEPSNSVIHCEQAFPI*		TTGGTTTCGC	TCAAGAACCT	0	S	0	0	NCU04087.1	0	0
4748	2531	af	AN5602.1	58.m07526	AO070328000002	0			-96	-13			ATGCCATTACTTTTGCAGAACCTAGTAACTCGGTTATCCACTGCGAGCAAGCCTTTCCGATATAATCAAGAACCTCCAGGTTAA		ATGCCATTACTTTTGCAGAACCTAGTAACTCGGTTATCCACTGCGAGCAAGCCTTTCCGATATAATCAAGAACCTCCAGGTTAA		MPLLLQNLVTRLSTASKPFRYNQEPPG*		MPLLLQNLVTRLSTASKPFRYNQEPPG*		TTGGTTACTA	CAAAATATCA	0	S	0	0	NCU04087.1	0	0
4743	2531	an	AN5602.1	58.m07526	AO070328000002	0	-293	-228					ATGATGAGACAATTAGCTGGCACCAGTCAGAGGAAGTGGGATATTCGTATCACCCTTCATTGCTGA	ATGATGAGACAATTAGCTGGCACCAGTCAGAGGAAGTGGGATATTCGTATCACCCTTCATTGCTGA			MMRQLAGTSQRKWDIRITLHC*	MMRQLAGTSQRKWDIRITLHC*			GCGTACTTTC	TTAGCTTCCT	0	S	0	0	NCU04087.1	0	0
4744	2531	an	AN5602.1	58.m07526	AO070328000002	0	-180	-115					ATGCCTCGATTCAGCATTTTTTCTTCCATTTTTGAGAAAGCCAATGCTAATTCGGACGCACGTTAG	ATGCCTCGATTCAGCATTTTTTCTTCCATTTTTGAGAAAGCCAATGCTAATTCGGACGCACGTTAG			MPRFSIFSSIFEKANANSDAR*	MPRFSIFSSIFEKANANSDAR*			ATTCACTTGC	CAGAACCCTT	0	S	0	0	NCU04087.1	0	0
4745	2531	an	AN5602.1	58.m07526	AO070328000002	0	-137	-99					ATGCTAATTCGGACGCACGTTAGCAGAACCCTTATCTAG	ATGCTAATTCGGACGCACGTTAGCAGAACCCTTATCTAG			MLIRTHVSRTLI*	MLIRTHVSRTLI*			GAGAAAGCCA	CGTTCAAGAT	0	S	0	0	NCU04087.1	0	0
4749	2531	ao	AN5602.1	58.m07526	AO070328000002	0					-413	-273	ATGCAGAGTTTTTTCTTTTCCCACCCACACAACCACATCCAACTACCCCACGGTTGGATAGGGTCTGCCCCCTCGATGATGAGATTATATAGCTGGCACCAGTCAGAGAAAAGATGGATTTCGATTTGTCTTTTGTGTTGA			ATGCAGAGTTTTTTCTTTTCCCACCCACACAACCACATCCAACTACCCCACGGTTGGATAGGGTCTGCCCCCTCGATGATGAGATTATATAGCTGGCACCAGTCAGAGAAAAGATGGATTTCGATTTGTCTTTTGTGTTGA	MQSFFFSHPHNHIQLPHGWIGSAPSMMRLYSWHQSEKRWISICLLC*			MQSFFFSHPHNHIQLPHGWIGSAPSMMRLYSWHQSEKRWISICLLC*	CTCCCCACCA	TTAGCTCCGG	0	S	0	0	NCU04087.1	0	0
4750	2531	ao	AN5602.1	58.m07526	AO070328000002	0					-338	-273	ATGATGAGATTATATAGCTGGCACCAGTCAGAGAAAAGATGGATTTCGATTTGTCTTTTGTGTTGA			ATGATGAGATTATATAGCTGGCACCAGTCAGAGAAAAGATGGATTTCGATTTGTCTTTTGTGTTGA	MMRLYSWHQSEKRWISICLLC*			MMRLYSWHQSEKRWISICLLC*	TGCCCCCTCG	TTAGCTCCGG	0	S	0	0	NCU04087.1	0	0
4751	2531	ao	AN5602.1	58.m07526	AO070328000002	0					-300	-184	ATGGATTTCGATTTGTCTTTTGTGTTGATTAGCTCCGGTCTGGGAACGCTACCCATGATCACTGAGAAATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAG			ATGGATTTCGATTTGTCTTTTGTGTTGATTAGCTCCGGTCTGGGAACGCTACCCATGATCACTGAGAAATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAG	MDFDLSFVLISSGLGTLPMITEKCLIHVVLYTSIGSSD*			MDFDLSFVLISSGLGTLPMITEKCLIHVVLYTSIGSSD*	CAGAGAAAAG	ATGGACTGAC	0	S	0	0	NCU04087.1	0	0
4752	2531	ao	AN5602.1	58.m07526	AO070328000002	0					-246	-184	ATGATCACTGAGAAATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAG			ATGATCACTGAGAAATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAG	MITEKCLIHVVLYTSIGSSD*			MITEKCLIHVVLYTSIGSSD*	AACGCTACCC	ATGGACTGAC	0	S	0	0	NCU04087.1	0	0
4753	2531	ao	AN5602.1	58.m07526	AO070328000002	0					-232	-137	ATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAGATGGACTGACTTGGATTTTACAGAACCTAGCATTGGAACAGTCTTAA			ATGTCTTATACACGTCGTCTTGTATACCTCAATTGGTTCTTCAGACTAGATGGACTGACTTGGATTTTACAGAACCTAGCATTGGAACAGTCTTAA	MSYTRRLVYLNWFFRLDGLTWILQNLALEQS*			MSYTRRLVYLNWFFRLDGLTWILQNLALEQS*	TCACTGAGAA	AGGAAAGACC	0	S	0	0	NCU04087.1	0	0
4742	2531	conserved	AN5602.1	58.m07526	AO070328000002	0	-290	-228	-257	-198	-335	-273	ATGAGAywwywwrsykGsmmCmrkymrrrsrrrdkrkdkATwhvbmwywbyCwyydkTGhTGA	ATGAGACAATTAGCTGGCACCAGTCAGAGGAAGTGGGATATTCGTATCACCCTTCATTGCTGA	ATGAGATATCATAGCTGGCACCAGTCAGACGGGGTGGTTATAAACCATATCCACTGTTGA	ATGAGATTATATAGCTGGCACCAGTCAGAGAAAAGATGGATTTCGATTTGTCTTTTGTGTTGA	MRqlagtsqrkwdiritlhc*	MRQLAGTSQRKWDIRITLHC*	MRYHSWHQSDGVVINHIHC*	MRLYSWHQSEKRWISICLLC*	bmyyyhbATG	TTAGCTyysk	0	S	0	0	NCU04087.1	0	0
4755	2532	af	AN4007.1	54.m06583	AO070328000146	0			-222	-208			ATGGAAGCTCCATAA		ATGGAAGCTCCATAA		MEAP*		MEAP*		CTCTTCTCCA	TCCTCAGGTA	0	C	0	0	0	0	0
4756	2532	af	AN4007.1	54.m06583	AO070328000146	0			-187	-59			ATGCCTACTTACGGAACATACCGAGCAGCTTCCCCAGCTGCCCCCCCAGAGCCGGCGGCGTTTCTTTTTCGTTGTCGGCTTCTGTTCTTCCCCGTCTCTTCTCTTATTTCTCATCCCTCTCTTCCTTAA		ATGCCTACTTACGGAACATACCGAGCAGCTTCCCCAGCTGCCCCCCCAGAGCCGGCGGCGTTTCTTTTTCGTTGTCGGCTTCTGTTCTTCCCCGTCTCTTCTCTTATTTCTCATCCCTCTCTTCCTTAA		MPTYGTYRAASPAAPPEPAAFLFRCRLLFFPVSSLISHPSLP*		MPTYGTYRAASPAAPPEPAAFLFRCRLLFFPVSSLISHPSLP*		ATCAGTTACT	AGTTCTATCC	0	C	0	0	0	0	0
4754	2532	an	AN4007.1	54.m06583	AO070328000146	0	-86	-18					ATGGAGCTCTTATTATTTCCCCAGTCGCCTGATCTCCAAGTCTTTCTCACTTCCCGTTCTCTCTCCTAG	ATGGAGCTCTTATTATTTCCCCAGTCGCCTGATCTCCAAGTCTTTCTCACTTCCCGTTCTCTCTCCTAG			MELLLFPQSPDLQVFLTSRSLS*	MELLLFPQSPDLQVFLTSRSLS*			CCGATCCGAC	CAGAACTGAC	0	C	0	0	0	0	0
4758	2532	ao	AN4007.1	54.m06583	AO070328000146	0					-147	-28	ATGTTGGGGTCGAAGCTGAGGTCGCTACTGTGGCGCCGCCGCCATGGATCTCTTTTTATTGCCCTCTCTTCTTCTTTCTTCTCTTTCCCTTCCTCAGTTTCATACTCCCTGCGGTTTTGA			ATGTTGGGGTCGAAGCTGAGGTCGCTACTGTGGCGCCGCCGCCATGGATCTCTTTTTATTGCCCTCTCTTCTTCTTTCTTCTCTTTCCCTTCCTCAGTTTCATACTCCCTGCGGTTTTGA	MLGSKLRSLLWRRRHGSLFIALSSSFFSFPSSVSYSLRF*			MLGSKLRSLLWRRRHGSLFIALSSSFFSFPSSVSYSLRF*	ATCGACCCTC	GTCAATTGTC	0	C	0	0	0	0	0
4759	2532	ao	AN4007.1	54.m06583	AO070328000146	0					-104	-9	ATGGATCTCTTTTTATTGCCCTCTCTTCTTCTTTCTTCTCTTTCCCTTCCTCAGTTTCATACTCCCTGCGGTTTTGAGTCAATTGTCAAAGGTTAG			ATGGATCTCTTTTTATTGCCCTCTCTTCTTCTTTCTTCTCTTTCCCTTCCTCAGTTTCATACTCCCTGCGGTTTTGAGTCAATTGTCAAAGGTTAG	MDLFLLPSLLLSSLSLPQFHTPCGFESIVKG*			MDLFLLPSLLLSSLSLPQFHTPCGFESIVKG*	CGCCGCCGCC	TCGACACGAT	0	C	0	0	0	0	0
4763	2533	af	AN8036.1	53.m03911	AO070330000011	0			-226	-161			ATGGCGTTATGCCCAAGAAGACTTTCGATAATGATGTCACATCACCTATATACGTTGATTGCATGA		ATGGCGTTATGCCCAAGAAGACTTTCGATAATGATGTCACATCACCTATATACGTTGATTGCATGA		MALCPRRLSIMMSHHLYTLIA*		MALCPRRLSIMMSHHLYTLIA*		GCTCTGAACT	TTGGTCCGGA	0	R	0	0	NCU01906.1	0	0
4764	2533	af	AN8036.1	53.m03911	AO070330000011	0			-196	-161			ATGATGTCACATCACCTATATACGTTGATTGCATGA		ATGATGTCACATCACCTATATACGTTGATTGCATGA		MMSHHLYTLIA*		MMSHHLYTLIA*		ACTTTCGATA	TTGGTCCGGA	0	R	0	0	NCU01906.1	0	0
4765	2533	af	AN8036.1	53.m03911	AO070330000011	0			-193	-161			ATGTCACATCACCTATATACGTTGATTGCATGA		ATGTCACATCACCTATATACGTTGATTGCATGA		MSHHLYTLIA*		MSHHLYTLIA*		TTCGATAATG	TTGGTCCGGA	0	R	0	0	NCU01906.1	0	0
4760	2533	an	AN8036.1	53.m03911	AO070330000011	0	-248	-222					ATGTCTTCCTGTTTGACCCATGAATAG	ATGTCTTCCTGTTTGACCCATGAATAG			MSSCLTHE*	MSSCLTHE*			CATTGCAGCA	CTGCCTATCA	0	R	0	0	NCU01906.1	0	0
4761	2533	an	AN8036.1	53.m03911	AO070330000011	0	-229	-179					ATGAATAGCTGCCTATCATGGTCCCCAGTGCGATTGCTGAATGGGCAATAA	ATGAATAGCTGCCTATCATGGTCCCCAGTGCGATTGCTGAATGGGCAATAA			MNSCLSWSPVRLLNGQ*	MNSCLSWSPVRLLNGQ*			TGTTTGACCC	AGACAAGGGA	0	R	0	0	NCU01906.1	0	0
4762	2533	an	AN8036.1	53.m03911	AO070330000011	0	-212	-159					ATGGTCCCCAGTGCGATTGCTGAATGGGCAATAAAGACAAGGGAATGGAGCTGA	ATGGTCCCCAGTGCGATTGCTGAATGGGCAATAAAGACAAGGGAATGGAGCTGA			MVPSAIAEWAIKTREWS*	MVPSAIAEWAIKTREWS*			GCTGCCTATC	TTGGGCCGGA	0	R	0	0	NCU01906.1	0	0
4766	2533	ao	AN8036.1	53.m03911	AO070330000011	0					-168	-55	ATGTCAGAACACCGACTTCTTGCAAACATATCATTGGCCAACGTACCCGAGTGGGCTAGCTACAGATGTTCTCCACCTCGACATACATCACTACTTCCATACTTCTTGATCTAA			ATGTCAGAACACCGACTTCTTGCAAACATATCATTGGCCAACGTACCCGAGTGGGCTAGCTACAGATGTTCTCCACCTCGACATACATCACTACTTCCATACTTCTTGATCTAA	MSEHRLLANISLANVPEWASYRCSPPRHTSLLPYFLI*			MSEHRLLANISLANVPEWASYRCSPPRHTSLLPYFLI*	CTCTTTTGAG	CAATACGCTA	0	R	0	0	NCU01906.1	0	0
4769	2534	af	AN9004.1	70.m15707	AO070330000107	0			-185	-18			ATGGACCATCAACAGGACGTGGTTGCGCATGACACTGAGGGATCTACTCCATACATAAGTGATTGCGACTCCGATTCTCGGCCTCTCTCTTGGGATATATCCTGTGAAAAGAAGAGAACGCCGCTTTCTGTATCTTCCAGCCTTTTTCCCTACCTCTTTTCCGGTTGA		ATGGACCATCAACAGGACGTGGTTGCGCATGACACTGAGGGATCTACTCCATACATAAGTGATTGCGACTCCGATTCTCGGCCTCTCTCTTGGGATATATCCTGTGAAAAGAAGAGAACGCCGCTTTCTGTATCTTCCAGCCTTTTTCCCTACCTCTTTTCCGGTTGA		MDHQQDVVAHDTEGSTPYISDCDSDSRPLSWDISCEKKRTPLSVSSSLFPYLFSG*		MDHQQDVVAHDTEGSTPYISDCDSDSRPLSWDISCEKKRTPLSVSSSLFPYLFSG*		GAAACCAAAA	TTAACACATC	0	C	0	0	0	0	0
4770	2534	af	AN9004.1	70.m15707	AO070330000107	0			-157	-128			ATGACACTGAGGGATCTACTCCATACATAA		ATGACACTGAGGGATCTACTCCATACATAA		MTLRDLLHT*		MTLRDLLHT*		GTGGTTGCGC	GTGATTGCGA	0	C	0	0	0	0	0
4767	2534	an	AN9004.1	70.m15707	AO070330000107	0	-169	-119					ATGAGCGCATGCGATTGCGTTTCCAAGAAAGGTGGGGGAGGGGTCCTATAA	ATGAGCGCATGCGATTGCGTTTCCAAGAAAGGTGGGGGAGGGGTCCTATAA			MSACDCVSKKGGGGVL*	MSACDCVSKKGGGGVL*			TACGAAAGCT	GTAGCAGGCG	0	C	0	0	0	0	0
4768	2534	an	AN9004.1	70.m15707	AO070330000107	0	-88	-71					ATGCGGGATTGTTGTTGA	ATGCGGGATTGTTGTTGA			MRDCC*	MRDCC*			GTCGCGAGCG	TACTATACAA	0	C	0	0	0	0	0
4771	2534	ao	AN9004.1	70.m15707	AO070330000107	0					-297	-226	ATGGTGTCATCGCGACCCACTTTGATGCTATATAGGACAAGGACACCACCCCTCGATCCCTGTCAAGGCTGA			ATGGTGTCATCGCGACCCACTTTGATGCTATATAGGACAAGGACACCACCCCTCGATCCCTGTCAAGGCTGA	MVSSRPTLMLYRTRTPPLDPCQG*			MVSSRPTLMLYRTRTPPLDPCQG*	CAGATCCCGC	GAATGAGGGG	0	C	0	0	0	0	0
4772	2534	ao	AN9004.1	70.m15707	AO070330000107	0					-273	-226	ATGCTATATAGGACAAGGACACCACCCCTCGATCCCTGTCAAGGCTGA			ATGCTATATAGGACAAGGACACCACCCCTCGATCCCTGTCAAGGCTGA	MLYRTRTPPLDPCQG*			MLYRTRTPPLDPCQG*	ACCCACTTTG	GAATGAGGGG	0	C	0	0	0	0	0

4773	2534	ao	AN9004.1	70.m15707	AO070330000107	0					-223	-122	ATGAGGGGAATTCGGGTAATGGTGCTGGCTAATATTAATACTGATAGAGGGGCACTTCGTCATATAGGCTTTAATTTCTCCTTGCTCAGTTGTTTCCCGTAG			ATGAGGGGAATTCGGGTAATGGTGCTGGCTAATATTAATACTGATAGAGGGGCACTTCGTCATATAGGCTTTAATTTCTCCTTGCTCAGTTGTTTCCCGTAG	MRGIRVMVLANINTDRGALRHIGFNFSLLSCFP*			MRGIRVMVLANINTDRGALRHIGFNFSLLSCFP*	AAGGCTGAGA	ACACTGGCGA	0	C	0	0	0	0	0
4774	2534	ao	AN9004.1	70.m15707	AO070330000107	0					-205	-122	ATGGTGCTGGCTAATATTAATACTGATAGAGGGGCACTTCGTCATATAGGCTTTAATTTCTCCTTGCTCAGTTGTTTCCCGTAG			ATGGTGCTGGCTAATATTAATACTGATAGAGGGGCACTTCGTCATATAGGCTTTAATTTCTCCTTGCTCAGTTGTTTCCCGTAG	MVLANINTDRGALRHIGFNFSLLSCFP*			MVLANINTDRGALRHIGFNFSLLSCFP*	AATTCGGGTA	ACACTGGCGA	0	C	0	0	0	0	0
4776	2535	af	AN1129.1	70.m15106	AO070331000121	0			-119	-45			ATGCTTCTGATATTAACCAGATGGGTGCATCGGAGGGTGTCCGGCCCCACGGGCAGATTCAGTCTATATATTTAG		ATGCTTCTGATATTAACCAGATGGGTGCATCGGAGGGTGTCCGGCCCCACGGGCAGATTCAGTCTATATATTTAG		MLLILTRWVHRRVSGPTGRFSLYI*		MLLILTRWVHRRVSGPTGRFSLYI*		TGTTGCAGCT	AATGTTGCTA	0	P	0	0	0	0	0
4777	2535	af	AN1129.1	70.m15106	AO070331000121	0			-99	-34			ATGGGTGCATCGGAGGGTGTCCGGCCCCACGGGCAGATTCAGTCTATATATTTAGAATGTTGCTAG		ATGGGTGCATCGGAGGGTGTCCGGCCCCACGGGCAGATTCAGTCTATATATTTAGAATGTTGCTAG		MGASEGVRPHGQIQSIYLECC*		MGASEGVRPHGQIQSIYLECC*		TATTAACCAG	ATCGTGGAAC	0	P	0	0	0	0	0
4775	2535	an	AN1129.1	70.m15106	AO070331000121	0	-108	-85					ATGTCTGAGCAATTCTGCGAGTAG	ATGTCTGAGCAATTCTGCGAGTAG			MSEQFCE*	MSEQFCE*			ATTTATACCA	AATCCTGCCT	0	P	0	0	0	0	0
4779	2535	ao	AN1129.1	70.m15106	AO070331000121	0					-152	-66	ATGCTGTATAAAGAGGACCTTCTGGCCAGGCTTCTGCCAGAGTCGCGTCGAAGAACACAATTCTATCAGACATTTATACGACCTTAA			ATGCTGTATAAAGAGGACCTTCTGGCCAGGCTTCTGCCAGAGTCGCGTCGAAGAACACAATTCTATCAGACATTTATACGACCTTAA	MLYKEDLLARLLPESRRRTQFYQTFIRP*			MLYKEDLLARLLPESRRRTQFYQTFIRP*	TCCCGCAGCG	CCCAAATTAT	0	P	0	0	0	0	0
4780	2537	af	AN0313.1	54.m06445	AO070334000019	0			-261	-232			ATGTCTTGGCTGGCGTCTTGTCCACTCTGA		ATGTCTTGGCTGGCGTCTTGTCCACTCTGA		MSWLASCPL*		MSWLASCPL*		CACTTTCTGG	ACATCGTACC	0	I	0	0	0	0	0
4781	2537	af	AN0313.1	54.m06445	AO070334000019	0			-194	-126			ATGATCCCTCGGTTCACTTCATCCATATCCAATCTCCAACATTCACGTTCTCCTCCTGTTTATTATTAG		ATGATCCCTCGGTTCACTTCATCCATATCCAATCTCCAACATTCACGTTCTCCTCCTGTTTATTATTAG		MIPRFTSSISNLQHSRSPPVYY*		MIPRFTSSISNLQHSRSPPVYY*		CCCAACCCCC	GTTTCGGGTC	0	I	0	0	0	0	0
4782	2537	ao	AN0313.1	54.m06445	AO070334000019	0					-83	-33	ATGGTCGTCTTTCCTTTCCCTTCCGATTCTCCAACATCCTCCAAAACTTAA			ATGGTCGTCTTTCCTTTCCCTTCCGATTCTCCAACATCCTCCAAAACTTAA	MVVFPFPSDSPTSSKT*			MVVFPFPSDSPTSSKT*	TCAATAATTC	TTGCCCCTTC	0	I	0	0	0	0	0
4783	2539	af	AN1485.1	55.m02991	AO070334000192	0			-158	-138			ATGCTCCTAGTCTTGCAGTAG		ATGCTCCTAGTCTTGCAGTAG		MLLVLQ*		MLLVLQ*		ACAGGCCTGT	CTGTTGTCTG	0	TDK	0	0	NCU03124.1	0	0
4784	2541	an	AN2985.1	59.m09028	AO070337000137	0	-186	-136					ATGTATACTCGATCTTTGCGATTCAAGCTAATATCCTGTTTGCGTGACTGA	ATGTATACTCGATCTTTGCGATTCAAGCTAATATCCTGTTTGCGTGACTGA			MYTRSLRFKLISCLRD*	MYTRSLRFKLISCLRD*			TCCGAGAGCG	TCTAGGCTCT	0	R	0	0	0	0	0
4786	2541	ao	AN2985.1	59.m09028	AO070337000137	0					-178	-161	ATGTCGATCTTTTACTAA			ATGTCGATCTTTTACTAA	MSIFY*			MSIFY*	CTCGTTCTTT	CCCTGAGTCA	0	R	0	0	0	0	0
4788	2546	ao	AN2875.1	59.m08724	AO070338000136	0					-199	-56	ATGACACTTTTATTAAATCCCCTGCTCCGTATTCGTCGTTCGGTAAAGATCCTTAGTTCGGAAGCTCCTACAGAACTTATTTCTAGCTGTTCACTTCCTCCTCCATCCTTTCCTTCTCCTCTTCCATTTCTTCTCCCAAACTAA			ATGACACTTTTATTAAATCCCCTGCTCCGTATTCGTCGTTCGGTAAAGATCCTTAGTTCGGAAGCTCCTACAGAACTTATTTCTAGCTGTTCACTTCCTCCTCCATCCTTTCCTTCTCCTCTTCCATTTCTTCTCCCAAACTAA	MTLLLNPLLRIRRSVKILSSEAPTELISSCSLPPPSFPSPLPFLLPN*			MTLLLNPLLRIRRSVKILSSEAPTELISSCSLPPPSFPSPLPFLLPN*	CCCTTTGCCA	TCCAATTCCT	0	G	0	MG00223.1	0	0	0
4790	2547	af	AN6073.1	72.m19947	AO070340000117	0			-248	-216			ATGAAATTACAGATATATGGTAGGATGTTCTAG		ATGAAATTACAGATATATGGTAGGATGTTCTAG		MKLQIYGRMF*		MKLQIYGRMF*		CAAACGTAAA	ATAAGTAACA	0	O	FG01119.1	0	NCU03310.1	0	0
4791	2547	af	AN6073.1	72.m19947	AO070340000117	0			-232	-212			ATGGTAGGATGTTCTAGATAA		ATGGTAGGATGTTCTAGATAA		MVGCSR*		MVGCSR*		TTACAGATAT	GTAACAATTT	0	O	FG01119.1	0	NCU03310.1	0	0
4792	2547	af	AN6073.1	72.m19947	AO070340000117	0			-152	-108			ATGAAGAAAAGCCGCGAGCAGGACCGAACGCTTTGTCTTGTTTGA		ATGAAGAAAAGCCGCGAGCAGGACCGAACGCTTTGTCTTGTTTGA		MKKSREQDRTLCLV*		MKKSREQDRTLCLV*		CCTTGCAACA	GCTGTCTGTC	0	O	FG01119.1	0	NCU03310.1	0	0
4789	2547	an	AN6073.1	72.m19947	AO070340000117	0	-146	-6					ATGGAGCAAACTACGTCTGATTCGGAGAGGGTCGAGAGCTGCCAAGGCGGTGTCCAAATCTGGAGAACTGCCGCAAGTTGCACGAACCTCAAGGGCTTTCCGACCTTGTCATCTGGACACCATCTTACATTTCCACCATAA	ATGGAGCAAACTACGTCTGATTCGGAGAGGGTCGAGAGCTGCCAAGGCGGTGTCCAAATCTGGAGAACTGCCGCAAGTTGCACGAACCTCAAGGGCTTTCCGACCTTGTCATCTGGACACCATCTTACATTTCCACCATAA			MEQTTSDSERVESCQGGVQIWRTAASCTNLKGFPTLSSGHHLTFPP*	MEQTTSDSERVESCQGGVQIWRTAASCTNLKGFPTLSSGHHLTFPP*			TCTTTTTCTG	CTATCATGTC	0	O	FG01119.1	0	NCU03310.1	0	0
4797	2548	af	AN6079.1	72.m19071	AO070340000129	0			-203	-180			ATGTCAAAGGAGGATTTGAATTGA		ATGTCAAAGGAGGATTTGAATTGA		MSKEDLN*		MSKEDLN*		ACTCATCAGT	AGTCTCCAGT	0	R	0	0	0	0	0
4793	2548	an	AN6079.1	72.m19071	AO070340000129	0	-214	-131					ATGTTTACAAATAAATGTAAATATAACCAATCAATGTCCATTATTGAGGCCACTTCGAAGTTGCGTTGGCTACTGGCTTTCTAG	ATGTTTACAAATAAATGTAAATATAACCAATCAATGTCCATTATTGAGGCCACTTCGAAGTTGCGTTGGCTACTGGCTTTCTAG			MFTNKCKYNQSMSIIEATSKLRWLLAF*	MFTNKCKYNQSMSIIEATSKLRWLLAF*			TGCCAACACT	AAGCCCTAGA	0	R	0	0	0	0	0
4794	2548	an	AN6079.1	72.m19071	AO070340000129	0	-181	-131					ATGTCCATTATTGAGGCCACTTCGAAGTTGCGTTGGCTACTGGCTTTCTAG	ATGTCCATTATTGAGGCCACTTCGAAGTTGCGTTGGCTACTGGCTTTCTAG			MSIIEATSKLRWLLAF*	MSIIEATSKLRWLLAF*			TAACCAATCA	AAGCCCTAGA	0	R	0	0	0	0	0
4795	2548	an	AN6079.1	72.m19071	AO070340000129	0	-120	-103					ATGATTCAGAATGAGTGA	ATGATTCAGAATGAGTGA			MIQNE*	MIQNE*			AAGCCCTAGA	GAAATGCCCC	0	R	0	0	0	0	0
4796	2548	an	AN6079.1	72.m19071	AO070340000129	0	-110	-75					ATGAGTGAGAAATGCCCCGCATACGTCACGTCTTAA	ATGAGTGAGAAATGCCCCGCATACGTCACGTCTTAA			MSEKCPAYVTS*	MSEKCPAYVTS*			ATGATTCAGA	AGTCGGGCCT	0	R	0	0	0	0	0
4798	2548	ao	AN6079.1	72.m19071	AO070340000129	0					-221	-15	ATGATATTCTCCACAATTTTGTGGGCTGGGCTTATGCGGTTAAAACCACTATCGAATGGCATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA			ATGATATTCTCCACAATTTTGTGGGCTGGGCTTATGCGGTTAAAACCACTATCGAATGGCATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA	MIFSTILWAGLMRLKPLSNGMEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*			MIFSTILWAGLMRLKPLSNGMEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*	GAATTCAATC	ATTTAGAAAA	0	R	0	0	0	0	0
4799	2548	ao	AN6079.1	72.m19071	AO070340000129	0					-188	-15	ATGCGGTTAAAACCACTATCGAATGGCATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA			ATGCGGTTAAAACCACTATCGAATGGCATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA	MRLKPLSNGMEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*			MRLKPLSNGMEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*	GGCTGGGCTT	ATTTAGAAAA	0	R	0	0	0	0	0
4800	2548	ao	AN6079.1	72.m19071	AO070340000129	0					-166	-143	ATGGCATGGAAAAGCGATCGATAA			ATGGCATGGAAAAGCGATCGATAA	MAWKSDR*			MAWKSDR*	CCACTATCGA	ATAGTGAAAA	0	R	0	0	0	0	0
4801	2548	ao	AN6079.1	72.m19071	AO070340000129	0					-161	-15	ATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA			ATGGAAAAGCGATCGATAAATAGTGAAAAACTGCCCCGCATACGTCACGCTCTTTGCCTACGCTGGTCCCATTTTGGTCTTTGCAAACTTCTTGCTCACCAGCCACTTTTCGCCGTACTGGCTCATTTTCCTGGAGTCTCAAGCTAA	MEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*			MEKRSINSEKLPRIRHALCLRWSHFGLCKLLAHQPLFAVLAHFPGVSS*	ATCGAATGGC	ATTTAGAAAA	0	R	0	0	0	0	0
4808	2550	af	AN5755.1	69.m14853	AO070341000014	0			-608	-594			ATGTGCCCTTTCTGA		ATGTGCCCTTTCTGA		MCPF*		MCPF*		TCCTGAATCC	GATTTTCCAA	0		0	0	0	0	0
4802	2550	an	AN5755.1	69.m14853	AO070341000014	0	-703	-611					ATGGCCATAATAATGAATTGGAAAGAGAAATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGA	ATGGCCATAATAATGAATTGGAAAGAGAAATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGA			MAIIMNWKEKWHHSSNRCQSTYLSGAPTSA*	MAIIMNWKEKWHHSSNRCQSTYLSGAPTSA*			CAAGTTGACT	TAGGCGGGCG	0		0	0	0	0	0
4803	2550	an	AN5755.1	69.m14853	AO070341000014	0	-691	-611					ATGAATTGGAAAGAGAAATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGA	ATGAATTGGAAAGAGAAATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGA			MNWKEKWHHSSNRCQSTYLSGAPTSA*	MNWKEKWHHSSNRCQSTYLSGAPTSA*			GGCCATAATA	TAGGCGGGCG	0		0	0	0	0	0
4804	2550	an	AN5755.1	69.m14853	AO070341000014	0	-674	-579					ATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGATAGGCGGGCGTTTGGCAAGGTTCTGGCTCTGA	ATGGCATCATTCTTCAAATCGCTGCCAATCGACTTATCTGAGTGGGGCACCGACCTCGGCCTGATAGGCGGGCGTTTGGCAAGGTTCTGGCTCTGA			MASFFKSLPIDLSEWGTDLGLIGGRLARFWL*	MASFFKSLPIDLSEWGTDLGLIGGRLARFWL*			GGAAAGAGAA	GTGGATTGCT	0		0	0	0	0	0
4805	2550	an	AN5755.1	69.m14853	AO070341000014	0	-422	-390					ATGCCCGCCCGCTCTCCCTTTTCTTACTCTTGA	ATGCCCGCCCGCTCTCCCTTTTCTTACTCTTGA			MPARSPFSYS*	MPARSPFSYS*			AGTCCGTTAT	CTCTCTGTTT	0		0	0	0	0	0
4806	2550	an	AN5755.1	69.m14853	AO070341000014	0	-307	-287					ATGCGCTTATCCCACCAATGA	ATGCGCTTATCCCACCAATGA			MRLSHQ*	MRLSHQ*			CACTCTTGGG	TTCATCTCTC	0		0	0	0	0	0
4807	2550	an	AN5755.1	69.m14853	AO070341000014	0	-290	-198					ATGATTCATCTCTCTCGCGGCCTCGCTCTCTTTTCCCTCACTAACCGCCCTCCTTTTCCTCCAGTCCTCGTCACTTCGATCAGAATCATCTGA	ATGATTCATCTCTCTCGCGGCCTCGCTCTCTTTTCCCTCACTAACCGCCCTCCTTTTCCTCCAGTCCTCGTCACTTCGATCAGAATCATCTGA			MIHLSRGLALFSLTNRPPFPPVLVTSIRII*	MIHLSRGLALFSLTNRPPFPPVLVTSIRII*			TATCCCACCA	AAGTATCAAG	0		0	0	0	0	0
4809	2550	ao	AN5755.1	69.m14853	AO070341000014	0					-571	-515	ATGTTACATCCATATCTCGGCTACGGCACACGACTAATCAGTCCTTTTCCTCGATAG			ATGTTACATCCATATCTCGGCTACGGCACACGACTAATCAGTCCTTTTCCTCGATAG	MLHPYLGYGTRLISPFPR*			MLHPYLGYGTRLISPFPR*	AACTCCTTAC	CAGATCTCAC	0		0	0	0	0	0
4810	2552	af	AN4148.1	58.m07369	AO070342000182	0			-112	-86			ATGAGTCTGTCTGCTCTGGGATACTAG		ATGAGTCTGTCTGCTCTGGGATACTAG		MSLSALGY*		MSLSALGY*		TTTTCATCAC	GCTTCCCTAC	0	R	0	0	0	0	0
4811	2552	ao	AN4148.1	58.m07369	AO070342000182	0					-153	-121	ATGCATCTTTCTCCTCTCTTTCTTTCTCCTTAG			ATGCATCTTTCTCCTCTCTTTCTTTCTCCTTAG	MHLSPLFLSP*			MHLSPLFLSP*	TCTTGCGTTA	GTCTCCCTTC	0	R	0	0	0	0	0
4812	2552	ao	AN4148.1	58.m07369	AO070342000182	0					-102	-28	ATGAGACTGCCACTTCCTATCACCGCTCACCTGAAGCAGTCTCGTCCCGTTTGGGAATCTAGTCCAATTAGTTAG			ATGAGACTGCCACTTCCTATCACCGCTCACCTGAAGCAGTCTCGTCCCGTTTGGGAATCTAGTCCAATTAGTTAG	MRLPLPITAHLKQSRPVWESSPIS*			MRLPLPITAHLKQSRPVWESSPIS*	TCACTATCGC	GAGGGCACAG	0	R	0	0	0	0	0
4818	2556	af	AN4323.1	58.m08000	AO070230000015	0			-225	-199			ATGTCACACATATTGCTTGATGTATGA		ATGTCACACATATTGCTTGATGTATGA		MSHILLDV*		MSHILLDV*		AGTTTGAGGT	TACGCAATGT	0	E	0	MG02489.1	0	YHR208W	0
4819	2556	af	AN4323.1	58.m08000	AO070230000015	0			-206	-144			ATGTATGATACGCAATGTCGAGCTTTCGGAGTTGTCTCTTGGGTCCGGCGGGAGGAGTCATAG		ATGTATGATACGCAATGTCGAGCTTTCGGAGTTGTCTCTTGGGTCCGGCGGGAGGAGTCATAG		MYDTQCRAFGVVSWVRREES*		MYDTQCRAFGVVSWVRREES*		ATATTGCTTG	CCTCCGCTTT	0	E	0	MG02489.1	0	YHR208W	0
4820	2556	af	AN4323.1	58.m08000	AO070230000015	0			-192	-130			ATGTCGAGCTTTCGGAGTTGTCTCTTGGGTCCGGCGGGAGGAGTCATAGCCTCCGCTTTTTAA		ATGTCGAGCTTTCGGAGTTGTCTCTTGGGTCCGGCGGGAGGAGTCATAGCCTCCGCTTTTTAA		MSSFRSCLLGPAGGVIASAF*		MSSFRSCLLGPAGGVIASAF*		ATGATACGCA	GCTCCATTAT	0	E	0	MG02489.1	0	YHR208W	0
4813	2556	an	AN4323.1	58.m08000	AO070230000015	0	-178	-38					ATGTCAAATGTTGACATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAACTACCGCGGGTCACTTCTTCTGTCTCCCCTCAGCCGGCATTGATATGATCCCTTCGCTGTTTTGCTGA	ATGTCAAATGTTGACATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAACTACCGCGGGTCACTTCTTCTGTCTCCCCTCAGCCGGCATTGATATGATCCCTTCGCTGTTTTGCTGA			MSNVDMAIRSCYYGPESHAFIPFITTAGHFFCLPSAGIDMIPSLFC*	MSNVDMAIRSCYYGPESHAFIPFITTAGHFFCLPSAGIDMIPSLFC*			GTCTCCCTGG	GAATTGACTA	0	E	0	MG02489.1	0	YHR208W	0
4814	2556	an	AN4323.1	58.m08000	AO070230000015	0	-171	-106					ATGTTGACATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAA	ATGTTGACATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAA			MLTWPSGVVTTVRKVMHLFLL*	MLTWPSGVVTTVRKVMHLFLL*			TGGATGTCAA	CTACCGCGGG	0	E	0	MG02489.1	0	YHR208W	0
4815	2556	an	AN4323.1	58.m08000	AO070230000015	0	-163	-38					ATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAACTACCGCGGGTCACTTCTTCTGTCTCCCCTCAGCCGGCATTGATATGATCCCTTCGCTGTTTTGCTGA	ATGGCCATCCGGAGTTGTTACTACGGTCCGGAAAGTCATGCATTTATTCCTTTTATAACTACCGCGGGTCACTTCTTCTGTCTCCCCTCAGCCGGCATTGATATGATCCCTTCGCTGTTTTGCTGA			MAIRSCYYGPESHAFIPFITTAGHFFCLPSAGIDMIPSLFC*	MAIRSCYYGPESHAFIPFITTAGHFFCLPSAGIDMIPSLFC*			AAATGTTGAC	GAATTGACTA	0	E	0	MG02489.1	0	YHR208W	0
4816	2556	an	AN4323.1	58.m08000	AO070230000015	0	-126	-106					ATGCATTTATTCCTTTTATAA	ATGCATTTATTCCTTTTATAA			MHLFLL*	MHLFLL*			CCGGAAAGTC	CTACCGCGGG	0	E	0	MG02489.1	0	YHR208W	0
4821	2556	ao	AN4323.1	58.m08000	AO070230000015	0					-279	-187	ATGACAACTTTGCCATTCGAGATCGTGTGGGGCGCTTTTGGTAGGCTTCCGTATCAGTTCGGTTATCGCTGGATCTTCCGGAGTTGGACCTAG			ATGACAACTTTGCCATTCGAGATCGTGTGGGGCGCTTTTGGTAGGCTTCCGTATCAGTTCGGTTATCGCTGGATCTTCCGGAGTTGGACCTAG	MTTLPFEIVWGAFGRLPYQFGYRWIFRSWT*			MTTLPFEIVWGAFGRLPYQFGYRWIFRSWT*	CGAGACTTAT	GGTCCGTGGA	0	E	0	MG02489.1	0	YHR208W	0
4823	2557	af	AN1403.1	70.m14821	AO070233000018	0			-126	-106			ATGTCATTGGGCAGAATATGA		ATGTCATTGGGCAGAATATGA		MSLGRI*		MSLGRI*		GCATAACCAA	TGGGTGCCAA	0	H	0	0	0	YGL040C	0

4824	2557	af	AN1403.1	70.m14821	AO070233000018	0			-109	-17			ATGATGGGTGCCAAGGGGCAGGGACTGATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		ATGATGGGTGCCAAGGGGCAGGGACTGATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		MMGAKGQGLMGGISVLHSSTTTSQKVLNSP*		MMGAKGQGLMGGISVLHSSTTTSQKVLNSP*		TGGGCAGAAT	ATCCCTCATC	0	H	0	0	0	YGL040C	0
4825	2557	af	AN1403.1	70.m14821	AO070233000018	0			-106	-17			ATGGGTGCCAAGGGGCAGGGACTGATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		ATGGGTGCCAAGGGGCAGGGACTGATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		MGAKGQGLMGGISVLHSSTTTSQKVLNSP*		MGAKGQGLMGGISVLHSSTTTSQKVLNSP*		GCAGAATATG	ATCCCTCATC	0	H	0	0	0	YGL040C	0
4826	2557	af	AN1403.1	70.m14821	AO070233000018	0			-82	-17			ATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		ATGGGAGGAATATCCGTACTCCATAGTAGCACAACCACTTCTCAAAAAGTGCTCAACTCCCCATAA		MGGISVLHSSTTTSQKVLNSP*		MGGISVLHSSTTTSQKVLNSP*		GCAGGGACTG	ATCCCTCATC	0	H	0	0	0	YGL040C	0
4822	2557	an	AN1403.1	70.m14821	AO070233000018	0	-62	-39					ATGATACCTATTCGAATATACTGA	ATGATACCTATTCGAATATACTGA			MIPIRIY*	MIPIRIY*			GGAGGCTCCG	GTTACCATAT	0	H	0	0	0	YGL040C	0
4827	2557	ao	AN1403.1	70.m14821	AO070233000018	0					-185	-30	ATGATCCTTAAATCCTTACTTGTACCTGAAAATTGCAACAAATGTACTGACCTGGATCGCTGGCCATCTATATCATTGCCCTGCGAAGTCGTATTCTGCCAGTGGCACAGGCGCTATTCTCTTTTCTTCCCTCCACCGCGTTTCTATCTTCCATAG			ATGATCCTTAAATCCTTACTTGTACCTGAAAATTGCAACAAATGTACTGACCTGGATCGCTGGCCATCTATATCATTGCCCTGCGAAGTCGTATTCTGCCAGTGGCACAGGCGCTATTCTCTTTTCTTCCCTCCACCGCGTTTCTATCTTCCATAG	MILKSLLVPENCNKCTDLDRWPSISLPCEVVFCQWHRRYSLFFPPPRFYLP*			MILKSLLVPENCNKCTDLDRWPSISLPCEVVFCQWHRRYSLFFPPPRFYLP*	GCGTTGTTCT	CACCCCACTT	0	H	0	0	0	YGL040C	0
4830	2558	af	AN1428.1	55.m02927	AO070242000023	0			-270	-259			ATGTTTCTTTGA		ATGTTTCTTTGA		MFL*		MFL*		GCAACAGCGT	TGTCACCATC	0	G	0	MG00620.1	0	0	0
4831	2558	af	AN1428.1	55.m02927	AO070242000023	0			-259	-161			ATGTCACCATCATGTAGCCTGGCATTGTCATTGTTGTCCCTTGCTTCGCTTGTTGCCTCCAGACTCTGTCCATATACATCCGTGTGGATTTCATCTTGA		ATGTCACCATCATGTAGCCTGGCATTGTCATTGTTGTCCCTTGCTTCGCTTGTTGCCTCCAGACTCTGTCCATATACATCCGTGTGGATTTCATCTTGA		MSPSCSLALSLLSLASLVASRLCPYTSVWISS*		MSPSCSLALSLLSLASLVASRLCPYTSVWISS*		TGTTTCTTTG	TTTTTATTTC	0	G	0	MG00620.1	0	0	0
4828	2558	an	AN1428.1	55.m02927	AO070242000023	0	-191	-45					ATGGTGTCTCTTCCGCCCGCCATCGGCGTGGCCATGGATCGCCGCAGCCCTTACCGGTCTTTGTGTTCCCTTGTCGGCCTATATACTACTGACATCTCCACGGCTCTTTGCACGACTGCCTTCGTCCATACTAAATCGCCGGCTTGA	ATGGTGTCTCTTCCGCCCGCCATCGGCGTGGCCATGGATCGCCGCAGCCCTTACCGGTCTTTGTGTTCCCTTGTCGGCCTATATACTACTGACATCTCCACGGCTCTTTGCACGACTGCCTTCGTCCATACTAAATCGCCGGCTTGA			MVSLPPAIGVAMDRRSPYRSLCSLVGLYTTDISTALCTTAFVHTKSPA*	MVSLPPAIGVAMDRRSPYRSLCSLVGLYTTDISTALCTTAFVHTKSPA*			CAGGTACCAC	CAGCACACGA	0	G	0	MG00620.1	0	0	0
4829	2558	an	AN1428.1	55.m02927	AO070242000023	0	-158	-45					ATGGATCGCCGCAGCCCTTACCGGTCTTTGTGTTCCCTTGTCGGCCTATATACTACTGACATCTCCACGGCTCTTTGCACGACTGCCTTCGTCCATACTAAATCGCCGGCTTGA	ATGGATCGCCGCAGCCCTTACCGGTCTTTGTGTTCCCTTGTCGGCCTATATACTACTGACATCTCCACGGCTCTTTGCACGACTGCCTTCGTCCATACTAAATCGCCGGCTTGA			MDRRSPYRSLCSLVGLYTTDISTALCTTAFVHTKSPA*	MDRRSPYRSLCSLVGLYTTDISTALCTTAFVHTKSPA*			CGGCGTGGCC	CAGCACACGA	0	G	0	MG00620.1	0	0	0
4832	2558	ao	AN1428.1	55.m02927	AO070242000023	0					-215	-192	ATGGATGCTACTATCTATCCATGA			ATGGATGCTACTATCTATCCATGA	MDATIYP*			MDATIYP*	GCCCGCCGTA	TGTAGCCTTT	0	G	0	MG00620.1	0	0	0
4834	2561	af	AN2648.1	54.m06312	AO070263000025	0			-206	-195			ATGCCGAGGTAG		ATGCCGAGGTAG		MPR*		MPR*		CTACGGAAGA	CTAGCTGGAC	0	C	0	0	0	0	0
4835	2561	af	AN2648.1	54.m06312	AO070263000025	0			-105	-85			ATGATCAACCGACGATCTTGA		ATGATCAACCGACGATCTTGA		MINRRS*		MINRRS*		CAGGATCGGC	GAATCTTCCC	0	C	0	0	0	0	0
4833	2561	an	AN2648.1	54.m06312	AO070263000025	0	-197	-84					ATGTGCGACGGTGCCTCAATAGTACCGGGGCCTAACGCTTCGGGGAACAACTCCGACACGTGGCCGTGTCAGTCTTCAGCGCTGGCGCCATACCTTGGAGAACGACGAGTATAA	ATGTGCGACGGTGCCTCAATAGTACCGGGGCCTAACGCTTCGGGGAACAACTCCGACACGTGGCCGTGTCAGTCTTCAGCGCTGGCGCCATACCTTGGAGAACGACGAGTATAA			MCDGASIVPGPNASGNNSDTWPCQSSALAPYLGERRV*	MCDGASIVPGPNASGNNSDTWPCQSSALAPYLGERRV*			AGCAGATTCG	GACATCAACC	0	C	0	0	0	0	0
4836	2561	ao	AN2648.1	54.m06312	AO070263000025	0					-263	-234	ATGACTCTTCGGTTCCTCCGCCCAGACTAG			ATGACTCTTCGGTTCCTCCGCCCAGACTAG	MTLRFLRPD*			MTLRFLRPD*	CACCCCGTCC	ACGCTCTTGG	0	C	0	0	0	0	0
4837	2561	ao	AN2648.1	54.m06312	AO070263000025	0					-200	-129	ATGAGGTTCCTGTCTAGGATGCCTCCGCCACGGACGATAGATGAAGATGCCTCCCCTGGTGCCTCGGTGTAG			ATGAGGTTCCTGTCTAGGATGCCTCCGCCACGGACGATAGATGAAGATGCCTCCCCTGGTGCCTCGGTGTAG	MRFLSRMPPPRTIDEDASPGASV*			MRFLSRMPPPRTIDEDASPGASV*	GACGCTGCTC	TGCAAAAGCG	0	C	0	0	0	0	0
4838	2561	ao	AN2648.1	54.m06312	AO070263000025	0					-182	-129	ATGCCTCCGCCACGGACGATAGATGAAGATGCCTCCCCTGGTGCCTCGGTGTAG			ATGCCTCCGCCACGGACGATAGATGAAGATGCCTCCCCTGGTGCCTCGGTGTAG	MPPPRTIDEDASPGASV*			MPPPRTIDEDASPGASV*	CCTGTCTAGG	TGCAAAAGCG	0	C	0	0	0	0	0
4839	2561	ao	AN2648.1	54.m06312	AO070263000025	0					-160	-110	ATGAAGATGCCTCCCCTGGTGCCTCGGTGTAGTGCAAAAGCGCCAAATTAA			ATGAAGATGCCTCCCCTGGTGCCTCGGTGTAGTGCAAAAGCGCCAAATTAA	MKMPPLVPRCSAKAPN*			MKMPPLVPRCSAKAPN*	CGGACGATAG	TATGTGATAT	0	C	0	0	0	0	0
4840	2561	ao	AN2648.1	54.m06312	AO070263000025	0					-154	-110	ATGCCTCCCCTGGTGCCTCGGTGTAGTGCAAAAGCGCCAAATTAA			ATGCCTCCCCTGGTGCCTCGGTGTAGTGCAAAAGCGCCAAATTAA	MPPLVPRCSAKAPN*			MPPLVPRCSAKAPN*	ATAGATGAAG	TATGTGATAT	0	C	0	0	0	0	0
4841	2563	ao	AN4417.1	58.m07906	AO070273000038	0					-210	-67	ATGCTTTTCCCAAAAAGCTTCATTTTATCGTCGCATGCTGCCGTCGCTGCTCGGAATTTCAGTTGCCCGTTCAGCTCATACGTCGAATTGCCTCTTGATTTCCTAGTTCTGGCATATAAGAATAGTACTGCGCAGCAGTTCTGA			ATGCTTTTCCCAAAAAGCTTCATTTTATCGTCGCATGCTGCCGTCGCTGCTCGGAATTTCAGTTGCCCGTTCAGCTCATACGTCGAATTGCCTCTTGATTTCCTAGTTCTGGCATATAAGAATAGTACTGCGCAGCAGTTCTGA	MLFPKSFILSSHAAVAARNFSCPFSSYVELPLDFLVLAYKNSTAQQF*			MLFPKSFILSSHAAVAARNFSCPFSSYVELPLDFLVLAYKNSTAQQF*	GTGTGTTTTG	TCATGCTGTG	0	S	FG10865.1	MG03886.1	0	0	0
4842	2563	ao	AN4417.1	58.m07906	AO070273000038	0					-176	-105	ATGCTGCCGTCGCTGCTCGGAATTTCAGTTGCCCGTTCAGCTCATACGTCGAATTGCCTCTTGATTTCCTAG			ATGCTGCCGTCGCTGCTCGGAATTTCAGTTGCCCGTTCAGCTCATACGTCGAATTGCCTCTTGATTTCCTAG	MLPSLLGISVARSAHTSNCLLIS*			MLPSLLGISVARSAHTSNCLLIS*	TTATCGTCGC	TTCTGGCATA	0	S	FG10865.1	MG03886.1	0	0	0
4844	2564	af	AN8805.1	71.m15612	AO070276000053	0			-158	-126			ATGAAAAAGGAAAAATTTTATAATGATAACTAA		ATGAAAAAGGAAAAATTTTATAATGATAACTAA		MKKEKFYNDN*		MKKEKFYNDN*		ATCGTTTCAT	CCAAATCACA	0	R	FG05948.1	0	0	0	0
4845	2564	af	AN8805.1	71.m15612	AO070276000053	0			-136	-95			ATGATAACTAACCAAATCACAGATACCAAACCACCGCATTGA		ATGATAACTAACCAAATCACAGATACCAAACCACCGCATTGA		MITNQITDTKPPH*		MITNQITDTKPPH*		AAATTTTATA	CCTGCATCTG	0	R	FG05948.1	0	0	0	0
4843	2564	an	AN8805.1	71.m15612	AO070276000053	0	-169	-86					ATGAGTACAAGACAGACTAACTACCCCTCAGATCAATCCAAATCGGGATCCAAAAAAGCCATTCTACGATTGTGTCTACCATAG	ATGAGTACAAGACAGACTAACTACCCCTCAGATCAATCCAAATCGGGATCCAAAAAAGCCATTCTACGATTGTGTCTACCATAG			MSTRQTNYPSDQSKSGSKKAILRLCLP*	MSTRQTNYPSDQSKSGSKKAILRLCLP*			TCTATTTATA	GGCATCATCT	0	R	FG05948.1	0	0	0	0
4846	2564	ao	AN8805.1	71.m15612	AO070276000053	0					-208	-62	ATGACATCTGTTGGGCATCAAATACATATAAACCTCTATAACATCCCACCCCACCATCGCCATCAAAAACCACACCATCCAGAAGAAACCACTAACAAACCCCCAGATACCCAAAAATCCCAAATTCAAGAGTCACACAGACTTTGA			ATGACATCTGTTGGGCATCAAATACATATAAACCTCTATAACATCCCACCCCACCATCGCCATCAAAAACCACACCATCCAGAAGAAACCACTAACAAACCCCCAGATACCCAAAAATCCCAAATTCAAGAGTCACACAGACTTTGA	MTSVGHQIHINLYNIPPHHRHQKPHHPEETTNKPPDTQKSQIQESHRL*			MTSVGHQIHINLYNIPPHHRHQKPHHPEETTNKPPDTQKSQIQESHRL*	AATCTTTAAT	ACAAACTCGT	0	R	FG05948.1	0	0	0	0
4848	2566	af	AN0590.1	69.m15259	AO070280000012	0			-193	-146			ATGTTAATCTTTTGGTCGGCAATGAAGCAATCCGCCGTCGGGCGGTGA		ATGTTAATCTTTTGGTCGGCAATGAAGCAATCCGCCGTCGGGCGGTGA		MLIFWSAMKQSAVGR*		MLIFWSAMKQSAVGR*		GGTATAGATT	AGCAACTTTT	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4849	2566	af	AN0590.1	69.m15259	AO070280000012	0			-172	-146			ATGAAGCAATCCGCCGTCGGGCGGTGA		ATGAAGCAATCCGCCGTCGGGCGGTGA		MKQSAVGR*		MKQSAVGR*		TTGGTCGGCA	AGCAACTTTT	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4847	2566	an	AN0590.1	69.m15259	AO070280000012	0	-136	-98					ATGCGTCGCAGTTCGCAATCCCAGTTGTTGACGAGCTAA	ATGCGTCGCAGTTCGCAATCCCAGTTGTTGACGAGCTAA			MRRSSQSQLLTS*	MRRSSQSQLLTS*			CGATAGCCTC	CGAAACATTT	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4850	2566	ao	AN0590.1	69.m15259	AO070280000012	0					-227	-144	ATGCGAAAGAAATCGCGGGCGGTGTATCAGTTACTTTTTTTTCTGCCGGACACTACTTTGCTGAGTCAGCGTGCGATAAGATGA			ATGCGAAAGAAATCGCGGGCGGTGTATCAGTTACTTTTTTTTCTGCCGGACACTACTTTGCTGAGTCAGCGTGCGATAAGATGA	MRKKSRAVYQLLFFLPDTTLLSQRAIR*			MRKKSRAVYQLLFFLPDTTLLSQRAIR*	GCTGTTTCGA	AGGCTTATCG	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4851	2566	ao	AN0590.1	69.m15259	AO070280000012	0					-147	-28	ATGAAGGCTTATCGATGGTTATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAGGGATTGA			ATGAAGGCTTATCGATGGTTATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAGGGATTGA	MKAYRWLWRHATISILHAELLSVASESVTASLTSFQHRD*			MKAYRWLWRHATISILHAELLSVASESVTASLTSFQHRD*	GTGCGATAAG	GATTGGTTTA	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4852	2566	ao	AN0590.1	69.m15259	AO070280000012	0					-133	-35	ATGGTTATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAG			ATGGTTATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAG	MVMETCDHLYSPCGAFISSIRICYCIPHLFST*			MVMETCDHLYSPCGAFISSIRICYCIPHLFST*	AGGCTTATCG	GGATTGAGAT	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4853	2566	ao	AN0590.1	69.m15259	AO070280000012	0					-127	-35	ATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAG			ATGGAGACATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAGCATCCGAATCTGTTACTGCATCCCTCACCTCTTTTCAACATAG	METCDHLYSPCGAFISSIRICYCIPHLFST*			METCDHLYSPCGAFISSIRICYCIPHLFST*	ATCGATGGTT	GGATTGAGAT	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4854	2566	ao	AN0590.1	69.m15259	AO070280000012	0					-119	-78	ATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAG			ATGCGACCATCTCTATTCTCCATGCGGAGCTTTTATCAGTAG	MRPSLFSMRSFYQ*			MRPSLFSMRSFYQ*	TTATGGAGAC	CATCCGAATC	0	O	FG09767.1	MG04180.1	NCU07713.1	0	0
4862	2572	af	AN8488.1	58.m08926	AO070299000105	0			-198	-157			ATGGCAAGCGATCGAGTAATGCCGAAGGGTCATCGATTGTAG		ATGGCAAGCGATCGAGTAATGCCGAAGGGTCATCGATTGTAG		MASDRVMPKGHRL*		MASDRVMPKGHRL*		TAATCTCATC	CCGTGGACAG	0	U	0	0	0	0	0
4863	2572	af	AN8488.1	58.m08926	AO070299000105	0			-180	-157			ATGCCGAAGGGTCATCGATTGTAG		ATGCCGAAGGGTCATCGATTGTAG		MPKGHRL*		MPKGHRL*		CGATCGAGTA	CCGTGGACAG	0	U	0	0	0	0	0
4857	2572	an	AN8488.1	58.m08926	AO070299000105	0	-263	-246					ATGCCACCAAAAAATTTGA	ATGCCACCAAAAAATTTGA			MPPKI*	MPPKI*			TTACTATATT	GTGATAATAT	0	U	0	0	0	0	0
4858	2572	an	AN8488.1	58.m08926	AO070299000105	0	-226	-185					ATGGTTGAATTGCTTCATGTTTGTTGTGCTGGTGGTGGTTGA	ATGGTTGAATTGCTTCATGTTTGTTGTGCTGGTGGTGGTTGA			MVELLHVCCAGGG*	MVELLHVCCAGGG*			TTAGTTGTAT	AATCGATCGT	0	U	0	0	0	0	0
4859	2572	an	AN8488.1	58.m08926	AO070299000105	0	-210	-151					ATGTTTGTTGTGCTGGTGGTGGTTGAAATCGATCGTCAGGTGGGAACGATCGTCAGGTGA	ATGTTTGTTGTGCTGGTGGTGGTTGAAATCGATCGTCAGGTGGGAACGATCGTCAGGTGA			MFVVLVVVEIDRQVGTIVR*	MFVVLVVVEIDRQVGTIVR*			GAATTGCTTC	TCAACCACTG	0	U	0	0	0	0	0
4860	2572	an	AN8488.1	58.m08926	AO070299000105	0	-138	-43					ATGGTCTCGGCTCATGAACTGCTAAGCTACCCTTACATATTCTGCCGCATCCCACCGCCTTCACGGTCCCATTCACAAAGCCTCCCCATTCCTTGA	ATGGTCTCGGCTCATGAACTGCTAAGCTACCCTTACATATTCTGCCGCATCCCACCGCCTTCACGGTCCCATTCACAAAGCCTCCCCATTCCTTGA			MVSAHELLSYPYIFCRIPPSRSHSQSLPIP*	MVSAHELLSYPYIFCRIPPSRSHSQSLPIP*			AACCACTGTA	CACCCCACAT	0	U	0	0	0	0	0
4861	2572	an	AN8488.1	58.m08926	AO070299000105	0	-125	-114					ATGAACTGCTAA	ATGAACTGCTAA			MNC*	MNC*			GTCTCGGCTC	GCTACCCTTA	0	U	0	0	0	0	0
4864	2572	ao	AN8488.1	58.m08926	AO070299000105	0					-259	-224	ATGACTTGGATAATTTTTGTATATAGAATCCTGTAG			ATGACTTGGATAATTTTTGTATATAGAATCCTGTAG	MTWIIFVYRIL*			MTWIIFVYRIL*	ACTTGGATAT	TAATACAATA	0	U	0	0	0	0	0
4865	2572	ao	AN8488.1	58.m08926	AO070299000105	0					-211	-179	ATGAAAGGGACGAATATGAATCTGCCTAATTGA			ATGAAAGGGACGAATATGAATCTGCCTAATTGA	MKGTNMNLPN*			MKGTNMNLPN*	ATACAATATC	TGAGGCTAAT	0	U	0	0	0	0	0
4866	2572	ao	AN8488.1	58.m08926	AO070299000105	0					-196	-179	ATGAATCTGCCTAATTGA			ATGAATCTGCCTAATTGA	MNLPN*			MNLPN*	AGGGACGAAT	TGAGGCTAAT	0	U	0	0	0	0	0
4867	2572	ao	AN8488.1	58.m08926	AO070299000105	0					-179	-153	ATGAGGCTAATTGAACTGAGCATGTGA			ATGAGGCTAATTGAACTGAGCATGTGA	MRLIELSM*			MRLIELSM*	TGCCTAATTG	GTGGTTGCCT	0	U	0	0	0	0	0
4868	2572	ao	AN8488.1	58.m08926	AO070299000105	0					-92	-3	ATGCTTTTCCGCCTCCGAGATTATATCCCCGCAAACTTCAGCCAACTGTCAACGACGTCAGTCATCCTTGAAACCCCTCGGAGCCCGTAA			ATGCTTTTCCGCCTCCGAGATTATATCCCCGCAAACTTCAGCCAACTGTCAACGACGTCAGTCATCCTTGAAACCCCTCGGAGCCCGTAA	MLFRLRDYIPANFSQLSTTSVILETPRSP*			MLFRLRDYIPANFSQLSTTSVILETPRSP*	GTGAGGCGAG	AAATGAAGAT	0	U	0	0	0	0	0
4871	2576	af	AN6462.1	69.m15712	AO070306000002	0			-104	-63			ATGGCTACGTGGGGGAGTGGGCGTGGTATTGGCCGGGTATAA		ATGGCTACGTGGGGGAGTGGGCGTGGTATTGGCCGGGTATAA		MATWGSGRGIGRV*		MATWGSGRGIGRV*		TTTGATCTAC	TAAGGACGGC	0	R	0	0	0	0	0
4869	2576	an	AN6462.1	69.m15712	AO070306000002	0	-192	-4					ATGATTCATTACGAGATAGTATTCGAGTACCGATTAGACTGCCGAACTGTCTCCAACCGTCCATCAGGAGCGACGTACGCGAGTCGGGGAATGCGGACCTATCCCGCCTCCACTCATATATGGGACGACACCCTGTTCAGTCCCAGTCTCAGCTCCGCGAGGAGATCGCATCCACTTACATTGTGTTAA	ATGATTCATTACGAGATAGTATTCGAGTACCGATTAGACTGCCGAACTGTCTCCAACCGTCCATCAGGAGCGACGTACGCGAGTCGGGGAATGCGGACCTATCCCGCCTCCACTCATATATGGGACGACACCCTGTTCAGTCCCAGTCTCAGCTCCGCGAGGAGATCGCATCCACTTACATTGTGTTAA			MIHYEIVFEYRLDCRTVSNRPSGATYASRGMRTYPASTHIWDDTLFSPSLSSARRSHPLTLC*	MIHYEIVFEYRLDCRTVSNRPSGATYASRGMRTYPASTHIWDDTLFSPSLSSARRSHPLTLC*			TATCTCACCC	GCCATGGCGA	0	R	0	0	0	0	0

4870	2576	an	AN6462.1	69.m15712	AO070306000002	0	-102	-4					ATGCGGACCTATCCCGCCTCCACTCATATATGGGACGACACCCTGTTCAGTCCCAGTCTCAGCTCCGCGAGGAGATCGCATCCACTTACATTGTGTTAA	ATGCGGACCTATCCCGCCTCCACTCATATATGGGACGACACCCTGTTCAGTCCCAGTCTCAGCTCCGCGAGGAGATCGCATCCACTTACATTGTGTTAA			MRTYPASTHIWDDTLFSPSLSSARRSHPLTLC*	MRTYPASTHIWDDTLFSPSLSSARRSHPLTLC*			GAGTCGGGGA	GCCATGGCGA	0	R	0	0	0	0	0
4875	2578	af	AN5698.1	65.m07509	AO070309000118	0			-135	-64			ATGCTGCTCCTTGAAGGTGTTTTGGAGGATATATCACACAGCTTCGCCCACCTTGACTCTCTCGAAAGTTAG		ATGCTGCTCCTTGAAGGTGTTTTGGAGGATATATCACACAGCTTCGCCCACCTTGACTCTCTCGAAAGTTAG		MLLLEGVLEDISHSFAHLDSLES*		MLLLEGVLEDISHSFAHLDSLES*		AAATTAACTA	AAATAATCGA	0	I	0	0	0	0	0
4872	2578	an	AN5698.1	65.m07509	AO070309000118	0	-267	-148					ATGGGGGGAAGGCCCTGGCCTTTTAAGAATGGACCCAAGATCCGGAGTCCAGACGGACGGCTCATTTTCCAATCTTTTGTAAATTTCCTAAACGCCGTATTCCCAGTGAGGCGTTCGTGA	ATGGGGGGAAGGCCCTGGCCTTTTAAGAATGGACCCAAGATCCGGAGTCCAGACGGACGGCTCATTTTCCAATCTTTTGTAAATTTCCTAAACGCCGTATTCCCAGTGAGGCGTTCGTGA			MGGRPWPFKNGPKIRSPDGRLIFQSFVNFLNAVFPVRRS*	MGGRPWPFKNGPKIRSPDGRLIFQSFVNFLNAVFPVRRS*			TGGCAATTAC	CTTGGATTGC	0	I	0	0	0	0	0
4873	2578	an	AN5698.1	65.m07509	AO070309000118	0	-239	-186					ATGGACCCAAGATCCGGAGTCCAGACGGACGGCTCATTTTCCAATCTTTTGTAA	ATGGACCCAAGATCCGGAGTCCAGACGGACGGCTCATTTTCCAATCTTTTGTAA			MDPRSGVQTDGSFSNLL*	MDPRSGVQTDGSFSNLL*			CCTTTTAAGA	ATTTCCTAAA	0	I	0	0	0	0	0
4874	2578	an	AN5698.1	65.m07509	AO070309000118	0	-66	-4					ATGTCTGACTATCTAGCGAAGGCAGATCATAGATTACTTGAGTCGAAGACTGTCCCTTTATAA	ATGTCTGACTATCTAGCGAAGGCAGATCATAGATTACTTGAGTCGAAGACTGTCCCTTTATAA			MSDYLAKADHRLLESKTVPL*	MSDYLAKADHRLLESKTVPL*			TACGTGCATT	ATAATGGCCT	0	I	0	0	0	0	0
4876	2578	ao	AN5698.1	65.m07509	AO070309000118	0					-72	-22	ATGTTCTTCTATTTCTTGTTTCCCCGGAATTCAGCTTGTTGTGCGCGTTGA			ATGTTCTTCTATTTCTTGTTTCCCCGGAATTCAGCTTGTTGTGCGCGTTGA	MFFYFLFPRNSACCAR*			MFFYFLFPRNSACCAR*	ATTCATATAA	AACCCACTAC	0	I	0	0	0	0	0
4880	2579	af	AN8396.1	63.m00597	AO070312000154	0			-232	-182			ATGTCGGCGAGTAGCAGCCAATCACCGCTCGGGATCTTGAGATCTGATTGA		ATGTCGGCGAGTAGCAGCCAATCACCGCTCGGGATCTTGAGATCTGATTGA		MSASSSQSPLGILRSD*		MSASSSQSPLGILRSD*		GCCTTATCGG	GTAATGGCCA	0	EH	0	0	0	0	0
4881	2579	af	AN8396.1	63.m00597	AO070312000154	0			-178	-146			ATGGCCAGCCGAGGATGCCCCAAAGAGGACTAG		ATGGCCAGCCGAGGATGCCCCAAAGAGGACTAG		MASRGCPKED*		MASRGCPKED*		TGATTGAGTA	CGTATATGCC	0	EH	0	0	0	0	0
4882	2579	af	AN8396.1	63.m00597	AO070312000154	0			-164	-120			ATGCCCCAAAGAGGACTAGCGTATATGCCCCCCGCATCTTTTTGA		ATGCCCCAAAGAGGACTAGCGTATATGCCCCCCGCATCTTTTTGA		MPQRGLAYMPPASF*		MPQRGLAYMPPASF*		CCAGCCGAGG	TGTCGCAGAT	0	EH	0	0	0	0	0
4883	2579	af	AN8396.1	63.m00597	AO070312000154	0			-140	-120			ATGCCCCCCGCATCTTTTTGA		ATGCCCCCCGCATCTTTTTGA		MPPASF*		MPPASF*		ACTAGCGTAT	TGTCGCAGAT	0	EH	0	0	0	0	0
4884	2579	af	AN8396.1	63.m00597	AO070312000154	0			-120	-97			ATGTCGCAGATTCCCCATTGTTGA		ATGTCGCAGATTCCCCATTGTTGA		MSQIPHC*		MSQIPHC*		CATCTTTTTG	TCTTCCTTCT	0	EH	0	0	0	0	0
4877	2579	an	AN8396.1	63.m00597	AO070312000154	0	-229	-59					ATGAGCTCTCCAAAATCAATGGCTCACCATATATCTGTCGAGCAGAATATTATTATTTGGAATCATGTTTCATCCTGCTTTTGGAGACGTTTAATTACGATTAGTGTTCCACGCTCTGGGGTCGGCTATTATCGGCGATACAGCGATAGCGGGGAAAGGCACCCGCGATAA	ATGAGCTCTCCAAAATCAATGGCTCACCATATATCTGTCGAGCAGAATATTATTATTTGGAATCATGTTTCATCCTGCTTTTGGAGACGTTTAATTACGATTAGTGTTCCACGCTCTGGGGTCGGCTATTATCGGCGATACAGCGATAGCGGGGAAAGGCACCCGCGATAA			MSSPKSMAHHISVEQNIIIWNHVSSCFWRRLITISVPRSGVGYYRRYSDSGERHPR*	MSSPKSMAHHISVEQNIIIWNHVSSCFWRRLITISVPRSGVGYYRRYSDSGERHPR*			TCCTCCTGAT	GAGTATATAA	0	EH	0	0	0	0	0
4878	2579	an	AN8396.1	63.m00597	AO070312000154	0	-211	-59					ATGGCTCACCATATATCTGTCGAGCAGAATATTATTATTTGGAATCATGTTTCATCCTGCTTTTGGAGACGTTTAATTACGATTAGTGTTCCACGCTCTGGGGTCGGCTATTATCGGCGATACAGCGATAGCGGGGAAAGGCACCCGCGATAA	ATGGCTCACCATATATCTGTCGAGCAGAATATTATTATTTGGAATCATGTTTCATCCTGCTTTTGGAGACGTTTAATTACGATTAGTGTTCCACGCTCTGGGGTCGGCTATTATCGGCGATACAGCGATAGCGGGGAAAGGCACCCGCGATAA			MAHHISVEQNIIIWNHVSSCFWRRLITISVPRSGVGYYRRYSDSGERHPR*	MAHHISVEQNIIIWNHVSSCFWRRLITISVPRSGVGYYRRYSDSGERHPR*			TCCAAAATCA	GAGTATATAA	0	EH	0	0	0	0	0
4879	2579	an	AN8396.1	63.m00597	AO070312000154	0	-165	-136					ATGTTTCATCCTGCTTTTGGAGACGTTTAA	ATGTTTCATCCTGCTTTTGGAGACGTTTAA			MFHPAFGDV*	MFHPAFGDV*			ATTTGGAATC	TTACGATTAG	0	EH	0	0	0	0	0
4885	2579	ao	AN8396.1	63.m00597	AO070312000154	0					-113	-21	ATGTATAGGACCATTGAAATTCCTTCTGTCATATATAAAAGAGAAGATGTGTACAGTACTGAAGAGAGCAACGCAAGTAACGTAACAGTCTAG			ATGTATAGGACCATTGAAATTCCTTCTGTCATATATAAAAGAGAAGATGTGTACAGTACTGAAGAGAGCAACGCAAGTAACGTAACAGTCTAG	MYRTIEIPSVIYKREDVYSTEESNASNVTV*			MYRTIEIPSVIYKREDVYSTEESNASNVTV*	ATTACGATCG	TTCACTCTGA	0	EH	0	0	0	0	0
4886	2579	ao	AN8396.1	63.m00597	AO070312000154	0					-67	-29	ATGTGTACAGTACTGAAGAGAGCAACGCAAGTAACGTAA			ATGTGTACAGTACTGAAGAGAGCAACGCAAGTAACGTAA	MCTVLKRATQVT*			MCTVLKRATQVT*	AAAAGAGAAG	CAGTCTAGTT	0	EH	0	0	0	0	0
4891	2581	af	AN0774.1	70.m15380	AO070316000064	0			-238	-224			ATGTTATGTTGGTAA		ATGTTATGTTGGTAA		MLCW*		MLCW*		TAAATACACC	TCTAGACTGT	0	Q	0	MG01176.1	0	0	0
4892	2581	af	AN0774.1	70.m15380	AO070316000064	0			-233	-219			ATGTTGGTAATCTAG		ATGTTGGTAATCTAG		MLVI*		MLVI*		ACACCATGTT	ACTGTCGGCT	0	Q	0	MG01176.1	0	0	0
4893	2581	af	AN0774.1	70.m15380	AO070316000064	0			-149	-114			ATGGCCGACGAGGGGAAGAGGAAATGGAATGACTGA		ATGGCCGACGAGGGGAAGAGGAAATGGAATGACTGA		MADEGKRKWND*		MADEGKRKWND*		ACGTTGTTCA	TGAGGCTTCA	0	Q	0	MG01176.1	0	0	0
4894	2581	af	AN0774.1	70.m15380	AO070316000064	0			-121	-74			ATGACTGATGAGGCTTCAGAATCATCCATAATAGTTCTTCTACCATGA		ATGACTGATGAGGCTTCAGAATCATCCATAATAGTTCTTCTACCATGA		MTDEASESSIIVLLP*		MTDEASESSIIVLLP*		AGGAAATGGA	GCAATGTGAA	0	Q	0	MG01176.1	0	0	0
4895	2581	af	AN0774.1	70.m15380	AO070316000064	0			-114	-91			ATGAGGCTTCAGAATCATCCATAA		ATGAGGCTTCAGAATCATCCATAA		MRLQNHP*		MRLQNHP*		GGAATGACTG	TAGTTCTTCT	0	Q	0	MG01176.1	0	0	0
4887	2581	an	AN0774.1	70.m15380	AO070316000064	0	-230	-192					ATGCATGGCAGTGGGTGGCCTTCACCAGCAATTGTATGA	ATGCATGGCAGTGGGTGGCCTTCACCAGCAATTGTATGA			MHGSGWPSPAIV*	MHGSGWPSPAIV*			GTCTGCGTTA	CCTGCAATTG	0	Q	0	MG01176.1	0	0	0
4888	2581	an	AN0774.1	70.m15380	AO070316000064	0	-226	-167					ATGGCAGTGGGTGGCCTTCACCAGCAATTGTATGACCTGCAATTGAAGGTCGGCTATTGA	ATGGCAGTGGGTGGCCTTCACCAGCAATTGTATGACCTGCAATTGAAGGTCGGCTATTGA			MAVGGLHQQLYDLQLKVGY*	MAVGGLHQQLYDLQLKVGY*			GCGTTAATGC	CCTGGCTTTT	0	Q	0	MG01176.1	0	0	0
4889	2581	an	AN0774.1	70.m15380	AO070316000064	0	-195	-181					ATGACCTGCAATTGA	ATGACCTGCAATTGA			MTCN*	MTCN*			CAGCAATTGT	AGGTCGGCTA	0	Q	0	MG01176.1	0	0	0
4890	2581	an	AN0774.1	70.m15380	AO070316000064	0	-87	-76					ATGAACAAATAA	ATGAACAAATAA			MNK*	MNK*			GGCAGCCACC	ATACCCAACA	0	Q	0	MG01176.1	0	0	0
4896	2581	ao	AN0774.1	70.m15380	AO070316000064	0					-101	-69	ATGGCCGACAAGCAAGTCATGCTGTGCATATAA			ATGGCCGACAAGCAAGTCATGCTGTGCATATAA	MADKQVMLCI*			MADKQVMLCI*	AGCGGAGTCA	TAGCATTGTC	0	Q	0	MG01176.1	0	0	0
4897	2581	ao	AN0774.1	70.m15380	AO070316000064	0					-83	-69	ATGCTGTGCATATAA			ATGCTGTGCATATAA	MLCI*			MLCI*	CAAGCAAGTC	TAGCATTGTC	0	Q	0	MG01176.1	0	0	0
4898	2582	af	AN4577.1	57.m05504	AO070316000168	0			-274	-170			ATGCGCTCAGTCCACTTTGGAGTAACATCTGCAGTTTGGAGTAGCATCTTATCCTACCTATCATCCCCGCCTGCGGGGTATGCTCGACATCGGATGAAAGGATAG		ATGCGCTCAGTCCACTTTGGAGTAACATCTGCAGTTTGGAGTAGCATCTTATCCTACCTATCATCCCCGCCTGCGGGGTATGCTCGACATCGGATGAAAGGATAG		MRSVHFGVTSAVWSSILSYLSSPPAGYARHRMKG*		MRSVHFGVTSAVWSSILSYLSSPPAGYARHRMKG*		ACATCGCGTA	GTTCACAGGA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4899	2582	af	AN4577.1	57.m05504	AO070316000168	0			-195	-178			ATGCTCGACATCGGATGA		ATGCTCGACATCGGATGA		MLDIG*		MLDIG*		CCTGCGGGGT	AAGGATAGGT	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4900	2582	af	AN4577.1	57.m05504	AO070316000168	0			-181	-170			ATGAAAGGATAG		ATGAAAGGATAG		MKG*		MKG*		TCGACATCGG	GTTCACAGGA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4901	2582	af	AN4577.1	57.m05504	AO070316000168	0			-117	-52			ATGCGTTGTTCCTGTGCGATCCTATCAATCTTAGGTTGGTTGACTATGCGCGCCCTCGAACCATAA		ATGCGTTGTTCCTGTGCGATCCTATCAATCTTAGGTTGGTTGACTATGCGCGCCCTCGAACCATAA		MRCSCAILSILGWLTMRALEP*		MRCSCAILSILGWLTMRALEP*		ATTCAAAAGG	CACTACCCTT	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4902	2582	af	AN4577.1	57.m05504	AO070316000168	0			-72	-52			ATGCGCGCCCTCGAACCATAA		ATGCGCGCCCTCGAACCATAA		MRALEP*		MRALEP*		TTGGTTGACT	CACTACCCTT	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4903	2582	ao	AN4577.1	57.m05504	AO070316000168	0					-185	-36	ATGAATCAGTCAAGAGATAATCATGCAGCCATGAGGGGAAAAGAGTTACCCTCTCCTCCTCACTTGGAGTTGCAATCCGAACCTTCTTATATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA			ATGAATCAGTCAAGAGATAATCATGCAGCCATGAGGGGAAAAGAGTTACCCTCTCCTCCTCACTTGGAGTTGCAATCCGAACCTTCTTATATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA	MNQSRDNHAAMRGKELPSPPHLELQSEPSYMRHSLLENLHLSFSPWIRT*			MNQSRDNHAAMRGKELPSPPHLELQSEPSYMRHSLLENLHLSFSPWIRT*	TGGTAAAACA	CCAAACATCA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4904	2582	ao	AN4577.1	57.m05504	AO070316000168	0					-163	-152	ATGCAGCCATGA			ATGCAGCCATGA	MQP*			MQP*	AGAGATAATC	GGGGAAAAGA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4905	2582	ao	AN4577.1	57.m05504	AO070316000168	0					-155	-36	ATGAGGGGAAAAGAGTTACCCTCTCCTCCTCACTTGGAGTTGCAATCCGAACCTTCTTATATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA			ATGAGGGGAAAAGAGTTACCCTCTCCTCCTCACTTGGAGTTGCAATCCGAACCTTCTTATATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA	MRGKELPSPPHLELQSEPSYMRHSLLENLHLSFSPWIRT*			MRGKELPSPPHLELQSEPSYMRHSLLENLHLSFSPWIRT*	TCATGCAGCC	CCAAACATCA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4906	2582	ao	AN4577.1	57.m05504	AO070316000168	0					-95	-36	ATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA			ATGCGCCATTCCCTCCTTGAGAACCTCCATCTTAGCTTCTCACCGTGGATACGTACATAA	MRHSLLENLHLSFSPWIRT*			MRHSLLENLHLSFSPWIRT*	ACCTTCTTAT	CCAAACATCA	0	C	FG09042.1	MG03533.1	NCU02361.1	0	0
4912	2584	af	AN0131.1	71.m15415	AO070321000122	0			-233	-222			ATGGCACGATGA		ATGGCACGATGA		MAR*		MAR*		GACCCCAGCG	TGCGGAATTC	0		0	0	0	YLR250W	0
4913	2584	af	AN0131.1	71.m15415	AO070321000122	0			-172	-29			ATGCAAACAGCCAAGCAGTCGAGGTCCAAGAAGATGCGGACAGGCAATTGTTCTGTTTCTCGTCCCATTCATCATATTTACCAATTCGGTGCTGGATACATTCTGTTCTGTAAGTATCCGGGATTCTGTACATCTTGTGTTTAG		ATGCAAACAGCCAAGCAGTCGAGGTCCAAGAAGATGCGGACAGGCAATTGTTCTGTTTCTCGTCCCATTCATCATATTTACCAATTCGGTGCTGGATACATTCTGTTCTGTAAGTATCCGGGATTCTGTACATCTTGTGTTTAG		MQTAKQSRSKKMRTGNCSVSRPIHHIYQFGAGYILFCKYPGFCTSCV*		MQTAKQSRSKKMRTGNCSVSRPIHHIYQFGAGYILFCKYPGFCTSCV*		GATACAAACA	ATTCGTCATT	0		0	0	0	YLR250W	0
4914	2584	af	AN0131.1	71.m15415	AO070321000122	0			-139	-29			ATGCGGACAGGCAATTGTTCTGTTTCTCGTCCCATTCATCATATTTACCAATTCGGTGCTGGATACATTCTGTTCTGTAAGTATCCGGGATTCTGTACATCTTGTGTTTAG		ATGCGGACAGGCAATTGTTCTGTTTCTCGTCCCATTCATCATATTTACCAATTCGGTGCTGGATACATTCTGTTCTGTAAGTATCCGGGATTCTGTACATCTTGTGTTTAG		MRTGNCSVSRPIHHIYQFGAGYILFCKYPGFCTSCV*		MRTGNCSVSRPIHHIYQFGAGYILFCKYPGFCTSCV*		GTCCAAGAAG	ATTCGTCATT	0		0	0	0	YLR250W	0
4907	2584	an	AN0131.1	71.m15415	AO070321000122	0	-233	-3					ATGATGATAGTTATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA	ATGATGATAGTTATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA			MMIVMVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*	MMIVMVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*			GCTGGGTGGT	CAATGCTGAT	0		0	0	0	YLR250W	0
4908	2584	an	AN0131.1	71.m15415	AO070321000122	0	-230	-3					ATGATAGTTATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA	ATGATAGTTATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA			MIVMVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*	MIVMVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*			GGGTGGTATG	CAATGCTGAT	0		0	0	0	YLR250W	0
4909	2584	an	AN0131.1	71.m15415	AO070321000122	0	-221	-3					ATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA	ATGGTTGTGCTATCGGGGAAAAAGTTGGAGATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA			MVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*	MVVLSGKKLEMPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*			GATGATAGTT	CAATGCTGAT	0		0	0	0	YLR250W	0

4910	2584	an	AN0131.1	71.m15415	AO070321000122	0	-191	-3					ATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA	ATGCCGGAAAGCAAACACTGCAAACAGCCTGTATCCCCAAGCCGGCGGACAGCTGGTCCCCCGGAGGCTCCTCTTTCGAAGGTCAACCCCGGGGGAGCTGCTTGTTCTATATTATGCTCTTATTTTCAGCTATATTTTCTTGAAATAGCTTGGCTCTGGTTAGCCAACATCTTAACTTTCTGCAATTGA			MPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*	MPESKHCKQPVSPSRRTAGPPEAPLSKVNPGGAACSILCSYFQLYFLEIAWLWLANILTFCN*			AAAGTTGGAG	CAATGCTGAT	0		0	0	0	YLR250W	0
4911	2584	an	AN0131.1	71.m15415	AO070321000122	0	-78	-49					ATGCTCTTATTTTCAGCTATATTTTCTTGA	ATGCTCTTATTTTCAGCTATATTTTCTTGA			MLLFSAIFS*	MLLFSAIFS*			GTTCTATATT	AATAGCTTGG	0		0	0	0	YLR250W	0
4915	2584	ao	AN0131.1	71.m15415	AO070321000122	0					-177	-43	ATGCAAACACTGCAAACAGTATATCTTCTGATTGGGCAGTTCGTTCTCCGAATCCAGGTGCTAGCACTCGAAGAAAAGGCCACATCAACAGGGTTGAAATTATTCGTTCCTGCTTGTATACTGGAACGATTTTGA			ATGCAAACACTGCAAACAGTATATCTTCTGATTGGGCAGTTCGTTCTCCGAATCCAGGTGCTAGCACTCGAAGAAAAGGCCACATCAACAGGGTTGAAATTATTCGTTCCTGCTTGTATACTGGAACGATTTTGA	MQTLQTVYLLIGQFVLRIQVLALEEKATSTGLKLFVPACILERF*			MQTLQTVYLLIGQFVLRIQVLALEEKATSTGLKLFVPACILERF*	GAGCGGATTT	TATTTTTCTT	0		0	0	0	YLR250W	0
4916	2586	an	AN2316.1	71.m15518	AO070323000038	0	-209	-75					ATGAGTCGCTGCCCGCTAGTGCACGTGATTTGTAGGTGGTGCGATGTCCTCGAACTTCCCACGAACGTCTTTCATCGCGACTCACCTCCTGTCCTCGTCACTCACATCAGTACATCCTCGGTCCCGAGGCATTGA	ATGAGTCGCTGCCCGCTAGTGCACGTGATTTGTAGGTGGTGCGATGTCCTCGAACTTCCCACGAACGTCTTTCATCGCGACTCACCTCCTGTCCTCGTCACTCACATCAGTACATCCTCGGTCCCGAGGCATTGA			MSRCPLVHVICRWCDVLELPTNVFHRDSPPVLVTHISTSSVPRH*	MSRCPLVHVICRWCDVLELPTNVFHRDSPPVLVTHISTSSVPRH*			TCTTCTTCCA	CCTTGTCGCT	0	C	FG04315.1	0	0	0	0
4917	2586	an	AN2316.1	71.m15518	AO070323000038	0	-166	-35					ATGTCCTCGAACTTCCCACGAACGTCTTTCATCGCGACTCACCTCCTGTCCTCGTCACTCACATCAGTACATCCTCGGTCCCGAGGCATTGACCTTGTCGCTTTTACAAGAGCTAAAAAATTCACCATTTAA	ATGTCCTCGAACTTCCCACGAACGTCTTTCATCGCGACTCACCTCCTGTCCTCGTCACTCACATCAGTACATCCTCGGTCCCGAGGCATTGACCTTGTCGCTTTTACAAGAGCTAAAAAATTCACCATTTAA			MSSNFPRTSFIATHLLSSLTSVHPRSRGIDLVAFTRAKKFTI*	MSSNFPRTSFIATHLLSSLTSVHPRSRGIDLVAFTRAKKFTI*			AGGTGGTGCG	TTATTTTCTA	0	C	FG04315.1	0	0	0	0
4918	2586	ao	AN2316.1	71.m15518	AO070323000038	0					-230	-45	ATGAGGGCGCAGGCAAAACGGACTAACCTAACCGGCCGGATACTCGACTTTCCACCTCAAACCACAGTCGAACGACGTCTTCGTTTCCCATCGCGAAGTCTCGATCACCTCCTCCACTTCCATCCCACCTTAATTCATCCTCAATCCCGAGGCATTACATCTCTCGTTCACGGAGAGTGTATTTGA			ATGAGGGCGCAGGCAAAACGGACTAACCTAACCGGCCGGATACTCGACTTTCCACCTCAAACCACAGTCGAACGACGTCTTCGTTTCCCATCGCGAAGTCTCGATCACCTCCTCCACTTCCATCCCACCTTAATTCATCCTCAATCCCGAGGCATTACATCTCTCGTTCACGGAGAGTGTATTTGA	MRAQAKRTNLTGRILDFPQTTVERRLRFPSRSLDHLLHFHPTLIHPQSRGITSLVHGECI*			MRAQAKRTNLTGRILDFPQTTVERRLRFPSRSLDHLLHFHPTLIHPQSRGITSLVHGECI*	ACGTGGACCA	TTTCTAATTG	0	C	FG04315.1	0	0	0	0
4920	2587	af	AN3894.1	54.m07025	AO070324000132	0			-231	-220			ATGCCTGCCTGA		ATGCCTGCCTGA		MPA*		MPA*		ACTACTTAGA	CCTCAAAATG	0	CE	FG10198.1	0	0	0	0
4921	2587	af	AN3894.1	54.m07025	AO070324000132	0			-212	-171			ATGCCCTGGATGATACCTTATCCACAAGTATTTCTGTCATAA		ATGCCCTGGATGATACCTTATCCACAAGTATTTCTGTCATAA		MPWMIPYPQVFLS*		MPWMIPYPQVFLS*		TGACCTCAAA	CGTAACGTAT	0	CE	FG10198.1	0	0	0	0
4922	2587	af	AN3894.1	54.m07025	AO070324000132	0			-203	-171			ATGATACCTTATCCACAAGTATTTCTGTCATAA		ATGATACCTTATCCACAAGTATTTCTGTCATAA		MIPYPQVFLS*		MIPYPQVFLS*		AATGCCCTGG	CGTAACGTAT	0	CE	FG10198.1	0	0	0	0
4923	2587	af	AN3894.1	54.m07025	AO070324000132	0			-154	-122			ATGACACCGACCCCGGCATCGGCGTCGTCATAA		ATGACACCGACCCCGGCATCGGCGTCGTCATAA		MTPTPASASS*		MTPTPASASS*		GTATTGTAAG	CCAATCAGAT	0	CE	FG10198.1	0	0	0	0
4919	2587	an	AN3894.1	54.m07025	AO070324000132	0	-161	-144					ATGTCTGAGAACGGCTAG	ATGTCTGAGAACGGCTAG			MSENG*	MSENG*			CCTGAGGTGG	CGCCACTCAG	0	CE	FG10198.1	0	0	0	0
4924	2587	ao	AN3894.1	54.m07025	AO070324000132	0					-186	-97	ATGGGGCCCCGAGTAAAGTACGGTAAGATGGGTCCTTTGGAATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAA			ATGGGGCCCCGAGTAAAGTACGGTAAGATGGGTCCTTTGGAATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAA	MGPRVKYGKMGPLECRPGIGEGTVQSAWR*			MGPRVKYGKMGPLECRPGIGEGTVQSAWR*	CAGTAGAGAT	AAGGCAGCCG	0	CE	FG10198.1	0	0	0	0
4925	2587	ao	AN3894.1	54.m07025	AO070324000132	0					-159	-97	ATGGGTCCTTTGGAATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAA			ATGGGTCCTTTGGAATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAA	MGPLECRPGIGEGTVQSAWR*			MGPLECRPGIGEGTVQSAWR*	GTACGGTAAG	AAGGCAGCCG	0	CE	FG10198.1	0	0	0	0
4926	2587	ao	AN3894.1	54.m07025	AO070324000132	0					-145	-74	ATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAAAAGGCAGCCGAAGGCCAAAATAA			ATGTCGGCCCGGCATCGGCGAAGGGACCGTCCAATCAGCATGGAGGTAAAAGGCAGCCGAAGGCCAAAATAA	MSARHRRRDRPISMEVKGSRRPK*			MSARHRRRDRPISMEVKGSRRPK*	GTCCTTTGGA	AAGAATATCG	0	CE	FG10198.1	0	0	0	0
4927	2587	ao	AN3894.1	54.m07025	AO070324000132	0					-106	-74	ATGGAGGTAAAAGGCAGCCGAAGGCCAAAATAA			ATGGAGGTAAAAGGCAGCCGAAGGCCAAAATAA	MEVKGSRRPK*			MEVKGSRRPK*	TCCAATCAGC	AAGAATATCG	0	CE	FG10198.1	0	0	0	0
4928	2591	af	AN8040.1	53.m03906	AO070330000006	0			-244	-218			ATGAGGCCAATTGACAAACTACTGTAA		ATGAGGCCAATTGACAAACTACTGTAA		MRPIDKLL*		MRPIDKLL*		CTGCCTGAGG	TGCAATAGTT	0	P	0	0	0	0	0
4929	2591	af	AN8040.1	53.m03906	AO070330000006	0			-145	-2			ATGGACAGCTGTTCGACTTTCTGGGGCTCCAGGTCTGCGCTTTGTCCGAAAGTTCTGCCTGCACGCGCCTCCTTCCTCGACCCTTCAGTTTCAATTCCAGTCCTGCCCATATTTGATCTTCTTGTCAAAGGACCTTGTTGCTAA		ATGGACAGCTGTTCGACTTTCTGGGGCTCCAGGTCTGCGCTTTGTCCGAAAGTTCTGCCTGCACGCGCCTCCTTCCTCGACCCTTCAGTTTCAATTCCAGTCCTGCCCATATTTGATCTTCTTGTCAAAGGACCTTGTTGCTAA		MDSCSTFWGSRSALCPKVLPARASFLDPSVSIPVLPIFDLLVKGPCC*		MDSCSTFWGSRSALCPKVLPARASFLDPSVSIPVLPIFDLLVKGPCC*		CTCACACCTT	AATGAATCCT	0	P	0	0	0	0	0
4931	2592	ao	AN9086.1	66.m04759	AO070332000191	0					-170	-42	ATGCGCTCCGTCGATCCACCGACTCGGGCGGGGAGGAATATCCATCAACAACATTTTGATAGCTGCCGGACCTTCAACTCATGCCGTTGCCATATCACGCCGGAACGCCTTATTTCAAGCTGTGTATAA			ATGCGCTCCGTCGATCCACCGACTCGGGCGGGGAGGAATATCCATCAACAACATTTTGATAGCTGCCGGACCTTCAACTCATGCCGTTGCCATATCACGCCGGAACGCCTTATTTCAAGCTGTGTATAA	MRSVDPPTRAGRNIHQQHFDSCRTFNSCRCHITPERLISSCV*			MRSVDPPTRAGRNIHQQHFDSCRTFNSCRCHITPERLISSCV*	CCGGTCCACT	GTTCTTTGGC	0	U	FG02649.1	MG04694.1	0	YKR068C	0
4932	2592	ao	AN9086.1	66.m04759	AO070332000191	0					-90	-25	ATGCCGTTGCCATATCACGCCGGAACGCCTTATTTCAAGCTGTGTATAAGTTCTTTGGCAATCTAA			ATGCCGTTGCCATATCACGCCGGAACGCCTTATTTCAAGCTGTGTATAAGTTCTTTGGCAATCTAA	MPLPYHAGTPYFKLCISSLAI*			MPLPYHAGTPYFKLCISSLAI*	CCTTCAACTC	GTAATAGAAG	0	U	FG02649.1	MG04694.1	0	YKR068C	0
4934	2595	af	AN0261.1	54.m06965	AO070334000097	0			-231	-163			ATGCTGCAACCTGGCCTCATGCCAACAGGACCAGCTTCACACAACATACAACCCCAGATCCACATCTAA		ATGCTGCAACCTGGCCTCATGCCAACAGGACCAGCTTCACACAACATACAACCCCAGATCCACATCTAA		MLQPGLMPTGPASHNIQPQIHI*		MLQPGLMPTGPASHNIQPQIHI*		GCAACCAAGG	ATCCCGGACA	0	U	FG01917.1	0	NCU01318.1	0	0
4935	2595	af	AN0261.1	54.m06965	AO070334000097	0			-213	-163			ATGCCAACAGGACCAGCTTCACACAACATACAACCCCAGATCCACATCTAA		ATGCCAACAGGACCAGCTTCACACAACATACAACCCCAGATCCACATCTAA		MPTGPASHNIQPQIHI*		MPTGPASHNIQPQIHI*		ACCTGGCCTC	ATCCCGGACA	0	U	FG01917.1	0	NCU01318.1	0	0
4936	2595	af	AN0261.1	54.m06965	AO070334000097	0			-117	-88			ATGCTACAGAAATTTGTTCTCACTATATAG		ATGCTACAGAAATTTGTTCTCACTATATAG		MLQKFVLTI*		MLQKFVLTI*		ACATAAGATT	TTAAAGTGAT	0	U	FG01917.1	0	NCU01318.1	0	0
4933	2595	an	AN0261.1	54.m06965	AO070334000097	0	-236	-81					ATGCCGCTGTGCTGCAACCTGGCCTTAAACAACACTCCGGCTCACACAACCTGGAACTCCCCGCATTGCCTAGCTTCCGGACAACTTCAATTGTCGGCGTGCTTTATTCTAAACAGTGCTGGAGTAGAATCCCTGAGCTTGAAATATACGAGTTAA	ATGCCGCTGTGCTGCAACCTGGCCTTAAACAACACTCCGGCTCACACAACCTGGAACTCCCCGCATTGCCTAGCTTCCGGACAACTTCAATTGTCGGCGTGCTTTATTCTAAACAGTGCTGGAGTAGAATCCCTGAGCTTGAAATATACGAGTTAA			MPLCCNLALNNTPAHTTWNSPHCLASGQLQLSACFILNSAGVESLSLKYTS*	MPLCCNLALNNTPAHTTWNSPHCLASGQLQLSACFILNSAGVESLSLKYTS*			TAGCGGACCC	GGGATAATCG	0	U	FG01917.1	0	NCU01318.1	0	0
4937	2595	ao	AN0261.1	54.m06965	AO070334000097	0					-224	-171	ATGCTGCAACCTGGCCTTATGGCAACAACACAGGTTCACACAACATACGCCTAG			ATGCTGCAACCTGGCCTTATGGCAACAACACAGGTTCACACAACATACGCCTAG	MLQPGLMATTQVHTTYA*			MLQPGLMATTQVHTTYA*	GCCGCCTAAC	TCCCCGCATA	0	U	FG01917.1	0	NCU01318.1	0	0
4938	2595	ao	AN0261.1	54.m06965	AO070334000097	0					-206	-171	ATGGCAACAACACAGGTTCACACAACATACGCCTAG			ATGGCAACAACACAGGTTCACACAACATACGCCTAG	MATTQVHTTYA*			MATTQVHTTYA*	ACCTGGCCTT	TCCCCGCATA	0	U	FG01917.1	0	NCU01318.1	0	0
4939	2595	ao	AN0261.1	54.m06965	AO070334000097	0					-113	-75	ATGGTACAGGATACTCTTTCACAGTTTGAAATTTCTTAA			ATGGTACAGGATACTCTTTCACAGTTTGAAATTTCTTAA	MVQDTLSQFEIS*			MVQDTLSQFEIS*	AGACCGGGTT	TCATCCGGGT	0	U	FG01917.1	0	NCU01318.1	0	0
4948	2598	an	AN1602.1	55.m03185	AO070339000250	0	-253	-140					ATGCCCTTGGCAGGGGTCTCTCGTTACAGACTGCATCGGTACCAGGACAGAGGCGGAGGACCGAGGAGTAGCCCTAGTATAAAGGCCCTCCAAGCTGCTGGCTCTAGTCTTTGA	ATGCCCTTGGCAGGGGTCTCTCGTTACAGACTGCATCGGTACCAGGACAGAGGCGGAGGACCGAGGAGTAGCCCTAGTATAAAGGCCCTCCAAGCTGCTGGCTCTAGTCTTTGA			MPLAGVSRYRLHRYQDRGGGPRSSPSIKALQAAGSSL*	MPLAGVSRYRLHRYQDRGGGPRSSPSIKALQAAGSSL*			TAGATGAAGC	TTCTGTTCTG	0	GO	0	0	0	0	0
4949	2598	ao	AN1602.1	55.m03185	AO070339000250	0					-205	-95	ATGAGAACCATGAAGGGGTGCTGGAAGCTGGAAGCTTTCGTCGATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAGGTCTCTCTCATTCCTCAAGCCTGGATAGCTAA			ATGAGAACCATGAAGGGGTGCTGGAAGCTGGAAGCTTTCGTCGATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAGGTCTCTCTCATTCCTCAAGCCTGGATAGCTAA	MRTMKGCWKLEAFVDVYKRPSSGPSIGLSHSSSLDS*			MRTMKGCWKLEAFVDVYKRPSSGPSIGLSHSSSLDS*	CGTCTAATCT	CCATTCATTC	0	GO	0	0	0	0	0
4950	2598	ao	AN1602.1	55.m03185	AO070339000250	0					-196	-95	ATGAAGGGGTGCTGGAAGCTGGAAGCTTTCGTCGATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAGGTCTCTCTCATTCCTCAAGCCTGGATAGCTAA			ATGAAGGGGTGCTGGAAGCTGGAAGCTTTCGTCGATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAGGTCTCTCTCATTCCTCAAGCCTGGATAGCTAA	MKGCWKLEAFVDVYKRPSSGPSIGLSHSSSLDS*			MKGCWKLEAFVDVYKRPSSGPSIGLSHSSSLDS*	TATGAGAACC	CCATTCATTC	0	GO	0	0	0	0	0
4951	2598	ao	AN1602.1	55.m03185	AO070339000250	0					-162	-127	ATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAG			ATGTGTATAAAAGGCCCTCATCCGGACCCTCGATAG	MCIKGPHPDPR*			MCIKGPHPDPR*	GCTTTCGTCG	GTCTCTCTCA	0	GO	0	0	0	0	0
4953	2599	af	AN5932.1	72.m19197	AO070340000348	0			-207	-85			ATGGGGATTGGCGGAGGCGCGTCCAAACCGCGTCCCCAACGCGTTGTCATTTCCTTGCGCGATAGCCCGCATGGCCCGCCATCCCTTCCCCAGTCCACACCATTCAAGATATCAAGAAAATAA		ATGGGGATTGGCGGAGGCGCGTCCAAACCGCGTCCCCAACGCGTTGTCATTTCCTTGCGCGATAGCCCGCATGGCCCGCCATCCCTTCCCCAGTCCACACCATTCAAGATATCAAGAAAATAA		MGIGGGASKPRPQRVVISLRDSPHGPPSLPQSTPFKISRK*		MGIGGGASKPRPQRVVISLRDSPHGPPSLPQSTPFKISRK*		CTTTAACCGA	TTACTGGATA	0	L	FG05421.1	MG06397.1	0	0	0
4954	2599	af	AN5932.1	72.m19197	AO070340000348	0			-137	-48			ATGGCCCGCCATCCCTTCCCCAGTCCACACCATTCAAGATATCAAGAAAATAATTACTGGATAATTGCAAAACCCAGTCACTACTGGTGA		ATGGCCCGCCATCCCTTCCCCAGTCCACACCATTCAAGATATCAAGAAAATAATTACTGGATAATTGCAAAACCCAGTCACTACTGGTGA		MARHPFPSPHHSRYQENNYWIIAKPSHYW*		MARHPFPSPHHSRYQENNYWIIAKPSHYW*		GATAGCCCGC	GGTCATTGAT	0	L	FG05421.1	MG06397.1	0	0	0
4956	2599	ao	AN5932.1	72.m19197	AO070340000348	0					-226	-188	ATGGAACTAACCACTAACGGTAATGGAAAAACCACTTAA			ATGGAACTAACCACTAACGGTAATGGAAAAACCACTTAA	MELTTNGNGKTT*			MELTTNGNGKTT*	GGTAAAGCAG	CGGCGATTGG	0	L	FG05421.1	MG06397.1	0	0	0
4957	2599	ao	AN5932.1	72.m19197	AO070340000348	0					-204	-109	ATGGAAAAACCACTTAACGGCGATTGGGCGGTGAGCGCGTACATCTCGCGTTCCGCTCACGCGTTGTCTCCGCGACGCCCGCCTTTGAACCACTAG			ATGGAAAAACCACTTAACGGCGATTGGGCGGTGAGCGCGTACATCTCGCGTTCCGCTCACGCGTTGTCTCCGCGACGCCCGCCTTTGAACCACTAG	MEKPLNGDWAVSAYISRSAHALSPRRPPLNH*			MEKPLNGDWAVSAYISRSAHALSPRRPPLNH*	ACTAACGGTA	ACCCTTTCTC	0	L	FG05421.1	MG06397.1	0	0	0
4965	2600	af	AN1913.1	69.m14928	AO070341000134	0			-198	-163			ATGACCGTTATCGGTGGTAGAGGCTCCAAGCAATAG		ATGACCGTTATCGGTGGTAGAGGCTCCAAGCAATAG		MTVIGGRGSKQ*		MTVIGGRGSKQ*		TAGTATCCAT	CCAATGACAG	0	J	FG08761.1	0	0	0	0
4966	2600	af	AN1913.1	69.m14928	AO070341000134	0			-159	-139			ATGACAGTCGCCGATCCATGA		ATGACAGTCGCCGATCCATGA		MTVADP*		MTVADP*		GCAATAGCCA	GTCAGGCCCG	0	J	FG08761.1	0	0	0	0
4959	2600	an	AN1913.1	69.m14928	AO070341000134	0	-271	-197					ATGAGAACTGTAACAATGGAAGTTAAATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAG	ATGAGAACTGTAACAATGGAAGTTAAATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAG			MRTVTMEVKCRRCWDCTMSHLLTV*	MRTVTMEVKCRRCWDCTMSHLLTV*			TATTATCAAG	TAGGACTGAT	0	J	FG08761.1	0	0	0	0
4960	2600	an	AN1913.1	69.m14928	AO070341000134	0	-256	-197					ATGGAAGTTAAATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAG	ATGGAAGTTAAATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAG			MEVKCRRCWDCTMSHLLTV*	MEVKCRRCWDCTMSHLLTV*			AACTGTAACA	TAGGACTGAT	0	J	FG08761.1	0	0	0	0
4961	2600	an	AN1913.1	69.m14928	AO070341000134	0	-245	-30					ATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAGTAGGACTGATAATACCCAATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAGAGAACAATCATCCACGCCCGCAATTTTTCTCTTCTATTACTCGCACCGCTCGGAGTGAGTAG	ATGCAGGAGATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAGTAGGACTGATAATACCCAATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAGAGAACAATCATCCACGCCCGCAATTTTTCTCTTCTATTACTCGCACCGCTCGGAGTGAGTAG			MQEMLGLYNESSAHSVVGLIIPNDSHPASDSRPKIFGTFSPSRISPPTLPLENNHPRPQFFSSITRTARSE*	MQEMLGLYNESSAHSVVGLIIPNDSHPASDSRPKIFGTFSPSRISPPTLPLENNHPRPQFFSSITRTARSE*			TGGAAGTTAA	ATAGAGCGTG	0	J	FG08761.1	0	0	0	0

4962	2600	an	AN1913.1	69.m14928	AO070341000134	0	-236	-30					ATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAGTAGGACTGATAATACCCAATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAGAGAACAATCATCCACGCCCGCAATTTTTCTCTTCTATTACTCGCACCGCTCGGAGTGAGTAG	ATGCTGGGATTGTACAATGAGTCATCTGCTCACAGTGTAGTAGGACTGATAATACCCAATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAGAGAACAATCATCCACGCCCGCAATTTTTCTCTTCTATTACTCGCACCGCTCGGAGTGAGTAG			MLGLYNESSAHSVVGLIIPNDSHPASDSRPKIFGTFSPSRISPPTLPLENNHPRPQFFSSITRTARSE*	MLGLYNESSAHSVVGLIIPNDSHPASDSRPKIFGTFSPSRISPPTLPLENNHPRPQFFSSITRTARSE*			AATGCAGGAG	ATAGAGCGTG	0	J	FG08761.1	0	0	0	0
4963	2600	an	AN1913.1	69.m14928	AO070341000134	0	-220	-197					ATGAGTCATCTGCTCACAGTGTAG	ATGAGTCATCTGCTCACAGTGTAG			MSHLLTV*	MSHLLTV*			GGATTGTACA	TAGGACTGAT	0	J	FG08761.1	0	0	0	0
4964	2600	an	AN1913.1	69.m14928	AO070341000134	0	-178	-92					ATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAG	ATGATAGCCACCCCGCCAGTGACTCCCGCCCAAAAATCTTTGGCACGTTTTCTCCATCTCGGATCTCCCCTCCCACTTTGCCTTTAG			MIATPPVTPAQKSLARFLHLGSPLPLCL*	MIATPPVTPAQKSLARFLHLGSPLPLCL*			ATAATACCCA	AGAACAATCA	0	J	FG08761.1	0	0	0	0
4967	2600	ao	AN1913.1	69.m14928	AO070341000134	0					-191	-132	ATGAAGAATATCATGACTCATAGGAATTGTAGGATGTCATTGATTCTTAACGTGGGGTAA			ATGAAGAATATCATGACTCATAGGAATTGTAGGATGTCATTGATTCTTAACGTGGGGTAA	MKNIMTHRNCRMSLILNVG*			MKNIMTHRNCRMSLILNVG*	AAGCTTAAGC	TTAATGACCC	0	J	FG08761.1	0	0	0	0
4968	2600	ao	AN1913.1	69.m14928	AO070341000134	0					-179	-132	ATGACTCATAGGAATTGTAGGATGTCATTGATTCTTAACGTGGGGTAA			ATGACTCATAGGAATTGTAGGATGTCATTGATTCTTAACGTGGGGTAA	MTHRNCRMSLILNVG*			MTHRNCRMSLILNVG*	GAAGAATATC	TTAATGACCC	0	J	FG08761.1	0	0	0	0
4969	2600	ao	AN1913.1	69.m14928	AO070341000134	0					-158	-132	ATGTCATTGATTCTTAACGTGGGGTAA			ATGTCATTGATTCTTAACGTGGGGTAA	MSLILNVG*			MSLILNVG*	GAATTGTAGG	TTAATGACCC	0	J	FG08761.1	0	0	0	0
4970	2600	ao	AN1913.1	69.m14928	AO070341000134	0					-128	-117	ATGACCCAATGA			ATGACCCAATGA	MTQ*			MTQ*	GGGGTAATTA	AAAAAAAGTT	0	J	FG08761.1	0	0	0	0
4971	2600	ao	AN1913.1	69.m14928	AO070341000134	0					-120	-103	ATGAAAAAAAAGTTGTGA			ATGAAAAAAAAGTTGTGA	MKKKL*			MKKKL*	TAATGACCCA	CTCCCGCCCA	0	J	FG08761.1	0	0	0	0
4974	2603	af	AN0673.1	70.m15275	AO070343000547	0			-265	-239			ATGCAAAGGACTCAATGTGATACTTAA		ATGCAAAGGACTCAATGTGATACTTAA		MQRTQCDT*		MQRTQCDT*		CGAGACTGAA	GACTCCATTT	0	Z	0	0	NCU07171.1	0	0
4975	2603	af	AN0673.1	70.m15275	AO070343000547	0			-226	-158			ATGCGTTCCGTTGCTGATGGAATGAGGCTCGGCGCGCTAATGACGACTATGGGGAAGCCCATCGACTGA		ATGCGTTCCGTTGCTGATGGAATGAGGCTCGGCGCGCTAATGACGACTATGGGGAAGCCCATCGACTGA		MRSVADGMRLGALMTTMGKPID*		MRSVADGMRLGALMTTMGKPID*		CTCCATTTAC	AGACACACCT	0	Z	0	0	NCU07171.1	0	0
4976	2603	af	AN0673.1	70.m15275	AO070343000547	0			-205	-158			ATGAGGCTCGGCGCGCTAATGACGACTATGGGGAAGCCCATCGACTGA		ATGAGGCTCGGCGCGCTAATGACGACTATGGGGAAGCCCATCGACTGA		MRLGALMTTMGKPID*		MRLGALMTTMGKPID*		TGCTGATGGA	AGACACACCT	0	Z	0	0	NCU07171.1	0	0
4977	2603	af	AN0673.1	70.m15275	AO070343000547	0			-187	-158			ATGACGACTATGGGGAAGCCCATCGACTGA		ATGACGACTATGGGGAAGCCCATCGACTGA		MTTMGKPID*		MTTMGKPID*		CGGCGCGCTA	AGACACACCT	0	Z	0	0	NCU07171.1	0	0
4978	2603	af	AN0673.1	70.m15275	AO070343000547	0			-178	-158			ATGGGGAAGCCCATCGACTGA		ATGGGGAAGCCCATCGACTGA		MGKPID*		MGKPID*		AATGACGACT	AGACACACCT	0	Z	0	0	NCU07171.1	0	0
4972	2603	an	AN0673.1	70.m15275	AO070343000547	0	-220	-197					ATGAGGTTGGGGCTGCCTGGTTAA	ATGAGGTTGGGGCTGCCTGGTTAA			MRLGLPG*	MRLGLPG*			ACGTAAACTA	TAGTGCCTGA	0	Z	0	0	NCU07171.1	0	0
4981	2604	af	AN0654.1	70.m15258	AO070343000572	0			-246	-220			ATGGCCACTGATGCGGGGTGCATGTGA		ATGGCCACTGATGCGGGGTGCATGTGA		MATDAGCM*		MATDAGCM*		AAGGCTCTTC	TAAATTCATT	0	H	FG10097.1	0	0	0	0
4982	2604	af	AN0654.1	70.m15258	AO070343000572	0			-236	-27			ATGCGGGGTGCATGTGATAAATTCATTCACAAAGTTATTCTTCCACCATGCATATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGATGGATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGACACCTCGTGGGCAGAGCACGTTCTAA		ATGCGGGGTGCATGTGATAAATTCATTCACAAAGTTATTCTTCCACCATGCATATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGATGGATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGACACCTCGTGGGCAGAGCACGTTCTAA		MRGACDKFIHKVILPPCIWNVLAYPCALSPTPQYLNRVLRIVDGCNRSQILCSPTISRACLTPRGQSTF*		MRGACDKFIHKVILPPCIWNVLAYPCALSPTPQYLNRVLRIVDGCNRSQILCSPTISRACLTPRGQSTF*		ATGGCCACTG	AGTGAGAGCC	0	H	FG10097.1	0	0	0	0
4983	2604	af	AN0654.1	70.m15258	AO070343000572	0			-189	-109			ATGCATATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		ATGCATATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		MHMECAGIPMRSVTDTSVFKQSFEDR*		MHMECAGIPMRSVTDTSVFKQSFEDR*		TTCTTCCACC	TGGATGCAAC	0	H	FG10097.1	0	0	0	0
4984	2604	af	AN0654.1	70.m15258	AO070343000572	0			-183	-109			ATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		ATGGAATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		MECAGIPMRSVTDTSVFKQSFEDR*		MECAGIPMRSVTDTSVFKQSFEDR*		CACCATGCAT	TGGATGCAAC	0	H	FG10097.1	0	0	0	0
4985	2604	af	AN0654.1	70.m15258	AO070343000572	0			-178	-131			ATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAA		ATGTGCTGGCATACCCATGCGCTCTGTCACCGACACCTCAGTATTTAA		MCWHTHALCHRHLSI*		MCWHTHALCHRHLSI*		TGCATATGGA	ACAGAGTTTT	0	H	FG10097.1	0	0	0	0
4986	2604	af	AN0654.1	70.m15258	AO070343000572	0			-162	-109			ATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		ATGCGCTCTGTCACCGACACCTCAGTATTTAAACAGAGTTTTGAGGATCGTTGA		MRSVTDTSVFKQSFEDR*		MRSVTDTSVFKQSFEDR*		TGGCATACCC	TGGATGCAAC	0	H	FG10097.1	0	0	0	0
4987	2604	af	AN0654.1	70.m15258	AO070343000572	0			-109	-53			ATGGATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGA		ATGGATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGA		MDATVLKFFVRQPFHVHV*		MDATVLKFFVRQPFHVHV*		AGGATCGTTG	CACCTCGTGG	0	H	FG10097.1	0	0	0	0
4988	2604	af	AN0654.1	70.m15258	AO070343000572	0			-105	-22			ATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGACACCTCGTGGGCAGAGCACGTTCTAAAGTGA		ATGCAACCGTTCTCAAATTCTTTGTTCGCCAACCATTTCACGTGCATGTTTGACACCTCGTGGGCAGAGCACGTTCTAAAGTGA		MQPFSNSLFANHFTCMFDTSWAEHVLK*		MQPFSNSLFANHFTCMFDTSWAEHVLK*		TCGTTGATGG	GAGCCGTTGA	0	H	FG10097.1	0	0	0	0
4980	2604	an	AN0654.1	70.m15258	AO070343000572	0	-113	-78					ATGCCGTCCACCTACAGGGCTTCACTTATAAATTAG	ATGCCGTCCACCTACAGGGCTTCACTTATAAATTAG			MPSTYRASLIN*	MPSTYRASLIN*			TTTCTAGTAC	GCAACCACGA	0	H	FG10097.1	0	0	0	0
4991	2606	af	AN4211.1	54.m06770	AO070231000013	0			-209	-123			ATGTTTCTACCACTTATGGTCCGGGCTTTCTCTTCTATCATCTTTTCGGTCTTTTCCAGACAGTCCTACAGGCCCTCCGCTCGATAG		ATGTTTCTACCACTTATGGTCCGGGCTTTCTCTTCTATCATCTTTTCGGTCTTTTCCAGACAGTCCTACAGGCCCTCCGCTCGATAG		MFLPLMVRAFSSIIFSVFSRQSYRPSAR*		MFLPLMVRAFSSIIFSVFSRQSYRPSAR*		TCCTCATTTT	TCTCTCCTTT	0	R	0	0	0	0	0
4992	2606	af	AN4211.1	54.m06770	AO070231000013	0			-194	-123			ATGGTCCGGGCTTTCTCTTCTATCATCTTTTCGGTCTTTTCCAGACAGTCCTACAGGCCCTCCGCTCGATAG		ATGGTCCGGGCTTTCTCTTCTATCATCTTTTCGGTCTTTTCCAGACAGTCCTACAGGCCCTCCGCTCGATAG		MVRAFSSIIFSVFSRQSYRPSAR*		MVRAFSSIIFSVFSRQSYRPSAR*		TCTACCACTT	TCTCTCCTTT	0	R	0	0	0	0	0
4993	2606	af	AN4211.1	54.m06770	AO070231000013	0			-82	-71			ATGATCATCTAA		ATGATCATCTAA		MII*		MII*		TTTCCCCGTC	TTTGGGACAC	0	R	0	0	0	0	0
4990	2606	an	AN4211.1	54.m06770	AO070231000013	0	-84	-67					ATGGTCAATTATTGTTGA	ATGGTCAATTATTGTTGA			MVNYC*	MVNYC*			TGACCGCGAC	TCGATCAAAT	0	R	0	0	0	0	0
4994	2606	ao	AN4211.1	54.m06770	AO070231000013	0					-179	-126	ATGTGTCCTTCTTTTAACAGAATCCGGCCCTTTTCTGTCTGCGATTTTAGCTAG			ATGTGTCCTTCTTTTAACAGAATCCGGCCCTTTTCTGTCTGCGATTTTAGCTAG	MCPSFNRIRPFSVCDFS*			MCPSFNRIRPFSVCDFS*	TTGCACTTCC	GTTGATAGTC	0	R	0	0	0	0	0
4995	2606	ao	AN4211.1	54.m06770	AO070231000013	0					-86	-69	ATGAACAATTACTCTTGA			ATGAACAATTACTCTTGA	MNNYS*			MNNYS*	TTCCCTCGTC	TTGTCCAAGA	0	R	0	0	0	0	0
4996	2607	ao	AN5450.1	69.m15482	AO070239000029	0					-166	-152	ATGGGGACGGTCTAG			ATGGGGACGGTCTAG	MGTV*			MGTV*	GGCTTGTTAA	GGTAGCTTCA	0	U	0	0	0	0	0
4997	2607	ao	AN5450.1	69.m15482	AO070239000029	0					-68	-57	ATGCTTCCTTGA			ATGCTTCCTTGA	MLP*			MLP*	CTGTCGGTGC	TAGCATCCGT	0	U	0	0	0	0	0
5003	2608	af	AN5908.1	72.m19223	AO070245000002	0			-405	-316			ATGACATGTTTTAGGGATAGGGATATTCAGATTAGATCTTCTATTTTTCCTCGTCGGCCCATCAAACACAATTTCTGGGATGAAGTGTAA		ATGACATGTTTTAGGGATAGGGATATTCAGATTAGATCTTCTATTTTTCCTCGTCGGCCCATCAAACACAATTTCTGGGATGAAGTGTAA		MTCFRDRDIQIRSSIFPRRPIKHNFWDEV*		MTCFRDRDIQIRSSIFPRRPIKHNFWDEV*		TCTAGACTCA	GGCGTGAAAC	0	G	FG06702.1	0	NCU07550.1	0	0
5004	2608	af	AN5908.1	72.m19223	AO070245000002	0			-326	-309			ATGAAGTGTAAGGCGTGA		ATGAAGTGTAAGGCGTGA		MKCKA*		MKCKA*		AATTTCTGGG	AACACATACC	0	G	FG06702.1	0	NCU07550.1	0	0
5005	2608	af	AN5908.1	72.m19223	AO070245000002	0			-294	-277			ATGCCAATCAATCAGTGA		ATGCCAATCAATCAGTGA		MPINQ*		MPINQ*		CATACCGTGG	CATCACCCCG	0	G	FG06702.1	0	NCU07550.1	0	0
5006	2608	af	AN5908.1	72.m19223	AO070245000002	0			-266	-237			ATGAGACACTGGATAATTGCTCCTCATTGA		ATGAGACACTGGATAATTGCTCCTCATTGA		MRHWIIAPH*		MRHWIIAPH*		CATCACCCCG	CAATCTATCC	0	G	FG06702.1	0	NCU07550.1	0	0
4998	2608	an	AN5908.1	72.m19223	AO070245000002	0	-366	-217					ATGGGTACATGCGTTGCGTGGGACGATCTTTGTGTGTCTCTCCTCTCACTAGGTAAGTCCACCGAGTGCAGCTCCATTCTCTCGCTTTTCAGAGTGGTTTTGCTAGTCGCCAATGAGATTGTTAACCGTCGAGAATGGATCATTCACTAA	ATGGGTACATGCGTTGCGTGGGACGATCTTTGTGTGTCTCTCCTCTCACTAGGTAAGTCCACCGAGTGCAGCTCCATTCTCTCGCTTTTCAGAGTGGTTTTGCTAGTCGCCAATGAGATTGTTAACCGTCGAGAATGGATCATTCACTAA			MGTCVAWDDLCVSLLSLGKSTECSSILSLFRVVLLVANEIVNRREWIIH*	MGTCVAWDDLCVSLLSLGKSTECSSILSLFRVVLLVANEIVNRREWIIH*			GCCTCATTGG	TAGACACTCT	0	G	FG06702.1	0	NCU07550.1	0	0
4999	2608	an	AN5908.1	72.m19223	AO070245000002	0	-358	-311					ATGCGTTGCGTGGGACGATCTTTGTGTGTCTCTCCTCTCACTAGGTAA	ATGCGTTGCGTGGGACGATCTTTGTGTGTCTCTCCTCTCACTAGGTAA			MRCVGRSLCVSPLTR*	MRCVGRSLCVSPLTR*			GGATGGGTAC	GTCCACCGAG	0	G	FG06702.1	0	NCU07550.1	0	0
5000	2608	an	AN5908.1	72.m19223	AO070245000002	0	-254	-114					ATGAGATTGTTAACCGTCGAGAATGGATCATTCACTAATAGACACTCTGCAGTGATTGGCAAGCTCTGTTCTGGTCTGGGTACAATAACATTCGATTCATTTCGCCATCATTCTTCTGGTGTCGCCACTTCTCGAGCATAA	ATGAGATTGTTAACCGTCGAGAATGGATCATTCACTAATAGACACTCTGCAGTGATTGGCAAGCTCTGTTCTGGTCTGGGTACAATAACATTCGATTCATTTCGCCATCATTCTTCTGGTGTCGCCACTTCTCGAGCATAA			MRLLTVENGSFTNRHSAVIGKLCSGLGTITFDSFRHHSSGVATSRA*	MRLLTVENGSFTNRHSAVIGKLCSGLGTITFDSFRHHSSGVATSRA*			CTAGTCGCCA	TCCGCGACCC	0	G	FG06702.1	0	NCU07550.1	0	0
5001	2608	an	AN5908.1	72.m19223	AO070245000002	0	-232	-200					ATGGATCATTCACTAATAGACACTCTGCAGTGA	ATGGATCATTCACTAATAGACACTCTGCAGTGA			MDHSLIDTLQ*	MDHSLIDTLQ*			ACCGTCGAGA	TTGGCAAGCT	0	G	FG06702.1	0	NCU07550.1	0	0
5015	2609	af	AN0827.1	70.m15428	AO070255000018	0			-84	-34			ATGCAGTCTGTAGTTGAGATTGACTCTTCTGGAGGAGTGATCTCCAAATAA		ATGCAGTCTGTAGTTGAGATTGACTCTTCTGGAGGAGTGATCTCCAAATAA		MQSVVEIDSSGGVISK*		MQSVVEIDSSGGVISK*		TCCTCCCTTC	AGAAAGGTGC	0	S	0	0	NCU00913.1	YJL091C	0
5010	2609	an	AN0827.1	70.m15428	AO070255000018	0	-177	-139					ATGGCAGTTGCAGTATTTATGCGTAACAGACTTACATAA	ATGGCAGTTGCAGTATTTATGCGTAACAGACTTACATAA			MAVAVFMRNRLT*	MAVAVFMRNRLT*			CAGCTTCTTT	TGCGGGAAGG	0	S	0	0	NCU00913.1	YJL091C	0
5011	2609	an	AN0827.1	70.m15428	AO070255000018	0	-159	-139					ATGCGTAACAGACTTACATAA	ATGCGTAACAGACTTACATAA			MRNRLT*	MRNRLT*			TGCAGTATTT	TGCGGGAAGG	0	S	0	0	NCU00913.1	YJL091C	0
5012	2609	an	AN0827.1	70.m15428	AO070255000018	0	-139	-53					ATGCGGGAAGGCCAGATGGTCAGCGTCACTGGCCGAGTTGAACAACAACTGTCAATATCCTCAATTCTGCAGCTCGATCAACAATGA	ATGCGGGAAGGCCAGATGGTCAGCGTCACTGGCCGAGTTGAACAACAACTGTCAATATCCTCAATTCTGCAGCTCGATCAACAATGA			MREGQMVSVTGRVEQQLSISSILQLDQQ*	MREGQMVSVTGRVEQQLSISSILQLDQQ*			GACTTACATA	CCCCTTAACG	0	S	0	0	NCU00913.1	YJL091C	0
5013	2609	an	AN0827.1	70.m15428	AO070255000018	0	-124	-53					ATGGTCAGCGTCACTGGCCGAGTTGAACAACAACTGTCAATATCCTCAATTCTGCAGCTCGATCAACAATGA	ATGGTCAGCGTCACTGGCCGAGTTGAACAACAACTGTCAATATCCTCAATTCTGCAGCTCGATCAACAATGA			MVSVTGRVEQQLSISSILQLDQQ*	MVSVTGRVEQQLSISSILQLDQQ*			GGAAGGCCAG	CCCCTTAACG	0	S	0	0	NCU00913.1	YJL091C	0
5016	2609	ao	AN0827.1	70.m15428	AO070255000018	0					-172	-53	ATGCACTCCGATTGCAAGTTGTCATCATCTTATCCGATAGCTTTTCCCCCTCGAATGTGCAGCTTCTCGTTTGGTATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA			ATGCACTCCGATTGCAAGTTGTCATCATCTTATCCGATAGCTTTTCCCCCTCGAATGTGCAGCTTCTCGTTTGGTATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA	MHSDCKLSSSYPIAFPPRMCSFSFGMGRLMTRLNPNLQN*			MHSDCKLSSSYPIAFPPRMCSFSFGMGRLMTRLNPNLQN*	ATATGCTTTG	ATCGAATCGA	0	S	0	0	NCU00913.1	YJL091C	0
5017	2609	ao	AN0827.1	70.m15428	AO070255000018	0					-118	-53	ATGTGCAGCTTCTCGTTTGGTATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA			ATGTGCAGCTTCTCGTTTGGTATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA	MCSFSFGMGRLMTRLNPNLQN*			MCSFSFGMGRLMTRLNPNLQN*	TCCCCCTCGA	ATCGAATCGA	0	S	0	0	NCU00913.1	YJL091C	0
5018	2609	ao	AN0827.1	70.m15428	AO070255000018	0					-97	-53	ATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA			ATGGGCCGACTGATGACGAGATTAAATCCAAATCTCCAGAACTGA	MGRLMTRLNPNLQN*			MGRLMTRLNPNLQN*	CTCGTTTGGT	ATCGAATCGA	0	S	0	0	NCU00913.1	YJL091C	0
5019	2609	ao	AN0827.1	70.m15428	AO070255000018	0					-85	-53	ATGACGAGATTAAATCCAAATCTCCAGAACTGA			ATGACGAGATTAAATCCAAATCTCCAGAACTGA	MTRLNPNLQN*			MTRLNPNLQN*	GGGCCGACTG	ATCGAATCGA	0	S	0	0	NCU00913.1	YJL091C	0
5023	2610	af	AN3973.1	55.m03215	AO070263000041	0			-217	-194			ATGGTCAACCAAGGACATAGGTAG		ATGGTCAACCAAGGACATAGGTAG		MVNQGHR*		MVNQGHR*		ACATACATCC	ATGGAAGAAA	0	O	0	0	0	0	0
5024	2610	af	AN3973.1	55.m03215	AO070263000041	0			-193	-131			ATGGAAGAAATGTTCTGCCTCAGGCATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAG		ATGGAAGAAATGTTCTGCCTCAGGCATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAG		MEEMFCLRHARHSEWVSQYG*		MEEMFCLRHARHSEWVSQYG*		ACATAGGTAG	CACCTGGTAC	0	O	0	0	0	0	0

5025	2610	af	AN3973.1	55.m03215	AO070263000041	0			-184	-131			ATGTTCTGCCTCAGGCATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAG		ATGTTCTGCCTCAGGCATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAG		MFCLRHARHSEWVSQYG*		MFCLRHARHSEWVSQYG*		GATGGAAGAA	CACCTGGTAC	0	O	0	0	0	0	0
5026	2610	af	AN3973.1	55.m03215	AO070263000041	0			-168	-37			ATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAGCACCTGGTACTGCCGTGCCCCTCCGATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		ATGCACGGCATTCCGAGTGGGTTTCCCAATATGGTTAGCACCTGGTACTGCCGTGCCCCTCCGATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		MHGIPSGFPNMVSTWYCRAPPMLLRQSSTDKSHRRYTLVSALN*		MHGIPSGFPNMVSTWYCRAPPMLLRQSSTDKSHRRYTLVSALN*		TGCCTCAGGC	CTGCCCAGAA	0	O	0	0	0	0	0
5027	2610	af	AN3973.1	55.m03215	AO070263000041	0			-138	-37			ATGGTTAGCACCTGGTACTGCCGTGCCCCTCCGATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		ATGGTTAGCACCTGGTACTGCCGTGCCCCTCCGATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		MVSTWYCRAPPMLLRQSSTDKSHRRYTLVSALN*		MVSTWYCRAPPMLLRQSSTDKSHRRYTLVSALN*		GTTTCCCAAT	CTGCCCAGAA	0	O	0	0	0	0	0
5028	2610	af	AN3973.1	55.m03215	AO070263000041	0			-105	-37			ATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		ATGTTGTTGCGTCAGTCGAGCACCGACAAAAGCCATCGAAGGTACACTCTCGTTTCCGCCCTCAATTGA		MLLRQSSTDKSHRRYTLVSALN*		MLLRQSSTDKSHRRYTLVSALN*		TGCCCCTCCG	CTGCCCAGAA	0	O	0	0	0	0	0
5020	2610	an	AN3973.1	55.m03215	AO070263000041	0	-202	-122					ATGGCATCTTCTAGTATGATAAGCAGCGACAATCGTAAACACAGCCAAGCTATTCAGAATATTGTCGAGGACAAATATTGA	ATGGCATCTTCTAGTATGATAAGCAGCGACAATCGTAAACACAGCCAAGCTATTCAGAATATTGTCGAGGACAAATATTGA			MASSSMISSDNRKHSQAIQNIVEDKY*	MASSSMISSDNRKHSQAIQNIVEDKY*			AGTTTTGACA	ATAAAGGCGG	0	O	0	0	0	0	0
5021	2610	an	AN3973.1	55.m03215	AO070263000041	0	-187	-122					ATGATAAGCAGCGACAATCGTAAACACAGCCAAGCTATTCAGAATATTGTCGAGGACAAATATTGA	ATGATAAGCAGCGACAATCGTAAACACAGCCAAGCTATTCAGAATATTGTCGAGGACAAATATTGA			MISSDNRKHSQAIQNIVEDKY*	MISSDNRKHSQAIQNIVEDKY*			ATCTTCTAGT	ATAAAGGCGG	0	O	0	0	0	0	0
5022	2610	an	AN3973.1	55.m03215	AO070263000041	0	-79	-11					ATGGCGTCACCTCCACCAACTTTCTGCTTCCAGTGTTTCCATTGCCATTGGAATCCCTCATTGCTGTGA	ATGGCGTCACCTCCACCAACTTTCTGCTTCCAGTGTTTCCATTGCCATTGGAATCCCTCATTGCTGTGA			MASPPPTFCFQCFHCHWNPSLL*	MASPPPTFCFQCFHCHWNPSLL*			TGTTCAAATC	AAATATCAAA	0	O	0	0	0	0	0
5029	2610	ao	AN3973.1	55.m03215	AO070263000041	0					-223	-182	ATGATTGCCTTTTCTGGACAGGTGAATATACATCATGCCTGA			ATGATTGCCTTTTCTGGACAGGTGAATATACATCATGCCTGA	MIAFSGQVNIHHA*			MIAFSGQVNIHHA*	CACGTCTACA	GGCCAACTAC	0	O	0	0	0	0	0
5030	2610	ao	AN3973.1	55.m03215	AO070263000041	0					-189	-16	ATGCCTGAGGCCAACTACCCACGTGCCAAGGTCGACCGAAAAGGGGATAGTCTGGGGATCTGCGACCTGACGCAATCACGCAATCGGCAATTAGCTCAAGACACCATAGTGATTGATATAATTCTTGGGACATTCTTTCCAGCTTCAACCTCAATTGACCCTCTCAACTCTTAA			ATGCCTGAGGCCAACTACCCACGTGCCAAGGTCGACCGAAAAGGGGATAGTCTGGGGATCTGCGACCTGACGCAATCACGCAATCGGCAATTAGCTCAAGACACCATAGTGATTGATATAATTCTTGGGACATTCTTTCCAGCTTCAACCTCAATTGACCCTCTCAACTCTTAA	MPEANYPRAKVDRKGDSLGICDLTQSRNRQLAQDTIVIDIILGTFFPASTSIDPLNS*			MPEANYPRAKVDRKGDSLGICDLTQSRNRQLAQDTIVIDIILGTFFPASTSIDPLNS*	AATATACATC	TTACCATCCT	0	O	0	0	0	0	0
5031	2615	an	AN6360.1	72.m19498	AO070279000048	0	-207	-154					ATGAATGTATTCCGAGTAATTGCGTATGTATCATCACGACGTAAGTATTCCTGA	ATGAATGTATTCCGAGTAATTGCGTATGTATCATCACGACGTAAGTATTCCTGA			MNVFRVIAYVSSRRKYS*	MNVFRVIAYVSSRRKYS*			AAGCCGTAGG	GAATCTCGAC	0		0	MG07667.1	0	0	0
5032	2615	an	AN6360.1	72.m19498	AO070279000048	0	-203	-189					ATGTATTCCGAGTAA	ATGTATTCCGAGTAA			MYSE*	MYSE*			CGTAGGATGA	TTGCGTATGT	0		0	MG07667.1	0	0	0
5033	2615	an	AN6360.1	72.m19498	AO070279000048	0	-133	-122					ATGCGGCTGTGA	ATGCGGCTGTGA			MRL*	MRL*			AGGTCCCGTG	ACCTGGGCTT	0		0	MG07667.1	0	0	0
5034	2615	ao	AN6360.1	72.m19498	AO070279000048	0					-208	-197	ATGATGGCCTAA			ATGATGGCCTAA	MMA*			MMA*	CAATGGAGTG	GTCTACGCAG	0		0	MG07667.1	0	0	0
5035	2615	ao	AN6360.1	72.m19498	AO070279000048	0					-69	-19	ATGCAAATCAGTTGCGGCATTTTCCAATCATTTGTTTGCTCGACGGATTGA			ATGCAAATCAGTTGCGGCATTTTCCAATCATTTGTTTGCTCGACGGATTGA	MQISCGIFQSFVCSTD*			MQISCGIFQSFVCSTD*	AAATTATCTT	TCTGGAACGT	0		0	MG07667.1	0	0	0
5041	2617	af	AN7505.1	57.m05948	AO070287000005	0			-134	-24			ATGAGGAGAACTGAGAATGATGACCTGACATATAATATCCGGTCTTTCCTACATTGCAGCGTTCTTCTTTCAACCGTGCAGTGTCTATCACATTGTTCAACCCAAGCTTGA		ATGAGGAGAACTGAGAATGATGACCTGACATATAATATCCGGTCTTTCCTACATTGCAGCGTTCTTCTTTCAACCGTGCAGTGTCTATCACATTGTTCAACCCAAGCTTGA		MRRTENDDLTYNIRSFLHCSVLLSTVQCLSHCSTQA*		MRRTENDDLTYNIRSFLHCSVLLSTVQCLSHCSTQA*		AAGGAGGAGA	GTGATTCATT	0	G	0	0	0	0	0
5042	2617	af	AN7505.1	57.m05948	AO070287000005	0			-118	-107			ATGATGACCTGA		ATGATGACCTGA		MMT*		MMT*		AGAACTGAGA	CATATAATAT	0	G	0	0	0	0	0
5037	2617	an	AN7505.1	57.m05948	AO070287000005	0	-180	-70					ATGTGGACCAGGAGAGCTCTAATGCAAGACGGAGTCTTGCCCTTTGCGGATGAGGGAATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA	ATGTGGACCAGGAGAGCTCTAATGCAAGACGGAGTCTTGCCCTTTGCGGATGAGGGAATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA			MWTRRALMQDGVLPFADEGMLGVDIPPAVPPLLFWL*	MWTRRALMQDGVLPFADEGMLGVDIPPAVPPLLFWL*			ACAACCTGGC	TACTTTTCTC	0	G	0	0	0	0	0
5038	2617	an	AN7505.1	57.m05948	AO070287000005	0	-159	-70					ATGCAAGACGGAGTCTTGCCCTTTGCGGATGAGGGAATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA	ATGCAAGACGGAGTCTTGCCCTTTGCGGATGAGGGAATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA			MQDGVLPFADEGMLGVDIPPAVPPLLFWL*	MQDGVLPFADEGMLGVDIPPAVPPLLFWL*			GAGAGCTCTA	TACTTTTCTC	0	G	0	0	0	0	0
5039	2617	an	AN7505.1	57.m05948	AO070287000005	0	-131	-111					ATGAGGGAATGCTTGGGGTAG	ATGAGGGAATGCTTGGGGTAG			MRECLG*	MRECLG*			CCCTTTGCGG	ATATACCCCC	0	G	0	0	0	0	0
5040	2617	an	AN7505.1	57.m05948	AO070287000005	0	-123	-70					ATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA	ATGCTTGGGGTAGATATACCCCCCGCGGTCCCTCCGCTGCTGTTCTGGCTCTAA			MLGVDIPPAVPPLLFWL*	MLGVDIPPAVPPLLFWL*			GGATGAGGGA	TACTTTTCTC	0	G	0	0	0	0	0
5043	2617	ao	AN7505.1	57.m05948	AO070287000005	0					-206	-120	ATGTCCCCTTGCTCTCATGTGAGGGGCTTGAAAGTCCTACGAACAAATGCGCTAGACCGAGATACCGCTACTGGGTCTAATACATAG			ATGTCCCCTTGCTCTCATGTGAGGGGCTTGAAAGTCCTACGAACAAATGCGCTAGACCGAGATACCGCTACTGGGTCTAATACATAG	MSPCSHVRGLKVLRTNALDRDTATGSNT*			MSPCSHVRGLKVLRTNALDRDTATGSNT*	TTAAAGCTAG	AGGTGATTCT	0	G	0	0	0	0	0
5044	2619	ao	AN5184.1	54.m07057	AO070291000019	0					-210	-196	ATGGGGACGCTATAA			ATGGGGACGCTATAA	MGTL*			MGTL*	AGGCACCTTT	GGACGATGAA	0	IT	0	0	0	0	0
5045	2619	ao	AN5184.1	54.m07057	AO070291000019	0					-190	-158	ATGAATGGCCGAAAATCTTACCCGACAAGGTAA			ATGAATGGCCGAAAATCTTACCCGACAAGGTAA	MNGRKSYPTR*			MNGRKSYPTR*	TATAAGGACG	TTAAACTAAG	0	IT	0	0	0	0	0
5046	2619	ao	AN5184.1	54.m07057	AO070291000019	0					-186	-154	ATGGCCGAAAATCTTACCCGACAAGGTAATTAA			ATGGCCGAAAATCTTACCCGACAAGGTAATTAA	MAENLTRQGN*			MAENLTRQGN*	AGGACGATGA	ACTAAGGTAC	0	IT	0	0	0	0	0
5047	2619	ao	AN5184.1	54.m07057	AO070291000019	0					-137	-102	ATGAATTGTTGTTCAAAACATTCTCCTTCTCCCTGA			ATGAATTGTTGTTCAAAACATTCTCCTTCTCCCTGA	MNCCSKHSPSP*			MNCCSKHSPSP*	GTACGGAGTA	CTCTGGCTTT	0	IT	0	0	0	0	0
5048	2620	af	AN7388.1	56.m02393	AO070293000057	0			-159	-136			ATGTTGAACTGGGCGTGTTATTAA		ATGTTGAACTGGGCGTGTTATTAA		MLNWACY*		MLNWACY*		TCGGATTAAC	TGAGACCTGG	0	P	0	0	0	0	0
5049	2620	af	AN7388.1	56.m02393	AO070293000057	0			-136	-98			ATGAGACCTGGCCTAGACGAGGACATCCCAGCTTTATAA		ATGAGACCTGGCCTAGACGAGGACATCCCAGCTTTATAA		MRPGLDEDIPAL*		MRPGLDEDIPAL*		CGTGTTATTA	GGTTTCATCT	0	P	0	0	0	0	0
5050	2620	ao	AN7388.1	56.m02393	AO070293000057	0					-186	-175	ATGAATACCTAG			ATGAATACCTAG	MNT*			MNT*	CGCTTAGGTG	AGCGCCTTAC	0	P	0	0	0	0	0
5051	2620	ao	AN7388.1	56.m02393	AO070293000057	0					-162	-85	ATGAAGCCATACTCATGGGTGTTGAAGAAACAATATAAAGACCATGGTTGTTCACTACCAGCTGCTGAAGTGTCATGA			ATGAAGCCATACTCATGGGTGTTGAAGAAACAATATAAAGACCATGGTTGTTCACTACCAGCTGCTGAAGTGTCATGA	MKPYSWVLKKQYKDHGCSLPAAEVS*			MKPYSWVLKKQYKDHGCSLPAAEVS*	CGCCTTACTA	CACAATCAAA	0	P	0	0	0	0	0
5052	2620	ao	AN7388.1	56.m02393	AO070293000057	0					-148	-125	ATGGGTGTTGAAGAAACAATATAA			ATGGGTGTTGAAGAAACAATATAA	MGVEETI*			MGVEETI*	AGCCATACTC	AGACCATGGT	0	P	0	0	0	0	0
5054	2622	af	AN2406.1	72.m19527	AO070298000039	0			-198	-169			ATGCGTCGAGACGTGCAGTACCTGAACTAG		ATGCGTCGAGACGTGCAGTACCTGAACTAG		MRRDVQYLN*		MRRDVQYLN*		TAGACCTGTT	CTGTCATCGG	0		0	0	0	0	0
5053	2622	an	AN2406.1	72.m19527	AO070298000039	0	-142	-122					ATGTCATCACCAGTTCCCTGA	ATGTCATCACCAGTTCCCTGA			MSSPVP*	MSSPVP*			CACCGGTCCA	CTCCCAGCCT	0		0	0	0	0	0
5055	2622	ao	AN2406.1	72.m19527	AO070298000039	0					-206	-189	ATGGTGGTCGGCAATTGA			ATGGTGGTCGGCAATTGA	MVVGN*			MVVGN*	GAAGAGTGAG	AAGGGTTCGC	0		0	0	0	0	0
5056	2622	ao	AN2406.1	72.m19527	AO070298000039	0					-151	-107	ATGGATTCGAATGCGTTTCTCTGCAGTCTTGGCGGCCGGAGGTGA			ATGGATTCGAATGCGTTTCTCTGCAGTCTTGGCGGCCGGAGGTGA	MDSNAFLCSLGGRR*			MDSNAFLCSLGGRR*	TGTTGTTTAC	TTCGTCCGCC	0		0	0	0	0	0
5057	2623	an	AN8095.1	70.m15204	AO070298000078	0	-228	-175					ATGATGGCCCCGAACCACGAAATCGGGCTGAGACCTGAGTCACTCTCCGTCTAG	ATGATGGCCCCGAACCACGAAATCGGGCTGAGACCTGAGTCACTCTCCGTCTAG			MMAPNHEIGLRPESLSV*	MMAPNHEIGLRPESLSV*			TTCGGCGAGA	GGAAATATCG	0	GEPR	0	0	0	0	0
5058	2623	an	AN8095.1	70.m15204	AO070298000078	0	-225	-175					ATGGCCCCGAACCACGAAATCGGGCTGAGACCTGAGTCACTCTCCGTCTAG	ATGGCCCCGAACCACGAAATCGGGCTGAGACCTGAGTCACTCTCCGTCTAG			MAPNHEIGLRPESLSV*	MAPNHEIGLRPESLSV*			GGCGAGAATG	GGAAATATCG	0	GEPR	0	0	0	0	0
5059	2623	an	AN8095.1	70.m15204	AO070298000078	0	-117	-82					ATGGGGAATTCAACTGACGAAGATGATGTTTTATAA	ATGGGGAATTCAACTGACGAAGATGATGTTTTATAA			MGNSTDEDDVL*	MGNSTDEDDVL*			TAGGCTACCT	AGAGGCACCT	0	GEPR	0	0	0	0	0
5060	2623	an	AN8095.1	70.m15204	AO070298000078	0	-95	-54					ATGATGTTTTATAAAGAGGCACCTGGAAGAGTCCCAATCTGA	ATGATGTTTTATAAAGAGGCACCTGGAAGAGTCCCAATCTGA			MMFYKEAPGRVPI*	MMFYKEAPGRVPI*			ACTGACGAAG	TATCCCCCAG	0	GEPR	0	0	0	0	0
5061	2623	an	AN8095.1	70.m15204	AO070298000078	0	-92	-54					ATGTTTTATAAAGAGGCACCTGGAAGAGTCCCAATCTGA	ATGTTTTATAAAGAGGCACCTGGAAGAGTCCCAATCTGA			MFYKEAPGRVPI*	MFYKEAPGRVPI*			GACGAAGATG	TATCCCCCAG	0	GEPR	0	0	0	0	0
5062	2623	ao	AN8095.1	70.m15204	AO070298000078	0					-163	-74	ATGTCTTGCTGTTTTTGTACCAGAGCACCGGTTTATAAATCCCCTATCACGCAAACCTTCAGTGCAATGCTGCGATATTTATTCATATGA			ATGTCTTGCTGTTTTTGTACCAGAGCACCGGTTTATAAATCCCCTATCACGCAAACCTTCAGTGCAATGCTGCGATATTTATTCATATGA	MSCCFCTRAPVYKSPITQTFSAMLRYLFI*			MSCCFCTRAPVYKSPITQTFSAMLRYLFI*	AGGTACGCTC	GGAATCTCAA	0	GEPR	0	0	0	0	0
5063	2623	ao	AN8095.1	70.m15204	AO070298000078	0					-97	-74	ATGCTGCGATATTTATTCATATGA			ATGCTGCGATATTTATTCATATGA	MLRYLFI*			MLRYLFI*	CTTCAGTGCA	GGAATCTCAA	0	GEPR	0	0	0	0	0
5066	2624	af	AN1629.1	58.m08929	AO070299000059	0			-247	-227			ATGATTTGTCTTTCTATTTGA		ATGATTTGTCTTTCTATTTGA		MICLSI*		MICLSI*		TCGTGTAAAT	GATCCCACTA	0	U	0	0	0	0	0
5064	2624	an	AN1629.1	58.m08929	AO070299000059	0	-151	-104					ATGACAGCACATTCTTTGGTAAATATGTGCTGCTTATCCGCTCGTTAA	ATGACAGCACATTCTTTGGTAAATATGTGCTGCTTATCCGCTCGTTAA			MTAHSLVNMCCLSAR*	MTAHSLVNMCCLSAR*			CAATAGACTT	TTCTGTACAT	0	U	0	0	0	0	0
5065	2624	an	AN1629.1	58.m08929	AO070299000059	0	-127	-104					ATGTGCTGCTTATCCGCTCGTTAA	ATGTGCTGCTTATCCGCTCGTTAA			MCCLSAR*	MCCLSAR*			TTTGGTAAAT	TTCTGTACAT	0	U	0	0	0	0	0
5067	2624	ao	AN1629.1	58.m08929	AO070299000059	0					-207	-187	ATGATTTGCCTCTTCGCCTAA			ATGATTTGCCTCTTCGCCTAA	MICLFA*			MICLFA*	CGAAGAAAAT	AACAATTCCG	0	U	0	0	0	0	0
5068	2625	af	AN9518.1	69.m15586	AO070300000007	0			-141	-106			ATGTGCGTTTCCCTTTCTGGACCCCGCTATCGATAA		ATGTGCGTTTCCCTTTCTGGACCCCGCTATCGATAA		MCVSLSGPRYR*		MCVSLSGPRYR*		CGGCAGGCGC	GCCTGCACTA	0	R	0	0	0	0	0
5069	2625	ao	AN9518.1	69.m15586	AO070300000007	0					-140	-75	ATGTCCAAAACCCCGCAGTTAAGGACAAAGACAGAGATAAATAGCAGGGATGACACCTTGTTGTAG			ATGTCCAAAACCCCGCAGTTAAGGACAAAGACAGAGATAAATAGCAGGGATGACACCTTGTTGTAG	MSKTPQLRTKTEINSRDDTLL*			MSKTPQLRTKTEINSRDDTLL*	AAGTCCGATA	TCACTGTACT	0	R	0	0	0	0	0
5079	2628	af	AN3744.1	65.m07391	AO070309000079	0			-138	-127			ATGTTGCTCTGA		ATGTTGCTCTGA		MLL*		MLL*		AAGTTCGAAA	GACCCCAGCC	0	J	FG07106.1	0	0	0	0
5078	2628	an	AN3744.1	65.m07391	AO070309000079	0	-122	-33					ATGTGCTCTGACCTTCAGTTCTCTCCCGGTCTTGCGGCGTACCCCCGGTCCAGCGTCCACAATCGCCGTTTCGTCAACATTATCAAATAA	ATGTGCTCTGACCTTCAGTTCTCTCCCGGTCTTGCGGCGTACCCCCGGTCCAGCGTCCACAATCGCCGTTTCGTCAACATTATCAAATAA			MCSDLQFSPGLAAYPRSSVHNRRFVNIIK*	MCSDLQFSPGLAAYPRSSVHNRRFVNIIK*			ACGACCAAAA	CACTGGCCGT	0	J	FG07106.1	0	0	0	0
5080	2628	ao	AN3744.1	65.m07391	AO070309000079	0					-227	-162	ATGAGCACAATATTGACAGACCGCCTTCGGAGTTGGGCTTGCGGCAACTACACTAAACTCGAATAG			ATGAGCACAATATTGACAGACCGCCTTCGGAGTTGGGCTTGCGGCAACTACACTAAACTCGAATAG	MSTILTDRLRSWACGNYTKLE*			MSTILTDRLRSWACGNYTKLE*	CCGCTTTAAG	GTAATCTGAG	0	J	FG07106.1	0	0	0	0
5083	2630	af	AN6902.1	71.m15234	AO070314000013	0			-252	-169			ATGACAATGGTGATCTTGGAGTCCAAGGTTGAAGCCCCAACTTCATCAGCTCATTTCCTTATACGACTTAGTGTAATCGGATAA		ATGACAATGGTGATCTTGGAGTCCAAGGTTGAAGCCCCAACTTCATCAGCTCATTTCCTTATACGACTTAGTGTAATCGGATAA		MTMVILESKVEAPTSSAHFLIRLSVIG*		MTMVILESKVEAPTSSAHFLIRLSVIG*		TGGATAATTA	GCCCCGCATC	0	A	FG06705.1	MG08908.1	0	0	0
5084	2630	af	AN6902.1	71.m15234	AO070314000013	0			-246	-169			ATGGTGATCTTGGAGTCCAAGGTTGAAGCCCCAACTTCATCAGCTCATTTCCTTATACGACTTAGTGTAATCGGATAA		ATGGTGATCTTGGAGTCCAAGGTTGAAGCCCCAACTTCATCAGCTCATTTCCTTATACGACTTAGTGTAATCGGATAA		MVILESKVEAPTSSAHFLIRLSVIG*		MVILESKVEAPTSSAHFLIRLSVIG*		ATTAATGACA	GCCCCGCATC	0	A	FG06705.1	MG08908.1	0	0	0
5081	2630	an	AN6902.1	71.m15234	AO070314000013	0	-248	-168					ATGGAAGTAGACCATGACAAGAATCCCAGCCGCGGGCCAGGAACCGTATCAGCTCATTCCCCCTTTGGGCGAGTCGGATAA	ATGGAAGTAGACCATGACAAGAATCCCAGCCGCGGGCCAGGAACCGTATCAGCTCATTCCCCCTTTGGGCGAGTCGGATAA			MEVDHDKNPSRGPGTVSAHSPFGRVG*	MEVDHDKNPSRGPGTVSAHSPFGRVG*			AATTGCTGAA	GCCTCGCATC	0	A	FG06705.1	MG08908.1	0	0	0

5082	2630	an	AN6902.1	71.m15234	AO070314000013	0	-235	-122					ATGACAAGAATCCCAGCCGCGGGCCAGGAACCGTATCAGCTCATTCCCCCTTTGGGCGAGTCGGATAAGCCTCGCATCATCATTGATCCGTCGTTATCAGCGAAGAAAAAATAA	ATGACAAGAATCCCAGCCGCGGGCCAGGAACCGTATCAGCTCATTCCCCCTTTGGGCGAGTCGGATAAGCCTCGCATCATCATTGATCCGTCGTTATCAGCGAAGAAAAAATAA			MTRIPAAGQEPYQLIPPLGESDKPRIIIDPSLSAKKK*	MTRIPAAGQEPYQLIPPLGESDKPRIIIDPSLSAKKK*			GAAGTAGACC	TTCCACTTCA	0	A	FG06705.1	MG08908.1	0	0	0
5085	2630	ao	AN6902.1	71.m15234	AO070314000013	0					-252	-223	ATGTCAGTCGGCGGAGGCATTTACAGCTGA			ATGTCAGTCGGCGGAGGCATTTACAGCTGA	MSVGGGIYS*			MSVGGGIYS*	GAGAGTTGAT	TTTCCCCATG	0	A	FG06705.1	MG08908.1	0	0	0
5086	2631	af	AN0061.1	71.m15337	AO070314000148	0			-202	-155			ATGTCAAATTCTGTAAAGCTTAATTCATTTAGGACATTATATCATTGA		ATGTCAAATTCTGTAAAGCTTAATTCATTTAGGACATTATATCATTGA		MSNSVKLNSFRTLYH*		MSNSVKLNSFRTLYH*		GTGCCCTGCT	TCTCTGTCAG	0		0	0	0	0	0
5087	2633	an	AN8683.1	62.m03388	AO070315000103	0	-195	-166					ATGGTTACCAACGAACTCTCTGCTCAATGA	ATGGTTACCAACGAACTCTCTGCTCAATGA			MVTNELSAQ*	MVTNELSAQ*			TCAAAGTGCT	TTTGACTGAG	0	PQ	0	0	0	0	0
5088	2633	ao	AN8683.1	62.m03388	AO070315000103	0					-196	-185	ATGCGGCGTTGA			ATGCGGCGTTGA	MRR*			MRR*	AAGCTAACAG	ATGCTTTCCA	0	PQ	0	0	0	0	0
5089	2633	ao	AN8683.1	62.m03388	AO070315000103	0					-184	-161	ATGCTTTCCAGTGCTCTGTCATAG			ATGCTTTCCAGTGCTCTGTCATAG	MLSSALS*			MLSSALS*	GCGGCGTTGA	TTGATACATC	0	PQ	0	0	0	0	0
5090	2635	af	AN2311.1	71.m15506	AO070323000049	0			-182	-114			ATGTGCGTCCGATTTGATAGTGTCTCGTACATGTGTGCGGAGCAATTGGCTTGCTTGCAGAAATGCTGA		ATGTGCGTCCGATTTGATAGTGTCTCGTACATGTGTGCGGAGCAATTGGCTTGCTTGCAGAAATGCTGA		MCVRFDSVSYMCAEQLACLQKC*		MCVRFDSVSYMCAEQLACLQKC*		TCTGTCAGAC	CGCCATGTTA	0	I	FG09764.1	0	NCU08671.1	YMR220W	YMR220W
5091	2635	af	AN2311.1	71.m15506	AO070323000049	0			-152	-114			ATGTGTGCGGAGCAATTGGCTTGCTTGCAGAAATGCTGA		ATGTGTGCGGAGCAATTGGCTTGCTTGCAGAAATGCTGA		MCAEQLACLQKC*		MCAEQLACLQKC*		TGTCTCGTAC	CGCCATGTTA	0	I	FG09764.1	0	NCU08671.1	YMR220W	YMR220W
5092	2635	af	AN2311.1	71.m15506	AO070323000049	0			-120	-61			ATGCTGACGCCATGTTACTCTAGCTCCCATCAAACCCCTGATACCGGACCACCACATTAA		ATGCTGACGCCATGTTACTCTAGCTCCCATCAAACCCCTGATACCGGACCACCACATTAA		MLTPCYSSSHQTPDTGPPH*		MLTPCYSSSHQTPDTGPPH*		GCTTGCAGAA	CATCTCGGTC	0	I	FG09764.1	0	NCU08671.1	YMR220W	YMR220W
5093	2635	af	AN2311.1	71.m15506	AO070323000049	0			-109	-98			ATGTTACTCTAG		ATGTTACTCTAG		MLL*		MLL*		TGCTGACGCC	CTCCCATCAA	0	I	FG09764.1	0	NCU08671.1	YMR220W	YMR220W
5094	2638	af	AN5530.1	58.m07476	AO070328000063	0			-99	-16			ATGGCGATCTCCGAATTTCCAGTCGAAGCTTATCGATGCGTATCACCCGTTTTTGTCCACTCGCTCAGTTTTTCTGATTCTTAG		ATGGCGATCTCCGAATTTCCAGTCGAAGCTTATCGATGCGTATCACCCGTTTTTGTCCACTCGCTCAGTTTTTCTGATTCTTAG		MAISEFPVEAYRCVSPVFVHSLSFSDS*		MAISEFPVEAYRCVSPVFVHSLSFSDS*		ACTCAAATAT	TGGACGTGAT	0	A	FG01187.1	MG05375.1	0	0	0
5095	2638	af	AN5530.1	58.m07476	AO070328000063	0			-64	-23			ATGCGTATCACCCGTTTTTGTCCACTCGCTCAGTTTTTCTGA		ATGCGTATCACCCGTTTTTGTCCACTCGCTCAGTTTTTCTGA		MRITRFCPLAQFF*		MRITRFCPLAQFF*		AAGCTTATCG	TTCTTAGTGG	0	A	FG01187.1	MG05375.1	0	0	0
5096	2638	ao	AN5530.1	58.m07476	AO070328000063	0					-154	-113	ATGGGCTGTCAATTAGGACAAAGAGTTCCTCTCATCCAATGA			ATGGGCTGTCAATTAGGACAAAGAGTTCCTCTCATCCAATGA	MGCQLGQRVPLIQ*			MGCQLGQRVPLIQ*	CTTGAAGCCC	CAGTCGACGA	0	A	FG01187.1	MG05375.1	0	0	0
5097	2638	ao	AN5530.1	58.m07476	AO070328000063	0					-116	-78	ATGACAGTCGACGAGATTGCTGACATAATATTTCCATAG			ATGACAGTCGACGAGATTGCTGACATAATATTTCCATAG	MTVDEIADIIFP*			MTVDEIADIIFP*	CTCTCATCCA	AATTTCCCTT	0	A	FG01187.1	MG05375.1	0	0	0
5098	2640	an	AN8063.1	53.m03914	AO070330000019	0	-210	-124					ATGGCGTTCCGCGGACACCCATTGCTTGATAAAGATAAGAAATCCGAGGAGAATGATGGCGGACCCCGCCTATGTAAAGCTAGTTAG	ATGGCGTTCCGCGGACACCCATTGCTTGATAAAGATAAGAAATCCGAGGAGAATGATGGCGGACCCCGCCTATGTAAAGCTAGTTAG			MAFRGHPLLDKDKKSEENDGGPRLCKAS*	MAFRGHPLLDKDKKSEENDGGPRLCKAS*			GGAACCTTCA	CTGATGATAA	0		0	0	0	0	0
5099	2640	an	AN8063.1	53.m03914	AO070330000019	0	-158	-120					ATGATGGCGGACCCCGCCTATGTAAAGCTAGTTAGCTGA	ATGATGGCGGACCCCGCCTATGTAAAGCTAGTTAGCTGA			MMADPAYVKLVS*	MMADPAYVKLVS*			TCCGAGGAGA	TGATAAGGCA	0		0	0	0	0	0
5100	2640	an	AN8063.1	53.m03914	AO070330000019	0	-155	-120					ATGGCGGACCCCGCCTATGTAAAGCTAGTTAGCTGA	ATGGCGGACCCCGCCTATGTAAAGCTAGTTAGCTGA			MADPAYVKLVS*	MADPAYVKLVS*			GAGGAGAATG	TGATAAGGCA	0		0	0	0	0	0
5101	2640	an	AN8063.1	53.m03914	AO070330000019	0	-120	-85					ATGATAAGGCAACGGGCGGGACTGTTTCCTGCGTAG	ATGATAAGGCAACGGGCGGGACTGTTTCCTGCGTAG			MIRQRAGLFPA*	MIRQRAGLFPA*			TAGTTAGCTG	CTACTTAAAG	0		0	0	0	0	0
5102	2640	ao	AN8063.1	53.m03914	AO070330000019	0					-174	-142	ATGATCACAGAACCTTCTCTATGGTGGATGTGA			ATGATCACAGAACCTTCTCTATGGTGGATGTGA	MITEPSLWWM*			MITEPSLWWM*	AGGGGTCATA	AGACCCTAAC	0		0	0	0	0	0
5105	2642	af	AN1138.1	70.m15099	AO070331000129	0			-88	-47			ATGCCTCCATCAGCTTTCTTCTCACCTTCCAGTCATCCTTAG		ATGCCTCCATCAGCTTTCTTCTCACCTTCCAGTCATCCTTAG		MPPSAFFSPSSHP*		MPPSAFFSPSSHP*		GATACAGTTG	TACCATTGCG	0	R	0	0	0	0	0
5103	2642	an	AN1138.1	70.m15099	AO070331000129	0	-175	-11					ATGCTTTCCCCACAATCTCTGCTCGAGTCATGCCCAGTGAAATCCTTTCATCCCCGGGTTTCCTTTACCCAGGCCGCCCTCCCCCCGGCCGCATATAAGGTTCCCTTGAGTCTCCGCTATTTTCCTCCCCTTCTCCATCACCACGTCCTATTCTTCTACCTTTAA	ATGCTTTCCCCACAATCTCTGCTCGAGTCATGCCCAGTGAAATCCTTTCATCCCCGGGTTTCCTTTACCCAGGCCGCCCTCCCCCCGGCCGCATATAAGGTTCCCTTGAGTCTCCGCTATTTTCCTCCCCTTCTCCATCACCACGTCCTATTCTTCTACCTTTAA			MLSPQSLLESCPVKSFHPRVSFTQAALPPAAYKVPLSLRYFPPLLHHHVLFFYL*	MLSPQSLLESCPVKSFHPRVSFTQAALPPAAYKVPLSLRYFPPLLHHHVLFFYL*			AGGGTGGTAA	TCAGGGCAAA	0	R	0	0	0	0	0
5104	2642	an	AN1138.1	70.m15099	AO070331000129	0	-146	-78					ATGCCCAGTGAAATCCTTTCATCCCCGGGTTTCCTTTACCCAGGCCGCCCTCCCCCCGGCCGCATATAA	ATGCCCAGTGAAATCCTTTCATCCCCGGGTTTCCTTTACCCAGGCCGCCCTCCCCCCGGCCGCATATAA			MPSEILSSPGFLYPGRPPGRI*	MPSEILSSPGFLYPGRPPGRI*			TGCTCGAGTC	GGTTCCCTTG	0	R	0	0	0	0	0
5106	2643	af	AN9108.1	66.m04760	AO070332000164	0			-257	-231			ATGGCCGGAAATAATACCGGCCTCTGA		ATGGCCGGAAATAATACCGGCCTCTGA		MAGNNTGL*		MAGNNTGL*		TGGCATGCCC	TATTATAAGA	0		0	MG00755.1	NCU01402.1	0	0
5108	2644	af	AN1478.1	55.m02985	AO070334000161	0			-271	-185			ATGCCATCTCCCTTCAACCATCCAAATCACTACAGGCAGCTTGCAACCCTGCAACAACGAGTAAGCGTGCCTGCTGCAAGAGGATGA		ATGCCATCTCCCTTCAACCATCCAAATCACTACAGGCAGCTTGCAACCCTGCAACAACGAGTAAGCGTGCCTGCTGCAAGAGGATGA		MPSPFNHPNHYRQLATLQQRVSVPAARG*		MPSPFNHPNHYRQLATLQQRVSVPAARG*		CAACTTTCAG	TCCAGGTTTG	0	A	0	0	0	0	0
5109	2644	af	AN1478.1	55.m02985	AO070334000161	0			-188	-153			ATGATCCAGGTTTGTGAAACCTTCACGGACACTTAA		ATGATCCAGGTTTGTGAAACCTTCACGGACACTTAA		MIQVCETFTDT*		MIQVCETFTDT*		CTGCAAGAGG	TTATTTCCAC	0	A	0	0	0	0	0
5107	2644	an	AN1478.1	55.m02985	AO070334000161	0	-169	-47					ATGGTCCAGGTTTGTGCAGACTCACGAATCTCAACTTTGCCACAGAATTCATCTCCATTCGCAGGTGTCTCGACGCGCCGCCGATTCCTGAGCCTGAGCTCCATTGAGCCAGTGACGATTTAA	ATGGTCCAGGTTTGTGCAGACTCACGAATCTCAACTTTGCCACAGAATTCATCTCCATTCGCAGGTGTCTCGACGCGCCGCCGATTCCTGAGCCTGAGCTCCATTGAGCCAGTGACGATTTAA			MVQVCADSRISTLPQNSSPFAGVSTRRRFLSLSSIEPVTI*	MVQVCADSRISTLPQNSSPFAGVSTRRRFLSLSSIEPVTI*			CTGCAGGACG	ACGGTCACCT	0	A	0	0	0	0	0
5110	2644	ao	AN1478.1	55.m02985	AO070334000161	0					-198	-160	ATGCTCCAGGTTTGTGAAACCTTCTGGAATCTCATATAA			ATGCTCCAGGTTTGTGAAACCTTCTGGAATCTCATATAA	MLQVCETFWNLI*			MLQVCETFWNLI*	CTGCAGGAGG	TTGCAGGATT	0	A	0	0	0	0	0
5112	2650	an	AN8144.1	69.m15536	AO070340000167	0	-191	-180					ATGGGTTCTTAG	ATGGGTTCTTAG			MGS*	MGS*			GAGCGTTACA	ACAAATGCAG	0		0	MG08671.1	NCU09400.1	0	0
5113	2650	an	AN8144.1	69.m15536	AO070340000167	0	-175	-158					ATGCAGGGTCTAATTTAG	ATGCAGGGTCTAATTTAG			MQGLI*	MQGLI*			TCTTAGACAA	CCGTAATAAG	0		0	MG08671.1	NCU09400.1	0	0
5114	2650	an	AN8144.1	69.m15536	AO070340000167	0	-137	-33					ATGCTAAAACCGAGAAGTAAGCAATTGTGTCTATGGAGTGGAACATCTGAGCACCCAACTGTCCTCAGGGCTCGATCGAATTTCTCCCCAGATTGTTGGAGTTAG	ATGCTAAAACCGAGAAGTAAGCAATTGTGTCTATGGAGTGGAACATCTGAGCACCCAACTGTCCTCAGGGCTCGATCGAATTTCTCCCCAGATTGTTGGAGTTAG			MLKPRSKQLCLWSGTSEHPTVLRARSNFSPDCWS*	MLKPRSKQLCLWSGTSEHPTVLRARSNFSPDCWS*			TCTGTCCTTT	ATCTTATACT	0		0	MG08671.1	NCU09400.1	0	0
5115	2650	an	AN8144.1	69.m15536	AO070340000167	0	-105	-88					ATGGAGTGGAACATCTGA	ATGGAGTGGAACATCTGA			MEWNI*	MEWNI*			AATTGTGTCT	GCACCCAACT	0		0	MG08671.1	NCU09400.1	0	0
5116	2650	ao	AN8144.1	69.m15536	AO070340000167	0					-224	-201	ATGCCGCGCTTTGCACCTGAATAA			ATGCCGCGCTTTGCACCTGAATAA	MPRFAPE*			MPRFAPE*	AAGGGCGTTC	TATCTCGCTG	0		0	MG08671.1	NCU09400.1	0	0
5117	2650	ao	AN8144.1	69.m15536	AO070340000167	0					-179	-15	ATGATTGGCTATCTTTACGCGTGGCAACGGATTAGTGATATCGTTAGAAGTATTAAACTGGTTCCTGTGCCATTGGACTGTCTGAATAAACTCTCTCTGATTCTTTATTACATTTTTATAAGAGTAGAGTCTAGGACAAACAACACCCACGCGACCATACTTTGA			ATGATTGGCTATCTTTACGCGTGGCAACGGATTAGTGATATCGTTAGAAGTATTAAACTGGTTCCTGTGCCATTGGACTGTCTGAATAAACTCTCTCTGATTCTTTATTACATTTTTATAAGAGTAGAGTCTAGGACAAACAACACCCACGCGACCATACTTTGA	MIGYLYAWQRISDIVRSIKLVPVPLDCLNKLSLILYYIFIRVESRTNNTHATIL*			MIGYLYAWQRISDIVRSIKLVPVPLDCLNKLSLILYYIFIRVESRTNNTHATIL*	AGCACATAGG	ATCCCACATC	0		0	MG08671.1	NCU09400.1	0	0
5119	2652	af	AN6032.1	72.m19949	AO070340000256	0			-266	-252			ATGTACGTATCTTAG		ATGTACGTATCTTAG		MYVS*		MYVS*		CTTCCAGTTC	AGACATAAGC	0	H	FG09710.1	MG01474.1	NCU09930.1	0	0
5120	2652	af	AN6032.1	72.m19949	AO070340000256	0			-80	-60			ATGTCAAAAATGTGTCTTTAA		ATGTCAAAAATGTGTCTTTAA		MSKMCL*		MSKMCL*		AAACTCGGGA	AGCACGTGTC	0	H	FG09710.1	MG01474.1	NCU09930.1	0	0
5118	2652	conserved	AN6032.1	72.m19949	AO070340000256	0	-71	-60	-71	-60	-71	-60	ATGdryCkbTrA	ATGAACCGGTGA	ATGTGTCTTTAA	ATGGATCTCTAA	Mnr*	MNR*	MCL*	MDL*	rvTdysmrmm	rvhmskysbm	0	H	FG09710.1	MG01474.1	NCU09930.1	0	0
5122	2653	af	AN5988.1	72.m19152	AO070340000290	0			-223	-131			ATGTCATTGCTCACCCATCGTTTATCAATTTCGCGCTCTTTTTCCATCTGTGCAGTGTTGTCAACAGTCGATGGCTTCATTTCTGACTGGTAA		ATGTCATTGCTCACCCATCGTTTATCAATTTCGCGCTCTTTTTCCATCTGTGCAGTGTTGTCAACAGTCGATGGCTTCATTTCTGACTGGTAA		MSLLTHRLSISRSFSICAVLSTVDGFISDW*		MSLLTHRLSISRSFSICAVLSTVDGFISDW*		ATTATCCTGT	TCGTTGACGG	0	A	0	0	0	0	0
5123	2653	af	AN5988.1	72.m19152	AO070340000290	0			-153	-124			ATGGCTTCATTTCTGACTGGTAATCGTTGA		ATGGCTTCATTTCTGACTGGTAATCGTTGA		MASFLTGNR*		MASFLTGNR*		TCAACAGTCG	CGGCGTAGCG	0	A	0	0	0	0	0
5121	2653	an	AN5988.1	72.m19152	AO070340000290	0	-117	-55					ATGTTCCCGCCAACCCACTGTATCACCTGCGCGCTTGATTCTGACTTCGAAAGACTGGATTGA	ATGTTCCCGCCAACCCACTGTATCACCTGCGCGCTTGATTCTGACTTCGAAAGACTGGATTGA			MFPPTHCITCALDSDFERLD*	MFPPTHCITCALDSDFERLD*			GGTCATTCTT	GCGGCACTCG	0	A	0	0	0	0	0
5124	2653	ao	AN5988.1	72.m19152	AO070340000290	0					-231	-202	ATGCAGCCCTCTTGTGGCGACGGCCCATAG			ATGCAGCCCTCTTGTGGCGACGGCCCATAG	MQPSCGDGP*			MQPSCGDGP*	TGATCGATTC	TTGCCAGTGA	0	A	0	0	0	0	0
5125	2653	ao	AN5988.1	72.m19152	AO070340000290	0					-188	-126	ATGATTCTGACTCGTAAGATTGACCTAGTATCAGCGGAATACATGCGTCCATCTGATCTGTAA			ATGATTCTGACTCGTAAGATTGACCTAGTATCAGCGGAATACATGCGTCCATCTGATCTGTAA	MILTRKIDLVSAEYMRPSDL*			MILTRKIDLVSAEYMRPSDL*	CCAGTGACAT	CCCCTTTACG	0	A	0	0	0	0	0
5126	2653	ao	AN5988.1	72.m19152	AO070340000290	0					-146	-126	ATGCGTCCATCTGATCTGTAA			ATGCGTCCATCTGATCTGTAA	MRPSDL*			MRPSDL*	AGCGGAATAC	CCCCTTTACG	0	A	0	0	0	0	0
5132	2655	af	AN5528.1	69.m15427	AO070341000360	0			-100	-59			ATGGCCTGTGAGCTATTTACACCCAAGAACACACGCCTATGA		ATGGCCTGTGAGCTATTTACACCCAAGAACACACGCCTATGA		MACELFTPKNTRL*		MACELFTPKNTRL*		GGCGGTTTGC	TGGTCTCTTG	0	U	0	0	NCU05029.1	0	0
5134	2657	af	AN3593.1	58.m08903	AO070342000145	0			-63	-49			ATGCCATTATCCTAG		ATGCCATTATCCTAG		MPLS*		MPLS*		TTGGCAATTT	CAATCGACTG	0	G	0	0	0	0	0
5135	2657	ao	AN3593.1	58.m08903	AO070342000145	0					-222	-100	ATGGAGTTCTTCACGTTGCCCCTCTCCCCGCCGACGTTCTTTTCCCCTCCTCACTCACTTTGCAAAACTTCAGACCACACTGGTTTAGGTGTCAACGGCAATTATCTTACCACTCTTACCTGA			ATGGAGTTCTTCACGTTGCCCCTCTCCCCGCCGACGTTCTTTTCCCCTCCTCACTCACTTTGCAAAACTTCAGACCACACTGGTTTAGGTGTCAACGGCAATTATCTTACCACTCTTACCTGA	MEFFTLPLSPPTFFSPPHSLCKTSDHTGLGVNGNYLTTLT*			MEFFTLPLSPPTFFSPPHSLCKTSDHTGLGVNGNYLTTLT*	AAAAAAAAAA	GGAAAGGGCC	0	G	0	0	0	0	0
5136	2659	an	AN5644.1	58.m07332	AO070342000235	0	-225	-211					ATGCTTGCGAGCTAG	ATGCTTGCGAGCTAG			MLAS*	MLAS*			TGTCCTGGCA	AGACAGCCAA	0	C	0	0	0	0	0
5137	2659	an	AN5644.1	58.m07332	AO070342000235	0	-123	-28					ATGTGCCTCCCCAATAAAAGATGCAGCCACCTCCCTGTCCCTTTCATTCTTGTGCAACGCTCGCCTTTGGGGAATAAAATCAGTTTATATCGTTGA	ATGTGCCTCCCCAATAAAAGATGCAGCCACCTCCCTGTCCCTTTCATTCTTGTGCAACGCTCGCCTTTGGGGAATAAAATCAGTTTATATCGTTGA			MCLPNKRCSHLPVPFILVQRSPLGNKISLYR*	MCLPNKRCSHLPVPFILVQRSPLGNKISLYR*			CTGGAGCTGC	ATAATCGCTC	0	C	0	0	0	0	0
5138	2659	an	AN5644.1	58.m07332	AO070342000235	0	-103	-47					ATGCAGCCACCTCCCTGTCCCTTTCATTCTTGTGCAACGCTCGCCTTTGGGGAATAA	ATGCAGCCACCTCCCTGTCCCTTTCATTCTTGTGCAACGCTCGCCTTTGGGGAATAA			MQPPPCPFHSCATLAFGE*	MQPPPCPFHSCATLAFGE*			CCAATAAAAG	AATCAGTTTA	0	C	0	0	0	0	0
5143	2664	af	AN2163.1	72.m19677	AO070343000222	0			-647	-507			ATGAAATACCTAATTCGTACTCTGTACTCCGTACCTTGTTCAGGTTCCGGACTATTCCCGCCCCTCCCCTCCATGTCATCCATATCTTTCTGCCCACTAAATTACAGACTAAAAAAGACCTCTTCTTTTCATTACAATTAG		ATGAAATACCTAATTCGTACTCTGTACTCCGTACCTTGTTCAGGTTCCGGACTATTCCCGCCCCTCCCCTCCATGTCATCCATATCTTTCTGCCCACTAAATTACAGACTAAAAAAGACCTCTTCTTTTCATTACAATTAG		MKYLIRTLYSVPCSGSGLFPPLPSMSSISFCPLNYRLKKTSSFHYN*		MKYLIRTLYSVPCSGSGLFPPLPSMSSISFCPLNYRLKKTSSFHYN*		TCACCCACCG	TTACTACTGA	0	D	0	0	0	0	0
5144	2664	af	AN2163.1	72.m19677	AO070343000222	0			-575	-507			ATGTCATCCATATCTTTCTGCCCACTAAATTACAGACTAAAAAAGACCTCTTCTTTTCATTACAATTAG		ATGTCATCCATATCTTTCTGCCCACTAAATTACAGACTAAAAAAGACCTCTTCTTTTCATTACAATTAG		MSSISFCPLNYRLKKTSSFHYN*		MSSISFCPLNYRLKKTSSFHYN*		CCTCCCCTCC	TTACTACTGA	0	D	0	0	0	0	0

5145	2664	af	AN2163.1	72.m19677	AO070343000222	0			-497	-483			ATGTTCATTCCTTAA		ATGTTCATTCCTTAA		MFIP*		MFIP*		GTTACTACTG	CTCCTCACCT	0	D	0	0	0	0	0
5146	2664	af	AN2163.1	72.m19677	AO070343000222	0			-454	-320			ATGTTCTCTGCTTCCCAATCTTACCCTCAGACTCTCAGACTTAACCTAGCCACCAACCACCACCACCAAACCCCCCTCCTCCCCCTCCCCGCCTCCATCCCTACTCAGCACTTTCAATATCATACAACACGTTGA		ATGTTCTCTGCTTCCCAATCTTACCCTCAGACTCTCAGACTTAACCTAGCCACCAACCACCACCACCAAACCCCCCTCCTCCCCCTCCCCGCCTCCATCCCTACTCAGCACTTTCAATATCATACAACACGTTGA		MFSASQSYPQTLRLNLATNHHHQTPLLPLPASIPTQHFQYHTTR*		MFSASQSYPQTLRLNLATNHHHQTPLLPLPASIPTQHFQYHTTR*		TCAGTCATCC	TTCTCTTCTC	0	D	0	0	0	0	0
5147	2664	af	AN2163.1	72.m19677	AO070343000222	0			-149	-138			ATGGTTTGGTGA		ATGGTTTGGTGA		MVW*		MVW*		GTCATCTCCC	GAGAAATAGT	0	D	0	0	0	0	0
5140	2664	an	AN2163.1	72.m19677	AO070343000222	0	-318	-280					ATGGCCAGCACCATGATCCTGCCTAATCTTGAGCCTTGA	ATGGCCAGCACCATGATCCTGCCTAATCTTGAGCCTTGA			MASTMILPNLEP*	MASTMILPNLEP*			TTGACCTAGC	CCTTGTTTCT	0	D	0	0	0	0	0
5141	2664	an	AN2163.1	72.m19677	AO070343000222	0	-306	-280					ATGATCCTGCCTAATCTTGAGCCTTGA	ATGATCCTGCCTAATCTTGAGCCTTGA			MILPNLEP*	MILPNLEP*			GGCCAGCACC	CCTTGTTTCT	0	D	0	0	0	0	0
5148	2664	ao	AN2163.1	72.m19677	AO070343000222	0					-740	-564	ATGTTTAATCCGAACAGTTGCTTCCTTACTTTAACTTACAAACCACAATCCACCGTCACCCCTCCTCCCTCCCTCTTTCCCTCCCTCTCTCTTCCTTTCCCTTTTCTCACCTTCGGACAAACACCCATTTCATCATCCACTTTATTCCCGTTGGACTTCCCACAATTTTCACCCTAA			ATGTTTAATCCGAACAGTTGCTTCCTTACTTTAACTTACAAACCACAATCCACCGTCACCCCTCCTCCCTCCCTCTTTCCCTCCCTCTCTCTTCCTTTCCCTTTTCTCACCTTCGGACAAACACCCATTTCATCATCCACTTTATTCCCGTTGGACTTCCCACAATTTTCACCCTAA	MFNPNSCFLTLTYKPQSTVTPPPSLFPSLSLPFPFLTFGQTPISSSTLFPLDFPQFSP*			MFNPNSCFLTLTYKPQSTVTPPPSLFPSLSLPFPFLTFGQTPISSSTLFPLDFPQFSP*	CACCCAACGT	TTTGGTGTAC	0	D	0	0	0	0	0
5149	2664	ao	AN2163.1	72.m19677	AO070343000222	0					-241	-215	ATGCGTGGCAGAAAAGACAGTTGTTGA			ATGCGTGGCAGAAAAGACAGTTGTTGA	MRGRKDSC*			MRGRKDSC*	GTTCCATTTC	CCCATCGTCT	0	D	0	0	0	0	0
5153	2666	af	AN5207.1	69.m14904	AO070199000007	0			-217	-62			ATGACGTCGGTAGGCGTTCATCAAGAGCCACCAGCTGGGATAGAACCAAGAATATCAAGGACGATCATGCACCTGGGTTTTGTAGAGCCGTATAAAGCGCTTCGAGCTCTAACACTAGTGTATCTGTTCTTTTACGTATACTTATGCAGCGATTGA		ATGACGTCGGTAGGCGTTCATCAAGAGCCACCAGCTGGGATAGAACCAAGAATATCAAGGACGATCATGCACCTGGGTTTTGTAGAGCCGTATAAAGCGCTTCGAGCTCTAACACTAGTGTATCTGTTCTTTTACGTATACTTATGCAGCGATTGA		MTSVGVHQEPPAGIEPRISRTIMHLGFVEPYKALRALTLVYLFFYVYLCSD*		MTSVGVHQEPPAGIEPRISRTIMHLGFVEPYKALRALTLVYLFFYVYLCSD*		CGTTCAGCAG	TATATGTGTA	0		0	0	0	0	0
5154	2666	af	AN5207.1	69.m14904	AO070199000007	0			-151	-62			ATGCACCTGGGTTTTGTAGAGCCGTATAAAGCGCTTCGAGCTCTAACACTAGTGTATCTGTTCTTTTACGTATACTTATGCAGCGATTGA		ATGCACCTGGGTTTTGTAGAGCCGTATAAAGCGCTTCGAGCTCTAACACTAGTGTATCTGTTCTTTTACGTATACTTATGCAGCGATTGA		MHLGFVEPYKALRALTLVYLFFYVYLCSD*		MHLGFVEPYKALRALTLVYLFFYVYLCSD*		AAGGACGATC	TATATGTGTA	0		0	0	0	0	0
5155	2666	af	AN5207.1	69.m14904	AO070199000007	0			-74	-51			ATGCAGCGATTGATATATGTGTAA		ATGCAGCGATTGATATATGTGTAA		MQRLIYV*		MQRLIYV*		ACGTATACTT	TACCAGGATT	0		0	0	0	0	0
5150	2666	an	AN5207.1	69.m14904	AO070199000007	0	-200	-90					ATGCAACGTTCATTATCTTATCGCATCTATGACGTCTTTTCTACGAAGGCCCCAGGGTTCAGGTCGAACCTTGAAAATGTACTGTACTCCATAGGTGGTGGTTGTATTTAA	ATGCAACGTTCATTATCTTATCGCATCTATGACGTCTTTTCTACGAAGGCCCCAGGGTTCAGGTCGAACCTTGAAAATGTACTGTACTCCATAGGTGGTGGTTGTATTTAA			MQRSLSYRIYDVFSTKAPGFRSNLENVLYSIGGGCI*	MQRSLSYRIYDVFSTKAPGFRSNLENVLYSIGGGCI*			CTAGTGGTCA	CTTTGTGACT	0		0	0	0	0	0
5151	2666	an	AN5207.1	69.m14904	AO070199000007	0	-172	-107					ATGACGTCTTTTCTACGAAGGCCCCAGGGTTCAGGTCGAACCTTGAAAATGTACTGTACTCCATAG	ATGACGTCTTTTCTACGAAGGCCCCAGGGTTCAGGTCGAACCTTGAAAATGTACTGTACTCCATAG			MTSFLRRPQGSGRTLKMYCTP*	MTSFLRRPQGSGRTLKMYCTP*			TATCGCATCT	GTGGTGGTTG	0		0	0	0	0	0
5152	2666	an	AN5207.1	69.m14904	AO070199000007	0	-124	-107					ATGTACTGTACTCCATAG	ATGTACTGTACTCCATAG			MYCTP*	MYCTP*			AACCTTGAAA	GTGGTGGTTG	0		0	0	0	0	0
5156	2666	ao	AN5207.1	69.m14904	AO070199000007	0					-228	-175	ATGACGTCGATGGGCGTCAATCCTTCGATTAACCTTCGATATGCATTCTTTTAA			ATGACGTCGATGGGCGTCAATCCTTCGATTAACCTTCGATATGCATTCTTTTAA	MTSMGVNPSINLRYAFF*			MTSMGVNPSINLRYAFF*	TATCGGAGCG	ATACTTCTCT	0		0	0	0	0	0
5157	2666	ao	AN5207.1	69.m14904	AO070199000007	0					-219	-175	ATGGGCGTCAATCCTTCGATTAACCTTCGATATGCATTCTTTTAA			ATGGGCGTCAATCCTTCGATTAACCTTCGATATGCATTCTTTTAA	MGVNPSINLRYAFF*			MGVNPSINLRYAFF*	GATGACGTCG	ATACTTCTCT	0		0	0	0	0	0
5158	2666	ao	AN5207.1	69.m14904	AO070199000007	0					-188	-144	ATGCATTCTTTTAAATACTTCTCTGCCATTGCGATTTCAATTTAA			ATGCATTCTTTTAAATACTTCTCTGCCATTGCGATTTCAATTTAA	MHSFKYFSAIAISI*			MHSFKYFSAIAISI*	AACCTTCGAT	AGATACTGTG	0		0	0	0	0	0
5161	2669	af	AN4333.1	58.m09007	AO070240000012	0			-173	-96			ATGATTCTTGCTCCTCCAGAAGGTATACAATGGACCTCTGATTGGCCAACATTAAGCGCCTCTTGGCATCAGCGATAA		ATGATTCTTGCTCCTCCAGAAGGTATACAATGGACCTCTGATTGGCCAACATTAAGCGCCTCTTGGCATCAGCGATAA		MILAPPEGIQWTSDWPTLSASWHQR*		MILAPPEGIQWTSDWPTLSASWHQR*		ACTGGCCAAA	GATCAGGAAT	0		0	0	NCU10035.1	0	0
5162	2669	af	AN4333.1	58.m09007	AO070240000012	0			-144	-133			ATGGACCTCTGA		ATGGACCTCTGA		MDL*		MDL*		AAGGTATACA	TTGGCCAACA	0		0	0	NCU10035.1	0	0
5163	2669	af	AN4333.1	58.m09007	AO070240000012	0			-85	-14			ATGGCCATCAGCCTCATCCACTTAGCTGTCATCCATCTCAAAGGACATGTGGCAGCCAGGTTGTTGAAATAA		ATGGCCATCAGCCTCATCCACTTAGCTGTCATCCATCTCAAAGGACATGTGGCAGCCAGGTTGTTGAAATAA		MAISLIHLAVIHLKGHVAARLLK*		MAISLIHLAVIHLKGHVAARLLK*		GATCAGGAAT	ATTGATGGGC	0		0	0	NCU10035.1	0	0
5159	2669	an	AN4333.1	58.m09007	AO070240000012	0	-161	-54					ATGTGCCTGGCAACCATACTACAGTTGCCTGAGGACCCTGGCCGAACAAAGCCCGCCAAACGGGTCTTGGCGCTTAAAGTCCCAAGACAGCTCATGCCAACTAACTAA	ATGTGCCTGGCAACCATACTACAGTTGCCTGAGGACCCTGGCCGAACAAAGCCCGCCAAACGGGTCTTGGCGCTTAAAGTCCCAAGACAGCTCATGCCAACTAACTAA			MCLATILQLPEDPGRTKPAKRVLALKVPRQLMPTN*	MCLATILQLPEDPGRTKPAKRVLALKVPRQLMPTN*			ACTACAGCGA	CCTTCCCCAA	0		0	0	NCU10035.1	0	0
5160	2669	an	AN4333.1	58.m09007	AO070240000012	0	-68	-54					ATGCCAACTAACTAA	ATGCCAACTAACTAA			MPTN*	MPTN*			AAGACAGCTC	CCTTCCCCAA	0		0	0	NCU10035.1	0	0
5168	2671	af	AN3144.1	59.m08521	AO070256000047	0			-201	-163			ATGGCCCGGATATTTCTGCCTCTATGCCTAAGGCATTAA		ATGGCCCGGATATTTCTGCCTCTATGCCTAAGGCATTAA		MARIFLPLCLRH*		MARIFLPLCLRH*		TGATGATTTG	ATATCTGCCT	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5169	2671	af	AN3144.1	59.m08521	AO070256000047	0			-178	-104			ATGCCTAAGGCATTAAATATCTGCCTCAGGCTAGTGCATTCCCCCTCAAATAAGCTCCGCAGCCTGATTGCCTGA		ATGCCTAAGGCATTAAATATCTGCCTCAGGCTAGTGCATTCCCCCTCAAATAAGCTCCGCAGCCTGATTGCCTGA		MPKALNICLRLVHSPSNKLRSLIA*		MPKALNICLRLVHSPSNKLRSLIA*		TTCTGCCTCT	GCTAGGCAGG	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5166	2671	an	AN3144.1	59.m08521	AO070256000047	0	-171	-154					ATGGGCGGATCACCATGA	ATGGGCGGATCACCATGA			MGGSP*	MGGSP*			CGCCCCCTCA	CCGATTAGCA	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5167	2671	an	AN3144.1	59.m08521	AO070256000047	0	-157	-146					ATGACCGATTAG	ATGACCGATTAG			MTD*	MTD*			GCGGATCACC	CAGGCGCTCC	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5170	2671	ao	AN3144.1	59.m08521	AO070256000047	0					-257	-12	ATGGATGTTTCTGCCTCAGGCATCATAGGGGATCCGCGCCCCTCATCAGCCAGGATCAGCTGCCTTACGTGCTACTTTACTCGCATCCCCAAAGCTCCGCCTCGATCCAGAACTGAAACATCACAGCTGCGCTGCATGCACGGCTGGTTGTCCCACTATTCCCTTTACTCTTCCCTTCTTCTACCTTCCCGCCCGGATCGCCTTATCTGCCGCTTTCCGCGGAATTTTCCTCCCATGCTCTACTAA			ATGGATGTTTCTGCCTCAGGCATCATAGGGGATCCGCGCCCCTCATCAGCCAGGATCAGCTGCCTTACGTGCTACTTTACTCGCATCCCCAAAGCTCCGCCTCGATCCAGAACTGAAACATCACAGCTGCGCTGCATGCACGGCTGGTTGTCCCACTATTCCCTTTACTCTTCCCTTCTTCTACCTTCCCGCCCGGATCGCCTTATCTGCCGCTTTCCGCGGAATTTTCCTCCCATGCTCTACTAA	MDVSASGIIGDPRPSSARISCLTCYFTRIPKAPPRSRTETSQLRCMHGWLSHYSLYSSLLLPSRPDRLICRFPRNFPPMLY*			MDVSASGIIGDPRPSSARISCLTCYFTRIPKAPPRSRTETSQLRCMHGWLSHYSLYSSLLLPSRPDRLICRFPRNFPPMLY*	TTCAAGTGCC	TCTGAGCCAA	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5171	2671	ao	AN3144.1	59.m08521	AO070256000047	0					-253	-230	ATGTTTCTGCCTCAGGCATCATAG			ATGTTTCTGCCTCAGGCATCATAG	MFLPQAS*			MFLPQAS*	AGTGCCATGG	GGGATCCGCG	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5172	2671	ao	AN3144.1	59.m08521	AO070256000047	0					-122	-12	ATGCACGGCTGGTTGTCCCACTATTCCCTTTACTCTTCCCTTCTTCTACCTTCCCGCCCGGATCGCCTTATCTGCCGCTTTCCGCGGAATTTTCCTCCCATGCTCTACTAA			ATGCACGGCTGGTTGTCCCACTATTCCCTTTACTCTTCCCTTCTTCTACCTTCCCGCCCGGATCGCCTTATCTGCCGCTTTCCGCGGAATTTTCCTCCCATGCTCTACTAA	MHGWLSHYSLYSSLLLPSRPDRLICRFPRNFPPMLY*			MHGWLSHYSLYSSLLLPSRPDRLICRFPRNFPPMLY*	GCTGCGCTGC	TCTGAGCCAA	0	R	FG04221.1	MG09837.1	0	YDR323C	0
5179	2672	af	AN5808.1	72.m18938	AO070260000039	0			-108	-28			ATGCAAAGAGTACAGTTTCATGCCAATTTTACTTCCTTCCATATCTCCAAAGTCTGGGCAAAGGACCTTCCCTCATTGTGA		ATGCAAAGAGTACAGTTTCATGCCAATTTTACTTCCTTCCATATCTCCAAAGTCTGGGCAAAGGACCTTCCCTCATTGTGA		MQRVQFHANFTSFHISKVWAKDLPSL*		MQRVQFHANFTSFHISKVWAKDLPSL*		TACTCAGCCC	TATGAAAGAA	0		0	0	0	0	0
5174	2672	an	AN5808.1	72.m18938	AO070260000039	0	-287	-120					ATGTTGACCTGGGCTACAGTGGCGTTCGCTGGTGCCTTGCCTACACATACAGCAATAATTACCGCAATTGTTCGAATATCTTACATCTTGCCCTTTCTACCGGGAAAATGCCTTAAATCTTGGAGCGTAAGTCCAAGACTGTGGAGCATTGCCGTGCGAAAACGCTGA	ATGTTGACCTGGGCTACAGTGGCGTTCGCTGGTGCCTTGCCTACACATACAGCAATAATTACCGCAATTGTTCGAATATCTTACATCTTGCCCTTTCTACCGGGAAAATGCCTTAAATCTTGGAGCGTAAGTCCAAGACTGTGGAGCATTGCCGTGCGAAAACGCTGA			MLTWATVAFAGALPTHTAIITAIVRISYILPFLPGKCLKSWSVSPRLWSIAVRKR*	MLTWATVAFAGALPTHTAIITAIVRISYILPFLPGKCLKSWSVSPRLWSIAVRKR*			GCAGTTACCC	TTTCGATGAT	0		0	0	0	0	0
5175	2672	an	AN5808.1	72.m18938	AO070260000039	0	-114	-70					ATGATATGCAAAGTTTACTTGATAAGACCAGAAGTCGCTTCTTGA	ATGATATGCAAAGTTTACTTGATAAGACCAGAAGTCGCTTCTTGA			MICKVYLIRPEVAS*	MICKVYLIRPEVAS*			GCTGATTTCG	ACTTTCGTAT	0		0	0	0	0	0
5176	2672	an	AN5808.1	72.m18938	AO070260000039	0	-109	-47					ATGCAAAGTTTACTTGATAAGACCAGAAGTCGCTTCTTGAACTTTCGTATCAACTCATCCTAA	ATGCAAAGTTTACTTGATAAGACCAGAAGTCGCTTCTTGAACTTTCGTATCAACTCATCCTAA			MQSLLDKTRSRFLNFRINSS*	MQSLLDKTRSRFLNFRINSS*			TTTCGATGAT	TCACACTTGG	0		0	0	0	0	0
5181	2672	ao	AN5808.1	72.m18938	AO070260000039	0					-258	-76	ATGATAATTAAGTGCTCAAATGAACTTCTGTCCTTATTTTCGTCCAATGCAGCTATGAGACACTCCACTGTTTATTTTGCATCAAATACCGTCGGTTATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG			ATGATAATTAAGTGCTCAAATGAACTTCTGTCCTTATTTTCGTCCAATGCAGCTATGAGACACTCCACTGTTTATTTTGCATCAAATACCGTCGGTTATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG	MIIKCSNELLSLFSSNAAMRHSTVYFASNTVGYGNPTAAYFTRPPHILMNNRQRTLKAVM*			MIIKCSNELLSLFSSNAAMRHSTVYFASNTVGYGNPTAAYFTRPPHILMNNRQRTLKAVM*	CCCCAGTATT	AATGTACCTG	0		0	0	0	0	0
5184	2672	ao	AN5808.1	72.m18938	AO070260000039	0					-204	-76	ATGAGACACTCCACTGTTTATTTTGCATCAAATACCGTCGGTTATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG			ATGAGACACTCCACTGTTTATTTTGCATCAAATACCGTCGGTTATGGTAATCCAACTGCTGCTTACTTCACTCGTCCCCCACACATACTGATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG	MRHSTVYFASNTVGYGNPTAAYFTRPPHILMNNRQRTLKAVM*			MRHSTVYFASNTVGYGNPTAAYFTRPPHILMNNRQRTLKAVM*	CAATGCAGCT	AATGTACCTG	0		0	0	0	0	0
5186	2672	ao	AN5808.1	72.m18938	AO070260000039	0					-114	-76	ATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG			ATGAACAACAGACAACGGACGTTGAAGGCTGTCATGTAG	MNNRQRTLKAVM*			MNNRQRTLKAVM*	ACACATACTG	AATGTACCTG	0		0	0	0	0	0
5187	2672	ao	AN5808.1	72.m18938	AO070260000039	0					-74	-18	ATGTACCTGCTTTCAGAAGACCGACTGTTTCTGCTTCGCATCCAATTTATGTTGTAG			ATGTACCTGCTTTCAGAAGACCGACTGTTTCTGCTTCGCATCCAATTTATGTTGTAG	MYLLSEDRLFLLRIQFML*			MYLLSEDRLFLLRIQFML*	GTCATGTAGA	TATCTCGGTT	0		0	0	0	0	0
5190	2673	ao	AN3439.1	59.m09299	AO070265000013	0					-66	-13	ATGCTACCCTGCCCTTCCTCAGTCCATTTATTCCGTGTCCCAGCGCTTTTTTAA			ATGCTACCCTGCCCTTCCTCAGTCCATTTATTCCGTGTCCCAGCGCTTTTTTAA	MLPCPSSVHLFRVPALF*			MLPCPSSVHLFRVPALF*	ATAAAGATAC	AACTGCGCAA	0	S	0	0	0	0	0
5191	2677	af	AN8369.1	58.m07277	AO070281000009	0			-159	-148			ATGTATCATTGA		ATGTATCATTGA		MYH*		MYH*		TATCATAGAG	GTTCCATCAG	0	M	0	0	0	0	0
5192	2677	af	AN8369.1	58.m07277	AO070281000009	0			-63	-52			ATGCACCTGTAG		ATGCACCTGTAG		MHL*		MHL*		CCGCACGCCC	TCTTCTGCAT	0	M	0	0	0	0	0
5193	2677	ao	AN8369.1	58.m07277	AO070281000009	0					-109	-98	ATGTTAACATAG			ATGTTAACATAG	MLT*			MLT*	GCACTGTATC	TAGTAGAAAA	0	M	0	0	0	0	0
5200	2681	af	AN1570.1	66.m04699	AO070290000058	0			-120	-67			ATGTCACTCCACTATCAGACTTCCCGGCACATTCCACCTACAAAAGGACTGTAG		ATGTCACTCCACTATCAGACTTCCCGGCACATTCCACCTACAAAAGGACTGTAG		MSLHYQTSRHIPPTKGL*		MSLHYQTSRHIPPTKGL*		GCAGTGACTG	TGTATTGTAC	0	C	0	0	0	0	0
5197	2681	an	AN1570.1	66.m04699	AO070290000058	0	-212	-162					ATGCCTACCGGACTTGGCAAACGGGAATTGGCCTTCCCTGCCCGGAGATGA	ATGCCTACCGGACTTGGCAAACGGGAATTGGCCTTCCCTGCCCGGAGATGA			MPTGLGKRELAFPARR*	MPTGLGKRELAFPARR*			TATAAAGGTT	TTTCATCGTG	0	C	0	0	0	0	0
5198	2681	an	AN1570.1	66.m04699	AO070290000058	0	-165	-106					ATGATTTCATCGTGCGGGGACTCCGAGGAAGCAGCGGAACAACCGATAAAGTCCGGCTAA	ATGATTTCATCGTGCGGGGACTCCGAGGAAGCAGCGGAACAACCGATAAAGTCCGGCTAA			MISSCGDSEEAAEQPIKSG*	MISSCGDSEEAAEQPIKSG*			CTGCCCGGAG	GTCCGCATAC	0	C	0	0	0	0	0
5199	2681	an	AN1570.1	66.m04699	AO070290000058	0	-70	-20					ATGATAGTCCTTCGTCGTCTTATCTTCCCACAGTATTCTCAGCTCAGTTGA	ATGATAGTCCTTCGTCGTCTTATCTTCCCACAGTATTCTCAGCTCAGTTGA			MIVLRRLIFPQYSQLS*	MIVLRRLIFPQYSQLS*			AAAGAACCGA	TTCCTCGTAT	0	C	0	0	0	0	0
5201	2681	ao	AN1570.1	66.m04699	AO070290000058	0					-214	-137	ATGCTGGACTCAATCAATGTCTGGCGGTCCGTCGGATGCCCGGATAAACGGTGTAGATCGACGGAGTTATGCGGGTAA			ATGCTGGACTCAATCAATGTCTGGCGGTCCGTCGGATGCCCGGATAAACGGTGTAGATCGACGGAGTTATGCGGGTAA	MLDSINVWRSVGCPDKRCRSTELCG*			MLDSINVWRSVGCPDKRCRSTELCG*	CTGCTCCGGA	AGTCCTATGT	0	C	0	0	0	0	0

5202	2681	ao	AN1570.1	66.m04699	AO070290000058	0					-198	-91	ATGTCTGGCGGTCCGTCGGATGCCCGGATAAACGGTGTAGATCGACGGAGTTATGCGGGTAAAGTCCTATGTCCGCCAATACTATCATCGACCGCAAAGTATAAATAA			ATGTCTGGCGGTCCGTCGGATGCCCGGATAAACGGTGTAGATCGACGGAGTTATGCGGGTAAAGTCCTATGTCCGCCAATACTATCATCGACCGCAAAGTATAAATAA	MSGGPSDARINGVDRRSYAGKVLCPPILSSTAKYK*			MSGGPSDARINGVDRRSYAGKVLCPPILSSTAKYK*	GACTCAATCA	GAGGAGTAAG	0	C	0	0	0	0	0
5203	2681	ao	AN1570.1	66.m04699	AO070290000058	0					-179	-168	ATGCCCGGATAA			ATGCCCGGATAA	MPG*			MPG*	GGTCCGTCGG	ACGGTGTAGA	0	C	0	0	0	0	0
5204	2681	ao	AN1570.1	66.m04699	AO070290000058	0					-130	-95	ATGTCCGCCAATACTATCATCGACCGCAAAGTATAA			ATGTCCGCCAATACTATCATCGACCGCAAAGTATAA	MSANTIIDRKV*			MSANTIIDRKV*	GTAAAGTCCT	ATAAGAGGAG	0	C	0	0	0	0	0
5208	2682	af	AN7636.1	57.m05400	AO070294000081	0			-193	-50			ATGGGACAAAGTTTACTGCAGAGAATGGAAAAAACTGTCGGATATCTCCAAGACTCCAAGACTCCAACTGCGGGGCGACTCCACAATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGAACCTCGAAAGATTTTGA		ATGGGACAAAGTTTACTGCAGAGAATGGAAAAAACTGTCGGATATCTCCAAGACTCCAAGACTCCAACTGCGGGGCGACTCCACAATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGAACCTCGAAAGATTTTGA		MGQSLLQRMEKTVGYLQDSKTPTAGRLHNDALFQHILSHRQLNLERF*		MGQSLLQRMEKTVGYLQDSKTPTAGRLHNDALFQHILSHRQLNLERF*		GTCAACGGCA	GGTTCTGGGG	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5209	2682	af	AN7636.1	57.m05400	AO070294000081	0			-169	-50			ATGGAAAAAACTGTCGGATATCTCCAAGACTCCAAGACTCCAACTGCGGGGCGACTCCACAATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGAACCTCGAAAGATTTTGA		ATGGAAAAAACTGTCGGATATCTCCAAGACTCCAAGACTCCAACTGCGGGGCGACTCCACAATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGAACCTCGAAAGATTTTGA		MEKTVGYLQDSKTPTAGRLHNDALFQHILSHRQLNLERF*		MEKTVGYLQDSKTPTAGRLHNDALFQHILSHRQLNLERF*		ACTGCAGAGA	GGTTCTGGGG	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5210	2682	af	AN7636.1	57.m05400	AO070294000081	0			-108	-67			ATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGA		ATGACGCACTTTTCCAGCATATTCTTTCTCACCGTCAACTGA		MTHFSSIFFLTVN*		MTHFSSIFFLTVN*		CGACTCCACA	ACCTCGAAAG	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5205	2682	an	AN7636.1	57.m05400	AO070294000081	0	-232	-203					ATGAGTACATGCTCAGTCAGGTACAACTGA	ATGAGTACATGCTCAGTCAGGTACAACTGA			MSTCSVRYN*	MSTCSVRYN*			CTATATGCTC	ACCTGCGCCG	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5206	2682	an	AN7636.1	57.m05400	AO070294000081	0	-224	-45					ATGCTCAGTCAGGTACAACTGAACCTGCGCCGACGGTTCCGAGACCTTCTTGGGTCGTTGTTGATTCTGGTTCTGTGGGGCGTGCAGCTCCGGCGACGATTATTAATGGAGTGCTCTAGTGGACCATTTAAATGTGAGGTCATTCCTTATCTTGAACTGTTTTCTGCCGTTGAGGGGTAG	ATGCTCAGTCAGGTACAACTGAACCTGCGCCGACGGTTCCGAGACCTTCTTGGGTCGTTGTTGATTCTGGTTCTGTGGGGCGTGCAGCTCCGGCGACGATTATTAATGGAGTGCTCTAGTGGACCATTTAAATGTGAGGTCATTCCTTATCTTGAACTGTTTTCTGCCGTTGAGGGGTAG			MLSQVQLNLRRRFRDLLGSLLILVLWGVQLRRRLLMECSSGPFKCEVIPYLELFSAVEG*	MLSQVQLNLRRRFRDLLGSLLILVLWGVQLRRRLLMECSSGPFKCEVIPYLELFSAVEG*			TCATGAGTAC	GTAGCTCGTC	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5207	2682	an	AN7636.1	57.m05400	AO070294000081	0	-119	-45					ATGGAGTGCTCTAGTGGACCATTTAAATGTGAGGTCATTCCTTATCTTGAACTGTTTTCTGCCGTTGAGGGGTAG	ATGGAGTGCTCTAGTGGACCATTTAAATGTGAGGTCATTCCTTATCTTGAACTGTTTTCTGCCGTTGAGGGGTAG			MECSSGPFKCEVIPYLELFSAVEG*	MECSSGPFKCEVIPYLELFSAVEG*			ACGATTATTA	GTAGCTCGTC	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5211	2682	ao	AN7636.1	57.m05400	AO070294000081	0					-215	-144	ATGCCATGCCATACGCTGGGAAGGTCGCGATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGA			ATGCCATGCCATACGCTGGGAAGGTCGCGATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGA	MPCHTLGRSRWVSAFFAVGHSPP*			MPCHTLGRSRWVSAFFAVGHSPP*	CTTCTCCAAA	CGTCGAGACA	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5212	2682	ao	AN7636.1	57.m05400	AO070294000081	0					-210	-127	ATGCCATACGCTGGGAAGGTCGCGATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGACGTCGAGACATTATTAA			ATGCCATACGCTGGGAAGGTCGCGATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGACGTCGAGACATTATTAA	MPYAGKVAMGLGILRSGALPTVTSRHY*			MPYAGKVAMGLGILRSGALPTVTSRHY*	CCAAAATGCC	TCGTCTCCAA	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5213	2682	ao	AN7636.1	57.m05400	AO070294000081	0					-186	-127	ATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGACGTCGAGACATTATTAA			ATGGGTCTCGGCATTCTTCGCAGTGGGGCACTCCCCACCGTGACGTCGAGACATTATTAA	MGLGILRSGALPTVTSRHY*			MGLGILRSGALPTVTSRHY*	GAAGGTCGCG	TCGTCTCCAA	0	CR	FG01630.1	MG07773.1	NCU06303.1	0	0
5214	2683	ao	AN5625.1	58.m07547	AO070301000023	0					-187	-119	ATGTGGCCGAAAGACCAACAACATCATACGCAACAGGTCGTTATCTATAAGGCTGTGCCAACTCACTAG			ATGTGGCCGAAAGACCAACAACATCATACGCAACAGGTCGTTATCTATAAGGCTGTGCCAACTCACTAG	MWPKDQQHHTQQVVIYKAVPTH*			MWPKDQQHHTQQVVIYKAVPTH*	AATCACTTTC	CTGGTATAGC	0	B	0	0	0	0	0
5215	2684	an	AN1969.1	58.m07574	AO070301000053	0	-151	-110					ATGATCCCAGCGGGACTGAGCCTTGTTATCCGCATCCGGTAG	ATGATCCCAGCGGGACTGAGCCTTGTTATCCGCATCCGGTAG			MIPAGLSLVIRIR*	MIPAGLSLVIRIR*			CGGTCCAAGG	TAGTATCATG	0	GM	FG04412.1	0	0	0	0
5216	2684	an	AN1969.1	58.m07574	AO070301000053	0	-102	-73					ATGTCGGCTGAAGCTTTGCTTCACTTCTGA	ATGTCGGCTGAAGCTTTGCTTCACTTCTGA			MSAEALLHF*	MSAEALLHF*			TAGTAGTATC	CTCCCACTTC	0	GM	FG04412.1	0	0	0	0
5217	2684	ao	AN1969.1	58.m07574	AO070301000053	0					-234	-205	ATGAAATTACCTCAGGAATGTCTTGGATAA			ATGAAATTACCTCAGGAATGTCTTGGATAA	MKLPQECLG*			MKLPQECLG*	ACAACCAACT	TATGTCGGGC	0	GM	FG04412.1	0	0	0	0
5218	2684	ao	AN1969.1	58.m07574	AO070301000053	0					-217	-152	ATGTCTTGGATAATATGTCGGGCCGTTTATGATCCGCATTTAATTTCCGGATGCGGCAGATACTAG			ATGTCTTGGATAATATGTCGGGCCGTTTATGATCCGCATTTAATTTCCGGATGCGGCAGATACTAG	MSWIICRAVYDPHLISGCGRY*			MSWIICRAVYDPHLISGCGRY*	TACCTCAGGA	ATAAGACCGT	0	GM	FG04412.1	0	0	0	0
5219	2684	ao	AN1969.1	58.m07574	AO070301000053	0					-203	-186	ATGTCGGGCCGTTTATGA			ATGTCGGGCCGTTTATGA	MSGRL*			MSGRL*	CTTGGATAAT	TCCGCATTTA	0	GM	FG04412.1	0	0	0	0
5220	2684	ao	AN1969.1	58.m07574	AO070301000053	0					-189	-175	ATGATCCGCATTTAA			ATGATCCGCATTTAA	MIRI*			MIRI*	CGGGCCGTTT	TTTCCGGATG	0	GM	FG04412.1	0	0	0	0
5221	2684	ao	AN1969.1	58.m07574	AO070301000053	0					-167	-69	ATGCGGCAGATACTAGATAAGACCGTTCCAGAAGTACTGCAACGCTGCAAACTACATTTCCACTCAGCCCAGGGTGTACTTCCTACTAGAATGCACTGA			ATGCGGCAGATACTAGATAAGACCGTTCCAGAAGTACTGCAACGCTGCAAACTACATTTCCACTCAGCCCAGGGTGTACTTCCTACTAGAATGCACTGA	MRQILDKTVPEVLQRCKLHFHSAQGVLPTRMH*			MRQILDKTVPEVLQRCKLHFHSAQGVLPTRMH*	TAATTTCCGG	TCGATAGTTT	0	GM	FG04412.1	0	0	0	0
5224	2685	af	AN3971.1	70.m15745	AO070303000052	0			-213	-145			ATGTTAGCTGGTCACCAAGGCAGAGATTTTGTACGTCGAACTGACGTTACTTTAAGATCACGGCTTTGA		ATGTTAGCTGGTCACCAAGGCAGAGATTTTGTACGTCGAACTGACGTTACTTTAAGATCACGGCTTTGA		MLAGHQGRDFVRRTDVTLRSRL*		MLAGHQGRDFVRRTDVTLRSRL*		CTCTGGCCTG	TTTCCTGCCT	0	R	0	0	0	0	0
5222	2685	an	AN3971.1	70.m15745	AO070303000052	0	-156	-130					ATGTTCATGCTGTATACATCAGTTTGA	ATGTTCATGCTGTATACATCAGTTTGA			MFMLYTSV*	MFMLYTSV*			ACACAACGTC	CGTCAACACC	0	R	0	0	0	0	0
5223	2685	an	AN3971.1	70.m15745	AO070303000052	0	-150	-130					ATGCTGTATACATCAGTTTGA	ATGCTGTATACATCAGTTTGA			MLYTSV*	MLYTSV*			CGTCATGTTC	CGTCAACACC	0	R	0	0	0	0	0
5225	2685	ao	AN3971.1	70.m15745	AO070303000052	0					-131	-114	ATGGACATTCTTGACTAG			ATGGACATTCTTGACTAG	MDILD*			MDILD*	TCCTATTAAA	ACCTGCTCCA	0	R	0	0	0	0	0
5226	2685	ao	AN3971.1	70.m15745	AO070303000052	0					-101	-87	ATGAAATATATATAG			ATGAAATATATATAG	MKYI*			MKYI*	CTGCTCCAGT	AGGACATTGT	0	R	0	0	0	0	0
5227	2686	af	AN2812.1	52.m03911	AO070303000084	0			-214	-92			ATGTGGACTGCTTTGGATCTGGTTCGTACGCCTCTCGCACGTTTTTTTCCTTTTTCTTTTTCTTTTTTTCTTGGAAAGGCCTGCCTCTACGAAGCCGATGGCAGCTGTGTGCTAAGTATATAA		ATGTGGACTGCTTTGGATCTGGTTCGTACGCCTCTCGCACGTTTTTTTCCTTTTTCTTTTTCTTTTTTTCTTGGAAAGGCCTGCCTCTACGAAGCCGATGGCAGCTGTGTGCTAAGTATATAA		MWTALDLVRTPLARFFPFSFSFFLGKACLYEADGSCVLSI*		MWTALDLVRTPLARFFPFSFSFFLGKACLYEADGSCVLSI*		TAGCGAAGGG	GCACTATGCA	0	P	0	0	0	0	0
5228	2686	af	AN2812.1	52.m03911	AO070303000084	0			-117	-100			ATGGCAGCTGTGTGCTAA		ATGGCAGCTGTGTGCTAA		MAAVC*		MAAVC*		TACGAAGCCG	GTATATAAGC	0	P	0	0	0	0	0
5229	2686	af	AN2812.1	52.m03911	AO070303000084	0			-86	-24			ATGCACGCTGCAATACTAGCATGGGGAACGATCTTCTCTGCAAGTTGTAAGGACACGATATAG		ATGCACGCTGCAATACTAGCATGGGGAACGATCTTCTCTGCAAGTTGTAAGGACACGATATAG		MHAAILAWGTIFSASCKDTI*		MHAAILAWGTIFSASCKDTI*		TATAAGCACT	GATATCCAAC	0	P	0	0	0	0	0
5230	2686	af	AN2812.1	52.m03911	AO070303000084	0			-66	-37			ATGGGGAACGATCTTCTCTGCAAGTTGTAA		ATGGGGAACGATCTTCTCTGCAAGTTGTAA		MGNDLLCKL*		MGNDLLCKL*		CAATACTAGC	GGACACGATA	0	P	0	0	0	0	0
5231	2686	ao	AN2812.1	52.m03911	AO070303000084	0					-253	-41	ATGAATGGACTGACCTCGCCTAATGTTACATGGAGGGTGGGCGGATGCTGTCAAAGAGTATGGAAACGCTGGGCAATCGTATTAGGGTTTGGCCTAGGTTTCTTATCCTACTTCTCGCCCGTAAGAAATCGCCAATGGTATATAAAAGAGCCTTGCACACCCCTCTGCTTGTGGGGAAAAACGGACTACGGTGCTGGAATATCTGTAGCTTGA			ATGAATGGACTGACCTCGCCTAATGTTACATGGAGGGTGGGCGGATGCTGTCAAAGAGTATGGAAACGCTGGGCAATCGTATTAGGGTTTGGCCTAGGTTTCTTATCCTACTTCTCGCCCGTAAGAAATCGCCAATGGTATATAAAAGAGCCTTGCACACCCCTCTGCTTGTGGGGAAAAACGGACTACGGTGCTGGAATATCTGTAGCTTGA	MNGLTSPNVTWRVGGCQRVWKRWAIVLGFGLGFLSYFSPVRNRQWYIKEPCTPLCLWGKTDYGAGISVA*			MNGLTSPNVTWRVGGCQRVWKRWAIVLGFGLGFLSYFSPVRNRQWYIKEPCTPLCLWGKTDYGAGISVA*	CAATTCGCGA	CTCAAGACCA	0	P	0	0	0	0	0
5232	2686	ao	AN2812.1	52.m03911	AO070303000084	0					-231	-169	ATGTTACATGGAGGGTGGGCGGATGCTGTCAAAGAGTATGGAAACGCTGGGCAATCGTATTAG			ATGTTACATGGAGGGTGGGCGGATGCTGTCAAAGAGTATGGAAACGCTGGGCAATCGTATTAG	MLHGGWADAVKEYGNAGQSY*			MLHGGWADAVKEYGNAGQSY*	ACCTCGCCTA	GGTTTGGCCT	0	P	0	0	0	0	0
5235	2687	af	AN6229.1	72.m19424	AO070304000080	0			-103	-29			ATGGGCGTTGGGGTAGAATTTCCAAACCTCAAATTTCCATTTCTCTCGTCTATCGCTGCTGATTATACGTACTGA		ATGGGCGTTGGGGTAGAATTTCCAAACCTCAAATTTCCATTTCTCTCGTCTATCGCTGCTGATTATACGTACTGA		MGVGVEFPNLKFPFLSSIAADYTY*		MGVGVEFPNLKFPFLSSIAADYTY*		CTGATCATCG	ACTGATAGAC	0	CR	0	0	0	0	0
5233	2687	an	AN6229.1	72.m19424	AO070304000080	0	-215	-201					ATGCTGTTCATATAA	ATGCTGTTCATATAA			MLFI*	MLFI*			TATTTGCAGC	AGTGTGACTG	0	CR	0	0	0	0	0
5234	2687	an	AN6229.1	72.m19424	AO070304000080	0	-178	-155					ATGTCCTCTTGTGATCAGTATTGA	ATGTCCTCTTGTGATCAGTATTGA			MSSCDQY*	MSSCDQY*			AACGGGGAAC	GGCCGGACAG	0	CR	0	0	0	0	0
5239	2688	af	AN6182.1	72.m19274	AO070308000124	0			-204	-109			ATGAATGGAACCAAAATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGACCGGTCTCCTGGTTGGGCAGTGCCATTGA		ATGAATGGAACCAAAATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGACCGGTCTCCTGGTTGGGCAGTGCCATTGA		MNGTKMDRGETPRQLFRSPAALTGLLVGQCH*		MNGTKMDRGETPRQLFRSPAALTGLLVGQCH*		GCGCGCTCAA	ACCATCTCTC	0	C	FG05668.1	MG05098.1	0	0	0
5240	2688	af	AN6182.1	72.m19274	AO070308000124	0			-200	-138			ATGGAACCAAAATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGA		ATGGAACCAAAATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGA		MEPKWTGGRPRDNFSGAPPH*		MEPKWTGGRPRDNFSGAPPH*		GCTCAAATGA	CCGGTCTCCT	0	C	FG05668.1	MG05098.1	0	0	0
5241	2688	af	AN6182.1	72.m19274	AO070308000124	0			-189	-109			ATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGACCGGTCTCCTGGTTGGGCAGTGCCATTGA		ATGGACCGGGGGGAGACCCCGCGACAACTTTTCCGGAGCCCCGCCGCATTGACCGGTCTCCTGGTTGGGCAGTGCCATTGA		MDRGETPRQLFRSPAALTGLLVGQCH*		MDRGETPRQLFRSPAALTGLLVGQCH*		TGGAACCAAA	ACCATCTCTC	0	C	FG05668.1	MG05098.1	0	0	0
5236	2688	an	AN6182.1	72.m19274	AO070308000124	0	-169	-32					ATGCCCCTCCGCGCCCGGAAGAATTCACCTCTCGGTTCCCCGCGGTCTTCACCTCCACATGTCCTTAAACCCAAGGGCTCGCCCTTAATAAATTCTCTCCTCTCAATTAGTCACTCCTCTTCCCCTACTGTATCTTGA	ATGCCCCTCCGCGCCCGGAAGAATTCACCTCTCGGTTCCCCGCGGTCTTCACCTCCACATGTCCTTAAACCCAAGGGCTCGCCCTTAATAAATTCTCTCCTCTCAATTAGTCACTCCTCTTCCCCTACTGTATCTTGA			MPLRARKNSPLGSPRSSPPHVLKPKGSPLINSLLSISHSSSPTVS*	MPLRARKNSPLGSPRSSPPHVLKPKGSPLINSLLSISHSSSPTVS*			ATGACAGGAA	TGTTAATTCA	0	C	FG05668.1	MG05098.1	0	0	0
5237	2688	an	AN6182.1	72.m19274	AO070308000124	0	-111	-82					ATGTCCTTAAACCCAAGGGCTCGCCCTTAA	ATGTCCTTAAACCCAAGGGCTCGCCCTTAA			MSLNPRARP*	MSLNPRARP*			TCACCTCCAC	TAAATTCTCT	0	C	FG05668.1	MG05098.1	0	0	0
5242	2688	ao	AN6182.1	72.m19274	AO070308000124	0					-138	-55	ATGTGCCCCGCCGCCGTCGCTTCATCTTCGCTGACTTTCTCTCCTACCTTTTTCTTCCCCTCTTTTCTTCTCTTCTTCCTGTAG			ATGTGCCCCGCCGCCGTCGCTTCATCTTCGCTGACTTTCTCTCCTACCTTTTTCTTCCCCTCTTTTCTTCTCTTCTTCCTGTAG	MCPAAVASSSLTFSPTFFFPSFLLFFL*			MCPAAVASSSLTFSPTFFFPSFLLFFL*	GAAACAGACC	CTTGCCCTTC	0	C	FG05668.1	MG05098.1	0	0	0
5244	2691	af	AN9522.1	53.m04094	AO070310000070	0			-114	-37			ATGCACATCGCGCCGCAGGCCAGCGGGTTGGCTACATCTGTTATTCCCTATCGAGGTTTCTCGGGATTGGACGTCTAG		ATGCACATCGCGCCGCAGGCCAGCGGGTTGGCTACATCTGTTATTCCCTATCGAGGTTTCTCGGGATTGGACGTCTAG		MHIAPQASGLATSVIPYRGFSGLDV*		MHIAPQASGLATSVIPYRGFSGLDV*		AACCATCATC	TGACAGATCA	0	I	FG07173.1	MG09516.1	0	0	0
5243	2691	an	AN9522.1	53.m04094	AO070310000070	0	-200	-135					ATGATCAGCCTCGCTAGAGCGGTACTCCTTAGAAGAGGGTTTTGTCCCACGGTCCGGGGTAGATAG	ATGATCAGCCTCGCTAGAGCGGTACTCCTTAGAAGAGGGTTTTGTCCCACGGTCCGGGGTAGATAG			MISLARAVLLRRGFCPTVRGR*	MISLARAVLLRRGFCPTVRGR*			ACCGATATCG	ATATTCCCCG	0	I	FG07173.1	MG09516.1	0	0	0
5248	2696	af	AN2359.1	70.m15643	AO070318000132	0			-213	-193			ATGTGGGGGAAGTCGGGGTAA		ATGTGGGGGAAGTCGGGGTAA		MWGKSG*		MWGKSG*		GGGCATCCGC	CAAGTCCAGA	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5249	2696	af	AN2359.1	70.m15643	AO070318000132	0			-153	-79			ATGGGGTACAAGATGCCGACTATCGAGGAGGACAGACAGAACCCATTCTGCCGGTGTTGCCGAAGCATACTATAA		ATGGGGTACAAGATGCCGACTATCGAGGAGGACAGACAGAACCCATTCTGCCGGTGTTGCCGAAGCATACTATAA		MGYKMPTIEEDRQNPFCRCCRSIL*		MGYKMPTIEEDRQNPFCRCCRSIL*		CGCGGCATTG	CTATAAATTC	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5250	2696	af	AN2359.1	70.m15643	AO070318000132	0			-141	-79			ATGCCGACTATCGAGGAGGACAGACAGAACCCATTCTGCCGGTGTTGCCGAAGCATACTATAA		ATGCCGACTATCGAGGAGGACAGACAGAACCCATTCTGCCGGTGTTGCCGAAGCATACTATAA		MPTIEEDRQNPFCRCCRSIL*		MPTIEEDRQNPFCRCCRSIL*		GGGGTACAAG	CTATAAATTC	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5245	2696	an	AN2359.1	70.m15643	AO070318000132	0	-187	-41					ATGCCGGTATCCTTGGATCACCGGCGGGCGAGATGGCGATCGTCACTGCGTGAGCTGGAGCTCCCTTTATCCATCGGCAATAGTCCGGGACATTATGACAATAAGCAAGGTATAAGAAACGCTCGACGCTCGCGGCAGTCACAGTAG	ATGCCGGTATCCTTGGATCACCGGCGGGCGAGATGGCGATCGTCACTGCGTGAGCTGGAGCTCCCTTTATCCATCGGCAATAGTCCGGGACATTATGACAATAAGCAAGGTATAAGAAACGCTCGACGCTCGCGGCAGTCACAGTAG			MPVSLDHRRARWRSSLRELELPLSIGNSPGHYDNKQGIRNARRSRQSQ*	MPVSLDHRRARWRSSLRELELPLSIGNSPGHYDNKQGIRNARRSRQSQ*			GCATCTCCAA	CGGACCAGAG	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0

5246	2696	an	AN2359.1	70.m15643	AO070318000132	0	-155	-135					ATGGCGATCGTCACTGCGTGA	ATGGCGATCGTCACTGCGTGA			MAIVTA*	MAIVTA*			GGCGGGCGAG	GCTGGAGCTC	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5247	2696	an	AN2359.1	70.m15643	AO070318000132	0	-93	-73					ATGACAATAAGCAAGGTATAA	ATGACAATAAGCAAGGTATAA			MTISKV*	MTISKV*			CCGGGACATT	GAAACGCTCG	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5251	2696	ao	AN2359.1	70.m15643	AO070318000132	0					-184	-140	ATGTTGGAGATGCTGCGGCAATGCCGACTTTTTATCCAGAGATAG			ATGTTGGAGATGCTGCGGCAATGCCGACTTTTTATCCAGAGATAG	MLEMLRQCRLFIQR*			MLEMLRQCRLFIQR*	TGAAGTCAAA	ATGACGTACA	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5252	2696	ao	AN2359.1	70.m15643	AO070318000132	0					-175	-140	ATGCTGCGGCAATGCCGACTTTTTATCCAGAGATAG			ATGCTGCGGCAATGCCGACTTTTTATCCAGAGATAG	MLRQCRLFIQR*			MLRQCRLFIQR*	AATGTTGGAG	ATGACGTACA	0	G	FG07993.1	MG08985.1	NCU09923.1	0	0
5254	2698	af	AN0942.1	70.m15574	AO070320000137	0			-244	-230			ATGGATCTTCGATAA		ATGGATCTTCGATAA		MDLR*		MDLR*		CTGGCCACCT	CCATAGTAAT	0	Q	0	MG01231.1	NCU00643.1	0	0
5255	2698	af	AN0942.1	70.m15574	AO070320000137	0			-218	-186			ATGGAGGATTATCATTCGGCCAGCGGTATCTGA		ATGGAGGATTATCATTCGGCCAGCGGTATCTGA		MEDYHSASGI*		MEDYHSASGI*		CATAGTAATC	ATATCCATCA	0	Q	0	MG01231.1	NCU00643.1	0	0
5256	2698	af	AN0942.1	70.m15574	AO070320000137	0			-176	-150			ATGAACTTTGTGTACTCTTTTCCTTAG		ATGAACTTTGTGTACTCTTTTCCTTAG		MNFVYSFP*		MNFVYSFP*		AATATCCATC	AGGGGCAACC	0	Q	0	MG01231.1	NCU00643.1	0	0
5253	2698	an	AN0942.1	70.m15574	AO070320000137	0	-136	-8					ATGGAGGGGCAGGTATTTAATCTGGTTGTACCCCAACTTAGATCTCCCAACCTTTACTCTCTTCACCTCTCCTCGCTCTCGTTCTTCGGTCTGCGTGTTTTCAACTCCTCCAACCGCGGACTCTCCTGA	ATGGAGGGGCAGGTATTTAATCTGGTTGTACCCCAACTTAGATCTCCCAACCTTTACTCTCTTCACCTCTCCTCGCTCTCGTTCTTCGGTCTGCGTGTTTTCAACTCCTCCAACCGCGGACTCTCCTGA			MEGQVFNLVVPQLRSPNLYSLHLSSLSFFGLRVFNSSNRGLS*	MEGQVFNLVVPQLRSPNLYSLHLSSLSFFGLRVFNSSNRGLS*			CCCGTACAAC	TTGAAACATG	0	Q	0	MG01231.1	NCU00643.1	0	0
5257	2698	ao	AN0942.1	70.m15574	AO070320000137	0					-249	-220	ATGGAAAATGGAGCAGTGGTATCGGTTTGA			ATGGAAAATGGAGCAGTGGTATCGGTTTGA	MENGAVVSV*			MENGAVVSV*	AAGATGGAGC	CGGTTGACCG	0	Q	0	MG01231.1	NCU00643.1	0	0
5258	2698	ao	AN0942.1	70.m15574	AO070320000137	0					-242	-213	ATGGAGCAGTGGTATCGGTTTGACGGTTGA			ATGGAGCAGTGGTATCGGTTTGACGGTTGA	MEQWYRFDG*			MEQWYRFDG*	AGCATGGAAA	CCGTCTTTCG	0	Q	0	MG01231.1	NCU00643.1	0	0
5259	2698	ao	AN0942.1	70.m15574	AO070320000137	0					-181	-161	ATGCAAGCTGGGTCTGATTAA			ATGCAAGCTGGGTCTGATTAA	MQAGSD*			MQAGSD*	CTCAGTGACA	AAAAAAAAAT	0	Q	0	MG01231.1	NCU00643.1	0	0
5260	2698	ao	AN0942.1	70.m15574	AO070320000137	0					-143	-102	ATGCTCCGTCTTGGAGGGGTAGCTCCGTCGGGCAGCTATTAA			ATGCTCCGTCTTGGAGGGGTAGCTCCGTCGGGCAGCTATTAA	MLRLGGVAPSGSY*			MLRLGGVAPSGSY*	AATATTCTCA	AGCTTGTTGG	0	Q	0	MG01231.1	NCU00643.1	0	0
5262	2703	af	AN7707.1	71.m16102	AO070325000113	0			-248	-183			ATGCCGAATCCAGCCACCTTCAAATTGGTCTGTGGTGAAGATCTTGCCCTTTCCATCCCAGGCTAG		ATGCCGAATCCAGCCACCTTCAAATTGGTCTGTGGTGAAGATCTTGCCCTTTCCATCCCAGGCTAG		MPNPATFKLVCGEDLALSIPG*		MPNPATFKLVCGEDLALSIPG*		ATCTCCATCG	TTTATCGGGG	0	Z	FG07284.1	0	0	0	0
5263	2703	af	AN7707.1	71.m16102	AO070325000113	0			-110	-93			ATGAACGTTCGTTCTTAA		ATGAACGTTCGTTCTTAA		MNVRS*		MNVRS*		TTTTCAATTC	CACTGACAAG	0	Z	FG07284.1	0	0	0	0
5261	2703	an	AN7707.1	71.m16102	AO070325000113	0	-151	-107					ATGAAGATCTTGCCCATTTTATCCCGGCGATCCCTCTATCAATAG	ATGAAGATCTTGCCCATTTTATCCCGGCGATCCCTCTATCAATAG			MKILPILSRRSLYQ*	MKILPILSRRSLYQ*			TCTCATTTCT	AAATCTAGCA	0	Z	FG07284.1	0	0	0	0
5272	2712	af	AN5440.1	69.m15495	AO070333000102	0			-207	-193			ATGTGCGACAACTGA		ATGTGCGACAACTGA		MCDN*		MCDN*		TTTGTCCTTC	CAAGAAAAAG	0	P	0	0	0	0	0
5273	2712	af	AN5440.1	69.m15495	AO070333000102	0			-177	-52			ATGCCTCCCAGGCTCGGTGACCTTGACCTTCTTTTCTCTCCTTCATTGTCCATTCTTTACCTTTTGACGATCGATACCCGTCGTGTTCTGTCTCTCTTTTTGGATTGGATTTTGCATTCGACTTGA		ATGCCTCCCAGGCTCGGTGACCTTGACCTTCTTTTCTCTCCTTCATTGTCCATTCTTTACCTTTTGACGATCGATACCCGTCGTGTTCTGTCTCTCTTTTTGGATTGGATTTTGCATTCGACTTGA		MPPRLGDLDLLFSPSLSILYLLTIDTRRVLSLFLDWILHST*		MPPRLGDLDLLFSPSLSILYLLTIDTRRVLSLFLDWILHST*		AAAAGAGTCG	AAAGGCTGTT	0	P	0	0	0	0	0
5271	2712	an	AN5440.1	69.m15495	AO070333000102	0	-103	-83					ATGTGTTGGTCGCCATCCTGA	ATGTGTTGGTCGCCATCCTGA			MCWSPS*	MCWSPS*			GTCGGAGTGC	ATATACCTTC	0	P	0	0	0	0	0
5274	2712	ao	AN5440.1	69.m15495	AO070333000102	0					-224	-132	ATGTGCGACCAGCAAGACATCGCCTCCTGGACCGACAGACTTCTCTCATATTTCTTCCTTAACAACATCTTCAATCTCTTTCTCTTTCTGTAA			ATGTGCGACCAGCAAGACATCGCCTCCTGGACCGACAGACTTCTCTCATATTTCTTCCTTAACAACATCTTCAATCTCTTTCTCTTTCTGTAA	MCDQQDIASWTDRLLSYFFLNNIFNLFLFL*			MCDQQDIASWTDRLLSYFFLNNIFNLFLFL*	GCCTCTCTTC	TCAAATTTGT	0	P	0	0	0	0	0
5278	2713	af	AN3972.1	69.m15765	AO070333000216	0			-196	-104			ATGTCGTTATCAGTGATGGCCCTCTTTCGGCCCTTTAAAGTCGGAGAGCGAACGAGCTTAGTGTTTGCCAGACTTTGGAGTGGCATATTATAA		ATGTCGTTATCAGTGATGGCCCTCTTTCGGCCCTTTAAAGTCGGAGAGCGAACGAGCTTAGTGTTTGCCAGACTTTGGAGTGGCATATTATAA		MSLSVMALFRPFKVGERTSLVFARLWSGIL*		MSLSVMALFRPFKVGERTSLVFARLWSGIL*		CAGTGATGTG	ATTGGTGATA	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5279	2713	af	AN3972.1	69.m15765	AO070333000216	0			-181	-104			ATGGCCCTCTTTCGGCCCTTTAAAGTCGGAGAGCGAACGAGCTTAGTGTTTGCCAGACTTTGGAGTGGCATATTATAA		ATGGCCCTCTTTCGGCCCTTTAAAGTCGGAGAGCGAACGAGCTTAGTGTTTGCCAGACTTTGGAGTGGCATATTATAA		MALFRPFKVGERTSLVFARLWSGIL*		MALFRPFKVGERTSLVFARLWSGIL*		GTTATCAGTG	ATTGGTGATA	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5275	2713	an	AN3972.1	69.m15765	AO070333000216	0	-214	-203					ATGTACTATTAG	ATGTACTATTAG			MYY*	MYY*			TCTGAATAGA	AACTGCTTGC	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5276	2713	an	AN3972.1	69.m15765	AO070333000216	0	-112	-98					ATGTCGTCATTTTGA	ATGTCGTCATTTTGA			MSSF*	MSSF*			AAGGCGGCAG	TTCATCGATG	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5277	2713	an	AN3972.1	69.m15765	AO070333000216	0	-90	-22					ATGACTAAGCCTGACTGGGGAACCCCTCATGTTCTCCAAATCCTGTCAAGATCCAGATTCCATCTTTGA	ATGACTAAGCCTGACTGGGGAACCCCTCATGTTCTCCAAATCCTGTCAAGATCCAGATTCCATCTTTGA			MTKPDWGTPHVLQILSRSRFHL*	MTKPDWGTPHVLQILSRSRFHL*			TGATTCATCG	GACAGCGGAG	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5280	2713	ao	AN3972.1	69.m15765	AO070333000216	0					-191	-126	ATGAGGGAGGGTTCCATGGTGTGTCCCGCTGTCGTTATCATCGTCCCGCACCAGGACTGCGGATAA			ATGAGGGAGGGTTCCATGGTGTGTCCCGCTGTCGTTATCATCGTCCCGCACCAGGACTGCGGATAA	MREGSMVCPAVVIIVPHQDCG*			MREGSMVCPAVVIIVPHQDCG*	AGCGACCAAA	ATCATAAAGG	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5281	2713	ao	AN3972.1	69.m15765	AO070333000216	0					-176	-126	ATGGTGTGTCCCGCTGTCGTTATCATCGTCCCGCACCAGGACTGCGGATAA			ATGGTGTGTCCCGCTGTCGTTATCATCGTCCCGCACCAGGACTGCGGATAA	MVCPAVVIIVPHQDCG*			MVCPAVVIIVPHQDCG*	GGAGGGTTCC	ATCATAAAGG	0	E	FG10203.1	MG00771.1	0	YKL215C	0
5283	2715	af	AN5228.1	57.m05703	AO070337000249	0			-126	-7			ATGCTCTCCAGAGCTTGTAGGATAAAAAGCCAACGGCCTCCCTCCCCGTACTGCCTCGCCCCAATCAGTACCATACAGAGTATAAGTTGCGCTATCATCACGCCTCGGAGTGATCCCTAG		ATGCTCTCCAGAGCTTGTAGGATAAAAAGCCAACGGCCTCCCTCCCCGTACTGCCTCGCCCCAATCAGTACCATACAGAGTATAAGTTGCGCTATCATCACGCCTCGGAGTGATCCCTAG		MLSRACRIKSQRPPSPYCLAPISTIQSISCAIITPRSDP*		MLSRACRIKSQRPPSPYCLAPISTIQSISCAIITPRSDP*		TCAAGGCACA	ATCCAAATGC	0	CR	0	0	0	0	0
5284	2715	ao	AN5228.1	57.m05703	AO070337000249	0					-166	-119	ATGGCGAAAAACAAATGGAAAAAAAAAAGTCTCCGAAGTATAGTATAA			ATGGCGAAAAACAAATGGAAAAAAAAAAGTCTCCGAAGTATAGTATAA	MAKNKWKKKSLRSIV*			MAKNKWKKKSLRSIV*	TTGGAAATCA	AAGGAAGTCG	0	CR	0	0	0	0	0
5285	2715	ao	AN5228.1	57.m05703	AO070337000249	0					-96	-73	ATGGACCTCCAGTATACAATATAA			ATGGACCTCCAGTATACAATATAA	MDLQYTI*			MDLQYTI*	CATTTGCTCC	AACACCAATT	0	CR	0	0	0	0	0
5286	2716	af	AN2882.1	59.m08729	AO070338000132	0			-247	-203			ATGTTTGGACTCTACGGAGAAGGCAACTCTGCCGATGCTGATTAG		ATGTTTGGACTCTACGGAGAAGGCAACTCTGCCGATGCTGATTAG		MFGLYGEGNSADAD*		MFGLYGEGNSADAD*		AGAGCAGTAA	ATAACCGTGT	0	E	0	0	0	0	0
5287	2716	af	AN2882.1	59.m08729	AO070338000132	0			-213	-199			ATGCTGATTAGATAA		ATGCTGATTAGATAA		MLIR*		MLIR*		AACTCTGCCG	CCGTGTATGC	0	E	0	0	0	0	0
5288	2716	af	AN2882.1	59.m08729	AO070338000132	0			-192	-169			ATGCCTCAGGCACCACTCAGATAA		ATGCCTCAGGCACCACTCAGATAA		MPQAPLR*		MPQAPLR*		ATAACCGTGT	TCGCTGCCCC	0	E	0	0	0	0	0
5289	2716	ao	AN2882.1	59.m08729	AO070338000132	0					-238	-215	ATGGCCGTAATCGATAAGACGTGA			ATGGCCGTAATCGATAAGACGTGA	MAVIDKT*			MAVIDKT*	AGGTACAGGA	TTGACCTAAA	0	E	0	0	0	0	0
5290	2716	ao	AN2882.1	59.m08729	AO070338000132	0					-179	-30	ATGACTAAGGTCCATAGATGGCCCCGCGGAAACCCCTCCAGACTTGTCCTTCTATTTCCCATCGACATATTCTCTGTTTGTACCTTGTCTTTCTGGAGGAGCTTGTTCTCTTGTTGGATATTTGGTATACTTCTTCCGGTTACCATTTAA			ATGACTAAGGTCCATAGATGGCCCCGCGGAAACCCCTCCAGACTTGTCCTTCTATTTCCCATCGACATATTCTCTGTTTGTACCTTGTCTTTCTGGAGGAGCTTGTTCTCTTGTTGGATATTTGGTATACTTCTTCCGGTTACCATTTAA	MTKVHRWPRGNPSRLVLLFPIDIFSVCTLSFWRSLFSCWIFGILLPVTI*			MTKVHRWPRGNPSRLVLLFPIDIFSVCTLSFWRSLFSCWIFGILLPVTI*	ATAGGCAGGT	GCCCAGTGCC	0	E	0	0	0	0	0
5291	2718	an	AN6078.1	72.m19069	AO070340000126	0	-143	-132					ATGTTGGAGTAG	ATGTTGGAGTAG			MLE*	MLE*			CATTACCCGG	AACTCTACTC	0	F	0	0	0	YNL141W	0
5292	2718	ao	AN6078.1	72.m19069	AO070340000126	0					-212	-189	ATGATCCATATAATGAGTAGTTGA			ATGATCCATATAATGAGTAGTTGA	MIHIMSS*			MIHIMSS*	ATTTGTATAC	CTCAAACTTC	0	F	0	0	0	YNL141W	0
5293	2718	ao	AN6078.1	72.m19069	AO070340000126	0					-200	-189	ATGAGTAGTTGA			ATGAGTAGTTGA	MSS*			MSS*	GATCCATATA	CTCAAACTTC	0	F	0	0	0	YNL141W	0
5295	2719	an	AN5925.1	72.m19206	AO070340000359	0	-262	-245					ATGATACCTTCTGAATGA	ATGATACCTTCTGAATGA			MIPSE*	MIPSE*			CACACGTGCG	GATGGGAGGC	0	A	0	0	NCU06365.1	YDR291W	0
5296	2719	an	AN5925.1	72.m19206	AO070340000359	0	-248	-210					ATGAGATGGGAGGCCTGCGCTGGATTCAGACGGCGGTAG	ATGAGATGGGAGGCCTGCGCTGGATTCAGACGGCGGTAG			MRWEACAGFRRR*	MRWEACAGFRRR*			TACCTTCTGA	TTGGCTTTTC	0	A	0	0	NCU06365.1	YDR291W	0
5297	2719	an	AN5925.1	72.m19206	AO070340000359	0	-243	-196					ATGGGAGGCCTGCGCTGGATTCAGACGGCGGTAGTTGGCTTTTCTTGA	ATGGGAGGCCTGCGCTGGATTCAGACGGCGGTAGTTGGCTTTTCTTGA			MGGLRWIQTAVVGFS*	MGGLRWIQTAVVGFS*			TCTGAATGAG	AGCCTTTTCT	0	A	0	0	NCU06365.1	YDR291W	0
5298	2719	an	AN5925.1	72.m19206	AO070340000359	0	-184	-110					ATGTTGAACAACTCGTTTGATCGAACTCCGATATTGAATGGTGCGTTAATCATAGGCATTGCAGGTTCCGTTTAG	ATGTTGAACAACTCGTTTGATCGAACTCCGATATTGAATGGTGCGTTAATCATAGGCATTGCAGGTTCCGTTTAG			MLNNSFDRTPILNGALIIGIAGSV*	MLNNSFDRTPILNGALIIGIAGSV*			GCCTTTTCTT	CCTCGTCGCT	0	A	0	0	NCU06365.1	YDR291W	0
5299	2719	an	AN5925.1	72.m19206	AO070340000359	0	-147	-136					ATGGTGCGTTAA	ATGGTGCGTTAA			MVR*	MVR*			CCGATATTGA	TCATAGGCAT	0	A	0	0	NCU06365.1	YDR291W	0
5301	2722	an	AN5231.1	65.m07188	AO070343000100	0	-224	-174					ATGCCGCCACGGAATGCAGGCACAACTGTAACGGTTAATCGTCTAGCCTGA	ATGCCGCCACGGAATGCAGGCACAACTGTAACGGTTAATCGTCTAGCCTGA			MPPRNAGTTVTVNRLA*	MPPRNAGTTVTVNRLA*			CCACATTGCC	TGACGACGCG	0		0	0	0	0	0
5302	2722	an	AN5231.1	65.m07188	AO070343000100	0	-211	-194					ATGCAGGCACAACTGTAA	ATGCAGGCACAACTGTAA			MQAQL*	MQAQL*			CCGCCACGGA	CGGTTAATCG	0		0	0	0	0	0
5303	2722	an	AN5231.1	65.m07188	AO070343000100	0	-174	-97					ATGACGACGCGTCGAATAATATCCCCGTGTAAACCACTGTTTCAGTCAAATTTCCTCCCCAACGGCAATTTTCAATGA	ATGACGACGCGTCGAATAATATCCCCGTGTAAACCACTGTTTCAGTCAAATTTCCTCCCCAACGGCAATTTTCAATGA			MTTRRIISPCKPLFQSNFLPNGNFQ*	MTTRRIISPCKPLFQSNFLPNGNFQ*			GTCTAGCCTG	TGTCATAATG	0		0	0	0	0	0
5304	2722	an	AN5231.1	65.m07188	AO070343000100	0	-100	-89					ATGATGTCATAA	ATGATGTCATAA			MMS*	MMS*			GCAATTTTCA	TGGCGCTGGA	0		0	0	0	0	0
5305	2722	an	AN5231.1	65.m07188	AO070343000100	0	-89	-33					ATGGCGCTGGAATGTCAGCAGAAGGCAGCAACAATCTCGTCCTATTATTCCCCCTGA	ATGGCGCTGGAATGTCAGCAGAAGGCAGCAACAATCTCGTCCTATTATTCCCCCTGA			MALECQQKAATISSYYSP*	MALECQQKAATISSYYSP*			TGATGTCATA	ACCTTGCAAC	0		0	0	0	0	0
5306	2722	an	AN5231.1	65.m07188	AO070343000100	0	-78	-10					ATGTCAGCAGAAGGCAGCAACAATCTCGTCCTATTATTCCCCCTGAACCTTGCAACATCTTTCAATTGA	ATGTCAGCAGAAGGCAGCAACAATCTCGTCCTATTATTCCCCCTGAACCTTGCAACATCTTTCAATTGA			MSAEGSNNLVLLFPLNLATSFN*	MSAEGSNNLVLLFPLNLATSFN*			TGGCGCTGGA	AGCAACACCA	0		0	0	0	0	0
5307	2722	ao	AN5231.1	65.m07188	AO070343000100	0					-203	-162	ATGAGGCAACCAGGCAGCCGTGTTTCAACGGGGCTTGGATGA			ATGAGGCAACCAGGCAGCCGTGTTTCAACGGGGCTTGGATGA	MRQPGSRVSTGLG*			MRQPGSRVSTGLG*	GAGATCAACA	CGTCATCCAT	0		0	0	0	0	0
5308	2722	ao	AN5231.1	65.m07188	AO070343000100	0					-165	-127	ATGACGTCATCCATGTCAATCACTTCGATAAACAGATGA			ATGACGTCATCCATGTCAATCACTTCGATAAACAGATGA	MTSSMSITSINR*			MTSSMSITSINR*	CGGGGCTTGG	ACTATCGGTG	0		0	0	0	0	0
5309	2722	ao	AN5231.1	65.m07188	AO070343000100	0					-153	-127	ATGTCAATCACTTCGATAAACAGATGA			ATGTCAATCACTTCGATAAACAGATGA	MSITSINR*			MSITSINR*	GACGTCATCC	ACTATCGGTG	0		0	0	0	0	0
5310	2722	ao	AN5231.1	65.m07188	AO070343000100	0					-130	-116	ATGAACTATCGGTGA			ATGAACTATCGGTGA	MNYR*			MNYR*	CGATAAACAG	ACAAGTGGCT	0		0	0	0	0	0
5311	2723	af	AN0746.1	70.m15362	AO070343000434	0			-263	-213			ATGGCCACAGCTAATGACAGTAATGCCGATGGCGTCGAGACGGAGAAATAA		ATGGCCACAGCTAATGACAGTAATGCCGATGGCGTCGAGACGGAGAAATAA		MATANDSNADGVETEK*		MATANDSNADGVETEK*		TAATCCCGCG	TGGTGGACGT	0	MG	0	0	0	0	0
5312	2723	af	AN0746.1	70.m15362	AO070343000434	0			-250	-89			ATGACAGTAATGCCGATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		ATGACAGTAATGCCGATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		MTVMPMASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		MTVMPMASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		GCCACAGCTA	GTTTGAGTGT	0	MG	0	0	0	0	0
5313	2723	af	AN0746.1	70.m15362	AO070343000434	0			-241	-89			ATGCCGATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		ATGCCGATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		MPMASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		MPMASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		AATGACAGTA	GTTTGAGTGT	0	MG	0	0	0	0	0

5314	2723	af	AN0746.1	70.m15362	AO070343000434	0			-235	-89			ATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		ATGGCGTCGAGACGGAGAAATAATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAAACCATCAGCAATGGGATAAAACTGCCGGGGGAAACATGGTATCTGAATGA		MASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		MASRRRNNGGRGGAFTSSLHRPRIHRQHGDYINHQQWDKTAGGNMVSE*		AGTAATGCCG	GTTTGAGTGT	0	MG	0	0	0	0	0
5315	2723	af	AN0746.1	70.m15362	AO070343000434	0			-213	-139			ATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAA		ATGGTGGACGTGGGGGAGCATTCACAAGTTCTCTCCACCGACCCCGCATACATAGACAGCATGGAGACTATATAA		MVDVGEHSQVLSTDPAYIDSMETI*		MVDVGEHSQVLSTDPAYIDSMETI*		CGGAGAAATA	ACCATCAGCA	0	MG	0	0	0	0	0
5316	2723	af	AN0746.1	70.m15362	AO070343000434	0			-153	-139			ATGGAGACTATATAA		ATGGAGACTATATAA		METI*		METI*		CATAGACAGC	ACCATCAGCA	0	MG	0	0	0	0	0
5317	2723	af	AN0746.1	70.m15362	AO070343000434	0			-103	-89			ATGGTATCTGAATGA		ATGGTATCTGAATGA		MVSE*		MVSE*		CGGGGGAAAC	GTTTGAGTGT	0	MG	0	0	0	0	0
5318	2723	af	AN0746.1	70.m15362	AO070343000434	0			-92	-45			ATGAGTTTGAGTGTCCGTGCGATATTCAGTTTCTCTTCTATTTTCTAG		ATGAGTTTGAGTGTCCGTGCGATATTCAGTTTCTCTTCTATTTTCTAG		MSLSVRAIFSFSSIF*		MSLSVRAIFSFSSIF*		TGGTATCTGA	TCAAATCACT	0	MG	0	0	0	0	0
5319	2723	ao	AN0746.1	70.m15362	AO070343000434	0					-261	-112	ATGATTATGGGGGCTTGCAGAGACCGAGAGCGGGGATCATCCCACGCTGAGAATTACTTTCTCCCTCTGACCCCGCAGTATCTTGACAACTGGGATAATTGCTATTTAAGTCACGGTAATATTCTCATCGGATTTCAGGCAGTCTCGTGA			ATGATTATGGGGGCTTGCAGAGACCGAGAGCGGGGATCATCCCACGCTGAGAATTACTTTCTCCCTCTGACCCCGCAGTATCTTGACAACTGGGATAATTGCTATTTAAGTCACGGTAATATTCTCATCGGATTTCAGGCAGTCTCGTGA	MIMGACRDRERGSSHAENYFLPLTPQYLDNWDNCYLSHGNILIGFQAVS*			MIMGACRDRERGSSHAENYFLPLTPQYLDNWDNCYLSHGNILIGFQAVS*	TGACACCATC	GAAACTATAT	0	MG	0	0	0	0	0
5320	2723	ao	AN0746.1	70.m15362	AO070343000434	0					-255	-112	ATGGGGGCTTGCAGAGACCGAGAGCGGGGATCATCCCACGCTGAGAATTACTTTCTCCCTCTGACCCCGCAGTATCTTGACAACTGGGATAATTGCTATTTAAGTCACGGTAATATTCTCATCGGATTTCAGGCAGTCTCGTGA			ATGGGGGCTTGCAGAGACCGAGAGCGGGGATCATCCCACGCTGAGAATTACTTTCTCCCTCTGACCCCGCAGTATCTTGACAACTGGGATAATTGCTATTTAAGTCACGGTAATATTCTCATCGGATTTCAGGCAGTCTCGTGA	MGACRDRERGSSHAENYFLPLTPQYLDNWDNCYLSHGNILIGFQAVS*			MGACRDRERGSSHAENYFLPLTPQYLDNWDNCYLSHGNILIGFQAVS*	CATCATGATT	GAAACTATAT	0	MG	0	0	0	0	0
5321	2725	an	AN4303.1	58.m08021	AO070207000007	0	-149	-9					ATGATGTTCTCCGCAATTCATACCCCTCTTAGCCCCTCTTATATATCCAACCCTAGATCATCCTCCACCGAGCGTCGTGTGTTGAAGACGAATCACCCGTTGATAGACCTTTGCGCCATCAATCACAAACCGCTTTCTTGA	ATGATGTTCTCCGCAATTCATACCCCTCTTAGCCCCTCTTATATATCCAACCCTAGATCATCCTCCACCGAGCGTCGTGTGTTGAAGACGAATCACCCGTTGATAGACCTTTGCGCCATCAATCACAAACCGCTTTCTTGA			MMFSAIHTPLSPSYISNPRSSSTERRVLKTNHPLIDLCAINHKPLS*	MMFSAIHTPLSPSYISNPRSSSTERRVLKTNHPLIDLCAINHKPLS*			GGCGGTCAGG	CACGCACAAT	0	I	FG04571.1	0	0	YGR007W	0
5322	2725	an	AN4303.1	58.m08021	AO070207000007	0	-146	-9					ATGTTCTCCGCAATTCATACCCCTCTTAGCCCCTCTTATATATCCAACCCTAGATCATCCTCCACCGAGCGTCGTGTGTTGAAGACGAATCACCCGTTGATAGACCTTTGCGCCATCAATCACAAACCGCTTTCTTGA	ATGTTCTCCGCAATTCATACCCCTCTTAGCCCCTCTTATATATCCAACCCTAGATCATCCTCCACCGAGCGTCGTGTGTTGAAGACGAATCACCCGTTGATAGACCTTTGCGCCATCAATCACAAACCGCTTTCTTGA			MFSAIHTPLSPSYISNPRSSSTERRVLKTNHPLIDLCAINHKPLS*	MFSAIHTPLSPSYISNPRSSSTERRVLKTNHPLIDLCAINHKPLS*			GGTCAGGATG	CACGCACAAT	0	I	FG04571.1	0	0	YGR007W	0
5323	2725	ao	AN4303.1	58.m08021	AO070207000007	0					-110	-90	ATGGAAGGAGGACAATTATAA			ATGGAAGGAGGACAATTATAA	MEGGQL*			MEGGQL*	TTCTCAAGAA	TAAAATTATA	0	I	FG04571.1	0	0	YGR007W	0
5324	2725	ao	AN4303.1	58.m08021	AO070207000007	0					-73	-53	ATGCTAATCATCAATTGCTGA			ATGCTAATCATCAATTGCTGA	MLIINC*			MLIINC*	TATAATCATC	CAGCAAGTGT	0	I	FG04571.1	0	0	YGR007W	0
5327	2728	af	AN7430.1	57.m05914	AO070229000001	0			-275	-237			ATGTGGGCGGAAAGAGGAAAAAAGAGCAAAAAAAAGTAG		ATGTGGGCGGAAAGAGGAAAAAAGAGCAAAAAAAAGTAG		MWAERGKKSKKK*		MWAERGKKSKKK*		GAGAATATTA	GTTATCATTT	0	E	FG09984.1	0	NCU07156.1	0	0
5328	2728	af	AN7430.1	57.m05914	AO070229000001	0			-221	-171			ATGACTCAGCTAAATGTCCCCGCCGTGGTGGGGAGTGATGGTCGACAATAA		ATGACTCAGCTAAATGTCCCCGCCGTGGTGGGGAGTGATGGTCGACAATAA		MTQLNVPAVVGSDGRQ*		MTQLNVPAVVGSDGRQ*		CATTTGAACA	ATGAGGGTGA	0	E	FG09984.1	0	NCU07156.1	0	0
5329	2728	af	AN7430.1	57.m05914	AO070229000001	0			-208	-167			ATGTCCCCGCCGTGGTGGGGAGTGATGGTCGACAATAAATGA		ATGTCCCCGCCGTGGTGGGGAGTGATGGTCGACAATAAATGA		MSPPWWGVMVDNK*		MSPPWWGVMVDNK*		ACTCAGCTAA	GGGTGATTAT	0	E	FG09984.1	0	NCU07156.1	0	0
5330	2728	af	AN7430.1	57.m05914	AO070229000001	0			-184	-167			ATGGTCGACAATAAATGA		ATGGTCGACAATAAATGA		MVDNK*		MVDNK*		GTGGGGAGTG	GGGTGATTAT	0	E	FG09984.1	0	NCU07156.1	0	0
5331	2728	af	AN7430.1	57.m05914	AO070229000001	0			-170	-18			ATGAGGGTGATTATTCTTCTTACCAAGTCACTTTCATTCATTCTCTCTGTCCCCGAATGTTTGTGGCCTTCCCGAAGCCAGACAAAGCGTGTGATTCAGTCTCTACTCGACATTAGTATTGAAGTACAGTCAGTACCTTGTCTTACGGCTTGA		ATGAGGGTGATTATTCTTCTTACCAAGTCACTTTCATTCATTCTCTCTGTCCCCGAATGTTTGTGGCCTTCCCGAAGCCAGACAAAGCGTGTGATTCAGTCTCTACTCGACATTAGTATTGAAGTACAGTCAGTACCTTGTCTTACGGCTTGA		MRVIILLTKSLSFILSVPECLWPSRSQTKRVIQSLLDISIEVQSVPCLTA*		MRVIILLTKSLSFILSVPECLWPSRSQTKRVIQSLLDISIEVQSVPCLTA*		TCGACAATAA	GGTACCGGAC	0	E	FG09984.1	0	NCU07156.1	0	0
5332	2728	af	AN7430.1	57.m05914	AO070229000001	0			-114	-55			ATGTTTGTGGCCTTCCCGAAGCCAGACAAAGCGTGTGATTCAGTCTCTACTCGACATTAG		ATGTTTGTGGCCTTCCCGAAGCCAGACAAAGCGTGTGATTCAGTCTCTACTCGACATTAG		MFVAFPKPDKACDSVSTRH*		MFVAFPKPDKACDSVSTRH*		CTGTCCCCGA	TATTGAAGTA	0	E	FG09984.1	0	NCU07156.1	0	0
5325	2728	an	AN7430.1	57.m05914	AO070229000001	0	-158	-69					ATGAGTCAGCCCCTCCGTTCCTCTGGTGGGGTGGCGTGGAAAGATACGATGGTATTGAGTAGTCAAAACTTGGGTCTACGAAGCCATTGA	ATGAGTCAGCCCCTCCGTTCCTCTGGTGGGGTGGCGTGGAAAGATACGATGGTATTGAGTAGTCAAAACTTGGGTCTACGAAGCCATTGA			MSQPLRSSGGVAWKDTMVLSSQNLGLRSH*	MSQPLRSSGGVAWKDTMVLSSQNLGLRSH*			AAAAACTTGT	GCTTTTCTAT	0	E	FG09984.1	0	NCU07156.1	0	0
5326	2728	an	AN7430.1	57.m05914	AO070229000001	0	-110	-69					ATGGTATTGAGTAGTCAAAACTTGGGTCTACGAAGCCATTGA	ATGGTATTGAGTAGTCAAAACTTGGGTCTACGAAGCCATTGA			MVLSSQNLGLRSH*	MVLSSQNLGLRSH*			GAAAGATACG	GCTTTTCTAT	0	E	FG09984.1	0	NCU07156.1	0	0
5333	2728	ao	AN7430.1	57.m05914	AO070229000001	0					-219	-85	ATGAGTCAGCTAGCTCTTGGTGGGGTATTGAAGACAGGATCCCATTCTTTCAAAGCTCCAATTCAACCCCCCAGTAAAATCTTGTCTACCCTAAAAAGATACTGGAAAGATAATAGAACAAATCAAGGAGCGTAG			ATGAGTCAGCTAGCTCTTGGTGGGGTATTGAAGACAGGATCCCATTCTTTCAAAGCTCCAATTCAACCCCCCAGTAAAATCTTGTCTACCCTAAAAAGATACTGGAAAGATAATAGAACAAATCAAGGAGCGTAG	MSQLALGGVLKTGSHSFKAPIQPPSKILSTLKRYWKDNRTNQGA*			MSQLALGGVLKTGSHSFKAPIQPPSKILSTLKRYWKDNRTNQGA*	ATTGTAGATT	ATTTTCTATT	0	E	FG09984.1	0	NCU07156.1	0	0
5335	2729	af	AN1437.1	55.m03263	AO070232000002	0			-96	-70			ATGCTTTCCGGAGAGCGTCGTCTCTGA		ATGCTTTCCGGAGAGCGTCGTCTCTGA		MLSGERRL*		MLSGERRL*		ACACAGAAAT	TTTCGTTGGC	0		0	0	0	0	0
5334	2729	an	AN1437.1	55.m03263	AO070232000002	0	-141	-109					ATGCCACTTTGTACCCTTCTCATCAGGTACTAG	ATGCCACTTTGTACCCTTCTCATCAGGTACTAG			MPLCTLLIRY*	MPLCTLLIRY*			CGTGCTAGAC	TGCTACGTAC	0		0	0	0	0	0
5336	2729	ao	AN1437.1	55.m03263	AO070232000002	0					-195	-184	ATGGCTTTCTAG			ATGGCTTTCTAG	MAF*			MAF*	CTGCTCATCG	ACATGCGTCC	0		0	0	0	0	0
5337	2729	ao	AN1437.1	55.m03263	AO070232000002	0					-181	-149	ATGCGTCCTCAACTCTGCTTTCCATCTCAGTGA			ATGCGTCCTCAACTCTGCTTTCCATCTCAGTGA	MRPQLCFPSQ*			MRPQLCFPSQ*	CTTTCTAGAC	GGTCTACCG	0		0	0	0	0	0
5338	2730	af	AN5175.1	69.m14872	AO070247000006	0			-282	-253			ATGCCTTATCAGTTGGCTCTTTCCCATTAA		ATGCCTTATCAGTTGGCTCTTTCCCATTAA		MPYQLALSH*		MPYQLALSH*		TGATGATTTG	CTGATAAGAT	0	R	0	0	0	0	0
5340	2730	ao	AN5175.1	69.m14872	AO070247000006	0					-177	-82	ATGCAGCCGAGACGGACCGTCGGCACTTCTCTTCATTCTTCCTTCACTTCCACCTACAGTCTTTCTTACTGCATTCATTTGTTGAGCACAGATTGA			ATGCAGCCGAGACGGACCGTCGGCACTTCTCTTCATTCTTCCTTCACTTCCACCTACAGTCTTTCTTACTGCATTCATTTGTTGAGCACAGATTGA	MQPRRTVGTSLHSSFTSTYSLSYCIHLLSTD*			MQPRRTVGTSLHSSFTSTYSLSYCIHLLSTD*	AAAAGGAAAG	TTTCTCTATT	0	R	0	0	0	0	0
5343	2731	af	AN0824.1	70.m15426	AO070255000021	0			-250	-230			ATGGCCAAATTCGGGTTATAG		ATGGCCAAATTCGGGTTATAG		MAKFGL*		MAKFGL*		TTTTTCTAAG	CGAATGATCA	0	I	FG09661.1	0	0	0	0
5344	2731	af	AN0824.1	70.m15426	AO070255000021	0			-226	-173			ATGATCACGCTGCCATTGATCCAGTCAGCGTTCCCTTTGGACAGCCGCGGTTAA		ATGATCACGCTGCCATTGATCCAGTCAGCGTTCCCTTTGGACAGCCGCGGTTAA		MITLPLIQSAFPLDSRG*		MITLPLIQSAFPLDSRG*		GTTATAGCGA	CCGAGGCATA	0	I	FG09661.1	0	0	0	0
5341	2731	an	AN0824.1	70.m15426	AO070255000021	0	-176	-147					ATGCCAAGACCCGCTTTTAACCGAGGCTGA	ATGCCAAGACCCGCTTTTAACCGAGGCTGA			MPRPAFNRG*	MPRPAFNRG*			CGGACGTACA	CATTCCCTCC	0	I	FG09661.1	0	0	0	0
5342	2731	an	AN0824.1	70.m15426	AO070255000021	0	-87	-40					ATGATTTTCTCCTTCTCCCTTTCTTTTCTTCCGCATTTTCTAGCGTGA	ATGATTTTCTCCTTCTCCCTTTCTTTTCTTCCGCATTTTCTAGCGTGA			MIFSFSLSFLPHFLA*	MIFSFSLSFLPHFLA*			CCTTTTTCCC	CCCTTTGCAA	0	I	FG09661.1	0	0	0	0
5345	2731	ao	AN0824.1	70.m15426	AO070255000021	0					-200	-132	ATGGGGAAGCAAGCTTACATGCTGGGGGCAGCCGCGGTTAACCGAGGTTCATCAGCAGCGCCCTCGTGA			ATGGGGAAGCAAGCTTACATGCTGGGGGCAGCCGCGGTTAACCGAGGTTCATCAGCAGCGCCCTCGTGA	MGKQAYMLGAAAVNRGSSAAPS*			MGKQAYMLGAAAVNRGSSAAPS*	CGGACAACCC	TTTCGCTCCA	0	I	FG09661.1	0	0	0	0
5346	2731	ao	AN0824.1	70.m15426	AO070255000021	0					-182	-132	ATGCTGGGGGCAGCCGCGGTTAACCGAGGTTCATCAGCAGCGCCCTCGTGA			ATGCTGGGGGCAGCCGCGGTTAACCGAGGTTCATCAGCAGCGCCCTCGTGA	MLGAAAVNRGSSAAPS*			MLGAAAVNRGSSAAPS*	GCAAGCTTAC	TTTCGCTCCA	0	I	FG09661.1	0	0	0	0
5351	2735	af	AN1858.1	58.m07652	AO070292000035	0			-191	-99			ATGCCACCATGTTATCGTTCCGGGTTGGATCCGGCACTCTTCCGCCCAAGCAGTTCGTCCCCTTATATTCTGGCTTCGACATGGACAGAGTGA		ATGCCACCATGTTATCGTTCCGGGTTGGATCCGGCACTCTTCCGCCCAAGCAGTTCGTCCCCTTATATTCTGGCTTCGACATGGACAGAGTGA		MPPCYRSGLDPALFRPSSSPYILASTWTE*		MPPCYRSGLDPALFRPSSSPYILASTWTE*		TCCTGTGCTC	ATATTTCTAT	0		0	MG00755.1	0	0	0
5352	2735	af	AN1858.1	58.m07652	AO070292000035	0			-183	-61			ATGTTATCGTTCCGGGTTGGATCCGGCACTCTTCCGCCCAAGCAGTTCGTCCCCTTATATTCTGGCTTCGACATGGACAGAGTGAATATTTCTATTTCTAAAGTTCACTCCAAGAATCTTTGA		ATGTTATCGTTCCGGGTTGGATCCGGCACTCTTCCGCCCAAGCAGTTCGTCCCCTTATATTCTGGCTTCGACATGGACAGAGTGAATATTTCTATTTCTAAAGTTCACTCCAAGAATCTTTGA		MLSFRVGSGTLPPKQFVPLYSGFDMDRVNISISKVHSKNL*		MLSFRVGSGTLPPKQFVPLYSGFDMDRVNISISKVHSKNL*		TCATGCCACC	CTATAAAGAC	0		0	MG00755.1	0	0	0
5353	2735	af	AN1858.1	58.m07652	AO070292000035	0			-111	-61			ATGGACAGAGTGAATATTTCTATTTCTAAAGTTCACTCCAAGAATCTTTGA		ATGGACAGAGTGAATATTTCTATTTCTAAAGTTCACTCCAAGAATCTTTGA		MDRVNISISKVHSKNL*		MDRVNISISKVHSKNL*		TGGCTTCGAC	CTATAAAGAC	0		0	MG00755.1	0	0	0
5347	2735	an	AN1858.1	58.m07652	AO070292000035	0	-260	-225					ATGGCTAGTGCTAACTCACTGGCATTGTCACAGTGA	ATGGCTAGTGCTAACTCACTGGCATTGTCACAGTGA			MASANSLALSQ*	MASANSLALSQ*			TAACGAGCCT	GCAAGGGCGT	0		0	MG00755.1	0	0	0
5348	2735	an	AN1858.1	58.m07652	AO070292000035	0	-190	-119					ATGTCAACGTCTTCCGGGCCCGCTTCCATCATACCATTTAGAGACACTATTATATTGGATAACCATATTTAA	ATGTCAACGTCTTCCGGGCCCGCTTCCATCATACCATTTAGAGACACTATTATATTGGATAACCATATTTAA			MSTSSGPASIIPFRDTIILDNHI*	MSTSSGPASIIPFRDTIILDNHI*			GATAAGATCC	GGGGGGCCGT	0		0	MG00755.1	0	0	0
5349	2735	an	AN1858.1	58.m07652	AO070292000035	0	-85	-32					ATGCTCATGCATTTAAAGACCATTCTATCTATTTCTCCAATAGCATCCTCCTAG	ATGCTCATGCATTTAAAGACCATTCTATCTATTTCTCCAATAGCATCCTCCTAG			MLMHLKTILSISPIASS*	MLMHLKTILSISPIASS*			TCAGCGCCTC	CTTTAGAGTC	0		0	MG00755.1	0	0	0
5350	2735	an	AN1858.1	58.m07652	AO070292000035	0	-79	-32					ATGCATTTAAAGACCATTCTATCTATTTCTCCAATAGCATCCTCCTAG	ATGCATTTAAAGACCATTCTATCTATTTCTCCAATAGCATCCTCCTAG			MHLKTILSISPIASS*	MHLKTILSISPIASS*			CCTCATGCTC	CTTTAGAGTC	0		0	MG00755.1	0	0	0
5354	2735	ao	AN1858.1	58.m07652	AO070292000035	0					-103	-89	ATGTATAAGAGTTGA			ATGTATAAGAGTTGA	MYKS*			MYKS*	ATTGATAGAC	AGTTTCTAAC	0		0	MG00755.1	0	0	0
5358	2737	af	AN3341.1	56.m02301	AO070294000055	0			-113	-102			ATGAGAAATTGA		ATGAGAAATTGA		MRN*		MRN*		ATAAGGGAAG	GAATGTTTAA	0	P	0	0	0	0	0
5355	2737	an	AN3341.1	56.m02301	AO070294000055	0	-207	-163					ATGCCAAGATTTGAGCTGAAAGCCCAGCCCTTGGCAACCATGTGA	ATGCCAAGATTTGAGCTGAAAGCCCAGCCCTTGGCAACCATGTGA			MPRFELKAQPLATM*	MPRFELKAQPLATM*			GACATCTACA	ACATTGACTG	0	P	0	0	0	0	0
5356	2737	an	AN3341.1	56.m02301	AO070294000055	0	-140	-12					ATGAACTTTAAAGTCGATTCTAACCTTAAAGGTCCGCCATATCCCCAGCTTATGATTTCAAGCCATCGTGAGGAGTTGTTCACTCCTTTCTTTCTCCAAGATCTGGAAGTCTTACCGGTTTATCAATAG	ATGAACTTTAAAGTCGATTCTAACCTTAAAGGTCCGCCATATCCCCAGCTTATGATTTCAAGCCATCGTGAGGAGTTGTTCACTCCTTTCTTTCTCCAAGATCTGGAAGTCTTACCGGTTTATCAATAG			MNFKVDSNLKGPPYPQLMISSHREELFTPFFLQDLEVLPVYQ*	MNFKVDSNLKGPPYPQLMISSHREELFTPFFLQDLEVLPVYQ*			CTCGTATTGG	ACGAAGCAAG	0	P	0	0	0	0	0
5357	2737	an	AN3341.1	56.m02301	AO070294000055	0	-89	-12					ATGATTTCAAGCCATCGTGAGGAGTTGTTCACTCCTTTCTTTCTCCAAGATCTGGAAGTCTTACCGGTTTATCAATAG	ATGATTTCAAGCCATCGTGAGGAGTTGTTCACTCCTTTCTTTCTCCAAGATCTGGAAGTCTTACCGGTTTATCAATAG			MISSHREELFTPFFLQDLEVLPVYQ*	MISSHREELFTPFFLQDLEVLPVYQ*			TCCCCAGCTT	ACGAAGCAAG	0	P	0	0	0	0	0
5359	2737	ao	AN3341.1	56.m02301	AO070294000055	0					-70	-23	ATGCCTTTTCGCCTTCAGTCTGGAATTAGAAGAGATTTCACCCCTTGA			ATGCCTTTTCGCCTTCAGTCTGGAATTAGAAGAGATTTCACCCCTTGA	MPFRLQSGIRRDFTP*			MPFRLQSGIRRDFTP*	ATGTCATGAA	ACATTGTGGT	0	P	0	0	0	0	0
5360	2738	an	AN2294.1	71.m15943	AO070295000074	0	-143	-90					ATGGTCGATGCGAGTCAAACGCTTCAAAAACAGTGTTACTACTCCACGCGTTAA	ATGGTCGATGCGAGTCAAACGCTTCAAAAACAGTGTTACTACTCCACGCGTTAA			MVDASQTLQKQCYYSTR*	MVDASQTLQKQCYYSTR*			TCCGCTATCG	TCCTTTTTCT	0	BK	FG02040.1	MG05481.1	NCU01229.1	0	0
5363	2743	af	AN1701.1	58.m07777	AO070305000027	0			-264	-250			ATGGAGAACAGGTGA		ATGGAGAACAGGTGA		MENR*		MENR*		TTACGATAGA	ACAGTTGGCG	0	S	0	0	0	0	0
5364	2743	af	AN1701.1	58.m07777	AO070305000027	0			-223	-212			ATGTCAACATGA		ATGTCAACATGA		MST*		MST*		CCAAGGCAAA	CCACCTTCGC	0	S	0	0	0	0	0
5365	2743	af	AN1701.1	58.m07777	AO070305000027	0			-215	-156			ATGACCACCTTCGCAGATGATCATTCTTTCCTTGCGTTGTTTGGCGTTCTGTGGCGTTAA		ATGACCACCTTCGCAGATGATCATTCTTTCCTTGCGTTGTTTGGCGTTCTGTGGCGTTAA		MTTFADDHSFLALFGVLWR*		MTTFADDHSFLALFGVLWR*		AAATGTCAAC	CGTTCCTTTT	0	S	0	0	0	0	0

5366	2743	af	AN1701.1	58.m07777	AO070305000027	0			-199	-119			ATGATCATTCTTTCCTTGCGTTGTTTGGCGTTCTGTGGCGTTAACGTTCCTTTTCTTTGTTTCCCTTTTCTTCTGGTTTGA		ATGATCATTCTTTCCTTGCGTTGTTTGGCGTTCTGTGGCGTTAACGTTCCTTTTCTTTGTTTCCCTTTTCTTCTGGTTTGA		MIILSLRCLAFCGVNVPFLCFPFLLV*		MIILSLRCLAFCGVNVPFLCFPFLLV*		ACCTTCGCAG	CATCCACCGA	0	S	0	0	0	0	0
5361	2743	an	AN1701.1	58.m07777	AO070305000027	0	-206	-75					ATGTCACGTGCCAACAGGCACTCGATGGGAAGCCGCGTGAGCTCAGCTCTAACTTGTGCACGAGGACAAAAGGCCGGTGGTTCAATCTTCAATAAGCGATCGCTTCCTAATGCTGATATCCCTACTAGATAA	ATGTCACGTGCCAACAGGCACTCGATGGGAAGCCGCGTGAGCTCAGCTCTAACTTGTGCACGAGGACAAAAGGCCGGTGGTTCAATCTTCAATAAGCGATCGCTTCCTAATGCTGATATCCCTACTAGATAA			MSRANRHSMGSRVSSALTCARGQKAGGSIFNKRSLPNADIPTR*	MSRANRHSMGSRVSSALTCARGQKAGGSIFNKRSLPNADIPTR*			CCCTACCGAA	TATACTCTGC	0	S	0	0	0	0	0
5362	2743	an	AN1701.1	58.m07777	AO070305000027	0	-182	-75					ATGGGAAGCCGCGTGAGCTCAGCTCTAACTTGTGCACGAGGACAAAAGGCCGGTGGTTCAATCTTCAATAAGCGATCGCTTCCTAATGCTGATATCCCTACTAGATAA	ATGGGAAGCCGCGTGAGCTCAGCTCTAACTTGTGCACGAGGACAAAAGGCCGGTGGTTCAATCTTCAATAAGCGATCGCTTCCTAATGCTGATATCCCTACTAGATAA			MGSRVSSALTCARGQKAGGSIFNKRSLPNADIPTR*	MGSRVSSALTCARGQKAGGSIFNKRSLPNADIPTR*			CAGGCACTCG	TATACTCTGC	0	S	0	0	0	0	0
5367	2743	ao	AN1701.1	58.m07777	AO070305000027	0					-237	-172	ATGATGGCATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGA			ATGATGGCATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGA	MMAWVSSSPKGSRAHREDNNI*			MMAWVSSSPKGSRAHREDNNI*	CACGTGATCT	GCTACCACGG	0	S	0	0	0	0	0
5368	2743	ao	AN1701.1	58.m07777	AO070305000027	0					-234	-172	ATGGCATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGA			ATGGCATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGA	MAWVSSSPKGSRAHREDNNI*			MAWVSSSPKGSRAHREDNNI*	GTGATCTATG	GCTACCACGG	0	S	0	0	0	0	0
5369	2743	ao	AN1701.1	58.m07777	AO070305000027	0					-229	-128	ATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGAGCTACCACGGAGGTCACACATCCAAGTCAGGCTCAATGCCTTGA			ATGGGTTTCAAGCTCCCCGAAAGGGTCACGAGCCCACCGAGAAGACAACAACATTTGAGCTACCACGGAGGTCACACATCCAAGTCAGGCTCAATGCCTTGA	MGFKLPERVTSPPRRQQHLSYHGGHTSKSGSMP*			MGFKLPERVTSPPRRQQHLSYHGGHTSKSGSMP*	CTATGATGGC	CTTGCTTTTA	0	S	0	0	0	0	0
5370	2743	ao	AN1701.1	58.m07777	AO070305000027	0					-83	-36	ATGGTATTTTTGTCTTATAGTTTTAATGTCCGAGTAGCTTCTATCTAG			ATGGTATTTTTGTCTTATAGTTTTAATGTCCGAGTAGCTTCTATCTAG	MVFLSYSFNVRVASI*			MVFLSYSFNVRVASI*	TGAATTCGAT	CCCATAAACC	0	S	0	0	0	0	0
5372	2745	af	AN3830.1	58.m07808	AO070305000068	0			-195	-151			ATGAGTCAACAATTCCGCTCCGATCACGGCATTCCAGAAGGGTAG		ATGAGTCAACAATTCCGCTCCGATCACGGCATTCCAGAAGGGTAG		MSQQFRSDHGIPEG*		MSQQFRSDHGIPEG*		GTGAGGGCTG	GTAGCCCCCC	0	E	0	MG07224.1	0	0	0
5373	2745	af	AN3830.1	58.m07808	AO070305000068	0			-129	-85			ATGTTTGTCGAAGGCGTGATTGTGCCACTGCCGGCGAATTTTTGA		ATGTTTGTCGAAGGCGTGATTGTGCCACTGCCGGCGAATTTTTGA		MFVEGVIVPLPANF*		MFVEGVIVPLPANF*		GGAAGGATTA	AATCTCGCCG	0	E	0	MG07224.1	0	0	0
5374	2745	ao	AN3830.1	58.m07808	AO070305000068	0					-247	-173	ATGCCTATCAAAGTATGGATATACTACTCTGCGGCGGGGACGCAAGGATTTAGGGCTGAGGATGAGGGTTGCTGA			ATGCCTATCAAAGTATGGATATACTACTCTGCGGCGGGGACGCAAGGATTTAGGGCTGAGGATGAGGGTTGCTGA	MPIKVWIYYSAAGTQGFRAEDEGC*			MPIKVWIYYSAAGTQGFRAEDEGC*	TGTTCTCTAC	CATAACCTCA	0	E	0	MG07224.1	0	0	0
5375	2745	ao	AN3830.1	58.m07808	AO070305000068	0					-233	-195	ATGGATATACTACTCTGCGGCGGGGACGCAAGGATTTAG			ATGGATATACTACTCTGCGGCGGGGACGCAAGGATTTAG	MDILLCGGDARI*			MDILLCGGDARI*	CTATCAAAGT	GGCTGAGGAT	0	E	0	MG07224.1	0	0	0
5379	2746	af	AN8558.1	52.m03760	AO070306000055	0			-180	-94			ATGAGGGGCCCGAGTACAGAGTACGAGTGGGATAAAAGTCCTCGAGTACTCCAGCTCTTGACCCCTTCCCGCGGGTTCAACTCGTAG		ATGAGGGGCCCGAGTACAGAGTACGAGTGGGATAAAAGTCCTCGAGTACTCCAGCTCTTGACCCCTTCCCGCGGGTTCAACTCGTAG		MRGPSTEYEWDKSPRVLQLLTPSRGFNS*		MRGPSTEYEWDKSPRVLQLLTPSRGFNS*		CCTCCTGATT	AGTCAACGTT	0		0	0	0	0	0
5376	2746	an	AN8558.1	52.m03760	AO070306000055	0	-208	-182					ATGAGAATCAAGTATCACGTCCATTAG	ATGAGAATCAAGTATCACGTCCATTAG			MRIKYHVH*	MRIKYHVH*			TGAAGAACGA	ACTACCAACC	0		0	0	0	0	0
5377	2746	an	AN8558.1	52.m03760	AO070306000055	0	-156	-49					ATGCCGGTACCCCTGGCAGAGTGCTCTTCCGCGTGGAAGAGATGGGCCATTGGGGGGCATGCGTCAGCGCCTGCATCACGGCATCTTGGCGTCCAAACGGCCATTTAA	ATGCCGGTACCCCTGGCAGAGTGCTCTTCCGCGTGGAAGAGATGGGCCATTGGGGGGCATGCGTCAGCGCCTGCATCACGGCATCTTGGCGTCCAAACGGCCATTTAA			MPVPLAECSSAWKRWAIGGHASAPASRHLGVQTAI*	MPVPLAECSSAWKRWAIGGHASAPASRHLGVQTAI*			TGCCGCGTGG	CAGCAGGTGT	0		0	0	0	0	0
5378	2746	an	AN8558.1	52.m03760	AO070306000055	0	-98	-21					ATGCGTCAGCGCCTGCATCACGGCATCTTGGCGTCCAAACGGCCATTTAACAGCAGGTGTTCGCAGCTTCGGCTGTAG	ATGCGTCAGCGCCTGCATCACGGCATCTTGGCGTCCAAACGGCCATTTAACAGCAGGTGTTCGCAGCTTCGGCTGTAG			MRQRLHHGILASKRPFNSRCSQLRL*	MRQRLHHGILASKRPFNSRCSQLRL*			ATTGGGGGGC	ACAAGGTGTC	0		0	0	0	0	0
5382	2747	af	AN8232.1	53.m03737	AO070310000076	0			-179	-141			ATGCGGCTTGTTGCTCAGAAATCATCCCGCATGTTTTAA		ATGCGGCTTGTTGCTCAGAAATCATCCCGCATGTTTTAA		MRLVAQKSSRMF*		MRLVAQKSSRMF*		AACTGTCAGA	TAGATCAGGG	0	K	0	MG04877.1	NCU07757.1	YGL112C	0
5380	2747	an	AN8232.1	53.m03737	AO070310000076	0	-142	-101					ATGCCTCTTACCCTCCGCGATTCGATGTCCTCCCCAATCTGA	ATGCCTCTTACCCTCCGCGATTCGATGTCCTCCCCAATCTGA			MPLTLRDSMSSPI*	MPLTLRDSMSSPI*			AGAGACCAGA	TTGATTGATT	0	K	0	MG04877.1	NCU07757.1	YGL112C	0
5381	2747	an	AN8232.1	53.m03737	AO070310000076	0	-118	-101					ATGTCCTCCCCAATCTGA	ATGTCCTCCCCAATCTGA			MSSPI*	MSSPI*			CCGCGATTCG	TTGATTGATT	0	K	0	MG04877.1	NCU07757.1	YGL112C	0
5383	2747	ao	AN8232.1	53.m03737	AO070310000076	0					-137	-90	ATGCCCCTCACCCTCCTCGAATCCTCTCTTTTTTTTGCGATAATCTGA			ATGCCCCTCACCCTCCTCGAATCCTCTCTTTTTTTTGCGATAATCTGA	MPLTLLESSLFFAII*			MPLTLLESSLFFAII*	TGCAACCAGA	TTACTCTCTA	0	K	0	MG04877.1	NCU07757.1	YGL112C	0
5385	2749	af	AN4504.1	57.m05627	AO070311000057	0			-192	-118			ATGACAATATCTCTTATTGTCCTCGATTGGTCGCAGGTCGCCTTTTGTGGTCTCCATCGTCTCCTCTGTCTATAG		ATGACAATATCTCTTATTGTCCTCGATTGGTCGCAGGTCGCCTTTTGTGGTCTCCATCGTCTCCTCTGTCTATAG		MTISLIVLDWSQVAFCGLHRLLCL*		MTISLIVLDWSQVAFCGLHRLLCL*		ACGTCATGGC	ACTCCGCATA	0	O	0	0	0	0	0
5384	2749	an	AN4504.1	57.m05627	AO070311000057	0	-215	-177					ATGCACGACGGTCCCAGGGGAATACACTCAGTTATGTGA	ATGCACGACGGTCCCAGGGGAATACACTCAGTTATGTGA			MHDGPRGIHSVM*	MHDGPRGIHSVM*			AGACACTTGA	GATTCCCCTG	0	O	0	0	0	0	0
5386	2749	ao	AN4504.1	57.m05627	AO070311000057	0					-294	-265	ATGGTGAGTGCGACATCGTCGTACAACTGA			ATGGTGAGTGCGACATCGTCGTACAACTGA	MVSATSSYN*			MVSATSSYN*	TTCCTTGACT	GAGAGCATGA	0	O	0	0	0	0	0
5388	2750	af	AN2493.1	59.m08496	AO070312000127	0			-143	-99			ATGCACTCCTTATGCATCATGGAGGGACGGTCCTTGGCACCCTGA		ATGCACTCCTTATGCATCATGGAGGGACGGTCCTTGGCACCCTGA		MHSLCIMEGRSLAP*		MHSLCIMEGRSLAP*		CGGAAATGCA	CTAAGTTTGT	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5389	2750	af	AN2493.1	59.m08496	AO070312000127	0			-132	-82			ATGCATCATGGAGGGACGGTCCTTGGCACCCTGACTAAGTTTGTATTATGA		ATGCATCATGGAGGGACGGTCCTTGGCACCCTGACTAAGTTTGTATTATGA		MHHGGTVLGTLTKFVL*		MHHGGTVLGTLTKFVL*		TGCACTCCTT	CTTATAAAGG	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5390	2750	af	AN2493.1	59.m08496	AO070312000127	0			-125	-99			ATGGAGGGACGGTCCTTGGCACCCTGA		ATGGAGGGACGGTCCTTGGCACCCTGA		MEGRSLAP*		MEGRSLAP*		CTTATGCATC	CTAAGTTTGT	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5391	2750	af	AN2493.1	59.m08496	AO070312000127	0			-85	-50			ATGACTTATAAAGGGAGTGGTACCCTCGACGGTTGA		ATGACTTATAAAGGGAGTGGTACCCTCGACGGTTGA		MTYKGSGTLDG*		MTYKGSGTLDG*		AGTTTGTATT	ATCTGCTGTC	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5387	2750	an	AN2493.1	59.m08496	AO070312000127	0	-134	-54					ATGCGAGCACAATCTGTCGGACTCGCCCGCCTCTTGGTTCGCTCGGTCATAATAAATAGAGGAGACCGTCCCCCTGATTGA	ATGCGAGCACAATCTGTCGGACTCGCCCGCCTCTTGGTTCGCTCGGTCATAATAAATAGAGGAGACCGTCCCCCTGATTGA			MRAQSVGLARLLVRSVIINRGDRPPD*	MRAQSVGLARLLVRSVIINRGDRPPD*			CGCAGCTGCC	GATCTGTACC	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5392	2750	ao	AN2493.1	59.m08496	AO070312000127	0					-175	-101	ATGTACACAGGAGATGAGATAGCCATGCGAGGGTGGTATCTGGCCGTCGCATTCCCTTGGCATTCCACCTTTTAA			ATGTACACAGGAGATGAGATAGCCATGCGAGGGTGGTATCTGGCCGTCGCATTCCCTTGGCATTCCACCTTTTAA	MYTGDEIAMRGWYLAVAFPWHSTF*			MYTGDEIAMRGWYLAVAFPWHSTF*	GATGCATGAA	AAAGGCGCGT	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5393	2750	ao	AN2493.1	59.m08496	AO070312000127	0					-151	-101	ATGCGAGGGTGGTATCTGGCCGTCGCATTCCCTTGGCATTCCACCTTTTAA			ATGCGAGGGTGGTATCTGGCCGTCGCATTCCCTTGGCATTCCACCTTTTAA	MRGWYLAVAFPWHSTF*			MRGWYLAVAFPWHSTF*	TGAGATAGCC	AAAGGCGCGT	0	P	FG07375.1	MG04900.1	NCU01376.1	0	0
5405	2756	af	AN4576.1	57.m05496	AO070316000158	0			-203	-111			ATGTGGGACTGTGGGAGTTCCCTCCGGAAAAGTATTCAACCGGCCCATCATCATCATTCATCAATGCCAAAGTCAAGCCATGGATGGGCCTGA		ATGTGGGACTGTGGGAGTTCCCTCCGGAAAAGTATTCAACCGGCCCATCATCATCATTCATCAATGCCAAAGTCAAGCCATGGATGGGCCTGA		MWDCGSSLRKSIQPAHHHSSMPKSSHGWA*		MWDCGSSLRKSIQPAHHHSSMPKSSHGWA*		CGTCTGTGGG	ACACGAGGCC	0	HC	0	0	NCU08315.1	0	0
5406	2756	af	AN4576.1	57.m05496	AO070316000158	0			-140	-111			ATGCCAAAGTCAAGCCATGGATGGGCCTGA		ATGCCAAAGTCAAGCCATGGATGGGCCTGA		MPKSSHGWA*		MPKSSHGWA*		TCATTCATCA	ACACGAGGCC	0	HC	0	0	NCU08315.1	0	0
5407	2756	af	AN4576.1	57.m05496	AO070316000158	0			-124	-92			ATGGATGGGCCTGAACACGAGGCCTTTATTTAA		ATGGATGGGCCTGAACACGAGGCCTTTATTTAA		MDGPEHEAFI*		MDGPEHEAFI*		AAGTCAAGCC	GATATCAAAC	0	HC	0	0	NCU08315.1	0	0
5403	2756	an	AN4576.1	57.m05496	AO070316000158	0	-173	-156					ATGACACTGATAAAATGA	ATGACACTGATAAAATGA			MTLIK*	MTLIK*			GCACTGTAGA	CCCCATAAAT	0	HC	0	0	NCU08315.1	0	0
5404	2756	an	AN4576.1	57.m05496	AO070316000158	0	-159	-148					ATGACCCCATAA	ATGACCCCATAA			MTP*	MTP*			CACTGATAAA	ATGTGATTGT	0	HC	0	0	NCU08315.1	0	0
5408	2756	ao	AN4576.1	57.m05496	AO070316000158	0					-104	-60	ATGGCCGAGGACCGTGCCCAGCATTTAAATAAATCTACATCTTAA			ATGGCCGAGGACCGTGCCCAGCATTTAAATAAATCTACATCTTAA	MAEDRAQHLNKSTS*			MAEDRAQHLNKSTS*	TTCCCGCCTT	CGACATCTCG	0	HC	0	0	NCU08315.1	0	0
5411	2757	af	AN0885.1	70.m15498	AO070320000053	0			-243	-148			ATGCTTCTGATACCCCAGACGAAGACACCTAATATCGGACCTTGCCTACTGGACTGTCTGTCCACTTCCCTCCATCAGCTCCTCCATCCACTCTGA		ATGCTTCTGATACCCCAGACGAAGACACCTAATATCGGACCTTGCCTACTGGACTGTCTGTCCACTTCCCTCCATCAGCTCCTCCATCCACTCTGA		MLLIPQTKTPNIGPCLLDCLSTSLHQLLHPL*		MLLIPQTKTPNIGPCLLDCLSTSLHQLLHPL*		GTACTTCGGC	ACTTTCAATC	0	K	0	0	0	0	0
5409	2757	an	AN0885.1	70.m15498	AO070320000053	0	-229	-191					ATGCTTTTCATACCCCAGACGAAAAACATGGGCTTTTGA	ATGCTTTTCATACCCCAGACGAAAAACATGGGCTTTTGA			MLFIPQTKNMGF*	MLFIPQTKNMGF*			GGGGTCCGGC	TATCTCCACC	0	K	0	0	0	0	0
5410	2757	an	AN0885.1	70.m15498	AO070320000053	0	-202	-191					ATGGGCTTTTGA	ATGGGCTTTTGA			MGF*	MGF*			GACGAAAAAC	TATCTCCACC	0	K	0	0	0	0	0
5412	2757	ao	AN0885.1	70.m15498	AO070320000053	0					-231	-58	ATGCTTTTGATACCCCAGACGAAAAAAACCGTATCCTACTTCTCAGACCCCTCGTCCATCTTCCCCCCACTACCCATCTTCTCTCAGTATCACCTGTTATCTTTATTCTCCGGCGATTTGTTTCCCACTGAGACTGCATTGATTATTACCACTTCCCCTGACTGGTGTCATTGA			ATGCTTTTGATACCCCAGACGAAAAAAACCGTATCCTACTTCTCAGACCCCTCGTCCATCTTCCCCCCACTACCCATCTTCTCTCAGTATCACCTGTTATCTTTATTCTCCGGCGATTTGTTTCCCACTGAGACTGCATTGATTATTACCACTTCCCCTGACTGGTGTCATTGA	MLLIPQTKKTVSYFSDPSSIFPPLPIFSQYHLLSLFSGDLFPTETALIITTSPDWCH*			MLLIPQTKKTVSYFSDPSSIFPPLPIFSQYHLLSLFSGDLFPTETALIITTSPDWCH*	TGGTTTCGGC	AGCACCACAG	0	K	0	0	0	0	0
5415	2758	af	AN8757.1	62.m03452	AO070321000005	0			-247	-104			ATGTTAGGAAAGGCAGGTCTCGCCGATCTCTGGTCTGATACGAGTGTTCTCATATTGGTCGTTTATCGTGGTTTGTTTGTTATATACGAAGTAGTCCGCATGGTTATAACTCTACCCTGGAAGCCAAGCAGGCTATTTGGGTAA		ATGTTAGGAAAGGCAGGTCTCGCCGATCTCTGGTCTGATACGAGTGTTCTCATATTGGTCGTTTATCGTGGTTTGTTTGTTATATACGAAGTAGTCCGCATGGTTATAACTCTACCCTGGAAGCCAAGCAGGCTATTTGGGTAA		MLGKAGLADLWSDTSVLILVVYRGLFVIYEVVRMVITLPWKPSRLFG*		MLGKAGLADLWSDTSVLILVVYRGLFVIYEVVRMVITLPWKPSRLFG*		ATGGGGTAAG	CATGCTCTCA	0	P	0	0	0	0	0
5416	2758	af	AN8757.1	62.m03452	AO070321000005	0			-148	-104			ATGGTTATAACTCTACCCTGGAAGCCAAGCAGGCTATTTGGGTAA		ATGGTTATAACTCTACCCTGGAAGCCAAGCAGGCTATTTGGGTAA		MVITLPWKPSRLFG*		MVITLPWKPSRLFG*		AGTAGTCCGC	CATGCTCTCA	0	P	0	0	0	0	0
5417	2758	af	AN8757.1	62.m03452	AO070321000005	0			-102	-88			ATGCTCTCAGCATAG		ATGCTCTCAGCATAG		MLSA*		MLSA*		TTTGGGTAAC	TGCATCTTGA	0	P	0	0	0	0	0
5413	2758	an	AN8757.1	62.m03452	AO070321000005	0	-245	-165					ATGTACGGATGGAGACTCCGCACTTTTGCCTGGTCGAGAGAGGCGCTAGTCTGGTTAACTTTTTCGGCTCTGAGGAGTTGA	ATGTACGGATGGAGACTCCGCACTTTTGCCTGGTCGAGAGAGGCGCTAGTCTGGTTAACTTTTTCGGCTCTGAGGAGTTGA			MYGWRLRTFAWSREALVWLTFSALRS*	MYGWRLRTFAWSREALVWLTFSALRS*			TGGGAGTGTG	GGAGTTGGCG	0	P	0	0	0	0	0
5414	2758	an	AN8757.1	62.m03452	AO070321000005	0	-237	-61					ATGGAGACTCCGCACTTTTGCCTGGTCGAGAGAGGCGCTAGTCTGGTTAACTTTTTCGGCTCTGAGGAGTTGAGGAGTTGGCGTGTATCCTCCGGGGGGGAGCCATTCAGCGTTTCCACCGCAGAACGGGCCCCTGACCCTTGTCTCCTGTTGATTTATATACCTCGCTCGCTGTGA	ATGGAGACTCCGCACTTTTGCCTGGTCGAGAGAGGCGCTAGTCTGGTTAACTTTTTCGGCTCTGAGGAGTTGAGGAGTTGGCGTGTATCCTCCGGGGGGGAGCCATTCAGCGTTTCCACCGCAGAACGGGCCCCTGACCCTTGTCTCCTGTTGATTTATATACCTCGCTCGCTGTGA			METPHFCLVERGASLVNFFGSEELRSWRVSSGGEPFSVSTAERAPDPCLLLIYIPRSL*	METPHFCLVERGASLVNFFGSEELRSWRVSSGGEPFSVSTAERAPDPCLLLIYIPRSL*			TGATGTACGG	TACCCGACTT	0	P	0	0	0	0	0
5418	2758	ao	AN8757.1	62.m03452	AO070321000005	0					-250	-209	ATGGGTGTAGGAGAGGCATTTGGGTTCTCTGAGTGGTTGTAA			ATGGGTGTAGGAGAGGCATTTGGGTTCTCTGAGTGGTTGTAA	MGVGEAFGFSEWL*			MGVGEAFGFSEWL*	CAGGCAGTTT	GTAAGGCAGT	0	P	0	0	0	0	0

5419	2758	ao	AN8757.1	62.m03452	AO070321000005	0					-196	-125	ATGCTGACCCGAATCGTCTATAAAAACCGGTCAAAAGGCACATGCGGCATTCCTGACCTGCATTCTAAATAA			ATGCTGACCCGAATCGTCTATAAAAACCGGTCAAAAGGCACATGCGGCATTCCTGACCTGCATTCTAAATAA	MLTRIVYKNRSKGTCGIPDLHSK*			MLTRIVYKNRSKGTCGIPDLHSK*	AAGGCAGTGG	GTGTTCGCAA	0	P	0	0	0	0	0
5420	2758	ao	AN8757.1	62.m03452	AO070321000005	0					-155	-141	ATGCGGCATTCCTGA			ATGCGGCATTCCTGA	MRHS*			MRHS*	CAAAAGGCAC	CCTGCATTCT	0	P	0	0	0	0	0
5425	2759	af	AN0142.1	71.m15425	AO070321000107	0			-209	-174			ATGGAGAGGTACCACAAAAAATGGTGGAGGAAATGA		ATGGAGAGGTACCACAAAAAATGGTGGAGGAAATGA		MERYHKKWWRK*		MERYHKKWWRK*		GTACACTGGG	AGTGTTGCGG	0	J	0	0	0	0	0
5426	2759	af	AN0142.1	71.m15425	AO070321000107	0			-189	-55			ATGGTGGAGGAAATGAAGTGTTGCGGAAAGGGCGGACGCGGATTGGCTGGAGGCTCTCCGCTGAGAATTTCACCATCCCGTCGATTGTTCCCTTCTGCCATCTCTCACTTACTCCATCACGCGGCCCATCTATAG		ATGGTGGAGGAAATGAAGTGTTGCGGAAAGGGCGGACGCGGATTGGCTGGAGGCTCTCCGCTGAGAATTTCACCATCCCGTCGATTGTTCCCTTCTGCCATCTCTCACTTACTCCATCACGCGGCCCATCTATAG		MVEEMKCCGKGGRGLAGGSPLRISPSRRLFPSAISHLLHHAAHL*		MVEEMKCCGKGGRGLAGGSPLRISPSRRLFPSAISHLLHHAAHL*		ACCACAAAAA	CGCCAATTCC	0	J	0	0	0	0	0
5427	2759	af	AN0142.1	71.m15425	AO070321000107	0			-177	-55			ATGAAGTGTTGCGGAAAGGGCGGACGCGGATTGGCTGGAGGCTCTCCGCTGAGAATTTCACCATCCCGTCGATTGTTCCCTTCTGCCATCTCTCACTTACTCCATCACGCGGCCCATCTATAG		ATGAAGTGTTGCGGAAAGGGCGGACGCGGATTGGCTGGAGGCTCTCCGCTGAGAATTTCACCATCCCGTCGATTGTTCCCTTCTGCCATCTCTCACTTACTCCATCACGCGGCCCATCTATAG		MKCCGKGGRGLAGGSPLRISPSRRLFPSAISHLLHHAAHL*		MKCCGKGGRGLAGGSPLRISPSRRLFPSAISHLLHHAAHL*		GGTGGAGGAA	CGCCAATTCC	0	J	0	0	0	0	0
5421	2759	an	AN0142.1	71.m15425	AO070321000107	0	-249	-142					ATGGAGAAGAAAAGCAGCATCAAAAATGAAGAAGAGGAAGTCGAGAATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGATTGGCCAGCTTGGATGCTGA	ATGGAGAAGAAAAGCAGCATCAAAAATGAAGAAGAGGAAGTCGAGAATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGATTGGCCAGCTTGGATGCTGA			MEKKSSIKNEEEEVENGRKSIPSKKGRALIGQLGC*	MEKKSSIKNEEEEVENGRKSIPSKKGRALIGQLGC*			TTCCTAAATT	GCTGAGATTT	0	J	0	0	0	0	0
5422	2759	an	AN0142.1	71.m15425	AO070321000107	0	-224	-162					ATGAAGAAGAGGAAGTCGAGAATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGA	ATGAAGAAGAGGAAGTCGAGAATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGA			MKKRKSRMGGNPSQAKKDEL*	MKKRKSRMGGNPSQAKKDEL*			AGCATCAAAA	TTGGCCAGCT	0	J	0	0	0	0	0
5423	2759	an	AN0142.1	71.m15425	AO070321000107	0	-203	-162					ATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGA	ATGGGCGGAAATCCATCCCAAGCAAAAAAGGACGAGCTTTGA			MGGNPSQAKKDEL*	MGGNPSQAKKDEL*			GAAGTCGAGA	TTGGCCAGCT	0	J	0	0	0	0	0
5424	2759	an	AN0142.1	71.m15425	AO070321000107	0	-148	-137					ATGCTGAGCTGA	ATGCTGAGCTGA			MLS*	MLS*			GCCAGCTTGG	GATTTTCTCT	0	J	0	0	0	0	0
5428	2759	ao	AN0142.1	71.m15425	AO070321000107	0					-206	-138	ATGAGTGACCAAAAAAAGGTGGGCGGCAATTGGTCGAACCGCTCCGCTGAGAATTTCGCCGGCTTTTAG			ATGAGTGACCAAAAAAAGGTGGGCGGCAATTGGTCGAACCGCTCCGCTGAGAATTTCGCCGGCTTTTAG	MSDQKKVGGNWSNRSAENFAGF*			MSDQKKVGGNWSNRSAENFAGF*	GAGGGACAAG	TCCTTCAGTT	0	J	0	0	0	0	0
5431	2760	af	AN8004.1	53.m04146	AO070322000036	0			-194	-150			ATGCAGGGTGAGCTCAGCTGGAGATGTGTTACACAAATCAGGTAG		ATGCAGGGTGAGCTCAGCTGGAGATGTGTTACACAAATCAGGTAG		MQGELSWRCVTQIR*		MQGELSWRCVTQIR*		TGATACAGCT	CAGGTGCAAA	0	Q	0	0	0	0	0
5432	2760	af	AN8004.1	53.m04146	AO070322000036	0			-171	-28			ATGTGTTACACAAATCAGGTAGCAGGTGCAAAGGAACCTGCCGTCATGAACCTTCTGGGGAAGTCCATTGGATTTAAGTCGCAGTATTCCCCTCCCGCGCGGTCAGTATGTATCCTTTCAGCTTTGTTTGGGAATTGTTTCTGA		ATGTGTTACACAAATCAGGTAGCAGGTGCAAAGGAACCTGCCGTCATGAACCTTCTGGGGAAGTCCATTGGATTTAAGTCGCAGTATTCCCCTCCCGCGCGGTCAGTATGTATCCTTTCAGCTTTGTTTGGGAATTGTTTCTGA		MCYTNQVAGAKEPAVMNLLGKSIGFKSQYSPPARSVCILSALFGNCF*		MCYTNQVAGAKEPAVMNLLGKSIGFKSQYSPPARSVCILSALFGNCF*		TCAGCTGGAG	TTGAGTGGTG	0	Q	0	0	0	0	0
5433	2760	af	AN8004.1	53.m04146	AO070322000036	0			-126	-28			ATGAACCTTCTGGGGAAGTCCATTGGATTTAAGTCGCAGTATTCCCCTCCCGCGCGGTCAGTATGTATCCTTTCAGCTTTGTTTGGGAATTGTTTCTGA		ATGAACCTTCTGGGGAAGTCCATTGGATTTAAGTCGCAGTATTCCCCTCCCGCGCGGTCAGTATGTATCCTTTCAGCTTTGTTTGGGAATTGTTTCTGA		MNLLGKSIGFKSQYSPPARSVCILSALFGNCF*		MNLLGKSIGFKSQYSPPARSVCILSALFGNCF*		ACCTGCCGTC	TTGAGTGGTG	0	Q	0	0	0	0	0
5429	2760	an	AN8004.1	53.m04146	AO070322000036	0	-177	-112					ATGGCTGATTATTCCAGCTCTGCAGATTCATCGTCGTGGCACGGCTGGCTGGTTAAAAGCTGCTGA	ATGGCTGATTATTCCAGCTCTGCAGATTCATCGTCGTGGCACGGCTGGCTGGTTAAAAGCTGCTGA			MADYSSSADSSSWHGWLVKSC*	MADYSSSADSSSWHGWLVKSC*			GGGCGAATCA	GCTTCCCCGT	0	Q	0	0	0	0	0
5430	2760	an	AN8004.1	53.m04146	AO070322000036	0	-99	-37					ATGGTACCGAGATCTGGAGTCTACTTTTCCACGGTTCACTTATCTATTCATCCATACGCTTAA	ATGGTACCGAGATCTGGAGTCTACTTTTCCACGGTTCACTTATCTATTCATCCATACGCTTAA			MVPRSGVYFSTVHLSIHPYA*	MVPRSGVYFSTVHLSIHPYA*			TTCCCCGTTG	TATCTAATTA	0	Q	0	0	0	0	0
5434	2760	ao	AN8004.1	53.m04146	AO070322000036	0					-162	-85	ATGGCTGGCGCCAGTGGTTGCACGGGCAAGAACGGGGACGAATGTGTAGGATGGGGCAGGAGAGCACCTGGCGGATAG			ATGGCTGGCGCCAGTGGTTGCACGGGCAAGAACGGGGACGAATGTGTAGGATGGGGCAGGAGAGCACCTGGCGGATAG	MAGASGCTGKNGDECVGWGRRAPGG*			MAGASGCTGKNGDECVGWGRRAPGG*	TTCACAAATC	GAAATTTAAA	0	Q	0	0	0	0	0
5435	2760	ao	AN8004.1	53.m04146	AO070322000036	0					-121	-53	ATGTGTAGGATGGGGCAGGAGAGCACCTGGCGGATAGGAAATTTAAATTGCCTGCCCACTGGCACCTGA			ATGTGTAGGATGGGGCAGGAGAGCACCTGGCGGATAGGAAATTTAAATTGCCTGCCCACTGGCACCTGA	MCRMGQESTWRIGNLNCLPTGT*			MCRMGQESTWRIGNLNCLPTGT*	ACGGGGACGA	ACCTCCTCCC	0	Q	0	0	0	0	0
5436	2760	ao	AN8004.1	53.m04146	AO070322000036	0					-112	-53	ATGGGGCAGGAGAGCACCTGGCGGATAGGAAATTTAAATTGCCTGCCCACTGGCACCTGA			ATGGGGCAGGAGAGCACCTGGCGGATAGGAAATTTAAATTGCCTGCCCACTGGCACCTGA	MGQESTWRIGNLNCLPTGT*			MGQESTWRIGNLNCLPTGT*	AATGTGTAGG	ACCTCCTCCC	0	Q	0	0	0	0	0
5437	2761	an	AN8056.1	53.m03887	AO070322000144	0	-208	-167					ATGCTCCGCCCCGTGACTCTCAGCAACGGTTATAACGAGTAG	ATGCTCCGCCCCGTGACTCTCAGCAACGGTTATAACGAGTAG			MLRPVTLSNGYNE*	MLRPVTLSNGYNE*			GTGTTTGTTT	TGGCAGCAGC	0	BD	0	MG08841.1	0	0	0
5446	2762	af	AN1735.1	69.m15034	AO070324000065	0			-223	-203			ATGACGTCTCCTCCGCCGTGA		ATGACGTCTCCTCCGCCGTGA		MTSPPP*		MTSPPP*		AAAGGCACCG	TGTAATTCCA	0	F	0	0	0	0	0
5447	2762	af	AN1735.1	69.m15034	AO070324000065	0			-171	-115			ATGCGCTGTCCGATTGCCACTGGATGTTCGTTCAATAAGAGATCCTGGTCCATGTAA		ATGCGCTGTCCGATTGCCACTGGATGTTCGTTCAATAAGAGATCCTGGTCCATGTAA		MRCPIATGCSFNKRSWSM*		MRCPIATGCSFNKRSWSM*		TTCAAGCCGG	AGTAGTCAAT	0	F	0	0	0	0	0
5448	2762	af	AN1735.1	69.m15034	AO070324000065	0			-148	-134			ATGTTCGTTCAATAA		ATGTTCGTTCAATAA		MFVQ*		MFVQ*		TTGCCACTGG	GAGATCCTGG	0	F	0	0	0	0	0
5444	2762	an	AN1735.1	69.m15034	AO070324000065	0	-105	-28					ATGCTTGTGATGCTATTTATCTTCCAACCATCTGCGTACACCTTCATTCCAAGCTATATCCTCTCCAAACAAAAATAG	ATGCTTGTGATGCTATTTATCTTCCAACCATCTGCGTACACCTTCATTCCAAGCTATATCCTCTCCAAACAAAAATAG			MLVMLFIFQPSAYTFIPSYILSKQK*	MLVMLFIFQPSAYTFIPSYILSKQK*			ATGTAAGATA	CGATTCACAA	0	F	0	0	0	0	0
5445	2762	an	AN1735.1	69.m15034	AO070324000065	0	-96	-28					ATGCTATTTATCTTCCAACCATCTGCGTACACCTTCATTCCAAGCTATATCCTCTCCAAACAAAAATAG	ATGCTATTTATCTTCCAACCATCTGCGTACACCTTCATTCCAAGCTATATCCTCTCCAAACAAAAATAG			MLFIFQPSAYTFIPSYILSKQK*	MLFIFQPSAYTFIPSYILSKQK*			AATGCTTGTG	CGATTCACAA	0	F	0	0	0	0	0
5449	2762	ao	AN1735.1	69.m15034	AO070324000065	0					-81	-61	ATGCGCGGAATTCAGCGATGA			ATGCGCGGAATTCAGCGATGA	MRGIQR*			MRGIQR*	CTATTCAAGT	TCTTCAACAC	0	F	0	0	0	0	0
5452	2764	af	AN7751.1	71.m15782	AO070325000182	0			-210	-157			ATGCAAACTTTCCGCTGGAGCTCAGCAAAAAGTCCACCGAAATTGCCCTGTTGA		ATGCAAACTTTCCGCTGGAGCTCAGCAAAAAGTCCACCGAAATTGCCCTGTTGA		MQTFRWSSAKSPPKLPC*		MQTFRWSSAKSPPKLPC*		GTGCACCGCC	ATATTCCAAC	0	I	0	0	0	0	0
5451	2764	an	AN7751.1	71.m15782	AO070325000182	0	-63	-49					ATGAGCAATTGGTGA	ATGAGCAATTGGTGA			MSNW*	MSNW*			TTTATCCTGC	TATTCCAACA	0	I	0	0	0	0	0
5454	2764	ao	AN7751.1	71.m15782	AO070325000182	0					-232	-83	ATGGGACCACAAGCAGTACGGCGGCCGGAAGAAACCAATGTTACTCCGTACTTGCAAACTTTCCGCCGAAAATCATCTATCTCAAAACTCCGACCGTCAATTGCGATAGTTCCCCAGCTTGCTCTCTTGGCTTGCACTACTCAGAATTAA			ATGGGACCACAAGCAGTACGGCGGCCGGAAGAAACCAATGTTACTCCGTACTTGCAAACTTTCCGCCGAAAATCATCTATCTCAAAACTCCGACCGTCAATTGCGATAGTTCCCCAGCTTGCTCTCTTGGCTTGCACTACTCAGAATTAA	MGPQAVRRPEETNVTPYLQTFRRKSSISKLRPSIAIVPQLALLACTTQN*			MGPQAVRRPEETNVTPYLQTFRRKSSISKLRPSIAIVPQLALLACTTQN*	AAAGGAACGA	ACGTCAATCT	0	I	0	0	0	0	0
5455	2764	ao	AN7751.1	71.m15782	AO070325000182	0					-195	-124	ATGTTACTCCGTACTTGCAAACTTTCCGCCGAAAATCATCTATCTCAAAACTCCGACCGTCAATTGCGATAG			ATGTTACTCCGTACTTGCAAACTTTCCGCCGAAAATCATCTATCTCAAAACTCCGACCGTCAATTGCGATAG	MLLRTCKLSAENHLSQNSDRQLR*			MLLRTCKLSAENHLSQNSDRQLR*	GAAGAAACCA	TTCCCCAGCT	0	I	0	0	0	0	0
5459	2765	af	AN6570.1	62.m03157	AO070326000013	0			-93	-79			ATGCTGGCATCCTAA		ATGCTGGCATCCTAA		MLAS*		MLAS*		TGGCGCGCTG	CATACAGTAG	0	G	0	0	0	0	0
5457	2765	an	AN6570.1	62.m03157	AO070326000013	0	-266	-132					ATGTGTACCCTGCTTATACATGATAGACTATTTATTTCCTTCTCTCCCCGCATTCCCTCCCTTGACTCACCGAGCAACCTCCGTCCGCTCACGTTGATCCTTTGGCCTTGTGCCCCTCCGAGGTCGACGGCTTAA	ATGTGTACCCTGCTTATACATGATAGACTATTTATTTCCTTCTCTCCCCGCATTCCCTCCCTTGACTCACCGAGCAACCTCCGTCCGCTCACGTTGATCCTTTGGCCTTGTGCCCCTCCGAGGTCGACGGCTTAA			MCTLLIHDRLFISFSPRIPSLDSPSNLRPLTLILWPCAPPRSTA*	MCTLLIHDRLFISFSPRIPSLDSPSNLRPLTLILWPCAPPRSTA*			CTCTTACCCT	TACGGATGTC	0	G	0	0	0	0	0
5458	2765	an	AN6570.1	62.m03157	AO070326000013	0	-247	-170					ATGATAGACTATTTATTTCCTTCTCTCCCCGCATTCCCTCCCTTGACTCACCGAGCAACCTCCGTCCGCTCACGTTGA	ATGATAGACTATTTATTTCCTTCTCTCCCCGCATTCCCTCCCTTGACTCACCGAGCAACCTCCGTCCGCTCACGTTGA			MIDYLFPSLPAFPPLTHRATSVRSR*	MIDYLFPSLPAFPPLTHRATSVRSR*			CTGCTTATAC	TCCTTTGGCC	0	G	0	0	0	0	0
5465	2767	an	AN4834.1	59.m09144	AO070327000147	0	-184	-47					ATGAGCGTTGCGCGATCGGTGTCTTCCTCGTCGACCCTCTCCCCGTCGCTGGACCTGTCGCTCGACCTGTCGCATATAGCGGGTTCCTTCTTCATTGCCGGTCGATTCCAACCCCGCCTAATAACACCTTGCGGATAA	ATGAGCGTTGCGCGATCGGTGTCTTCCTCGTCGACCCTCTCCCCGTCGCTGGACCTGTCGCTCGACCTGTCGCATATAGCGGGTTCCTTCTTCATTGCCGGTCGATTCCAACCCCGCCTAATAACACCTTGCGGATAA			MSVARSVSSSSTLSPSLDLSLDLSHIAGSFFIAGRFQPRLITPCG*	MSVARSVSSSSTLSPSLDLSLDLSHIAGSFFIAGRFQPRLITPCG*			GGACGAGCCG	GTGCGCTGCA	0		0	0	0	0	0
5467	2768	an	AN3634.1	58.m07467	AO070328000078	0	-194	-183					ATGGCGGTGTGA	ATGGCGGTGTGA			MAV*	MAV*			CGTATTTGCT	TTTTGCCGTG	0	E	FG00598.1	MG05168.1	NCU04411.1	0	0
5468	2768	an	AN3634.1	58.m07467	AO070328000078	0	-135	-49					ATGTGTCACAGGGCGATCGTCAATTATTGGAACAAAGCACTTATAAAGCCGCGCAGCCGGCAGTTGAAGGCTCACTGTTTCGAATAA	ATGTGTCACAGGGCGATCGTCAATTATTGGAACAAAGCACTTATAAAGCCGCGCAGCCGGCAGTTGAAGGCTCACTGTTTCGAATAA			MCHRAIVNYWNKALIKPRSRQLKAHCFE*	MCHRAIVNYWNKALIKPRSRQLKAHCFE*			CGAGAGTAGT	CTGTTCGCCA	0	E	FG00598.1	MG05168.1	NCU04411.1	0	0
5473	2770	af	AN3224.1	67.m02932	AO070330000074	0			-166	-149			ATGAGCATACAACCATAG		ATGAGCATACAACCATAG		MSIQP*		MSIQP*		TATCATCAGC	TCGACTGACT	0		0	0	0	0	0
5474	2770	af	AN3224.1	67.m02932	AO070330000074	0			-119	-27			ATGTCTGAGCTCTGGCTGTCACGTGCCTCGGCGTCACTTCCATCTTCATTTCCAGCCTTGAGAAATCTTTCAGCGCTGCTCACAAGTCGTTGA		ATGTCTGAGCTCTGGCTGTCACGTGCCTCGGCGTCACTTCCATCTTCATTTCCAGCCTTGAGAAATCTTTCAGCGCTGCTCACAAGTCGTTGA		MSELWLSRASASLPSSFPALRNLSALLTSR*		MSELWLSRASASLPSSFPALRNLSALLTSR*		GAATTTGGCG	CGCAGGGCGC	0		0	0	0	0	0
5472	2770	an	AN3224.1	67.m02932	AO070330000074	0	-184	-173					ATGAGGTCGTAA	ATGAGGTCGTAA			MRS*	MRS*			TAATGGAATA	CCACCCTTTA	0		0	0	0	0	0
5475	2770	ao	AN3224.1	67.m02932	AO070330000074	0					-208	-191	ATGTTCCGATTGTTTTAA			ATGTTCCGATTGTTTTAA	MFRLF*			MFRLF*	GTTAAACAAG	AAAAGTATAC	0		0	0	0	0	0
5476	2770	ao	AN3224.1	67.m02932	AO070330000074	0					-175	-158	ATGAAATTGCTGTTTTAA			ATGAAATTGCTGTTTTAA	MKLLF*			MKLLF*	TATACCACCA	GGGCTACACA	0		0	0	0	0	0
5478	2774	af	AN3498.1	58.m07225	AO070333000036	0			-241	-131			ATGGAGTACGTTGGGACACGGTGTCGCCCGAAACTGCTCCAAAACGCCCAATTTGGTTTTCTGGATCGGTTTGGGATGGAGTGCAGGATTAGGGCTGAGACTATTATTTAA		ATGGAGTACGTTGGGACACGGTGTCGCCCGAAACTGCTCCAAAACGCCCAATTTGGTTTTCTGGATCGGTTTGGGATGGAGTGCAGGATTAGGGCTGAGACTATTATTTAA		MEYVGTRCRPKLLQNAQFGFLDRFGMECRIRAETII*		MEYVGTRCRPKLLQNAQFGFLDRFGMECRIRAETII*		GCGCGGACAG	ATCGATCTCT	0	R	0	0	0	0	0
5479	2774	af	AN3498.1	58.m07225	AO070333000036	0			-166	-131			ATGGAGTGCAGGATTAGGGCTGAGACTATTATTTAA		ATGGAGTGCAGGATTAGGGCTGAGACTATTATTTAA		MECRIRAETII*		MECRIRAETII*		TCGGTTTGGG	ATCGATCTCT	0	R	0	0	0	0	0
5477	2774	an	AN3498.1	58.m07225	AO070333000036	0	-182	-102					ATGCGGAACAGAATCCTCAGTTTCTGCACCACACTTCTGGAGTTCGGGCGTTTCTGTGGAGGCGGAGCACTTATGGGCTAG	ATGCGGAACAGAATCCTCAGTTTCTGCACCACACTTCTGGAGTTCGGGCGTTTCTGTGGAGGCGGAGCACTTATGGGCTAG			MRNRILSFCTTLLEFGRFCGGGALMG*	MRNRILSFCTTLLEFGRFCGGGALMG*			TGCTCCACCA	TAATTGCCTC	0	R	0	0	0	0	0
5481	2774	ao	AN3498.1	58.m07225	AO070333000036	0					-146	-117	ATGCAATCTCAAAATTCATTCATATTATAG			ATGCAATCTCAAAATTCATTCATATTATAG	MQSQNSFIL*			MQSQNSFIL*	TAATTCAGGA	GCCACGGTAT	0	R	0	0	0	0	0
5485	2775	af	AN0295.1	54.m06466	AO070334000046	0			-245	-210			ATGTGGCTGCAGTGTAACACACTGGTAACACCGTGA		ATGTGGCTGCAGTGTAACACACTGGTAACACCGTGA		MWLQCNTLVTP*		MWLQCNTLVTP*		CTGGCTTGCA	CGGGCGATGA	0	YU	FG01216.1	0	0	0	0
5486	2775	af	AN0295.1	54.m06466	AO070334000046	0			-203	-162			ATGACGATAGAGCTCCGTTGCCTTTTGCCCGCCTTTGGATAA		ATGACGATAGAGCTCCGTTGCCTTTTGCCCGCCTTTGGATAA		MTIELRCLLPAFG*		MTIELRCLLPAFG*		GTGACGGGCG	GCACCTCCAC	0	YU	FG01216.1	0	0	0	0
5482	2775	an	AN0295.1	54.m06466	AO070334000046	0	-173	-150					ATGAACTGTGCTGACTTGACTTAG	ATGAACTGTGCTGACTTGACTTAG			MNCADLT*	MNCADLT*			CCATTACGAC	TTTCCACCAT	0	YU	FG01216.1	0	0	0	0
5483	2775	an	AN0295.1	54.m06466	AO070334000046	0	-118	-68					ATGTCCTCTACTTCTCAGAAATTACTCAATCTATGGAATGAGCATAAGTGA	ATGTCCTCTACTTCTCAGAAATTACTCAATCTATGGAATGAGCATAAGTGA			MSSTSQKLLNLWNEHK*	MSSTSQKLLNLWNEHK*			TTTCCTGCAT	GATAGACATA	0	YU	FG01216.1	0	0	0	0

5484	2775	an	AN0295.1	54.m06466	AO070334000046	0	-81	-43					ATGAGCATAAGTGAGATAGACATAATTCTCATCCTCTAA	ATGAGCATAAGTGAGATAGACATAATTCTCATCCTCTAA			MSISEIDIILIL*	MSISEIDIILIL*			AATCTATGGA	ACACCTCTAC	0	YU	FG01216.1	0	0	0	0
5487	2775	ao	AN0295.1	54.m06466	AO070334000046	0					-213	-100	ATGACGATAGAGCTCTTCCGCCTTCTCGTCTTCTCCAGCTTGAGCTCTCACTCTCACTCGTGTCTCCAAACCCGCCACTGCCTCACTATACCTTATGCTTTCCCACCGTCATGA			ATGACGATAGAGCTCTTCCGCCTTCTCGTCTTCTCCAGCTTGAGCTCTCACTCTCACTCGTGTCTCCAAACCCGCCACTGCCTCACTATACCTTATGCTTTCCCACCGTCATGA	MTIELFRLLVFSSLSSHSHSCLQTRHCLTIPYAFPPS*			MTIELFRLLVFSSLSSHSHSCLQTRHCLTIPYAFPPS*	ACCGGCGGCG	TTCCATGAAC	0	YU	FG01216.1	0	0	0	0
5488	2775	ao	AN0295.1	54.m06466	AO070334000046	0					-119	-81	ATGCTTTCCCACCGTCATGATTCCATGAACGCAATCTAG			ATGCTTTCCCACCGTCATGATTCCATGAACGCAATCTAG	MLSHRHDSMNAI*			MLSHRHDSMNAI*	ACTATACCTT	TTTTCCGTAT	0	YU	FG01216.1	0	0	0	0
5489	2775	ao	AN0295.1	54.m06466	AO070334000046	0					-103	-92	ATGATTCCATGA			ATGATTCCATGA	MIP*			MIP*	TCCCACCGTC	ACGCAATCTA	0	YU	FG01216.1	0	0	0	0
5490	2775	ao	AN0295.1	54.m06466	AO070334000046	0					-95	-81	ATGAACGCAATCTAG			ATGAACGCAATCTAG	MNAI*			MNAI*	TCATGATTCC	TTTTCCGTAT	0	YU	FG01216.1	0	0	0	0
5494	2776	af	AN0294.1	54.m06492	AO070334000047	0			-227	-198			ATGAACCACTGTCTGCTGCGTTCGCCATGA		ATGAACCACTGTCTGCTGCGTTCGCCATGA		MNHCLLRSP*		MNHCLLRSP*		GCTCGACCTA	CGTCAATTTC	0	R	0	0	0	0	0
5495	2776	af	AN0294.1	54.m06492	AO070334000047	0			-201	-148			ATGACGTCAATTTCACCTGGCTTAGTATCAGTAGCAGGTACCCCTCTATTGTAA		ATGACGTCAATTTCACCTGGCTTAGTATCAGTAGCAGGTACCCCTCTATTGTAA		MTSISPGLVSVAGTPLL*		MTSISPGLVSVAGTPLL*		TGCGTTCGCC	TTATATATTG	0	R	0	0	0	0	0
5491	2776	an	AN0294.1	54.m06492	AO070334000047	0	-202	-143					ATGAATTCAATGCAGGCCTGTCCAACAGCAACAATCAGCTTAGTCAAGCACAGCAACTAG	ATGAATTCAATGCAGGCCTGTCCAACAGCAACAATCAGCTTAGTCAAGCACAGCAACTAG			MNSMQACPTATISLVKHSN*	MNSMQACPTATISLVKHSN*			GTCACAAACA	TTATCAACAT	0	R	0	0	0	0	0
5492	2776	an	AN0294.1	54.m06492	AO070334000047	0	-193	-143					ATGCAGGCCTGTCCAACAGCAACAATCAGCTTAGTCAAGCACAGCAACTAG	ATGCAGGCCTGTCCAACAGCAACAATCAGCTTAGTCAAGCACAGCAACTAG			MQACPTATISLVKHSN*	MQACPTATISLVKHSN*			AATGAATTCA	TTATCAACAT	0	R	0	0	0	0	0
5493	2776	an	AN0294.1	54.m06492	AO070334000047	0	-134	-69					ATGGTGGGTGGTGCATGCAATGACGTCAGCACCGTCATATCAATATCCGCCACGGGCAGTTTATAA	ATGGTGGGTGGTGCATGCAATGACGTCAGCACCGTCATATCAATATCCGCCACGGGCAGTTTATAA			MVGGACNDVSTVISISATGSL*	MVGGACNDVSTVISISATGSL*			AGTTATCAAC	CGTGTCTTTC	0	R	0	0	0	0	0
5496	2776	ao	AN0294.1	54.m06492	AO070334000047	0					-180	-166	ATGTCCTACCCATGA			ATGTCCTACCCATGA	MSYP*			MSYP*	CTGGAGGCGC	CGTCACCTCA	0	R	0	0	0	0	0
5497	2776	ao	AN0294.1	54.m06492	AO070334000047	0					-169	-149	ATGACGTCACCTCAGCTCTGA			ATGACGTCACCTCAGCTCTGA	MTSPQL*			MTSPQL*	TGTCCTACCC	GGAATCTCGG	0	R	0	0	0	0	0
5502	2777	af	AN8412.1	56.m02506	AO070336000018	0			-226	-152			ATGCCACCAATCGTATCGGGTGTCGGAAGGCCGAAGATTGGGGAGAACGCTGAGAGTAAGGCTCCTGAGGTCTAG		ATGCCACCAATCGTATCGGGTGTCGGAAGGCCGAAGATTGGGGAGAACGCTGAGAGTAAGGCTCCTGAGGTCTAG		MPPIVSGVGRPKIGENAESKAPEV*		MPPIVSGVGRPKIGENAESKAPEV*		GGTGGTTGTG	GGGATTTGAC	0	Q	0	0	0	0	0
5503	2777	af	AN8412.1	56.m02506	AO070336000018	0			-124	-50			ATGCAGCCTATTCCAATCTCTGTGTGTAGCTCAAGGTCTAGAACAATAACAAAACACGTTCCATGCCCGACCTGA		ATGCAGCCTATTCCAATCTCTGTGTGTAGCTCAAGGTCTAGAACAATAACAAAACACGTTCCATGCCCGACCTGA		MQPIPISVCSSRSRTITKHVPCPT*		MQPIPISVCSSRSRTITKHVPCPT*		AAGGGTGAAT	CACACATCTC	0	Q	0	0	0	0	0
5504	2777	af	AN8412.1	56.m02506	AO070336000018	0			-62	-27			ATGCCCGACCTGACACACATCTCCCCTGTTCAGTGA		ATGCCCGACCTGACACACATCTCCCCTGTTCAGTGA		MPDLTHISPVQ*		MPDLTHISPVQ*		AACACGTTCC	TACGATTCCA	0	Q	0	0	0	0	0
5498	2777	an	AN8412.1	56.m02506	AO070336000018	0	-184	-152					ATGACCTATGTATACCTTGGTGATGCAGTATAG	ATGACCTATGTATACCTTGGTGATGCAGTATAG			MTYVYLGDAV*	MTYVYLGDAV*			TGCGTTGCGG	GTACCAGCTG	0	Q	0	0	0	0	0
5499	2777	an	AN8412.1	56.m02506	AO070336000018	0	-177	-133					ATGTATACCTTGGTGATGCAGTATAGGTACCAGCTGGATGTATAA	ATGTATACCTTGGTGATGCAGTATAGGTACCAGCTGGATGTATAA			MYTLVMQYRYQLDV*	MYTLVMQYRYQLDV*			CGGATGACCT	CCTTTCAAGA	0	Q	0	0	0	0	0
5500	2777	an	AN8412.1	56.m02506	AO070336000018	0	-162	-133					ATGCAGTATAGGTACCAGCTGGATGTATAA	ATGCAGTATAGGTACCAGCTGGATGTATAA			MQYRYQLDV*	MQYRYQLDV*			TACCTTGGTG	CCTTTCAAGA	0	Q	0	0	0	0	0
5501	2777	an	AN8412.1	56.m02506	AO070336000018	0	-140	-21					ATGTATAACCTTTCAAGAAACATTCTACCACCAGGCGGCTACGAGGCAGTCGAAGCGACTGCCATCGAAACCCCAGTTTTACTTGATACTTGCCGCCCTCTTCTTCGTTACTGTGCATAA	ATGTATAACCTTTCAAGAAACATTCTACCACCAGGCGGCTACGAGGCAGTCGAAGCGACTGCCATCGAAACCCCAGTTTTACTTGATACTTGCCGCCCTCTTCTTCGTTACTGTGCATAA			MYNLSRNILPPGGYEAVEATAIETPVLLDTCRPLLRYCA*	MYNLSRNILPPGGYEAVEATAIETPVLLDTCRPLLRYCA*			TACCAGCTGG	ACATACATTA	0	Q	0	0	0	0	0
5505	2777	ao	AN8412.1	56.m02506	AO070336000018	0					-168	-154	ATGTATTTGTGGTGA			ATGTATTTGTGGTGA	MYLW*			MYLW*	TCAGGCCTCT	CACTTTCCTG	0	Q	0	0	0	0	0
5507	2780	an	AN5216.1	69.m14914	AO070337000263	0	-165	-145					ATGGTGCCGAATCAGGTATAA	ATGGTGCCGAATCAGGTATAA			MVPNQV*	MVPNQV*			GCTTATCGCT	TTTTCACGTG	0	L	0	0	0	0	0
5508	2780	an	AN5216.1	69.m14914	AO070337000263	0	-126	-70					ATGCTCGTGCCTAGTGGCGACGCGGAGAGTCGTGCCTCAATAGATGATCTCATCTGA	ATGCTCGTGCCTAGTGGCGACGCGGAGAGTCGTGCCTCAATAGATGATCTCATCTGA			MLVPSGDAESRASIDDLI*	MLVPSGDAESRASIDDLI*			TGATCTCGTG	GCAGCCGTGT	0	L	0	0	0	0	0
5511	2780	ao	AN5216.1	69.m14914	AO070337000263	0					-249	-235	ATGAGGCATAATTGA			ATGAGGCATAATTGA	MRHN*			MRHN*	AAATATCCAG	GCACGTGATA	0	L	0	0	0	0	0
5512	2780	ao	AN5216.1	69.m14914	AO070337000263	0					-87	-22	ATGGTCTGGCCTATAAGTCTGTCACAAGGTCATGTCGTCGAGAGTACTACTATGACGCAACCTTAG			ATGGTCTGGCCTATAAGTCTGTCACAAGGTCATGTCGTCGAGAGTACTACTATGACGCAACCTTAG	MVWPISLSQGHVVESTTMTQP*			MVWPISLSQGHVVESTTMTQP*	TATACTGCTC	ATCCGCCATT	0	L	0	0	0	0	0
5517	2782	af	AN2872.1	59.m08720	AO070338000142	0			-127	-113			ATGTGTGTTGCCTGA		ATGTGTGTTGCCTGA		MCVA*		MCVA*		CGCTCAGGTG	GGCTTGGGTT	0		0	0	0	0	0
5515	2782	an	AN2872.1	59.m08720	AO070338000142	0	-102	-25					ATGTCGAGATCACAACGGTCATCGTACGATCACAGCATTGGCTTGAAAATCCCCAATGCCAATCACCGACACCTCTGA	ATGTCGAGATCACAACGGTCATCGTACGATCACAGCATTGGCTTGAAAATCCCCAATGCCAATCACCGACACCTCTGA			MSRSQRSSYDHSIGLKIPNANHRHL*	MSRSQRSSYDHSIGLKIPNANHRHL*			TCAGTGTCCG	AATTTGACAG	0		0	0	0	0	0
5518	2784	an	AN1543.1	55.m03061	AO070339000311	0	-208	-161					ATGCCGGTCGGACTCAGCAGGCCGTACCGTGTGGCAGACCGTCAGTGA	ATGCCGGTCGGACTCAGCAGGCCGTACCGTGTGGCAGACCGTCAGTGA			MPVGLSRPYRVADRQ*	MPVGLSRPYRVADRQ*			AACTCTGTAC	GCCTCGGCCG	0	C	0	0	0	YJR051W	0
5519	2784	an	AN1543.1	55.m03061	AO070339000311	0	-123	-76					ATGAACGAGTCCTGCCTTTTAAGACCGTCTACTTTCCCTCCGCCCTGA	ATGAACGAGTCCTGCCTTTTAAGACCGTCTACTTTCCCTCCGCCCTGA			MNESCLLRPSTFPPP*	MNESCLLRPSTFPPP*			CCGTCGGCTT	ATTCTTCCTC	0	C	0	0	0	YJR051W	0
5520	2784	ao	AN1543.1	55.m03061	AO070339000311	0					-246	-163	ATGGATAGCGAAACGGTACCAGTACGGTACAGGGACATTCTCTCGAGCGATGAGCCTCGGCCGAAAAGCATTGTCGGCTTCTGA			ATGGATAGCGAAACGGTACCAGTACGGTACAGGGACATTCTCTCGAGCGATGAGCCTCGGCCGAAAAGCATTGTCGGCTTCTGA	MDSETVPVRYRDILSSDEPRPKSIVGF*			MDSETVPVRYRDILSSDEPRPKSIVGF*	GAAGTGGTCC	ACCTTACCCA	0	C	0	0	0	YJR051W	0
5523	2787	af	AN5757.1	69.m14854	AO070341000016	0			-257	-237			ATGAATGGTCCGGCTTGGTGA		ATGAATGGTCCGGCTTGGTGA		MNGPAW*		MNGPAW*		GAACTCGTTC	AGGAACAAAA	0	T	0	0	NCU04005.1	0	0
5524	2787	af	AN5757.1	69.m14854	AO070341000016	0			-253	-188			ATGGTCCGGCTTGGTGAAGGAACAAAACCTGTTCTTATTCCTACGTGGCTCGACGAACATCTGTAA		ATGGTCCGGCTTGGTGAAGGAACAAAACCTGTTCTTATTCCTACGTGGCTCGACGAACATCTGTAA		MVRLGEGTKPVLIPTWLDEHL*		MVRLGEGTKPVLIPTWLDEHL*		TCGTTCATGA	GTAGACTGCA	0	T	0	0	NCU04005.1	0	0
5525	2787	af	AN5757.1	69.m14854	AO070341000016	0			-129	-76			ATGGTCATCTCAGTTGCTGACAGCTCAATTGAGTGCAGTCCGTCTTCCACGTGA		ATGGTCATCTCAGTTGCTGACAGCTCAATTGAGTGCAGTCCGTCTTCCACGTGA		MVISVADSSIECSPSST*		MVISVADSSIECSPSST*		TCGCCATTTC	TAATATATCG	0	T	0	0	NCU04005.1	0	0
5521	2787	an	AN5757.1	69.m14854	AO070341000016	0	-191	-174					ATGAATGGTATAGCATAG	ATGAATGGTATAGCATAG			MNGIA*	MNGIA*			CCGTTGTTGC	AATCTCGGGC	0	T	0	0	NCU04005.1	0	0
5522	2787	an	AN5757.1	69.m14854	AO070341000016	0	-141	-91					ATGTACCTTTCCTTTGTATCGCTGTGGAGTTCCTGTTTTGTCTTCCGCTAA	ATGTACCTTTCCTTTGTATCGCTGTGGAGTTCCTGTTTTGTCTTCCGCTAA			MYLSFVSLWSSCFVFR*	MYLSFVSLWSSCFVFR*			CACCAATCTC	CGACTGCTAG	0	T	0	0	NCU04005.1	0	0
5526	2787	ao	AN5757.1	69.m14854	AO070341000016	0					-250	-179	ATGAATGGTCTAGATTGCAAACAGGCTTTCTGTGAGCCTCTCCTCCCTTTCTTTTGCTTCCAATGCAAATAA			ATGAATGGTCTAGATTGCAAACAGGCTTTCTGTGAGCCTCTCCTCCCTTTCTTTTGCTTCCAATGCAAATAA	MNGLDCKQAFCEPLLPFFCFQCK*			MNGLDCKQAFCEPLLPFFCFQCK*	AAACTCGTGA	TCATCCCATT	0	T	0	0	NCU04005.1	0	0
5527	2787	ao	AN5757.1	69.m14854	AO070341000016	0					-188	-99	ATGCAAATAATCATCCCATTCCGGTCGATCGGTGTTAATCGACGTTCCCCTTGTTACCTTGCTGACTGTTTCGATCTATTCGCAGACTAG			ATGCAAATAATCATCCCATTCCGGTCGATCGGTGTTAATCGACGTTCCCCTTGTTACCTTGCTGACTGTTTCGATCTATTCGCAGACTAG	MQIIIPFRSIGVNRRSPCYLADCFDLFAD*			MQIIIPFRSIGVNRRSPCYLADCFDLFAD*	TTTGCTTCCA	TCTTTCACGT	0	T	0	0	NCU04005.1	0	0
5529	2789	ao	AN2090.1	57.m05792	AO070341000248	0					-187	-122	ATGGTATTCGTTTTACACGTAACCAAACGAGGGGAATTAATTTTTTTTCTGAACCCCGCGCTGTAG			ATGGTATTCGTTTTACACGTAACCAAACGAGGGGAATTAATTTTTTTTCTGAACCCCGCGCTGTAG	MVFVLHVTKRGELIFFLNPAL*			MVFVLHVTKRGELIFFLNPAL*	GGGACTTGAT	AATGTTATCA	0	R	0	0	0	YPL263C	0
5530	2789	ao	AN2090.1	57.m05792	AO070341000248	0					-120	-10	ATGTTATCAACCCCACGCATTAAAAACGCCATTGAATTGGCAGTCTATATACATATAGAGTGTCGCTATCCGATAAACATATCGGGCCATTATAAACAGACAACTAAGTGA			ATGTTATCAACCCCACGCATTAAAAACGCCATTGAATTGGCAGTCTATATACATATAGAGTGTCGCTATCCGATAAACATATCGGGCCATTATAAACAGACAACTAAGTGA	MLSTPRIKNAIELAVYIHIECRYPINISGHYKQTTK*			MLSTPRIKNAIELAVYIHIECRYPINISGHYKQTTK*	GCGCTGTAGA	TTTCACAACA	0	R	0	0	0	YPL263C	0
5533	2799	an	AN8785.1	65.m07308	AO070289000010	0	-248	-225					ATGAAAACGCTTGTCAGTTGCTGA	ATGAAAACGCTTGTCAGTTGCTGA			MKTLVSC*	MKTLVSC*			AGATTCGGAG	TCCATCTCTC	0	C	0	0	0	0	0
5536	2801	af	AN1660.1	58.m08995	AO070299000020	0			-104	-87			ATGTTCAGCTTGGCCTGA		ATGTTCAGCTTGGCCTGA		MFSLA*		MFSLA*		AGGCATTCGC	GCCTTGTAGC	0	RP	0	0	0	0	0
5537	2801	af	AN1660.1	58.m08995	AO070299000020	0			-62	-21			ATGCTTTTTGTTCTCTTGCCGCCCCTGTCCTCATTTCCTTGA		ATGCTTTTTGTTCTCTTGCCGCCCCTGTCCTCATTTCCTTGA		MLFVLLPPLSSFP*		MLFVLLPPLSSFP*		CCATATCGCC	TCATTCGATC	0	RP	0	0	0	0	0
5534	2801	an	AN1660.1	58.m08995	AO070299000020	0	-141	-4					ATGGTCTCCGTCAATCTTCAATCTGCCATCTTCAGTGCTACGGCGTGGTTAGGAACAGGCCTGAGTTCGCTCCTGGAGCTTGGCCGTCTCGCAATGTTCCGTTTTCTCTCCTCCTTCTACCACTGCTTCTTGTCTTGA	ATGGTCTCCGTCAATCTTCAATCTGCCATCTTCAGTGCTACGGCGTGGTTAGGAACAGGCCTGAGTTCGCTCCTGGAGCTTGGCCGTCTCGCAATGTTCCGTTTTCTCTCCTCCTTCTACCACTGCTTCTTGTCTTGA			MVSVNLQSAIFSATAWLGTGLSSLLELGRLAMFRFLSSFYHCFLS*	MVSVNLQSAIFSATAWLGTGLSSLLELGRLAMFRFLSSFYHCFLS*			TCAATTCTTC	ACTATGGTTG	0	RP	0	0	0	0	0
5538	2801	ao	AN1660.1	58.m08995	AO070299000020	0					-99	-82	ATGGATATTGCGGTCTGA			ATGGATATTGCGGTCTGA	MDIAV*			MDIAV*	AACCCGAGCA	GTTTACTGCT	0	RP	0	0	0	0	0
5544	2802	af	AN1665.1	58.m07733	AO070299000047	0			-232	-218			ATGGGCAGTACCTAA		ATGGGCAGTACCTAA		MGST*		MGST*		TAGAAGCCAA	GCACGTAGAG	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5545	2802	af	AN1665.1	58.m07733	AO070299000047	0			-92	-27			ATGGTGTTTTCGGTGGAACTAGCGTCCATGACTACAACTATAATTCTTCATGTCTCTATTCTCTAG		ATGGTGTTTTCGGTGGAACTAGCGTCCATGACTACAACTATAATTCTTCATGTCTCTATTCTCTAG		MVFSVELASMTTTIILHVSIL*		MVFSVELASMTTTIILHVSIL*		AGTCACCTGC	AGAGATGTGC	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5546	2802	af	AN1665.1	58.m07733	AO070299000047	0			-65	-27			ATGACTACAACTATAATTCTTCATGTCTCTATTCTCTAG		ATGACTACAACTATAATTCTTCATGTCTCTATTCTCTAG		MTTTIILHVSIL*		MTTTIILHVSIL*		ACTAGCGTCC	AGAGATGTGC	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5539	2802	an	AN1665.1	58.m07733	AO070299000047	0	-258	-244					ATGATAGGTAAATAA	ATGATAGGTAAATAA			MIGK*	MIGK*			CTGGATTCTT	AATGTATAGG	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5540	2802	an	AN1665.1	58.m07733	AO070299000047	0	-242	-165					ATGTATAGGAGGCAAGCAGTAAGACGAATTGGCTGGACACTAGCTCACCGCCGTCACGTGGGGCAGTCATTTTCATAA	ATGTATAGGAGGCAAGCAGTAAGACGAATTGGCTGGACACTAGCTCACCGCCGTCACGTGGGGCAGTCATTTTCATAA			MYRRQAVRRIGWTLAHRRHVGQSFS*	MYRRQAVRRIGWTLAHRRHVGQSFS*			GGTAAATAAA	ATCCCCACCG	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5541	2802	an	AN1665.1	58.m07733	AO070299000047	0	-125	-75					ATGGGCAACTGCCTCACTTTGTGGAGGACGGATCACCTCCCTTCACTTTAA	ATGGGCAACTGCCTCACTTTGTGGAGGACGGATCACCTCCCTTCACTTTAA			MGNCLTLWRTDHLPSL*	MGNCLTLWRTDHLPSL*			CGTTCATATC	ACGACCATAA	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5547	2802	ao	AN1665.1	58.m07733	AO070299000047	0					-215	-141	ATGGTTATTGTTTATGCGCTAGTGCTTCACCGCCGTAGCTCACGTGGGGCCACCCCAGCCTCGCTTTCATCATAG			ATGGTTATTGTTTATGCGCTAGTGCTTCACCGCCGTAGCTCACGTGGGGCCACCCCAGCCTCGCTTTCATCATAG	MVIVYALVLHRRSSRGATPASLSS*			MVIVYALVLHRRSSRGATPASLSS*	TACTTGAATT	CTCTTCTGGG	0	T	FG07520.1	MG00700.1	0	YJL057C	0
5551	2804	af	AN4460.1	58.m07864	AO070305000133	0			-232	-170			ATGGCGGCTACTGCGCTTGTTGCACGGACCAACGTTTATCGTTCTTTTTTTCTGTCCGTTTGA		ATGGCGGCTACTGCGCTTGTTGCACGGACCAACGTTTATCGTTCTTTTTTTCTGTCCGTTTGA		MAATALVARTNVYRSFFLSV*		MAATALVARTNVYRSFFLSV*		GTGTGAACTG	CAAACAGAAC	0	A	FG06788.1	0	NCU03628.1	0	0
5550	2804	an	AN4460.1	58.m07864	AO070305000133	0	-203	-180					ATGCCTGCTGGGCGGTTTGTTTGA	ATGCCTGCTGGGCGGTTTGTTTGA			MPAGRFV*	MPAGRFV*			AGTGGATACC	CAGCTTCACA	0	A	FG06788.1	0	NCU03628.1	0	0
5554	2805	af	AN8215.1	53.m03758	AO070310000097	0			-249	-190			ATGATCCCAAGACGTAGCGAGTGTCATGGTATAGCCCCTATTATCCTGGAAAATGAATGA		ATGATCCCAAGACGTAGCGAGTGTCATGGTATAGCCCCTATTATCCTGGAAAATGAATGA		MIPRRSECHGIAPIILENE*		MIPRRSECHGIAPIILENE*		GAACGATTTG	GCTGTAAATG	0	E	0	0	0	0	0
5555	2805	af	AN8215.1	53.m03758	AO070310000097	0			-197	-183			ATGAATGAGCTGTAA		ATGAATGAGCTGTAA		MNEL*		MNEL*		ATCCTGGAAA	ATGGACGTCA	0	E	0	0	0	0	0
5556	2805	af	AN8215.1	53.m03758	AO070310000097	0			-182	-153			ATGGACGTCATCAACCTCTCGTTGGGCTGA		ATGGACGTCATCAACCTCTCGTTGGGCTGA		MDVINLSLG*		MDVINLSLG*		TGAGCTGTAA	CCATCTATGG	0	E	0	0	0	0	0
5557	2805	af	AN8215.1	53.m03758	AO070310000097	0			-146	-111			ATGGTCGGCATTCGGGCGTCTTTCCGTCTCCGTTAA		ATGGTCGGCATTCGGGCGTCTTTCCGTCTCCGTTAA		MVGIRASFRLR*		MVGIRASFRLR*		CTGACCATCT	TAGGAGGGGG	0	E	0	0	0	0	0
5553	2805	an	AN8215.1	53.m03758	AO070310000097	0	-159	-31					ATGGCCGGACTGAGGTACGGGGCCTCGAGGGGGCGAGGATACTCCGAACAAAAACCCACCAGCAGTCCCCCCCGAATTCGTCATATTCTTCCCCCCCCTTTCTTCTTCCTCTCTCTTCACACCACCTAA	ATGGCCGGACTGAGGTACGGGGCCTCGAGGGGGCGAGGATACTCCGAACAAAAACCCACCAGCAGTCCCCCCCGAATTCGTCATATTCTTCCCCCCCCTTTCTTCTTCCTCTCTCTTCACACCACCTAA			MAGLRYGASRGRGYSEQKPTSSPPRIRHILPPPFFLSLHTT*	MAGLRYGASRGRGYSEQKPTSSPPRIRHILPPPFFLSLHTT*			CGGCAGGCCA	ACATTCAGAC	0	E	0	0	0	0	0
5558	2805	ao	AN8215.1	53.m03758	AO070310000097	0					-214	-188	ATGAGATCACAAAAGTACCGATCTTAG			ATGAGATCACAAAAGTACCGATCTTAG	MRSQKYRS*			MRSQKYRS*	TCAGAGCCAA	TCGCTCTCGA	0	E	0	0	0	0	0

5559	2805	ao	AN8215.1	53.m03758	AO070310000097	0					-175	-104	ATGTCATGTAATCCTACTTTATGGAGATGTCATGGGCATGTTTCCCTTTCCGTTAATCGGAGGGCCCGTTAA			ATGTCATGTAATCCTACTTTATGGAGATGTCATGGGCATGTTTCCCTTTCCGTTAATCGGAGGGCCCGTTAA	MSCNPTLWRCHGHVSLSVNRRAR*			MSCNPTLWRCHGHVSLSVNRRAR*	GCTCTCGACC	ACTCCGGCCC	0	E	0	0	0	0	0
5560	2805	ao	AN8215.1	53.m03758	AO070310000097	0					-155	-120	ATGGAGATGTCATGGGCATGTTTCCCTTTCCGTTAA			ATGGAGATGTCATGGGCATGTTTCCCTTTCCGTTAA	MEMSWACFPFR*			MEMSWACFPFR*	ATCCTACTTT	TCGGAGGGCC	0	E	0	0	0	0	0
5561	2805	ao	AN8215.1	53.m03758	AO070310000097	0					-149	-120	ATGTCATGGGCATGTTTCCCTTTCCGTTAA			ATGTCATGGGCATGTTTCCCTTTCCGTTAA	MSWACFPFR*			MSWACFPFR*	CTTTATGGAG	TCGGAGGGCC	0	E	0	0	0	0	0
5562	2805	ao	AN8215.1	53.m03758	AO070310000097	0					-76	-29	ATGGATATCGCCCCAGTCATCCCTCTTCAACTACCACCTTTCCCGTAA			ATGGATATCGCCCCAGTCATCCCTCTTCAACTACCACCTTTCCCGTAA	MDIAPVIPLQLPPFP*			MDIAPVIPLQLPPFP*	TCCCTCCCCG	CTTCGCCGGA	0	E	0	0	0	0	0
5564	2813	af	AN5839.1	72.m18975	AO070340000003	0			-175	-65			ATGGAGACCTTTTCATCATTCAACACTCGCATTCACACTCTAAAAACCCTACGGGCCCAAGGATCTCCGTCGATATTTCAACGCCAATTTTTGTGCGGCTCGTGGGGGTGA		ATGGAGACCTTTTCATCATTCAACACTCGCATTCACACTCTAAAAACCCTACGGGCCCAAGGATCTCCGTCGATATTTCAACGCCAATTTTTGTGCGGCTCGTGGGGGTGA		METFSSFNTRIHTLKTLRAQGSPSIFQRQFLCGSWG*		METFSSFNTRIHTLKTLRAQGSPSIFQRQFLCGSWG*		TCTCGCACCC	ATCGGTCTTA	0	A	FG09875.1	MG04709.1	NCU05802.1	0	0
5565	2813	ao	AN5839.1	72.m18975	AO070340000003	0					-281	-267	ATGGAATTGAGTTGA			ATGGAATTGAGTTGA	MELS*			MELS*	CGGGGAGGGA	ATTGCCTTTC	0	A	FG09875.1	MG04709.1	NCU05802.1	0	0
5566	2813	ao	AN5839.1	72.m18975	AO070340000003	0					-184	-170	ATGACCACCATTTAA			ATGACCACCATTTAA	MTTI*			MTTI*	GCTCCAGTTG	TTCCCACACT	0	A	FG09875.1	MG04709.1	NCU05802.1	0	0
5567	2813	ao	AN5839.1	72.m18975	AO070340000003	0					-154	-119	ATGTTGCATTCCACTAACACTCCCTTACTCACTTAA			ATGTTGCATTCCACTAACACTCCCTTACTCACTTAA	MLHSTNTPLLT*			MLHSTNTPLLT*	ACACTTCTTA	TAGACTAATA	0	A	FG09875.1	MG04709.1	NCU05802.1	0	0
5563	2813	conserved	AN5839.1	72.m18975	AO070340000003	0	-175	-164	-256	-245	-246	-235	ATGyTGTCATAA	ATGTTGTCATAA	ATGCTGTCATAA	ATGTTGTCATAA	MLS*	MLS*	MLS*	MLS*	ssTbsyssyr	rAGTTTTCGr	0	A	FG09875.1	MG04709.1	NCU05802.1	0	0
5570	2819	af	AN3657.1	58.m07443	AO070342000031	0			-266	-252			ATGAGTGCGTTTTAA		ATGAGTGCGTTTTAA		MSAF*		MSAF*		AGGCTAGTCT	TAGAAAAGTG	0	J	0	MG00193.1	0	0	0
5571	2819	af	AN3657.1	58.m07443	AO070342000031	0			-213	-166			ATGGGTTGTAGGATGGTGACTGCTGATAGAGTACCGATAACAGTCTGA		ATGGGTTGTAGGATGGTGACTGCTGATAGAGTACCGATAACAGTCTGA		MGCRMVTADRVPITV*		MGCRMVTADRVPITV*		ACAACGAATA	TAGTGATAGA	0	J	0	MG00193.1	0	0	0
5572	2819	af	AN3657.1	58.m07443	AO070342000031	0			-201	-166			ATGGTGACTGCTGATAGAGTACCGATAACAGTCTGA		ATGGTGACTGCTGATAGAGTACCGATAACAGTCTGA		MVTADRVPITV*		MVTADRVPITV*		GGGTTGTAGG	TAGTGATAGA	0	J	0	MG00193.1	0	0	0
5573	2819	af	AN3657.1	58.m07443	AO070342000031	0			-95	-3			ATGCACAAAACGTTAATCACTGCGCTGCGGCTGGAAGTACACAGTGTTTATTCAAAACCAGATCTGACAGGAGTTAGATCACTTTTTAAATAA		ATGCACAAAACGTTAATCACTGCGCTGCGGCTGGAAGTACACAGTGTTTATTCAAAACCAGATCTGACAGGAGTTAGATCACTTTTTAAATAA		MHKTLITALRLEVHSVYSKPDLTGVRSLFK*		MHKTLITALRLEVHSVYSKPDLTGVRSLFK*		GGAGCAGATC	ATATGAGGAG	0	J	0	MG00193.1	0	0	0
5568	2819	an	AN3657.1	58.m07443	AO070342000031	0	-233	-192					ATGAGCAACCTACCAGGTTTTACAAGATACAACACAATATAA	ATGAGCAACCTACCAGGTTTTACAAGATACAACACAATATAA			MSNLPGFTRYNTI*	MSNLPGFTRYNTI*			TGAGCCAAGG	AATCACGTCT	0	J	0	MG00193.1	0	0	0
5569	2819	an	AN3657.1	58.m07443	AO070342000031	0	-179	-12					ATGGTTGGGGTGACTAACGGCGAAGGGAGCTATTGCGGGACACTTGCCGGATTCGGACAGGCCATCAAGACTGCGGAATTAGCAGATAATCGCCGCCCACACCACATCGAAATAACTACAACAACCAGCTTTGCTCCAGACAATCTGATCCGCAAAGTCGGGTCTTGA	ATGGTTGGGGTGACTAACGGCGAAGGGAGCTATTGCGGGACACTTGCCGGATTCGGACAGGCCATCAAGACTGCGGAATTAGCAGATAATCGCCGCCCACACCACATCGAAATAACTACAACAACCAGCTTTGCTCCAGACAATCTGATCCGCAAAGTCGGGTCTTGA			MVGVTNGEGSYCGTLAGFGQAIKTAELADNRRPHHIEITTTTSFAPDNLIRKVGS*	MVGVTNGEGSYCGTLAGFGQAIKTAELADNRRPHHIEITTTTSFAPDNLIRKVGS*			TCACGTCTTC	ATCGGGGCAC	0	J	0	MG00193.1	0	0	0
5574	2819	ao	AN3657.1	58.m07443	AO070342000031	0					-236	-177	ATGCCATCTATTGGAAAGGTAGTTGTACTAACTGGTGAAGCACGTTATCTGATACTATGA			ATGCCATCTATTGGAAAGGTAGTTGTACTAACTGGTGAAGCACGTTATCTGATACTATGA	MPSIGKVVVLTGEARYLIL*			MPSIGKVVVLTGEARYLIL*	ATTAGAGTGT	TTAGTGAGGT	0	J	0	MG00193.1	0	0	0
5575	2819	ao	AN3657.1	58.m07443	AO070342000031	0					-180	-94	ATGATTAGTGAGGTAATCGGCAGACTTTCCCTTTTTGGGACAACATTTATCTCTGGAGCTGCGCTCCAGCAGCGAAACCGATTCTGA			ATGATTAGTGAGGTAATCGGCAGACTTTCCCTTTTTGGGACAACATTTATCTCTGGAGCTGCGCTCCAGCAGCGAAACCGATTCTGA	MISEVIGRLSLFGTTFISGAALQQRNRF*			MISEVIGRLSLFGTTFISGAALQQRNRF*	ATCTGATACT	ACGAACGTCA	0	J	0	MG00193.1	0	0	0
5579	2820	af	AN0756.1	70.m15358	AO070343000444	0			-221	-81			ATGGACCATGACGATAGGCACGGTGCAATCCTGGCAGACTTGTGGATGGCTAGGATCGAACTTTCTCTCATTTTACATCTCGGAGGATCATGCGGAGTGGCAAGTCCGTCATATATTAAGCCGAAGCTCCTGCCCCTGTAG		ATGGACCATGACGATAGGCACGGTGCAATCCTGGCAGACTTGTGGATGGCTAGGATCGAACTTTCTCTCATTTTACATCTCGGAGGATCATGCGGAGTGGCAAGTCCGTCATATATTAAGCCGAAGCTCCTGCCCCTGTAG		MDHDDRHGAILADLWMARIELSLILHLGGSCGVASPSYIKPKLLPL*		MDHDDRHGAILADLWMARIELSLILHLGGSCGVASPSYIKPKLLPL*		GTCGTGCTTG	TCAAGCTCCC	0	G	0	0	0	0	0
5580	2820	af	AN0756.1	70.m15358	AO070343000444	0			-176	-81			ATGGCTAGGATCGAACTTTCTCTCATTTTACATCTCGGAGGATCATGCGGAGTGGCAAGTCCGTCATATATTAAGCCGAAGCTCCTGCCCCTGTAG		ATGGCTAGGATCGAACTTTCTCTCATTTTACATCTCGGAGGATCATGCGGAGTGGCAAGTCCGTCATATATTAAGCCGAAGCTCCTGCCCCTGTAG		MARIELSLILHLGGSCGVASPSYIKPKLLPL*		MARIELSLILHLGGSCGVASPSYIKPKLLPL*		AGACTTGTGG	TCAAGCTCCC	0	G	0	0	0	0	0
5581	2820	af	AN0756.1	70.m15358	AO070343000444	0			-132	-103			ATGCGGAGTGGCAAGTCCGTCATATATTAA		ATGCGGAGTGGCAAGTCCGTCATATATTAA		MRSGKSVIY*		MRSGKSVIY*		TCGGAGGATC	GCCGAAGCTC	0	G	0	0	0	0	0
5576	2820	an	AN0756.1	70.m15358	AO070343000444	0	-152	-102					ATGCAGGTGTTTACCGACGTAGTCGGACGAAATCAGCCAACCCAGTCCTGA	ATGCAGGTGTTTACCGACGTAGTCGGACGAAATCAGCCAACCCAGTCCTGA			MQVFTDVVGRNQPTQS*	MQVFTDVVGRNQPTQS*			GACCAGCTCA	AAGGCGGGGT	0	G	0	0	0	0	0
5577	2820	an	AN0756.1	70.m15358	AO070343000444	0	-69	-52					ATGATGGACTCCCTCTGA	ATGATGGACTCCCTCTGA			MMDSL*	MMDSL*			AGAGATAAAT	GATCGACCAT	0	G	0	0	0	0	0
5578	2820	an	AN0756.1	70.m15358	AO070343000444	0	-66	-52					ATGGACTCCCTCTGA	ATGGACTCCCTCTGA			MDSL*	MDSL*			GATAAATATG	GATCGACCAT	0	G	0	0	0	0	0
5582	2820	ao	AN0756.1	70.m15358	AO070343000444	0					-227	-213	ATGATGTTAAGATGA			ATGATGTTAAGATGA	MMLR*			MMLR*	CGACCTCTAC	AATCGTACGG	0	G	0	0	0	0	0
5583	2820	ao	AN0756.1	70.m15358	AO070343000444	0					-224	-213	ATGTTAAGATGA			ATGTTAAGATGA	MLR*			MLR*	CCTCTACATG	AATCGTACGG	0	G	0	0	0	0	0
5584	2820	ao	AN0756.1	70.m15358	AO070343000444	0					-216	-124	ATGAAATCGTACGGGACTCCACTTTCGGCTAAGGACTCTATTGGACCATTCCCTCCTCTATACATCATCAACGCAAGGTGTCGGACATTTTAA			ATGAAATCGTACGGGACTCCACTTTCGGCTAAGGACTCTATTGGACCATTCCCTCCTCTATACATCATCAACGCAAGGTGTCGGACATTTTAA	MKSYGTPLSAKDSIGPFPPLYIINARCRTF*			MKSYGTPLSAKDSIGPFPPLYIINARCRTF*	TGATGTTAAG	TTAACGAAGT	0	G	0	0	0	0	0
5586	2825	an	AN4297.1	58.m08027	AO070189000005	0	-248	-234					ATGTGTAATAGTTAA	ATGTGTAATAGTTAA			MCNS*	MCNS*			TATGCATGTA	CCCAATGAGG	0	C	0	0	0	0	0
5587	2825	an	AN4297.1	58.m08027	AO070189000005	0	-229	-218					ATGAGGTCTTAG	ATGAGGTCTTAG			MRS*	MRS*			AGTTAACCCA	GTTTTGTAAT	0	C	0	0	0	0	0
5588	2825	an	AN4297.1	58.m08027	AO070189000005	0	-82	-62					ATGAGTGGCCAAACTCCATAA	ATGAGTGGCCAAACTCCATAA			MSGQTP*	MSGQTP*			AATTTCACTG	CTTCGACAAC	0	C	0	0	0	0	0
5589	2825	ao	AN4297.1	58.m08027	AO070189000005	0					-183	-169	ATGACAGTAAAGTAA			ATGACAGTAAAGTAA	MTVK*			MTVK*	TCCTTGTATT	AGGCTAGTGT	0	C	0	0	0	0	0
5593	2826	af	AN3679.1	58.m08026	AO070189000006	0			-256	-176			ATGGCTATATCTCGAAGATGCTTCGTGGCTCTCAATTCCTGGATTCTTATGTTGCTTGAAAACGTCATCCTGACGCTGTGA		ATGGCTATATCTCGAAGATGCTTCGTGGCTCTCAATTCCTGGATTCTTATGTTGCTTGAAAACGTCATCCTGACGCTGTGA		MAISRRCFVALNSWILMLLENVILTL*		MAISRRCFVALNSWILMLLENVILTL*		TTGTACGTGC	CATTGCAGCA	0	R	0	0	0	0	0
5594	2826	af	AN3679.1	58.m08026	AO070189000006	0			-239	-198			ATGCTTCGTGGCTCTCAATTCCTGGATTCTTATGTTGCTTGA		ATGCTTCGTGGCTCTCAATTCCTGGATTCTTATGTTGCTTGA		MLRGSQFLDSYVA*		MLRGSQFLDSYVA*		TATCTCGAAG	AAACGTCATC	0	R	0	0	0	0	0
5595	2826	af	AN3679.1	58.m08026	AO070189000006	0			-208	-176			ATGTTGCTTGAAAACGTCATCCTGACGCTGTGA		ATGTTGCTTGAAAACGTCATCCTGACGCTGTGA		MLLENVILTL*		MLLENVILTL*		CTGGATTCTT	CATTGCAGCA	0	R	0	0	0	0	0
5596	2826	af	AN3679.1	58.m08026	AO070189000006	0			-162	-124			ATGGCCGTATGCGCCGGATTTTGTGATGCTATAATTTGA		ATGGCCGTATGCGCCGGATTTTGTGATGCTATAATTTGA		MAVCAGFCDAII*		MAVCAGFCDAII*		TGCAGCAGAC	CCCGATTATC	0	R	0	0	0	0	0
5597	2826	af	AN3679.1	58.m08026	AO070189000006	0			-154	-137			ATGCGCCGGATTTTGTGA		ATGCGCCGGATTTTGTGA		MRRIL*		MRRIL*		ACATGGCCGT	TGCTATAATT	0	R	0	0	0	0	0
5590	2826	an	AN3679.1	58.m08026	AO070189000006	0	-165	-13					ATGTCTAGTGTCATGATCAGACGTCATACTGACGCCCTAGAGGGCCTCGGTGTTACTATAACTGCTTTAACCGTCGATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAA	ATGTCTAGTGTCATGATCAGACGTCATACTGACGCCCTAGAGGGCCTCGGTGTTACTATAACTGCTTTAACCGTCGATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAA			MSSVMIRRHTDALEGLGVTITALTVDDLRFSLKPRFPVTVFPCSNPSVLD*	MSSVMIRRHTDALEGLGVTITALTVDDLRFSLKPRFPVTVFPCSNPSVLD*			AGTGTTGAGT	TTAAGTGCCA	0	R	0	0	0	0	0
5591	2826	an	AN3679.1	58.m08026	AO070189000006	0	-153	-13					ATGATCAGACGTCATACTGACGCCCTAGAGGGCCTCGGTGTTACTATAACTGCTTTAACCGTCGATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAA	ATGATCAGACGTCATACTGACGCCCTAGAGGGCCTCGGTGTTACTATAACTGCTTTAACCGTCGATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAA			MIRRHTDALEGLGVTITALTVDDLRFSLKPRFPVTVFPCSNPSVLD*	MIRRHTDALEGLGVTITALTVDDLRFSLKPRFPVTVFPCSNPSVLD*			GTCTAGTGTC	TTAAGTGCCA	0	R	0	0	0	0	0
5592	2826	an	AN3679.1	58.m08026	AO070189000006	0	-89	-9					ATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAATTAA	ATGATCTTAGGTTTTCCCTTAAGCCACGATTTCCAGTTACTGTATTTCCTTGCAGTAATCCCTCTGTACTTGATTAATTAA			MILGFPLSHDFQLLYFLAVIPLYLIN*	MILGFPLSHDFQLLYFLAVIPLYLIN*			TTAACCGTCG	GTGCCAACAT	0	R	0	0	0	0	0
5598	2826	ao	AN3679.1	58.m08026	AO070189000006	0					-130	-95	ATGCTGCATAGTAGCCACAGATATACTCAATTATAG			ATGCTGCATAGTAGCCACAGATATACTCAATTATAG	MLHSSHRYTQL*			MLHSSHRYTQL*	GGGGATATTT	ACTTGGGTCA	0	R	0	0	0	0	0
5607	2829	af	AN4307.1	58.m09013	AO070207000012	0			-68	-3			ATGACGGTTGTCTACTCGTTACTCGTCTTTTCTCGGCGCCTTTTAGTCCTTTCACAACTAATCTGA		ATGACGGTTGTCTACTCGTTACTCGTCTTTTCTCGGCGCCTTTTAGTCCTTTCACAACTAATCTGA		MTVVYSLLVFSRRLLVLSQLI*		MTVVYSLLVFSRRLLVLSQLI*		CGCTCACTGC	CAATGGCACT	0		0	MG02512.1	0	0	0
5606	2829	an	AN4307.1	58.m09013	AO070207000012	0	-158	-135					ATGCCCCAAGTTTGTCTTGTTTGA	ATGCCCCAAGTTTGTCTTGTTTGA			MPQVCLV*	MPQVCLV*			GCCACATCAT	TTTCACCTCC	0		0	MG02512.1	0	0	0
5608	2829	ao	AN4307.1	58.m09013	AO070207000012	0					-216	-100	ATGACGTTGCATCCATATATTGCTGGGTCATCTCTACCTCCGCAGTTTGTCTTGTTTGGTTGTTCCTCTCCGCCACACAAGCTACATCTGCCTGGGAAGGAACTGCCAAGTTGCTAA			ATGACGTTGCATCCATATATTGCTGGGTCATCTCTACCTCCGCAGTTTGTCTTGTTTGGTTGTTCCTCTCCGCCACACAAGCTACATCTGCCTGGGAAGGAACTGCCAAGTTGCTAA	MTLHPYIAGSSLPPQFVLFGCSSPPHKLHLPGKELPSC*			MTLHPYIAGSSLPPQFVLFGCSSPPHKLHLPGKELPSC*	ACAGCGGAAG	CATATCTACT	0		0	MG02512.1	0	0	0
5609	2829	ao	AN4307.1	58.m09013	AO070207000012	0					-77	-57	ATGCTATCGACATATGACTAA			ATGCTATCGACATATGACTAA	MLSTYD*			MLSTYD*	TGTCGTGCCC	GCTCGCCTCT	0		0	MG02512.1	0	0	0
5610	2829	ao	AN4307.1	58.m09013	AO070207000012	0					-64	-2	ATGACTAAGCTCGCCTCTGTACCATATCATTTAGCTAGCCATCTAGACTTGCATTTACCCTAA			ATGACTAAGCTCGCCTCTGTACCATATCATTTAGCTAGCCATCTAGACTTGCATTTACCCTAA	MTKLASVPYHLASHLDLHLP*			MTKLASVPYHLASHLDLHLP*	CTATCGACAT	AATGGCTCTG	0		0	MG02512.1	0	0	0
5611	2831	af	AN9465.1	70.m14852	AO070215000004	0			-196	-143			ATGTCCGCCGCTGGCAGAGCCCTAGAAAACGCGCTAAGCCGGAATGGTCGTTAA		ATGTCCGCCGCTGGCAGAGCCCTAGAAAACGCGCTAAGCCGGAATGGTCGTTAA		MSAAGRALENALSRNGR*		MSAAGRALENALSRNGR*		GGAGTAAAGG	GCGACGCACA	0	J	FG01154.1	0	0	0	0
5612	2831	af	AN9465.1	70.m14852	AO070215000004	0			-153	-82			ATGGTCGTTAAGCGACGCACAACCCGCCCACCCTCGATTTTCGCTCCACCAAGACCAGGCCGTCTCCGTTGA		ATGGTCGTTAAGCGACGCACAACCCGCCCACCCTCGATTTTCGCTCCACCAAGACCAGGCCGTCTCCGTTGA		MVVKRRTTRPPSIFAPPRPGRLR*		MVVKRRTTRPPSIFAPPRPGRLR*		CTAAGCCGGA	ATTTCGATCC	0	J	FG01154.1	0	0	0	0
5613	2831	ao	AN9465.1	70.m14852	AO070215000004	0					-253	-230	ATGCCAGGTTCGGGCCTTGGGTAG			ATGCCAGGTTCGGGCCTTGGGTAG	MPGSGLG*			MPGSGLG*	TAAATAGGAA	GTGAATGGAG	0	J	FG01154.1	0	0	0	0
5614	2831	ao	AN9465.1	70.m14852	AO070215000004	0					-225	-211	ATGGAGAGGTCATAG			ATGGAGAGGTCATAG	MERS*			MERS*	GGGTAGGTGA	AACTAGTACT	0	J	FG01154.1	0	0	0	0
5615	2833	af	AN6911.1	71.m15221	AO070219000015	0			-78	-55			ATGCCCACTACTGCATTGGACTGA		ATGCCCACTACTGCATTGGACTGA		MPTTALD*		MPTTALD*		CAATCAGTCC	TACGTGTCTC	0	U	0	0	0	0	0
5617	2834	af	AN6506.1	62.m03093	AO070222000022	0			-142	-116			ATGTTTTATCTTCTTTCTTGTCTCTAG		ATGTTTTATCTTCTTTCTTGTCTCTAG		MFYLLSCL*		MFYLLSCL*		CCCTCCGCCA	ATTCATACCG	0	I	0	MG08832.1	0	0	0
5618	2834	ao	AN6506.1	62.m03093	AO070222000022	0					-259	-170	ATGCCGAGCTTGTTTCTCATAGGCTATTTTCCTTTTATTCATTCCCGTCCATACTTCACATCAATTTCCTCTTCTCTCCACTTTACTTAA			ATGCCGAGCTTGTTTCTCATAGGCTATTTTCCTTTTATTCATTCCCGTCCATACTTCACATCAATTTCCTCTTCTCTCCACTTTACTTAA	MPSLFLIGYFPFIHSRPYFTSISSSLHFT*			MPSLFLIGYFPFIHSRPYFTSISSSLHFT*	GCCTGGTGTG	TTTCCAAACT	0	I	0	MG08832.1	0	0	0
5622	2835	af	AN1246.1	70.m14974	AO070223000009	0			-272	-261			ATGGAACACTGA		ATGGAACACTGA		MEH*		MEH*		GTCATCGATC	CATCAGTCCC	0	G	0	MG05063.1	0	0	0
5619	2835	an	AN1246.1	70.m14974	AO070223000009	0	-228	-151					ATGACATCAGTGGTCCGACTCCCGCCGAACCCTCCTCCTTCACCGGCAGCCCCACCATGTCGCCAAAGCAAATGGTAG	ATGACATCAGTGGTCCGACTCCCGCCGAACCCTCCTCCTTCACCGGCAGCCCCACCATGTCGCCAAAGCAAATGGTAG			MTSVVRLPPNPPPSPAAPPCRQSKW*	MTSVVRLPPNPPPSPAAPPCRQSKW*			CGTCGTGGAC	CTCTGCGATT	0	G	0	MG05063.1	0	0	0
5620	2835	an	AN1246.1	70.m14974	AO070223000009	0	-172	-116					ATGTCGCCAAAGCAAATGGTAGCTCTGCGATTCTGGATACCCCGCCACTCACCGTGA	ATGTCGCCAAAGCAAATGGTAGCTCTGCGATTCTGGATACCCCGCCACTCACCGTGA			MSPKQMVALRFWIPRHSP*	MSPKQMVALRFWIPRHSP*			CAGCCCCACC	TACAATTTCA	0	G	0	MG05063.1	0	0	0
5621	2835	an	AN1246.1	70.m14974	AO070223000009	0	-157	-116					ATGGTAGCTCTGCGATTCTGGATACCCCGCCACTCACCGTGA	ATGGTAGCTCTGCGATTCTGGATACCCCGCCACTCACCGTGA			MVALRFWIPRHSP*	MVALRFWIPRHSP*			GCCAAAGCAA	TACAATTTCA	0	G	0	MG05063.1	0	0	0

5623	2835	ao	AN1246.1	70.m14974	AO070223000009	0					-235	-164	ATGCGTCAGCGAATCTCTCACCGGTGGCCCCACCAAACGAGACAAAACAATGTTCCTCTACCCCGCCGCTGA			ATGCGTCAGCGAATCTCTCACCGGTGGCCCCACCAAACGAGACAAAACAATGTTCCTCTACCCCGCCGCTGA	MRQRISHRWPHQTRQNNVPLPRR*			MRQRISHRWPHQTRQNNVPLPRR*	CAACAGTCCG	ACCGATCGCT	0	G	0	MG05063.1	0	0	0
5624	2835	ao	AN1246.1	70.m14974	AO070223000009	0					-186	-106	ATGTTCCTCTACCCCGCCGCTGAACCGATCGCTTCTATCAGGAGACTGGCGTTCACCGTGAAACGTATTGAGTATTTCTAA			ATGTTCCTCTACCCCGCCGCTGAACCGATCGCTTCTATCAGGAGACTGGCGTTCACCGTGAAACGTATTGAGTATTTCTAA	MFLYPAAEPIASIRRLAFTVKRIEYF*			MFLYPAAEPIASIRRLAFTVKRIEYF*	AGACAAAACA	ACATCCCACT	0	G	0	MG05063.1	0	0	0
5625	2838	af	AN4316.1	58.m08008	AO070230000004	0			-79	-65			ATGCGACAGCAGTAG		ATGCGACAGCAGTAG		MRQQ*		MRQQ*		CAACAACCTC	ACCACTGTCT	0	R	0	0	0	0	0
5627	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-280	-134	ATGAATGGCAGTAGAACTGGGCAAGTTTTTTCAAAGCCACGAGATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGATGAATGTATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG			ATGAATGGCAGTAGAACTGGGCAAGTTTTTTCAAAGCCACGAGATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGATGAATGTATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG	MNGSRTGQVFSKPRDGKPNGFDQFYQALMNVCPRYYNMKMCLPQELSH*			MNGSRTGQVFSKPRDGKPNGFDQFYQALMNVCPRYYNMKMCLPQELSH*	TATCACTTGA	TGGGTCCCGT	0	R	0	0	0	0	0
5628	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-276	-196	ATGGCAGTAGAACTGGGCAAGTTTTTTCAAAGCCACGAGATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGA			ATGGCAGTAGAACTGGGCAAGTTTTTTCAAAGCCACGAGATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGA	MAVELGKFFQSHEMVSRTDLISFIKL*			MAVELGKFFQSHEMVSRTDLISFIKL*	ACTTGAATGA	TGAATGTATG	0	R	0	0	0	0	0
5629	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-237	-196	ATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGA			ATGGTAAGCCGAACGGATTTGATCAGTTTTATCAAGCTTTGA	MVSRTDLISFIKL*			MVSRTDLISFIKL*	AAGCCACGAG	TGAATGTATG	0	R	0	0	0	0	0
5630	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-196	-134	ATGAATGTATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG			ATGAATGTATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG	MNVCPRYYNMKMCLPQELSH*			MNVCPRYYNMKMCLPQELSH*	TCAAGCTTTG	TGGGTCCCGT	0	R	0	0	0	0	0
5631	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-192	-166	ATGTATGCCCGAGGTACTACAACATGA			ATGTATGCCCGAGGTACTACAACATGA	MYARGTTT*			MYARGTTT*	GCTTTGATGA	AGATGTGTTT	0	R	0	0	0	0	0
5632	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-188	-108	ATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAGTGGGTCCCGTGAGATGCCAAAGCTAA			ATGCCCGAGGTACTACAACATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAGTGGGTCCCGTGAGATGCCAAAGCTAA	MPEVLQHEDVFASGIKPLVGPVRCQS*			MPEVLQHEDVFASGIKPLVGPVRCQS*	TGATGAATGT	ACCTCTTCCG	0	R	0	0	0	0	0
5633	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-169	-134	ATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG			ATGAAGATGTGTTTGCCTCAGGAATTAAGCCATTAG	MKMCLPQELSH*			MKMCLPQELSH*	GTACTACAAC	TGGGTCCCGT	0	R	0	0	0	0	0
5634	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-163	-134	ATGTGTTTGCCTCAGGAATTAAGCCATTAG			ATGTGTTTGCCTCAGGAATTAAGCCATTAG	MCLPQELSH*			MCLPQELSH*	CAACATGAAG	TGGGTCCCGT	0	R	0	0	0	0	0
5635	2838	ao	AN4316.1	58.m08008	AO070230000004	0					-89	-18	ATGCTTCCCTTGGCATCCAGTTCCTACCGCTCAGTCAACGTCTCTGCGTGGGTTGGCACTGTTTATTATTAG			ATGCTTCCCTTGGCATCCAGTTCCTACCGCTCAGTCAACGTCTCTGCGTGGGTTGGCACTGTTTATTATTAG	MLPLASSSYRSVNVSAWVGTVYY*			MLPLASSSYRSVNVSAWVGTVYY*	CGTAGCTCCC	GAATATCCTT	0	R	0	0	0	0	0
5636	2840	an	AN4215.1	54.m06772	AO070231000009	0	-177	-145					ATGATGACCAAACCCCTCTTTCGTCATTCCTGA	ATGATGACCAAACCCCTCTTTCGTCATTCCTGA			MMTKPLFRHS*	MMTKPLFRHS*			TCCCCCATCT	TTCCTCCAAC	0	O	FG02097.1	0	0	0	0
5637	2840	an	AN4215.1	54.m06772	AO070231000009	0	-174	-145					ATGACCAAACCCCTCTTTCGTCATTCCTGA	ATGACCAAACCCCTCTTTCGTCATTCCTGA			MTKPLFRHS*	MTKPLFRHS*			CCCATCTATG	TTCCTCCAAC	0	O	FG02097.1	0	0	0	0
5638	2842	af	AN4233.1	54.m06783	AO070234000013	0			-236	-144			ATGATATTATTGGGAATAAAAGCAAGTCCCAATAGCTTCCTCCGCTGTCTGGACAAGAGTGTGACTTCTCTCTCAGGTCCAGAAAAAAAGTAG		ATGATATTATTGGGAATAAAAGCAAGTCCCAATAGCTTCCTCCGCTGTCTGGACAAGAGTGTGACTTCTCTCTCAGGTCCAGAAAAAAAGTAG		MILLGIKASPNSFLRCLDKSVTSLSGPEKK*		MILLGIKASPNSFLRCLDKSVTSLSGPEKK*		AAGTCCAGAT	ATTTGTCGGA	0	A	0	0	0	YHR065C	0
5639	2842	ao	AN4233.1	54.m06783	AO070234000013	0					-227	-78	ATGGTAGGTATGTGGTTCGAGGGAAATGTTATTCAACGTCTAATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA			ATGGTAGGTATGTGGTTCGAGGGAAATGTTATTCAACGTCTAATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA	MVGMWFEGNVIQRLMKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*			MVGMWFEGNVIQRLMKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*	CAGGAAATAT	TATCGAACTA	0	A	0	0	0	YHR065C	0
5640	2842	ao	AN4233.1	54.m06783	AO070234000013	0					-218	-78	ATGTGGTTCGAGGGAAATGTTATTCAACGTCTAATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA			ATGTGGTTCGAGGGAAATGTTATTCAACGTCTAATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA	MWFEGNVIQRLMKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*			MWFEGNVIQRLMKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*	TATGGTAGGT	TATCGAACTA	0	A	0	0	0	YHR065C	0
5641	2842	ao	AN4233.1	54.m06783	AO070234000013	0					-202	-185	ATGTTATTCAACGTCTAA			ATGTTATTCAACGTCTAA	MLFNV*			MLFNV*	TTCGAGGGAA	TGAAAGACGG	0	A	0	0	0	YHR065C	0
5642	2842	ao	AN4233.1	54.m06783	AO070234000013	0					-185	-78	ATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA			ATGAAAGACGGACTTTTTTTTCTTGGCCGAAAAAGTAGATCGGCGGAAACCAGGCCGCGGAGCAACTCCGGACCAACTGTTTTACCGGGACCCACACTGATTTTTTGA	MKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*			MKDGLFFLGRKSRSAETRPRSNSGPTVLPGPTLIF*	TCAACGTCTA	TATCGAACTA	0	A	0	0	0	YHR065C	0
5643	2843	an	AN4231.1	54.m06785	AO070234000015	0	-142	-119					ATGCTCCTGATATGGCACGTGTAA	ATGCTCCTGATATGGCACGTGTAA			MLLIWHV*	MLLIWHV*			GTAACTCGCG	GCGCTGACAA	0	H	0	0	0	0	0
5644	2843	an	AN4231.1	54.m06785	AO070234000015	0	-131	-105					ATGGCACGTGTAAGCGCTGACAAATAG	ATGGCACGTGTAAGCGCTGACAAATAG			MARVSADK*	MARVSADK*			TGCTCCTGAT	ACGCCGGATC	0	H	0	0	0	0	0
5645	2843	ao	AN4231.1	54.m06785	AO070234000015	0					-220	-209	ATGAAAATGTAA			ATGAAAATGTAA	MKM*			MKM*	TCTATATTAG	GTATATCGCT	0	H	0	0	0	0	0
5646	2845	af	AN1357.1	70.m14873	AO070237000003	0			-78	-61			ATGGTTTTTCTCAACTAA		ATGGTTTTTCTCAACTAA		MVFLN*		MVFLN*		GGAATCTCTC	ATACCTTATA	0	I	0	MG01003.1	0	0	0
5650	2849	af	AN5196.1	69.m14895	AO070237000026	0			-229	-194			ATGGATGTGGTTTTTTGTCTATGGTTGCGTGGTTGA		ATGGATGTGGTTTTTTGTCTATGGTTGCGTGGTTGA		MDVVFCLWLRG*		MDVVFCLWLRG*		AATACGAAGA	TTTCATCCTG	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5651	2849	af	AN5196.1	69.m14895	AO070237000026	0			-225	-103			ATGTGGTTTTTTGTCTATGGTTGCGTGGTTGATTTCATCCTGCGTTCTCCATCGATCTTCACTCTTCGCTGGTGGGTGTCACCGTCGCCCGTAAAATCCCAGAAACTCGCCGACTTCCTGTAG		ATGTGGTTTTTTGTCTATGGTTGCGTGGTTGATTTCATCCTGCGTTCTCCATCGATCTTCACTCTTCGCTGGTGGGTGTCACCGTCGCCCGTAAAATCCCAGAAACTCGCCGACTTCCTGTAG		MWFFVYGCVVDFILRSPSIFTLRWWVSPSPVKSQKLADFL*		MWFFVYGCVVDFILRSPSIFTLRWWVSPSPVKSQKLADFL*		CGAAGAATGG	CGGCTCACTT	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5652	2849	af	AN5196.1	69.m14895	AO070237000026	0			-209	-132			ATGGTTGCGTGGTTGATTTCATCCTGCGTTCTCCATCGATCTTCACTCTTCGCTGGTGGGTGTCACCGTCGCCCGTAA		ATGGTTGCGTGGTTGATTTCATCCTGCGTTCTCCATCGATCTTCACTCTTCGCTGGTGGGTGTCACCGTCGCCCGTAA		MVAWLISSCVLHRSSLFAGGCHRRP*		MVAWLISSCVLHRSSLFAGGCHRRP*		TTTTTTGTCT	AATCCCAGAA	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5647	2849	an	AN5196.1	69.m14895	AO070237000026	0	-163	-122					ATGGCAGTATGTCTCCAATCAGCTGTGAACATTCAACCTTAA	ATGGCAGTATGTCTCCAATCAGCTGTGAACATTCAACCTTAA			MAVCLQSAVNIQP*	MAVCLQSAVNIQP*			AAACTCTTGT	AAAAGGCCGA	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5648	2849	an	AN5196.1	69.m14895	AO070237000026	0	-155	-66					ATGTCTCCAATCAGCTGTGAACATTCAACCTTAAAAAAGGCCGAGTGGCTGATGGCGGGTTTGCGTTCTTGGCGCTACCGGCACCCGTAA	ATGTCTCCAATCAGCTGTGAACATTCAACCTTAAAAAAGGCCGAGTGGCTGATGGCGGGTTTGCGTTCTTGGCGCTACCGGCACCCGTAA			MSPISCEHSTLKKAEWLMAGLRSWRYRHP*	MSPISCEHSTLKKAEWLMAGLRSWRYRHP*			GTATGGCAGT	AACGTCAAAC	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5649	2849	an	AN5196.1	69.m14895	AO070237000026	0	-104	-66					ATGGCGGGTTTGCGTTCTTGGCGCTACCGGCACCCGTAA	ATGGCGGGTTTGCGTTCTTGGCGCTACCGGCACCCGTAA			MAGLRSWRYRHP*	MAGLRSWRYRHP*			CGAGTGGCTG	AACGTCAAAC	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5653	2849	ao	AN5196.1	69.m14895	AO070237000026	0					-247	-137	ATGATCGTTGTAAAAGTGGTGTGGAATGGGCAGAGCGCCGGTGGTGTAGAAACGGCAGTGTTCGCAGTGGGACACTCGCCGCCCGAAAAATTAGACTCGCCGCCTTTGTAA			ATGATCGTTGTAAAAGTGGTGTGGAATGGGCAGAGCGCCGGTGGTGTAGAAACGGCAGTGTTCGCAGTGGGACACTCGCCGCCCGAAAAATTAGACTCGCCGCCTTTGTAA	MIVVKVVWNGQSAGGVETAVFAVGHSPPEKLDSPPL*			MIVVKVVWNGQSAGGVETAVFAVGHSPPEKLDSPPL*	TCCATACCAA	CTTAGCTTAT	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5654	2849	ao	AN5196.1	69.m14895	AO070237000026	0					-222	-199	ATGGGCAGAGCGCCGGTGGTGTAG			ATGGGCAGAGCGCCGGTGGTGTAG	MGRAPVV*			MGRAPVV*	GTGGTGTGGA	AAACGGCAGT	0	S	FG01399.1	MG08133.1	NCU06921.1	0	0
5656	2850	af	AN4353.1	58.m07978	AO070240000022	0			-190	-152			ATGGGGATGCTTTCAAACAACTACTGGTCTAACCACTAA		ATGGGGATGCTTTCAAACAACTACTGGTCTAACCACTAA		MGMLSNNYWSNH*		MGMLSNNYWSNH*		AAACCCAAGA	TCACAACAGT	0	I	FG10853.1	MG02409.1	0	0	0
5657	2850	af	AN4353.1	58.m07978	AO070240000022	0			-184	-152			ATGCTTTCAAACAACTACTGGTCTAACCACTAA		ATGCTTTCAAACAACTACTGGTCTAACCACTAA		MLSNNYWSNH*		MLSNNYWSNH*		AAGAATGGGG	TCACAACAGT	0	I	FG10853.1	MG02409.1	0	0	0
5658	2850	af	AN4353.1	58.m07978	AO070240000022	0			-111	-97			ATGTTATATCTATGA		ATGTTATATCTATGA		MLYL*		MLYL*		CAGACGGCAA	CAATCATCTC	0	I	FG10853.1	MG02409.1	0	0	0
5655	2850	an	AN4353.1	58.m07978	AO070240000022	0	-95	-84					ATGTCCTGTTGA	ATGTCCTGTTGA			MSC*	MSC*			TATCATCCAC	ACTATACATA	0	I	FG10853.1	MG02409.1	0	0	0
5659	2850	ao	AN4353.1	58.m07978	AO070240000022	0					-162	-91	ATGCTTGCTCCTGGACCGATCGTTATATATACTTTAAACCAGAACAATAGTTTCATAGTTCTCCATTTCTAG			ATGCTTGCTCCTGGACCGATCGTTATATATACTTTAAACCAGAACAATAGTTTCATAGTTCTCCATTTCTAG	MLAPGPIVIYTLNQNNSFIVLHF*			MLAPGPIVIYTLNQNNSFIVLHF*	AGAGATTCAT	ACAACCTACA	0	I	FG10853.1	MG02409.1	0	0	0
5660	2852	an	AN1430.1	55.m02925	AO070242000021	0	-146	-108					ATGCAGTGGGTGCGAGTGGGACCCAGATCTTGGAGATGA	ATGCAGTGGGTGCGAGTGGGACCCAGATCTTGGAGATGA			MQWVRVGPRSWR*	MQWVRVGPRSWR*			TGCAGCGCGC	CCAACTTTTT	0	C	0	0	0	0	0
5661	2854	ao	AN1379.1	70.m14844	AO070243000010	0					-218	-174	ATGTGTCGCGGCTGCAGAACGCGCGCCTTCCCAAATCTACGCTGA			ATGTGTCGCGGCTGCAGAACGCGCGCCTTCCCAAATCTACGCTGA	MCRGCRTRAFPNLR*			MCRGCRTRAFPNLR*	TAAGGCATTA	GCTCTTTCTC	0	A	FG10280.1	0	0	0	0
5662	2855	af	AN1382.1	70.m14839	AO070243000014	0			-133	-119			ATGTCTGCTTGTTAA		ATGTCTGCTTGTTAA		MSAC*		MSAC*		GCCAAGCTCG	AAGGTCAGAT	0		0	0	0	0	0
5667	2857	af	AN1385.1	70.m14836	AO070243000019	0			-146	-132			ATGATCCGCTATTAG		ATGATCCGCTATTAG		MIRY*		MIRY*		AGTTCTATCA	AAGAACCCCA	0	R	0	MG03150.1	0	0	0
5663	2857	an	AN1385.1	70.m14836	AO070243000019	0	-243	-223					ATGCCGATTGGATGTGCGTAA	ATGCCGATTGGATGTGCGTAA			MPIGCA*	MPIGCA*			AGTACCTTAT	TAACCATTTG	0	R	0	MG03150.1	0	0	0
5664	2857	an	AN1385.1	70.m14836	AO070243000019	0	-232	-170					ATGTGCGTAATAACCATTTGTGTACCTTTGTTTTGGGATCAAATTCATGCGCTTGTGTCTTGA	ATGTGCGTAATAACCATTTGTGTACCTTTGTTTTGGGATCAAATTCATGCGCTTGTGTCTTGA			MCVITICVPLFWDQIHALVS*	MCVITICVPLFWDQIHALVS*			TGCCGATTGG	TCTGTACTTC	0	R	0	MG03150.1	0	0	0
5665	2857	an	AN1385.1	70.m14836	AO070243000019	0	-186	-22					ATGCGCTTGTGTCTTGATCTGTACTTCGTACTCCGTATCTGTATCTATATTGTTGGAGACTTCCGCGGACATGTCTGGAACCCCACCAAACCTGAGTTTCTCTCTCCGCCCTCAGTCTTCAGCAACGACACCAAGATTCCTTTAAAGAACGACTCATTGCATTGA	ATGCGCTTGTGTCTTGATCTGTACTTCGTACTCCGTATCTGTATCTATATTGTTGGAGACTTCCGCGGACATGTCTGGAACCCCACCAAACCTGAGTTTCTCTCTCCGCCCTCAGTCTTCAGCAACGACACCAAGATTCCTTTAAAGAACGACTCATTGCATTGA			MRLCLDLYFVLRICIYIVGDFRGHVWNPTKPEFLSPPSVFSNDTKIPLKNDSLH*	MRLCLDLYFVLRICIYIVGDFRGHVWNPTKPEFLSPPSVFSNDTKIPLKNDSLH*			GATCAAATTC	TACCAAATCG	0	R	0	MG03150.1	0	0	0
5666	2857	an	AN1385.1	70.m14836	AO070243000019	0	-116	-42					ATGTCTGGAACCCCACCAAACCTGAGTTTCTCTCTCCGCCCTCAGTCTTCAGCAACGACACCAAGATTCCTTTAA	ATGTCTGGAACCCCACCAAACCTGAGTTTCTCTCTCCGCCCTCAGTCTTCAGCAACGACACCAAGATTCCTTTAA			MSGTPPNLSFSLRPQSSATTPRFL*	MSGTPPNLSFSLRPQSSATTPRFL*			TTCCGCGGAC	AGAACGACTC	0	R	0	MG03150.1	0	0	0
5668	2857	ao	AN1385.1	70.m14836	AO070243000019	0					-183	-43	ATGCTACTCAACGCTCCGAGGTCGCTTCTGTGGCCAGTCGGTACCTTTGGATTAATCTACCATCTAACCCCACCCTCCCCCCACTACAGCAAATATTCTGTCCGCCCCCAGACCGCAATTCCGGCAAGCCTTCTAAACTAG			ATGCTACTCAACGCTCCGAGGTCGCTTCTGTGGCCAGTCGGTACCTTTGGATTAATCTACCATCTAACCCCACCCTCCCCCCACTACAGCAAATATTCTGTCCGCCCCCAGACCGCAATTCCGGCAAGCCTTCTAAACTAG	MLLNAPRSLLWPVGTFGLIYHLTPPSPHYSKYSVRPQTAIPASLLN*			MLLNAPRSLLWPVGTFGLIYHLTPPSPHYSKYSVRPQTAIPASLLN*	CAATAAGTAA	GACGATACAA	0	R	0	MG03150.1	0	0	0
5673	2858	af	AN5178.1	69.m14875	AO070247000009	0			-253	-173			ATGACGTTGAATGGGATTCGTACCCCCTCTTACTGGTGGGGTGTGGGGAGAAGAGGTTATTCACTTATTATTCATGGCTGA		ATGACGTTGAATGGGATTCGTACCCCCTCTTACTGGTGGGGTGTGGGGAGAAGAGGTTATTCACTTATTATTCATGGCTGA		MTLNGIRTPSYWWGVGRRGYSLIIHG*		MTLNGIRTPSYWWGVGRRGYSLIIHG*		CAATCGCTCC	TCAAGCCCCA	0	C	0	0	0	0	0
5674	2858	af	AN5178.1	69.m14875	AO070247000009	0			-243	-148			ATGGGATTCGTACCCCCTCTTACTGGTGGGGTGTGGGGAGAAGAGGTTATTCACTTATTATTCATGGCTGATCAAGCCCCATTACCGAACGGCTGA		ATGGGATTCGTACCCCCTCTTACTGGTGGGGTGTGGGGAGAAGAGGTTATTCACTTATTATTCATGGCTGATCAAGCCCCATTACCGAACGGCTGA		MGFVPPLTGGVWGEEVIHLLFMADQAPLPNG*		MGFVPPLTGGVWGEEVIHLLFMADQAPLPNG*		ATGACGTTGA	TGGACTAGAG	0	C	0	0	0	0	0
5675	2858	af	AN5178.1	69.m14875	AO070247000009	0			-180	-148			ATGGCTGATCAAGCCCCATTACCGAACGGCTGA		ATGGCTGATCAAGCCCCATTACCGAACGGCTGA		MADQAPLPNG*		MADQAPLPNG*		CTTATTATTC	TGGACTAGAG	0	C	0	0	0	0	0
5676	2858	af	AN5178.1	69.m14875	AO070247000009	0			-120	-88			ATGTTGCCCTGGTCTCATCCAATGTTTCATTGA		ATGTTGCCCTGGTCTCATCCAATGTTTCATTGA		MLPWSHPMFH*		MLPWSHPMFH*		ACTTATAGCC	TCTAAGAGTC	0	C	0	0	0	0	0
5677	2858	af	AN5178.1	69.m14875	AO070247000009	0			-99	-88			ATGTTTCATTGA		ATGTTTCATTGA		MFH*		MFH*		GTCTCATCCA	TCTAAGAGTC	0	C	0	0	0	0	0
5669	2858	an	AN5178.1	69.m14875	AO070247000009	0	-146	-93					ATGACGTTCCAAACGCTGCCGGTGGGGTGTGGGGAGAATGCCGATTATTCATGA	ATGACGTTCCAAACGCTGCCGGTGGGGTGTGGGGAGAATGCCGATTATTCATGA			MTFQTLPVGCGENADYS*	MTFQTLPVGCGENADYS*			TACAAGCTTC	TGATCAAGCG	0	C	0	0	0	0	0

5670	2858	an	AN5178.1	69.m14875	AO070247000009	0	-109	-14					ATGCCGATTATTCATGATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGA	ATGCCGATTATTCATGATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGA			MPIIHDDQALKVLYQTVDFLLPFSSFPICTF*	MPIIHDDQALKVLYQTVDFLLPFSSFPICTF*			TGTGGGGAGA	CCAATAATCC	0	C	0	0	0	0	0
5671	2858	an	AN5178.1	69.m14875	AO070247000009	0	-96	-7					ATGATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGACCAATAA	ATGATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGACCAATAA			MMIKRSKFYIKPWTSSSRFLLSPSALSDQ*	MMIKRSKFYIKPWTSSSRFLLSPSALSDQ*			CCGATTATTC	TCCACAATGG	0	C	0	0	0	0	0
5672	2858	an	AN5178.1	69.m14875	AO070247000009	0	-93	-7					ATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGACCAATAA	ATGATCAAGCGCTCAAAGTTCTATATCAAACCGTGGACTTCCTCCTCCCGTTTTCTTCTTTCCCCATCTGCACTTTCTGACCAATAA			MIKRSKFYIKPWTSSSRFLLSPSALSDQ*	MIKRSKFYIKPWTSSSRFLLSPSALSDQ*			ATTATTCATG	TCCACAATGG	0	C	0	0	0	0	0
5678	2858	ao	AN5178.1	69.m14875	AO070247000009	0					-173	-144	ATGATGATCAAAGCTTCGTCTAAAACATAA			ATGATGATCAAAGCTTCGTCTAAAACATAA	MMIKASSKT*			MMIKASSKT*	GAGATTATTC	GGTCTCGGTA	0	C	0	0	0	0	0
5679	2858	ao	AN5178.1	69.m14875	AO070247000009	0					-170	-144	ATGATCAAAGCTTCGTCTAAAACATAA			ATGATCAAAGCTTCGTCTAAAACATAA	MIKASSKT*			MIKASSKT*	ATTATTCATG	GGTCTCGGTA	0	C	0	0	0	0	0
5683	2859	af	AN5181.1	69.m14878	AO070247000011	0			-114	-85			ATGGAGTACCCCGGCGCAAACAACGGCTAA		ATGGAGTACCCCGGCGCAAACAACGGCTAA		MEYPGANNG*		MEYPGANNG*		AAATGCGACT	CCCCACACCT	0	T	FG09165.1	MG03604.1	0	0	0
5680	2859	an	AN5181.1	69.m14878	AO070247000011	0	-227	-165					ATGCCAAGTTCTAGTATTTATAATAAGGTCTACATGAGCAAGGGTTTTTGTTGTAGTGTGTAG	ATGCCAAGTTCTAGTATTTATAATAAGGTCTACATGAGCAAGGGTTTTTGTTGTAGTGTGTAG			MPSSSIYNKVYMSKGFCSV*	MPSSSIYNKVYMSKGFCSV*			TTGCAGCGAT	GTGGACGGAC	0	T	FG09165.1	MG03604.1	0	0	0
5681	2859	an	AN5181.1	69.m14878	AO070247000011	0	-194	-165					ATGAGCAAGGGTTTTTGTTGTAGTGTGTAG	ATGAGCAAGGGTTTTTGTTGTAGTGTGTAG			MSKGFCCSV*	MSKGFCCSV*			TAAGGTCTAC	GTGGACGGAC	0	T	FG09165.1	MG03604.1	0	0	0
5682	2859	an	AN5181.1	69.m14878	AO070247000011	0	-153	-70					ATGGAAGCACCCAGAACAACAAACGGAGCCTCAACATGCCCCACCTCCGCTCCGCGCCGCAGCTCCTCGAAATATCGCAGCTAA	ATGGAAGCACCCAGAACAACAAACGGAGCCTCAACATGCCCCACCTCCGCTCCGCGCCGCAGCTCCTCGAAATATCGCAGCTAA			MEAPRTTNGASTCPTSAPRRSSSKYRS*	MEAPRTTNGASTCPTSAPRRSSSKYRS*			TGGACGGACT	TTCCAACTTT	0	T	FG09165.1	MG03604.1	0	0	0
5684	2861	ao	AN1345.1	70.m14888	AO070247000019	0					-221	-195	ATGTATATTGTTGCTGCTATTTTTTGA			ATGTATATTGTTGCTGCTATTTTTTGA	MYIVAAIF*			MYIVAAIF*	ATCAGTCGGT	TGAAATATAT	0	J	0	0	0	0	0
5685	2861	ao	AN1345.1	70.m14888	AO070247000019	0					-195	-175	ATGAAATATATTCGTGTCTAG			ATGAAATATATTCGTGTCTAG	MKYIRV*			MKYIRV*	CTATTTTTTG	GGACTCCCGT	0	J	0	0	0	0	0
5686	2861	ao	AN1345.1	70.m14888	AO070247000019	0					-120	-109	ATGTACTTCTGA			ATGTACTTCTGA	MYF*			MYF*	CGCCCCGGCC	AATCCACGTC	0	J	0	0	0	0	0
5688	2862	an	AN1341.1	70.m15733	AO070247000023	0	-216	-160					ATGGATAGGGCTCAGGGTTTGCCAAACCCGTGGCAGACCCAGTTTTCCCCGCGGTAG	ATGGATAGGGCTCAGGGTTTGCCAAACCCGTGGCAGACCCAGTTTTCCCCGCGGTAG			MDRAQGLPNPWQTQFSPR*	MDRAQGLPNPWQTQFSPR*			AGTTCAGCAC	CTTCACCGTT	0	U	FG01552.1	0	0	0	0
5689	2864	af	AN5769.1	69.m14829	AO070249000006	0			-239	-225			ATGGGGCTAGGCTGA		ATGGGGCTAGGCTGA		MGLG*		MGLG*		TACGACCCAA	AGGTTCCAAT	0	U	0	0	0	0	0
5696	2867	af	AN5784.1	69.m14813	AO070249000029	0			-257	-198			ATGGTGTGCCTGTTCAACCAACTCAAGCAAGCCAGCCACATCAAGCCACCTGTGGCGTAA		ATGGTGTGCCTGTTCAACCAACTCAAGCAAGCCAGCCACATCAAGCCACCTGTGGCGTAA		MVCLFNQLKQASHIKPPVA*		MVCLFNQLKQASHIKPPVA*		TCCGGTATTC	GCTATTAAAT	0	O	FG01160.1	0	0	0	0
5695	2867	an	AN5784.1	69.m14813	AO070249000029	0	-197	-135					ATGGGACGGCTGCTAGCACATTACATAATCCAAAGGAAGCTCCAGCACCGCTTCAGTAGGTGA	ATGGGACGGCTGCTAGCACATTACATAATCCAAAGGAAGCTCCAGCACCGCTTCAGTAGGTGA			MGRLLAHYIIQRKLQHRFSR*	MGRLLAHYIIQRKLQHRFSR*			AAGCTGTACA	GAGCTCCATT	0	O	FG01160.1	0	0	0	0
5697	2867	ao	AN5784.1	69.m14813	AO070249000029	0					-252	-214	ATGTTCCAGTGGAGAAGTGAAAGCTATCGGCTTATATAA			ATGTTCCAGTGGAGAAGTGAAAGCTATCGGCTTATATAA	MFQWRSESYRLI*			MFQWRSESYRLI*	AAGACAGTTC	GCCGAAGGCA	0	O	FG01160.1	0	0	0	0
5699	2868	af	AN8745.1	62.m03335	AO070250000030	0			-177	-163			ATGTCAATTATGTAA		ATGTCAATTATGTAA		MSIM*		MSIM*		GGAACCTTCC	ACCATAGCCT	0	G	0	0	0	0	0
5700	2868	af	AN8745.1	62.m03335	AO070250000030	0			-101	-90			ATGAGTCAATAA		ATGAGTCAATAA		MSQ*		MSQ*		TGATCACCTG	CAGACAAACA	0	G	0	0	0	0	0
5698	2868	an	AN8745.1	62.m03335	AO070250000030	0	-166	-128					ATGGGCGCTGCCAGAACGAGTGCCGGTAAATCCCGTTAA	ATGGGCGCTGCCAGAACGAGTGCCGGTAAATCCCGTTAA			MGAARTSAGKSR*	MGAARTSAGKSR*			ATAAGCGAGC	ATTCGCCTCC	0	G	0	0	0	0	0
5702	2868	ao	AN8745.1	62.m03335	AO070250000030	0					-155	-135	ATGCAAGGACTGTCGGTGTGA			ATGCAAGGACTGTCGGTGTGA	MQGLSV*			MQGLSV*	CTTCTGCGCA	TTGTGTGTTC	0	G	0	0	0	0	0
5707	2870	af	AN7201.1	69.m15184	AO070252000010	0			-251	-222			ATGATAGCAGGGGCTGATCCTCCATCTTAG		ATGATAGCAGGGGCTGATCCTCCATCTTAG		MIAGADPPS*		MIAGADPPS*		GTCGATCGAC	CATGTGCACG	0	O	0	0	0	0	0
5708	2870	af	AN7201.1	69.m15184	AO070252000010	0			-220	-155			ATGTGCACGATTCTAATAGCTCCGCTCTGTACTAGTGCTAAGCCCCACTGCAACGTTCCATCATAA		ATGTGCACGATTCTAATAGCTCCGCTCTGTACTAGTGCTAAGCCCCACTGCAACGTTCCATCATAA		MCTILIAPLCTSAKPHCNVPS*		MCTILIAPLCTSAKPHCNVPS*		CCATCTTAGC	TAGTCAACAT	0	O	0	0	0	0	0
5709	2870	af	AN7201.1	69.m15184	AO070252000010	0			-135	-4			ATGCATGATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		ATGCATGATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		MHDGYDMRVVRGSLMSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		MHDGYDMRVVRGSLMSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		TCAGGGTCTA	ATAATGCGAC	0	O	0	0	0	0	0
5710	2870	af	AN7201.1	69.m15184	AO070252000010	0			-131	-93			ATGATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGA		ATGATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGA		MMGMICESCGGR*		MMGMICESCGGR*		GGTCTAATGC	TGTCGATCAG	0	O	0	0	0	0	0
5711	2870	af	AN7201.1	69.m15184	AO070252000010	0			-128	-93			ATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGA		ATGGGTATGATATGCGAGTCGTGCGGGGGTCGTTGA		MGMICESCGGR*		MGMICESCGGR*		CTAATGCATG	TGTCGATCAG	0	O	0	0	0	0	0
5712	2870	af	AN7201.1	69.m15184	AO070252000010	0			-122	-93			ATGATATGCGAGTCGTGCGGGGGTCGTTGA		ATGATATGCGAGTCGTGCGGGGGTCGTTGA		MICESCGGR*		MICESCGGR*		CATGATGGGT	TGTCGATCAG	0	O	0	0	0	0	0
5713	2870	af	AN7201.1	69.m15184	AO070252000010	0			-117	-4			ATGCGAGTCGTGCGGGGGTCGTTGATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		ATGCGAGTCGTGCGGGGGTCGTTGATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		MRVVRGSLMSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		MRVVRGSLMSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		TGGGTATGAT	ATAATGCGAC	0	O	0	0	0	0	0
5714	2870	af	AN7201.1	69.m15184	AO070252000010	0			-93	-4			ATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		ATGTCGATCAGGAGAGATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAGGTACACACAAGCTATTCTTGCGCTGA		MSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		MSIRRDGSKHLYEAVPQAVLLGTHKLFLR*		GGGGTCGTTG	ATAATGCGAC	0	O	0	0	0	0	0
5715	2870	af	AN7201.1	69.m15184	AO070252000010	0			-77	-30			ATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAG		ATGGGTCCAAACATTTATATGAAGCGGTTCCCCAGGCCGTCTTGCTAG		MGPNIYMKRFPRPSC*		MGPNIYMKRFPRPSC*		ATCAGGAGAG	GTACACACAA	0	O	0	0	0	0	0
5703	2870	an	AN7201.1	69.m15184	AO070252000010	0	-281	-156					ATGGGACAAGGCAAGCAAATGCTATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA	ATGGGACAAGGCAAGCAAATGCTATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA			MGQGKQMLCRQKAASILLLFFYLFSMVEPISFRPNIDRIWE*	MGQGKQMLCRQKAASILLLFFYLFSMVEPISFRPNIDRIWE*			TGACTCGATT	CCACATACCC	0	O	0	0	0	0	0
5704	2870	an	AN7201.1	69.m15184	AO070252000010	0	-263	-156					ATGCTATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA	ATGCTATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA			MLCRQKAASILLLFFYLFSMVEPISFRPNIDRIWE*	MLCRQKAASILLLFFYLFSMVEPISFRPNIDRIWE*			AGGCAAGCAA	CCACATACCC	0	O	0	0	0	0	0
5705	2870	an	AN7201.1	69.m15184	AO070252000010	0	-258	-190					ATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAG	ATGCCGCCAGAAGGCGGCGAGTATTTTACTCCTTTTTTTTTATCTGTTTTCTATGGTCGAACCCATTAG			MPPEGGEYFTPFFLSVFYGRTH*	MPPEGGEYFTPFFLSVFYGRTH*			AGCAAATGCT	CTTTCGCCCT	0	O	0	0	0	0	0
5706	2870	an	AN7201.1	69.m15184	AO070252000010	0	-206	-156					ATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA	ATGGTCGAACCCATTAGCTTTCGCCCTAATATTGATCGTATCTGGGAGTAA			MVEPISFRPNIDRIWE*	MVEPISFRPNIDRIWE*			TCTGTTTTCT	CCACATACCC	0	O	0	0	0	0	0
5717	2870	ao	AN7201.1	69.m15184	AO070252000010	0					-206	-168	ATGCTCCTTCAGGAGAACAATGCGATTCTAAACTGCTAA			ATGCTCCTTCAGGAGAACAATGCGATTCTAAACTGCTAA	MLLQENNAILNC*			MLLQENNAILNC*	GCGCACACTA	CCCCGAGAGC	0	O	0	0	0	0	0
5718	2870	ao	AN7201.1	69.m15184	AO070252000010	0					-187	-176	ATGCGATTCTAA			ATGCGATTCTAA	MRF*			MRF*	CAGGAGAACA	ACTGCTAACC	0	O	0	0	0	0	0
5719	2870	ao	AN7201.1	69.m15184	AO070252000010	0					-139	-86	ATGAGCTTGGGCCCTCTGCGAGCGGGGAATGGGGCTTTCCAGACAGGTATATGA			ATGAGCTTGGGCCCTCTGCGAGCGGGGAATGGGGCTTTCCAGACAGGTATATGA	MSLGPLRAGNGAFQTGI*			MSLGPLRAGNGAFQTGI*	TGCTTGTTGA	AAGGGCAGAG	0	O	0	0	0	0	0
5720	2870	ao	AN7201.1	69.m15184	AO070252000010	0					-111	-25	ATGGGGCTTTCCAGACAGGTATATGAAAGGGCAGAGTCCGTCTATACTAGTCCTTGCTTCACCTCTGTTCTCTGTGTTCAGGGTTGA			ATGGGGCTTTCCAGACAGGTATATGAAAGGGCAGAGTCCGTCTATACTAGTCCTTGCTTCACCTCTGTTCTCTGTGTTCAGGGTTGA	MGLSRQVYERAESVYTSPCFTSVLCVQG*			MGLSRQVYERAESVYTSPCFTSVLCVQG*	CGAGCGGGGA	AGAACCCCAA	0	O	0	0	0	0	0
5722	2872	af	AN5006.1	59.m08904	AO070255000034	0			-223	-191			ATGGAAAACATCAATTCAGGGCAAAACTGTTGA		ATGGAAAACATCAATTCAGGGCAAAACTGTTGA		MENINSGQNC*		MENINSGQNC*		CACTACGATA	TTGTGCTTCG	0	L	0	0	0	0	0
5721	2872	an	AN5006.1	59.m08904	AO070255000034	0	-256	-203					ATGATAGTTTATACCAATAATTATCCAAAGAATTCTGCCAACTGCACACCATAA	ATGATAGTTTATACCAATAATTATCCAAAGAATTCTGCCAACTGCACACCATAA			MIVYTNNYPKNSANCTP*	MIVYTNNYPKNSANCTP*			GTTATCCTAT	TTAGTTACTC	0	L	0	0	0	0	0
5723	2872	ao	AN5006.1	59.m08904	AO070255000034	0					-232	-197	ATGATGAACATGAAGTACTTCAGTTCCTATGTGTAG			ATGATGAACATGAAGTACTTCAGTTCCTATGTGTAG	MMNMKYFSSYV*			MMNMKYFSSYV*	CATATCAATC	GCGTTTTTTG	0	L	0	0	0	0	0
5724	2872	ao	AN5006.1	59.m08904	AO070255000034	0					-229	-197	ATGAACATGAAGTACTTCAGTTCCTATGTGTAG			ATGAACATGAAGTACTTCAGTTCCTATGTGTAG	MNMKYFSSYV*			MNMKYFSSYV*	ATCAATCATG	GCGTTTTTTG	0	L	0	0	0	0	0
5725	2872	ao	AN5006.1	59.m08904	AO070255000034	0					-223	-197	ATGAAGTACTTCAGTTCCTATGTGTAG			ATGAAGTACTTCAGTTCCTATGTGTAG	MKYFSSYV*			MKYFSSYV*	CATGATGAAC	GCGTTTTTTG	0	L	0	0	0	0	0
5726	2872	ao	AN5006.1	59.m08904	AO070255000034	0					-204	-139	ATGTGTAGGCGTTTTTTGGACCTATCACTTTGTAGAGTTCTAACGGGTGCTATTATTGGCCAATGA			ATGTGTAGGCGTTTTTTGGACCTATCACTTTGTAGAGTTCTAACGGGTGCTATTATTGGCCAATGA	MCRRFLDLSLCRVLTGAIIGQ*			MCRRFLDLSLCRVLTGAIIGQ*	TTCAGTTCCT	TACTTCAATA	0	L	0	0	0	0	0
5728	2874	af	AN3173.1	59.m08563	AO070256000017	0			-203	-159			ATGTGTACCGCCCGCGTAATTTCTCTGTATTGCTGTAATCTTTGA		ATGTGTACCGCCCGCGTAATTTCTCTGTATTGCTGTAATCTTTGA		MCTARVISLYCCNL*		MCTARVISLYCCNL*		CAATTACCAG	GGCTCCAATC	0	J	0	MG07006.1	0	0	0
5729	2874	af	AN3173.1	59.m08563	AO070256000017	0			-102	-70			ATGTCGGGCGGTCTCAAGATTTCGTTTCAGTAG		ATGTCGGGCGGTCTCAAGATTTCGTTTCAGTAG		MSGGLKISFQ*		MSGGLKISFQ*		GGACTAGTGC	CATCAAAGTC	0	J	0	MG07006.1	0	0	0
5727	2874	an	AN3173.1	59.m08563	AO070256000017	0	-194	-177					ATGTTAGGGCTAGCCTAG	ATGTTAGGGCTAGCCTAG			MLGLA*	MLGLA*			GGGTTTGTGA	GGTTGACAAA	0	J	0	MG07006.1	0	0	0
5735	2875	af	AN3172.1	59.m08562	AO070256000018	0			-282	-187			ATGGGGGAAAATATTTCACGTGATACAATGGGCGGATTGGAGCCTCAAAGATTACAGCAATACAGAGAAATTACGCGGGCGGTACACATCTGGTAA		ATGGGGGAAAATATTTCACGTGATACAATGGGCGGATTGGAGCCTCAAAGATTACAGCAATACAGAGAAATTACGCGGGCGGTACACATCTGGTAA		MGENISRDTMGGLEPQRLQQYREITRAVHIW*		MGENISRDTMGGLEPQRLQQYREITRAVHIW*		ACTAGTCCAG	TTGACCTTAC	0	J	0	0	0	0	0
5736	2875	af	AN3172.1	59.m08562	AO070256000018	0			-255	-187			ATGGGCGGATTGGAGCCTCAAAGATTACAGCAATACAGAGAAATTACGCGGGCGGTACACATCTGGTAA		ATGGGCGGATTGGAGCCTCAAAGATTACAGCAATACAGAGAAATTACGCGGGCGGTACACATCTGGTAA		MGGLEPQRLQQYREITRAVHIW*		MGGLEPQRLQQYREITRAVHIW*		ACGTGATACA	TTGACCTTAC	0	J	0	0	0	0	0
5730	2875	an	AN3172.1	59.m08562	AO070256000018	0	-209	-162					ATGATGAGTAATCGAGAAGATGATGATGATTTGTCAACCCTAGGCTAG	ATGATGAGTAATCGAGAAGATGATGATGATTTGTCAACCCTAGGCTAG			MMSNREDDDDLSTLG*	MMSNREDDDDLSTLG*			TGGAGAAGGC	CCCTAACATT	0	J	0	0	0	0	0
5731	2875	an	AN3172.1	59.m08562	AO070256000018	0	-206	-162					ATGAGTAATCGAGAAGATGATGATGATTTGTCAACCCTAGGCTAG	ATGAGTAATCGAGAAGATGATGATGATTTGTCAACCCTAGGCTAG			MSNREDDDDLSTLG*	MSNREDDDDLSTLG*			AGAAGGCATG	CCCTAACATT	0	J	0	0	0	0	0
5732	2875	an	AN3172.1	59.m08562	AO070256000018	0	-190	-167					ATGATGATGATTTGTCAACCCTAG	ATGATGATGATTTGTCAACCCTAG			MMMICQP*	MMMICQP*			AATCGAGAAG	GCTAGCCCTA	0	J	0	0	0	0	0
5733	2875	an	AN3172.1	59.m08562	AO070256000018	0	-187	-167					ATGATGATTTGTCAACCCTAG	ATGATGATTTGTCAACCCTAG			MMICQP*	MMICQP*			CGAGAAGATG	GCTAGCCCTA	0	J	0	0	0	0	0
5734	2875	an	AN3172.1	59.m08562	AO070256000018	0	-184	-167					ATGATTTGTCAACCCTAG	ATGATTTGTCAACCCTAG			MICQP*	MICQP*			GAAGATGATG	GCTAGCCCTA	0	J	0	0	0	0	0
5737	2875	ao	AN3172.1	59.m08562	AO070256000018	0					-190	-104	ATGGCAAAGTGGAGGCCTGAGGCTCCGAATATTCGTACCCTAGCCCTAAAATTCACAAACGAAAATCATCCAAACGCGGAGGGCTAA			ATGGCAAAGTGGAGGCCTGAGGCTCCGAATATTCGTACCCTAGCCCTAAAATTCACAAACGAAAATCATCCAAACGCGGAGGGCTAA	MAKWRPEAPNIRTLALKFTNENHPNAEG*			MAKWRPEAPNIRTLALKFTNENHPNAEG*	ACGTGATTTG	AGTTCACCTT	0	J	0	0	0	0	0
5740	2876	af	AN3153.1	59.m08513	AO070256000033	0			-240	-205			ATGAGTTCTATTTCTTCCACCGAGGACAATTGCTAA		ATGAGTTCTATTTCTTCCACCGAGGACAATTGCTAA		MSSISSTEDNC*		MSSISSTEDNC*		GTGCATCTCC	AGGTCCTCTT	0	BK	0	0	0	0	0
5738	2876	an	AN3153.1	59.m08513	AO070256000033	0	-140	-111					ATGGATGACCTAGGCTTTCTTTCATGTTAA	ATGGATGACCTAGGCTTTCTTTCATGTTAA			MDDLGFLSC*	MDDLGFLSC*			ATAGCCAGCG	CGGTCAAAAA	0	BK	0	0	0	0	0
5739	2876	an	AN3153.1	59.m08513	AO070256000033	0	-117	-82					ATGTTAACGGTCAAAAACCAAAAGGTGATTTACTAG	ATGTTAACGGTCAAAAACCAAAAGGTGATTTACTAG			MLTVKNQKVIY*	MLTVKNQKVIY*			GCTTTCTTTC	ATTTCTTGAA	0	BK	0	0	0	0	0
5742	2876	ao	AN3153.1	59.m08513	AO070256000033	0					-208	-188	ATGACAGCTCCCAAAGATTAG			ATGACAGCTCCCAAAGATTAG	MTAPKD*			MTAPKD*	ACCACGAGCG	CATTACCGTT	0	BK	0	0	0	0	0
5743	2877	af	AN3156.1	59.m08547	AO070256000036	0			-235	-200			ATGCGGGCTGCAACAAAGCCCAAAAGTGGGTTTTGA		ATGCGGGCTGCAACAAAGCCCAAAAGTGGGTTTTGA		MRAATKPKSGF*		MRAATKPKSGF*		CCCGAATTCG	ACCGCCACAA	0	J	0	0	0	0	0

5744	2877	ao	AN3156.1	59.m08547	AO070256000036	0					-235	-131	ATGACTCACCACCAGCCCAAAGTGGGTTTTGAGCCGCCACAAAGTGATTTGAAGTGTGCTCTGATTCTCATCAGTGGTCTGCCGTTAATCTCTTTTTCCAGTTGA			ATGACTCACCACCAGCCCAAAGTGGGTTTTGAGCCGCCACAAAGTGATTTGAAGTGTGCTCTGATTCTCATCAGTGGTCTGCCGTTAATCTCTTTTTCCAGTTGA	MTHHQPKVGFEPPQSDLKCALILISGLPLISFSS*			MTHHQPKVGFEPPQSDLKCALILISGLPLISFSS*	GATGCACGTG	ACCAACCTCC	0	J	0	0	0	0	0
5750	2878	af	AN2378.1	69.m15152	AO070258000021	0			-190	-104			ATGAAAAATCGAGAAAATGGAGCCCTCAGTCGTTGCCTGTCTATAAAGCTGCTCGAATTCCTTGATGAACCGACTCCCATGAGATGA		ATGAAAAATCGAGAAAATGGAGCCCTCAGTCGTTGCCTGTCTATAAAGCTGCTCGAATTCCTTGATGAACCGACTCCCATGAGATGA		MKNRENGALSRCLSIKLLEFLDEPTPMR*		MKNRENGALSRCLSIKLLEFLDEPTPMR*		CCTCTCCGCG	GCAAAGCTCT	0	R	0	0	0	0	0
5751	2878	af	AN2378.1	69.m15152	AO070258000021	0			-174	-145			ATGGAGCCCTCAGTCGTTGCCTGTCTATAA		ATGGAGCCCTCAGTCGTTGCCTGTCTATAA		MEPSVVACL*		MEPSVVACL*		AATCGAGAAA	AGCTGCTCGA	0	R	0	0	0	0	0
5752	2878	af	AN2378.1	69.m15152	AO070258000021	0			-126	-109			ATGAACCGACTCCCATGA		ATGAACCGACTCCCATGA		MNRLP*		MNRLP*		GAATTCCTTG	GATGAGCAAA	0	R	0	0	0	0	0
5753	2878	af	AN2378.1	69.m15152	AO070258000021	0			-107	-60			ATGAGCAAAGCTCTGAAGGTTCCTCTTTGTCAACTTTATAGCGAATAG		ATGAGCAAAGCTCTGAAGGTTCCTCTTTGTCAACTTTATAGCGAATAG		MSKALKVPLCQLYSE*		MSKALKVPLCQLYSE*		CTCCCATGAG	CTAGCGAATC	0	R	0	0	0	0	0
5745	2878	an	AN2378.1	69.m15152	AO070258000021	0	-154	-122					ATGACCATAACGGGGATGCATGAGGATGCATGA	ATGACCATAACGGGGATGCATGAGGATGCATGA			MTITGMHEDA*	MTITGMHEDA*			CAAAACGTAC	AGAGGTGAAG	0	R	0	0	0	0	0
5746	2878	an	AN2378.1	69.m15152	AO070258000021	0	-139	-122					ATGCATGAGGATGCATGA	ATGCATGAGGATGCATGA			MHEDA*	MHEDA*			CATAACGGGG	AGAGGTGAAG	0	R	0	0	0	0	0
5747	2878	an	AN2378.1	69.m15152	AO070258000021	0	-135	-49					ATGAGGATGCATGAAGAGGTGAAGAGGAGACCTGGCCAGGGAATCCAAAGCTATAAAGCCCTTCATGGCCCCGTCCCTGCTGTCTAA	ATGAGGATGCATGAAGAGGTGAAGAGGAGACCTGGCCAGGGAATCCAAAGCTATAAAGCCCTTCATGGCCCCGTCCCTGCTGTCTAA			MRMHEEVKRRPGQGIQSYKALHGPVPAV*	MRMHEEVKRRPGQGIQSYKALHGPVPAV*			ACGGGGATGC	ATCAAGAGAG	0	R	0	0	0	0	0
5748	2878	an	AN2378.1	69.m15152	AO070258000021	0	-129	-49					ATGCATGAAGAGGTGAAGAGGAGACCTGGCCAGGGAATCCAAAGCTATAAAGCCCTTCATGGCCCCGTCCCTGCTGTCTAA	ATGCATGAAGAGGTGAAGAGGAGACCTGGCCAGGGAATCCAAAGCTATAAAGCCCTTCATGGCCCCGTCCCTGCTGTCTAA			MHEEVKRRPGQGIQSYKALHGPVPAV*	MHEEVKRRPGQGIQSYKALHGPVPAV*			ATGCATGAGG	ATCAAGAGAG	0	R	0	0	0	0	0
5749	2878	an	AN2378.1	69.m15152	AO070258000021	0	-125	-114					ATGAAGAGGTGA	ATGAAGAGGTGA			MKR*	MKR*			ATGAGGATGC	AGAGGAGACC	0	R	0	0	0	0	0
5754	2878	ao	AN2378.1	69.m15152	AO070258000021	0					-225	-166	ATGCACAGCAGGCGGGTATTCTTGCCTCACACCATAATGGTCCAGTTTTCCATTTTGTGA			ATGCACAGCAGGCGGGTATTCTTGCCTCACACCATAATGGTCCAGTTTTCCATTTTGTGA	MHSRRVFLPHTIMVQFSIL*			MHSRRVFLPHTIMVQFSIL*	TATATCCAAG	GCCCCATGTA	0	R	0	0	0	0	0
5755	2878	ao	AN2378.1	69.m15152	AO070258000021	0					-189	-166	ATGGTCCAGTTTTCCATTTTGTGA			ATGGTCCAGTTTTCCATTTTGTGA	MVQFSIL*			MVQFSIL*	TCACACCATA	GCCCCATGTA	0	R	0	0	0	0	0
5756	2878	ao	AN2378.1	69.m15152	AO070258000021	0					-160	-17	ATGTATTCCAGTTATATAAGGAGCGCAAAGGTGCTCCTCGAGTCACAACAACCAGCTCAGGAATTCCTTTTGCAACATCTCTCTCTTCCATTTTATCGCATAACGTCTATTTTCTGCTTGTATACCGATTGCGATTACATCTGA			ATGTATTCCAGTTATATAAGGAGCGCAAAGGTGCTCCTCGAGTCACAACAACCAGCTCAGGAATTCCTTTTGCAACATCTCTCTCTTCCATTTTATCGCATAACGTCTATTTTCTGCTTGTATACCGATTGCGATTACATCTGA	MYSSYIRSAKVLLESQQPAQEFLLQHLSLPFYRITSIFCLYTDCDYI*			MYSSYIRSAKVLLESQQPAQEFLLQHLSLPFYRITSIFCLYTDCDYI*	TGTGAGCCCC	AACGCCGTCT	0	R	0	0	0	0	0
5757	2882	an	AN4382.1	58.m07943	AO070261000027	0	-104	-51					ATGCCTCGAATATCGCGAGCTGCCCGTCCGACTGAGACTTTGGATCCTCGCTGA	ATGCCTCGAATATCGCGAGCTGCCCGTCCGACTGAGACTTTGGATCCTCGCTGA			MPRISRAARPTETLDPR*	MPRISRAARPTETLDPR*			TTGCTCCTGC	GCTTATACGT	0	FH	0	0	0	0	0
5758	2882	ao	AN4382.1	58.m07943	AO070261000027	0					-98	-69	ATGAGCTACGACTCGGGGTATTTGGATTGA			ATGAGCTACGACTCGGGGTATTTGGATTGA	MSYDSGYLD*			MSYDSGYLD*	GTTTATCCGC	TTTTCTATAC	0	FH	0	0	0	0	0
5762	2885	af	AN2441.1	69.m15217	AO070264000038	0			-245	-108			ATGTTCCAAAGTGCCTCAGGCGTCTCAGGCCACAACATCACATGGGCGCGCCTGGCTCTTGGTCATGTGATCACATCACAGTTATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAG		ATGTTCCAAAGTGCCTCAGGCGTCTCAGGCCACAACATCACATGGGCGCGCCTGGCTCTTGGTCATGTGATCACATCACAGTTATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAG		MFQSASGVSGHNITWARLALGHVITSQLCPTIINTSRCIAMIFGG*		MFQSASGVSGHNITWARLALGHVITSQLCPTIINTSRCIAMIFGG*		GTCATACCTT	GGCCCGTCGA	0	O	0	0	NCU08040.1	YPL003W	0
5763	2885	af	AN2441.1	69.m15217	AO070264000038	0			-204	-61			ATGGGCGCGCCTGGCTCTTGGTCATGTGATCACATCACAGTTATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		ATGGGCGCGCCTGGCTCTTGGTCATGTGATCACATCACAGTTATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		MGAPGSWSCDHITVMPDNHQHKQMHCYDLWWIGPVESALVLVIAFFL*		MGAPGSWSCDHITVMPDNHQHKQMHCYDLWWIGPVESALVLVIAFFL*		ACAACATCAC	ATTTGAAGAG	0	O	0	0	NCU08040.1	YPL003W	0
5764	2885	af	AN2441.1	69.m15217	AO070264000038	0			-162	-61			ATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		ATGCCCGACAATCATCAACACAAGCAGATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		MPDNHQHKQMHCYDLWWIGPVESALVLVIAFFL*		MPDNHQHKQMHCYDLWWIGPVESALVLVIAFFL*		CATCACAGTT	ATTTGAAGAG	0	O	0	0	NCU08040.1	YPL003W	0
5765	2885	af	AN2441.1	69.m15217	AO070264000038	0			-135	-61			ATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		ATGCATTGCTATGATCTTTGGTGGATAGGGCCCGTCGAATCTGCCCTTGTATTGGTTATCGCTTTTTTCCTTTGA		MHCYDLWWIGPVESALVLVIAFFL*		MHCYDLWWIGPVESALVLVIAFFL*		ACACAAGCAG	ATTTGAAGAG	0	O	0	0	NCU08040.1	YPL003W	0
5766	2885	af	AN2441.1	69.m15217	AO070264000038	0			-125	-108			ATGATCTTTGGTGGATAG		ATGATCTTTGGTGGATAG		MIFGG*		MIFGG*		ATGCATTGCT	GGCCCGTCGA	0	O	0	0	NCU08040.1	YPL003W	0
5759	2885	an	AN2441.1	69.m15217	AO070264000038	0	-106	-2					ATGATGCTTGTCCGAGGAGAGTGCATTTACGTCTACATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA	ATGATGCTTGTCCGAGGAGAGTGCATTTACGTCTACATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA			MMLVRGECIYVYMTKIAADFTARFFHSVLHYTLG*	MMLVRGECIYVYMTKIAADFTARFFHSVLHYTLG*			CGGATCATCA	AATGACATCG	0	O	0	0	NCU08040.1	YPL003W	0
5760	2885	an	AN2441.1	69.m15217	AO070264000038	0	-103	-2					ATGCTTGTCCGAGGAGAGTGCATTTACGTCTACATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA	ATGCTTGTCCGAGGAGAGTGCATTTACGTCTACATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA			MLVRGECIYVYMTKIAADFTARFFHSVLHYTLG*	MLVRGECIYVYMTKIAADFTARFFHSVLHYTLG*			ATCATCAATG	AATGACATCG	0	O	0	0	NCU08040.1	YPL003W	0
5761	2885	an	AN2441.1	69.m15217	AO070264000038	0	-70	-2					ATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA	ATGACCAAGATCGCTGCTGATTTTACTGCCCGTTTCTTTCATTCTGTCTTACATTACACCCTGGGTTGA			MTKIAADFTARFFHSVLHYTLG*	MTKIAADFTARFFHSVLHYTLG*			TTACGTCTAC	AATGACATCG	0	O	0	0	NCU08040.1	YPL003W	0
5767	2885	ao	AN2441.1	69.m15217	AO070264000038	0					-192	-130	ATGCAGCGTCTACTACGGATTACTGCAGAACCATTGTCAACAACTACAAGCTTTCAACGATAG			ATGCAGCGTCTACTACGGATTACTGCAGAACCATTGTCAACAACTACAAGCTTTCAACGATAG	MQRLLRITAEPLSTTTSFQR*			MQRLLRITAEPLSTTTSFQR*	TCACGTGGGC	TCAGATGCTT	0	O	0	0	NCU08040.1	YPL003W	0
5768	2885	ao	AN2441.1	69.m15217	AO070264000038	0					-125	-87	ATGCTTGCCATTCTATTCTCTGTCCGAGGCAGGTACTAG			ATGCTTGCCATTCTATTCTCTGTCCGAGGCAGGTACTAG	MLAILFSVRGRY*			MLAILFSVRGRY*	CGATAGTCAG	TATCCCGGCT	0	O	0	0	NCU08040.1	YPL003W	0
5770	2888	af	AN4594.1	57.m05517	AO070267000010	0			-215	-132			ATGGAATTCATTCGTCTGTTGCATTTCACGATAGCTCTTCAACGGCCATCATCACCTTACCGAACCTCGAAGTTCAGGTCTTGA		ATGGAATTCATTCGTCTGTTGCATTTCACGATAGCTCTTCAACGGCCATCATCACCTTACCGAACCTCGAAGTTCAGGTCTTGA		MEFIRLLHFTIALQRPSSPYRTSKFRS*		MEFIRLLHFTIALQRPSSPYRTSKFRS*		GATAAAAAAA	TTGGCAACTA	0	J	0	0	0	0	YHL015W
5771	2888	af	AN4594.1	57.m05517	AO070267000010	0			-108	-73			ATGATTCTTCTGTCATTTCTGTCTAGTTTTTCTTGA		ATGATTCTTCTGTCATTTCTGTCTAGTTTTTCTTGA		MILLSFLSSFS*		MILLSFLSSFS*		TCATACAGGT	GCAGCGACTA	0	J	0	0	0	0	YHL015W
5769	2888	an	AN4594.1	57.m05517	AO070267000010	0	-92	-51					ATGTCCATTCCTCAATCCAATTCACCCGCTACCACAAGCTAA	ATGTCCATTCCTCAATCCAATTCACCCGCTACCACAAGCTAA			MSIPQSNSPATTS*	MSIPQSNSPATTS*			CATCTGCAGT	CTGGTCCTCA	0	J	0	0	0	0	YHL015W
5773	2891	af	AN7657.1	57.m05419	AO070268000020	0			-249	-142			ATGGTTGACTACTCTCCCTGCCTCTTTGTTTCCGTTTCCTGCATCATCCCTTCGGTCGTTCATCTCCATTCTTCCTTTCTTTACTCCTGTCCTTCATACCTCTTTTAA		ATGGTTGACTACTCTCCCTGCCTCTTTGTTTCCGTTTCCTGCATCATCCCTTCGGTCGTTCATCTCCATTCTTCCTTTCTTTACTCCTGTCCTTCATACCTCTTTTAA		MVDYSPCLFVSVSCIIPSVVHLHSSFLYSCPSYLF*		MVDYSPCLFVSVSCIIPSVVHLHSSFLYSCPSYLF*		TGGGTATTCC	TCCTCGATAT	0		0	0	0	0	0
5772	2891	an	AN7657.1	57.m05419	AO070268000020	0	-231	-97					ATGATCCCTCTTTCTCCTCTCCTTGCCTCCTCTTCTTCCCTTCTTTCCCTCCATCCCTTCCATCGCTTGACTTCTTCTTTCTTGTTTATCCTACATCAAATCGTCCCAGTCACTCGTTTGGACTTGCCTTTTTAA	ATGATCCCTCTTTCTCCTCTCCTTGCCTCCTCTTCTTCCCTTCTTTCCCTCCATCCCTTCCATCGCTTGACTTCTTCTTTCTTGTTTATCCTACATCAAATCGTCCCAGTCACTCGTTTGGACTTGCCTTTTTAA			MIPLSPLLASSSSLLSLHPFHRLTSSFLFILHQIVPVTRLDLPF*	MIPLSPLLASSSSLLSLHPFHRLTSSFLFILHQIVPVTRLDLPF*			CCAGCAGTCC	TTCTCACACT	0		0	0	0	0	0
5776	2892	af	AN7663.1	57.m05430	AO070268000034	0			-154	-92			ATGGGCGGGTTGGATGTCGGAGATCTGCTGTGTCGGCTATCGGTTTTTGATCTCGGCAATTGA		ATGGGCGGGTTGGATGTCGGAGATCTGCTGTGTCGGCTATCGGTTTTTGATCTCGGCAATTGA		MGGLDVGDLLCRLSVFDLGN*		MGGLDVGDLLCRLSVFDLGN*		ACGGCTATAG	TCGGGGCGGG	0	C	0	0	0	0	0
5777	2892	af	AN7663.1	57.m05430	AO070268000034	0			-141	-40			ATGTCGGAGATCTGCTGTGTCGGCTATCGGTTTTTGATCTCGGCAATTGATCGGGGCGGGATACTTTTGTATAAGACAACTCCCATGGAGGACAAGCCGTAG		ATGTCGGAGATCTGCTGTGTCGGCTATCGGTTTTTGATCTCGGCAATTGATCGGGGCGGGATACTTTTGTATAAGACAACTCCCATGGAGGACAAGCCGTAG		MSEICCVGYRFLISAIDRGGILLYKTTPMEDKP*		MSEICCVGYRFLISAIDRGGILLYKTTPMEDKP*		GGCGGGTTGG	CCCTAGTATA	0	C	0	0	0	0	0
5774	2892	an	AN7663.1	57.m05430	AO070268000034	0	-185	-78					ATGATACGGCAATCTCAAAACCCGCTTGCACCCATCGGCAATCGGCCTTTGAAGCAACCCCCGGCTATTGACCGCACCGCCGTATCCGTATCCGAAGTATACTTATAA	ATGATACGGCAATCTCAAAACCCGCTTGCACCCATCGGCAATCGGCCTTTGAAGCAACCCCCGGCTATTGACCGCACCGCCGTATCCGTATCCGAAGTATACTTATAA			MIRQSQNPLAPIGNRPLKQPPAIDRTAVSVSEVYL*	MIRQSQNPLAPIGNRPLKQPPAIDRTAVSVSEVYL*			TCACTGGGAG	CCCTAACTAT	0	C	0	0	0	0	0
5779	2892	ao	AN7663.1	57.m05430	AO070268000034	0					-249	-217	ATGGGGAAAAGCAGCTCCCAGCAGCAGCGGTGA			ATGGGGAAAAGCAGCTCCCAGCAGCAGCGGTGA	MGKSSSQQQR*			MGKSSSQQQR*	ATCGCCCCAT	CGGCAATACG	0	C	0	0	0	0	0
5781	2893	af	AN2561.1	59.m08407	AO070268000055	0			-150	-127			ATGATGCTTGACTCGCAGCCATGA		ATGATGCTTGACTCGCAGCCATGA		MMLDSQP*		MMLDSQP*		GCTTGCTAAG	CGTGCTGGTC	0		FG00828.1	0	0	0	0
5782	2893	af	AN2561.1	59.m08407	AO070268000055	0			-147	-127			ATGCTTGACTCGCAGCCATGA		ATGCTTGACTCGCAGCCATGA		MLDSQP*		MLDSQP*		TGCTAAGATG	CGTGCTGGTC	0		FG00828.1	0	0	0	0
5783	2893	af	AN2561.1	59.m08407	AO070268000055	0			-130	-65			ATGACGTGCTGGTCTGACAAATGCTACCCCGCAAGAGAACTCGGTGATATAAGACCAGTTCAATGA		ATGACGTGCTGGTCTGACAAATGCTACCCCGCAAGAGAACTCGGTGATATAAGACCAGTTCAATGA		MTCWSDKCYPARELGDIRPVQ*		MTCWSDKCYPARELGDIRPVQ*		ACTCGCAGCC	ATGGCCGATT	0		FG00828.1	0	0	0	0
5784	2893	af	AN2561.1	59.m08407	AO070268000055	0			-110	-84			ATGCTACCCCGCAAGAGAACTCGGTGA		ATGCTACCCCGCAAGAGAACTCGGTGA		MLPRKRTR*		MLPRKRTR*		GGTCTGACAA	TATAAGACCA	0		FG00828.1	0	0	0	0
5780	2893	an	AN2561.1	59.m08407	AO070268000055	0	-216	-172					ATGATTGCGTGCTGGTCTGACAAATTGGCATTGCGCATTGTCTGA	ATGATTGCGTGCTGGTCTGACAAATTGGCATTGCGCATTGTCTGA			MIACWSDKLALRIV*	MIACWSDKLALRIV*			TGTCACATTG	CCCCTCATCT	0		FG00828.1	0	0	0	0
5785	2893	ao	AN2561.1	59.m08407	AO070268000055	0					-203	-180	ATGACACATGCATCTGAAACCTAG			ATGACACATGCATCTGAAACCTAG	MTHASET*			MTHASET*	CCCGAATCGA	GTGATGGCGT	0		FG00828.1	0	0	0	0
5786	2893	ao	AN2561.1	59.m08407	AO070268000055	0					-196	-176	ATGCATCTGAAACCTAGGTGA			ATGCATCTGAAACCTAGGTGA	MHLKPR*			MHLKPR*	CGAATGACAC	TGGCGTGCGA	0		FG00828.1	0	0	0	0
5787	2893	ao	AN2561.1	59.m08407	AO070268000055	0					-176	-96	ATGGCGTGCGAATCTGACAAATGCCAATTCTTCTCCACGTTTCACCAACGGCCGTGTATAAAAAGTAGCTATTCACCTTAA			ATGGCGTGCGAATCTGACAAATGCCAATTCTTCTCCACGTTTCACCAACGGCCGTGTATAAAAAGTAGCTATTCACCTTAA	MACESDKCQFFSTFHQRPCIKSSYSP*			MACESDKCQFFSTFHQRPCIKSSYSP*	AACCTAGGTG	ATCCATAGTG	0		FG00828.1	0	0	0	0
5788	2893	ao	AN2561.1	59.m08407	AO070268000055	0					-156	-109	ATGCCAATTCTTCTCCACGTTTCACCAACGGCCGTGTATAAAAAGTAG			ATGCCAATTCTTCTCCACGTTTCACCAACGGCCGTGTATAAAAAGTAG	MPILLHVSPTAVYKK*			MPILLHVSPTAVYKK*	AATCTGACAA	CTATTCACCT	0		FG00828.1	0	0	0	0
5789	2894	af	AN6650.1	62.m03250	AO070269000001	0			-108	-16			ATGCTTGCTCTTTTCCTCCTTGTTTCGCTGAGCTTTTTCTTTCGCTCTCTTCTCTCGTTTCCCCCGCCATCTTTTTCTCAGACCATCCCTTGA		ATGCTTGCTCTTTTCCTCCTTGTTTCGCTGAGCTTTTTCTTTCGCTCTCTTCTCTCGTTTCCCCCGCCATCTTTTTCTCAGACCATCCCTTGA		MLALFLLVSLSFFFRSLLSFPPPSFSQTIP*		MLALFLLVSLSFFFRSLLSFPPPSFSQTIP*		TGCCGAGCTC	TAGCATCCCA	0	C	FG00175.1	0	0	0	0
5792	2895	af	AN6653.1	62.m03255	AO070269000013	0			-273	-181			ATGGAAATGGATATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		ATGGAAATGGATATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		MEMDMGDLPRFPCFAHGWSKLPMGRGCSSF*		MEMDMGDLPRFPCFAHGWSKLPMGRGCSSF*		GATGACTGGA	CGTATGTCTT	0	C	0	0	0	YIR031C	YIR031C
5793	2895	af	AN6653.1	62.m03255	AO070269000013	0			-267	-181			ATGGATATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		ATGGATATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		MDMGDLPRFPCFAHGWSKLPMGRGCSSF*		MDMGDLPRFPCFAHGWSKLPMGRGCSSF*		TGGAATGGAA	CGTATGTCTT	0	C	0	0	0	YIR031C	YIR031C

5794	2895	af	AN6653.1	62.m03255	AO070269000013	0			-261	-181			ATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		ATGGGTGACCTCCCAAGGTTTCCGTGTTTCGCCCATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGA		MGDLPRFPCFAHGWSKLPMGRGCSSF*		MGDLPRFPCFAHGWSKLPMGRGCSSF*		GGAAATGGAT	CGTATGTCTT	0	C	0	0	0	YIR031C	YIR031C
5795	2895	af	AN6653.1	62.m03255	AO070269000013	0			-227	-75			ATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGACGTATGTCTTTCTTCGTACTCCCGAAGGACCTATGCATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGATTTCTTTCCTTCTTCTTCTTGA		ATGGTTGGTCCAAACTTCCAATGGGCCGCGGTTGTTCATCGTTCTGACGTATGTCTTTCTTCGTACTCCCGAAGGACCTATGCATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGATTTCTTTCCTTCTTCTTCTTGA		MVGPNFQWAAVVHRSDVCLSSYSRRTYACDPSIYCRLGAAPGFDFFPSSS*		MVGPNFQWAAVVHRSDVCLSSYSRRTYACDPSIYCRLGAAPGFDFFPSSS*		TGTTTCGCCC	ACTTTATTTG	0	C	0	0	0	YIR031C	YIR031C
5796	2895	af	AN6653.1	62.m03255	AO070269000013	0			-207	-181			ATGGGCCGCGGTTGTTCATCGTTCTGA		ATGGGCCGCGGTTGTTCATCGTTCTGA		MGRGCSSF*		MGRGCSSF*		CAAACTTCCA	CGTATGTCTT	0	C	0	0	0	YIR031C	YIR031C
5797	2895	af	AN6653.1	62.m03255	AO070269000013	0			-177	-97			ATGTCTTTCTTCGTACTCCCGAAGGACCTATGCATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGA		ATGTCTTTCTTCGTACTCCCGAAGGACCTATGCATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGA		MSFFVLPKDLCMRSFYILSSRCCAGL*		MSFFVLPKDLCMRSFYILSSRCCAGL*		GTTCTGACGT	TTTCTTTCCT	0	C	0	0	0	YIR031C	YIR031C
5798	2895	af	AN6653.1	62.m03255	AO070269000013	0			-148	-116			ATGCATGCGATCCTTCTATATATTGTCGTCTAG		ATGCATGCGATCCTTCTATATATTGTCGTCTAG		MHAILLYIVV*		MHAILLYIVV*		CGAAGGACCT	GTGCTGCGCC	0	C	0	0	0	YIR031C	YIR031C
5799	2895	af	AN6653.1	62.m03255	AO070269000013	0			-144	-97			ATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGA		ATGCGATCCTTCTATATATTGTCGTCTAGGTGCTGCGCCGGGCTTTGA		MRSFYILSSRCCAGL*		MRSFYILSSRCCAGL*		GGACCTATGC	TTTCTTTCCT	0	C	0	0	0	YIR031C	YIR031C
5790	2895	an	AN6653.1	62.m03255	AO070269000013	0	-153	-106					ATGTGCTCCTGCCGAACTGACTGTTATCGGCATGCTTCATATATATAA	ATGTGCTCCTGCCGAACTGACTGTTATCGGCATGCTTCATATATATAA			MCSCRTDCYRHASYI*	MCSCRTDCYRHASYI*			CGTAGTCACA	GTCTGGTCTA	0	C	0	0	0	YIR031C	YIR031C
5791	2895	an	AN6653.1	62.m03255	AO070269000013	0	-122	-75					ATGCTTCATATATATAAGTCTGGTCTAGGCTCGCCCCCGGATTCTTGA	ATGCTTCATATATATAAGTCTGGTCTAGGCTCGCCCCCGGATTCTTGA			MLHIYKSGLGSPPDS*	MLHIYKSGLGSPPDS*			TGTTATCGGC	TTGACTTTTC	0	C	0	0	0	YIR031C	YIR031C
5800	2897	ao	AN6515.1	62.m03102	AO070270000010	0					-284	-225	ATGCGGAATATTACATATAGTACTTTGGTTCTATTCGTCCCTCCGGGGTTCTGGATTTGA			ATGCGGAATATTACATATAGTACTTTGGTTCTATTCGTCCCTCCGGGGTTCTGGATTTGA	MRNITYSTLVLFVPPGFWI*			MRNITYSTLVLFVPPGFWI*	AAACACGAGC	GAGCCGAAAG	0	S	FG07320.1	MG08069.1	0	YOR164C	0
5801	2898	an	AN6549.1	62.m03124	AO070270000036	0	-210	-172					ATGCCTGAACCTTTACCTAACCTATTTTCTTTCGATTGA	ATGCCTGAACCTTTACCTAACCTATTTTCTTTCGATTGA			MPEPLPNLFSFD*	MPEPLPNLFSFD*			GAATCGCGCG	TTATACTTAT	0	K	0	0	0	0	0
5802	2898	an	AN6549.1	62.m03124	AO070270000036	0	-145	-41					ATGCAAACTGTGCAAACAGGGCCTCATAGTCGCGGAGAGCAAGGTATCGAACCGAGCTTCTCTTCTGCAGAACTACGTCTTCCATTAGAGATTGTATTATTTTGA	ATGCAAACTGTGCAAACAGGGCCTCATAGTCGCGGAGAGCAAGGTATCGAACCGAGCTTCTCTTCTGCAGAACTACGTCTTCCATTAGAGATTGTATTATTTTGA			MQTVQTGPHSRGEQGIEPSFSSAELRLPLEIVLF*	MQTVQTGPHSRGEQGIEPSFSSAELRLPLEIVLF*			CAGACTGGAG	CTCCTCATTC	0	K	0	0	0	0	0
5803	2898	ao	AN6549.1	62.m03124	AO070270000036	0					-227	-186	ATGAACCTACCAACTGGCGCGGATAGAACTTCAATTAAATAA			ATGAACCTACCAACTGGCGCGGATAGAACTTCAATTAAATAA	MNLPTGADRTSIK*			MNLPTGADRTSIK*	AGGGTTAGAC	ACAATGCAAA	0	K	0	0	0	0	0
5804	2898	ao	AN6549.1	62.m03124	AO070270000036	0					-182	-141	ATGCAAACAAGTCAAACATCGCTTTTCTTTCTGTGGGGATAA			ATGCAAACAAGTCAAACATCGCTTTTCTTTCTGTGGGGATAA	MQTSQTSLFFLWG*			MQTSQTSLFFLWG*	TAAATAAACA	TACATCATAG	0	K	0	0	0	0	0
5805	2898	ao	AN6549.1	62.m03124	AO070270000036	0					-102	-52	ATGGTCTTGAGGTGTAGACTAGCATTTGCACTCCTGGCTGTTGTTTTGTAA			ATGGTCTTGAGGTGTAGACTAGCATTTGCACTCCTGGCTGTTGTTTTGTAA	MVLRCRLAFALLAVVL*			MVLRCRLAFALLAVVL*	TATACACTTC	GTCGGGATCT	0	K	0	0	0	0	0
5810	2901	af	AN6536.1	62.m03136	AO070270000048	0			-176	-165			ATGTTCCGCTAA		ATGTTCCGCTAA		MFR*		MFR*		AACGCGGGAC	AAAGAAGTGA	0	E	0	MG07528.1	0	YOR202W	0
5813	2903	af	AN8868.1	71.m16007	AO070271000003	0			-259	-215			ATGCACCTTATTAACTTGGTAGTCCCCGGGAAAACAGCAAACTAA		ATGCACCTTATTAACTTGGTAGTCCCCGGGAAAACAGCAAACTAA		MHLINLVVPGKTAN*		MHLINLVVPGKTAN*		ACTTGGGAAC	TGGGTGTTTC	0	R	0	0	NCU01444.1	0	0
5814	2903	af	AN8868.1	71.m16007	AO070271000003	0			-215	-189			ATGGGTGTTTCGATTATTGTAATTTAA		ATGGGTGTTTCGATTATTGTAATTTAA		MGVSIIVI*		MGVSIIVI*		CAGCAAACTA	CCACTTCACT	0	R	0	0	NCU01444.1	0	0
5815	2903	af	AN8868.1	71.m16007	AO070271000003	0			-164	-123			ATGTCATTGGGACACAGTGCTTATTTCCCCCAGTCTGGCTAA		ATGTCATTGGGACACAGTGCTTATTTCCCCCAGTCTGGCTAA		MSLGHSAYFPQSG*		MSLGHSAYFPQSG*		CTGACAGTTC	TCGGCGTGAT	0	R	0	0	NCU01444.1	0	0
5811	2903	an	AN8868.1	71.m16007	AO070271000003	0	-175	-155					ATGGGGTTTACTATTTCCTGA	ATGGGGTTTACTATTTCCTGA			MGFTIS*	MGFTIS*			CGAGAGTTAA	CGTCGTTCCC	0	R	0	0	NCU01444.1	0	0
5812	2903	an	AN8868.1	71.m16007	AO070271000003	0	-125	-105					ATGATCTTTAGCGGTCAGTAA	ATGATCTTTAGCGGTCAGTAA			MIFSGQ*	MIFSGQ*			TTGGTTATTC	CCATCCGCCG	0	R	0	0	NCU01444.1	0	0
5818	2904	af	AN8867.1	71.m16006	AO070271000004	0			-249	-235			ATGTCCCTACGGTAG		ATGTCCCTACGGTAG		MSLR*		MSLR*		AGTTACATAA	TACGTTACCT	0	J	0	0	0	0	0
5819	2904	af	AN8867.1	71.m16006	AO070271000004	0			-202	-191			ATGCACATATGA		ATGCACATATGA		MHI*		MHI*		ACTTTTCCTT	CTACTCAATA	0	J	0	0	0	0	0
5820	2904	af	AN8867.1	71.m16006	AO070271000004	0			-194	-180			ATGACTACTCAATAA		ATGACTACTCAATAA		MTTQ*		MTTQ*		TTATGCACAT	CCCCAAGCGA	0	J	0	0	0	0	0
5821	2904	af	AN8867.1	71.m16006	AO070271000004	0			-126	-67			ATGACACAGGGTTCGATTGTGTCAAAGCCTTCCCACAGTTTTCCTCCATCTGTCTTTTGA		ATGACACAGGGTTCGATTGTGTCAAAGCCTTCCCACAGTTTTCCTCCATCTGTCTTTTGA		MTQGSIVSKPSHSFPPSVF*		MTQGSIVSKPSHSFPPSVF*		GCCTAATTAG	ATATCTTCAT	0	J	0	0	0	0	0
5816	2904	an	AN8867.1	71.m16006	AO070271000004	0	-144	-58					ATGTCGACCAAAATTCGTGCCCCTCACCCCGCCCAGGCCGAAGTCAATGCACATTTGATCAAACAGCCAGCAACAGCGACATTTTGA	ATGTCGACCAAAATTCGTGCCCCTCACCCCGCCCAGGCCGAAGTCAATGCACATTTGATCAAACAGCCAGCAACAGCGACATTTTGA			MSTKIRAPHPAQAEVNAHLIKQPATATF*	MSTKIRAPHPAQAEVNAHLIKQPATATF*			TATCGGAGAA	CTGACCCGAC	0	J	0	0	0	0	0
5817	2904	an	AN8867.1	71.m16006	AO070271000004	0	-98	-87					ATGCACATTTGA	ATGCACATTTGA			MHI*	MHI*			GCCGAAGTCA	TCAAACAGCC	0	J	0	0	0	0	0
5822	2904	ao	AN8867.1	71.m16006	AO070271000004	0					-164	-108	ATGCATAGTTTATGCCCTAATGTCTCGAGGCACCCAAGTTTTTACCCCTCACATTGA			ATGCATAGTTTATGCCCTAATGTCTCGAGGCACCCAAGTTTTTACCCCTCACATTGA	MHSLCPNVSRHPSFYPSH*			MHSLCPNVSRHPSFYPSH*	AACTACTTTC	CCGTGAAGAA	0	J	0	0	0	0	0
5823	2904	ao	AN8867.1	71.m16006	AO070271000004	0					-145	-59	ATGTCTCGAGGCACCCAAGTTTTTACCCCTCACATTGACCGTGAAGAACCTCTGGGGCTCCTGTTCAACTTCACTCCACATTGTTAG			ATGTCTCGAGGCACCCAAGTTTTTACCCCTCACATTGACCGTGAAGAACCTCTGGGGCTCCTGTTCAACTTCACTCCACATTGTTAG	MSRGTQVFTPHIDREEPLGLLFNFTPHC*			MSRGTQVFTPHIDREEPLGLLFNFTPHC*	TTATGCCCTA	AATCTGAGAG	0	J	0	0	0	0	0
5824	2906	af	AN8844.1	71.m15978	AO070271000032	0			-210	-91			ATGACCTCTTATCAGTTCTATACTCCTACTAGAAAGGTATATCGCCAGAAAACTTACGTCAGTACCCCAGCCTACACCGCAACATCCGATAATACCCTGCCATCACTCCCAACTACGTAG		ATGACCTCTTATCAGTTCTATACTCCTACTAGAAAGGTATATCGCCAGAAAACTTACGTCAGTACCCCAGCCTACACCGCAACATCCGATAATACCCTGCCATCACTCCCAACTACGTAG		MTSYQFYTPTRKVYRQKTYVSTPAYTATSDNTLPSLPTT*		MTSYQFYTPTRKVYRQKTYVSTPAYTATSDNTLPSLPTT*		AACTCCTCAG	TTCGAGACTA	0	O	0	0	NCU06224.1	YOL133W	YOL133W
5826	2907	af	AN8834.1	71.m15964	AO070271000043	0			-245	-231			ATGAAACGAACGTGA		ATGAAACGAACGTGA		MKRT*		MKRT*		TAGGTAAGAG	GTTAGAAAAA	0	A	FG05466.1	MG06322.1	0	0	0
5825	2907	an	AN8834.1	71.m15964	AO070271000043	0	-90	-7					ATGTTTCTCCACAAAAAATTATCTCCGCTCCAAAAGTCTGGACGGATTGAAGCTTCAGTAACACCACCAAGTATACGTCTATAA	ATGTTTCTCCACAAAAAATTATCTCCGCTCCAAAAGTCTGGACGGATTGAAGCTTCAGTAACACCACCAAGTATACGTCTATAA			MFLHKKLSPLQKSGRIEASVTPPSIRL*	MFLHKKLSPLQKSGRIEASVTPPSIRL*			CGCCGGTCAA	CCCAACATGG	0	A	FG05466.1	MG06322.1	0	0	0
5827	2907	ao	AN8834.1	71.m15964	AO070271000043	0					-63	-40	ATGGCTTCTCATGTCCATTTCTAA			ATGGCTTCTCATGTCCATTTCTAA	MASHVHF*			MASHVHF*	AACTACATCC	AGAGCGCCTC	0	A	FG05466.1	MG06322.1	0	0	0
5833	2910	af	AN0993.1	69.m15282	AO070272000042	0			-158	-15			ATGGTGTGCGGTGTCCTGTGTGCCATACGGCGCTTGATGACCTCTCAGAACCTTAATAGTCACCTATTGTCCGTCCTGGCGATACCGTTCTACCTAAAAGTTCCCTTAACTGTCCCCTTGTCGCGCAAAACCTCCACCAGGTAG		ATGGTGTGCGGTGTCCTGTGTGCCATACGGCGCTTGATGACCTCTCAGAACCTTAATAGTCACCTATTGTCCGTCCTGGCGATACCGTTCTACCTAAAAGTTCCCTTAACTGTCCCCTTGTCGCGCAAAACCTCCACCAGGTAG		MVCGVLCAIRRLMTSQNLNSHLLSVLAIPFYLKVPLTVPLSRKTSTR*		MVCGVLCAIRRLMTSQNLNSHLLSVLAIPFYLKVPLTVPLSRKTSTR*		TACGGCAACG	AGTTGCTCGA	0	G	FG04668.1	0	0	0	0
5834	2910	af	AN0993.1	69.m15282	AO070272000042	0			-122	-15			ATGACCTCTCAGAACCTTAATAGTCACCTATTGTCCGTCCTGGCGATACCGTTCTACCTAAAAGTTCCCTTAACTGTCCCCTTGTCGCGCAAAACCTCCACCAGGTAG		ATGACCTCTCAGAACCTTAATAGTCACCTATTGTCCGTCCTGGCGATACCGTTCTACCTAAAAGTTCCCTTAACTGTCCCCTTGTCGCGCAAAACCTCCACCAGGTAG		MTSQNLNSHLLSVLAIPFYLKVPLTVPLSRKTSTR*		MTSQNLNSHLLSVLAIPFYLKVPLTVPLSRKTSTR*		ACGGCGCTTG	AGTTGCTCGA	0	G	FG04668.1	0	0	0	0
5828	2910	an	AN0993.1	69.m15282	AO070272000042	0	-253	-137					ATGGGCCCCCTTGCGATTCGCAGCTGCCATCACCATCATCGCGTGAATTGCATCTATGATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAA	ATGGGCCCCCTTGCGATTCGCAGCTGCCATCACCATCATCGCGTGAATTGCATCTATGATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAA			MGPLAIRSCHHHHRVNCIYDDVLSAMRGAPCGRHRWQL*	MGPLAIRSCHHHHRVNCIYDDVLSAMRGAPCGRHRWQL*			CCCCCACGAC	AATATCCTAA	0	G	FG04668.1	0	0	0	0
5829	2910	an	AN0993.1	69.m15282	AO070272000042	0	-198	-127					ATGATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA	ATGATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA			MMMCFPPCAVRRAGDTVGSFKIS*	MMMCFPPCAVRRAGDTVGSFKIS*			AATTGCATCT	CGGGCCCTCA	0	G	FG04668.1	0	0	0	0
5830	2910	an	AN0993.1	69.m15282	AO070272000042	0	-195	-127					ATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA	ATGATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA			MMCFPPCAVRRAGDTVGSFKIS*	MMCFPPCAVRRAGDTVGSFKIS*			TGCATCTATG	CGGGCCCTCA	0	G	FG04668.1	0	0	0	0
5831	2910	an	AN0993.1	69.m15282	AO070272000042	0	-192	-127					ATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA	ATGTGCTTTCCGCCATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAAAATATCCTAA			MCFPPCAVRRAGDTVGSFKIS*	MCFPPCAVRRAGDTVGSFKIS*			ATCTATGATG	CGGGCCCTCA	0	G	FG04668.1	0	0	0	0
5832	2910	an	AN0993.1	69.m15282	AO070272000042	0	-178	-137					ATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAA	ATGCGCGGTGCGCCGTGCGGGAGACACCGTTGGCAGCTTTAA			MRGAPCGRHRWQL*	MRGAPCGRHRWQL*			GCTTTCCGCC	AATATCCTAA	0	G	FG04668.1	0	0	0	0
5835	2910	ao	AN0993.1	69.m15282	AO070272000042	0					-184	-158	ATGTCATTCGCTGCCTTTATCGCGTGA			ATGTCATTCGCTGCCTTTATCGCGTGA	MSFAAFIA*			MSFAAFIA*	CTGCGACTAT	AATGCTGGGG	0	G	FG04668.1	0	0	0	0
5836	2910	ao	AN0993.1	69.m15282	AO070272000042	0					-156	-142	ATGCTGGGGCGATGA			ATGCTGGGGCGATGA	MLGR*			MLGR*	ATCGCGTGAA	TGTGCTGTCT	0	G	FG04668.1	0	0	0	0
5837	2910	ao	AN0993.1	69.m15282	AO070272000042	0					-128	-93	ATGTGGTACCCCAAATCTTCTGCTTATATTTTATAA			ATGTGGTACCCCAAATCTTCTGCTTATATTTTATAA	MWYPKSSAYIL*			MWYPKSSAYIL*	GCTGTCTGCC	CCAGCCTTTG	0	G	FG04668.1	0	0	0	0
5839	2913	af	AN4437.1	58.m07889	AO070273000018	0			-203	-45			ATGGAAGGGATAGCTGATCGACCTAGCAAAAGTGTCCAGGGCTATTATGGTGTCTTGATTACATCGGAGGGATTGGACTACTCAGTGGTCGTGAATCATACAATTAAATCCGCGACGCCCAGACAGATCTATACCGCTCTCCAGAGGATTGATCATTGA		ATGGAAGGGATAGCTGATCGACCTAGCAAAAGTGTCCAGGGCTATTATGGTGTCTTGATTACATCGGAGGGATTGGACTACTCAGTGGTCGTGAATCATACAATTAAATCCGCGACGCCCAGACAGATCTATACCGCTCTCCAGAGGATTGATCATTGA		MEGIADRPSKSVQGYYGVLITSEGLDYSVVVNHTIKSATPRQIYTALQRIDH*		MEGIADRPSKSVQGYYGVLITSEGLDYSVVVNHTIKSATPRQIYTALQRIDH*		CAAAGGGCTA	TCATTGTTCA	0	T	0	0	0	0	0
5840	2913	af	AN4437.1	58.m07889	AO070273000018	0			-157	-146			ATGGTGTCTTGA		ATGGTGTCTTGA		MVS*		MVS*		CAGGGCTATT	TTACATCGGA	0	T	0	0	0	0	0
5838	2913	an	AN4437.1	58.m07889	AO070273000018	0	-139	-113					ATGCTCGTGACCCTGGCAACTACTTAG	ATGCTCGTGACCCTGGCAACTACTTAG			MLVTLATT*	MLVTLATT*			TAAAGAGGAC	CGCGCTGCCA	0	T	0	0	0	0	0
5841	2913	ao	AN4437.1	58.m07889	AO070273000018	0					-144	-121	ATGCCCGTGACCCCCACGAGATAA			ATGCCCGTGACCCCCACGAGATAA	MPVTPTR*			MPVTPTR*	CAGAAGAGAA	CGCTCTCCAC	0	T	0	0	0	0	0
5842	2914	af	AN4414.1	58.m07903	AO070273000035	0			-103	-92			ATGGTCAAATAA		ATGGTCAAATAA		MVK*		MVK*		AACGCCCGAG	TCCACAGCCC	0	I	0	0	0	0	0
5843	2915	ao	AN4415.1	58.m07904	AO070273000036	0					-252	-241	ATGGATCAATGA			ATGGATCAATGA	MDQ*			MDQ*	AGAAGCCTAA	GTCTCAGAAG	0	CO	0	0	0	0	0
5844	2915	ao	AN4415.1	58.m07904	AO070273000036	0					-244	-200	ATGAGTCTCAGAAGGGTGCCGTATCCTAGTTACTACTCGATATGA			ATGAGTCTCAGAAGGGTGCCGTATCCTAGTTACTACTCGATATGA	MSLRRVPYPSYYSI*			MSLRRVPYPSYYSI*	AAATGGATCA	TGAATCGAGA	0	CO	0	0	0	0	0
5845	2915	ao	AN4415.1	58.m07904	AO070273000036	0					-203	-93	ATGATGAATCGAGAGACCGCCTTTCCAACAGAGAAGAAATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGAAACTGTCAGGACTTCTCTCTCCGCCTTCCGCAAGTAA			ATGATGAATCGAGAGACCGCCTTTCCAACAGAGAAGAAATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGAAACTGTCAGGACTTCTCTCTCCGCCTTCCGCAAGTAA	MMNRETAFPTEKKCGANSIPLEGGETVRTSLSAFRK*			MMNRETAFPTEKKCGANSIPLEGGETVRTSLSAFRK*	ACTACTCGAT	ATCTTCTTCC	0	CO	0	0	0	0	0
5846	2915	ao	AN4415.1	58.m07904	AO070273000036	0					-200	-93	ATGAATCGAGAGACCGCCTTTCCAACAGAGAAGAAATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGAAACTGTCAGGACTTCTCTCTCCGCCTTCCGCAAGTAA			ATGAATCGAGAGACCGCCTTTCCAACAGAGAAGAAATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGAAACTGTCAGGACTTCTCTCTCCGCCTTCCGCAAGTAA	MNRETAFPTEKKCGANSIPLEGGETVRTSLSAFRK*			MNRETAFPTEKKCGANSIPLEGGETVRTSLSAFRK*	ACTCGATATG	ATCTTCTTCC	0	CO	0	0	0	0	0
5847	2915	ao	AN4415.1	58.m07904	AO070273000036	0					-165	-130	ATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGA			ATGCGGAGCAAATTCAATTCCACTAGAAGGCGGTGA	MRSKFNSTRRR*			MRSKFNSTRRR*	CAGAGAAGAA	AACTGTCAGG	0	CO	0	0	0	0	0
5848	2918	af	AN9408.1	52.m04035	AO070274000009	0			-136	-83			ATGAGCGAAAGAAGAGACATACCCATTTATTTGACTTGCCTTTCTGATATCTGA		ATGAGCGAAAGAAGAGACATACCCATTTATTTGACTTGCCTTTCTGATATCTGA		MSERRDIPIYLTCLSDI*		MSERRDIPIYLTCLSDI*		GACTGCAGGA	TCAATCGCAG	0	I	0	MG04118.1	0	0	0

5849	2919	an	AN9407.1	52.m04034	AO070274000010	0	-158	-105					ATGTTATATCTGCTTGCGCCGACGACAAGCGTACAGGGTGCTGAATCGACTTGA	ATGTTATATCTGCTTGCGCCGACGACAAGCGTACAGGGTGCTGAATCGACTTGA			MLYLLAPTTSVQGAEST*	MLYLLAPTTSVQGAEST*			TTTTGTGCCA	TGCTGACATC	0	I	0	0	0	0	0
5850	2919	ao	AN9407.1	52.m04034	AO070274000010	0					-294	-262	ATGCCCGGCAAGCAAAGGCACTGCAAAACATGA			ATGCCCGGCAAGCAAAGGCACTGCAAAACATGA	MPGKQRHCKT*			MPGKQRHCKT*	TAAAGTGGTT	CTTTTTAATA	0	I	0	0	0	0	0
5851	2919	ao	AN9407.1	52.m04034	AO070274000010	0					-265	-254	ATGACTTTTTAA			ATGACTTTTTAA	MTF*			MTF*	ACTGCAAAAC	TAAACCTCTA	0	I	0	0	0	0	0
5855	2922	af	AN1133.1	71.m15635	AO070276000007	0			-210	-70			ATGTTCGACGACTTCTCGACTTTTCGTTCTATTCTGCGGCGGCACCACGTGATAGAAGACGTCACATGGCCTGGAAGCTCTCCCCGGCCTTTCATCATCATATCGAGCCTATCTGTCGCCTCCCCATCCTCGTCCATTTGA		ATGTTCGACGACTTCTCGACTTTTCGTTCTATTCTGCGGCGGCACCACGTGATAGAAGACGTCACATGGCCTGGAAGCTCTCCCCGGCCTTTCATCATCATATCGAGCCTATCTGTCGCCTCCCCATCCTCGTCCATTTGA		MFDDFSTFRSILRRHHVIEDVTWPGSSPRPFIIISSLSVASPSSSI*		MFDDFSTFRSILRRHHVIEDVTWPGSSPRPFIIISSLSVASPSSSI*		TGTTTCTTTC	GGCCTCATCG	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5852	2922	an	AN1133.1	71.m15635	AO070276000007	0	-193	-149					ATGAGAGTGGTTGCTGGACTGATTATGTCAGAACGAAATCGATGA	ATGAGAGTGGTTGCTGGACTGATTATGTCAGAACGAAATCGATGA			MRVVAGLIMSERNR*	MRVVAGLIMSERNR*			AGAAGCAAGT	CAGGACCCAC	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5853	2922	an	AN1133.1	71.m15635	AO070276000007	0	-169	-149					ATGTCAGAACGAAATCGATGA	ATGTCAGAACGAAATCGATGA			MSERNR*	MSERNR*			TGGACTGATT	CAGGACCCAC	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5854	2922	an	AN1133.1	71.m15635	AO070276000007	0	-152	-84					ATGACAGGACCCACTTGGGCGGTGAGCTGTCGCGGATGTCATAGAGCCGTGCCATTCCCCCCATCCTAG	ATGACAGGACCCACTTGGGCGGTGAGCTGTCGCGGATGTCATAGAGCCGTGCCATTCCCCCCATCCTAG			MTGPTWAVSCRGCHRAVPFPPS*	MTGPTWAVSCRGCHRAVPFPPS*			AACGAAATCG	AGCTTCGATT	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5856	2922	ao	AN1133.1	71.m15635	AO070276000007	0					-260	-129	ATGAGGGTTTGTCTAATATATTGTTTTAGGGCGAAATCCAAATATTGGTGGAAGAAAGATACAAGCCGATGTATGTCTCCGCCTGAGGCAGTGGCCATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG			ATGAGGGTTTGTCTAATATATTGTTTTAGGGCGAAATCCAAATATTGGTGGAAGAAAGATACAAGCCGATGTATGTCTCCGCCTGAGGCAGTGGCCATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG	MRVCLIYCFRAKSKYWWKKDTSRCMSPPEAVAMHHVTPSDVTF*			MRVCLIYCFRAKSKYWWKKDTSRCMSPPEAVAMHHVTPSDVTF*	ACGTGTAAGA	AAGCTCCCGT	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5857	2922	ao	AN1133.1	71.m15635	AO070276000007	0					-192	-175	ATGTATGTCTCCGCCTGA			ATGTATGTCTCCGCCTGA	MYVSA*			MYVSA*	ATACAAGCCG	GGCAGTGGCC	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5858	2922	ao	AN1133.1	71.m15635	AO070276000007	0					-188	-129	ATGTCTCCGCCTGAGGCAGTGGCCATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG			ATGTCTCCGCCTGAGGCAGTGGCCATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG	MSPPEAVAMHHVTPSDVTF*			MSPPEAVAMHHVTPSDVTF*	AAGCCGATGT	AAGCTCCCGT	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5859	2922	ao	AN1133.1	71.m15635	AO070276000007	0					-164	-129	ATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG			ATGCATCATGTGACTCCCTCCGACGTCACGTTCTAG	MHHVTPSDVTF*			MHHVTPSDVTF*	GGCAGTGGCC	AAGCTCCCGT	0	T	FG09422.1	MG03089.1	NCU02463.1	0	0
5865	2924	af	AN8810.1	71.m15616	AO070276000047	0			-89	-57			ATGGTACTACGACGTCTCGACATCAATCTCTAA		ATGGTACTACGACGTCTCGACATCAATCTCTAA		MVLRRLDINL*		MVLRRLDINL*		CCATCTCCGA	GTGACTTGTA	0		FG06805.1	0	0	YHR045W	0
5862	2924	an	AN8810.1	71.m15616	AO070276000047	0	-166	-131					ATGCTGGACACCTTAAGCGCTAGTAACCCCACATGA	ATGCTGGACACCTTAAGCGCTAGTAACCCCACATGA			MLDTLSASNPT*	MLDTLSASNPT*			ATCAGGAGAT	CAGTTGCTCA	0		FG06805.1	0	0	YHR045W	0
5863	2924	an	AN8810.1	71.m15616	AO070276000047	0	-134	-72					ATGACAGTTGCTCAACCATTCCAGCTCGTCATCCAAACACCTCAGCTATATCGTGTCAATTAG	ATGACAGTTGCTCAACCATTCCAGCTCGTCATCCAAACACCTCAGCTATATCGTGTCAATTAG			MTVAQPFQLVIQTPQLYRVN*	MTVAQPFQLVIQTPQLYRVN*			GTAACCCCAC	ACTGTTGTGT	0		FG06805.1	0	0	YHR045W	0
5866	2924	ao	AN8810.1	71.m15616	AO070276000047	0					-159	-88	ATGTCTCCACATCTACCCTCAGCTGTGGTCACGTCACCATCTAACTGCAGCCTAGAACCCGGCCCTTACTAG			ATGTCTCCACATCTACCCTCAGCTGTGGTCACGTCACCATCTAACTGCAGCCTAGAACCCGGCCCTTACTAG	MSPHLPSAVVTSPSNCSLEPGPY*			MSPHLPSAVVTSPSNCSLEPGPY*	GACCCGCGAA	GGAAATAAGG	0		FG06805.1	0	0	YHR045W	0
5868	2925	af	AN8797.1	71.m15604	AO070276000063	0			-210	-181			ATGTGCACTGTCTCCTTTCGCCTTCAGTGA		ATGTGCACTGTCTCCTTTCGCCTTCAGTGA		MCTVSFRLQ*		MCTVSFRLQ*		TCATTATTCG	AATTTGGCCG	0		0	0	0	0	0
5869	2925	ao	AN8797.1	71.m15604	AO070276000063	0					-225	-145	ATGCGTTTTCCCCTTCTGGGTGGCCTTCTTTGTCCGGTATCTCTCCCGGTTCCAGTAGTTGTGAATTACCTACTGGTGTAA			ATGCGTTTTCCCCTTCTGGGTGGCCTTCTTTGTCCGGTATCTCTCCCGGTTCCAGTAGTTGTGAATTACCTACTGGTGTAA	MRFPLLGGLLCPVSLPVPVVVNYLLV*			MRFPLLGGLLCPVSLPVPVVVNYLLV*	TCCTCTGTTT	CTCCTGTTCG	0		0	0	0	0	0
5874	2926	af	AN8283.1	65.m07459	AO070277000005	0			-212	-150			ATGCCTATCCTTTTTCTTCCCATCCTCATTTCATCCTCCCCAATTCCTGTACTCTCTGTTTGA		ATGCCTATCCTTTTTCTTCCCATCCTCATTTCATCCTCCCCAATTCCTGTACTCTCTGTTTGA		MPILFLPILISSSPIPVLSV*		MPILFLPILISSSPIPVLSV*		CAACGAGTAG	TCGCGGATTC	0	Q	0	MG04432.1	0	0	0
5870	2926	an	AN8283.1	65.m07459	AO070277000005	0	-214	-68					ATGAATTTATGCCTGAAAAAACCTCAGCATCACATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAGTGCCAACTTTTCCTTCGACTCCTGTAAGTGCCTCTCCGTTGACACTTAA	ATGAATTTATGCCTGAAAAAACCTCAGCATCACATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAGTGCCAACTTTTCCTTCGACTCCTGTAAGTGCCTCTCCGTTGACACTTAA			MNLCLKKPQHHMTDLPLALPWAPRIGPNPFKVSANFSFDSCKCLSVDT*	MNLCLKKPQHHMTDLPLALPWAPRIGPNPFKVSANFSFDSCKCLSVDT*			CCCCGAAGCC	CCACCCTCGT	0	Q	0	MG04432.1	0	0	0
5871	2926	an	AN8283.1	65.m07459	AO070277000005	0	-206	-117					ATGCCTGAAAAAACCTCAGCATCACATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAG	ATGCCTGAAAAAACCTCAGCATCACATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAG			MPEKTSASHDRFAPGPAMGATDRTQSIQG*	MPEKTSASHDRFAPGPAMGATDRTQSIQG*			CCATGAATTT	TGCCAACTTT	0	Q	0	MG04432.1	0	0	0
5872	2926	an	AN8283.1	65.m07459	AO070277000005	0	-181	-68					ATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAGTGCCAACTTTTCCTTCGACTCCTGTAAGTGCCTCTCCGTTGACACTTAA	ATGACCGATTTGCCCCTGGCCCTGCCATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAGTGCCAACTTTTCCTTCGACTCCTGTAAGTGCCTCTCCGTTGACACTTAA			MTDLPLALPWAPRIGPNPFKVSANFSFDSCKCLSVDT*	MTDLPLALPWAPRIGPNPFKVSANFSFDSCKCLSVDT*			TCAGCATCAC	CCACCCTCGT	0	Q	0	MG04432.1	0	0	0
5873	2926	an	AN8283.1	65.m07459	AO070277000005	0	-155	-117					ATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAG	ATGGGCGCCACGGATCGGACCCAATCCATTCAAGGTTAG			MGATDRTQSIQG*	MGATDRTQSIQG*			TGGCCCTGCC	TGCCAACTTT	0	Q	0	MG04432.1	0	0	0
5878	2928	af	AN2133.1	72.m19708	AO070278000026	0			-193	-176			ATGGAGAGGAGCGGATGA		ATGGAGAGGAGCGGATGA		MERSG*		MERSG*		TAAAGGACAG	GGGGGGCTAA	0	TZ	0	0	0	0	0
5879	2928	af	AN2133.1	72.m19708	AO070278000026	0			-144	-16			ATGCTTTACTGCAGCTCATTCAAACTCCGACAGCGATACAACTCATCAGCCCCTCTCTATCCCCCTCTTCATCCCTTCCTCGAATCCCTCCTCGTTATCTGCTTCACTTCTGCATCTCACAGTAACTAG		ATGCTTTACTGCAGCTCATTCAAACTCCGACAGCGATACAACTCATCAGCCCCTCTCTATCCCCCTCTTCATCCCTTCCTCGAATCCCTCCTCGTTATCTGCTTCACTTCTGCATCTCACAGTAACTAG		MLYCSSFKLRQRYNSSAPLYPPLHPFLESLLVICFTSASHSN*		MLYCSSFKLRQRYNSSAPLYPPLHPFLESLLVICFTSASHSN*		TTCCTGCGGC	TCACTTGAAT	0	TZ	0	0	0	0	0
5876	2928	an	AN2133.1	72.m19708	AO070278000026	0	-221	-165					ATGGAGGAGATAGGATCGTCGATGAGGCCGGAGGAGGCCGCAAGGGCGCATTTTTAA	ATGGAGGAGATAGGATCGTCGATGAGGCCGGAGGAGGCCGCAAGGGCGCATTTTTAA			MEEIGSSMRPEEAARAHF*	MEEIGSSMRPEEAARAHF*			CCGGGGGAGT	AAGAGCAGCC	0	TZ	0	0	0	0	0
5877	2928	an	AN2133.1	72.m19708	AO070278000026	0	-200	-165					ATGAGGCCGGAGGAGGCCGCAAGGGCGCATTTTTAA	ATGAGGCCGGAGGAGGCCGCAAGGGCGCATTTTTAA			MRPEEAARAHF*	MRPEEAARAHF*			AGGATCGTCG	AAGAGCAGCC	0	TZ	0	0	0	0	0
5880	2928	ao	AN2133.1	72.m19708	AO070278000026	0					-239	-183	ATGACAAGAGAGAGATTGACTTGGAAATCTGAGCGGAGAAGAAGAAAGGGACGCTGA			ATGACAAGAGAGAGATTGACTTGGAAATCTGAGCGGAGAAGAAGAAAGGGACGCTGA	MTRERLTWKSERRRRKGR*			MTRERLTWKSERRRRKGR*	GAGAGAAGGA	CATCAAGGTA	0	TZ	0	0	0	0	0
5881	2928	ao	AN2133.1	72.m19708	AO070278000026	0					-171	-142	ATGCATACCGTACAGTACCTGAGCAGGTGA			ATGCATACCGTACAGTACCTGAGCAGGTGA	MHTVQYLSR*			MHTVQYLSR*	ATCAAGGTAC	CACGACACAC	0	TZ	0	0	0	0	0
5882	2928	ao	AN2133.1	72.m19708	AO070278000026	0					-111	-34	ATGTGTATATATTTCTTGCTTCTCTCCCCCCTCACAAGCTTTCATTTTCTTATCTCTCTATTTTCCTACGACCTCTAG			ATGTGTATATATTTCTTGCTTCTCTCCCCCCTCACAAGCTTTCATTTTCTTATCTCTCTATTTTCCTACGACCTCTAG	MCIYFLLLSPLTSFHFLISLFSYDL*			MCIYFLLLSPLTSFHFLISLFSYDL*	CACTTCTCTG	AACCATACGA	0	TZ	0	0	0	0	0
5885	2930	ao	AN7354.1	72.m19725	AO070278000046	0					-62	-18	ATGTTCTATGCCGGGATGATGGCTTTATATTGTCGTTATTCTTGA			ATGTTCTATGCCGGGATGATGGCTTTATATTGTCGTTATTCTTGA	MFYAGMMALYCRYS*			MFYAGMMALYCRYS*	CCGACAAGGT	TACTAATTGG	0	J	0	MG05248.1	0	0	0
5889	2931	af	AN6364.1	72.m19496	AO070279000050	0			-201	-70			ATGGTTGATCGGCCTCGCGTTTCGATGGTTCTTACCGTCGCATACGGAAGATCACCTTCACAGACTATTGCTTGCCTTTCATCGAAGGTAATTCTGACGGCCACAGGCAGGGGCTCAGAGCGTCTTCTTTGA		ATGGTTGATCGGCCTCGCGTTTCGATGGTTCTTACCGTCGCATACGGAAGATCACCTTCACAGACTATTGCTTGCCTTTCATCGAAGGTAATTCTGACGGCCACAGGCAGGGGCTCAGAGCGTCTTCTTTGA		MVDRPRVSMVLTVAYGRSPSQTIACLSSKVILTATGRGSERLL*		MVDRPRVSMVLTVAYGRSPSQTIACLSSKVILTATGRGSERLL*		GCTTCAGTGG	AATCGCTGGC	0	D	0	MG04988.1	NCU07554.1	YJL074C	YJL074C
5890	2931	af	AN6364.1	72.m19496	AO070279000050	0			-177	-70			ATGGTTCTTACCGTCGCATACGGAAGATCACCTTCACAGACTATTGCTTGCCTTTCATCGAAGGTAATTCTGACGGCCACAGGCAGGGGCTCAGAGCGTCTTCTTTGA		ATGGTTCTTACCGTCGCATACGGAAGATCACCTTCACAGACTATTGCTTGCCTTTCATCGAAGGTAATTCTGACGGCCACAGGCAGGGGCTCAGAGCGTCTTCTTTGA		MVLTVAYGRSPSQTIACLSSKVILTATGRGSERLL*		MVLTVAYGRSPSQTIACLSSKVILTATGRGSERLL*		TCGCGTTTCG	AATCGCTGGC	0	D	0	MG04988.1	NCU07554.1	YJL074C	YJL074C
5893	2934	af	AN0595.1	69.m15252	AO070280000021	0			-190	-146			ATGAGGATCGCCACAGTTGCCCGATCCTTCATTTCTCATTCTTAA		ATGAGGATCGCCACAGTTGCCCGATCCTTCATTTCTCATTCTTAA		MRIATVARSFISHS*		MRIATVARSFISHS*		CTCCCCGTTG	TTTTTTCTTT	0	C	FG09786.1	0	0	0	0
5895	2937	af	AN1104.1	70.m15128	AO070285000034	0			-250	-149			ATGTTTCCAGAAACCATCAAGCCACACAGAGAACTATTTACTGATTTGAGATACTGGTCATTTTTATCATCATTGTCCTTGTCTACCAGAGTGATTGATTAG		ATGTTTCCAGAAACCATCAAGCCACACAGAGAACTATTTACTGATTTGAGATACTGGTCATTTTTATCATCATTGTCCTTGTCTACCAGAGTGATTGATTAG		MFPETIKPHRELFTDLRYWSFLSSLSLSTRVID*		MFPETIKPHRELFTDLRYWSFLSSLSLSTRVID*		CTAATCCTAA	ATAAGCCATC	0	O	FG02563.1	MG05258.1	0	0	0
5894	2937	an	AN1104.1	70.m15128	AO070285000034	0	-135	-103					ATGACGTTGGAAAGGCCGGAAACGCTTAGATAA	ATGACGTTGGAAAGGCCGGAAACGCTTAGATAA			MTLERPETLR*	MTLERPETLR*			GTAGAAGTTC	GCCGGTTTTC	0	O	FG02563.1	MG05258.1	0	0	0
5896	2937	ao	AN1104.1	70.m15128	AO070285000034	0					-203	-144	ATGAAAAGGAGGAAAATATTTCCAGTCGACGTCATTTTCGTTGGTTTGATTAAGGAATGA			ATGAAAAGGAGGAAAATATTTCCAGTCGACGTCATTTTCGTTGGTTTGATTAAGGAATGA	MKRRKIFPVDVIFVGLIKE*			MKRRKIFPVDVIFVGLIKE*	TTGAAATGAA	AAACAGACCG	0	O	FG02563.1	MG05258.1	0	0	0
5897	2937	ao	AN1104.1	70.m15128	AO070285000034	0					-147	-124	ATGAAAACAGACCGGATTAGATAA			ATGAAAACAGACCGGATTAGATAA	MKTDRIR*			MKTDRIR*	TGATTAAGGA	GCCATGGGAT	0	O	FG02563.1	MG05258.1	0	0	0
5899	2939	af	AN1069.1	70.m15145	AO070285000067	0			-220	-179			ATGATCCGGACTGGGGCTCGCCGTCGTTTGTTGGACGCTTGA		ATGATCCGGACTGGGGCTCGCCGTCGTTTGTTGGACGCTTGA		MIRTGARRRLLDA*		MIRTGARRRLLDA*		CTAACTCCTG	AATCGCCTTG	0		0	0	0	0	0
5901	2942	af	AN7498.1	57.m05843	AO070287000016	0			-101	-75			ATGCTTATGCTCTCTGAGTACGTTTGA		ATGCTTATGCTCTCTGAGTACGTTTGA		MLMLSEYV*		MLMLSEYV*		GAAAATTTAG	TGCTCTAATC	0	R	0	0	0	0	0
5902	2942	af	AN7498.1	57.m05843	AO070287000016	0			-95	-75			ATGCTCTCTGAGTACGTTTGA		ATGCTCTCTGAGTACGTTTGA		MLSEYV*		MLSEYV*		TTAGATGCTT	TGCTCTAATC	0	R	0	0	0	0	0
5900	2942	an	AN7498.1	57.m05843	AO070287000016	0	-206	-3					ATGTATCTGCCAAGAACGGGAAGCCAAAAACCTAGGTATCGTTCGACACGGATCATTATAAGAAAAAGCAGGCCTAGCCGTAGGTTTGGGCCCCGCCACCCCGCCAAAAAATTATTATCTACGCAGATAAGATCGAAAAATAATACTTCACCTCACGATCCAGTCCATTTGTTTCTTATCTATAATAAATACGGCCATTATTGA	ATGTATCTGCCAAGAACGGGAAGCCAAAAACCTAGGTATCGTTCGACACGGATCATTATAAGAAAAAGCAGGCCTAGCCGTAGGTTTGGGCCCCGCCACCCCGCCAAAAAATTATTATCTACGCAGATAAGATCGAAAAATAATACTTCACCTCACGATCCAGTCCATTTGTTTCTTATCTATAATAAATACGGCCATTATTGA			MYLPRTGSQKPRYRSTRIIIRKSRPSRRFGPRHPAKKLLSTQIRSKNNTSPHDPVHLFLIYNKYGHY*	MYLPRTGSQKPRYRSTRIIIRKSRPSRRFGPRHPAKKLLSTQIRSKNNTSPHDPVHLFLIYNKYGHY*			TCAATCCCCA	AAATGACAAC	0	R	0	0	0	0	0
5903	2944	af	AN7493.1	57.m05851	AO070287000024	0			-206	-108			ATGGCGCATTTCCATTTTCCTATCCACTTAACACGGGCAACGCGTTGTGTCGCGTTGTTCCGAAGAGCAACCACACCATTGCAGCAAAACACCCCTTAA		ATGGCGCATTTCCATTTTCCTATCCACTTAACACGGGCAACGCGTTGTGTCGCGTTGTTCCGAAGAGCAACCACACCATTGCAGCAAAACACCCCTTAA		MAHFHFPIHLTRATRCVALFRRATTPLQQNTP*		MAHFHFPIHLTRATRCVALFRRATTPLQQNTP*		CGTTTTTGGG	GGAAGTGCAG	0		0	0	0	0	0
5904	2944	ao	AN7493.1	57.m05851	AO070287000024	0					-197	-102	ATGCTCTGGGTTCGGAAATTTCCGCTCTTAACGGCACTTAAATCACTTTACGCGACGCGTGCGCCAGTTTACTCCCATCCATCATCCAGCTCATAG			ATGCTCTGGGTTCGGAAATTTCCGCTCTTAACGGCACTTAAATCACTTTACGCGACGCGTGCGCCAGTTTACTCCCATCCATCATCCAGCTCATAG	MLWVRKFPLLTALKSLYATRAPVYSHPSSSS*			MLWVRKFPLLTALKSLYATRAPVYSHPSSSS*	CGATCCGGTG	AACAACACCC	0		0	0	0	0	0
5905	2946	af	AN7459.1	57.m05882	AO070287000066	0			-242	-168			ATGATCAACGGCCACTGCGATTTCATCGTTCTGTGCGGGGCCTTTCTTCGGTGGCTGCCCCACGGTGTCCCCTAG		ATGATCAACGGCCACTGCGATTTCATCGTTCTGTGCGGGGCCTTTCTTCGGTGGCTGCCCCACGGTGTCCCCTAG		MINGHCDFIVLCGAFLRWLPHGVP*		MINGHCDFIVLCGAFLRWLPHGVP*		AGGGAATCGG	ATACACCTCA	0	G	0	0	NCU02542.1	0	0
5906	2946	ao	AN7459.1	57.m05882	AO070287000066	0					-192	-130	ATGCGTATTTTAGGGTCAACTTGCTGCCTGCCCCACGCCCAAGCGCTGATATCATACAACTAA			ATGCGTATTTTAGGGTCAACTTGCTGCCTGCCCCACGCCCAAGCGCTGATATCATACAACTAA	MRILGSTCCLPHAQALISYN*			MRILGSTCCLPHAQALISYN*	TTCTTGGGTG	CTCTCTGACC	0	G	0	0	NCU02542.1	0	0

5910	2947	af	AN1319.1	57.m05886	AO070287000068	0			-271	-233			ATGGGGTCATTGCCTCACTGCCTTATAATTAAGGTATGA		ATGGGGTCATTGCCTCACTGCCTTATAATTAAGGTATGA		MGSLPHCLIIKV*		MGSLPHCLIIKV*		GTGTACTGGC	AATAGATTCC	0	AJ	0	MG02467.1	0	0	0
5911	2947	af	AN1319.1	57.m05886	AO070287000068	0			-120	-49			ATGAAGTCTGCTCTCAAGCATCTCTTTCCACCTGTTCTTTTGATACCCTGCAATACGGCAGTGATCCTTTGA		ATGAAGTCTGCTCTCAAGCATCTCTTTCCACCTGTTCTTTTGATACCCTGCAATACGGCAGTGATCCTTTGA		MKSALKHLFPPVLLIPCNTAVIL*		MKSALKHLFPPVLLIPCNTAVIL*		TGCTCTTATC	GTGAGCCATT	0	AJ	0	MG02467.1	0	0	0
5907	2947	an	AN1319.1	57.m05886	AO070287000068	0	-218	-156					ATGGTACGTCAAGTTCTCAAGTTGGGGCTACCGGTCGACCGCCTTCTAGTTACATTCACGTGA	ATGGTACGTCAAGTTCTCAAGTTGGGGCTACCGGTCGACCGCCTTCTAGTTACATTCACGTGA			MVRQVLKLGLPVDRLLVTFT*	MVRQVLKLGLPVDRLLVTFT*			TGTCCGTACC	TACCATGCCA	0	AJ	0	MG02467.1	0	0	0
5908	2947	an	AN1319.1	57.m05886	AO070287000068	0	-151	-140					ATGCCAGATTAG	ATGCCAGATTAG			MPD*	MPD*			ACGTGATACC	GACTAGCTCC	0	AJ	0	MG02467.1	0	0	0
5909	2947	an	AN1319.1	57.m05886	AO070287000068	0	-128	-27					ATGCTTGATCGGAAGAAAAAAAAAGATCTTGAGCTCCGCAAGAATTCTCAAGCCAAACCTCAACCTATCTCTCACATCAACGGCCGTGATCCGCAGTCGTGA	ATGCTTGATCGGAAGAAAAAAAAAGATCTTGAGCTCCGCAAGAATTCTCAAGCCAAACCTCAACCTATCTCTCACATCAACGGCCGTGATCCGCAGTCGTGA			MLDRKKKKDLELRKNSQAKPQPISHINGRDPQS*	MLDRKKKKDLELRKNSQAKPQPISHINGRDPQS*			ACTAGCTCCC	GCCACTAAAT	0	AJ	0	MG02467.1	0	0	0
5913	2950	af	AN8782.1	71.m15582	AO070289000007	0			-196	-164			ATGAATCTGGCTTTGCGCCTAGTGGTACGATAA		ATGAATCTGGCTTTGCGCCTAGTGGTACGATAA		MNLALRLVVR*		MNLALRLVVR*		CTTGAGCAAT	TTCAAAATCT	0	R	0	0	0	0	0
5912	2950	an	AN8782.1	71.m15582	AO070289000007	0	-121	-65					ATGCCAAGCCTGCCCCTCATTCCCCTCATCACTTCTCTTCAACTTCCAGGGACTTGA	ATGCCAAGCCTGCCCCTCATTCCCCTCATCACTTCTCTTCAACTTCCAGGGACTTGA			MPSLPLIPLITSLQLPGT*	MPSLPLIPLITSLQLPGT*			AGAGGCTGCC	CCAACTTCAC	0	R	0	0	0	0	0
5914	2950	ao	AN8782.1	71.m15582	AO070289000007	0					-178	-146	ATGTGGGGGGTTGTTTTTCTGCCCCTCATTTAA			ATGTGGGGGGTTGTTTTTCTGCCCCTCATTTAA	MWGVVFLPLI*			MWGVVFLPLI*	GTAGATTTAA	ATCAATTCTT	0	R	0	0	0	0	0
5916	2951	af	AN7087.1	55.m03219	AO070289000031	0			-212	-180			ATGTCTGCCAAGACAGTGTTATTTCCTCTTTAA		ATGTCTGCCAAGACAGTGTTATTTCCTCTTTAA		MSAKTVLFPL*		MSAKTVLFPL*		GATTACGGAT	GCTACATTCT	0		0	0	0	0	0
5917	2951	af	AN7087.1	55.m03219	AO070289000031	0			-155	-87			ATGCCCAAAGCTTCGATACTTCCAATGTTCTTTACTCCGTATTGGGAGAGCAATGATCGTTGTATATAA		ATGCCCAAAGCTTCGATACTTCCAATGTTCTTTACTCCGTATTGGGAGAGCAATGATCGTTGTATATAA		MPKASILPMFFTPYWESNDRCI*		MPKASILPMFFTPYWESNDRCI*		CTCTATCGTG	GCTTCCTCCG	0		0	0	0	0	0
5918	2951	af	AN7087.1	55.m03219	AO070289000031	0			-131	-87			ATGTTCTTTACTCCGTATTGGGAGAGCAATGATCGTTGTATATAA		ATGTTCTTTACTCCGTATTGGGAGAGCAATGATCGTTGTATATAA		MFFTPYWESNDRCI*		MFFTPYWESNDRCI*		GATACTTCCA	GCTTCCTCCG	0		0	0	0	0	0
5915	2951	an	AN7087.1	55.m03219	AO070289000031	0	-177	-73					ATGCTTTTATACAGCGAATTGGAAGACGCCCTCGTTGCTATTCGGCTGCTGAGCCACCATTCATACCCATCATTCTCGTATAAATATCACGCACAGCCTAGGTGA	ATGCTTTTATACAGCGAATTGGAAGACGCCCTCGTTGCTATTCGGCTGCTGAGCCACCATTCATACCCATCATTCTCGTATAAATATCACGCACAGCCTAGGTGA			MLLYSELEDALVAIRLLSHHSYPSFSYKYHAQPR*	MLLYSELEDALVAIRLLSHHSYPSFSYKYHAQPR*			CGAGATTGCG	ACGGTCTATA	0		0	0	0	0	0
5919	2951	ao	AN7087.1	55.m03219	AO070289000031	0					-270	-208	ATGTTGATCGTCATTTCCACTGTTCCACTCAGAGAAGGACCTTCATATATCCTGACCCGTTAG			ATGTTGATCGTCATTTCCACTGTTCCACTCAGAGAAGGACCTTCATATATCCTGACCCGTTAG	MLIVISTVPLREGPSYILTR*			MLIVISTVPLREGPSYILTR*	GTACGATCTG	ACCGTATGGC	0		0	0	0	0	0
5920	2951	ao	AN7087.1	55.m03219	AO070289000031	0					-202	-125	ATGGCCAAGCTTGCAATGCTCGCATCATGGGCACATAATAGGTTAGTCGCGAGAAGGGTACGGCGCAGAGACATATAA			ATGGCCAAGCTTGCAATGCTCGCATCATGGGCACATAATAGGTTAGTCGCGAGAAGGGTACGGCGCAGAGACATATAA	MAKLAMLASWAHNRLVARRVRRRDI*			MAKLAMLASWAHNRLVARRVRRRDI*	GTTAGACCGT	GAAAGTTATA	0		0	0	0	0	0
5921	2951	ao	AN7087.1	55.m03219	AO070289000031	0					-187	-125	ATGCTCGCATCATGGGCACATAATAGGTTAGTCGCGAGAAGGGTACGGCGCAGAGACATATAA			ATGCTCGCATCATGGGCACATAATAGGTTAGTCGCGAGAAGGGTACGGCGCAGAGACATATAA	MLASWAHNRLVARRVRRRDI*			MLASWAHNRLVARRVRRRDI*	CAAGCTTGCA	GAAAGTTATA	0		0	0	0	0	0
5922	2951	ao	AN7087.1	55.m03219	AO070289000031	0					-176	-165	ATGGGCACATAA			ATGGGCACATAA	MGT*			MGT*	TGCTCGCATC	TAGGTTAGTC	0		0	0	0	0	0
5925	2953	af	AN2201.1	56.m02346	AO070290000004	0			-222	-19			ATGGGGCCTCTTCCCCAGTTTTGTGCGCCCCTTATCGCCCTTGTGATCGGATTGGATCTGGCTCTCCGATGGCGGACGATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAACTGCAACCGTCGCCCAGCCGGCCGTGGTGCTGTCGCATCGTGGCCACTGCCCTCATCGTTCCTTCATTATTGTCCATAG		ATGGGGCCTCTTCCCCAGTTTTGTGCGCCCCTTATCGCCCTTGTGATCGGATTGGATCTGGCTCTCCGATGGCGGACGATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAACTGCAACCGTCGCCCAGCCGGCCGTGGTGCTGTCGCATCGTGGCCACTGCCCTCATCGTTCCTTCATTATTGTCCATAG		MGPLPQFCAPLIALVIGLDLALRWRTMPITLFAGCGGLEEYNCNRRPAGRGAVASWPLPSSFLHYCP*		MGPLPQFCAPLIALVIGLDLALRWRTMPITLFAGCGGLEEYNCNRRPAGRGAVASWPLPSSFLHYCP*		TGGCCATATC	TCTATTGTCC	0	E	0	0	0	0	0
5926	2953	af	AN2201.1	56.m02346	AO070290000004	0			-154	-98			ATGGCGGACGATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAA		ATGGCGGACGATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAA		MADDANNFIRGVRRTRGV*		MADDANNFIRGVRRTRGV*		TGGCTCTCCG	CTGCAACCGT	0	E	0	0	0	0	0
5927	2953	af	AN2201.1	56.m02346	AO070290000004	0			-144	-19			ATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAACTGCAACCGTCGCCCAGCCGGCCGTGGTGCTGTCGCATCGTGGCCACTGCCCTCATCGTTCCTTCATTATTGTCCATAG		ATGCCAATAACTTTATTCGCGGGGTGCGGAGGACTCGAGGAGTATAACTGCAACCGTCGCCCAGCCGGCCGTGGTGCTGTCGCATCGTGGCCACTGCCCTCATCGTTCCTTCATTATTGTCCATAG		MPITLFAGCGGLEEYNCNRRPAGRGAVASWPLPSSFLHYCP*		MPITLFAGCGGLEEYNCNRRPAGRGAVASWPLPSSFLHYCP*		ATGGCGGACG	TCTATTGTCC	0	E	0	0	0	0	0
5923	2953	an	AN2201.1	56.m02346	AO070290000004	0	-146	-135					ATGGTTCGCTGA	ATGGTTCGCTGA			MVR*	MVR*			CGGCAGGGGT	TGGCGGACGG	0	E	0	0	0	0	0
5924	2953	an	AN2201.1	56.m02346	AO070290000004	0	-135	-28					ATGGCGGACGGTAACTTTGTATCGCGAGGAGCGGCGGAGTATAACTGCAGCCGTCGCCCGGCCGGTGCGGCGCTTTCGCATCGTGGCGTTCTCATTCATTGTCCATAG	ATGGCGGACGGTAACTTTGTATCGCGAGGAGCGGCGGAGTATAACTGCAGCCGTCGCCCGGCCGGTGCGGCGCTTTCGCATCGTGGCGTTCTCATTCATTGTCCATAG			MADGNFVSRGAAEYNCSRRPAGAALSHRGVLIHCP*	MADGNFVSRGAAEYNCSRRPAGAALSHRGVLIHCP*			TGGTTCGCTG	TTCTCTGTTC	0	E	0	0	0	0	0
5928	2956	af	AN5129.1	54.m06894	AO070291000048	0			-207	-25			ATGTTTTCTCTCGCACAATTTCCTGACTCTCCCAGACTCAATTTTCTCACACACAATCTTCTCACTGAAATTATCTCCATCTTTCCTGTTGTCTCCCTCTCCCCCCGCGCTAGAGACTGTACAGTAATTACCTCTCTCCTAACTCTACCTTCACGATCCACCTCTATCCTCTTTCTATTTTAA		ATGTTTTCTCTCGCACAATTTCCTGACTCTCCCAGACTCAATTTTCTCACACACAATCTTCTCACTGAAATTATCTCCATCTTTCCTGTTGTCTCCCTCTCCCCCCGCGCTAGAGACTGTACAGTAATTACCTCTCTCCTAACTCTACCTTCACGATCCACCTCTATCCTCTTTCTATTTTAA		MFSLAQFPDSPRLNFLTHNLLTEIISIFPVVSLSPRARDCTVITSLLTLPSRSTSILFLF*		MFSLAQFPDSPRLNFLTHNLLTEIISIFPVVSLSPRARDCTVITSLLTLPSRSTSILFLF*		CACTATATCA	CGAAACCCTC	0	O	0	0	0	0	0
5930	2957	af	AN5102.1	54.m06919	AO070291000077	0			-171	-100			ATGGCCCTGTGCATCGTCACATCCTCAAAATCTTGTGTTTACCATAGTCGCGTTACCGAATCCAGAGCTTAA		ATGGCCCTGTGCATCGTCACATCCTCAAAATCTTGTGTTTACCATAGTCGCGTTACCGAATCCAGAGCTTAA		MALCIVTSSKSCVYHSRVTESRA*		MALCIVTSSKSCVYHSRVTESRA*		CTGTCCTTAC	GGCAACCAGA	0	E	0	MG07316.1	0	0	0
5929	2957	an	AN5102.1	54.m06919	AO070291000077	0	-220	-149					ATGCCTAAAAAATCCACAAGGATAACAGGCTTTTATCATCTGAACCTGCCACAACCATTACATATCATTTAA	ATGCCTAAAAAATCCACAAGGATAACAGGCTTTTATCATCTGAACCTGCCACAACCATTACATATCATTTAA			MPKKSTRITGFYHLNLPQPLHII*	MPKKSTRITGFYHLNLPQPLHII*			ATTCATTTAT	GCAACTTAAA	0	E	0	MG07316.1	0	0	0
5931	2957	ao	AN5102.1	54.m06919	AO070291000077	0					-192	-118	ATGTCGCTTGCTTCCACAACCACATACCAACCTAAAGTAGCCGTGCCATTACTGGCTACTTGGGTGACTGTCTGA			ATGTCGCTTGCTTCCACAACCACATACCAACCTAAAGTAGCCGTGCCATTACTGGCTACTTGGGTGACTGTCTGA	MSLASTTTYQPKVAVPLLATWVTV*			MSLASTTTYQPKVAVPLLATWVTV*	GCTTCTACCT	TACATGCCCA	0	E	0	MG07316.1	0	0	0
5932	2957	ao	AN5102.1	54.m06919	AO070291000077	0					-114	-49	ATGCCCAGTGATATATTGCTTCCCTTTTACTTCATACTACCGTCCCCCTACCCAGACTTTGGTTGA			ATGCCCAGTGATATATTGCTTCCCTTTTACTTCATACTACCGTCCCCCTACCCAGACTTTGGTTGA	MPSDILLPFYFILPSPYPDFG*			MPSDILLPFYFILPSPYPDFG*	TGTCTGATAC	ATACCAGGAG	0	E	0	MG07316.1	0	0	0
5934	2958	af	AN2051.1	58.m07639	AO070292000018	0			-260	-180			ATGCATGTGACTTATTATAACGAGGTCTACCTTTGTTTTGAAGCTACTAATACTCCTGCTGGTCTTGGTCGAATAGCTTGA		ATGCATGTGACTTATTATAACGAGGTCTACCTTTGTTTTGAAGCTACTAATACTCCTGCTGGTCTTGGTCGAATAGCTTGA		MHVTYYNEVYLCFEATNTPAGLGRIA*		MHVTYYNEVYLCFEATNTPAGLGRIA*		AGAGCTTTCG	GTCATTCAAA	0	D	0	0	0	0	0
5935	2958	af	AN2051.1	58.m07639	AO070292000018	0			-165	-82			ATGATCTCCAACAGCTTTTCTTTGATTCGCACATCTTGTGAACATAATTGTCTCTTTACCATTCATCGTCTATTACTGTTATAG		ATGATCTCCAACAGCTTTTCTTTGATTCGCACATCTTGTGAACATAATTGTCTCTTTACCATTCATCGTCTATTACTGTTATAG		MISNSFSLIRTSCEHNCLFTIHRLLLL*		MISNSFSLIRTSCEHNCLFTIHRLLLL*		TTCAAACTTT	TACTTTGTTT	0	D	0	0	0	0	0
5933	2958	an	AN2051.1	58.m07639	AO070292000018	0	-179	-66					ATGTCGAGCTGCTTGTTGGCATATCTGGTACGTTCTCGCGGCGTTGATAAAGCTGAAGGGACACTGACAACAACGGTTCCTAGTTTTTATCGCCCCGAGCTCTATTTCCTATAA	ATGTCGAGCTGCTTGTTGGCATATCTGGTACGTTCTCGCGGCGTTGATAAAGCTGAAGGGACACTGACAACAACGGTTCCTAGTTTTTATCGCCCCGAGCTCTATTTCCTATAA			MSSCLLAYLVRSRGVDKAEGTLTTTVPSFYRPELYFL*	MSSCLLAYLVRSRGVDKAEGTLTTTVPSFYRPELYFL*			AGCCTTTTCG	GATACTGATC	0	D	0	0	0	0	0
5936	2958	ao	AN2051.1	58.m07639	AO070292000018	0					-216	-148	ATGAGCTCCATTTGGGACGATACGTTGATTTGGAGCCTATTTTGTGAGGTCCTATATAGTCACTGGTAG			ATGAGCTCCATTTGGGACGATACGTTGATTTGGAGCCTATTTTGTGAGGTCCTATATAGTCACTGGTAG	MSSIWDDTLIWSLFCEVLYSHW*			MSSIWDDTLIWSLFCEVLYSHW*	AGAGCTTTCG	GGTTCTCCAT	0	D	0	0	0	0	0
5937	2958	ao	AN2051.1	58.m07639	AO070292000018	0					-134	-45	ATGCGACAAGTTACAAGTGTCCCTGACCAATTTCTCACATATAATTTGAACCCAATTTTTTCTCCATTTACTATTTCATCTATCATTTAG			ATGCGACAAGTTACAAGTGTCCCTGACCAATTTCTCACATATAATTTGAACCCAATTTTTTCTCCATTTACTATTTCATCTATCATTTAG	MRQVTSVPDQFLTYNLNPIFSPFTISSII*			MRQVTSVPDQFLTYNLNPIFSPFTISSII*	TCTCCATTGA	TATTTACCCC	0	D	0	0	0	0	0
5940	2959	af	AN1851.1	58.m07660	AO070292000043	0			-261	-250			ATGAAACCATGA		ATGAAACCATGA		MKP*		MKP*		ACGTATAAAT	GTCATGCAAA	0	O	FG06761.1 0	NCU07567.1	0	0	
5941	2959	af	AN1851.1	58.m07660	AO070292000043	0			-253	-230			ATGAGTCATGCAAATGAAACATAA		ATGAGTCATGCAAATGAAACATAA		MSHANET*		MSHANET*		ATATGAAACC	TTGCCAGGAT	0	O	FG06761.1 0	NCU07567.1	0	0	
5942	2959	af	AN1851.1	58.m07660	AO070292000043	0			-246	-205			ATGCAAATGAAACATAATTGCCAGGATAAGTCCTCTGTATGA		ATGCAAATGAAACATAATTGCCAGGATAAGTCCTCTGTATGA		MQMKHNCQDKSSV*		MQMKHNCQDKSSV*		ACCATGAGTC	GTGCAAAGTA	0	O	FG06761.1 0	NCU07567.1	0	0	
5943	2959	af	AN1851.1	58.m07660	AO070292000043	0			-240	-205			ATGAAACATAATTGCCAGGATAAGTCCTCTGTATGA		ATGAAACATAATTGCCAGGATAAGTCCTCTGTATGA		MKHNCQDKSSV*		MKHNCQDKSSV*		AGTCATGCAA	GTGCAAAGTA	0	O	FG06761.1 0	NCU07567.1	0	0	
5944	2959	af	AN1851.1	58.m07660	AO070292000043	0			-208	-77			ATGAGTGCAAAGTATTATTATATGTCCCGTAAAAGGAAGTGCCCTAGCCCCTCCGGATGCAAACCATCCAAACACCTGCCGCCGCCTGACCATCTCGAAAGCTCCATCAAAAATTCCCGGAGCAGCACTTAG		ATGAGTGCAAAGTATTATTATATGTCCCGTAAAAGGAAGTGCCCTAGCCCCTCCGGATGCAAACCATCCAAACACCTGCCGCCGCCTGACCATCTCGAAAGCTCCATCAAAAATTCCCGGAGCAGCACTTAG		MSAKYYYMSRKRKCPSPSGCKPSKHLPPPDHLESSIKNSRSST*		MSAKYYYMSRKRKCPSPSGCKPSKHLPPPDHLESSIKNSRSST*		AGTCCTCTGT	CTTGTGTGAT	0	O	FG06761.1 0	NCU07567.1	0	0	
5945	2959	af	AN1851.1	58.m07660	AO070292000043	0			-187	-77			ATGTCCCGTAAAAGGAAGTGCCCTAGCCCCTCCGGATGCAAACCATCCAAACACCTGCCGCCGCCTGACCATCTCGAAAGCTCCATCAAAAATTCCCGGAGCAGCACTTAG		ATGTCCCGTAAAAGGAAGTGCCCTAGCCCCTCCGGATGCAAACCATCCAAACACCTGCCGCCGCCTGACCATCTCGAAAGCTCCATCAAAAATTCCCGGAGCAGCACTTAG		MSRKRKCPSPSGCKPSKHLPPPDHLESSIKNSRSST*		MSRKRKCPSPSGCKPSKHLPPPDHLESSIKNSRSST*		GTATTATTAT	CTTGTGTGAT	0	O	FG06761.1 0	NCU07567.1	0	0	
5946	2959	af	AN1851.1	58.m07660	AO070292000043	0			-152	-120			ATGCAAACCATCCAAACACCTGCCGCCGCCTGA		ATGCAAACCATCCAAACACCTGCCGCCGCCTGA		MQTIQTPAAA*		MQTIQTPAAA*		GCCCCTCCGG	CCATCTCGAA	0	O	FG06761.1 0	NCU07567.1	0	0	
5938	2959	an	AN1851.1	58.m07660	AO070292000043	0	-241	-188					ATGAATAATCTCCTATCAATTGTCTTTGCCAATACGGAGTGTAACAGGCGATAA	ATGAATAATCTCCTATCAATTGTCTTTGCCAATACGGAGTGTAACAGGCGATAA			MNNLLSIVFANTECNRR*	MNNLLSIVFANTECNRR*			TTATGATATA	TCGACAGGGC	0	O	FG06761.1 0	NCU07567.1	0	0	
5939	2959	an	AN1851.1	58.m07660	AO070292000043	0	-177	-139					ATGCCAAGAGCCCCTCGTGGTGCAAACCAAGCAAACTAG	ATGCCAAGAGCCCCTCGTGGTGCAAACCAAGCAAACTAG			MPRAPRGANQAN*	MPRAPRGANQAN*			TCGACAGGGC	TAACCGCAGA	0	O	FG06761.1 0	NCU07567.1	0	0	
5947	2959	ao	AN1851.1	58.m07660	AO070292000043	0					-248	-237	ATGATAATATAA			ATGATAATATAA	MII*			MII*	ACCCTGTACA	CGAGCAATTC	0	O	FG06761.1 0	NCU07567.1	0	0	
5948	2959	ao	AN1851.1	58.m07660	AO070292000043	0					-213	-187	ATGCGATGTATAAACATTAGTCAGTGA			ATGCGATGTATAAACATTAGTCAGTGA	MRCINISQ*			MRCINISQ*	TCTCACTTTT	CCCAAAAGGG	0	O	FG06761.1 0	NCU07567.1	0	0	
5949	2959	ao	AN1851.1	58.m07660	AO070292000043	0					-208	-194	ATGTATAAACATTAG			ATGTATAAACATTAG	MYKH*			MYKH*	CTTTTATGCG	TCAGTGACCC	0	O	FG06761.1 0	NCU07567.1	0	0	
5950	2960	ao	AN8049.1	53.m03895	AO070292000101	0					-250	-227	ATGTATCGTGCTATAACCATGTAG			ATGTATCGTGCTATAACCATGTAG	MYRAITM*			MYRAITM*	ACTTTTCTTG	GTACAACCAT	0	C	0	0	0	0	0

5951	2960	ao	AN8049.1	53.m03895	AO070292000101	0					-218	-18	ATGAAGAAAGCGCGACAAGAAAAACATGAGCCAAAAGCGGAACAAATTCGCAAGCGGCAGAATTGGGTCAGCAGCCGCAGGAGAGACGCCGATTGGCTCTTCAAGCGGCGGCGCGAGCTCCCGCAAACCTCACCCTTTGAAGCCGACTTCTCACCTCCGCTTCACCCGCCATCCACAATTGCCCTCTACACCAAGTCCTAG			ATGAAGAAAGCGCGACAAGAAAAACATGAGCCAAAAGCGGAACAAATTCGCAAGCGGCAGAATTGGGTCAGCAGCCGCAGGAGAGACGCCGATTGGCTCTTCAAGCGGCGGCGCGAGCTCCCGCAAACCTCACCCTTTGAAGCCGACTTCTCACCTCCGCTTCACCCGCCATCCACAATTGCCCTCTACACCAAGTCCTAG	MKKARQEKHEPKAEQIRKRQNWVSSRRRDADWLFKRRRELPQTSPFEADFSPPLHPPSTIALYTKS*			MKKARQEKHEPKAEQIRKRQNWVSSRRRDADWLFKRRRELPQTSPFEADFSPPLHPPSTIALYTKS*	AGGTACAACC	GGACTCAATT	0	C	0	0	0	0	0
5954	2961	af	AN8877.1	56.m03107	AO070293000006	0			-91	-2			ATGGTGACTGCTACCTACTTGGATTCTTGGATTCCTGGATGTCCGATGGCATACTACGACGCTCGGTCACACACGGAGCAACTCGTCTGA		ATGGTGACTGCTACCTACTTGGATTCTTGGATTCCTGGATGTCCGATGGCATACTACGACGCTCGGTCACACACGGAGCAACTCGTCTGA		MVTATYLDSWIPGCPMAYYDARSHTEQLV*		MVTATYLDSWIPGCPMAYYDARSHTEQLV*		CAAATATTGG	AATGGAGGGC	0	T	0	0	NCU03264.1	0	0
5952	2961	an	AN8877.1	56.m03107	AO070293000006	0	-92	-54					ATGGGGCGTCATCGCACGGTTCGGCACATGTGGGTATAA	ATGGGGCGTCATCGCACGGTTCGGCACATGTGGGTATAA			MGRHRTVRHMWV*	MGRHRTVRHMWV*			TTTGTCTGGC	ATTAACCACT	0	T	0	0	NCU03264.1	0	0
5953	2961	an	AN8877.1	56.m03107	AO070293000006	0	-65	-54					ATGTGGGTATAA	ATGTGGGTATAA			MWV*	MWV*			GGTTCGGCAC	ATTAACCACT	0	T	0	0	NCU03264.1	0	0
5956	2961	ao	AN8877.1	56.m03107	AO070293000006	0					-170	-99	ATGCCGTTGATATTACCGAGCATATGGCTGTCGCCTTCCACGATCAATGTCACTTGCCTTCTTAAGAAATAA			ATGCCGTTGATATTACCGAGCATATGGCTGTCGCCTTCCACGATCAATGTCACTTGCCTTCTTAAGAAATAA	MPLILPSIWLSPSTINVTCLLKK*			MPLILPSIWLSPSTINVTCLLKK*	AGGAGTGTGT	CTCTCGTGAC	0	T	0	0	NCU03264.1	0	0
5957	2961	ao	AN8877.1	56.m03107	AO070293000006	0					-147	-106	ATGGCTGTCGCCTTCCACGATCAATGTCACTTGCCTTCTTAA			ATGGCTGTCGCCTTCCACGATCAATGTCACTTGCCTTCTTAA	MAVAFHDQCHLPS*			MAVAFHDQCHLPS*	TACCGAGCAT	GAAATAACTC	0	T	0	0	NCU03264.1	0	0
5958	2961	ao	AN8877.1	56.m03107	AO070293000006	0					-124	-71	ATGTCACTTGCCTTCTTAAGAAATAACTCTCGTGACGCAGAAGCGGCTTTTTGA			ATGTCACTTGCCTTCTTAAGAAATAACTCTCGTGACGCAGAAGCGGCTTTTTGA	MSLAFLRNNSRDAEAAF*			MSLAFLRNNSRDAEAAF*	TCCACGATCA	CTCGCCTTGT	0	T	0	0	NCU03264.1	0	0
5964	2962	af	AN8896.1	56.m02307	AO070293000029	0			-163	-107			ATGTTACGCCTGTGCCTCGGTACTATGCAGGAACACTTGTATATGAGCTTGACATGA		ATGTTACGCCTGTGCCTCGGTACTATGCAGGAACACTTGTATATGAGCTTGACATGA		MLRLCLGTMQEHLYMSLT*		MLRLCLGTMQEHLYMSLT*		GATCTGCATT	TCCATAAAGA	0	Q	0	0	0	0	0
5965	2962	af	AN8896.1	56.m02307	AO070293000029	0			-139	-107			ATGCAGGAACACTTGTATATGAGCTTGACATGA		ATGCAGGAACACTTGTATATGAGCTTGACATGA		MQEHLYMSLT*		MQEHLYMSLT*		CCTCGGTACT	TCCATAAAGA	0	Q	0	0	0	0	0
5966	2962	af	AN8896.1	56.m02307	AO070293000029	0			-121	-107			ATGAGCTTGACATGA		ATGAGCTTGACATGA		MSLT*		MSLT*		ACACTTGTAT	TCCATAAAGA	0	Q	0	0	0	0	0
5967	2962	af	AN8896.1	56.m02307	AO070293000029	0			-87	-67			ATGCGTATACATATGGCATAG		ATGCGTATACATATGGCATAG		MRIHMA*		MRIHMA*		ACGCTGCAGC	GCCATCCATT	0	Q	0	0	0	0	0
5959	2962	an	AN8896.1	56.m02307	AO070293000029	0	-137	-72					ATGCGAATGCCTCGGTTCGGTCGTCCGATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA	ATGCGAATGCCTCGGTTCGGTCGTCCGATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA			MRMPRFGRPMAIKVQAGYLIL*	MRMPRFGRPMAIKVQAGYLIL*			TGGGAACCCC	TCATGCAATC	0	Q	0	0	0	0	0
5960	2962	an	AN8896.1	56.m02307	AO070293000029	0	-131	-72					ATGCCTCGGTTCGGTCGTCCGATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA	ATGCCTCGGTTCGGTCGTCCGATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA			MPRFGRPMAIKVQAGYLIL*	MPRFGRPMAIKVQAGYLIL*			CCCCATGCGA	TCATGCAATC	0	Q	0	0	0	0	0
5961	2962	an	AN8896.1	56.m02307	AO070293000029	0	-110	-72					ATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA	ATGGCGATCAAGGTCCAAGCTGGATATTTAATATTGTGA			MAIKVQAGYLIL*	MAIKVQAGYLIL*			CGGTCGTCCG	TCATGCAATC	0	Q	0	0	0	0	0
5962	2962	an	AN8896.1	56.m02307	AO070293000029	0	-69	-46					ATGCAATCTAGTCATGCCACCTGA	ATGCAATCTAGTCATGCCACCTGA			MQSSHAT*	MQSSHAT*			TATTGTGATC	TTACTCTTCC	0	Q	0	0	0	0	0
5968	2962	ao	AN8896.1	56.m02307	AO070293000029	0					-181	-146	ATGGGGCAAAAATCGTCGCACCGAAGGCCCTTGTGA			ATGGGGCAAAAATCGTCGCACCGAAGGCCCTTGTGA	MGQKSSHRRPL*			MGQKSSHRRPL*	CCCTTGCCGG	GTACCTCGGT	0	Q	0	0	0	0	0
5969	2962	ao	AN8896.1	56.m02307	AO070293000029	0					-80	-69	ATGTACATATAA			ATGTACATATAA	MYI*			MYI*	ATATATAAAC	GTTATAATGA	0	Q	0	0	0	0	0
5971	2964	af	AN3337.1	55.m03098	AO070293000073	0			-251	-171			ATGGCGGAAATGGGGTCTATCACCGCTGTTTCGTGTTTGAATATATGCCTCATTAAGTGTAGAGCACAGGTATCGCAGTGA		ATGGCGGAAATGGGGTCTATCACCGCTGTTTCGTGTTTGAATATATGCCTCATTAAGTGTAGAGCACAGGTATCGCAGTGA		MAEMGSITAVSCLNICLIKCRAQVSQ*		MAEMGSITAVSCLNICLIKCRAQVSQ*		GCTGGTGTCA	GACAGACCAA	0		0	0	0	0	0
5972	2964	af	AN3337.1	55.m03098	AO070293000073	0			-242	-171			ATGGGGTCTATCACCGCTGTTTCGTGTTTGAATATATGCCTCATTAAGTGTAGAGCACAGGTATCGCAGTGA		ATGGGGTCTATCACCGCTGTTTCGTGTTTGAATATATGCCTCATTAAGTGTAGAGCACAGGTATCGCAGTGA		MGSITAVSCLNICLIKCRAQVSQ*		MGSITAVSCLNICLIKCRAQVSQ*		AATGGCGGAA	GACAGACCAA	0		0	0	0	0	0
5973	2964	af	AN3337.1	55.m03098	AO070293000073	0			-207	-196			ATGCCTCATTAA		ATGCCTCATTAA		MPH*		MPH*		GTTTGAATAT	GTGTAGAGCA	0		0	0	0	0	0
5970	2964	an	AN3337.1	55.m03098	AO070293000073	0	-208	-167					ATGTATTCTTCATTAAACGCAGAGGACCAAGTGTTGCAGTGA	ATGTATTCTTCATTAAACGCAGAGGACCAAGTGTTGCAGTGA			MYSSLNAEDQVLQ*	MYSSLNAEDQVLQ*			TTTCATTTTG	GATATACCAA	0		0	0	0	0	0
5974	2964	ao	AN3337.1	55.m03098	AO070293000073	0					-199	-179	ATGCCGTGTGTGGTAAACTGA			ATGCCGTGTGTGGTAAACTGA	MPCVVN*			MPCVVN*	TTTTTCAACC	AACAAGACAT	0		0	0	0	0	0
5976	2965	af	AN2208.1	71.m15856	AO070294000014	0			-235	-203			ATGGAGCCCCGCCCGATCCAGAGGTTGCGGTAG		ATGGAGCCCCGCCCGATCCAGAGGTTGCGGTAG		MEPRPIQRLR*		MEPRPIQRLR*		CGGCTTCTGG	TTGCCCCTCG	0	R	0	0	0	0	0
5977	2965	af	AN2208.1	71.m15856	AO070294000014	0			-160	-92			ATGACGACTCTGGAAGAGAATCTCGACAGCTTGCCAAAGTGGCACGGAGCATCCATTTTGTGTATATAA		ATGACGACTCTGGAAGAGAATCTCGACAGCTTGCCAAAGTGGCACGGAGCATCCATTTTGTGTATATAA		MTTLEENLDSLPKWHGASILCI*		MTTLEENLDSLPKWHGASILCI*		CTCCTTTTCT	GACATTAAGA	0	R	0	0	0	0	0
5975	2965	an	AN2208.1	71.m15856	AO070294000014	0	-105	-76					ATGTCCTTATATAAACTGTCAATATCTTAA	ATGTCCTTATATAAACTGTCAATATCTTAA			MSLYKLSIS*	MSLYKLSIS*			AAGCGATCGC	CTTCAACCCT	0	R	0	0	0	0	0
5978	2965	ao	AN2208.1	71.m15856	AO070294000014	0					-211	-161	ATGTCCGCCGGACCCAAAGGTTCCTATCGCGAGGACCTTCCCCCGCACTAG			ATGTCCGCCGGACCCAAAGGTTCCTATCGCGAGGACCTTCCCCCGCACTAG	MSAGPKGSYREDLPPH*			MSAGPKGSYREDLPPH*	TTGCCCCGCC	CTGTGTTTCT	0	R	0	0	0	0	0
5979	2965	ao	AN2208.1	71.m15856	AO070294000014	0					-136	-125	ATGACTTCTTGA			ATGACTTCTTGA	MTS*			MTS*	CATCACTAAT	GTAATTTTCC	0	R	0	0	0	0	0
5981	2966	af	AN7641.1	71.m15823	AO070294000037	0			-189	-58			ATGAGGTGTTGCTGCAATCATGCAGTCATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAGGGAGGATATTTCTTTTAAGTGTTTCAGTCAGACACCTGGCACAGTCGTATCTTATAAGAGGACATTGA		ATGAGGTGTTGCTGCAATCATGCAGTCATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAGGGAGGATATTTCTTTTAAGTGTTTCAGTCAGACACCTGGCACAGTCGTATCTTATAAGAGGACATTGA		MRCCCNHAVMAPVYNLRWPLLGRIFLLSVSVRHLAQSYLIRGH*		MRCCCNHAVMAPVYNLRWPLLGRIFLLSVSVRHLAQSYLIRGH*		GTGGTCGAGG	TAATTACCCT	0	Q	0	0	0	0	0
5982	2966	af	AN7641.1	71.m15823	AO070294000037	0			-170	-126			ATGCAGTCATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAG		ATGCAGTCATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAG		MQSWLQFIICVGPY*		MQSWLQFIICVGPY*		TGCTGCAATC	GGAGGATATT	0	Q	0	0	0	0	0
5983	2966	af	AN7641.1	71.m15823	AO070294000037	0			-162	-58			ATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAGGGAGGATATTTCTTTTAAGTGTTTCAGTCAGACACCTGGCACAGTCGTATCTTATAAGAGGACATTGA		ATGGCTCCAGTTTATAATTTGCGTTGGCCCCTACTAGGGAGGATATTTCTTTTAAGTGTTTCAGTCAGACACCTGGCACAGTCGTATCTTATAAGAGGACATTGA		MAPVYNLRWPLLGRIFLLSVSVRHLAQSYLIRGH*		MAPVYNLRWPLLGRIFLLSVSVRHLAQSYLIRGH*		TCATGCAGTC	TAATTACCCT	0	Q	0	0	0	0	0
5980	2966	an	AN7641.1	71.m15823	AO070294000037	0	-185	-69					ATGCTACAGTTGGGGGTTTATAAGCGCATCTCATCCCCTCACGGGATATTCTTGTCTGTCTCTAGATCATCTAATCATATTCTTTTCGCGCTCTCTGGAGTTGCGGTGTCTACTTAA	ATGCTACAGTTGGGGGTTTATAAGCGCATCTCATCCCCTCACGGGATATTCTTGTCTGTCTCTAGATCATCTAATCATATTCTTTTCGCGCTCTCTGGAGTTGCGGTGTCTACTTAA			MLQLGVYKRISSPHGIFLSVSRSSNHILFALSGVAVST*	MLQLGVYKRISSPHGIFLSVSRSSNHILFALSGVAVST*			CGAAAGCAAG	GCTCTCCGCT	0	Q	0	0	0	0	0
5984	2966	ao	AN7641.1	71.m15823	AO070294000037	0					-219	-49	ATGCTGCAACTTAAAAAGCAAGGGCCCCCTTCCTGGTCATGGACTCTTTTTTTGCTGCGTTGTGTCACTTTCCTGCATTCTATCTGGTTGTTGGTTACACCGACATTGATACCCGGGGACTTTACCAAACTATATAACCCGGTTGACAACCTCCTACTTGAACATTCCTAA			ATGCTGCAACTTAAAAAGCAAGGGCCCCCTTCCTGGTCATGGACTCTTTTTTTGCTGCGTTGTGTCACTTTCCTGCATTCTATCTGGTTGTTGGTTACACCGACATTGATACCCGGGGACTTTACCAAACTATATAACCCGGTTGACAACCTCCTACTTGAACATTCCTAA	MLQLKKQGPPSWSWTLFLLRCVTFLHSIWLLVTPTLIPGDFTKLYNPVDNLLLEHS*			MLQLKKQGPPSWSWTLFLLRCVTFLHSIWLLVTPTLIPGDFTKLYNPVDNLLLEHS*	AAACCCAACC	GAATCTCTAT	0	Q	0	0	0	0	0
5985	2966	ao	AN7641.1	71.m15823	AO070294000037	0					-181	-83	ATGGACTCTTTTTTTGCTGCGTTGTGTCACTTTCCTGCATTCTATCTGGTTGTTGGTTACACCGACATTGATACCCGGGGACTTTACCAAACTATATAA			ATGGACTCTTTTTTTGCTGCGTTGTGTCACTTTCCTGCATTCTATCTGGTTGTTGGTTACACCGACATTGATACCCGGGGACTTTACCAAACTATATAA	MDSFFAALCHFPAFYLVVGYTDIDTRGLYQTI*			MDSFFAALCHFPAFYLVVGYTDIDTRGLYQTI*	CTTCCTGGTC	CCCGGTTGAC	0	Q	0	0	0	0	0
5987	2967	af	AN7646.1	57.m05380	AO070294000051	0			-226	-143			ATGCACTGCCCCATTGGGAAATATATGGGGGCCATTCCCCAAATAAGCAGTACAGGGGCTCCCGGGGTATGTAAAGCTCACTGA		ATGCACTGCCCCATTGGGAAATATATGGGGGCCATTCCCCAAATAAGCAGTACAGGGGCTCCCGGGGTATGTAAAGCTCACTGA		MHCPIGKYMGAIPQISSTGAPGVCKAH*		MHCPIGKYMGAIPQISSTGAPGVCKAH*		AGATATACGT	TGCCGCCTGC	0	G	0	0	0	0	0
5988	2967	af	AN7646.1	57.m05380	AO070294000051	0			-202	-143			ATGGGGGCCATTCCCCAAATAAGCAGTACAGGGGCTCCCGGGGTATGTAAAGCTCACTGA		ATGGGGGCCATTCCCCAAATAAGCAGTACAGGGGCTCCCGGGGTATGTAAAGCTCACTGA		MGAIPQISSTGAPGVCKAH*		MGAIPQISSTGAPGVCKAH*		TGGGAAATAT	TGCCGCCTGC	0	G	0	0	0	0	0
5989	2967	af	AN7646.1	57.m05380	AO070294000051	0			-143	-111			ATGCCGCCTGCGACGAGGTTTTCGTTTCAGTAG		ATGCCGCCTGCGACGAGGTTTTCGTTTCAGTAG		MPPATRFSFQ*		MPPATRFSFQ*		AAGCTCACTG	GCTCAACAGG	0	G	0	0	0	0	0
5986	2967	an	AN7646.1	57.m05380	AO070294000051	0	-222	-193					ATGGCCATATTCAGGAGTCAGAAGGGGTGA	ATGGCCATATTCAGGAGTCAGAAGGGGTGA			MAIFRSQKG*	MAIFRSQKG*			ACTAGCTTCT	TCGTTTCAGT	0	G	0	0	0	0	0
5990	2967	ao	AN7646.1	57.m05380	AO070294000051	0					-261	-247	ATGACGATCTCTTGA			ATGACGATCTCTTGA	MTIS*			MTIS*	GGGGTAAACG	TTCTGTTCCA	0	G	0	0	0	0	0
5991	2967	ao	AN7646.1	57.m05380	AO070294000051	0					-233	-159	ATGGCAATTATGTTGGTCCTAGCTCGAGTTTCCATAGCTCGGATATGCGGTACCGAGCTCTATAGAGATGAATAA			ATGGCAATTATGTTGGTCCTAGCTCGAGTTTCCATAGCTCGGATATGCGGTACCGAGCTCTATAGAGATGAATAA	MAIMLVLARVSIARICGTELYRDE*			MAIMLVLARVSIARICGTELYRDE*	TGTTCCACCT	TATAGAAAAT	0	G	0	0	0	0	0
5992	2967	ao	AN7646.1	57.m05380	AO070294000051	0					-224	-159	ATGTTGGTCCTAGCTCGAGTTTCCATAGCTCGGATATGCGGTACCGAGCTCTATAGAGATGAATAA			ATGTTGGTCCTAGCTCGAGTTTCCATAGCTCGGATATGCGGTACCGAGCTCTATAGAGATGAATAA	MLVLARVSIARICGTELYRDE*			MLVLARVSIARICGTELYRDE*	TATGGCAATT	TATAGAAAAT	0	G	0	0	0	0	0
5993	2967	ao	AN7646.1	57.m05380	AO070294000051	0					-189	-169	ATGCGGTACCGAGCTCTATAG			ATGCGGTACCGAGCTCTATAG	MRYRAL*			MRYRAL*	TAGCTCGGAT	AGATGAATAA	0	G	0	0	0	0	0
5994	2967	ao	AN7646.1	57.m05380	AO070294000051	0					-166	-143	ATGAATAATATAGAAAATCCTTAA			ATGAATAATATAGAAAATCCTTAA	MNNIENP*			MNNIENP*	CTCTATAGAG	GCGCCAGACG	0	G	0	0	0	0	0
5996	2969	af	AN7648.1	57.m05388	AO070294000077	0			-221	-96			ATGGCTATCTGCTTATCTTCACATCGAACAGTTGATGATACTCTGCCTTTGGATCAGCAGAATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGA		ATGGCTATCTGCTTATCTTCACATCGAACAGTTGATGATACTCTGCCTTTGGATCAGCAGAATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGA		MAICLSSHRTVDDTLPLDQQNDKRDDSMVQIYVDCPCMPFP*		MAICLSSHRTVDDTLPLDQQNDKRDDSMVQIYVDCPCMPFP*		CCGTGTCACC	TTGACATCCC	0	G	0	0	0	0	0
5997	2969	af	AN7648.1	57.m05388	AO070294000077	0			-187	-92			ATGATACTCTGCCTTTGGATCAGCAGAATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		ATGATACTCTGCCTTTGGATCAGCAGAATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		MILCLWISRMISAMIQWCRYMSTALACHFLD*		MILCLWISRMISAMIQWCRYMSTALACHFLD*		CGAACAGTTG	CATCCCCCTC	0	G	0	0	0	0	0
5998	2969	af	AN7648.1	57.m05388	AO070294000077	0			-160	-92			ATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		ATGATAAGCGCGATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		MISAMIQWCRYMSTALACHFLD*		MISAMIQWCRYMSTALACHFLD*		GATCAGCAGA	CATCCCCCTC	0	G	0	0	0	0	0
5999	2969	af	AN7648.1	57.m05388	AO070294000077	0			-148	-92			ATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		ATGATTCAATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		MIQWCRYMSTALACHFLD*		MIQWCRYMSTALACHFLD*		GATAAGCGCG	CATCCCCCTC	0	G	0	0	0	0	0
6000	2969	af	AN7648.1	57.m05388	AO070294000077	0			-140	-96			ATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGA		ATGGTGCAGATATATGTCGACTGCCCTTGCATGCCATTTCCTTGA		MVQIYVDCPCMPFP*		MVQIYVDCPCMPFP*		CGATGATTCA	TTGACATCCC	0	G	0	0	0	0	0
6001	2969	af	AN7648.1	57.m05388	AO070294000077	0			-127	-92			ATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		ATGTCGACTGCCCTTGCATGCCATTTCCTTGATTGA		MSTALACHFLD*		MSTALACHFLD*		GTGCAGATAT	CATCCCCCTC	0	G	0	0	0	0	0
6002	2969	af	AN7648.1	57.m05388	AO070294000077	0			-110	-96			ATGCCATTTCCTTGA		ATGCCATTTCCTTGA		MPFP*		MPFP*		CTGCCCTTGC	TTGACATCCC	0	G	0	0	0	0	0
5995	2969	an	AN7648.1	57.m05388	AO070294000077	0	-135	-79					ATGACGAACAGTTATCTATCCCTTGCTTCATCATCTCCTGCCCTGCAAAACTCGTGA	ATGACGAACAGTTATCTATCCCTTGCTTCATCATCTCCTGCCCTGCAAAACTCGTGA			MTNSYLSLASSSPALQNS*	MTNSYLSLASSSPALQNS*			ATCCATCGCC	AATCGCTTCA	0	G	0	0	0	0	0
6003	2969	ao	AN7648.1	57.m05388	AO070294000077	0					-188	-147	ATGACGATGATACTCTGCCTTCCGACCTGCATGACGATGTGA			ATGACGATGATACTCTGCCTTCCGACCTGCATGACGATGTGA	MTMILCLPTCMTM*			MTMILCLPTCMTM*	CTTATCACCC	GGAGAAGCTT	0	G	0	0	0	0	0
6004	2969	ao	AN7648.1	57.m05388	AO070294000077	0					-182	-147	ATGATACTCTGCCTTCCGACCTGCATGACGATGTGA			ATGATACTCTGCCTTCCGACCTGCATGACGATGTGA	MILCLPTCMTM*			MILCLPTCMTM*	ACCCATGACG	GGAGAAGCTT	0	G	0	0	0	0	0
6005	2969	ao	AN7648.1	57.m05388	AO070294000077	0					-158	-147	ATGACGATGTGA			ATGACGATGTGA	MTM*			MTM*	TCCGACCTGC	GGAGAAGCTT	0	G	0	0	0	0	0

6010	2970	af	AN4336.1	70.m15045	AO070295000006	0			-133	-35			ATGTTTCCATTGCGCCAAATCATGCTGCGCTCGGTCGTCGCTCAGGGTGTCTCTGTTGAGATATGTCTATATATCCTCCGATTCCAGAATGGAGCCTGA		ATGTTTCCATTGCGCCAAATCATGCTGCGCTCGGTCGTCGCTCAGGGTGTCTCTGTTGAGATATGTCTATATATCCTCCGATTCCAGAATGGAGCCTGA		MFPLRQIMLRSVVAQGVSVEICLYILRFQNGA*		MFPLRQIMLRSVVAQGVSVEICLYILRFQNGA*		GGAGCCGGAG	TTGATCACCA	0	Q	0	MG01231.1	NCU00643.1	0	0
6011	2970	af	AN4336.1	70.m15045	AO070295000006	0			-112	-35			ATGCTGCGCTCGGTCGTCGCTCAGGGTGTCTCTGTTGAGATATGTCTATATATCCTCCGATTCCAGAATGGAGCCTGA		ATGCTGCGCTCGGTCGTCGCTCAGGGTGTCTCTGTTGAGATATGTCTATATATCCTCCGATTCCAGAATGGAGCCTGA		MLRSVVAQGVSVEICLYILRFQNGA*		MLRSVVAQGVSVEICLYILRFQNGA*		GCGCCAAATC	TTGATCACCA	0	Q	0	MG01231.1	NCU00643.1	0	0
6006	2970	an	AN4336.1	70.m15045	AO070295000006	0	-184	-134					ATGCGTCGAAGCACTCTAATTGTATCCGTCACTCTCATGTACTCCAAGTAG	ATGCGTCGAAGCACTCTAATTGTATCCGTCACTCTCATGTACTCCAAGTAG			MRRSTLIVSVTLMYSK*	MRRSTLIVSVTLMYSK*			ACTGGATTAG	AGTCTAGATG	0	Q	0	MG01231.1	NCU00643.1	0	0
6007	2970	an	AN4336.1	70.m15045	AO070295000006	0	-148	-134					ATGTACTCCAAGTAG	ATGTACTCCAAGTAG			MYSK*	MYSK*			CGTCACTCTC	AGTCTAGATG	0	Q	0	MG01231.1	NCU00643.1	0	0
6008	2970	an	AN4336.1	70.m15045	AO070295000006	0	-126	-100					ATGTGCTGGCTCGGGGATGCCCCGTAG	ATGTGCTGGCTCGGGGATGCCCCGTAG			MCWLGDAP*	MCWLGDAP*			TAGAGTCTAG	GAACCGACCC	0	Q	0	MG01231.1	NCU00643.1	0	0
6009	2970	an	AN4336.1	70.m15045	AO070295000006	0	-110	-78					ATGCCCCGTAGGAACCGACCCTCGACCACGTAA	ATGCCCCGTAGGAACCGACCCTCGACCACGTAA			MPRRNRPSTT*	MPRRNRPSTT*			TGGCTCGGGG	CCGAGACCGG	0	Q	0	MG01231.1	NCU00643.1	0	0
6013	2970	ao	AN4336.1	70.m15045	AO070295000006	0					-270	-250	ATGCCGAAGTGCCTTTCCTAA			ATGCCGAAGTGCCTTTCCTAA	MPKCLS*			MPKCLS*	TTCGGAGGTG	GTGACGATAA	0	Q	0	MG01231.1	NCU00643.1	0	0
6014	2970	ao	AN4336.1	70.m15045	AO070295000006	0					-197	-171	ATGATCTTCTGCAGGAGGATGGCATGA			ATGATCTTCTGCAGGAGGATGGCATGA	MIFCRRMA*			MIFCRRMA*	GGATCGACAC	ACATTGGCCA	0	Q	0	MG01231.1	NCU00643.1	0	0
6015	2970	ao	AN4336.1	70.m15045	AO070295000006	0					-174	-67	ATGAACATTGGCCAGCAACCCACCAATTCGGCGGTATGTCCGAAGAGCTATCCCACCGGATACGATTCCCCAATATGGGAGCCTTTCGGCCTCCGAAGCAAGATATAA			ATGAACATTGGCCAGCAACCCACCAATTCGGCGGTATGTCCGAAGAGCTATCCCACCGGATACGATTCCCCAATATGGGAGCCTTTCGGCCTCCGAAGCAAGATATAA	MNIGQQPTNSAVCPKSYPTGYDSPIWEPFGLRSKI*			MNIGQQPTNSAVCPKSYPTGYDSPIWEPFGLRSKI*	GGAGGATGGC	GTAGCTCCTC	0	Q	0	MG01231.1	NCU00643.1	0	0
6016	2971	af	AN6645.1	62.m03456	AO070295000020	0			-193	-107			ATGATTCCTAAATGTACCTACTATCCAGTCCACAGATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAG		ATGATTCCTAAATGTACCTACTATCCAGTCCACAGATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAG		MIPKCTYYPVHRWAPLRCVAFGRSVFIS*		MIPKCTYYPVHRWAPLRCVAFGRSVFIS*		GTCATATCGC	TCTATCTATC	0	H	0	0	0	0	0
6017	2971	af	AN6645.1	62.m03456	AO070295000020	0			-182	-39			ATGTACCTACTATCCAGTCCACAGATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAGTCTATCTATCTATCTACCCCAGATCAGCTGTCTCTTGTGTCACTGTGTCAGAGTGTCGACGTTTTTGA		ATGTACCTACTATCCAGTCCACAGATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAGTCTATCTATCTATCTACCCCAGATCAGCTGTCTCTTGTGTCACTGTGTCAGAGTGTCGACGTTTTTGA		MYLLSSPQMGSTPVCCIWTVRLYFLVYLSIYPRSAVSCVTVSECRRF*		MYLLSSPQMGSTPVCCIWTVRLYFLVYLSIYPRSAVSCVTVSECRRF*		TGATTCCTAA	ATAATCTGTT	0	H	0	0	0	0	0
6018	2971	af	AN6645.1	62.m03456	AO070295000020	0			-158	-39			ATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAGTCTATCTATCTATCTACCCCAGATCAGCTGTCTCTTGTGTCACTGTGTCAGAGTGTCGACGTTTTTGA		ATGGGCTCCACTCCGGTGTGTTGCATTTGGACGGTCCGTCTTTATTTCTTAGTCTATCTATCTATCTACCCCAGATCAGCTGTCTCTTGTGTCACTGTGTCAGAGTGTCGACGTTTTTGA		MGSTPVCCIWTVRLYFLVYLSIYPRSAVSCVTVSECRRF*		MGSTPVCCIWTVRLYFLVYLSIYPRSAVSCVTVSECRRF*		CAGTCCACAG	ATAATCTGTT	0	H	0	0	0	0	0
6019	2971	ao	AN6645.1	62.m03456	AO070295000020	0					-228	-199	ATGACGGGAAAGAGTAGCTCCACTCTTTAG			ATGACGGGAAAGAGTAGCTCCACTCTTTAG	MTGKSSSTL*			MTGKSSSTL*	AAGCCACCAA	GCGCAGTTCA	0	H	0	0	0	0	0
6023	2972	af	AN2268.1	71.m15913	AO070295000040	0			-253	-233			ATGATTCCGGAACAGAAGTAG		ATGATTCCGGAACAGAAGTAG		MIPEQK*		MIPEQK*		AGCCATAAGA	TGGATACCTC	0	J	FG07333.1	0	0	0	0
6024	2972	af	AN2268.1	71.m15913	AO070295000040	0			-217	-206			ATGTATATCTAG		ATGTATATCTAG		MYI*		MYI*		ACCTCTTGAA	CTTGCTATCT	0	J	FG07333.1	0	0	0	0
6025	2972	af	AN2268.1	71.m15913	AO070295000040	0			-183	-142			ATGAAGCTGATCACATGTGGAACCTCTTGTTATGCGGAGTGA		ATGAAGCTGATCACATGTGGAACCTCTTGTTATGCGGAGTGA		MKLITCGTSCYAE*		MKLITCGTSCYAE*		TGGTGGGGTG	GCTCTGTTGC	0	J	FG07333.1	0	0	0	0
6026	2972	af	AN2268.1	71.m15913	AO070295000040	0			-169	-107			ATGTGGAACCTCTTGTTATGCGGAGTGAGCTCTGTTGCCTTGCGTGGATGCCAGATCGTTTAG		ATGTGGAACCTCTTGTTATGCGGAGTGAGCTCTGTTGCCTTGCGTGGATGCCAGATCGTTTAG		MWNLLLCGVSSVALRGCQIV*		MWNLLLCGVSSVALRGCQIV*		AGCTGATCAC	GCAAAAACCC	0	J	FG07333.1	0	0	0	0
6027	2972	af	AN2268.1	71.m15913	AO070295000040	0			-152	-81			ATGCGGAGTGAGCTCTGTTGCCTTGCGTGGATGCCAGATCGTTTAGGCAAAAACCCCTGCCCCTGCACGTGA		ATGCGGAGTGAGCTCTGTTGCCTTGCGTGGATGCCAGATCGTTTAGGCAAAAACCCCTGCCCCTGCACGTGA		MRSELCCLAWMPDRLGKNPCPCT*		MRSELCCLAWMPDRLGKNPCPCT*		ACCTCTTGTT	CCATCTGAGA	0	J	FG07333.1	0	0	0	0
6028	2972	af	AN2268.1	71.m15913	AO070295000040	0			-122	-81			ATGCCAGATCGTTTAGGCAAAAACCCCTGCCCCTGCACGTGA		ATGCCAGATCGTTTAGGCAAAAACCCCTGCCCCTGCACGTGA		MPDRLGKNPCPCT*		MPDRLGKNPCPCT*		CCTTGCGTGG	CCATCTGAGA	0	J	FG07333.1	0	0	0	0
6020	2972	an	AN2268.1	71.m15913	AO070295000040	0	-186	-142					ATGGCGGGGAATCGGGATGCGGGCCGATTGTGCCTGGCCCTTTAG	ATGGCGGGGAATCGGGATGCGGGCCGATTGTGCCTGGCCCTTTAG			MAGNRDAGRLCLAL*	MAGNRDAGRLCLAL*			AACCAAATAA	GCATTAGCAA	0	J	FG07333.1	0	0	0	0
6021	2972	an	AN2268.1	71.m15913	AO070295000040	0	-170	-135					ATGCGGGCCGATTGTGCCTGGCCCTTTAGGCATTAG	ATGCGGGCCGATTGTGCCTGGCCCTTTAGGCATTAG			MRADCAWPFRH*	MRADCAWPFRH*			GGGAATCGGG	CAAAATAACA	0	J	FG07333.1	0	0	0	0
6022	2972	an	AN2268.1	71.m15913	AO070295000040	0	-123	-103					ATGCCAGATTTGTCAGGCTAG	ATGCCAGATTTGTCAGGCTAG			MPDLSG*	MPDLSG*			AAAATAACAT	TAATTTCACG	0	J	FG07333.1	0	0	0	0
6029	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-281	-234	ATGACTCTGGCACCGGATCGGCAGCGATCTAAAGTTATGGATGCCTAG			ATGACTCTGGCACCGGATCGGCAGCGATCTAAAGTTATGGATGCCTAG	MTLAPDRQRSKVMDA*			MTLAPDRQRSKVMDA*	TCAATAACCC	CTTGCTGGAT	0	J	FG07333.1	0	0	0	0
6030	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-245	-234	ATGGATGCCTAG			ATGGATGCCTAG	MDA*			MDA*	ATCTAAAGTT	CTTGCTGGAT	0	J	FG07333.1	0	0	0	0
6031	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-241	-209	ATGCCTAGCTTGCTGGATGTGGTGCGGGGATGA			ATGCCTAGCTTGCTGGATGTGGTGCGGGGATGA	MPSLLDVVRG*			MPSLLDVVRG*	AAAGTTATGG	TTGAAGCTGA	0	J	FG07333.1	0	0	0	0
6032	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-225	-205	ATGTGGTGCGGGGATGATTGA			ATGTGGTGCGGGGATGATTGA	MWCGDD*			MWCGDD*	AGCTTGCTGG	AGCTGATCAC	0	J	FG07333.1	0	0	0	0
6033	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-212	-141	ATGATTGAAGCTGATCACATGTGGATCCTCCCGCTGCCTTTTCTCTCTGCGGAGCTTTTGTTCGTTGCCTGA			ATGATTGAAGCTGATCACATGTGGATCCTCCCGCTGCCTTTTCTCTCTGCGGAGCTTTTGTTCGTTGCCTGA	MIEADHMWILPLPFLSAELLFVA*			MIEADHMWILPLPFLSAELLFVA*	TGGTGCGGGG	GATTGCCGCC	0	J	FG07333.1	0	0	0	0
6034	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-194	-141	ATGTGGATCCTCCCGCTGCCTTTTCTCTCTGCGGAGCTTTTGTTCGTTGCCTGA			ATGTGGATCCTCCCGCTGCCTTTTCTCTCTGCGGAGCTTTTGTTCGTTGCCTGA	MWILPLPFLSAELLFVA*			MWILPLPFLSAELLFVA*	AGCTGATCAC	GATTGCCGCC	0	J	FG07333.1	0	0	0	0
6035	2972	ao	AN2268.1	71.m15913	AO070295000040	0					-94	-32	ATGTCCCGAACTCGATGTCTCCGATCCGGAAAACAATTTTTGGGATGCCCAATCTTGAACTAG			ATGTCCCGAACTCGATGTCTCCGATCCGGAAAACAATTTTTGGGATGCCCAATCTTGAACTAG	MSRTRCLRSGKQFLGCPILN*			MSRTRCLRSGKQFLGCPILN*	CCACGTGATC	TCTACAGCGA	0	J	FG07333.1	0	0	0	0
6036	2974	ao	AN2293.1	71.m15941	AO070295000072	0					-136	-104	ATGGCGGCCAACTTGAACCTATCTTTTTCATAG			ATGGCGGCCAACTTGAACCTATCTTTTTCATAG	MAANLNLSFS*			MAANLNLSFS*	GAAGCATTTC	TCACGTGTGA	0	E	0	0	0	0	0
6037	2976	an	AN1677.1	58.m07754	AO070299000001	0	-203	-78					ATGACCTCCCACCGAGTCTGCCATCGTGAGTATAAAGTCTGGCTTCAAATCGCTCGAGGAATTTCCCATCATCAATTCCATTCCTCAATCTCTCTTCCACCTCGAGCTTCTCAGCGTTCGACCTAG	ATGACCTCCCACCGAGTCTGCCATCGTGAGTATAAAGTCTGGCTTCAAATCGCTCGAGGAATTTCCCATCATCAATTCCATTCCTCAATCTCTCTTCCACCTCGAGCTTCTCAGCGTTCGACCTAG			MTSHRVCHREYKVWLQIARGISHHQFHSSISLPPRASQRST*	MTSHRVCHREYKVWLQIARGISHHQFHSSISLPPRASQRST*			ATGAGCTCCC	CGCAACACCT	0	IQR	0	0	0	0	0
6038	2976	ao	AN1677.1	58.m07754	AO070299000001	0					-287	-183	ATGACTCTCCCGGACCCAGAGTCATTCTTTCCCCTAGCAGTCTCCAATGCCCATCGTGAAGTATATAAGTGTGATATTCCTCGCCGTGTTGGAGTGACTGACTAG			ATGACTCTCCCGGACCCAGAGTCATTCTTTCCCCTAGCAGTCTCCAATGCCCATCGTGAAGTATATAAGTGTGATATTCCTCGCCGTGTTGGAGTGACTGACTAG	MTLPDPESFFPLAVSNAHREVYKCDIPRRVGVTD*			MTLPDPESFFPLAVSNAHREVYKCDIPRRVGVTD*	ATGAGGCCTC	ACATCATCAA	0	IQR	0	0	0	0	0
6039	2976	ao	AN1677.1	58.m07754	AO070299000001	0					-241	-191	ATGCCCATCGTGAAGTATATAAGTGTGATATTCCTCGCCGTGTTGGAGTGA			ATGCCCATCGTGAAGTATATAAGTGTGATATTCCTCGCCGTGTTGGAGTGA	MPIVKYISVIFLAVLE*			MPIVKYISVIFLAVLE*	GCAGTCTCCA	CTGACTAGAC	0	IQR	0	0	0	0	0
6040	2978	af	AN1667.1	58.m07731	AO070299000049	0			-203	-21			ATGTGCAAGAAAATCCGCTTCATCTTTTCTAACTCCTATGATATTGAGACCGCCGTCTTCGGTCGTTCATTGCTTGCTACCTTCTTATCTGGCCACTTGCCAAGGCTGGAGATCGCTTGCTCCTCAATCTCCGCTGGCCCCTTTTCTATTCAAAAGAGACTTGCCGCTTTCTCGGGACCCTGA		ATGTGCAAGAAAATCCGCTTCATCTTTTCTAACTCCTATGATATTGAGACCGCCGTCTTCGGTCGTTCATTGCTTGCTACCTTCTTATCTGGCCACTTGCCAAGGCTGGAGATCGCTTGCTCCTCAATCTCCGCTGGCCCCTTTTCTATTCAAAAGAGACTTGCCGCTTTCTCGGGACCCTGA		MCKKIRFIFSNSYDIETAVFGRSLLATFLSGHLPRLEIACSSISAGPFSIQKRLAAFSGP*		MCKKIRFIFSNSYDIETAVFGRSLLATFLSGHLPRLEIACSSISAGPFSIQKRLAAFSGP*		TGCACGGACC	GAAAACTGCG	0		0	0	0	0	0
6041	2978	ao	AN1667.1	58.m07731	AO070299000049	0					-111	-100	ATGGAGAGTTGA			ATGGAGAGTTGA	MES*			MES*	CGAATTGCGG	TTTGTTTGAT	0		0	0	0	0	0
6042	2979	an	AN1636.1	58.m07726	AO070299000057	0	-213	-121					ATGAAACAAACACCTCGGATCCCCAGCCACGGAGTCGAACCTGAGCCCGCGCTTCGCCGCCCTTTTTTTCTGCCGATACCAATTTCGGTTTAG	ATGAAACAAACACCTCGGATCCCCAGCCACGGAGTCGAACCTGAGCCCGCGCTTCGCCGCCCTTTTTTTCTGCCGATACCAATTTCGGTTTAG			MKQTPRIPSHGVEPEPALRRPFFLPIPISV*	MKQTPRIPSHGVEPEPALRRPFFLPIPISV*			AGACGGAGAA	TGCCGATTTC	0		0	0	0	0	0
6043	2979	ao	AN1636.1	58.m07726	AO070299000057	0					-149	-57	ATGTGGCTTAGCGCCCATTTCAATTTCAACTTGGACGAGCATCTGGAAGCGCTCCCCGTGATCAATCAACAAGATCCCATTCTCACCCACTGA			ATGTGGCTTAGCGCCCATTTCAATTTCAACTTGGACGAGCATCTGGAAGCGCTCCCCGTGATCAATCAACAAGATCCCATTCTCACCCACTGA	MWLSAHFNFNLDEHLEALPVINQQDPILTH*			MWLSAHFNFNLDEHLEALPVINQQDPILTH*	CCTCACCCAA	CCTGATCGGA	0		0	0	0	0	0
6044	2980	af	AN2351.1	65.m07205	AO070299000101	0			-199	-116			ATGACCGCCACTTCTACTTGGATTGGCCATGCGAATCGTCATTTCAGGTTCTCCCCCCCCCCGACCGTAAAGAAACCCGTTTAG		ATGACCGCCACTTCTACTTGGATTGGCCATGCGAATCGTCATTTCAGGTTCTCCCCCCCCCCGACCGTAAAGAAACCCGTTTAG		MTATSTWIGHANRHFRFSPPPTVKKPV*		MTATSTWIGHANRHFRFSPPPTVKKPV*		GAACGGCCGA	AATCTCCAAC	0	CR	0	MG09007.1	0	0	0
6045	2980	af	AN2351.1	65.m07205	AO070299000101	0			-171	-130			ATGCGAATCGTCATTTCAGGTTCTCCCCCCCCCCGACCGTAA		ATGCGAATCGTCATTTCAGGTTCTCCCCCCCCCCGACCGTAA		MRIVISGSPPPRP*		MRIVISGSPPPRP*		TGGATTGGCC	AGAAACCCGT	0	CR	0	MG09007.1	0	0	0
6046	2980	ao	AN2351.1	65.m07205	AO070299000101	0					-167	-114	ATGCCTCTGCGCTCAGCGGGTATCCGTGAAGACTCTCTAAACGCAGATGTATAA			ATGCCTCTGCGCTCAGCGGGTATCCGTGAAGACTCTCTAAACGCAGATGTATAA	MPLRSAGIREDSLNADV*			MPLRSAGIREDSLNADV*	CCATTTTTGC	AGCATGGTCT	0	CR	0	MG09007.1	0	0	0
6047	2980	ao	AN2351.1	65.m07205	AO070299000101	0					-121	-14	ATGTATAAAGCATGGTCTCTCTCGAGTATGCTCTATTTCCAAAAAGCACTGCACTTCATCGCACCTACACTTCGTCCATTCTCTGTCAGCCGAACAGGACACACATAA			ATGTATAAAGCATGGTCTCTCTCGAGTATGCTCTATTTCCAAAAAGCACTGCACTTCATCGCACCTACACTTCGTCCATTCTCTGTCAGCCGAACAGGACACACATAA	MYKAWSLSSMLYFQKALHFIAPTLRPFSVSRTGHT*			MYKAWSLSSMLYFQKALHFIAPTLRPFSVSRTGHT*	CTAAACGCAG	CCTTTCTCCC	0	CR	0	MG09007.1	0	0	0
6048	2980	ao	AN2351.1	65.m07205	AO070299000101	0					-94	-14	ATGCTCTATTTCCAAAAAGCACTGCACTTCATCGCACCTACACTTCGTCCATTCTCTGTCAGCCGAACAGGACACACATAA			ATGCTCTATTTCCAAAAAGCACTGCACTTCATCGCACCTACACTTCGTCCATTCTCTGTCAGCCGAACAGGACACACATAA	MLYFQKALHFIAPTLRPFSVSRTGHT*			MLYFQKALHFIAPTLRPFSVSRTGHT*	TCTCTCGAGT	CCTTTCTCCC	0	CR	0	MG09007.1	0	0	0
6052	2982	af	AN2532.1	59.m08443	AO070300000057	0			-280	-101			ATGAACCCGATCGCGTGTCATATCCCAGAAATGGTTAGGCGCTCCCAGAGTGGGGCAGCCCACTCCGGCACTGTCGACCAACCACAACGTAAGGCACGGAAAGCTTCCGTTGTGAAACCGATTCCGAAATTCCGAGGCTCCGATATCCTTGGGCCTCCCCCTCACATCCCAATCAGGTAA		ATGAACCCGATCGCGTGTCATATCCCAGAAATGGTTAGGCGCTCCCAGAGTGGGGCAGCCCACTCCGGCACTGTCGACCAACCACAACGTAAGGCACGGAAAGCTTCCGTTGTGAAACCGATTCCGAAATTCCGAGGCTCCGATATCCTTGGGCCTCCCCCTCACATCCCAATCAGGTAA		MNPIACHIPEMVRRSQSGAAHSGTVDQPQRKARKASVVKPIPKFRGSDILGPPPHIPIR*		MNPIACHIPEMVRRSQSGAAHSGTVDQPQRKARKASVVKPIPKFRGSDILGPPPHIPIR*		GCTAGGTGCA	GAAATACGCC	0	Q	0	0	0	0	0
6053	2982	af	AN2532.1	59.m08443	AO070300000057	0			-250	-101			ATGGTTAGGCGCTCCCAGAGTGGGGCAGCCCACTCCGGCACTGTCGACCAACCACAACGTAAGGCACGGAAAGCTTCCGTTGTGAAACCGATTCCGAAATTCCGAGGCTCCGATATCCTTGGGCCTCCCCCTCACATCCCAATCAGGTAA		ATGGTTAGGCGCTCCCAGAGTGGGGCAGCCCACTCCGGCACTGTCGACCAACCACAACGTAAGGCACGGAAAGCTTCCGTTGTGAAACCGATTCCGAAATTCCGAGGCTCCGATATCCTTGGGCCTCCCCCTCACATCCCAATCAGGTAA		MVRRSQSGAAHSGTVDQPQRKARKASVVKPIPKFRGSDILGPPPHIPIR*		MVRRSQSGAAHSGTVDQPQRKARKASVVKPIPKFRGSDILGPPPHIPIR*		TATCCCAGAA	GAAATACGCC	0	Q	0	0	0	0	0
6049	2982	an	AN2532.1	59.m08443	AO070300000057	0	-207	-166					ATGAGCTTTAAACTGTATCCAGCAAGTCCAGCCGACTTCTGA	ATGAGCTTTAAACTGTATCCAGCAAGTCCAGCCGACTTCTGA			MSFKLYPASPADF*	MSFKLYPASPADF*			TGATATAGCC	AGCTCCCCTC	0	Q	0	0	0	0	0
6050	2982	an	AN2532.1	59.m08443	AO070300000057	0	-94	-71					ATGGGCCGTTGCCAAAGTACCTGA	ATGGGCCGTTGCCAAAGTACCTGA			MGRCQST*	MGRCQST*			GAGGGGTCGG	ATGATTTACT	0	Q	0	0	0	0	0

6051	2982	an	AN2532.1	59.m08443	AO070300000057	0	-70	-5					ATGATTTACTACAAAGCGACTGCTTCCCTCGTTGTAGATTCTTTCAATAATTCTTTTCACAACTGA	ATGATTTACTACAAAGCGACTGCTTCCCTCGTTGTAGATTCTTTCAATAATTCTTTTCACAACTGA			MIYYKATASLVVDSFNNSFHN*	MIYYKATASLVVDSFNNSFHN*			AAGTACCTGA	AACTATGGCC	0	Q	0	0	0	0	0
6054	2982	ao	AN2532.1	59.m08443	AO070300000057	0					-74	-3	ATGCATAATAAGCGCGCCTCTTCCTACCTTTCGTCCTCTTTTTTCCTCAGACTATCAACAGATCCAAATTAA			ATGCATAATAAGCGCGCCTCTTCCTACCTTTCGTCCTCTTTTTTCCTCAGACTATCAACAGATCCAAATTAA	MHNKRASSYLSSSFFLRLSTDPN*			MHNKRASSYLSSSFFLRLSTDPN*	CGCTGGCTTC	CCATGGCGCC	0	Q	0	0	0	0	0
6055	2985	af	AN5613.1	58.m07536	AO070301000012	0			-227	-204			ATGGATTCATCTGGTGCTACTTGA		ATGGATTCATCTGGTGCTACTTGA		MDSSGAT*		MDSSGAT*		ACTTCAGGTG	TTCATCATCA	0	F	0	0	0	0	0
6056	2985	af	AN5613.1	58.m07536	AO070301000012	0			-119	-69			ATGCGAACCAGCTTCTCCATTCGACTATACACAAAGGAAGCTACTGCCTGA		ATGCGAACCAGCTTCTCCATTCGACTATACACAAAGGAAGCTACTGCCTGA		MRTSFSIRLYTKEATA*		MRTSFSIRLYTKEATA*		CGCTAGACTC	GCTGGGAGAG	0	F	0	0	0	0	0
6057	2985	ao	AN5613.1	58.m07536	AO070301000012	0					-181	-110	ATGAATACTACCCTATGCCTCCTCGATTCTCTCCCCACTTATAAATATATGTCCTTCGTCAGACCCTCGTGA			ATGAATACTACCCTATGCCTCCTCGATTCTCTCCCCACTTATAAATATATGTCCTTCGTCAGACCCTCGTGA	MNTTLCLLDSLPTYKYMSFVRPS*			MNTTLCLLDSLPTYKYMSFVRPS*	GCTGTACGGC	ACGTCTTACA	0	F	0	0	0	0	0
6058	2985	ao	AN5613.1	58.m07536	AO070301000012	0					-167	-138	ATGCCTCCTCGATTCTCTCCCCACTTATAA			ATGCCTCCTCGATTCTCTCCCCACTTATAA	MPPRFSPHL*			MPPRFSPHL*	ATACTACCCT	ATATATGTCC	0	F	0	0	0	0	0
6059	2985	ao	AN5613.1	58.m07536	AO070301000012	0					-133	-110	ATGTCCTTCGTCAGACCCTCGTGA			ATGTCCTTCGTCAGACCCTCGTGA	MSFVRPS*			MSFVRPS*	TTATAAATAT	ACGTCTTACA	0	F	0	0	0	0	0
6060	2986	af	AN5626.1	58.m07549	AO070301000025	0			-139	-59			ATGTGCATGCTTCCGGTGCTCACAAAAGCTGACCCCCGCATCTTTAGCAGCTTGTCCCAACCTTTCCTACTTTTCTCCTGA		ATGTGCATGCTTCCGGTGCTCACAAAAGCTGACCCCCGCATCTTTAGCAGCTTGTCCCAACCTTTCCTACTTTTCTCCTGA		MCMLPVLTKADPRIFSSLSQPFLLFS*		MCMLPVLTKADPRIFSSLSQPFLLFS*		GCTCACGGGC	AACTTTGCAA	0	I	0	0	0	0	0
6061	2986	af	AN5626.1	58.m07549	AO070301000025	0			-133	-59			ATGCTTCCGGTGCTCACAAAAGCTGACCCCCGCATCTTTAGCAGCTTGTCCCAACCTTTCCTACTTTTCTCCTGA		ATGCTTCCGGTGCTCACAAAAGCTGACCCCCGCATCTTTAGCAGCTTGTCCCAACCTTTCCTACTTTTCTCCTGA		MLPVLTKADPRIFSSLSQPFLLFS*		MLPVLTKADPRIFSSLSQPFLLFS*		GGGCATGTGC	AACTTTGCAA	0	I	0	0	0	0	0
6062	2987	af	AN5632.1	58.m07556	AO070301000031	0			-254	-201			ATGCCGGATTCAGGGAACCATACTCATGAAATCCAGTTCTGGAAGTTTAATTAG		ATGCCGGATTCAGGGAACCATACTCATGAAATCCAGTTCTGGAAGTTTAATTAG		MPDSGNHTHEIQFWKFN*		MPDSGNHTHEIQFWKFN*		CTGATCAGCG	TATGCGAAGT	0	U	0	0	NCU04541.1	0	0
6063	2987	af	AN5632.1	58.m07556	AO070301000031	0			-229	-119			ATGAAATCCAGTTCTGGAAGTTTAATTAGTATGCGAAGTAATGTGAAGCTGCTGTCGAGGTCTACTAAGGTTTTGACAGCTCCAAGACCTTTGTTCGATCTTCGTTGCTAG		ATGAAATCCAGTTCTGGAAGTTTAATTAGTATGCGAAGTAATGTGAAGCTGCTGTCGAGGTCTACTAAGGTTTTGACAGCTCCAAGACCTTTGTTCGATCTTCGTTGCTAG		MKSSSGSLISMRSNVKLLSRSTKVLTAPRPLFDLRC*		MKSSSGSLISMRSNVKLLSRSTKVLTAPRPLFDLRC*		AACCATACTC	CCTGGGGCAT	0	U	0	0	NCU04541.1	0	0
6064	2987	af	AN5632.1	58.m07556	AO070301000031	0			-199	-119			ATGCGAAGTAATGTGAAGCTGCTGTCGAGGTCTACTAAGGTTTTGACAGCTCCAAGACCTTTGTTCGATCTTCGTTGCTAG		ATGCGAAGTAATGTGAAGCTGCTGTCGAGGTCTACTAAGGTTTTGACAGCTCCAAGACCTTTGTTCGATCTTCGTTGCTAG		MRSNVKLLSRSTKVLTAPRPLFDLRC*		MRSNVKLLSRSTKVLTAPRPLFDLRC*		TTTAATTAGT	CCTGGGGCAT	0	U	0	0	NCU04541.1	0	0
6065	2987	ao	AN5632.1	58.m07556	AO070301000031	0					-263	-228	ATGCGAATCCTTGAAACCTATGGAGTTGCCAGTTAA			ATGCGAATCCTTGAAACCTATGGAGTTGCCAGTTAA	MRILETYGVAS*			MRILETYGVAS*	CTGTCAGGTG	TCATATGAAA	0	U	0	0	NCU04541.1	0	0
6066	2987	ao	AN5632.1	58.m07556	AO070301000031	0					-244	-170	ATGGAGTTGCCAGTTAATCATATGAAACAGGCTACTCCAGTGCTAATACTCCGTAGACTACAGAGTACCACTTAG			ATGGAGTTGCCAGTTAATCATATGAAACAGGCTACTCCAGTGCTAATACTCCGTAGACTACAGAGTACCACTTAG	MELPVNHMKQATPVLILRRLQSTT*			MELPVNHMKQATPVLILRRLQSTT*	CTTGAAACCT	TATTCGAAGC	0	U	0	0	NCU04541.1	0	0
6067	2987	ao	AN5632.1	58.m07556	AO070301000031	0					-223	-170	ATGAAACAGGCTACTCCAGTGCTAATACTCCGTAGACTACAGAGTACCACTTAG			ATGAAACAGGCTACTCCAGTGCTAATACTCCGTAGACTACAGAGTACCACTTAG	MKQATPVLILRRLQSTT*			MKQATPVLILRRLQSTT*	AGTTAATCAT	TATTCGAAGC	0	U	0	0	NCU04541.1	0	0
6069	2988	af	AN5646.1	58.m07559	AO070301000034	0			-236	-171			ATGTTGATGCGGCTGAACCTCGGTACTTTCACAGGTTCCTGGATACACGAACACTGCAAAGGGTAA		ATGTTGATGCGGCTGAACCTCGGTACTTTCACAGGTTCCTGGATACACGAACACTGCAAAGGGTAA		MLMRLNLGTFTGSWIHEHCKG*		MLMRLNLGTFTGSWIHEHCKG*		AGCCGGAACA	CAGGACCGAG	0	I	0	0	0	0	0
6070	2988	af	AN5646.1	58.m07559	AO070301000034	0			-230	-171			ATGCGGCTGAACCTCGGTACTTTCACAGGTTCCTGGATACACGAACACTGCAAAGGGTAA		ATGCGGCTGAACCTCGGTACTTTCACAGGTTCCTGGATACACGAACACTGCAAAGGGTAA		MRLNLGTFTGSWIHEHCKG*		MRLNLGTFTGSWIHEHCKG*		AACAATGTTG	CAGGACCGAG	0	I	0	0	0	0	0
6068	2988	an	AN5646.1	58.m07559	AO070301000034	0	-179	-168					ATGGCTACATAA	ATGGCTACATAA			MAT*	MAT*			TTTTCACAGG	TCAATAAGGA	0	I	0	0	0	0	0
6071	2988	ao	AN5646.1	58.m07559	AO070301000034	0					-227		ATGACGCGGGTGAGCCTCGGTACTTTCACAGGACCGGCGATGAGCATACAAAAAGGCAACAGAACCGACCAAGTGGATTCTACTCCACGTTGTCTCCCCCGGGTTCACGATATAAAGAGGAATCCTGTCGCTTCTCTTTTCTCTCTCTATCCCCCTACTATCTATTTGATTGTTGATACCCATTTCATTCCTCTTCTGTATTTTCTCAAAATTTCACTGACGTCATAA			ATGACGCGGGTGAGCCTCGGTACTTTCACAGGACCGGCGATGAGCATACAAAAAGGCAACAGAACCGACCAAGTGGATTCTACTCCACGTTGTCTCCCCCGGGTTCACGATATAAAGAGGAATCCTGTCGCTTCTCTTTTCTCTCTCTATCCCCCTACTATCTATTTGATTGTTGATACCCATTTCATTCCTCTTCTGTATTTTCTCAAAATTTCACTGACGTCATAA	MTRVSLGTFTGPAMSIQKGNRTDQVDSTPRCLPRVHDIKRNPVASLFSLYPPTIYLIVDTHFIPLLYFLKISLTS*			MTRVSLGTFTGPAMSIQKGNRTDQVDSTPRCLPRVHDIKRNPVASLFSLYPPTIYLIVDTHFIPLLYFLKISLTS*	CGGAATAACG	TGTCTTCTGG	0	I	0	0	0	0	0
6072	2988	ao	AN5646.1	58.m07559	AO070301000034	0					-188		ATGAGCATACAAAAAGGCAACAGAACCGACCAAGTGGATTCTACTCCACGTTGTCTCCCCCGGGTTCACGATATAAAGAGGAATCCTGTCGCTTCTCTTTTCTCTCTCTATCCCCCTACTATCTATTTGATTGTTGATACCCATTTCATTCCTCTTCTGTATTTTCTCAAAATTTCACTGACGTCATAA			ATGAGCATACAAAAAGGCAACAGAACCGACCAAGTGGATTCTACTCCACGTTGTCTCCCCCGGGTTCACGATATAAAGAGGAATCCTGTCGCTTCTCTTTTCTCTCTCTATCCCCCTACTATCTATTTGATTGTTGATACCCATTTCATTCCTCTTCTGTATTTTCTCAAAATTTCACTGACGTCATAA	MSIQKGNRTDQVDSTPRCLPRVHDIKRNPVASLFSLYPPTIYLIVDTHFIPLLYFLKISLTS*			MSIQKGNRTDQVDSTPRCLPRVHDIKRNPVASLFSLYPPTIYLIVDTHFIPLLYFLKISLTS*	AGGACCGGCG	TGTCTTCTGG	0	I	0	0	0	0	0
6074	2989	af	AN1964.1	58.m07569	AO070301000045	0			-242	-144			ATGGATCGCTTCACCAAAGATGAAGATTGGTTAGAAATCCGGGTAGGAGGGGCTGACATAAGAAGCCCTACCGACAGGCGCTGTACCCGACTCGGCTAG		ATGGATCGCTTCACCAAAGATGAAGATTGGTTAGAAATCCGGGTAGGAGGGGCTGACATAAGAAGCCCTACCGACAGGCGCTGTACCCGACTCGGCTAG		MDRFTKDEDWLEIRVGGADIRSPTDRRCTRLG*		MDRFTKDEDWLEIRVGGADIRSPTDRRCTRLG*		AATTAATAAG	TACACCTTAG	0	J	0	0	NCU08502.1	0	0
6075	2989	af	AN1964.1	58.m07569	AO070301000045	0			-223	-209			ATGAAGATTGGTTAG		ATGAAGATTGGTTAG		MKIG*		MKIG*		TTCACCAAAG	AAATCCGGGT	0	J	0	0	NCU08502.1	0	0
6073	2989	an	AN1964.1	58.m07569	AO070301000045	0	-242	-231					ATGCCTGAATAA	ATGCCTGAATAA			MPE*	MPE*			ATCAGAATCG	AGGATTACCT	0	J	0	0	NCU08502.1	0	0
6076	2989	ao	AN1964.1	58.m07569	AO070301000045	0					-249	-190	ATGATCATCTCGAATGGGCATCCTTACAGTCTGGAAATTCCCAAAAGGGAAAGCGGCTGA			ATGATCATCTCGAATGGGCATCCTTACAGTCTGGAAATTCCCAAAAGGGAAAGCGGCTGA	MIISNGHPYSLEIPKRESG*			MIISNGHPYSLEIPKRESG*	AAGAAGTTTG	CATAAGAAGC	0	J	0	0	NCU08502.1	0	0
6077	2989	ao	AN1964.1	58.m07569	AO070301000045	0					-236	-171	ATGGGCATCCTTACAGTCTGGAAATTCCCAAAAGGGAAAGCGGCTGACATAAGAAGCCCTATTTAG			ATGGGCATCCTTACAGTCTGGAAATTCCCAAAAGGGAAAGCGGCTGACATAAGAAGCCCTATTTAG	MGILTVWKFPKGKAADIRSPI*			MGILTVWKFPKGKAADIRSPI*	ATCATCTCGA	CGGCACTAAC	0	J	0	0	NCU08502.1	0	0
6078	2989	ao	AN1964.1	58.m07569	AO070301000045	0					-149	-60	ATGGTGGATGTTAGTCAGCCGCCCACAGAGGGAAATCTCGCTACACCACAGCGGCCAAAAATCCCAAGTACTGAATCTCCGACGACCTAA			ATGGTGGATGTTAGTCAGCCGCCCACAGAGGGAAATCTCGCTACACCACAGCGGCCAAAAATCCCAAGTACTGAATCTCCGACGACCTAA	MVDVSQPPTEGNLATPQRPKIPSTESPTT*			MVDVSQPPTEGNLATPQRPKIPSTESPTT*	CCGAACGGGG	CCTCCTCGAC	0	J	0	0	NCU08502.1	0	0
6080	2990	af	AN1965.1	58.m07570	AO070301000046	0			-244	-158			ATGGTTTCATTGGGGAAAAAAAGTTCGATCAAAGTTGCCCGCGGGGCTTCATTTTGGATCTTCATCCTTGAATTCACCGAGATTTAG		ATGGTTTCATTGGGGAAAAAAAGTTCGATCAAAGTTGCCCGCGGGGCTTCATTTTGGATCTTCATCCTTGAATTCACCGAGATTTAG		MVSLGKKSSIKVARGASFWIFILEFTEI*		MVSLGKKSSIKVARGASFWIFILEFTEI*		CGGGACGGCA	ATCGTTCCCT	0	FE	0	MG07148.1	0	0	0
6085	2991	af	AN1967.1	58.m07572	AO070301000051	0			-151	-59			ATGATGTCCCACAAGCTCAGCACATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		ATGATGTCCCACAAGCTCAGCACATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		MMSHKLSTWWMYWMLQASCIFFSQRCPVLM*		MMSHKLSTWWMYWMLQASCIFFSQRCPVLM*		GTGAGTCGCA	CTTGGTAGTT	0	R	0	0	0	0	0
6086	2991	af	AN1967.1	58.m07572	AO070301000051	0			-148	-59			ATGTCCCACAAGCTCAGCACATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		ATGTCCCACAAGCTCAGCACATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		MSHKLSTWWMYWMLQASCIFFSQRCPVLM*		MSHKLSTWWMYWMLQASCIFFSQRCPVLM*		AGTCGCAATG	CTTGGTAGTT	0	R	0	0	0	0	0
6087	2991	af	AN1967.1	58.m07572	AO070301000051	0			-128	-51			ATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGACTTGGTAG		ATGGTGGATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGACTTGGTAG		MVDVLDAAGLMHFLLAKVPSADVTW*		MVDVLDAAGLMHFLLAKVPSADVTW*		AGCTCAGCAC	TTTATTTGTA	0	R	0	0	0	0	0
6088	2991	af	AN1967.1	58.m07572	AO070301000051	0			-121	-59			ATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		ATGTATTGGATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		MYWMLQASCIFFSQRCPVLM*		MYWMLQASCIFFSQRCPVLM*		CACATGGTGG	CTTGGTAGTT	0	R	0	0	0	0	0
6089	2991	af	AN1967.1	58.m07572	AO070301000051	0			-112	-59			ATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		ATGCTGCAGGCCTCATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGA		MLQASCIFFSQRCPVLM*		MLQASCIFFSQRCPVLM*		GATGTATTGG	CTTGGTAGTT	0	R	0	0	0	0	0
6090	2991	af	AN1967.1	58.m07572	AO070301000051	0			-98	-51			ATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGACTTGGTAG		ATGCATTTTCTTCTCGCAAAGGTGCCCAGTGCTGATGTGACTTGGTAG		MHFLLAKVPSADVTW*		MHFLLAKVPSADVTW*		TGCAGGCCTC	TTTATTTGTA	0	R	0	0	0	0	0
6083	2991	an	AN1967.1	58.m07572	AO070301000051	0	-141	-121					ATGCCTCTTTCCTTCACGTGA	ATGCCTCTTTCCTTCACGTGA			MPLSFT*	MPLSFT*			TTAATAAGGT	GCTTAGCCAG	0	R	0	0	0	0	0
6084	2991	an	AN1967.1	58.m07572	AO070301000051	0	-82	-65					ATGGCTGACATTGCATAG	ATGGCTGACATTGCATAG			MADIA*	MADIA*			TACTAAAAGC	GCAGGCTTTA	0	R	0	0	0	0	0
6091	2991	ao	AN1967.1	58.m07572	AO070301000051	0					-244	-80	ATGTGCCCCTCGTGCCATGGAAATCTTTCTCTATTGCTCTCCTGGCTTTGCTCAATCTCTACGACGACCTTATGGTTATCTCTTCTTCCTTTGCTTATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAAGATCATCAGCACTGATATTCGATAG			ATGTGCCCCTCGTGCCATGGAAATCTTTCTCTATTGCTCTCCTGGCTTTGCTCAATCTCTACGACGACCTTATGGTTATCTCTTCTTCCTTTGCTTATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAAGATCATCAGCACTGATATTCGATAG	MCPSCHGNLSLLLSWLCSISTTTLWLSLLPLLMKEDIGGKGATVVSKIISTDIR*			MCPSCHGNLSLLLSWLCSISTTTLWLSLLPLLMKEDIGGKGATVVSKIISTDIR*	GTGGGTGACT	CAGTTAATAT	0	R	0	0	0	0	0
6092	2991	ao	AN1967.1	58.m07572	AO070301000051	0					-228	-145	ATGGAAATCTTTCTCTATTGCTCTCCTGGCTTTGCTCAATCTCTACGACGACCTTATGGTTATCTCTTCTTCCTTTGCTTATGA			ATGGAAATCTTTCTCTATTGCTCTCCTGGCTTTGCTCAATCTCTACGACGACCTTATGGTTATCTCTTCTTCCTTTGCTTATGA	MEIFLYCSPGFAQSLRRPYGYLFFLCL*			MEIFLYCSPGFAQSLRRPYGYLFFLCL*	CCCTCGTGCC	AAGAAGATAT	0	R	0	0	0	0	0
6093	2991	ao	AN1967.1	58.m07572	AO070301000051	0					-173	-105	ATGGTTATCTCTTCTTCCTTTGCTTATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAA			ATGGTTATCTCTTCTTCCTTTGCTTATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAA	MVISSSFAYERRYWRERSHRCF*			MVISSSFAYERRYWRERSHRCF*	CGACGACCTT	GATCATCAGC	0	R	0	0	0	0	0
6094	2991	ao	AN1967.1	58.m07572	AO070301000051	0					-148	-80	ATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAAGATCATCAGCACTGATATTCGATAG			ATGAAAGAAGATATTGGAGGGAAAGGAGCCACCGTTGTTTCTAAGATCATCAGCACTGATATTCGATAG	MKEDIGGKGATVVSKIISTDIR*			MKEDIGGKGATVVSKIISTDIR*	TCCTTTGCTT	CAGTTAATAT	0	R	0	0	0	0	0
6099	2992	af	AN1970.1	58.m07575	AO070301000054	0			-277	-254			ATGCTTTATTATCCAGCGAGGTGA		ATGCTTTATTATCCAGCGAGGTGA		MLYYPAR*		MLYYPAR*		AAGGAAATAA	TGCTGCTGGC	0	J	0	0	0	0	0
6100	2992	af	AN1970.1	58.m07575	AO070301000054	0			-254	-9			ATGCTGCTGGCCGAATTTCAACCGCGCAGCTCAAAGGGTTCAAGCAATGATAGCGGTGCGTTGCCAAGGCGGTCAGCACCCCAAAGAATCCGCCCAAATTCTTTCCATCTAGCACACTTTCCGATCATTTTACTAGCGGACGGTGCTCTATCGGGCTACGATTTCCCTCATCAGCAGTCTTTTGTCGGCTGTCTACACTTGATTTCCTACTGTCATGCCATTGCTCATGCAGTTTCTATAACTTGA		ATGCTGCTGGCCGAATTTCAACCGCGCAGCTCAAAGGGTTCAAGCAATGATAGCGGTGCGTTGCCAAGGCGGTCAGCACCCCAAAGAATCCGCCCAAATTCTTTCCATCTAGCACACTTTCCGATCATTTTACTAGCGGACGGTGCTCTATCGGGCTACGATTTCCCTCATCAGCAGTCTTTTGTCGGCTGTCTACACTTGATTTCCTACTGTCATGCCATTGCTCATGCAGTTTCTATAACTTGA		MLLAEFQPRSSKGSSNDSGALPRRSAPQRIRPNSFHLAHFPIILLADGALSGYDFPHQQSFVGCLHLISYCHAIAHAVSIT*		MLLAEFQPRSSKGSSNDSGALPRRSAPQRIRPNSFHLAHFPIILLADGALSGYDFPHQQSFVGCLHLISYCHAIAHAVSIT*		CAGCGAGGTG	TTATCAAAAT	0	J	0	0	0	0	0
6101	2992	af	AN1970.1	58.m07575	AO070301000054	0			-208	-143			ATGATAGCGGTGCGTTGCCAAGGCGGTCAGCACCCCAAAGAATCCGCCCAAATTCTTTCCATCTAG		ATGATAGCGGTGCGTTGCCAAGGCGGTCAGCACCCCAAAGAATCCGCCCAAATTCTTTCCATCTAG		MIAVRCQGGQHPKESAQILSI*		MIAVRCQGGQHPKESAQILSI*		GGTTCAAGCA	CACACTTTCC	0	J	0	0	0	0	0
6095	2992	an	AN1970.1	58.m07575	AO070301000054	0	-195	-166					ATGAGGAGTCTAGAATGCAGCTGTTGCTGA	ATGAGGAGTCTAGAATGCAGCTGTTGCTGA			MRSLECSCC*	MRSLECSCC*			ATTATTGATA	AATCCGTTCG	0	J	0	0	0	0	0

6096	2992	an	AN1970.1	58.m07575	AO070301000054	0	-181	-101					ATGCAGCTGTTGCTGAAATCCGTTCGCTATTATGCCAAGGCGGTCAGCAACTCCAAATTCTTCCAACCAAATTGTCTCTAG	ATGCAGCTGTTGCTGAAATCCGTTCGCTATTATGCCAAGGCGGTCAGCAACTCCAAATTCTTCCAACCAAATTGTCTCTAG			MQLLLKSVRYYAKAVSNSKFFQPNCL*	MQLLLKSVRYYAKAVSNSKFFQPNCL*			GGAGTCTAGA	CCTCATCAAC	0	J	0	0	0	0	0
6097	2992	an	AN1970.1	58.m07575	AO070301000054	0	-150	-67					ATGCCAAGGCGGTCAGCAACTCCAAATTCTTCCAACCAAATTGTCTCTAGCCTCATCAACAGCACTACTCGTCCTGCCTCCTGA	ATGCCAAGGCGGTCAGCAACTCCAAATTCTTCCAACCAAATTGTCTCTAGCCTCATCAACAGCACTACTCGTCCTGCCTCCTGA			MPRRSATPNSSNQIVSSLINSTTRPAS*	MPRRSATPNSSNQIVSSLINSTTRPAS*			GTTCGCTATT	CCTTGCCATG	0	J	0	0	0	0	0
6104	2992	ao	AN1970.1	58.m07575	AO070301000054	0					-237	-169	ATGGATGCTTCTGGCCGAAATTCAAAGCGCAGCTTAAGGGACCGCTCAATGATAGCCGTCCGTTGCTAA			ATGGATGCTTCTGGCCGAAATTCAAAGCGCAGCTTAAGGGACCGCTCAATGATAGCCGTCCGTTGCTAA	MDASGRNSKRSLRDRSMIAVRC*			MDASGRNSKRSLRDRSMIAVRC*	GACGATAGCG	GGCGGTGAAG	0	J	0	0	0	0	0
6105	2992	ao	AN1970.1	58.m07575	AO070301000054	0					-233	-201	ATGCTTCTGGCCGAAATTCAAAGCGCAGCTTAA			ATGCTTCTGGCCGAAATTCAAAGCGCAGCTTAA	MLLAEIQSAA*			MLLAEIQSAA*	ATAGCGATGG	GGGACCGCTC	0	J	0	0	0	0	0
6106	2992	ao	AN1970.1	58.m07575	AO070301000054	0					-189	-169	ATGATAGCCGTCCGTTGCTAA			ATGATAGCCGTCCGTTGCTAA	MIAVRC*			MIAVRC*	GGACCGCTCA	GGCGGTGAAG	0	J	0	0	0	0	0
6108	2993	af	AN1971.1	58.m07576	AO070301000055	0			-267	-232			ATGGAAAGAATTTGGGCGGATTCTTTGGGGTGCTGA		ATGGAAAGAATTTGGGCGGATTCTTTGGGGTGCTGA		MERIWADSLGC*		MERIWADSLGC*		AGTGTGCTAG	CCGCCTTGGC	0	L	0	0	0	YDR190C	YDR190C
6110	2996	ao	AN1976.1	58.m07581	AO070301000061	0					-182	-165	ATGGCACGTGGTCTTTAA			ATGGCACGTGGTCTTTAA	MARGL*			MARGL*	GATTGATTGC	GAGGAACAGC	0	BK	0	0	0	0	0
6111	2997	ao	AN1988.1	58.m07595	AO070301000075	0					-82	-71	ATGATCCTGTAG			ATGATCCTGTAG	MIL*			MIL*	ACCGAGTTGA	CAGGCAAAGC	0	U	FG05181.1	0	0	YIL068C	0
6112	2998	af	AN1989.1	58.m07597	AO070301000077	0			-180	-148			ATGTGGAAGAAGAACCGAGGCAGGTTCGACTAA		ATGTGGAAGAAGAACCGAGGCAGGTTCGACTAA		MWKKNRGRFD*		MWKKNRGRFD*		CAGGATTAAC	CTCTCTTTTA	0	E	0	MG07162.1	NCU06761.1	0	0
6113	3001	af	AN6234.1	52.m04099	AO070302000121	0			-261	-250			ATGGCGCCTTAA		ATGGCGCCTTAA		MAP*		MAP*		GACTGGATTT	GCAGTCTGTT	0	J	0	0	0	0	0
6114	3001	af	AN6234.1	52.m04099	AO070302000121	0			-228	-184			ATGAGGAATAGTGTTCTTATACTCTTGTCCATAGGGATCAAGTAA		ATGAGGAATAGTGTTCTTATACTCTTGTCCATAGGGATCAAGTAA		MRNSVLILLSIGIK*		MRNSVLILLSIGIK*		ACGATTCTCA	TTTAAGTCAT	0	J	0	0	0	0	0
6115	3001	ao	AN6234.1	52.m04099	AO070302000121	0					-223	-158	ATGGACCAATGCACAATTCTAGCCAAAGTTCCGGCTTTCTTGTGCTCGGCTTTCCGTATAGTGTAA			ATGGACCAATGCACAATTCTAGCCAAAGTTCCGGCTTTCTTGTGCTCGGCTTTCCGTATAGTGTAA	MDQCTILAKVPAFLCSAFRIV*			MDQCTILAKVPAFLCSAFRIV*	CCAGCTTCAC	ACTTTCTCCA	0	J	0	0	0	0	0
6116	3001	ao	AN6234.1	52.m04099	AO070302000121	0					-111	-73	ATGTCTTATATATATACCAGGCCCAGATCCTTGCGCTTTGA			ATGTCTTATATATATACCAGGCCCAGATCCTTGCGCTTTGA	MSYIYQAQILAL*			MSYIYQAQILAL*	ATCTCTCTCC	GAGCCACTGT	0	J	0	0	0	0	0
6117	3005	ao	AN3113.1	59.m09373	AO070303000036	0					-269	-246	ATGCTTCCCATCTCTCCTTCGTGA			ATGCTTCCCATCTCTCCTTCGTGA	MLPISPS*			MLPISPS*	TTCTTCTCTC	GCGCCAAGTT	0	GE	0	0	0	0	0
6118	3006	af	AN6265.1	72.m19392	AO070304000023	0			-243	-178			ATGATAGACAAGACAAGATCTCGGAGAGCGGGTCTTTTCTGCCAGGGAAAAAAAATTATCTATTAG		ATGATAGACAAGACAAGATCTCGGAGAGCGGGTCTTTTCTGCCAGGGAAAAAAAATTATCTATTAG		MIDKTRSRRAGLFCQGKKIIY*		MIDKTRSRRAGLFCQGKKIIY*		AAGCTGCTGT	TTTAAGGTGT	0	A	0	MG01100.1	NCU01502.1	0	0
6119	3006	af	AN6265.1	72.m19392	AO070304000023	0			-142	-65			ATGAATTTTCCTTCAAGACCCGCAGATAACCTTACCTCCGATCATCTTTTCAGACAGCAACACTTCTGGCTCAGCTGA		ATGAATTTTCCTTCAAGACCCGCAGATAACCTTACCTCCGATCATCTTTTCAGACAGCAACACTTCTGGCTCAGCTGA		MNFPSRPADNLTSDHLFRQQHFWLS*		MNFPSRPADNLTSDHLFRQQHFWLS*		AAATCTTGGC	ATTTTTTTGC	0	A	0	MG01100.1	NCU01502.1	0	0
6120	3006	ao	AN6265.1	72.m19392	AO070304000023	0					-239	-84	ATGAGATCGCCTGGCGGTCAGTTTGCAGAAAAAAAAATCCGCTGTGGTGGACAAGCGAAAGGGAAAAAAAAGTCTTGGCATGAATTTTCCTGCGAAAGACCCGCAAAACCTCCGGATCGTTGCTCCAACACTTTTCTTCTTACCTTTACGCTTTTGA			ATGAGATCGCCTGGCGGTCAGTTTGCAGAAAAAAAATCCGCTGTGGTGGACAAGCGAAAGGGAAAAAAAAGTCTTGGCATGAATTTTCCTGCGAAAGACCCGCAAAACCTCCGGATCGTTGCTCCAACACTTTTCTTCTTACCTTTACGCTTTTGA	MRSPGGQFAEKKSAVVDKRKGKKSLGMNFPAKDPQNLRIVAPTLFFLPLRF*			MRSPGGQFAEKKSAVVDKRKGKKSLGMNFPAKDPQNLRIVAPTLFFLPLRF*	CCAGTGGGCA	TTGTTTTGCT	0	A	0	MG01100.1	NCU01502.1	0	0
6121	3006	ao	AN6265.1	72.m19392	AO070304000023	0					-161	-84	ATGAATTTTCCTGCGAAAGACCCGCAAAACCTCCGGATCGTTGCTCCAACACTTTTCTTCTTACCTTTACGCTTTTGA			ATGAATTTTCCTGCGAAAGACCCGCAAAACCTCCGGATCGTTGCTCCAACACTTTTCTTCTTACCTTTACGCTTTTGA	MNFPAKDPQNLRIVAPTLFFLPLRF*			MNFPAKDPQNLRIVAPTLFFLPLRF*	AAGTCTTGGC	TTGTTTTGCT	0	A	0	MG01100.1	NCU01502.1	0	0
6122	3008	af	AN6256.1	72.m19400	AO070304000032	0			-265	-212			ATGCCTTGGGCTCAAGCAACCAAGTGTCCTTCTGGAGGGGGACCGGGGGAGTGA		ATGCCTTGGGCTCAAGCAACCAAGTGTCCTTCTGGAGGGGGACCGGGGGAGTGA		MPWAQATKCPSGGGPGE*		MPWAQATKCPSGGGPGE*		GAACGATCCG	CGCTAAGCTC	0	O	0	MG01109.1	NCU06739.1	0	0
6123	3008	af	AN6256.1	72.m19400	AO070304000032	0			-173	-12			ATGCACGTGACATCATTCATGCCACTGAAGGGCCCAGGCAAAGAAATCTACCTGGGGGAGGGAGGAACAGATATCAACCAGGCGATCGTGACGCAAGGCCTGTTCGCTCATTCTCTGACGGTTCTCATATGGCTCAATAATCAGTCTCATCAAAGTTTTTGA		ATGCACGTGACATCATTCATGCCACTGAAGGGCCCAGGCAAAGAAATCTACCTGGGGGAGGGAGGAACAGATATCAACCAGGCGATCGTGACGCAAGGCCTGTTCGCTCATTCTCTGACGGTTCTCATATGGCTCAATAATCAGTCTCATCAAAGTTTTTGA		MHVTSFMPLKGPGKEIYLGEGGTDINQAIVTQGLFAHSLTVLIWLNNQSHQSF*		MHVTSFMPLKGPGKEIYLGEGGTDINQAIVTQGLFAHSLTVLIWLNNQSHQSF*		ACATCTGCGG	TCGGCTACAC	0	O	0	MG01109.1	NCU06739.1	0	0
6124	3008	af	AN6256.1	72.m19400	AO070304000032	0			-155	-12			ATGCCACTGAAGGGCCCAGGCAAAGAAATCTACCTGGGGGAGGGAGGAACAGATATCAACCAGGCGATCGTGACGCAAGGCCTGTTCGCTCATTCTCTGACGGTTCTCATATGGCTCAATAATCAGTCTCATCAAAGTTTTTGA		ATGCCACTGAAGGGCCCAGGCAAAGAAATCTACCTGGGGGAGGGAGGAACAGATATCAACCAGGCGATCGTGACGCAAGGCCTGTTCGCTCATTCTCTGACGGTTCTCATATGGCTCAATAATCAGTCTCATCAAAGTTTTTGA		MPLKGPGKEIYLGEGGTDINQAIVTQGLFAHSLTVLIWLNNQSHQSF*		MPLKGPGKEIYLGEGGTDINQAIVTQGLFAHSLTVLIWLNNQSHQSF*		GACATCATTC	TCGGCTACAC	0	O	0	MG01109.1	NCU06739.1	0	0
6129	3009	af	AN6232.1	72.m19422	AO070304000085	0			-277	-206			ATGATAATAATTTATGACAAAACATCATTCTCTCCTGGAATCTTGACAGGCCTGTATACTAGACAGCCTTGA		ATGATAATAATTTATGACAAAACATCATTCTCTCCTGGAATCTTGACAGGCCTGTATACTAGACAGCCTTGA		MIIIYDKTSFSPGILTGLYTRQP*		MIIIYDKTSFSPGILTGLYTRQP*		AGAAAAAAAA	AGGAGATCAC	0	C	FG00637.1	MG03244.1	0	0	0
6130	3009	af	AN6232.1	72.m19422	AO070304000085	0			-264	-232			ATGACAAAACATCATTCTCTCCTGGAATCTTGA		ATGACAAAACATCATTCTCTCCTGGAATCTTGA		MTKHHSLLES*		MTKHHSLLES*		ATAATAATTT	CAGGCCTGTA	0	C	FG00637.1	MG03244.1	0	0	0
6131	3009	af	AN6232.1	72.m19422	AO070304000085	0			-167	-45			ATGCGTCACCGCCAAGCTAGAGCTGCGGGCGTGGATCCCTCCCTCATCGATCACATACGGACGACCACTTGGCCCCCTCGTCAGGAGCAGCTCTTCCTGACCTTTCATCGCCCTCTCCTATAG		ATGCGTCACCGCCAAGCTAGAGCTGCGGGCGTGGATCCCTCCCTCATCGATCACATACGGACGACCACTTGGCCCCCTCGTCAGGAGCAGCTCTTCCTGACCTTTCATCGCCCTCTCCTATAG		MRHRQARAAGVDPSLIDHIRTTTWPPRQEQLFLTFHRPLL*		MRHRQARAAGVDPSLIDHIRTTTWPPRQEQLFLTFHRPLL*		CATCACGTGC	CTTCCTTCAG	0	C	FG00637.1	MG03244.1	0	0	0
6127	3009	an	AN6232.1	72.m19422	AO070304000085	0	-243	-232					ATGAGACGATGA	ATGAGACGATGA			MRR*	MRR*			GAAGAAGATA	GTTTACTGTA	0	C	FG00637.1	MG03244.1	0	0	0
6128	3009	an	AN6232.1	72.m19422	AO070304000085	0	-235	-191					ATGAGTTTACTGTACCTCCCACTACTACGGAATACTGGACATTGA	ATGAGTTTACTGTACCTCCCACTACTACGGAATACTGGACATTGA			MSLLYLPLLRNTGH*	MSLLYLPLLRNTGH*			TAATGAGACG	GTTGTGCTAT	0	C	FG00637.1	MG03244.1	0	0	0
6132	3009	ao	AN6232.1	72.m19422	AO070304000085	0					-267	-196	ATGAGTTGGGACAAATTCCCTAGACAACCAAAATTGTGCCTCACAAGTTATGTATGTGTACTCCGTATGTAG			ATGAGTTGGGACAAATTCCCTAGACAACCAAAATTGTGCCTCACAAGTTATGTATGTGTACTCCGTATGTAG	MSWDKFPRQPKLCLTSYVCVLRM*			MSWDKFPRQPKLCLTSYVCVLRM*	ATAAAACATA	ACGATGTCAT	0	C	FG00637.1	MG03244.1	0	0	0
6133	3012	an	AN3839.1	58.m07815	AO070305000074	0	-179	-75					ATGTTTACTTTGATTAGAAAGAAATATCCAAGTCCAGTCTCTCAGTTACTGTCACGGGAGCATAGTGTGTCAGACTTCGCAAAAACAGAGGCCACCTTTCTGTGA	ATGTTTACTTTGATTAGAAAGAAATATCCAAGTCCAGTCTCTCAGTTACTGTCACGGGAGCATAGTGTGTCAGACTTCGCAAAAACAGAGGCCACCTTTCTGTGA			MFTLIRKKYPSPVSQLLSREHSVSDFAKTEATFL*	MFTLIRKKYPSPVSQLLSREHSVSDFAKTEATFL*			TCCGCGCTTT	CGTGGGGCCT	0	I	0	0	0	0	0
6134	3012	ao	AN3839.1	58.m07815	AO070305000074	0					-205	-149	ATGCTAGAGAATGCGCCAAGTGGATTTTGGCTCCATCGTTGTGGTTTAAGTGAGTGA			ATGCTAGAGAATGCGCCAAGTGGATTTTGGCTCCATCGTTGTGGTTTAAGTGAGTGA	MLENAPSGFWLHRCGLSE*			MLENAPSGFWLHRCGLSE*	GGAGAAAAAT	ATTGTTTACT	0	I	0	0	0	0	0
6135	3012	ao	AN3839.1	58.m07815	AO070305000074	0					-195	-157	ATGCGCCAAGTGGATTTTGGCTCCATCGTTGTGGTTTAA			ATGCGCCAAGTGGATTTTGGCTCCATCGTTGTGGTTTAA	MRQVDFGSIVVV*			MRQVDFGSIVVV*	ATGCTAGAGA	GTGAGTGAAT	0	I	0	0	0	0	0
6136	3012	ao	AN3839.1	58.m07815	AO070305000074	0					-133	-122	ATGAATTTATGA			ATGAATTTATGA	MNL*			MNL*	TTACTTATCA	TTACTACTAT	0	I	0	0	0	0	0
6137	3012	ao	AN3839.1	58.m07815	AO070305000074	0					-125	-105	ATGATTACTACTATTTATTAA			ATGATTACTACTATTTATTAA	MITTIY*			MITTIY*	CAATGAATTT	GCTTGACCCC	0	I	0	0	0	0	0
6138	3016	an	AN4462.1	58.m07847	AO070305000113	0	-157	-140					ATGGTCCATATTTATTGA	ATGGTCCATATTTATTGA			MVHIY*	MVHIY*			TCTTCAACTA	AGACCTCTAG	0	C	0	0	0	0	0
6139	3017	an	AN4464.1	58.m07849	AO070305000118	0	-228	-190					ATGCAATCGACTCATCTTCTTCTATCACAGTGGCTCTAA	ATGCAATCGACTCATCTTCTTCTATCACAGTGGCTCTAA			MQSTHLLLSQWL*	MQSTHLLLSQWL*			TTTAAAAAAA	GCATATACTC	0	F	0	MG04435.1	NCU02629.1	0	0
6141	3020	an	AN6219.1	72.m19318	AO070308000071	0	-238	-215					ATGCATTACTGCTTCGGGTTCTGA	ATGCATTACTGCTTCGGGTTCTGA			MHYCFGF*	MHYCFGF*			CACATACTGC	CGACATAGCC	0	C	0	0	0	0	0
6142	3020	ao	AN6219.1	72.m19318	AO070308000071	0					-208	-134	ATGTCTACACATTCTTGGGGAATTTGGGACGATTCCTCCCTTCACCATAGTCAATTAATTCTTTTATCAGCTTAG			ATGTCTACACATTCTTGGGGAATTTGGGACGATTCCTCCCTTCACCATAGTCAATTAATTCTTTTATCAGCTTAG	MSTHSWGIWDDSSLHHSQLILLSA*			MSTHSWGIWDDSSLHHSQLILLSA*	ACCCTGCTTT	AATACTTCTT	0	C	0	0	0	0	0
6145	3021	af	AN6193.1	72.m19291	AO070308000106	0			-207	-79			ATGCGCCGGGTGCTGTTGATGATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		ATGCGCCGGGTGCTGTTGATGATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		MRRVLLMMKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		MRRVLLMMKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		AGAAACGATG	CTCTCTTCGC	0	O	0	0	0	0	0
6146	3021	af	AN6193.1	72.m19291	AO070308000106	0			-189	-79			ATGATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		ATGATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		MMKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		MMKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		GGTGCTGTTG	CTCTCTTCGC	0	O	0	0	0	0	0
6147	3021	af	AN6193.1	72.m19291	AO070308000106	0			-186	-79			ATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		ATGAAAGCACCTGTTCAGCTACCGAAAGTGTCGCTCGGCTTCTGTTCGAGTAATCCTTTCTCTGGTCTTTATCTATTATCTTGTACTACAACTCCTTTTTCTATCTAA		MKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		MKAPVQLPKVSLGFCSSNPFSGLYLLSCTTTPFSI*		GCTGTTGATG	CTCTCTTCGC	0	O	0	0	0	0	0
6143	3021	an	AN6193.1	72.m19291	AO070308000106	0	-199	-110					ATGATGGAACTGCTTGCTTCGGTAATCAATCGCCTGAGCTCGCCATCGCCTCCTCTTTGTCATTGCCTGGCCGGACAGGGACTATTGTGA	ATGATGGAACTGCTTGCTTCGGTAATCAATCGCCTGAGCTCGCCATCGCCTCCTCTTTGTCATTGCCTGGCCGGACAGGGACTATTGTGA			MMELLASVINRLSSPSPPLCHCLAGQGLL*	MMELLASVINRLSSPSPPLCHCLAGQGLL*			CACCGAGGGA	TATTCTCTTG	0	O	0	0	0	0	0
6144	3021	an	AN6193.1	72.m19291	AO070308000106	0	-196	-110					ATGGAACTGCTTGCTTCGGTAATCAATCGCCTGAGCTCGCCATCGCCTCCTCTTTGTCATTGCCTGGCCGGACAGGGACTATTGTGA	ATGGAACTGCTTGCTTCGGTAATCAATCGCCTGAGCTCGCCATCGCCTCCTCTTTGTCATTGCCTGGCCGGACAGGGACTATTGTGA			MELLASVINRLSSPSPPLCHCLAGQGLL*	MELLASVINRLSSPSPPLCHCLAGQGLL*			CGAGGGAATG	TATTCTCTTG	0	O	0	0	0	0	0
6148	3021	ao	AN6193.1	72.m19291	AO070308000106	0					-212	-186	ATGATGAAAGGCTTCTTGCTTCGGTAA			ATGATGAAAGGCTTCTTGCTTCGGTAA	MMKGFLLR*			MMKGFLLR*	CGAGACGACG	TCAAGCACTC	0	O	0	0	0	0	0
6149	3021	ao	AN6193.1	72.m19291	AO070308000106	0					-209	-186	ATGAAAGGCTTCTTGCTTCGGTAA			ATGAAAGGCTTCTTGCTTCGGTAA	MKGFLLR*			MKGFLLR*	GACGACGATG	TCAAGCACTC	0	O	0	0	0	0	0
6150	3022	af	AN5862.1	72.m19273	AO070308000125	0			-254	-123			ATGCGACATATTACTCTCAAACTTAATATCGAGGATTCAATATCCATAAGGGAGTCTATGACGATTCAGCGGTATTCAAATTTGTCTAAAGTTCCCTATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAG		ATGCGACATATTACTCTCAAACTTAATATCGAGGATTCAATATCCATAAGGGAGTCTATGACGATTCAGCGGTATTCAAATTTGTCTAAAGTTCCCTATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAG		MRHITLKLNIEDSISIRESMTIQRYSNLSKVPYAGWLKFYLSQ*		MRHITLKLNIEDSISIRESMTIQRYSNLSKVPYAGWLKFYLSQ*		GGACACTGGA	TCAGCCGCAC	0	S	0	0	0	0	0
6151	3022	af	AN5862.1	72.m19273	AO070308000125	0			-197	-123			ATGACGATTCAGCGGTATTCAAATTTGTCTAAAGTTCCCTATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAG		ATGACGATTCAGCGGTATTCAAATTTGTCTAAAGTTCCCTATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAG		MTIQRYSNLSKVPYAGWLKFYLSQ*		MTIQRYSNLSKVPYAGWLKFYLSQ*		AAGGGAGTCT	TCAGCCGCAC	0	S	0	0	0	0	0
6152	3022	af	AN5862.1	72.m19273	AO070308000125	0			-157	-68			ATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAGTCAGCCGCACCTCGGGCCCTTAGTCTGGTGTTCATCTTCATCGTCCACAAGGTAG		ATGCGGGGTGGCTTAAGTTTTATCTGTCCCAATAGTCAGCCGCACCTCGGGCCCTTAGTCTGGTGTTCATCTTCATCGTCCACAAGGTAG		MRGGLSFICPNSQPHLGPLVWCSSSSSTR*		MRGGLSFICPNSQPHLGPLVWCSSSSSTR*		AAAGTTCCCT	ATGCATATGA	0	S	0	0	0	0	0
6153	3022	af	AN5862.1	72.m19273	AO070308000125	0			-67	-23			ATGCATATGACAAGCAAACTCGCTGTAACCTCATCCATTCAATAG		ATGCATATGACAAGCAAACTCGCTGTAACCTCATCCATTCAATAG		MHMTSKLAVTSSIQ*		MHMTSKLAVTSSIQ*		CACAAGGTAG	CAATTGCATT	0	S	0	0	0	0	0
6154	3022	af	AN5862.1	72.m19273	AO070308000125	0			-61	-23			ATGACAAGCAAACTCGCTGTAACCTCATCCATTCAATAG		ATGACAAGCAAACTCGCTGTAACCTCATCCATTCAATAG		MTSKLAVTSSIQ*		MTSKLAVTSSIQ*		GTAGATGCAT	CAATTGCATT	0	S	0	0	0	0	0
6155	3023	an	AN3756.1	65.m07368	AO070309000050	0	-231	-145					ATGAGAGTCCCAGTTGCCCTGACCGCCTGGCGGAATCAGCTCCAGCTTGCTTGCCCACGTAAGGCTCGCCTGCCTGAGCTCTGCTGA	ATGAGAGTCCCAGTTGCCCTGACCGCCTGGCGGAATCAGCTCCAGCTTGCTTGCCCACGTAAGGCTCGCCTGCCTGAGCTCTGCTGA			MRVPVALTAWRNQLQLACPRKARLPELC*	MRVPVALTAWRNQLQLACPRKARLPELC*			GGCTTGACCA	AGCTGTTTCT	0	O	0	0	0	0	0

6156	3023	ao	AN3756.1	65.m07368	AO070309000050	0					-269	-213	ATGGAATTGTTGTTCCTACTCACCGCCCGGCGGAACCAGCTTCAGCTGCCAACGTAA			ATGGAATTGTTGTTCCTACTCACCGCCCGGCGGAACCAGCTTCAGCTGCCAACGTAA	MELLFLLTARRNQLQLPT*			MELLFLLTARRNQLQLPT*	CATCTGGCCA	CGCGTTCGCC	0	O	0	0	0	0	0
6160	3026	af	AN3741.1	65.m07395	AO070309000082	0			-174	-16			ATGAAGATCAAAATAGATAAAGAGGGGTCCGAAGACCGTGGGACTGTAGGAGGGTTTGAACCATTCGGATTGCCACCTACACAGTACACTTCTTCGCGACTCGTCTCTTTCGCTTTTCCGTCAACGCTGCACGTATACCACCAGAACAGCACCACATAA		ATGAAGATCAAAATAGATAAAGAGGGGTCCGAAGACCGTGGGACTGTAGGAGGGTTTGAACCATTCGGATTGCCACCTACACAGTACACTTCTTCGCGACTCGTCTCTTTCGCTTTTCCGTCAACGCTGCACGTATACCACCAGAACAGCACCACATAA		MKIKIDKEGSEDRGTVGGFEPFGLPPTQYTSSRLVSFAFPSTLHVYHQNSTT*		MKIKIDKEGSEDRGTVGGFEPFGLPPTQYTSSRLVSFAFPSTLHVYHQNSTT*		AGACTTGACA	GCTCATATTG	0	Q	0	MG03880.1	NCU01754.1	0	0
6157	3026	an	AN3741.1	65.m07395	AO070309000082	0	-210	-157					ATGCCCTTTCCCCTCATTTTCATATCAGCAATCAGACTACCTGACTGCTTCTAA	ATGCCCTTTCCCCTCATTTTCATATCAGCAATCAGACTACCTGACTGCTTCTAA			MPFPLIFISAIRLPDCF*	MPFPLIFISAIRLPDCF*			CCCTGCGGAG	GGTTATGGTC	0	Q	0	MG03880.1	NCU01754.1	0	0
6158	3026	an	AN3741.1	65.m07395	AO070309000082	0	-152	-96					ATGGTCAGGCTAGAGATGATAGTCGACTTGGCGTTACGTTGCTCTGGTCTGGGATAG	ATGGTCAGGCTAGAGATGATAGTCGACTTGGCGTTACGTTGCTCTGGTCTGGGATAG			MVRLEMIVDLALRCSGLG*	MVRLEMIVDLALRCSGLG*			TTCTAAGGTT	CCATATAAAG	0	Q	0	MG03880.1	NCU01754.1	0	0
6159	3026	an	AN3741.1	65.m07395	AO070309000082	0	-137	-96					ATGATAGTCGACTTGGCGTTACGTTGCTCTGGTCTGGGATAG	ATGATAGTCGACTTGGCGTTACGTTGCTCTGGTCTGGGATAG			MIVDLALRCSGLG*	MIVDLALRCSGLG*			CAGGCTAGAG	CCATATAAAG	0	Q	0	MG03880.1	NCU01754.1	0	0
6161	3030	an	AN1797.1	72.m19549	AO070309000134	0	-166	-83					ATGGTCAACTCCTGGCTGTTTCCTCCGCATCTCTGGTCGGGATATAAAAGACTACCCCGTGCCCACTGGTGGAGAGAATGTTGA	ATGGTCAACTCCTGGCTGTTTCCTCCGCATCTCTGGTCGGGATATAAAAGACTACCCCGTGCCCACTGGTGGAGAGAATGTTGA			MVNSWLFPPHLWSGYKRLPRAHWWREC*	MVNSWLFPPHLWSGYKRLPRAHWWREC*			CCGGCCGGGC	TCGTCTTGTT	0	R	0	0	0	0	0
6162	3030	an	AN1797.1	72.m19549	AO070309000134	0	-89	-15					ATGTTGATCGTCTTGTTTTGCTTCCCCTCCATTATTCTTCCCCGCCGCCGGCCTATATCATTGTTTATCTGTTAG	ATGTTGATCGTCTTGTTTTGCTTCCCCTCCATTATTCTTCCCCGCCGCCGGCCTATATCATTGTTTATCTGTTAG			MLIVLFCFPSIILPRRRPISLFIC*	MLIVLFCFPSIILPRRRPISLFIC*			GGTGGAGAGA	CGTCTTCGTT	0	R	0	0	0	0	0
6163	3030	ao	AN1797.1	72.m19549	AO070309000134	0					-141	-61	ATGGCCCCTTCCCCATGGAGATTGTGTATCTCATTTTTCTCTCCACTTGTCATTCCTACGTTCTCCCCATCTGCGTGTTGA			ATGGCCCCTTCCCCATGGAGATTGTGTATCTCATTTTTCTCTCCACTTGTCATTCCTACGTTCTCCCCATCTGCGTGTTGA	MAPSPWRLCISFFSPLVIPTFSPSAC*			MAPSPWRLCISFFSPLVIPTFSPSAC*	AAACTCTGTC	TCTACAGCCG	0	R	0	0	0	0	0
6164	3030	ao	AN1797.1	72.m19549	AO070309000134	0					-127	-35	ATGGAGATTGTGTATCTCATTTTTCTCTCCACTTGTCATTCCTACGTTCTCCCCATCTGCGTGTTGATCTACAGCCGAAGAATCTTTTCATAG			ATGGAGATTGTGTATCTCATTTTTCTCTCCACTTGTCATTCCTACGTTCTCCCCATCTGCGTGTTGATCTACAGCCGAAGAATCTTTTCATAG	MEIVYLIFLSTCHSYVLPICVLIYSRRIFS*			MEIVYLIFLSTCHSYVLPICVLIYSRRIFS*	CCCCTTCCCC	ATTGAGCCAG	0	R	0	0	0	0	0
6165	3033	af	AN8280.1	53.m03681	AO070310000020	0			-64	-35			ATGTCTTCTGAATGCTTTTGTACCTTCTAA		ATGTCTTCTGAATGCTTTTGTACCTTCTAA		MSSECFCTF*		MSSECFCTF*		GAAACAACTT	CTCAAATGGA	0	I	0	0	NCU01654.1	0	0
6166	3033	ao	AN8280.1	53.m03681	AO070310000020	0					-110	-84	ATGATAAGATTTCGCCCTCGACGTTGA			ATGATAAGATTTCGCCCTCGACGTTGA	MIRFRPRR*			MIRFRPRR*	GAGTATTGGT	GACATTTATA	0	I	0	0	NCU01654.1	0	0
6168	3034	af	AN8275.1	53.m03685	AO070310000026	0			-282	-247			ATGCTCCATGTTCCCTTGGGTTGGGGGTTACCGTAA		ATGCTCCATGTTCCCTTGGGTTGGGGGTTACCGTAA		MLHVPLGWGLP*		MLHVPLGWGLP*		GTCCGGCTCC	TGTACGGAAT	0	C	0	0	0	0	0
6169	3034	af	AN8275.1	53.m03685	AO070310000026	0			-247	-107			ATGTACGGAATGCACACCATTGCCCATCATTGCCTGGCTTCCCTGCCGGGAGTTACGGTCACAATCATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		ATGTACGGAATGCACACCATTGCCCATCATTGCCTGGCTTCCCTGCCGGGAGTTACGGTCACAATCATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		MYGMHTIAHHCLASLPGVTVTIMYRLYQYGQMEKRAAKEQLPQLNF*		MYGMHTIAHHCLASLPGVTVTIMYRLYQYGQMEKRAAKEQLPQLNF*		GGTTACCGTA	ACACCTCCCT	0	C	0	0	0	0	0
6170	3034	af	AN8275.1	53.m03685	AO070310000026	0			-238	-107			ATGCACACCATTGCCCATCATTGCCTGGCTTCCCTGCCGGGAGTTACGGTCACAATCATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		ATGCACACCATTGCCCATCATTGCCTGGCTTCCCTGCCGGGAGTTACGGTCACAATCATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		MHTIAHHCLASLPGVTVTIMYRLYQYGQMEKRAAKEQLPQLNF*		MHTIAHHCLASLPGVTVTIMYRLYQYGQMEKRAAKEQLPQLNF*		AATGTACGGA	ACACCTCCCT	0	C	0	0	0	0	0
6171	3034	af	AN8275.1	53.m03685	AO070310000026	0			-181	-107			ATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		ATGTACCGGCTGTATCAATACGGTCAGATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		MYRLYQYGQMEKRAAKEQLPQLNF*		MYRLYQYGQMEKRAAKEQLPQLNF*		GGTCACAATC	ACACCTCCCT	0	C	0	0	0	0	0
6172	3034	af	AN8275.1	53.m03685	AO070310000026	0			-154	-107			ATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		ATGGAAAAAAGGGCCGCAAAAGAGCAGCTCCCTCAACTCAACTTTTGA		MEKRAAKEQLPQLNF*		MEKRAAKEQLPQLNF*		ATACGGTCAG	ACACCTCCCT	0	C	0	0	0	0	0
6167	3034	an	AN8275.1	53.m03685	AO070310000026	0	-157	-107					ATGGAAAAAAGATGGGACCGAAAACAGCTTTCACGTTCTCCCGAAACCTGA	ATGGAAAAAAGATGGGACCGAAAACAGCTTTCACGTTCTCCCGAAACCTGA			MEKRWDRKQLSRSPET*	MEKRWDRKQLSRSPET*			TTACGGCCAG	ACTTCTTCTC	0	C	0	0	0	0	0
6173	3034	ao	AN8275.1	53.m03685	AO070310000026	0					-164	-18	ATGTACCGGCTGTACCGTTACGGTCATATGGAAAAAAAAAAAAGAGCTTCTCCCGAGACCTCAGCATCTTTTCTTCTTTTCTCTCTGTCACTATCTCGATATACCCAGACCCTCTCCATTCTTCAATTATACTCAGCCGCTCAATAA			ATGTACCGGCTGTACCGTTACGGTCATATGGAAAAAAAAAAAAGAGCTTCTCCCGAGACCTCAGCATCTTTTCTTCTTTTCTCTCTGTCACTATCTCGATATACCCAGACCCTCTCCATTCTTCAATTATACTCAGCCGCTCAATAA	MYRLYRYGHMEKKKRASPETSASFLLFSLSLSRYTQTLSILQLYSAAQ*			MYRLYRYGHMEKKKRASPETSASFLLFSLSLSRYTQTLSILQLYSAAQ*	TGTACCGCCC	AGGTTGTTTG	0	C	0	0	0	0	0
6174	3034	ao	AN8275.1	53.m03685	AO070310000026	0					-137	-18	ATGGAAAAAAAAAAAAAGAGCTTCTCCCGAGACCTCAGCATCTTTTCTTCTTTTCTCTCTGTCACTATCTCGATATACCCAGACCCTCTCCATTCTTCAATTATACTCAGCCGCTCAATAA			ATGGAAAAAAAAAAAAAGAGCTTCTCCCGAGACCTCAGCATCTTTTCTTCTTTTCTCTCTGTCACTATCTCGATATACCCAGACCCTCTCCATTCTTCAATTATACTCAGCCGCTCAATAA	MEKKKRASPETSASFLLFSLSLSRYTQTLSILQLYSAAQ*			MEKKKRASPETSASFLLFSLSLSRYTQTLSILQLYSAAQ*	TTACGGTCAT	AGGTTGTTTG	0	C	0	0	0	0	0
6176	3035	af	AN8273.1	53.m03687	AO070310000028	0			-223	-149			ATGGAAAAGCCGGTTCCGCCCGCACTCGTCATTTCGACCAATCAGCAAACGAGTAATCAAGACGCCGGCATCTGA		ATGGAAAAGCCGGTTCCGCCCGCACTCGTCATTTCGACCAATCAGCAAACGAGTAATCAAGACGCCGGCATCTGA		MEKPVPPALVISTNQQTSNQDAGI*		MEKPVPPALVISTNQQTSNQDAGI*		ACAGAGGGCG	AGCTTTTCAG	0	C	0	MG03226.1	0	0	0
6175	3035	an	AN8273.1	53.m03687	AO070310000028	0	-183	-148					ATGAAGCGAGTAATCACAACGCCGGCATCAACTTGA	ATGAAGCGAGTAATCACAACGCCGGCATCAACTTGA			MKRVITTPAST*	MKRVITTPAST*			TTGACCAATC	AGCTTTTCAG	0	C	0	MG03226.1	0	0	0
6177	3035	ao	AN8273.1	53.m03687	AO070310000028	0					-283	-233	ATGCTTTTGCCGGGGCTCACGTGCAGCCATGCATCATGTGACATCAGCTGA			ATGCTTTTGCCGGGGCTCACGTGCAGCCATGCATCATGTGACATCAGCTGA	MLLPGLTCSHASCDIS*			MLLPGLTCSHASCDIS*	TCTTATCGCA	CACGGAGGAG	0	C	0	MG03226.1	0	0	0
6178	3038	af	AN8204.1	53.m03770	AO070310000113	0			-214	-119			ATGCACATCCTCGGCCAGAATCGGATGACTAATCCTCTCTTAACAATCTGTGAGGGACAGCTTAGAAAGCGTGGTGCTAGTGTGATGATACCTTAA		ATGCACATCCTCGGCCAGAATCGGATGACTAATCCTCTCTTAACAATCTGTGAGGGACAGCTTAGAAAGCGTGGTGCTAGTGTGATGATACCTTAA		MHILGQNRMTNPLLTICEGQLRKRGASVMIP*		MHILGQNRMTNPLLTICEGQLRKRGASVMIP*		CGGCAGGGCC	TTGGGTTGCC	0	L	FG05580.1	MG04697.1	0	0	0
6179	3038	af	AN8204.1	53.m03770	AO070310000113	0			-190	-119			ATGACTAATCCTCTCTTAACAATCTGTGAGGGACAGCTTAGAAAGCGTGGTGCTAGTGTGATGATACCTTAA		ATGACTAATCCTCTCTTAACAATCTGTGAGGGACAGCTTAGAAAGCGTGGTGCTAGTGTGATGATACCTTAA		MTNPLLTICEGQLRKRGASVMIP*		MTNPLLTICEGQLRKRGASVMIP*		CCAGAATCGG	TTGGGTTGCC	0	L	FG05580.1	MG04697.1	0	0	0
6180	3038	af	AN8204.1	53.m03770	AO070310000113	0			-130	-119			ATGATACCTTAA		ATGATACCTTAA		MIP*		MIP*		TGCTAGTGTG	TTGGGTTGCC	0	L	FG05580.1	MG04697.1	0	0	0
6181	3038	ao	AN8204.1	53.m03770	AO070310000113	0					-220	-173	ATGCATGCGGTGATAGTATCCGGAATACGTCATTTGCCGGCGTGTTGA			ATGCATGCGGTGATAGTATCCGGAATACGTCATTTGCCGGCGTGTTGA	MHAVIVSGIRHLPAC*			MHAVIVSGIRHLPAC*	GATCTCTGAA	TCCTCGGATA	0	L	FG05580.1	MG04697.1	0	0	0
6182	3038	ao	AN8204.1	53.m03770	AO070310000113	0					-158	-144	ATGAGAAGCAGCTGA			ATGAGAAGCAGCTGA	MRSS*			MRSS*	CGGATAAGTT	TTAATCACTG	0	L	FG05580.1	MG04697.1	0	0	0
6184	3039	af	AN8180.1	53.m03800	AO070310000147	0			-179	-45			ATGCAGGGCTCTACTCCATACCCAGTAGGAAATTCTTATGCAGGACAGCTATTACGGCAATCCACACGAGCCACTGACGCACTTCCGCCTGTTCGCCGCCAAACGAAAAGCAACCATCACCATCCAAAAGTTTGA		ATGCAGGGCTCTACTCCATACCCAGTAGGAAATTCTTATGCAGGACAGCTATTACGGCAATCCACACGAGCCACTGACGCACTTCCGCCTGTTCGCCGCCAAACGAAAAGCAACCATCACCATCCAAAAGTTTGA		MQGSTPYPVGNSYAGQLLRQSTRATDALPPVRRQTKSNHHHPKV*		MQGSTPYPVGNSYAGQLLRQSTRATDALPPVRRQTKSNHHHPKV*		CTCCTTGATT	CCATCAACGT	0	AB	0	0	0	0	0
6183	3039	an	AN8180.1	53.m03800	AO070310000147	0	-144	-115					ATGTTATCTAATCGTAGGGTGCGCGGGTGA	ATGTTATCTAATCGTAGGGTGCGCGGGTGA			MLSNRRVRG*	MLSNRRVRG*			TCCCGTCAGG	GACCATTCGC	0	AB	0	0	0	0	0
6185	3039	ao	AN8180.1	53.m03800	AO070310000147	0					-233	-216	ATGTTTGTTGATATTTAG			ATGTTTGTTGATATTTAG	MFVDI*			MFVDI*	CAGTGGTGAT	TGATAAACTA	0	AB	0	0	0	0	0
6186	3039	ao	AN8180.1	53.m03800	AO070310000147	0					-206	-171	ATGAAAACGGACGTCTTCCCAATCGGGAAACAATGA			ATGAAAACGGACGTCTTCCCAATCGGGAAACAATGA	MKTDVFPIGKQ*			MKTDVFPIGKQ*	GTGATAAACT	CGACGAGACG	0	AB	0	0	0	0	0
6187	3040	af	AN4717.1	71.m15705	AO070311000004	0			-201	-190			ATGAAGGATTGA		ATGAAGGATTGA		MKD*		MKD*		CTTACCTCCC	TCAAGGCTTG	0	T	0	0	0	0	0
6188	3040	af	AN4717.1	71.m15705	AO070311000004	0			-145	-107			ATGACCGATCTTCCAATTTCTGCCTGCTTTGGCCAGTAG		ATGACCGATCTTCCAATTTCTGCCTGCTTTGGCCAGTAG		MTDLPISACFGQ*		MTDLPISACFGQ*		AGGCAGTTTA	CCTTCGAAAT	0	T	0	0	0	0	0
6189	3040	ao	AN4717.1	71.m15705	AO070311000004	0					-158	-129	ATGGAATATTACGTTTACATCGCATTCTAG			ATGGAATATTACGTTTACATCGCATTCTAG	MEYYVYIAF*			MEYYVYIAF*	TACATACTCA	TCTTAATTTT	0	T	0	0	0	0	0
6191	3041	af	AN4716.1	71.m15704	AO070311000005	0			-183	-166			ATGCCTGGCCGACACTGA		ATGCCTGGCCGACACTGA		MPGRH*		MPGRH*		AGGCGCAGAT	ATTGAGTTGA	0		0	0	0	YJR075W	0
6190	3041	an	AN4716.1	71.m15704	AO070311000005	0	-180	-151					ATGAACGGCTGTCAGGGGGTCTCTCAGTGA	ATGAACGGCTGTCAGGGGGTCTCTCAGTGA			MNGCQGVSQ*	MNGCQGVSQ*			ACGAGCAGAC	AGGCAACACT	0		0	0	0	YJR075W	0
6192	3041	ao	AN4716.1	71.m15704	AO070311000005	0					-220	-197	ATGCGCGATTTCAATGACCATTGA			ATGCGCGATTTCAATGACCATTGA	MRDFNDH*			MRDFNDH*	AAGTGCAGAT	GTGGGATGCA	0		0	0	0	YJR075W	0
6193	3041	ao	AN4716.1	71.m15704	AO070311000005	0					-207	-181	ATGACCATTGAGTGGGATGCAAATTGA			ATGACCATTGAGTGGGATGCAAATTGA	MTIEWDAN*			MTIEWDAN*	CGCGATTTCA	GATCTATACC	0		0	0	0	YJR075W	0
6194	3041	ao	AN4716.1	71.m15704	AO070311000005	0					-191	-123	ATGCAAATTGAGATCTATACCGAATCCCACTGGTTGTCGCCGCATCTCAAAGTCGCTGTCATTCACTGA			ATGCAAATTGAGATCTATACCGAATCCCACTGGTTGTCGCCGCATCTCAAAGTCGCTGTCATTCACTGA	MQIEIYTESHWLSPHLKVAVIH*			MQIEIYTESHWLSPHLKVAVIH*	ATTGAGTGGG	TCGTCGGCGG	0		0	0	0	YJR075W	0
6197	3042	af	AN3824.1	57.m05656	AO070311000023	0			-248	-219			ATGATTGAACTTGATGCACGAAGTAGATAA		ATGATTGAACTTGATGCACGAAGTAGATAA		MIELDARSR*		MIELDARSR*		CAGACGTGGA	CGGCTTATGC	0	J	FG01104.1	MG04425.1	0	0	0
6198	3042	af	AN3824.1	57.m05656	AO070311000023	0			-235	-206			ATGCACGAAGTAGATAACGGCTTATGCTGA		ATGCACGAAGTAGATAACGGCTTATGCTGA		MHEVDNGLC*		MHEVDNGLC*		ATTGAACTTG	TGATGACTAA	0	J	FG01104.1	MG04425.1	0	0	0
6199	3042	af	AN3824.1	57.m05656	AO070311000023	0			-212	-168			ATGCTGATGATGACTAATTATGATGATGGCGGGGTACCTGGATAG		ATGCTGATGATGACTAATTATGATGATGGCGGGGTACCTGGATAG		MLMMTNYDDGGVPG*		MLMMTNYDDGGVPG*		ATAACGGCTT	AATCACGTGA	0	J	FG01104.1	MG04425.1	0	0	0
6200	3042	af	AN3824.1	57.m05656	AO070311000023	0			-206	-168			ATGATGACTAATTATGATGATGGCGGGGTACCTGGATAG		ATGATGACTAATTATGATGATGGCGGGGTACCTGGATAG		MMTNYDDGGVPG*		MMTNYDDGGVPG*		GCTTATGCTG	AATCACGTGA	0	J	FG01104.1	MG04425.1	0	0	0
6201	3042	af	AN3824.1	57.m05656	AO070311000023	0			-203	-168			ATGACTAATTATGATGATGGCGGGGTACCTGGATAG		ATGACTAATTATGATGATGGCGGGGTACCTGGATAG		MTNYDDGGVPG*		MTNYDDGGVPG*		TATGCTGATG	AATCACGTGA	0	J	FG01104.1	MG04425.1	0	0	0
6202	3042	af	AN3824.1	57.m05656	AO070311000023	0			-193	-158			ATGATGATGGCGGGGTACCTGGATAGAATCACGTGA		ATGATGATGGCGGGGTACCTGGATAGAATCACGTGA		MMMAGYLDRIT*		MMMAGYLDRIT*		ATGACTAATT	ATGCGTCTAT	0	J	FG01104.1	MG04425.1	0	0	0
6203	3042	af	AN3824.1	57.m05656	AO070311000023	0			-190	-158			ATGATGGCGGGGTACCTGGATAGAATCACGTGA		ATGATGGCGGGGTACCTGGATAGAATCACGTGA		MMAGYLDRIT*		MMAGYLDRIT*		ACTAATTATG	ATGCGTCTAT	0	J	FG01104.1	MG04425.1	0	0	0
6204	3042	af	AN3824.1	57.m05656	AO070311000023	0			-187	-158			ATGGCGGGGTACCTGGATAGAATCACGTGA		ATGGCGGGGTACCTGGATAGAATCACGTGA		MAGYLDRIT*		MAGYLDRIT*		AATTATGATG	ATGCGTCTAT	0	J	FG01104.1	MG04425.1	0	0	0
6205	3042	af	AN3824.1	57.m05656	AO070311000023	0			-157	-32			ATGCGTCTATGGTTTGAACTGTCTCCCGTAAGAGGGCCCGAAAAGAGTCACAATTTAGTTGGAGACACAGTGGTCGACATCCCAGAGTTCTCGTTACAGTCCCCGCCACGCAGTTCTTTATCTTGA		ATGCGTCTATGGTTTGAACTGTCTCCCGTAAGAGGGCCCGAAAAGAGTCACAATTTAGTTGGAGACACAGTGGTCGACATCCCAGAGTTCTCGTTACAGTCCCCGCCACGCAGTTCTTTATCTTGA		MRLWFELSPVRGPEKSHNLVGDTVVDIPEFSLQSPPRSSLS*		MRLWFELSPVRGPEKSHNLVGDTVVDIPEFSLQSPPRSSLS*		AATCACGTGA	CCTCTGTTAT	0	J	FG01104.1	MG04425.1	0	0	0
6195	3042	an	AN3824.1	57.m05656	AO070311000023	0	-229	-161					ATGTCTCACAAGTGGAAAGTAAAGAAACAGCAAGAGACAGGTAATATTAGCGGGGTAGTCACGGGATGA	ATGTCTCACAAGTGGAAAGTAAAGAAACAGCAAGAGACAGGTAATATTAGCGGGGTAGTCACGGGATGA			MSHKWKVKKQQETGNISGVVTG*	MSHKWKVKKQQETGNISGVVTG*			ATTGTTTGAG	CGCACTTGGC	0	J	FG01104.1	MG04425.1	0	0	0
6196	3042	an	AN3824.1	57.m05656	AO070311000023	0	-164	-72					ATGACGCACTTGGCACGGCTGCCCCGCCGTAATTTTGAGGGCCGAAAAAGAGGTGGGCGGGATGCTTTGAGTCAATCGTACATCAAGCCCTAG	ATGACGCACTTGGCACGGCTGCCCCGCCGTAATTTTGAGGGCCGAAAAAGAGGTGGGCGGGATGCTTTGAGTCAATCGTACATCAAGCCCTAG			MTHLARLPRRNFEGRKRGGRDALSQSYIKP*	MTHLARLPRRNFEGRKRGGRDALSQSYIKP*			TAGTCACGGG	TCAACTCTCT	0	J	FG01104.1	MG04425.1	0	0	0

6206	3042	ao	AN3824.1	57.m05656	AO070311000023	0					-169	-80	ATGGCGTCTATGGTCCGCGTCACTTACCGTAACCACACAAGAGCCGCCAAAGAGTCACAATTCGGAAAGTGGGCAGTATCTGTTGCATAA			ATGGCGTCTATGGTCCGCGTCACTTACCGTAACCACACAAGAGCCGCCAAAGAGTCACAATTCGGAAAGTGGGCAGTATCTGTTGCATAA	MASMVRVTYRNHTRAAKESQFGKWAVSVA*			MASMVRVTYRNHTRAAKESQFGKWAVSVA*	AAGTCACGGG	TTCGAGTCCT	0	J	FG01104.1	MG04425.1	0	0	0
6207	3042	ao	AN3824.1	57.m05656	AO070311000023	0					-160	-80	ATGGTCCGCGTCACTTACCGTAACCACACAAGAGCCGCCAAAGAGTCACAATTCGGAAAGTGGGCAGTATCTGTTGCATAA			ATGGTCCGCGTCACTTACCGTAACCACACAAGAGCCGCCAAAGAGTCACAATTCGGAAAGTGGGCAGTATCTGTTGCATAA	MVRVTYRNHTRAAKESQFGKWAVSVA*			MVRVTYRNHTRAAKESQFGKWAVSVA*	GATGGCGTCT	TTCGAGTCCT	0	J	FG01104.1	MG04425.1	0	0	0
6210	3045	af	AN4508.1	57.m05622	AO070311000061	0			-122	-102			ATGCCGCACGGAGGTAGCTGA		ATGCCGCACGGAGGTAGCTGA		MPHGGS*		MPHGGS*		CCCGTAGTGG	TATCACCGGC	0	T	FG09422.1	0	0	0	0
6208	3045	an	AN4508.1	57.m05622	AO070311000061	0	-190	-77					ATGGTTATGGCCGAGCTTAGTCAGAAGCCATGTGACAGATGGTTGCGCTTCTCGAACGTTCGGGTCGCCGTAGTAAGCAAAGTGATATCACTGGCTGTATTCTGTATCCTATAA	ATGGTTATGGCCGAGCTTAGTCAGAAGCCATGTGACAGATGGTTGCGCTTCTCGAACGTTCGGGTCGCCGTAGTAAGCAAAGTGATATCACTGGCTGTATTCTGTATCCTATAA			MVMAELSQKPCDRWLRFSNVRVAVVSKVISLAVFCIL*	MVMAELSQKPCDRWLRFSNVRVAVVSKVISLAVFCIL*			GGAGTTAGTG	ATACCCGAGC	0	T	FG09422.1	0	0	0	0
6209	3045	an	AN4508.1	57.m05622	AO070311000061	0	-184	-77					ATGGCCGAGCTTAGTCAGAAGCCATGTGACAGATGGTTGCGCTTCTCGAACGTTCGGGTCGCCGTAGTAAGCAAAGTGATATCACTGGCTGTATTCTGTATCCTATAA	ATGGCCGAGCTTAGTCAGAAGCCATGTGACAGATGGTTGCGCTTCTCGAACGTTCGGGTCGCCGTAGTAAGCAAAGTGATATCACTGGCTGTATTCTGTATCCTATAA			MAELSQKPCDRWLRFSNVRVAVVSKVISLAVFCIL*	MAELSQKPCDRWLRFSNVRVAVVSKVISLAVFCIL*			AGTGATGGTT	ATACCCGAGC	0	T	FG09422.1	0	0	0	0
6211	3045	ao	AN4508.1	57.m05622	AO070311000061	0					-258	-235	ATGACATCGGAGAAAGGAAACTAG			ATGACATCGGAGAAAGGAAACTAG	MTSEKGN*			MTSEKGN*	CTCCCCCACT	TTATCGCCGA	0	T	FG09422.1	0	0	0	0
6212	3045	ao	AN4508.1	57.m05622	AO070311000061	0					-193	-59	ATGGCGATTGCACTTCTCGAACTTTCGGGTAGCCGTAGCGCCAGAGAGCGGAGCAAACATGCAGAGGTTCGGGAGCGAACACTCCTAATCCGGAAAAGGGCGGAAAGACTGATATCACCGGCCCGCGGCTTTTAA			ATGGCGATTGCACTTCTCGAACTTTCGGGTAGCCGTAGCGCCAGAGAGCGGAGCAAACATGCAGAGGTTCGGGAGCGAACACTCCTAATCCGGAAAAGGGCGGAAAGACTGATATCACCGGCCCGCGGCTTTTAA	MAIALLELSGSRSARERSKHAEVRERTLLIRKRAERLISPARGF*			MAIALLELSGSRSARERSKHAEVRERTLLIRKRAERLISPARGF*	GTCACACGTG	ATAGCTGCTC	0	T	FG09422.1	0	0	0	0
6213	3045	ao	AN4508.1	57.m05622	AO070311000061	0					-135	-106	ATGCAGAGGTTCGGGAGCGAACACTCCTAA			ATGCAGAGGTTCGGGAGCGAACACTCCTAA	MQRFGSEHS*			MQRFGSEHS*	CGGAGCAAAC	TCCGGAAAAG	0	T	FG09422.1	0	0	0	0
6214	3046	an	AN4513.1	57.m05616	AO070311000069	0	-180	-154					ATGGGGTCCTCGGGAGAGGCCCACTAG	ATGGGGTCCTCGGGAGAGGCCCACTAG			MGSSGEAH*	MGSSGEAH*			GGGGTAAGTT	TGTCAACAAT	0	Z	0	0	0	0	0
6215	3046	ao	AN4513.1	57.m05616	AO070311000069	0					-180	-70	ATGAGCTCGTTCTCCAATTCTTATCTCTTCGTCGCCTCATCGTTGTTTCGACACGCCGCCGGTGTAGGGCGTCGCTGGATATTTCGACAACTGCCCTCCCCGCGCCGATAA			ATGAGCTCGTTCTCCAATTCTTATCTCTTCGTCGCCTCATCGTTGTTTCGACACGCCGCCGGTGTAGGGCGTCGCTGGATATTTCGACAACTGCCCTCCCCGCGCCGATAA	MSSFSNSYLFVASSLFRHAAGVGRRWIFRQLPSPRR*			MSSFSNSYLFVASSLFRHAAGVGRRWIFRQLPSPRR*	TTCTTCGTCG	ATCTCGACTT	0	Z	0	0	0	0	0
6218	3047	af	AN0116.1	71.m15395	AO070311000103	0			-180	-124			ATGATTCCTTTTCCATCGTCTTTTTGTGGCCGGTCGGAAGATGACCCAGAGCGGTAA		ATGATTCCTTTTCCATCGTCTTTTTGTGGCCGGTCGGAAGATGACCCAGAGCGGTAA		MIPFPSSFCGRSEDDPER*		MIPFPSSFCGRSEDDPER*		CCATTCAAGA	GAAACTCCGG	0	J	FG06204.1	MG06071.1	0	0	0
6219	3047	af	AN0116.1	71.m15395	AO070311000103	0			-140	-69			ATGACCCAGAGCGGTAAGAAACTCCGGCCCTGGGGCTTACCTGAATCCGAACAAAACTCGGGCCGCAAATAG		ATGACCCAGAGCGGTAAGAAACTCCGGCCCTGGGGCTTACCTGAATCCGAACAAAACTCGGGCCGCAAATAG		MTQSGKKLRPWGLPESEQNSGRK*		MTQSGKKLRPWGLPESEQNSGRK*		CGGTCGGAAG	TTGGCAGATC	0	J	FG06204.1	MG06071.1	0	0	0
6216	3047	an	AN0116.1	71.m15395	AO070311000103	0	-201	-154					ATGACGTCCAGCATTTTGCGCTCAGCGCCGGACGTGCCCGTCCACTGA	ATGACGTCCAGCATTTTGCGCTCAGCGCCGGACGTGCCCGTCCACTGA			MTSSILRSAPDVPVH*	MTSSILRSAPDVPVH*			ACGGTTTGTT	GGGCTGACTT	0	J	FG06204.1	MG06071.1	0	0	0
6217	3047	an	AN0116.1	71.m15395	AO070311000103	0	-124	-59					ATGCCGATTCCGGCCGCCCGTCCATCTCGAAAATCTTGGCCGCAGGAAGGGCAACAGATCAGTTGA	ATGCCGATTCCGGCCGCCCGTCCATCTCGAAAATCTTGGCCGCAGGAAGGGCAACAGATCAGTTGA			MPIPAARPSRKSWPQEGQQIS*	MPIPAARPSRKSWPQEGQQIS*			AAGGATAGAA	CATTGACGAA	0	J	FG06204.1	MG06071.1	0	0	0
6220	3047	ao	AN0116.1	71.m15395	AO070311000103	0					-219	-178	ATGACGTTCAGCATTTCATTTCGTTTCTTCGCTTGCGGTTAA			ATGACGTTCAGCATTTCATTTCGTTTCTTCGCTTGCGGTTAA	MTFSISFRFFACG*			MTFSISFRFFACG*	CAATGTTTTA	TACGGTAAGT	0	J	FG06204.1	MG06071.1	0	0	0
6224	3048	af	AN1014.1	70.m15232	AO070312000004	0			-249	-94			ATGCCAGTGCTTCCATCCATCCATCCACCATCCACCATCTTATCACTCTATCCATCTGCTCTTCCCCCTCCTCCTTCCGCTATCTCCATATCACCATTCTCCGGAGTCCAATGCAGTAGTAGTATAGATATGTTCGCCTTCGCCGACCCTGGATAG		ATGCCAGTGCTTCCATCCATCCATCCACCATCCACCATCTTATCACTCTATCCATCTGCTCTTCCCCCTCCTCCTTCCGCTATCTCCATATCACCATTCTCCGGAGTCCAATGCAGTAGTAGTATAGATATGTTCGCCTTCGCCGACCCTGGATAG		MPVLPSIHPPSTILSLYPSALPPPPSAISISPFSGVQCSSSIDMFAFADPG*		MPVLPSIHPPSTILSLYPSALPPPPSAISISPFSGVQCSSSIDMFAFADPG*		GGAAGTTCAC	TCCCTAAAGC	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6222	3048	an	AN1014.1	70.m15232	AO070312000004	0	-155	-51					ATGCATGGGGCACTTCAGCTATCTCACCATTCTTCAAGCAACATCCAACAATATCATCACTTTCCTCAAAGAAGTATCGCCGCTGGTCATGTTGCCTTACGTTGA	ATGCATGGGGCACTTCAGCTATCTCACCATTCTTCAAGCAACATCCAACAATATCATCACTTTCCTCAAAGAAGTATCGCCGCTGGTCATGTTGCCTTACGTTGA			MHGALQLSHHSSSNIQQYHHFPQRSIAAGHVALR*	MHGALQLSHHSSSNIQQYHHFPQRSIAAGHVALR*			TCGCGTTCAC	TTCCGGATAA	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6223	3048	an	AN1014.1	70.m15232	AO070312000004	0	-151	-41					ATGGGGCACTTCAGCTATCTCACCATTCTTCAAGCAACATCCAACAATATCATCACTTTCCTCAAAGAAGTATCGCCGCTGGTCATGTTGCCTTACGTTGATTCCGGATAA	ATGGGGCACTTCAGCTATCTCACCATTCTTCAAGCAACATCCAACAATATCATCACTTTCCTCAAAGAAGTATCGCCGCTGGTCATGTTGCCTTACGTTGATTCCGGATAA			MGHFSYLTILQATSNNIITFLKEVSPLVMLPYVDSG*	MGHFSYLTILQATSNNIITFLKEVSPLVMLPYVDSG*			GTTCACATGC	AGTCATTTTT	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6225	3048	ao	AN1014.1	70.m15232	AO070312000004	0					-220	-47	ATGATCCGTTCACATGTCATTCCCCGGGTTCTTCTCATCCATCATCCCTCTGATTCTCTCTCCTCCTCCACCTTCTTTTCCCTCCCGAAAGAACAAGGTGGCACTATACTTCCTCCCCCGGCAACTAAATTAATCCGCTTCATGGCCATGTTATCCCAAGTTGACTCTGGCTGA			ATGATCCGTTCACATGTCATTCCCCGGGTTCTTCTCATCCATCATCCCTCTGATTCTCTCTCCTCCTCCACCTTCTTTTCCCTCCCGAAAGAACAAGGTGGCACTATACTTCCTCCCCCGGCAACTAAATTAATCCGCTTCATGGCCATGTTATCCCAAGTTGACTCTGGCTGA	MIRSHVIPRVLLIHHPSDSLSSSTFFSLPKEQGGTILPPPATKLIRFMAMLSQVDSG*			MIRSHVIPRVLLIHHPSDSLSSSTFFSLPKEQGGTILPPPATKLIRFMAMLSQVDSG*	AAGTCGGGGG	AATTAATTCT	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6226	3048	ao	AN1014.1	70.m15232	AO070312000004	0					-207	-88	ATGTCATTCCCCGGGTTCTTCTCATCCATCATCCCTCTGATTCTCTCTCCTCCTCCACCTTCTTTTCCCTCCCGAAAGAACAAGGTGGCACTATACTTCCTCCCCCGGCAACTAAATTAA			ATGTCATTCCCCGGGTTCTTCTCATCCATCATCCCTCTGATTCTCTCTCCTCCTCCACCTTCTTTTCCCTCCCGAAAGAACAAGGTGGCACTATACTTCCTCCCCCGGCAACTAAATTAA	MSFPGFFSSIIPLILSPPPPSFPSRKNKVALYFLPRQLN*			MSFPGFFSSIIPLILSPPPPSFPSRKNKVALYFLPRQLN*	ATCCGTTCAC	TCCGCTTCAT	0	I	0	0	NCU01751.1	YKL188C	YKL188C
6228	3049	af	AN1012.1	70.m15229	AO070312000018	0			-185	-72			ATGGTTTACGCTCTACTTTCATCTAACCTCGGCAAACCACCAGGTGTCCTGGCCTGGTCAATACTCCGCAGTAACAAATACCGGCCTCAGGCCCAGCAAGCTGATACGGAGTGA		ATGGTTTACGCTCTACTTTCATCTAACCTCGGCAAACCACCAGGTGTCCTGGCCTGGTCAATACTCCGCAGTAACAAATACCGGCCTCAGGCCCAGCAAGCTGATACGGAGTGA		MVYALLSSNLGKPPGVLAWSILRSNKYRPQAQQADTE*		MVYALLSSNLGKPPGVLAWSILRSNKYRPQAQQADTE*		ATTGATGTAG	CTTGGTTGAC	0	R	0	0	0	0	0
6229	3050	af	AN1003.1	70.m15221	AO070312000031	0			-252	-217			ATGGGGCCAGTCGGACCGGCCACTGTGCGTACTTGA		ATGGGGCCAGTCGGACCGGCCACTGTGCGTACTTGA		MGPVGPATVRT*		MGPVGPATVRT*		GGCTTCCCGA	TACCTCAGGT	0	E	0	0	0	0	0
6230	3050	ao	AN1003.1	70.m15221	AO070312000031	0					-180	-19	ATGCCATGCCGGTCGGTCGGCAGCGGCGGTGCCGAGAGAGGTCAAGATTGGCCTGAGGAACCTTCTCTCACTTCCCGCACAAGCAACCCGCCGCCTTTCTTCTTTCTCTCCTTCCCATCCTCCACATACTCTCCTCTCCAGCCCTGTGTTGTTCGTCGCTGA			ATGCCATGCCGGTCGGTCGGCAGCGGCGGTGCCGAGAGAGGTCAAGATTGGCCTGAGGAACCTTCTCTCACTTCCCGCACAAGCAACCCGCCGCCTTTCTTCTTTCTCTCCTTCCCATCCTCCACATACTCTCCTCTCCAGCCCTGTGTTGTTCGTCGCTGA	MPCRSVGSGGAERGQDWPEEPSLTSRTSNPPPFFFLSFPSSTYSPLPQPCVVRR*			MPCRSVGSGGAERGQDWPEEPSLTSRTSNPPPFFFLSFPSSTYSPLPQPCVVRR*	CACGGAATCC	CCCCGGGGAT	0	E	0	0	0	0	0
6231	3050	ao	AN1003.1	70.m15221	AO070312000031	0					-175	-125	ATGCCGGTCGGTCGGCAGCGGCGGTGCCGAGAGAGGTCAAGATTGGCCTGA			ATGCCGGTCGGTCGGCAGCGGCGGTGCCGAGAGAGGTCAAGATTGGCCTGA	MPVGRQRRCRERSRLA*			MPVGRQRRCRERSRLA*	AATCCATGCC	GGAACCTTCT	0	E	0	0	0	0	0
6239	3054	af	AN6906.1	71.m15231	AO070314000008	0			-248	-159			ATGGTTATATCATGGTCTAAGCATGCAGAGATACTAGCACGCAGAGTAGGATTGCTTGAAAACGAACTGATCCAAAATGCTGTGCAGTGA		ATGGTTATATCATGGTCTAAGCATGCAGAGATACTAGCACGCAGAGTAGGATTGCTTGAAAACGAACTGATCCAAAATGCTGTGCAGTGA		MVISWSKHAEILARRVGLLENELIQNAVQ*		MVISWSKHAEILARRVGLLENELIQNAVQ*		TAAAGCATAG	CTGAGTCGCA	0	R	0	0	0	YLL036C	0
6240	3054	af	AN6906.1	71.m15231	AO070314000008	0			-226	-212			ATGCAGAGATACTAG		ATGCAGAGATACTAG		MQRY*		MQRY*		TGGTCTAAGC	CACGCAGAGT	0	R	0	0	0	YLL036C	0
6241	3054	af	AN6906.1	71.m15231	AO070314000008	0			-172	-155			ATGCTGTGCAGTGACTGA		ATGCTGTGCAGTGACTGA		MLCSD*		MLCSD*		CTGATCCAAA	GTCGCATGAG	0	R	0	0	0	YLL036C	0
6242	3054	af	AN6906.1	71.m15231	AO070314000008	0			-149	-21			ATGAGTGCCAAGAATGGACGATCAGCCAACTTTGCGGTGCGGCTAAACCAGATAGGGCGGAAGGGTTATCTCGTCGAAAAGTCCAATGCGGCGACAGCTCTCGCGTCAAGCAACCTCTCTCTAGACTAA		ATGAGTGCCAAGAATGGACGATCAGCCAACTTTGCGGTGCGGCTAAACCAGATAGGGCGGAAGGGTTATCTCGTCGAAAAGTCCAATGCGGCGACAGCTCTCGCGTCAAGCAACCTCTCTCTAGACTAA		MSAKNGRSANFAVRLNQIGRKGYLVEKSNAATALASSNLSLD*		MSAKNGRSANFAVRLNQIGRKGYLVEKSNAATALASSNLSLD*		ACTGAGTCGC	CCAACTCATC	0	R	0	0	0	YLL036C	0
6243	3054	af	AN6906.1	71.m15231	AO070314000008	0			-136	-104			ATGGACGATCAGCCAACTTTGCGGTGCGGCTAA		ATGGACGATCAGCCAACTTTGCGGTGCGGCTAA		MDDQPTLRCG*		MDDQPTLRCG*		AGTGCCAAGA	ACCAGATAGG	0	R	0	0	0	YLL036C	0
6244	3054	af	AN6906.1	71.m15231	AO070314000008	0			-64	-26			ATGCGGCGACAGCTCTCGCGTCAAGCAACCTCTCTCTAG		ATGCGGCGACAGCTCTCGCGTCAAGCAACCTCTCTCTAG		MRRQLSRQATSL*		MRRQLSRQATSL*		GAAAAGTCCA	ACTAACCAAC	0	R	0	0	0	YLL036C	0
6234	3054	an	AN6906.1	71.m15231	AO070314000008	0	-233	-129					ATGGCAATAGCCTCTAGCTTATGTCAAGCGCACTGTTCCATTGGAGGGACCCTATGGAAAATCCGCAGCGTCATGGGTGACGGGTGGTTGGGCGTTTCGGGATGA	ATGGCAATAGCCTCTAGCTTATGTCAAGCGCACTGTTCCATTGGAGGGACCCTATGGAAAATCCGCAGCGTCATGGGTGACGGGTGGTTGGGCGTTTCGGGATGA			MAIASSLCQAHCSIGGTLWKIRSVMGDGWLGVSG*	MAIASSLCQAHCSIGGTLWKIRSVMGDGWLGVSG*			TTGACTCTAG	CCGCCAAGCA	0	R	0	0	0	YLL036C	0
6235	3054	an	AN6906.1	71.m15231	AO070314000008	0	-213	-154					ATGTCAAGCGCACTGTTCCATTGGAGGGACCCTATGGAAAATCCGCAGCGTCATGGGTGA	ATGTCAAGCGCACTGTTCCATTGGAGGGACCCTATGGAAAATCCGCAGCGTCATGGGTGA			MSSALFHWRDPMENPQRHG*	MSSALFHWRDPMENPQRHG*			CCTCTAGCTT	CGGGTGGTTG	0	R	0	0	0	YLL036C	0
6236	3054	an	AN6906.1	71.m15231	AO070314000008	0	-180	-154					ATGGAAAATCCGCAGCGTCATGGGTGA	ATGGAAAATCCGCAGCGTCATGGGTGA			MENPQRHG*	MENPQRHG*			GAGGGACCCT	CGGGTGGTTG	0	R	0	0	0	YLL036C	0
6237	3054	an	AN6906.1	71.m15231	AO070314000008	0	-161	-129					ATGGGTGACGGGTGGTTGGGCGTTTCGGGATGA	ATGGGTGACGGGTGGTTGGGCGTTTCGGGATGA			MGDGWLGVSG*	MGDGWLGVSG*			CCGCAGCGTC	CCGCCAAGCA	0	R	0	0	0	YLL036C	0
6238	3054	an	AN6906.1	71.m15231	AO070314000008	0	-132	-88					ATGACCGCCAAGCATGAATCACCGATCGGCCAGAGGTGGCACTAG	ATGACCGCCAAGCATGAATCACCGATCGGCCAGAGGTGGCACTAG			MTAKHESPIGQRWH*	MTAKHESPIGQRWH*			GCGTTTCGGG	TCCGAATTCA	0	R	0	0	0	YLL036C	0
6245	3054	ao	AN6906.1	71.m15231	AO070314000008	0					-216	-178	ATGAATAAGTGTACAGGAAAAACGAATACAACGAATTGA			ATGAATAAGTGTACAGGAAAAACGAATACAACGAATTGA	MNKCTGKTNTTN*			MNKCTGKTNTTN*	AGTCGTAAGA	GAAGAAAAGA	0	R	0	0	0	YLL036C	0
6246	3054	ao	AN6906.1	71.m15231	AO070314000008	0					-141	-109	ATGGTTGCTTGCCGCCAAGAGATCTGCGGCTAA			ATGGTTGCTTGCCGCCAAGAGATCTGCGGCTAA	MVACRQEICG*			MVACRQEICG*	TCGTTTGCGC	ACCCAAAAGA	0	R	0	0	0	YLL036C	0
6249	3055	af	AN6904.1	71.m15232	AO070314000010	0			-247	-227			ATGAGGGGAAACGATAGGTAA		ATGAGGGGAAACGATAGGTAA		MRGNDR*		MRGNDR*		AACTGAAGTC	TAATCTAGGT	0	J	FG06703.1	MG08906.1	0	0	0
6250	3055	af	AN6904.1	71.m15232	AO070314000010	0			-94	-41			ATGGTGAACCACCTTGCTTGCGTCTCGAAAAGTCACCGAACTGTTCCTGGATGA		ATGGTGAACCACCTTGCTTGCGTCTCGAAAAGTCACCGAACTGTTCCTGGATGA		MVNHLACVSKSHRTVPG*		MVNHLACVSKSHRTVPG*		ACGCCAGCCA	CTTGTTTAAC	0	J	FG06703.1	MG08906.1	0	0	0
6247	3055	an	AN6904.1	71.m15232	AO070314000010	0	-249	-181					ATGAGAGTTCTAGCAACTGAGATAAGGGGCATATGTGGAGGGAGGGAGTTGATACCTTGTCTTGAGTAG	ATGAGAGTTCTAGCAACTGAGATAAGGGGCATATGTGGAGGGAGGGAGTTGATACCTTGTCTTGAGTAG			MRVLATEIRGICGGRELIPCLE*	MRVLATEIRGICGGRELIPCLE*			GAGAATAAGA	TTGGATTATT	0	J	FG06703.1	MG08906.1	0	0	0
6248	3055	an	AN6904.1	71.m15232	AO070314000010	0	-217	-185					ATGTGGAGGGAGGGAGTTGATACCTTGTCTTGA	ATGTGGAGGGAGGGAGTTGATACCTTGTCTTGA			MWREGVDTLS*	MWREGVDTLS*			TAAGGGGCAT	GTAGTTGGAT	0	J	FG06703.1	MG08906.1	0	0	0
6251	3055	ao	AN6904.1	71.m15232	AO070314000010	0					-246	-220	ATGCGCAATGGGCATAAGCAACGATGA			ATGCGCAATGGGCATAAGCAACGATGA	MRNGHKQR*			MRNGHKQR*	TTCGATTCCC	GCGTTGGAAT	0	J	FG06703.1	MG08906.1	0	0	0
6252	3055	ao	AN6904.1	71.m15232	AO070314000010	0					-239	-90	ATGGGCATAAGCAACGATGAGCGTTGGAATTATTCTGAGACACTACCGCAGGCCTCGTTTGTCGAGTTCGCGTTCCTACGTGACTTGGCAGCTCAATTGCAGTTCTGGAAGCCACTAGGCGCGCTAACCGACATAGCCGCGGACCAATGA			ATGGGCATAAGCAACGATGAGCGTTGGAATTATTCTGAGACACTACCGCAGGCCTCGTTTGTCGAGTTCGCGTTCCTACGTGACTTGGCAGCTCAATTGCAGTTCTGGAAGCCACTAGGCGCGCTAACCGACATAGCCGCGGACCAATGA	MGISNDERWNYSETLPQASFVEFAFLRDLAAQLQFWKPLGALTDIAADQ*			MGISNDERWNYSETLPQASFVEFAFLRDLAAQLQFWKPLGALTDIAADQ*	CCCATGCGCA	CAGCCACGCT	0	J	FG06703.1	MG08906.1	0	0	0

6253	3055	ao	AN6904.1	71.m15232	AO070314000010	0					-223	-122	ATGAGCGTTGGAATTATTCTGAGACACTACCGCAGGCCTCGTTTGTCGAGTTCGCGTTCCTACGTGACTTGGCAGCTCAATTGCAGTTCTGGAAGCCACTAG			ATGAGCGTTGGAATTATTCTGAGACACTACCGCAGGCCTCGTTTGTCGAGTTCGCGTTCCTACGTGACTTGGCAGCTCAATTGCAGTTCTGGAAGCCACTAG	MSVGIILRHYRRPRLSSSRSYVTWQLNCSSGSH*			MSVGIILRHYRRPRLSSSRSYVTWQLNCSSGSH*	ATAAGCAACG	GCGCGCTAAC	0	J	FG06703.1	MG08906.1	0	0	0
6254	3055	ao	AN6904.1	71.m15232	AO070314000010	0					-93	-61	ATGACAGCCACGCTCAGAGGTGCTGAAAAGTGA			ATGACAGCCACGCTCAGAGGTGCTGAAAAGTGA	MTATLRGAEK*			MTATLRGAEK*	CCGCGGACCA	ACTATCTCTC	0	J	FG06703.1	MG08906.1	0	0	0
6256	3056	af	AN6888.1	71.m15251	AO070314000034	0			-157	-101			ATGGACAAGGGAACAAAAAAAAACTATATAAAGGAGGCATGTTCACCAGCTGTTGA		ATGGACAAGGGAACAAAAAAAAACTATATAAAGGAGGCATGTTCACCAGCTGTTGA		MDKGTKKKLYKGGMFTSC*		MDKGTKKKLYKGGMFTSC*		TCCTGGGCCC	CCGAATATCA	0	O	0	0	0	0	0
6257	3056	af	AN6888.1	71.m15251	AO070314000034	0			-118	-101			ATGTTCACCAGCTGTTGA		ATGTTCACCAGCTGTTGA		MFTSC*		MFTSC*		TAAAGGAGGC	CCGAATATCA	0	O	0	0	0	0	0
6255	3056	an	AN6888.1	71.m15251	AO070314000034	0	-213	-190					ATGCTCTCCTTCTGTTCCTCCTAG	ATGCTCTCCTTCTGTTCCTCCTAG			MLSFCSS*	MLSFCSS*			GCAGATTGCG	CTCTTGAGGG	0	O	0	0	0	0	0
6258	3056	ao	AN6888.1	71.m15251	AO070314000034	0					-233	-75	ATGTGGACCGCTTCTCTCCTGAGCCGGAGTCCGTTGATTATCACCACTACCTTCATGATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG			ATGTGGACCGCTTCTCTCCTGAGCCGGAGTCCGTTGATTATCACCACTACCTTCATGATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG	MWTASLLSRSPLIITTTFMMTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*			MWTASLLSRSPLIITTTFMMTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*	AGTGCTGCTG	GCTTGTGCTT	0	O	0	0	0	0	0
6259	3056	ao	AN6888.1	71.m15251	AO070314000034	0					-179	-75	ATGATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG			ATGATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG	MMTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*			MMTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*	CACTACCTTC	GCTTGTGCTT	0	O	0	0	0	0	0
6260	3056	ao	AN6888.1	71.m15251	AO070314000034	0					-176	-75	ATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG			ATGACCACCAGAGTAGACAAAGCTATAAAGGAGCGCCTTCCAGCTGCCCTGAGTAGCTCATCACTCTCCCATCCTCTCCAACAAGAGTCTGAGTTCGTCTAG	MTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*			MTTRVDKAIKERLPAALSSSSLSHPLQQESEFV*	TACCTTCATG	GCTTGTGCTT	0	O	0	0	0	0	0
6262	3057	af	AN6866.1	71.m15266	AO070314000070	0			-117	-64			ATGAAGCTGTCCGACCATCGGCGCCGATTTCTTCCCCTTCTTAGCTCAGAATAG		ATGAAGCTGTCCGACCATCGGCGCCGATTTCTTCCCCTTCTTAGCTCAGAATAG		MKLSDHRRRFLPLLSSE*		MKLSDHRRRFLPLLSSE*		CATAAACTGG	CCCAAGATCC	0	E	FG09602.1	0	NCU07725.1	0	0
6261	3057	an	AN6866.1	71.m15266	AO070314000070	0	-186	-133					ATGAATTGGACTGCTTTTCCTGGTTGGCAAAACACAGAAAGACGGTGTTCCTGA	ATGAATTGGACTGCTTTTCCTGGTTGGCAAAACACAGAAAGACGGTGTTCCTGA			MNWTAFPGWQNTERRCS*	MNWTAFPGWQNTERRCS*			CCTCCATGAT	ATTCGGTCAG	0	E	FG09602.1	0	NCU07725.1	0	0
6263	3059	af	AN6842.1	71.m15299	AO070314000097	0			-204	-124			ATGCCCTATATTGCTTGTGTTATCGAGCCAGGGCAGAGGAAGCAAAAGTTCAATCCGGGGGTTTGCGGTGGTCCGCGCTAG		ATGCCCTATATTGCTTGTGTTATCGAGCCAGGGCAGAGGAAGCAAAAGTTCAATCCGGGGGTTTGCGGTGGTCCGCGCTAG		MPYIACVIEPGQRKQKFNPGVCGGPR*		MPYIACVIEPGQRKQKFNPGVCGGPR*		TTGCAGTTTG	TTGGGTGAGG	0	R	0	0	NCU01473.1	0	0
6264	3059	ao	AN6842.1	71.m15299	AO070314000097	0					-182	-159	ATGGGGTTGCCAAATGGGCGATGA			ATGGGGTTGCCAAATGGGCGATGA	MGLPNGR*			MGLPNGR*	TGATGGGGGA	AGCAAAAGTT	0	R	0	0	NCU01473.1	0	0
6265	3059	ao	AN6842.1	71.m15299	AO070314000097	0					-162	-124	ATGAAGCAAAAGTTCAGACGGGAGGCGCTAACCCGCTGA			ATGAAGCAAAAGTTCAGACGGGAGGCGCTAACCCGCTGA	MKQKFRREALTR*			MKQKFRREALTR*	CAAATGGGCG	GGCTTGGCTC	0	R	0	0	NCU01473.1	0	0
6272	3060	af	AN6841.1	71.m15298	AO070314000098	0			-161	-120			ATGAAGCCGCAAGTGCGAAGAATTTTTAAACGAAGACAGTAA		ATGAAGCCGCAAGTGCGAAGAATTTTTAAACGAAGACAGTAA		MKPQVRRIFKRRQ*		MKPQVRRIFKRRQ*		CAAAAGTAGA	CACGTGACTT	0	O	0	0	0	YMR150C	YMR150C
6266	3060	an	AN6841.1	71.m15298	AO070314000098	0	-271	-212					ATGAAATGTGAAATGCGATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGA	ATGAAATGTGAAATGCGATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGA			MKCEMRCRWSLDSKSLVDR*	MKCEMRCRWSLDSKSLVDR*			TTGTCAGTAA	AGGAAAGAAG	0	O	0	0	0	YMR150C	YMR150C
6267	3060	an	AN6841.1	71.m15298	AO070314000098	0	-259	-212					ATGCGATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGA	ATGCGATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGA			MRCRWSLDSKSLVDR*	MRCRWSLDSKSLVDR*			GAAATGTGAA	AGGAAAGAAG	0	O	0	0	0	YMR150C	YMR150C
6268	3060	an	AN6841.1	71.m15298	AO070314000098	0	-254	-174					ATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGAAGGAAAGAAGAAAATTATCCAATCCGAAGAAAATTTAA	ATGTCGTTGGTCACTCGACTCAAAATCCTTGGTGGACAGATGAAGGAAAGAAGAAAATTATCCAATCCGAAGAAAATTTAA			MSLVTRLKILGGQMKERRKLSNPKKI*	MSLVTRLKILGGQMKERRKLSNPKKI*			GTGAAATGCG	AGCTATGTCA	0	O	0	0	0	YMR150C	YMR150C
6269	3060	an	AN6841.1	71.m15298	AO070314000098	0	-215	-174					ATGAAGGAAAGAAGAAAATTATCCAATCCGAAGAAAATTTAA	ATGAAGGAAAGAAGAAAATTATCCAATCCGAAGAAAATTTAA			MKERRKLSNPKKI*	MKERRKLSNPKKI*			TGGTGGACAG	AGCTATGTCA	0	O	0	0	0	YMR150C	YMR150C
6270	3060	an	AN6841.1	71.m15298	AO070314000098	0	-169	-77					ATGTCAAATCACGTGTTATCTACCTCCGGGCCGGCTCCGCTCCAGAGGTCTGCATACAGCACTAAATCTACATCGGCTCACTCCGACTCATAA	ATGTCAAATCACGTGTTATCTACCTCCGGGCCGGCTCCGCTCCAGAGGTCTGCATACAGCACTAAATCTACATCGGCTCACTCCGACTCATAA			MSNHVLSTSGPAPLQRSAYSTKSTSAHSDS*	MSNHVLSTSGPAPLQRSAYSTKSTSAHSDS*			ATTTAAAGCT	ACAAGCTCTC	0	O	0	0	0	YMR150C	YMR150C
6273	3060	ao	AN6841.1	71.m15298	AO070314000098	0					-192	-64	ATGACAATAAAGAACAGAAGAAAAAAGGAATCGAAAAAAAAAAAGTTCCCGCACTTTTATACCACCTACCCACGTGACCAACCCGAAGCTCCGCCGGAGATGAGCAGCCAAAGCACCCACCATACGTAG			ATGACAATAAAGAACAGAAGAAAAAAGGAATCGAAAAAAAAAAAGTTCCCGCACTTTTATACCACCTACCCACGTGACCAACCCGAAGCTCCGCCGGAGATGAGCAGCCAAAGCACCCACCATACGTAG	MTIKNRRKKESKKKFPHFYTTYPRDQPEAPPEMSSQSTHHT*			MTIKNRRKKESKKKFPHFYTTYPRDQPEAPPEMSSQSTHHT*	GAAGTCCTGC	TAATTGGTAA	0	O	0	0	0	YMR150C	YMR150C
6274	3060	ao	AN6841.1	71.m15298	AO070314000098	0					-93	-64	ATGAGCAGCCAAAGCACCCACCATACGTAG			ATGAGCAGCCAAAGCACCCACCATACGTAG	MSSQSTHHT*			MSSQSTHHT*	TCCGCCGGAG	TAATTGGTAA	0	O	0	0	0	YMR150C	YMR150C
6276	3063	af	AN0051.1	71.m15331	AO070314000138	0			-232	-158			ATGGCTGCTGTCCTTCCAACTCTATTGATCTGCTTAATTTCCTTTTCTTCTCCTTGGTTCATGATCAAGTCGTGA		ATGGCTGCTGTCCTTCCAACTCTATTGATCTGCTTAATTTCCTTTTCTTCTCCTTGGTTCATGATCAAGTCGTGA		MAAVLPTLLICLISFSSPWFMIKS*		MAAVLPTLLICLISFSSPWFMIKS*		CTCCGGAACC	TTTCACGAAG	0	R	FG07303.1	MG06487.1	NCU06416.1	0	0
6277	3063	af	AN0051.1	71.m15331	AO070314000138	0			-172	-158			ATGATCAAGTCGTGA		ATGATCAAGTCGTGA		MIKS*		MIKS*		TCCTTGGTTC	TTTCACGAAG	0	R	FG07303.1	MG06487.1	NCU06416.1	0	0
6278	3063	af	AN0051.1	71.m15331	AO070314000138	0			-92	-81			ATGCCGTTCTAA		ATGCCGTTCTAA		MPF*		MPF*		GAGACGCCTA	CACCTTAGAA	0	R	FG07303.1	MG06487.1	NCU06416.1	0	0
6275	3063	an	AN0051.1	71.m15331	AO070314000138	0	-184	-71					ATGATATATTTGACGGACTTCCCCGCTCCCCGGCCTCCTCCATCCATTTCCTTATCACCTTTTCGTTTTTCTGCAGCTTTTACCCCAGGTCTTTTACTCTGTTCTACCGCGTAA	ATGATATATTTGACGGACTTCCCCGCTCCCCGGCCTCCTCCATCCATTTCCTTATCACCTTTTCGTTTTTCTGCAGCTTTTACCCCAGGTCTTTTACTCTGTTCTACCGCGTAA			MIYLTDFPAPRPPPSISLSPFRFSAAFTPGLLLCSTA*	MIYLTDFPAPRPPPSISLSPFRFSAAFTPGLLLCSTA*			GTCTGCGGTG	TCTTTGAATA	0	R	FG07303.1	MG06487.1	NCU06416.1	0	0
6279	3063	ao	AN0051.1	71.m15331	AO070314000138	0					-191	-102	ATGTCCCGCCTTCTGGTCCAGTGGAGTAGAAGTGACTTCACCAAGTCATTTCACTCTTCACCTTGCGCCACCACTCTATTTAACGTTTAA			ATGTCCCGCCTTCTGGTCCAGTGGAGTAGAAGTGACTTCACCAAGTCATTTCACTCTTCACCTTGCGCCACCACTCTATTTAACGTTTAA	MSRLLVQWSRSDFTKSFHSSPCATTLFNV*			MSRLLVQWSRSDFTKSFHSSPCATTLFNV*	ATCTCTCTCA	CCTCTACCCT	0	R	FG07303.1	MG06487.1	NCU06416.1	0	0
6280	3065	ao	AN9360.1	52.m03843	AO070315000040	0					-272	-246	ATGAGGCGCGTATTGAACCAGATCTGA			ATGAGGCGCGTATTGAACCAGATCTGA	MRRVLNQI*			MRRVLNQI*	TCTCCCCGGC	ACTAACCCAA	0	A	0	0	0	0	0
6281	3065	ao	AN9360.1	52.m03843	AO070315000040	0					-191	-132	ATGCTTATCTTATTTCCGCCTCAGCCTGTCTCCGCTGTCGCGACTTTCCCACGATACTAA			ATGCTTATCTTATTTCCGCCTCAGCCTGTCTCCGCTGTCGCGACTTTCCCACGATACTAA	MLILFPPQPVSAVATFPRY*			MLILFPPQPVSAVATFPRY*	CAGGATAAGG	ATTATACGGC	0	A	0	0	0	0	0
6284	3066	af	AN9357.1	52.m04075	AO070315000043	0			-176	-90			ATGCTGTTAACAATATTTTTCATTAATTCCTACAACACGATTGGCTCTGCGCATTCATCTTTGAGAGTAACAGAAAGTCCAACTTGA		ATGCTGTTAACAATATTTTTCATTAATTCCTACAACACGATTGGCTCTGCGCATTCATCTTTGAGAGTAACAGAAAGTCCAACTTGA		MLLTIFFINSYNTIGSAHSSLRVTESPT*		MLLTIFFINSYNTIGSAHSSLRVTESPT*		AATTACATCA	ATTCCTCTGG	0	Q	0	0	0	YIR035C	0
6282	3066	an	AN9357.1	52.m04075	AO070315000043	0	-227	-213					ATGTCTAAGCTATAG	ATGTCTAAGCTATAG			MSKL*	MSKL*			GATTGGGTCG	ACATGACCAC	0	Q	0	0	0	YIR035C	0
6283	3066	an	AN9357.1	52.m04075	AO070315000043	0	-210	-184					ATGACCACTGTTAGGAGATTCATCTAA	ATGACCACTGTTAGGAGATTCATCTAA			MTTVRRFI*	MTTVRRFI*			AGCTATAGAC	TTGGACCTTT	0	Q	0	0	0	YIR035C	0
6285	3066	ao	AN9357.1	52.m04075	AO070315000043	0					-117	-61	ATGGGAGCTCGTTGCTTTCCACATCTTCGGCCTCGGTCCCTTCGAAGTCAATCCTAA			ATGGGAGCTCGTTGCTTTCCACATCTTCGGCCTCGGTCCCTTCGAAGTCAATCCTAA	MGARCFPHLRPRSLRSQS*			MGARCFPHLRPRSLRSQS*	ATCACCGCCA	CCAAACAACT	0	Q	0	0	0	YIR035C	0
6286	3068	ao	AN8676.1	62.m03394	AO070315000096	0					-285	-79	ATGGGCCGTCCGGCACACGTGACAGACCGCCTGCCTGTCCCAACCGGCACTTTGCCTTCTTCGAACTCCTCCTCCCCGTTTCTCTTTCCTCTTCTTGTCCTGAACCCAAACCCTGCGAAGCAAACGCGTTACTCGATTTGGTCATTCTTCCTCCCCCTCAAAAGCATCATTCCTCTTTGGGCATCTGTCTTCACTTCCCCCAGATAA			ATGGGCCGTCCGGCACACGTGACAGACCGCCTGCCTGTCCCAACCGGCACTTTGCCTTCTTCGAACTCCTCCTCCCCGTTTCTCTTTCCTCTTCTTGTCCTGAACCCAAACCCTGCGAAGCAAACGCGTTACTCGATTTGGTCATTCTTCCTCCCCCTCAAAAGCATCATTCCTCTTTGGGCATCTGTCTTCACTTCCCCCAGATAA	MGRPAHVTDRLPVPTGTLPSSNSSSPFLFPLLVLNPNPAKQTRYSIWSFFLPLKSIIPLWASVFTSPR*			MGRPAHVTDRLPVPTGTLPSSNSSSPFLFPLLVLNPNPAKQTRYSIWSFFLPLKSIIPLWASVFTSPR*	TAAGGAGGGA	TCCCCATTAC	0	K	0	0	0	0	0
6288	3069	af	AN8680.1	62.m03391	AO070315000100	0			-133	-41			ATGATAGATGCCAAGACAAGCATCTTCATTCCCGCCGCGAGATCATTAGGAAGCTCGAATACAACCTTCTACTCTGTTGGAAGAACGATTTGA		ATGATAGATGCCAAGACAAGCATCTTCATTCCCGCCGCGAGATCATTAGGAAGCTCGAATACAACCTTCTACTCTGTTGGAAGAACGATTTGA		MIDAKTSIFIPAARSLGSSNTTFYSVGRTI*		MIDAKTSIFIPAARSLGSSNTTFYSVGRTI*		GTGTTTCCCA	AGTCGTCTGA	0	O	0	0	0	0	0
6289	3069	af	AN8680.1	62.m03391	AO070315000100	0			-126	-85			ATGCCAAGACAAGCATCTTCATTCCCGCCGCGAGATCATTAG		ATGCCAAGACAAGCATCTTCATTCCCGCCGCGAGATCATTAG		MPRQASSFPPRDH*		MPRQASSFPPRDH*		CCAATGATAG	GAAGCTCGAA	0	O	0	0	0	0	0
6287	3069	an	AN8680.1	62.m03391	AO070315000100	0	-140	-108					ATGGTTCAAAGAAACCAGTCCAACAACATTTGA	ATGGTTCAAAGAAACCAGTCCAACAACATTTGA			MVQRNQSNNI*	MVQRNQSNNI*			GGTGTTGTCG	TGCCAAGACC	0	O	0	0	0	0	0
6290	3069	ao	AN8680.1	62.m03391	AO070315000100	0					-249	-169	ATGCGATTTGAAGCCCTCGTAGCGTTGATCCAGGTTAGTAGGGTGTACGGTCCAATGTCAGGTTTATTAATCCATGGCTGA			ATGCGATTTGAAGCCCTCGTAGCGTTGATCCAGGTTAGTAGGGTGTACGGTCCAATGTCAGGTTTATTAATCCATGGCTGA	MRFEALVALIQVSRVYGPMSGLLIHG*			MRFEALVALIQVSRVYGPMSGLLIHG*	GTGCGATAGA	AGGTTGTGTT	0	O	0	0	0	0	0
6291	3069	ao	AN8680.1	62.m03391	AO070315000100	0					-195	-169	ATGTCAGGTTTATTAATCCATGGCTGA			ATGTCAGGTTTATTAATCCATGGCTGA	MSGLLIHG*			MSGLLIHG*	GTACGGTCCA	AGGTTGTGTT	0	O	0	0	0	0	0
6292	3069	ao	AN8680.1	62.m03391	AO070315000100	0					-176	-153	ATGGCTGAAGGTTGTGTTTACTGA			ATGGCTGAAGGTTGTGTTTACTGA	MAEGCVY*			MAEGCVY*	TTATTAATCC	GGAAAGAATA	0	O	0	0	0	0	0
6295	3070	af	AN8692.1	62.m03473	AO070315000113	0			-256	-113			ATGGATGTCTCCAGCGGCCCGTTGGCACATCATTTGCCGGCTTTGTCAGGGGCTGCTCCAACCGTCCGCGGACCAGATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAGTTCCATAA		ATGGATGTCTCCAGCGGCCCGTTGGCACATCATTTGCCGGCTTTGTCAGGGGCTGCTCCAACCGTCCGCGGACCAGATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAGTTCCATAA		MDVSSGPLAHHLPALSGAAPTVRGPDGVYIDRYGPLTRLIFFSLLVP*		MDVSSGPLAHHLPALSGAAPTVRGPDGVYIDRYGPLTRLIFFSLLVP*		GGATCACCTT	TAAATCACCC	0	O	0	0	0	0	0
6296	3070	af	AN8692.1	62.m03473	AO070315000113	0			-252	-121			ATGTCTCCAGCGGCCCGTTGGCACATCATTTGCCGGCTTTGTCAGGGGCTGCTCCAACCGTCCGCGGACCAGATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		ATGTCTCCAGCGGCCCGTTGGCACATCATTTGCCGGCTTTGTCAGGGGCTGCTCCAACCGTCCGCGGACCAGATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		MSPAARWHIICRLCQGLLQPSADQMVYILTAMDPSPASSSFLF*		MSPAARWHIICRLCQGLLQPSADQMVYILTAMDPSPASSSFLF*		CACCTTATGG	TTCCATAATA	0	O	0	0	0	0	0
6297	3070	af	AN8692.1	62.m03473	AO070315000113	0			-180	-121			ATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		ATGGTGTATATATTGACCGCTATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		MVYILTAMDPSPASSSFLF*		MVYILTAMDPSPASSSFLF*		CGCGGACCAG	TTCCATAATA	0	O	0	0	0	0	0
6298	3070	af	AN8692.1	62.m03473	AO070315000113	0			-159	-121			ATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		ATGGACCCCTCACCCGCCTCATCTTCTTTTCTCTTCTAG		MDPSPASSSFLF*		MDPSPASSSFLF*		ATTGACCGCT	TTCCATAATA	0	O	0	0	0	0	0
6293	3070	an	AN8692.1	62.m03473	AO070315000113	0	-248	-219					ATGGATGGCGCCTCTGCAGCCCGGGACTGA	ATGGATGGCGCCTCTGCAGCCCGGGACTGA			MDGASAARD*	MDGASAARD*			ACTACGGAGT	GCCAATTCGA	0	O	0	0	0	0	0
6294	3070	an	AN8692.1	62.m03473	AO070315000113	0	-244	-164					ATGGCGCCTCTGCAGCCCGGGACTGAGCCAATTCGATTCTTCCTGGAGCGCGATCTCCAATCCGAACGGCAACTCTGGTAA	ATGGCGCCTCTGCAGCCCGGGACTGAGCCAATTCGATTCTTCCTGGAGCGCGATCTCCAATCCGAACGGCAACTCTGGTAA			MAPLQPGTEPIRFFLERDLQSERQLW*	MAPLQPGTEPIRFFLERDLQSERQLW*			CGGAGTATGG	CCGTCCCAAT	0	O	0	0	0	0	0
6299	3070	ao	AN8692.1	62.m03473	AO070315000113	0					-131	-102	ATGCTCCTGCCCCTCGCTCCTACCTTCTGA			ATGCTCCTGCCCCTCGCTCCTACCTTCTGA	MLLPLAPTF*			MLLPLAPTF*	TAACCGCCAC	CTTTCCACAT	0	O	0	0	0	0	0

6302	3072	af	AN8701.1	62.m03367	AO070315000129	0			-226	-185			ATGCGCGCAATGGATGGTCCCTTACAGTTATATCTGCCATAA		ATGCGCGCAATGGATGGTCCCTTACAGTTATATCTGCCATAA		MRAMDGPLQLYLP*		MRAMDGPLQLYLP*		GCCTCAGATA	TTCGTTGATG	0	S	0	0	0	YDR128W	0
6303	3072	af	AN8701.1	62.m03367	AO070315000129	0			-217	-185			ATGGATGGTCCCTTACAGTTATATCTGCCATAA		ATGGATGGTCCCTTACAGTTATATCTGCCATAA		MDGPLQLYLP*		MDGPLQLYLP*		AATGCGCGCA	TTCGTTGATG	0	S	0	0	0	YDR128W	0
6304	3072	af	AN8701.1	62.m03367	AO070315000129	0			-213	-151			ATGGTCCCTTACAGTTATATCTGCCATAATTCGTTGATGGCCAATTGCCATGTTCCGAGATGA		ATGGTCCCTTACAGTTATATCTGCCATAATTCGTTGATGGCCAATTGCCATGTTCCGAGATGA		MVPYSYICHNSLMANCHVPR*		MVPYSYICHNSLMANCHVPR*		CGCGCAATGG	GAGCACCTCA	0	S	0	0	0	YDR128W	0
6305	3072	af	AN8701.1	62.m03367	AO070315000129	0			-177	-151			ATGGCCAATTGCCATGTTCCGAGATGA		ATGGCCAATTGCCATGTTCCGAGATGA		MANCHVPR*		MANCHVPR*		TAATTCGTTG	GAGCACCTCA	0	S	0	0	0	YDR128W	0
6306	3072	af	AN8701.1	62.m03367	AO070315000129	0			-164	-87			ATGTTCCGAGATGAGAGCACCTCAGATCTCCCTACCGCTCATCCTGTCCTCGAGCGATTTTTTAATTTCTACTTCTAG		ATGTTCCGAGATGAGAGCACCTCAGATCTCCCTACCGCTCATCCTGTCCTCGAGCGATTTTTTAATTTCTACTTCTAG		MFRDESTSDLPTAHPVLERFFNFYF*		MFRDESTSDLPTAHPVLERFFNFYF*		GCCAATTGCC	CTCACGTCCG	0	S	0	0	0	YDR128W	0
6307	3072	af	AN8701.1	62.m03367	AO070315000129	0			-154	-50			ATGAGAGCACCTCAGATCTCCCTACCGCTCATCCTGTCCTCGAGCGATTTTTTAATTTCTACTTCTAGCTCACGTCCGAGGTGGACGCGAGACTGCACGGTTTAG		ATGAGAGCACCTCAGATCTCCCTACCGCTCATCCTGTCCTCGAGCGATTTTTTAATTTCTACTTCTAGCTCACGTCCGAGGTGGACGCGAGACTGCACGGTTTAG		MRAPQISLPLILSSSDFLISTSSSRPRWTRDCTV*		MRAPQISLPLILSSSDFLISTSSSRPRWTRDCTV*		ATGTTCCGAG	GAAGCGCTTT	0	S	0	0	0	YDR128W	0
6301	3072	an	AN8701.1	62.m03367	AO070315000129	0	-85	-65					ATGTGTCCACCAGTCTGTTGA	ATGTGTCCACCAGTCTGTTGA			MCPPVC*	MCPPVC*			CTTGCGGTCA	AAACCGTCTC	0	S	0	0	0	YDR128W	0
6308	3072	ao	AN8701.1	62.m03367	AO070315000129	0					-155	-96	ATGAAAGCACTTCCTAGTGTCGTACAATCCTTTCTATTAATGAGTTGTAGGAAGACTTGA			ATGAAAGCACTTCCTAGTGTCGTACAATCCTTTCTATTAATGAGTTGTAGGAAGACTTGA	MKALPSVVQSFLLMSCRKT*			MKALPSVVQSFLLMSCRKT*	ATCCATCGAG	AACCCGACAC	0	S	0	0	0	YDR128W	0
6309	3072	ao	AN8701.1	62.m03367	AO070315000129	0					-116	-96	ATGAGTTGTAGGAAGACTTGA			ATGAGTTGTAGGAAGACTTGA	MSCRKT*			MSCRKT*	CTTTCTATTA	AACCCGACAC	0	S	0	0	0	YDR128W	0
6310	3073	an	AN8702.1	62.m03366	AO070315000130	0	-245	-114					ATGCCCCTCGTCCGTTACGTCGTTGAATCCTTTTGCGATGAGTTCTATTTGGAAGGGCAGGACCAACACCGTCATTTTCTGACAGCCCGTCGGTTTCTTCACCCTAGGACTTTCTCCGCGCTCCGATTTTAG	ATGCCCCTCGTCCGTTACGTCGTTGAATCCTTTTGCGATGAGTTCTATTTGGAAGGGCAGGACCAACACCGTCATTTTCTGACAGCCCGTCGGTTTCTTCACCCTAGGACTTTCTCCGCGCTCCGATTTTAG			MPLVRYVVESFCDEFYLEGQDQHRHFLTARRFLHPRTFSALRF*	MPLVRYVVESFCDEFYLEGQDQHRHFLTARRFLHPRTFSALRF*			CTAAAGTGCA	TTGTCTTCGT	0	O	0	MG02568.1	0	0	0
6311	3073	an	AN8702.1	62.m03366	AO070315000130	0	-208	-164					ATGAGTTCTATTTGGAAGGGCAGGACCAACACCGTCATTTTCTGA	ATGAGTTCTATTTGGAAGGGCAGGACCAACACCGTCATTTTCTGA			MSSIWKGRTNTVIF*	MSSIWKGRTNTVIF*			TCCTTTTGCG	CAGCCCGTCG	0	O	0	MG02568.1	0	0	0
6312	3073	ao	AN8702.1	62.m03366	AO070315000130	0					-258	-235	ATGCATCTGCTGATGGCTTGGTAA			ATGCATCTGCTGATGGCTTGGTAA	MHLLMAW*			MHLLMAW*	CCTCTGCCCG	CCTTCATAGG	0	O	0	MG02568.1	0	0	0
6313	3073	ao	AN8702.1	62.m03366	AO070315000130	0					-246	-235	ATGGCTTGGTAA			ATGGCTTGGTAA	MAW*			MAW*	GCATCTGCTG	CCTTCATAGG	0	O	0	MG02568.1	0	0	0
6315	3075	af	AN0775.1	70.m15785	AO070316000063	0			-219	-61			ATGATAACCAAGATGAAGTCAAGAAACAATATCGATAAAACAAGATCAGGATCCAGATACAAGTCAGGTGAATCCTCTCAATTAGCTCTTGATATCTCCTATCCTTCTTTTCTTCTCATCATCTCAATTGCTTTGTCTCTCCCTACGCTCTGTTCTTGA		ATGATAACCAAGATGAAGTCAAGAAACAATATCGATAAAACAAGATCAGGATCCAGATACAAGTCAGGTGAATCCTCTCAATTAGCTCTTGATATCTCCTATCCTTCTTTTCTTCTCATCATCTCAATTGCTTTGTCTCTCCCTACGCTCTGTTCTTGA		MITKMKSRNNIDKTRSGSRYKSGESSQLALDISYPSFLLIISIALSLPTLCS*		MITKMKSRNNIDKTRSGSRYKSGESSQLALDISYPSFLLIISIALSLPTLCS*		ACTCCGGAAA	ACATCGGATT	0	C	0	MG08725.1	0	0	0
6316	3075	af	AN0775.1	70.m15785	AO070316000063	0			-207	-61			ATGAAGTCAAGAAACAATATCGATAAAACAAGATCAGGATCCAGATACAAGTCAGGTGAATCCTCTCAATTAGCTCTTGATATCTCCTATCCTTCTTTTCTTCTCATCATCTCAATTGCTTTGTCTCTCCCTACGCTCTGTTCTTGA		ATGAAGTCAAGAAACAATATCGATAAAACAAGATCAGGATCCAGATACAAGTCAGGTGAATCCTCTCAATTAGCTCTTGATATCTCCTATCCTTCTTTTCTTCTCATCATCTCAATTGCTTTGTCTCTCCCTACGCTCTGTTCTTGA		MKSRNNIDKTRSGSRYKSGESSQLALDISYPSFLLIISIALSLPTLCS*		MKSRNNIDKTRSGSRYKSGESSQLALDISYPSFLLIISIALSLPTLCS*		GATAACCAAG	ACATCGGATT	0	C	0	MG08725.1	0	0	0
6314	3075	an	AN0775.1	70.m15785	AO070316000063	0	-196	-155					ATGAACCCCACGGACGCGGAGGAGCTCCTCGCCAGTCCATAA	ATGAACCCCACGGACGCGGAGGAGCTCCTCGCCAGTCCATAA			MNPTDAEELLASP*	MNPTDAEELLASP*			GCTCTAGTAA	CCGGTTCCCT	0	C	0	MG08725.1	0	0	0
6317	3075	ao	AN0775.1	70.m15785	AO070316000063	0					-256	-170	ATGATAACGGTAATACATACAGTAAAAGGGCCACCCCACGCCAACCGGAATTGGGGGGCAACAATCAATCAATCAATCACTCAGTGA			ATGATAACGGTAATACATACAGTAAAAGGGCCACCCCACGCCAACCGGAATTGGGGGGCAACAATCAATCAATCAATCACTCAGTGA	MITVIHTVKGPPHANRNWGATINQSITQ*			MITVIHTVKGPPHANRNWGATINQSITQ*	ACCGATATCC	AACATAATCA	0	C	0	MG08725.1	0	0	0
6320	3077	af	AN4648.1	57.m05479	AO070316000120	0			-207	-142			ATGAATACAGATAAATTACTAGCGGTATCTGCCAATCGGCGTTGCGATAGAACTTTTACTGTTTGA		ATGAATACAGATAAATTACTAGCGGTATCTGCCAATCGGCGTTGCGATAGAACTTTTACTGTTTGA		MNTDKLLAVSANRRCDRTFTV*		MNTDKLLAVSANRRCDRTFTV*		CAAATACACA	TGTAACAGAA	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6318	3077	an	AN4648.1	57.m05479	AO070316000120	0	-198	-175					ATGAGTTCGTTGTTGATTGTATGA	ATGAGTTCGTTGTTGATTGTATGA			MSSLLIV*	MSSLLIV*			GTAGGAAATA	GCGAGCAAGC	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6319	3077	an	AN4648.1	57.m05479	AO070316000120	0	-178	-161					ATGAGCGAGCAAGCGTAA	ATGAGCGAGCAAGCGTAA			MSEQA*	MSEQA*			TGTTGATTGT	GTTGAATACA	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6321	3077	ao	AN4648.1	57.m05479	AO070316000120	0					-262	-251	ATGAGCCATTAA			ATGAGCCATTAA	MSH*			MSH*	GATGAAAGGA	TGTCTTATAG	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6322	3077	ao	AN4648.1	57.m05479	AO070316000120	0					-251	-216	ATGTCTTATAGCCACTATGTAACAAAAACGCACTAG			ATGTCTTATAGCCACTATGTAACAAAAACGCACTAG	MSYSHYVTKTH*			MSYSHYVTKTH*	TGAGCCATTA	CGCATTGCTT	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6323	3077	ao	AN4648.1	57.m05479	AO070316000120	0					-175	-128	ATGCGATTTTATCAGAAAATCTTCCAGACCATCACAAAATTCCCATAA			ATGCGATTTTATCAGAAAATCTTCCAGACCATCACAAAATTCCCATAA	MRFYQKIFQTITKFP*			MRFYQKIFQTITKFP*	ACTTTTCCCG	ACGCCCTGCA	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6324	3077	ao	AN4648.1	57.m05479	AO070316000120	0					-98	-24	ATGAGCTGCCTTTTGTCGTATCACGTCTGTCCGATCTTACAGTCAACTACCATTGCGGTAATACCCGATAATTAA			ATGAGCTGCCTTTTGTCGTATCACGTCTGTCCGATCTTACAGTCAACTACCATTGCGGTAATACCCGATAATTAA	MSCLLSYHVCPILQSTTIAVIPDN*			MSCLLSYHVCPILQSTTIAVIPDN*	CAGCTGGTGG	TTACAACATA	0	S	FG10060.1	0	NCU09843.1	YMR093W	0
6326	3078	af	AN4647.1	57.m05486	AO070316000121	0			-165	-136			ATGGTGTCAACGTGCCATGACCATCATTGA		ATGGTGTCAACGTGCCATGACCATCATTGA		MVSTCHDHH*		MVSTCHDHH*		GTCTTTCTAT	TGCATTCGGG	0	I	0	0	0	0	0
6327	3078	af	AN4647.1	57.m05486	AO070316000121	0			-136	-113			ATGCATTCGGGCATCTCCGACTGA		ATGCATTCGGGCATCTCCGACTGA		MHSGISD*		MHSGISD*		ACCATCATTG	TACTGATAAG	0	I	0	0	0	0	0
6325	3078	an	AN4647.1	57.m05486	AO070316000121	0	-156	-25					ATGAAGCTATCGCGACCAATCCAGAACCCCGCAGATAAGCGTTGTATCTTCCCACCATCGTACGGCCGTTTCTCCAACTTTCGCTTCATTTCTGCTCTTGCTTCTCTACCCACATTCAGTGCCTCAAAATAG	ATGAAGCTATCGCGACCAATCCAGAACCCCGCAGATAAGCGTTGTATCTTCCCACCATCGTACGGCCGTTTCTCCAACTTTCGCTTCATTTCTGCTCTTGCTTCTCTACCCACATTCAGTGCCTCAAAATAG			MKLSRPIQNPADKRCIFPPSYGRFSNFRFISALSLPTFSASK*	MKLSRPIQNPADKRCIFPPSYGRFSNFRFISALSLPTFSASK*			TACGGATAGC	AAATTGAGAA	0	I	0	0	0	0	0
6328	3078	ao	AN4647.1	57.m05486	AO070316000121	0					-177	-166	ATGAGTACCTGA			ATGAGTACCTGA	MST*			MST*	AATCAGCATC	AGCTCGGCCA	0	I	0	0	0	0	0
6338	3084	af	AN0634.1	70.m15648	AO070318000124	0			-259	-221			ATGCCCTACTTACCCGATGTGGACACAGCTGACGCATGA		ATGCCCTACTTACCCGATGTGGACACAGCTGACGCATGA		MPYLPDVDTADA*		MPYLPDVDTADA*		AGAAGACCCT	TCCATTCCTA	0	U	0	0	0	0	0
6339	3084	af	AN0634.1	70.m15648	AO070318000124	0			-243	-67			ATGTGGACACAGCTGACGCATGATCCATTCCTAGGGCCTCCTTGGATCCTGGGGATCGTCCGTTCCGGAGTGGGAGGGACGAGCGATGGAAGATTCGAAGACATTCAGGAAGTCGGGGCCGAAAGTCTCTGTGCTGCCATGATTGTCTCACCAAGGGCTTGGCTACCTGTTTCATAA		ATGTGGACACAGCTGACGCATGATCCATTCCTAGGGCCTCCTTGGATCCTGGGGATCGTCCGTTCCGGAGTGGGAGGGACGAGCGATGGAAGATTCGAAGACATTCAGGAAGTCGGGGCCGAAAGTCTCTGTGCTGCCATGATTGTCTCACCAAGGGCTTGGCTACCTGTTTCATAA		MWTQLTHDPFLGPPWILGIVRSGVGGTSDGRFEDIQEVGAESLCAAMIVSPRAWLPVS*		MWTQLTHDPFLGPPWILGIVRSGVGGTSDGRFEDIQEVGAESLCAAMIVSPRAWLPVS*		TACTTACCCG	TTGGAAATTA	0	U	0	0	0	0	0
6340	3084	af	AN0634.1	70.m15648	AO070318000124	0			-224	-210			ATGATCCATTCCTAG		ATGATCCATTCCTAG		MIHS*		MIHS*		CAGCTGACGC	GGCCTCCTTG	0	U	0	0	0	0	0
6341	3084	af	AN0634.1	70.m15648	AO070318000124	0			-158	-102			ATGGAAGATTCGAAGACATTCAGGAAGTCGGGGCCGAAAGTCTCTGTGCTGCCATGA		ATGGAAGATTCGAAGACATTCAGGAAGTCGGGGCCGAAAGTCTCTGTGCTGCCATGA		MEDSKTFRKSGPKVSVLP*		MEDSKTFRKSGPKVSVLP*		GGGACGAGCG	TTGTCTCACC	0	U	0	0	0	0	0
6342	3084	af	AN0634.1	70.m15648	AO070318000124	0			-105	-67			ATGATTGTCTCACCAAGGGCTTGGCTACCTGTTTCATAA		ATGATTGTCTCACCAAGGGCTTGGCTACCTGTTTCATAA		MIVSPRAWLPVS*		MIVSPRAWLPVS*		CTGTGCTGCC	TTGGAAATTA	0	U	0	0	0	0	0
6336	3084	an	AN0634.1	70.m15648	AO070318000124	0	-113	-93					ATGGCTCTCAAACTGTCATGA	ATGGCTCTCAAACTGTCATGA			MALKLS*	MALKLS*			TTAGCAGAGA	TTTCTCCGCT	0	U	0	0	0	0	0
6337	3084	an	AN0634.1	70.m15648	AO070318000124	0	-96	-52					ATGATTTCTCCGCTCTATTCGTGCTTATACCTCAATAATCCCTAG	ATGATTTCTCCGCTCTATTCGTGCTTATACCTCAATAATCCCTAG			MISPLYSCLYLNNP*	MISPLYSCLYLNNP*			TCAAACTGTC	ACTGAGGCTG	0	U	0	0	0	0	0
6343	3084	ao	AN0634.1	70.m15648	AO070318000124	0					-165	-73	ATGATCGTCACCAGAGGCAGAACGACGCTGAAATCGAAAGAGAAAGTGAAAAGAGAAGGGCTAGGGAATCAGAGGCAAGTTGCGCTGCCATGA			ATGATCGTCACCAGAGGCAGAACGACGCTGAAATCGAAAGAGAAAGTGAAAAGAGAAGGGCTAGGGAATCAGAGGCAAGTTGCGCTGCCATGA	MIVTRGRTTLKSKEKVKREGLGNQRQVALP*			MIVTRGRTTLKSKEKVKREGLGNQRQVALP*	AGGCGGGTGA	TTCTGTTATT	0	U	0	0	0	0	0
6344	3084	ao	AN0634.1	70.m15648	AO070318000124	0					-76	-38	ATGATTCTGTTATTCCGACTCTCGTTACGCCCGTTTTGA			ATGATTCTGTTATTCCGACTCTCGTTACGCCCGTTTTGA	MILLFRLSLRPF*			MILLFRLSLRPF*	TTGCGCTGCC	TACCAGGAGT	0	U	0	0	0	0	0
6348	3085	af	AN8597.1	70.m15665	AO070319000106	0			-269	-108			ATGATTGGTGCCGGCTATATTGGCAAAATGGAAATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		ATGATTGGTGCCGGCTATATTGGCAAAATGGAAATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		MIGAGYIGKMEMVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		MIGAGYIGKMEMVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		GAAGCCAGCC	AAGGTAGAGC	0	C	0	0	0	0	0
6349	3085	af	AN8597.1	70.m15665	AO070319000106	0			-242	-108			ATGGAAATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		ATGGAAATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		MEMVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		MEMVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		TATTGGCAAA	AAGGTAGAGC	0	C	0	0	0	0	0
6350	3085	af	AN8597.1	70.m15665	AO070319000106	0			-236	-108			ATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		ATGGTGCTCGTTTTGCACTGCAACCATCATTGGCTTGGGGCCATCCCGCTTTACAAACAATACGTTGACCGATTTCCCTTTCAGGTCCCCGATCCGCTTATTCTGTCGACGTTTTGCGACTTGCGATAG		MVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		MVLVLHCNHHWLGAIPLYKQYVDRFPFQVPDPLILSTFCDLR*		CAAAATGGAA	AAGGTAGAGC	0	C	0	0	0	0	0
6345	3085	an	AN8597.1	70.m15665	AO070319000106	0	-281	-261					ATGCTGGTCTGGGTGGTGTAG	ATGCTGGTCTGGGTGGTGTAG			MLVWVV*	MLVWVV*			GTATATATCG	ATGGAGGTCG	0	C	0	0	0	0	0
6346	3085	an	AN8597.1	70.m15665	AO070319000106	0	-260	-195					ATGGAGGTCGCTGCCTCACCTTGCGACTGTCTCCCGCGGTGGTTGGGCGCAGTCGCGGCTCCGTAG	ATGGAGGTCGCTGCCTCACCTTGCGACTGTCTCCCGCGGTGGTTGGGCGCAGTCGCGGCTCCGTAG			MEVAASPCDCLPRWLGAVAAP*	MEVAASPCDCLPRWLGAVAAP*			GGTGGTGTAG	AACAACTCCA	0	C	0	0	0	0	0
6347	3085	an	AN8597.1	70.m15665	AO070319000106	0	-78	-46					ATGAAGGTGTGTGCCCACGTAAAACCGCATTAA	ATGAAGGTGTGTGCCCACGTAAAACCGCATTAA			MKVCAHVKPH*	MKVCAHVKPH*			GCCCTTTTAA	ACCCTCATTA	0	C	0	0	0	0	0
6351	3086	af	AN0856.1	70.m15473	AO070320000003	0			-241	-215			ATGCCAGCATCGGTCGGAATTCTTTGA		ATGCCAGCATCGGTCGGAATTCTTTGA		MPASVGIL*		MPASVGIL*		GAGGTGATAT	CAGTCGCCAT	0	E	0	0	0	0	0
6352	3086	ao	AN0856.1	70.m15473	AO070320000003	0					-235	-215	ATGCCCGGCCAATCTTGCTAA			ATGCCCGGCCAATCTTGCTAA	MPGQSC*			MPGQSC*	TTTAGAAGCA	CTAAATCCCA	0	E	0	0	0	0	0
6353	3088	af	AN0873.1	70.m15476	AO070320000032	0			-299	-213			ATGGACAAGTCTGACACTAACGAACTAAAGTCAACATGGCTTATCCACAAGGCATCCGGCCACCCAAAACTTCCAAGTAAGTGTTAG		ATGGACAAGTCTGACACTAACGAACTAAAGTCAACATGGCTTATCCACAAGGCATCCGGCCACCCAAAACTTCCAAGTAAGTGTTAG		MDKSDTNELKSTWLIHKASGHPKLPSKC*		MDKSDTNELKSTWLIHKASGHPKLPSKC*		ACTTGGGTGG	GATTTCTGTT	0	R	0	0	0	0	0
6354	3088	af	AN0873.1	70.m15476	AO070320000032	0			-264	-220			ATGGCTTATCCACAAGGCATCCGGCCACCCAAAACTTCCAAGTAA		ATGGCTTATCCACAAGGCATCCGGCCACCCAAAACTTCCAAGTAA		MAYPQGIRPPKTSK*		MAYPQGIRPPKTSK*		TAAAGTCAAC	GTGTTAGGAT	0	R	0	0	0	0	0
6355	3088	af	AN0873.1	70.m15476	AO070320000032	0			-196	-65			ATGAGATGTTTTTGTTTTAGTGCGGACTTCGGCGAGTGCTCCGACCCAAGAAACGGAGTTTCCCCGCATATCAAATGCCCCCGCAATAGAGTCAATTGCCCGGGGTGTCTCCGTATGGGCCTGAGTATTTGA		ATGAGATGTTTTTGTTTTAGTGCGGACTTCGGCGAGTGCTCCGACCCAAGAAACGGAGTTTCCCCGCATATCAAATGCCCCCGCAATAGAGTCAATTGCCCGGGGTGTCTCCGTATGGGCCTGAGTATTTGA		MRCFCFSADFGECSDPRNGVSPHIKCPRNRVNCPGCLRMGLSI*		MRCFCFSADFGECSDPRNGVSPHIKCPRNRVNCPGCLRMGLSI*		TGTTTCGTGC	GAGCATGGAG	0	R	0	0	0	0	0
6356	3088	af	AN0873.1	70.m15476	AO070320000032	0			-191	-177			ATGTTTTTGTTTTAG		ATGTTTTTGTTTTAG		MFLF*		MFLF*		CGTGCATGAG	TGCGGACTTC	0	R	0	0	0	0	0
6357	3088	af	AN0873.1	70.m15476	AO070320000032	0			-122	-108			ATGCCCCCGCAATAG		ATGCCCCCGCAATAG		MPPQ*		MPPQ*		CGCATATCAA	AGTCAATTGC	0	R	0	0	0	0	0

6358	3088	af	AN0873.1	70.m15476	AO070320000032	0			-82	-65			ATGGGCCTGAGTATTTGA		ATGGGCCTGAGTATTTGA		MGLSI*		MGLSI*		GTGTCTCCGT	GAGCATGGAG	0	R	0	0	0	0	0
6362	3089	af	AN0886.1	70.m15496	AO070320000055	0			-282	-262			ATGGCAGATAATGAGGTATGA		ATGGCAGATAATGAGGTATGA		MADNEV*		MADNEV*		TCTGGAGTCA	TCGTCGTGGG	0	R	0	0	0	0	0
6363	3089	af	AN0886.1	70.m15496	AO070320000055	0			-272	-183			ATGAGGTATGATCGTCGTGGGGTATGGTCACAGCTCGGCGTTTGTTGGAGAGTTGGAGAAAATGCGGAGAATCCGTCTATGCGGTCATAA		ATGAGGTATGATCGTCGTGGGGTATGGTCACAGCTCGGCGTTTGTTGGAGAGTTGGAGAAAATGCGGAGAATCCGTCTATGCGGTCATAA		MRYDRRGVWSQLGVCWRVGENAENPSMRS*		MRYDRRGVWSQLGVCWRVGENAENPSMRS*		ATGGCAGATA	ATGATAGGCT	0	R	0	0	0	0	0
6364	3089	af	AN0886.1	70.m15496	AO070320000055	0			-265	-179			ATGATCGTCGTGGGGTATGGTCACAGCTCGGCGTTTGTTGGAGAGTTGGAGAAAATGCGGAGAATCCGTCTATGCGGTCATAAATGA		ATGATCGTCGTGGGGTATGGTCACAGCTCGGCGTTTGTTGGAGAGTTGGAGAAAATGCGGAGAATCCGTCTATGCGGTCATAAATGA		MIVVGYGHSSAFVGELEKMRRIRLCGHK*		MIVVGYGHSSAFVGELEKMRRIRLCGHK*		ATAATGAGGT	TAGGCTCCAA	0	R	0	0	0	0	0
6365	3089	af	AN0886.1	70.m15496	AO070320000055	0			-211	-179			ATGCGGAGAATCCGTCTATGCGGTCATAAATGA		ATGCGGAGAATCCGTCTATGCGGTCATAAATGA		MRRIRLCGHK*		MRRIRLCGHK*		GTTGGAGAAA	TAGGCTCCAA	0	R	0	0	0	0	0
6366	3089	af	AN0886.1	70.m15496	AO070320000055	0			-194	-183			ATGCGGTCATAA		ATGCGGTCATAA		MRS*		MRS*		GAATCCGTCT	ATGATAGGCT	0	R	0	0	0	0	0
6367	3089	af	AN0886.1	70.m15496	AO070320000055	0			-182	-126			ATGATAGGCTCCAAACCCCTCGGTCACAAAGTCTCATTCAGCCGAGCGAGGAGTTGA		ATGATAGGCTCCAAACCCCTCGGTCACAAAGTCTCATTCAGCCGAGCGAGGAGTTGA		MIGSKPLGHKVSFSRARS*		MIGSKPLGHKVSFSRARS*		GCGGTCATAA	AAGGACTGAA	0	R	0	0	0	0	0
6360	3089	an	AN0886.1	70.m15496	AO070320000055	0	-236	-222					ATGATTGCACGATGA	ATGATTGCACGATGA			MIAR*	MIAR*			CGGCGTTGCT	CGCCGAAGAC	0	R	0	0	0	0	0
6361	3089	an	AN0886.1	70.m15496	AO070320000055	0	-225	-127					ATGACGCCGAAGACTTTGGAGCTTCGGCTTGACGGAGAGGATCGGCACAAAACGATAGGGACAACCTCCCCGAGGCCCCCACCCTGCCCCAACTACTGA	ATGACGCCGAAGACTTTGGAGCTTCGGCTTGACGGAGAGGATCGGCACAAAACGATAGGGACAACCTCCCCGAGGCCCCCACCCTGCCCCAACTACTGA			MTPKTLELRLDGEDRHKTIGTTSPRPPPCPNY*	MTPKTLELRLDGEDRHKTIGTTSPRPPPCPNY*			TGATTGCACG	AGAATTCCCC	0	R	0	0	0	0	0
6368	3089	ao	AN0886.1	70.m15496	AO070320000055	0					-214	-131	ATGACAATAAGGTTGGAGAAATTGGAGGCGTGTGGAGTCAATGCAGCGATAAGAGTGGGACACACCCCTCTTTTGTGTAGCTAG			ATGACAATAAGGTTGGAGAAATTGGAGGCGTGTGGAGTCAATGCAGCGATAAGAGTGGGACACACCCCTCTTTTGTGTAGCTAG	MTIRLEKLEACGVNAAIRVGHTPLLCS*			MTIRLEKLEACGVNAAIRVGHTPLLCS*	GCGTAGATCG	GGTAGGAAGC	0	R	0	0	0	0	0
6369	3089	ao	AN0886.1	70.m15496	AO070320000055	0					-174	-163	ATGCAGCGATAA			ATGCAGCGATAA	MQR*			MQR*	TGTGGAGTCA	GAGTGGGACA	0	R	0	0	0	0	0
6370	3090	an	AN0893.1	70.m15488	AO070320000065	0	-139	-56					ATGGTTTTTTGTTCGCTCCGTGCGAGTTTGCGCAATTGGGTTGTCTATTCCGACTCCAGGCTAACTGCGTACACTTCTCTGTAG	ATGGTTTTTTGTTCGCTCCGTGCGAGTTTGCGCAATTGGGTTGTCTATTCCGACTCCAGGCTAACTGCGTACACTTCTCTGTAG			MVFCSLRASLRNWVVYSDSRLTAYTSL*	MVFCSLRASLRNWVVYSDSRLTAYTSL*			TTTTAGTCAT	AGAACTCGTT	0	F	FG05187.1	0	0	0	0
6371	3090	ao	AN0893.1	70.m15488	AO070320000065	0					-147	-79	ATGTCAGTCTCCATCCGGTGGACCCCGCCATCTCTCTTCAATACACCACATCGAGCCACACGTCTATGA			ATGTCAGTCTCCATCCGGTGGACCCCGCCATCTCTCTTCAATACACCACATCGAGCCACACGTCTATGA	MSVSIRWTPPSLFNTPHRATRL*			MSVSIRWTPPSLFNTPHRATRL*	TATCGGAATC	TTATCAATTG	0	F	FG05187.1	0	0	0	0
6372	3090	ao	AN0893.1	70.m15488	AO070320000065	0					-82	-68	ATGATTATCAATTGA			ATGATTATCAATTGA	MIIN*			MIIN*	CCACACGTCT	AGACTGATAC	0	F	FG05187.1	0	0	0	0
6373	3094	ao	AN0907.1	70.m15516	AO070320000083	0					-129	-115	ATGAAAAAATTCTTAA			ATGAAAAAATTCTTAA	MKNS*			MKNS*	AGAACCCTTG	AGGGGCACTC	0	J	FG07291.1	MG06479.1	NCU06431.1	YJL190C	0
6374	3097	an	AN0927.1	70.m15536	AO070320000116	0	-222	-208					ATGGCAAATCCATAA	ATGGCAAATCCATAA			MANP*	MANP*			CTTCTCACTC	TGTAGATCGC	0	O	0	0	0	0	0
6375	3097	an	AN0927.1	70.m15536	AO070320000116	0	-155	-69					ATGAGGAAAGTCCGAAGATTGCCCGTCCCCAAACTCAAGCTTACTTGCTCCAACCTCCCAAAGGCCCATCTAGACGGGTGGGGGTGA	ATGAGGAAAGTCCGAAGATTGCCCGTCCCCAAACTCAAGCTTACTTGCTCCAACCTCCCAAAGGCCCATCTAGACGGGTGGGGGTGA			MRKVRRLPVPKLKLTCSNLPKAHLDGWG*	MRKVRRLPVPKLKLTCSNLPKAHLDGWG*			TTCTCATTAC	TAGTGGATAT	0	O	0	0	0	0	0
6379	3099	af	AN0943.1	70.m15575	AO070320000138	0			-286	-164			ATGACAAGAATGCCATGGGTGATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		ATGACAAGAATGCCATGGGTGATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		MTRMPWVMLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		MTRMPWVMLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		ACAGAGTGCC	AGTTCCCGAG	0	C	0	0	0	YPR020W	0
6380	3099	af	AN0943.1	70.m15575	AO070320000138	0			-277	-164			ATGCCATGGGTGATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		ATGCCATGGGTGATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		MPWVMLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		MPWVMLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		CATGACAAGA	AGTTCCCGAG	0	C	0	0	0	YPR020W	0
6381	3099	af	AN0943.1	70.m15575	AO070320000138	0			-272	-255			ATGGGTGATGTTGCTTGA		ATGGGTGATGTTGCTTGA		MGDVA*		MGDVA*		CAAGAATGCC	TGGAGGGATG	0	C	0	0	0	YPR020W	0
6382	3099	af	AN0943.1	70.m15575	AO070320000138	0			-265	-164			ATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		ATGTTGCTTGATGGAGGGATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		MLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		MLLDGGMNGSHVAKTLKVHHHHVTPKAAFSIP*		GCCATGGGTG	AGTTCCCGAG	0	C	0	0	0	YPR020W	0
6383	3099	af	AN0943.1	70.m15575	AO070320000138	0			-255	-244			ATGGAGGGATGA		ATGGAGGGATGA		MEG*		MEG*		ATGTTGCTTG	ATGGAAGTCA	0	C	0	0	0	YPR020W	0
6384	3099	af	AN0943.1	70.m15575	AO070320000138	0			-247	-164			ATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		ATGAATGGAAGTCACGTTGCCAAAACCTTGAAAGTGCACCATCATCACGTGACCCCCAAAGCGGCGGCCTTTTCCATTCCCTGA		MNGSHVAKTLKVHHHHVTPKAAFSIP*		MNGSHVAKTLKVHHHHVTPKAAFSIP*		TGATGGAGGG	AGTTCCCGAG	0	C	0	0	0	YPR020W	0
6385	3099	af	AN0943.1	70.m15575	AO070320000138	0			-243	-217			ATGGAAGTCACGTTGCCAAAACCTTGA		ATGGAAGTCACGTTGCCAAAACCTTGA		MEVTLPKP*		MEVTLPKP*		GGAGGGATGA	AAGTGCACCA	0	C	0	0	0	YPR020W	0
6376	3099	an	AN0943.1	70.m15575	AO070320000138	0	-186	-94					ATGCTGTCACGTGATGCGATGTGGGCGAATTCCCTGAACTTCCCGAGCTTCAAATCTCAGATTCTAGTCCTGCAATTGCGCGACGGCTCTTGA	ATGCTGTCACGTGATGCGATGTGGGCGAATTCCCTGAACTTCCCGAGCTTCAAATCTCAGATTCTAGTCCTGCAATTGCGCGACGGCTCTTGA			MLSRDAMWANSLNFPSFKSQILVLQLRDGS*	MLSRDAMWANSLNFPSFKSQILVLQLRDGS*			GGTGGTAAGG	CCAACCCGCC	0	C	0	0	0	YPR020W	0
6377	3099	an	AN0943.1	70.m15575	AO070320000138	0	-173	-150					ATGCGATGTGGGCGAATTCCCTGA	ATGCGATGTGGGCGAATTCCCTGA			MRCGRIP*	MRCGRIP*			CTGTCACGTG	ACTTCCCGAG	0	C	0	0	0	YPR020W	0
6378	3099	an	AN0943.1	70.m15575	AO070320000138	0	-168	-94					ATGTGGGCGAATTCCCTGAACTTCCCGAGCTTCAAATCTCAGATTCTAGTCCTGCAATTGCGCGACGGCTCTTGA	ATGTGGGCGAATTCCCTGAACTTCCCGAGCTTCAAATCTCAGATTCTAGTCCTGCAATTGCGCGACGGCTCTTGA			MWANSLNFPSFKSQILVLQLRDGS*	MWANSLNFPSFKSQILVLQLRDGS*			ACGTGATGCG	CCAACCCGCC	0	C	0	0	0	YPR020W	0
6386	3099	ao	AN0943.1	70.m15575	AO070320000138	0					-217	-191	ATGTCAACAGTGCTGTTGTGCACGTGA			ATGTCAACAGTGCTGTTGTGCACGTGA	MSTVLLCT*			MSTVLLCT*	TGTGGATGGC	CCCAATGGAG	0	C	0	0	0	YPR020W	0
6391	3100	af	AN5015.1	62.m03287	AO070320000151	0			-261	-97			ATGATGTCGTCTGGCCGCATCTTCAGTATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		ATGATGTCGTCTGGCCGCATCTTCAGTATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		MMSSGRIFSMRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		MMSSGRIFSMRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		GGCCCCACAG	ATACCTGCCT	0	R	0	0	0	0	0
6392	3100	af	AN5015.1	62.m03287	AO070320000151	0			-258	-97			ATGTCGTCTGGCCGCATCTTCAGTATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		ATGTCGTCTGGCCGCATCTTCAGTATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		MSSGRIFSMRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		MSSGRIFSMRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		CCCACAGATG	ATACCTGCCT	0	R	0	0	0	0	0
6393	3100	af	AN5015.1	62.m03287	AO070320000151	0			-234	-97			ATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		ATGCGGAGAGAAGTCACTCAGAGTGCATCAGAGTGGATACAGCGGGTCGATCAACGTCTCCCCACGGGAATAGTGACTGCATCACTGACAGACCACCAGCTACATCATGATGTAGTCAGCTCGCTCTTTCCAGCATAA		MRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		MRREVTQSASEWIQRVDQRLPTGIVTASLTDHQLHHDVVSSLFPA*		CATCTTCAGT	ATACCTGCCT	0	R	0	0	0	0	0
6387	3100	an	AN5015.1	62.m03287	AO070320000151	0	-219	-205					ATGACTGTACCATGA	ATGACTGTACCATGA			MTVP*	MTVP*			CAAACCCACA	TGCTTTAGTA	0	R	0	0	0	0	0
6388	3100	an	AN5015.1	62.m03287	AO070320000151	0	-208	-197					ATGATGCTTTAG	ATGATGCTTTAG			MML*	MML*			TGACTGTACC	TACTCACCAT	0	R	0	0	0	0	0
6389	3100	an	AN5015.1	62.m03287	AO070320000151	0	-188	-171					ATGCTTCTCCCCTCATGA	ATGCTTCTCCCCTCATGA			MLLPS*	MLLPS*			AGTACTCACC	CCTCACTCGT	0	R	0	0	0	0	0
6390	3100	an	AN5015.1	62.m03287	AO070320000151	0	-174	-121					ATGACCTCACTCGTCATCATCGCAGACGAAGATCCAGGTACTCACCGGCTATAA	ATGACCTCACTCGTCATCATCGCAGACGAAGATCCAGGTACTCACCGGCTATAA			MTSLVIIADEDPGTHRL*	MTSLVIIADEDPGTHRL*			TTCTCCCCTC	GTACCACCTT	0	R	0	0	0	0	0
6394	3100	ao	AN5015.1	62.m03287	AO070320000151	0					-159	-118	ATGACCTCACATCGCTCATGTATAGGGACTCGAGAAGTATAA			ATGACCTCACATCGCTCATGTATAGGGACTCGAGAAGTATAA	MTSHRSCIGTREV*			MTSHRSCIGTREV*	CGGGTATACC	GAATGGCAGA	0	R	0	0	0	0	0
6395	3100	ao	AN5015.1	62.m03287	AO070320000151	0					-142	-92	ATGTATAGGGACTCGAGAAGTATAAGAATGGCAGAAGCGAACCGCTACTAG			ATGTATAGGGACTCGAGAAGTATAAGAATGGCAGAAGCGAACCGCTACTAG	MYRDSRSIRMAEANRY*			MYRDSRSIRMAEANRY*	CACATCGCTC	GAGTGTTATA	0	R	0	0	0	0	0
6396	3100	ao	AN5015.1	62.m03287	AO070320000151	0					-115	-92	ATGGCAGAAGCGAACCGCTACTAG			ATGGCAGAAGCGAACCGCTACTAG	MAEANRY*			MAEANRY*	AAGTATAAGA	GAGTGTTATA	0	R	0	0	0	0	0
6400	3101	af	AN0191.1	71.m15461	AO070321000052	0			-211	-98			ATGGATAACGAGAAGCCACAAGATCGTGTGAATGTCGATTGTCAAGGAACTAGCGAAGCGGTCTTGGGATCGGAGAGAATTGAACAGCAGCTTTTTTTTTGTTCAACTTTTTAG		ATGGATAACGAGAAGCCACAAGATCGTGTGAATGTCGATTGTCAAGGAACTAGCGAAGCGGTCTTGGGATCGGAGAGAATTGAACAGCAGCTTTTTTTTTGTTCAACTTTTTAG		MDNEKPQDRVNVDCQGTSEAVLGSERIEQQLFFCSTF*		MDNEKPQDRVNVDCQGTSEAVLGSERIEQQLFFCSTF*		TCTTGTATTG	CGTACCGCCG	0	BK	0	0	0	0	0
6401	3101	af	AN0191.1	71.m15461	AO070321000052	0			-180	-82			ATGTCGATTGTCAAGGAACTAGCGAAGCGGTCTTGGGATCGGAGAGAATTGAACAGCAGCTTTTTTTTTGTTCAACTTTTTAGCGTACCGCCGCTTTAG		ATGTCGATTGTCAAGGAACTAGCGAAGCGGTCTTGGGATCGGAGAGAATTGAACAGCAGCTTTTTTTTTGTTCAACTTTTTAGCGTACCGCCGCTTTAG		MSIVKELAKRSWDRRELNSSFFFVQLFSVPPL*		MSIVKELAKRSWDRRELNSSFFFVQLFSVPPL*		GATCGTGTGA	TTTCCTTCCA	0	BK	0	0	0	0	0
6397	3101	an	AN0191.1	71.m15461	AO070321000052	0	-190	-176					ATGACGGTAAGATGA	ATGACGGTAAGATGA			MTVR*	MTVR*			AGGCGCTGAA	ATGTGCCGGT	0	BK	0	0	0	0	0
6398	3101	an	AN0191.1	71.m15461	AO070321000052	0	-179	-150					ATGAATGTGCCGGTAGTGCACGATTGTTAG	ATGAATGTGCCGGTAGTGCACGATTGTTAG			MNVPVVHDC*	MNVPVVHDC*			TGACGGTAAG	CTGTAGCGGT	0	BK	0	0	0	0	0
6399	3101	an	AN0191.1	71.m15461	AO070321000052	0	-175	-164					ATGTGCCGGTAG	ATGTGCCGGTAG			MCR*	MCR*			GGTAAGATGA	TGCACGATTG	0	BK	0	0	0	0	0
6403	3102	af	AN0189.1	71.m15459	AO070321000054	0			-186	-139			ATGCAGTTGTCAGGTCTGCAGAGTGTGAGCATGAAGCGCTATCTATAA		ATGCAGTTGTCAGGTCTGCAGAGTGTGAGCATGAAGCGCTATCTATAA		MQLSGLQSVSMKRYL*		MQLSGLQSVSMKRYL*		ACTTAACAAG	CCCATATAGG	0	A	0	MG01893.1	0	0	0
6404	3102	af	AN0189.1	71.m15459	AO070321000054	0			-156	-139			ATGAAGCGCTATCTATAA		ATGAAGCGCTATCTATAA		MKRYL*		MKRYL*		GAGTGTGAGC	CCCATATAGG	0	A	0	MG01893.1	0	0	0
6405	3102	af	AN0189.1	71.m15459	AO070321000054	0			-104	-93			ATGGACAGTTGA		ATGGACAGTTGA		MDS*		MDS*		GGTCTTCCGC	AATACTCCTC	0	A	0	MG01893.1	0	0	0
6406	3102	ao	AN0189.1	71.m15459	AO070321000054	0					-248	-207	ATGGACTACGATACTTCAAGTGATATACCAAGTAGACTGTAA			ATGGACTACGATACTTCAAGTGATATACCAAGTAGACTGTAA	MDYDTSSDIPSRL*			MDYDTSSDIPSRL*	TAGAAAGCCC	CTGCTGGAGT	0	A	0	MG01893.1	0	0	0
6408	3104	an	AN0174.1	71.m15447	AO070321000070	0	-196	-167					ATGAGAACCATCCACAATGGATTGGGGTAG	ATGAGAACCATCCACAATGGATTGGGGTAG			MRTIHNGLG*	MRTIHNGLG*			CCGATTGATA	CTCTCGATTG	0	E	0	MG08011.1	NCU06558.1	0	0
6409	3104	an	AN0174.1	71.m15447	AO070321000070	0	-180	-100					ATGGATTGGGGTAGCTCTCGATTGCTACGTAGTGGTCCTTGGCGATTGTACCATATATTCTCTCCAACTCGTATTGCATGA	ATGGATTGGGGTAGCTCTCGATTGCTACGTAGTGGTCCTTGGCGATTGTACCATATATTCTCTCCAACTCGTATTGCATGA			MDWGSSRLLRSGPWRLYHIFSPTRIA*	MDWGSSRLLRSGPWRLYHIFSPTRIA*			ACCATCCACA	TTGTTTCCTT	0	E	0	MG08011.1	NCU06558.1	0	0
6410	3104	an	AN0174.1	71.m15447	AO070321000070	0	-103	-77					ATGATTGTTTCCTTTTTTTTTCTCTGA	ATGATTGTTTCCTTTTTTTTTCTCTGA			MIVSFFFL*	MIVSFFFL*			CTCGTATTGC	TTATATCTTC	0	E	0	MG08011.1	NCU06558.1	0	0
6411	3104	ao	AN0174.1	71.m15447	AO070321000070	0					-134	-120	ATGACGATTATTTAA			ATGACGATTATTTAA	MTII*			MTII*	ATCCTTGATA	TTCAACTCGC	0	E	0	MG08011.1	NCU06558.1	0	0
6412	3104	ao	AN0174.1	71.m15447	AO070321000070	0					-108	-70	ATGTACTGGATCTTCAATTCCTCTTTTTTCTCTATATAG			ATGTACTGGATCTTCAATTCCTCTTTTTTCTCTATATAG	MYWIFNSSFFSI*			MYWIFNSSFFSI*	TCAACTCGCC	TCTTCATCTC	0	E	0	MG08011.1	NCU06558.1	0	0
6414	3114	an	AN7994.1	53.m03853	AO070322000052	0	-179	-132					ATGTTCCGAGGTCGGTACCTGAAAATATACCTTATATGTCAGGCATAA	ATGTTCCGAGGTCGGTACCTGAAAATATACCTTATATGTCAGGCATAA			MFRGRYLKIYLICQA*	MFRGRYLKIYLICQA*			GGCAAAATTG	ACCACTTAAC	0	L	FG06777.1	MG08646.1	0	YLR274W	0
6415	3114	ao	AN7994.1	53.m03853	AO070322000052	0					-163	-140	ATGCCTAAGGCCAAAACCACTTAA			ATGCCTAAGGCCAAAACCACTTAA	MPKAKTT*			MPKAKTT*	CAACTATTAG	CGCGTGCGAC	0	L	FG06777.1	MG08646.1	0	YLR274W	0
6434	3118	af	AN8057.1	53.m03886	AO070322000143	0			-230	-141			ATGTTGTATTGCGAAGACGAACTCAACAGAGGAAGAAATGGCTGGCTTCATTACGCCCAACTACTTGTTAGAAACCTCATCACGCCATAG		ATGTTGTATTGCGAAGACGAACTCAACAGAGGAAGAAATGGCTGGCTTCATTACGCCCAACTACTTGTTAGAAACCTCATCACGCCATAG		MLYCEDELNRGRNGWLHYAQLLVRNLITP*		MLYCEDELNRGRNGWLHYAQLLVRNLITP*		TGTAAGGCCT	TTCACGTGAC	0	E	FG07287.1	0	0	0	0
6435	3118	af	AN8057.1	53.m03886	AO070322000143	0			-193	-122			ATGGCTGGCTTCATTACGCCCAACTACTTGTTAGAAACCTCATCACGCCATAGTTCACGTGACCAAAGATGA		ATGGCTGGCTTCATTACGCCCAACTACTTGTTAGAAACCTCATCACGCCATAGTTCACGTGACCAAAGATGA		MAGFITPNYLLETSSRHSSRDQR*		MAGFITPNYLLETSSRHSSRDQR*		AGAGGAAGAA	CTAATGCCGA	0	E	FG07287.1	0	0	0	0

6436	3118	af	AN8057.1	53.m03886	AO070322000143	0			-125	-81			ATGACTAATGCCGATCTTCGGCGTCCGAGAATCTGGGGTTCTTAG		ATGACTAATGCCGATCTTCGGCGTCCGAGAATCTGGGGTTCTTAG		MTNADLRRPRIWGS*		MTNADLRRPRIWGS*		GTGACCAAAG	ACTCGCAAGT	0	E	FG07287.1	0	0	0	0
6437	3118	af	AN8057.1	53.m03886	AO070322000143	0			-118	-38			ATGCCGATCTTCGGCGTCCGAGAATCTGGGGTTCTTAGACTCGCAAGTCATTTTGTCTTTTTCCGGCGTGCATACCGTTGA		ATGCCGATCTTCGGCGTCCGAGAATCTGGGGTTCTTAGACTCGCAAGTCATTTTGTCTTTTTCCGGCGTGCATACCGTTGA		MPIFGVRESGVLRLASHFVFFRRAYR*		MPIFGVRESGVLRLASHFVFFRRAYR*		AAGATGACTA	ACGGGTGTCG	0	E	FG07287.1	0	0	0	0
6431	3118	an	AN8057.1	53.m03886	AO070322000143	0	-249	-223					ATGAATACAATGCCTCAGCTATCCTAA	ATGAATACAATGCCTCAGCTATCCTAA			MNTMPQLS*	MNTMPQLS*			TTCCTGATAC	TCACACACTG	0	E	FG07287.1	0	0	0	0
6432	3118	an	AN8057.1	53.m03886	AO070322000143	0	-240	-223					ATGCCTCAGCTATCCTAA	ATGCCTCAGCTATCCTAA			MPQLS*	MPQLS*			CATGAATACA	TCACACACTG	0	E	FG07287.1	0	0	0	0
6433	3118	an	AN8057.1	53.m03886	AO070322000143	0	-140	-102					ATGCCTTGCATACTAGCTAGCACGCCATCTTTCACGTGA	ATGCCTTGCATACTAGCTAGCACGCCATCTTTCACGTGA			MPCILASTPSFT*	MPCILASTPSFT*			CTGAGCCGAA	CCTCTTACTA	0	E	FG07287.1	0	0	0	0
6438	3118	ao	AN8057.1	53.m03886	AO070322000143	0					-251	-228	ATGTCACTCCATCAACTGGATTAA			ATGTCACTCCATCAACTGGATTAA	MSLHQLD*			MSLHQLD*	AGTTATCGTT	ATTAATATCA	0	E	FG07287.1	0	0	0	0
6439	3118	ao	AN8057.1	53.m03886	AO070322000143	0					-197	-138	ATGCGCAATGTACAATTGAGGGTCCTCTTCGTCCAAGCTATCACGCCATCGCTCACGTGA			ATGCGCAATGTACAATTGAGGGTCCTCTTCGTCCAAGCTATCACGCCATCGCTCACGTGA	MRNVQLRVLFVQAITPSLT*			MRNVQLRVLFVQAITPSLT*	AGTCAACGTT	TGCGCTATCG	0	E	FG07287.1	0	0	0	0
6440	3118	ao	AN8057.1	53.m03886	AO070322000143	0					-190	-179	ATGTACAATTGA			ATGTACAATTGA	MYN*			MYN*	GTTATGCGCA	GGGTCCTCTT	0	E	FG07287.1	0	0	0	0
6441	3118	ao	AN8057.1	53.m03886	AO070322000143	0					-138	-124	ATGCGCTATCGCTGA			ATGCGCTATCGCTGA	MRYR*			MRYR*	CGCTCACGTG	CTAAGGCCGA	0	E	FG07287.1	0	0	0	0
6442	3118	ao	AN8057.1	53.m03886	AO070322000143	0					-83	-66	ATGGTCTTCTTCCATTAA			ATGGTCTTCTTCCATTAA	MVFFH*			MVFFH*	GGGGAATGGA	TTGTCTCTTG	0	E	FG07287.1	0	0	0	0
6443	3119	an	AN8055.1	53.m03888	AO070322000145	0	-178	-161					ATGTTTTTTGTTGCTTGA	ATGTTTTTTGTTGCTTGA			MFFVA*	MFFVA*			CTTTCGCTGT	TTCACGACTT	0	R	0	0	0	0	0
6444	3121	an	AN4727.1	71.m15496	AO070323000057	0	-212	-120					ATGACGGATAAATCGATAGGTGGTCTGCCCCTCCACGAGGCTAGCCTGGCCGCTACACCCCCCCCACTATCCTCCTGCATCTGTACTCCGTAG	ATGACGGATAAATCGATAGGTGGTCTGCCCCTCCACGAGGCTAGCCTGGCCGCTACACCCCCCCCACTATCCTCCTGCATCTGTACTCCGTAG			MTDKSIGGLPLHEASLAATPPPLSSCICTP*	MTDKSIGGLPLHEASLAATPPPLSSCICTP*			AATGGCTGCA	CTCGCCATCG	0	M	FG05689.1	0	NCU04442.1	0	0
6445	3121	ao	AN4727.1	71.m15496	AO070323000057	0					-219	-172	ATGAAAATGAAATCCACCCGAACGCATGCCCCTCCGCAATTGTCCTAA			ATGAAAATGAAATCCACCCGAACGCATGCCCCTCCGCAATTGTCCTAA	MKMKSTRTHAPPQLS*			MKMKSTRTHAPPQLS*	TCCAAGTGGT	TTGTCCTCCC	0	M	FG05689.1	0	NCU04442.1	0	0
6446	3121	ao	AN4727.1	71.m15496	AO070323000057	0					-213	-172	ATGAAATCCACCCGAACGCATGCCCCTCCGCAATTGTCCTAA			ATGAAATCCACCCGAACGCATGCCCCTCCGCAATTGTCCTAA	MKSTRTHAPPQLS*			MKSTRTHAPPQLS*	TGGTATGAAA	TTGTCCTCCC	0	M	FG05689.1	0	NCU04442.1	0	0
6451	3122	af	AN8528.1	71.m15589	AO070323000191	0			-128	-84			ATGTTTATAGCGGGGGCTTACTGTATCTGCTTGCTAAGGAACTGA		ATGTTTATAGCGGGGGCTTACTGTATCTGCTTGCTAAGGAACTGA		MFIAGAYCICLLRN*		MFIAGAYCICLLRN*		TATATCAGCG	ACAACTCTAC	0	V	0	0	0	0	0
6447	3122	an	AN8528.1	71.m15589	AO070323000191	0	-216	-166					ATGGCAAGGCTTTCGAAGGTCGATGTGCTAGACAGGACACAGGACCTATGA	ATGGCAAGGCTTTCGAAGGTCGATGTGCTAGACAGGACACAGGACCTATGA			MARLSKVDVLDRTQDL*	MARLSKVDVLDRTQDL*			TTAACCATAG	GTCGCTATCA	0	V	0	0	0	0	0
6448	3122	an	AN8528.1	71.m15589	AO070323000191	0	-169	-122					ATGAGTCGCTATCATACTGGGTATGCGCGCAAGGAGGATCTACGCTAG	ATGAGTCGCTATCATACTGGGTATGCGCGCAAGGAGGATCTACGCTAG			MSRYHTGYARKEDLR*	MSRYHTGYARKEDLR*			CACAGGACCT	GAGTGGGCTA	0	V	0	0	0	0	0
6449	3122	an	AN8528.1	71.m15589	AO070323000191	0	-147	-43					ATGCGCGCAAGGAGGATCTACGCTAGGAGTGGGCTAGATCGAGAAAGAGCTCCACATGCTGCCGCTGACCAATGTTGTTATACCGAGGGACACTTATCTATTTAA	ATGCGCGCAAGGAGGATCTACGCTAGGAGTGGGCTAGATCGAGAAAGAGCTCCACATGCTGCCGCTGACCAATGTTGTTATACCGAGGGACACTTATCTATTTAA			MRARRIYARSGLDRERAPHAAADQCCYTEGHLSI*	MRARRIYARSGLDRERAPHAAADQCCYTEGHLSI*			CATACTGGGT	CCGGCTTCCC	0	V	0	0	0	0	0
6450	3122	an	AN8528.1	71.m15589	AO070323000191	0	-92	-18					ATGCTGCCGCTGACCAATGTTGTTATACCGAGGGACACTTATCTATTTAACCGGCTTCCCCTCTTCCACTTCTGA	ATGCTGCCGCTGACCAATGTTGTTATACCGAGGGACACTTATCTATTTAACCGGCTTCCCCTCTTCCACTTCTGA			MLPLTNVVIPRDTYLFNRLPLFHF*	MLPLTNVVIPRDTYLFNRLPLFHF*			AGAGCTCCAC	TTTCAACTTC	0	V	0	0	0	0	0
6452	3122	ao	AN8528.1	71.m15589	AO070323000191	0					-189	-145	ATGGAGTTACTTACAAGAATAAGCACTAAACGTTTTAGCTCCTAA			ATGGAGTTACTTACAAGAATAAGCACTAAACGTTTTAGCTCCTAA	MELLTRISTKRFSS*			MELLTRISTKRFSS*	CGGGGCGGTT	CATGACAAAT	0	V	0	0	0	0	0
6453	3122	ao	AN8528.1	71.m15589	AO070323000191	0					-143	-93	ATGACAAATTTAGTTCCCTCACTCAACGAGGCCAAAGAAAAGGATAAATAG			ATGACAAATTTAGTTCCCTCACTCAACGAGGCCAAAGAAAAGGATAAATAG	MTNLVPSLNEAKEKDK*			MTNLVPSLNEAKEKDK*	AGCTCCTAAC	CACCATGGGA	0	V	0	0	0	0	0
6454	3122	ao	AN8528.1	71.m15589	AO070323000191	0					-88	-71	ATGGGATCATTCAAATAA			ATGGGATCATTCAAATAA	MGSFK*			MGSFK*	AAATAGCACC	CGAATAAATT	0	V	0	0	0	0	0
6455	3124	af	AN1782.1	69.m15081	AO070324000013	0			-155	-57			ATGGAAAAACTGACAGCTCAACCGTCAGTTAATAGTATAGATATGAGTTTCACATTTGAATTTAAATCAAACTGGCTTGCTGAAGATATTCTTCTCTGA		ATGGAAAAACTGACAGCTCAACCGTCAGTTAATAGTATAGATATGAGTTTCACATTTGAATTTAAATCAAACTGGCTTGCTGAAGATATTCTTCTCTGA		MEKLTAQPSVNSIDMSFTFEFKSNWLAEDILL*		MEKLTAQPSVNSIDMSFTFEFKSNWLAEDILL*		AGGACAAGCA	TTCTGTTTTT	0	BK	0	0	0	0	0
6456	3124	af	AN1782.1	69.m15081	AO070324000013	0			-113	-57			ATGAGTTTCACATTTGAATTTAAATCAAACTGGCTTGCTGAAGATATTCTTCTCTGA		ATGAGTTTCACATTTGAATTTAAATCAAACTGGCTTGCTGAAGATATTCTTCTCTGA		MSFTFEFKSNWLAEDILL*		MSFTFEFKSNWLAEDILL*		TAGTATAGAT	TTCTGTTTTT	0	BK	0	0	0	0	0
6458	3124	ao	AN1782.1	69.m15081	AO070324000013	0					-231	-193	ATGCCACGCACTACCGACAGGGCCAACGTCATAATTTAA			ATGCCACGCACTACCGACAGGGCCAACGTCATAATTTAA	MPRTTDRANVII*			MPRTTDRANVII*	TACGGTTCAA	ACATCAACAT	0	BK	0	0	0	0	0
6459	3124	ao	AN1782.1	69.m15081	AO070324000013	0					-135	-115	ATGTTTCTACCCTTTTTTTAA			ATGTTTCTACCCTTTTTTTAA	MFLPFF*			MFLPFF*	GTCCGTGTAC	ATAAGAAAAA	0	BK	0	0	0	0	0
6460	3128	ao	AN1752.1	69.m15053	AO070324000041	0					-222	-76	ATGCCGATAAAAAATCTAATCGATAAGAGAGAACGAAAGAATCACGCAATTCACGCTAACCGCAATAGGCAAGGGCTCCCTGGGGATTTCTATAGACTGCGGATGGGGGGTTCGACTCTTTTTACCCCATTGCCTCCCACTTTGTGA			ATGCCGATAAAAAATCTAATCGATAAGAGAGAACGAAAGAATCACGCAATTCACGCTAACCGCAATAGGCAAGGGCTCCCTGGGGATTTCTATAGACTGCGGATGGGGGGTTCGACTCTTTTTACCCCATTGCCTCCCACTTTGTGA	MPIKNLIDKRERKNHAIHANRNRQGLPGDFYRLRMGGSTLFTPLPPTL*			MPIKNLIDKRERKNHAIHANRNRQGLPGDFYRLRMGGSTLFTPLPPTL*	ACCGCTGTAG	TTCATTCCTT	0	C	FG08463.1	MG00929.1	0	0	YFR030W
6461	3128	ao	AN1752.1	69.m15053	AO070324000041	0					-120	-76	ATGGGGGGTTCGACTCTTTTTACCCCATTGCCTCCCACTTTGTGA			ATGGGGGGTTCGACTCTTTTTACCCCATTGCCTCCCACTTTGTGA	MGGSTLFTPLPPTL*			MGGSTLFTPLPPTL*	TAGACTGCGG	TTCATTCCTT	0	C	FG08463.1	MG00929.1	0	0	YFR030W
6465	3133	af	AN7708.1	71.m15732	AO070325000115	0			-240	-64			ATGGGTAATCACCTGAGAAGCCTAGGAAATGATATCATTTGCACCAAGACCGACGGGGCGGGGCAAGTTGGAGGGGCTGGACACCGACCATCAGCGCCTACCAAATCTTCCTCTCCCCGCTCCATGTCCATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		ATGGGTAATCACCTGAGAAGCCTAGGAAATGATATCATTTGCACCAAGACCGACGGGGCGGGGCAAGTTGGAGGGGCTGGACACCGACCATCAGCGCCTACCAAATCTTCCTCTCCCCGCTCCATGTCCATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		MGNHLRSLGNDIICTKTDGAGQVGGAGHRPSAPTKSSSPRSMSMPLSHSSGQLISFRN*		MGNHLRSLGNDIICTKTDGAGQVGGAGHRPSAPTKSSSPRSMSMPLSHSSGQLISFRN*		GTAATAAATA	ATATATTCGA	0	R	FG07908.1	0	0	0	0
6466	3133	af	AN7708.1	71.m15732	AO070325000115	0			-212	-102			ATGATATCATTTGCACCAAGACCGACGGGGCGGGGCAAGTTGGAGGGGCTGGACACCGACCATCAGCGCCTACCAAATCTTCCTCTCCCCGCTCCATGTCCATGCCATTGA		ATGATATCATTTGCACCAAGACCGACGGGGCGGGGCAAGTTGGAGGGGCTGGACACCGACCATCAGCGCCTACCAAATCTTCCTCTCCCCGCTCCATGTCCATGCCATTGA		MISFAPRPTGRGKLEGLDTDHQRLPNLPLPAPCPCH*		MISFAPRPTGRGKLEGLDTDHQRLPNLPLPAPCPCH*		AGCCTAGGAA	GTCACTCTTC	0	R	FG07908.1	0	0	0	0
6467	3133	af	AN7708.1	71.m15732	AO070325000115	0			-117	-64			ATGTCCATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		ATGTCCATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		MSMPLSHSSGQLISFRN*		MSMPLSHSSGQLISFRN*		TCCCCGCTCC	ATATATTCGA	0	R	FG07908.1	0	0	0	0
6468	3133	af	AN7708.1	71.m15732	AO070325000115	0			-111	-64			ATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		ATGCCATTGAGTCACTCTTCTGGCCAACTTATAAGCTTCAGAAACTGA		MPLSHSSGQLISFRN*		MPLSHSSGQLISFRN*		CTCCATGTCC	ATATATTCGA	0	R	FG07908.1	0	0	0	0
6462	3133	an	AN7708.1	71.m15732	AO070325000115	0	-150	-7					ATGGAACGGGCGTATGATATCATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAATTTTTTTTGTCCCTAGAATCTCACGCTATTCAGCAAGATAA	ATGGAACGGGCGTATGATATCATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAATTTTTTTTGTCCCTAGAATCTCACGCTATTCAGCAAGATAA			MERAYDIMGSSGAPTEFLPANVYITSSQPTRDHVIFFVPRISRYSAR*	MERAYDIMGSSGAPTEFLPANVYITSSQPTRDHVIFFVPRISRYSAR*			ATCGCAAGCA	CAAGCCATGT	0	R	FG07908.1	0	0	0	0
6463	3133	an	AN7708.1	71.m15732	AO070325000115	0	-137	-48					ATGATATCATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAA	ATGATATCATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAA			MISWAAAGHQPNFSPPTSISPRRSPRETT*	MISWAAAGHQPNFSPPTSISPRRSPRETT*			GAACGGGCGT	TTTTTTTTGT	0	R	FG07908.1	0	0	0	0
6464	3133	an	AN7708.1	71.m15732	AO070325000115	0	-129	-7					ATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAATTTTTTTTGTCCCTAGAATCTCACGCTATTCAGCAAGATAA	ATGGGCAGCAGCGGGGCACCAACCGAATTTCTCCCCGCCAACGTCTATATCACCTCGTCGCAGCCCACGAGAGACCACGTAATTTTTTTTGTCCCTAGAATCTCACGCTATTCAGCAAGATAA			MGSSGAPTEFLPANVYITSSQPTRDHVIFFVPRISRYSAR*	MGSSGAPTEFLPANVYITSSQPTRDHVIFFVPRISRYSAR*			GTATGATATC	CAAGCCATGT	0	R	FG07908.1	0	0	0	0
6469	3133	ao	AN7708.1	71.m15732	AO070325000115	0					-232	-8	ATGATATCATTTTCGGGGCGGGGCAATTGTCTCCCACGCGCAACCTACCACAGCCGAATCCCTTCTGCTCGCTGCTTCCGGGTCTCGAGTTACCTGGTTACATTTTTGTTCTTTGAATCGGTCGGCTATTACGGGATTGTCTTGAGCTTGTACTCTCTTTTTATTTATTTATTTTTTTTTATTTTTTTATTTGACTTTTGGGTTTTGTTTGCCGGCCTTGCCTGA			ATGATATCATTTTCGGGGCGGGGCAATTGTCTCCCACGCGCAACCTACCACAGCCGAATCCCTTCTGCTCGCTGCTTCCGGGTCTCGAGTTACCTGGTTACATTTTTGTTCTTTGAATCGGTCGGCTATTACGGGATTGTCTTGAGCTTGTACTCTCTTTTTATTTATTTATTTTTTTTTATTTTTTTATTTGACTTTTGGGTTTTGTTTGCCGGCCTTGCCTGA	MISFSGRGNCLPRATYHSRIPSARCFRVSSYLVTFLFFESVGYYGIVLSLYSLFIYLFFFIFLFDFWVLFAGLA*			MISFSGRGNCLPRATYHSRIPSARCFRVSSYLVTFLFFESVGYYGIVLSLYSLFIYLFFFIFLFDFWVLFAGLA*	CCCTTTCGGT	TTTTATCATG	0	R	FG07908.1	0	0	0	0
6471	3136	af	AN6569.1	62.m03156	AO070326000012	0			-82	-44			ATGAGCCAACTTCTAATGGATATGATTATTTTCCCTTGA		ATGAGCCAACTTCTAATGGATATGATTATTTTCCCTTGA		MSQLLMDMIIFP*		MSQLLMDMIIFP*		CCTGTAACGA	AATTTGAATC	0	O	0	0	0	0	0
6472	3136	af	AN6569.1	62.m03156	AO070326000012	0			-67	-44			ATGGATATGATTATTTTCCCTTGA		ATGGATATGATTATTTTCCCTTGA		MDMIIFP*		MDMIIFP*		CCAACTTCTA	AATTTGAATC	0	O	0	0	0	0	0
6473	3136	af	AN6569.1	62.m03156	AO070326000012	0			-61	-44			ATGATTATTTTCCCTTGA		ATGATTATTTTCCCTTGA		MIIFP*		MIIFP*		TCTAATGGAT	AATTTGAATC	0	O	0	0	0	0	0
6474	3136	ao	AN6569.1	62.m03156	AO070326000012	0					-115	-92	ATGAAAATAATCTCCTCATTGTAA			ATGAAAATAATCTCCTCATTGTAA	MKIISSL*			MKIISSL*	TGGCTCATCA	ACCCCCCTCC	0	O	0	0	0	0	0
6475	3137	af	AN6589.1	62.m03178	AO070326000037	0			-163	-149			ATGAAGTCCATTTGA		ATGAAGTCCATTTGA		MKSI*		MKSI*		TACAATATCA	GTAATCAAAT	0	T	FG05591.1	0	0	0	0
6476	3137	ao	AN6589.1	62.m03178	AO070326000037	0					-188	-156	ATGTGTCCAGTTTCAATTTCTAAAATTCTTTGA			ATGTGTCCAGTTTCAATTTCTAAAATTCTTTGA	MCPVSISKIL*			MCPVSISKIL*	TTCAATTTCA	CACCCCTATC	0	T	FG05591.1	0	0	0	0
6479	3139	af	AN6636.1	62.m03467	AO070326000087	0			-246	-211			ATGATTTTTGTTTCCTGTCCGACTACACCATCTTGA		ATGATTTTTGTTTCCTGTCCGACTACACCATCTTGA		MIFVSCPTTPS*		MIFVSCPTTPS*		CAACTGCGCT	CTACACTTCA	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6480	3139	af	AN6636.1	62.m03467	AO070326000087	0			-107	-9			ATGGGGCCACTCTTCTGGCCTTCCTCTACCGGGTTCCGTCCAGGTACGAACCACACATCCTCCGAGAGAGGCTCTGGGAATCAATTGAGCTGCAATTGA		ATGGGGCCACTCTTCTGGCCTTCCTCTACCGGGTTCCGTCCAGGTACGAACCACACATCCTCCGAGAGAGGCTCTGGGAATCAATTGAGCTGCAATTGA		MGPLFWPSSTGFRPGTNHTSSERGSGNQLSCN*		MGPLFWPSSTGFRPGTNHTSSERGSGNQLSCN*		CGATAAAAAG	TTGCAAAGAT	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6478	3139	an	AN6636.1	62.m03467	AO070326000087	0	-151	-131					ATGAATGTGTCGAGTACCTAG	ATGAATGTGTCGAGTACCTAG			MNVSST*	MNVSST*			AAGGTAGTTA	AGACCGGCAC	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6481	3139	ao	AN6636.1	62.m03467	AO070326000087	0					-182	-111	ATGTATTGTCTGATGTATGTACTATTCTATTCTATAGGATGGGTGGCACGTGCACCCTATCGGAGTGGCTGA			ATGTATTGTCTGATGTATGTACTATTCTATTCTATAGGATGGGTGGCACGTGCACCCTATCGGAGTGGCTGA	MYCLMYVLFYSIGWVARAPYRSG*			MYCLMYVLFYSIGWVARAPYRSG*	GGGGAAGGAA	TAAAACAATG	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6482	3139	ao	AN6636.1	62.m03467	AO070326000087	0					-170	-111	ATGTATGTACTATTCTATTCTATAGGATGGGTGGCACGTGCACCCTATCGGAGTGGCTGA			ATGTATGTACTATTCTATTCTATAGGATGGGTGGCACGTGCACCCTATCGGAGTGGCTGA	MYVLFYSIGWVARAPYRSG*			MYVLFYSIGWVARAPYRSG*	GTATTGTCTG	TAAAACAATG	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6483	3139	ao	AN6636.1	62.m03467	AO070326000087	0					-166	-146	ATGTACTATTCTATTCTATAG			ATGTACTATTCTATTCTATAG	MYYSIL*			MYYSIL*	TGTCTGATGT	GATGGGTGGC	0	C	FG08596.1	MG02766.1	0	YHR039C	0
6503	3142	af	AN2234.1	71.m15831	AO070326000145	0			-148	-35			ATGGAAGCTACGGTTTGTGTTTGCGCTGTTTGCAATACTGTTGAGCTTCCCCGCTATTGTCCGGGCCATCTCTACAGTCCCACTTTATCGTTCGAAAGTGTTCCGGCAGCTTGA		ATGGAAGCTACGGTTTGTGTTTGCGCTGTTTGCAATACTGTTGAGCTTCCCCGCTATTGTCCGGGCCATCTCTACAGTCCCACTTTATCGTTCGAAAGTGTTCCGGCAGCTTGA		MEATVCVCAVCNTVELPRYCPGHLYSPTLSFESVPAA*		MEATVCVCAVCNTVELPRYCPGHLYSPTLSFESVPAA*		GCCCAAGTTG	GAAGCGGTTA	0		0	0	0	0	0
6501	3142	an	AN2234.1	71.m15831	AO070326000145	0	-217	-203					ATGCGTGTTGTTTAA	ATGCGTGTTGTTTAA			MRVV*	MRVV*			GCGTGTGTGT	AGGTGCGATT	0		0	0	0	0	0
6502	3142	an	AN2234.1	71.m15831	AO070326000145	0	-146	-78					ATGGTTGATAAGCTCTCTCCCCGGCTCAAGAGGGGGCCCAGGTCGGCCGAGTTTGCTTTGTTTGCATGA	ATGGTTGATAAGCTCTCTCCCCGGCTCAAGAGGGGGCCCAGGTCGGCCGAGTTTGCTTTGTTTGCATGA			MVDKLSPRLKRGPRSAEFALFA*	MVDKLSPRLKRGPRSAEFALFA*			TTTGGTGGTC	GAAGCTTCCC	0		0	0	0	0	0

6504	3142	ao	AN2234.1	71.m15831	AO070326000145	0					-206	-174	ATGGCTGTTCCTAGAACTGCGTTTGGAGGTTGA			ATGGCTGTTCCTAGAACTGCGTTTGGAGGTTGA	MAVPRTAFGG*			MAVPRTAFGG*	GGGGCTACAA	CTTGTAGAGG	0		0	0	0	0	0
6505	3142	ao	AN2234.1	71.m15831	AO070326000145	0					-154	-20	ATGGAGAGTGCGGAGCTATCGTTGCTGTTTGTCGTGTTTGCATTGAGCTTCCCCACCATCACAAAGGATAGATGCGGCGTTCCTGAGCAACCATCTTCTATCTATCCATCAGCTGTGGGAGAGGGTCGCTTGTGA			ATGGAGAGTGCGGAGCTATCGTTGCTGTTTGTCGTGTTTGCATTGAGCTTCCCCACCATCACAAAGGATAGATGCGGCGTTCCTGAGCAACCATCTTCTATCTATCCATCAGCTGTGGGAGAGGGTCGCTTGTGA	MESAELSLLFVVFALSFPTITKDRCGVPEQPSSIYPSAVGEGRL*			MESAELSLLFVVFALSFPTITKDRCGVPEQPSSIYPSAVGEGRL*	GAACTAAACC	ATGAAATATT	0		0	0	0	0	0
6506	3142	ao	AN2234.1	71.m15831	AO070326000145	0					-83	-69	ATGCGGCGTTCCTGA			ATGCGGCGTTCCTGA	MRRS*			MRRS*	CAAAGGATAG	GCAACCATCT	0		0	0	0	0	0
6507	3143	an	AN2227.1	71.m15838	AO070326000160	0	-204	-181					ATGGAGAACTGGGGTTGGGATTAG	ATGGAGAACTGGGGTTGGGATTAG			MENWGWD*	MENWGWD*			AGACGGTGCA	TACGTATATC	0	G	0	0	0	0	0
6508	3143	an	AN2227.1	71.m15838	AO070326000160	0	-115	-98					ATGCTTGTCAATTTCTGA	ATGCTTGTCAATTTCTGA			MLVNF*	MLVNF*			TTGTCATTTT	CCTGGTTTGC	0	G	0	0	0	0	0
6509	3143	ao	AN2227.1	71.m15838	AO070326000160	0					-211	-113	ATGCCTCGTAGTCCTTCGTATTCTGGTTTTCTTATCCTTTTATCCTTTATACCTCTTCCTACCTTTTCATCTATCGTTTTTGCACTATTCCACCCATAG			ATGCCTCGTAGTCCTTCGTATTCTGGTTTTCTTATCCTTTTATCCTTTATACCTCTTCCTACCTTTTCATCTATCGTTTTTGCACTATTCCACCCATAG	MPRSPSYSGFLILLSFIPLPTFSSIVFALFHP*			MPRSPSYSGFLILLSFIPLPTFSSIVFALFHP*	ATATATTTGT	TTTTGGTCGG	0	G	0	0	0	0	0
6510	3144	af	AN3423.1	59.m09501	AO070327000008	0			-249	-67			ATGGGCGACGGAGGCGCTACTGAAGGAGAGGAGCAGCAGCATACTCCGTACTCCGTTCTAGTTTTCCATCTCCATCTTATTTCCCATACCCAGCCACTGTCTGGTGTCCTTTCTCGTGTGTTCATTCTTCTTGTTCATCGCTTCTTCTACTTTCCCTTACCATTTTCTCCTTCCTCTCATTAG		ATGGGCGACGGAGGCGCTACTGAAGGAGAGGAGCAGCAGCATACTCCGTACTCCGTTCTAGTTTTCCATCTCCATCTTATTTCCCATACCCAGCCACTGTCTGGTGTCCTTTCTCGTGTGTTCATTCTTCTTGTTCATCGCTTCTTCTACTTTCCCTTACCATTTTCTCCTTCCTCTCATTAG		MGDGGATEGEEQQHTPYSVLVFHLHLISHTQPLSGVLSRVFILLVHRFFYFPLPFSPSSH*		MGDGGATEGEEQQHTPYSVLVFHLHLISHTQPLSGVLSRVFILLVHRFFYFPLPFSPSSH*		AGTCTCTCTG	ATTTTACATT	0	A	0	0	0	0	0
6511	3145	ao	AN2761.1	59.m09263	AO070327000023	0					-213	-67	ATGTATTCCTTCTCTTCCTTCTCATTACATCCTATAGATAATATTAGTCTTCCATCACCTCCAGCCTTAAAAGTACTGACCGGATTGTGTTGTGCAGATTTCTTAAATTCGATACCAACCGCTCTTTCGACTGAGCGGTCGCTTTAA			ATGTATTCCTTCTCTTCCTTCTCATTACATCCTATAGATAATATTAGTCTTCCATCACCTCCAGCCTTAAAAGTACTGACCGGATTGTGTTGTGCAGATTTCTTAAATTCGATACCAACCGCTCTTTCGACTGAGCGGTCGCTTTAA	MYSFSSFSLHPIDNISLPSPPALKVLTGLCCADFLNSIPTALSTERSL*			MYSFSSFSLHPIDNISLPSPPALKVLTGLCCADFLNSIPTALSTERSL*	TTGATTTTTG	AAGCCTCTCT	0	O	0	0	0	0	0
6512	3148	af	AN4819.1	59.m09156	AO070327000168	0			-179	-144			ATGAGCCCCTTGTTCGACCGTTTTGGTCATTTCTAG		ATGAGCCCCTTGTTCGACCGTTTTGGTCATTTCTAG		MSPLFDRFGHF*		MSPLFDRFGHF*		TTAAATCCAC	TGCTCCTTTG	0	E	0	0	0	0	0
6513	3148	af	AN4819.1	59.m09156	AO070327000168	0			-94	-83			ATGACGCATTAG		ATGACGCATTAG		MTH*		MTH*		CACTTCTTCC	CCTTCATCGT	0	E	0	0	0	0	0
6514	3148	ao	AN4819.1	59.m09156	AO070327000168	0					-88	-62	ATGAACATACTATCATTTATCTCATAA			ATGAACATACTATCATTTATCTCATAA	MNILSFIS*			MNILSFIS*	CTATTCTGTG	TTACGACACT	0	E	0	0	0	0	0
6519	3149	af	AN5601.1	58.m07525	AO070328000003	0			-143	-129			ATGGATCACACGTGA		ATGGATCACACGTGA		MDHT*		MDHT*		ACTGCACCAT	CTTCACATGA	0	E	0	MG08564.1	0	YNR050C	0
6515	3149	an	AN5601.1	58.m07525	AO070328000003	0	-224	-30					ATGACAAATGAGGCTTGTTTTTCTGGACCACTTCATTTTGATAGAGATAACAACAGAACTATAATTATCATTGGGTGCTTCTATTGGCATAAATGCCGGAGCTGTCTCCGATACCGCCCTGAATTAGTTCACGTGATCATCCCTATGGCGGGGATAACTTTTGAATCAGGTCTTCTTGACTCATTTGATTCTTAG	ATGACAAATGAGGCTTGTTTTTCTGGACCACTTCATTTTGATAGAGATAACAACAGAACTATAATTATCATTGGGTGCTTCTATTGGCATAAATGCCGGAGCTGTCTCCGATACCGCCCTGAATTAGTTCACGTGATCATCCCTATGGCGGGGATAACTTTTGAATCAGGTCTTCTTGACTCATTTGATTCTTAG			MTNEACFSGPLHFDRDNNRTIIIIGCFYWHKCRSCLRYRPELVHVIIPMAGITFESGLLDSFDS*	MTNEACFSGPLHFDRDNNRTIIIIGCFYWHKCRSCLRYRPELVHVIIPMAGITFESGLLDSFDS*			TTCCATAGCA	TACAATCAAT	0	E	0	MG08564.1	0	YNR050C	0
6516	3149	an	AN5601.1	58.m07525	AO070328000003	0	-217	-161					ATGAGGCTTGTTTTTCTGGACCACTTCATTTTGATAGAGATAACAACAGAACTATAA	ATGAGGCTTGTTTTTCTGGACCACTTCATTTTGATAGAGATAACAACAGAACTATAA			MRLVFLDHFILIEITTEL*	MRLVFLDHFILIEITTEL*			GCAATGACAA	TTATCATTGG	0	E	0	MG08564.1	0	YNR050C	0
6517	3149	an	AN5601.1	58.m07525	AO070328000003	0	-132	-103					ATGCCGGAGCTGTCTCCGATACCGCCCTGA	ATGCCGGAGCTGTCTCCGATACCGCCCTGA			MPELSPIPP*	MPELSPIPP*			ATTGGCATAA	ATTAGTTCAC	0	E	0	MG08564.1	0	YNR050C	0
6518	3149	an	AN5601.1	58.m07525	AO070328000003	0	-80	-30					ATGGCGGGGATAACTTTTGAATCAGGTCTTCTTGACTCATTTGATTCTTAG	ATGGCGGGGATAACTTTTGAATCAGGTCTTCTTGACTCATTTGATTCTTAG			MAGITFESGLLDSFDS*	MAGITFESGLLDSFDS*			GATCATCCCT	TACAATCAAT	0	E	0	MG08564.1	0	YNR050C	0
6520	3149	ao	AN5601.1	58.m07525	AO070328000003	0					-164	-9	ATGATAATCCACACCTCCGATACCGCCGTCCCCAGGTGGACCCACGTGACTGAGTCATCACACAACTGCCGGCGGGGAAGACCAGCGAGATCACTGACTCTCTTTCTTTTCCTTCTCAATCCTTTGACACATACTACTTCCTATCTTCTTCCCTAA			ATGATAATCCACACCTCCGATACCGCCGTCCCCAGGTGGACCCACGTGACTGAGTCATCACACAACTGCCGGCGGGGAAGACCAGCGAGATCACTGACTCTCTTTCTTTTCCTTCTCAATCCTTTGACACATACTACTTCCTATCTTCTTCCCTAA	MIIHTSDTAVPRWTHVTESSHNCRRGRPARSLTLFLFLLNPLTHTTSYLLP*			MIIHTSDTAVPRWTHVTESSHNCRRGRPARSLTLFLFLLNPLTHTTSYLLP*	TTTAGTTAAT	TCGTCACAAT	0	E	0	MG08564.1	0	YNR050C	0
6526	3154	af	AN5558.1	58.m07484	AO070328000053	0			-251	-237			ATGTTACCCTGTTAG		ATGTTACCCTGTTAG		MLPC*		MLPC*		CAGAGTTGCA	TTCCCACTGC	0	O	0	0	0	0	0
6527	3154	af	AN5558.1	58.m07484	AO070328000053	0			-158	-99			ATGAAAATGGCACAAGTGCTGAAGAACATGAATGGAACACGAAGAGACAAAAAGTTATAA		ATGAAAATGGCACAAGTGCTGAAGAACATGAATGGAACACGAAGAGACAAAAAGTTATAA		MKMAQVLKNMNGTRRDKKL*		MKMAQVLKNMNGTRRDKKL*		ATTCTGAGGC	ATACCTGCCT	0	O	0	0	0	0	0
6528	3154	af	AN5558.1	58.m07484	AO070328000053	0			-152	-99			ATGGCACAAGTGCTGAAGAACATGAATGGAACACGAAGAGACAAAAAGTTATAA		ATGGCACAAGTGCTGAAGAACATGAATGGAACACGAAGAGACAAAAAGTTATAA		MAQVLKNMNGTRRDKKL*		MAQVLKNMNGTRRDKKL*		AGGCATGAAA	ATACCTGCCT	0	O	0	0	0	0	0
6529	3154	af	AN5558.1	58.m07484	AO070328000053	0			-131	-99			ATGAATGGAACACGAAGAGACAAAAAGTTATAA		ATGAATGGAACACGAAGAGACAAAAAGTTATAA		MNGTRRDKKL*		MNGTRRDKKL*		GCTGAAGAAC	ATACCTGCCT	0	O	0	0	0	0	0
6522	3154	an	AN5558.1	58.m07484	AO070328000053	0	-220	-182					ATGTCACCCTGTGAGTTTTCACGAGTCGACCCTGGTTAA	ATGTCACCCTGTGAGTTTTCACGAGTCGACCCTGGTTAA			MSPCEFSRVDPG*	MSPCEFSRVDPG*			GAAGGACGCA	TTCGTGATGG	0	O	0	0	0	0	0
6523	3154	an	AN5558.1	58.m07484	AO070328000053	0	-175	-119					ATGGACGAGGTCAATGACGCAGAATTGGAGGTGATGAAGTGGGCGCGAAAGGTATAA	ATGGACGAGGTCAATGACGCAGAATTGGAGGTGATGAAGTGGGCGCGAAAGGTATAA			MDEVNDAELEVMKWARKV*	MDEVNDAELEVMKWARKV*			TTAATTCGTG	GAGTGGGGTT	0	O	0	0	0	0	0
6524	3154	an	AN5558.1	58.m07484	AO070328000053	0	-162	-142					ATGACGCAGAATTGGAGGTGA	ATGACGCAGAATTGGAGGTGA			MTQNWR*	MTQNWR*			GACGAGGTCA	TGAAGTGGGC	0	O	0	0	0	0	0
6525	3154	an	AN5558.1	58.m07484	AO070328000053	0	-142	-119					ATGAAGTGGGCGCGAAAGGTATAA	ATGAAGTGGGCGCGAAAGGTATAA			MKWARKV*	MKWARKV*			ATTGGAGGTG	GAGTGGGGTT	0	O	0	0	0	0	0
6530	3154	ao	AN5558.1	58.m07484	AO070328000053	0					-236	-198	ATGCAATGTCACCCTGTAAGTTTCAACTACAATCTGTAG			ATGCAATGTCACCCTGTAAGTTTCAACTACAATCTGTAG	MQCHPVSFNYNL*			MQCHPVSFNYNL*	GTCCTCTGAG	TACAGAGCAT	0	O	0	0	0	0	0
6531	3154	ao	AN5558.1	58.m07484	AO070328000053	0					-231	-148	ATGTCACCCTGTAAGTTTCAACTACAATCTGTAGTACAGAGCATCCTTGTCATTGCATGCTGTGCAAGTGATCCAAATCCGTAG			ATGTCACCCTGTAAGTTTCAACTACAATCTGTAGTACAGAGCATCCTTGTCATTGCATGCTGTGCAAGTGATCCAAATCCGTAG	MSPCKFQLQSVVQSILVIACCASDPNP*			MSPCKFQLQSVVQSILVIACCASDPNP*	CTGAGATGCA	AACTTGCTCG	0	O	0	0	0	0	0
6532	3154	ao	AN5558.1	58.m07484	AO070328000053	0					-175	-161	ATGCTGTGCAAGTGA			ATGCTGTGCAAGTGA	MLCK*			MLCK*	TTGTCATTGC	TCCAAATCCG	0	O	0	0	0	0	0
6533	3158	af	AN3644.1	58.m08910	AO070328000090	0			-190	-137			ATGACTCCTCGAAAACATGGCAGCGGTGACAAGTACCTCAGGCACCCAGGCTAA		ATGACTCCTCGAAAACATGGCAGCGGTGACAAGTACCTCAGGCACCCAGGCTAA		MTPRKHGSGDKYLRHPG*		MTPRKHGSGDKYLRHPG*		ATCACGTGAT	CTAAAATTAA	0	O	0	0	0	0	0
6534	3158	af	AN3644.1	58.m08910	AO070328000090	0			-174	-133			ATGGCAGCGGTGACAAGTACCTCAGGCACCCAGGCTAACTAA		ATGGCAGCGGTGACAAGTACCTCAGGCACCCAGGCTAACTAA		MAAVTSTSGTQAN*		MAAVTSTSGTQAN*		CCTCGAAAAC	AATTAACAGT	0	O	0	0	0	0	0
6536	3160	af	AN4023.1	54.m06548	AO070328000112	0			-219	-136			ATGTATGTCAAGGAAACGTTCAGGGCTCGGAAGTTGAAGGTTGTGCGAAACCAATTGCATTCATCTTTCCATTTCATCCTCTAA		ATGTATGTCAAGGAAACGTTCAGGGCTCGGAAGTTGAAGGTTGTGCGAAACCAATTGCATTCATCTTTCCATTTCATCCTCTAA		MYVKETFRARKLKVVRNQLHSSFHFIL*		MYVKETFRARKLKVVRNQLHSSFHFIL*		TGATTATTGA	GGTAGGTCTA	0	S	0	0	0	0	0
6537	3160	af	AN4023.1	54.m06548	AO070328000112	0			-215	-183			ATGTCAAGGAAACGTTCAGGGCTCGGAAGTTGA		ATGTCAAGGAAACGTTCAGGGCTCGGAAGTTGA		MSRKRSGLGS*		MSRKRSGLGS*		TATTGAATGT	AGGTTGTGCG	0	S	0	0	0	0	0
6538	3160	af	AN4023.1	54.m06548	AO070328000112	0			-107	-93			ATGATGACTCACTGA		ATGATGACTCACTGA		MMTH*		MMTH*		GATTTGTTAT	GTACTACATA	0	S	0	0	0	0	0
6539	3160	af	AN4023.1	54.m06548	AO070328000112	0			-104	-93			ATGACTCACTGA		ATGACTCACTGA		MTH*		MTH*		TTGTTATATG	GTACTACATA	0	S	0	0	0	0	0
6535	3160	an	AN4023.1	54.m06548	AO070328000112	0	-116	-87					ATGATCATACTGATTTCATGGCGTAGCTAA	ATGATCATACTGATTTCATGGCGTAGCTAA			MIILISWRS*	MIILISWRS*			GTGCCATCAT	CAGACTCTAG	0	S	0	0	0	0	0
6541	3165	af	AN4793.1	59.m09188	AO070329000053	0			-312	-259			ATGTTTCTGTGCCTGGAAATTGCTTCTGTGCTGCGTTTGTCAAAAGCGATATGA		ATGTTTCTGTGCCTGGAAATTGCTTCTGTGCTGCGTTTGTCAAAAGCGATATGA		MFLCLEIASVLRLSKAI*		MFLCLEIASVLRLSKAI*		GTTAGTGGAT	TGTCCGTCGC	0	E	FG08498.1	MG03051.1	0	0	0
6542	3165	af	AN4793.1	59.m09188	AO070329000053	0			-262	-245			ATGATGTCCGTCGCTTGA		ATGATGTCCGTCGCTTGA		MMSVA*		MMSVA*		CAAAAGCGAT	AGAAGGGGCA	0	E	FG08498.1	MG03051.1	0	0	0
6543	3165	af	AN4793.1	59.m09188	AO070329000053	0			-259	-245			ATGTCCGTCGCTTGA		ATGTCCGTCGCTTGA		MSVA*		MSVA*		AAGCGATATG	AGAAGGGGCA	0	E	FG08498.1	MG03051.1	0	0	0
6544	3165	af	AN4793.1	59.m09188	AO070329000053	0			-144	-118			ATGTCATTCCATTCTTTTTATGACTGA		ATGTCATTCCATTCTTTTTATGACTGA		MSFHSFYD*		MSFHSFYD*		AAGGCTTTGC	TTGATAAATG	0	E	FG08498.1	MG03051.1	0	0	0
6545	3165	af	AN4793.1	59.m09188	AO070329000053	0			-125	-114			ATGACTGATTGA		ATGACTGATTGA		MTD*		MTD*		CATTCTTTTT	TAAATGGACT	0	E	FG08498.1	MG03051.1	0	0	0
6546	3165	af	AN4793.1	59.m09188	AO070329000053	0			-110	-84			ATGGACTTTTCATGCTTCGAATTTTAG		ATGGACTTTTCATGCTTCGAATTTTAG		MDFSCFEF*		MDFSCFEF*		TGATTGATAA	CTCATCCCTA	0	E	FG08498.1	MG03051.1	0	0	0
6547	3165	af	AN4793.1	59.m09188	AO070329000053	0			-99	-64			ATGCTTCGAATTTTAGCTCATCCCTATTATATCTAG		ATGCTTCGAATTTTAGCTCATCCCTATTATATCTAG		MLRILAHPYYI*		MLRILAHPYYI*		TGGACTTTTC	CTAATTGACT	0	E	FG08498.1	MG03051.1	0	0	0
6540	3165	an	AN4793.1	59.m09188	AO070329000053	0	-147	-70					ATGAGTTTACTGTTAAATCACTTCAGCCACTGTTCTGGTGTTGTCTCTACTCTGTCTATCAGGAGTCTTCTGATTTAA	ATGAGTTTACTGTTAAATCACTTCAGCCACTGTTCTGGTGTTGTCTCTACTCTGTCTATCAGGAGTCTTCTGATTTAA			MSLLLNHFSHCSGVVSTLSIRSLLI*	MSLLLNHFSHCSGVVSTLSIRSLLI*			TTGGCCCTGA	AGTCTTCTTA	0	E	FG08498.1	MG03051.1	0	0	0
6548	3165	ao	AN4793.1	59.m09188	AO070329000053	0					-116	-93	ATGGTTGTTACTCCAATCAATTAG			ATGGTTGTTACTCCAATCAATTAG	MVVTPIN*			MVVTPIN*	AGGGGCATCG	CACCATTGAT	0	E	FG08498.1	MG03051.1	0	0	0
6549	3165	ao	AN4793.1	59.m09188	AO070329000053	0					-84	-61	ATGATCTCTACATTAGTCTCTTGA			ATGATCTCTACATTAGTCTCTTGA	MISTLVS*			MISTLVS*	AGCACCATTG	ATTTCTCGGC	0	E	FG08498.1	MG03051.1	0	0	0
6550	3166	af	AN4777.1	59.m09469	AO070329000074	0			-232	-194			ATGGGACGAGCACACGGCCCGTGTCAAAATTACCAGTAA		ATGGGACGAGCACACGGCCCGTGTCAAAATTACCAGTAA		MGRAHGPCQNYQ*		MGRAHGPCQNYQ*		TTGGGCGGGG	GAGGAAGGTA	0	J	FG06407.1	MG02872.1	0	YHR021C	0
6551	3166	ao	AN4777.1	59.m09469	AO070329000074	0					-235	-11	ATGGTACGGGGTAAAGCTGCCGGGTACGCCAAGACTCCTGAAAGGAGTATTGTTAGCGAGGGCTTGAGCCCTATTTTCCCAGAAAGGGCCAGTGGGTTGAACGGGAGCAGTGAATTCCCTTCAGAGTTTGCCCTCTCCACGAGACCACCTTCTTCGTTCCTCACCCTTCAAGCAGGCCATCTCCATCAGCGCACCATTCAACTTTTATCGCTGATCGACTTTTAG			ATGGTACGGGGTAAAGCTGCCGGGTACGCCAAGACTCCTGAAAGGAGTATTGTTAGCGAGGGCTTGAGCCCTATTTTCCCAGAAAGGGCCAGTGGGTTGAACGGGAGCAGTGAATTCCCTTCAGAGTTTGCCCTCTCCACGAGACCACCTTCTTCGTTCCTCACCCTTCAAGCAGGCCATCTCCATCAGCGCACCATTCAACTTTTATCGCTGATCGACTTTTAG	MVRGKAAGYAKTPERSIVSEGLSPIFPERASGLNGSSEFPSEFALSTRPPSSFLTLQAGHLHQRTIQLLSLIDF*			MVRGKAAGYAKTPERSIVSEGLSPIFPERASGLNGSSEFPSEFALSTRPPSSFLTLQAGHLHQRTIQLLSLIDF*	CAGGCTCGAA	TCTCGTCAAG	0	J	FG06407.1	MG02872.1	0	YHR021C	0
6552	3167	an	AN4770.1	59.m09215	AO070329000086	0	-180	-169					ATGATGTCGTGA	ATGATGTCGTGA			MMS*	MMS*			TCAACTGCCG	TTGCCCCTGT	0	E	0	0	0	0	0
6553	3167	ao	AN4770.1	59.m09215	AO070329000086	0					-227	-195	ATGTCGTGCTCGCCCCTGTTTTCTTATATCTGA			ATGTCGTGCTCGCCCCTGTTTTCTTATATCTGA	MSCSPLFSYI*			MSCSPLFSYI*	ATTGCCGCTG	CCGGTCGTGG	0	E	0	0	0	0	0
6554	3167	ao	AN4770.1	59.m09215	AO070329000086	0					-164	-93	ATGATTACTATCCTACATCATCTCACGCAAATTGGACCTGGTCATTTGTCATCCTCTTCCATTCATCCATAG			ATGATTACTATCCTACATCATCTCACGCAAATTGGACCTGGTCATTTGTCATCCTCTTCCATTCATCCATAG	MITILHHLTQIGPGHLSSSSIHP*			MITILHHLTQIGPGHLSSSSIHP*	CCGTGTTGTG	ACATATAGAC	0	E	0	0	0	0	0
6555	3168	af	AN2917.1	59.m09096	AO070329000154	0			-223	-206			ATGCTTGGCGGCCACTAG		ATGCTTGGCGGCCACTAG		MLGGH*		MLGGH*		GGCGGTGGTG	CGTCAGCAGC	0	O	0	0	0	YKL145W	YKL145W
6559	3170	af	AN4709.1	71.m15697	AO070329000166	0			-290	-222			ATGAATGATATCTGCCCGCGCGACGCGTGCCTGTCCAAAGCGGATAAGAACCATCTACTACATCGATAA		ATGAATGATATCTGCCCGCGCGACGCGTGCCTGTCCAAAGCGGATAAGAACCATCTACTACATCGATAA		MNDICPRDACLSKADKNHLLHR*		MNDICPRDACLSKADKNHLLHR*		GAGCATCATC	CAGTCACGTG	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6560	3170	af	AN4709.1	71.m15697	AO070329000166	0			-286	-152			ATGATATCTGCCCGCGCGACGCGTGCCTGTCCAAAGCGGATAAGAACCATCTACTACATCGATAACAGTCACGTGGTAAGGAAGACTGCTCCCAGTCATTATGCAACAAGCAGCCAATCAGATGTGCTCGCATGA		ATGATATCTGCCCGCGCGACGCGTGCCTGTCCAAAGCGGATAAGAACCATCTACTACATCGATAACAGTCACGTGGTAAGGAAGACTGCTCCCAGTCATTATGCAACAAGCAGCCAATCAGATGTGCTCGCATGA		MISARATRACPKRIRTIYYIDNSHVVRKTAPSHYATSSQSDVLA*		MISARATRACPKRIRTIYYIDNSHVVRKTAPSHYATSSQSDVLA*		ATCATCATGA	TCTTCCCCAG	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6561	3170	af	AN4709.1	71.m15697	AO070329000166	0			-186	-121			ATGCAACAAGCAGCCAATCAGATGTGCTCGCATGATCTTCCCCAGTTAAGCTCCATAGCTAGTTAA		ATGCAACAAGCAGCCAATCAGATGTGCTCGCATGATCTTCCCCAGTTAAGCTCCATAGCTAGTTAA		MQQAANQMCSHDLPQLSSIAS*		MQQAANQMCSHDLPQLSSIAS*		CCCAGTCATT	GTCACCGACC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6562	3170	af	AN4709.1	71.m15697	AO070329000166	0			-165	-121			ATGTGCTCGCATGATCTTCCCCAGTTAAGCTCCATAGCTAGTTAA		ATGTGCTCGCATGATCTTCCCCAGTTAAGCTCCATAGCTAGTTAA		MCSHDLPQLSSIAS*		MCSHDLPQLSSIAS*		AGCCAATCAG	GTCACCGACC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0

6563	3170	af	AN4709.1	71.m15697	AO070329000166	0			-155	-138			ATGATCTTCCCCAGTTAA		ATGATCTTCCCCAGTTAA		MIFPS*		MIFPS*		ATGTGCTCGC	GCTCCATAGC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6556	3170	an	AN4709.1	71.m15697	AO070329000166	0	-167	-129					ATGGATTGTCTGGACGCGTCCGAAATACACTGCACGTGA	ATGGATTGTCTGGACGCGTCCGAAATACACTGCACGTGA			MDCLDASEIHCT*	MDCLDASEIHCT*			ATTGAAATCA	TGTCTCCGGC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6557	3170	an	AN4709.1	71.m15697	AO070329000166	0	-129	-31					ATGTCTCCGGCCTCCCCGCGTCATCTCCAAATTGGAGCTGGGCTCTCTTTAATGGCACAGGCGTTGTCCACACGTCAACTTTCCCTAATCATGCCTTAA	ATGTCTCCGGCCTCCCCGCGTCATCTCCAAATTGGAGCTGGGCTCTCTTTAATGGCACAGGCGTTGTCCACACGTCAACTTTCCCTAATCATGCCTTAA			MSPASPRHLQIGAGLSLMAQALSTRQLSLIMP*	MSPASPRHLQIGAGLSLMAQALSTRQLSLIMP*			ACTGCACGTG	GCAGCCGGAC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6558	3170	an	AN4709.1	71.m15697	AO070329000166	0	-78	-31					ATGGCACAGGCGTTGTCCACACGTCAACTTTCCCTAATCATGCCTTAA	ATGGCACAGGCGTTGTCCACACGTCAACTTTCCCTAATCATGCCTTAA			MAQALSTRQLSLIMP*	MAQALSTRQLSLIMP*			GCTCTCTTTA	GCAGCCGGAC	0	TU	FG08522.1	MG03069.1	NCU00656.1	0	0
6566	3174	ao	AN5399.1	72.m19996	AO070330000231	0					-226	-131	ATGAGAGTCACCTTTCCCAAGGATACGAGGTCAACGGTAACCAATTGGACAATCCGACATTGGCTCAGCCACTTCCATTTCATCAGCCACGTTTAA			ATGAGAGTCACCTTTCCCAAGGATACGAGGTCAACGGTAACCAATTGGACAATCCGACATTGGCTCAGCCACTTCCATTTCATCAGCCACGTTTAA	MRVTFPKDTRSTVTNWTIRHWLSHFHFISHV*			MRVTFPKDTRSTVTNWTIRHWLSHFHFISHV*	TTCTGCCACG	GGTTTCGGAA	0		0	0	0	0	0
6567	3174	ao	AN5399.1	72.m19996	AO070330000231	0					-71	-21	ATGCATCTCCCTCTGTCTCCTTCGTTATTAGCCGGAAACTACCATCTCTAA			ATGCATCTCCCTCTGTCTCCTTCGTTATTAGCCGGAAACTACCATCTCTAA	MHLPLSPSLLAGNYHL*			MHLPLSPSLLAGNYHL*	TCGCGAATTG	TTTCTCACCG	0		0	0	0	0	0
6569	3176	an	AN1122.1	70.m15112	AO070331000114	0	-236	-189					ATGTATCAGCCTAAAGACGGCAACAGTAGATGCAAATCCGATAGATGA	ATGTATCAGCCTAAAGACGGCAACAGTAGATGCAAATCCGATAGATGA			MYQPKDGNSRCKSDR*	MYQPKDGNSRCKSDR*			TTCTCAGCTC	GTCATCAAGG	0	J	0	0	0	YPL220W	YPL220W
6570	3176	an	AN1122.1	70.m15112	AO070331000114	0	-207	-193					ATGCAAATCCGATAG	ATGCAAATCCGATAG			MQIR*	MQIR*			GCAACAGTAG	ATGAGTCATC	0	J	0	0	0	YPL220W	YPL220W
6571	3176	an	AN1122.1	70.m15112	AO070331000114	0	-192	-175					ATGAGTCATCAAGGCTAG	ATGAGTCATCAAGGCTAG			MSHQG*	MSHQG*			AATCCGATAG	ATTAGGGCAA	0	J	0	0	0	YPL220W	YPL220W
6573	3177	af	AN1140.1	70.m15097	AO070331000131	0			-230	-123			ATGTCAGTTCAATGTCAGGACTGGAGATATATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		ATGTCAGTTCAATGTCAGGACTGGAGATATATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		MSVQCQDWRYMMIEFCLGCRYRLASALGVTRTSRQ*		MSVQCQDWRYMMIEFCLGCRYRLASALGVTRTSRQ*		AAAACGAGAG	AGTGACTGTT	0	G	0	0	0	0	0
6574	3177	af	AN1140.1	70.m15097	AO070331000131	0			-219	-118			ATGTCAGGACTGGAGATATATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAAAGTGA		ATGTCAGGACTGGAGATATATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAAAGTGA		MSGLEIYDDRILSWLPLSIGLGARCDAYKSPIK*		MSGLEIYDDRILSWLPLSIGLGARCDAYKSPIK*		TGTCAGTTCA	CTGTTGACAT	0	G	0	0	0	0	0
6575	3177	af	AN1140.1	70.m15097	AO070331000131	0			-200	-123			ATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		ATGATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		MMIEFCLGCRYRLASALGVTRTSRQ*		MMIEFCLGCRYRLASALGVTRTSRQ*		CTGGAGATAT	AGTGACTGTT	0	G	0	0	0	0	0
6576	3177	af	AN1140.1	70.m15097	AO070331000131	0			-197	-123			ATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		ATGATAGAATTCTGTCTTGGCTGCCGCTATCGATTGGCCTCGGCGCTCGGTGTGACGCGTACAAGTCGCCAATAA		MIEFCLGCRYRLASALGVTRTSRQ*		MIEFCLGCRYRLASALGVTRTSRQ*		GAGATATATG	AGTGACTGTT	0	G	0	0	0	0	0
6572	3177	an	AN1140.1	70.m15097	AO070331000131	0	-209	-162					ATGCAGATTGCCTTTACTTCAGCTGCATTTGATCAGCCACAGCTCTAA	ATGCAGATTGCCTTTACTTCAGCTGCATTTGATCAGCCACAGCTCTAA			MQIAFTSAAFDQPQL*	MQIAFTSAAFDQPQL*			TACGTATCAC	GAGCAAACAT	0	G	0	0	0	0	0
6577	3177	ao	AN1140.1	70.m15097	AO070331000131	0					-170	-144	ATGACGCGGCAGTTCGCGTGTCTTTAG			ATGACGCGGCAGTTCGCGTGTCTTTAG	MTRQFACL*			MTRQFACL*	AACACGAGAC	CAGTTTCATA	0	G	0	0	0	0	0
6581	3179	af	AN1186.1	70.m15034	AO070331000186	0			-132	-73			ATGGTAAGACCGATGCTAACTGCGAGAGCAAAACAGAGAGGGAATTCGCACCCCTGGTAG		ATGGTAAGACCGATGCTAACTGCGAGAGCAAAACAGAGAGGGAATTCGCACCCCTGGTAG		MVRPMLTARAKQRGNSHPW*		MVRPMLTARAKQRGNSHPW*		TCATTCTGTG	GAAAGACGAG	0	F	0	0	0	0	0
6582	3179	af	AN1186.1	70.m15034	AO070331000186	0			-120	-73			ATGCTAACTGCGAGAGCAAAACAGAGAGGGAATTCGCACCCCTGGTAG		ATGCTAACTGCGAGAGCAAAACAGAGAGGGAATTCGCACCCCTGGTAG		MLTARAKQRGNSHPW*		MLTARAKQRGNSHPW*		GGTAAGACCG	GAAAGACGAG	0	F	0	0	0	0	0
6580	3179	an	AN1186.1	70.m15034	AO070331000186	0	-137	-120					ATGCAGATAAGAGTATGA	ATGCAGATAAGAGTATGA			MQIRV*	MQIRV*			CTGGGCATGG	GCTCACCGTC	0	F	0	0	0	0	0
6583	3180	an	AN1194.1	70.m15765	AO070331000198	0	-220	-11					ATGATCGCCACCTTCGCGTGGGATGAGAACAACCTTGAAAGTCTTGGACTCCGCCCCGAAGTCGGTGACAACCCCCGCGGTTTCAGGAGCCCCGCCAAACCCATTTTTATTACGCGGCAGTCTATCTCCTCTTCCTATTACTTTTCTCTCCTTCAACTTCCCTTTATCACATCAATTTCCCTGAGACCCAGTACCAGGTCACATAGCTGA	ATGATCGCCACCTTCGCGTGGGATGAGAACAACCTTGAAAGTCTTGGACTCCGCCCCGAAGTCGGTGACAACCCCCGCGGTTTCAGGAGCCCCGCCAAACCCATTTTTATTACGCGGCAGTCTATCTCCTCTTCCTATTACTTTTCTCTCCTTCAACTTCCCTTTATCACATCAATTTCCCTGAGACCCAGTACCAGGTCACATAGCTGA			MIATFAWDENNLESLGLRPEVGDNPRGFRSPAKPIFITRQSISSSYYFSLLQLPFITSISLRPSTRSHS*	MIATFAWDENNLESLGLRPEVGDNPRGFRSPAKPIFITRQSISSSYYFSLLQLPFITSISLRPSTRSHS*			TAACTAATTA	ATTCTCCAAA	0	P	FG01329.1	MG06348.1	0	0	0
6584	3180	an	AN1194.1	70.m15765	AO070331000198	0	-198	-37					ATGAGAACAACCTTGAAAGTCTTGGACTCCGCCCCGAAGTCGGTGACAACCCCCGCGGTTTCAGGAGCCCCGCCAAACCCATTTTTATTACGCGGCAGTCTATCTCCTCTTCCTATTACTTTTCTCTCCTTCAACTTCCCTTTATCACATCAATTTCCCTGA	ATGAGAACAACCTTGAAAGTCTTGGACTCCGCCCCGAAGTCGGTGACAACCCCCGCGGTTTCAGGAGCCCCGCCAAACCCATTTTTATTACGCGGCAGTCTATCTCCTCTTCCTATTACTTTTCTCTCCTTCAACTTCCCTTTATCACATCAATTTCCCTGA			MRTTLKVLDSAPKSVTTPAVSGAPPNPFLLRGSLSPLPITFLSFNFPLSHQFP*	MRTTLKVLDSAPKSVTTPAVSGAPPNPFLLRGSLSPLPITFLSFNFPLSHQFP*			TTCGCGTGGG	GACCCAGTAC	0	P	FG01329.1	MG06348.1	0	0	0
6586	3181	ao	AN1222.1	70.m15003	AO070331000222	0					-255	-70	ATGTCAGAATGCGCACTTTTTCTGCCGAGGGTGACCGCCGGAGGAAGATGGCGCCATCGGCGGCACATTAATACGGCCAGATTCCCCTCGATTTCTTTTCCCTCCTCCCGCCCCCCCTCTTCTTTTTCCCTCAGATCTCATCTCATCTCACTGATATCTCTTCTCTCTCCCCCTTTGTGGAATTGA			ATGTCAGAATGCGCACTTTTTCTGCCGAGGGTGACCGCCGGAGGAAGATGGCGCCATCGGCGGCACATTAATACGGCCAGATTCCCCTCGATTTCTTTTCCCTCCTCCCGCCCCCCCTCTTCTTTTTCCCTCAGATCTCATCTCATCTCACTGATATCTCTTCTCTCTCCCCCTTTGTGGAATTGA	MSECALFLPRVTAGGRWRHRRHINTARFPSISFPSSRPPSSFSLRSHLISLISLLSPPLWN*			MSECALFLPRVTAGGRWRHRRHINTARFPSISFPSSRPPSSFSLRSHLISLISLLSPPLWN*	ATTGGCGCAG	CGCTCCTTCT	0	H	0	MG00383.1	0	0	0
6589	3182	af	AN1237.1	70.m14981	AO070331000251	0			-215	-165			ATGAGCTGCAACTTATCCTGTCAAGCTATATTGCCGAATCATCTGTGGTAG		ATGAGCTGCAACTTATCCTGTCAAGCTATATTGCCGAATCATCTGTGGTAG		MSCNLSCQAILPNHLW*		MSCNLSCQAILPNHLW*		TGCCACATTA	CGCCTTCGAG	0	L	FG01157.1	0	NCU02741.1	0	0
6590	3183	af	AN1265.1	70.m15737	AO070332000012	0			-161	-150			ATGTGGGACTGA		ATGTGGGACTGA		MWD*		MWD*		TGTGAAGCCA	GTCGTGCTAA	0	R	0	0	0	0	0
6591	3183	ao	AN1265.1	70.m15737	AO070332000012	0					-227	-165	ATGTGGGCTAACGCTTGTGAAGTCTGGAGTGCTCAAGGACAAACACCCCATACCGCCGAGTGA			ATGTGGGCTAACGCTTGTGAAGTCTGGAGTGCTCAAGGACAAACACCCCATACCGCCGAGTGA	MWANACEVWSAQGQTPHTAE*			MWANACEVWSAQGQTPHTAE*	CGCGGTGGCG	TCTCCCCGCC	0	R	0	0	0	0	0
6592	3185	af	AN9138.1	66.m04601	AO070332000122	0			-124	-107			ATGCTTTCCCCGCAATAA		ATGCTTTCCCCGCAATAA		MLSPQ*		MLSPQ*		ATTAGTGTCC	ATAGCAACGG	0	JIT	0	0	0	0	0
6593	3185	ao	AN9138.1	66.m04601	AO070332000122	0					-262	-227	ATGCATAGCAATCTAGTCTATGAGTGTCTCCTCTAA			ATGCATAGCAATCTAGTCTATGAGTGTCTCCTCTAA	MHSNLVYECLL*			MHSNLVYECLL*	GAAGCATACA	TAAGTGTCAT	0	JIT	0	0	0	0	0
6594	3185	ao	AN9138.1	66.m04601	AO070332000122	0					-243	-202	ATGAGTGTCTCCTCTAATAAGTGTCATATGGGAGGTGCGTAG			ATGAGTGTCTCCTCTAATAAGTGTCATATGGGAGGTGCGTAG	MSVSSNKCHMGGA*			MSVSSNKCHMGGA*	AATCTAGTCT	TAGCTTTATG	0	JIT	0	0	0	0	0
6595	3185	ao	AN9138.1	66.m04601	AO070332000122	0					-216	-202	ATGGGAGGTGCGTAG			ATGGGAGGTGCGTAG	MGGA*			MGGA*	TAAGTGTCAT	TAGCTTTATG	0	JIT	0	0	0	0	0
6596	3185	ao	AN9138.1	66.m04601	AO070332000122	0					-194	-174	ATGGAGCTTGAAGTGCCTTAA			ATGGAGCTTGAAGTGCCTTAA	MELEVP*			MELEVP*	TAGTAGCTTT	CGGCTCACAT	0	JIT	0	0	0	0	0
6598	3186	an	AN9125.1	66.m04585	AO070332000149	0	-205	-188					ATGGATAGACCACGCTAA	ATGGATAGACCACGCTAA			MDRPR*	MDRPR*			TAATCCTTTT	GCCAGAAAGA	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
6600	3186	ao	AN9125.1	66.m04585	AO070332000149	0					-208	-68	ATGGAAAAGCCGTCAAAAACATCTTTTTCTGCCGCTGTCGCACTCGTCAAGTTCTCCTCTCACAGGCTCTTCTTCAACCCGTCCGGGTATTCTTTGGCACTCCTTGGTATAGATAGATGCTGGTCTAATATGCATCTCTGA			ATGGAAAAGCCGTCAAAAACATCTTTTTCTGCCGCTGTCGCACTCGTCAAGTTCTCCTCTCACAGGCTCTTCTTCAACCCGTCCGGGTATTCTTTGGCACTCCTTGGTATAGATAGATGCTGGTCTAATATGCATCTCTGA	MEKPSKTSFSAAVALVKFSSHRLFFNPSGYSLALLGIDRCWSNMHL*			MEKPSKTSFSAAVALVKFSSHRLFFNPSGYSLALLGIDRCWSNMHL*	CAAAAAGGGA	ATATGCCAGT	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
6603	3187	an	AN9126.1	66.m04583	AO070332000150	0	-208	-137					ATGAGTGGTCGGCCGGATAATCAAGCACCCGCTCCGGCGGCGAGATATCCTGGACCAGACGCAGATGGATGA	ATGAGTGGTCGGCCGGATAATCAAGCACCCGCTCCGGCGGCGAGATATCCTGGACCAGACGCAGATGGATGA			MSGRPDNQAPAPAARYPGPDADG*	MSGRPDNQAPAPAARYPGPDADG*			ATACAGACCA	TTAACCAACC	0	B	0	0	0	0	0
6604	3187	an	AN9126.1	66.m04583	AO070332000150	0	-144	-133					ATGGATGATTAA	ATGGATGATTAA			MDD*	MDD*			CCAGACGCAG	CCAACCCATC	0	B	0	0	0	0	0
6605	3187	ao	AN9126.1	66.m04583	AO070332000150	0					-169	-62	ATGCGTTCTGCTAGTTGCGATTACGACCGGTCCTCGCCTTGTCCCTACTTTATACAAAATAACAAGACGTCTGCTCTCAAAGCTAACTACATCAGGAACTCTGGCTAG			ATGCGTTCTGCTAGTTGCGATTACGACCGGTCCTCGCCTTGTCCCTACTTTATACAAAATAACAAGACGTCTGCTCTCAAAGCTAACTACATCAGGAACTCTGGCTAG	MRSASCDYDRSSPCPYFIQNNKTSALKANYIRNSG*			MRSASCDYDRSSPCPYFIQNNKTSALKANYIRNSG*	CGCTTGGTTC	CCTGAACCAC	0	B	0	0	0	0	0
6610	3188	af	AN9116.1	66.m04582	AO070332000151	0			-255	-235			ATGCAAATTGTGCTCATATGA		ATGCAAATTGTGCTCATATGA		MQIVLI*		MQIVLI*		TCCCCATCAG	CGTCGCGTGC	0	H	0	0	0	0	0
6611	3188	af	AN9116.1	66.m04582	AO070332000151	0			-238	-218			ATGACGTCGCGTGCTCCATGA		ATGACGTCGCGTGCTCCATGA		MTSRAP*		MTSRAP*		TTGTGCTCAT	CATATATGTA	0	H	0	0	0	0	0
6612	3188	af	AN9116.1	66.m04582	AO070332000151	0			-221	-102			ATGACATATATGTACAGGTGCAAACAGTGCAAACCACTTCTTATTTCATTGATTCCCCGCGCAAGACGACTGACTAGCCAACGACAACGGACTTTTGTACCAGCCCTATCTGATATCTAG		ATGACATATATGTACAGGTGCAAACAGTGCAAACCACTTCTTATTTCATTGATTCCCCGCGCAAGACGACTGACTAGCCAACGACAACGGACTTTTGTACCAGCCCTATCTGATATCTAG		MTYMYRCKQCKPLLISLIPRARRLTSQRQRTFVPALSDI*		MTYMYRCKQCKPLLISLIPRARRLTSQRQRTFVPALSDI*		CGCGTGCTCC	TGACTTTGGG	0	H	0	0	0	0	0
6613	3188	af	AN9116.1	66.m04582	AO070332000151	0			-212	-102			ATGTACAGGTGCAAACAGTGCAAACCACTTCTTATTTCATTGATTCCCCGCGCAAGACGACTGACTAGCCAACGACAACGGACTTTTGTACCAGCCCTATCTGATATCTAG		ATGTACAGGTGCAAACAGTGCAAACCACTTCTTATTTCATTGATTCCCCGCGCAAGACGACTGACTAGCCAACGACAACGGACTTTTGTACCAGCCCTATCTGATATCTAG		MYRCKQCKPLLISLIPRARRLTSQRQRTFVPALSDI*		MYRCKQCKPLLISLIPRARRLTSQRQRTFVPALSDI*		CATGACATAT	TGACTTTGGG	0	H	0	0	0	0	0
6614	3188	af	AN9116.1	66.m04582	AO070332000151	0			-61	-47			ATGCTGATCTGCTGA		ATGCTGATCTGCTGA		MLIC*		MLIC*		TCTCATCTGG	GTTTGTAGAT	0	H	0	0	0	0	0
6606	3188	an	AN9116.1	66.m04582	AO070332000151	0	-245	-126					ATGTACAATGACGTCGCTGTGATATGCGCCTCATGGGCTTATGAACTAGTGCAAACATTGCAAACATCCCTCTTCTCTCCCCCACCCCCCGCAGTGGGCTTAAATAAACTCATCCTTTGA	ATGTACAATGACGTCGCTGTGATATGCGCCTCATGGGCTTATGAACTAGTGCAAACATTGCAAACATCCCTCTTCTCTCCCCCACCCCCCGCAGTGGGCTTAAATAAACTCATCCTTTGA			MYNDVAVICASWAYELVQTLQTSLFSPPPPAVGLNKLIL*	MYNDVAVICASWAYELVQTLQTSLFSPPPPAVGLNKLIL*			AGCAAACAAA	CAGACTCAAT	0	H	0	0	0	0	0
6607	3188	an	AN9116.1	66.m04582	AO070332000151	0	-238	-224					ATGACGTCGCTGTGA	ATGACGTCGCTGTGA			MTSL*	MTSL*			AAAATGTACA	TATGCGCCTC	0	H	0	0	0	0	0
6608	3188	an	AN9116.1	66.m04582	AO070332000151	0	-222	-202					ATGCGCCTCATGGGCTTATGA	ATGCGCCTCATGGGCTTATGA			MRLMGL*	MRLMGL*			TCGCTGTGAT	ACTAGTGCAA	0	H	0	0	0	0	0
6609	3188	an	AN9116.1	66.m04582	AO070332000151	0	-213	-202					ATGGGCTTATGA	ATGGGCTTATGA			MGL*	MGL*			TATGCGCCTC	ACTAGTGCAA	0	H	0	0	0	0	0
6615	3188	ao	AN9116.1	66.m04582	AO070332000151	0					-240	-220	ATGACGTCGCCCACAGCATGA			ATGACGTCGCCCACAGCATGA	MTSPTA*			MTSPTA*	GCATCTCAAT	CGAAGATTAT	0	H	0	0	0	0	0
6616	3188	ao	AN9116.1	66.m04582	AO070332000151	0					-223	-173	ATGACGAAGATTATACAATGCAAACAGTACAAACATGGTCTTTTTGGTAG			ATGACGAAGATTATACAATGCAAACAGTACAAACATGGTCTTTTTGGTAG	MTKIIQCKQYKHGLFW*			MTKIIQCKQYKHGLFW*	CGCCCACAGC	TTCCCCGCAG	0	H	0	0	0	0	0
6617	3188	ao	AN9116.1	66.m04582	AO070332000151	0					-206	-132	ATGCAAACAGTACAAACATGGTCTTTTTTGGTAGTTCCCCGCAGCAGCGTGGATATGACTGTTTTCAGCTGCTGA			ATGCAAACAGTACAAACATGGTCTTTTTTGGTAGTTCCCCGCAGCAGCGTGGATATGACTGTTTTCAGCTGCTGA	MQTVQTWSFLVVPRSSVDMTVFSC*			MQTVQTWSFLVVPRSSVDMTVFSC*	AGATTATACA	TAAACTTCTC	0	H	0	0	0	0	0
6618	3188	ao	AN9116.1	66.m04582	AO070332000151	0					-189	-46	ATGGTCTTTTTTGGTAGTTCCCCGCAGCAGCGTGGATATGACTGTTTTCAGCTGCTGATAAACTTCTCTACTACACAATTACTTTCCTTTGACTGGGGCTTTTACCCCATTGAATTGAATTTCGCACATTTTATTCACTTCTAG			ATGGTCTTTTTTGGTAGTTCCCCGCAGCAGCGTGGATATGACTGTTTTCAGCTGCTGATAAACTTCTCTACTACACAATTACTTTCCTTTGACTGGGGCTTTTACCCCATTGAATTGAATTTCGCACATTTTATTCACTTCTAG	MVFFGSSPQQRGYDCFQLLINFSTTQLLSFDWGFYPIELNFAHFIHF*			MVFFGSSPQQRGYDCFQLLINFSTTQLLSFDWGFYPIELNFAHFIHF*	CAGTACAAAC	CCACTGCAGC	0	H	0	0	0	0	0
6619	3188	ao	AN9116.1	66.m04582	AO070332000151	0					-152	-132	ATGACTGTTTTCAGCTGCTGA			ATGACTGTTTTCAGCTGCTGA	MTVFSC*			MTVFSC*	CAGCGTGGAT	TAAACTTCTC	0	H	0	0	0	0	0
6621	3190	an	AN9078.1	66.m04536	AO070332000201	0	-135	-124					ATGGTCAATTGA	ATGGTCAATTGA			MVN*	MVN*			ACTTCATCCC	GCCTTTCGCT	0		0	0	0	0	0
6624	3190	ao	AN9078.1	66.m04536	AO070332000201	0					-217	-203	ATGCCTAAGGCATAA			ATGCCTAAGGCATAA	MPKA*			MPKA*	CTCTGAGTTT	AGTACCGGCC	0		0	0	0	0	0

6627	3192	af	AN3312.1	69.m15522	AO070333000132	0			-78	-67			ATGCGGGGTTGA		ATGCGGGGTTGA		MRG*		MRG*		AGGGCCTCCG	CATCTTGGTC	0	R	0	0	0	0	0
6625	3192	an	AN3312.1	69.m15522	AO070333000132	0	-167	-150					ATGCCCGTAACGAGTTGA	ATGCCCGTAACGAGTTGA			MPVTS*	MPVTS*			CGGACCTCAG	GTGAACGGGA	0	R	0	0	0	0	0
6626	3192	an	AN3312.1	69.m15522	AO070333000132	0	-136	-53					ATGCGGGGTGGCTGCGCGGGGTGGCTGCAACCCTCACCCCCACGCTTGACGCTCTCTTATTACATCTTTCCTTCTTTAACATAG	ATGCGGGGTGGCTGCGCGGGGTGGCTGCAACCCTCACCCCCACGCTTGACGCTCTCTTATTACATCTTTCCTTCTTTAACATAG			MRGGCAGWLQPSPPRLTLSYYIFPSLT*	MRGGCAGWLQPSPPRLTLSYYIFPSLT*			AACGGGAAGA	ATACTCTACA	0	R	0	0	0	0	0
6628	3192	ao	AN3312.1	69.m15522	AO070333000132	0					-198	-169	ATGTTTTCCTTCTATACCATGCTAAACTAA			ATGTTTTCCTTCTATACCATGCTAAACTAA	MFSFYTMLN*			MFSFYTMLN*	CCAGAACTTC	TAAGAAAGAT	0	R	0	0	0	0	0
6629	3192	ao	AN3312.1	69.m15522	AO070333000132	0					-180	-169	ATGCTAAACTAA			ATGCTAAACTAA	MLN*			MLN*	CTTCTATACC	TAAGAAAGAT	0	R	0	0	0	0	0
6630	3192	ao	AN3312.1	69.m15522	AO070333000132	0					-160	-149	ATGCTTTGCTAG			ATGCTTTGCTAG	MLC*			MLC*	AATAAGAAAG	TAGTTGATAT	0	R	0	0	0	0	0
6631	3192	ao	AN3312.1	69.m15522	AO070333000132	0					-123	-40	ATGCGGGGATTGAAGTATCTGCGGGGTTGCCCGAAGCCATGTCCAGACATTAAAAGAGAACCCACATTCTTACAGTTATCTTAA			ATGCGGGGATTGAAGTATCTGCGGGGTTGCCCGAAGCCATGTCCAGACATTAAAAGAGAACCCACATTCTTACAGTTATCTTAA	MRGLKYLRGCPKPCPDIKREPTFLQLS*			MRGLKYLRGCPKPCPDIKREPTFLQLS*	AGAATCTCCG	ACCTGGATAG	0	R	0	0	0	0	0
6632	3192	ao	AN3312.1	69.m15522	AO070333000132	0					-85	-71	ATGTCCAGACATTAA			ATGTCCAGACATTAA	MSRH*			MSRH*	GCCCGAAGCC	AAGAGAACCC	0	R	0	0	0	0	0
6633	3193	an	AN5344.1	69.m15562	AO070333000180	0	-217	-134					ATGGGGAGCAGTCTTATCATCATCCATGACCCATCAATCCTCCTAGAACTCACATCATCTCACCTTTTTCTCACCACTTATAA	ATGGGGAGCAGTCTTATCATCATCCATGACCCATCAATCCTCCTAGAACTCACATCATCTCACCTTTTTCTCACCACTTATAA			MGSSLIIIHDPSILLELTSSHLFSHHL*	MGSSLIIIHDPSILLELTSSHLFSHHL*			CTGTTTAGAT	CGACGAAGGA	0	O	0	0	0	0	0
6634	3193	an	AN5344.1	69.m15562	AO070333000180	0	-192	-172					ATGACCCATCAATCCTCCTAG	ATGACCCATCAATCCTCCTAG			MTHQSS*	MTHQSS*			ATCATCATCC	AACTCACATC	0	O	0	0	0	0	0
6635	3194	af	AN0316.1	54.m06442	AO070334000016	0			-178	-116			ATGTTGTGTGCTGTCCTGCCCACCACATTCTATGTTTTGTGGTGTCCGTTTACTAACCCCTGA		ATGTTGTGTGCTGTCCTGCCCACCACATTCTATGTTTTGTGGTGTCCGTTTACTAACCCCTGA		MLCAVLPTTFYVLWCPFTNP*		MLCAVLPTTFYVLWCPFTNP*		CCCCTCTTCA	AACACCCATA	0	Z	0	0	0	0	0
6636	3194	af	AN0316.1	54.m06442	AO070334000016	0			-147	-19			ATGTTTTGTGGTGTCCGTTTACTAACCCCTGAAACACCCATACAGCAGATCGTCTTGGGTTTTTTTCGTCCTTCATTCCTCCCTCCTCCACCCACCTTTCTTAATTTATCCTTTGTGAACGGAATTTAG		ATGTTTTGTGGTGTCCGTTTACTAACCCCTGAAACACCCATACAGCAGATCGTCTTGGGTTTTTTTCGTCCTTCATTCCTCCCTCCTCCACCCACCTTTCTTAATTTATCCTTTGTGAACGGAATTTAG		MFCGVRLLTPETPIQQIVLGFFRPSFLPPPPTFLNLSFVNGI*		MFCGVRLLTPETPIQQIVLGFFRPSFLPPPPTFLNLSFVNGI*		ACCACATTCT	TCAATCGAAT	0	Z	0	0	0	0	0
6639	3196	af	AN0272.1	54.m06471	AO070334000078	0			-199	-146			ATGGGGTTGCTGCCAATTGGACTGTTTTGCCTCGGTCCGCAGCTCTGGAGCTGA		ATGGGGTTGCTGCCAATTGGACTGTTTTGCCTCGGTCCGCAGCTCTGGAGCTGA		MGLLPIGLFCLGPQLWS*		MGLLPIGLFCLGPQLWS*		GGCCAGAGAG	CCTGGAGCAT	0	R	0	0	0	0	0
6640	3196	af	AN0272.1	54.m06471	AO070334000078	0			-137	-63			ATGTCCTGCTTTTTCATTACCGGGGCTATTTCTGTCCCCAGGCTCCTCCGGTTTTTCTACACCTATCCGACTTGA		ATGTCCTGCTTTTTCATTACCGGGGCTATTTCTGTCCCCAGGCTCCTCCGGTTTTTCTACACCTATCCGACTTGA		MSCFFITGAISVPRLLRFFYTYPT*		MSCFFITGAISVPRLLRFFYTYPT*		GACCTGGAGC	CGCTGGGGAG	0	R	0	0	0	0	0
6637	3196	an	AN0272.1	54.m06471	AO070334000078	0	-146	-54					ATGCTGGGGACGCATTCTCACCGAGCGCCCTCCTATTGCCTTGACACGACTATGGACTTGTTTCTAATAACAATTCCTCTCTCCGTACTGTGA	ATGCTGGGGACGCATTCTCACCGAGCGCCCTCCTATTGCCTTGACACGACTATGGACTTGTTTCTAATAACAATTCCTCTCTCCGTACTGTGA			MLGTHSHRAPSYCLDTTMDLFLITIPLSVL*	MLGTHSHRAPSYCLDTTMDLFLITIPLSVL*			GTCCGGGGGT	GAGGACTGAT	0	R	0	0	0	0	0
6638	3196	an	AN0272.1	54.m06471	AO070334000078	0	-95	-54					ATGGACTTGTTTCTAATAACAATTCCTCTCTCCGTACTGTGA	ATGGACTTGTTTCTAATAACAATTCCTCTCTCCGTACTGTGA			MDLFLITIPLSVL*	MDLFLITIPLSVL*			TGACACGACT	GAGGACTGAT	0	R	0	0	0	0	0
6641	3196	ao	AN0272.1	54.m06471	AO070334000078	0					-219	-205	ATGCCAATGAGGTAG			ATGCCAATGAGGTAG	MPMR*			MPMR*	CGCCCCGCAA	TATTGCTGTT	0	R	0	0	0	0	0
6642	3196	ao	AN0272.1	54.m06471	AO070334000078	0					-109	-62	ATGATCCCGCTAACATCCCTGCGAACTAGGTATCTAGCTCGCAGATAA			ATGATCCCGCTAACATCCCTGCGAACTAGGTATCTAGCTCGCAGATAA	MIPLTSLRTRYLARR*			MIPLTSLRTRYLARR*	TGTCTTCAGA	CTATCAATAC	0	R	0	0	0	0	0
6646	3197	af	AN0260.1	54.m06521	AO070334000098	0			-199	-188			ATGGAGGCCTGA		ATGGAGGCCTGA		MEA*		MEA*		GCTGTCGAAA	GGCTGCTAAA	0	L	0	0	0	0	0
6647	3197	af	AN0260.1	54.m06521	AO070334000098	0			-137	-108			ATGAACGCGTGTCGAGCGCGTCTCGCGTGA		ATGAACGCGTGTCGAGCGCGTCTCGCGTGA		MNACRARLA*		MNACRARLA*		GCTATTAGTG	TGCTCGTGAA	0	L	0	0	0	0	0
6648	3197	af	AN0260.1	54.m06521	AO070334000098	0			-108	-52			ATGCTCGTGAAAGTGGTCGATTGGAGTCTCGATAGTATTTTACAGACTACCATTTGA		ATGCTCGTGAAAGTGGTCGATTGGAGTCTCGATAGTATTTTACAGACTACCATTTGA		MLVKVVDWSLDSILQTTI*		MLVKVVDWSLDSILQTTI*		GTCTCGCGTG	ACACAATAAT	0	L	0	0	0	0	0
6643	3197	an	AN0260.1	54.m06521	AO070334000098	0	-182	-147					ATGATGGTGCTCCTCGGTTTAAGCCAAGCCCACTAA	ATGATGGTGCTCCTCGGTTTAAGCCAAGCCCACTAA			MMVLLGLSQAH*	MMVLLGLSQAH*			CTGCCTTAAA	GGAGATCCCG	0	L	0	0	0	0	0
6644	3197	an	AN0260.1	54.m06521	AO070334000098	0	-179	-147					ATGGTGCTCCTCGGTTTAAGCCAAGCCCACTAA	ATGGTGCTCCTCGGTTTAAGCCAAGCCCACTAA			MVLLGLSQAH*	MVLLGLSQAH*			CCTTAAAATG	GGAGATCCCG	0	L	0	0	0	0	0
6645	3197	an	AN0260.1	54.m06521	AO070334000098	0	-83	-60					ATGCCGATAACAATTTCGATATAG	ATGCCGATAACAATTTCGATATAG			MPITISI*	MPITISI*			GCGTCGTCCA	GTTCAAGACC	0	L	0	0	0	0	0
6651	3201	af	AN3090.1	59.m08656	AO070334000130	0			-88	-74			ATGCCATTCCACTGA		ATGCCATTCCACTGA		MPFH*		MPFH*		CGTTTCATCG	CCATATTTCT	0	DT	0	0	NCU06493.1	0	0
6649	3201	an	AN3090.1	59.m08656	AO070334000130	0	-168	-115					ATGGTGTCCCGCCGCGGCTTGAGGACACTCCTGATTCGGTACGGCGACTGTTAG	ATGGTGTCCCGCCGCGGCTTGAGGACACTCCTGATTCGGTACGGCGACTGTTAG			MVSRRGLRTLLIRYGDC*	MVSRRGLRTLLIRYGDC*			TCCTCTTTTT	CAATGGTGTT	0	DT	0	0	NCU06493.1	0	0
6650	3201	an	AN3090.1	59.m08656	AO070334000130	0	-112	-95					ATGGTGTTGAAGTTTTAA	ATGGTGTTGAAGTTTTAA			MVLKF*	MVLKF*			ACTGTTAGCA	GTCCGTATCT	0	DT	0	0	NCU06493.1	0	0
6652	3201	ao	AN3090.1	59.m08656	AO070334000130	0					-161	-63	ATGAGCATTTGTCAGGCGTGTCCCCTGATTCACCTGCTGCCATTGGACTTCGCCCGTTCCCCTCCCATGTGTACACCAACGCTGAAGTTCTTAAACTAA			ATGAGCATTTGTCAGGCGTGTCCCCTGATTCACCTGCTGCCATTGGACTTCGCCCGTTCCCCTCCCATGTGTACACCAACGCTGAAGTTCTTAAACTAA	MSICQACPLIHLLPLDFARSPPMCTPTLKFLN*			MSICQACPLIHLLPLDFARSPPMCTPTLKFLN*	TTGAGTGGTC	TTGGCACCTT	0	DT	0	0	NCU06493.1	0	0
6653	3201	ao	AN3090.1	59.m08656	AO070334000130	0					-95	-63	ATGTGTACACCAACGCTGAAGTTCTTAAACTAA			ATGTGTACACCAACGCTGAAGTTCTTAAACTAA	MCTPTLKFLN*			MCTPTLKFLN*	TTCCCCTCCC	TTGGCACCTT	0	DT	0	0	NCU06493.1	0	0
6656	3206	af	AN1522.1	55.m03041	AO070334000240	0			-142	-119			ATGTCTTATTTCTCCACCACGTAG		ATGTCTTATTTCTCCACCACGTAG		MSYFSTT*		MSYFSTT*		ACTACTTAAA	CTGGCCTGAT	0	S	0	0	0	YGL010W	0
6657	3206	af	AN1522.1	55.m03041	AO070334000240	0			-65	-51			ATGCTATTCCTTTGA		ATGCTATTCCTTTGA		MLFL*		MLFL*		AAGTCTCTCC	TTCAATAAAG	0	S	0	0	0	YGL010W	0
6654	3206	an	AN1522.1	55.m03041	AO070334000240	0	-130	-104					ATGATCTGGGGTTGGCTCATACGATGA	ATGATCTGGGGTTGGCTCATACGATGA			MIWGWLIR*	MIWGWLIR*			AGCGGCTTTG	CTTTCACACT	0	S	0	0	0	YGL010W	0
6655	3206	an	AN1522.1	55.m03041	AO070334000240	0	-107	-87					ATGACTTTCACACTTCATTAA	ATGACTTTCACACTTCATTAA			MTFTLH*	MTFTLH*			GGCTCATACG	TCCTGCGGGG	0	S	0	0	0	YGL010W	0
6658	3206	ao	AN1522.1	55.m03041	AO070334000240	0					-257	-201	ATGACAATACATTGTAACGGCCCCCGTATCCTCGGCATTCGACTCCCCAGCACATGA			ATGACAATACATTGTAACGGCCCCCGTATCCTCGGCATTCGACTCCCCAGCACATGA	MTIHCNGPRILGIRLPST*			MTIHCNGPRILGIRLPST*	CGACAATGGC	CGTCTGTCTA	0	S	0	0	0	YGL010W	0
6659	3206	ao	AN1522.1	55.m03041	AO070334000240	0					-204	-190	ATGACGTCTGTCTAG			ATGACGTCTGTCTAG	MTSV*			MTSV*	TCCCCAGCAC	GAATACTTTA	0	S	0	0	0	YGL010W	0
6660	3206	ao	AN1522.1	55.m03041	AO070334000240	0					-157	-92	ATGCGAAAATGTCTGATTCTCCACCTCTTGGCTGGCCTGATCAGGCATAATCCTTATCCAGTCTAA			ATGCGAAAATGTCTGATTCTCCACCTCTTGGCTGGCCTGATCAGGCATAATCCTTATCCAGTCTAA	MRKCLILHLLAGLIRHNPYPV*			MRKCLILHLLAGLIRHNPYPV*	CGAGTAGCGC	CTGGCAGAAA	0	S	0	0	0	YGL010W	0
6661	3206	ao	AN1522.1	55.m03041	AO070334000240	0					-149	-108	ATGTCTGATTCTCCACCTCTTGGCTGGCCTGATCAGGCATAA			ATGTCTGATTCTCCACCTCTTGGCTGGCCTGATCAGGCATAA	MSDSPPLGWPDQA*			MSDSPPLGWPDQA*	GCATGCGAAA	TCCTTATCCA	0	S	0	0	0	YGL010W	0
6662	3206	ao	AN1522.1	55.m03041	AO070334000240	0					-68	-9	ATGGTTACCTTCGAGCATCGACAATTTCATTTCTTGGAGACGACAAACCATCAGGTCTGA			ATGGTTACCTTCGAGCATCGACAATTTCATTTCTTGGAGACGACAAACCATCAGGTCTGA	MVTFEHRQFHFLETTNHQV*			MVTFEHRQFHFLETTNHQV*	GGTCTCCTGC	TTACCAATAT	0	S	0	0	0	YGL010W	0
6664	3207	af	AN1523.1	55.m03042	AO070334000241	0			-266	-225			ATGGATCGAGAGTGCTGTGGGAAAACGACATCATTGACCTGA		ATGGATCGAGAGTGCTGTGGGAAAACGACATCATTGACCTGA		MDRECCGKTTSLT*		MDRECCGKTTSLT*		AGAATATTTT	ATTTCTCTGG	0	C	FG00637.1	0	0	0	0
6663	3207	an	AN1523.1	55.m03042	AO070334000241	0	-254	-231					ATGAGTTGGTTAAATCAATTTTGA	ATGAGTTGGTTAAATCAATTTTGA			MSWLNQF*	MSWLNQF*			TAGCAAAGAC	CCCGAGGAGG	0	C	FG00637.1	0	0	0	0
6665	3207	ao	AN1523.1	55.m03042	AO070334000241	0					-225	-13	ATGTTTTCTTGGGGCGGGTGGGTGTCCCGTGAACGCACTAGGGCGGCTTCGGAGGTTGCTGAGGCTCGGCAAACTGGGTTTAGTGGCAGTCCTGAGAATCCTCCCAACCCCGACGACAAAAGCTCTCCTTCCATCCATCCACAATCCTCTCTCCTCTTCCACCTCCCCCCAATTACATCTCTTCTTCAGAGAAACCACTCTCCCACTCCTCTGA			ATGTTTTCTTGGGGCGGGTGGGTGTCCCGTGAACGCACTAGGGCGGCTTCGGAGGTTGCTGAGGCTCGGCAAACTGGGTTTAGTGGCAGTCCTGAGAATCCTCCCAACCCCGACGACAAAGCTCTCCTTCCATCCATCCACAATCCTCTCTCCTCTTCCACCTCCCCCCAATTACATCTCTTCTTCAGAGAAACCACTCTCCCACTCCTCTGA	MFSWGGWVSRERTRAASEVAEARQTGFSGSPENPPNPDDKALLPSIHNPLSSSTSPQLHLFFRETTLPLL*			MFSWGGWVSRERTRAASEVAEARQTGFSGSPENPPNPDDKALLPSIHNPLSSSTSPQLHLFFRETTLPLL*	CAAAGCAGCG	ACCCCATTCA	0	C	FG00637.1	0	0	0	0
6667	3209	af	AN1539.1	55.m03058	AO070334000263	0			-252	-208			ATGTCCACAGAGTTGGAGTCTTCTACGTTTTACGCATGGTTCTAA		ATGTCCACAGAGTTGGAGTCTTCTACGTTTTACGCATGGTTCTAA		MSTELESSTFYAWF*		MSTELESSTFYAWF*		TAGAGTCAGT	TTCCCTTGTT	0	OT	FG00623.1	MG00336.1	0	0	0
6668	3209	af	AN1539.1	55.m03058	AO070334000263	0			-217	-35			ATGGTTCTAATTCCCTTGTTCTCTCTGCATGTTGTATTGTTTCATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGA		ATGGTTCTAATTCCCTTGTTCTCTCTGCATGTTGTATTGTTTCATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGA		MVLIPLFSLHVVLFHVPSTTSLIDKRSSNSSALCQASLSTHQALFFSHLLANCTTIESTN*		MVLIPLFSLHVVLFHVPSTTSLIDKRSSNSSALCQASLSTHQALFFSHLLANCTTIESTN*		CGTTTTACGC	CTAGGCTTGC	0	OT	FG00623.1	MG00336.1	0	0	0
6669	3209	af	AN1539.1	55.m03058	AO070334000263	0			-189	-31			ATGTTGTATTGTTTCATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGACTAG		ATGTTGTATTGTTTCATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGACTAG		MLYCFMSPARPALSINGAPTPPLFAKRHFQPIKRSSSRICSLIVLLLNQLID*		MLYCFMSPARPALSINGAPTPPLFAKRHFQPIKRSSSRICSLIVLLLNQLID*		TTCTCTCTGC	GCTTGCACTC	0	OT	FG00623.1	MG00336.1	0	0	0
6670	3209	af	AN1539.1	55.m03058	AO070334000263	0			-174	-31			ATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGACTAG		ATGTCCCCAGCACGACCAGCCTTATCGATAAACGGAGCTCCAACTCCTCCGCTCTTTGCCAAGCGTCACTTTCAACCCATCAAGCGCTCTTCTTCTCGCATCTGCTCGCTAATTGTACTACTATTGAATCAACTAATTGACTAG		MSPARPALSINGAPTPPLFAKRHFQPIKRSSSRICSLIVLLLNQLID*		MSPARPALSINGAPTPPLFAKRHFQPIKRSSSRICSLIVLLLNQLID*		GTATTGTTTC	GCTTGCACTC	0	OT	FG00623.1	MG00336.1	0	0	0
6666	3209	an	AN1539.1	55.m03058	AO070334000263	0	-145	-68					ATGCGGCAGTGGCTGCTCCTGTCTCCTGTAGAGATACGTCTTATCGATAAGTGCGTATTGATTGATCTTCAGGCTTGA	ATGCGGCAGTGGCTGCTCCTGTCTCCTGTAGAGATACGTCTTATCGATAAGTGCGTATTGATTGATCTTCAGGCTTGA			MRQWLLLSPVEIRLIDKCVLIDLQA*	MRQWLLLSPVEIRLIDKCVLIDLQA*			TGCGACAATA	GCTTCACGCA	0	OT	FG00623.1	MG00336.1	0	0	0
6671	3209	ao	AN1539.1	55.m03058	AO070334000263	0					-217	-89	ATGGTGGTGATGCTATTGTTGCACCCTCAGCCCCCTCTTATCGATAAGCCAAGCTTGTCATCGTTTGTGTCCGCAGTAAGTTCAAGGTACAACATCTTCTCCGTCACACCGATCCCAAAAGACAAATAA			ATGGTGGTGATGCTATTGTTGCACCCTCAGCCCCCTCTTATCGATAAGCCAAGCTTGTCATCGTTTGTGTCCGCAGTAAGTTCAAGGTACAACATCTTCTCCGTCACACCGATCCCAAAAGACAAATAA	MVVMLLLHPQPPLIDKPSLSSFVSAVSSRYNIFSVTPIPKDK*			MVVMLLLHPQPPLIDKPSLSSFVSAVSSRYNIFSVTPIPKDK*	AAAACCCCGC	TAGCCAACCT	0	OT	FG00623.1	MG00336.1	0	0	0
6672	3209	ao	AN1539.1	55.m03058	AO070334000263	0					-208	-89	ATGCTATTGTTGCACCCTCAGCCCCCTCTTATCGATAAGCCAAGCTTGTCATCGTTTGTGTCCGCAGTAAGTTCAAGGTACAACATCTTCTCCGTCACACCGATCCCAAAAGACAAATAA			ATGCTATTGTTGCACCCTCAGCCCCCTCTTATCGATAAGCCAAGCTTGTCATCGTTTGTGTCCGCAGTAAGTTCAAGGTACAACATCTTCTCCGTCACACCGATCCCAAAAGACAAATAA	MLLLHPQPPLIDKPSLSSFVSAVSSRYNIFSVTPIPKDK*			MLLLHPQPPLIDKPSLSSFVSAVSSRYNIFSVTPIPKDK*	CATGGTGGTG	TAGCCAACCT	0	OT	FG00623.1	MG00336.1	0	0	0
6673	3213	ao	AN3070.1	59.m08929	AO070337000004	0					-168	-43	ATGTGGGCTTTTTGCCAAAACTACGAGCTCACCGCATTCGACGGCAAACACCACCAGCTTTGTGCCAGTGCGGGCGATTCTTTGGGGCCGATAGCACCAGCAAGCCTGTTTTTTTTTACGAGTTAG			ATGTGGGCTTTTTGCCAAAACTACGAGCTCACCGCATTCGACGGCAAACACCACCAGCTTTGTGCCAGTGCGGGCGATTCTTTGGGGCCGATAGCACCAGCAAGCCTGTTTTTTTTTACGAGTTAG	MWAFCQNYELTAFDGKHHQLCASAGDSLGPIAPASLFFFTS*			MWAFCQNYELTAFDGKHHQLCASAGDSLGPIAPASLFFFTS*	CGAATACTGA	TTCGCTGGGG	0	O	0	MG03857.1	NCU09709.1	0	0

6674	3214	af	AN3069.1	59.m08928	AO070337000005	0			-211	-47			ATGTTCGCACTAGCGCCGCCGCGAAAGAAAAAAAAGAGCTCTGATGGTTCGGACACTCCAAATCCACCTTCCAGCCCTTTTTCAACTCCACGTCGGGACACAACAAGGCTGCAATCGCAGGTGACCAGTGACTGCGCAGTGGGCTTGGGTACTCGGCTCAATTAA		ATGTTCGCACTAGCGCCGCCGCGAAAGAAAAAAAAGAGCTCTGATGGTTCGGACACTCCAAATCCACCTTCCAGCCCTTTTTCAACTCCACGTCGGGACACAACAAGGCTGCAATCGCAGGTGACCAGTGACTGCGCAGTGGGCTTGGGTACTCGGCTCAATTAA		MFALAPPRKKKKSSDGSDTPNPPSSPFSTPRRDTTRLQSQVTSDCAVGLGTRLN*		MFALAPPRKKKKSSDGSDTPNPPSSPFSTPRRDTTRLQSQVTSDCAVGLGTRLN*		CCCACATTCG	CTGACTTTTC	0	AJ	0	0	0	0	0
6675	3214	af	AN3069.1	59.m08928	AO070337000005	0			-168	-88			ATGGTTCGGACACTCCAAATCCACCTTCCAGCCCTTTTTCAACTCCACGTCGGGACACAACAAGGCTGCAATCGCAGGTGA		ATGGTTCGGACACTCCAAATCCACCTTCCAGCCCTTTTTCAACTCCACGTCGGGACACAACAAGGCTGCAATCGCAGGTGA		MVRTLQIHLPALFQLHVGTQQGCNRR*		MVRTLQIHLPALFQLHVGTQQGCNRR*		AAGAGCTCTG	CCAGTGACTG	0	AJ	0	0	0	0	0
6676	3218	an	AN3026.1	59.m09001	AO070337000068	0	-111	-91					ATGAGGTGGTCGCCTTTGTGA	ATGAGGTGGTCGCCTTTGTGA			MRWSPL*	MRWSPL*			TGTGCAGTGG	TTCCTCTGTC	0	U	0	0	0	0	0
6677	3218	ao	AN3026.1	59.m09001	AO070337000068	0					-87	-67	ATGAGGTGGTCGCTTTTGTGA			ATGAGGTGGTCGCTTTTGTGA	MRWSLL*			MRWSLL*	GTAGCAGTGG	TCTCTTTATA	0	U	0	0	0	0	0
6679	3220	af	AN3013.1	59.m09003	AO070337000103	0			-219	-190			ATGACCAACCTTCTTAATTGTTGTTGCTGA		ATGACCAACCTTCTTAATTGTTGTTGCTGA		MTNLLNCCC*		MTNLLNCCC*		TCACTTGATC	CTTTCCTAAG	0		FG06325.1	MG00882.1	0	0	0
6678	3220	an	AN3013.1	59.m09003	AO070337000103	0	-142	-116					ATGGTCAAAACTAAGAAGCCAGATTGA	ATGGTCAAAACTAAGAAGCCAGATTGA			MVKTKKPD*	MVKTKKPD*			CGTCTAACAT	TATCCAGCGC	0		FG06325.1	MG00882.1	0	0	0
6680	3220	ao	AN3013.1	59.m09003	AO070337000103	0					-127	-113	ATGTATCATTGTTGA			ATGTATCATTGTTGA	MYHC*			MYHC*	CTCATCAGCA	GCTATTCCCT	0		FG06325.1	MG00882.1	0	0	0
6682	3221	af	AN2996.1	59.m09439	AO070337000121	0			-253	-212			ATGATGTCAGCAACGCTAGTCCCAGAGAGGAATAGTGCATGA		ATGATGTCAGCAACGCTAGTCCCAGAGAGGAATAGTGCATGA		MMSATLVPERNSA*		MMSATLVPERNSA*		CCCGAATGAG	CTCCCCTCCA	0	K	0	0	0	0	0
6683	3221	af	AN2996.1	59.m09439	AO070337000121	0			-250	-212			ATGTCAGCAACGCTAGTCCCAGAGAGGAATAGTGCATGA		ATGTCAGCAACGCTAGTCCCAGAGAGGAATAGTGCATGA		MSATLVPERNSA*		MSATLVPERNSA*		GAATGAGATG	CTCCCCTCCA	0	K	0	0	0	0	0
6684	3221	af	AN2996.1	59.m09439	AO070337000121	0			-215	-156			ATGACTCCCCTCCAAATTGCGTCGCTCAGGGCTCGAGAAGCTTCTGTGTCATCAGTATAA		ATGACTCCCCTCCAAATTGCGTCGCTCAGGGCTCGAGAAGCTTCTGTGTCATCAGTATAA		MTPLQIASLRAREASVSSV*		MTPLQIASLRAREASVSSV*		GGAATAGTGC	ATTCGGTGGC	0	K	0	0	0	0	0
6685	3221	ao	AN2996.1	59.m09439	AO070337000121	0					-270	-259	ATGAACGAATGA			ATGAACGAATGA	MNE*			MNE*	GCCCGAGCGA	TGTCAGTGGG	0	K	0	0	0	0	0
6686	3221	ao	AN2996.1	59.m09439	AO070337000121	0					-262	-221	ATGATGTCAGTGGGGCAGAACCCAAAGAGGGGACCGAAATAG			ATGATGTCAGTGGGGCAGAACCCAAAGAGGGGACCGAAATAG	MMSVGQNPKRGPK*			MMSVGQNPKRGPK*	GAATGAACGA	GACTAGGGCA	0	K	0	0	0	0	0
6687	3221	ao	AN2996.1	59.m09439	AO070337000121	0					-259	-221	ATGTCAGTGGGGCAGAACCCAAAGAGGGGACCGAAATAG			ATGTCAGTGGGGCAGAACCCAAAGAGGGGACCGAAATAG	MSVGQNPKRGPK*			MSVGQNPKRGPK*	TGAACGAATG	GACTAGGGCA	0	K	0	0	0	0	0
6688	3222	af	AN2976.1	59.m09037	AO070337000145	0			-87	-16			ATGGTCCGCAGTCGACTCACTGCTGAACGCTATTCTGCCCCTCATCCTAAAACACCCCTCCTGAATCCGTGA		ATGGTCCGCAGTCGACTCACTGCTGAACGCTATTCTGCCCCTCATCCTAAAACACCCCTCCTGAATCCGTGA		MVRSRLTAERYSAPHPKTPLLNP*		MVRSRLTAERYSAPHPKTPLLNP*		CCATTGATTG	CACTTTTCTC	0		0	0	0	0	0
6692	3223	af	AN2971.1	59.m09046	AO070337000157	0			-218	-207			ATGAGGAGGTAG		ATGAGGAGGTAG		MRR*		MRR*		TAAGGCCATC	TTGATCAGTT	0		0	0	0	0	0
6693	3223	af	AN2971.1	59.m09046	AO070337000157	0			-143	-105			ATGGTTGTAGAAGAAAGGACTGGTCAGGATTTGGAGTAG		ATGGTTGTAGAAGAAAGGACTGGTCAGGATTTGGAGTAG		MVVEERTGQDLE*		MVVEERTGQDLE*		GGATACTGCT	GAGTCGGAGA	0		0	0	0	0	0
6689	3223	an	AN2971.1	59.m09046	AO070337000157	0	-152	-138					ATGGAGAAGGTATGA	ATGGAGAAGGTATGA			MEKV*	MEKV*			GGTGAAGGGG	GGTTAGCAAA	0		0	0	0	0	0
6690	3223	an	AN2971.1	59.m09046	AO070337000157	0	-141	-94					ATGAGGTTAGCAAAACTGATGGGTGAAGCTCCGCAGTGTTGGAGTTGA	ATGAGGTTAGCAAAACTGATGGGTGAAGCTCCGCAGTGTTGGAGTTGA			MRLAKLMGEAPQCWS*	MRLAKLMGEAPQCWS*			TGGAGAAGGT	GAGTTGGATT	0		0	0	0	0	0
6691	3223	an	AN2971.1	59.m09046	AO070337000157	0	-123	-94					ATGGGTGAAGCTCCGCAGTGTTGGAGTTGA	ATGGGTGAAGCTCCGCAGTGTTGGAGTTGA			MGEAPQCWS*	MGEAPQCWS*			AGCAAAACTG	GAGTTGGATT	0		0	0	0	0	0
6694	3223	ao	AN2971.1	59.m09046	AO070337000157	0					-193	-104	ATGGAAGCGAAGACAACCGTACTCCGATCGCATCTGAGCAGAAGGTCCGCCGCCAAGCATCGGAGCTTGAACAGCATGGAAGCGGTTTAG			ATGGAAGCGAAGACAACCGTACTCCGATCGCATCTGAGCAGAAGGTCCGCCGCCAAGCATCGGAGCTTGAACAGCATGGAAGCGGTTTAG	MEAKTTVLRSHLSRRSAAKHRSLNSMEAV*			MEAKTTVLRSHLSRRSAAKHRSLNSMEAV*	CGAGGAAAGA	CGCCGCGGAT	0		0	0	0	0	0
6695	3223	ao	AN2971.1	59.m09046	AO070337000157	0					-118	-104	ATGGAAGCGGTTTAG			ATGGAAGCGGTTTAG	MEAV*			MEAV*	CTTGAACAGC	CGCCGCGGAT	0		0	0	0	0	0
6696	3226	an	AN4714.1	71.m16089	AO070337000217	0	-104	-69					ATGAAATGCGATATTGACAAACTTCCTAAGATCTAG	ATGAAATGCGATATTGACAAACTTCCTAAGATCTAG			MKCDIDKLPKI*	MKCDIDKLPKI*			CCTGGGTTTT	GAACAGCACA	0	O	FG09413.1	MG02856.1	NCU00605.1	YKL027W	0
6697	3226	an	AN4714.1	71.m16089	AO070337000217	0	-99	-88					ATGCGATATTGA	ATGCGATATTGA			MRY*	MRY*			GTTTTATGAA	CAAACTTCCT	0	O	FG09413.1	MG02856.1	NCU00605.1	YKL027W	0
6698	3226	ao	AN4714.1	71.m16089	AO070337000217	0					-122	-96	ATGCGCAGTGGCCTGACGAATTACTAG			ATGCGCAGTGGCCTGACGAATTACTAG	MRSGLTNY*			MRSGLTNY*	CTTAAAACTT	GTCGTTTGAA	0	O	FG09413.1	MG02856.1	NCU00605.1	YKL027W	0
6700	3227	af	AN8343.1	57.m05682	AO070337000229	0			-207	-166			ATGCTGGATGGTGATAATGTTTGGTTCACGGACTCCGCATAG		ATGCTGGATGGTGATAATGTTTGGTTCACGGACTCCGCATAG		MLDGDNVWFTDSA*		MLDGDNVWFTDSA*		ATCATCAAAC	TAAGCAAACT	0	O	0	0	0	0	0
6701	3227	af	AN8343.1	57.m05682	AO070337000229	0			-200	-93			ATGGTGATAATGTTTGGTTCACGGACTCCGCATAGTAAGCAAACTCCGGCAGATCGCCATCTAACCACGTTACCTAGACCGGAGCACATCGCTCCCAACAACAGCTGA		ATGGTGATAATGTTTGGTTCACGGACTCCGCATAGTAAGCAAACTCCGGCAGATCGCCATCTAACCACGTTACCTAGACCGGAGCACATCGCTCCCAACAACAGCTGA		MVIMFGSRTPHSKQTPADRHLTTLPRPEHIAPNNS*		MVIMFGSRTPHSKQTPADRHLTTLPRPEHIAPNNS*		AACATGCTGG	GCAAACCACA	0	O	0	0	0	0	0
6702	3227	af	AN8343.1	57.m05682	AO070337000229	0			-191	-93			ATGTTTGGTTCACGGACTCCGCATAGTAAGCAAACTCCGGCAGATCGCCATCTAACCACGTTACCTAGACCGGAGCACATCGCTCCCAACAACAGCTGA		ATGTTTGGTTCACGGACTCCGCATAGTAAGCAAACTCCGGCAGATCGCCATCTAACCACGTTACCTAGACCGGAGCACATCGCTCCCAACAACAGCTGA		MFGSRTPHSKQTPADRHLTTLPRPEHIAPNNS*		MFGSRTPHSKQTPADRHLTTLPRPEHIAPNNS*		GATGGTGATA	GCAAACCACA	0	O	0	0	0	0	0
6699	3227	an	AN8343.1	57.m05682	AO070337000229	0	-100	-89					ATGCCCAACTAG	ATGCCCAACTAG			MPN*	MPN*			GCCACGTTAC	CTCCACGCTT	0	O	0	0	0	0	0
6703	3227	ao	AN8343.1	57.m05682	AO070337000229	0					-170	-153	ATGCCAAACCACATCTAA			ATGCCAAACCACATCTAA	MPNHI*			MPNHI*	GCCCGGAGTT	TCTCCGCATA	0	O	0	0	0	0	0
6704	3229	ao	AN5210.1	69.m14907	AO070337000270	0					-247	-23	ATGAGAAAGCGGCCAACAACATTTTCCCTCCCGGGCACACACCCACTCCCGCAAATCAAACCAAACCCAAAGCAGCCCCTCGCTCACCGGCTCTCTTTCTCTGGCCAACCTCTCCGATCTTTTTTTATCGCCCATCCCCCCCCTCTTCCCCCCCCAATTCTTCCATTCATCCACATCACAACTTCCTCTCCCCCCCAAACCATCTTCTCCTCTTCATCCTTCTAG			ATGAGAAAGCGGCCAACAACATTTTCCCTCCCGGGCACACACCCACTCCCGCAAATCAAACCAAACCCAAAGCAGCCCCTCGCTCACCGGCTCTCTTTCTCTGGCCAACCTCTCCGATCTTTTTTTATCGCCCATCCCCCCCCTCTTCCCCCCCCAATTCTTCCATTCATCCACATCACAACTTCCTCTCCCCCCCAAACCATCTTCTCCTCTTCATCCTTCTAG	MRKRPTTFSLPGTHPLPQIKPNPKQPLAHRLSFSGQPLRSFFIAHPPPLPPPILPFIHITTSSPPQTIFSSSSF*			MRKRPTTFSLPGTHPLPQIKPNPKQPLAHRLSFSGQPLRSFFIAHPPPLPPPILPFIHITTSSPPQTIFSSSSF*	CCTCTCTCAA	TGTAGACAGA	0	G	FG07528.1	0	0	0	0
6705	3231	af	AN4923.1	59.m08826	AO070338000020	0			-232	-80			ATGATTTGGGCAATCAGTCGGCCATTGCTTCTTTCTCTCGTCCTACCTACTGCTTTAAAGGTACACCTGGCCCTCCCTCCTTCTCTTCCTTCTGTTTCTCCTCCCAAGTTTCACCTTCTTTGCAATCATTGTCTGTTTCCTTTTTGTGCTTGA		ATGATTTGGGCAATCAGTCGGCCATTGCTTCTTTCTCTCGTCCTACCTACTGCTTTAAAGGTACACCTGGCCCTCCCTCCTTCTCTTCCTTCTGTTTCTCCTCCCAAGTTTCACCTTCTTTGCAATCATTGTCTGTTTCCTTTTTGTGCTTGA		MIWAISRPLLLSLVLPTALKVHLALPPSLPSVSPPKFHLLCNHCLFPFCA*		MIWAISRPLLLSLVLPTALKVHLALPPSLPSVSPPKFHLLCNHCLFPFCA*		AGCAGGTAAG	GAGTCTGCCT	0	I	0	MG01026.1	NCU03922.1	0	0
6706	3231	ao	AN4923.1	59.m08826	AO070338000020	0					-185	-84	ATGCTCCTCCCTGCTCCTTCTTTTTGTTCTCTTGCCCAGCTGTCTTCCCTCCTCATTCTCTTCTTCTACTTCTTCTTTGCTACCGTTTCCCTTATACCTTAA			ATGCTCCTCCCTGCTCCTTCTTTTTGTTCTCTTGCCCAGCTGTCTTCCCTCCTCATTCTCTTCTTCTACTTCTTCTTTGCTACCGTTTCCCTTATACCTTAA	MLLPAPSFCSLAQLSSLLILFFYFFFATVSLIP*			MLLPAPSFCSLAQLSSLLILFFYFFFATVSLIP*	GTTCTTATAT	TAACCAAATA	0	I	0	MG01026.1	NCU03922.1	0	0
6707	3232	af	AN4919.1	59.m08822	AO070338000024	0			-153	-127			ATGTGCTCTTCTAGAATTTCTCGCTAA		ATGTGCTCTTCTAGAATTTCTCGCTAA		MCSSRISR*		MCSSRISR*		TAGACAAGGT	CAGGCTAATA	0	Z	0	MG09495.1	0	0	0
6708	3232	ao	AN4919.1	59.m08822	AO070338000024	0					-164	-123	ATGACGGTGCCTGACCGTGAATTGAGCCTAGCTAACATATAA			ATGACGGTGCCTGACCGTGAATTGAGCCTAGCTAACATATAA	MTVPDRELSLANI*			MTVPDRELSLANI*	GGACTGGATA	ACAGCCCCAG	0	Z	0	MG09495.1	0	0	0
6710	3233	af	AN4916.1	59.m08819	AO070338000027	0			-228	-115			ATGAGCGTTCCCCTAAGAGGGCAGAGGCTAACCCCACAACGGCAAAGCGCAATACCGCTAAGCGAGGCGCCGAGACTCCGATCCCACACCAGCACGACCGAGCGCAAATTGTAG		ATGAGCGTTCCCCTAAGAGGGCAGAGGCTAACCCCACAACGGCAAAGCGCAATACCGCTAAGCGAGGCGCCGAGACTCCGATCCCACACCAGCACGACCGAGCGCAAATTGTAG		MSVPLRGQRLTPQRQSAIPLSEAPRLRSHTSTTERKL*		MSVPLRGQRLTPQRQSAIPLSEAPRLRSHTSTTERKL*		AAGTCACGGG	GGTAGGAACT	0	J	FG06587.1	0	0	0	0
6709	3233	an	AN4916.1	59.m08819	AO070338000027	0	-201	-190					ATGACACGCTAA	ATGACACGCTAA			MTR*	MTR*			TCTAAGTCAC	GCCAAAACAG	0	J	FG06587.1	0	0	0	0
6711	3233	ao	AN4916.1	59.m08819	AO070338000027	0					-257	-192	ATGTTCCTGATATCGAGGGCAGACCGGTCACGGGACCAGGCTTTCCCTAGGAGAGTAATGCGCTAA			ATGTTCCTGATATCGAGGGCAGACCGGTCACGGGACCAGGCTTTCCCTAGGAGAGTAATGCGCTAA	MFLISRADRSRDQAFPRRVMR*			MFLISRADRSRDQAFPRRVMR*	CTGATAAGAG	CCGGGAGGGG	0	J	FG06587.1	0	0	0	0
6715	3237	af	AN2886.1	59.m08733	AO070338000128	0			-265	-230			ATGACAAGGCGAGAATCATATCACATACGGAGGTAG		ATGACAAGGCGAGAATCATATCACATACGGAGGTAG		MTRRESYHIRR*		MTRRESYHIRR*		GGAGGGGAAG	ACGCCAGCCT	0		0	0	0	0	0
6712	3237	an	AN2886.1	59.m08733	AO070338000128	0	-201	-22					ATGATAAGAGACCGCTGGTTAAGGCTTAGATGCCTGAGAAGCTTCCCCGGCCTAGGCTGGATTTGGATGACGCGGGCCCGGGAGCACACGCCGGGGACTCCACCGCCCAGCGTGCAGTCATTCCTTGGAACCCAGGGTCTCTATATTCGAGATCACGAGATGCTTCCTTTGAGTCTCTGA	ATGATAAGAGACCGCTGGTTAAGGCTTAGATGCCTGAGAAGCTTCCCCGGCCTAGGCTGGATTTGGATGACGCGGGCCCGGGAGCACACGCCGGGGACTCCACCGCCCAGCGTGCAGTCATTCCTTGGAACCCAGGGTCTCTATATTCGAGATCACGAGATGCTTCCTTTGAGTCTCTGA			MIRDRWLRLRCLRSFPGLGWIWMTRAREHTPGTPPPSVQSFLGTQGLYIRDHEMLPLSL*	MIRDRWLRLRCLRSFPGLGWIWMTRAREHTPGTPPPSVQSFLGTQGLYIRDHEMLPLSL*			TGGTGTCGGA	CCTGCCACGA	0		0	0	0	0	0
6713	3237	an	AN2886.1	59.m08733	AO070338000128	0	-135	-22					ATGACGCGGGCCCGGGAGCACACGCCGGGGACTCCACCGCCCAGCGTGCAGTCATTCCTTGGAACCCAGGGTCTCTATATTCGAGATCACGAGATGCTTCCTTTGAGTCTCTGA	ATGACGCGGGCCCGGGAGCACACGCCGGGGACTCCACCGCCCAGCGTGCAGTCATTCCTTGGAACCCAGGGTCTCTATATTCGAGATCACGAGATGCTTCCTTTGAGTCTCTGA			MTRAREHTPGTPPPSVQSFLGTQGLYIRDHEMLPLSL*	MTRAREHTPGTPPPSVQSFLGTQGLYIRDHEMLPLSL*			CTGGATTTGG	CCTGCCACGA	0		0	0	0	0	0
6717	3240	an	AN5020.1	59.m09512	AO070338000180	0	-206	-117					ATGACAAGGACCACGTTCGCTGATTTGAACTCGACTAAACAGGCCCCTTGCTTCGAATTGATTTCACGGTCCCTCTTCTCCCTTACCTAG	ATGACAAGGACCACGTTCGCTGATTTGAACTCGACTAAACAGGCCCCTTGCTTCGAATTGATTTCACGGTCCCTCTTCTCCCTTACCTAG			MTRTTFADLNSTKQAPCFELISRSLFSLT*	MTRTTFADLNSTKQAPCFELISRSLFSLT*			TGCGCATGAA	ACTACGCTCG	0	U	0	0	0	0	0
6718	3243	af	AN2734.1	54.m06676	AO070338000217	0			-183	-160			ATGCGGCGGGTGGAGCTCACGTGA		ATGCGGCGGGTGGAGCTCACGTGA		MRRVELT*		MRRVELT*		CATTTTTGCA	CTGTCTCGCT	0	J	FG06827.1	MG04467.1	0	0	0
6719	3243	af	AN2734.1	54.m06676	AO070338000217	0			-119	-30			ATGACCGCCGGCGGAAATTCTCTTGAACTTTCAACGTCACGATTCATATCGGACAACAACACATTTCACAAATCTCCTCCTTGCCCTTAA		ATGACCGCCGGCGGAAATTCTCTTGAACTTTCAACGTCACGATTCATATCGGACAACAACACATTTCACAAATCTCCTCCTTGCCCTTAA		MTAGGNSLELSTSRFISDNNTFHKSPPCP*		MTAGGNSLELSTSRFISDNNTFHKSPPCP*		TTTCCCCAAA	ATAACCTATC	0	J	FG06827.1	MG04467.1	0	0	0
6720	3243	ao	AN2734.1	54.m06676	AO070338000217	0					-229	-161	ATGCATGCTTGCATGCCCTATCTGATCTCTCTGCGGACATTTTTTTCTGCCGGGCGGAGCTCCACGTGA			ATGCATGCTTGCATGCCCTATCTGATCTCTCTGCGGACATTTTTTTCTGCCGGGCGGAGCTCCACGTGA	MHACMPYLISLRTFFSAGRSST*			MHACMPYLISLRTFFSAGRSST*	ATACCACTAA	CTACCTCGCT	0	J	FG06827.1	MG04467.1	0	0	0
6721	3243	ao	AN2734.1	54.m06676	AO070338000217	0					-225	-205	ATGCTTGCATGCCCTATCTGA			ATGCTTGCATGCCCTATCTGA	MLACPI*			MLACPI*	CACTAAATGC	TCTCTCTGCG	0	J	FG06827.1	MG04467.1	0	0	0
6722	3243	ao	AN2734.1	54.m06676	AO070338000217	0					-217	-161	ATGCCCTATCTGATCTCTCTGCGGACATTTTTTTCTGCCGGGCGGAGCTCCACGTGA			ATGCCCTATCTGATCTCTCTGCGGACATTTTTTTCTGCCGGGCGGAGCTCCACGTGA	MPYLISLRTFFSAGRSST*			MPYLISLRTFFSAGRSST*	GCATGCTTGC	CTACCTCGCT	0	J	FG06827.1	MG04467.1	0	0	0
6726	3245	af	AN0408.1	54.m06666	AO070338000251	0			-98	-57			ATGTCAAGCTACTCGCGGCTTCCAAACAGGCTTTGGGAATAG		ATGTCAAGCTACTCGCGGCTTCCAAACAGGCTTTGGGAATAG		MSSYSRLPNRLWE*		MSSYSRLPNRLWE*		TCTGACGTCG	CATCTCAGCA	0	R	0	0	0	0	0
6723	3245	an	AN0408.1	54.m06666	AO070338000251	0	-206	-111					ATGTTATTCCGAGTCCCCGCGCTATGCCCAGTTTGGCCATACCGGCCGTCTTTTCAAGGAAATCCGGGCCGGGCGGTCAAGTGCAGGGGCCCGTGA	ATGTTATTCCGAGTCCCCGCGCTATGCCCAGTTTGGCCATACCGGCCGTCTTTTCAAGGAAATCCGGGCCGGGCGGTCAAGTGCAGGGGCCCGTGA			MLFRVPALCPVWPYRPSFQGNPGRAVKCRGP*	MLFRVPALCPVWPYRPSFQGNPGRAVKCRGP*			TTCCGCAACG	CGTCGATGTC	0	R	0	0	0	0	0
6724	3245	an	AN0408.1	54.m06666	AO070338000251	0	-183	-52					ATGCCCAGTTTGGCCATACCGGCCGTCTTTTCAAGGAAATCCGGGCCGGGCGGTCAAGTGCAGGGGCCCGTGACGTCGATGTCGTCAGTGTCAGTCCATGGCTGTCTATCTTGGTGGTCCCAACACTGTTGA	ATGCCCAGTTTGGCCATACCGGCCGTCTTTTCAAGGAAATCCGGGCCGGGCGGTCAAGTGCAGGGGCCCGTGACGTCGATGTCGTCAGTGTCAGTCCATGGCTGTCTATCTTGGTGGTCCCAACACTGTTGA			MPSLAIPAVFSRKSGPGGQVQGPVTSMSSVSVHGCLSWWSQHC*	MPSLAIPAVFSRKSGPGGQVQGPVTSMSSVSVHGCLSWWSQHC*			TCCCCGCGCT	TACCAGCATT	0	R	0	0	0	0	0

6725	3245	an	AN0408.1	54.m06666	AO070338000251	0	-105	-52					ATGTCGTCAGTGTCAGTCCATGGCTGTCTATCTTGGTGGTCCCAACACTGTTGA	ATGTCGTCAGTGTCAGTCCATGGCTGTCTATCTTGGTGGTCCCAACACTGTTGA			MSSVSVHGCLSWWSQHC*	MSSVSVHGCLSWWSQHC*			CGTGACGTCG	TACCAGCATT	0	R	0	0	0	0	0
6727	3245	ao	AN0408.1	54.m06666	AO070338000251	0					-216	-160	ATGCCAAGCCCCTCTAAGCCCGTTCGCCACAGAGACCTGTGGCTGGTGGCCCCATGA			ATGCCAAGCCCCTCTAAGCCCGTTCGCCACAGAGACCTGTGGCTGGTGGCCCCATGA	MPSPSKPVRHRDLWLVAP*			MPSPSKPVRHRDLWLVAP*	TAGAGCCAGA	GGCGGTGTAA	0	R	0	0	0	0	0
6728	3245	ao	AN0408.1	54.m06666	AO070338000251	0					-163	-143	ATGAGGCGGTGTAACTTCTGA			ATGAGGCGGTGTAACTTCTGA	MRRCNF*			MRRCNF*	TGGTGGCCCC	CGTGACGTCG	0	R	0	0	0	0	0
6729	3246	af	AN0411.1	54.m06663	AO070338000254	0			-246	-229			ATGTGGTTGCAGGATTAG		ATGTGGTTGCAGGATTAG		MWLQD*		MWLQD*		GCAAGTGGTC	AGTTGATCTT	0	U	0	0	0	0	0
6733	3247	af	AN3191.1	59.m08411	AO070338000263	0			-217	-128			ATGTTGAATCTCCGTATAGTCTACCGCAGTAATCTCGGCTACGTGTCTATTTCAGTAGGATTCAGTAGGATCTATTCAAGGACGCCATGA		ATGTTGAATCTCCGTATAGTCTACCGCAGTAATCTCGGCTACGTGTCTATTTCAGTAGGATTCAGTAGGATCTATTCAAGGACGCCATGA		MLNLRIVYRSNLGYVSISVGFSRIYSRTP*		MLNLRIVYRSNLGYVSISVGFSRIYSRTP*		GGCAGTGTGA	GAAACCCCAT	0	I	0	0	0	0	0
6734	3247	af	AN3191.1	59.m08411	AO070338000263	0			-131	-27			ATGAGAAACCCCATTCGGCATATGCTGTCGGCGTTCGGTTATCATCTCCGATCGACTGATATAACCCCGCCGTCCCTCTCCGCAAGATCGAATACCGAATACTGA		ATGAGAAACCCCATTCGGCATATGCTGTCGGCGTTCGGTTATCATCTCCGATCGACTGATATAACCCCGCCGTCCCTCTCCGCAAGATCGAATACCGAATACTGA		MRNPIRHMLSAFGYHLRSTDITPPSLSARSNTEY*		MRNPIRHMLSAFGYHLRSTDITPPSLSARSNTEY*		CAAGGACGCC	TCTTTGAAGA	0	I	0	0	0	0	0
6735	3247	af	AN3191.1	59.m08411	AO070338000263	0			-110	-27			ATGCTGTCGGCGTTCGGTTATCATCTCCGATCGACTGATATAACCCCGCCGTCCCTCTCCGCAAGATCGAATACCGAATACTGA		ATGCTGTCGGCGTTCGGTTATCATCTCCGATCGACTGATATAACCCCGCCGTCCCTCTCCGCAAGATCGAATACCGAATACTGA		MLSAFGYHLRSTDITPPSLSARSNTEY*		MLSAFGYHLRSTDITPPSLSARSNTEY*		CATTCGGCAT	TCTTTGAAGA	0	I	0	0	0	0	0
6731	3247	an	AN3191.1	59.m08411	AO070338000263	0	-226	-194					ATGGAGATAACCTGGTCCGCTTATGTACGATGA	ATGGAGATAACCTGGTCCGCTTATGTACGATGA			MEITWSAYVR*	MEITWSAYVR*			GATATACATA	GATTGCAATT	0	I	0	0	0	0	0
6732	3247	an	AN3191.1	59.m08411	AO070338000263	0	-197	-168					ATGAGATTGCAATTGCGATTGCGACAGTGA	ATGAGATTGCAATTGCGATTGCGACAGTGA			MRLQLRLRQ*	MRLQLRLRQ*			CTTATGTACG	CTGCGGGGTA	0	I	0	0	0	0	0
6736	3247	ao	AN3191.1	59.m08411	AO070338000263	0					-252	-172	ATGGTGTGTACTAGTGATCATCTATACCTCGGGTGTACGCGTAAGACAGTGCAAAGAAATAGGATTTATAAACTTATCTAG			ATGGTGTGTACTAGTGATCATCTATACCTCGGGTGTACGCGTAAGACAGTGCAAAGAAATAGGATTTATAAACTTATCTAG	MVCTSDHLYLGCTRKTVQRNRIYKLI*			MVCTSDHLYLGCTRKTVQRNRIYKLI*	ATTTAGAAGT	TAATCCCAAG	0	I	0	0	0	0	0
6742	3250	af	AN9171.1	72.m19835	AO070339000050	0			-191	-81			ATGCGTGTCTCATCCCTCGGCCGGATCGAGCATTGCCCAAACGGGAAATCTGGATGGCTGCGAGCATCTGCGGTGGTTCGTAAACATCTCAACCTTCCACAAAGGGTATAA		ATGCGTGTCTCATCCCTCGGCCGGATCGAGCATTGCCCAAACGGGAAATCTGGATGGCTGCGAGCATCTGCGGTGGTTCGTAAACATCTCAACCTTCCACAAAGGGTATAA		MRVSSLGRIEHCPNGKSGWLRASAVVRKHLNLPQRV*		MRVSSLGRIEHCPNGKSGWLRASAVVRKHLNLPQRV*		AACGTGCTGC	GTAGAGCACA	0	R	0	0	0	0	0
6743	3250	af	AN9171.1	72.m19835	AO070339000050	0			-138	-109			ATGGCTGCGAGCATCTGCGGTGGTTCGTAA		ATGGCTGCGAGCATCTGCGGTGGTTCGTAA		MAASICGGS*		MAASICGGS*		GGAAATCTGG	ACATCTCAAC	0	R	0	0	0	0	0
6739	3250	an	AN9171.1	72.m19835	AO070339000050	0	-204	-139					ATGCATTGCAATGCAACATCGTGCATTGAGTTCCCTGGTTGGAATGCCGGGTGCCCTGATTTGTGA	ATGCATTGCAATGCAACATCGTGCATTGAGTTCCCTGGTTGGAATGCCGGGTGCCCTGATTTGTGA			MHCNATSCIEFPGWNAGCPDL*	MHCNATSCIEFPGWNAGCPDL*			TTCCTGAAGA	AGAATGATTC	0	R	0	0	0	0	0
6740	3250	an	AN9171.1	72.m19835	AO070339000050	0	-194	-132					ATGCAACATCGTGCATTGAGTTCCCTGGTTGGAATGCCGGGTGCCCTGATTTGTGAAGAATGA	ATGCAACATCGTGCATTGAGTTCCCTGGTTGGAATGCCGGGTGCCCTGATTTGTGAAGAATGA			MQHRALSSLVGMPGALICEE*	MQHRALSSLVGMPGALICEE*			ATGCATTGCA	TTCAATATAT	0	R	0	0	0	0	0
6741	3250	an	AN9171.1	72.m19835	AO070339000050	0	-161	-132					ATGCCGGGTGCCCTGATTTGTGAAGAATGA	ATGCCGGGTGCCCTGATTTGTGAAGAATGA			MPGALICEE*	MPGALICEE*			CCTGGTTGGA	TTCAATATAT	0	R	0	0	0	0	0
6744	3250	ao	AN9171.1	72.m19835	AO070339000050	0					-214	-188	ATGTACAGTGAATTAGAGGGAGCGTGA			ATGTACAGTGAATTAGAGGGAGCGTGA	MYSELEGA*			MYSELEGA*	CTATTGGCAA	TTCGTGAAGT	0	R	0	0	0	0	0
6745	3250	ao	AN9171.1	72.m19835	AO070339000050	0					-80	-3	ATGCTTCTAACTCCAGCCCTCCTTCTACTACCACAGGCCAAGGATTCATTCAGACCTCAGTTTATTCCACATTTATAA			ATGCTTCTAACTCCAGCCCTCCTTCTACTACCACAGGCCAAGGATTCATTCAGACCTCAGTTTATTCCACATTTATAA	MLLTPALLLLPQAKDSFRPQFIPHL*			MLLTPALLLLPQAKDSFRPQFIPHL*	CAAATTTACT	AAATGCCTAA	0	R	0	0	0	0	0
6746	3251	an	AN6688.1	65.m07502	AO070339000095	0	-703	-611					ATGGCTTCTTTCTTAACATCGCCATTCCTCCGTTCCACAGAACATCTGCGGGTGTTGTGGTTTCATCCGACTTGCTGGACATTGTTGCTTTGA	ATGGCTTCTTTCTTAACATCGCCATTCCTCCGTTCCACAGAACATCTGCGGGTGTTGTGGTTTCATCCGACTTGCTGGACATTGTTGCTTTGA			MASFLTSPFLRSTEHLRVLWFHPTCWTLLL*	MASFLTSPFLRSTEHLRVLWFHPTCWTLLL*			CCAAGGTAAG	GCCCCTCTCC	0	DZU	FG05315.1	MG01521.1	0	0	0
6747	3251	ao	AN6688.1	65.m07502	AO070339000095	0					-754	-488	ATGGTGGCACTTCTTGCCTGCGCTCCTTCCCTCAATCCACCCCCCTCAAAATCACTTCCCCCTCCCCTCCCTTGGAAAGAATTACCTGGTTCCAGATGCCTTCCTGATTCTATTATCAACCCCTCGCCTAAATTTCCATCTCTGCAAGGGTGTTTGTCTGCTAACCAAGAAGGTGCGACCTGCTCAGGGGAACTTCCTCATCAACGCTCGCTACTTCCGACATTTTTTCCAAACCGTCCACGCTCGCTTCCTAAACCGATCCCTTAA			ATGGTGGCACTTCTTGCCTGCGCTCCTTCCCTCAATCCACCCCCCTCAAAATCACTTCCCCCTCCCCTCCCTTGGAAAGAATTACCTGGTTCCAGATGCCTTCCTGATTCTATTATCAACCCCTCGCCTAAATTTCCATCTCTGCAAGGGTGTTTGTCTGCTAACCAAGAAGGTGCGACCTGCTCAGGGGAACTTCCTCATCAACGCTCGCTACTTCCGACATTTTTTCCAAACCGTCCACGCTCGCTTCCTAAACCGATCCCTTAA	MVALLACAPSLNPPPSKSLPPPLPWKELPGSRCLPDSIINPSPKFPSLQGCLSANQEGATCSGELPHQRSLLPTFFPNRPRSLPKPIP*			MVALLACAPSLNPPPSKSLPPPLPWKELPGSRCLPDSIINPSPKFPSLQGCLSANQEGATCSGELPHQRSLLPTFFPNRPRSLPKPIP*	TTTTCCAGGT	CATTCACAAT	0	DZU	FG05315.1	MG01521.1	0	0	0
6748	3251	ao	AN6688.1	65.m07502	AO070339000095	0					-659	-648	ATGCCTTCCTGA			ATGCCTTCCTGA	MPS*			MPS*	CTGGTTCCAG	TTCTATTATC	0	DZU	FG05315.1	MG01521.1	0	0	0
6750	3252	af	AN6717.1	65.m07257	AO070339000157	0			-194	-171			ATGGTCGGAAACGGAGCGAATTAG		ATGGTCGGAAACGGAGCGAATTAG		MVGNGAN*		MVGNGAN*		GGCTGTGGAG	CCGCCCCAAA	0	C	0	MG09367.1	NCU04899.1	0	0
6749	3252	an	AN6717.1	65.m07257	AO070339000157	0	-210	-157					ATGCCTTGTAGCTTCAGTTGCTCGAGCTTAGCTGGCTGTTCCGTTGCCATGTGA	ATGCCTTGTAGCTTCAGTTGCTCGAGCTTAGCTGGCTGTTCCGTTGCCATGTGA			MPCSFSCSSLAGCSVAM*	MPCSFSCSSLAGCSVAM*			AGAAAGCACC	CCGGAACGGG	0	C	0	MG09367.1	NCU04899.1	0	0
6753	3253	af	AN6723.1	65.m07247	AO070339000166	0			-182	-105			ATGATGATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		ATGATGATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		MMMYTISQYKASKCSATDPCNSPSK*		MMMYTISQYKASKCSATDPCNSPSK*		ATAGATAGGT	TCTGTTGAAT	0	R	0	0	0	0	0
6754	3253	af	AN6723.1	65.m07247	AO070339000166	0			-179	-105			ATGATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		ATGATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		MMYTISQYKASKCSATDPCNSPSK*		MMYTISQYKASKCSATDPCNSPSK*		GATAGGTATG	TCTGTTGAAT	0	R	0	0	0	0	0
6755	3253	af	AN6723.1	65.m07247	AO070339000166	0			-176	-105			ATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		ATGTATACTATCTCGCAGTATAAAGCGTCGAAGTGTTCAGCAACCGATCCTTGCAACAGTCCATCCAAATAA		MYTISQYKASKCSATDPCNSPSK*		MYTISQYKASKCSATDPCNSPSK*		AGGTATGATG	TCTGTTGAAT	0	R	0	0	0	0	0
6756	3253	af	AN6723.1	65.m07247	AO070339000166	0			-96	-85			ATGAGAGTCTGA		ATGAGAGTCTGA		MRV*		MRV*		AATCTGTTGA	TCATTCACTA	0	R	0	0	0	0	0
6751	3253	an	AN6723.1	65.m07247	AO070339000166	0	-165	-151					ATGATCACTTCCTAA	ATGATCACTTCCTAA			MITS*	MITS*			CATCCTGGTC	CCCCTCTCAA	0	R	0	0	0	0	0
6752	3253	an	AN6723.1	65.m07247	AO070339000166	0	-63	-10					ATGGGCGTTTCTTTCTCTCCGCATTCTCTTACTCTCTCATTCTTCCAAAACTAA	ATGGGCGTTTCTTTCTCTCCGCATTCTCTTACTCTCTCATTCTTCCAAAACTAA			MGVSFSPHSLTLSFFQN*	MGVSFSPHSLTLSFFQN*			CGACAATCCT	GAAAGCAAGA	0	R	0	0	0	0	0
6757	3253	ao	AN6723.1	65.m07247	AO070339000166	0					-173	-153	ATGACCCGTCCATTCAAATGA			ATGACCCGTCCATTCAAATGA	MTRPFK*			MTRPFK*	CACATCCGCC	TATAAAGCTG	0	R	0	0	0	0	0
6758	3255	af	AN8651.1	69.m15171	AO070339000265	0			-253	-197			ATGTCTCATTGGCATTGCATTGTTACACTGATAGGCGCAAAGTGTTCACCTCCTTGA		ATGTCTCATTGGCATTGCATTGTTACACTGATAGGCGCAAAGTGTTCACCTCCTTGA		MSHWHCIVTLIGAKCSPP*		MSHWHCIVTLIGAKCSPP*		CCTAGAATTT	AGGTTTCGGG	0	CR	0	0	0	0	0
6759	3255	ao	AN8651.1	69.m15171	AO070339000265	0					-213	-163	ATGCCGTGGGGAGTCTCCCAGCTCACGATACCTACCACCGATTGGCCATAG			ATGCCGTGGGGAGTCTCCCAGCTCACGATACCTACCACCGATTGGCCATAG	MPWGVSQLTIPTTDWP*			MPWGVSQLTIPTTDWP*	ATTATAAATC	AACTGGTAAC	0	CR	0	0	0	0	0
6760	3255	ao	AN8651.1	69.m15171	AO070339000265	0					-121	-104	ATGGGGAGGAATTTCTAA			ATGGGGAGGAATTTCTAA	MGRNF*			MGRNF*	TTTGTAATAC	GCCTTTCGTT	0	CR	0	0	0	0	0
6763	3256	af	AN6176.1	72.m18993	AO070340000023	0			-278	-255			ATGACCCCATCTACGGAATTTTGA		ATGACCCCATCTACGGAATTTTGA		MTPSTEF*		MTPSTEF*		TGATATTTGC	GCCATACATT	0		0	0	0	0	0
6764	3256	af	AN6176.1	72.m18993	AO070340000023	0			-173	-81			ATGGTTATACATGAGTTGTCTACGGACTTATGCGTTGTAGCTCTTGCACATGTTGAGCACCTGAGAAGCAATTACTTGCATGACATCATCTGA		ATGGTTATACATGAGTTGTCTACGGACTTATGCGTTGTAGCTCTTGCACATGTTGAGCACCTGAGAAGCAATTACTTGCATGACATCATCTGA		MVIHELSTDLCVVALAHVEHLRSNYLHDII*		MVIHELSTDLCVVALAHVEHLRSNYLHDII*		CTGCCTTTCA	GATATAATTG	0		0	0	0	0	0
6765	3256	af	AN6176.1	72.m18993	AO070340000023	0			-163	-134			ATGAGTTGTCTACGGACTTATGCGTTGTAG		ATGAGTTGTCTACGGACTTATGCGTTGTAG		MSCLRTYAL*		MSCLRTYAL*		ATGGTTATAC	CTCTTGCACA	0		0	0	0	0	0
6766	3256	af	AN6176.1	72.m18993	AO070340000023	0			-144	-118			ATGCGTTGTAGCTCTTGCACATGTTGA		ATGCGTTGTAGCTCTTGCACATGTTGA		MRCSSCTC*		MRCSSCTC*		CTACGGACTT	GCACCTGAGA	0		0	0	0	0	0
6767	3256	af	AN6176.1	72.m18993	AO070340000023	0			-124	-110			ATGTTGAGCACCTGA		ATGTTGAGCACCTGA		MLST*		MLST*		GCTCTTGCAC	GAAGCAATTA	0		0	0	0	0	0
6768	3256	af	AN6176.1	72.m18993	AO070340000023	0			-94	-74			ATGACATCATCTGAGATATAA		ATGACATCATCTGAGATATAA		MTSSEI*		MTSSEI*		AATTACTTGC	TTGCCCGCCT	0		0	0	0	0	0
6761	3256	an	AN6176.1	72.m18993	AO070340000023	0	-125	-93					ATGCTCCCCGCGACAACCGTACTCAAACATTGA	ATGCTCCCCGCGACAACCGTACTCAAACATTGA			MLPATTVLKH*	MLPATTVLKH*			GCTTTTCACT	CCAGGTCTGG	0		0	0	0	0	0
6770	3256	ao	AN6176.1	72.m18993	AO070340000023	0					-243	-157	ATGGTTTTCATCTTAGCAACCACAAAACCTTGTCGAAATCAAAAGGACTGCAGCGGAGTACATGGCAGCTCGCTTTTTGTTGTCTAG			ATGGTTTTCATCTTAGCAACCACAAAACCTTGTCGAAATCAAAAGGACTGCAGCGGAGTACATGGCAGCTCGCTTTTTGTTGTCTAG	MVFILATTKPCRNQKDCSGVHGSSLFVV*			MVFILATTKPCRNQKDCSGVHGSSLFVV*	TACGCTCTGC	GATACCTGAT	0		0	0	0	0	0
6771	3256	ao	AN6176.1	72.m18993	AO070340000023	0					-182	-117	ATGGCAGCTCGCTTTTTGTTGTCTAGGATACCTGATCCTAACTACAATCATGCTCCTACATCGTGA			ATGGCAGCTCGCTTTTTGTTGTCTAGGATACCTGATCCTAACTACAATCATGCTCCTACATCGTGA	MAARFLLSRIPDPNYNHAPTS*			MAARFLLSRIPDPNYNHAPTS*	AGCGGAGTAC	CTTCAAATAT	0		0	0	0	0	0
6772	3256	ao	AN6176.1	72.m18993	AO070340000023	0					-133	-32	ATGCTCCTACATCGTGACTTCAAATATAAACTCCCTTCAGCATCACCAGCTCTGAATAACCCATTAATTCACACTCATATATACAGACTCCCCGTGAGTTAA			ATGCTCCTACATCGTGACTTCAAATATAAACTCCCTTCAGCATCACCAGCTCTGAATAACCCATTAATTCACACTCATATATACAGACTCCCCGTGAGTTAA	MLLHRDFKYKLPSASPALNNPLIHTHIYRLPVS*			MLLHRDFKYKLPSASPALNNPLIHTHIYRLPVS*	AACTACAATC	TGGCTAACTA	0		0	0	0	0	0
6776	3258	af	AN6139.1	72.m19025	AO070340000063	0			-191	-171			ATGGCCATTGCCGCTTTCTGA		ATGGCCATTGCCGCTTTCTGA		MAIAAF*		MAIAAF*		AACTCGGGTC	AGTCTCCTGC	0	I	0	0	NCU00168.1	0	0
6774	3258	an	AN6139.1	72.m19025	AO070340000063	0	-184	-164					ATGCCTTTGGTCGAATTGTAA	ATGCCTTTGGTCGAATTGTAA			MPLVEL*	MPLVEL*			GCCGTCTGCC	ATATTTAGTC	0	I	0	0	NCU00168.1	0	0
6775	3258	an	AN6139.1	72.m19025	AO070340000063	0	-87	-67					ATGCGAGGGCCTGAAAATTGA	ATGCGAGGGCCTGAAAATTGA			MRGPEN*	MRGPEN*			GTTATCATTC	GTGCTCGATA	0	I	0	0	NCU00168.1	0	0
6777	3258	ao	AN6139.1	72.m19025	AO070340000063	0					-254	-240	ATGTTCTTCTTCTAA			ATGTTCTTCTTCTAA	MFFF*			MFFF*	AATATTCCTA	GTGTTCCTGG	0	I	0	0	NCU00168.1	0	0
6778	3258	ao	AN6139.1	72.m19025	AO070340000063	0					-189	-169	ATGCCCCAACCGCTTTTGTGA			ATGCCCCAACCGCTTTTGTGA	MPQPLL*			MPQPLL*	GGCCATTGCC	TTCTCCCGTG	0	I	0	0	NCU00168.1	0	0
6779	3258	ao	AN6139.1	72.m19025	AO070340000063	0					-94	-62	ATGTGCCTTTCTTACCTTGGACCGCCTATATAG			ATGTGCCTTTCTTACCTTGGACCGCCTATATAG	MCLSYLGPPI*			MCLSYLGPPI*	CCAAGTAAGG	TGCTGACGCT	0	I	0	0	NCU00168.1	0	0
6784	3261	af	AN6111.1	72.m19047	AO070340000094	0			-256	-122			ATGGGCTGTCACGGATGGGCTGTTGTCTGTTTTATGCTGGATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAA		ATGGGCTGTCACGGATGGGCTGTTGTCTGTTTTATGCTGGATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAA		MGCHGWAVVCFMLDDLFLPKDDNVNVAASGYPLYQPFSPPSGYY*		MGCHGWAVVCFMLDDLFLPKDDNVNVAASGYPLYQPFSPPSGYY*		TGTAGTCATG	TATAATTGGC	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6785	3261	af	AN6111.1	72.m19047	AO070340000094	0			-242	-213			ATGGGCTGTTGTCTGTTTTATGCTGGATGA		ATGGGCTGTTGTCTGTTTTATGCTGGATGA		MGCCLFYAG*		MGCCLFYAG*		GCTGTCACGG	TCTATTCTTG	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6786	3261	af	AN6111.1	72.m19047	AO070340000094	0			-223	-122			ATGCTGGATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAA		ATGCTGGATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAA		MLDDLFLPKDDNVNVAASGYPLYQPFSPPSGYY*		MLDDLFLPKDDNVNVAASGYPLYQPFSPPSGYY*		TGTCTGTTTT	TATAATTGGC	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W

6787	3261	af	AN6111.1	72.m19047	AO070340000094	0			-216	-76			ATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		ATGATCTATTCTTGCCAAAGGATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		MIYSCQRMIMSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		MIYSCQRMIMSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		TTTATGCTGG	CGCTGCAGAA	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6788	3261	af	AN6111.1	72.m19047	AO070340000094	0			-195	-76			ATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		ATGATAATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		MIMSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		MIMSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		TTGCCAAAGG	CGCTGCAGAA	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6789	3261	af	AN6111.1	72.m19047	AO070340000094	0			-189	-76			ATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		ATGTCAATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		MSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		MSMLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		AAGGATGATA	CGCTGCAGAA	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6790	3261	af	AN6111.1	72.m19047	AO070340000094	0			-183	-76			ATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		ATGTTGCGGCCTCAGGCTACCCGCTGTACCAGCCATTCTCACCGCCTTCAGGCTACTACTAATATAATTGGCTTATCTGGAAGATTGATGATCCGCTGCATTGAATGA		MLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		MLRPQATRCTSHSHRLQATTNIIGLSGRLMIRCIE*		GATAATGTCA	CGCTGCAGAA	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6791	3261	af	AN6111.1	72.m19047	AO070340000094	0			-96	-76			ATGATCCGCTGCATTGAATGA		ATGATCCGCTGCATTGAATGA		MIRCIE*		MIRCIE*		TGGAAGATTG	CGCTGCAGAA	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6782	3261	an	AN6111.1	72.m19047	AO070340000094	0	-98	-33					ATGAACCGCTTTCATCAAATGACGCTGCCGGACAGGAAATTTCCCAAGCCCGCTCGTCTGTCTTGA	ATGAACCGCTTTCATCAAATGACGCTGCCGGACAGGAAATTTCCCAAGCCCGCTCGTCTGTCTTGA			MNRFHQMTLPDRKFPKPARLS*	MNRFHQMTLPDRKFPKPARLS*			CGGAACATCA	CCCCCTCATC	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6783	3261	an	AN6111.1	72.m19047	AO070340000094	0	-80	-33					ATGACGCTGCCGGACAGGAAATTTCCCAAGCCCGCTCGTCTGTCTTGA	ATGACGCTGCCGGACAGGAAATTTCCCAAGCCCGCTCGTCTGTCTTGA			MTLPDRKFPKPARLS*	MTLPDRKFPKPARLS*			CTTTCATCAA	CCCCCTCATC	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6792	3261	ao	AN6111.1	72.m19047	AO070340000094	0					-241	-221	ATGGTTGTCGTTCAAGGTTGA			ATGGTTGTCGTTCAAGGTTGA	MVVVQG*			MVVVQG*	GAAATTTCCG	ATGACCGCCG	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6793	3261	ao	AN6111.1	72.m19047	AO070340000094	0					-220	-173	ATGACCGCCGAAGCAGCGCTCCGCCGACGGCCTCAGGTTAGAAGCTGA			ATGACCGCCGAAGCAGCGCTCCGCCGACGGCCTCAGGTTAGAAGCTGA	MTAEAALRRRPQVRS*			MTAEAALRRRPQVRS*	TCAAGGTTGA	ATCAGCGAGT	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6794	3261	ao	AN6111.1	72.m19047	AO070340000094	0					-120	-49	ATGATCGACAGTCTTAGGAACAACTTTGGCCCGCTCTTCAATGACGCTGCGGAGTGCAGGAAATTTCTATAG			ATGATCGACAGTCTTAGGAACAACTTTGGCCCGCTCTTCAATGACGCTGCGGAGTGCAGGAAATTTCTATAG	MIDSLRNNFGPLFNDAAECRKFL*			MIDSLRNNFGPLFNDAAECRKFL*	TGGGTTTCTG	AAAGTCCGTC	0	J	FG05509.1	MG08860.1	NCU00334.1	YDR280W	YDR280W
6795	3262	af	AN6080.1	72.m19927	AO070340000130	0			-236	-222			ATGCATTTTCTCTGA		ATGCATTTTCTCTGA		MHFL*		MHFL*		TCCTTTCTAG	AAAATCTCTC	0	U	0	0	0	0	0
6796	3262	af	AN6080.1	72.m19927	AO070340000130	0			-136	-41			ATGTTGCAGCGGAATCCGAATTGCGGACAGCTTGACAGTACTCCGTACTCTGGAAATAGCAATTCATGTTGGACTTCGGACCAGGCGATTGATTGA		ATGTTGCAGCGGAATCCGAATTGCGGACAGCTTGACAGTACTCCGTACTCTGGAAATAGCAATTCATGTTGGACTTCGGACCAGGCGATTGATTGA		MLQRNPNCGQLDSTPYSGNSNSCWTSDQAID*		MLQRNPNCGQLDSTPYSGNSNSCWTSDQAID*		GTCCGGAATA	TAAATTGAAC	0	U	0	0	0	0	0
6797	3262	af	AN6080.1	72.m19927	AO070340000130	0			-71	-45			ATGTTGGACTTCGGACCAGGCGATTGA		ATGTTGGACTTCGGACCAGGCGATTGA		MLDFGPGD*		MLDFGPGD*		ATAGCAATTC	TTGATAAATT	0	U	0	0	0	0	0
6798	3262	ao	AN6080.1	72.m19927	AO070340000130	0					-293	-282	ATGTCTCAATAA			ATGTCTCAATAA	MSQ*			MSQ*	AATAGGTACA	TACGATCTAG	0	U	0	0	0	0	0
6799	3262	ao	AN6080.1	72.m19927	AO070340000130	0					-234	-91	ATGTTTCACTTATTTTTTGTTAACCTCAAAGAAAAAACTCACTTAAAAACTCACCCATGGCTAATAAAAACGGTGTCCTCCATCCTATACTCCGGAACAACATTAATACGACCTCCGGATACCGGCCAGCGTGACAGTAAATAG			ATGTTTCACTTATTTTTTGTTAACCTCAAAGAAAAAACTCACTTAAAAACTCACCCATGGCTAATAAAAACGGTGTCCTCCATCCTATACTCCGGAACAACATTAATACGACCTCCGGATACCGGCCAGCGTGACAGTAAATAG	MFHLFFVNLKEKTHLKTHPWLIKTVSSILYSGTTLIRPPDTGQRDSK*			MFHLFFVNLKEKTHLKTHPWLIKTVSSILYSGTTLIRPPDTGQRDSK*	ACCCTAGAGC	ATAGTACCAA	0	U	0	0	0	0	0
6800	3262	ao	AN6080.1	72.m19927	AO070340000130	0					-178	-101	ATGGCTAATAAAAACGGTGTCCTCCATCCTATACTCCGGAACAACATTAATACGACCTCCGGATACCGGCCAGCGTGA			ATGGCTAATAAAAACGGTGTCCTCCATCCTATACTCCGGAACAACATTAATACGACCTCCGGATACCGGCCAGCGTGA	MANKNGVLHPILRNNINTTSGYRPA*			MANKNGVLHPILRNNINTTSGYRPA*	AAACTCACCC	CAGTAAATAG	0	U	0	0	0	0	0
6802	3263	af	AN6082.1	72.m19923	AO070340000132	0			-290	-246			ATGCACCTCAAATGGTTGGATGCGATAACGGAAAGATACCCGTAA		ATGCACCTCAAATGGTTGGATGCGATAACGGAAAGATACCCGTAA		MHLKWLDAITERYP*		MHLKWLDAITERYP*		TGCCCATAGG	TTGGATTTCA	0	J	0	0	0	YGL030W	0
6803	3263	af	AN6082.1	72.m19923	AO070340000132	0			-279	-100			ATGGTTGGATGCGATAACGGAAAGATACCCGTAATTGGATTTCAGCCCCTTGTACTCCGTACGAAAACAGCGGGGTTACTCAGCAGCTTCTGGCGGAGCGGAATATCTCTGCTCCGGCCGGCACTAGGGCAAACCCACAAGAAAATTATCATGAAAATCAATCTGGGAAGCGCTTCTTGA		ATGGTTGGATGCGATAACGGAAAGATACCCGTAATTGGATTTCAGCCCCTTGTACTCCGTACGAAAACAGCGGGGTTACTCAGCAGCTTCTGGCGGAGCGGAATATCTCTGCTCCGGCCGGCACTAGGGCAAACCCACAAGAAAATTATCATGAAAATCAATCTGGGAAGCGCTTCTTGA		MVGCDNGKIPVIGFQPLVLRTKTAGLLSSFWRSGISLLRPALGQTHKKIIMKINLGSAS*		MVGCDNGKIPVIGFQPLVLRTKTAGLLSSFWRSGISLLRPALGQTHKKIIMKINLGSAS*		TGCACCTCAA	TCGCATCCCA	0	J	0	0	0	YGL030W	0
6804	3263	af	AN6082.1	72.m19923	AO070340000132	0			-129	-100			ATGAAAATCAATCTGGGAAGCGCTTCTTGA		ATGAAAATCAATCTGGGAAGCGCTTCTTGA		MKINLGSAS*		MKINLGSAS*		GAAAATTATC	TCGCATCCCA	0	J	0	0	0	YGL030W	0
6801	3263	an	AN6082.1	72.m19923	AO070340000132	0	-161	-3					ATGACTAAGCACCGCGGAAACGGAGAAACAAGCGATCCGGGTCCTCGCCAAACCCACAAAAAATCACCTTACCGTCTTTTGCATCTCATCCCAATCAAAGACACGGCCGGAGCGCACGTTTTTCGATTCACCCCAGAAACACATCTACAACAGCGTAA	ATGACTAAGCACCGCGGAAACGGAGAAACAAGCGATCCGGGTCCTCGCCAAACCCACAAAAAATCACCTTACCGTCTTTTGCATCTCATCCCAATCAAAGACACGGCCGGAGCGCACGTTTTTCGATTCACCCCAGAAACACATCTACAACAGCGTAA			MTKHRGNGETSDPGPRQTHKKSPYRLFASHPNQRHGRSARFSIHPRNTSTA*	MTKHRGNGETSDPGPRQTHKKSPYRLFASHPNQRHGRSARFSIHPRNTSTA*			TGTATTCAAA	CGATGGCCCC	0	J	0	0	0	YGL030W	0
6805	3263	ao	AN6082.1	72.m19923	AO070340000132	0					-167	-3	ATGACTCAGCAACGACGGAACGGATCAGGAATAGTCCGAGCGAATATAACGCTCGACCGCCAAACCCCACAAAGGAAAGAAAAAACTCAACTTCACGATAAGGCCGGAGCGCACCTTTTCAGACTACTCTCAAAGCATACCGAACTACTCAGTTCAACAGCGTAA			ATGACTCAGCAACGACGGAACGGATCAGGAATAGTCCGAGCGAATATAACGCTCGACCGCCAAACCCCACAAAGGAAAGAAAAAACTCAACTTCACGATAAGGCCGGAGCGCACCTTTTCAGACTACTCTCAAAGCATACCGAACTACTCAGTTCAACAGCGTAA	MTQQRRNGSGIVRANITLDRQTPQRKEKTQLHDKAGAHLFRLLSKHTELLSSTA*			MTQQRRNGSGIVRANITLDRQTPQRKEKTQLHDKAGAHLFRLLSKHTELLSSTA*	AGAAGGCGGA	CGATGGCCCC	0	J	0	0	0	YGL030W	0
6807	3267	af	AN6039.1	72.m19118	AO070340000246	0			-216	-145			ATGTTGAGTCGTTTGGCCTGTGGAGCATCTACAGCCATGGTCAAGTCACGTGAGTGCAGATTTCCGTCTTGA		ATGTTGAGTCGTTTGGCCTGTGGAGCATCTACAGCCATGGTCAAGTCACGTGAGTGCAGATTTCCGTCTTGA		MLSRLACGASTAMVKSRECRFPS*		MLSRLACGASTAMVKSRECRFPS*		ATATTCTCGG	GAATGTCCGC	0		0	0	0	0	0
6808	3267	af	AN6039.1	72.m19118	AO070340000246	0			-180	-145			ATGGTCAAGTCACGTGAGTGCAGATTTCCGTCTTGA		ATGGTCAAGTCACGTGAGTGCAGATTTCCGTCTTGA		MVKSRECRFPS*		MVKSRECRFPS*		ATCTACAGCC	GAATGTCCGC	0		0	0	0	0	0
6809	3267	af	AN6039.1	72.m19118	AO070340000246	0			-142	-62			ATGTCCGCATATTTCCAACGAGATATAGCTACGCCGAGCACTGGTCTGTATCTTCACGAAACAACCATATTTCCTTTTGA		ATGTCCGCATATTTCCAACGAGATATAGCTACGCCGAGCACTGGTCTGTATCTTCACGAAACAACCATATTTCCTTTTGA		MSAYFQRDIATPSTGLYLHETTIFSF*		MSAYFQRDIATPSTGLYLHETTIFSF*		CGTCTTGAGA	GATTTAGCGA	0		0	0	0	0	0
6806	3267	an	AN6039.1	72.m19118	AO070340000246	0	-98	-84					ATGCCTCACGTTTGA	ATGCCTCACGTTTGA			MPHV*	MPHV*			GCTCCTTCCC	GTCAAGAAGG	0		0	0	0	0	0
6810	3267	ao	AN6039.1	72.m19118	AO070340000246	0					-230	-198	ATGTCGTGGTGTAGAAGGAAGTATGTAACATAA			ATGTCGTGGTGTAGAAGGAAGTATGTAACATAA	MSWCRRKYVT*			MSWCRRKYVT*	AAGAAAAAGA	TACGGAGTCA	0		0	0	0	0	0
6811	3268	ao	AN6037.1	72.m19944	AO070340000248	0					-127	-65	ATGTCTTTCTTGGGTCAAGCTCGTTCATCTAGGACTCTTCTTTTCTTGATTACTTGCTGTTGA			ATGTCTTTCTTGGGTCAAGCTCGTTCATCTAGGACTCTTCTTTTCTTGATTACTTGCTGTTGA	MSFLGQARSSRTLLFLITCC*			MSFLGQARSSRTLLFLITCC*	ATAACCAGGT	GAGCTTCCCC	0	G	0	0	0	0	0
6812	3269	af	AN6034.1	72.m19950	AO070340000254	0			-241	-59			ATGTATTGCAATTACAGCACAAAACTGTCCCTGAAAGTTTCGAACCGATGTTGGAACAAGGCTTCCCACGTGACCCACTGTATCCAGGGCCGTCCCCACATGGCCGAGTTTCGATATCGCATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		ATGTATTGCAATTACAGCACAAAACTGTCCCTGAAAGTTTCGAACCGATGTTGGAACAAGGCTTCCCACGTGACCCACTGTATCCAGGGCCGTCCCCACATGGCCGAGTTTCGATATCGCATGCAATGCTTTGATGGATTATTTGCCGGATTTGAAACGAATGGTAATACAATTCAGGCTTGA		MYCNYSTKLSLKVSNRCWNKASHVTHCIQGRPHMAEFRYRMQCFDGLFAGFETNGNTIQA*		MYCNYSTKLSLKVSNRCWNKASHVTHCIQGRPHMAEFRYRMQCFDGLFAGFETNGNTIQA*		GCAATCCGAG	CGTTGGACTT	0		0	0	0	0	0
6823	3270	af	AN6031.1	72.m19125	AO070340000257	0			-201	-115			ATGCTATCGTTCTCCTCTCCTCGGTTCCCCGGCTTAGCCTTGCTCTTCTCCAGATTCTCCTTATTATTATTAGAGTTGCGCCGTTGA		ATGCTATCGTTCTCCTCTCCTCGGTTCCCCGGCTTAGCCTTGCTCTTCTCCAGATTCTCCTTATTATTATTAGAGTTGCGCCGTTGA		MLSFSSPRFPGLALLFSRFSLLLLELRR*		MLSFSSPRFPGLALLFSRFSLLLLELRR*		CAAACAGATC	TACCCTCCAC	0	R	FG05919.1	0	0	0	0
6824	3270	ao	AN6031.1	72.m19125	AO070340000257	0					-213	-40	ATGGGGAAATTAAGTTCATTCGGAGGTCCCGTGTTGAAGTTGCAACCGAGGCTGTCATGCTCATGCTTCCTCCTCGGTTCATGCCAACCTCTTCTTCTCCTATATTTAGGACTTATTCTCCATACTCTCCACATTTCATTGTTCCTGATCATCTTCACTACATCTATCTTTTGA			ATGGGGAAATTAAGTTCATTCGGAGGTCCCGTGTTGAAGTTGCAACCGAGGCTGTCATGCTCATGCTTCCTCCTCGGTTCATGCCAACCTCTTCTTCTCCTATATTTAGGACTTATTCTCCATACTCTCCACATTTCATTGTTCCTGATCATCTTCACTACATCTATCTTTTGA	MGKLSSFGGPVLKLQPRLSCSCFLLGSCQPLLLLYLGLILHTLHISLFLIIFTTSIF*			MGKLSSFGGPVLKLQPRLSCSCFLLGSCQPLLLLYLGLILHTLHISLFLIIFTTSIF*	TCTGGCAATT	TTCTCGATTA	0	R	FG05919.1	0	0	0	0
6826	3273	af	AN5989.1	72.m19151	AO070340000288	0			-251	-231			ATGATAAGTGAGCATCTATGA		ATGATAAGTGAGCATCTATGA		MISEHL*		MISEHL*		ACGTGCTCTG	GCTATCCATC	0	G	0	0	0	0	0
6827	3273	af	AN5989.1	72.m19151	AO070340000288	0			-234	-133			ATGAGCTATCCATCTGGTTGTAACAAATCCCAGGGGTTTATCAATCTATCACGCAACAAAGGCACCCGGCTCAAAATAATCAACCAGCTGCCAAGTCCATGA		ATGAGCTATCCATCTGGTTGTAACAAATCCCAGGGGTTTATCAATCTATCACGCAACAAAGGCACCCGGCTCAAAATAATCAACCAGCTGCCAAGTCCATGA		MSYPSGCNKSQGFINLSRNKGTRLKIINQLPSP*		MSYPSGCNKSQGFINLSRNKGTRLKIINQLPSP*		GTGAGCATCT	CGCAATAAGA	0	G	0	0	0	0	0
6828	3273	af	AN5989.1	72.m19151	AO070340000288	0			-136	-125			ATGACGCAATAA		ATGACGCAATAA		MTQ*		MTQ*		TGCCAAGTCC	GACACCACCA	0	G	0	0	0	0	0
6825	3273	an	AN5989.1	72.m19151	AO070340000288	0	-173	-108					ATGACGTTGTATTATTCATCTGCCCCCGCATCACGCAAGAGTTGCAGTAAACTCGAGGAACTTTGA	ATGACGTTGTATTATTCATCTGCCCCCGCATCACGCAAGAGTTGCAGTAAACTCGAGGAACTTTGA			MTLYYSSAPASRKSCSKLEEL*	MTLYYSSAPASRKSCSKLEEL*			TCGGCCGCCG	ACTTCAATTC	0	G	0	0	0	0	0
6829	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-263	-159	ATGTATGGGGCATCAGGAGATCAATCAATAATCAATATTGATTATGATTTTATCCCTTGGGAAACTGAGACATTGCGTCCTCAATACCTGAGGCATTCATCTTGA			ATGTATGGGGCATCAGGAGATCAATCAATAATCAATATTGATTATGATTTTATCCCTTGGGAAACTGAGACATTGCGTCCTCAATACCTGAGGCATTCATCTTGA	MYGASGDQSIINIDYDFIPWETETLRPQYLRHSS*			MYGASGDQSIINIDYDFIPWETETLRPQYLRHSS*	ACAGACACAA	AATGACGACA	0	G	0	0	0	0	0
6830	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-259	-233	ATGGGGCATCAGGAGATCAATCAATAA			ATGGGGCATCAGGAGATCAATCAATAA	MGHQEINQ*			MGHQEINQ*	ACACAAATGT	TCAATATTGA	0	G	0	0	0	0	0
6831	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-220	-173	ATGATTTTATCCCTTGGGAAACTGAGACATTGCGTCCTCAATACCTGA			ATGATTTTATCCCTTGGGAAACTGAGACATTGCGTCCTCAATACCTGA	MILSLGKLRHCVLNT*			MILSLGKLRHCVLNT*	AATATTGATT	GGCATTCATC	0	G	0	0	0	0	0
6832	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-157	-128	ATGACGACATCATTATTAATGCATCTATGA			ATGACGACATCATTATTAATGCATCTATGA	MTTSLLMHL*			MTTSLLMHL*	TCATCTTGAA	ATAACCTGAG	0	G	0	0	0	0	0
6833	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-139	-128	ATGCATCTATGA			ATGCATCTATGA	MHL*			MHL*	ATCATTATTA	ATAACCTGAG	0	G	0	0	0	0	0
6834	3273	ao	AN5989.1	72.m19151	AO070340000288	0					-131	-54	ATGAATAACCTGAGGCACCACATTGGTGCTGCCCCCTCACCAACAGAAACTAAATACCTCGCGATATCAGCCTACTAA			ATGAATAACCTGAGGCACCACATTGGTGCTGCCCCCTCACCAACAGAAACTAAATACCTCGCGATATCAGCCTACTAA	MNNLRHHIGAAPSPTETKYLAISAY*			MNNLRHHIGAAPSPTETKYLAISAY*	TAATGCATCT	ATAGCTTGAA	0	G	0	0	0	0	0
6837	3275	af	AN5954.1	72.m19170	AO070340000308	0			-225	-214			ATGTATAGATGA		ATGTATAGATGA		MYR*		MYR*		TGCGACATAA	CTCAGCTCAC	0	JK	FG02571.1	0	NCU06279.1	0	0
6838	3275	af	AN5954.1	72.m19170	AO070340000308	0			-217	-182			ATGACTCAGCTCACCTCCTATGCAGAGATAAGATAA		ATGACTCAGCTCACCTCCTATGCAGAGATAAGATAA		MTQLTSYAEIR*		MTQLTSYAEIR*		AAATGTATAG	ACACAAAACC	0	JK	FG02571.1	0	NCU06279.1	0	0

6839	3275	af	AN5954.1	72.m19170	AO070340000308	0			-198	-187			ATGCAGAGATAA		ATGCAGAGATAA		MQR*		MQR*		CTCACCTCCT	GATAAACACA	0	JK	FG02571.1	0	NCU06279.1	0	0
6835	3275	an	AN5954.1	72.m19170	AO070340000308	0	-220	-209					ATGCACATATAG	ATGCACATATAG			MHI*	MHI*			TGACAGACGA	ATGACTCAGC	0	JK	FG02571.1	0	NCU06279.1	0	0
6836	3275	an	AN5954.1	72.m19170	AO070340000308	0	-208	-179					ATGACTCAGCAACAACTTATCCGTAGATAA	ATGACTCAGCAACAACTTATCCGTAGATAA			MTQQQLIRR*	MTQQQLIRR*			GCACATATAG	GATAAGCACA	0	JK	FG02571.1	0	NCU06279.1	0	0
6840	3275	ao	AN5954.1	72.m19170	AO070340000308	0					-197	-186	ATGCGCAGATAA			ATGCGCAGATAA	MRR*			MRR*	CGGCTCCGTT	GATAAGCACA	0	JK	FG02571.1	0	NCU06279.1	0	0
6841	3277	an	AN9469.1	72.m19180	AO070340000318	0	-175	-53					ATGGTAGGGCTTCCGCTCGAGTCACGTGCCTACTGTTTTGAGTGCGGTGTATGGTTCATCCGGTCCGGACAGACTCCGCGGACGCAAGTTTGGTTTAGCTGTGTTGGTGCAGTGCTCTGTTAG	ATGGTAGGGCTTCCGCTCGAGTCACGTGCCTACTGTTTTGAGTGCGGTGTATGGTTCATCCGGTCCGGACAGACTCCGCGGACGCAAGTTTGGTTTAGCTGTGTTGGTGCAGTGCTCTGTTAG			MVGLPLESRAYCFECGVWFIRSGQTPRTQVWFSCVGAVLC*	MVGLPLESRAYCFECGVWFIRSGQTPRTQVWFSCVGAVLC*			TGGGTCAGGC	CAAGTCAGGC	0	J	0	0	0	YOR150W	0
6842	3277	an	AN9469.1	72.m19180	AO070340000318	0	-125	-78					ATGGTTCATCCGGTCCGGACAGACTCCGCGGACGCAAGTTTGGTTTAG	ATGGTTCATCCGGTCCGGACAGACTCCGCGGACGCAAGTTTGGTTTAG			MVHPVRTDSADASLV*	MVHPVRTDSADASLV*			AGTGCGGTGT	CTGTGTTGGT	0	J	0	0	0	YOR150W	0
6843	3277	ao	AN9469.1	72.m19180	AO070340000318	0					-157	-137	ATGCTCCGCCGGGGCGGCTGA			ATGCTCCGCCGGGGCGGCTGA	MLRRGG*			MLRRGG*	GTGTCACGTG	AGTTTGGGTC	0	J	0	0	0	YOR150W	0
6844	3279	an	AN5915.1	72.m19953	AO070340000372	0	-263	-234					ATGGTTCACGTGATAAGTGTCATTACGTAA	ATGGTTCACGTGATAAGTGTCATTACGTAA			MVHVISVIT*	MVHVISVIT*			CCCGAGGTAA	GCTATCAAGC	0	U	0	MG06273.1	0	0	0
6847	3280	af	AN4633.1	57.m05544	AO070340000373	0			-221	-186			ATGCACAGGATGTTCTTCCAGGTCACGTGCACCTGA		ATGCACAGGATGTTCTTCCAGGTCACGTGCACCTGA		MHRMFFQVTCT*		MHRMFFQVTCT*		CCGCTTCAAA	CGGAATAGGC	0	S	0	0	0	0	0
6848	3280	af	AN4633.1	57.m05544	AO070340000373	0			-212	-186			ATGTTCTTCCAGGTCACGTGCACCTGA		ATGTTCTTCCAGGTCACGTGCACCTGA		MFFQVTCT*		MFFQVTCT*		AATGCACAGG	CGGAATAGGC	0	S	0	0	0	0	0
6849	3280	ao	AN4633.1	57.m05544	AO070340000373	0					-197	-150	ATGATTTCCCCAAGAGGAAGGCGGTGTCACGTGTCGCCGGCGGAATAA			ATGATTTCCCCAAGAGGAAGGCGGTGTCACGTGTCGCCGGCGGAATAA	MISPRGRRCHVSPAE*			MISPRGRRCHVSPAE*	CGACACGGTC	CCCCGGTTTT	0	S	0	0	0	0	0
6853	3281	af	AN5746.1	69.m14844	AO070341000003	0			-419	-327			ATGCCTGGCTTTCCCAGTCTGAGATCATTAACATCTACCCCGCCATTCCACACCTGTACTGTTGACCCCTCCATCGCTCTTCGTCATCACTAA		ATGCCTGGCTTTCCCAGTCTGAGATCATTAACATCTACCCCGCCATTCCACACCTGTACTGTTGACCCCTCCATCGCTCTTCGTCATCACTAA		MPGFPSLRSLTSTPPFHTCTVDPSIALRHH*		MPGFPSLRSLTSTPPFHTCTVDPSIALRHH*		AGTGAATTTC	GAGGAATTGG	0	G	0	MG10607.1	0	0	0
6850	3281	an	AN5746.1	69.m14844	AO070341000003	0	-252	-187					ATGCCTCCTTCACATTGCGGTCTTCCTAAGGATGAGTCCAGGCGGTCTCGATCCATCAGCGATTGA	ATGCCTCCTTCACATTGCGGTCTTCCTAAGGATGAGTCCAGGCGGTCTCGATCCATCAGCGATTGA			MPPSHCGLPKDESRRSRSISD*	MPPSHCGLPKDESRRSRSISD*			ACCTGTCGGT	CCGGATGACT	0	G	0	MG10607.1	0	0	0
6851	3281	an	AN5746.1	69.m14844	AO070341000003	0	-221	-66					ATGAGTCCAGGCGGTCTCGATCCATCAGCGATTGACCGGATGACTCCATCGCTCACCTGCTGGCATCATTCTTTTTGGGCCATCGGTGAACGACATCCCCGCCTGCTAAATCACTCCCAGCAACTCTTCGCCTCCCCTTTCTGTTATATTTGTTAA	ATGAGTCCAGGCGGTCTCGATCCATCAGCGATTGACCGGATGACTCCATCGCTCACCTGCTGGCATCATTCTTTTTGGGCCATCGGTGAACGACATCCCCGCCTGCTAAATCACTCCCAGCAACTCTTCGCCTCCCCTTTCTGTTATATTTGTTAA			MSPGGLDPSAIDRMTPSLTCWHHSFWAIGERHPRLLNHSQQLFASPFCYIC*	MSPGGLDPSAIDRMTPSLTCWHHSFWAIGERHPRLLNHSQQLFASPFCYIC*			CTTCCTAAGG	CTTCTCCGTC	0	G	0	MG10607.1	0	0	0
6852	3281	an	AN5746.1	69.m14844	AO070341000003	0	-182	-66					ATGACTCCATCGCTCACCTGCTGGCATCATTCTTTTTGGGCCATCGGTGAACGACATCCCCGCCTGCTAAATCACTCCCAGCAACTCTTCGCCTCCCCTTTCTGTTATATTTGTTAA	ATGACTCCATCGCTCACCTGCTGGCATCATTCTTTTTGGGCCATCGGTGAACGACATCCCCGCCTGCTAAATCACTCCCAGCAACTCTTCGCCTCCCCTTTCTGTTATATTTGTTAA			MTPSLTCWHHSFWAIGERHPRLLNHSQQLFASPFCYIC*	MTPSLTCWHHSFWAIGERHPRLLNHSQQLFASPFCYIC*			GATTGACCGG	CTTCTCCGTC	0	G	0	MG10607.1	0	0	0
6854	3281	ao	AN5746.1	69.m14844	AO070341000003	0					-418	-374	ATGACCTCCTCCTACCCCACCATCCCACTATTTTTGTTACGGTAG			ATGACCTCCTCCTACCCCACCATCCCACTATTTTTGTTACGGTAG	MTSSYPTIPLFLLR*			MTSSYPTIPLFLLR*	CACTGAGATC	CCATGACCCC	0	G	0	MG10607.1	0	0	0
6855	3281	ao	AN5746.1	69.m14844	AO070341000003	0					-371	-282	ATGACCCCTCCATGGCAAAGAGAGAGGAGGACGAGGACGATCAGGAAACTGTGTCTCGCCGTCATACCACAATCGTGTTATCCTGATTGA			ATGACCCCTCCATGGCAAAGAGAGAGGAGGACGAGGACGATCAGGAAACTGTGTCTCGCCGTCATACCACAATCGTGTTATCCTGATTGA	MTPPWQRERRTRTIRKLCLAVIPQSCYPD*			MTPPWQRERRTRTIRKLCLAVIPQSCYPD*	TACGGTAGCC	CATCTTCTTA	0	G	0	MG10607.1	0	0	0
6856	3281	ao	AN5746.1	69.m14844	AO070341000003	0					-360	-286	ATGGCAAAGAGAGAGGAGGACGAGGACGATCAGGAAACTGTGTCTCGCCGTCATACCACAATCGTGTTATCCTGA			ATGGCAAAGAGAGAGGAGGACGAGGACGATCAGGAAACTGTGTCTCGCCGTCATACCACAATCGTGTTATCCTGA	MAKREEDEDDQETVSRRHTTIVLS*			MAKREEDEDDQETVSRRHTTIVLS*	TGACCCCTCC	TTGACATCTT	0	G	0	MG10607.1	0	0	0
6859	3282	af	AN5747.1	69.m14845	AO070341000004	0			-223	-212			ATGTTGGGCTAA		ATGTTGGGCTAA		MLG*		MLG*		CGTAATCGCC	GTCATGTGAC	0	O	FG01198.1	0	0	0	0
6857	3282	an	AN5747.1	69.m14845	AO070341000004	0	-222	-190					ATGGCCTATATTGGCCTGAATTTAATGGCATGA	ATGGCCTATATTGGCCTGAATTTAATGGCATGA			MAYIGLNLMA*	MAYIGLNLMA*			CGGCTTGAAC	ATATAGTCAT	0	O	FG01198.1	0	0	0	0
6858	3282	an	AN5747.1	69.m14845	AO070341000004	0	-193	-176					ATGAATATAGTCATGTGA	ATGAATATAGTCATGTGA			MNIVM*	MNIVM*			ATTTAATGGC	CCGAGTCCGT	0	O	FG01198.1	0	0	0	0
6860	3282	ao	AN5747.1	69.m14845	AO070341000004	0					-200	-180	ATGGGTTTGGTGGCTCCGTAA			ATGGGTTTGGTGGCTCCGTAA	MGLVAP*			MGLVAP*	AGGTGACCTC	GCTCCTCTAC	0	O	FG01198.1	0	0	0	0
6861	3283	af	AN5752.1	69.m14850	AO070341000009	0			-133	-107			ATGCCTCAGGCAGCAAGGCCACTCTGA		ATGCCTCAGGCAGCAAGGCCACTCTGA		MPQAARPL*		MPQAARPL*		CCGGTACTGA	TTGTTGGCCC	0		0	0	0	0	0
6862	3283	ao	AN5752.1	69.m14850	AO070341000009	0					-248	-234	ATGGAACCGTATTGA			ATGGAACCGTATTGA	MEPY*			MEPY*	CATTAAATAC	TTGGTATTGC	0		0	0	0	0	0
6863	3284	ao	AN5741.1	69.m14856	AO070341000018	0					-244	-125	ATGCCTTGTGTACGGTGTACGGAGTACAGTGCTATTACTATTTATCGAAGTATGCATATACTACTTCCACATCTACTAATACGGAGGCACCCCTATCGGATCTTCCCATTGGCTCCTTGA			ATGCCTTGTGTACGGTGTACGGAGTACAGTGCTATTACTATTTATCGAAGTATGCATATACTACTTCCACATCTACTAATACGGAGGCACCCCTATCGGATCTTCCCATTGGCTCCTTGA	MPCVRCTEYSAITIYRSMHILLPHLLIRRHPYRIFPLAP*			MPCVRCTEYSAITIYRSMHILLPHLLIRRHPYRIFPLAP*	GGCCAGGCAA	AACCTGAGCG	0		0	0	0	0	0
6864	3284	ao	AN5741.1	69.m14856	AO070341000018	0					-193	-125	ATGCATATACTACTTCCACATCTACTAATACGGAGGCACCCCTATCGGATCTTCCCATTGGCTCCTTGA			ATGCATATACTACTTCCACATCTACTAATACGGAGGCACCCCTATCGGATCTTCCCATTGGCTCCTTGA	MHILLPHLLIRRHPYRIFPLAP*			MHILLPHLLIRRHPYRIFPLAP*	TTATCGAAGT	AACCTGAGCG	0		0	0	0	0	0
6865	3284	ao	AN5741.1	69.m14856	AO070341000018	0					-109	-92	ATGGTCACGTGGTCGTGA			ATGGTCACGTGGTCGTGA	MVTWS*			MVTWS*	GAGCGACAAT	CGGCCGCAAT	0		0	0	0	0	0
6866	3285	af	AN5731.1	54.m06850	AO070341000029	0			-270	-220			ATGACTGTTGTTAAAAAGTCCCACTTCATCTCTTTTGCGACCTCAAACTAA		ATGACTGTTGTTAAAAAGTCCCACTTCATCTCTTTTGCGACCTCAAACTAA		MTVVKKSHFISFATSN*		MTVVKKSHFISFATSN*		AGCAACATCG	GGGCTGACAC	0	E	0	0	NCU05420.1	0	0
6867	3285	af	AN5731.1	54.m06850	AO070341000029	0			-84	-49			ATGATCCTCCCTTGCGAATGGCCCCACCAACAATAA		ATGATCCTCCCTTGCGAATGGCCCCACCAACAATAA		MILPCEWPHQQ*		MILPCEWPHQQ*		TAAGCATTGC	CATGAGTCAA	0	E	0	0	NCU05420.1	0	0
6868	3285	af	AN5731.1	54.m06850	AO070341000029	0			-67	-44			ATGGCCCCACCAACAATAACATGA		ATGGCCCCACCAACAATAACATGA		MAPPTIT*		MAPPTIT*		TCCCTTGCGA	GTCAAAAGCA	0	E	0	0	NCU05420.1	0	0
6869	3285	ao	AN5731.1	54.m06850	AO070341000029	0					-255	-199	ATGCCATATTTCTCACCTTATTTTCATCATGCAATCGTTGAGTGGATTTTTCTATGA			ATGCCATATTTCTCACCTTATTTTCATCATGCAATCGTTGAGTGGATTTTTCTATGA	MPYFSPYFHHAIVEWIFL*			MPYFSPYFHHAIVEWIFL*	CAGTGAAAAG	TCTCTTGTTC	0	E	0	0	NCU05420.1	0	0
6870	3285	ao	AN5731.1	54.m06850	AO070341000029	0					-227	-132	ATGCAATCGTTGAGTGGATTTTTCTATGATCTCTTGTTCGTTGAAGATCCTCGCGGGGTATCATTAGATCGACTTTCAGTTCAGTCGACCCTCTAA			ATGCAATCGTTGAGTGGATTTTTCTATGATCTCTTGTTCGTTGAAGATCCTCGCGGGGTATCATTAGATCGACTTTCAGTTCAGTCGACCCTCTAA	MQSLSGFFYDLLFVEDPRGVSLDRLSVQSTL*			MQSLSGFFYDLLFVEDPRGVSLDRLSVQSTL*	TATTTTCATC	ATCCTTTCTT	0	E	0	0	NCU05420.1	0	0
6871	3285	ao	AN5731.1	54.m06850	AO070341000029	0					-202	-161	ATGATCTCTTGTTCGTTGAAGATCCTCGCGGGGTATCATTAG			ATGATCTCTTGTTCGTTGAAGATCCTCGCGGGGTATCATTAG	MISCSLKILAGYH*			MISCSLKILAGYH*	GGATTTTTCT	ATCGACTTTC	0	E	0	0	NCU05420.1	0	0
6874	3286	af	AN3932.1	69.m14995	AO070341000043	0			-270	-172			ATGCCATTCAATGAAAGTTCAATATACTCTGTGTATATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGAGGGTTGATTGTAGTACTGTCACGTGA		ATGCCATTCAATGAAAGTTCAATATACTCTGTGTATATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGAGGGTTGATTGTAGTACTGTCACGTGA		MPFNESSIYSVYMHYQKLWKTPILRVDCSTVT*		MPFNESSIYSVYMHYQKLWKTPILRVDCSTVT*		GAAATGTTTT	CGCAGGCGGC	0	O	0	MG00170.1	0	0	0
6875	3286	af	AN3932.1	69.m14995	AO070341000043	0			-260	-198			ATGAAAGTTCAATATACTCTGTGTATATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGA		ATGAAAGTTCAATATACTCTGTGTATATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGA		MKVQYTLCICTIKSCGRLLF*		MKVQYTLCICTIKSCGRLLF*		ATGCCATTCA	GGGTTGATTG	0	O	0	MG00170.1	0	0	0
6876	3286	af	AN3932.1	69.m14995	AO070341000043	0			-234	-172			ATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGAGGGTTGATTGTAGTACTGTCACGTGA		ATGCACTATCAAAAGTTGTGGAAGACTCCTATTCTGAGGGTTGATTGTAGTACTGTCACGTGA		MHYQKLWKTPILRVDCSTVT*		MHYQKLWKTPILRVDCSTVT*		CTCTGTGTAT	CGCAGGCGGC	0	O	0	MG00170.1	0	0	0
6872	3286	an	AN3932.1	69.m14995	AO070341000043	0	-234	-220					ATGCAAAGTGTATAG	ATGCAAAGTGTATAG			MQSV*	MQSV*			TATCGTAAGG	TAGTAGAGGA	0	O	0	MG00170.1	0	0	0
6873	3286	an	AN3932.1	69.m14995	AO070341000043	0	-205	-188					ATGTTACGTGCCTGGTAA	ATGTTACGTGCCTGGTAA			MLRAW*	MLRAW*			AGAGGATCAA	TTGAGGCTGC	0	O	0	MG00170.1	0	0	0
6877	3286	ao	AN3932.1	69.m14995	AO070341000043	0					-240	-226	ATGTATGAAGTATGA			ATGTATGAAGTATGA	MYEV*			MYEV*	GTAGAGATAG	AGGGAAGGCA	0	O	0	MG00170.1	0	0	0
6878	3286	ao	AN3932.1	69.m14995	AO070341000043	0					-236	-210	ATGAAGTATGAAGGGAAGGCAAACTGA			ATGAAGTATGAAGGGAAGGCAAACTGA	MKYEGKAN*			MKYEGKAN*	AGATAGATGT	TAAAGGCGAT	0	O	0	MG00170.1	0	0	0
6879	3286	ao	AN3932.1	69.m14995	AO070341000043	0					-229	-191	ATGAAGGGAAGGCAAACTGATAAAGGCGATAAGGTGTGA			ATGAAGGGAAGGCAAACTGATAAAGGCGATAAGGTGTGA	MKGRQTDKGDKV*			MKGRQTDKGDKV*	TGTATGAAGT	AGTAAGCGAT	0	O	0	MG00170.1	0	0	0
6880	3286	ao	AN3932.1	69.m14995	AO070341000043	0					-180	-169	ATGATCACGTGA			ATGATCACGTGA	MIT*			MIT*	AGTAAGCGAT	CCCAGGCGGC	0	O	0	MG00170.1	0	0	0
6882	3289	af	AN4174.1	69.m14956	AO070341000088	0			-96	-82			ATGCGTCTCTCATAA		ATGCGTCTCTCATAA		MRLS*		MRLS*		CCTATCAGGT	TCAAGCCGTT	0	G	0	0	0	YML004C	0
6881	3289	an	AN4174.1	69.m14956	AO070341000088	0	-75	-46					ATGTCTAACTCATTAGGGTTCCCCGCTTGA	ATGTCTAACTCATTAGGGTTCCCCGCTTGA			MSNSLGFPA*	MSNSLGFPA*			TTCGTCATTC	GCAGTTGCAG	0	G	0	0	0	YML004C	0
6884	3290	af	AN1921.1	69.m14938	AO070341000116	0			-250	-86			ATGAACCCATCCTCCCCCAGACGCCATTCCGTATCCTTCCTACTAATTTCTCCCCGTCTTTCCTTTATTCTTCCTTTGTTTGGGGGGTTTTCGTCTCCGTCTTGCTATCTTTCTTCACAGATCTTGTTCTTCGGGACCCTATCAGCTGGCCTGTCATCTCCTTAG		ATGAACCCATCCTCCCCCAGACGCCATTCCGTATCCTTCCTACTAATTTCTCCCCGTCTTTCCTTTATTCTTCCTTTGTTTGGGGGGTTTTCGTCTCCGTCTTGCTATCTTTCTTCACAGATCTTGTTCTTCGGGACCCTATCAGCTGGCCTGTCATCTCCTTAG		MNPSSPRRHSVSFLLISPRLSFILPLFGGFSSPSCYLSSQILFFGTLSAGLSSP*		MNPSSPRRHSVSFLLISPRLSFILPLFGGFSSPSCYLSSQILFFGTLSAGLSSP*		TTTGCCGACC	TGGCACCTTG	0	U	0	MG08896.1	0	0	0
6885	3291	af	AN1897.1	57.m05721	AO070341000158	0			-195	-88			ATGGCCCATCACCTCATCAGCTTTGCAGTCGGGAATGCCGCGAAGATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAA		ATGGCCCATCACCTCATCAGCTTTGCAGTCGGGAATGCCGCGAAGATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAA		MAHHLISFAVGNAAKMAAAGFNGFLHFRAHEVFGS*		MAHHLISFAVGNAAKMAAAGFNGFLHFRAHEVFGS*		CCCAGTCTCG	GAAGGCCCGA	0	E	0	0	0	0	0
6886	3291	af	AN1897.1	57.m05721	AO070341000158	0			-161	-75			ATGCCGCGAAGATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAAGAAGGCCCGATAG		ATGCCGCGAAGATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAAGAAGGCCCGATAG		MPRRWPQLVLTASCIFVLTKYLVLKKAR*		MPRRWPQLVLTASCIFVLTKYLVLKKAR*		GCAGTCGGGA	TCCCTCTCAG	0	E	0	0	0	0	0
6887	3291	af	AN1897.1	57.m05721	AO070341000158	0			-150	-88			ATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAA		ATGGCCGCAGCTGGTTTTAACGGCTTCTTGCATTTTCGTGCTCACGAAGTATTTGGTTCTTAA		MAAAGFNGFLHFRAHEVFGS*		MAAAGFNGFLHFRAHEVFGS*		TGCCGCGAAG	GAAGGCCCGA	0	E	0	0	0	0	0
6888	3291	ao	AN1897.1	57.m05721	AO070341000158	0					-214	-173	ATGATCTGTTGGTTGCATTGTCAATGTTGCGCAATAGTTTGA			ATGATCTGTTGGTTGCATTGTCAATGTTGCGCAATAGTTTGA	MICWLHCQCCAIV*			MICWLHCQCCAIV*	TACTTTGGCT	ATTCCCGCGA	0	E	0	0	0	0	0
6889	3291	ao	AN1897.1	57.m05721	AO070341000158	0					-160	-116	ATGTCCGTGACTACCGGCAGGTCGCGACCGCCGTTAGTCTCATAA			ATGTCCGTGACTACCGGCAGGTCGCGACCGCCGTTAGTCTCATAA	MSVTTGRSRPPLVS*			MSVTTGRSRPPLVS*	TCCCGCGATC	AACGAGGCAC	0	E	0	0	0	0	0
6891	3292	af	AN1896.1	57.m05722	AO070341000159	0			-181	-131			ATGGAGGGGGAAGCAATAGGAGTCCCAGATATGAGGGGCAGACAGACTTGA		ATGGAGGGGGAAGCAATAGGAGTCCCAGATATGAGGGGCAGACAGACTTGA		MEGEAIGVPDMRGRQT*		MEGEAIGVPDMRGRQT*		GGAATCGTCC	AAACGATTTG	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0
6892	3292	af	AN1896.1	57.m05722	AO070341000159	0			-151	-131			ATGAGGGGCAGACAGACTTGA		ATGAGGGGCAGACAGACTTGA		MRGRQT*		MRGRQT*		AGTCCCAGAT	AAACGATTTG	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0
6893	3292	af	AN1896.1	57.m05722	AO070341000159	0			-114	-85			ATGTCGTTGGGTCGCTCTGGATCATCTTGA		ATGTCGTTGGGTCGCTCTGGATCATCTTGA		MSLGRSGSS*		MSLGRSGSS*		TTTGTTTTTA	GCAAGGCCAT	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0
6890	3292	an	AN1896.1	57.m05722	AO070341000159	0	-105	-22					ATGTCGACATCTCTCTCAGCAGCGTTTTATCTGTTATTTGGTCTTCGTTGTCTCCTGAATCATTCATCTACCATTCTCTCCTAA	ATGTCGACATCTCTCTCAGCAGCGTTTTATCTGTTATTTGGTCTTCGTTGTCTCCTGAATCATTCATCTACCATTCTCTCCTAA			MSTSLSAAFYLLFGLRCLLNHSSTILS*	MSTSLSAAFYLLFGLRCLLNHSSTILS*			GCCCCGTTCT	TTTTTGCTAG	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0
6894	3292	ao	AN1896.1	57.m05722	AO070341000159	0					-139	-68	ATGAGGGGCAGACTAAGTCAAAGCAACTTGTTTTTAACATCGCTTTCTTCGCCGTCGGAGCTTTTCACATGA			ATGAGGGGCAGACTAAGTCAAAGCAACTTGTTTTTAACATCGCTTTCTTCGCCGTCGGAGCTTTTCACATGA	MRGRLSQSNLFLTSLSSPSELFT*			MRGRLSQSNLFLTSLSSPSELFT*	CAATCAAGAG	GCACGTCGCT	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0

6895	3292	ao	AN1896.1	57.m05722	AO070341000159	0					-71	-54	ATGAGCACGTCGCTGTGA			ATGAGCACGTCGCTGTGA	MSTSL*			MSTSL*	AGCTTTTCAC	CTACCTTCTC	0	G	FG06449.1	MG00317.1	NCU05537.1	0	0
6898	3293	af	AN1895.1	57.m05723	AO070341000160	0			-173	-144			ATGTCTTATATTAAGTTATGCGTAGATTAA		ATGTCTTATATTAAGTTATGCGTAGATTAA		MSYIKLCVD*		MSYIKLCVD*		GAAAATAAGC	CATTGTTTAT	0	O	0	0	0	0	0
6899	3293	af	AN1895.1	57.m05723	AO070341000160	0			-156	-79			ATGCGTAGATTAACATTGTTTATACCCGACGTGACGTCCGCACCTCCGCATGTAAACGATCAGGAAACCTACATGTAG		ATGCGTAGATTAACATTGTTTATACCCGACGTGACGTCCGCACCTCCGCATGTAAACGATCAGGAAACCTACATGTAG		MRRLTLFIPDVTSAPPHVNDQETYM*		MRRLTLFIPDVTSAPPHVNDQETYM*		ATATTAAGTT	AGCTCTTTGC	0	O	0	0	0	0	0
6896	3293	an	AN1895.1	57.m05723	AO070341000160	0	-201	-130					ATGAATAGGAAATCGCCGTGGATACCCTTGGCCAGAGCCTTGAATACGAGCGATTCCGAGTTTATCCTCTAG	ATGAATAGGAAATCGCCGTGGATACCCTTGGCCAGAGCCTTGAATACGAGCGATTCCGAGTTTATCCTCTAG			MNRKSPWIPLARALNTSDSEFIL*	MNRKSPWIPLARALNTSDSEFIL*			GAAACTAGGA	ATAGAGAACT	0	O	0	0	0	0	0
6897	3293	an	AN1895.1	57.m05723	AO070341000160	0	-113	-45					ATGAACACTTCCAACGCACCACCTTTTCCCTCTAGCAGACTCAAACCGTTTCCAAGCAACAAACCCTAG	ATGAACACTTCCAACGCACCACCTTTTCCCTCTAGCAGACTCAAACCGTTTCCAAGCAACAAACCCTAG			MNTSNAPPFPSSRLKPFPSNKP*	MNTSNAPPFPSSRLKPFPSNKP*			AACTGCATCG	TCAAGACTGC	0	O	0	0	0	0	0
6900	3293	ao	AN1895.1	57.m05723	AO070341000160	0					-228	-145	ATGAGACGCAGTAACGGAAGTCTAAACCCAGTATTAATTTGTTACGTTGATGTATATTCCTCAAATAGTATTAAATTGCTGTAG			ATGAGACGCAGTAACGGAAGTCTAAACCCAGTATTAATTTGTTACGTTGATGTATATTCCTCAAATAGTATTAAATTGCTGTAG	MRRSNGSLNPVLICYVDVYSSNSIKLL*			MRRSNGSLNPVLICYVDVYSSNSIKLL*	GTGGTCAAGG	CGTAGAAACT	0	O	0	0	0	0	0
6901	3293	ao	AN1895.1	57.m05723	AO070341000160	0					-179	-120	ATGTATATTCCTCAAATAGTATTAAATTGCTGTAGCGTAGAAACTCTACTATTTGGGTAG			ATGTATATTCCTCAAATAGTATTAAATTGCTGTAGCGTAGAAACTCTACTATTTGGGTAG	MYIPQIVLNCCSVETLLFG*			MYIPQIVLNCCSVETLLFG*	TGTTACGTTG	TCTATCTCTC	0	O	0	0	0	0	0
6904	3294	af	AN1882.1	57.m05985	AO070341000166	0			-271	-245			ATGCACTCTTTGATCATCTTACGGTAG		ATGCACTCTTTGATCATCTTACGGTAG		MHSLIILR*		MHSLIILR*		ATTCAAGAAG	GTAGCTCTTC	0	CR	0	0	0	0	0
6905	3294	af	AN1882.1	57.m05985	AO070341000166	0			-135	-82			ATGGTGATATCAATCACCTTCAGTTGCACTGTCTTTGGGTCTCCTACTTCCTGA		ATGGTGATATCAATCACCTTCAGTTGCACTGTCTTTGGGTCTCCTACTTCCTGA		MVISITFSCTVFGSPTS*		MVISITFSCTVFGSPTS*		ACATTAGCGC	GCCGTTGCAT	0	CR	0	0	0	0	0
6902	3294	an	AN1882.1	57.m05985	AO070341000166	0	-127	-29					ATGATTTCTAAGCAGCTGCTAGGTCATGGAGTCCATTTAAACCCCCCAATCCTTGGTCTGCTCCTCAGTGTAATTGACACAGACCGAATCAAAGTTTAG	ATGATTTCTAAGCAGCTGCTAGGTCATGGAGTCCATTTAAACCCCCCAATCCTTGGTCTGCTCCTCAGTGTAATTGACACAGACCGAATCAAAGTTTAG			MISKQLLGHGVHLNPPILGLLLSVIDTDRIKV*	MISKQLLGHGVHLNPPILGLLLSVIDTDRIKV*			ACATCACTGC	CCCAAGCTAT	0	CR	0	0	0	0	0
6903	3294	an	AN1882.1	57.m05985	AO070341000166	0	-102	-88					ATGGAGTCCATTTAA	ATGGAGTCCATTTAA			MESI*	MESI*			CTGCTAGGTC	ACCCCCCAAT	0	CR	0	0	0	0	0
6906	3294	ao	AN1882.1	57.m05985	AO070341000166	0					-150	-133	ATGCATAGACCCAAATAG			ATGCATAGACCCAAATAG	MHRPK*			MHRPK*	CGCATTATTA	ACTTTATTAA	0	CR	0	0	0	0	0
6907	3297	ao	AN7967.1	57.m05767	AO070341000216	0					-227	-120	ATGACCTTGATAAGAGACCTTCCGTTCCACACATGGGTGGCGCTACCGGAAAAAATTGAAGATAAAAGAATTTCACCACAGCGAATGAGGGCTGTACCCCTACTTTAG			ATGACCTTGATAAGAGACCTTCCGTTCCACACATGGGTGGCGCTACCGGAAAAAATTGAAGATAAAAGAATTTCACCACAGCGAATGAGGGCTGTACCCCTACTTTAG	MTLIRDLPFHTWVALPEKIEDKRISPQRMRAVPLL*			MTLIRDLPFHTWVALPEKIEDKRISPQRMRAVPLL*	AGAAGAACAT	TTCGAGCTTA	0	F	0	0	0	0	0
6908	3297	ao	AN7967.1	57.m05767	AO070341000216	0					-195	-169	ATGGGTGGCGCTACCGGAAAAAATTGA			ATGGGTGGCGCTACCGGAAAAAATTGA	MGGATGKN*			MGGATGKN*	CGTTCCACAC	AGATAAAAGA	0	F	0	0	0	0	0
6909	3297	ao	AN7967.1	57.m05767	AO070341000216	0					-143	-120	ATGAGGGCTGTACCCCTACTTTAG			ATGAGGGCTGTACCCCTACTTTAG	MRAVPLL*			MRAVPLL*	ACCACAGCGA	TTCGAGCTTA	0	F	0	0	0	0	0
6911	3300	af	AN2104.1	57.m05805	AO070341000262	0			-281	-219			ATGGCGAATCATAGGGTCGGCATTCCACAGCGGTTGAACATTTTCCATTGTGTATGTAGGTAA		ATGGCGAATCATAGGGTCGGCATTCCACAGCGGTTGAACATTTTCCATTGTGTATGTAGGTAA		MANHRVGIPQRLNIFHCVCR*		MANHRVGIPQRLNIFHCVCR*		CGGCGAGGAG	GTTCTACGCA	0	J	0	MG04742.1	0	0	0
6912	3300	af	AN2104.1	57.m05805	AO070341000262	0			-189	-82			ATGAGCGCTGACTGTGTCAAGTCGCTATCTCAATTGATCTGGCACCATATACATGTACGCGTTGTACGGAGTAGGACAACGCGACATCGTCAATTGACGACTGAATAG		ATGAGCGCTGACTGTGTCAAGTCGCTATCTCAATTGATCTGGCACCATATACATGTACGCGTTGTACGGAGTAGGACAACGCGACATCGTCAATTGACGACTGAATAG		MSADCVKSLSQLIWHHIHVRVVRSRTTRHRQLTTE*		MSADCVKSLSQLIWHHIHVRVVRSRTTRHRQLTTE*		TCGCTTGGAA	CTTCGAGCTC	0	J	0	MG04742.1	0	0	0
6913	3300	af	AN2104.1	57.m05805	AO070341000262	0			-137	-93			ATGTACGCGTTGTACGGAGTAGGACAACGCGACATCGTCAATTGA		ATGTACGCGTTGTACGGAGTAGGACAACGCGACATCGTCAATTGA		MYALYGVGQRDIVN*		MYALYGVGQRDIVN*		CACCATATAC	CGACTGAATA	0	J	0	MG04742.1	0	0	0
6914	3300	ao	AN2104.1	57.m05805	AO070341000262	0					-115	-98	ATGTTGGTGTTCTATTGA			ATGTTGGTGTTCTATTGA	MLVFY*			MLVFY*	AGGACTGTGC	CGACTGTTCT	0	J	0	MG04742.1	0	0	0
6915	3300	ao	AN2104.1	57.m05805	AO070341000262	0					-87	-61	ATGATTATAACTGGGTATATTGAGTGA			ATGATTATAACTGGGTATATTGAGTGA	MIITGYIE*			MIITGYIE*	CGACTGTTCT	TCAACGCCAA	0	J	0	MG04742.1	0	0	0
6916	3302	af	AN3716.1	69.m15421	AO070341000345	0			-242	-177			ATGTCATCTCTCCACTACGGCGGCGCAGAGACACCGCCCAAGCTCCTACGTAACGCCGCCATCTAA		ATGTCATCTCTCCACTACGGCGGCGCAGAGACACCGCCCAAGCTCCTACGTAACGCCGCCATCTAA		MSSLHYGGAETPPKLLRNAAI*		MSSLHYGGAETPPKLLRNAAI*		ACAGATAGGG	GACCTAAGCA	0	O	0	MG03524.1	0	0	0
6917	3302	ao	AN3716.1	69.m15421	AO070341000345	0					-224	-183	ATGTCATGTGCTCGGGCGGTGCAAAGACACCGCCTTGAGTGA			ATGTCATGTGCTCGGGCGGTGCAAAGACACCGCCTTGAGTGA	MSCARAVQRHRLE*			MSCARAVQRHRLE*	CTATCCTTCG	GCTTCGCTCC	0	O	0	MG03524.1	0	0	0
6918	3302	ao	AN3716.1	69.m15421	AO070341000345	0					-219	-187	ATGTGCTCGGGCGGTGCAAAGACACCGCCTTGA			ATGTGCTCGGGCGGTGCAAAGACACCGCCTTGA	MCSGGAKTPP*			MCSGGAKTPP*	CTTCGATGTC	GTGAGCTTCG	0	O	0	MG03524.1	0	0	0
6920	3304	af	AN5457.1	69.m15475	AO070341000409	0			-160	-140			ATGATTTCAATCCGTATTTGA		ATGATTTCAATCCGTATTTGA		MISIRI*		MISIRI*		CATTGGTTTC	AAGAGTTTAG	0	PQ	0	0	0	0	0
6919	3304	an	AN5457.1	69.m15475	AO070341000409	0	-61	-11					ATGATCCAGTGCGCTGTCAAGATACACCGCGTTTCCTTACCGGGTCGGTAG	ATGATCCAGTGCGCTGTCAAGATACACCGCGTTTCCTTACCGGGTCGGTAG			MIQCAVKIHRVSLPGR*	MIQCAVKIHRVSLPGR*			TCGCCGGCCG	GCTTATCGCC	0	PQ	0	0	0	0	0
6921	3304	ao	AN5457.1	69.m15475	AO070341000409	0					-218	-171	ATGGATTGCAGACTGGAAGTATCTGAGCCATTTGCTCCTCTGATCTGA			ATGGATTGCAGACTGGAAGTATCTGAGCCATTTGCTCCTCTGATCTGA	MDCRLEVSEPFAPLI*			MDCRLEVSEPFAPLI*	TCGAGGTTGC	GGCACGGATA	0	PQ	0	0	0	0	0
6922	3304	ao	AN5457.1	69.m15475	AO070341000409	0					-84	-37	ATGACGCAGCTACCTTTTCCTTGTGCTTTTCTAGAGTTGCCCGCGTGA			ATGACGCAGCTACCTTTTCCTTGTGCTTTTCTAGAGTTGCCCGCGTGA	MTQLPFPCAFLELPA*			MTQLPFPCAFLELPA*	TTGCTGGTCG	ATTGACTACG	0	PQ	0	0	0	0	0
6923	3309	an	AN3622.1	58.m07409	AO070342000129	0	-251	-231					ATGTCCAAATTCTACGCCTAA	ATGTCCAAATTCTACGCCTAA			MSKFYA*	MSKFYA*			TCATCCTTTT	TTCGCTTTGT	0		0	MG03726.1	0	0	0
6924	3312	ao	AN4163.1	58.m07362	AO070342000193	0					-267	-121	ATGGCATTATATTGTTGGATGATCCACTATTATCGGAACCAGGAACTAGTAAGAGAACTAAGAGAACTAACCGCTGCACGTGACTCGCTTATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG			ATGGCATTATATTGTTGGATGATCCACTATTATCGGAACCAGGAACTAGTAAGAGAACTAAGAGAACTAACCGCTGCACGTGACTCGCTTATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG	MALYCWMIHYYRNQELVRELRELTAARDSLMLGFHVTTHTEGGKGVRA*			MALYCWMIHYYRNQELVRELRELTAARDSLMLGFHVTTHTEGGKGVRA*	CCGACAGCGA	GCGGGCACGC	0	T	FG09870.1	MG04719.1	0	0	0
6925	3312	ao	AN4163.1	58.m07362	AO070342000193	0					-249	-121	ATGATCCACTATTATCGGAACCAGGAACTAGTAAGAGAACTAAGAGAACTAACCGCTGCACGTGACTCGCTTATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG			ATGATCCACTATTATCGGAACCAGGAACTAGTAAGAGAACTAAGAGAACTAACCGCTGCACGTGACTCGCTTATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG	MIHYYRNQELVRELRELTAARDSLMLGFHVTTHTEGGKGVRA*			MIHYYRNQELVRELRELTAARDSLMLGFHVTTHTEGGKGVRA*	ATATTGTTGG	GCGGGCACGC	0	T	FG09870.1	MG04719.1	0	0	0
6926	3312	ao	AN4163.1	58.m07362	AO070342000193	0					-177	-121	ATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG			ATGTTAGGGTTCCATGTGACCACGCACACAGAGGGCGGTAAGGGAGTTAGGGCTTAG	MLGFHVTTHTEGGKGVRA*			MLGFHVTTHTEGGKGVRA*	TGACTCGCTT	GCGGGCACGC	0	T	FG09870.1	MG04719.1	0	0	0
6927	3313	ao	AN1953.1	58.m07342	AO070342000222	0					-232	-89	ATGCAAGACTCCAGATGTACGCGAAAGCTGCGGCCAGGAACATCTCCCTTTGTGCACTCCTCCCTCCCTCGATTTCTCCCGAGTTTCTCGACACCAAGGACTCCAATTAACTACAGGCTGTCGGAAACAATTCCTCCACTCTAG			ATGCAAGACTCCAGATGTACGCGAAAGCTGCGGCCAGGAACATCTCCCTTTGTGCACTCCTCCCTCCCTCGATTTCTCCCGAGTTTCTCGACACCAAGGACTCCAATTAACTACAGGCTGTCGGAAACAATTCCTCCACTCTAG	MQDSRCTRKLRPGTSPFVHSSLPRFLPSFSTPRTPINYRLSETIPPL*			MQDSRCTRKLRPGTSPFVHSSLPRFLPSFSTPRTPINYRLSETIPPL*	CACGGGAAAC	GACCTACGTG	0	Z	FG10385.1	0	NCU04247.1	0	0
6928	3313	ao	AN1953.1	58.m07342	AO070342000222	0					-218	-123	ATGTACGCGAAAGCTGCGGCCAGGAACATCTCCCTTTGTGCACTCCTCCCTCCCTCGATTTCTCCCGAGTTTCTCGACACCAAGGACTCCAATTAA			ATGTACGCGAAAGCTGCGGCCAGGAACATCTCCCTTTGTGCACTCCTCCCTCCCTCGATTTCTCCCGAGTTTCTCGACACCAAGGACTCCAATTAA	MYAKAAARNISLCALLPPSISPEFLDTKDSN*			MYAKAAARNISLCALLPPSISPEFLDTKDSN*	AAGACTCCAG	CTACAGGCTG	0	Z	FG10385.1	0	NCU04247.1	0	0
6929	3314	af	AN5634.1	58.m07331	AO070342000238	0			-269	-210			ATGGCGCATGCTTCAAAATGTAATAAGTACCCTGGTTTCTGGCTTGTGATTCTGGATTGA		ATGGCGCATGCTTCAAAATGTAATAAGTACCCTGGTTTCTGGCTTGTGATTCTGGATTGA		MAHASKCNKYPGFWLVILD*		MAHASKCNKYPGFWLVILD*		CGCATTCGCG	GACTGCAATT	0	C	FG09896.1	0	0	0	0
6930	3314	af	AN5634.1	58.m07331	AO070342000238	0			-262	-221			ATGCTTCAAAATGTAATAAGTACCCTGGTTTCTGGCTTGTGA		ATGCTTCAAAATGTAATAAGTACCCTGGTTTCTGGCTTGTGA		MLQNVISTLVSGL*		MLQNVISTLVSGL*		GCGATGGCGC	TTCTGGATTG	0	C	FG09896.1	0	0	0	0
6931	3314	af	AN5634.1	58.m07331	AO070342000238	0			-113	-96			ATGTTCCTCCTAGTGTAG		ATGTTCCTCCTAGTGTAG		MFLLV*		MFLLV*		CTTGTCTTGC	GGTTAGCTAC	0	C	FG09896.1	0	0	0	0
6932	3314	ao	AN5634.1	58.m07331	AO070342000238	0					-235	-215	ATGGCGCGTGCAACTCAATAA			ATGGCGCGTGCAACTCAATAA	MARATQ*			MARATQ*	ACGCATTTTC	GTACCTTGGC	0	C	FG09896.1	0	0	0	0
6934	3315	af	AN5637.1	58.m07326	AO070342000240	0			-124	-74			ATGAGGAGGGCTTCCCTCGCCTCGATCATGGTGAAGACAGGTCTTCCTTGA		ATGAGGAGGGCTTCCCTCGCCTCGATCATGGTGAAGACAGGTCTTCCTTGA		MRRASLASIMVKTGLP*		MRRASLASIMVKTGLP*		GCTAGACTAT	AACATTTTTT	0	IQR	0	0	0	0	0
6935	3315	af	AN5637.1	58.m07326	AO070342000240	0			-97	-74			ATGGTGAAGACAGGTCTTCCTTGA		ATGGTGAAGACAGGTCTTCCTTGA		MVKTGLP*		MVKTGLP*		CGCCTCGATC	AACATTTTTT	0	IQR	0	0	0	0	0
6933	3315	an	AN5637.1	58.m07326	AO070342000240	0	-151	-47					ATGAGCCTCGGCCCAGCTCGGTCTGGGGTGCTCTCGGTTGAGGTCGAGCTGGGGAGGAGGCAGTGCCTCGATCTTTCTGTACATAAGTCGCAAGATCTCCTGTAG	ATGAGCCTCGGCCCAGCTCGGTCTGGGGTGCTCTCGGTTGAGGTCGAGCTGGGGAGGAGGCAGTGCCTCGATCTTTCTGTACATAAGTCGCAAGATCTCCTGTAG			MSLGPARSGVLSVEVELGRRQCLDLSVHKSQDLL*	MSLGPARSGVLSVEVELGRRQCLDLSVHKSQDLL*			TGTTCCGCTC	AATAAATTCA	0	IQR	0	0	0	0	0
6936	3315	ao	AN5637.1	58.m07326	AO070342000240	0					-240	-154	ATGAATGTTTCTCCTTTCCCGGACGGCGTAGTACAGCCTCGGTATCTTCCGTTCAGTAATCTCGGCCGTCGGATAGCTAGGAGCTAG			ATGAATGTTTCTCCTTTCCCGGACGGCGTAGTACAGCCTCGGTATCTTCCGTTCAGTAATCTCGGCCGTCGGATAGCTAGGAGCTAG	MNVSPFPDGVVQPRYLPFSNLGRRIARS*			MNVSPFPDGVVQPRYLPFSNLGRRIARS*	CAAAGATCGC	AGTAGTAGTT	0	IQR	0	0	0	0	0
6937	3315	ao	AN5637.1	58.m07326	AO070342000240	0					-236	-210	ATGTTTCTCCTTTCCCGGACGGCGTAG			ATGTTTCTCCTTTCCCGGACGGCGTAG	MFLLSRTA*			MFLLSRTA*	GATCGCATGA	TACAGCCTCG	0	IQR	0	0	0	0	0
6938	3315	ao	AN5637.1	58.m07326	AO070342000240	0					-141	-79	ATGGCACGAAAGTCCATCTACTCCTGGATGTCCTTGACGTTAATCAGACTACATCCACATTAA			ATGGCACGAAAGTCCATCTACTCCTGGATGTCCTTGACGTTAATCAGACTACATCCACATTAA	MARKSIYSWMSLTLIRLHPH*			MARKSIYSWMSLTLIRLHPH*	TAGTAGTTAT	AATTATACTG	0	IQR	0	0	0	0	0
6939	3315	ao	AN5637.1	58.m07326	AO070342000240	0					-114	-79	ATGTCCTTGACGTTAATCAGACTACATCCACATTAA			ATGTCCTTGACGTTAATCAGACTACATCCACATTAA	MSLTLIRLHPH*			MSLTLIRLHPH*	CTACTCCTGG	AATTATACTG	0	IQR	0	0	0	0	0
6941	3318	af	AN3725.1	69.m15390	AO070342000290	0			-267	-187			ATGACAGGCTATGTGCCTGGGATAGTCGCAATCCTGGGTACATGTATCGCAATATGCAGGTTGCTCAAACGACGTCATTGA		ATGACAGGCTATGTGCCTGGGATAGTCGCAATCCTGGGTACATGTATCGCAATATGCAGGTTGCTCAAACGACGTCATTGA		MTGYVPGIVAILGTCIAICRLLKRRH*		MTGYVPGIVAILGTCIAICRLLKRRH*		CTTGTGAATT	AGCAGTCAAG	0		0	0	0	0	0
6942	3318	af	AN3725.1	69.m15390	AO070342000290	0			-257	-243			ATGTGCCTGGGATAG		ATGTGCCTGGGATAG		MCLG*		MCLG*		ATGACAGGCT	TCGCAATCCT	0		0	0	0	0	0
6943	3318	af	AN3725.1	69.m15390	AO070342000290	0			-226	-116			ATGTATCGCAATATGCAGGTTGCTCAAACGACGTCATTGAAGCAGTCAAGTTTCAGGGCTCCAGGAATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		ATGTATCGCAATATGCAGGTTGCTCAAACGACGTCATTGAAGCAGTCAAGTTTCAGGGCTCCAGGAATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		MYRNMQVAQTTSLKQSSFRAPGMAGSERYKGLVRPA*		MYRNMQVAQTTSLKQSSFRAPGMAGSERYKGLVRPA*		TCCTGGGTAC	AGCTCCTCAT	0		0	0	0	0	0
6944	3318	af	AN3725.1	69.m15390	AO070342000290	0			-214	-116			ATGCAGGTTGCTCAAACGACGTCATTGAAGCAGTCAAGTTTCAGGGCTCCAGGAATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		ATGCAGGTTGCTCAAACGACGTCATTGAAGCAGTCAAGTTTCAGGGCTCCAGGAATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		MQVAQTTSLKQSSFRAPGMAGSERYKGLVRPA*		MQVAQTTSLKQSSFRAPGMAGSERYKGLVRPA*		GTATCGCAAT	AGCTCCTCAT	0		0	0	0	0	0
6945	3318	af	AN3725.1	69.m15390	AO070342000290	0			-160	-116			ATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		ATGGCAGGCAGTGAAAGGTATAAAGGTCTTGTTCGGCCAGCGTAG		MAGSERYKGLVRPA*		MAGSERYKGLVRPA*		GGCTCCAGGA	AGCTCCTCAT	0		0	0	0	0	0
6940	3318	an	AN3725.1	69.m15390	AO070342000290	0	-152	-33					ATGGAGGACCAGAAAAGCTATATAAACTCCTTCCTTGACTGGATTTGCAAACCTCTCATCATCAGCTTTCACTTCGCGAACATCAAGAACCCCCCACTGAAAATCACATCGAATTTCTGA	ATGGAGGACCAGAAAAGCTATATAAACTCCTTCCTTGACTGGATTTGCAAACCTCTCATCATCAGCTTTCACTTCGCGAACATCAAGAACCCCCCACTGAAAATCACATCGAATTTCTGA			MEDQKSYINSFLDWICKPLIISFHFANIKNPPLKITSNF*	MEDQKSYINSFLDWICKPLIISFHFANIKNPPLKITSNF*			TCTGAGGTTT	AACTCAGAAC	0		0	0	0	0	0
6946	3318	ao	AN3725.1	69.m15390	AO070342000290	0					-216	-202	ATGTGCCTCGGGTGA			ATGTGCCTCGGGTGA	MCLG*			MCLG*	CTCAATATCC	ATTGCGTAGC	0		0	0	0	0	0

6947	3318	ao	AN3725.1	69.m15390	AO070342000290	0					-166	-149	ATGGAGGGACAGATATAG			ATGGAGGGACAGATATAG	MEGQI*			MEGQI*	CATCAACGTC	CAGCAGATGA	0		0	0	0	0	0
6948	3318	ao	AN3725.1	69.m15390	AO070342000290	0					-142	-128	ATGAAAGATATATAA			ATGAAAGATATATAA	MKDI*			MKDI*	ATAGCAGCAG	ACCATCAAAT	0		0	0	0	0	0
6949	3319	ao	AN1390.1	70.m14831	AO070342000349	0					-196	-83	ATGCCAACGGCTCGAGCTCTGGGCACAAATACCTCACCGGATAGAGGTATTTCTTGGCCTATAAGTAGAGAGATTATTCTTCATCCATTCACCAGGTCAGGTCCCGAGCACTAA			ATGCCAACGGCTCGAGCTCTGGGCACAAATACCTCACCGGATAGAGGTATTTCTTGGCCTATAAGTAGAGAGATTATTCTTCATCCATTCACCAGGTCAGGTCCCGAGCACTAA	MPTARALGTNTSPDRGISWPISREIILHPFTRSGPEH*			MPTARALGTNTSPDRGISWPISREIILHPFTRSGPEH*	GGACGAAGGG	CTCCTGCGTT	0	P	0	0	0	0	0
6950	3320	af	AN8496.1	52.m03744	AO070342000397	0			-292	-242			ATGGCCACGAGTAGAAATCACAGCGTCGTAACGATAACCATGGTCCGATGA		ATGGCCACGAGTAGAAATCACAGCGTCGTAACGATAACCATGGTCCGATGA		MATSRNHSVVTITMVR*		MATSRNHSVVTITMVR*		AAGCTAAATC	TTCGGTTGAT	0	G	0	0	0	0	0
6951	3320	af	AN8496.1	52.m03744	AO070342000397	0			-253	-242			ATGGTCCGATGA		ATGGTCCGATGA		MVR*		MVR*		AACGATAACC	TTCGGTTGAT	0	G	0	0	0	0	0
6952	3320	af	AN8496.1	52.m03744	AO070342000397	0			-245	-147			ATGATTCGGTTGATGGGTACTAGACCTCGGATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		ATGATTCGGTTGATGGGTACTAGACCTCGGATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		MIRLMGTRPRMLIGNAGVQTLQTYPACSDDSA*		MIRLMGTRPRMLIGNAGVQTLQTYPACSDDSA*		CCATGGTCCG	TCTGGGGTCG	0	G	0	0	0	0	0
6953	3320	af	AN8496.1	52.m03744	AO070342000397	0			-233	-147			ATGGGTACTAGACCTCGGATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		ATGGGTACTAGACCTCGGATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		MGTRPRMLIGNAGVQTLQTYPACSDDSA*		MGTRPRMLIGNAGVQTLQTYPACSDDSA*		GATTCGGTTG	TCTGGGGTCG	0	G	0	0	0	0	0
6954	3320	af	AN8496.1	52.m03744	AO070342000397	0			-215	-147			ATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		ATGCTGATCGGCAACGCAGGAGTTCAGACCCTGCAAACTTACCCCGCTTGCAGCGATGACTCCGCATAA		MLIGNAGVQTLQTYPACSDDSA*		MLIGNAGVQTLQTYPACSDDSA*		TAGACCTCGG	TCTGGGGTCG	0	G	0	0	0	0	0
6955	3320	af	AN8496.1	52.m03744	AO070342000397	0			-160	-80			ATGACTCCGCATAATCTGGGGTCGATGTCATGGTGGCACCACCTTATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		ATGACTCCGCATAATCTGGGGTCGATGTCATGGTGGCACCACCTTATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		MTPHNLGSMSWWHHLMWNPFSPFANI*		MTPHNLGSMSWWHHLMWNPFSPFANI*		GCTTGCAGCG	TACAGTACAA	0	G	0	0	0	0	0
6956	3320	af	AN8496.1	52.m03744	AO070342000397	0			-136	-80			ATGTCATGGTGGCACCACCTTATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		ATGTCATGGTGGCACCACCTTATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		MSWWHHLMWNPFSPFANI*		MSWWHHLMWNPFSPFANI*		TCTGGGGTCG	TACAGTACAA	0	G	0	0	0	0	0
6957	3320	af	AN8496.1	52.m03744	AO070342000397	0			-115	-80			ATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		ATGTGGAACCCATTCTCACCTTTCGCCAATATTTAA		MWNPFSPFANI*		MWNPFSPFANI*		GCACCACCTT	TACAGTACAA	0	G	0	0	0	0	0
6959	3321	af	AN6394.1	69.m15243	AO070343000149	0			-255	-214			ATGCCAAGAAGCTGGACCGTCCCAGACTTCCCAAAAGGGTAA		ATGCCAAGAAGCTGGACCGTCCCAGACTTCCCAAAAGGGTAA		MPRSWTVPDFPKG*		MPRSWTVPDFPKG*		GCCTACCGAC	CATCCTCGGC	0	I	FG10285.1	MG05949.1	0	0	0
6960	3321	af	AN6394.1	69.m15243	AO070343000149	0			-165	-61			ATGATTGGCAGTCTCTCACATCCCTCAGTATCTATCTATAATATTATTGCAAACCATTCTCAACCCAGACTCTGGACTAGTATTGACGCGATATTCGCTGGTTGA		ATGATTGGCAGTCTCTCACATCCCTCAGTATCTATCTATAATATTATTGCAAACCATTCTCAACCCAGACTCTGGACTAGTATTGACGCGATATTCGCTGGTTGA		MIGSLSHPSVSIYNIIANHSQPRLWTSIDAIFAG*		MIGSLSHPSVSIYNIIANHSQPRLWTSIDAIFAG*		TAGTCCCCGC	TCCTTATTCC	0	I	FG10285.1	MG05949.1	0	0	0
6958	3321	an	AN6394.1	69.m15243	AO070343000149	0	-228	-217					ATGAAGCAGTAG	ATGAAGCAGTAG			MKQ*	MKQ*			CCTCATCGAT	GAACCTCGGC	0	I	FG10285.1	MG05949.1	0	0	0
6961	3321	ao	AN6394.1	69.m15243	AO070343000149	0					-162	-148	ATGAAGTTCCCATGA			ATGAAGTTCCCATGA	MKFP*			MKFP*	CTTCTCCGTA	TTGGCGCACA	0	I	FG10285.1	MG05949.1	0	0	0
6962	3321	ao	AN6394.1	69.m15243	AO070343000149	0					-151	-110	ATGATTGGCGCACATCTCTTCCTCCCCCATATAAATCTATAA			ATGATTGGCGCACATCTCTTCCTCCCCCATATAAATCTATAA	MIGAHLFLPHINL*			MIGAHLFLPHINL*	TGAAGTTCCC	AACTATTATA	0	I	FG10285.1	MG05949.1	0	0	0
6963	3321	ao	AN6394.1	69.m15243	AO070343000149	0					-97	-65	ATGGCCTATCTTTCCCCGCAAAAAGAGTTTTAG			ATGGCCTATCTTTCCCCGCAAAAAGAGTTTTAG	MAYLSPQKEF*			MAYLSPQKEF*	CTATTATAGG	TCCTCCCCCA	0	I	FG10285.1	MG05949.1	0	0	0
6964	3324	af	AN2149.1	72.m19692	AO070343000198	0			-197	-72			ATGACTCGTCCGTGGGAGCAAATTCAGGGCCGCATTCCCCTCGCCAAAGTGGGATGCATCTTCGAAAACATTCACCGCCTCCGGACCGGCAGAACTTTTAGCGGGAGACCAACTGAGAGTGGGTAG		ATGACTCGTCCGTGGGAGCAAATTCAGGGCCGCATTCCCCTCGCCAAAGTGGGATGCATCTTCGAAAACATTCACCGCCTCCGGACCGGCAGAACTTTTAGCGGGAGACCAACTGAGAGTGGGTAG		MTRPWEQIQGRIPLAKVGCIFENIHRLRTGRTFSGRPTESG*		MTRPWEQIQGRIPLAKVGCIFENIHRLRTGRTFSGRPTESG*		GAAGCGAGAG	CAGAACGAGA	0	O	0	0	0	0	0
6965	3324	af	AN2149.1	72.m19692	AO070343000198	0			-144	-97			ATGCATCTTCGAAAACATTCACCGCCTCCGGACCGGCAGAACTTTTAG		ATGCATCTTCGAAAACATTCACCGCCTCCGGACCGGCAGAACTTTTAG		MHLRKHSPPPDRQNF*		MHLRKHSPPPDRQNF*		CCAAAGTGGG	CGGGAGACCA	0	O	0	0	0	0	0
6966	3324	ao	AN2149.1	72.m19692	AO070343000198	0					-190	-140	ATGCGGAGGCGAGGTTATAGATCCGTGGAGAGGAAAGGAACCCCTCGTTAA			ATGCGGAGGCGAGGTTATAGATCCGTGGAGAGGAAAGGAACCCCTCGTTAA	MRRRGYRSVERKGTPR*			MRRRGYRSVERKGTPR*	TAAACCAAGA	AGTGGGATGC	0	O	0	0	0	0	0
6967	3324	ao	AN2149.1	72.m19692	AO070343000198	0					-133	-53	ATGCGACTAGAAAACCTTCACCGCCAGGAACCGGCAGAATTCTTAGCGGAAGCACGACGAGCATCAACGACGACGAACTAG			ATGCGACTAGAAAACCTTCACCGCCAGGAACCGGCAGAATTCTTAGCGGAAGCACGACGAGCATCAACGACGACGAACTAG	MRLENLHRQEPAEFLAEARRASTTTN*			MRLENLHRQEPAEFLAEARRASTTTN*	TTAAAGTGGG	AGTCGGAGCT	0	O	0	0	0	0	0
6971	3325	af	AN0949.1	67.m02992	AO070343000236	0			-191	-129			ATGTGGACAAGATTTTGTTGGGAACCAAGATCCACATATTCTGACGCTGTGGGATGTTGCTAG		ATGTGGACAAGATTTTGTTGGGAACCAAGATCCACATATTCTGACGCTGTGGGATGTTGCTAG		MWTRFCWEPRSTYSDAVGCC*		MWTRFCWEPRSTYSDAVGCC*		TTCCATTCAT	TCTCTTCACA	0	I	0	0	0	0	0
6972	3325	af	AN0949.1	67.m02992	AO070343000236	0			-138	-91			ATGTTGCTAGTCTCTTCACATGTTCTGGTATCCCTGGACTGCCGATGA		ATGTTGCTAGTCTCTTCACATGTTCTGGTATCCCTGGACTGCCGATGA		MLLVSSHVLVSLDCR*		MLLVSSHVLVSLDCR*		ACGCTGTGGG	CCTGTAATCG	0	I	0	0	0	0	0
6973	3325	af	AN0949.1	67.m02992	AO070343000236	0			-119	-84			ATGTTCTGGTATCCCTGGACTGCCGATGACCTGTAA		ATGTTCTGGTATCCCTGGACTGCCGATGACCTGTAA		MFWYPWTADDL*		MFWYPWTADDL*		GTCTCTTCAC	TCGAGCCGAC	0	I	0	0	0	0	0
6974	3325	af	AN0949.1	67.m02992	AO070343000236	0			-94	-62			ATGACCTGTAATCGAGCCGACAAACCTACTTAA		ATGACCTGTAATCGAGCCGACAAACCTACTTAA		MTCNRADKPT*		MTCNRADKPT*		TGGACTGCCG	AGGAGCAGGT	0	I	0	0	0	0	0
6968	3325	an	AN0949.1	67.m02992	AO070343000236	0	-220	-56					ATGGACTGGGCGTCTGGATTTGTTGGGACAAGAGATCTGCAAACGCAAGATAGATCACAGGTTAGATCGTCAAGACTGAAGTTTCCATCACATGCTTGCTACGACCAGATCGCGTCTCCGAGCGTCAGATATCCACTAAACCACTATGGATATAAGGATTACTAG	ATGGACTGGGCGTCTGGATTTGTTGGGACAAGAGATCTGCAAACGCAAGATAGATCACAGGTTAGATCGTCAAGACTGAAGTTTCCATCACATGCTTGCTACGACCAGATCGCGTCTCCGAGCGTCAGATATCCACTAAACCACTATGGATATAAGGATTACTAG			MDWASGFVGTRDLQTQDRSQVRSSRLKFPSHACYDQIASPSVRYPLNHYGYKDY*	MDWASGFVGTRDLQTQDRSQVRSSRLKFPSHACYDQIASPSVRYPLNHYGYKDY*			ATGGACCCTG	ATCCCCTCCT	0	I	0	0	0	0	0
6969	3325	an	AN0949.1	67.m02992	AO070343000236	0	-129	-82					ATGCTTGCTACGACCAGATCGCGTCTCCGAGCGTCAGATATCCACTAA	ATGCTTGCTACGACCAGATCGCGTCTCCGAGCGTCAGATATCCACTAA			MLATTRSRLRASDIH*	MLATTRSRLRASDIH*			TTTCCATCAC	ACCACTATGG	0	I	0	0	0	0	0
6970	3325	an	AN0949.1	67.m02992	AO070343000236	0	-75	-34					ATGGATATAAGGATTACTAGATCCCCTCCTCACGGGGAGTAA	ATGGATATAAGGATTACTAGATCCCCTCCTCACGGGGAGTAA			MDIRITRSPPHGE*	MDIRITRSPPHGE*			CTAAACCACT	ACATCAGATA	0	I	0	0	0	0	0
6975	3325	ao	AN0949.1	67.m02992	AO070343000236	0					-277	-206	ATGGACCCTCATTACCGTAGCCCATTCAGGGGCCACATCTCTTTTTTGTTGGGAAAAAAGATCTACAGATGA			ATGGACCCTCATTACCGTAGCCCATTCAGGGGCCACATCTCTTTTTTGTTGGGAAAAAAGATCTACAGATGA	MDPHYRSPFRGHISFLLGKKIYR*			MDPHYRSPFRGHISFLLGKKIYR*	CTCTAGTTTG	TGATCTACAC	0	I	0	0	0	0	0
6976	3325	ao	AN0949.1	67.m02992	AO070343000236	0					-209	-84	ATGATGATCTACACTCCAGAACTTTTCATTCTGCACTCCAAAGCGGCCTCTTTTCTTTCTTCACTTTCACATGTAGAAACACACTCTCCGGAACTACCGGTGGCCCCTCTAGCGACAACAATTTAA			ATGATGATCTACACTCCAGAACTTTTCATTCTGCACTCCAAAGCGGCCTCTTTTCTTTCTTCACTTTCACATGTAGAAACACACTCTCCGGAACTACCGGTGGCCCCTCTAGCGACAACAATTTAA	MMIYTPELFILHSKAASFLSSLSHVETHSPELPVAPLATTI*			MMIYTPELFILHSKAASFLSSLSHVETHSPELPVAPLATTI*	AGATCTACAG	ACAATGGCTC	0	I	0	0	0	0	0
6977	3325	ao	AN0949.1	67.m02992	AO070343000236	0					-206	-84	ATGATCTACACTCCAGAACTTTTCATTCTGCACTCCAAAGCGGCCTCTTTTCTTTCTTCACTTTCACATGTAGAAACACACTCTCCGGAACTACCGGTGGCCCCTCTAGCGACAACAATTTAA			ATGATCTACACTCCAGAACTTTTCATTCTGCACTCCAAAGCGGCCTCTTTTCTTTCTTCACTTTCACATGTAGAAACACACTCTCCGGAACTACCGGTGGCCCCTCTAGCGACAACAATTTAA	MIYTPELFILHSKAASFLSSLSHVETHSPELPVAPLATTI*			MIYTPELFILHSKAASFLSSLSHVETHSPELPVAPLATTI*	TCTACAGATG	ACAATGGCTC	0	I	0	0	0	0	0
6980	3327	af	AN7606.1	72.m19640	AO070343000278	0			-209	-99			ATGAGCGCCTACTACCCTGTTGAAAATGGCTTATTGTATCTCTCTGTGTCTTTTTCATCTCACCTACTTAGATCCAAGGTTGCTTTTGTACAGGTGATGCTGTGTTATTGA		ATGAGCGCCTACTACCCTGTTGAAAATGGCTTATTGTATCTCTCTGTGTCTTTTTCATCTCACCTACTTAGATCCAAGGTTGCTTTTGTACAGGTGATGCTGTGTTATTGA		MSAYYPVENGLLYLSVSFSSHLLRSKVAFVQVMLCY*		MSAYYPVENGLLYLSVSFSSHLLRSKVAFVQVMLCY*		CGAATTATAT	GTATTCCTAT	0	HC	0	0	0	0	0
6981	3327	af	AN7606.1	72.m19640	AO070343000278	0			-184	-113			ATGGCTTATTGTATCTCTCTGTGTCTTTTTCATCTCACCTACTTAGATCCAAGGTTGCTTTTGTACAGGTGA		ATGGCTTATTGTATCTCTCTGTGTCTTTTTCATCTCACCTACTTAGATCCAAGGTTGCTTTTGTACAGGTGA		MAYCISLCLFHLTYLDPRLLLYR*		MAYCISLCLFHLTYLDPRLLLYR*		CCTGTTGAAA	TGCTGTGTTA	0	HC	0	0	0	0	0
6982	3327	af	AN7606.1	72.m19640	AO070343000278	0			-113	-99			ATGCTGTGTTATTGA		ATGCTGTGTTATTGA		MLCY*		MLCY*		TGTACAGGTG	GTATTCCTAT	0	HC	0	0	0	0	0
6978	3327	an	AN7606.1	72.m19640	AO070343000278	0	-174	-94					ATGAGCCCTTCAGCCCGTCTGCAAAATGACCACTATCACCACCATTCCTCCTCTATTATCTCGTTCCGTGCATTCCGGTAG	ATGAGCCCTTCAGCCCGTCTGCAAAATGACCACTATCACCACCATTCCTCCTCTATTATCTCGTTCCGTGCATTCCGGTAG			MSPSARLQNDHYHHHSSIISFRAFR*	MSPSARLQNDHYHHHSSIISFRAFR*			ATTATTATAT	TGCTAAAAGG	0	HC	0	0	0	0	0
6979	3327	an	AN7606.1	72.m19640	AO070343000278	0	-149						ATGACCACTATCACCACCATTCCTCCTCTATTATCTCGTTCCGTGCATTCCGGTAGTGCTAAAAGGTACATACCTGTTTTCCTATTCAAGCACTGCGAGGTCTGGATCTGGGCGATCATTTCATCAAATCTTCGGCTGTCTGCACCATAA	ATGACCACTATCACCACCATTCCTCCTCTATTATCTCGTTCCGTGCATTCCGGTAGTGCTAAAAGGTACATACCTGTTTTCCTATTCAAGCACTGCGAGGTCTGGATCTGGGCGATCATTTCATCAAATCTTCGGCTGTCTGCACCATAA			MTTITTIPPLLSRSVHSGSAKRYIPVFLFKHCEVWIWAIISSNLRLSAP*	MTTITTIPPLLSRSVHSGSAKRYIPVFLFKHCEVWIWAIISSNLRLSAP*			CGTCTGCAAA	TGACGACCGA	0	HC	0	0	0	0	0
6983	3327	ao	AN7606.1	72.m19640	AO070343000278	0					-198	-157	ATGAGCGCTTCACCCTTTGAGATTCACTTCTTCTCCTTGTAA			ATGAGCGCTTCACCCTTTGAGATTCACTTCTTCTCCTTGTAA	MSASPFEIHFFSL*			MSASPFEIHFFSL*	TTATTTATAA	CACTTTCACT	0	HC	0	0	0	0	0
6984	3327	ao	AN7606.1	72.m19640	AO070343000278	0					-130	-113	ATGTTGGTGATGGTTTAA			ATGTTGGTGATGGTTTAA	MLVMV*			MLVMV*	TTAACTATTC	TCTGTCCTAC	0	HC	0	0	0	0	0
6986	3328	af	AN7590.1	72.m19633	AO070343000286	0			-228	-217			ATGCTTGACTGA		ATGCTTGACTGA		MLD*		MLD*		TACCTTACTG	TGATGATTTT	0	R	0	0	0	0	0
6987	3328	af	AN7590.1	72.m19633	AO070343000286	0			-217	-188			ATGATGATTTTCTCCGAGGGGCTGAGTTAG		ATGATGATTTTCTCCGAGGGGCTGAGTTAG		MMIFSEGLS*		MMIFSEGLS*		TGCTTGACTG	CGAACTACGA	0	R	0	0	0	0	0
6988	3328	af	AN7590.1	72.m19633	AO070343000286	0			-214	-188			ATGATTTTCTCCGAGGGGCTGAGTTAG		ATGATTTTCTCCGAGGGGCTGAGTTAG		MIFSEGLS*		MIFSEGLS*		TTGACTGATG	CGAACTACGA	0	R	0	0	0	0	0
6989	3328	af	AN7590.1	72.m19633	AO070343000286	0			-162	-136			ATGCACCCTGTTTTAGCCACTTCATGA		ATGCACCCTGTTTTAGCCACTTCATGA		MHPVLATS*		MHPVLATS*		CTCCCTCAGT	CATCATCAAT	0	R	0	0	0	0	0
6990	3328	af	AN7590.1	72.m19633	AO070343000286	0			-139	-50			ATGACATCATCAATGACCATCACTGCTCCGCTCATTCCGGGGGATATAAACTGCCCCCTTCTTCTCTCATCCATCAAGTTGCCATCATAA		ATGACATCATCAATGACCATCACTGCTCCGCTCATTCCGGGGGATATAAACTGCCCCCTTCTTCTCTCATCCATCAAGTTGCCATCATAA		MTSSMTITAPLIPGDINCPLLLSSIKLPS*		MTSSMTITAPLIPGDINCPLLLSSIKLPS*		TAGCCACTTC	TCATCCCAAC	0	R	0	0	0	0	0
6991	3328	af	AN7590.1	72.m19633	AO070343000286	0			-127	-50			ATGACCATCACTGCTCCGCTCATTCCGGGGGATATAAACTGCCCCCTTCTTCTCTCATCCATCAAGTTGCCATCATAA		ATGACCATCACTGCTCCGCTCATTCCGGGGGATATAAACTGCCCCCTTCTTCTCTCATCCATCAAGTTGCCATCATAA		MTITAPLIPGDINCPLLLSSIKLPS*		MTITAPLIPGDINCPLLLSSIKLPS*		GACATCATCA	TCATCCCAAC	0	R	0	0	0	0	0
6985	3328	an	AN7590.1	72.m19633	AO070343000286	0	-210	-121					ATGAGCCTACTAGGTTCCTACTATCTTCCGGTTCCCGCCCTATCCAGTGAAATCAATTCGACGTCATCACCTGTTCAATCATTCTTATAA	ATGAGCCTACTAGGTTCCTACTATCTTCCGGTTCCCGCCCTATCCAGTGAAATCAATTCGACGTCATCACCTGTTCAATCATTCTTATAA			MSLLGSYYLPVPALSSEINSTSSPVQSFL*	MSLLGSYYLPVPALSSEINSTSSPVQSFL*			CCCAGTTTAA	CCATCCTGTC	0	R	0	0	0	0	0
6992	3328	ao	AN7590.1	72.m19633	AO070343000286	0					-262	-101	ATGCTTTCTAATGCGCCACTAAACACAACTTTACCCCGCGATTATGCATTGCCCAATAATCGTTCGTTGACCGGTCGGAAGGGGCAGGAGAGAAGTCGTGATATCATCAATCTAGAACAAGTCCCCATGACATCACTGCCATCCTGGATAAGCTACTTATAG			ATGCTTTCTAATGCGCCACTAAACACAACTTTACCCCGCGATTATGCATTGCCCAATAATCGTTCGTTGACCGGTCGGAAGGGGCAGGAGAGAAGTCGTGATATCATCAATCTAGAACAAGTCCCCATGACATCACTGCCATCCTGGATAAGCTACTTATAG	MLSNAPLNTTLPRDYALPNNRSLTGRKGQERSRDIINLEQVPMTSLPSWISYL*			MLSNAPLNTTLPRDYALPNNRSLTGRKGQERSRDIINLEQVPMTSLPSWISYL*	CGTTCTCGTA	CCCTAATACT	0	R	0	0	0	0	0
6993	3328	ao	AN7590.1	72.m19633	AO070343000286	0					-252	-241	ATGCGCCACTAA			ATGCGCCACTAA	MRH*			MRH*	ATGCTTTCTA	ACACAACTTT	0	R	0	0	0	0	0
6994	3328	ao	AN7590.1	72.m19633	AO070343000286	0					-219	-193	ATGCATTGCCCAATAATCGTTCGTTGA			ATGCATTGCCCAATAATCGTTCGTTGA	MHCPIIVR*			MHCPIIVR*	CCCCGCGATT	CCGGTCGGAA	0	R	0	0	0	0	0
6995	3328	ao	AN7590.1	72.m19633	AO070343000286	0					-136	-101	ATGACATCACTGCCATCCTGGATAAGCTACTTATAG			ATGACATCACTGCCATCCTGGATAAGCTACTTATAG	MTSLPSWISYL*			MTSLPSWISYL*	ACAAGTCCCC	CCCTAATACT	0	R	0	0	0	0	0

6996	3329	af	AN0747.1	70.m15361	AO070343000435	0			-244	-56			ATGCCGTCGAGCATGTCCTTTCGACAAACGTGCAGGATTATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		ATGCCGTCGAGCATGTCCTTTCGACAAACGTGCAGGATTATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		MPSSMSFRQTCRIMLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		MPSSMSFRQTCRIMLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		GACAATAATC	CAACCGTCCT	0	O	FG00863.1	MG03600.1	0	0	0
6997	3329	af	AN0747.1	70.m15361	AO070343000435	0			-232	-56			ATGTCCTTTCGACAAACGTGCAGGATTATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		ATGTCCTTTCGACAAACGTGCAGGATTATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		MSFRQTCRIMLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		MSFRQTCRIMLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		GCCGTCGAGC	CAACCGTCCT	0	O	FG00863.1	MG03600.1	0	0	0
6998	3329	af	AN0747.1	70.m15361	AO070343000435	0			-205	-56			ATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		ATGCTGGTTCTGTCTGTAGTGAAGGAAACAGTCGGGATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		MLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		MLVLSVVKETVGMQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		GTGCAGGATT	CAACCGTCCT	0	O	FG00863.1	MG03600.1	0	0	0
6999	3329	af	AN0747.1	70.m15361	AO070343000435	0			-169	-56			ATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		ATGCAACGCAGGCTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGGCGAGAGCTGGCGAACAATTTGACTCCCGAACTTCAACCTCGCATCTCCAGGACTGCCCCATTCTCTAG		MQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		MQRRLVWKSGSCDWLARAGEQFDSRTSTSHLQDCPIL*		AACAGTCGGG	CAACCGTCCT	0	O	FG00863.1	MG03600.1	0	0	0
7000	3329	ao	AN0747.1	70.m15361	AO070343000435	0					-202	-107	ATGGCCGAATCGAGCGTTAGGGAACAGTCGGGATCGAAAACAGTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGACGGGCTGGCGAACAATTTGA			ATGGCCGAATCGAGCGTTAGGGAACAGTCGGGATCGAAAACAGTGGTTTGGAAAAGCGGGTCATGTGATTGGCTGACGGGCTGGCGAACAATTTGA	MAESSVREQSGSKTVVWKSGSCDWLTGWRTI*			MAESSVREQSGSKTVVWKSGSCDWLTGWRTI*	TCGCGGTTCA	CTCCCGAACT	0	O	FG00863.1	MG03600.1	0	0	0
7004	3330	af	AN0720.1	70.m15343	AO070343000474	0			-269	-240			ATGCAAAAGAGTAAGGCTGATGAAGAATGA		ATGCAAAAGAGTAAGGCTGATGAAGAATGA		MQKSKADEE*		MQKSKADEE*		AGAAGCCGTA	CAACCCCATT	0	J	FG09628.1	0	NCU07266.1	0	0
7005	3330	af	AN0720.1	70.m15343	AO070343000474	0			-250	-194			ATGAAGAATGACAACCCCATTTACCAAACTGCACGATGCTCATGCCAAACTATATAG		ATGAAGAATGACAACCCCATTTACCAAACTGCACGATGCTCATGCCAAACTATATAG		MKNDNPIYQTARCSCQTI*		MKNDNPIYQTARCSCQTI*		AGTAAGGCTG	AATGATCGGA	0	J	FG09628.1	0	NCU07266.1	0	0
7006	3330	af	AN0720.1	70.m15343	AO070343000474	0			-243	-181			ATGACAACCCCATTTACCAAACTGCACGATGCTCATGCCAAACTATATAGAATGATCGGATAG		ATGACAACCCCATTTACCAAACTGCACGATGCTCATGCCAAACTATATAGAATGATCGGATAG		MTTPFTKLHDAHAKLYRMIG*		MTTPFTKLHDAHAKLYRMIG*		CTGATGAAGA	GAAGCGGACC	0	J	FG09628.1	0	NCU07266.1	0	0
7007	3330	af	AN0720.1	70.m15343	AO070343000474	0			-215	-189			ATGCTCATGCCAAACTATATAGAATGA		ATGCTCATGCCAAACTATATAGAATGA		MLMPNYIE*		MLMPNYIE*		AAACTGCACG	TCGGATAGGA	0	J	FG09628.1	0	NCU07266.1	0	0
7008	3330	af	AN0720.1	70.m15343	AO070343000474	0			-209	-189			ATGCCAAACTATATAGAATGA		ATGCCAAACTATATAGAATGA		MPNYIE*		MPNYIE*		CACGATGCTC	TCGGATAGGA	0	J	FG09628.1	0	NCU07266.1	0	0
7009	3330	af	AN0720.1	70.m15343	AO070343000474	0			-192	-181			ATGATCGGATAG		ATGATCGGATAG		MIG*		MIG*		ACTATATAGA	GAAGCGGACC	0	J	FG09628.1	0	NCU07266.1	0	0
7010	3330	af	AN0720.1	70.m15343	AO070343000474	0			-66	-13			ATGACCTTCCCCCTTCTACACGCGTCAAGCCTATTGACCGAATATTGCTTTTAA		ATGACCTTCCCCCTTCTACACGCGTCAAGCCTATTGACCGAATATTGCTTTTAA		MTFPLLHASSLLTEYCF*		MTFPLLHASSLLTEYCF*		CTGGACGGGA	CTTCCATTCA	0	J	FG09628.1	0	NCU07266.1	0	0
7001	3330	an	AN0720.1	70.m15343	AO070343000474	0	-231	-166					ATGAACTATAATCAGATATCACAATGTTCTCAATTAAAAGGAAGTAATAATCCAATCAAACCATAG	ATGAACTATAATCAGATATCACAATGTTCTCAATTAAAAGGAAGTAATAATCCAATCAAACCATAG			MNYNQISQCSQLKGSNNPIKP*	MNYNQISQCSQLKGSNNPIKP*			AACTTGTACA	TTAATGATAT	0	J	FG09628.1	0	NCU07266.1	0	0
7002	3330	an	AN0720.1	70.m15343	AO070343000474	0	-208	-185					ATGTTCTCAATTAAAAGGAAGTAA	ATGTTCTCAATTAAAAGGAAGTAA			MFSIKRK*	MFSIKRK*			AGATATCACA	TAATCCAATC	0	J	FG09628.1	0	NCU07266.1	0	0
7003	3330	an	AN0720.1	70.m15343	AO070343000474	0	-126	-28					ATGCGGTGCCCTACCAGGAACAATTGTTCCTCCGTCCGCCGCCCAGCGCTTCAATTTACATGGTGGGGTACCCAAAATTCGATTACAACAAACCATTGA	ATGCGGTGCCCTACCAGGAACAATTGTTCCTCCGTCCGCCGCCCAGCGCTTCAATTTACATGGTGGGGTACCCAAAATTCGATTACAACAAACCATTGA			MRCPTRNNCSSVRRPALQFTWWGTQNSITTNH*	MRCPTRNNCSSVRRPALQFTWWGTQNSITTNH*			GTCAGTCTCC	CTGAGTTATC	0	J	FG09628.1	0	NCU07266.1	0	0
7011	3330	ao	AN0720.1	70.m15343	AO070343000474	0					-236	-195	ATGATCGTGTCAAGACTGTGGGCCACGAAACGAGTGAATTGA			ATGATCGTGTCAAGACTGTGGGCCACGAAACGAGTGAATTGA	MIVSRLWATKRVN*			MIVSRLWATKRVN*	ATACAGATAG	AGTTGGTCGC	0	J	FG09628.1	0	NCU07266.1	0	0
7012	3330	ao	AN0720.1	70.m15343	AO070343000474	0					-173	-147	ATGGGGATGTCCAAAGGATCCCCGTGA			ATGGGGATGTCCAAAGGATCCCCGTGA	MGMSKGSP*			MGMSKGSP*	AAAGGCAACA	TTTGATGTCT	0	J	FG09628.1	0	NCU07266.1	0	0
7013	3330	ao	AN0720.1	70.m15343	AO070343000474	0					-167	-147	ATGTCCAAAGGATCCCCGTGA			ATGTCCAAAGGATCCCCGTGA	MSKGSP*			MSKGSP*	AACAATGGGG	TTTGATGTCT	0	J	FG09628.1	0	NCU07266.1	0	0
7014	3330	ao	AN0720.1	70.m15343	AO070343000474	0					-142	-68	ATGTCTAGTGACCTCCCCATATCCGGAACAACTCTTTACCCGCATCCCGTCATCCCGCCGCATTTGGTGGGGTGA			ATGTCTAGTGACCTCCCCATATCCGGAACAACTCTTTACCCGCATCCCGTCATCCCGCCGCATTTGGTGGGGTGA	MSSDLPISGTTLYPHPVIPPHLVG*			MSSDLPISGTTLYPHPVIPPHLVG*	CCGTGATTTG	TAGCGAAATA	0	J	FG09628.1	0	NCU07266.1	0	0
7015	3331	conserved	AN0733.1	70.m15320	AO070343000494	0	-249	-199	-266	-216	-242	-192	ATGGTGTGCTGsTTTCCGrvCrsTTTTTkkrwymrArrGAAAssrCGCTAA	ATGGTGTGCTGGTTTCCGGACGGTTTTTTTGATCAAAGGAAAGGGCGCTAA	ATGGTGTGCTGCTTTCCGACCACTTTTTGTGATCGAAAGAAACCGCGCTAA	ATGGTGTGCTGCTTTCCGAGCGCTTTTTTGATCAAAGGGAAACGACGCTAA	MVCwFPdgFfdqrKgR*	MVCWFPDGFFDQRKGR*	MVCCFPTTFCDRKKPR*	MVCCFPSAFLIKGKRR*	ATCAskrCTT	GrCCAyCCrd	0	B	FG04290.1	0	NCU01635.1	YNL031C	0
7016	3332	ao	AN0705.1	70.m15312	AO070343000504	0					-224	-186	ATGATGTACTGTACATACATAGAAGGGCAATTGCCTTAG			ATGATGTACTGTACATACATAGAAGGGCAATTGCCTTAG	MMYCTYIEGQLP*			MMYCTYIEGQLP*	TGTAGAAGTC	GTACCTACTA	0	J	0	0	0	0	0
7017	3332	ao	AN0705.1	70.m15312	AO070343000504	0					-221	-186	ATGTACTGTACATACATAGAAGGGCAATTGCCTTAG			ATGTACTGTACATACATAGAAGGGCAATTGCCTTAG	MYCTYIEGQLP*			MYCTYIEGQLP*	AGAAGTCATG	GTACCTACTA	0	J	0	0	0	0	0
7021	3334	af	AN0686.1	70.m15288	AO070343000532	0			-275	-258			ATGACCACCCATTGTTAA		ATGACCACCCATTGTTAA		MTTHC*		MTTHC*		TAGGATCAAG	TATTGCCGGA	0	O	0	MG06004.1	NCU08946.1	0	0
7022	3334	af	AN0686.1	70.m15288	AO070343000532	0			-215	-168			ATGTGCAGCACAGGTCGAGAGCAGCGGCAGAAAGAGAGACGAGGTTGA		ATGTGCAGCACAGGTCGAGAGCAGCGGCAGAAAGAGAGACGAGGTTGA		MCSTGREQRQKERRG*		MCSTGREQRQKERRG*		ACAAGCGTGG	CTCGGGCCAA	0	O	0	MG06004.1	NCU08946.1	0	0
7018	3334	an	AN0686.1	70.m15288	AO070343000532	0	-241	-182					ATGTATAAGACGAAACGAACGAGTTTGGAAACGCGACGTCGAGGTAAGGATGAGGTATGA	ATGTATAAGACGAAACGAACGAGTTTGGAAACGCGACGTCGAGGTAAGGATGAGGTATGA			MYKTKRTSLETRRRGKDEV*	MYKTKRTSLETRRRGKDEV*			CCCATTGTGA	CAACGAAAGA	0	O	0	MG06004.1	NCU08946.1	0	0
7019	3334	an	AN0686.1	70.m15288	AO070343000532	0	-192	-145					ATGAGGTATGACAACGAAAGAGAAGAATTGACGTTTCTCTCGGTCTGA	ATGAGGTATGACAACGAAAGAGAAGAATTGACGTTTCTCTCGGTCTGA			MRYDNEREELTFLSV*	MRYDNEREELTFLSV*			CGAGGTAAGG	GTCGGGCGAA	0	O	0	MG06004.1	NCU08946.1	0	0
7020	3334	an	AN0686.1	70.m15288	AO070343000532	0	-185	-162					ATGACAACGAAAGAGAAGAATTGA	ATGACAACGAAAGAGAAGAATTGA			MTTKEKN*	MTTKEKN*			AGGATGAGGT	CGTTTCTCTC	0	O	0	MG06004.1	NCU08946.1	0	0
7023	3334	ao	AN0686.1	70.m15288	AO070343000532	0					-237	-190	ATGCGTCTGGATATTAAACGACTGGAAATGCGGAGAAGGTGGAACTGA			ATGCGTCTGGATATTAAACGACTGGAAATGCGGAGAAGGTGGAACTGA	MRLDIKRLEMRRRWN*			MRLDIKRLEMRRRWN*	TTTTGAAGGA	AGAGACTAAG	0	O	0	MG06004.1	NCU08946.1	0	0
7024	3334	ao	AN0686.1	70.m15288	AO070343000532	0					-210	-190	ATGCGGAGAAGGTGGAACTGA			ATGCGGAGAAGGTGGAACTGA	MRRRWN*			MRRRWN*	ACGACTGGAA	AGAGACTAAG	0	O	0	MG06004.1	NCU08946.1	0	0
7025	3334	ao	AN0686.1	70.m15288	AO070343000532	0					-126	-22	ATGAGGTTTCCGCCCGGCACTAGTCCGCATCGGGACAGCATGCGAAAAGCCCGACATCATCAAGTTGATCCAACCCCTTTCAAGCTCCTCATCGACTAATCATTAG			ATGAGGTTTCCGCCCGGCACTAGTCCGCATCGGGACAGCATGCGAAAAGCCCGACATCATCAAGTTGATCCAACCCCTTTCAAGCTCCTCATCGACTAATCATTAG	MRFPPGTSPHRDSMRKARHHQVDPTLSSSSSTNH*			MRFPPGTSPHRDSMRKARHHQVDPTLSSSSSTNH*	AGTTGGGAAG	TGAACAATCC	0	O	0	MG06004.1	NCU08946.1	0	0
7026	3334	ao	AN0686.1	70.m15288	AO070343000532	0					-87	-22	ATGCGAAAAGCCCGACATCATCAAGTTGATCCAACCCCTTTCAAGCTCCTCATCGACTAATCATTAG			ATGCGAAAAGCCCGACATCATCAAGTTGATCCAACCCCTTTCAAGCTCCTCATCGACTAATCATTAG	MRKARHHQVDPTLSSSSSTNH*			MRKARHHQVDPTLSSSSSTNH*	TCGGGACAGC	TGAACAATCC	0	O	0	MG06004.1	NCU08946.1	0	0
7028	3336	af	AN0675.1	70.m15787	AO070343000544	0			-116	-39			ATGACCCCGAGCCTCGTCATCGCGCCGGAAAGTAGACCTGACCTCACTGTTCCATCAGATTCCGTCTTCGGCAGTTGA		ATGACCCCGAGCCTCGTCATCGCGCCGGAAAGTAGACCTGACCTCACTGTTCCATCAGATTCCGTCTTCGGCAGTTGA		MTPSLVIAPESRPDLTVPSDSVFGS*		MTPSLVIAPESRPDLTVPSDSVFGS*		AATAGCGACA	AGGGTTACCA	0	C	0	0	0	0	0
7027	3336	an	AN0675.1	70.m15787	AO070343000544	0	-148	-119					ATGTTTTGGTCCGTTTTAACATTCTTCTAG	ATGTTTTGGTCCGTTTTAACATTCTTCTAG			MFWSVLTFF*	MFWSVLTFF*			CTGATTCTTC	AGTGCCCAAA	0	C	0	0	0	0	0
7029	3336	ao	AN0675.1	70.m15787	AO070343000544	0					-177	-127	ATGTACCCCGCAAGCACATTTACTGGACGAGGCACTTCCCCTACCGTTTGA			ATGTACCCCGCAAGCACATTTACTGGACGAGGCACTTCCCCTACCGTTTGA	MYPASTFTGRGTSPTV*			MYPASTFTGRGTSPTV*	TTTCCACCAC	ATAACACCCA	0	C	0	0	0	0	0
7030	3336	ao	AN0675.1	70.m15787	AO070343000544	0					-97	-71	ATGTTATGCTGCCAGCCGGCAAGCTGA			ATGTTATGCTGCCAGCCGGCAAGCTGA	MLCCQPAS*			MLCCQPAS*	TGTTCAAGGT	GGACGGTAAA	0	C	0	0	0	0	0
7031	3336	ao	AN0675.1	70.m15787	AO070343000544	0					-92	-39	ATGCTGCCAGCCGGCAAGCTGAGGACGGTAAACGTGTTTGTTCGACGTGACTGA			ATGCTGCCAGCCGGCAAGCTGAGGACGGTAAACGTGTTTGTTCGACGTGACTGA	MLPAGKLRTVNVFVRRD*			MLPAGKLRTVNVFVRRD*	AAGGTATGTT	GATCCGGATA	0	C	0	0	0	0	0
7033	3337	af	AN0660.1	70.m15781	AO070343000564	0			-210	-91			ATGACGCAACATAATGTCTTATCTTATCCAAGGCATGGGGTGGTTAGTGTACCTGAGTTTATATTCATATGCATTTCTCTTGATGGTATGCAGTTGGTTGTGTTACTGGAGTGCGCGTGA		ATGACGCAACATAATGTCTTATCTTATCCAAGGCATGGGGTGGTTAGTGTACCTGAGTTTATATTCATATGCATTTCTCTTGATGGTATGCAGTTGGTTGTGTTACTGGAGTGCGCGTGA		MTQHNVLSYPRHGVVSVPEFIFICISLDGMQLVVLLECA*		MTQHNVLSYPRHGVVSVPEFIFICISLDGMQLVVLLECA*		TTATTGGGTC	ACTGTATAGA	0	FH	0	0	0	0	0
7034	3337	af	AN0660.1	70.m15781	AO070343000564	0			-142	-128			ATGCATTTCTCTTGA		ATGCATTTCTCTTGA		MHFS*		MHFS*		TTATATTCAT	TGGTATGCAG	0	FH	0	0	0	0	0
7035	3337	af	AN0660.1	70.m15781	AO070343000564	0			-123	-91			ATGCAGTTGGTTGTGTTACTGGAGTGCGCGTGA		ATGCAGTTGGTTGTGTTACTGGAGTGCGCGTGA		MQLVVLLECA*		MQLVVLLECA*		TCTTGATGGT	ACTGTATAGA	0	FH	0	0	0	0	0
7032	3337	an	AN0660.1	70.m15781	AO070343000564	0	-238	-212					ATGGCGCACCCCTGCGCCTTTTTATAA	ATGGCGCACCCCTGCGCCTTTTTATAA			MAHPCAFL*	MAHPCAFL*			TGCCCTTTAT	CTTGACGTCT	0	FH	0	0	0	0	0
7039	3338	af	AN0651.1	70.m15256	AO070343000576	0			-228	-109			ATGGGCATTTTTCCATTTGCAATTATTCTCTCCCATGGTGTATCACGTTCGATGTCGTTAACTGTCTCATCGGATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGA		ATGGGCATTTTTCCATTTGCAATTATTCTCTCCCATGGTGTATCACGTTCGATGTCGTTAACTGTCTCATCGGATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGA		MGIFPFAIILSHGVSRSMSLTVSSDGFVSVLVFFADVCY*		MGIFPFAIILSHGVSRSMSLTVSSDGFVSVLVFFADVCY*		TCCGTTTTCT	TAGGCTTCCA	0	DT	0	0	NCU06493.1	0	0
7040	3338	af	AN0651.1	70.m15256	AO070343000576	0			-194	-168			ATGGTGTATCACGTTCGATGTCGTTAA		ATGGTGTATCACGTTCGATGTCGTTAA		MVYHVRCR*		MVYHVRCR*		ATTCTCTCCC	CTGTCTCATC	0	DT	0	0	NCU06493.1	0	0
7041	3338	af	AN0651.1	70.m15256	AO070343000576	0			-177	-109			ATGTCGTTAACTGTCTCATCGGATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGA		ATGTCGTTAACTGTCTCATCGGATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGA		MSLTVSSDGFVSVLVFFADVCY*		MSLTVSSDGFVSVLVFFADVCY*		ATCACGTTCG	TAGGCTTCCA	0	DT	0	0	NCU06493.1	0	0
7042	3338	af	AN0651.1	70.m15256	AO070343000576	0			-155	-93			ATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGATAGGCTTCCAGAATAA		ATGGTTTCGTGTCGGTACTTGTCTTCTTTGCTGACGTCTGTTATTGATAGGCTTCCAGAATAA		MVSCRYLSSLLTSVIDRLPE*		MVSCRYLSSLLTSVIDRLPE*		GTCTCATCGG	TCAATACCGC	0	DT	0	0	NCU06493.1	0	0
7036	3338	an	AN0651.1	70.m15256	AO070343000576	0	-240	-187					ATGTTGGGTCTTCGCAGACTGTTCCGTTGTGCTTCTCGATTCTTTGTTTTCTGA	ATGTTGGGTCTTCGCAGACTGTTCCGTTGTGCTTCTCGATTCTTTGTTTTCTGA			MLGLRRLFRCASRFFVF*	MLGLRRLFRCASRFFVF*			TGAATCGAGG	CAGATGCCCC	0	DT	0	0	NCU06493.1	0	0
7037	3338	an	AN0651.1	70.m15256	AO070343000576	0	-183	-97					ATGCCCCCCTTCTCATGCCACATTCACGATAGCCTCGTCGCAGGAGTCCCGCGTACGGAGAATTTGCTGACAGTCAACATCCGATAG	ATGCCCCCCTTCTCATGCCACATTCACGATAGCCTCGTCGCAGGAGTCCCGCGTACGGAGAATTTGCTGACAGTCAACATCCGATAG			MPPFSCHIHDSLVAGVPRTENLLTVNIR*	MPPFSCHIHDSLVAGVPRTENLLTVNIR*			TTTCTGACAG	ACGCTTATCC	0	DT	0	0	NCU06493.1	0	0
7038	3338	an	AN0651.1	70.m15256	AO070343000576	0	-169	-152					ATGCCACATTCACGATAG	ATGCCACATTCACGATAG			MPHSR*	MPHSR*			CCCCCTTCTC	CCTCGTCGCA	0	DT	0	0	NCU06493.1	0	0
7044	3339	af	AN1023.1	70.m15244	AO070343000591	0			-216	-190			ATGGACATCACGTGCCCATGTAGTTAA		ATGGACATCACGTGCCCATGTAGTTAA		MDITCPCS*		MDITCPCS*		GAATAGGGGA	GTGTACCTTT	0	TU	FG09721.1	MG06180.1	0	0	0
7045	3339	af	AN1023.1	70.m15244	AO070343000591	0			-129	-64			ATGCCCGAAATGGGTAACGGGGTCTTATCAACATCACACCTCCAATACCCCGAACAGGATTCCTAA		ATGCCCGAAATGGGTAACGGGGTCTTATCAACATCACACCTCCAATACCCCGAACAGGATTCCTAA		MPEMGNGVLSTSHLQYPEQDS*		MPEMGNGVLSTSHLQYPEQDS*		CCACTGCGGG	GATCCGGATT	0	TU	FG09721.1	MG06180.1	0	0	0

7046	3339	af	AN1023.1	70.m15244	AO070343000591	0			-120	-64			ATGGGTAACGGGGTCTTATCAACATCACACCTCCAATACCCCGAACAGGATTCCTAA		ATGGGTAACGGGGTCTTATCAACATCACACCTCCAATACCCCGAACAGGATTCCTAA		MGNGVLSTSHLQYPEQDS*		MGNGVLSTSHLQYPEQDS*		GATGCCCGAA	GATCCGGATT	0	TU	FG09721.1	MG06180.1	0	0	0
7043	3339	an	AN1023.1	70.m15244	AO070343000591	0	-186	-175					ATGCATATATAG	ATGCATATATAG			MHI*	MHI*			GGGCTGCTGA	TCAAAAACGG	0	TU	FG09721.1	MG06180.1	0	0	0
7047	3339	ao	AN1023.1	70.m15244	AO070343000591	0					-255	-112	ATGAACATAGTGGATCCCCAGGTATTCCAGTTGGAGGAGTATGGAGCAATTGAACGGTTCCTGATTCTCTGCATATCACCTGCCGGATTTAACATGATCCGAGTGCCCCATGGGAGCCCGCCCGCGGGATGCCCGAAACGGTTAA			ATGAACATAGTGGATCCCCAGGTATTCCAGTTGGAGGAGTATGGAGCAATTGAACGGTTCCTGATTCTCTGCATATCACCTGCCGGATTTAACATGATCCGAGTGCCCCATGGGAGCCCGCCCGCGGGATGCCCGAAACGGTTAA	MNIVDPQVFQLEEYGAIERFLILCISPAGFNMIRVPHGSPPRDARNG*			MNIVDPQVFQLEEYGAIERFLILCISPAGFNMIRVPHGSPPRDARNG*	ATAACTTTCC	CTACTCAATA	0	TU	FG09721.1	MG06180.1	0	0	0
7048	3339	ao	AN1023.1	70.m15244	AO070343000591	0					-215	-192	ATGGAGCAATTGAACGGTTCCTGA			ATGGAGCAATTGAACGGTTCCTGA	MEQLNGS*			MEQLNGS*	TTGGAGGAGT	TTCTCTGCAT	0	TU	FG09721.1	MG06180.1	0	0	0
7049	3339	ao	AN1023.1	70.m15244	AO070343000591	0					-162	-112	ATGATCCGAGTGCCCCATGGGAGCCCGCCGCGGGATGCCCGAAACGGTTAA			ATGATCCGAGTGCCCCATGGGAGCCCGCCGCGGGATGCCCGAAACGGTTAA	MIRVPHGSPPRDARNG*			MIRVPHGSPPRDARNG*	CGGATTTAAC	CTACTCAATA	0	TU	FG09721.1	MG06180.1	0	0	0
7050	3339	ao	AN1023.1	70.m15244	AO070343000591	0					-146	-42	ATGGGAGCCCGCCGCGGGATGCCCGAAACGGTTAACTACTCAATAACCCATGAGCATCTCCAGCCAAACATCCTCTATAGTCGCTTCTCATTACTCGGTTCTTAA			ATGGGAGCCCGCCGCGGGATGCCCGAAACGGTTAACTACTCAATAACCCATGAGCATCTCCAGCCAAACATCCTCTATAGTCGCTTCTCATTACTCGGTTCTTAA	MGARRGMPETVNYSITHEHLQPNILYSRFSLLGS*			MGARRGMPETVNYSITHEHLQPNILYSRFSLLGS*	CGAGTGCCCC	TATCAAGTTT	0	TU	FG09721.1	MG06180.1	0	0	0
7051	3339	ao	AN1023.1	70.m15244	AO070343000591	0					-128	-42	ATGCCCGAAACGGTTAACTACTCAATAACCCATGAGCATCTCCAGCCAAACATCCTCTATAGTCGCTTCTCATTACTCGGTTCTTAA			ATGCCCGAAACGGTTAACTACTCAATAACCCATGAGCATCTCCAGCCAAACATCCTCTATAGTCGCTTCTCATTACTCGGTTCTTAA	MPETVNYSITHEHLQPNILYSRFSLLGS*			MPETVNYSITHEHLQPNILYSRFSLLGS*	CCGCCGCGGG	TATCAAGTTT	0	TU	FG09721.1	MG06180.1	0	0	0
7053	3341	af	AN0797.1	70.m15398	AO070239000020	0			-201	-43			ATGCGGGGCCAAAATTCCTTCCCCCGTCCAAAAAAAGAAATTCTCGCAATGATTCATTCTCCCCCTCGTCATCTCCCTCTCCCTTTCACCTTCTCTTCCCCCAGGCTAGGGACTTGGGGTTTGATCACTTTCATCACCTTTTTCATCGGATTTGATTGA		ATGCGGGGCCAAAATTCCTTCCCCCGTCCAAAAAAAGAAATTCTCGCAATGATTCATTCTCCCCCTCGTCATCTCCCTCTCCCTTTCACCTTCTCTTCCCCCAGGCTAGGGACTTGGGGTTTGATCACTTTCATCACCTTTTTCATCGGATTTGATTGA		MRGQNSFPRPKKEILAMIHSPPRHLPLPFTFSSPRLGTWGLITFITFFIGFD*		MRGQNSFPRPKKEILAMIHSPPRHLPLPFTFSSPRLGTWGLITFITFFIGFD*		GCTGACTCCG	TCTCTTGTCT	0	E	0	MG01309.1	0	0	0
7054	3341	af	AN0797.1	70.m15398	AO070239000020	0			-153	-43			ATGATTCATTCTCCCCCTCGTCATCTCCCTCTCCCTTTCACCTTCTCTTCCCCCAGGCTAGGGACTTGGGGTTTGATCACTTTCATCACCTTTTTCATCGGATTTGATTGA		ATGATTCATTCTCCCCCTCGTCATCTCCCTCTCCCTTTCACCTTCTCTTCCCCCAGGCTAGGGACTTGGGGTTTGATCACTTTCATCACCTTTTTCATCGGATTTGATTGA		MIHSPPRHLPLPFTFSSPRLGTWGLITFITFFIGFD*		MIHSPPRHLPLPFTFSSPRLGTWGLITFITFFIGFD*		AATTCTCGCA	TCTCTTGTCT	0	E	0	MG01309.1	0	0	0
7052	3341	an	AN0797.1	70.m15398	AO070239000020	0	-149	-93					ATGAATCACCGGCTACACAACAGTCAACGCATTCCCATTTCACTTTGCCCTTGTTAA	ATGAATCACCGGCTACACAACAGTCAACGCATTCCCATTTCACTTTGCCCTTGTTAA			MNHRLHNSQRIPISLCPC*	MNHRLHNSQRIPISLCPC*			TCTTGAAGGG	GCTCTCTCCA	0	E	0	MG01309.1	0	0	0
7055	3341	ao	AN0797.1	70.m15398	AO070239000020	0					-216	-142	ATGGCGATGAATCATCCCGCAATCAACTTGACTGACTCCCCGTTCCTTCTCCCCCAAGGCACCGGGCCTTTTTGA			ATGGCGATGAATCATCCCGCAATCAACTTGACTGACTCCCCGTTCCTTCTCCCCCAAGGCACCGGGCCTTTTTGA	MAMNHPAINLTDSPFLLPQGTGPF*			MAMNHPAINLTDSPFLLPQGTGPF*	TTCTTTTTCG	AATCTTAATT	0	E	0	MG01309.1	0	0	0
7056	3341	ao	AN0797.1	70.m15398	AO070239000020	0					-210	-142	ATGAATCATCCCGCAATCAACTTGACTGACTCCCCGTTCCTTCTCCCCCAAGGCACCGGGCCTTTTTGA			ATGAATCATCCCGCAATCAACTTGACTGACTCCCCGTTCCTTCTCCCCCAAGGCACCGGGCCTTTTTGA	MNHPAINLTDSPFLLPQGTGPF*			MNHPAINLTDSPFLLPQGTGPF*	TTCGATGGCG	AATCTTAATT	0	E	0	MG01309.1	0	0	0
7061	3344	af	AN4623.1	57.m05537	AO070267000035	0			-177	-154			ATGCTTCTCTTCATGCCTGATTAA		ATGCTTCTCTTCATGCCTGATTAA		MLLFMPD*		MLLFMPD*		ACGGAGACGA	GATTACGCAT	0	G	0	0	0	0	0
7062	3344	af	AN4623.1	57.m05537	AO070267000035	0			-165	-154			ATGCCTGATTAA		ATGCCTGATTAA		MPD*		MPD*		GCTTCTCTTC	GATTACGCAT	0	G	0	0	0	0	0
7063	3344	af	AN4623.1	57.m05537	AO070267000035	0			-86	-48			ATGCTTGCTATTCGGCTGCCGTTCCACATAGCAACTTGA		ATGCTTGCTATTCGGCTGCCGTTCCACATAGCAACTTGA		MLAIRLPFHIAT*		MLAIRLPFHIAT*		TCGGCCCGTT	TAAACAGTGC	0	G	0	0	0	0	0
7057	3344	an	AN4623.1	57.m05537	AO070267000035	0	-205	-134					ATGTGTTCGCTGCTAAGCAGCTGTTTTTATGATTCTGTTTTATTACTTCGGGCTGTACTGATGATTCTTTGA	ATGTGTTCGCTGCTAAGCAGCTGTTTTTATGATTCTGTTTTATTACTTCGGGCTGTACTGATGATTCTTTGA			MCSLLSSCFYDSVLLLRAVLMIL*	MCSLLSSCFYDSVLLLRAVLMIL*			CTCTTCGACA	TCGAATCATT	0	G	0	0	0	0	0
7058	3344	an	AN4623.1	57.m05537	AO070267000035	0	-177	-145					ATGATTCTGTTTTATTACTTCGGGCTGTACTGA	ATGATTCTGTTTTATTACTTCGGGCTGTACTGA			MILFYYFGLY*	MILFYYFGLY*			AGCTGTTTTT	TGATTCTTTG	0	G	0	0	0	0	0
7059	3344	an	AN4623.1	57.m05537	AO070267000035	0	-145	-134					ATGATTCTTTGA	ATGATTCTTTGA			MIL*	MIL*			GGCTGTACTG	TCGAATCATT	0	G	0	0	0	0	0
7060	3344	an	AN4623.1	57.m05537	AO070267000035	0	-100	-86					ATGTTAGGAGCTTGA	ATGTTAGGAGCTTGA			MLGA*	MLGA*			CCCCGTCGTG	ACACAGCTAT	0	G	0	0	0	0	0
7064	3344	ao	AN4623.1	57.m05537	AO070267000035	0					-192	-166	ATGTCATATCGAAATATCGTTGCATGA			ATGTCATATCGAAATATCGTTGCATGA	MSYRNIVA*			MSYRNIVA*	CATCTCCTCC	GATCTCATCC	0	G	0	0	0	0	0
7065	3344	ao	AN4623.1	57.m05537	AO070267000035	0					-169	-83	ATGAGATCTCATCCTCTGTTGCATCCCTCAAATATTGCCTGCCTCCTTCGCCCGTTATGCTTACTTTGCTTTGACTTGAGACTATAA			ATGAGATCTCATCCTCTGTTGCATCCCTCAAATATTGCCTGCCTCCTTCGCCCGTTATGCTTACTTTGCTTTGACTTGAGACTATAA	MRSHPLLHPSNIACLLRPLCLLCFDLRL*			MRSHPLLHPSNIACLLRPLCLLCFDLRL*	ATATCGTTGC	TTAGACCTGC	0	G	0	0	0	0	0
7066	3344	ao	AN4623.1	57.m05537	AO070267000035	0					-113	-96	ATGCTTACTTTGCTTTGA			ATGCTTACTTTGCTTTGA	MLTLL*			MLTLL*	TTCGCCCGTT	CTTGAGACTA	0	G	0	0	0	0	0
7068	3345	af	AN6551.1	62.m03122	AO070270000034	0			-261	-133			ATGCTTATTCTGCCTTTTTTTTCCATTCTGCTTTTCTTTGATTTTAGATTCGATCAAGTGTTAGGAAGCATATTGTTACAGTCTTATTTTCGTCGGTTGTCTGGGTACCCATGTTTATCGACCACATAA		ATGCTTATTCTGCCTTTTTTTTCCATTCTGCTTTTCTTTGATTTTAGATTCGATCAAGTGTTAGGAAGCATATTGTTACAGTCTTATTTTCGTCGGTTGTCTGGGTACCCATGTTTATCGACCACATAA		MLILPFFSILLFFDFRFDQVLGSILLQSYFRRLSGYPCLSTT*		MLILPFFSILLFFDFRFDQVLGSILLQSYFRRLSGYPCLSTT*		CTGGTTTTGC	TATCCGGACT	0		0	0	0	0	0
7069	3345	af	AN6551.1	62.m03122	AO070270000034	0			-151	-95			ATGTTTATCGACCACATAATATCCGGACTTCCAGATATTGAGGCATACACAGATTAA		ATGTTTATCGACCACATAATATCCGGACTTCCAGATATTGAGGCATACACAGATTAA		MFIDHIISGLPDIEAYTD*		MFIDHIISGLPDIEAYTD*		CTGGGTACCC	TACTCTTGCG	0		0	0	0	0	0
7067	3345	an	AN6551.1	62.m03122	AO070270000034	0	-181	-71					ATGACACGACTGGATCCACTGTCTACTTGCGTGTGCCATATTATCCCTTCGCGTTTCATTTGTATCCTTTGCGACCCTCTTTATTGCCATTCTCCGCTTTTGTTACCTTGA	ATGACACGACTGGATCCACTGTCTACTTGCGTGTGCCATATTATCCCTTCGCGTTTCATTTGTATCCTTTGCGACCCTCTTTATTGCCATTCTCCGCTTTTGTTACCTTGA			MTRLDPLSTCVCHIIPSRFICILCDPLYCHSPLLLP*	MTRLDPLSTCVCHIIPSRFICILCDPLYCHSPLLLP*			TAACTCTGAC	CGTTGGACCG	0		0	0	0	0	0
7070	3345	ao	AN6551.1	62.m03122	AO070270000034	0					-115	-104	ATGCTTGTTTGA			ATGCTTGTTTGA	MLV*			MLV*	ATAGTAACCT	GTTGTTCATT	0		0	0	0	0	0
7075	3347	af	AN8286.1	65.m07462	AO070277000002	0			-222	-184			ATGATGATGCTTCATATATCTACCCGATCTCCTATCTGA		ATGATGATGCTTCATATATCTACCCGATCTCCTATCTGA		MMMLHISTRSPI*		MMMLHISTRSPI*		TTGTGTCGCC	CTTTTGCCAG	0	Z	0	0	NCU02626.1	0	0
7076	3347	af	AN8286.1	65.m07462	AO070277000002	0			-219	-184			ATGATGCTTCATATATCTACCCGATCTCCTATCTGA		ATGATGCTTCATATATCTACCCGATCTCCTATCTGA		MMLHISTRSPI*		MMLHISTRSPI*		TGTCGCCATG	CTTTTGCCAG	0	Z	0	0	NCU02626.1	0	0
7077	3347	af	AN8286.1	65.m07462	AO070277000002	0			-216	-184			ATGCTTCATATATCTACCCGATCTCCTATCTGA		ATGCTTCATATATCTACCCGATCTCCTATCTGA		MLHISTRSPI*		MLHISTRSPI*		CGCCATGATG	CTTTTGCCAG	0	Z	0	0	NCU02626.1	0	0
7078	3347	af	AN8286.1	65.m07462	AO070277000002	0			-96	-79			ATGCCATTTCTAATCTGA		ATGCCATTTCTAATCTGA		MPFLI*		MPFLI*		CCCCATGACC	GCTCCTTCTG	0	Z	0	0	NCU02626.1	0	0
7079	3347	ao	AN8286.1	65.m07462	AO070277000002	0					-220	-182	ATGCACCACTACGGTCAGATGCTAACCCTAGCGCTTTAA			ATGCACCACTACGGTCAGATGCTAACCCTAGCGCTTTAA	MHHYGQMLTLAL*			MHHYGQMLTLAL*	AGTATAGCTT	ATATCAGAGG	0	Z	0	0	NCU02626.1	0	0
7080	3347	ao	AN8286.1	65.m07462	AO070277000002	0					-202	-182	ATGCTAACCCTAGCGCTTTAA			ATGCTAACCCTAGCGCTTTAA	MLTLAL*			MLTLAL*	CTACGGTCAG	ATATCAGAGG	0	Z	0	0	NCU02626.1	0	0
7074	3347	conserved	AN8286.1	65.m07462	AO070277000002	0	-112	-92	-102	-79	-113	-90	ATGrCyryssmrTyyCThdkhTGA	ATGGCTGCCGAATCCCTCTGA	ATGACCATGCCATTTCTAATCTGA	ATGGCCGCCGCGTTCCTTGGTTGA	MaaesL*	MAAESL*	MTMPFLI*	MAAAFLG*	wyywyCsybb	kyyymhdCdv	0	Z	0	0	NCU02626.1	0	0
7083	3349	af	AN0596.1	69.m15251	AO070280000022	0			-166	-116			ATGCAGCTTATTATTGCTGTATCTTCTGCACTTGATCCAAGGCTGATCTAA		ATGCAGCTTATTATTGCTGTATCTTCTGCACTTGATCCAAGGCTGATCTAA		MQLIIAVSSALDPRLI*		MQLIIAVSSALDPRLI*		CTGAAAAGCG	ACCTTGTCGC	0	L	0	0	0	0	0
7082	3349	an	AN0596.1	69.m15251	AO070280000022	0	-125	-114					ATGCTTTCTTGA	ATGCTTTCTTGA			MLS*	MLS*			GCAATTATAG	GGTCGACTTT	0	L	0	0	0	0	0
7084	3349	ao	AN0596.1	69.m15251	AO070280000022	0					-175	-152	ATGCGGATATCTTTCAAACATTAA			ATGCGGATATCTTTCAAACATTAA	MRISFKH*			MRISFKH*	GTAGTTAGAG	ATATACGATA	0	L	0	0	0	0	0
7090	3353	af	AN8874.1	56.m02287	AO070293000003	0			-237	-181			ATGAAGTGCTACGTATGTACCTCTGTGGTCATAGCTATCGTGTTCTCCATAGCATAG		ATGAAGTGCTACGTATGTACCTCTGTGGTCATAGCTATCGTGTTCTCCATAGCATAG		MKCYVCTSVVIAIVFSIA*		MKCYVCTSVVIAIVFSIA*		TAGTATTATT	CAAATTCTAT	0	UR	0	0	0	0	0
7091	3353	af	AN8874.1	56.m02287	AO070293000003	0			-223	-14			ATGTACCTCTGTGGTCATAGCTATCGTGTTCTCCATAGCATAGCAAATTCTATTGTCCTTTTCCATTGGTTTATCTGTCATTTTCAGACTCACTTACCCTTCGTCACTACTTTCCCTTCAAATTTTACTCATCCACCGCGAGGACATCTCTTAAAAAGGTCCCAAACCGGTTCACCAATCTCTGAACCACTAAGTGCTACCTGGGGTTGA		ATGTACCTCTGTGGTCATAGCTATCGTGTTCTCCATAGCATAGCAAATTCTATTGTCCTTTTCCATTGGTTTATCTGTCATTTTCAGACTCACTTACCCTTCGTCACTACTTTCCCTTCAAATTTTACTCATCCACCGCGAGGACATCTCTTAAAAAGGTCCCAAACCGGTTCACCAATCTCTGAACCACTAAGTGCTACCTGGGGTTGA		MYLCGHSYRVLHSIANSIVLFHWFICHFQTHLPFVTTFPSNFTHPPRGHLLKRSQTGSPISEPLSATWG*		MYLCGHSYRVLHSIANSIVLFHWFICHFQTHLPFVTTFPSNFTHPPRGHLLKRSQTGSPISEPLSATWG*		AGTGCTACGT	TTCTCAGGGC	0	UR	0	0	0	0	0
7089	3353	an	AN8874.1	56.m02287	AO070293000003	0	-209	-186					ATGAAAAAGCTTCATTTGCATTAG	ATGAAAAAGCTTCATTTGCATTAG			MKKLHLH*	MKKLHLH*			CTGTCAGGAG	ATATCCCAGC	0	UR	0	0	0	0	0
7092	3355	an	AN7325.1	72.m19745	AO070297000077	0	-187	-170					ATGTGCGCGCTCACGTGA	ATGTGCGCGCTCACGTGA			MCALT*	MCALT*			GGGACCGACG	CACCGCTCTA	0	L	0	MG08071.1	0	0	0
7094	3355	ao	AN7325.1	72.m19745	AO070297000077	0					-140	-126	ATGAATGGAGCATAA			ATGAATGGAGCATAA	MNGA*			MNGA*	CACGACCTGC	TTGCCCGCGA	0	L	0	MG08071.1	0	0	0
7095	3355	ao	AN7325.1	72.m19745	AO070297000077	0					-136	-104	ATGGAGCATAATTGCCCGCGACTCCGCCTATAG			ATGGAGCATAATTGCCCGCGACTCCGCCTATAG	MEHNCPRLRL*			MEHNCPRLRL*	ACCTGCATGA	TGCGTTCCAT	0	L	0	MG08071.1	0	0	0
7096	3355	ao	AN7325.1	72.m19745	AO070297000077	0					-95	-54	ATGTGTTGGTTTCTCACGACTCGCCAACCCTTCTTCACATAG			ATGTGTTGGTTTCTCACGACTCGCCAACCCTTCTTCACATAG	MCWFLTTRQPFFT*			MCWFLTTRQPFFT*	AGTGCGTTCC	GTCGCATAGT	0	L	0	MG08071.1	0	0	0
7097	3363	af	AN0122.1	71.m15403	AO070311000090	0			-168	-100			ATGGAGTTCTGGAACATCTCCGCGACTTTAAAACTGATCGTCTGGCCCCATACAGCCCATTTGTGTTAA		ATGGAGTTCTGGAACATCTCCGCGACTTTAAAACTGATCGTCTGGCCCCATACAGCCCATTTGTGTTAA		MEFWNISATLKLIVWPHTAHLC*		MEFWNISATLKLIVWPHTAHLC*		GACTACGTCT	TTGACTGGCT	0	O	FG09725.1	0	0	0	0
7100	3364	af	AN6886.1	71.m16031	AO070314000039	0			-105	-73			ATGGTCATCGAGAGCAGTCTTATCGCATGGTAA		ATGGTCATCGAGAGCAGTCTTATCGCATGGTAA		MVIESSLIAW*		MVIESSLIAW*		CGTTGCATTG	CCCGGCTTTA	0		0	0	0	0	0
7101	3364	af	AN6886.1	71.m16031	AO070314000039	0			-79	-62			ATGGTAACCCGGCTTTAA		ATGGTAACCCGGCTTTAA		MVTRL*		MVTRL*		GTCTTATCGC	TGAATCCCTC	0		0	0	0	0	0
7102	3364	af	AN6886.1	71.m16031	AO070314000039	0			-62	-27			ATGAATCCCTCGCCACCGACGACGACGACGACGTAA		ATGAATCCCTCGCCACCGACGACGACGACGACGTAA		MNPSPPTTTTT*		MNPSPPTTTTT*		CCCGGCTTTA	GAACGTCTTC	0		0	0	0	0	0
7098	3364	an	AN6886.1	71.m16031	AO070314000039	0	-91	-56					ATGCTTGCGATACAAATGTTTTCACGGCGTGCATGA	ATGCTTGCGATACAAATGTTTTCACGGCGTGCATGA			MLAIQMFSRRA*	MLAIQMFSRRA*			TTCAGTATTG	GCTGAGCTGC	0		0	0	0	0	0
7099	3364	an	AN6886.1	71.m16031	AO070314000039	0	-76	-56					ATGTTTTCACGGCGTGCATGA	ATGTTTTCACGGCGTGCATGA			MFSRRA*	MFSRRA*			TGCGATACAA	GCTGAGCTGC	0		0	0	0	0	0
7103	3364	ao	AN6886.1	71.m16031	AO070314000039	0					-85	-47	ATGGTGAGAGTAACTCGGATGGTCCTGTGGCATATATGA			ATGGTGAGAGTAACTCGGATGGTCCTGTGGCATATATGA	MVRVTRMVLWHI*			MVRVTRMVLWHI*	TCTGCTGGGA	GTGACTACAA	0		0	0	0	0	0
7104	3364	ao	AN6886.1	71.m16031	AO070314000039	0					-67	-47	ATGGTCCTGTGGCATATATGA			ATGGTCCTGTGGCATATATGA	MVLWHI*			MVLWHI*	AGTAACTCGG	GTGACTACAA	0		0	0	0	0	0
7106	3365	af	AN4547.1	57.m05557	AO070321000185	0			-185	-171			ATGAGGGCGCGTTAA		ATGAGGGCGCGTTAA		MRAR*		MRAR*		CTCACGGATA	TCGTTTACAC	0	U	FG08840.1	MG02634.1	NCU01992.1	0	0
7105	3365	an	AN4547.1	57.m05557	AO070321000185	0	-185	-174					ATGAGGATTTGA	ATGAGGATTTGA			MRI*	MRI*			TCACGAGATA	TACCGTTCAC	0	U	FG08840.1	MG02634.1	NCU01992.1	0	0
7107	3365	ao	AN4547.1	57.m05557	AO070321000185	0					-170	-156	ATGAGGGTGCGCTAA			ATGAGGGTGCGCTAA	MRVR*			MRVR*	CTAGAAGATA	TCGCTGTTTC	0	U	FG08840.1	MG02634.1	NCU01992.1	0	0
7108	3366	ao	AN5726.1	54.m06846	AO070324000125	0					-209	-198	ATGTGTGCCTGA			ATGTGTGCCTGA	MCA*			MCA*	CGTTTTCCCC	AATTGGCCAT	0	R	0	0	0	0	0
7110	3367	an	AN2246.1	71.m15880	AO070326000127	0	-201	-184					ATGCCCAATTGGTGTTGA	ATGCCCAATTGGTGTTGA			MPNWC*	MPNWC*			TCTGCTGTCA	AAGTACGCTT	0	J	0	0	0	0	0
7109	3367	conserved	AN2246.1	71.m15880	AO070326000127	0	-126	-106	-120	-100	-123	-103	ATGyyCywTwyhGArvyATAG	ATGTCCTATTCCGAGCCATAG	ATGCTCCTTTCAGAGATATAG	ATGTTCCTTATTGAAGCATAG	MsysEp*	MSYSEP*	MLLSEI*	MFLIEA*	mrdymTrrAy	AGGGCTGCAG	0	J	0	0	0	0	0
7111	3368	af	AN4018.1	54.m06553	AO070328000117	0			-111	-73			ATGCTTCTACCCAACTGCCATGGCACCTACCTAAACTAG		ATGCTTCTACCCAACTGCCATGGCACCTACCTAAACTAG		MLLPNCHGTYLN*		MLLPNCHGTYLN*		GGATCGACTC	TAGTGCTGTA	0	OPR	0	MG03702.1	0	0	0
7112	3368	af	AN4018.1	54.m06553	AO070328000117	0			-92	-78			ATGGCACCTACCTAA		ATGGCACCTACCTAA		MAPT*		MAPT*		CCCAACTGCC	ACTAGTAGTG	0	OPR	0	MG03702.1	0	0	0

7113	3368	af	AN4018.1	54.m06553	AO070328000117	0			-63	-46			ATGTCGAACACATTCTGA		ATGTCGAACACATTCTGA		MSNTF*		MSNTF*		GTAGTGCTGT	TTCCTACAGC	0	OPR	0	MG03702.1	0	0	0
7114	3368	ao	AN4018.1	54.m06553	AO070328000117	0					-234	-199	ATGACTGTCAATTACGTAGGGGCTCCGATTAGATAA			ATGACTGTCAATTACGTAGGGGCTCCGATTAGATAA	MTVNYVGAPIR*			MTVNYVGAPIR*	AAGAGATCCA	AAAGCCCTCC	0	OPR	0	MG03702.1	0	0	0
7115	3368	ao	AN4018.1	54.m06553	AO070328000117	0					-109	-47	ATGCGAGCGGTCGTCTGTTCCATGCCTGACCGCTATTTCCTCCAATTTCCTCAATTCACTTAG			ATGCGAGCGGTCGTCTGTTCCATGCCTGACCGCTATTTCCTCCAATTTCCTCAATTCACTTAG	MRAVVCSMPDRYFLQFPQFT*			MRAVVCSMPDRYFLQFPQFT*	AGACTGATCA	TTGAACCATG	0	OPR	0	MG03702.1	0	0	0
7116	3368	ao	AN4018.1	54.m06553	AO070328000117	0					-88	-47	ATGCCTGACCGCTATTTCCTCCAATTTCCTCAATTCACTTAG			ATGCCTGACCGCTATTTCCTCCAATTTCCTCAATTCACTTAG	MPDRYFLQFPQFT*			MPDRYFLQFPQFT*	CGTCTGTTCC	TTGAACCATG	0	OPR	0	MG03702.1	0	0	0
7121	3372	af	AN0268.1	54.m06475	AO070334000074	0			-136	-107			ATGGCATCCTACTTACTCAGGACTCTGTAA		ATGGCATCCTACTTACTCAGGACTCTGTAA		MASYLLRTL*		MASYLLRTL*		CAGATTGACC	TGTCCATTGA	0		0	0	0	0	0
7122	3372	af	AN0268.1	54.m06475	AO070334000074	0			-97	-80			ATGCGAGATATGCGGTGA		ATGCGAGATATGCGGTGA		MRDMR*		MRDMR*		ATGTCCATTG	TTATACCCAT	0		0	0	0	0	0
7119	3372	an	AN0268.1	54.m06475	AO070334000074	0	-205	-191					ATGCTTTCAGGCTAA	ATGCTTTCAGGCTAA			MLSG*	MLSG*			CCGGCAAGAC	GGGCTGATAA	0		0	0	0	0	0
7120	3372	an	AN0268.1	54.m06475	AO070334000074	0	-139	-101					ATGGATCATCTATCGCGTCTGTCTCCGTTGGCCCATTGA	ATGGATCATCTATCGCGTCTGTCTCCGTTGGCCCATTGA			MDHLSRLSPLAH*	MDHLSRLSPLAH*			AACTCGCTAA	ATGAGCATGC	0		0	0	0	0	0
7123	3372	ao	AN0268.1	54.m06475	AO070334000074	0					-202	-191	ATGACAGCTTGA			ATGACAGCTTGA	MTA*			MTA*	TTATTTGACC	CTTACGAGTC	0		0	0	0	0	0
7124	3372	ao	AN0268.1	54.m06475	AO070334000074	0					-120	-43	ATGCGGTTATTCCTTTGTTGCTCGTCTCCATTGTGCCTTGGCCACCAGAAACGCCCCGTTGATTTGCCCGCGATTTAA			ATGCGGTTATTCCTTTGTTGCTCGTCTCCATTGTGCCTTGGCCACCAGAAACGCCCCGTTGATTTGCCCGCGATTTAA	MRLFLCCSSPLCLGHQKRPVDLPAI*			MRLFLCCSSPLCLGHQKRPVDLPAI*	TCGGAGGAGC	TCCGAAACAT	0		0	0	0	0	0
7127	3373	af	AN1482.1	55.m02988	AO070334000186	0			-275	-258			ATGCAGCAGAAGGACTGA		ATGCAGCAGAAGGACTGA		MQQKD*		MQQKD*		CTATATCAGA	CAGGCCCGGA	0	I	0	MG05196.1	0	0	0
7128	3373	af	AN1482.1	55.m02988	AO070334000186	0			-233	-135			ATGTGGATTCTCCTGTTCTTCCCCGCATTCCCGCAACTCCGCAAAAACCGACTGGCATCAGCCATTTACCGAGGCCAGTTTGTCACTGATAGGAAATAA		ATGTGGATTCTCCTGTTCTTCCCCGCATTCCCGCAACTCCGCAAAAACCGACTGGCATCAGCCATTTACCGAGGCCAGTTTGTCACTGATAGGAAATAA		MWILLFFPAFPQLRKNRLASAIYRGQFVTDRK*		MWILLFFPAFPQLRKNRLASAIYRGQFVTDRK*		GACGCCTCTA	TAAGCGGACT	0	I	0	MG05196.1	0	0	0
7125	3373	an	AN1482.1	55.m02988	AO070334000186	0	-129	-112					ATGCCGAGGCCTAGATAG	ATGCCGAGGCCTAGATAG			MPRPR*	MPRPR*			TCCTACGGAT	GTCCCACCAC	0	I	0	MG05196.1	0	0	0
7126	3373	an	AN1482.1	55.m02988	AO070334000186	0	-76	-35					ATGGGAGCCTGGCGACAGTCAATCTACTCGATTTCCTCTTGA	ATGGGAGCCTGGCGACAGTCAATCTACTCGATTTCCTCTTGA			MGAWRQSIYSISS*	MGAWRQSIYSISS*			ATGGCCACGG	TATCTCATCC	0	I	0	MG05196.1	0	0	0
7129	3374	an	AN2936.1	59.m09058	AO070337000172	0	-182	-60					ATGCAACCAACAACGTCACCTGTTCCTGAATCCCTGCTCCAACCTCTTGCGTTCCGCTCTCGAATCGTCTTCTCTTGTCTCTTTCCAAAACCCTCTAGTTTTCGATCATCCCTTCATTTCTAA	ATGCAACCAACAACGTCACCTGTTCCTGAATCCCTGCTCCAACCTCTTGCGTTCCGCTCTCGAATCGTCTTCTCTTGTCTCTTTCCAAAACCCTCTAGTTTTCGATCATCCCTTCATTTCTAA			MQPTTSPVPESLLQPLAFRSRIVFSCLFPKPSSFRSSLHF*	MQPTTSPVPESLLQPLAFRSRIVFSCLFPKPSSFRSSLHF*			CCTTCTCCGC	AGTATTTGAA	0	G	0	0	NCU07404.1	0	0
7130	3374	ao	AN2936.1	59.m09058	AO070337000172	0					-217	-161	ATGCAGACAGCGTCACCTGCTTGTTTCGTTCCTGGATCCCACCCCGGAAGTGTTTAG			ATGCAGACAGCGTCACCTGCTTGTTTCGTTCCTGGATCCCACCCCGGAAGTGTTTAG	MQTASPACFVPGSHPGSV*			MQTASPACFVPGSHPGSV*	AGTACCTGGA	CTCTGGTTGC	0	G	0	0	NCU07404.1	0	0
7131	3374	ao	AN2936.1	59.m09058	AO070337000172	0					-71	-15	ATGCAGACATCATCACTCTCTGATATCCTGATAAGCTTAATTAATACCCACAATTGA			ATGCAGACATCATCACTCTCTGATATCCTGATAAGCTTAATTAATACCCACAATTGA	MQTSSLSDILISLINTHN*			MQTSSLSDILISLINTHN*	CCCTGCTCTG	TCTTATCCGT	0	G	0	0	NCU07404.1	0	0
7134	3376	af	AN0426.1	54.m06650	AO070338000276	0			-168	-121			ATGAAATCTGTCTCTCTTACTACATCATCAAGCGCGTCTAAACTGTAG		ATGAAATCTGTCTCTCTTACTACATCATCAAGCGCGTCTAAACTGTAG		MKSVSLTTSSSASKL*		MKSVSLTTSSSASKL*		TTCGACATTA	GCCTTCCCTT	0	I	0	0	0	0	0
7133	3376	an	AN0426.1	54.m06650	AO070338000276	0	-139	-104					ATGCATTTTACAGTCTCATCCGTCGCGTCTTGCTGA	ATGCATTTTACAGTCTCATCCGTCGCGTCTTGCTGA			MHFTVSSVASC*	MHFTVSSVASC*			ACGACTTTTC	TGCCTACGTC	0	I	0	0	0	0	0
7135	3376	ao	AN0426.1	54.m06650	AO070338000276	0					-75	-7	ATGTCGCCTTGGTTTAAAGAAGGGCGCTGTGTGAGCTACCCGCTCGACTTCAAGTGCCCCGGTAACTAA			ATGTCGCCTTGGTTTAAAGAAGGGCGCTGTGTGAGCTACCCGCTCGACTTCAAGTGCCCCGGTAACTAA	MSPWFKEGRCVSYPLDFKCPGN*			MSPWFKEGRCVSYPLDFKCPGN*	CTCATGGCCT	GTCACAATGG	0	I	0	0	0	0	0
7132	3376	conserved	AN0426.1	54.m06650	AO070338000276	0	-90	-67	-109	-86	-82	-59	ATGGCCwdyrwCGsCTTGGTwTAr	ATGGCCATCAACGGCTTGGTATAG	ATGGCCTGCGACGCCTTGGTATAG	ATGGCCTATGTCGCCTTGGTTTAA	MAingLV*	MAINGLV*	MACDALV*	MAYVALV*	CbhybyCyys	rswhkbdssy	0	I	0	0	0	0	0
7137	3377	af	AN3933.1	69.m14994	AO070341000044	0			-158	-147			ATGGGACATTGA		ATGGGACATTGA		MGH*		MGH*		TGGGCGAGGA	GTGTTTAAAT	0	K	0	MG01572.1	0	0	0
7138	3377	ao	AN3933.1	69.m14994	AO070341000044	0					-146	-135	ATGAGATCTTGA			ATGAGATCTTGA	MRS*			MRS*	GCAGGAGGGG	GGCACACCAG	0	K	0	MG01572.1	0	0	0
7140	3378	af	AN2107.1	57.m05807	AO070341000264	0			-146	-120			ATGTGCGTATTTTGCAACTTCGACTGA		ATGTGCGTATTTTGCAACTTCGACTGA		MCVFCNFD*		MCVFCNFD*		AATCTTTTGA	TACGAATATA	0	J	FG01359.1	MG00521.1	0	0	0
7139	3378	conserved	AN2107.1	57.m05807	AO070341000264	0	-191	-87	-222	-109	-177	-64	ATGACTmkAThmhhAhwrvmwhkChwmmryvwAkrwdwhrbwymCydmsswyryhsrymyhkAswbwdwyThTkvvhhsbkmrwrkwhykCrrhywmkhsTkdkACswATmTrA	ATGACTCTATACCAAAAACATAGCATACGTGAAGAATTTAGACACTGCCGACATACATCTCGACTGATATTCTGCGTACGTAAAGGTACGCGGATACTTGTTTGA	ATGACTATATCAATACAGAAACTCCTCCGCATATGTGAAACTCACTTCGCTCATCGACATATAGTTAATCTTTTGAATGTGCGTATTTTGCAACTTCGACTGATACGAATATAA	ATGACTCGATTATCATTAGCATTCTACAACCTATGTAACGTATCCCAAGCTTGCTGGCACTTACACTGTTTATTACCCCCTCGTATACCTCGGTCTAGCCTGGTACCTATCTGA	MTlyqkhsireefrhcrhtsrlifcvrkgtrilv*	MTLYQKHSIREEFRHCRHTSRLIFCVRKGTRILV*	MTISIQKLLRICETHFAHRHIVNLLNVRILQLRLIRI*	MTRLSLAFYNLCNVSQACWHLHCLLPPRIPRSSLVPI*	GdhyysmAAG	rdCwbhywyk	0	J	FG01359.1	MG00521.1	0	0	0
7141	3379	ao	AN4053.1	54.m06538	AO070342000038	0					-118	-80	ATGCTTCCACTGTGTCTTGGAGGTTCCTCTCTTGGCTGA			ATGCTTCCACTGTGTCTTGGAGGTTCCTCTCTTGGCTGA	MLPLCLGGSSLG*			MLPLCLGGSSLG*	CCCATATTCT	TATTGGGGTT	0	YU	FG00748.1	MG00744.1	0	0	0
7145	3380	af	AN3735.1	69.m15380	AO070342000272	0			-281	-231			ATGTGCGACTATACTCAGAATCTTTCGCTTGGACTCCATGCGTTCACTTAG		ATGTGCGACTATACTCAGAATCTTTCGCTTGGACTCCATGCGTTCACTTAG		MCDYTQNLSLGLHAFT*		MCDYTQNLSLGLHAFT*		TTCAAACCGA	CGATCCATTG	0	R	0	0	0	0	0
7146	3380	af	AN3735.1	69.m15380	AO070342000272	0			-244	-53			ATGCGTTCACTTAGCGATCCATTGGACGACAAAGGCCCTCAATTGTTCGAGGACGGTTGCGCAGCGTCATTTGGTTTCAGTGTGCTGCAAGGTAACACTCTGGAAGCGAAGACGTCGAGGTGTGCGTCTACTTGTACGTGCGTTTTGTGTGGTTTTGTGCTGGCCCTGATCTGCGTATCATACGTTTCCTAG		ATGCGTTCACTTAGCGATCCATTGGACGACAAAGGCCCTCAATTGTTCGAGGACGGTTGCGCAGCGTCATTTGGTTTCAGTGTGCTGCAAGGTAACACTCTGGAAGCGAAGACGTCGAGGTGTGCGTCTACTTGTACGTGCGTTTTGTGTGGTTTTGTGCTGGCCCTGATCTGCGTATCATACGTTTCCTAG		MRSLSDPLDDKGPQLFEDGCAASFGFSVLQGNTLEAKTSRCASTCTCVLCGFVLALICVSYVS*		MRSLSDPLDDKGPQLFEDGCAASFGFSVLQGNTLEAKTSRCASTCTCVLCGFVLALICVSYVS*		CTTGGACTCC	CAACCTCCTC	0	R	0	0	0	0	0
7142	3380	an	AN3735.1	69.m15380	AO070342000272	0	-227	-177					ATGTGCGACTTTATCAATCACCCCCTATCCGGACTCCATGCGTTCATCTAG	ATGTGCGACTTTATCAATCACCCCCTATCCGGACTCCATGCGTTCATCTAG			MCDFINHPLSGLHAFI*	MCDFINHPLSGLHAFI*			CCTCGACCGA	CGACCCATTG	0	R	0	0	0	0	0
7143	3380	an	AN3735.1	69.m15380	AO070342000272	0	-190	-92					ATGCGTTCATCTAGCGACCCATTGGACGACCAACGCTCTCAATTGTTCGAGGTCGGCTGCGCATTTTGTGTCGGGTCCCAGCCTGCCGCTGCAAGGTAA	ATGCGTTCATCTAGCGACCCATTGGACGACCAACGCTCTCAATTGTTCGAGGTCGGCTGCGCATTTTGTGTCGGGTCCCAGCCTGCCGCTGCAAGGTAA			MRSSSDPLDDQRSQLFEVGCAFCVGSQPAAAR*	MRSSSDPLDDQRSQLFEVGCAFCVGSQPAAAR*			TCCGGACTCC	CGTAACCAGA	0	R	0	0	0	0	0
7144	3380	an	AN3735.1	69.m15380	AO070342000272	0	-68	-3					ATGTGCTTTCGCCTGCTTGCGTCTTGTAGCGACTTCTCTTGGAGCGTCGCTGCCGCCCGCGGATAA	ATGTGCTTTCGCCTGCTTGCGTCTTGTAGCGACTTCTCTTGGAGCGTCGCTGCCGCCCGCGGATAA			MCFRLLASCSDFSWSVAAARG*	MCFRLLASCSDFSWSVAAARG*			TACTAGATAT	AGATGGAGTC	0	R	0	0	0	0	0
7147	3380	ao	AN3735.1	69.m15380	AO070342000272	0					-247	-194	ATGTGCGACTCGACTTGTCGACCTCTCCCCGGACTCCATGCGTTCAGCCCGTGA			ATGTGCGACTCGACTTGTCGACCTCTCCCCGGACTCCATGCGTTCAGCCCGTGA	MCDSTCRPLPGLHAFSP*			MCDSTCRPLPGLHAFSP*	CCTTGACCGA	CCCATTGGAC	0	R	0	0	0	0	0
7148	3380	ao	AN3735.1	69.m15380	AO070342000272	0					-210	-58	ATGCGTTCAGCCCGTGACCCATTGGACGACACAGACCCTCCATTGTTCGAGGACGGTTGCGCAGCGTACGTTGGGTGCCAACATCTGCAAGGTAACATTTTACATGAGTACATGTGTGTACGTGTGTCCGTCTGCGTCCTGCGTGTTTGGTAG			ATGCGTTCAGCCCGTGACCCATTGGACGACACAGACCCTCCATTGTTCGAGGACGGTTGCGCAGCGTACGTTGGGTGCCAACATCTGCAAGGTAACATTTTACATGAGTACATGTGTGTACGTGTGTCCGTCTGCGTCCTGCGTGTTTGGTAG	MRSARDPLDDTDPPLFEDGCAAYVGCQHLQGNILHEYMCVRVSVCVLRVW*			MRSARDPLDDTDPPLFEDGCAAYVGCQHLQGNILHEYMCVRVSVCVLRVW*	CCCGGACTCC	CGACCGCTCT	0	R	0	0	0	0	0
7149	3380	ao	AN3735.1	69.m15380	AO070342000272	0					-99	-58	ATGTGTGTACGTGTGTCCGTCTGCGTCCTGCGTGTTTGGTAG			ATGTGTGTACGTGTGTCCGTCTGCGTCCTGCGTGTTTGGTAG	MCVRVSVCVLRVW*			MCVRVSVCVLRVW*	ACATGAGTAC	CGACCGCTCT	0	R	0	0	0	0	0
7151	3381	af	AN1260.1	70.m14959	AO070214000005	0			-131	-96			ATGACTAAGCGGTGGCCCTCCCTTAGTGTAGTCTAG		ATGACTAAGCGGTGGCCCTCCCTTAGTGTAGTCTAG		MTKRWPSLSVV*		MTKRWPSLSVV*		CGCCACCCGG	TCCAGTCTAG	0	A	0	0	0	0	0
7150	3381	an	AN1260.1	70.m14959	AO070214000005	0	-72	-25					ATGGAAACCCAACCTTGTCAACCAGCAAACTACACGATCTTGTTATAA	ATGGAAACCCAACCTTGTCAACCAGCAAACTACACGATCTTGTTATAA			METQPCQPANYTILL*	METQPCQPANYTILL*			GGCGAGATTT	CTGCTTTGCT	0	A	0	0	0	0	0
7152	3381	ao	AN1260.1	70.m14959	AO070214000005	0					-215	-144	ATGTCGTTGCTGCTAGATCGACTTTTGGTTCTGCTAGCTAAGAGTCGGAAAAGCTGCATGTTAGGTTTGTAG			ATGTCGTTGCTGCTAGATCGACTTTTGGTTCTGCTAGCTAAGAGTCGGAAAAGCTGCATGTTAGGTTTGTAG	MSLLLDRLLVLLAKSRKSCMLGL*			MSLLLDRLLVLLAKSRKSCMLGL*	TCCAAGTCAG	CGCCACCCGA	0	A	0	0	0	0	0
7153	3381	ao	AN1260.1	70.m14959	AO070214000005	0					-158	-144	ATGTTAGGTTTGTAG			ATGTTAGGTTTGTAG	MLGL*			MLGL*	GAAAAGCTGC	CGCCACCCGA	0	A	0	0	0	0	0
7154	3383	af	AN7431.1	57.m05913	AO070229000002	0			-89	-48			ATGCTTCAATTTGAAGAAAAGTGTCGTCCCTTCTGTTTTTGA		ATGCTTCAATTTGAAGAAAAGTGTCGTCCCTTCTGTTTTTGA		MLQFEEKCRPFCF*		MLQFEEKCRPFCF*		TGTCACTTGT	TCTAATTACA	0	O	0	0	0	YKL059C	0
7155	3383	ao	AN7431.1	57.m05913	AO070229000002	0					-233	-54	ATGAGTTCGAGCAATATCGTCAATAGATATTGGGCTTGCGATCTCCAGGGTCTTATAACAAAGAGGATTCACGAATCAAAATCTGTCGTTGGCTGTTTGCCACACATTTCCCAAGTGCTGTTCCTTTTGCATTATTTTCTTTTCCTGTTGTGTATCCTTTCGCAAAAGATACCCCTTTAA			ATGAGTTCGAGCAATATCGTCAATAGATATTGGGCTTGCGATCTCCAGGGTCTTATAACAAAGAGGATTCACGAATCAAAATCTGTCGTTGGCTGTTTGCCACACATTTCCCAAGTGCTGTTCCTTTTGCATTATTTTCTTTTCCTGTTGTGTATCCTTTCGCAAAAGATACCCCTTTAA	MSSSNIVNRYWACDLQGLITKRIHESKSVVGCLPHISQVLFLLHYFLFLLCILSQKIPL*			MSSSNIVNRYWACDLQGLITKRIHESKSVVGCLPHISQVLFLLHYFLFLLCILSQKIPL*	CTTTAAATTT	TCTTGATTTA	0	O	0	0	0	YKL059C	0
7157	3387	af	AN5774.1	69.m14823	AO070249000018	0			-79	-8			ATGGTGGCTTGTACATCATCATCTTTCACATTATCCATGCGCCAGGTTAAGCATATTTTTTTCTCTATCTGA		ATGGTGGCTTGTACATCATCATCTTTCACATTATCCATGCGCCAGGTTAAGCATATTTTTTTCTCTATCTGA		MVACTSSSFTLSMRQVKHIFFSI*		MVACTSSSFTLSMRQVKHIFFSI*		CGCCTCTGGT	ATTCGTTATG	0	S	FG05736.1	0	NCU00770.1	0	0
7156	3387	an	AN5774.1	69.m14823	AO070249000018	0	-62	-36					ATGGTTTTTGCGTTGTTAAGTGGTTGA	ATGGTTTTTGCGTTGTTAAGTGGTTGA			MVFALLSG*	MVFALLSG*			TCTTGTTGAA	GATAATTCTG	0	S	FG05736.1	0	NCU00770.1	0	0
7159	3389	af	AN0832.1	70.m15433	AO070255000013	0			-159	-43			ATGCCCAAGAGAGTCTCCTTCATTGCATCCTCAATGCTAGCCCTTGATCGTCACGGCTCCTTGCCTTCCTGTTTCTTTCGCGGCCTAAAACACTCACTACCTTTTGACACCTTCTGA		ATGCCCAAGAGAGTCTCCTTCATTGCATCCTCAATGCTAGCCCTTGATCGTCACGGCTCCTTGCCTTCCTGTTTCTTTCGCGGCCTAAAACACTCACTACCTTTTGACACCTTCTGA		MPKRVSFIASSMLALDRHGSLPSCFFRGLKHSLPFDTF*		MPKRVSFIASSMLALDRHGSLPSCFFRGLKHSLPFDTF*		TAGACCTCTC	GACCTTTGGC	0	R	0	0	0	0	0
7160	3389	af	AN0832.1	70.m15433	AO070255000013	0			-126	-43			ATGCTAGCCCTTGATCGTCACGGCTCCTTGCCTTCCTGTTTCTTTCGCGGCCTAAAACACTCACTACCTTTTGACACCTTCTGA		ATGCTAGCCCTTGATCGTCACGGCTCCTTGCCTTCCTGTTTCTTTCGCGGCCTAAAACACTCACTACCTTTTGACACCTTCTGA		MLALDRHGSLPSCFFRGLKHSLPFDTF*		MLALDRHGSLPSCFFRGLKHSLPFDTF*		TGCATCCTCA	GACCTTTGGC	0	R	0	0	0	0	0
7161	3389	ao	AN0832.1	70.m15433	AO070255000013	0					-225	-163	ATGTACGATACCGTATCAGTAGGTGTACCCGACCTCAACTTAGCCGCCTCCAAATTAAAATAA			ATGTACGATACCGTATCAGTAGGTGTACCCGACCTCAACTTAGCCGCCTCCAAATTAAAATAA	MYDTVSVGVPDLNLAASKLK*			MYDTVSVGVPDLNLAASKLK*	AAAATACCGG	ACCAGCTGAG	0	R	0	0	0	0	0
7162	3389	ao	AN0832.1	70.m15433	AO070255000013	0					-150	-64	ATGATACATATCTCTTTGCTCCTGCGTTGCCTTCTCTTATTCTCCCTATTCTCGCGGTCTCTTGCAGCCCCTTGGCTTCTCATGTAG			ATGATACATATCTCTTTGCTCCTGCGTTGCCTTCTCTTATTCTCCCTATTCTCGCGGTCTCTTGCAGCCCCTTGGCTTCTCATGTAG	MIHISLLLRCLLLFSLFSRSLAAPWLLM*			MIHISLLLRCLLLFSLFSRSLAAPWLLM*	CAGCTGAGCG	ATATATAACT	0	R	0	0	0	0	0
7164	3395	af	AN6541.1	62.m03133	AO070270000044	0			-243	-226			ATGAGTGAGGGGCAGTAG		ATGAGTGAGGGGCAGTAG		MSEGQ*		MSEGQ*		TCAGCATGCA	CAAGGTGCCC	0	F	0	0	0	0	0
7165	3395	af	AN6541.1	62.m03133	AO070270000044	0			-196	-176			ATGATTGTCAGTCATCGATGA		ATGATTGTCAGTCATCGATGA		MIVSHR*		MIVSHR*		GTTGCGATTC	TCGCTGATTG	0	F	0	0	0	0	0
7166	3395	af	AN6541.1	62.m03133	AO070270000044	0			-179	-165			ATGATCGCTGATTGA		ATGATCGCTGATTGA		MIAD*		MIAD*		TCAGTCATCG	ATATTTCTGT	0	F	0	0	0	0	0
7163	3395	an	AN6541.1	62.m03133	AO070270000044	0	-74	-63					ATGAGTCACTGA	ATGAGTCACTGA			MSH*	MSH*			GCCGCTTTTA	AACCCTATCT	0	F	0	0	0	0	0
7167	3395	ao	AN6541.1	62.m03133	AO070270000044	0					-183	-142	ATGATAAAGAGAGGGGCACTCCTACTTTTTTCTATACTATGA			ATGATAAAGAGAGGGGCACTCCTACTTTTTTCTATACTATGA	MIKRGALLLFSIL*			MIKRGALLLFSIL*	GAACTTCAGA	ACTTGCCCCT	0	F	0	0	0	0	0

7168	3395	ao	AN6541.1	62.m03133	AO070270000044	0					-145	-44	ATGAACTTGCCCCTCCATTCTCTCCGCCCCGAGGAGCCATCCACCATATTCATTACCTCCCTGCAATGCTATTCTCGTGTGGGTAGGATATTCAGTTCCTAA			ATGAACTTGCCCCTCCATTCTCTCCGCCCCGAGGAGCCATCCACCATATTCATTACCTCCCTGCAATGCTATTCTCGTGTGGGTAGGATATTCAGTTCCTAA	MNLPLHSLRPEEPSTIFITSLQCYSRVGRIFSS*			MNLPLHSLRPEEPSTIFITSLQCYSRVGRIFSS*	TTTCTATACT	TGTTCCCCTT	0	F	0	0	0	0	0
7169	3395	ao	AN6541.1	62.m03133	AO070270000044	0					-80	-60	ATGCTATTCTCGTGTGGGTAG			ATGCTATTCTCGTGTGGGTAG	MLFSCG*			MLFSCG*	CCTCCCTGCA	GATATTCAGT	0	F	0	0	0	0	0
7171	3396	af	AN0577.1	69.m15692	AO070272000057	0			-263	-225			ATGAGCCCCGCATCATACTTCACCTGGTGTAGGCTATAA		ATGAGCCCCGCATCATACTTCACCTGGTGTAGGCTATAA		MSPASYFTWCRL*		MSPASYFTWCRL*		GTCAGGGTAC	GAAGGCCAGT	0		0	0	0	0	0
7172	3396	ao	AN0577.1	69.m15692	AO070272000057	0					-235	-71	ATGCTACTGATATCAGTCCGCAAAGAATTTCGTCGTCAATATACACCAAGGCCATCCTCCACTTTATTGAAGGTACAGAATCGGTCAAGAAGCTCCACGTTCCACGACCACGATCATGCTTCCAGTGATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAA			ATGCTACTGATATCAGTCCGCAAAGAATTTCGTCGTCAATATACACCAAGGCCATCCTCCACTTTATTGAAGGTACAGAATCGGTCAAGAAGCTCCACGTTCCACGACCACGATCATGCTTCCAGTGATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAA	MLLISVRKEFRRQYTPRPSSTLLKVQNRSRSSTFHDHDHASSDGVANYSQVPLS*			MLLISVRKEFRRQYTPRPSSTLLKVQNRSRSSTFHDHDHASSDGVANYSQVPLS*	CCTTGAGTCT	AGCCTACACT	0		0	0	0	0	0
7173	3396	ao	AN0577.1	69.m15692	AO070272000057	0					-120	-43	ATGCTTCCAGTGATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAAAGCCTACACTTGGGCTGAACGGCCCTGA			ATGCTTCCAGTGATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAAAGCCTACACTTGGGCTGAACGGCCCTGA	MLPVMVSLIIPRFLCRKAYTWAERP*			MLPVMVSLIIPRFLCRKAYTWAERP*	GACCACGATC	CATCGACCCC	0		0	0	0	0	0
7174	3396	ao	AN0577.1	69.m15692	AO070272000057	0					-108	-43	ATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAAAGCCTACACTTGGGCTGAACGGCCCTGA			ATGGTGTCGCTAATTATTCCCAGGTTCCTCTGTCGTAAAGCCTACACTTGGGCTGAACGGCCCTGA	MVSLIIPRFLCRKAYTWAERP*			MVSLIIPRFLCRKAYTWAERP*	GCTTCCAGTG	CATCGACCCC	0		0	0	0	0	0
7179	3397	af	AN4412.1	58.m08981	AO070273000032	0			-272	-198			ATGGACCACCCGGAAAGGAAGAGGATGAGTGGAATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		ATGGACCACCCGGAAAGGAAGAGGATGAGTGGAATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		MDHPERKRMSGMIQLRRLPGTAIT*		MDHPERKRMSGMIQLRRLPGTAIT*		GAACCCGATA	CTATTTCACC	0	A	0	MG03931.1	0	0	0
7180	3397	af	AN4412.1	58.m08981	AO070273000032	0			-248	-198			ATGAGTGGAATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		ATGAGTGGAATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		MSGMIQLRRLPGTAIT*		MSGMIQLRRLPGTAIT*		AAGGAAGAGG	CTATTTCACC	0	A	0	MG03931.1	0	0	0
7181	3397	af	AN4412.1	58.m08981	AO070273000032	0			-239	-198			ATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		ATGATACAGCTTCGGCGGCTCCCCGGGACCGCAATCACGTGA		MIQLRRLPGTAIT*		MIQLRRLPGTAIT*		GATGAGTGGA	CTATTTCACC	0	A	0	MG03931.1	0	0	0
7175	3397	an	AN4412.1	58.m08981	AO070273000032	0	-234	-220					ATGCGGGAAATGTAG	ATGCGGGAAATGTAG			MREM*	MREM*			TGATCGTGCC	GATGAAGATG	0	A	0	MG03931.1	0	0	0
7176	3397	an	AN4412.1	58.m08981	AO070273000032	0	-218	-198					ATGAAGATGGAGCCAAATTAG	ATGAAGATGGAGCCAAATTAG			MKMEPN*	MKMEPN*			GAAATGTAGG	TCACGTGATA	0	A	0	MG03931.1	0	0	0
7177	3397	an	AN4412.1	58.m08981	AO070273000032	0	-212	-198					ATGGAGCCAAATTAG	ATGGAGCCAAATTAG			MEPN*	MEPN*			TAGGATGAAG	TCACGTGATA	0	A	0	MG03931.1	0	0	0
7178	3397	an	AN4412.1	58.m08981	AO070273000032	0	-107	-66					ATGAAATTTCTTGGTCGCTCCAGTCGGTGGGAAGAAACATAG	ATGAAATTTCTTGGTCGCTCCAGTCGGTGGGAAGAAACATAG			MKFLGRSSRWEET*	MKFLGRSSRWEET*			CGAACGGGAC	CAGAAACCCG	0	A	0	MG03931.1	0	0	0
7182	3397	ao	AN4412.1	58.m08981	AO070273000032	0					-233	-153	ATGACAATCGTCGGCCCGGAGCCGGGTCACGTGTATACCATTCCGAACGGCAAGTTTGTCCGGCGGAAAGACCAGCAGTAG			ATGACAATCGTCGGCCCGGAGCCGGGTCACGTGTATACCATTCCGAACGGCAAGTTTGTCCGGCGGAAAGACCAGCAGTAG	MTIVGPEPGHVYTIPNGKFVRRKDQQ*			MTIVGPEPGHVYTIPNGKFVRRKDQQ*	GAGTGGTGGA	TGGCTCTGAC	0	A	0	MG03931.1	0	0	0
7183	3397	ao	AN4412.1	58.m08981	AO070273000032	0					-135	-76	ATGCCGCCCGCGTCAAAAGGAACATTGAAATTTCTCAGTGAATCGGCGAGTGCGACATAG			ATGCCGCCCGCGTCAAAAGGAACATTGAAATTTCTCAGTGAATCGGCGAGTGCGACATAG	MPPASKGTLKFLSESASAT*			MPPASKGTLKFLSESASAT*	GACCAATCAC	TGCGACGAGC	0	A	0	MG03931.1	0	0	0
7184	3398	af	AN9398.1	52.m04024	AO070274000018	0			-183	-151			ATGATCTTGAAATTTACACACGCCTTGAGTTGA		ATGATCTTGAAATTTACACACGCCTTGAGTTGA		MILKFTHALS*		MILKFTHALS*		CCTAAGTCAC	GAGGGGAAAA	0	W	0	0	0	0	0
7185	3398	ao	AN9398.1	52.m04024	AO070274000018	0					-119	-90	ATGTCAAAGCAGAGTTATACGACCATATAG			ATGTCAAAGCAGAGTTATACGACCATATAG	MSKQSYTTI*			MSKQSYTTI*	TTTCAATCCC	GCGGCCAGGC	0	W	0	0	0	0	0
7187	3402	af	AN0239.1	71.m15643	AO070284000068	0			-99	-22			ATGCAGATCACCTTCACCATAACGCCAAGAGCAGGTTCATGGTGTCTGATGGTTGTTGGCCATCAGGTCGATAGTTGA		ATGCAGATCACCTTCACCATAACGCCAAGAGCAGGTTCATGGTGTCTGATGGTTGTTGGCCATCAGGTCGATAGTTGA		MQITFTITPRAGSWCLMVVGHQVDS*		MQITFTITPRAGSWCLMVVGHQVDS*		ACACATACCA	GGGTAAAGCT	0	TU	FG00191.1	0	NCU00671.1	0	0
7188	3402	af	AN0239.1	71.m15643	AO070284000068	0			-61	-26			ATGGTGTCTGATGGTTGTTGGCCATCAGGTCGATAG		ATGGTGTCTGATGGTTGTTGGCCATCAGGTCGATAG		MVSDGCWPSGR*		MVSDGCWPSGR*		GAGCAGGTTC	TTGAGGGTAA	0	TU	FG00191.1	0	NCU00671.1	0	0
7190	3402	ao	AN0239.1	71.m15643	AO070284000068	0					-265	-221	ATGCTGAATTCGACACAATCGGCCTTGTCCTTATTCCTAGAGTAG			ATGCTGAATTCGACACAATCGGCCTTGTCCTTATTCCTAGAGTAG	MLNSTQSALSLFLE*			MLNSTQSALSLFLE*	CTCATCCCGG	TGCAATTGTT	0	TU	FG00191.1	0	NCU00671.1	0	0
7191	3402	ao	AN0239.1	71.m15643	AO070284000068	0					-152	-117	ATGTTGGAAAACTGTGTGGATTACATTCACGACTAG			ATGTTGGAAAACTGTGTGGATTACATTCACGACTAG	MLENCVDYIHD*			MLENCVDYIHD*	CGGCTGTGCC	CTACCATAAC	0	TU	FG00191.1	0	NCU00671.1	0	0
7192	3402	ao	AN0239.1	71.m15643	AO070284000068	0					-98	-15	ATGCAGACCGCCTTCATCCTTACACTAAGTGCTGGCTCATGGTGTCTGATGGTCTCTGGCCATCGAATAGGTAGTCGGGGATAA			ATGCAGACCGCCTTCATCCTTACACTAAGTGCTGGCTCATGGTGTCTGATGGTCTCTGGCCATCGAATAGGTAGTCGGGGATAA	MQTAFILTLSAGSWCLMVSGHRIGSRG*			MQTAFILTLSAGSWCLMVSGHRIGSRG*	ACGCATACCA	GCTTCAGCGG	0	TU	FG00191.1	0	NCU00671.1	0	0
7197	3405	af	AN0814.1	70.m15414	AO070288000089	0			-93	-73			ATGACCAGATCTGGCATTTGA		ATGACCAGATCTGGCATTTGA		MTRSGI*		MTRSGI*		TCTTCATTGA	GATCAAGGAG	0	DO	0	0	0	0	0
7196	3405	an	AN0814.1	70.m15414	AO070288000089	0	-84	-61					ATGGTTGGATTGAGGACAATCTGA	ATGGTTGGATTGAGGACAATCTGA			MVGLRTI*	MVGLRTI*			CGTCCTCCGC	AGCTCGAAAA	0	DO	0	0	0	0	0
7198	3405	ao	AN0814.1	70.m15414	AO070288000089	0					-74	-57	ATGACCGCATTGCCTTGA			ATGACCGCATTGCCTTGA	MTALP*			MTALP*	AGGTCATTGG	CCTTACTTCT	0	DO	0	0	0	0	0
7199	3406	an	AN5139.1	54.m07054	AO070291000038	0	-211	-122					ATGCCCGCATTTGCCCGAAACAGCAAAACGCGGCGCGTCCGACAACGCGTTCGACAACGCGTCTTGTCCAGTGCTTCTCGACTGCGATAA	ATGCCCGCATTTGCCCGAAACAGCAAAACGCGGCGCGTCCGACAACGCGTTCGACAACGCGTCTTGTCCAGTGCTTCTCGACTGCGATAA			MPAFARNSKTRRVRQRVRQRVLSSASRLR*	MPAFARNSKTRRVRQRVRQRVLSSASRLR*			CCTGTGCCCT	GGCATCTCCA	0	R	0	0	NCU08484.1	YPR135W	0
7204	3407	af	AN8051.1	53.m03891	AO070292000094	0			-282	-235			ATGTCTCTCTGCTTTCCAACTGTCCAATCCCCCAAGGTCGTCCGATAA		ATGTCTCTCTGCTTTCCAACTGTCCAATCCCCCAAGGTCGTCCGATAA		MSLCFPTVQSPKVVR*		MSLCFPTVQSPKVVR*		AAAGGGCTAT	TCCAACTCAC	0		0	0	0	0	0
7205	3407	af	AN8051.1	53.m03891	AO070292000094	0			-213	-199			ATGTCCCAATCATAA		ATGTCCCAATCATAA		MSQS*		MSQS*		ACGACAGTGC	CCGACTGTCT	0		0	0	0	0	0
7206	3407	af	AN8051.1	53.m03891	AO070292000094	0			-163	-125			ATGATCCTCCGGGCCTCCCCCTCCTTCGTCTTTATTTAA		ATGATCCTCCGGGCCTCCCCCTCCTTCGTCTTTATTTAA		MILRASPSFVFI*		MILRASPSFVFI*		CCTTAGTTTG	TTTCCAGTTG	0		0	0	0	0	0
7208	3408	af	AN7293.1	72.m19774	AO070297000034	0			-257	-72			ATGATATTCGATAAGTCCTTTCTACTTGCGGTTAGCTTGGAGAACCGAGGTATGACGACAACAAATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAATTCAAGATCTATGCCTGGGAATTGACATTTATATTCCTTGGAGGTCTTTATATTTGTACCATTTTGATGTCACATAG		ATGATATTCGATAAGTCCTTTCTACTTGCGGTTAGCTTGGAGAACCGAGGTATGACGACAACAAATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAATTCAAGATCTATGCCTGGGAATTGACATTTATATTCCTTGGAGGTCTTTATATTTGTACCATTTTGATGTCACATAG		MIFDKSFLLAVSLENRGMTTTNGYAWISNGLFIKDIIQDLCLGIDIYIPWRSLYLYHFDVT*		MIFDKSFLLAVSLENRGMTTTNGYAWISNGLFIKDIIQDLCLGIDIYIPWRSLYLYHFDVT*		TTATCGTCAC	TCAAGCTTTT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7209	3408	af	AN7293.1	72.m19774	AO070297000034	0			-206	-72			ATGACGACAACAAATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAATTCAAGATCTATGCCTGGGAATTGACATTTATATTCCTTGGAGGTCTTTATATTTGTACCATTTTGATGTCACATAG		ATGACGACAACAAATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAATTCAAGATCTATGCCTGGGAATTGACATTTATATTCCTTGGAGGTCTTTATATTTGTACCATTTTGATGTCACATAG		MTTTNGYAWISNGLFIKDIIQDLCLGIDIYIPWRSLYLYHFDVT*		MTTTNGYAWISNGLFIKDIIQDLCLGIDIYIPWRSLYLYHFDVT*		GAACCGAGGT	TCAAGCTTTT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7210	3408	af	AN7293.1	72.m19774	AO070297000034	0			-193	-149			ATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAA		ATGGGTACGCGTGGATATCCAATGGGTTGTTCATTAAGGACATAA		MGTRGYPMGCSLRT*		MGTRGYPMGCSLRT*		ACGACAACAA	TTCAAGATCT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7211	3408	af	AN7293.1	72.m19774	AO070297000034	0			-172	-149			ATGGGTTGTTCATTAAGGACATAA		ATGGGTTGTTCATTAAGGACATAA		MGCSLRT*		MGCSLRT*		TGGATATCCA	TTCAAGATCT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7212	3408	af	AN7293.1	72.m19774	AO070297000034	0			-138	-124			ATGCCTGGGAATTGA		ATGCCTGGGAATTGA		MPGN*		MPGN*		TTCAAGATCT	CATTTATATT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7213	3408	af	AN7293.1	72.m19774	AO070297000034	0			-82	-59			ATGTCACATAGTCAAGCTTTTTGA		ATGTCACATAGTCAAGCTTTTTGA		MSHSQAF*		MSHSQAF*		TACCATTTTG	GTTTTCAGTC	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7214	3408	ao	AN7293.1	72.m19774	AO070297000034	0					-212	-198	ATGAACGTGAAATGA			ATGAACGTGAAATGA	MNVK*			MNVK*	CCCTAGTCAC	CCCCATTCTA	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7215	3408	ao	AN7293.1	72.m19774	AO070297000034	0					-201	-103	ATGACCCCATTCTACTTTTGGTTAGTCTCACGGCCGAGGCGATCATCTCACATCACTGGGCAACTATGCTTAAGCTATGTGTATCTACGCGACTACTAG			ATGACCCCATTCTACTTTTGGTTAGTCTCACGGCCGAGGCGATCATCTCACATCACTGGGCAACTATGCTTAAGCTATGTGTATCTACGCGACTACTAG	MTPFYFWLVSRPRRSSHITGQLCLSYVYLRDY*			MTPFYFWLVSRPRRSSHITGQLCLSYVYLRDY*	TGAACGTGAA	TAGATCCTGT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7216	3408	ao	AN7293.1	72.m19774	AO070297000034	0					-136	-77	ATGCTTAAGCTATGTGTATCTACGCGACTACTAGTAGATCCTGTGTCCTTACTTGTTTGA			ATGCTTAAGCTATGTGTATCTACGCGACTACTAGTAGATCCTGTGTCCTTACTTGTTTGA	MLKLCVSTRLLVDPVSLLV*			MLKLCVSTRLLVDPVSLLV*	CTGGGCAACT	AGAATACATA	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7217	3408	ao	AN7293.1	72.m19774	AO070297000034	0					-125	-57	ATGTGTATCTACGCGACTACTAGTAGATCCTGTGTCCTTACTTGTTTGAAGAATACATACTTTATCTAA			ATGTGTATCTACGCGACTACTAGTAGATCCTGTGTCCTTACTTGTTTGAAGAATACATACTTTATCTAA	MCIYATTSRSCVLTCLKNTYFI*			MCIYATTSRSCVLTCLKNTYFI*	TGCTTAAGCT	TTGTCTGTGT	0	S	FG06758.1	MG00127.1	NCU07563.1	0	0
7218	3410	af	AN1635.1	58.m09022	AO070299000058	0			-201	-187			ATGTGTGGCTGGTGA		ATGTGTGGCTGGTGA		MCGW*		MCGW*		AAGGCGGCAG	GAGTGGCTTC	0	A	0	0	0	0	0
7219	3414	af	AN3134.1	59.m08591	AO070303000010	0			-254	-213			ATGACTTGGTTGATAGCTCAGGGGAAACTGCTGACGAACTAA		ATGACTTGGTTGATAGCTCAGGGGAAACTGCTGACGAACTAA		MTWLIAQGKLLTN*		MTWLIAQGKLLTN*		TACAATATCA	ACCCAAAGTA	0	O	0	0	0	0	0
7220	3414	af	AN3134.1	59.m08591	AO070303000010	0			-151	-14			ATGGTGGTGCGGGCACAACTCCACGTCTTCAAGCTCAGCAGGCCCATCGTTTGGCTGCTTTTAAACCGTGTTTGGAACAGTGATATTTGTTGCTCTATTGAACTCCATTTCTTGAAGCGTCTCGCCGAAGTAGCCTGA		ATGGTGGTGCGGGCACAACTCCACGTCTTCAAGCTCAGCAGGCCCATCGTTTGGCTGCTTTTAAACCGTGTTTGGAACAGTGATATTTGTTGCTCTATTGAACTCCATTTCTTGAAGCGTCTCGCCGAAGTAGCCTGA		MVVRAQLHVFKLSRPIVWLLLNRVWNSDICCSIELHFLKRLAEVA*		MVVRAQLHVFKLSRPIVWLLLNRVWNSDICCSIELHFLKRLAEVA*		TGGAAATTTG	AAACACCGCT	0	O	0	0	0	0	0
7221	3414	ao	AN3134.1	59.m08591	AO070303000010	0					-279	-55	ATGAGAATGTTTGGATTTGATAGGAGTGGATTTAATCAGGAGAAAGGTAGACTAAGCCTGAAGGGGATTAGTGGGGGTGAGCTTCCAATCCGCAATCCCACTTCGAGGTTCGCTGGAAATTTGATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG			ATGAGAATGTTTGGATTTGATAGGAGTGGATTTAATCAGGAGAAAGGTAGACTAAGCCTGAAGGGGATTAGTGGGGGTGAGCTTCCAATCCGCAATCCCACTTCGAGGTTCGCTGGAAATTTGATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG	MRMFGFDRSGFNQEKGRLSLKGISGGELPIRNPTSRFAGNLMVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*			MRMFGFDRSGFNQEKGRLSLKGISGGELPIRNPTSRFAGNLMVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*	AGTACATACA	GAATACCCAC	0	O	0	0	0	0	0
7222	3414	ao	AN3134.1	59.m08591	AO070303000010	0					-273	-55	ATGTTTGGATTTGATAGGAGTGGATTTAATCAGGAGAAAGGTAGACTAAGCCTGAAGGGGATTAGTGGGGGTGAGCTTCCAATCCGCAATCCCACTTCGAGGTTCGCTGGAAATTTGATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG			ATGTTTGGATTTGATAGGAGTGGATTTAATCAGGAGAAAGGTAGACTAAGCCTGAAGGGGATTAGTGGGGGTGAGCTTCCAATCCGCAATCCCACTTCGAGGTTCGCTGGAAATTTGATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG	MFGFDRSGFNQEKGRLSLKGISGGELPIRNPTSRFAGNLMVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*			MFGFDRSGFNQEKGRLSLKGISGGELPIRNPTSRFAGNLMVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*	TACAATGAGA	GAATACCCAC	0	O	0	0	0	0	0

7223	3414	ao	AN3134.1	59.m08591	AO070303000010	0					-156	-55	ATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG			ATGGTGAAGGCGGGCACAGCACTCCAGATCCCCCTAGCGAACACGCCCCTCATTTATCTTATTCTTCAGTTGTTTTTGAAGAACTCTTCCAGTAATTTTTAG	MVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*			MVKAGTALQIPLANTPLIYLILQLFLKNSSSNF*	TGGAAATTTG	GAATACCCAC	0	O	0	0	0	0	0
7226	3417	an	AN1715.1	58.m08959	AO070305000031	0	-184	-47					ATGGCGGACGGTCTCGGCTCCTGTTGCTGGATCATGACGAAAGATCTCTCGATTTGGGTGCTGAGTGTCCTGTCATGTCATGCATGCGGTTACAGGTACATAAAAGGCCTATCCAGGTCCACGTCGCAGTGGCATTAA	ATGGCGGACGGTCTCGGCTCCTGTTGCTGGATCATGACGAAAGATCTCTCGATTTGGGTGCTGAGTGTCCTGTCATGTCATGCATGCGGTTACAGGTACATAAAAGGCCTATCCAGGTCCACGTCGCAGTGGCATTAA			MADGLGSCCWIMTKDLSIWVLSVLSCHACGYRYIKGLSRSTSQWH*	MADGLGSCCWIMTKDLSIWVLSVLSCHACGYRYIKGLSRSTSQWH*			TCTTGGTGGA	ACCATCAATA	0	G	0	MG10677.1	0	0	0
7232	3417	ao	AN1715.1	58.m08959	AO070305000031	0					-280	-245	ATGGAAGTTCTTGAAGTCTTGGAGTCTTGGAGTTAG			ATGGAAGTTCTTGAAGTCTTGGAGTCTTGGAGTTAG	MEVLEVLESWS*			MEVLEVLESWS*	TCCTGGCTTC	GGCTCGGTGG	0	G	0	MG10677.1	0	0	0
7238	3419	af	AN3504.1	54.m06814	AO070306000123	0			-258	-172			ATGGACCGACGACATTCTGTGGGGGTAATAGTATGCCAACGGATATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGA		ATGGACCGACGACATTCTGTGGGGGTAATAGTATGCCAACGGATATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGA		MDRRHSVGVIVCQRIWRPRSDHILLMEY*		MDRRHSVGVIVCQRIWRPRSDHILLMEY*		GAAGACGGCG	CACCACTCGT	0	G	0	0	0	0	0
7239	3419	af	AN3504.1	54.m06814	AO070306000123	0			-226	-131			ATGCCAACGGATATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGACACCACTCGTAGGGTTATCCACCTTGCCCTTTCTTGAATGA		ATGCCAACGGATATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGACACCACTCGTAGGGTTATCCACCTTGCCCTTTCTTGAATGA		MPTDMEAEIRSYSPYGVLTPLVGLSTLPFLE*		MPTDMEAEIRSYSPYGVLTPLVGLSTLPFLE*		GGGTAATAGT	GGGGATGATG	0	G	0	0	0	0	0
7240	3419	af	AN3504.1	54.m06814	AO070306000123	0			-214	-131			ATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGACACCACTCGTAGGGTTATCCACCTTGCCCTTTCTTGAATGA		ATGGAGGCCGAGATCCGATCATATTCTCCTTATGGAGTACTGACACCACTCGTAGGGTTATCCACCTTGCCCTTTCTTGAATGA		MEAEIRSYSPYGVLTPLVGLSTLPFLE*		MEAEIRSYSPYGVLTPLVGLSTLPFLE*		GCCAACGGAT	GGGGATGATG	0	G	0	0	0	0	0
7241	3419	af	AN3504.1	54.m06814	AO070306000123	0			-183	-172			ATGGAGTACTGA		ATGGAGTACTGA		MEY*		MEY*		TATTCTCCTT	CACCACTCGT	0	G	0	0	0	0	0
7242	3419	af	AN3504.1	54.m06814	AO070306000123	0			-134	-123			ATGAGGGGATGA		ATGAGGGGATGA		MRG*		MRG*		CCTTTCTTGA	TGAGGGGAAG	0	G	0	0	0	0	0
7243	3419	af	AN3504.1	54.m06814	AO070306000123	0			-126	-64			ATGATGAGGGGAAGCATTGAAATAGATATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		ATGATGAGGGGAAGCATTGAAATAGATATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		MMRGSIEIDMMSPYCRLLLL*		MMRGSIEIDMMSPYCRLLLL*		GAATGAGGGG	ATTTTCCGCG	0	G	0	0	0	0	0
7244	3419	af	AN3504.1	54.m06814	AO070306000123	0			-123	-64			ATGAGGGGAAGCATTGAAATAGATATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		ATGAGGGGAAGCATTGAAATAGATATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		MRGSIEIDMMSPYCRLLLL*		MRGSIEIDMMSPYCRLLLL*		TGAGGGGATG	ATTTTCCGCG	0	G	0	0	0	0	0
7245	3419	af	AN3504.1	54.m06814	AO070306000123	0			-99	-64			ATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		ATGATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		MMSPYCRLLLL*		MMSPYCRLLLL*		TGAAATAGAT	ATTTTCCGCG	0	G	0	0	0	0	0
7246	3419	af	AN3504.1	54.m06814	AO070306000123	0			-96	-64			ATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		ATGTCGCCGTACTGTAGACTTCTGCTTCTGTAG		MSPYCRLLLL*		MSPYCRLLLL*		AATAGATATG	ATTTTCCGCG	0	G	0	0	0	0	0
7237	3419	an	AN3504.1	54.m06814	AO070306000123	0	-173	-99					ATGTCCCCCGAGTCCCGATGGAGCAGCCACCCTATTTGCCAGTGCAAGCCCCTCAGTGTGCCCCTCATAGAATGA	ATGTCCCCCGAGTCCCGATGGAGCAGCCACCCTATTTGCCAGTGCAAGCCCCTCAGTGTGCCCCTCATAGAATGA			MSPESRWSSHPICQCKPLSVPLIE*	MSPESRWSSHPICQCKPLSVPLIE*			TAGGTCGGAA	GGAGGAGCTG	0	G	0	0	0	0	0
7247	3419	ao	AN3504.1	54.m06814	AO070306000123	0					-161	-117	ATGAACCCGAAGTCCGATGTATACACGGTAGTTGTCCTTGAGTAG			ATGAACCCGAAGTCCGATGTATACACGGTAGTTGTCCTTGAGTAG	MNPKSDVYTVVVLE*			MNPKSDVYTVVVLE*	ACTGTCGGAG	TCCCGATGAC	0	G	0	0	0	0	0
7248	3419	ao	AN3504.1	54.m06814	AO070306000123	0					-145	-131	ATGTATACACGGTAG			ATGTATACACGGTAG	MYTR*			MYTR*	CCGAAGTCCG	TTGTCCTTGA	0	G	0	0	0	0	0
7249	3419	ao	AN3504.1	54.m06814	AO070306000123	0					-111	-79	ATGACGCAGATGTGCGTAATAACATTCAAATAG			ATGACGCAGATGTGCGTAATAACATTCAAATAG	MTQMCVITFK*			MTQMCVITFK*	AGTAGTCCCG	AGCTTCAAGT	0	G	0	0	0	0	0
7250	3419	ao	AN3504.1	54.m06814	AO070306000123	0					-102	-79	ATGTGCGTAATAACATTCAAATAG			ATGTGCGTAATAACATTCAAATAG	MCVITFK*			MCVITFK*	GATGACGCAG	AGCTTCAAGT	0	G	0	0	0	0	0
7252	3420	af	AN4255.1	65.m07427	AO070309000125	0			-157	-107			ATGCATCATTGTATAAATCGGTGTCAGCCTCGTCTTGTCTTCCACTATTGA		ATGCATCATTGTATAAATCGGTGTCAGCCTCGTCTTGTCTTCCACTATTGA		MHHCINRCQPRLVFHY*		MHHCINRCQPRLVFHY*		GAAGTTTCAG	ATATCGTCTC	0	G	0	0	0	0	0
7251	3420	an	AN4255.1	65.m07427	AO070309000125	0	-133	-122					ATGGCCTTCTAG	ATGGCCTTCTAG			MAF*	MAF*			TACCGTCCTC	ATTGTCCCCA	0	G	0	0	0	0	0
7253	3420	ao	AN4255.1	65.m07427	AO070309000125	0					-150	-100	ATGCATACACCTATGAGCTCATTTCATCTTGGACTTCACTTAAACATTTAA			ATGCATACACCTATGAGCTCATTTCATCTTGGACTTCACTTAAACATTTAA	MHTPMSSFHLGLHLNI*			MHTPMSSFHLGLHLNI*	CCTTCGGCAG	GCCCCGCTCG	0	G	0	0	0	0	0
7254	3420	ao	AN4255.1	65.m07427	AO070309000125	0					-138	-100	ATGAGCTCATTTCATCTTGGACTTCACTTAAACATTTAA			ATGAGCTCATTTCATCTTGGACTTCACTTAAACATTTAA	MSSFHLGLHLNI*			MSSFHLGLHLNI*	GCATACACCT	GCCCCGCTCG	0	G	0	0	0	0	0
7255	3421	af	AN8228.1	53.m03745	AO070310000083	0			-231	-157			ATGACCAATCAGGCAACAGTGACGTATCCTCATCAGCGCGGTGTTTGTCCCTTGGCGAAATCGGAGCTCCAGTGA		ATGACCAATCAGGCAACAGTGACGTATCCTCATCAGCGCGGTGTTTGTCCCTTGGCGAAATCGGAGCTCCAGTGA		MTNQATVTYPHQRGVCPLAKSELQ*		MTNQATVTYPHQRGVCPLAKSELQ*		CTTCGTCCGG	TAGTTTGGCA	0	D	0	0	0	0	0
7256	3421	ao	AN8228.1	53.m03745	AO070310000083	0					-250	-227	ATGGAAGATCCCCTCTTCCGATGA			ATGGAAGATCCCCTCTTCCGATGA	MEDPLFR*			MEDPLFR*	TGAGGCATCA	CCAATCAGGT	0	D	0	0	0	0	0
7257	3421	ao	AN8228.1	53.m03745	AO070310000083	0					-230	-159	ATGACCAATCAGGTAACAGTGACGTACCTCATTGGTCCCTCAATTGTTGTTCTTCAGCTTTCTCGGAGATGA			ATGACCAATCAGGTAACAGTGACGTACCTCATTGGTCCCTCAATTGTTGTTCTTCAGCTTTCTCGGAGATGA	MTNQVTVTYLIGPSIVVLQLSRR*			MTNQVTVTYLIGPSIVVLQLSRR*	CCCTCTTCCG	ACTAAGCATC	0	D	0	0	0	0	0
7263	3427	af	AN6857.1	71.m15270	AO070314000074	0			-178	-158			ATGGCTAGAATCCTCCATTAG		ATGGCTAGAATCCTCCATTAG		MARILH*		MARILH*		ACTACAGATA	CCATATAAAA	0		0	0	0	0	0
7264	3427	af	AN6857.1	71.m15270	AO070314000074	0			-148	-131			ATGTTCGTGCTATTCTAA		ATGTTCGTGCTATTCTAA		MFVLF*		MFVLF*		GCCATATAAA	TCTGGTCAGT	0		0	0	0	0	0
7261	3427	an	AN6857.1	71.m15270	AO070314000074	0	-272	-153					ATGATCTGCAGCGTGCCTTCTCTTATCGGCGGTGGTTCAGTCTCAGGGGTTCTGCCACCGCCTTCCGTATCGACACTCGCATCCAAAGGAACTAGGTGCTTTGTGCAGACCTGCTGCTGA	ATGATCTGCAGCGTGCCTTCTCTTATCGGCGGTGGTTCAGTCTCAGGGGTTCTGCCACCGCCTTCCGTATCGACACTCGCATCCAAAGGAACTAGGTGCTTTGTGCAGACCTGCTGCTGA			MICSVPSLIGGGSVSGVLPPPSVSTLASKGTRCFVQTCC*	MICSVPSLIGGGSVSGVLPPPSVSTLASKGTRCFVQTCC*			ACAACTCAGC	TCGGGATTTC	0		0	0	0	0	0
7265	3427	ao	AN6857.1	71.m15270	AO070314000074	0					-181	-158	ATGCTGAAATTCCTCAAGAATTAA			ATGCTGAAATTCCTCAAGAATTAA	MLKFLKN*			MLKFLKN*	GTCGCCTGTC	GACTGCTATT	0		0	0	0	0	0
7266	3427	ao	AN6857.1	71.m15270	AO070314000074	0					-136	-65	ATGATTGAGGTTCTCTCGTCAATTGTTAGGGCGTATCGTGTTTCCACCGCACCATTGGGTCGCATTGTGTAG			ATGATTGAGGTTCTCTCGTCAATTGTTAGGGCGTATCGTGTTTCCACCGCACCATTGGGTCGCATTGTGTAG	MIEVLSSIVRAYRVSTAPLGRIV*			MIEVLSSIVRAYRVSTAPLGRIV*	TCTGGGATCA	ACACCCAAGT	0		0	0	0	0	0
7267	3428	af	AN0067.1	71.m15344	AO070314000157	0			-245	-189			ATGGATTTTCCGCCAGCCACCGAGCCCAAAAAGCGCGCCAAGTCACGTGCGACGTGA		ATGGATTTTCCGCCAGCCACCGAGCCCAAAAAGCGCGCCAAGTCACGTGCGACGTGA		MDFPPATEPKKRAKSRAT*		MDFPPATEPKKRAKSRAT*		ATACGTAATA	CTTAGCCCGT	0	F	0	0	0	0	0
7270	3429	af	AN0871.1	70.m15455	AO070320000029	0			-99	-88			ATGTATATCTGA		ATGTATATCTGA		MYI*		MYI*		TTTCTTGCAG	CATTATCCGT	0	O	0	MG10490.1	0	0	0
7268	3429	an	AN0871.1	70.m15455	AO070320000029	0	-181	-74					ATGACAGCCCCGGAACAGCCACGTTCTCCCCACAGCAGCTTACAACAACCACAGTTCTTTCTCGATTCTACGATGGAAGCGGGATCAACAGTCCGCAGTGCAAGTTAG	ATGACAGCCCCGGAACAGCCACGTTCTCCCCACAGCAGCTTACAACAACCACAGTTCTTTCTCGATTCTACGATGGAAGCGGGATCAACAGTCCGCAGTGCAAGTTAG			MTAPEQPRSPHSSLQQPQFFLDSTMEAGSTVRSAS*	MTAPEQPRSPHSSLQQPQFFLDSTMEAGSTVRSAS*			ATAATCCGCT	TCAGCCGCGG	0	O	0	MG10490.1	0	0	0
7269	3429	an	AN0871.1	70.m15455	AO070320000029	0	-109	-74					ATGGAAGCGGGATCAACAGTCCGCAGTGCAAGTTAG	ATGGAAGCGGGATCAACAGTCCGCAGTGCAAGTTAG			MEAGSTVRSAS*	MEAGSTVRSAS*			CGATTCTACG	TCAGCCGCGG	0	O	0	MG10490.1	0	0	0
7271	3429	ao	AN0871.1	70.m15455	AO070320000029	0					-193	-158	ATGTGGCCCTCTTTCTGGCTGTCCTTTTCCACATGA			ATGTGGCCCTCTTTCTGGCTGTCCTTTTCCACATGA	MWPSFWLSFST*			MWPSFWLSFST*	GATCTTCCCG	ATTGATAAGC	0	O	0	MG10490.1	0	0	0
7272	3429	ao	AN0871.1	70.m15455	AO070320000029	0					-120	-103	ATGTATCCACCTACCTAG			ATGTATCCACCTACCTAG	MYPPT*			MYPPT*	ACTTCTTCAT	TTGTGCCCAC	0	O	0	MG10490.1	0	0	0
7279	3430	af	AN0161.1	71.m16051	AO070321000086	0			-246	-175			ATGTCTTTACTCCGTATTCTGGTAGCAATGGTATTCACGCATCAATTTATTTATATTGATGTCGAAGGATAA		ATGTCTTTACTCCGTATTCTGGTAGCAATGGTATTCACGCATCAATTTATTTATATTGATGTCGAAGGATAA		MSLLRILVAMVFTHQFIYIDVEG*		MSLLRILVAMVFTHQFIYIDVEG*		GTTGAATCAA	TACGGATTGA	0	A	0	0	0	0	0
7280	3430	af	AN0161.1	71.m16051	AO070321000086	0			-219	-175			ATGGTATTCACGCATCAATTTATTTATATTGATGTCGAAGGATAA		ATGGTATTCACGCATCAATTTATTTATATTGATGTCGAAGGATAA		MVFTHQFIYIDVEG*		MVFTHQFIYIDVEG*		TCTGGTAGCA	TACGGATTGA	0	A	0	0	0	0	0
7281	3430	af	AN0161.1	71.m16051	AO070321000086	0			-188	-165			ATGTCGAAGGATAATACGGATTGA		ATGTCGAAGGATAATACGGATTGA		MSKDNTD*		MSKDNTD*		ATTTATATTG	TCCGCATTGC	0	A	0	0	0	0	0
7282	3430	af	AN0161.1	71.m16051	AO070321000086	0			-128	-45			ATGGAGCTCCAGCACCACTTCTTGACCCTTGAGCTTCACATTCGGTCAGAAAAACAAAGACAAATATTTGTGTCAAGCTTGTGA		ATGGAGCTCCAGCACCACTTCTTGACCCTTGAGCTTCACATTCGGTCAGAAAAACAAAGACAAATATTTGTGTCAAGCTTGTGA		MELQHHFLTLELHIRSEKQRQIFVSSL*		MELQHHFLTLELHIRSEKQRQIFVSSL*		ACCGCAGTTC	AAACCGAGTG	0	A	0	0	0	0	0
7273	3430	an	AN0161.1	71.m16051	AO070321000086	0	-205	-41					ATGAATTGTAGTTCAGAAGCTGCATTGAAACGAGGGTGTCGGACCGGTTCGGACTGGAGCAAATGCAAACATGCAAACATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG	ATGAATTGTAGTTCAGAAGCTGCATTGAAACGAGGGTGTCGGACCGGTTCGGACTGGAGCAAATGCAAACATGCAAACATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG			MNCSSEAALKRGCRTGSDWSKCKHANMIMMFRQALFVAPISVATTTYLYLLSSV*	MNCSSEAALKRGCRTGSDWSKCKHANMIMMFRQALFVAPISVATTTYLYLLSSV*			TCAATTGTAC	ATTATTATAC	0	A	0	0	0	0	0
7274	3430	an	AN0161.1	71.m16051	AO070321000086	0	-143	-48					ATGCAAACATGCAAACATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAG	ATGCAAACATGCAAACATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAG			MQTCKHDHDVPPSTLCSANLGRNHYISVPSI*	MQTCKHDHDVPPSTLCSANLGRNHYISVPSI*			ACTGGAGCAA	TGTTTAGATT	0	A	0	0	0	0	0
7275	3430	an	AN0161.1	71.m16051	AO070321000086	0	-135	-124					ATGCAAACATGA	ATGCAAACATGA			MQT*	MQT*			AAATGCAAAC	TCATGATGTT	0	A	0	0	0	0	0
7276	3430	an	AN0161.1	71.m16051	AO070321000086	0	-127	-41					ATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG	ATGATCATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG			MIMMFRQALFVAPISVATTTYLYLLSSV*	MIMMFRQALFVAPISVATTTYLYLLSSV*			ACATGCAAAC	ATTATTATAC	0	A	0	0	0	0	0
7277	3430	an	AN0161.1	71.m16051	AO070321000086	0	-121	-41					ATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG	ATGATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG			MMFRQALFVAPISVATTTYLYLLSSV*	MMFRQALFVAPISVATTTYLYLLSSV*			AAACATGATC	ATTATTATAC	0	A	0	0	0	0	0
7278	3430	an	AN0161.1	71.m16051	AO070321000086	0	-118	-41					ATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG	ATGTTCCGCCAAGCACTCTTTGTAGCGCCAATCTCGGTCGCAACCACTACATATCTGTACCTTCTATCTAGTGTTTAG			MFRQALFVAPISVATTTYLYLLSSV*	MFRQALFVAPISVATTTYLYLLSSV*			CATGATCATG	ATTATTATAC	0	A	0	0	0	0	0
7283	3430	ao	AN0161.1	71.m16051	AO070321000086	0					-230	-207	ATGGTAGGTTGTACTCCAAAGTAG			ATGGTAGGTTGTACTCCAAAGTAG	MVGCTPK*			MVGCTPK*	AGTCTCCGAA	CGCATTTAGT	0	A	0	0	0	0	0
7284	3430	ao	AN0161.1	71.m16051	AO070321000086	0					-110	-69	ATGATCTTCAAGCTCCCCGAACATCCTGTCGTGGTACGTTAG			ATGATCTTCAAGCTCCCCGAACATCCTGTCGTGGTACGTTAG	MIFKLPEHPVVVR*			MIFKLPEHPVVVR*	AGCTCTGATA	AAGATAGAGC	0	A	0	0	0	0	0
7302	3435	af	AN2229.1	71.m15836	AO070326000151	0			-266	-234			ATGGGCACAGACATTCTGATAGGCCCAATATGA		ATGGGCACAGACATTCTGATAGGCCCAATATGA		MGTDILIGPI*		MGTDILIGPI*		CGCTTTAAAA	CGAGATCTCC	0	E	FG05658.1	MG01469.1	0	0	0
7303	3435	af	AN2229.1	71.m15836	AO070326000151	0			-237	-172			ATGACGAGATCTCCCTGCGGAGTCATAGTGGAACCCCCCCGATGTTCGGAGTTAAAGGATCAATAG		ATGACGAGATCTCCCTGCGGAGTCATAGTGGAACCCCCCCGATGTTCGGAGTTAAAGGATCAATAG		MTRSPCGVIVEPPRCSELKDQ*		MTRSPCGVIVEPPRCSELKDQ*		TAGGCCCAAT	GTACTCCGTA	0	E	FG05658.1	MG01469.1	0	0	0
7304	3435	af	AN2229.1	71.m15836	AO070326000151	0			-196	-86			ATGTTCGGAGTTAAAGGATCAATAGGTACTCCGTACCTCTTTGCCTCTCTAATTTGGATCTTCTTTTCTCGACGTCTTCTTTTCTCACAGATCTATCAGTTGCGAGGATAA		ATGTTCGGAGTTAAAGGATCAATAGGTACTCCGTACCTCTTTGCCTCTCTAATTTGGATCTTCTTTTCTCGACGTCTTCTTTTCTCACAGATCTATCAGTTGCGAGGATAA		MFGVKGSIGTPYLFASLIWIFFSRRLLFSQIYQLRG*		MFGVKGSIGTPYLFASLIWIFFSRRLLFSQIYQLRG*		AACCCCCCCG	GTTTCCAATC	0	E	FG05658.1	MG01469.1	0	0	0
7305	3435	ao	AN2229.1	71.m15836	AO070326000151	0					-241	-167	ATGGAGCCGCCGAAGTCGGGGTCAAGGAATTTCCAGTGCTCCTATTGGTTTCGTATGACGAATACGCATCTCTAG			ATGGAGCCGCCGAAGTCGGGGTCAAGGAATTTCCAGTGCTCCTATTGGTTTCGTATGACGAATACGCATCTCTAG	MEPPKSGSRNFQCSYWFRMTNTHL*			MEPPKSGSRNFQCSYWFRMTNTHL*	CGGAAAAACA	TGGGTCAGGC	0	E	FG05658.1	MG01469.1	0	0	0
7306	3435	ao	AN2229.1	71.m15836	AO070326000151	0					-187	-167	ATGACGAATACGCATCTCTAG			ATGACGAATACGCATCTCTAG	MTNTHL*			MTNTHL*	TTGGTTTCGT	TGGGTCAGGC	0	E	FG05658.1	MG01469.1	0	0	0
7310	3437	af	AN5579.1	58.m07506	AO070328000025	0			-234	-205			ATGGCTAAATCTATCGTTACTTGCGAGTGA		ATGGCTAAATCTATCGTTACTTGCGAGTGA		MAKSIVTCE*		MAKSIVTCE*		AACCACCTGG	ATCTAGTGCT	0	U	0	MG06537.1	0	0	0
7311	3437	af	AN5579.1	58.m07506	AO070328000025	0			-185	-129			ATGCCATTTCCTGCGAATCTATTCCTCAAGCATTCTATATTTTTGCCATCTATTAA		ATGCCATTTCCTGCGAATCTATTCCTCAAGCATTCTATATTTTTGCCATCTATTAA		MPFPANLFLKHSIFFAIY*		MPFPANLFLKHSIFFAIY*		TCGCGCAGGT	CGCGTCTAGA	0	U	0	MG06537.1	0	0	0
7307	3437	an	AN5579.1	58.m07506	AO070328000025	0	-245	-213					ATGCTTCCTTTAATATCTTGCGAGTGCAATTAG	ATGCTTCCTTTAATATCTTGCGAGTGCAATTAG			MLPLISCECN*	MLPLISCECN*			AATCTTGTGG	CCCTCGCCCA	0	U	0	MG06537.1	0	0	0

7308	3437	an	AN5579.1	58.m07506	AO070328000025	0	-203	-81					ATGTGCACCAGGTATTCCAACTTCACTGTCTACTGTTGCGCAACAGCCCCTCTTCGCTGGTCTACACCTTACGCGGCACTTCGCCCAACGGTACTGACAATTGTTATGCACATAGCCAGATAG	ATGTGCACCAGGTATTCCAACTTCACTGTCTACTGTTGCGCAACAGCCCCTCTTCGCTGGTCTACACCTTACGCGGCACTTCGCCCAACGGTACTGACAATTGTTATGCACATAGCCAGATAG			MCTRYSNFTVYCCATAPLRWSTPYAALRPTVLTIVMHIAR*	MCTRYSNFTVYCCATAPLRWSTPYAALRPTVLTIVMHIAR*			GCCCTCGCCC	GAGTTTCTCT	0	U	0	MG06537.1	0	0	0
7309	3437	an	AN5579.1	58.m07506	AO070328000025	0	-98	-81					ATGCACATAGCCAGATAG	ATGCACATAGCCAGATAG			MHIAR*	MHIAR*			GACAATTGTT	GAGTTTCTCT	0	U	0	MG06537.1	0	0	0
7312	3437	ao	AN5579.1	58.m07506	AO070328000025	0					-228	-199	ATGGCTCTGATTCATTCACTCTGCGAGTGA			ATGGCTCTGATTCATTCACTCTGCGAGTGA	MALIHSLCE*			MALIHSLCE*	AACCTCCTGG	ACTTAGAGCT	0	U	0	MG06537.1	0	0	0
7316	3440	af	AN2918.1	59.m09095	AO070329000153	0			-243	-154			ATGGAGTGTGAGGTGAAGCTTGATTGGGATAGTGATGTGATCGAGCTCTCAAGCTTGAGGTGCTGTCAGCGAACGGGTTCCAGCTGCTGA		ATGGAGTGTGAGGTGAAGCTTGATTGGGATAGTGATGTGATCGAGCTCTCAAGCTTGAGGTGCTGTCAGCGAACGGGTTCCAGCTGCTGA		MECEVKLDWDSDVIELSSLRCCQRTGSSC*		MECEVKLDWDSDVIELSSLRCCQRTGSSC*		GTCTGACGAG	CGCTAGTGGC	0	O	0	0	0	0	0
7313	3440	an	AN2918.1	59.m09095	AO070329000153	0	-246	-217					ATGAATAAGGTGCAAGTTGGGGTAGGATGA	ATGAATAAGGTGCAAGTTGGGGTAGGATGA			MNKVQVGVG*	MNKVQVGVG*			ATGAAATAAG	TGTCGAGAGC	0	O	0	0	0	0	0
7314	3440	an	AN2918.1	59.m09095	AO070329000153	0	-220	-170					ATGATGTCGAGAGCTGGCTGTTCTGACTTCAGGTCCAGCTTGAGCTGTTGA	ATGATGTCGAGAGCTGGCTGTTCTGACTTCAGGTCCAGCTTGAGCTGTTGA			MMSRAGCSDFRSSLSC*	MMSRAGCSDFRSSLSC*			TTGGGGTAGG	CGCTAGTGGC	0	O	0	0	0	0	0
7315	3440	an	AN2918.1	59.m09095	AO070329000153	0	-217	-170					ATGTCGAGAGCTGGCTGTTCTGACTTCAGGTCCAGCTTGAGCTGTTGA	ATGTCGAGAGCTGGCTGTTCTGACTTCAGGTCCAGCTTGAGCTGTTGA			MSRAGCSDFRSSLSC*	MSRAGCSDFRSSLSC*			GGGTAGGATG	CGCTAGTGGC	0	O	0	0	0	0	0
7317	3440	ao	AN2918.1	59.m09095	AO070329000153	0					-242	-228	ATGGATGGTAGATGA			ATGGATGGTAGATGA	MDGR*			MDGR*	AAAAAGGACG	GAGCTTGATC	0	O	0	0	0	0	0
7318	3440	ao	AN2918.1	59.m09095	AO070329000153	0					-238	-140	ATGGTAGATGAGAGCTTGATCGGAAGGAGGAGAGAGAGTGAAGTAATCAGGTGTGAGCTCCAGGTTGCTGCGGCGGTCGGTTCGAGCTGTTTGCGCTAG			ATGGTAGATGAGAGCTTGATCGGAAGGAGGAGAGAGAGTGAAGTAATCAGGTGTGAGCTCCAGGTTGCTGCGGCGGTCGGTTCGAGCTGTTTGCGCTAG	MVDESLIGRRRESEVIRCELQVAAAVGSSCLR*			MVDESLIGRRRESEVIRCELQVAAAVGSSCLR*	AGGACGATGG	TGGTGCCAAG	0	O	0	0	0	0	0
7319	3440	ao	AN2918.1	59.m09095	AO070329000153	0					-231	-220	ATGAGAGCTTGA			ATGAGAGCTTGA	MRA*			MRA*	TGGATGGTAG	TCGGAAGGAG	0	O	0	0	0	0	0
7323	3441	af	AN4706.1	71.m15694	AO070329000170	0			-260	-117			ATGCAGATGCGCAGGGTACTTTGGGTTCAAGCTGTGTTCACTCATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGA		ATGCAGATGCGCAGGGTACTTTGGGTTCAAGCTGTGTTCACTCATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGA		MQMRRVLWVQAVFTHALPSLHLHLFVPKAHWISFVLSLYYALVFPFH*		MQMRRVLWVQAVFTHALPSLHLHLFVPKAHWISFVLSLYYALVFPFH*		CCCCATCACA	AGATTAATGA	0	Z	0	0	0	0	0
7324	3441	af	AN4706.1	71.m15694	AO070329000170	0			-254	-117			ATGCGCAGGGTACTTTGGGTTCAAGCTGTGTTCACTCATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGA		ATGCGCAGGGTACTTTGGGTTCAAGCTGTGTTCACTCATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGA		MRRVLWVQAVFTHALPSLHLHLFVPKAHWISFVLSLYYALVFPFH*		MRRVLWVQAVFTHALPSLHLHLFVPKAHWISFVLSLYYALVFPFH*		CACAATGCAG	AGATTAATGA	0	Z	0	0	0	0	0
7325	3441	af	AN4706.1	71.m15694	AO070329000170	0			-217	-110			ATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGAAGATTAA		ATGCATTACCGAGTCTTCATCTGCACCTCTTCGTTCCCAAAGCACACTGGATCTCTTTTGTCTTGTCTTTATATTATGCTTTGGTTTTTCCTTTTCATTGAAGATTAA		MHYRVFICTSSFPKHTGSLLSCLYIMLWFFLFIED*		MHYRVFICTSSFPKHTGSLLSCLYIMLWFFLFIED*		GTGTTCACTC	TGACCTTGTT	0	Z	0	0	0	0	0
7326	3441	af	AN4706.1	71.m15694	AO070329000170	0			-142	-110			ATGCTTTGGTTTTTCCTTTTCATTGAAGATTAA		ATGCTTTGGTTTTTCCTTTTCATTGAAGATTAA		MLWFFLFIED*		MLWFFLFIED*		TCTTTATATT	TGACCTTGTT	0	Z	0	0	0	0	0
7327	3441	af	AN4706.1	71.m15694	AO070329000170	0			-110	-24			ATGACCTTGTTTGAAACAACTCCTAATGCCCGAAGCCTTTTTATGACCTTGATTGCATTGCCCTTGTCCCAATCTGTTTACAAATGA		ATGACCTTGTTTGAAACAACTCCTAATGCCCGAAGCCTTTTTATGACCTTGATTGCATTGCCCTTGTCCCAATCTGTTTACAAATGA		MTLFETTPNARSLFMTLIALPLSQSVYK*		MTLFETTPNARSLFMTLIALPLSQSVYK*		TTGAAGATTA	TGCTCCATTG	0	Z	0	0	0	0	0
7328	3441	af	AN4706.1	71.m15694	AO070329000170	0			-85	-65			ATGCCCGAAGCCTTTTTATGA		ATGCCCGAAGCCTTTTTATGA		MPEAFL*		MPEAFL*		ACAACTCCTA	CCTTGATTGC	0	Z	0	0	0	0	0
7329	3441	af	AN4706.1	71.m15694	AO070329000170	0			-68	-24			ATGACCTTGATTGCATTGCCCTTGTCCCAATCTGTTTACAAATGA		ATGACCTTGATTGCATTGCCCTTGTCCCAATCTGTTTACAAATGA		MTLIALPLSQSVYK*		MTLIALPLSQSVYK*		AAGCCTTTTT	TGCTCCATTG	0	Z	0	0	0	0	0
7320	3441	an	AN4706.1	71.m15694	AO070329000170	0	-124	-113					ATGCTGCGCTGA	ATGCTGCGCTGA			MLR*	MLR*			CGTGATTTGT	GCGGATCTTA	0	Z	0	0	0	0	0
7332	3441	ao	AN4706.1	71.m15694	AO070329000170	0					-253	-164	ATGGAGCAAGTGGTCAGTGACCTAGTCCTGTCTGTATCCAGGGACCACTTGCGGCTTTGCTGCAGCTTGCTTATTACCTCTTTACCTTAA			ATGGAGCAAGTGGTCAGTGACCTAGTCCTGTCTGTATCCAGGGACCACTTGCGGCTTTGCTGCAGCTTGCTTATTACCTCTTTACCTTAA	MEQVVSDLVLSVSRDHLRLCCSLLITSLP*			MEQVVSDLVLSVSRDHLRLCCSLLITSLP*	CCAATCGTGC	GGTTCTGTCA	0	Z	0	0	0	0	0
7335	3442	af	AN1208.1	70.m15013	AO070331000214	0			-284	-249			ATGGCAAATCGAAGGCCACTGCTGTCAAATTGCTAG		ATGGCAAATCGAAGGCCACTGCTGTCAAATTGCTAG		MANRRPLLSNC*		MANRRPLLSNC*		TCTCCGCCGA	CCTGACCATC	0	A	FG01337.1	MG05616.1	NCU02966.1	0	0
7338	3444	ao	AN5442.1	69.m15492	AO070333000105	0					-158	-18	ATGTTACAATCCCTACCATATCTCCTGTCTACCCCCATTAACAGCGTGATACTGATAAGCTACTTGCCTAGACCGCAAGGTACCCTCTTATCGTCATCTCGTCCTGCCATCATAAGCACCCCCCTTGTTACATCTCATTTAG			ATGTTACAATCCCTACCATATCTCCTGTCTACCCCCATTAACAGCGTGATACTGATAAGCTACTTGCCTAGACCGCAAGGTACCCTCTTATCGTCATCTCGTCCTGCCATCATAAGCACCCCCCTTGTTACATCTCATTTAG	MLQSLPYLLSTPINSVILISYLPRPQGTLLSSSRPAIISTPLLHLI*			MLQSLPYLLSTPINSVILISYLPRPQGTLLSSSRPAIISTPLLHLI*	TTTTTCCTGT	AGTCGAAGTG	0	OE	0	0	NCU00477.1	0	0
7339	3445	an	AN5447.1	69.m15487	AO070333000115	0	-175	-155					ATGATGCGGCACCAGGGGTAG	ATGATGCGGCACCAGGGGTAG			MMRHQG*	MMRHQG*			CGTCTAACTT	CGTGGCGGTT	0	E	0	MG02378.1	0	YMR250W	YMR250W
7340	3445	an	AN5447.1	69.m15487	AO070333000115	0	-172	-155					ATGCGGCACCAGGGGTAG	ATGCGGCACCAGGGGTAG			MRHQG*	MRHQG*			CTAACTTATG	CGTGGCGGTT	0	E	0	MG02378.1	0	YMR250W	YMR250W
7342	3447	af	AN0304.1	54.m06978	AO070334000034	0			-262	-236			ATGTCGCGAAAATCTTTTTTTCTTTGA		ATGTCGCGAAAATCTTTTTTTCTTTGA		MSRKSFFL*		MSRKSFFL*		CTCACATAGA	TATCTCTTTG	0	P	0	0	0	0	0
7341	3447	an	AN0304.1	54.m06978	AO070334000034	0	-118	-104					ATGAACATCTCGTAG	ATGAACATCTCGTAG			MNIS*	MNIS*			TTATCGAGAG	CTTCACAAGT	0	P	0	0	0	0	0
7344	3447	ao	AN0304.1	54.m06978	AO070334000034	0					-261	-211	ATGACGCGGCTTTCTTCTTTCACCTCCGACCTCCTTGGAAATCTCACTTAG			ATGACGCGGCTTTCTTCTTTCACCTCCGACCTCCTTGGAAATCTCACTTAG	MTRLSSFTSDLLGNLT*			MTRLSSFTSDLLGNLT*	ACTCAGGTTC	AGGATCTTCA	0	P	0	0	0	0	0
7346	3450	af	AN2973.1	59.m09039	AO070337000148	0			-131	-24			ATGGATTCTGGAGAAGCAGGCGAGCTCTCTTTTGGTGCTCCGTTGGGTTTTGCTCCTCTTTCATTGCTGCCTGATTTGTCCGTCTTTAATTCGATCTTTATTGCTTAA		ATGGATTCTGGAGAAGCAGGCGAGCTCTCTTTTGGTGCTCCGTTGGGTTTTGCTCCTCTTTCATTGCTGCCTGATTTGTCCGTCTTTAATTCGATCTTTATTGCTTAA		MDSGEAGELSFGAPLGFAPLSLLPDLSVFNSIFIA*		MDSGEAGELSFGAPLGFAPLSLLPDLSVFNSIFIA*		CAGTGATGGA	AAAGCTTGTT	0	B	0	0	0	0	0
7345	3450	an	AN2973.1	59.m09039	AO070337000148	0	-88	-29					ATGCTCTCTTTCAAAACGAACTCTAGGAGTGGAACAGGTAATAAGTACAGATTCACTTAA	ATGCTCTCTTTCAAAACGAACTCTAGGAGTGGAACAGGTAATAAGTACAGATTCACTTAA			MLSFKTNSRSGTGNKYRFT*	MLSFKTNSRSGTGNKYRFT*			AACGAGCTTG	TTTCACTTGC	0	B	0	0	0	0	0
7347	3450	ao	AN2973.1	59.m09039	AO070337000148	0					-218	-159	ATGAGACTGTCGCCACTGTTCCGCTGCCAAACTTTCAACAACCCGCAACCCAGTCGCTGA			ATGAGACTGTCGCCACTGTTCCGCTGCCAAACTTTCAACAACCCGCAACCCAGTCGCTGA	MRLSPLFRCQTFNNPQPSR*			MRLSPLFRCQTFNNPQPSR*	GAGGAAGGAT	CTCCGGCGAC	0	B	0	0	0	0	0
7352	3451	af	AN2905.1	59.m08756	AO070338000100	0			-275	-183			ATGACTTTTGTTTCTGTGGGGTCGTTGCTACTCAAATACCCGTGTCGCAGATTCAACAGCGCGACTCAACCACAACCCCCGACGCGTCTATAG		ATGACTTTTGTTTCTGTGGGGTCGTTGCTACTCAAATACCCGTGTCGCAGATTCAACAGCGCGACTCAACCACAACCCCCGACGCGTCTATAG		MTFVSVGSLLLKYPCRRFNSATQPQPPTRL*		MTFVSVGSLLLKYPCRRFNSATQPQPPTRL*		AATGTCAGCG	CCCCCAACCT	0	K	0	0	0	0	0
7353	3451	af	AN2905.1	59.m08756	AO070338000100	0			-159	-145			ATGACTTCCGTCTAG		ATGACTTCCGTCTAG		MTSV*		MTSV*		CCTTTCTGTG	TTGCCCCATC	0	K	0	0	0	0	0
7354	3451	af	AN2905.1	59.m08756	AO070338000100	0			-80	-12			ATGATGACCAAGCCTGTTCTGTGTGTGTCACATTCACTGACGATCATCGCCTTGCAGATGGGTTGGTAA		ATGATGACCAAGCCTGTTCTGTGTGTGTCACATTCACTGACGATCATCGCCTTGCAGATGGGTTGGTAA		MMTKPVLCVSHSLTIIALQMGW*		MMTKPVLCVSHSLTIIALQMGW*		AGTTGCTTCA	GACCACACGA	0	K	0	0	0	0	0
7355	3451	af	AN2905.1	59.m08756	AO070338000100	0			-77	-12			ATGACCAAGCCTGTTCTGTGTGTGTCACATTCACTGACGATCATCGCCTTGCAGATGGGTTGGTAA		ATGACCAAGCCTGTTCTGTGTGTGTCACATTCACTGACGATCATCGCCTTGCAGATGGGTTGGTAA		MTKPVLCVSHSLTIIALQMGW*		MTKPVLCVSHSLTIIALQMGW*		TGCTTCAATG	GACCACACGA	0	K	0	0	0	0	0
7349	3451	an	AN2905.1	59.m08756	AO070338000100	0	-80	-45					ATGATGGATATGTTGCATTTGTGTCATCTTCTCTGA	ATGATGGATATGTTGCATTTGTGTCATCTTCTCTGA			MMDMLHLCHLL*	MMDMLHLCHLL*			CGCGCGTTGA	CAGCTTCTTT	0	K	0	0	0	0	0
7350	3451	an	AN2905.1	59.m08756	AO070338000100	0	-77	-45					ATGGATATGTTGCATTTGTGTCATCTTCTCTGA	ATGGATATGTTGCATTTGTGTCATCTTCTCTGA			MDMLHLCHLL*	MDMLHLCHLL*			GCGTTGAATG	CAGCTTCTTT	0	K	0	0	0	0	0
7351	3451	an	AN2905.1	59.m08756	AO070338000100	0	-71	-45					ATGTTGCATTTGTGTCATCTTCTCTGA	ATGTTGCATTTGTGTCATCTTCTCTGA			MLHLCHLL*	MLHLCHLL*			AATGATGGAT	CAGCTTCTTT	0	K	0	0	0	0	0
7356	3451	ao	AN2905.1	59.m08756	AO070338000100	0					-123	-76	ATGATGGCTTTGATATCGCATCTATTGTTGATACTTATTGATGATTGA			ATGATGGCTTTGATATCGCATCTATTGTTGATACTTATTGATGATTGA	MMALISHLLLILIDD*			MMALISHLLLILIDD*	ATCTGGAACC	AATCAGTCTC	0	K	0	0	0	0	0
7357	3451	ao	AN2905.1	59.m08756	AO070338000100	0					-120	-76	ATGGCTTTGATATCGCATCTATTGTTGATACTTATTGATGATTGA			ATGGCTTTGATATCGCATCTATTGTTGATACTTATTGATGATTGA	MALISHLLLILIDD*			MALISHLLLILIDD*	TGGAACCATG	AATCAGTCTC	0	K	0	0	0	0	0
7358	3451	ao	AN2905.1	59.m08756	AO070338000100	0					-83	-48	ATGATTGAAATCAGTCTCTATTCTTATGTCTCATAA			ATGATTGAAATCAGTCTCTATTCTTATGTCTCATAA	MIEISLYSYVS*			MIEISLYSYVS*	ATACTTATTG	AGTCTGACAG	0	K	0	0	0	0	0
7360	3452	an	AN1558.1	55.m03276	AO070339000295	0	-123	-64					ATGAACATCTTGTTATCTGCGTTCATTCCTGTTTCTTGCGGTTTCTTTCATCTGCATTAA	ATGAACATCTTGTTATCTGCGTTCATTCCTGTTTCTTGCGGTTTCTTTCATCTGCATTAA			MNILLSAFIPVSCGFFHLH*	MNILLSAFIPVSCGFFHLH*			CCCGAGTGGA	ATTGATAGGC	0	Z	0	0	0	YMR109W	0
7361	3452	ao	AN1558.1	55.m03276	AO070339000295	0					-134	-93	ATGAGCGACCTTTCTTTTCCGCTGGTTCCCCTCAGTTCTTAA			ATGAGCGACCTTTCTTTTCCGCTGGTTCCCCTCAGTTCTTAA	MSDLSFPLVPLSS*			MSDLSFPLVPLSS*	TACACTTGGA	ACGCTTACTT	0	Z	0	0	0	YMR109W	0
7362	3453	af	AN6149.1	72.m19016	AO070340000053	0			-242	-183			ATGTTGACATTTTGGAGCGGCGGGTGTCTCCATAGCAACTGTTGCGGCCTCGCCGCCTGA		ATGTTGACATTTTGGAGCGGCGGGTGTCTCCATAGCAACTGTTGCGGCCTCGCCGCCTGA		MLTFWSGGCLHSNCCGLAA*		MLTFWSGGCLHSNCCGLAA*		AGGGCAGCAG	GAGCCTTATG	0	A	0	0	0	0	0
7363	3453	af	AN6149.1	72.m19016	AO070340000053	0			-175	-62			ATGGCCTTGTTTCCAAGGGTTGGCCTCCGATCTTCCTATGCCTATCTGGGGTTAGCGTGGTTTCGGGGTCGGCCAAGCCGCAAATTTCCAGGAAAGTTTCAGTCCACACAGTAG		ATGGCCTTGTTTCCAAGGGTTGGCCTCCGATCTTCCTATGCCTATCTGGGGTTAGCGTGGTTTCGGGGTCGGCCAAGCCGCAAATTTCCAGGAAAGTTTCAGTCCACACAGTAG		MALFPRVGLRSSYAYLGLAWFRGRPSRKFPGKFQSTQ*		MALFPRVGLRSSYAYLGLAWFRGRPSRKFPGKFQSTQ*		TGAGAGCCTT	ATAGCAATAT	0	A	0	0	0	0	0
7364	3453	af	AN6149.1	72.m19016	AO070340000053	0			-138	-121			ATGCCTATCTGGGGTTAG		ATGCCTATCTGGGGTTAG		MPIWG*		MPIWG*		CGATCTTCCT	CGTGGTTTCG	0	A	0	0	0	0	0
7365	3453	ao	AN6149.1	72.m19016	AO070340000053	0					-262	-203	ATGTTGACATTTGCTGGCGGGAGTCTCCATAGCAACACTTGTTTCGGCCTCGCCGCCTGA			ATGTTGACATTTGCTGGCGGGAGTCTCCATAGCAACACTTGTTTCGGCCTCGCCGCCTGA	MLTFAGGSLHSNTCFGLAA*			MLTFAGGSLHSNTCFGLAA*	TCGAGGTTCC	GCGCATTGGT	0	A	0	0	0	0	0
7367	3454	af	AN6107.1	72.m19051	AO070340000100	0			-164	-84			ATGTTTTTCAGTAAGTCGGATATGAGCAGATCCGGTTCCCTCAAGACGAGTCCTCCTTTGGTGTTTGTTTATTGTGCCTGA		ATGTTTTTCAGTAAGTCGGATATGAGCAGATCCGGTTCCCTCAAGACGAGTCCTCCTTTGGTGTTTGTTTATTGTGCCTGA		MFFSKSDMSRSGSLKTSPPLVFVYCA*		MFFSKSDMSRSGSLKTSPPLVFVYCA*		AGAGAGGGAT	GGAATGGTTA	0	P	0	0	0	0	0
7368	3454	af	AN6107.1	72.m19051	AO070340000100	0			-143	-84			ATGAGCAGATCCGGTTCCCTCAAGACGAGTCCTCCTTTGGTGTTTGTTTATTGTGCCTGA		ATGAGCAGATCCGGTTCCCTCAAGACGAGTCCTCCTTTGGTGTTTGTTTATTGTGCCTGA		MSRSGSLKTSPPLVFVYCA*		MSRSGSLKTSPPLVFVYCA*		TAAGTCGGAT	GGAATGGTTA	0	P	0	0	0	0	0
7369	3454	af	AN6107.1	72.m19051	AO070340000100	0			-80	-66			ATGGTTATAGTCTGA		ATGGTTATAGTCTGA		MVIV*		MVIV*		TGCCTGAGGA	CAAGGGTCTC	0	P	0	0	0	0	0
7366	3454	an	AN6107.1	72.m19051	AO070340000100	0	-94	-77					ATGTTGGTCGGTGAGTAA	ATGTTGGTCGGTGAGTAA			MLVGE*	MLVGE*			CAAGGGGATC	TCATAGCAGG	0	P	0	0	0	0	0
7370	3454	ao	AN6107.1	72.m19051	AO070340000100	0					-108	-52	ATGATATGTTTTGGTATACTCCGTTACTCTGGGTGCCTTGCGGGTGGCTTGTGTTAA			ATGATATGTTTTGGTATACTCCGTTACTCTGGGTGCCTTGCGGGTGGCTTGTGTTAA	MICFGILRYSGCLAGGLC*			MICFGILRYSGCLAGGLC*	TCTATAGCGA	CCAGGGAATC	0	P	0	0	0	0	0
7371	3454	ao	AN6107.1	72.m19051	AO070340000100	0					-103	-20	ATGTTTTGGTATACTCCGTTACTCTGGGTGCCTTGCGGGTGGCTTGTGTTAACCAGGGAATCAGATCACCACGTCGAACCGTGA			ATGTTTTGGTATACTCCGTTACTCTGGGTGCCTTGCGGGTGGCTTGTGTTAACCAGGGAATCAGATCACCACGTCGAACCGTGA	MFWYTPLLWVPCGWLVLTRESDHHVEP*			MFWYTPLLWVPCGWLVLTRESDHHVEP*	AGCGAATGAT	AGTACTTACC	0	P	0	0	0	0	0
7373	3456	af	AN1922.1	69.m14940	AO070341000114	0			-205	-167			ATGGAGGACAACAGTTGCCTCGGAGCGGAACTTCTTTGA		ATGGAGGACAACAGTTGCCTCGGAGCGGAACTTCTTTGA		MEDNSCLGAELL*		MEDNSCLGAELL*		TGGACCAACG	TCCAGATGAG	0	O	0	0	0	0	0
7374	3456	af	AN1922.1	69.m14940	AO070341000114	0			-139	-23			ATGTATCTGGTGCGACCAGATTCCCGTCAACAGACCTACCTACACAAGCATCGTTACTACTCACTAAGACCTATTTCCGCCATTCTCTTCCTCGGTCTCATCCATCTCTTATCATAG		ATGTATCTGGTGCGACCAGATTCCCGTCAACAGACCTACCTACACAAGCATCGTTACTACTCACTAAGACCTATTTCCGCCATTCTCTTCCTCGGTCTCATCCATCTCTTATCATAG		MYLVRPDSRQQTYLHKHRYYSLRPISAILFLGLIHLLS*		MYLVRPDSRQQTYLHKHRYYSLRPISAILFLGLIHLLS*		ATGTTAGGTG	TTTCCTTCAT	0	O	0	0	0	0	0
7372	3456	an	AN1922.1	69.m14940	AO070341000114	0	-113	-96					ATGCACGCGGCTTCCTGA	ATGCACGCGGCTTCCTGA			MHAAS*	MHAAS*			ACATCATCTC	CCCCATTCGG	0	O	0	0	0	0	0

7375	3456	ao	AN1922.1	69.m14940	AO070341000114	0					-214	-170	ATGGTGGTGACGGCTTCGGGACTGGAAAAACATTCCGCCAGCTGA			ATGGTGGTGACGGCTTCGGGACTGGAAAAACATTCCGCCAGCTGA	MVVTASGLEKHSAS*			MVVTASGLEKHSAS*	GATAACGGTG	GCTCAGGTCA	0	O	0	0	0	0	0
7376	3456	ao	AN1922.1	69.m14940	AO070341000114	0					-138	-106	ATGTATCTGCCTCTTCCGGTATCTCATTCATAA			ATGTATCTGCCTCTTCCGGTATCTCATTCATAA	MYLPLPVSHS*			MYLPLPVSHS*	TGGCTATGTG	GCAGTCTGGA	0	O	0	0	0	0	0
7378	3461	af	AN4187.1	54.m06748	AO070342000108	0			-107	-78			ATGGAACTTTTTAATACCCTGCGCGCATAA		ATGGAACTTTTTAATACCCTGCGCGCATAA		MELFNTLRA*		MELFNTLRA*		TTGTTTTCTT	TCTTTCATGA	0	K	0	0	0	YPL082C	0
7379	3461	af	AN4187.1	54.m06748	AO070342000108	0			-71	-48			ATGATTACAGTTTCCTCTCCCTGA		ATGATTACAGTTTCCTCTCCCTGA		MITVSSP*		MITVSSP*		ATAATCTTTC	TTTAATTTCC	0	K	0	0	0	YPL082C	0
7377	3461	conserved	AN4187.1	54.m06748	AO070342000108	0	-222	-202	-240	-220	-269	-249	ATGGCTGyGrCGyGsrwGTrA	ATGGCTGCGACGTGCAAGTGA	ATGGCTGTGGCGCGGGTGTAA	ATGGCTGTGACGTGGGTGTAA	MAatck*	MAATCK*	MAVARV*	MAVTWV*	hhybmbbyhv	CsrhyysGTr	0	K	0	0	0	YPL082C	0
7384	3464	af	AN3586.1	58.m07385	AO070342000163	0			-131	-48			ATGCTAATAATACCACATAGGGGAAGGTGTTTGTTGCGTTTGCATCTCCGTCGACCGGCTCGGCGTATCGCCAAAACGAGGTGA		ATGCTAATAATACCACATAGGGGAAGGTGTTTGTTGCGTTTGCATCTCCGTCGACCGGCTCGGCGTATCGCCAAAACGAGGTGA		MLIIPHRGRCLLRLHLRRPARRIAKTR*		MLIIPHRGRCLLRLHLRRPARRIAKTR*		TCATCGTCTT	TCTGATGATC	0	HC	0	0	0	0	0
7380	3464	an	AN3586.1	58.m07385	AO070342000163	0	-192	-136					ATGGTAGCTCAGATGCTAAGAATAGCGATCCATACAGGCCGGTTGGGACACGAGTAG	ATGGTAGCTCAGATGCTAAGAATAGCGATCCATACAGGCCGGTTGGGACACGAGTAG			MVAQMLRIAIHTGRLGHE*	MVAQMLRIAIHTGRLGHE*			GAGCAGGCTG	TGTAGCGTGT	0	HC	0	0	0	0	0
7381	3464	an	AN3586.1	58.m07385	AO070342000163	0	-180	-136					ATGCTAAGAATAGCGATCCATACAGGCCGGTTGGGACACGAGTAG	ATGCTAAGAATAGCGATCCATACAGGCCGGTTGGGACACGAGTAG			MLRIAIHTGRLGHE*	MLRIAIHTGRLGHE*			GGTAGCTCAG	TGTAGCGTGT	0	HC	0	0	0	0	0
7382	3464	an	AN3586.1	58.m07385	AO070342000163	0	-100	-53					ATGTGTGTTTGTCCTGTTTGCAGTTATCTCATGATCGCCCGAGCATGA	ATGTGTGTTTGTCCTGTTTGCAGTTATCTCATGATCGCCCGAGCATGA			MCVCPVCSYLMIARA*	MCVCPVCSYLMIARA*			GCGTCGAGTA	AATACTGTAT	0	HC	0	0	0	0	0
7383	3464	an	AN3586.1	58.m07385	AO070342000163	0	-70	-53					ATGATCGCCCGAGCATGA	ATGATCGCCCGAGCATGA			MIARA*	MIARA*			CAGTTATCTC	AATACTGTAT	0	HC	0	0	0	0	0
7386	3464	ao	AN3586.1	58.m07385	AO070342000163	0					-157	-20	ATGGTTTTCCACTCAGTGGATGGTAATCCGCGCATTAAAAATGTGCCATCAGTAGAAAGATTTCTGTTTGCGTTGTTTGCACATCATCACCCCATCGCCGACTGCTTTCTCCGAAGATTCAACTTCATTGTTTCCTGA			ATGGTTTTCCACTCAGTGGATGGTAATCCGCGCATTAAAAATGTGCCATCAGTAGAAAGATTTCTGTTTGCGTTGTTTGCACATCATCACCCCATCGCCGACTGCTTTCTCCGAAGATTCAACTTCATTGTTTCCTGA	MVFHSVDGNPRIKNVPSVERFLFALFAHHHPIADCFLRRFNFIVS*			MVFHSVDGNPRIKNVPSVERFLFALFAHHHPIADCFLRRFNFIVS*	GACATTATTA	ATCCAGACGC	0	HC	0	0	0	0	0
7387	3464	ao	AN3586.1	58.m07385	AO070342000163	0					-138	-103	ATGGTAATCCGCGCATTAAAAATGTGCCATCAGTAG			ATGGTAATCCGCGCATTAAAAATGTGCCATCAGTAG	MVIRALKMCHQ*			MVIRALKMCHQ*	CACTCAGTGG	AAAGATTTCT	0	HC	0	0	0	0	0
7388	3464	ao	AN3586.1	58.m07385	AO070342000163	0					-117	-103	ATGTGCCATCAGTAG			ATGTGCCATCAGTAG	MCHQ*			MCHQ*	CGCATTAAAA	AAAGATTTCT	0	HC	0	0	0	0	0
7389	3465	ao	AN2135.1	72.m19705	AO070343000180	0					-96	-85	ATGACCTCTTGA			ATGACCTCTTGA	MTS*			MTS*	TTTCAAGTCA	ACTATCGACC	0	K	0	0	0	0	0
7392	3466	af	AN2138.1	72.m20005	AO070343000183	0			-182	-126			ATGCGGAGAACGGGAAGGGTTGCGAGTCCCCGCAAGCTCCTGATAAAGCGGTTCTAG		ATGCGGAGAACGGGAAGGGTTGCGAGTCCCCGCAAGCTCCTGATAAAGCGGTTCTAG		MRRTGRVASPRKLLIKRF*		MRRTGRVASPRKLLIKRF*		CATTAGCAAG	TGCGGGACAG	0	A	0	0	0	0	0
7390	3466	an	AN2138.1	72.m20005	AO070343000183	0	-244	-101					ATGTATCCAGTCGAGACATTCGTCATGCTGGTTCATCGTTGGTACGTGTGCAGAACCTCGAAAACACCATCAGGCGGAGGCAATCTTGCTCCCCCGCAGCCGGCAGGGGAACGCTGCCTGAGGCGGGAACCCAAATCGGAATAG	ATGTATCCAGTCGAGACATTCGTCATGCTGGTTCATCGTTGGTACGTGTGCAGAACCTCGAAAACACCATCAGGCGGAGGCAATCTTGCTCCCCCGCAGCCGGCAGGGGAACGCTGCCTGAGGCGGGAACCCAAATCGGAATAG			MYPVETFVMLVHRWYVCRTSKTPSGGGNLAPPQPAGERCLRREPKSE*	MYPVETFVMLVHRWYVCRTSKTPSGGGNLAPPQPAGERCLRREPKSE*			TCGCGGAAAT	GAAATTATCT	0	A	0	0	0	0	0
7391	3466	an	AN2138.1	72.m20005	AO070343000183	0	-220	-101					ATGCTGGTTCATCGTTGGTACGTGTGCAGAACCTCGAAAACACCATCAGGCGGAGGCAATCTTGCTCCCCCGCAGCCGGCAGGGGAACGCTGCCTGAGGCGGGAACCCAAATCGGAATAG	ATGCTGGTTCATCGTTGGTACGTGTGCAGAACCTCGAAAACACCATCAGGCGGAGGCAATCTTGCTCCCCCGCAGCCGGCAGGGGAACGCTGCCTGAGGCGGGAACCCAAATCGGAATAG			MLVHRWYVCRTSKTPSGGGNLAPPQPAGERCLRREPKSE*	MLVHRWYVCRTSKTPSGGGNLAPPQPAGERCLRREPKSE*			GACATTCGTC	GAAATTATCT	0	A	0	0	0	0	0
7393	3466	ao	AN2138.1	72.m20005	AO070343000183	0					-221	-18	ATGGTTGTGTTCGGAGTAGCAAGTGACTGCGGAGGAAGCGAAGCTGAACCAGAAGGCGATCCGCGGCGACTTCCCCGCAGCCCTACGGTCCAAAAAAAGCGGCCCTGGTGCGGGACAACCAACTTCCGCTTTAACAGCAATTCACACCACTCCTTTTCTCTATCGAAAGGTGCGATTGCTCCACGGGCGTCTCCTTTAAGATAG			ATGGTTGTGTTCGGAGTAGCAAGTGACTGCGGAGGAAGCGAAGCTGAACCAGAAGGCGATCCGCGGCGACTTCCCCGCAGCCCTACGGTCCAAAAAAAGCGGCCCTGGTGCGGGACAACCAACTTCCGCTTTAACAGCAATTCACACCACTCCTTTTCTCTATCGAAAGGTGCGATTGCTCCACGGGCGTCTCCTTTAAGATAG	MVVFGVASDCGGSEAEPEGDPRRLPRSPTVQKKRPWCGTTNFRFNSNSHHSFSLSKGAIAPRASPLR*			MVVFGVASDCGGSEAEPEGDPRRLPRSPTVQKKRPWCGTTNFRFNSNSHHSFSLSKGAIAPRASPLR*	TCAGGTTGTC	CAAATAACCG	0	A	0	0	0	0	0
7396	3467	af	AN7620.1	72.m19654	AO070343000264	0			-286	-164			ATGCTGCATCATATTCAATCATTAGTAGTAGTCTTGTTCCTGAAGAATGCTCCGTCCAATTTCCCCCGATTTATTTCTTTTCTTGCATCTGATCCAGCAGCTCAGCTCTGTCATTTAAACTAG		ATGCTGCATCATATTCAATCATTAGTAGTAGTCTTGTTCCTGAAGAATGCTCCGTCCAATTTCCCCCGATTTATTTCTTTTCTTGCATCTGATCCAGCAGCTCAGCTCTGTCATTTAAACTAG		MLHHIQSLVVVLFLKNAPSNFPRFISFLASDPAAQLCHLN*		MLHHIQSLVVVLFLKNAPSNFPRFISFLASDPAAQLCHLN*		ACTAATCACC	TGCATTCCCC	0	S	0	0	0	0	0
7397	3467	af	AN7620.1	72.m19654	AO070343000264	0			-240	-169			ATGCTCCGTCCAATTTCCCCCGATTTATTTCTTTTCTTGCATCTGATCCAGCAGCTCAGCTCTGTCATTTAA		ATGCTCCGTCCAATTTCCCCCGATTTATTTCTTTTCTTGCATCTGATCCAGCAGCTCAGCTCTGTCATTTAA		MLRPISPDLFLFLHLIQQLSSVI*		MLRPISPDLFLFLHLIQQLSSVI*		TTCCTGAAGA	ACTAGTGCAT	0	S	0	0	0	0	0
7394	3467	an	AN7620.1	72.m19654	AO070343000264	0	-188	-141					ATGCTCTGCCATGCAATCAGTCCATTCCTCTCCTCTTCTTTGAAATAA	ATGCTCTGCCATGCAATCAGTCCATTCCTCTCCTCTTCTTTGAAATAA			MLCHAISPFLSSSLK*	MLCHAISPFLSSSLK*			ATTCTTCACG	CCCCCCATTT	0	S	0	0	0	0	0
7395	3467	an	AN7620.1	72.m19654	AO070343000264	0	-178	-146					ATGCAATCAGTCCATTCCTCTCCTCTTCTTTGA	ATGCAATCAGTCCATTCCTCTCCTCTTCTTTGA			MQSVHSSPLL*	MQSVHSSPLL*			ATGCTCTGCC	AATAACCCCC	0	S	0	0	0	0	0
7398	3467	ao	AN7620.1	72.m19654	AO070343000264	0					-220	-119	ATGTGTGTCATACCATCTGCAGGGTACTATCTGCAACTCCTCATTTACCCCTCATTGATCTGCCCTCCCAGAGTATATTCTTTATCTTTGCCTACCATATAA			ATGTGTGTCATACCATCTGCAGGGTACTATCTGCAACTCCTCATTTACCCCTCATTGATCTGCCCTCCCAGAGTATATTCTTTATCTTTGCCTACCATATAA	MCVIPSAGYYLQLLIYPSLICPPRVYSLSLPTI*			MCVIPSAGYYLQLLIYPSLICPPRVYSLSLPTI*	ATTGATTCCT	ACAACCCGGT	0	S	0	0	0	0	0
7401	3471	af	AN1249.1	70.m14972	AO070223000012	0			-247	-173			ATGTCGCTCGATTATTATTGTAGAGCTGAAGTGACCATTTTCCAATGTTATTTTATGCCCAACTCTGGCGAGTGA		ATGTCGCTCGATTATTATTGTAGAGCTGAAGTGACCATTTTCCAATGTTATTTTATGCCCAACTCTGGCGAGTGA		MSLDYYCRAEVTIFQCYFMPNSGE*		MSLDYYCRAEVTIFQCYFMPNSGE*		ACTCGAATAG	ATATGATAAG	0	A	0	0	0	YKL012W	0
7402	3471	af	AN1249.1	70.m14972	AO070223000012	0			-203	-132			ATGTTATTTTATGCCCAACTCTGGCGAGTGAATATGATAAGAAAGAGTTTAGGGGACCCGATGCAAACATAA		ATGTTATTTTATGCCCAACTCTGGCGAGTGAATATGATAAGAAAGAGTTTAGGGGACCCGATGCAAACATAA		MLFYAQLWRVNMIRKSLGDPMQT*		MLFYAQLWRVNMIRKSLGDPMQT*		CCATTTTCCA	CAAACAATAT	0	A	0	0	0	YKL012W	0
7403	3471	af	AN1249.1	70.m14972	AO070223000012	0			-193	-173			ATGCCCAACTCTGGCGAGTGA		ATGCCCAACTCTGGCGAGTGA		MPNSGE*		MPNSGE*		ATGTTATTTT	ATATGATAAG	0	A	0	0	0	YKL012W	0
7404	3471	af	AN1249.1	70.m14972	AO070223000012	0			-170	-132			ATGATAAGAAAGAGTTTAGGGGACCCGATGCAAACATAA		ATGATAAGAAAGAGTTTAGGGGACCCGATGCAAACATAA		MIRKSLGDPMQT*		MIRKSLGDPMQT*		GCGAGTGAAT	CAAACAATAT	0	A	0	0	0	YKL012W	0
7405	3471	af	AN1249.1	70.m14972	AO070223000012	0			-143	-132			ATGCAAACATAA		ATGCAAACATAA		MQT*		MQT*		AGGGGACCCG	CAAACAATAT	0	A	0	0	0	YKL012W	0
7399	3471	an	AN1249.1	70.m14972	AO070223000012	0	-144	-76					ATGGGGATGGTGGAGTTGTGCAAACAAGACAAACACTTGAAACCGGGGAGCTCTGTCGCGACGGTCTAA	ATGGGGATGGTGGAGTTGTGCAAACAAGACAAACACTTGAAACCGGGGAGCTCTGTCGCGACGGTCTAA			MGMVELCKQDKHLKPGSSVATV*	MGMVELCKQDKHLKPGSSVATV*			CACCGCGGAA	TTTTCTCGAA	0	A	0	0	0	YKL012W	0
7400	3471	an	AN1249.1	70.m14972	AO070223000012	0	-138	-76					ATGGTGGAGTTGTGCAAACAAGACAAACACTTGAAACCGGGGAGCTCTGTCGCGACGGTCTAA	ATGGTGGAGTTGTGCAAACAAGACAAACACTTGAAACCGGGGAGCTCTGTCGCGACGGTCTAA			MVELCKQDKHLKPGSSVATV*	MVELCKQDKHLKPGSSVATV*			GGAAATGGGG	TTTTCTCGAA	0	A	0	0	0	YKL012W	0
7406	3471	ao	AN1249.1	70.m14972	AO070223000012	0					-271	-200	ATGCCCATCTACCAAGTAGCGCTAGCAAGCGACACGGGACAATCACAAGAATTAAAGCGAACTGCCCAATAG			ATGCCCATCTACCAAGTAGCGCTAGCAAGCGACACGGGACAATCACAAGAATTAAAGCGAACTGCCCAATAG	MPIYQVALASDTGQSQELKRTAQ*			MPIYQVALASDTGQSQELKRTAQ*	CAACTACCGC	ACTCTGTCAA	0	A	0	0	0	YKL012W	0
7407	3471	ao	AN1249.1	70.m14972	AO070223000012	0					-190	-146	ATGTACGTCCAATTTAAAAAGAGTTTCGAGGATTGTCGGAGATGA			ATGTACGTCCAATTTAAAAAGAGTTTCGAGGATTGTCGGAGATGA	MYVQFKKSFEDCRR*			MYVQFKKSFEDCRR*	GACTCTGTCA	TGCTCGGTGT	0	A	0	0	0	YKL012W	0
7408	3471	ao	AN1249.1	70.m14972	AO070223000012	0					-149	-132	ATGATGCTCGGTGTATGA			ATGATGCTCGGTGTATGA	MMLGV*			MMLGV*	ATTGTCGGAG	GTGCAGGTGC	0	A	0	0	0	YKL012W	0
7409	3471	ao	AN1249.1	70.m14972	AO070223000012	0					-146	-132	ATGCTCGGTGTATGA			ATGCTCGGTGTATGA	MLGV*			MLGV*	GTCGGAGATG	GTGCAGGTGC	0	A	0	0	0	YKL012W	0
7411	3473	af	AN5011.1	59.m08914	AO070224000003	0			-220	-140			ATGTTGTCTACGCGCTCCTCCGCAGGTTACCGAGCTCCAACCTGGCCATTTCACATCTCAGGGGGTCTCGCTGACTGCTGA		ATGTTGTCTACGCGCTCCTCCGCAGGTTACCGAGCTCCAACCTGGCCATTTCACATCTCAGGGGGTCTCGCTGACTGCTGA		MLSTRSSAGYRAPTWPFHISGGLADC*		MLSTRSSAGYRAPTWPFHISGGLADC*		CTTTTGTTGC	CAGTTTTTCT	0	T	0	0	0	0	0
7410	3473	an	AN5011.1	59.m08914	AO070224000003	0	-170	-57					ATGCCTCGCTGGCCTCAGGGGTTCTCTTTACTTGCCTTCTCGTCTTCCCTTTCCAGATACTCTTCTTTCGTTTCTTTTTCTTTTCTTTTACTTTATTTTCTTGTCTCTCTCTAA	ATGCCTCGCTGGCCTCAGGGGTTCTCTTTACTTGCCTTCTCGTCTTCCCTTTCCAGATACTCTTCTTTCGTTTCTTTTTCTTTTCTTTTACTTTATTTTCTTGTCTCTCTCTAA			MPRWPQGFSLLAFSSSLSRYSSFVSFSFLLLYFLVSL*	MPRWPQGFSLLAFSSSLSRYSSFVSFSFLLLYFLVSL*			TTCAATTCTG	TAGCTTTTGA	0	T	0	0	0	0	0
7412	3473	ao	AN5011.1	59.m08914	AO070224000003	0					-190	-161	ATGTTCATCTGGCTGCTCAGGGGCTCCTGA			ATGTTCATCTGGCTGCTCAGGGGCTCCTGA	MFIWLLRGS*			MFIWLLRGS*	AATCCATCTC	CCATTGCAGT	0	T	0	0	0	0	0
7413	3475	af	AN1436.1	55.m02941	AO070232000009	0			-178	-119			ATGTTGAAACTCAAATGCCGCGGTGGACCTTCGCGTGTGCCACTAATCCAAATCAGGTAA		ATGTTGAAACTCAAATGCCGCGGTGGACCTTCGCGTGTGCCACTAATCCAAATCAGGTAA		MLKLKCRGGPSRVPLIQIR*		MLKLKCRGGPSRVPLIQIR*		AGAAACAATA	TAGTGGCTCT	0		0	0	0	0	0
7414	3475	af	AN1436.1	55.m02941	AO070232000009	0			-164	-42			ATGCCGCGGTGGACCTTCGCGTGTGCCACTAATCCAAATCAGGTAATAGTGGCTCTTTTCGCCGCGGAGCTTCAAGATCCTCCCCATCTATCCATTTTCTTTCTTGACGTCGCTGCTCTTTAG		ATGCCGCGGTGGACCTTCGCGTGTGCCACTAATCCAAATCAGGTAATAGTGGCTCTTTTCGCCGCGGAGCTTCAAGATCCTCCCCATCTATCCATTTTCTTTCTTGACGTCGCTGCTCTTTAG		MPRWTFACATNPNQVIVALFAAELQDPPHLSIFFLDVAAL*		MPRWTFACATNPNQVIVALFAAELQDPPHLSIFFLDVAAL*		TGAAACTCAA	CATCTCGACA	0		0	0	0	0	0
7415	3475	ao	AN1436.1	55.m02941	AO070232000009	0					-191	-180	ATGAATATGTAG			ATGAATATGTAG	MNM*			MNM*	CTGGGGAGGA	AATGATTTAC	0		0	0	0	0	0
7416	3475	ao	AN1436.1	55.m02941	AO070232000009	0					-178	-167	ATGATTTACTGA			ATGATTTACTGA	MIY*			MIY*	AATATGTAGA	AACCGCGGCG	0		0	0	0	0	0
7418	3477	af	AN5179.1	69.m14876	AO070247000010	0			-168	-46			ATGAAACCCTCCAAATACCATTACGTCCATTGGCCGTGGGTGGATGGCGGGGTGAAGTGGGGGATTTTCTCTCGCCATCACCAAAAAATAAAAATTTCCGCTATCACAATATCCCGCGTTTGA		ATGAAACCCTCCAAATACCATTACGTCCATTGGCCGTGGGTGGATGGCGGGGTGAAGTGGGGGATTTTCTCTCGCCATCACCAAAAAATAAAAATTTCCGCTATCACAATATCCCGCGTTTGA		MKPSKYHYVHWPWVDGGVKWGIFSRHHQKIKISAITISRV*		MKPSKYHYVHWPWVDGGVKWGIFSRHHQKIKISAITISRV*		TTATCGTACG	GAACGATTTC	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7419	3477	af	AN5179.1	69.m14876	AO070247000010	0			-125	-114			ATGGCGGGGTGA		ATGGCGGGGTGA		MAG*		MAG*		CCGTGGGTGG	AGTGGGGGAT	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7417	3477	an	AN5179.1	69.m14876	AO070247000010	0	-124	-110					ATGGCCCCTCAGTAA	ATGGCCCCTCAGTAA			MAPQ*	MAPQ*			GCTTGCTTAA	TTGGCCGCGG	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7420	3477	ao	AN5179.1	69.m14876	AO070247000010	0					-270	-247	ATGAATGAGAAAGGTAGAGAATGA			ATGAATGAGAAAGGTAGAGAATGA	MNEKGRE*			MNEKGRE*	CAGAGATATT	AAGGGAGACA	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7421	3477	ao	AN5179.1	69.m14876	AO070247000010	0					-250	-206	ATGAAAGGGAGACAGCATCGCATTTCATGCATACAACATCAGTAA			ATGAAAGGGAGACAGCATCGCATTTCATGCATACAACATCAGTAA	MKGRQHRISCIQHQ*			MKGRQHRISCIQHQ*	AAGGTAGAGA	TTGGTGTCCG	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7422	3477	ao	AN5179.1	69.m14876	AO070247000010	0					-157	-146	ATGGCGGGGTGA			ATGGCGGGGTGA	MAG*			MAG*	AGTAGTAGTA	AGTGGGGGAC	0	J	FG07484.1	MG08131.1	0	YKL191W	0
7423	3478	an	AN5911.1	72.m19954	AO070248000037	0	-262	-227					ATGGAGAACGGTCGGTGCCGTAGTTTGTCTGGATGA	ATGGAGAACGGTCGGTGCCGTAGTTTGTCTGGATGA			MENGRCRSLSG*	MENGRCRSLSG*			GCCGGAAAGT	CCGCAAGCGC	0	Z	0	0	0	0	0
7424	3478	an	AN5911.1	72.m19954	AO070248000037	0	-230	-36					ATGACCGCAAGCGCGCTCTTTCTCTATCTGCACCTCTTTCAATACTCAACTCTTTGTCACCCCACCATCTGTTCTCTGGATTCGCTCTGTATCCCCCATTTCACAGGAATTGATTTGGTGTTTCCATTAAGCGTGACGGACCTCTTGACCTGTCCTGATCCCAACAAGGTGATTCGGTCTTTGGCGCAACTCTGA	ATGACCGCAAGCGCGCTCTTTCTCTATCTGCACCTCTTTCAATACTCAACTCTTTGTCACCCCACCATCTGTTCTCTGGATTCGCTCTGTATCCCCCATTTCACAGGAATTGATTTGGTGTTTCCATTAAGCGTGACGGACCTCTTGACCTGTCCTGATCCCAACAAGGTGATTCGGTCTTTGGCGCAACTCTGA			MTASALFLYLHLFQYSTLCHPTICSLDSLCIPHFTGIDLVFPLSVTDLLTCPDPNKVIRSLAQL*	MTASALFLYLHLFQYSTLCHPTICSLDSLCIPHFTGIDLVFPLSVTDLLTCPDPNKVIRSLAQL*			GTTTGTCTGG	GAAGATTATT	0	Z	0	0	0	0	0
7427	3479	af	AN0834.1	70.m15804	AO070255000011	0			-229	-218			ATGATATGGTGA		ATGATATGGTGA		MIW*		MIW*		ACCCATCGTT	CTGGGTTGCT	0	O	0	MG05320.1	0	YOR254C	YOR254C

7428	3479	af	AN0834.1	70.m15804	AO070255000011	0			-224	-138			ATGGTGACTGGGTTGCTACATACTGGACAGCATTTTCCTTTGTCCTTTCCACTCCTTTGTTACATTTCTAGGAGATCATGCTTCTGA		ATGGTGACTGGGTTGCTACATACTGGACAGCATTTTCCTTTGTCCTTTCCACTCCTTTGTTACATTTCTAGGAGATCATGCTTCTGA		MVTGLLHTGQHFPLSFPLLCYISRRSCF*		MVTGLLHTGQHFPLSFPLLCYISRRSCF*		TCGTTATGAT	AGGTGAAATT	0	O	0	MG05320.1	0	YOR254C	YOR254C
7429	3479	af	AN0834.1	70.m15804	AO070255000011	0			-147	-124			ATGCTTCTGAAGGTGAAATTTTGA		ATGCTTCTGAAGGTGAAATTTTGA		MLLKVKF*		MLLKVKF*		CTAGGAGATC	CTTGTTTTGA	0	O	0	MG05320.1	0	YOR254C	YOR254C
7430	3479	af	AN0834.1	70.m15804	AO070255000011	0			-95	-57			ATGAGAGATATCTCTCATAGCTTGCCTTCTCTTTGCTAG		ATGAGAGATATCTCTCATAGCTTGCCTTCTCTTTGCTAG		MRDISHSLPSLC*		MRDISHSLPSLC*		TTTATCTTCC	CTCTAATACC	0	O	0	MG05320.1	0	YOR254C	YOR254C
7425	3479	an	AN0834.1	70.m15804	AO070255000011	0	-225	-211					ATGGCAATAAGATAG	ATGGCAATAAGATAG			MAIR*	MAIR*			ACAAAGCAAC	TCTGCCCCAG	0	O	0	MG05320.1	0	YOR254C	YOR254C
7426	3479	an	AN0834.1	70.m15804	AO070255000011	0	-190	-137					ATGTTGCTGGCCACCCTGTCTTTCCCTACCAAACTCTCTGCCTCGTCATATTAA	ATGTTGCTGGCCACCCTGTCTTTCCCTACCAAACTCTCTGCCTCGTCATATTAA			MLLATLSFPTKLSASSY*	MLLATLSFPTKLSASSY*			GTTCACGGAA	ACGATATTAC	0	O	0	MG05320.1	0	YOR254C	YOR254C
7431	3479	ao	AN0834.1	70.m15804	AO070255000011	0					-160	-137	ATGCTCCTGGGAACAGCCGCCTAA			ATGCTCCTGGGAACAGCCGCCTAA	MLLGTAA*			MLLGTAA*	GGAAGGGAAC	TTCTACATTT	0	O	0	MG05320.1	0	YOR254C	YOR254C
7434	3480	af	AN3157.1	59.m08548	AO070256000037	0			-281	-159			ATGGAGGTTCATCGTTTTCCCTACTGCCTTGGCCTACCCTCCGCCATTTCTCGGCTTACTTGGCCGAGCCGCTTCCACCGCCCTTCACATCTGCGGCAACACTTTGGTTGGACCTTGTTGTAA		ATGGAGGTTCATCGTTTTCCCTACTGCCTTGGCCTACCCTCCGCCATTTCTCGGCTTACTTGGCCGAGCCGCTTCCACCGCCCTTCACATCTGCGGCAACACTTTGGTTGGACCTTGTTGTAA		MEVHRFPYCLGLPSAISRLTWPSRFHRPSHLRQHFGWTLL*		MEVHRFPYCLGLPSAISRLTWPSRFHRPSHLRQHFGWTLL*		GCCGGTTCTG	CATTTAGCTA	0	P	0	0	0	YPR003C	0
7432	3480	an	AN3157.1	59.m08548	AO070256000037	0	-218	-114					ATGCATTGTATGCTCCCGGCTTTATCTTTACCCTCGACTCCAACTGACACTAGCGGTGTACCCACAGCACGGTATCAGCGACGCCGATTTATCTTTATTTCCTAG	ATGCATTGTATGCTCCCGGCTTTATCTTTACCCTCGACTCCAACTGACACTAGCGGTGTACCCACAGCACGGTATCAGCGACGCCGATTTATCTTTATTTCCTAG			MHCMLPALSLPSTPTDTSGVPTARYQRRRFIFIS*	MHCMLPALSLPSTPTDTSGVPTARYQRRRFIFIS*			ACCAAAAGCC	TCTTGGGTTT	0	P	0	0	0	YPR003C	0
7433	3480	an	AN3157.1	59.m08548	AO070256000037	0	-209	-114					ATGCTCCCGGCTTTATCTTTACCCTCGACTCCAACTGACACTAGCGGTGTACCCACAGCACGGTATCAGCGACGCCGATTTATCTTTATTTCCTAG	ATGCTCCCGGCTTTATCTTTACCCTCGACTCCAACTGACACTAGCGGTGTACCCACAGCACGGTATCAGCGACGCCGATTTATCTTTATTTCCTAG			MLPALSLPSTPTDTSGVPTARYQRRRFIFIS*	MLPALSLPSTPTDTSGVPTARYQRRRFIFIS*			CATGCATTGT	TCTTGGGTTT	0	P	0	0	0	YPR003C	0
7443	3482	af	AN9194.1	69.m15663	AO070259000004	0			-202	-110			ATGCCCGCAGACTGTCCGGAAAAGCTCTCCATTGGCCAGCATCTGTATCCCGAATCTGCCTGGAAGCACATCTTAATCATTTTGTTACCATGA		ATGCCCGCAGACTGTCCGGAAAAGCTCTCCATTGGCCAGCATCTGTATCCCGAATCTGCCTGGAAGCACATCTTAATCATTTTGTTACCATGA		MPADCPEKLSIGQHLYPESAWKHILIILLP*		MPADCPEKLSIGQHLYPESAWKHILIILLP*		CTATTAGGTC	CGCAGGTAGT	0	MG	0	0	0	0	0
7444	3482	af	AN9194.1	69.m15663	AO070259000004	0			-113	-36			ATGACGCAGGTAGTCAGGTTGTATAAAAGTCATACTACGTTCGCATCACCGCAACATAACACCAGTATATCCCCATAG		ATGACGCAGGTAGTCAGGTTGTATAAAAGTCATACTACGTTCGCATCACCGCAACATAACACCAGTATATCCCCATAG		MTQVVRLYKSHTTFASPQHNTSISP*		MTQVVRLYKSHTTFASPQHNTSISP*		TTTTGTTACC	CGTATCACCA	0	MG	0	0	0	0	0
7440	3482	an	AN9194.1	69.m15663	AO070259000004	0	-156	-112					ATGATGACCACTGCAGGATGTCAAACGCGGCATTCCCACGGGTAA	ATGATGACCACTGCAGGATGTCAAACGCGGCATTCCCACGGGTAA			MMTTAGCQTRHSHG*	MMTTAGCQTRHSHG*			TGGTTGCATC	GCTCTGGATA	0	MG	0	0	0	0	0
7441	3482	an	AN9194.1	69.m15663	AO070259000004	0	-153	-112					ATGACCACTGCAGGATGTCAAACGCGGCATTCCCACGGGTAA	ATGACCACTGCAGGATGTCAAACGCGGCATTCCCACGGGTAA			MTTAGCQTRHSHG*	MTTAGCQTRHSHG*			TTGCATCATG	GCTCTGGATA	0	MG	0	0	0	0	0
7442	3482	an	AN9194.1	69.m15663	AO070259000004	0	-139	-101					ATGTCAAACGCGGCATTCCCACGGGTAAGCTCTGGATAA	ATGTCAAACGCGGCATTCCCACGGGTAAGCTCTGGATAA			MSNAAFPRVSSG*	MSNAAFPRVSSG*			CCACTGCAGG	CCATTCACCA	0	MG	0	0	0	0	0
7445	3482	ao	AN9194.1	69.m15663	AO070259000004	0					-270	-244	ATGTCATGTGCACGACATCAGATATAA			ATGTCATGTGCACGACATCAGATATAA	MSCARHQI*			MSCARHQI*	AGGAGCACTT	TCATCCCCGT	0	MG	0	0	0	0	0
7446	3482	ao	AN9194.1	69.m15663	AO070259000004	0					-265	-221	ATGTGCACGACATCAGATATAATCATCCCCGTAAATAAAATGTAG			ATGTGCACGACATCAGATATAATCATCCCCGTAAATAAAATGTAG	MCTTSDIIIPVNKM*			MCTTSDIIIPVNKM*	CACTTATGTC	TAGAACCAAT	0	MG	0	0	0	0	0
7447	3482	ao	AN9194.1	69.m15663	AO070259000004	0					-184	-128	ATGGACATTGAGTCACCGTGGCAAGACGGAGGTAACATACGTATGATCTCAGAGTGA			ATGGACATTGAGTCACCGTGGCAAGACGGAGGTAACATACGTATGATCTCAGAGTGA	MDIESPWQDGGNIRMISE*			MDIESPWQDGGNIRMISE*	AACAAGCGAC	CACCGACTCA	0	MG	0	0	0	0	0
7448	3482	ao	AN9194.1	69.m15663	AO070259000004	0					-142	-128	ATGATCTCAGAGTGA			ATGATCTCAGAGTGA	MISE*			MISE*	TAACATACGT	CACCGACTCA	0	MG	0	0	0	0	0
7449	3482	ao	AN9194.1	69.m15663	AO070259000004	0					-99	-88	ATGAGTTTATAA			ATGAGTTTATAA	MSL*			MSL*	AGATCAAGCT	CATCGCTTAC	0	MG	0	0	0	0	0
7451	3485	af	AN6532.1	62.m03120	AO070270000032	0			-229	-197			ATGAATAGAATGAGAGAGCGCATAAATAAGTAA		ATGAATAGAATGAGAGAGCGCATAAATAAGTAA		MNRMRERINK*		MNRMRERINK*		CTCACAGTTC	ATGTCGATTT	0	IQR	0	MG08857.1	NCU00148.1	0	0
7452	3485	af	AN6532.1	62.m03120	AO070270000032	0			-220	-197			ATGAGAGAGCGCATAAATAAGTAA		ATGAGAGAGCGCATAAATAAGTAA		MRERINK*		MRERINK*		CATGAATAGA	ATGTCGATTT	0	IQR	0	MG08857.1	NCU00148.1	0	0
7453	3485	af	AN6532.1	62.m03120	AO070270000032	0			-196	-137			ATGTCGATTTTGTTTACTTGCGGAAATAAGCTGGCCATTCTATGCCTGTATACAGGGTGA		ATGTCGATTTTGTTTACTTGCGGAAATAAGCTGGCCATTCTATGCCTGTATACAGGGTGA		MSILFTCGNKLAILCLYTG*		MSILFTCGNKLAILCLYTG*		AAATAAGTAA	TCGTTGAGGT	0	IQR	0	MG08857.1	NCU00148.1	0	0
7450	3485	an	AN6532.1	62.m03120	AO070270000032	0	-80	-54					ATGCGGAGAAGCGGAGATCACAACTGA	ATGCGGAGAAGCGGAGATCACAACTGA			MRRSGDHN*	MRRSGDHN*			CAGAACCCCA	ATCCTCAGCA	0	IQR	0	MG08857.1	NCU00148.1	0	0
7455	3485	ao	AN6532.1	62.m03120	AO070270000032	0					-219	-187	ATGTGTATATATGTGTATTTAAATGCCGTGTGA			ATGTGTATATATGTGTATTTAAATGCCGTGTGA	MCIYVYLNAV*			MCIYVYLNAV*	CTACCTTGAG	GGATTGAGAT	0	IQR	0	MG08857.1	NCU00148.1	0	0
7456	3485	ao	AN6532.1	62.m03120	AO070270000032	0					-209	-198	ATGTGTATTTAA			ATGTGTATTTAA	MCI*			MCI*	ATGTGTATAT	ATGCCGTGTG	0	IQR	0	MG08857.1	NCU00148.1	0	0
7457	3485	ao	AN6532.1	62.m03120	AO070270000032	0					-197	-180	ATGCCGTGTGAGGATTGA			ATGCCGTGTGAGGATTGA	MPCED*			MPCED*	GTGTATTTAA	GATCATTTAA	0	IQR	0	MG08857.1	NCU00148.1	0	0
7458	3489	ao	AN8811.1	71.m15617	AO070276000046	0					-258	-64	ATGCGAGAAACAGACGGACCTCCGAGCGTGAAGTTTGCGGACCGGCAGAATTTCCGCCAAGCCTCAAATTACCTGTTTGGGTCAACGTCCAGAACTCGACTCCAGGAACTTTTCTGCCGCCGCGGACCAGCTTGCGCTTCACGTTGTGTTGATCTAATCTTTAAGTTTGTACAAGCGGGTTTTGCTTTTCTCTAG			ATGCGAGAAACAGACGGACCTCCGAGCGTGAAGTTTGCGGACCGGCAGAATTTCCGCCAAGCCTCAAATTACCTGTTTGGGTCAACGTCCAGAACTCGACTCCAGGAACTTTTCTGCCGCCGCGGACCAGCTTGCGCTTCACGTTGTGTTGATCTAATCTTTAAGTTTGTACAAGCGGGTTTTGCTTTTCTCTAG	MRETDGPPSVKFADRQNFRQASNYLFGSTSRTRLQELFCRRGPACASRCVDLIFKFVQAGFAFL*			MRETDGPPSVKFADRQNFRQASNYLFGSTSRTRLQELFCRRGPACASRCVDLIFKFVQAGFAFL*	AAAGAGAAAG	GAGGGTTCTC	0		0	0	0	0	0
7462	3491	af	AN7495.1	57.m05848	AO070287000021	0			-210	-31			ATGTGGTATCGCGGGGGCGATGCTAGGGCGGCTGCCGCGCTAATGTTCTTCCTGCTTGAATCTCGCTTTCTGGCCCGCGCCGATTTCCTATCGACTCTGGCCAGTGCAGTTTCATCTACTGCATCAGAGAAAACTCGAAGATTCTTCTATTTGTACATCAGTACCCATATATCTTGGTGA		ATGTGGTATCGCGGGGGCGATGCTAGGGCGGCTGCCGCGCTAATGTTCTTCCTGCTTGAATCTCGCTTTCTGGCCCGCGCCGATTTCCTATCGACTCTGGCCAGTGCAGTTTCATCTACTGCATCAGAGAAAACTCGAAGATTCTTCTATTTGTACATCAGTACCCATATATCTTGGTGA		MWYRGGDARAAAALMFFLLESRFLARADFLSTLASAVSSTASEKTRRFFYLYISTHISW*		MWYRGGDARAAAALMFFLLESRFLARADFLSTLASAVSSTASEKTRRFFYLYISTHISW*		GGCTTACCTA	AATCGTTCGC	0	AD	0	0	0	0	0
7463	3491	af	AN7495.1	57.m05848	AO070287000021	0			-191	-168			ATGCTAGGGCGGCTGCCGCGCTAA		ATGCTAGGGCGGCTGCCGCGCTAA		MLGRLPR*		MLGRLPR*		CGCGGGGGCG	TGTTCTTCCT	0	AD	0	0	0	0	0
7464	3491	af	AN7495.1	57.m05848	AO070287000021	0			-168	-31			ATGTTCTTCCTGCTTGAATCTCGCTTTCTGGCCCGCGCCGATTTCCTATCGACTCTGGCCAGTGCAGTTTCATCTACTGCATCAGAGAAAACTCGAAGATTCTTCTATTTGTACATCAGTACCCATATATCTTGGTGA		ATGTTCTTCCTGCTTGAATCTCGCTTTCTGGCCCGCGCCGATTTCCTATCGACTCTGGCCAGTGCAGTTTCATCTACTGCATCAGAGAAAACTCGAAGATTCTTCTATTTGTACATCAGTACCCATATATCTTGGTGA		MFFLLESRFLARADFLSTLASAVSSTASEKTRRFFYLYISTHISW*		MFFLLESRFLARADFLSTLASAVSSTASEKTRRFFYLYISTHISW*		TGCCGCGCTA	AATCGTTCGC	0	AD	0	0	0	0	0
7459	3491	an	AN7495.1	57.m05848	AO070287000021	0	-225	-205					ATGACTAATTGGGGAGGCTAG	ATGACTAATTGGGGAGGCTAG			MTNWGG*	MTNWGG*			GTCCGATCAC	ATGCGTCTAC	0	AD	0	0	0	0	0
7460	3491	an	AN7495.1	57.m05848	AO070287000021	0	-204	-187					ATGCGTCTACCGCGCTAA	ATGCGTCTACCGCGCTAA			MRLPR*	MRLPR*			GGGAGGCTAG	ACTGCCGCCG	0	AD	0	0	0	0	0
7465	3494	ao	AN8927.1	53.m03985	AO070292000086	0					-188	-66	ATGGATGAGCACCACTCCGGGTGGAGGCAGTTTCCTCCGGTGGGACGGTGGAAGGATTTCCTCTGCCATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAAACCCTTTCCCTCCGTAA			ATGGATGAGCACCACTCCGGGTGGAGGCAGTTTCCTCCGGTGGGACGGTGGAAGGATTTCCTCTGCCATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAAACCCTTTCCCTCCGTAA	MDEHHSGWRQFPPVGRWKDFLCHGHGNPPDGRAYINPFPP*			MDEHHSGWRQFPPVGRWKDFLCHGHGNPPDGRAYINPFPP*	TTCTTGCCCG	CAAAACCGGC	0		0	0	0	0	0
7466	3494	ao	AN8927.1	53.m03985	AO070292000086	0					-184	-83	ATGAGCACCACTCCGGGTGGAGGCAGTTTCCTCCGGTGGGACGGTGGAAGGATTTCCTCTGCCATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAA			ATGAGCACCACTCCGGGTGGAGGCAGTTTCCTCCGGTGGGACGGTGGAAGGATTTCCTCTGCCATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAA	MSTTPGGGSFLRWDGGRISSAMDMEILLMGGHI*			MSTTPGGGSFLRWDGGRISSAMDMEILLMGGHI*	TGCCCGATGG	ACCCTTTCCC	0		0	0	0	0	0
7467	3494	ao	AN8927.1	53.m03985	AO070292000086	0					-121	-83	ATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAA			ATGGACATGGAAATCCTCCTGATGGGAGGGCATATATAA	MDMEILLMGGHI*			MDMEILLMGGHI*	TTCCTCTGCC	ACCCTTTCCC	0		0	0	0	0	0
7468	3494	ao	AN8927.1	53.m03985	AO070292000086	0					-115	-83	ATGGAAATCCTCCTGATGGGAGGGCATATATAA			ATGGAAATCCTCCTGATGGGAGGGCATATATAA	MEILLMGGHI*			MEILLMGGHI*	TGCCATGGAC	ACCCTTTCCC	0		0	0	0	0	0
7469	3494	ao	AN8927.1	53.m03985	AO070292000086	0					-100	-83	ATGGGAGGGCATATATAA			ATGGGAGGGCATATATAA	MGGHI*			MGGHI*	AATCCTCCTG	ACCCTTTCCC	0		0	0	0	0	0
7471	3496	af	AN2295.1	71.m15944	AO070295000075	0			-238	-122			ATGGGAAAAAAAGGATCGCCGAGGGAGCAACCGACCGCCGCGACAAATCGGATCCGCTTAAAGCTTTGTCCCGAAAAGTCCAAACCCCAAACCCATCCCAGCGGGTTTTCCTACTGA		ATGGGAAAAAAAGGATCGCCGAGGGAGCAACCGACCGCCGCGACAAATCGGATCCGCTTAAAGCTTTGTCCCGAAAAGTCCAAACCCCAAACCCATCCCAGCGGGTTTTCCTACTGA		MGKKGSPREQPTAATNRIRLKLCPEKSKPQTHPSGFSY*		MGKKGSPREQPTAATNRIRLKLCPEKSKPQTHPSGFSY*		TAGGAGGGAG	AGTGTCCCAT	0	C	0	MG05480.1	0	0	0
7470	3496	an	AN2295.1	71.m15944	AO070295000075	0	-175	-92					ATGGCCGAACCCGTGTCTCAAACATCAATTGCTGCTCGCTTCCTATTGTCATCCTTTCTTTCCCACTCTCCCCTCCTCCTATAA	ATGGCCGAACCCGTGTCTCAAACATCAATTGCTGCTCGCTTCCTATTGTCATCCTTTCTTTCCCACTCTCCCCTCCTCCTATAA			MAEPVSQTSIAARFLLSSFLSHSPLLL*	MAEPVSQTSIAARFLLSSFLSHSPLLL*			TCCCGAACAG	TTTCAGTTCT	0	C	0	MG05480.1	0	0	0
7473	3496	ao	AN2295.1	71.m15944	AO070295000075	0					-222	-136	ATGCAAGAGGAAAAAAAAAGGCCGAGGAGACTGAGCCGACCGCCCGCGACAATTCGGGTCCGCTTAAAGCTTTGTCCCGAAAGTTGA			ATGCAAGAGGAAAAAAAAAGGCCGAGGAGACTGAGCCGACCGCCCGCGACAATTCGGGTCCGCTTAAAGCTTTGTCCCGAAAGTTGA	MQEEKKRPRRLSRPPATIRVRLKLCPES*			MQEEKKRPRRLSRPPATIRVRLKLCPES*	TCAAATCAGT	AATCCAAACC	0	C	0	MG05480.1	0	0	0
7474	3498	an	AN7311.1	72.m19752	AO070297000059	0	-215	-168					ATGTGCAGTGAGTTGGCTTCGACTAACTGCCGCGCTGCCTCACTTTAA	ATGTGCAGTGAGTTGGCTTCGACTAACTGCCGCGCTGCCTCACTTTAA			MCSELASTNCRAASL*	MCSELASTNCRAASL*			CTCCACGTTT	TTATCGCCGT	0	D	0	0	0	YDR108W	YDR108W
7478	3499	af	AN5607.1	58.m08908	AO070301000004	0			-232	-104			ATGCGAGCAGGACTGGCAGCAGCCTACTATCTGATATCGATATCTCCAGCTCGATATCCGGTTACAATCTTCATGACTAGTGTACAAGAAGCCCTACATTCTTGCTCGCTGGTTTGTTCCATTCGTTGA		ATGCGAGCAGGACTGGCAGCAGCCTACTATCTGATATCGATATCTCCAGCTCGATATCCGGTTACAATCTTCATGACTAGTGTACAAGAAGCCCTACATTCTTGCTCGCTGGTTTGTTCCATTCGTTGA		MRAGLAAAYYLISISPARYPVTIFMTSVQEALHSCSLVCSIR*		MRAGLAAAYYLISISPARYPVTIFMTSVQEALHSCSLVCSIR*		GAGCTGCCCC	CCGACGGGGT	0	S	0	0	0	0	0
7479	3499	af	AN5607.1	58.m08908	AO070301000004	0			-160	-104			ATGACTAGTGTACAAGAAGCCCTACATTCTTGCTCGCTGGTTTGTTCCATTCGTTGA		ATGACTAGTGTACAAGAAGCCCTACATTCTTGCTCGCTGGTTTGTTCCATTCGTTGA		MTSVQEALHSCSLVCSIR*		MTSVQEALHSCSLVCSIR*		TACAATCTTC	CCGACGGGGT	0	S	0	0	0	0	0
7475	3499	an	AN5607.1	58.m08908	AO070301000004	0	-215	-177					ATGCGAATAAACGACCTACAGCAGGCTACTGTCGGTTAA	ATGCGAATAAACGACCTACAGCAGGCTACTGTCGGTTAA			MRINDLQQATVG*	MRINDLQQATVG*			GATTCGTCCA	CGGTGATTAT	0	S	0	0	0	0	0
7476	3499	an	AN5607.1	58.m08908	AO070301000004	0	-141	-100					ATGAGTCAATGTATAGCGCTGCTTGTTGTACCGTCACTTTGA	ATGAGTCAATGTATAGCGCTGCTTGTTGTACCGTCACTTTGA			MSQCIALLVVPSL*	MSQCIALLVVPSL*			TTCGAGCTCT	CATCCGTGTA	0	S	0	0	0	0	0
7477	3499	an	AN5607.1	58.m08908	AO070301000004	0	-133	-89					ATGTATAGCGCTGCTTGTTGTACCGTCACTTTGACATCCGTGTAG	ATGTATAGCGCTGCTTGTTGTACCGTCACTTTGACATCCGTGTAG			MYSAACCTVTLTSV*	MYSAACCTVTLTSV*			CTATGAGTCA	CTGACATCAG	0	S	0	0	0	0	0
7480	3499	ao	AN5607.1	58.m08908	AO070301000004	0					-237	-226	ATGCAGACATAA			ATGCAGACATAA	MQT*			MQT*	CCTGTTACCC	TTGGCAGTAA	0	S	0	0	0	0	0
7481	3499	ao	AN5607.1	58.m08908	AO070301000004	0					-165	-139	ATGTCCGATGTAAGTTCATACCGCTAA			ATGTCCGATGTAAGTTCATACCGCTAA	MSDVSSYR*			MSDVSSYR*	TACAATCTTC	ACGCCCATCT	0	S	0	0	0	0	0
7482	3499	ao	AN5607.1	58.m08908	AO070301000004	0					-109	-86	ATGTTATTGAACGAAAGTAGTTAA			ATGTTATTGAACGAAAGTAGTTAA	MLLNESS*			MLLNESS*	CATTATTCCA	CACTTATTGT	0	S	0	0	0	0	0
7485	3500	af	AN5610.1	58.m07534	AO070301000010	0			-234	-202			ATGCCTCGATGCCTCGATGCCTTCATGCCTTGA		ATGCCTCGATGCCTCGATGCCTTCATGCCTTGA		MPRCLDAFMP*		MPRCLDAFMP*		TAATACCTTG	TGCCGTGATG	0	Q	0	0	0	0	0
7486	3500	af	AN5610.1	58.m07534	AO070301000010	0			-226	-194			ATGCCTCGATGCCTTCATGCCTTGATGCCGTGA		ATGCCTCGATGCCTTCATGCCTTGATGCCGTGA		MPRCLHALMP*		MPRCLHALMP*		TGATGCCTCG	TGCCTGGAAC	0	Q	0	0	0	0	0

7487	3500	af	AN5610.1	58.m07534	AO070301000010	0			-218	-111			ATGCCTTCATGCCTTGATGCCGTGATGCCTGGAACCCCAAAAGGCGGTGACCGTGACAAAAAGATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		ATGCCTTCATGCCTTGATGCCGTGATGCCTGGAACCCCAAAAGGCGGTGACCGTGACAAAAAGATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		MPSCLDAVMPGTPKGGDRDKKMVVGPGAAKSALFL*		MPSCLDAVMPGTPKGGDRDKKMVVGPGAAKSALFL*		CGATGCCTCG	ATGCCCCTCT	0	Q	0	0	0	0	0
7488	3500	af	AN5610.1	58.m07534	AO070301000010	0			-194	-111			ATGCCTGGAACCCCAAAAGGCGGTGACCGTGACAAAAAGATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		ATGCCTGGAACCCCAAAAGGCGGTGACCGTGACAAAAAGATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		MPGTPKGGDRDKKMVVGPGAAKSALFL*		MPGTPKGGDRDKKMVVGPGAAKSALFL*		TGATGCCGTG	ATGCCCCTCT	0	Q	0	0	0	0	0
7489	3500	af	AN5610.1	58.m07534	AO070301000010	0			-155	-111			ATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		ATGGTTGTGGGGCCTGGGGCAGCGAAATCGGCACTTTTCTTGTAG		MVVGPGAAKSALFL*		MVVGPGAAKSALFL*		TGACAAAAAG	ATGCCCCTCT	0	Q	0	0	0	0	0
7490	3500	af	AN5610.1	58.m07534	AO070301000010	0			-110				ATGCCCCTCTTGACTCATACTAATATCCTTCTGTTCTGTCACCCGATATCCAGCCCCAGTTGTGAAAGTCGAGTGCCCAAACAAGAGTTTCGGGCCTCTGGACCGCAATAA		ATGCCCCTCTTGACTCATACTAATATCCTTCTGTTCTGTCACCCGATATCCAGCCCCAGTTGTGAAAGTCGAGTGCCCAAACAAGAGTTTCGGGCCTCTGGACCGCAATAA		MPLLTHTNILLFCHPISSPSCESRVPKQEFRASGPQ*		MPLLTHTNILLFCHPISSPSCESRVPKQEFRASGPQ*		TTTCTTGTAG	TGGGTGTTGA	0	Q	0	0	0	0	0
7483	3500	an	AN5610.1	58.m07534	AO070301000010	0	-203	-135					ATGCCTCAGGCATTAGGCTTATTGCCTTGTTGCCTGAACCTCTATCAAATGTGGGGAAATTTTCGATAG	ATGCCTCAGGCATTAGGCTTATTGCCTTGTTGCCTGAACCTCTATCAAATGTGGGGAAATTTTCGATAG			MPQALGLLPCCLNLYQMWGNFR*	MPQALGLLPCCLNLYQMWGNFR*			CACACATTTA	CGAAATCGGC	0	Q	0	0	0	0	0
7484	3500	an	AN5610.1	58.m07534	AO070301000010	0	-155	-135					ATGTGGGGAAATTTTCGATAG	ATGTGGGGAAATTTTCGATAG			MWGNFR*	MWGNFR*			CCTCTATCAA	CGAAATCGGC	0	Q	0	0	0	0	0
7491	3500	ao	AN5610.1	58.m07534	AO070301000010	0					-255	-232	ATGCGCACAACCACTTGTGCCTGA			ATGCGCACAACCACTTGTGCCTGA	MRTTTCA*			MRTTTCA*	TGCATTTGGT	ATGCCTCACC	0	Q	0	0	0	0	0
7492	3500	ao	AN5610.1	58.m07534	AO070301000010	0					-231	-97	ATGCCTCACCGTTCTGGGTCTAACCGGGATCGGCCTAGTCGGAGGTGGAAGGCGGTAAGTGGTGATGATGTGAGTGTGGGGTTTCAGAAGCTTGGCCGCTATGACTGGCTGCGAAATCGGCACTTTTTCTCTTAG			ATGCCTCACCGTTCTGGGTCTAACCGGGATCGGCCTAGTCGGAGGTGGAAGGCGGTAAGTGGTGATGATGTGAGTGTGGGGTTTCAGAAGCTTGGCCGCTATGACTGGCTGCGAAATCGGCACTTTTTCTCTTAG	MPHRSGSNRDRPSRRWKAVSGDDVSVGFQKLGRYDWLRNRHFFS*			MPHRSGSNRDRPSRRWKAVSGDDVSVGFQKLGRYDWLRNRHFFS*	TTGTGCCTGA	TGCCCCTCCA	0	Q	0	0	0	0	0
7493	3500	ao	AN5610.1	58.m07534	AO070301000010	0					-131	-78	ATGACTGGCTGCGAAATCGGCACTTTTTCTCTTAGTGCCCCTCCAATTGACTGA			ATGACTGGCTGCGAAATCGGCACTTTTTCTCTTAGTGCCCCTCCAATTGACTGA	MTGCEIGTFSLSAPPID*			MTGCEIGTFSLSAPPID*	CTTGGCCGCT	GTCACAATAG	0	Q	0	0	0	0	0
7495	3502	af	AN1455.1	55.m02957	AO070302000021	0			-249	-193			ATGTTAATCGATTTAGTAAGATGCGGATACGGACACAAACTAGGCTATGTTACGTAG		ATGTTAATCGATTTAGTAAGATGCGGATACGGACACAAACTAGGCTATGTTACGTAG		MLIDLVRCGYGHKLGYVT*		MLIDLVRCGYGHKLGYVT*		AGCTTCTCCG	ACTGACTGCG	0	O	FG00430.1	0	NCU02708.1	0	0
7496	3502	af	AN1455.1	55.m02957	AO070302000021	0			-229	-188			ATGCGGATACGGACACAAACTAGGCTATGTTACGTAGACTGA		ATGCGGATACGGACACAAACTAGGCTATGTTACGTAGACTGA		MRIRTQTRLCYVD*		MRIRTQTRLCYVD*		ATTTAGTAAG	CTGCGTACTG	0	O	FG00430.1	0	NCU02708.1	0	0
7497	3502	af	AN1455.1	55.m02957	AO070302000021	0			-203	-171			ATGTTACGTAGACTGACTGCGTACTGTACCTGA		ATGTTACGTAGACTGACTGCGTACTGTACCTGA		MLRRLTAYCT*		MLRRLTAYCT*		AAACTAGGCT	TGCCAAGCCT	0	O	FG00430.1	0	NCU02708.1	0	0
7498	3502	af	AN1455.1	55.m02957	AO070302000021	0			-171	-28			ATGCCAAGCCTCCAGAAGAGACCACCTTGCGAAGCTCTCCCCCCAAATCAGTATACTGGCGAGACTAAACGTCCAACTACCTCTCTCTTTTCGGCTACAAAGCACGTCGAGAGAGACATACTCTCCTTTGTTTTTTCCAATTGA		ATGCCAAGCCTCCAGAAGAGACCACCTTGCGAAGCTCTCCCCCCAAATCAGTATACTGGCGAGACTAAACGTCCAACTACCTCTCTCTTTTCGGCTACAAAGCACGTCGAGAGAGACATACTCTCCTTTGTTTTTTCCAATTGA		MPSLQKRPPCEALPPNQYTGETKRPTTSLFSATKHVERDILSFVFSN*		MPSLQKRPPCEALPPNQYTGETKRPTTSLFSATKHVERDILSFVFSN*		ACTGTACCTG	TATTCCTTTT	0	O	FG00430.1	0	NCU02708.1	0	0
7494	3502	an	AN1455.1	55.m02957	AO070302000021	0	-181	-122					ATGATTGCGAAGTACCTAGTGCCAAGACTTCCAAAAGAGACCACCTTGCGCAGCTCCTAG	ATGATTGCGAAGTACCTAGTGCCAAGACTTCCAAAAGAGACCACCTTGCGCAGCTCCTAG			MIAKYLVPRLPKETTLRSS*	MIAKYLVPRLPKETTLRSS*			GTCCGAATGA	TCGTCGTCAA	0	O	FG00430.1	0	NCU02708.1	0	0
7502	3503	af	AN3827.1	58.m07803	AO070305000064	0			-198	-124			ATGCTCCAGCTGTCCTTCGGCCTGCCGCGCCAAGACTCCGCGCATTTCCCTTTTCCGCAGCGCACGGGCCAATAG		ATGCTCCAGCTGTCCTTCGGCCTGCCGCGCCAAGACTCCGCGCATTTCCCTTTTCCGCAGCGCACGGGCCAATAG		MLQLSFGLPRQDSAHFPFPQRTGQ*		MLQLSFGLPRQDSAHFPFPQRTGQ*		GTTGGTTTGT	AGCTTGTGAT	0	A	0	0	0	YGR103W	0
7499	3503	an	AN3827.1	58.m07803	AO070305000064	0	-188	-3					ATGAAAGGGTGTTCATATGAAGTGGTTTCGCTCCACCTGTCCCTTGTCCGCTATTCAAACGCCAAGACTCCGCGGTCTTTCGTGCACGGGCCACCCGAGTTTTCTCTGCGGAAAAAAAGTTCAAATTTTTGGATGACTAGAAGACCTTCCTCCCATCATTCTTCCATTCTACCATCAAAGTCGTAA	ATGAAAGGGTGTTCATATGAAGTGGTTTCGCTCCACCTGTCCCTTGTCCGCTATTCAAACGCCAAGACTCCGCGGTCTTTCGTGCACGGGCCACCCGAGTTTTCTCTGCGGAAAAAAAGTTCAAATTTTTGGATGACTAGAAGACCTTCCTCCCATCATTCTTCCATTCTACCATCAAAGTCGTAA			MKGCSYEVVSLHLSLVRYSNAKTPRSFVHGPPEFSLRKKSSNFWMTRRPSSHHSSILPSKS*	MKGCSYEVVSLHLSLVRYSNAKTPRSFVHGPPEFSLRKKSSNFWMTRRPSSHHSSILPSKS*			CTTCCCTTCG	TCATGGCGAA	0	A	0	0	0	YGR103W	0
7500	3503	an	AN3827.1	58.m07803	AO070305000064	0	-172	-53					ATGAAGTGGTTTCGCTCCACCTGTCCCTTGTCCGCTATTCAAACGCCAAGACTCCGCGGTCTTTCGTGCACGGGCCACCCGAGTTTTCTCTGCGGAAAAAAAGTTCAAATTTTTGGATGA	ATGAAGTGGTTTCGCTCCACCTGTCCCTTGTCCGCTATTCAAACGCCAAGACTCCGCGGTCTTTCGTGCACGGGCCACCCGAGTTTTCTCTGCGGAAAAAAAGTTCAAATTTTTGGATGA			MKWFRSTCPLSAIQTPRLRGLSCTGHPSFLCGKKVQIFG*	MKWFRSTCPLSAIQTPRLRGLSCTGHPSFLCGKKVQIFG*			GGGTGTTCAT	CTAGAAGACC	0	A	0	0	0	YGR103W	0
7503	3503	ao	AN3827.1	58.m07803	AO070305000064	0					-212	-192	ATGCTAGAGAGCACGGAGTAG			ATGCTAGAGAGCACGGAGTAG	MLESTE*			MLESTE*	TTGTATAATC	CAAGGCATCT	0	A	0	0	0	YGR103W	0
7505	3507	af	AN8242.1	53.m03728	AO070310000066	0			-86	-39			ATGACTCACTATTCAAGTCCTCTCTGCTCAAACTCATATCACCCATAA		ATGACTCACTATTCAAGTCCTCTCTGCTCAAACTCATATCACCCATAA		MTHYSSPLCSNSYHP*		MTHYSSPLCSNSYHP*		GCCTGGTCCA	GCTGCTCGGT	0	V	0	0	0	0	0
7506	3507	ao	AN8242.1	53.m03728	AO070310000066	0					-189	-130	ATGGCATGGAAACCCCCACTCCCTTGCTTCGGAACGAACCCCATCGACTCTGGAATGTAA			ATGGCATGGAAACCCCCACTCCCTTGCTTCGGAACGAACCCCATCGACTCTGGAATGTAA	MAWKPPLPCFGTNPIDSGM*			MAWKPPLPCFGTNPIDSGM*	ATCAGGATAA	CGATCTGCGT	0	V	0	0	0	0	0
7507	3507	ao	AN8242.1	53.m03728	AO070310000066	0					-184	-86	ATGGAAACCCCCACTCCCTTGCTTCGGAACGAACCCCATCGACTCTGGAATGTAACGATCTGCGTGAGGAGGTACCGAGGCCGATACGTAAGAAGGTAA			ATGGAAACCCCCACTCCCTTGCTTCGGAACGAACCCCATCGACTCTGGAATGTAACGATCTGCGTGAGGAGGTACCGAGGCCGATACGTAAGAAGGTAA	METPTPLLRNEPHRLWNVTICVRRYRGRYVRR*			METPTPLLRNEPHRLWNVTICVRRYRGRYVRR*	GATAAATGGC	ACAAAAGGGG	0	V	0	0	0	0	0
7509	3511	af	AN1016.1	70.m15234	AO070312000002	0			-122	-81			ATGAGTCCTACCCCGAGTGTCTCGGGTGTCAGTGTCTCGTAA		ATGAGTCCTACCCCGAGTGTCTCGGGTGTCAGTGTCTCGTAA		MSPTPSVSGVSVS*		MSPTPSVSGVSVS*		TGCCTAGTAC	ATTGATGCCG	0	DT	0	0	0	0	0
7510	3511	ao	AN1016.1	70.m15234	AO070312000002	0					-63	-7	ATGCCGTTCACTTCCGCAGGCAGCTCATGGTTTAGTCGTTCGCTGTCTAGAATATAA			ATGCCGTTCACTTCCGCAGGCAGCTCATGGTTTAGTCGTTCGCTGTCTAGAATATAA	MPFTSAGSSWFSRSLSRI*			MPFTSAGSSWFSRSLSRI*	TGCTAGGTTG	TCCGAGATGG	0	DT	0	0	0	0	0
7512	3513	af	AN0049.1	71.m15323	AO070314000128	0			-237	-217			ATGCTTCATTATCATTGCTGA		ATGCTTCATTATCATTGCTGA		MLHYHC*		MLHYHC*		TCAAGCTCAT	TGATAGCAGA	0	M	0	MG05020.1	0	0	0
7513	3513	af	AN0049.1	71.m15323	AO070314000128	0			-217	-143			ATGATAGCAGACAGAGCTTCAAAGCTGAGACGGACTGGACTGGTGGAGTTGATGATGCGGAATCCCCACCTGTAA		ATGATAGCAGACAGAGCTTCAAAGCTGAGACGGACTGGACTGGTGGAGTTGATGATGCGGAATCCCCACCTGTAA		MIADRASKLRRTGLVELMMRNPHL*		MIADRASKLRRTGLVELMMRNPHL*		ATCATTGCTG	TCCGCAACCA	0	M	0	MG05020.1	0	0	0
7514	3513	af	AN0049.1	71.m15323	AO070314000128	0			-166	-143			ATGATGCGGAATCCCCACCTGTAA		ATGATGCGGAATCCCCACCTGTAA		MMRNPHL*		MMRNPHL*		GGTGGAGTTG	TCCGCAACCA	0	M	0	MG05020.1	0	0	0
7515	3513	af	AN0049.1	71.m15323	AO070314000128	0			-163	-143			ATGCGGAATCCCCACCTGTAA		ATGCGGAATCCCCACCTGTAA		MRNPHL*		MRNPHL*		GGAGTTGATG	TCCGCAACCA	0	M	0	MG05020.1	0	0	0
7511	3513	an	AN0049.1	71.m15323	AO070314000128	0	-180	-124					ATGGTGACTTCAGACGTTGTGTTGAATGGATTGATCTACCTGGAGCCGAAAATGTAG	ATGGTGACTTCAGACGTTGTGTTGAATGGATTGATCTACCTGGAGCCGAAAATGTAG			MVTSDVVLNGLIYLEPKM*	MVTSDVVLNGLIYLEPKM*			TGGTTAGGAC	GTATAGCTCC	0	M	0	MG05020.1	0	0	0
7516	3513	ao	AN0049.1	71.m15323	AO070314000128	0					-247	-224	ATGCTGCAATTGAGTTGCTATTGA			ATGCTGCAATTGAGTTGCTATTGA	MLQLSCY*			MLQLSCY*	TTAAAAAGCC	CTGGCTCCAT	0	M	0	MG05020.1	0	0	0
7517	3513	ao	AN0049.1	71.m15323	AO070314000128	0					-158	-129	ATGTCGGATGCGCCTCCAGTACAGTCATAG			ATGTCGGATGCGCCTCCAGTACAGTCATAG	MSDAPPVQS*			MSDAPPVQS*	GTGTGAGAGA	CCAATCTGCG	0	M	0	MG05020.1	0	0	0
7518	3513	ao	AN0049.1	71.m15323	AO070314000128	0					-151	-92	ATGCGCCTCCAGTACAGTCATAGCCAATCTGCGTTTGATCCTCCGATCCATACTTCTTAA			ATGCGCCTCCAGTACAGTCATAGCCAATCTGCGTTTGATCCTCCGATCCATACTTCTTAA	MRLQYSHSQSAFDPPIHTS*			MRLQYSHSQSAFDPPIHTS*	AGAATGTCGG	ACATAACCTT	0	M	0	MG05020.1	0	0	0
7519	3514	af	AN0771.1	70.m15374	AO070316000073	0			-67	-23			ATGTGTATACCTATTGTGACGCAACCACTCCCGAATCGAGACTGA		ATGTGTATACCTATTGTGACGCAACCACTCCCGAATCGAGACTGA		MCIPIVTQPLPNRD*		MCIPIVTQPLPNRD*		TCGACTGTTT	GTGTCTCACT	0	Q	0	0	0	0	0
7520	3514	ao	AN0771.1	70.m15374	AO070316000073	0					-197	-117	ATGGCCCCCTCTTCGTTCTCCCTCCTGATTATCTACGTTCTTTTCTTTTACAGATCTGAACACATGGACGAACACTTGTAA			ATGGCCCCCTCTTCGTTCTCCCTCCTGATTATCTACGTTCTTTTCTTTTACAGATCTGAACACATGGACGAACACTTGTAA	MAPSSFSLLIIYVLFFYRSEHMDEHL*			MAPSSFSLLIIYVLFFYRSEHMDEHL*	TTATTATTAG	TAATATCTAC	0	Q	0	0	0	0	0
7521	3514	ao	AN0771.1	70.m15374	AO070316000073	0					-134	-117	ATGGACGAACACTTGTAA			ATGGACGAACACTTGTAA	MDEHL*			MDEHL*	ATCTGAACAC	TAATATCTAC	0	Q	0	0	0	0	0
7522	3515	an	AN0370.1	54.m06986	AO070318000048	0	-285	-271					ATGCATCGAAAGTAG	ATGCATCGAAAGTAG			MHRK*	MHRK*			GTGTGGTGCC	TACTGTACTG	0	I	0	0	0	0	0
7523	3515	an	AN0370.1	54.m06986	AO070318000048	0	-257	-231					ATGAGCTCTCCGCATTTGCGGGGTTAG	ATGAGCTCTCCGCATTTGCGGGGTTAG			MSSPHLRG*	MSSPHLRG*			TGTACTGTAC	AGCTCCGCAA	0	I	0	0	0	0	0
7524	3515	an	AN0370.1	54.m06986	AO070318000048	0	-158	-63					ATGAGCATACCACCAGTTGCACGGGGCAGCCGACAACCGTCAGCCTTGAAGCCGAGACAGAGGGGTTGTCTCACCAGTCTTCCGCCCTTTAAATAA	ATGAGCATACCACCAGTTGCACGGGGCAGCCGACAACCGTCAGCCTTGAAGCCGAGACAGAGGGGTTGTCTCACCAGTCTTCCGCCCTTTAAATAA			MSIPPVARGSRQPSALKPRQRGCLTSLPPFK*	MSIPPVARGSRQPSALKPRQRGCLTSLPPFK*			TATAATCTAG	CCTCTGCCGT	0	I	0	0	0	0	0
7525	3517	af	AN8907.1	56.m02323	AO070319000030	0			-111	-91			ATGCCATCCCGGGTAACTTGA		ATGCCATCCCGGGTAACTTGA		MPSRVT*		MPSRVT*		CATTCGGATC	CATATCTGCG	0	I	0	0	0	0	0
7526	3517	ao	AN8907.1	56.m02323	AO070319000030	0					-166	-65	ATGATTAAATTCTTCCCGGATCCGAGTGGTCTGTCCCGTCAGACCATTCGGGATGTCCACTCGTCTTGGCTTCGTTCCAACACAATGGTAAACGTTATATAA			ATGATTAAATTCTTCCCGGATCCGAGTGGTCTGTCCCGTCAGACCATTCGGGATGTCCACTCGTCTTGGCTTCGTTCCAACACAATGGTAAACGTTATATAA	MIKFFPDPSGLSRQTIRDVHSSWLRSNTMVNVI*			MIKFFPDPSGLSRQTIRDVHSSWLRSNTMVNVI*	GCCTGATCAT	TGCATGAAAA	0	I	0	0	0	0	0
7527	3517	ao	AN8907.1	56.m02323	AO070319000030	0					-114	-76	ATGTCCACTCGTCTTGGCTTCGTTCCAACACAATGGTAA			ATGTCCACTCGTCTTGGCTTCGTTCCAACACAATGGTAA	MSTRLGFVPTQW*			MSTRLGFVPTQW*	ACCATTCGGG	ACGTTATATA	0	I	0	0	0	0	0
7528	3517	ao	AN8907.1	56.m02323	AO070319000030	0					-82	-65	ATGGTAAACGTTATATAA			ATGGTAAACGTTATATAA	MVNVI*			MVNVI*	TTCCAACACA	TGCATGAAAA	0	I	0	0	0	0	0
7529	3517	ao	AN8907.1	56.m02323	AO070319000030	0					-65	-27	ATGCATGAAAATCATCTGAACGGTGATTGGAACTTCTAA			ATGCATGAAAATCATCTGAACGGTGATTGGAACTTCTAA	MHENHLNGDWNF*			MHENHLNGDWNF*	ACGTTATATA	ATCACCCAGC	0	I	0	0	0	0	0
7530	3517	ao	AN8907.1	56.m02323	AO070319000030	0					-61	-47	ATGAAAATCATCTGA			ATGAAAATCATCTGA	MKII*			MKII*	TATATAATGC	ACGGTGATTG	0	I	0	0	0	0	0
7533	3518	af	AN0872.1	70.m15474	AO070320000030	0			-151	-137			ATGGAGCCGATATAA		ATGGAGCCGATATAA		MEPI*		MEPI*		GACAGGAACG	CGCGATTGAG	0	L	0	0	0	0	0
7531	3518	an	AN0872.1	70.m15474	AO070320000030	0	-127	-83					ATGACCTACCACGCCATTCTTATAAATGTCCTCTCGACGCGTTAA	ATGACCTACCACGCCATTCTTATAAATGTCCTCTCGACGCGTTAA			MTYHAILINVLSTR*	MTYHAILINVLSTR*			TTTCTCTTTT	TATACCAGCA	0	L	0	0	0	0	0
7532	3518	an	AN0872.1	70.m15474	AO070320000030	0	-102	-28					ATGTCCTCTCGACGCGTTAATATACCAGCACCAACAATATCGACGCAATCGGCTGTGACCCGGACGAAGAAATAA	ATGTCCTCTCGACGCGTTAATATACCAGCACCAACAATATCGACGCAATCGGCTGTGACCCGGACGAAGAAATAA			MSSRRVNIPAPTISTQSAVTRTKK*	MSSRRVNIPAPTISTQSAVTRTKK*			ATTCTTATAA	ACAGATTACC	0	L	0	0	0	0	0
7534	3518	ao	AN0872.1	70.m15474	AO070320000030	0					-151	-113	ATGGAGCCAACCAAAACACCATTGACTTTGTTTGTGTGA			ATGGAGCCAACCAAAACACCATTGACTTTGTTTGTGTGA	MEPTKTPLTLFV*			MEPTKTPLTLFV*	ACACCTGGGA	ACAGTCCGTG	0	L	0	0	0	0	0
7535	3520	af	AN0912.1	70.m15521	AO070320000093	0			-241	-209			ATGATCAGTAACAATTTACTGTTCTTCAGATAG		ATGATCAGTAACAATTTACTGTTCTTCAGATAG		MISNNLLFFR*		MISNNLLFFR*		CTATTTTTAT	CTATTTCAAT	0	E	0	0	0	0	0
7536	3520	af	AN0912.1	70.m15521	AO070320000093	0			-200	-180			ATGTATGAGTGTTTTGTATAG		ATGTATGAGTGTTTTGTATAG		MYECFV*		MYECFV*		AGCTATTTCA	CTCCAAGTCC	0	E	0	0	0	0	0
7537	3520	af	AN0912.1	70.m15521	AO070320000093	0			-196	-83			ATGAGTGTTTTGTATAGCTCCAAGTCCAATCGGCTTGAAGTGGATTCCAAAGGATCTCCGTCCGTCACTCTCCGGTGTCGGCGCGCGGGGTGCATCCACCCCTCCATATTTTGA		ATGAGTGTTTTGTATAGCTCCAAGTCCAATCGGCTTGAAGTGGATTCCAAAGGATCTCCGTCCGTCACTCTCCGGTGTCGGCGCGCGGGGTGCATCCACCCCTCCATATTTTGA		MSVLYSSKSNRLEVDSKGSPSVTLRCRRAGCIHPSIF*		MSVLYSSKSNRLEVDSKGSPSVTLRCRRAGCIHPSIF*		ATTTCAATGT	AGGGATATTT	0	E	0	0	0	0	0
7538	3520	ao	AN0912.1	70.m15521	AO070320000093	0					-223	-164	ATGCTGGACTCCCTTAGTAATTCGCATGATCCTACTAGCGTTGCAGTTGCAGTTGCATGA			ATGCTGGACTCCCTTAGTAATTCGCATGATCCTACTAGCGTTGCAGTTGCAGTTGCATGA	MLDSLSNSHDPTSVAVAVA*			MLDSLSNSHDPTSVAVAVA*	ACAGTTGAAA	GGCGGCGGTT	0	E	0	0	0	0	0

7539	3520	ao	AN0912.1	70.m15521	AO070320000093	0					-198	-106	ATGATCCTACTAGCGTTGCAGTTGCAGTTGCATGAGGCGGCGGTTAATCACGGGGAAGTCCGACTGCGGCTCCGGTGTCGGCGCGCGGGGTGA			ATGATCCTACTAGCGTTGCAGTTGCAGTTGCATGAGGCGGCGGTTAATCACGGGGAAGTCCGACTGCGGCTCCGGTGTCGGCGCGCGGGGTGA	MILLALQLQLHEAAVNHGEVRLRLRCRRAG*			MILLALQLQLHEAAVNHGEVRLRLRCRRAG*	AGTAATTCGC	CTCGAGATCC	0	E	0	0	0	0	0
7540	3520	ao	AN0912.1	70.m15521	AO070320000093	0					-167	-54	ATGAGGCGGCGGTTAATCACGGGGAAGTCCGACTGCGGCTCCGGTGTCGGCGCGCGGGGTGACTCGAGATCCACCCCTCATCGCCATATAACTCTCGATGCTTTCGGTCTTTGA			ATGAGGCGGCGGTTAATCACGGGGAAGTCCGACTGCGGCTCCGGTGTCGGCGCGCGGGGTGACTCGAGATCCACCCCTCATCGCCATATAACTCTCGATGCTTTCGGTCTTTGA	MRRRLITGKSDCGSGVGARGDSRSTPHRHITLDAFGL*			MRRRLITGKSDCGSGVGARGDSRSTPHRHITLDAFGL*	TTGCAGTTGC	GCTTGGTCTC	0	E	0	0	0	0	0
7541	3520	ao	AN0912.1	70.m15521	AO070320000093	0					-70	-29	ATGCTTTCGGTCTTTGAGCTTGGTCTCTCGTCAGTGTTATAG			ATGCTTTCGGTCTTTGAGCTTGGTCTCTCGTCAGTGTTATAG	MLSVFELGLSSVL*			MLSVFELGLSSVL*	ATAACTCTCG	TCCATTGTAC	0	E	0	0	0	0	0
7543	3522	af	AN8126.1	70.m15699	AO070322000018	0			-264	-250			ATGGCTAACGCATAA		ATGGCTAACGCATAA		MANA*		MANA*		GATAACATAC	GAGATATCCT	0	R	0	0	0	0	0
7542	3522	an	AN8126.1	70.m15699	AO070322000018	0	-205	-194					ATGCGACGCTAG	ATGCGACGCTAG			MRR*	MRR*			GTAGTGAAGA	AGTGTAACAT	0	R	0	0	0	0	0
7544	3522	ao	AN8126.1	70.m15699	AO070322000018	0					-234	-205	ATGCCGAACAAGAGTGCAAGACTAAAGTGA			ATGCCGAACAAGAGTGCAAGACTAAAGTGA	MPNKSARLK*			MPNKSARLK*	TAAGTCTTGA	GCTACTGCAC	0	R	0	0	0	0	0
7545	3522	ao	AN8126.1	70.m15699	AO070322000018	0					-156	-109	ATGTCGGTCACCGAGTTCCACTTCTCGCCATATCTCGACGATTTCTAG			ATGTCGGTCACCGAGTTCCACTTCTCGCCATATCTCGACGATTTCTAG	MSVTEFHFSPYLDDF*			MSVTEFHFSPYLDDF*	TATCGCGCGG	TATATGGCGA	0	R	0	0	0	0	0
7546	3522	ao	AN8126.1	70.m15699	AO070322000018	0					-105	-61	ATGGCGACCCTGGTTGAAAAGCACGTTAAATCTTTCCAAAATAA			ATGGCGACCCTGGTTGAAAAGCACGTTAAATCTTTCCAAAATAA	MATLVEKHVKSFQK*			MATLVEKHVKSFQK*	TTTCTAGTAT	CAATATACAA	0	R	0	0	0	0	0
7548	3523	ao	AN1768.1	69.m15068	AO070324000027	0					-128	-60	ATGTATAGGGGTCAGGTGGTGATTGACTATTTGAGTCTTCGTCCCTCGTGTGGCTGCTATCGGTCTTGA			ATGTATAGGGGTCAGGTGGTGATTGACTATTTGAGTCTTCGTCCCTCGTGTGGCTGCTATCGGTCTTGA	MYRGQVVIDYLSLRPSCGCYRS*			MYRGQVVIDYLSLRPSCGCYRS*	CTGCACGTTG	GTATTTGTTT	0	U	0	0	0	0	0
7549	3524	an	AN1745.1	69.m15048	AO070324000051	0	-82	-44					ATGCCGCTCTCGACTGAAATATTCAGTCTCTTGCTCTGA	ATGCCGCTCTCGACTGAAATATTCAGTCTCTTGCTCTGA			MPLSTEIFSLLL*	MPLSTEIFSLLL*			CTTCATCTTC	TTTACAGTTA	0	H	0	0	0	0	0
7550	3526	af	AN7699.1	71.m15724	AO070325000105	0			-187	-104			ATGCCCGGCTGTCCTTCTCCCACTATCACAAACACCAGTGCTGTACTTCACCACCACTCGCGGCTGGCATTTTTAATACTATAG		ATGCCCGGCTGTCCTTCTCCCACTATCACAAACACCAGTGCTGTACTTCACCACCACTCGCGGCTGGCATTTTTAATACTATAG		MPGCPSPTITNTSAVLHHHSRLAFLIL*		MPGCPSPTITNTSAVLHHHSRLAFLIL*		TTCTTTCGAA	ACGCTCAATT	0		FG08949.1	0	0	0	0
7551	3526	ao	AN7699.1	71.m15724	AO070325000105	0					-68	-27	ATGCAAGCCCATTGTGACCTGATATCCCCTTTTGATACTTAG			ATGCAAGCCCATTGTGACCTGATATCCCCTTTTGATACTTAG	MQAHCDLISPFDT*			MQAHCDLISPFDT*	ACCTGCATTG	ATAGTGTTCT	0		FG08949.1	0	0	0	0
7553	3529	af	AN4003.1	54.m06586	AO070328000160	0			-190	-17			ATGAGAGCATCATCATCTCTGGGAAATGTAACTGCAAGGATGAAACTTCAGGCTCATTACGCTCATCTCTTTCGACCAAGAACTACCCTGTTTATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		ATGAGAGCATCATCATCTCTGGGAAATGTAACTGCAAGGATGAAACTTCAGGCTCATTACGCTCATCTCTTTCGACCAAGAACTACCCTGTTTATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		MRASSSLGNVTARMKLQAHYAHLFRPRTTLFMKGMTSVYIEDGARLAPQHSHPYELI*		MRASSSLGNVTARMKLQAHYAHLFRPRTTLFMKGMTSVYIEDGARLAPQHSHPYELI*		CAGTAATACA	CAGAGAATAA	0	CE	0	0	0	0	0
7554	3529	af	AN4003.1	54.m06586	AO070328000160	0			-151	-17			ATGAAACTTCAGGCTCATTACGCTCATCTCTTTCGACCAAGAACTACCCTGTTTATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		ATGAAACTTCAGGCTCATTACGCTCATCTCTTTCGACCAAGAACTACCCTGTTTATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		MKLQAHYAHLFRPRTTLFMKGMTSVYIEDGARLAPQHSHPYELI*		MKLQAHYAHLFRPRTTLFMKGMTSVYIEDGARLAPQHSHPYELI*		AACTGCAAGG	CAGAGAATAA	0	CE	0	0	0	0	0
7555	3529	af	AN4003.1	54.m06586	AO070328000160	0			-97	-17			ATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		ATGAAAGGCATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		MKGMTSVYIEDGARLAPQHSHPYELI*		MKGMTSVYIEDGARLAPQHSHPYELI*		TACCCTGTTT	CAGAGAATAA	0	CE	0	0	0	0	0
7556	3529	af	AN4003.1	54.m06586	AO070328000160	0			-88	-17			ATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		ATGACATCGGTATATATAGAGGACGGGGCCCGATTGGCTCCTCAGCACTCCCATCCATATGAACTTATTTAG		MTSVYIEDGARLAPQHSHPYELI*		MTSVYIEDGARLAPQHSHPYELI*		TATGAAAGGC	CAGAGAATAA	0	CE	0	0	0	0	0
7552	3529	an	AN4003.1	54.m06586	AO070328000160	0	-140	-57					ATGAACTCTCACGGTGACCCAACTTACAGGTTGCAGAGTCGGCTGAAGGATCAGCCGAATTGTTCTCCCGTCTACGACACATAA	ATGAACTCTCACGGTGACCCAACTTACAGGTTGCAGAGTCGGCTGAAGGATCAGCCGAATTGTTCTCCCGTCTACGACACATAA			MNSHGDPTYRLQSRLKDQPNCSPVYDT*	MNSHGDPTYRLQSRLKDQPNCSPVYDT*			ACTTGGGAGG	GAGGATGCAG	0	CE	0	0	0	0	0
7558	3529	ao	AN4003.1	54.m06586	AO070328000160	0					-194	-147	ATGAGTATGAGTATACGTGGGGCAGCTGCCCTACTCCGCAACGGGTAA			ATGAGTATGAGTATACGTGGGGCAGCTGCCCTACTCCGCAACGGGTAA	MSMSIRGAAALLRNG*			MSMSIRGAAALLRNG*	GAGTTGTTGA	ACCTTCAGCC	0	CE	0	0	0	0	0
7559	3529	ao	AN4003.1	54.m06586	AO070328000160	0					-188	-147	ATGAGTATACGTGGGGCAGCTGCCCTACTCCGCAACGGGTAA			ATGAGTATACGTGGGGCAGCTGCCCTACTCCGCAACGGGTAA	MSIRGAAALLRNG*			MSIRGAAALLRNG*	TTGAATGAGT	ACCTTCAGCC	0	CE	0	0	0	0	0
7560	3529	ao	AN4003.1	54.m06586	AO070328000160	0					-131	-93	ATGGCCGATGAAGTATGCTTAGCTTCATCCACGTCATGA			ATGGCCGATGAAGTATGCTTAGCTTCATCCACGTCATGA	MADEVCLASSTS*			MADEVCLASSTS*	CAGCCAGAAC	AGATTAAGGA	0	CE	0	0	0	0	0
7561	3529	ao	AN4003.1	54.m06586	AO070328000160	0					-124	-110	ATGAAGTATGCTTAG			ATGAAGTATGCTTAG	MKYA*			MKYA*	AACATGGCCG	CTTCATCCAC	0	CE	0	0	0	0	0
7562	3529	ao	AN4003.1	54.m06586	AO070328000160	0					-61	-47	ATGCAGGGTCTCTGA			ATGCAGGGTCTCTGA	MQGL*			MQGL*	TTTATAGTAG	TCTGACAAGT	0	CE	0	0	0	0	0
7563	3530	an	AN8038.1	53.m03908	AO070330000008	0	-120	-109					ATGACTAAGTAG	ATGACTAAGTAG			MTK*	MTK*			GATCGCTCCT	TCCGCTTGCA	0	A	0	0	0	0	0
7564	3530	ao	AN8038.1	53.m03908	AO070330000008	0					-143	-132	ATGTTTGAGTAG			ATGTTTGAGTAG	MFE*			MFE*	GGTCGCTCCT	CCCGTTCACG	0	A	0	0	0	0	0
7568	3531	af	AN8066.1	53.m03917	AO070330000022	0			-322	-266			ATGGTAAATACATGCATCAGCCACATTGCATGTGCCGTGACGTACGGAGTACTGTGA		ATGGTAAATACATGCATCAGCCACATTGCATGTGCCGTGACGTACGGAGTACTGTGA		MVNTCISHIACAVTYGVL*		MVNTCISHIACAVTYGVL*		TCGGTATTGT	CTTGATCGTA	0	J	0	MG00308.1	NCU09571.1	0	0
7569	3531	af	AN8066.1	53.m03917	AO070330000022	0			-311	-261			ATGCATCAGCCACATTGCATGTGCCGTGACGTACGGAGTACTGTGACTTGA		ATGCATCAGCCACATTGCATGTGCCGTGACGTACGGAGTACTGTGACTTGA		MHQPHCMCRDVRSTVT*		MHQPHCMCRDVRSTVT*		TGGTAAATAC	TCGTAAGATC	0	J	0	MG00308.1	NCU09571.1	0	0
7570	3531	af	AN8066.1	53.m03917	AO070330000022	0			-293	-261			ATGTGCCGTGACGTACGGAGTACTGTGACTTGA		ATGTGCCGTGACGTACGGAGTACTGTGACTTGA		MCRDVRSTVT*		MCRDVRSTVT*		GCCACATTGC	TCGTAAGATC	0	J	0	MG00308.1	NCU09571.1	0	0
7571	3531	af	AN8066.1	53.m03917	AO070330000022	0			-232	-44			ATGACGGACAGCTTATGTAATCTGTTATCAAGATTGCATCCTGATGTGGCCCCGTGCGTTTGCATCATGCGAAAGAAAAAAGAGTAGGGCAATTTTTGGTTATCAGTGCGTGATACGGCAGAATTTGTTGTGCAACATTTCCAAGTCCGCACTTCCCCGTAGCGGTATGTCTATCGCGAGACATGTGTGA		ATGACGGACAGCTTATGTAATCTGTTATCAAGATTGCATCCTGATGTGGCCCCGTGCGTTTGCATCATGCGAAAGAAAAAAGAGTAGGGCAATTTTTGGTTATCAGTGCGTGATACGGCAGAATTTGTTGTGCAACATTTCCAAGTCCGCACTTCCCCGTAGCGGTATGTCTATCGCGAGACATGTGTGA		MTDSLCNLLSRLHPDVARAFASCERKKSRAIFGYQCVIRQNLLCNISKSALPRSGMSIARHV*		MTDSLCNLLSRLHPDVARAFASCERKKSRAIFGYQCVIRQNLLCNISKSALPRSGMSIARHV*		GAGATCTACA	CTGCTGAAGC	0	J	0	MG00308.1	NCU09571.1	0	0
7572	3531	af	AN8066.1	53.m03917	AO070330000022	0			-189	-121			ATGTGGCCCGTGCGTTTGCATCATGCGAAAGAAAAAAGAGTAGGGCAATTTTTGGTTATCAGTGCGTGA		ATGTGGCCCGTGCGTTTGCATCATGCGAAAGAAAAAAGAGTAGGGCAATTTTTGGTTATCAGTGCGTGA		MWPVRLHHAKEKRVGQFLVISA*		MWPVRLHHAKEKRVGQFLVISA*		TTGCATCCTG	TACGGCAGAA	0	J	0	MG00308.1	NCU09571.1	0	0
7573	3531	af	AN8066.1	53.m03917	AO070330000022	0			-167	-147			ATGCGAAAGAAAAAAGAGTAG		ATGCGAAAGAAAAAAGAGTAG		MRKKKE*		MRKKKE*		CGTTTGCATC	GGCAATTTTT	0	J	0	MG00308.1	NCU09571.1	0	0
7574	3531	af	AN8066.1	53.m03917	AO070330000022	0			-67	-44			ATGTCTATCGCGAGACATGTGTGA		ATGTCTATCGCGAGACATGTGTGA		MSIARHV*		MSIARHV*		CCGTAGCGGT	CTGCTGAAGC	0	J	0	MG00308.1	NCU09571.1	0	0
7565	3531	an	AN8066.1	53.m03917	AO070330000022	0	-232	-197					ATGATTTTCAATACAACGGTATTGCGTCGTAACTAG	ATGATTTTCAATACAACGGTATTGCGTCGTAACTAG			MIFNTTVLRRN*	MIFNTTVLRRN*			CTGGCAGTTA	GGACTCTCTT	0	J	0	MG00308.1	NCU09571.1	0	0
7566	3531	an	AN8066.1	53.m03917	AO070330000022	0	-140	-63					ATGTCAGCCATCTTATCAAGATTCAATGGTCCGTGCGCCATCGCAAAGAAAAAAAGTCAAGAAATCTGCGACGGTTGA	ATGTCAGCCATCTTATCAAGATTCAATGGTCCGTGCGCCATCGCAAAGAAAAAAAGTCAAGAAATCTGCGACGGTTGA			MSAILSRFNGPCAIAKKKSQEICDG*	MSAILSRFNGPCAIAKKKSQEICDG*			TCCGCAAATT	CGGAAGCTCT	0	J	0	MG00308.1	NCU09571.1	0	0
7567	3531	an	AN8066.1	53.m03917	AO070330000022	0	-115	-20					ATGGTCCGTGCGCCATCGCAAAGAAAAAAAGTCAAGAAATCTGCGACGGTTGACGGAAGCTCTATACTTGACTGGAGCAAGATTGACCTGAATTAA	ATGGTCCGTGCGCCATCGCAAAGAAAAAAAGTCAAGAAATCTGCGACGGTTGACGGAAGCTCTATACTTGACTGGAGCAAGATTGACCTGAATTAA			MVRAPSQRKKVKKSATVDGSSILDWSKIDLN*	MVRAPSQRKKVKKSATVDGSSILDWSKIDLN*			TCAAGATTCA	GATCATATCG	0	J	0	MG00308.1	NCU09571.1	0	0
7576	3531	ao	AN8066.1	53.m03917	AO070330000022	0					-287	-213	ATGTTGCATGCCAAGCCACCGGGGATCAACCGCCACGCACGAACACCGTTAGCCATCGGACGGAATAACCTCTGA			ATGTTGCATGCCAAGCCACCGGGGATCAACCGCCACGCACGAACACCGTTAGCCATCGGACGGAATAACCTCTGA	MLHAKPPGINRHARTPLAIGRNNL*			MLHAKPPGINRHARTPLAIGRNNL*	CTGTATGCTT	TCCGAATAAA	0	J	0	MG00308.1	NCU09571.1	0	0
7577	3531	ao	AN8066.1	53.m03917	AO070330000022	0					-280	-236	ATGCCAAGCCACCGGGGATCAACCGCCACGCACGAACACCGTTAG			ATGCCAAGCCACCGGGGATCAACCGCCACGCACGAACACCGTTAG	MPSHRGSTATHEHR*			MPSHRGSTATHEHR*	CTTATGTTGC	CCATCGGACG	0	J	0	MG00308.1	NCU09571.1	0	0
7578	3531	ao	AN8066.1	53.m03917	AO070330000022	0					-186	-157	ATGGTCCGTGCGCTATCGCAAAAAAAGTAA			ATGGTCCGTGCGCTATCGCAAAAAAAGTAA	MVRALSQKK*			MVRALSQKK*	ATAATATCAT	AAAGAGCATT	0	J	0	MG00308.1	NCU09571.1	0	0
7579	3531	ao	AN8066.1	53.m03917	AO070330000022	0					-133	-113	ATGTCGTACGCGGTTTCTTAA			ATGTCGTACGCGGTTTCTTAA	MSYAVS*			MSYAVS*	ACACCCGCGC	CTTTGCGGAG	0	J	0	MG00308.1	NCU09571.1	0	0
7580	3531	ao	AN8066.1	53.m03917	AO070330000022	0					-95	-54	ATGGTCCATTCTAGTATAATTTTGTGCTACTGGAGATCATGA			ATGGTCCATTCTAGTATAATTTTGTGCTACTGGAGATCATGA	MVHSSIILCYWRS*			MVHSSIILCYWRS*	GAGAATTTTT	TCTAATACCC	0	J	0	MG00308.1	NCU09571.1	0	0
7582	3532	af	AN1230.1	70.m14989	AO070331000242	0			-140	-54			ATGACCTTAAATCAATTAACTTACTCTCTTTGTCAAACAGTTATCGGCTGTCGGCGATCCGGCGAGCTCGAGATTACCTTAGTGTAG		ATGACCTTAAATCAATTAACTTACTCTCTTTGTCAAACAGTTATCGGCTGTCGGCGATCCGGCGAGCTCGAGATTACCTTAGTGTAG		MTLNQLTYSLCQTVIGCRRSGELEITLV*		MTLNQLTYSLCQTVIGCRRSGELEITLV*		ACCAAGTCAC	TCCCAACCTA	0	O	0	0	0	0	0
7581	3532	an	AN1230.1	70.m14989	AO070331000242	0	-202	-176					ATGACAAGTCCCAGAGACTGGATTTGA	ATGACAAGTCCCAGAGACTGGATTTGA			MTSPRDWI*	MTSPRDWI*			ATACCTGACG	TTTTCTTCAG	0	O	0	0	0	0	0
7583	3532	ao	AN1230.1	70.m14989	AO070331000242	0					-178	-119	ATGCAAAAAACACGCCGGAAGGCAACCACGCGCCGGGAGAGACACGAAAATGCCGCCTAG			ATGCAAAAAACACGCCGGAAGGCAACCACGCGCCGGGAGAGACACGAAAATGCCGCCTAG	MQKTRRKATTRRERHENAA*			MQKTRRKATTRRERHENAA*	AGGGAATACT	TCACGGGATT	0	O	0	0	0	0	0
7584	3532	ao	AN1230.1	70.m14989	AO070331000242	0					-129	-58	ATGCCGCCTAGTCACGGGATTGTGGGCTTTCAATTTAACTTTCCGAAAGGTAAGCATGTGGATCTTTCTTAG			ATGCCGCCTAGTCACGGGATTGTGGGCTTTCAATTTAACTTTCCGAAAGGTAAGCATGTGGATCTTTCTTAG	MPPSHGIVGFQFNFPKGKHVDLS*			MPPSHGIVGFQFNFPKGKHVDLS*	AGACACGAAA	CAGATAGACC	0	O	0	0	0	0	0
7585	3532	ao	AN1230.1	70.m14989	AO070331000242	0					-74	-51	ATGTGGATCTTTCTTAGCAGATAG			ATGTGGATCTTTCTTAGCAGATAG	MWIFLSR*			MWIFLSR*	AAAGGTAAGC	ACCGAGTCTA	0	O	0	0	0	0	0
7586	3534	ao	AN9149.1	66.m04586	AO070332000147	0					-175	-128	ATGTTTAACATTTCCTACTTATCTTTGTTATTTGCAATTCCGCGTTAG			ATGTTTAACATTTCCTACTTATCTTTGTTATTTGCAATTCCGCGTTAG	MFNISYLSLLFAIPR*			MFNISYLSLLFAIPR*	ATATAATTTG	CTTATAAGAA	0	R	0	0	0	0	0
7587	3535	af	AN9075.1	66.m04774	AO070332000206	0			-155	-111			ATGCACTTTCTGTGCATCTGCTCTCTTTACGCCCTTTTCCACTGA		ATGCACTTTCTGTGCATCTGCTCTCTTTACGCCCTTTTCCACTGA		MHFLCICSLYALFH*		MHFLCICSLYALFH*		AGCTTGCAGC	GTCTATCGAC	0	CR	0	0	0	0	0
7593	3538	af	AN5013.1	59.m08664	AO070334000121	0			-165	-133			ATGTGTCCTCAGGATTACTCATATTTGATATAG		ATGTGTCCTCAGGATTACTCATATTTGATATAG		MCPQDYSYLI*		MCPQDYSYLI*		GGCAAGGAAG	ATTTGGACTC	0	L	0	MG06005.1	0	0	0
7588	3538	an	AN5013.1	59.m08664	AO070334000121	0	-276	-202					ATGATCAGACTTAATATCGTTATGACCTTAAGGATATCTCATAGCAAAACAGCAGATCCCTGTCCAACGTCATGA	ATGATCAGACTTAATATCGTTATGACCTTAAGGATATCTCATAGCAAAACAGCAGATCCCTGTCCAACGTCATGA			MIRLNIVMTLRISHSKTADPCPTS*	MIRLNIVMTLRISHSKTADPCPTS*			CCTTAATGCT	TCTCGTTATG	0	L	0	MG06005.1	0	0	0
7589	3538	an	AN5013.1	59.m08664	AO070334000121	0	-255	-202					ATGACCTTAAGGATATCTCATAGCAAAACAGCAGATCCCTGTCCAACGTCATGA	ATGACCTTAAGGATATCTCATAGCAAAACAGCAGATCCCTGTCCAACGTCATGA			MTLRISHSKTADPCPTS*	MTLRISHSKTADPCPTS*			TAATATCGTT	TCTCGTTATG	0	L	0	MG06005.1	0	0	0
7594	3542	af	AN5215.1	69.m14913	AO070337000264	0			-228	-190			ATGAAGCTTCGAGGATCGCGGTGTCACGTGAATAGTTAA		ATGAAGCTTCGAGGATCGCGGTGTCACGTGAATAGTTAA		MKLRGSRCHVNS*		MKLRGSRCHVNS*		TCGCCACCTG	CCCGCTTCAG	0	R	FG00848.1	0	NCU07492.1	YPL183C	YPL183C

7596	3542	ao	AN5215.1	69.m14913	AO070337000264	0					-195	-148	ATGCCTCATCTGGATATTTGCCTAAGGCGAGACTTGTGTATTACATAA			ATGCCTCATCTGGATATTTGCCTAAGGCGAGACTTGTGTATTACATAA	MPHLDICLRRDLCIT*			MPHLDICLRRDLCIT*	GTGCTCAATT	TCCGCCTCGC	0	R	FG00848.1	0	NCU07492.1	YPL183C	YPL183C
7597	3542	ao	AN5215.1	69.m14913	AO070337000264	0					-95	-66	ATGTGGGGAAGTGCTGCTGTACAAATTTGA			ATGTGGGGAAGTGCTGCTGTACAAATTTGA	MWGSAAVQI*			MWGSAAVQI*	TAATCGAGGC	GCGTCAGGAA	0	R	FG00848.1	0	NCU07492.1	YPL183C	YPL183C
7601	3543	af	AN2903.1	59.m08754	AO070338000102	0			-246	-214			ATGTTGATTTGCGGATCAAGAGCAGGGGCGTAG		ATGTTGATTTGCGGATCAAGAGCAGGGGCGTAG		MLICGSRAGA*		MLICGSRAGA*		CAGTTGCATC	CTCCGCAACC	0	O	FG10782.1	0	0	0	0
7598	3543	an	AN2903.1	59.m08754	AO070338000102	0	-236	-213					ATGACGCAGCCGGTGCTCCGATGA	ATGACGCAGCCGGTGCTCCGATGA			MTQPVLR*	MTQPVLR*			GCCGAGTCCG	TTGGCTGGGC	0	O	FG10782.1	0	0	0	0
7599	3543	an	AN2903.1	59.m08754	AO070338000102	0	-216	-157					ATGATTGGCTGGGCCCCCATGTCGCTCCGCAACCAGAGCAAGTCACCCGGGGCCGCCTGA	ATGATTGGCTGGGCCCCCATGTCGCTCCGCAACCAGAGCAAGTCACCCGGGGCCGCCTGA			MIGWAPMSLRNQSKSPGAA*	MIGWAPMSLRNQSKSPGAA*			CGGTGCTCCG	GCAGTGCATC	0	O	FG10782.1	0	0	0	0
7600	3543	an	AN2903.1	59.m08754	AO070338000102	0	-198	-157					ATGTCGCTCCGCAACCAGAGCAAGTCACCCGGGGCCGCCTGA	ATGTCGCTCCGCAACCAGAGCAAGTCACCCGGGGCCGCCTGA			MSLRNQSKSPGAA*	MSLRNQSKSPGAA*			CTGGGCCCCC	GCAGTGCATC	0	O	FG10782.1	0	0	0	0
7602	3543	ao	AN2903.1	59.m08754	AO070338000102	0					-255	-232	ATGACGCATCGAGTTGCTCCCTGA			ATGACGCATCGAGTTGCTCCCTGA	MTHRVAP*			MTHRVAP*	CTTCAATCCA	TTGGTTGATA	0	O	FG10782.1	0	0	0	0
7604	3544	af	AN7836.1	66.m04663	AO070338000245	0			-140	-18			ATGGCTGCTGGCAGCTACAAGTACACAGAGTGCACTGGCCGAAATATAAAACGAGCAAAACCCACGGCCAGAAACCTCTCACTAATCAGTAACCAACCCACAAGACATCCCATCCAGCTTTAG		ATGGCTGCTGGCAGCTACAAGTACACAGAGTGCACTGGCCGAAATATAAAACGAGCAAAACCCACGGCCAGAAACCTCTCACTAATCAGTAACCAACCCACAAGACATCCCATCCAGCTTTAG		MAAGSYKYTECTGRNIKRAKPTARNLSLISNQPTRHPIQL*		MAAGSYKYTECTGRNIKRAKPTARNLSLISNQPTRHPIQL*		TGAGAACATC	TTGAACAATC	0		0	0	0	0	0
7603	3544	an	AN7836.1	66.m04663	AO070338000245	0	-148	-137					ATGTTCCGATGA	ATGTTCCGATGA			MFR*	MFR*			GTAGACTGGG	TGAAGTTGTT	0		0	0	0	0	0
7605	3544	ao	AN7836.1	66.m04663	AO070338000245	0					-178	-164	ATGTTGTGGAGCTGA			ATGTTGTGGAGCTGA	MLWS*			MLWS*	AGGGTGCGAG	GAGTATGGTA	0		0	0	0	0	0
7606	3544	ao	AN7836.1	66.m04663	AO070338000245	0					-159	-100	ATGGTATGGGGGGTTCCTACCCCCAACAATTCCAAATATCCAAGTCTCACAATTCTATAA			ATGGTATGGGGGGTTCCTACCCCCAACAATTCCAAATATCCAAGTCTCACAATTCTATAA	MVWGVPTPNNSKYPSLTIL*			MVWGVPTPNNSKYPSLTIL*	AGCTGAGAGT	GAAGAGCATC	0		0	0	0	0	0
7613	3545	af	AN3313.1	65.m07345	AO070339000070	0			-121	-65			ATGACCCGTCAAGTGTCTAACCTAATCAGGAAATGTCCTTATCTGATAAACTTTTGA		ATGACCCGTCAAGTGTCTAACCTAATCAGGAAATGTCCTTATCTGATAAACTTTTGA		MTRQVSNLIRKCPYLINF*		MTRQVSNLIRKCPYLINF*		CATAAATCAC	TAAAAAATTT	0	A	0	0	0	0	0
7607	3545	an	AN3313.1	65.m07345	AO070339000070	0	-257	-243					ATGCATCATCCGTGA	ATGCATCATCCGTGA			MHHP*	MHHP*			GGAAAGTCCA	ATCGAACACG	0	A	0	0	0	0	0
7608	3545	an	AN3313.1	65.m07345	AO070339000070	0	-222	-76					ATGGCAACGATGAATTCTACCACTAGACCAATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA	ATGGCAACGATGAATTCTACCACTAGACCAATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA			MATMNSTTRPMMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*	MATMNSTTRPMMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*			GGCCTCATCG	GCAAAAAAGA	0	A	0	0	0	0	0
7609	3545	an	AN3313.1	65.m07345	AO070339000070	0	-213	-76					ATGAATTCTACCACTAGACCAATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA	ATGAATTCTACCACTAGACCAATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA			MNSTTRPMMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*	MNSTTRPMMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*			GATGGCAACG	GCAAAAAAGA	0	A	0	0	0	0	0
7610	3545	an	AN3313.1	65.m07345	AO070339000070	0	-192	-76					ATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA	ATGATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA			MMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*	MMLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*			CACTAGACCA	GCAAAAAAGA	0	A	0	0	0	0	0
7611	3545	an	AN3313.1	65.m07345	AO070339000070	0	-189	-76					ATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA	ATGCTTTTTTTCATAAAACATATAAATTTTGACAAAATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA			MLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*	MLFFIKHINFDKMFRILNSLKLRPYHHVLAPPPHLGR*			TAGACCAATG	GCAAAAAAGA	0	A	0	0	0	0	0
7612	3545	an	AN3313.1	65.m07345	AO070339000070	0	-153	-76					ATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA	ATGTTCCGAATATTAAACAGCCTGAAATTACGTCCTTATCACCACGTGCTCGCTCCACCGCCGCACCTGGGCCGATAA			MFRILNSLKLRPYHHVLAPPPHLGR*	MFRILNSLKLRPYHHVLAPPPHLGR*			TTTTGACAAA	GCAAAAAAGA	0	A	0	0	0	0	0
7614	3545	ao	AN3313.1	65.m07345	AO070339000070	0					-168	-136	ATGCATTCTCAGGTGACCTCGGTCCCTGAATGA			ATGCATTCTCAGGTGACCTCGGTCCCTGAATGA	MHSQVTSVPE*			MHSQVTSVPE*	TAACAGCTTT	CTCAGCATCC	0	A	0	0	0	0	0
7615	3545	ao	AN3313.1	65.m07345	AO070339000070	0					-139	-74	ATGACTCAGCATCCTATCAGAACATCAGGTGATTTATCAGTACAGTCACGTGCCACATCCCGCTGA			ATGACTCAGCATCCTATCAGAACATCAGGTGATTTATCAGTACAGTCACGTGCCACATCCCGCTGA	MTQHPIRTSGDLSVQSRATSR*			MTQHPIRTSGDLSVQSRATSR*	CGGTCCCTGA	TAACGCATGA	0	A	0	0	0	0	0
7616	3545	ao	AN3313.1	65.m07345	AO070339000070	0					-67	-23	ATGAATTTTTTGGAGATCAACAAAATTCCCGCGGTGACGAATTAA			ATGAATTTTTTGGAGATCAACAAAATTCCCGCGGTGACGAATTAA	MNFLEINKIPAVTN*			MNFLEINKIPAVTN*	CTGATAACGC	AATAACCACC	0	A	0	0	0	0	0
7618	3547	af	AN6116.1	72.m19043	AO070340000088	0			-187	-65			ATGAATGCAGTGTTAATTTGGGGTGTTGTGATTTGGGCTGATTGTGATGGTGTCATTCCCCTCTTTGGCTCGCGAGGCATTTATTATCTGCCCTCGTCCTGGACCACTTGTCCCTCCTTCTGA		ATGAATGCAGTGTTAATTTGGGGTGTTGTGATTTGGGCTGATTGTGATGGTGTCATTCCCCTCTTTGGCTCGCGAGGCATTTATTATCTGCCCTCGTCCTGGACCACTTGTCCCTCCTTCTGA		MNAVLIWGVVIWADCDGVIPLFGSRGIYYLPSSWTTCPSF*		MNAVLIWGVVIWADCDGVIPLFGSRGIYYLPSSWTTCPSF*		CACTTGTGGG	CGGTGAAGAA	0		0	0	0	0	0
7619	3547	af	AN6116.1	72.m19043	AO070340000088	0			-183	-172			ATGCAGTGTTAA		ATGCAGTGTTAA		MQC*		MQC*		TGTGGGATGA	TTTGGGGTGT	0		0	0	0	0	0
7620	3547	af	AN6116.1	72.m19043	AO070340000088	0			-141	-31			ATGGTGTCATTCCCCTCTTTGGCTCGCGAGGCATTTATTATCTGCCCTCGTCCTGGACCACTTGTCCCTCCTTCTGACGGTGAAGAAGATTTCCTTCTCAGCCTGCTCTAG		ATGGTGTCATTCCCCTCTTTGGCTCGCGAGGCATTTATTATCTGCCCTCGTCCTGGACCACTTGTCCCTCCTTCTGACGGTGAAGAAGATTTCCTTCTCAGCCTGCTCTAG		MVSFPSLAREAFIICPRPGPLVPPSDGEEDFLLSLL*		MVSFPSLAREAFIICPRPGPLVPPSDGEEDFLLSLL*		GCTGATTGTG	AGACGAGAAA	0		0	0	0	0	0
7617	3547	an	AN6116.1	72.m19043	AO070340000088	0	-127	-38					ATGGAGGGGAGGTTATTTATCGATCCAGTCCCTGCTGCGCGTCCCCTGTCACAGCTGCTTGTGCAACTCACCATCTTCAAATTCTACTAA	ATGGAGGGGAGGTTATTTATCGATCCAGTCCCTGCTGCGCGTCCCCTGTCACAGCTGCTTGTGCAACTCACCATCTTCAAATTCTACTAA			MEGRLFIDPVPAARPLSQLLVQLTIFKFY*	MEGRLFIDPVPAARPLSQLLVQLTIFKFY*			GAGAGCCTGC	GCATTCAAAG	0		0	0	0	0	0
7621	3547	ao	AN6116.1	72.m19043	AO070340000088	0					-203	-162	ATGACAATAATCCCATCTGGCATGACGAGGAAAAAAATATAA			ATGACAATAATCCCATCTGGCATGACGAGGAAAAAAATATAA	MTIIPSGMTRKKI*			MTIIPSGMTRKKI*	GTTGACTCTC	TAAGATCTTG	0		0	0	0	0	0
7622	3547	ao	AN6116.1	72.m19043	AO070340000088	0					-182	-162	ATGACGAGGAAAAAAATATAA			ATGACGAGGAAAAAAATATAA	MTRKKI*			MTRKKI*	CCCATCTGGC	TAAGATCTTG	0		0	0	0	0	0
7623	3547	ao	AN6116.1	72.m19043	AO070340000088	0					-151	-14	ATGGGTTTCCCCAGGCCTTCCTTCCTCTTCTCCTTTTCATCATCAAACCCTCCAGAGAATAACCTGGGGTTGTCCGTGGTTTGGAACCACGTTACTCTCTCTGAACAACCCTATCCTATACTTCATCTGTTCTTTTGA			ATGGGTTTCCCCAGGCCTTCCTTCCTCTTCTCCTTTTCATCATCAAACCCTCCAGAGAATAACCTGGGGTTGTCCGTGGTTTGGAACCACGTTACTCTCTCTGAACAACCCTATCCTATACTTCATCTGTTCTTTTGA	MGFPRPSFLFSFSSSNPPENNLGLSVVWNHVTLSEQPYPILHLFF*			MGFPRPSFLFSFSSSNPPENNLGLSVVWNHVTLSEQPYPILHLFF*	TAAGATCTTG	TCAATCATCC	0		0	0	0	0	0
7624	3548	ao	AN6112.1	72.m19046	AO070340000093	0					-165	-109	ATGATTATTGGTTTTTTCTCTTGCACTCCCTTGCGCAATCCAAAACCCCAGCTATAG			ATGATTATTGGTTTTTTCTCTTGCACTCCCTTGCGCAATCCAAAACCCCAGCTATAG	MIIGFFSCTPLRNPKPQL*			MIIGFFSCTPLRNPKPQL*	TTCAAGTTTC	TCGTTCCATA	0	R	0	0	0	YAL026C	YAL026C
7625	3550	an	AN3953.1	69.m14967	AO070341000070	0	-88	-62					ATGACTGCTGCGTCAGTCAAGCCCTGA	ATGACTGCTGCGTCAGTCAAGCCCTGA			MTAASVKP*	MTAASVKP*			CGTCTGGCGT	AGGTACGTGT	0	R	0	0	0	0	0
7629	3551	af	AN2099.1	57.m05801	AO070341000258	0			-271	-149			ATGATGAGAAAATTTCCTTGTTTCATTCCAGATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAGATATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		ATGATGAGAAAATTTCCTTGTTTCATTCCAGATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAGATATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		MMRKFPCFIPDECPLFLFGSASLPVFAIDMTLQIFGRLRI*		MMRKFPCFIPDECPLFLFGSASLPVFAIDMTLQIFGRLRI*		GAGATTTTCT	AGGACATGAC	0		0	0	0	0	0
7630	3551	af	AN2099.1	57.m05801	AO070341000258	0			-268	-149			ATGAGAAAATTTCCTTGTTTCATTCCAGATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAGATATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		ATGAGAAAATTTCCTTGTTTCATTCCAGATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAGATATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		MRKFPCFIPDECPLFLFGSASLPVFAIDMTLQIFGRLRI*		MRKFPCFIPDECPLFLFGSASLPVFAIDMTLQIFGRLRI*		ATTTTCTATG	AGGACATGAC	0		0	0	0	0	0
7631	3551	af	AN2099.1	57.m05801	AO070341000258	0			-240	-187			ATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAG		ATGAGTGCCCACTGTTTTTGTTTGGTTCCGCATCGCTTCCGGTTTTTGCCATAG		MSAHCFCLVPHRFRFLP*		MSAHCFCLVPHRFRFLP*		TTCATTCCAG	ATATGACTCT	0		0	0	0	0	0
7632	3551	af	AN2099.1	57.m05801	AO070341000258	0			-184	-149			ATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		ATGACTCTGCAAATATTTGGTCGGTTGCGTATATAA		MTLQIFGRLRI*		MTLQIFGRLRI*		TGCCATAGAT	AGGACATGAC	0		0	0	0	0	0
7633	3551	af	AN2099.1	57.m05801	AO070341000258	0			-143	-132			ATGACTGTATAG		ATGACTGTATAG		MTV*		MTV*		TATAAAGGAC	ACCATAAGCT	0		0	0	0	0	0
7626	3551	an	AN2099.1	57.m05801	AO070341000258	0	-265	-158					ATGAAAAGTTCTGTTCGGCGGCGAGCGTGTGACTCCTGTGTGCGGGTACTCAGCCCTGAGAGTTCCGATTCCTGCCTCAGATTGCCTCTGGTTGAATTTTTTTTATAG	ATGAAAAGTTCTGTTCGGCGGCGAGCGTGTGACTCCTGTGTGCGGGTACTCAGCCCTGAGAGTTCCGATTCCTGCCTCAGATTGCCTCTGGTTGAATTTTTTTTATAG			MKSSVRRRACDSCVRVLSPESSDSCLRLPLVEFFL*	MKSSVRRRACDSCVRVLSPESSDSCLRLPLVEFFL*			CTTTCGGTGA	GTCTTTGTAT	0		0	0	0	0	0
7634	3551	ao	AN2099.1	57.m05801	AO070341000258	0					-207	-154	ATGACAGTATATTGTTCTCATTTGGTTCCGGCCTTATTCCGATTTCTGCCATAA			ATGACAGTATATTGTTCTCATTTGGTTCCGGCCTTATTCCGATTTCTGCCATAA	MTVYCSHLVPALFRFLP*			MTVYCSHLVPALFRFLP*	TTTGCGCCCT	GCTTCTTATC	0		0	0	0	0	0
7635	3551	ao	AN2099.1	57.m05801	AO070341000258	0					-102	-28	ATGTCCAGTAAACAGCAAGCCTTTTGTGATCAAAGCACGACTCTTTCTACTACTACTTCACCCCAAGACCATTAA			ATGTCCAGTAAACAGCAAGCCTTTTGTGATCAAAGCACGACTCTTTCTACTACTACTTCACCCCAAGACCATTAA	MSSKQQAFCDQSTTLSTTTSPQDH*			MSSKQQAFCDQSTTLSTTTSPQDH*	TAGCTTCCCA	TCAGTTTATC	0		0	0	0	0	0
7639	3552	af	AN9054.1	57.m05358	AO070341000361	0			-107	-51			ATGCGTGCATTCCAGGGAGCCTCCGTCACCAGTAACCATAAATCAAGAAATGTATAA		ATGCGTGCATTCCAGGGAGCCTCCGTCACCAGTAACCATAAATCAAGAAATGTATAA		MRAFQGASVTSNHKSRNV*		MRAFQGASVTSNHKSRNV*		CGCGTTGTTG	AACGAGGAAT	0		0	0	0	0	0
7636	3552	an	AN9054.1	57.m05358	AO070341000361	0	-255	-127					ATGGGAGCCAGAAGCTTTCCCCAGCCAACGCAATTCTTGGATTTTCAAACCTTGATCCTGGACGATCCCTCCCATGGGCTAATCCTTTCGGATATCAAGGAATGTATGTGTCACCACACTAACCAATAA	ATGGGAGCCAGAAGCTTTCCCCAGCCAACGCAATTCTTGGATTTTCAAACCTTGATCCTGGACGATCCCTCCCATGGGCTAATCCTTTCGGATATCAAGGAATGTATGTGTCACCACACTAACCAATAA			MGARSFPQPTQFLDFQTLILDDPSHGLILSDIKECMCHHTNQ*	MGARSFPQPTQFLDFQTLILDDPSHGLILSDIKECMCHHTNQ*			TTCCCTCATC	TATTTCCTCC	0		0	0	0	0	0
7637	3552	an	AN9054.1	57.m05358	AO070341000361	0	-154	-134					ATGTATGTGTCACCACACTAA	ATGTATGTGTCACCACACTAA			MYVSPH*	MYVSPH*			ATATCAAGGA	CCAATAATAT	0		0	0	0	0	0
7638	3552	an	AN9054.1	57.m05358	AO070341000361	0	-150	-127					ATGTGTCACCACACTAACCAATAA	ATGTGTCACCACACTAACCAATAA			MCHHTNQ*	MCHHTNQ*			CAAGGAATGT	TATTTCCTCC	0		0	0	0	0	0
7640	3552	ao	AN9054.1	57.m05358	AO070341000361	0					-219	-166	ATGCGCCACGAATACATGTCAGATCACCAAGTTCCAGGCCAGCTGATAATATAG			ATGCGCCACGAATACATGTCAGATCACCAAGTTCCAGGCCAGCTGATAATATAG	MRHEYMSDHQVPGQLII*			MRHEYMSDHQVPGQLII*	CGTATTTCAG	CATTCCAGAC	0		0	0	0	0	0
7641	3552	ao	AN9054.1	57.m05358	AO070341000361	0					-204	-166	ATGTCAGATCACCAAGTTCCAGGCCAGCTGATAATATAG			ATGTCAGATCACCAAGTTCCAGGCCAGCTGATAATATAG	MSDHQVPGQLII*			MSDHQVPGQLII*	CCACGAATAC	CATTCCAGAC	0		0	0	0	0	0
7642	3552	ao	AN9054.1	57.m05358	AO070341000361	0					-100	-74	ATGTTTGCAGGGAAGTGGCGTATATAA			ATGTTTGCAGGGAAGTGGCGTATATAA	MFAGKWRI*			MFAGKWRI*	CTTGAAGACC	GATCCTTTCG	0		0	0	0	0	0
7643	3553	af	AN4065.1	54.m06709	AO070342000055	0			-157	-92			ATGGCAGGCGGTGAGCACCGGATGAATATTTTTTCTTTTTCTGCCAGTAACTCCAACTTTTTCTGA		ATGGCAGGCGGTGAGCACCGGATGAATATTTTTTCTTTTTCTGCCAGTAACTCCAACTTTTTCTGA		MAGGEHRMNIFSFSASNSNFF*		MAGGEHRMNIFSFSASNSNFF*		TGCAGGGCGG	TTAAAAAGCA	0	J	0	0	0	0	0
7644	3553	af	AN4065.1	54.m06709	AO070342000055	0			-136	-92			ATGAATATTTTTTCTTTTTCTGCCAGTAACTCCAACTTTTTCTGA		ATGAATATTTTTTCTTTTTCTGCCAGTAACTCCAACTTTTTCTGA		MNIFSFSASNSNFF*		MNIFSFSASNSNFF*		TGAGCACCGG	TTAAAAAGCA	0	J	0	0	0	0	0
7648	3555	af	AN5662.1	58.m07312	AO070342000256	0			-242	-168			ATGGAGATGTCTGGAGTTCGGAGTCCGGAGAAGTTTTCAAATGGTGGGAGCCTCGAAACGGTAAAGTGTCGCTAG		ATGGAGATGTCTGGAGTTCGGAGTCCGGAGAAGTTTTCAAATGGTGGGAGCCTCGAAACGGTAAAGTGTCGCTAG		MEMSGVRSPEKFSNGGSLETVKCR*		MEMSGVRSPEKFSNGGSLETVKCR*		GTTGGAATTG	CCGCCAGGGC	0	J	0	0	0	YIL078W	YIL078W
7649	3555	af	AN5662.1	58.m07312	AO070342000256	0			-236	-168			ATGTCTGGAGTTCGGAGTCCGGAGAAGTTTTCAAATGGTGGGAGCCTCGAAACGGTAAAGTGTCGCTAG		ATGTCTGGAGTTCGGAGTCCGGAGAAGTTTTCAAATGGTGGGAGCCTCGAAACGGTAAAGTGTCGCTAG		MSGVRSPEKFSNGGSLETVKCR*		MSGVRSPEKFSNGGSLETVKCR*		ATTGATGGAG	CCGCCAGGGC	0	J	0	0	0	YIL078W	YIL078W

7650	3555	af	AN5662.1	58.m07312	AO070342000256	0			-202	-179			ATGGTGGGAGCCTCGAAACGGTAA		ATGGTGGGAGCCTCGAAACGGTAA		MVGASKR*		MVGASKR*		AAGTTTTCAA	AGTGTCGCTA	0	J	0	0	0	YIL078W	YIL078W
7651	3555	af	AN5662.1	58.m07312	AO070342000256	0			-151	-110			ATGTCACGTGCTTCACCGCCTTCCTTCCCCTCACCGTTCTGA		ATGTCACGTGCTTCACCGCCTTCCTTCCCCTCACCGTTCTGA		MSRASPPSFPSPF*		MSRASPPSFPSPF*		GGGCAGTTTA	ATTATTACGA	0	J	0	0	0	YIL078W	YIL078W
7645	3555	an	AN5662.1	58.m07312	AO070342000256	0	-230	-99					ATGTTGGGGTTGTTCTTGTCGACCTGGTGCGGACTGAAGCGGAGAAGTTTTCAAACGGCGGGAGCCTCAAAGGAAAATGTTGCTAGCCGAGTTACTCACCGCCTTCCGGGTAGGTATGATTCACAGATCTGA	ATGTTGGGGTTGTTCTTGTCGACCTGGTGCGGACTGAAGCGGAGAAGTTTTCAAACGGCGGGAGCCTCAAAGGAAAATGTTGCTAGCCGAGTTACTCACCGCCTTCCGGGTAGGTATGATTCACAGATCTGA			MLGLFLSTWCGLKRRSFQTAGASKENVASRVTHRLPGRYDSQI*	MLGLFLSTWCGLKRRSFQTAGASKENVASRVTHRLPGRYDSQI*			TGACATCTTG	GTCAACTTTC	0	J	0	0	0	YIL078W	YIL078W
7646	3555	an	AN5662.1	58.m07312	AO070342000256	0	-154	-86					ATGTTGCTAGCCGAGTTACTCACCGCCTTCCGGGTAGGTATGATTCACAGATCTGAGTCAACTTTCTAG	ATGTTGCTAGCCGAGTTACTCACCGCCTTCCGGGTAGGTATGATTCACAGATCTGAGTCAACTTTCTAG			MLLAELLTAFRVGMIHRSESTF*	MLLAELLTAFRVGMIHRSESTF*			TCAAAGGAAA	AGGCTTGAGA	0	J	0	0	0	YIL078W	YIL078W
7647	3555	an	AN5662.1	58.m07312	AO070342000256	0	-115	-86					ATGATTCACAGATCTGAGTCAACTTTCTAG	ATGATTCACAGATCTGAGTCAACTTTCTAG			MIHRSESTF*	MIHRSESTF*			CCGGGTAGGT	AGGCTTGAGA	0	J	0	0	0	YIL078W	YIL078W
7652	3555	ao	AN5662.1	58.m07312	AO070342000256	0					-205	-182	ATGGTGGGAAGCTCGAAACGGTAA			ATGGTGGGAAGCTCGAAACGGTAA	MVGSSKR*			MVGSSKR*	AAGTTTTCAA	AGTGTCGCTA	0	J	0	0	0	YIL078W	YIL078W
7653	3556	af	AN3738.1	69.m15377	AO070342000269	0			-279	-247			ATGAAGATGACTCATTATCCGCAATCAAGGTAA		ATGAAGATGACTCATTATCCGCAATCAAGGTAA		MKMTHYPQSR*		MKMTHYPQSR*		ATCGATTGAA	AGTATGATTC	0	S	0	0	0	0	0
7654	3556	af	AN3738.1	69.m15377	AO070342000269	0			-273	-247			ATGACTCATTATCCGCAATCAAGGTAA		ATGACTCATTATCCGCAATCAAGGTAA		MTHYPQSR*		MTHYPQSR*		TGAAATGAAG	AGTATGATTC	0	S	0	0	0	0	0
7655	3556	af	AN3738.1	69.m15377	AO070342000269	0			-243	-202			ATGATTCCATGGCTAATTGCTGTGACCTGGACTGCCTGCTGA		ATGATTCCATGGCTAATTGCTGTGACCTGGACTGCCTGCTGA		MIPWLIAVTWTAC*		MIPWLIAVTWTAC*		AAGGTAAAGT	ATTGGTCAAG	0	S	0	0	0	0	0
7656	3556	af	AN3738.1	69.m15377	AO070342000269	0			-235	-179			ATGGCTAATTGCTGTGACCTGGACTGCCTGCTGAATTGGTCAAGAATGCATTCATGA		ATGGCTAATTGCTGTGACCTGGACTGCCTGCTGAATTGGTCAAGAATGCATTCATGA		MANCCDLDCLLNWSRMHS*		MANCCDLDCLLNWSRMHS*		GTATGATTCC	CAGGAAGATC	0	S	0	0	0	0	0
7657	3556	af	AN3738.1	69.m15377	AO070342000269	0			-190	-179			ATGCATTCATGA		ATGCATTCATGA		MHS*		MHS*		TTGGTCAAGA	CAGGAAGATC	0	S	0	0	0	0	0
7658	3556	af	AN3738.1	69.m15377	AO070342000269	0			-182	-84			ATGACAGGAAGATCAGTTTGGCTCAGCTCAGACCACCGCTTATACCAAGATTCCTTCTCCGGCTGGCCCGACGTTCCATCCTATTCATCAAGCCACTAG		ATGACAGGAAGATCAGTTTGGCTCAGCTCAGACCACCGCTTATACCAAGATTCCTTCTCCGGCTGGCCCGACGTTCCATCCTATTCATCAAGCCACTAG		MTGRSVWLSSDHRLYQDSFSGWPDVPSYSSSH*		MTGRSVWLSSDHRLYQDSFSGWPDVPSYSSSH*		GAATGCATTC	TAACTTTGCC	0	S	0	0	0	0	0
7660	3558	ao	AN0661.1	70.m15264	AO070343000559	0					-230	-153	ATGACCCAGAGTTTCACCAGCACTAATTTTCTGTCTTTCATCCTTCCTTGCCCACCGAGCTCTGCTCTCTCCTTTTGA			ATGACCCAGAGTTTCACCAGCACTAATTTTCTGTCTTTCATCCTTCCTTGCCCACCGAGCTCTGCTCTCTCCTTTTGA	MTQSFTSTNFLSFILPCPPSSALSF*			MTQSFTSTNFLSFILPCPPSSALSF*	CTTAGCATAT	CTCTAAACGG	0		0	0	0	0	0
7662	3562	af	AN1434.1	55.m02940	AO070232000012	0			-200	-51			ATGGCAATGCAGGTTCTCAAAGGACATATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		ATGGCAATGCAGGTTCTCAAAGGACATATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		MAMQVLKGHMRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		MAMQVLKGHMRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		CCATATTGCT	AAATTTCGGT	0	J	0	0	0	0	0
7663	3562	af	AN1434.1	55.m02940	AO070232000012	0			-194	-51			ATGCAGGTTCTCAAAGGACATATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		ATGCAGGTTCTCAAAGGACATATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		MQVLKGHMRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		MQVLKGHMRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		TGCTATGGCA	AAATTTCGGT	0	J	0	0	0	0	0
7664	3562	af	AN1434.1	55.m02940	AO070232000012	0			-173	-51			ATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		ATGCGTGTGAGGAGAAAGCGGAGTAGTTCGGTCATCTCAAAAGCGGTGCGGCAGAATTTCCCCCCGGCGAGAGCGGTGAGCCTACTTTTTTGCGGACAATCATTGAAAAATGCATCGTCTTAA		MRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		MRVRRKRSSSVISKAVRQNFPPARAVSLLFCGQSLKNASS*		CAAAGGACAT	AAATTTCGGT	0	J	0	0	0	0	0
7661	3562	an	AN1434.1	55.m02940	AO070232000012	0	-141	-106					ATGTCATCGAGGGTGACGCCCGGAAAGCGGAGATAA	ATGTCATCGAGGGTGACGCCCGGAAAGCGGAGATAA			MSSRVTPGKRR*	MSSRVTPGKRR*			TCCATTGTCG	GAAGCGGCAA	0	J	0	0	0	0	0
7665	3562	ao	AN1434.1	55.m02940	AO070232000012	0					-186	-124	ATGAGAACAAGAACGATCTATACTCATGGTATTGTAGAAAAGCGGAGAGTAATGACGATCTAA			ATGAGAACAAGAACGATCTATACTCATGGTATTGTAGAAAAGCGGAGAGTAATGACGATCTAA	MRTRTIYTHGIVEKRRVMTI*			MRTRTIYTHGIVEKRRVMTI*	ATGGTTCGGT	AGACAAACCG	0	J	0	0	0	0	0
7666	3562	ao	AN1434.1	55.m02940	AO070232000012	0					-161	-150	ATGGTATTGTAG			ATGGTATTGTAG	MVL*			MVL*	ATCTATACTC	AAAAGCGGAG	0	J	0	0	0	0	0
7667	3562	ao	AN1434.1	55.m02940	AO070232000012	0					-135	-124	ATGACGATCTAA			ATGACGATCTAA	MTI*			MTI*	GCGGAGAGTA	AGACAAACCG	0	J	0	0	0	0	0
7668	3563	af	AN4236.1	54.m06779	AO070234000007	0			-226	-197			ATGAGCGGAGGCGGTCGAGGACGCCAGTAG		ATGAGCGGAGGCGGTCGAGGACGCCAGTAG		MSGGGRGRQ*		MSGGGRGRQ*		TCAGTTCGTA	AGATCAATAT	0	O	0	0	0	0	0
7669	3563	ao	AN4236.1	54.m06779	AO070234000007	0					-255	-211	ATGGTACCATCGTGTAGGATGCGAACTATACCATTCATGACCTGA			ATGGTACCATCGTGTAGGATGCGAACTATACCATTCATGACCTGA	MVPSCRMRTIPFMT*			MVPSCRMRTIPFMT*	CACAATTCAA	GGCACCAACA	0	O	0	0	0	0	0
7670	3563	ao	AN4236.1	54.m06779	AO070234000007	0					-237	-211	ATGCGAACTATACCATTCATGACCTGA			ATGCGAACTATACCATTCATGACCTGA	MRTIPFMT*			MRTIPFMT*	ATCGTGTAGG	GGCACCAACA	0	O	0	0	0	0	0
7673	3564	af	AN5892.1	72.m19236	AO070245000010	0			-255	-244			ATGCCTACCTAG		ATGCCTACCTAG		MPT*		MPT*		TAATGTCGAA	GTGATTCGGT	0	L	0	0	0	0	0
7674	3564	af	AN5892.1	72.m19236	AO070245000010	0			-194	-114			ATGCTTGGTTTGGATGTGTCCCATGGGCATCAACACCGGCCATTGACCTTCGACAACGCTCAATGTCTGTCTAACGTTTAA		ATGCTTGGTTTGGATGTGTCCCATGGGCATCAACACCGGCCATTGACCTTCGACAACGCTCAATGTCTGTCTAACGTTTAA		MLGLDVSHGHQHRPLTFDNAQCLSNV*		MLGLDVSHGHQHRPLTFDNAQCLSNV*		TAAGCGGTTT	GGAAATTTTA	0	L	0	0	0	0	0
7675	3564	af	AN5892.1	72.m19236	AO070245000010	0			-181	-149			ATGTGTCCCATGGGCATCAACACCGGCCATTGA		ATGTGTCCCATGGGCATCAACACCGGCCATTGA		MCPMGINTGH*		MCPMGINTGH*		CTTGGTTTGG	CCTTCGACAA	0	L	0	0	0	0	0
7676	3564	af	AN5892.1	72.m19236	AO070245000010	0			-172	-149			ATGGGCATCAACACCGGCCATTGA		ATGGGCATCAACACCGGCCATTGA		MGINTGH*		MGINTGH*		GATGTGTCCC	CCTTCGACAA	0	L	0	0	0	0	0
7677	3564	af	AN5892.1	72.m19236	AO070245000010	0			-132	-121			ATGTCTGTCTAA		ATGTCTGTCTAA		MSV*		MSV*		ACAACGCTCA	CGTTTAAGGA	0	L	0	0	0	0	0
7671	3564	an	AN5892.1	72.m19236	AO070245000010	0	-254	-177					ATGCTCCCCTTTGCTGATGAACAAGATATCCTCTCACGATCCGTCTCTGCAATTTCCCCCGGCGGACGTTTCGTCTAA	ATGCTCCCCTTTGCTGATGAACAAGATATCCTCTCACGATCCGTCTCTGCAATTTCCCCCGGCGGACGTTTCGTCTAA			MLPFADEQDILSRSVSAISPGGRFV*	MLPFADEQDILSRSVSAISPGGRFV*			CCCATTCTAT	GAACCGCCGA	0	L	0	0	0	0	0
7672	3564	an	AN5892.1	72.m19236	AO070245000010	0	-238	-146					ATGAACAAGATATCCTCTCACGATCCGTCTCTGCAATTTCCCCCGGCGGACGTTTCGTCTAAGAACCGCCGAGCACTTTTTGAACCGACCTAG	ATGAACAAGATATCCTCTCACGATCCGTCTCTGCAATTTCCCCCGGCGGACGTTTCGTCTAAGAACCGCCGAGCACTTTTTGAACCGACCTAG			MNKISSHDPSLQFPPADVSSKNRRALFEPT*	MNKISSHDPSLQFPPADVSSKNRRALFEPT*			CCCTTTGCTG	CTTGATTTCT	0	L	0	0	0	0	0
7678	3564	ao	AN5892.1	72.m19236	AO070245000010	0					-185	-135	ATGCTCAAATCCGGTCGACGTGCCATTGACGCTTCGATTTACTCGATTTGA			ATGCTCAAATCCGGTCGACGTGCCATTGACGCTTCGATTTACTCGATTTGA	MLKSGRRAIDASIYSI*			MLKSGRRAIDASIYSI*	GCTTCCTTCG	TTCAACGGAT	0	L	0	0	0	0	0
7680	3565	af	AN5785.1	69.m14812	AO070249000030	0			-179	-135			ATGAAATCATCCCGCACACCAGATGTTTGTCTTGTTTGCAACTGA		ATGAAATCATCCCGCACACCAGATGTTTGTCTTGTTTGCAACTGA		MKSSRTPDVCLVCN*		MKSSRTPDVCLVCN*		AAATCTTTCC	AAAATCCACG	0	O	FG01345.1	0	0	0	0
7681	3565	af	AN5785.1	69.m14812	AO070249000030	0			-157	-20			ATGTTTGTCTTGTTTGCAACTGAAAAATCCACGACCCACATGCACATTTCCCTACCGCTGCCCATAAAATTTGTGATAACAAGCCCCTCAGGTGATCATCAGGGATTCCTATCTACAGAGATTCAATACTGGAGATAG		ATGTTTGTCTTGTTTGCAACTGAAAAATCCACGACCCACATGCACATTTCCCTACCGCTGCCCATAAAATTTGTGATAACAAGCCCCTCAGGTGATCATCAGGGATTCCTATCTACAGAGATTCAATACTGGAGATAG		MFVLFATEKSTTHMHISLPLPIKFVITSPSGDHQGFLSTEIQYWR*		MFVLFATEKSTTHMHISLPLPIKFVITSPSGDHQGFLSTEIQYWR*		CGCACACCAG	CGATAGATAG	0	O	FG01345.1	0	0	0	0
7682	3565	af	AN5785.1	69.m14812	AO070249000030	0			-118	-20			ATGCACATTTCCCTACCGCTGCCCATAAAATTTGTGATAACAAGCCCCTCAGGTGATCATCAGGGATTCCTATCTACAGAGATTCAATACTGGAGATAG		ATGCACATTTCCCTACCGCTGCCCATAAAATTTGTGATAACAAGCCCCTCAGGTGATCATCAGGGATTCCTATCTACAGAGATTCAATACTGGAGATAG		MHISLPLPIKFVITSPSGDHQGFLSTEIQYWR*		MHISLPLPIKFVITSPSGDHQGFLSTEIQYWR*		CACGACCCAC	CGATAGATAG	0	O	FG01345.1	0	0	0	0
7679	3565	an	AN5785.1	69.m14812	AO070249000030	0	-191	-132					ATGAAATCATCCCGCTGCTGTTATCAAGGAGTGTTTGACCTGTTTGCAATAAAAATTTAA	ATGAAATCATCCCGCTGCTGTTATCAAGGAGTGTTTGACCTGTTTGCAATAAAAATTTAA			MKSSRCCYQGVFDLFAIKI*	MKSSRCCYQGVFDLFAIKI*			GCAAATTTGG	AGCCTCCCGC	0	O	FG01345.1	0	0	0	0
7683	3565	ao	AN5785.1	69.m14812	AO070249000030	0					-130	-14	ATGCATGAAATCATCAACCCGCGCCTAAAGACGTTTGTCTTGTTTGCAACCGAAAACTCTAGATTTCCCACTACATCCACCATCCATCCTTTTACAGTTCCCGAAAATCATTACTAG			ATGCATGAAATCATCAACCCGCGCCTAAAGACGTTTGTCTTGTTTGCAACCGAAAACTCTAGATTTCCCACTACATCCACCATCCATCCTTTTACAGTTCCCGAAAATCATTACTAG	MHEIINPRLKTFVLFATENSRFPTTSTIHPFTVPENHY*			MHEIINPRLKTFVLFATENSRFPTTSTIHPFTVPENHY*	CGGACAAAAT	CAACCCAAGC	0	O	FG01345.1	0	0	0	0
7684	3565	ao	AN5785.1	69.m14812	AO070249000030	0					-126	-103	ATGAAATCATCAACCCGCGCCTAA			ATGAAATCATCAACCCGCGCCTAA	MKSSTRA*			MKSSTRA*	CAAAATATGC	AGACGTTTGT	0	O	FG01345.1	0	0	0	0
7685	3566	af	AN8748.1	62.m03453	AO070250000024	0			-172	-146			ATGTGGGGCGGTGAAGGGCGCATGTAA		ATGTGGGGCGGTGAAGGGCGCATGTAA		MWGGEGRM*		MWGGEGRM*		TACGTCTGGA	CGTCGGCGGC	0	I	FG06404.1	0	NCU02027.1	YLR118C	0
7686	3566	ao	AN8748.1	62.m03453	AO070250000024	0					-202	-179	ATGCATTATCATACTAGGCGGTGA			ATGCATTATCATACTAGGCGGTGA	MHYHTRR*			MHYHTRR*	TTGAGGCACA	GAGCTTAGGC	0	I	FG06404.1	0	NCU02027.1	YLR118C	0
7687	3566	ao	AN8748.1	62.m03453	AO070250000024	0					-151	-128	ATGTTTATCGCGTTATCGTCTTAG			ATGTTTATCGCGTTATCGTCTTAG	MFIALSS*			MFIALSS*	ATCGCGGGGA	TTATCTAGCA	0	I	FG06404.1	0	NCU02027.1	YLR118C	0
7689	3567	af	AN5296.1	69.m15183	AO070252000014	0			-88	-71			ATGCGTATTTTGAAGTAG		ATGCGTATTTTGAAGTAG		MRILK*		MRILK*		CACTCTCCTC	CGAGTTCTCG	0	T	0	0	0	0	0
7688	3567	an	AN5296.1	69.m15183	AO070252000014	0	-88	-32					ATGCGTTCCGGCCATTTTCTGCCTGCCTTCAGACTTGTCAAAGAAATCCACGAATGA	ATGCGTTCCGGCCATTTTCTGCCTGCCTTCAGACTTGTCAAAGAAATCCACGAATGA			MRSGHFLPAFRLVKEIHE*	MRSGHFLPAFRLVKEIHE*			TCATCTCGTC	GGCCAATGCT	0	T	0	0	0	0	0
7690	3567	ao	AN5296.1	69.m15183	AO070252000014	0					-154	-125	ATGAACGGGTTTCACGAGGTCACAACGTAA			ATGAACGGGTTTCACGAGGTCACAACGTAA	MNGFHEVTT*			MNGFHEVTT*	TTTTACTGGT	CCTAGATCGT	0	T	0	0	0	0	0
7694	3568	af	AN5827.1	72.m18954	AO070260000019	0			-94	-74			ATGCGCGATAGCATCTACTAG		ATGCGCGATAGCATCTACTAG		MRDSIY*		MRDSIY*		CAGTCCAATC	AGCAAAGGGC	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7691	3568	an	AN5827.1	72.m18954	AO070260000019	0	-168	-145					ATGCCAATGCATATCAAACATTAA	ATGCCAATGCATATCAAACATTAA			MPMHIKH*	MPMHIKH*			CGTTTTATTT	AGACAATTAT	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7692	3568	an	AN5827.1	72.m18954	AO070260000019	0	-162	-145					ATGCATATCAAACATTAA	ATGCATATCAAACATTAA			MHIKH*	MHIKH*			ATTTATGCCA	AGACAATTAT	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7693	3568	an	AN5827.1	72.m18954	AO070260000019	0	-116	-99					ATGCATGCTTGCTTCTGA	ATGCATGCTTGCTTCTGA			MHACF*	MHACF*			CAAGGCGACA	CAGCCGAAAC	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7695	3568	ao	AN5827.1	72.m18954	AO070260000019	0					-154	-95	ATGCTTACTGTTGTTCTTGTTTTTAAAGCACATTCTGATATGACGCGCGGCTTTCTCTGA			ATGCTTACTGTTGTTCTTGTTTTTAAAGCACATTCTGATATGACGCGCGGCTTTCTCTGA	MLTVVLVFKAHSDMTRGFL*			MLTVVLVFKAHSDMTRGFL*	CAGTTCACCA	GGGTTACAAT	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7696	3568	ao	AN5827.1	72.m18954	AO070260000019	0					-115	-95	ATGACGCGCGGCTTTCTCTGA			ATGACGCGCGGCTTTCTCTGA	MTRGFL*			MTRGFL*	ACATTCTGAT	GGGTTACAAT	0	A	FG10391.1	MG07501.1	NCU08928.1	0	0
7700	3569	af	AN4360.1	58.m07961	AO070261000003	0			-246	-193			ATGGCTCAATGGGGTGTTTTGGAGTTAGAAGCCCTCCACAAGAGTGGGAAATAG		ATGGCTCAATGGGGTGTTTTGGAGTTAGAAGCCCTCCACAAGAGTGGGAAATAG		MAQWGVLELEALHKSGK*		MAQWGVLELEALHKSGK*		CAACTTCATG	CAATCGGTAA	0		0	0	0	0	0
7701	3569	af	AN4360.1	58.m07961	AO070261000003	0			-238	-152			ATGGGGTGTTTTGGAGTTAGAAGCCCTCCACAAGAGTGGGAAATAGCAATCGGTAATAACGTGACGTTTCTGCTTATCTCCACGTGA		ATGGGGTGTTTTGGAGTTAGAAGCCCTCCACAAGAGTGGGAAATAGCAATCGGTAATAACGTGACGTTTCTGCTTATCTCCACGTGA		MGCFGVRSPPQEWEIAIGNNVTFLLIST*		MGCFGVRSPPQEWEIAIGNNVTFLLIST*		TGATGGCTCA	CTCATCTGCT	0		0	0	0	0	0
7697	3569	an	AN4360.1	58.m07961	AO070261000003	0	-134	-45					ATGCTCGGCGGCTTTAAAGTGGGCTCTCAAAACAAACTGCTGCTCGGCGAGCAACGACTCTTGCCAAATGCGAGGCAAGAAACAGTTTGA	ATGCTCGGCGGCTTTAAAGTGGGCTCTCAAAACAAACTGCTGCTCGGCGAGCAACGACTCTTGCCAAATGCGAGGCAAGAAACAGTTTGA			MLGGFKVGSQNKLLLGEQRLLPNARQETV*	MLGGFKVGSQNKLLLGEQRLLPNARQETV*			GCGAGTGCTG	ACAGTTTACA	0		0	0	0	0	0
7698	3569	an	AN4360.1	58.m07961	AO070261000003	0	-67	-17					ATGCGAGGCAAGAAACAGTTTGAACAGTTTACAGACATGAGTCTGAAGTGA	ATGCGAGGCAAGAAACAGTTTGAACAGTTTACAGACATGAGTCTGAAGTGA			MRGKKQFEQFTDMSLK*	MRGKKQFEQFTDMSLK*			CTCTTGCCAA	TCCTAGATTA	0		0	0	0	0	0
7704	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-172	-134	ATGATTATGTCCCTATCACCACGTGACTGTATCTACTGA			ATGATTATGTCCCTATCACCACGTGACTGTATCTACTGA	MIMSLSPRDCIY*			MIMSLSPRDCIY*	CTTATCGACG	TGGCCCGTGC	0		0	0	0	0	0

7705	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-166	-134	ATGTCCCTATCACCACGTGACTGTATCTACTGA			ATGTCCCTATCACCACGTGACTGTATCTACTGA	MSLSPRDCIY*			MSLSPRDCIY*	GACGATGATT	TGGCCCGTGC	0		0	0	0	0	0
7706	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-134	-54	ATGGCCCGTGCAAATGAAGTCGTCTTGATGGAACATCCCACAACCTGTCTTTCAACCATACCTGTATCCGCGGCGGGATAA			ATGGCCCGTGCAAATGAAGTCGTCTTGATGGAACATCCCACAACCTGTCTTTCAACCATACCTGTATCCGCGGCGGGATAA	MARANEVVLMEHPTTCLSTIPVSAAG*			MARANEVVLMEHPTTCLSTIPVSAAG*	GTATCTACTG	TGCGCAAGAA	0		0	0	0	0	0
7707	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-121	-107	ATGAAGTCGTCTTGA			ATGAAGTCGTCTTGA	MKSS*			MKSS*	GCCCGTGCAA	TGGAACATCC	0		0	0	0	0	0
7708	3569	ao	AN4360.1	58.m07961	AO070261000003	0					-107	-54	ATGGAACATCCCACAACCTGTCTTTCAACCATACCTGTATCCGCGGCGGGATAA			ATGGAACATCCCACAACCTGTCTTTCAACCATACCTGTATCCGCGGCGGGATAA	MEHPTTCLSTIPVSAAG*			MEHPTTCLSTIPVSAAG*	AGTCGTCTTG	TGCGCAAGAA	0		0	0	0	0	0
7710	3573	af	AN6934.1	62.m03423	AO070269000048	0			-131	-90			ATGGATCACTTTGGCTGCAGTCCGTGCAGTCGGAGCTCATAA		ATGGATCACTTTGGCTGCAGTCCGTGCAGTCGGAGCTCATAA		MDHFGCSPCSRSS*		MDHFGCSPCSRSS*		CTTGATCTGA	CCCCGGACAT	0	G	0	0	0	0	0
7712	3574	an	AN8869.1	71.m16009	AO070271000002	0	-166	-74					ATGAAGCATTCGCCAATCACGCCGTTTTTGCAGAAACAAAACCCACTTTCGATATTTAGTCATCCATACGCTAAGGCCTTTTCGCATACCTAA	ATGAAGCATTCGCCAATCACGCCGTTTTTGCAGAAACAAAACCCACTTTCGATATTTAGTCATCCATACGCTAAGGCCTTTTCGCATACCTAA			MKHSPITPFLQKQNPLSIFSHPYAKAFSHT*	MKHSPITPFLQKQNPLSIFSHPYAKAFSHT*			AGGACGACTC	CAGTCTGCGT	0	TZ	FG07475.1	0	0	0	0
7713	3574	ao	AN8869.1	71.m16009	AO070271000002	0					-247	-197	ATGTTGTACTTCGTAGTCCAATTAGAAAACCACCCCGCCCGCCAGCCATGA			ATGTTGTACTTCGTAGTCCAATTAGAAAACCACCCCGCCCGCCAGCCATGA	MLYFVVQLENHPARQP*			MLYFVVQLENHPARQP*	TGCTGGTTTT	TTAGTCCAGG	0	TZ	FG07475.1	0	0	0	0
7714	3574	ao	AN8869.1	71.m16009	AO070271000002	0					-200	-90	ATGATTAGTCCAGGCTACTTATCGTACATATTCATGCACAGTCTGTACCTGCTTGATCTCTCTCTTTTCCTTGCTACAACTTCATTACATAGTGCTTCCACGCGAGATTAG			ATGATTAGTCCAGGCTACTTATCGTACATATTCATGCACAGTCTGTACCTGCTTGATCTCTCTCTTTTCCTTGCTACAACTTCATTACATAGTGCTTCCACGCGAGATTAG	MISPGYLSYIFMHSLYLLDLSLFLATTSLHSASTRD*			MISPGYLSYIFMHSLYLLDLSLFLATTSLHSASTRD*	CCCGCCAGCC	TAGACCCTCA	0	TZ	FG07475.1	0	0	0	0
7715	3574	ao	AN8869.1	71.m16009	AO070271000002	0					-167	-90	ATGCACAGTCTGTACCTGCTTGATCTCTCTCTTTTCCTTGCTACAACTTCATTACATAGTGCTTCCACGCGAGATTAG			ATGCACAGTCTGTACCTGCTTGATCTCTCTCTTTTCCTTGCTACAACTTCATTACATAGTGCTTCCACGCGAGATTAG	MHSLYLLDLSLFLATTSLHSASTRD*			MHSLYLLDLSLFLATTSLHSASTRD*	GTACATATTC	TAGACCCTCA	0	TZ	FG07475.1	0	0	0	0
7716	3575	af	AN8841.1	71.m15972	AO070271000036	0			-110	-57			ATGCGGTCACTGACTATCAGCATGCGATTGTCATTTGATCAACCACTGTTGTGA		ATGCGGTCACTGACTATCAGCATGCGATTGTCATTTGATCAACCACTGTTGTGA		MRSLTISMRLSFDQPLL*		MRSLTISMRLSFDQPLL*		CAAGGAAACC	ACAGGCTCTT	0	R	FG07396.1	MG06940.1	0	0	0
7717	3575	af	AN8841.1	71.m15972	AO070271000036	0			-89	-57			ATGCGATTGTCATTTGATCAACCACTGTTGTGA		ATGCGATTGTCATTTGATCAACCACTGTTGTGA		MRLSFDQPLL*		MRLSFDQPLL*		GACTATCAGC	ACAGGCTCTT	0	R	FG07396.1	MG06940.1	0	0	0
7718	3575	ao	AN8841.1	71.m15972	AO070271000036	0					-83	-33	ATGTTCTTAACAGGTTTTTTAGCTGAACGAAGTCATATTCATTTGCGTTGA			ATGTTCTTAACAGGTTTTTTAGCTGAACGAAGTCATATTCATTTGCGTTGA	MFLTGFLAERSHIHLR*			MFLTGFLAERSHIHLR*	ATGTAGTATT	TCTTTCTAGG	0	R	FG07396.1	MG06940.1	0	0	0
7722	3576	af	AN4407.1	58.m08972	AO070273000067	0			-167	-147			ATGTGGGCTTCAATGATCTGA		ATGTGGGCTTCAATGATCTGA		MWASMI*		MWASMI*		AGCATAATAC	TATTTGCAGT	0	L	0	0	0	0	0
7723	3576	af	AN4407.1	58.m08972	AO070273000067	0			-101	-87			ATGCGCCATCCTTAA		ATGCGCCATCCTTAA		MRHP*		MRHP*		GCGTAAGCTA	TCGTATTGTT	0	L	0	0	0	0	0
7720	3576	an	AN4407.1	58.m08972	AO070273000067	0	-223	-188					ATGGGCTTCAGCCTAAGCCTGAGCGACCCCACATGA	ATGGGCTTCAGCCTAAGCCTGAGCGACCCCACATGA			MGFSLSLSDPT*	MGFSLSLSDPT*			CGTTTCCACG	GTTAGAACAT	0	L	0	0	0	0	0
7721	3576	an	AN4407.1	58.m08972	AO070273000067	0	-168	-148					ATGATAGCTCTCATAGAGTAA	ATGATAGCTCTCATAGAGTAA			MIALIE*	MIALIE*			TCAACTCCTT	CTCATAGAGT	0	L	0	0	0	0	0
7724	3576	ao	AN4407.1	58.m08972	AO070273000067	0					-159	-139	ATGATACCCTTTCTTAACTAG			ATGATACCCTTTCTTAACTAG	MIPFLN*			MIPFLN*	GTGTATACCA	TGTAACATTT	0	L	0	0	0	0	0
7719	3576	conserved	AN4407.1	58.m08972	AO070273000067	0	-116	-105	-117	-106	-113	-102	ATGCCmGCGTrA	ATGCCAGCGTGA	ATGCCCGCGTAA	ATGCCCGCGTGA	MPA*	MPA*	MPA*	MPA*	wmwyTkAATh	Gyymmysmds	0	L	0	0	0	0	0
7726	3579	af	AN6363.1	72.m19497	AO070279000049	0			-115	-92			ATGGTTCGCACCAAATTATGGTAA		ATGGTTCGCACCAAATTATGGTAA		MVRTKLW*		MVRTKLW*		AAGTCAACAC	AAAAAAGTGT	0	TD	0	0	0	YOR119C	0
7727	3579	af	AN6363.1	72.m19497	AO070279000049	0			-98	-6			ATGGTAAAAAAAAGTGTTGGCGGCAAGAGTTCCACCACGGTTACCAACTCGATTGCTGGAATATCCTCAATACAAACGAGTAGGACATTCTAG		ATGGTAAAAAAAAGTGTTGGCGGCAAGAGTTCCACCACGGTTACCAACTCGATTGCTGGAATATCCTCAATACAAACGAGTAGGACATTCTAG		MVKKSVGGKSSTTVTNSIAGISSIQTSRTF*		MVKKSVGGKSSTTVTNSIAGISSIQTSRTF*		GCACCAAATT	CAGTCATGTC	0	TD	0	0	0	YOR119C	0
7725	3579	an	AN6363.1	72.m19497	AO070279000049	0	-229	-77					ATGCCTCGACGTGCGACAGCCTCAACACTGAGACGCGATCAACGCGTTTCTCTTCAGCCAGCGGGGTTCTGCCGGGCGGTCAAGACAATCAAGTCCACCCACAGCTCGTCCAATCAGCAGCTCGGAACCGATAAGGCACTTTTTCCTACCTAA	ATGCCTCGACGTGCGACAGCCTCAACACTGAGACGCGATCAACGCGTTTCTCTTCAGCCAGCGGGGTTCTGCCGGGCGGTCAAGACAATCAAGTCCACCCACAGCTCGTCCAATCAGCAGCTCGGAACCGATAAGGCACTTTTTCCTACCTAA			MPRRATASTLRRDQRVSLQPAGFCRAVKTIKSTHSSSNQQLGTDKALFPT*	MPRRATASTLRRDQRVSLQPAGFCRAVKTIKSTHSSSNQQLGTDKALFPT*			TCAAGCGTCA	ATTTCTTGAG	0	TD	0	0	0	YOR119C	0
7728	3580	conserved	AN7455.1	57.m05888	AO070287000070	0	-163	-128	-147	-112	-145	-110	ATGACTyTCywTyyrCCTGCGGTGGyCyyyyyhTAG	ATGACTTTCCATTCACCTGCGGTGGTCCTCTCTTAG	ATGACTCTCTTTCTGCCTGCGGTGGCCTCTCTCTAG	ATGACTCTCCATTTGCCTGCGGTGGCCTCTCTATAG	MTfhsPAVvls*	MTFHSPAVVLS*	MTLFLPAVASL*	MTLHLPAVASL*	yyyGCCAGGA	CCCGyGTGGT	0	B	0	0	0	0	0
7732	3581	af	AN0818.1	70.m15418	AO070288000084	0			-196	-125			ATGCAAACAATGCAAAATTCACTATCTCCGCCGTCTCTAATTGGAATTTTTTGTATTCAACCACTTCGATAA		ATGCAAACAATGCAAAATTCACTATCTCCGCCGTCTCTAATTGGAATTTTTTGTATTCAACCACTTCGATAA		MQTMQNSLSPPSLIGIFCIQPLR*		MQTMQNSLSPPSLIGIFCIQPLR*		CACCTCCCGC	GACGTTCCAG	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7733	3581	af	AN0818.1	70.m15418	AO070288000084	0			-187	-125			ATGCAAAATTCACTATCTCCGCCGTCTCTAATTGGAATTTTTTGTATTCAACCACTTCGATAA		ATGCAAAATTCACTATCTCCGCCGTCTCTAATTGGAATTTTTTGTATTCAACCACTTCGATAA		MQNSLSPPSLIGIFCIQPLR*		MQNSLSPPSLIGIFCIQPLR*		CATGCAAACA	GACGTTCCAG	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7729	3581	an	AN0818.1	70.m15418	AO070288000084	0	-156	-58					ATGCAAACAATACAAACCATGGGCTACTCCGCGGCGGGTCTTCAAAAATTGTCCGCATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAG	ATGCAAACAATACAAACCATGGGCTACTCCGCGGCGGGTCTTCAAAAATTGTCCGCATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAG			MQTIQTMGYSAAGLQKLSACEAEIYLLICYPI*	MQTIQTMGYSAAGLQKLSACEAEIYLLICYPI*			ACATCTAAAG	CTTAGATTTT	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7730	3581	an	AN0818.1	70.m15418	AO070288000084	0	-138	-58					ATGGGCTACTCCGCGGCGGGTCTTCAAAAATTGTCCGCATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAG	ATGGGCTACTCCGCGGCGGGTCTTCAAAAATTGTCCGCATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAG			MGYSAAGLQKLSACEAEIYLLICYPI*	MGYSAAGLQKLSACEAEIYLLICYPI*			AATACAAACC	CTTAGATTTT	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7731	3581	an	AN0818.1	70.m15418	AO070288000084	0	-100	-53					ATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAGCTTAG	ATGCGAAGCCGAAATCTACCTGTTAATCTGCTACCCCATCTAGCTTAG			MRSRNLPVNLLPHLA*	MRSRNLPVNLLPHLA*			AATTGTCCGC	ATTTTTTGAT	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7734	3581	ao	AN0818.1	70.m15418	AO070288000084	0					-207	-112	ATGCAAAATTTCATTCATACTCCGCGGTGGGATGTGAGAGCCGAAATTTTTGTCGGCATTAATCGAGGCAGAAGGCTTGTTTGCGCTAAGCATTGA			ATGCAAAATTTCATTCATACTCCGCGGTGGGATGTGAGAGCCGAAATTTTTGTCGGCATTAATCGAGGCAGAAGGCTTGTTTGCGCTAAGCATTGA	MQNFIHTPRWDVRAEIFVGINRGRRLVCAKH*			MQNFIHTPRWDVRAEIFVGINRGRRLVCAKH*	ACTGCAAACA	ACCTAGCTGC	0	R	FG00665.1	MG01205.1	NCU02619.1	YLR401C	YLR401C
7737	3585	af	AN2290.1	71.m15938	AO070295000069	0			-111	-64			ATGACACCAATCCTTCCATCCAAATACGAAATGCCTCCTTGGGCCTAA		ATGACACCAATCCTTCCATCCAAATACGAAATGCCTCCTTGGGCCTAA		MTPILPSKYEMPPWA*		MTPILPSKYEMPPWA*		ACTAAAACCT	TGCCTATAAT	0	R	0	0	0	0	0
7738	3585	af	AN2290.1	71.m15938	AO070295000069	0			-81	-64			ATGCCTCCTTGGGCCTAA		ATGCCTCCTTGGGCCTAA		MPPWA*		MPPWA*		CAAATACGAA	TGCCTATAAT	0	R	0	0	0	0	0
7739	3585	af	AN2290.1	71.m15938	AO070295000069	0			-64	-38			ATGCCTATAATCTCCGCGCTCGGCTGA		ATGCCTATAATCTCCGCGCTCGGCTGA		MPIISALG*		MPIISALG*		CTTGGGCCTA	CGATTATCCA	0	R	0	0	0	0	0
7740	3585	ao	AN2290.1	71.m15938	AO070295000069	0					-73	-29	ATGCCGCTTATCTTTGATTCAAACATTCCTCTAGCACCTGATTAA			ATGCCGCTTATCTTTGATTCAAACATTCCTCTAGCACCTGATTAA	MPLIFDSNIPLAPD*			MPLIFDSNIPLAPD*	CAGCTTGTCA	TACGATATAC	0	R	0	0	0	0	0
7743	3587	af	AN7335.1	72.m19736	AO070297000108	0			-183	-142			ATGTCAGTGTGTAGATCACGTGATGTTTCCTTCCGCCGGTGA		ATGTCAGTGTGTAGATCACGTGATGTTTCCTTCCGCCGGTGA		MSVCRSRDVSFRR*		MSVCRSRDVSFRR*		GAATACGTTA	TGTCATGTGT	0		0	MG04671.1	NCU00295.1	0	0
7744	3587	af	AN7335.1	72.m19736	AO070297000108	0			-161	-105			ATGTTTCCTTCCGCCGGTGATGTCATGTGTTGGATAAACCCCCACTTTCAGCCTTAG		ATGTTTCCTTCCGCCGGTGATGTCATGTGTTGGATAAACCCCCACTTTCAGCCTTAG		MFPSAGDVMCWINPHFQP*		MFPSAGDVMCWINPHFQP*		AGATCACGTG	GTATCCATAG	0		0	MG04671.1	NCU00295.1	0	0
7745	3587	af	AN7335.1	72.m19736	AO070297000108	0			-142	-125			ATGTCATGTGTTGGATAA		ATGTCATGTGTTGGATAA		MSCVG*		MSCVG*		TCCGCCGGTG	ACCCCCACTT	0		0	MG04671.1	NCU00295.1	0	0
7746	3587	af	AN7335.1	72.m19736	AO070297000108	0			-137	-105			ATGTGTTGGATAAACCCCCACTTTCAGCCTTAG		ATGTGTTGGATAAACCCCCACTTTCAGCCTTAG		MCWINPHFQP*		MCWINPHFQP*		CGGTGATGTC	GTATCCATAG	0		0	MG04671.1	NCU00295.1	0	0
7741	3587	an	AN7335.1	72.m19736	AO070297000108	0	-243	-142					ATGCCTTTTATTGTAAGTTCATCGCAAATTTCAAATTTCGATATTATTTACTGTTTCGTGAGTATAGAGGACTGCTCTCTGTTGATATTGAATTGTACCTGA	ATGCCTTTTATTGTAAGTTCATCGCAAATTTCAAATTTCGATATTATTTACTGTTTCGTGAGTATAGAGGACTGCTCTCTGTTGATATTGAATTGTACCTGA			MPFIVSSSQISNFDIIYCFVSIEDCSLLILNCT*	MPFIVSSSQISNFDIIYCFVSIEDCSLLILNCT*			GGCGTCTCCT	GCTGCTGGTG	0		0	MG04671.1	NCU00295.1	0	0
7742	3587	an	AN7335.1	72.m19736	AO070297000108	0	-126	-28					ATGCGTGCCCCGCTGCCAAGCTTTGGAGCTTACGCAGCTACAACGGCGAGGACCCTTCTTCCCTCCTCTACTCCCCCCAAAACTTCATATTTCCGTTAA	ATGCGTGCCCCGCTGCCAAGCTTTGGAGCTTACGCAGCTACAACGGCGAGGACCCTTCTTCCCTCCTCTACTCCCCCCAAAACTTCATATTTCCGTTAA			MRAPLPSFGAYAATTARTLLPSSTPPKTSYFR*	MRAPLPSFGAYAATTARTLLPSSTPPKTSYFR*			TGGTGATGTC	ATGTCATCGG	0		0	MG04671.1	NCU00295.1	0	0
7747	3587	ao	AN7335.1	72.m19736	AO070297000108	0					-164	-66	ATGATCAGGGGAAGGGATGACATCATAGGGCCCGTGCATCATGTGAGTATCAAACTGTCCCGCGCTTACGCACTCACGCTGGTCGATCTAGACTCCTGA			ATGATCAGGGGAAGGGATGACATCATAGGGCCCGTGCATCATGTGAGTATCAAACTGTCCCGCGCTTACGCACTCACGCTGGTCGATCTAGACTCCTGA	MIRGRDDIIGPVHHVSIKLSRAYALTLVDLDS*			MIRGRDDIIGPVHHVSIKLSRAYALTLVDLDS*	CCTTATATTA	GTCCTATTCC	0		0	MG04671.1	NCU00295.1	0	0
7748	3587	ao	AN7335.1	72.m19736	AO070297000108	0					-148	-137	ATGACATCATAG			ATGACATCATAG	MTS*			MTS*	AGGGGAAGGG	GGCCCGTGCA	0		0	MG04671.1	NCU00295.1	0	0
7749	3588	an	AN7773.1	65.m07171	AO070298000072	0	-74	-48					ATGGTTCTTCCCTTGCAGGGAGTGTGA	ATGGTTCTTCCCTTGCAGGGAGTGTGA			MVLPLQGV*	MVLPLQGV*			TTTTCTCTCC	GGCTGACCAG	0	Q	0	0	0	0	0
7750	3588	ao	AN7773.1	65.m07171	AO070298000072	0					-151	-107	ATGATGCACAGTTTCCACGACAATCGTCGGCTATTTCTGGCATAA			ATGATGCACAGTTTCCACGACAATCGTCGGCTATTTCTGGCATAA	MMHSFHDNRRLFLA*			MMHSFHDNRRLFLA*	CATAAGTGAA	GCCATACTGG	0	Q	0	0	0	0	0
7751	3588	ao	AN7773.1	65.m07171	AO070298000072	0					-148	-107	ATGCACAGTTTCCACGACAATCGTCGGCTATTTCTGGCATAA			ATGCACAGTTTCCACGACAATCGTCGGCTATTTCTGGCATAA	MHSFHDNRRLFLA*			MHSFHDNRRLFLA*	AAGTGAAATG	GCCATACTGG	0	Q	0	0	0	0	0
7752	3590	an	AN4477.1	58.m07843	AO070305000107	0	-225	-211					ATGCTGCATCGGTAG	ATGCTGCATCGGTAG			MLHR*	MLHR*			GAGTCTGTAA	AAGAAGATCA	0	E	0	0	0	0	0
7753	3590	an	AN4477.1	58.m07843	AO070305000107	0	-167	-129					ATGATTCAGTCCCCTACCGCGCACCTCGATTGCACGTGA	ATGATTCAGTCCCCTACCGCGCACCTCGATTGCACGTGA			MIQSPTAHLDCT*	MIQSPTAHLDCT*			TATCAATCGG	TCGTAAGCTA	0	E	0	0	0	0	0
7754	3592	af	AN6310.1	72.m19324	AO070308000065	0			-224	-72			ATGAGGGATGGTGTGACTCGTACAGACCTTCAGGCCACCAGCTATTACACTCGCCAAATACTTGATTTTGAGACCGCCTACTTTTCATGGACAAGCGTCTTCTACCACCAGGGCAGGCGGTGGAAAAGACGGCCAGTTTCTTCCGTAAAATAA		ATGAGGGATGGTGTGACTCGTACAGACCTTCAGGCCACCAGCTATTACACTCGCCAAATACTTGATTTTGAGACCGCCTACTTTTCATGGACAAGCGTCTTCTACCACCAGGGCAGGCGGTGGAAAAGACGGCCAGTTTCTTCCGTAAAATAA		MRDGVTRTDLQATSYYTRQILDFETAYFSWTSVFYHQGRRWKRRPVSSVK*		MRDGVTRTDLQATSYYTRQILDFETAYFSWTSVFYHQGRRWKRRPVSSVK*		ATCAGAGGCC	TATCGTGATA	0	R	0	0	0	0	0
7755	3592	af	AN6310.1	72.m19324	AO070308000065	0			-138	-64			ATGGACAAGCGTCTTCTACCACCAGGGCAGGCGGTGGAAAAGACGGCCAGTTTCTTCCGTAAAATAATATCGTGA		ATGGACAAGCGTCTTCTACCACCAGGGCAGGCGGTGGAAAAGACGGCCAGTTTCTTCCGTAAAATAATATCGTGA		MDKRLLPPGQAVEKTASFFRKIIS*		MDKRLLPPGQAVEKTASFFRKIIS*		CCTACTTTTC	TACTACAAAT	0	R	0	0	0	0	0
7756	3592	ao	AN6310.1	72.m19324	AO070308000065	0					-125	-54	ATGTGGGGCTGCGCCACATTTAGCGGCAGAAAACGGCTTGGAAAAAAAAGTTACTGTTATCGGCATCGATAA			ATGTGGGGCTGCGCCACATTTAGCGGCAGAAAACGGCTTGGAAAAAAAAGTTACTGTTATCGGCATCGATAA	MWGCATFSGRKRLGKKSYCYRHR*			MWGCATFSGRKRLGKKSYCYRHR*	AGAACACTAA	TTTCCTTCTC	0	R	0	0	0	0	0
7759	3593	af	AN7621.1	65.m07418	AO070309000109	0			-274	-251			ATGAAGTTCATCAAACTGATCTAA		ATGAAGTTCATCAAACTGATCTAA		MKFIKLI*		MKFIKLI*		TCGATTGGCC	AGCAACACTA	0	C	0	0	0	0	0
7760	3593	af	AN7621.1	65.m07418	AO070309000109	0			-226	-161			ATGGCGCCATTTCCCCGAAGGTGGGCATCCGCCCCATGGGTTAGAAATCAATTCCAGAATAAATAA		ATGGCGCCATTTCCCCGAAGGTGGGCATCCGCCCCATGGGTTAGAAATCAATTCCAGAATAAATAA		MAPFPRRWASAPWVRNQFQNK*		MAPFPRRWASAPWVRNQFQNK*		AACCCAGCCC	TAATGGCTCG	0	C	0	0	0	0	0
7761	3593	af	AN7621.1	65.m07418	AO070309000109	0			-158	-99			ATGGCTCGCCTTCGCGCCCCTCCTAACAAATATTTCTTTCCTTCTTATCTCCACGACTGA		ATGGCTCGCCTTCGCGCCCCTCCTAACAAATATTTCTTTCCTTCTTATCTCCACGACTGA		MARLRAPPNKYFFPSYLHD*		MARLRAPPNKYFFPSYLHD*		ATAAATAATA	TCACTGGCTT	0	C	0	0	0	0	0

7757	3593	an	AN7621.1	65.m07418	AO070309000109	0	-235	-56					ATGCTAATCGGGTCCAGCCATGGCGCCATCCGGTGGGGATCCTCCGTTCTCTCGGCTGGAGATTTAGTCAAAAGACCAAAATATTTTGCCCCGCGGCTTCCCTTATCAATCGTGAATTTCTCGCCCTCCCCTTCTGTTTTCACATATCCGGCGAGATTTCTCATCATAGCGAGTGCATAG	ATGCTAATCGGGTCCAGCCATGGCGCCATCCGGTGGGGATCCTCCGTTCTCTCGGCTGGAGATTTAGTCAAAAGACCAAAATATTTTGCCCCGCGGCTTCCCTTATCAATCGTGAATTTCTCGCCCTCCCCTTCTGTTTTCACATATCCGGCGAGATTTCTCATCATAGCGAGTGCATAG			MLIGSSHGAIRWGSSVLSAGDLVKRPKYFAPRLPLSIVNFSPSPSVFTYPARFLIIASA*	MLIGSSHGAIRWGSSVLSAGDLVKRPKYFAPRLPLSIVNFSPSPSVFTYPARFLIIASA*			CGCTCCCATC	CACCGCTGCC	0	C	0	0	0	0	0
7758	3593	an	AN7621.1	65.m07418	AO070309000109	0	-216	-169					ATGGCGCCATCCGGTGGGGATCCTCCGTTCTCTCGGCTGGAGATTTAG	ATGGCGCCATCCGGTGGGGATCCTCCGTTCTCTCGGCTGGAGATTTAG			MAPSGGDPPFSRLEI*	MAPSGGDPPFSRLEI*			GGGTCCAGCC	TCAAAAGACC	0	C	0	0	0	0	0
7762	3593	ao	AN7621.1	65.m07418	AO070309000109	0					-227	-174	ATGGGGGTTCAACTATGGCGCCATCCCGAGCGGAGGTTCCGCGCCGATGGTTAG			ATGGGGGTTCAACTATGGCGCCATCCCGAGCGGAGGTTCCGCGCCGATGGTTAG	MGVQLWRHPERRFRADG*			MGVQLWRHPERRFRADG*	CCGGGTGCCC	AAATCCAAAA	0	C	0	0	0	0	0
7763	3593	ao	AN7621.1	65.m07418	AO070309000109	0					-213	-145	ATGGCGCCATCCCGAGCGGAGGTTCCGCGCCGATGGTTAGAAATCCAAAAAAGTCCGGCCACTGTCTAG			ATGGCGCCATCCCGAGCGGAGGTTCCGCGCCGATGGTTAGAAATCCAAAAAAGTCCGGCCACTGTCTAG	MAPSRAEVPRRWLEIQKSPATV*			MAPSRAEVPRRWLEIQKSPATV*	GGGTTCAACT	ATATCCGATC	0	C	0	0	0	0	0
7764	3593	ao	AN7621.1	65.m07418	AO070309000109	0					-72	-58	ATGCTCACAGAGTAG			ATGCTCACAGAGTAG	MLTE*			MLTE*	CATACTGTTG	TCCACAACTG	0	C	0	0	0	0	0
7767	3595	af	AN0084.1	71.m16061	AO070311000132	0			-191	-177			ATGATTATTTTGTGA		ATGATTATTTTGTGA		MIIL*		MIIL*		GGGCCCAGGC	GCGGGACGAA	0	U	0	MG05203.1	0	0	0
7765	3595	an	AN0084.1	71.m16061	AO070311000132	0	-237	-208					ATGAAAGAACTAGCAACCTTTATTGCCTGA	ATGAAAGAACTAGCAACCTTTATTGCCTGA			MKELATFIA*	MKELATFIA*			GAGGGGTGAA	GGCCACATGC	0	U	0	MG05203.1	0	0	0
7766	3595	an	AN0084.1	71.m16061	AO070311000132	0	-201	-91					ATGCACGAACCAACCCAACCCACTTGCGACCAAAACCAGGCCGCCCATAATTTTCCCCTCCTTCTCTCCCTCCTCAGTGATACCCACCTCATAGAATCTTCTGTCTTTTAA	ATGCACGAACCAACCCAACCCACTTGCGACCAAAACCAGGCCGCCCATAATTTTCCCCTCCTTCTCTCCCTCCTCAGTGATACCCACCTCATAGAATCTTCTGTCTTTTAA			MHEPTQPTCDQNQAAHNFPLLLSLLSDTHLIESSVF*	MHEPTQPTCDQNQAAHNFPLLLSLLSDTHLIESSVF*			CTGAGGCCAC	GAATATCCAT	0	U	0	MG05203.1	0	0	0
7768	3595	ao	AN0084.1	71.m16061	AO070311000132	0					-180	-118	ATGAACTACCCCCCACCTTTTACAACAAAAACAGCCGACCATATTTTCTTCCCCTCTCTATAA			ATGAACTACCCCCCACCTTTTACAACAAAAACAGCCGACCATATTTTCTTCCCCTCTCTATAA	MNYPPPFTTKTADHIFFPSL*			MNYPPPFTTKTADHIFFPSL*	GCCGGAGGCA	CCATCTCCTA	0	U	0	MG05203.1	0	0	0
7769	3596	af	AN1008.1	70.m15226	AO070312000025	0			-175	-140			ATGACAGTCCGCCGAACAGATCTAGACAACAATTAA		ATGACAGTCCGCCGAACAGATCTAGACAACAATTAA		MTVRRTDLDNN*		MTVRRTDLDNN*		ACTCTTGTCC	GCTTCCTATA	0	P	0	0	0	0	0
7770	3596	ao	AN1008.1	70.m15226	AO070312000025	0					-216	-160	ATGATATGCCTGCATTTGTTTACACTCGCCAATATCTGTCAAAGAGTCTATATATGA			ATGATATGCCTGCATTTGTTTACACTCGCCAATATCTGTCAAAGAGTCTATATATGA	MICLHLFTLANICQRVYI*			MICLHLFTLANICQRVYI*	CAAATCTTAT	GATCTAATTC	0	P	0	0	0	0	0
7771	3596	ao	AN1008.1	70.m15226	AO070312000025	0					-211	-131	ATGCCTGCATTTGTTTACACTCGCCAATATCTGTCAAAGAGTCTATATATGAGATCTAATTCCCTGTCTAGAGCTATCTAA			ATGCCTGCATTTGTTTACACTCGCCAATATCTGTCAAAGAGTCTATATATGAGATCTAATTCCCTGTCTAGAGCTATCTAA	MPAFVYTRQYLSKSLYMRSNSLSRAI*			MPAFVYTRQYLSKSLYMRSNSLSRAI*	CTTATATGAT	ATCACAGCTC	0	P	0	0	0	0	0
7772	3596	ao	AN1008.1	70.m15226	AO070312000025	0					-163	-131	ATGAGATCTAATTCCCTGTCTAGAGCTATCTAA			ATGAGATCTAATTCCCTGTCTAGAGCTATCTAA	MRSNSLSRAI*			MRSNSLSRAI*	GAGTCTATAT	ATCACAGCTC	0	P	0	0	0	0	0
7776	3599	af	AN3613.1	52.m03647	AO070315000027	0			-160	-134			ATGTCGCGAGGTGGGCTTGGCCGGTAG		ATGTCGCGAGGTGGGCTTGGCCGGTAG		MSRGGLGR*		MSRGGLGR*		CGGTTCCAGG	TTGCTCACTC	0		0	0	0	0	0
7773	3599	an	AN3613.1	52.m03647	AO070315000027	0	-232	-155					ATGGGCTCTAGCACATGCACAGCTTGCAGTTGCTGCTACGCTATCTGGGAAAACGAATGGCTATTCAGGAGTTTATAA	ATGGGCTCTAGCACATGCACAGCTTGCAGTTGCTGCTACGCTATCTGGGAAAACGAATGGCTATTCAGGAGTTTATAA			MGSSTCTACSCCYAIWENEWLFRSL*	MGSSTCTACSCCYAIWENEWLFRSL*			CTTTGCCCGC	CCAAAAGAGC	0		0	0	0	0	0
7774	3599	an	AN3613.1	52.m03647	AO070315000027	0	-218	-66					ATGCACAGCTTGCAGTTGCTGCTACGCTATCTGGGAAAACGAATGGCTATTCAGGAGTTTATAACCAAAAGAGCCGGAAACAGGCTGATTGCCCTCTCACGGGGAGACGTTGTACTTCTGATCCAGAGGCTATTAACCGGACACTACCTATAA	ATGCACAGCTTGCAGTTGCTGCTACGCTATCTGGGAAAACGAATGGCTATTCAGGAGTTTATAACCAAAAGAGCCGGAAACAGGCTGATTGCCCTCTCACGGGGAGACGTTGTACTTCTGATCCAGAGGCTATTAACCGGACACTACCTATAA			MHSLQLLLRYLGKRMAIQEFITKRAGNRLIALSRGDVVLLIQRLLTGHYL*	MHSLQLLLRYLGKRMAIQEFITKRAGNRLIALSRGDVVLLIQRLLTGHYL*			GCTCTAGCAC	AGGAGGTAGC	0		0	0	0	0	0
7775	3599	an	AN3613.1	52.m03647	AO070315000027	0	-176	-66					ATGGCTATTCAGGAGTTTATAACCAAAAGAGCCGGAAACAGGCTGATTGCCCTCTCACGGGGAGACGTTGTACTTCTGATCCAGAGGCTATTAACCGGACACTACCTATAA	ATGGCTATTCAGGAGTTTATAACCAAAAGAGCCGGAAACAGGCTGATTGCCCTCTCACGGGGAGACGTTGTACTTCTGATCCAGAGGCTATTAACCGGACACTACCTATAA			MAIQEFITKRAGNRLIALSRGDVVLLIQRLLTGHYL*	MAIQEFITKRAGNRLIALSRGDVVLLIQRLLTGHYL*			GGGAAAACGA	AGGAGGTAGC	0		0	0	0	0	0
7777	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-223	-158	ATGTTCATCATTCTGGCAACGGAAATGATCACCGACATGCCTAAACTGAAATCATCCTTCCGATGA			ATGTTCATCATTCTGGCAACGGAAATGATCACCGACATGCCTAAACTGAAATCATCCTTCCGATGA	MFIILATEMITDMPKLKSSFR*			MFIILATEMITDMPKLKSSFR*	TACTCGCCGG	CTCCCCACAC	0		0	0	0	0	0
7778	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-199	-158	ATGATCACCGACATGCCTAAACTGAAATCATCCTTCCGATGA			ATGATCACCGACATGCCTAAACTGAAATCATCCTTCCGATGA	MITDMPKLKSSFR*			MITDMPKLKSSFR*	GGCAACGGAA	CTCCCCACAC	0		0	0	0	0	0
7779	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-187	-158	ATGCCTAAACTGAAATCATCCTTCCGATGA			ATGCCTAAACTGAAATCATCCTTCCGATGA	MPKLKSSFR*			MPKLKSSFR*	GATCACCGAC	CTCCCCACAC	0		0	0	0	0	0
7780	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-161	-84	ATGACTCCCCACACTTGGCACCTGTTGTTAATACAGGTAGCAGAGGGTATGTGCCGGACTGGGGGGAAACATGTATAA			ATGACTCCCCACACTTGGCACCTGTTGTTAATACAGGTAGCAGAGGGTATGTGCCGGACTGGGGGGAAACATGTATAA	MTPHTWHLLLIQVAEGMCRTGGKHV*			MTPHTWHLLLIQVAEGMCRTGGKHV*	CATCCTTCCG	ATGCCAGTCA	0		0	0	0	0	0
7781	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-113	-84	ATGTGCCGGACTGGGGGGAAACATGTATAA			ATGTGCCGGACTGGGGGGAAACATGTATAA	MCRTGGKHV*			MCRTGGKHV*	AGCAGAGGGT	ATGCCAGTCA	0		0	0	0	0	0
7782	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-91	-2	ATGTATAAATGCCAGTCAATTCCACAACAAGCCAACATTGTATCTCATCGCAGTCACACACAACCAACGAACTCTAGCACAGTCACATAA			ATGTATAAATGCCAGTCAATTCCACAACAAGCCAACATTGTATCTCATCGCAGTCACACACAACCAACGAACTCTAGCACAGTCACATAA	MYKCQSIPQQANIVSHRSHTQPTNSSTVT*			MYKCQSIPQQANIVSHRSHTQPTNSSTVT*	GGGGGGAAAC	CATGGTGTCC	0		0	0	0	0	0
7783	3599	ao	AN3613.1	52.m03647	AO070315000027	0					-83	-15	ATGCCAGTCAATTCCACAACAAGCCAACATTGTATCTCATCGCAGTCACACACAACCAACGAACTCTAG			ATGCCAGTCAATTCCACAACAAGCCAACATTGTATCTCATCGCAGTCACACACAACCAACGAACTCTAG	MPVNSTTSQHCISSQSHTTNEL*			MPVNSTTSQHCISSQSHTTNEL*	ACATGTATAA	CACAGTCACA	0		0	0	0	0	0
7786	3601	af	AN9504.1	62.m03341	AO070315000153	0			-274	-236			ATGTCTTGCTGCGTTGCTCAGCAACAACACTGCATCTAA		ATGTCTTGCTGCGTTGCTCAGCAACAACACTGCATCTAA		MSCCVAQQQHCI*		MSCCVAQQQHCI*		GAATAGAGCC	ACATCCAAAA	0	V	0	MG03026.1	0	0	0
7787	3601	af	AN9504.1	62.m03341	AO070315000153	0			-100	-80			ATGCATTGCATGCCTGTATAA		ATGCATTGCATGCCTGTATAA		MHCMPV*		MHCMPV*		AGGCTAGTAA	TATCTATTCG	0	V	0	MG03026.1	0	0	0
7788	3601	af	AN9504.1	62.m03341	AO070315000153	0			-91	-80			ATGCCTGTATAA		ATGCCTGTATAA		MPV*		MPV*		AATGCATTGC	TATCTATTCG	0	V	0	MG03026.1	0	0	0
7784	3601	an	AN9504.1	62.m03341	AO070315000153	0	-159	-130					ATGTTCCCATCCGACTTCTTCGACTACTAA	ATGTTCCCATCCGACTTCTTCGACTACTAA			MFPSDFFDY*	MFPSDFFDY*			AACCTTCTCC	CCTGCAGAAA	0	V	0	MG03026.1	0	0	0
7785	3601	an	AN9504.1	62.m03341	AO070315000153	0	-94	-32					ATGCGCCAGGACCATCATCTTTCCCATCCACCATTCTCTCCTTCGATAACCTTTACCTGCTGA	ATGCGCCAGGACCATCATCTTTCCCATCCACCATTCTCTCCTTCGATAACCTTTACCTGCTGA			MRQDHHLSHPPFSPSITFTC*	MRQDHHLSHPPFSPSITFTC*			CGAATTGTCA	AGCGACGCTC	0	V	0	MG03026.1	0	0	0
7789	3601	ao	AN9504.1	62.m03341	AO070315000153	0					-222	-184	ATGGCCTCCGTCCCGTTGCATGAAGACTTACTTCTTTAA			ATGGCCTCCGTCCCGTTGCATGAAGACTTACTTCTTTAA	MASVPLHEDLLL*			MASVPLHEDLLL*	CTAAACATTC	ATCTACCAAT	0	V	0	MG03026.1	0	0	0
7790	3601	ao	AN9504.1	62.m03341	AO070315000153	0					-203	-96	ATGAAGACTTACTTCTTTAAATCTACCAATTTTGCTCCATGTCCAAAGCCGACCTCGTTGTCTACTAACCAAACAGGTTCTACAAAAATAAGATCAATTCATGAATGA			ATGAAGACTTACTTCTTTAAATCTACCAATTTTGCTCCATGTCCAAAGCCGACCTCGTTGTCTACTAACCAAACAGGTTCTACAAAAATAAGATCAATTCATGAATGA	MKTYFFKSTNFAPCPKPTSLSTNQTGSTKIRSIHE*			MKTYFFKSTNFAPCPKPTSLSTNQTGSTKIRSIHE*	GTCCCGTTGC	GCTGATCACT	0	V	0	MG03026.1	0	0	0
7791	3601	ao	AN9504.1	62.m03341	AO070315000153	0					-165	-136	ATGTCCAAAGCCGACCTCGTTGTCTACTAA			ATGTCCAAAGCCGACCTCGTTGTCTACTAA	MSKADLVVY*			MSKADLVVY*	ATTTTGCTCC	CCAAACAGGT	0	V	0	MG03026.1	0	0	0
7793	3602	af	AN4569.1	57.m05490	AO070316000152	0			-276	-175			ATGGCTTTTGAGGTGAAGAGAAGCAATCGGACGGAGTGCATGGCGGCATCCGCACGATTTGGTTCGTCCATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		ATGGCTTTTGAGGTGAAGAGAAGCAATCGGACGGAGTGCATGGCGGCATCCGCACGATTTGGTTCGTCCATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		MAFEVKRSNRTECMAASARFGSSMTFQPQDPRD*		MAFEVKRSNRTECMAASARFGSSMTFQPQDPRD*		AAGAGGACGG	TGCCTTGCCA	0	R	0	0	0	0	0
7794	3602	af	AN4569.1	57.m05490	AO070316000152	0			-237	-175			ATGGCGGCATCCGCACGATTTGGTTCGTCCATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		ATGGCGGCATCCGCACGATTTGGTTCGTCCATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		MAASARFGSSMTFQPQDPRD*		MAASARFGSSMTFQPQDPRD*		GACGGAGTGC	TGCCTTGCCA	0	R	0	0	0	0	0
7795	3602	af	AN4569.1	57.m05490	AO070316000152	0			-207	-175			ATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		ATGACGTTCCAGCCGCAGGACCCCCGAGATTGA		MTFQPQDPRD*		MTFQPQDPRD*		TGGTTCGTCC	TGCCTTGCCA	0	R	0	0	0	0	0
7796	3602	af	AN4569.1	57.m05490	AO070316000152	0			-175	-53			ATGCCTTGCCAAGAAGGCCGCAAGCGCGCGTCTGCAGCCATGCGTTTGGATTGGACCACCTCGGAATATCCGGTATATCAGCACCTCAGGCCTACAATTGCTGATGATTTACCCATCTATTAA		ATGCCTTGCCAAGAAGGCCGCAAGCGCGCGTCTGCAGCCATGCGTTTGGATTGGACCACCTCGGAATATCCGGTATATCAGCACCTCAGGCCTACAATTGCTGATGATTTACCCATCTATTAA		MPCQEGRKRASAAMRLDWTTSEYPVYQHLRPTIADDLPIY*		MPCQEGRKRASAAMRLDWTTSEYPVYQHLRPTIADDLPIY*		CCCGAGATTG	CTGTTCGTGA	0	R	0	0	0	0	0
7797	3602	af	AN4569.1	57.m05490	AO070316000152	0			-136	-53			ATGCGTTTGGATTGGACCACCTCGGAATATCCGGTATATCAGCACCTCAGGCCTACAATTGCTGATGATTTACCCATCTATTAA		ATGCGTTTGGATTGGACCACCTCGGAATATCCGGTATATCAGCACCTCAGGCCTACAATTGCTGATGATTTACCCATCTATTAA		MRLDWTTSEYPVYQHLRPTIADDLPIY*		MRLDWTTSEYPVYQHLRPTIADDLPIY*		GTCTGCAGCC	CTGTTCGTGA	0	R	0	0	0	0	0
7798	3602	af	AN4569.1	57.m05490	AO070316000152	0			-72	-43			ATGATTTACCCATCTATTAACTGTTCGTGA		ATGATTTACCCATCTATTAACTGTTCGTGA		MIYPSINCS*		MIYPSINCS*		ACAATTGCTG	TATTACCCAA	0	R	0	0	0	0	0
7792	3602	an	AN4569.1	57.m05490	AO070316000152	0	-148	-95					ATGACGTCCAGCCACAGTACCGCGTGCCGGCCCGAGCTAAGGCTGGATACTTAG	ATGACGTCCAGCCACAGTACCGCGTGCCGGCCCGAGCTAAGGCTGGATACTTAG			MTSSHSTACRPELRLDT*	MTSSHSTACRPELRLDT*			GGGGCCCAGA	GCGCGCGGCT	0	R	0	0	0	0	0
7799	3602	ao	AN4569.1	57.m05490	AO070316000152	0					-196	-134	ATGACGTCCGTCGTGCCAAGCCCTTTTCGGGCCTTTAAGCGCGCGTCTGCGGATTTCAATTGA			ATGACGTCCGTCGTGCCAAGCCCTTTTCGGGCCTTTAAGCGCGCGTCTGCGGATTTCAATTGA	MTSVVPSPFRAFKRASADFN*			MTSVVPSPFRAFKRASADFN*	CGCGGTCGGC	GCGGGTTGGA	0	R	0	0	0	0	0
7800	3602	ao	AN4569.1	57.m05490	AO070316000152	0					-113	-39	ATGAATGTCTTTACTCCGTCTCTGGTGAATTTCTTTCTACCTTCTTTTCTGTTCCTCTTCCTATCGCTTCCCTAA			ATGAATGTCTTTACTCCGTCTCTGGTGAATTTCTTTCTACCTTCTTTTCTGTTCCTCTTCCTATCGCTTCCCTAA	MNVFTPSLVNFFLPSFLFLFLSLP*			MNVFTPSLVNFFLPSFLFLFLSLP*	CCACCTCGGA	TACTCACTCA	0	R	0	0	0	0	0
7801	3602	ao	AN4569.1	57.m05490	AO070316000152	0					-109	-86	ATGTCTTTACTCCGTCTCTGGTGA			ATGTCTTTACTCCGTCTCTGGTGA	MSLLRLW*			MSLLRLW*	CTCGGAATGA	ATTTCTTTCT	0	R	0	0	0	0	0
7807	3604	af	AN0629.1	70.m15652	AO070318000119	0			-166	-152			ATGAGAGAAATGTAG		ATGAGAGAAATGTAG		MREM*		MREM*		GCCGTGAACC	ATCAATGATA	0	O	0	0	0	YIR038C	0
7808	3604	af	AN0629.1	70.m15652	AO070318000119	0			-147	-64			ATGATAAAGCCTTGTATCTGCTGTTGCCGACTAAGCTTTCGACGGTCGTCTCGTCCTGTTGTTTCAACAGAATCAGCTCCGTAG		ATGATAAAGCCTTGTATCTGCTGTTGCCGACTAAGCTTTCGACGGTCGTCTCGTCCTGTTGTTTCAACAGAATCAGCTCCGTAG		MIKPCICCCRLSFRRSSRPVVSTESAP*		MIKPCICCCRLSFRRSSRPVVSTESAP*		ATGTAGATCA	ACCAACATTT	0	O	0	0	0	YIR038C	0
7802	3604	an	AN0629.1	70.m15652	AO070318000119	0	-237	-175					ATGATAATGGTGGCCGGAGGACATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGATTTAG	ATGATAATGGTGGCCGGAGGACATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGATTTAG			MIMVAGGHASNVAKSNDGLI*	MIMVAGGHASNVAKSNDGLI*			CAAAGAGCTC	ATCTACCGCT	0	O	0	0	0	YIR038C	0
7803	3604	an	AN0629.1	70.m15652	AO070318000119	0	-231	-175					ATGGTGGCCGGAGGACATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGATTTAG	ATGGTGGCCGGAGGACATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGATTTAG			MVAGGHASNVAKSNDGLI*	MVAGGHASNVAKSNDGLI*			GCTCATGATA	ATCTACCGCT	0	O	0	0	0	YIR038C	0
7804	3604	an	AN0629.1	70.m15652	AO070318000119	0	-215	-180					ATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGA	ATGCCTCGAACGTCGCCAAGAGTAATGACGGTCTGA			MPRTSPRVMTV*	MPRTSPRVMTV*			GCCGGAGGAC	TTTAGATCTA	0	O	0	0	0	YIR038C	0
7805	3604	an	AN0629.1	70.m15652	AO070318000119	0	-191	-180					ATGACGGTCTGA	ATGACGGTCTGA			MTV*	MTV*			GCCAAGAGTA	TTTAGATCTA	0	O	0	0	0	YIR038C	0
7806	3604	an	AN0629.1	70.m15652	AO070318000119	0	-100	-80					ATGGTTCAGGCACGGATCTAA	ATGGTTCAGGCACGGATCTAA			MVQARI*	MVQARI*			TCGGTCTGTG	GGGATAAGAA	0	O	0	0	0	YIR038C	0
7809	3606	af	AN0917.1	70.m15524	AO070320000097	0			-218	-186			ATGAATCAAGTGATCAACTGCCCCCGCCTTTGA		ATGAATCAAGTGATCAACTGCCCCCGCCTTTGA		MNQVINCPRL*		MNQVINCPRL*		TGCGACACAC	CTCTCTGACT	0	K	0	0	0	0	0
7811	3608	af	AN0938.1	70.m15570	AO070320000129	0			-220	-56			ATGTGCTTTTCCGCCCCCATGCAAATTTATCCCAAGTTCCAGCGGAAGATACCGATCTCAATCTTCCAGAACGAGGCCTTGGTGGGTAATCCATTATCTGATTGCCCAAATCACACCAATCAATTGGTGAATTCCATCAAGGCTATCCTCGCGAGCTTGAATTAG		ATGTGCTTTTCCGCCCCCATGCAAATTTATCCCAAGTTCCAGCGGAAGATACCGATCTCAATCTTCCAGAACGAGGCCTTGGTGGGTAATCCATTATCTGATTGCCCAAATCACACCAATCAATTGGTGAATTCCATCAAGGCTATCCTCGCGAGCTTGAATTAG		MCFSAPMQIYPKFQRKIPISIFQNEALVGNPLSDCPNHTNQLVNSIKAILASLN*		MCFSAPMQIYPKFQRKIPISIFQNEALVGNPLSDCPNHTNQLVNSIKAILASLN*		GAGCCGTGTC	TGGTACTTGC	0	R	0	0	0	0	0

7812	3608	af	AN0938.1	70.m15570	AO070320000129	0			-202	-56			ATGCAAATTTATCCCAAGTTCCAGCGGAAGATACCGATCTCAATCTTCCAGAACGAGGCCTTGGTGGGTAATCCATTATCTGATTGCCCAAATCACACCAATCAATTGGTGAATTCCATCAAGGCTATCCTCGCGAGCTTGAATTAG		ATGCAAATTTATCCCAAGTTCCAGCGGAAGATACCGATCTCAATCTTCCAGAACGAGGCCTTGGTGGGTAATCCATTATCTGATTGCCCAAATCACACCAATCAATTGGTGAATTCCATCAAGGCTATCCTCGCGAGCTTGAATTAG		MQIYPKFQRKIPISIFQNEALVGNPLSDCPNHTNQLVNSIKAILASLN*		MQIYPKFQRKIPISIFQNEALVGNPLSDCPNHTNQLVNSIKAILASLN*		TTCCGCCCCC	TGGTACTTGC	0	R	0	0	0	0	0
7810	3608	an	AN0938.1	70.m15570	AO070320000129	0	-135	-97					ATGATCCTCCCGAGGACCGAGCCCTCTGCCGAAACCTGA	ATGATCCTCCCGAGGACCGAGCCCTCTGCCGAAACCTGA			MILPRTEPSAET*	MILPRTEPSAET*			CCAACACCTC	ACGTCGAATG	0	R	0	0	0	0	0
7813	3608	ao	AN0938.1	70.m15570	AO070320000129	0					-266	-81	ATGGCGACAGAGCGGAAGTTGACCGAGGCGGAGGGGGGCGTGACTAGGAAGCCCTCTTTTAAAACTCTTCGCCGTCCAGTTTGCCCCCATCGCGCCGAAAGAGTACCCGACCTCGTTTATACTGCCGCCCCCGATAATAATAATAATAATATATCGAAGGATCGCTTAGCTGTTGTCATCGTCTGA			ATGGCGACAGAGCGGAAGTTGACCGAGGCGGAGGGGGGCGTGACTAGGAAGCCCTCTTTTAAAACTCTTCGCCGTCCAGTTTGCCCCCATCGCGCCGAAAGAGTACCCGACCTCGTTTATACTGCCGCCCCCGATAATAATAATAATAATATATCGAAGGATCGCTTAGCTGTTGTCATCGTCTGA	MATERKLTEAEGGVTRKPSFKTLRRPVCPHRAERVPDLVYTAAPDNNNNNISKDRLAVVIV*			MATERKLTEAEGGVTRKPSFKTLRRPVCPHRAERVPDLVYTAAPDNNNNNISKDRLAVVIV*	GAGGAGAAGC	TTTCCCCGGA	0	R	0	0	0	0	0
7815	3610	af	AN4639.1	57.m05552	AO070321000194	0			-204	-112			ATGATAGGCATCTACAACGTACAAGGTAGGAATTTCAATCTCTGCTACCCCGCCGGCAAAGAATTTACTTTGAACTTGTGGTCAATGTCATAG		ATGATAGGCATCTACAACGTACAAGGTAGGAATTTCAATCTCTGCTACCCCGCCGGCAAAGAATTTACTTTGAACTTGTGGTCAATGTCATAG		MIGIYNVQGRNFNLCYPAGKEFTLNLWSMS*		MIGIYNVQGRNFNLCYPAGKEFTLNLWSMS*		CAGAGGAGGC	CAGACATGAT	0	D	0	MG02874.1	0	0	0
7816	3610	af	AN4639.1	57.m05552	AO070321000194	0			-106	-77			ATGATACCTAGCGATATGACCGGCGGCTAA		ATGATACCTAGCGATATGACCGGCGGCTAA		MIPSDMTGG*		MIPSDMTGG*		CATAGCAGAC	TAAAGCGCAA	0	D	0	MG02874.1	0	0	0
7817	3610	af	AN4639.1	57.m05552	AO070321000194	0			-91	-77			ATGACCGGCGGCTAA		ATGACCGGCGGCTAA		MTGG*		MTGG*		ACCTAGCGAT	TAAAGCGCAA	0	D	0	MG02874.1	0	0	0
7814	3610	an	AN4639.1	57.m05552	AO070321000194	0	-175	-14					ATGATAGTCGGTCTGGACTCGGTGCATGCGCTGACTTCTGATAAGGTGAGCGCCCCACTGTCGAAAAACGGCTCTCCAGAGCCCCTGCACAGGGTAACCTCACTAACAGCGATTGCGACTGTAAGTGACGGCCGACGTTCCTACGATAGACGCACACGATGA	ATGATAGTCGGTCTGGACTCGGTGCATGCGCTGACTTCTGATAAGGTGAGCGCCCCACTGTCGAAAAACGGCTCTCCAGAGCCCCTGCACAGGGTAACCTCACTAACAGCGATTGCGACTGTAAGTGACGGCCGACGTTCCTACGATAGACGCACACGATGA			MIVGLDSVHALTSDKVSAPLSKNGSPEPLHRVTSLTAIATVSDGRRSYDRRTR*	MIVGLDSVHALTSDKVSAPLSKNGSPEPLHRVTSLTAIATVSDGRRSYDRRTR*			CTTCATACCG	GCATCGCTGT	0	D	0	MG02874.1	0	0	0
7818	3610	ao	AN4639.1	57.m05552	AO070321000194	0					-232	-170	ATGATAATTGATAAGGTGAGAGCATACATGTGCATCTGCCCCACAATCAGATACATCGAATAG			ATGATAATTGATAAGGTGAGAGCATACATGTGCATCTGCCCCACAATCAGATACATCGAATAG	MIIDKVRAYMCICPTIRYIE*			MIIDKVRAYMCICPTIRYIE*	GCACCGTGGC	CTATAATATA	0	D	0	MG02874.1	0	0	0
7819	3610	ao	AN4639.1	57.m05552	AO070321000194	0					-205	-170	ATGTGCATCTGCCCCACAATCAGATACATCGAATAG			ATGTGCATCTGCCCCACAATCAGATACATCGAATAG	MCICPTIRYIE*			MCICPTIRYIE*	GAGAGCATAC	CTATAATATA	0	D	0	MG02874.1	0	0	0
7821	3612	an	AN8053.1	53.m04098	AO070322000147	0	-63	-40					ATGATTCTGATCGAAAGCCTATGA	ATGATTCTGATCGAAAGCCTATGA			MILIESL*	MILIESL*			GGGTGCTGTA	TCCAGCTTTC	0	U	0	0	0	0	0
7824	3614	af	AN1742.1	69.m15045	AO070324000056	0			-157	-137			ATGCTTGTTTACTACACTTGA		ATGCTTGTTTACTACACTTGA		MLVYYT*		MLVYYT*		CAGTGGCTGA	CATCGGATTA	0	G	0	0	0	0	0
7822	3614	an	AN1742.1	69.m15045	AO070324000056	0	-136	-119					ATGCTTTTCCTCTTCTAA	ATGCTTTTCCTCTTCTAA			MLFLF*	MLFLF*			TTGGTCCCCG	CACGGCCTTC	0	G	0	0	0	0	0
7823	3614	an	AN1742.1	69.m15045	AO070324000056	0	-88	-56					ATGCCTCGCTCACTATATATTCTTGGCCCGTAA	ATGCCTCGCTCACTATATATTCTTGGCCCGTAA			MPRSLYILGP*	MPRSLYILGP*			CATCTCATAT	GCCAAGAAGT	0	G	0	0	0	0	0
7825	3614	ao	AN1742.1	69.m15045	AO070324000056	0					-220	-167	ATGATACTTTCCCTTTTTCAACACGGTTTGGCTTCCGTCTACTCTATGCCGTGA			ATGATACTTTCCCTTTTTCAACACGGTTTGGCTTCCGTCTACTCTATGCCGTGA	MILSLFQHGLASVYSMP*			MILSLFQHGLASVYSMP*	AACCCCACTC	CCCGAATCGT	0	G	0	0	0	0	0
7826	3614	ao	AN1742.1	69.m15045	AO070324000056	0					-133	-83	ATGACGGCTGGTAGAAATCTAGTGACTGAAATGATACTTAGCGAAGTATAA			ATGACGGCTGGTAGAAATCTAGTGACTGAAATGATACTTAGCGAAGTATAA	MTAGRNLVTEMILSEV*			MTAGRNLVTEMILSEV*	GGAGTCCTGC	AACGGACCTG	0	G	0	0	0	0	0
7827	3614	ao	AN1742.1	69.m15045	AO070324000056	0					-103	-83	ATGATACTTAGCGAAGTATAA			ATGATACTTAGCGAAGTATAA	MILSEV*			MILSEV*	AGTGACTGAA	AACGGACCTG	0	G	0	0	0	0	0
7828	3615	ao	AN1731.1	69.m15037	AO070324000062	0					-199	-56	ATGACTTTTTACTATGGTCAAAGAAATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAACCATCTTCCTGTCTACTTGA			ATGACTTTTTACTATGGTCAAAGAAATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAACCATCTTCCTGTCTACTTGA	MTFYYGQRNVMESYRSNFSPSITVDSSGSTYSYFRTFIPYLTIFLST*			MTFYYGQRNVMESYRSNFSPSITVDSSGSTYSYFRTFIPYLTIFLST*	ATCTCTAATC	CTTGTCCACA	0	E	0	0	0	0	0
7829	3615	ao	AN1731.1	69.m15037	AO070324000062	0					-186	-76	ATGGTCAAAGAAATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAA			ATGGTCAAAGAAATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAA	MVKEMSWKATGLIFPPQLRWIPPEVLIHISVLLFPT*			MVKEMSWKATGLIFPPQLRWIPPEVLIHISVLLFPT*	ACTTTTTACT	CCATCTTCCT	0	E	0	0	0	0	0
7830	3615	ao	AN1731.1	69.m15037	AO070324000062	0					-174	-76	ATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAA			ATGTCATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAA	MSWKATGLIFPPQLRWIPPEVLIHISVLLFPT*			MSWKATGLIFPPQLRWIPPEVLIHISVLLFPT*	GGTCAAAGAA	CCATCTTCCT	0	E	0	0	0	0	0
7831	3615	ao	AN1731.1	69.m15037	AO070324000062	0					-169	-56	ATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAACCATCTTCCTGTCTACTTGA			ATGGAAAGCTACCGGTCTAATTTTTCCCCCTCAATTACGGTGGATTCCTCCGGAAGTACTTATTCATATTTCCGTACTTTTATTCCCTACTTAACCATCTTCCTGTCTACTTGA	MESYRSNFSPSITVDSSGSTYSYFRTFIPYLTIFLST*			MESYRSNFSPSITVDSSGSTYSYFRTFIPYLTIFLST*	AAGAAATGTC	CTTGTCCACA	0	E	0	0	0	0	0
7832	3616	af	AN3923.1	69.m15006	AO070324000119	0			-261	-247			ATGTTTTTGTTTTGA		ATGTTTTTGTTTTGA		MFLF*		MFLF*		ACATACAGTT	GTTTAGGTTT	0	O	0	0	0	0	0
7837	3619	af	AN6634.1	62.m03229	AO070326000086	0			-200	-117			ATGTTATGCCATGAACTGTCAGATTCCCAGGTGTCAAAAGATATCGTCATTGCACCCCTGCCAGCCCCAGCCCAACTGGGCTAA		ATGTTATGCCATGAACTGTCAGATTCCCAGGTGTCAAAAGATATCGTCATTGCACCCCTGCCAGCCCCAGCCCAACTGGGCTAA		MLCHELSDSQVSKDIVIAPLPAPAQLG*		MLCHELSDSQVSKDIVIAPLPAPAQLG*		CTTTGTGGTG	ACTGAGGTCA	0		0	0	0	0	0
7838	3619	af	AN6634.1	62.m03229	AO070326000086	0			-190	-41			ATGAACTGTCAGATTCCCAGGTGTCAAAAGATATCGTCATTGCACCCCTGCCAGCCCCAGCCCAACTGGGCTAAACTGAGGTCAACCCGGGACGTGTACATTCCTCGAGAATCTACAGGCTCGCTTGTCATGGCGCAAAGACAACCTTAA		ATGAACTGTCAGATTCCCAGGTGTCAAAAGATATCGTCATTGCACCCCTGCCAGCCCCAGCCCAACTGGGCTAAACTGAGGTCAACCCGGGACGTGTACATTCCTCGAGAATCTACAGGCTCGCTTGTCATGGCGCAAAGACAACCTTAA		MNCQIPRCQKISSLHPCQPQPNWAKLRSTRDVYIPRESTGSLVMAQRQP*		MNCQIPRCQKISSLHPCQPQPNWAKLRSTRDVYIPRESTGSLVMAQRQP*		ATGTTATGCC	CTCTCGTCAG	0		0	0	0	0	0
7839	3619	af	AN6634.1	62.m03229	AO070326000086	0			-61	-41			ATGGCGCAAAGACAACCTTAA		ATGGCGCAAAGACAACCTTAA		MAQRQP*		MAQRQP*		CTCGCTTGTC	CTCTCGTCAG	0		0	0	0	0	0
7840	3619	ao	AN6634.1	62.m03229	AO070326000086	0					-83	-33	ATGCCCGATAACCTCCCCTCCCATCCAATGGCCCGCGACAACAAAATTTGA			ATGCCCGATAACCTCCCCTCCCATCCAATGGCCCGCGACAACAAAATTTGA	MPDNLPSHPMARDNKI*			MPDNLPSHPMARDNKI*	CCGACCCGCC	GTGACAAGAC	0		0	0	0	0	0
7843	3620	af	AN4854.1	59.m09119	AO070327000089	0			-95	-75			ATGATCACGAGGAAAAAATAA		ATGATCACGAGGAAAAAATAA		MITRKK*		MITRKK*		AGGCATTACT	AAGCTTCATT	0		0	0	0	0	0
7842	3620	an	AN4854.1	59.m09119	AO070327000089	0	-69	-58					ATGTCTTTATAA	ATGTCTTTATAA			MSL*	MSL*			AACTCTTTGA	CATCATTTGA	0		0	0	0	0	0
7844	3620	ao	AN4854.1	59.m09119	AO070327000089	0					-163	-101	ATGCTAAAAATACCCCTGACCAGCCACACGCTAACCCCTTCTAGGCAAGTATCTACTTGTTAG			ATGCTAAAAATACCCCTGACCAGCCACACGCTAACCCCTTCTAGGCAAGTATCTACTTGTTAG	MLKIPLTSHTLTPSRQVSTC*			MLKIPLTSHTLTPSRQVSTC*	ACGTACAAAC	ACGCGTAAGG	0		0	0	0	0	0
7845	3620	ao	AN4854.1	59.m09119	AO070327000089	0					-66	-55	ATGATACAATAA			ATGATACAATAA	MIQ*			MIQ*	ATTCCACCCC	ACAGCACAAA	0		0	0	0	0	0
7852	3624	af	AN7918.1	55.m03095	AO070330000118	0			-132	-31			ATGGCCCCGTCACTCCACTCTACATCTCCACATAAAACAACCCCTCCCCTCCCCTCACTCATCCCCTTTCCCAAATCAATTGAAACAAATTGCATTGAATAA		ATGGCCCCGTCACTCCACTCTACATCTCCACATAAAACAACCCCTCCCCTCCCCTCACTCATCCCCTTTCCCAAATCAATTGAAACAAATTGCATTGAATAA		MAPSLHSTSPHKTTPPLPSLIPFPKSIETNCIE*		MAPSLHSTSPHKTTPPLPSLIPFPKSIETNCIE*		GTCCAAGACC	TCTACAGTCC	0		0	0	0	0	0
7853	3624	ao	AN7918.1	55.m03095	AO070330000118	0					-301	-152	ATGCCGGCGACGATAACAAGAGTATCAGTGATAGCGGGGAAAGCTCTCGATAAGGTCTATCCCGGTAAACAGCTTCCTCCGTTATCGGTTCCAGTGTCAGCACAACCTCGACTCATGGTATTTACCACGTGGACGGTCATTCTAGGGTGA			ATGCCGGCGACGATAACAAGAGTATCAGTGATAGCGGGGAAAGCTCTCGATAAGGTCTATCCCGGTAAACAGCTTCCTCCGTTATCGGTTCCAGTGTCAGCACAACCTCGACTCATGGTATTTACCACGTGGACGGTCATTCTAGGGTGA	MPATITRVSVIAGKALDKVYPGKQLPPLSVPVSAQPRLMVFTTWTVILG*			MPATITRVSVIAGKALDKVYPGKQLPPLSVPVSAQPRLMVFTTWTVILG*	GGTATTGCAA	GAACATGACT	0		0	0	0	0	0
7854	3624	ao	AN7918.1	55.m03095	AO070330000118	0					-187	-152	ATGGTATTTACCACGTGGACGGTCATTCTAGGGTGA			ATGGTATTTACCACGTGGACGGTCATTCTAGGGTGA	MVFTTWTVILG*			MVFTTWTVILG*	ACCTCGACTC	GAACATGACT	0		0	0	0	0	0
7855	3624	ao	AN7918.1	55.m03095	AO070330000118	0					-147	-118	ATGACTCAAAGGCCAATTGAGTATAAATAA			ATGACTCAAAGGCCAATTGAGTATAAATAA	MTQRPIEYK*			MTQRPIEYK*	GGGTGAGAAC	GTGACTAGAG	0		0	0	0	0	0
7856	3625	af	AN1182.1	70.m15763	AO070331000182	0			-227	-153			ATGTTGACTTGTTGTCTGTTGATCCTTGAGAGACCAGCCCGCACAACGAACAACTCCTTCTCTCCTCACCGCTAA		ATGTTGACTTGTTGTCTGTTGATCCTTGAGAGACCAGCCCGCACAACGAACAACTCCTTCTCTCCTCACCGCTAA		MLTCCLLILERPARTTNNSFSPHR*		MLTCCLLILERPARTTNNSFSPHR*		CCAACAGCAA	ACTTCAACCC	0	Z	0	0	0	0	0
7857	3625	ao	AN1182.1	70.m15763	AO070331000182	0					-221	-207	ATGTTGACTTGTTGA			ATGTTGACTTGTTGA	MLTC*			MLTC*	AACTAAGCCA	TCCCCTGACG	0	Z	0	0	0	0	0
7859	3627	af	AN9079.1	66.m04537	AO070332000200	0			-142	-44			ATGAAACTTGATTTGACTCAGTACGCGCTGGCTAGTGCTTTGGTCCTAAAACCTCTATCCATGGTCTCCGCATCTTCCCCTCTCCTAAAGTGCAGTTGA		ATGAAACTTGATTTGACTCAGTACGCGCTGGCTAGTGCTTTGGTCCTAAAACCTCTATCCATGGTCTCCGCATCTTCCCCTCTCCTAAAGTGCAGTTGA		MKLDLTQYALASALVLKPLSMVSASSPLLKCS*		MKLDLTQYALASALVLKPLSMVSASSPLLKCS*		TCGCGGCTTA	ATTCTAAATA	0	R	0	0	0	0	0
7860	3627	af	AN9079.1	66.m04537	AO070332000200	0			-82	-44			ATGGTCTCCGCATCTTCCCCTCTCCTAAAGTGCAGTTGA		ATGGTCTCCGCATCTTCCCCTCTCCTAAAGTGCAGTTGA		MVSASSPLLKCS*		MVSASSPLLKCS*		ACCTCTATCC	ATTCTAAATA	0	R	0	0	0	0	0
7858	3627	an	AN9079.1	66.m04537	AO070332000200	0	-224	-186					ATGATCTTCCACCGCAACAACGCGCCCCCTTCTTATTGA	ATGATCTTCCACCGCAACAACGCGCCCCCTTCTTATTGA			MIFHRNNAPPSY*	MIFHRNNAPPSY*			CAGCAAGACA	CTTCACCTGC	0	R	0	0	0	0	0
7863	3631	af	AN3791.1	57.m05695	AO070337000241	0			-126	-103			ATGGAACCCATCGTGGTCTGCTGA		ATGGAACCCATCGTGGTCTGCTGA		MEPIVVC*		MEPIVVC*		TTTCAAAACC	GATGCAGTGT	0		0	0	0	0	0
7864	3631	af	AN3791.1	57.m05695	AO070337000241	0			-101	-81			ATGCAGTGTGGGTTGAGCTGA		ATGCAGTGTGGGTTGAGCTGA		MQCGLS*		MQCGLS*		GTCTGCTGAG	GCTAGATTGG	0		0	0	0	0	0
7861	3631	an	AN3791.1	57.m05695	AO070337000241	0	-135	-106					ATGAACCGACACGTCTTCTGTTCGACGTGA	ATGAACCGACACGTCTTCTGTTCGACGTGA			MNRHVFCST*	MNRHVFCST*			CCCGAGGCCC	TCATTAATAT	0		0	0	0	0	0
7862	3631	an	AN3791.1	57.m05695	AO070337000241	0	-97	-86					ATGATTTATTGA	ATGATTTATTGA			MIY*	MIY*			GATCATTAAT	CGCGGATTTT	0		0	0	0	0	0
7865	3631	ao	AN3791.1	57.m05695	AO070337000241	0					-149	-120	ATGTCGTTCGTGAAGACCATGATCTATTAA			ATGTCGTTCGTGAAGACCATGATCTATTAA	MSFVKTMIY*			MSFVKTMIY*	TCTGGCGGTT	AATGTCGTCG	0		0	0	0	0	0
7866	3631	ao	AN3791.1	57.m05695	AO070337000241	0					-131	-120	ATGATCTATTAA			ATGATCTATTAA	MIY*			MIY*	CGTGAAGACC	AATGTCGTCG	0		0	0	0	0	0
7867	3631	ao	AN3791.1	57.m05695	AO070337000241	0					-118	-101	ATGTCGTCGGACAAGTGA			ATGTCGTCGGACAAGTGA	MSSDK*			MSSDK*	ATCTATTAAA	GCGGTCGTCA	0		0	0	0	0	0
7868	3633	af	AN2880.1	59.m08727	AO070338000135	0			-273	-250			ATGCAGGCGGTCTTGTCCTCTTGA		ATGCAGGCGGTCTTGTCCTCTTGA		MQAVLSS*		MQAVLSS*		CCGAACCCAC	TTGCTGCTGT	0	R	0	0	0	0	0
7870	3633	ao	AN2880.1	59.m08727	AO070338000135	0					-124	-29	ATGTCTTATTGCTCTTGCAATATTATCATTCTTTTTTTTTTTTACCTTACCCTTTCGCCTTGCCCTTTCCTCTATACTCTAATTTATTGCCCTTAA			ATGTCTTATTGCTCTTGCAATATTATCATTCTTTTTTTTTTTTACCTTACCCTTTCGCCTTGCCCTTTCCTCTATACTCTAATTTATTGCCCTTAA	MSYCSCNIIILFFFYLTLSPCPFLYTLIYCP*			MSYCSCNIIILFFFYLTLSPCPFLYTLIYCP*	CCTCTTTTGG	TCCATGTCGC	0	R	0	0	0	0	0
7872	3634	ao	AN1548.1	55.m03068	AO070339000306	0					-183	-88	ATGTATAATTTCCAAACTTGCGAGATCGAGATGACAAATATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA			ATGTATAATTTCCAAACTTGCGAGATCGAGATGACAAATATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA	MYNFQTCEIEMTNMSMATSIQKAIKMEYPCD*			MYNFQTCEIEMTNMSMATSIQKAIKMEYPCD*	GAAATAGCCC	ACTGGCAAAC	0	IQR	0	0	0	0	0
7873	3634	ao	AN1548.1	55.m03068	AO070339000306	0					-153	-88	ATGACAAATATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA			ATGACAAATATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA	MTNMSMATSIQKAIKMEYPCD*			MTNMSMATSIQKAIKMEYPCD*	CGAGATCGAG	ACTGGCAAAC	0	IQR	0	0	0	0	0
7874	3634	ao	AN1548.1	55.m03068	AO070339000306	0					-144	-88	ATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA			ATGTCCATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA	MSMATSIQKAIKMEYPCD*			MSMATSIQKAIKMEYPCD*	GATGACAAAT	ACTGGCAAAC	0	IQR	0	0	0	0	0

7875	3634	ao	AN1548.1	55.m03068	AO070339000306	0					-138	-88	ATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA			ATGGCTACATCAATACAGAAGGCTATAAAGATGGAATATCCTTGCGACTAA	MATSIQKAIKMEYPCD*			MATSIQKAIKMEYPCD*	AAATATGTCC	ACTGGCAAAC	0	IQR	0	0	0	0	0
7876	3634	ao	AN1548.1	55.m03068	AO070339000306	0					-108	-88	ATGGAATATCCTTGCGACTAA			ATGGAATATCCTTGCGACTAA	MEYPCD*			MEYPCD*	GGCTATAAAG	ACTGGCAAAC	0	IQR	0	0	0	0	0
7878	3635	af	AN6136.1	72.m19029	AO070340000066	0			-181	-152			ATGGTGACTGCTTGTTACTCCTTTCTGTGA		ATGGTGACTGCTTGTTACTCCTTTCTGTGA		MVTACYSFL*		MVTACYSFL*		CTCATATTTC	CTTGGGACAA	0	A	0	0	0	0	0
7879	3635	af	AN6136.1	72.m19029	AO070340000066	0			-63	-40			ATGACAAATTGCGACTCCTCCTAA		ATGACAAATTGCGACTCCTCCTAA		MTNCDSS*		MTNCDSS*		CCCTCTTATC	GAATCGTCGG	0	A	0	0	0	0	0
7877	3635	an	AN6136.1	72.m19029	AO070340000066	0	-68	-54					ATGGTAACCGAGTAG	ATGGTAACCGAGTAG			MVTE*	MVTE*			TCTCCGAATC	CTGTCTGCTG	0	A	0	0	0	0	0
7880	3635	ao	AN6136.1	72.m19029	AO070340000066	0					-201	-190	ATGGTAAACTGA			ATGGTAAACTGA	MVN*			MVN*	ATCATCGCCT	CATCGATGCT	0	A	0	0	0	0	0
7881	3635	ao	AN6136.1	72.m19029	AO070340000066	0					-184	-131	ATGCTTGTCATCAATTCTCAAGGATTCTTTGTTTTCGAGGGTAAGGGGACTTAG			ATGCTTGTCATCAATTCTCAAGGATTCTTTGTTTTCGAGGGTAAGGGGACTTAG	MLVINSQGFFVFEGKGT*			MLVINSQGFFVFEGKGT*	ACTGACATCG	CATAGGTACC	0	A	0	0	0	0	0
7887	3638	af	AN1865.1	57.m05754	AO070341000202	0			-270	-121			ATGGCAGCAATGCAAGGCCCCTATCAGGAGACGGGATCATCCGCAAGCTTTCCTGTTCAGCCGAAGCTTCGTGTTGCGGGTGTGACACTGACATTGACACCGTCGGATCACGCAACGGCAGGGATGATTGGCATGCGATCGATGCATTGA		ATGGCAGCAATGCAAGGCCCCTATCAGGAGACGGGATCATCCGCAAGCTTTCCTGTTCAGCCGAAGCTTCGTGTTGCGGGTGTGACACTGACATTGACACCGTCGGATCACGCAACGGCAGGGATGATTGGCATGCGATCGATGCATTGA		MAAMQGPYQETGSSASFPVQPKLRVAGVTLTLTPSDHATAGMIGMRSMH*		MAAMQGPYQETGSSASFPVQPKLRVAGVTLTLTPSDHATAGMIGMRSMH*		ACTCAATCGT	CCGGTCTTCG	0	R	0	MG04225.1	0	0	0
7888	3638	af	AN1865.1	57.m05754	AO070341000202	0			-261	-121			ATGCAAGGCCCCTATCAGGAGACGGGATCATCCGCAAGCTTTCCTGTTCAGCCGAAGCTTCGTGTTGCGGGTGTGACACTGACATTGACACCGTCGGATCACGCAACGGCAGGGATGATTGGCATGCGATCGATGCATTGA		ATGCAAGGCCCCTATCAGGAGACGGGATCATCCGCAAGCTTTCCTGTTCAGCCGAAGCTTCGTGTTGCGGGTGTGACACTGACATTGACACCGTCGGATCACGCAACGGCAGGGATGATTGGCATGCGATCGATGCATTGA		MQGPYQETGSSASFPVQPKLRVAGVTLTLTPSDHATAGMIGMRSMH*		MQGPYQETGSSASFPVQPKLRVAGVTLTLTPSDHATAGMIGMRSMH*		TATGGCAGCA	CCGGTCTTCG	0	R	0	MG04225.1	0	0	0
7889	3638	af	AN1865.1	57.m05754	AO070341000202	0			-147	-121			ATGATTGGCATGCGATCGATGCATTGA		ATGATTGGCATGCGATCGATGCATTGA		MIGMRSMH*		MIGMRSMH*		AACGGCAGGG	CCGGTCTTCG	0	R	0	MG04225.1	0	0	0
7890	3638	af	AN1865.1	57.m05754	AO070341000202	0			-138	-121			ATGCGATCGATGCATTGA		ATGCGATCGATGCATTGA		MRSMH*		MRSMH*		GATGATTGGC	CCGGTCTTCG	0	R	0	MG04225.1	0	0	0
7891	3638	ao	AN1865.1	57.m05754	AO070341000202	0					-257	-147	ATGGATTTCATACCATATGTTGTTCTGTCACCTAAGTGGATAGGTAAACTCCTAGCCTCCCCACAGCCTTGTGCAAACGACACGCGGCAGCGGCAGTTGCGCAAGGGGTGA			ATGGATTTCATACCATATGTTGTTCTGTCACCTAAGTGGATAGGTAAACTCCTAGCCTCCCCACAGCCTTGTGCAAACGACACGCGGCAGCGGCAGTTGCGCAAGGGGTGA	MDFIPYVVLSPKWIGKLLASPQPCANDTRQRQLRKG*			MDFIPYVVLSPKWIGKLLASPQPCANDTRQRQLRKG*	TTATTGCACC	CAACAAGCTT	0	R	0	MG04225.1	0	0	0
7892	3638	ao	AN1865.1	57.m05754	AO070341000202	0					-241	-215	ATGTTGTTCTGTCACCTAAGTGGATAG			ATGTTGTTCTGTCACCTAAGTGGATAG	MLFCHLSG*			MLFCHLSG*	TTCATACCAT	GTAAACTCCT	0	R	0	MG04225.1	0	0	0
7894	3639	af	AN3712.1	69.m15419	AO070341000341	0			-137	-120			ATGGATCTTCCTTCATAA		ATGGATCTTCCTTCATAA		MDLPS*		MDLPS*		CCTGTGTTGG	TTCTTCGGGC	0	R	0	0	0	0	0
7893	3639	an	AN3712.1	69.m15419	AO070341000341	0	-136	-89					ATGGAGGGGCAAAGTGGGGATCCGTGCTGCTGCAGAAGCGGCAAATAA	ATGGAGGGGCAAAGTGGGGATCCGTGCTGCTGCAGAAGCGGCAAATAA			MEGQSGDPCCCRSGK*	MEGQSGDPCCCRSGK*			GCAAGTGGAC	ATATCCTCCT	0	R	0	0	0	0	0
7895	3639	ao	AN3712.1	69.m15419	AO070341000341	0					-204	-187	ATGTATATACCGTATTAA			ATGTATATACCGTATTAA	MYIPY*			MYIPY*	AATGTAACTT	TAATGCCGAT	0	R	0	0	0	0	0
7896	3639	ao	AN3712.1	69.m15419	AO070341000341	0					-184	-65	ATGCCGATGAGAAAGTGGGGGAGTGGAGGGGAACTGCAAAATGGGTATTATTTAAAGATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG			ATGCCGATGAGAAAGTGGGGGAGTGGAGGGGAACTGCAAAATGGGTATTATTTAAAGATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG	MPMRKWGSGGELQNGYYLKMGRSVPSELVISQCLYISPA*			MPMRKWGSGGELQNGYYLKMGRSVPSELVISQCLYISPA*	CGTATTAATA	TAAGAAACTC	0	R	0	0	0	0	0
7897	3639	ao	AN3712.1	69.m15419	AO070341000341	0					-178	-65	ATGAGAAAGTGGGGGAGTGGAGGGGAACTGCAAAATGGGTATTATTTAAAGATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG			ATGAGAAAGTGGGGGAGTGGAGGGGAACTGCAAAATGGGTATTATTTAAAGATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG	MRKWGSGGELQNGYYLKMGRSVPSELVISQCLYISPA*			MRKWGSGGELQNGYYLKMGRSVPSELVISQCLYISPA*	AATAATGCCG	TAAGAAACTC	0	R	0	0	0	0	0
7898	3639	ao	AN3712.1	69.m15419	AO070341000341	0					-144	-130	ATGGGTATTATTTAA			ATGGGTATTATTTAA	MGII*			MGII*	GAACTGCAAA	AGATGGGCCG	0	R	0	0	0	0	0
7899	3639	ao	AN3712.1	69.m15419	AO070341000341	0					-127	-65	ATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG			ATGGGCCGCAGTGTTCCCTCGGAGCTTGTGATTTCGCAATGTTTATATATTTCGCCAGCATAG	MGRSVPSELVISQCLYISPA*			MGRSVPSELVISQCLYISPA*	TTATTTAAAG	TAAGAAACTC	0	R	0	0	0	0	0
7901	3641	af	AN4094.1	54.m06498	AO070342000095	0			-85	-29			ATGGTCTTGCGACAGCTGTCATCACTCCAACGCTACCCCAATACTTTGTCTTGTTGA		ATGGTCTTGCGACAGCTGTCATCACTCCAACGCTACCCCAATACTTTGTCTTGTTGA		MVLRQLSSLQRYPNTLSC*		MVLRQLSSLQRYPNTLSC*		TGGTAAACGT	CGTATATCCC	0	IT	0	0	0	0	0
7900	3641	an	AN4094.1	54.m06498	AO070342000095	0	-82	-71					ATGTCGACATAA	ATGTCGACATAA			MST*	MST*			GGTCAGCCCA	ATACCACGCT	0	IT	0	0	0	0	0
7903	3642	af	AN3624.1	58.m07411	AO070342000127	0			-225	-145			ATGATATGCCCTTGTCGGACTTCCGACCACATCCGTCCCTGTGCTCCCTTCATTGGTCTTTTGTCCGCTATTTATCTTTGA		ATGATATGCCCTTGTCGGACTTCCGACCACATCCGTCCCTGTGCTCCCTTCATTGGTCTTTTGTCCGCTATTTATCTTTGA		MICPCRTSDHIRPCAPFIGLLSAIYL*		MICPCRTSDHIRPCAPFIGLLSAIYL*		AAGGGATGAA	CGTCAACCCA	0	P	0	0	0	0	0
7904	3642	af	AN3624.1	58.m07411	AO070342000127	0			-220	-26			ATGCCCTTGTCGGACTTCCGACCACATCCGTCCCTGTGCTCCCTTCATTGGTCTTTTGTCCGCTATTTATCTTTGACGTCAACCCAGCTTGCTGGAGGCGCTGGCTCCTGGTCTTTCTTTTCATACAGTCTTGGTCTCCCTTCCATAACAGACCCTCATGCGGTAACACACTGCAGTACAGCTTCCGTTGCGTAG		ATGCCCTTGTCGGACTTCCGACCACATCCGTCCCTGTGCTCCCTTCATTGGTCTTTTGTCCGCTATTTATCTTTGACGTCAACCCAGCTTGCTGGAGGCGCTGGCTCCTGGTCTTTCTTTTCATACAGTCTTGGTCTCCCTTCCATAACAGACCCTCATGCGGTAACACACTGCAGTACAGCTTCCGTTGCGTAG		MPLSDFRPHPSLCSLHWSFVRYLSLTSTQLAGGAGSWSFFSYSLGLPSITDPHAVTHCSTASVA*		MPLSDFRPHPSLCSLHWSFVRYLSLTSTQLAGGAGSWSFFSYSLGLPSITDPHAVTHCSTASVA*		ATGAAATGAT	CTTTAGTGAA	0	P	0	0	0	0	0
7902	3642	an	AN3624.1	58.m07411	AO070342000127	0	-218	-156					ATGCGGGATTCAAGGATTAAGCCCAGGCGCGTCAGCTCCGCAAGTTCCGACCCGTCTGATTAA	ATGCGGGATTCAAGGATTAAGCCCAGGCGCGTCAGCTCCGCAAGTTCCGACCCGTCTGATTAA			MRDSRIKPRRVSSASSDPSD*	MRDSRIKPRRVSSASSDPSD*			TCAGCAATAA	TCCCCATTCT	0	P	0	0	0	0	0
7907	3643	af	AN3583.1	58.m07381	AO070342000166	0			-261	-151			ATGTTGTCTCAGTCATCGACATTGACAAAGCAGGAGTTTTTCGTGAAGCAAGAACTGATATTCAAATTCTTCTTCTTCTTCCTATTATCATTGTTACTTGTTAATAACTGA		ATGTTGTCTCAGTCATCGACATTGACAAAGCAGGAGTTTTTCGTGAAGCAAGAACTGATATTCAAATTCTTCTTCTTCTTCCTATTATCATTGTTACTTGTTAATAACTGA		MLSQSSTLTKQEFFVKQELIFKFFFFFLLSLLLVNN*		MLSQSSTLTKQEFFVKQELIFKFFFFFLLSLLLVNN*		CGCAACCACT	CTTGAACTTG	0	O	FG09156.1	0	NCU03219.1	YNL238W	0
7908	3643	af	AN3583.1	58.m07381	AO070342000166	0			-85	-47			ATGGCAGCCAAGTCGTCGTCCTTTATTCCGCCTGACTGA		ATGGCAGCCAAGTCGTCGTCCTTTATTCCGCCTGACTGA		MAAKSSSFIPPD*		MAAKSSSFIPPD*		CTTTCCGTTC	GAGGACGTTT	0	O	FG09156.1	0	NCU03219.1	YNL238W	0
7905	3643	an	AN3583.1	58.m07381	AO070342000166	0	-165	-64					ATGAATAGACGGTTGTTTCTATCCTCAATCAATTCTTGTGGCGTATTGTCATCATTGCTCTCCAGTCTCTGCTTGCGCTGTCCTCCGATGTCAGGCTGTTAG	ATGAATAGACGGTTGTTTCTATCCTCAATCAATTCTTGTGGCGTATTGTCATCATTGCTCTCCAGTCTCTGCTTGCGCTGTCCTCCGATGTCAGGCTGTTAG			MNRRLFLSSINSCGVLSSLLSSLCLRCPPMSGC*	MNRRLFLSSINSCGVLSSLLSSLCLRCPPMSGC*			GTATCTGTGG	CTGTCCTTAA	0	O	FG09156.1	0	NCU03219.1	YNL238W	0
7906	3643	an	AN3583.1	58.m07381	AO070342000166	0	-78	-64					ATGTCAGGCTGTTAG	ATGTCAGGCTGTTAG			MSGC*	MSGC*			CTGTCCTCCG	CTGTCCTTAA	0	O	FG09156.1	0	NCU03219.1	YNL238W	0
7909	3643	ao	AN3583.1	58.m07381	AO070342000166	0					-75	-34	ATGGCAACTATCTTATTTGTCCTCATCTCGCCTTACTACTGA			ATGGCAACTATCTTATTTGTCCTCATCTCGCCTTACTACTGA	MATILFVLISPYY*			MATILFVLISPYY*	GTTCTTATTG	TAGGAGCCTA	0	O	FG09156.1	0	NCU03219.1	YNL238W	0
7911	3644	af	AN3578.1	58.m07376	AO070342000171	0			-176	-159			ATGGATTTTCATCTCTGA		ATGGATTTTCATCTCTGA		MDFHL*		MDFHL*		TTGGAGAGCA	GGGCCTGCTC	0	L	0	0	0	0	0
7910	3644	an	AN3578.1	58.m07376	AO070342000171	0	-195	-178					ATGGACTCGAAGCTTTGA	ATGGACTCGAAGCTTTGA			MDSKL*	MDSKL*			CTGAAGGACA	GCTCCTTCTT	0	L	0	0	0	0	0
7912	3644	ao	AN3578.1	58.m07376	AO070342000171	0					-174	-157	ATGATATCTGAATGTTAA			ATGATATCTGAATGTTAA	MISEC*			MISEC*	ACAGGGAACA	ACGCCCTTCT	0	L	0	0	0	0	0
7914	3645	af	AN3737.1	69.m15379	AO070342000271	0			-231	-181			ATGTATTCTTTTCCTATGACTGTATTCACCAATGGCACCAAGGAAGAATAA		ATGTATTCTTTTCCTATGACTGTATTCACCAATGGCACCAAGGAAGAATAA		MYSFPMTVFTNGTKEE*		MYSFPMTVFTNGTKEE*		CTTATTTATC	CCGCACTGCA	0	S	0	0	0	0	0
7915	3645	af	AN3737.1	69.m15379	AO070342000271	0			-216	-181			ATGACTGTATTCACCAATGGCACCAAGGAAGAATAA		ATGACTGTATTCACCAATGGCACCAAGGAAGAATAA		MTVFTNGTKEE*		MTVFTNGTKEE*		TTCTTTTCCT	CCGCACTGCA	0	S	0	0	0	0	0
7916	3645	af	AN3737.1	69.m15379	AO070342000271	0			-200	-54			ATGGCACCAAGGAAGAATAACCGCACTGCATCATTTGTTTGTTCCGATCTCATTCAACATATTCCCATTACATCACGTGATAGCGCGACATTTCAGGACGCGTTTCCTCAGTCAGAAGCGCGGGTTCAGCCTGTGACACTGACCTGA		ATGGCACCAAGGAAGAATAACCGCACTGCATCATTTGTTTGTTCCGATCTCATTCAACATATTCCCATTACATCACGTGATAGCGCGACATTTCAGGACGCGTTTCCTCAGTCAGAAGCGCGGGTTCAGCCTGTGACACTGACCTGA		MAPRKNNRTASFVCSDLIQHIPITSRDSATFQDAFPQSEARVQPVTLT*		MAPRKNNRTASFVCSDLIQHIPITSRDSATFQDAFPQSEARVQPVTLT*		GTATTCACCA	GCCCCCTACA	0	S	0	0	0	0	0
7913	3645	an	AN3737.1	69.m15379	AO070342000271	0	-69	-19					ATGACTGAACAACTGGCATCCCACTCAATACATCCTTTCGCAGTCGATTGA	ATGACTGAACAACTGGCATCCCACTCAATACATCCTTTCGCAGTCGATTGA			MTEQLASHSIHPFAVD*	MTEQLASHSIHPFAVD*			TGACTCTCCG	CTCTTCTACA	0	S	0	0	0	0	0
7918	3646	af	AN8489.1	52.m03751	AO070342000405	0			-236	-141			ATGGCATGCACCATCATGATTGGTGAGCACAGCCTTGGGACTTGTATTTCTATTGATGCTGTGAGAATCGGGGCCCTGGTCTGTTTAGACCGCTGA		ATGGCATGCACCATCATGATTGGTGAGCACAGCCTTGGGACTTGTATTTCTATTGATGCTGTGAGAATCGGGGCCCTGGTCTGTTTAGACCGCTGA		MACTIMIGEHSLGTCISIDAVRIGALVCLDR*		MACTIMIGEHSLGTCISIDAVRIGALVCLDR*		ATTGATCACA	CCCACTCGGC	0	Q	0	0	0	0	0
7919	3646	af	AN8489.1	52.m03751	AO070342000405	0			-231	-211			ATGCACCATCATGATTGGTGA		ATGCACCATCATGATTGGTGA		MHHHDW*		MHHHDW*		TCACAATGGC	GCACAGCCTT	0	Q	0	0	0	0	0
7920	3646	af	AN8489.1	52.m03751	AO070342000405	0			-221	-141			ATGATTGGTGAGCACAGCCTTGGGACTTGTATTTCTATTGATGCTGTGAGAATCGGGGCCCTGGTCTGTTTAGACCGCTGA		ATGATTGGTGAGCACAGCCTTGGGACTTGTATTTCTATTGATGCTGTGAGAATCGGGGCCCTGGTCTGTTTAGACCGCTGA		MIGEHSLGTCISIDAVRIGALVCLDR*		MIGEHSLGTCISIDAVRIGALVCLDR*		ATGCACCATC	CCCACTCGGC	0	Q	0	0	0	0	0
7921	3646	af	AN8489.1	52.m03751	AO070342000405	0			-114	-103			ATGGCAAGCTAA		ATGGCAAGCTAA		MAS*		MAS*		ATTTTGCAAA	TATATACCTT	0	Q	0	0	0	0	0
7917	3646	an	AN8489.1	52.m03751	AO070342000405	0	-173	-144					ATGTGGGCCTCTAGGGCGGATTCGGGCTGA	ATGTGGGCCTCTAGGGCGGATTCGGGCTGA			MWASRADSG*	MWASRADSG*			TAGGGGAGCC	TTATCACGCC	0	Q	0	0	0	0	0
7922	3646	ao	AN8489.1	52.m03751	AO070342000405	0					-246	-82	ATGACGCCCCTAACAAATCCCAATAAACTATGGAGTCCGCTGGAGCCTCGATCCATCCCTGGTGGGTCGCTTAAATGTGAACTCGGTGCCGGTCTGGTTTCAGGCCCCCAGACCCACTCAAGGGCAATGTGCTTATATACTTCGTTGCCCGTCCCATCCTCGTGA			ATGACGCCCCTAACAAATCCCAATAAACTATGGAGTCCGCTGGAGCCTCGATCCATCCCTGGTGGGTCGCTTAAATGTGAACTCGGTGCCGGTCTGGTTTCAGGCCCCCAGACCCACTCAAGGGCAATGTGCTTATATACTTCGTTGCCCGTCCCATCCTCGTGA	MTPLTNPNKLWSPLEPRSIPGGSLKCELGAGLVSGPQTHSRAMCLYTSLPVPSS*			MTPLTNPNKLWSPLEPRSIPGGSLKCELGAGLVSGPQTHSRAMCLYTSLPVPSS*	TCTAAGCAAG	GGGAGGATTT	0	Q	0	0	0	0	0
7923	3646	ao	AN8489.1	52.m03751	AO070342000405	0					-217	-173	ATGGAGTCCGCTGGAGCCTCGATCCATCCCTGGTGGGTCGCTTAA			ATGGAGTCCGCTGGAGCCTCGATCCATCCCTGGTGGGTCGCTTAA	MESAGASIHPWWVA*			MESAGASIHPWWVA*	CCAATAAACT	ATGTGAACTC	0	Q	0	0	0	0	0
7924	3646	ao	AN8489.1	52.m03751	AO070342000405	0					-120	-82	ATGTGCTTATATACTTCGTTGCCCGTCCCATCCTCGTGA			ATGTGCTTATATACTTCGTTGCCCGTCCCATCCTCGTGA	MCLYTSLPVPSS*			MCLYTSLPVPSS*	CTCAAGGGCA	GGGAGGATTT	0	Q	0	0	0	0	0
7925	3647	af	AN2164.1	72.m20017	AO070343000224	0			-245	-30			ATGAACAATATACTCACCGCCTCCCCTTTTGCGTTGTGTGCGTCCACCATCTTCTGCCCCTCCTACGCGACAATAATCATTCACGTCGTATCAATTTGTATCTTCAATCGCAGGTCAATTGCAGGCGCCATCGATCAGCAGGCGTTTTTCTCTACAGGTAGCTGCTCTGAGGCCTTGGCTTCAATTTGTGGAACATCTACCATTCTCTTCCGGTAG		ATGAACAATATACTCACCGCCTCCCCTTTTGCGTTGTGTGCGTCCACCATCTTCTGCCCCTCCTACGCGACAATAATCATTCACGTCGTATCAATTTGTATCTTCAATCGCAGGTCAATTGCAGGCGCCATCGATCAGCAGGCGTTTTTCTCTACAGGTAGCTGCTCTGAGGCCTTGGCTTCAATTTGTGGAACATCTACCATTCTCTTCCGGTAG		MNNILTASPFALCASTIFCPSYATIIIHVVSICIFNRRSIAGAIDQQAFFSTGSCSEALASICGTSTILFR*		MNNILTASPFALCASTIFCPSYATIIIHVVSICIFNRRSIAGAIDQQAFFSTGSCSEALASICGTSTILFR*		AGTCGTTATA	CCTGCACTAC	0	UY	0	0	0	0	0
7926	3647	ao	AN2164.1	72.m20017	AO070343000224	0					-229	-173	ATGAAATTCCACTCACCGCTTCCTTTTCTGCCTGGTTCTATCATCTGCCCCTCCTAA			ATGAAATTCCACTCACCGCTTCCTTTTCTGCCTGGTTCTATCATCTGCCCCTCCTAA	MKFHSPLPFLPGSIICPS*			MKFHSPLPFLPGSIICPS*	GTTTGCTCCC	CAACGCGCCA	0	UY	0	0	0	0	0
7927	3648	an	AN2017.1	58.m07625	AO070202000010	0	-168	-130					ATGGATGATCGCCGCGGGACGTGCCACAGCATGGTTTGA	ATGGATGATCGCCGCGGGACGTGCCACAGCATGGTTTGA			MDDRRGTCHSMV*	MDDRRGTCHSMV*			CTAAAGTCAA	CTCTTGCTTG	0	G	0	0	0	0	0
7928	3648	an	AN2017.1	58.m07625	AO070202000010	0	-164	-66					ATGATCGCCGCGGGACGTGCCACAGCATGGTTTGACTCTTGCTTGTCTTGTGAATCCGTGATTTTCCCGTCGAGTTCGAAACCTCGAAGATTAAATTGA	ATGATCGCCGCGGGACGTGCCACAGCATGGTTTGACTCTTGCTTGTCTTGTGAATCCGTGATTTTCCCGTCGAGTTCGAAACCTCGAAGATTAAATTGA			MIAAGRATAWFDSCLSCESVIFPSSSKPRRLN*	MIAAGRATAWFDSCLSCESVIFPSSSKPRRLN*			AGTCAAATGG	GTCAAGGCCG	0	G	0	0	0	0	0
7929	3648	ao	AN2017.1	58.m07625	AO070202000010	0					-196	-173	ATGTTTTGCCTTCACGGCAGGTAG			ATGTTTTGCCTTCACGGCAGGTAG	MFCLHGR*			MFCLHGR*	TTGACGGGGA	CACAAATCGA	0	G	0	0	0	0	0

7930	3648	ao	AN2017.1	58.m07625	AO070202000010	0					-163	-47	ATGGGAACGGGACGGGCCATCAATTGTGAGGGATTTCCCGTGGACACCTGGTTCGTCAAGACATATACATCTAGCTACAATTCCGGTTCGGAGACGGCAGAGGGGTCCGTTTCTTAA			ATGGGAACGGGACGGGCCATCAATTGTGAGGGATTTCCCGTGGACACCTGGTTCGTCAAGACATATACATCTAGCTACAATTCCGGTTCGGAGACGGCAGAGGGGTCCGTTTCTTAA	MGTGRAINCEGFPVDTWFVKTYTSSYNSGSETAEGSVS*			MGTGRAINCEGFPVDTWFVKTYTSSYNSGSETAEGSVS*	GCACAAATCG	AAGAACAACT	0	G	0	0	0	0	0
7934	3649	af	AN3080.1	59.m08918	AO070224000006	0			-153	-7			ATGATGTCGAACAAGATCCTCGGTGATCCCAACTTCATAGAAGACGCTTTCTGCGCGTCTGAATTTACTGCTGGTGCTCGACGGATTGATGCATTGATCAGTCATTGTCCCTTCTCTCCTCTCAGTCCCACGGTATCCGCGTTATGA		ATGATGTCGAACAAGATCCTCGGTGATCCCAACTTCATAGAAGACGCTTTCTGCGCGTCTGAATTTACTGCTGGTGCTCGACGGATTGATGCATTGATCAGTCATTGTCCCTTCTCTCCTCTCAGTCCCACGGTATCCGCGTTATGA		MMSNKILGDPNFIEDAFCASEFTAGARRIDALISHCPFSPLSPTVSAL*		MMSNKILGDPNFIEDAFCASEFTAGARRIDALISHCPFSPLSPTVSAL*		CAGTTGCTTG	AGCAGCATGG	0	U	0	0	0	0	0
7935	3649	af	AN3080.1	59.m08918	AO070224000006	0			-150	-7			ATGTCGAACAAGATCCTCGGTGATCCCAACTTCATAGAAGACGCTTTCTGCGCGTCTGAATTTACTGCTGGTGCTCGACGGATTGATGCATTGATCAGTCATTGTCCCTTCTCTCCTCTCAGTCCCACGGTATCCGCGTTATGA		ATGTCGAACAAGATCCTCGGTGATCCCAACTTCATAGAAGACGCTTTCTGCGCGTCTGAATTTACTGCTGGTGCTCGACGGATTGATGCATTGATCAGTCATTGTCCCTTCTCTCCTCTCAGTCCCACGGTATCCGCGTTATGA		MSNKILGDPNFIEDAFCASEFTAGARRIDALISHCPFSPLSPTVSAL*		MSNKILGDPNFIEDAFCASEFTAGARRIDALISHCPFSPLSPTVSAL*		TTGCTTGATG	AGCAGCATGG	0	U	0	0	0	0	0
7931	3649	an	AN3080.1	59.m08918	AO070224000006	0	-160	-137					ATGATTTGTTTAGGATGGCCTTGA	ATGATTTGTTTAGGATGGCCTTGA			MICLGWP*	MICLGWP*			AGTAATTCCG	AAGGTGGTCA	0	U	0	0	0	0	0
7932	3649	an	AN3080.1	59.m08918	AO070224000006	0	-146	-51					ATGGCCTTGAAAGGTGGTCATTTCAGATCAGAGCATCCTCTCCTCATAGCTTTTCTGAGGGCGCATATTCTCTTCTCAGTAATGGCCCGGTGCTGA	ATGGCCTTGAAAGGTGGTCATTTCAGATCAGAGCATCCTCTCCTCATAGCTTTTCTGAGGGCGCATATTCTCTTCTCAGTAATGGCCCGGTGCTGA			MALKGGHFRSEHPLLIAFLRAHILFSVMARC*	MALKGGHFRSEHPLLIAFLRAHILFSVMARC*			TTTGTTTAGG	GACTCTTTAC	0	U	0	0	0	0	0
7933	3649	an	AN3080.1	59.m08918	AO070224000006	0	-65	-51					ATGGCCCGGTGCTGA	ATGGCCCGGTGCTGA			MARC*	MARC*			CTTCTCAGTA	GACTCTTTAC	0	U	0	0	0	0	0
7936	3649	ao	AN3080.1	59.m08918	AO070224000006	0					-223	-158	ATGCCCCGTGCCAGCTTCGGAACAACATATGTCCGTCGGCTTCAGATTAGGTGGTCAGTTGCTTGA			ATGCCCCGTGCCAGCTTCGGAACAACATATGTCCGTCGGCTTCAGATTAGGTGGTCAGTTGCTTGA	MPRASFGTTYVRRLQIRWSVA*			MPRASFGTTYVRRLQIRWSVA*	AGGGTGTAGC	TTGGGTTAAC	0	U	0	0	0	0	0
7937	3649	ao	AN3080.1	59.m08918	AO070224000006	0					-195	-10	ATGTCCGTCGGCTTCAGATTAGGTGGTCAGTTGCTTGATTGGGTTAACGGATTTGTTTGGATATACTCCGTACTTGTCGCCCTTTTCGCCGAAACTCCCTTTAGTGATGGTCCGGTGCTGATCGGTGTGGGCTGTAAAAGACCTACCTTCCTCATTTCTCCTTCCCTGAGTCTGTTCACAAAATAA			ATGTCCGTCGGCTTCAGATTAGGTGGTCAGTTGCTTGATTGGGTTAACGGATTTGTTTGGATATACTCCGTACTTGTCGCCCTTTTCGCCGAAACTCCCTTTAGTGATGGTCCGGTGCTGATCGGTGTGGGCTGTAAAAGACCTACCTTCCTCATTTCTCCTTCCCTGAGTCTGTTCACAAAATAA	MSVGFRLGGQLLDWVNGFVWIYSVLVALFAETPFSDGPVLIGVGCKRPTFLISPSLSLFTK*			MSVGFRLGGQLLDWVNGFVWIYSVLVALFAETPFSDGPVLIGVGCKRPTFLISPSLSLFTK*	GGAACAACAT	TGAAGCACTA	0	U	0	0	0	0	0
7938	3649	ao	AN3080.1	59.m08918	AO070224000006	0					-89	-75	ATGGTCCGGTGCTGA			ATGGTCCGGTGCTGA	MVRC*			MVRC*	CCCTTTAGTG	TCGGTGTGGG	0	U	0	0	0	0	0
7944	3651	af	AN1349.1	70.m14884	AO070237000012	0			-287	-183			ATGCACGCAATAGATCTGACGTTGAACAGCTTTCCATATGGCGAACTTCCCTTTTCAGAGATATGTCGTCATTCTTTTTGGGCTTGTGTGAAGTGGGATTTCTGA		ATGCACGCAATAGATCTGACGTTGAACAGCTTTCCATATGGCGAACTTCCCTTTTCAGAGATATGTCGTCATTCTTTTTGGGCTTGTGTGAAGTGGGATTTCTGA		MHAIDLTLNSFPYGELPFSEICRHSFWACVKWDF*		MHAIDLTLNSFPYGELPFSEICRHSFWACVKWDF*		ACAGCTCATT	GTGGCTTCTT	0	A	0	0	0	0	0
7941	3651	an	AN1349.1	70.m14884	AO070237000012	0	-391	-329					ATGTTTTATTTTTCATTCTCGATACACAGCTTTCGTTCCTTTGCCCCAACATTCATTGCCTGA	ATGTTTTATTTTTCATTCTCGATACACAGCTTTCGTTCCTTTGCCCCAACATTCATTGCCTGA			MFYFSFSIHSFRSFAPTFIA*	MFYFSFSIHSFRSFAPTFIA*			ACAACAGTGT	ATATTTTTTT	0	A	0	0	0	0	0
7961	3653	af	AN1407.1	55.m02914	AO070242000010	0			-255	-202			ATGAGTCCCACGGTTCTGATTGGTACCGGGGTCCCTGTGTCGCTGGTAAACTAA		ATGAGTCCCACGGTTCTGATTGGTACCGGGGTCCCTGTGTCGCTGGTAAACTAA		MSPTVLIGTGVPVSLVN*		MSPTVLIGTGVPVSLVN*		TTACCAATTC	TAGATGGTGT	0	S	0	0	0	0	0
7962	3653	af	AN1407.1	55.m02914	AO070242000010	0			-198	-175			ATGGTGTCTGTTTTGGTGTGGTAG		ATGGTGTCTGTTTTGGTGTGGTAG		MVSVLVW*		MVSVLVW*		AAACTAATAG	CCTCCTCGGC	0	S	0	0	0	0	0
7963	3653	af	AN1407.1	55.m02914	AO070242000010	0			-122	-60			ATGGAAGCATGCCTAGACTACATAAAATATTGCCTCCCCCCACTCTTCTGTAAGAAATGCTGA		ATGGAAGCATGCCTAGACTACATAAAATATTGCCTCCCCCCACTCTTCTGTAAGAAATGCTGA		MEACLDYIKYCLPPLFCKKC*		MEACLDYIKYCLPPLFCKKC*		GGAGCTTTGC	CGTTTAGCAT	0	S	0	0	0	0	0
7964	3653	af	AN1407.1	55.m02914	AO070242000010	0			-114	-70			ATGCCTAGACTACATAAAATATTGCCTCCCCCCACTCTTCTGTAA		ATGCCTAGACTACATAAAATATTGCCTCCCCCCACTCTTCTGTAA		MPRLHKILPPPTLL*		MPRLHKILPPPTLL*		GCATGGAAGC	GAAATGCTGA	0	S	0	0	0	0	0
7960	3653	an	AN1407.1	55.m02914	AO070242000010	0	-128	-84					ATGTTATTCCGAGACCCCCCCTCCCCCCGCCACCACTATCATTGA	ATGTTATTCCGAGACCCCCCCTCCCCCCGCCACCACTATCATTGA			MLFRDPPSPRHHYH*	MLFRDPPSPRHHYH*			TCTTGGGGCA	GTTTTGACTT	0	S	0	0	0	0	0
7965	3653	ao	AN1407.1	55.m02914	AO070242000010	0					-194	-180	ATGTTTGGGTTTTAG			ATGTTTGGGTTTTAG	MFGF*			MFGF*	ATTCTATCGG	ATCTTTTATA	0	S	0	0	0	0	0
7966	3653	ao	AN1407.1	55.m02914	AO070242000010	0					-156	-145	ATGGATTCATAG			ATGGATTCATAG	MDS*			MDS*	AATTCTTGAG	AGTTTAGACT	0	S	0	0	0	0	0
7967	3653	ao	AN1407.1	55.m02914	AO070242000010	0					-108	-49	ATGGCCGTTCTCCATCCCCATAGTAAATTTACCCCTCGTCTAGAAAACATACAATTGTGA			ATGGCCGTTCTCCATCCCCATAGTAAATTTACCCCTCGTCTAGAAAACATACAATTGTGA	MAVLHPHSKFTPRLENIQL*			MAVLHPHSKFTPRLENIQL*	ATTGTTCCAC	TTTCCTACCC	0	S	0	0	0	0	0
7969	3658	af	AN3837.1	62.m03106	AO070270000016	0			-173	-153			ATGCAATGGCAGCTACTCTAA		ATGCAATGGCAGCTACTCTAA		MQWQLL*		MQWQLL*		CAGTTGAGCA	TGACCGTGAC	0	G	0	0	0	0	0
7970	3658	af	AN3837.1	62.m03106	AO070270000016	0			-168	-124			ATGGCAGCTACTCTAATGACCGTGACAGCATCAACGAATTCATGA		ATGGCAGCTACTCTAATGACCGTGACAGCATCAACGAATTCATGA		MAATLMTVTASTNS*		MAATLMTVTASTNS*		GAGCAATGCA	CGGGTGGCTA	0	G	0	0	0	0	0
7971	3658	af	AN3837.1	62.m03106	AO070270000016	0			-153	-124			ATGACCGTGACAGCATCAACGAATTCATGA		ATGACCGTGACAGCATCAACGAATTCATGA		MTVTASTNS*		MTVTASTNS*		AGCTACTCTA	CGGGTGGCTA	0	G	0	0	0	0	0
7972	3658	af	AN3837.1	62.m03106	AO070270000016	0			-127	-113			ATGACGGGTGGCTAG		ATGACGGGTGGCTAG		MTGG*		MTGG*		CAACGAATTC	AGTCTATTTA	0	G	0	0	0	0	0
7968	3658	an	AN3837.1	62.m03106	AO070270000016	0	-63	-22					ATGTTCTTTATTGGCAAACATTTCTTTCGACATCGACACTGA	ATGTTCTTTATTGGCAAACATTTCTTTCGACATCGACACTGA			MFFIGKHFFRHRH*	MFFIGKHFFRHRH*			ATCGGTGACG	GCATCTTTCT	0	G	0	0	0	0	0
7973	3658	ao	AN3837.1	62.m03106	AO070270000016	0					-220	-194	ATGCATACCTGCACCACCATACTATAG			ATGCATACCTGCACCACCATACTATAG	MHTCTTIL*			MHTCTTIL*	CAACCCGTTT	GCTTTCTGCC	0	G	0	0	0	0	0
7975	3659	af	AN6550.1	62.m03123	AO070270000035	0			-165	-88			ATGAAGTCTGGCTATCGCCTATATACGCTCTTGAGGTCTTTGATTCATTTTTACTTGGCTGATCGCTGTGTTGGATAA		ATGAAGTCTGGCTATCGCCTATATACGCTCTTGAGGTCTTTGATTCATTTTTACTTGGCTGATCGCTGTGTTGGATAA		MKSGYRLYTLLRSLIHFYLADRCVG*		MKSGYRLYTLLRSLIHFYLADRCVG*		TCATTGGTCG	TCGCATCCAA	0	J	0	0	0	0	0
7974	3659	an	AN6550.1	62.m03123	AO070270000035	0	-179	-120					ATGGTGGTGCCACCTGCCAGTCATCTTTTAGTGTTGTCGATCCGCTGTTTTCTGATATAG	ATGGTGGTGCCACCTGCCAGTCATCTTTTAGTGTTGTCGATCCGCTGTTTTCTGATATAG			MVVPPASHLLVLSIRCFLI*	MVVPPASHLLVLSIRCFLI*			AGATATAAGG	AAGAGCCTGA	0	J	0	0	0	0	0
7976	3659	ao	AN6550.1	62.m03123	AO070270000035	0					-229	-212	ATGAGTGTGGTGCACTGA			ATGAGTGTGGTGCACTGA	MSVVH*			MSVVH*	TTGGTGAGTC	ATAAAGAACT	0	J	0	0	0	0	0
7977	3659	ao	AN6550.1	62.m03123	AO070270000035	0					-160	-146	ATGAACCTCCGTTGA			ATGAACCTCCGTTGA	MNLR*			MNLR*	TCATTCCACT	CCTTTAGTGC	0	J	0	0	0	0	0
7978	3659	ao	AN6550.1	62.m03123	AO070270000035	0					-121	-104	ATGCATTGTGCTTGTTAG			ATGCATTGTGCTTGTTAG	MHCAC*			MHCAC*	GTTTCGTCTC	TCATTTACAC	0	J	0	0	0	0	0
7980	3661	an	AN1096.1	70.m15136	AO070285000048	0	-195	-139					ATGTTGTTACTGGATCCGCCTGGCCTGGTTACGACCTACTGCTACTATACTAGTTGA	ATGTTGTTACTGGATCCGCCTGGCCTGGTTACGACCTACTGCTACTATACTAGTTGA			MLLLDPPGLVTTYCYYTS*	MLLLDPPGLVTTYCYYTS*			CCGACGCTGA	GTGTCAATAA	0	WV	0	0	0	0	0
7981	3661	ao	AN1096.1	70.m15136	AO070285000048	0					-87	-67	ATGCCAATGGGAGTTCCATGA			ATGCCAATGGGAGTTCCATGA	MPMGVP*			MPMGVP*	TTCGCGGTTG	GAAGCTGTGT	0	WV	0	0	0	0	0
7979	3661	conserved	AN1096.1	70.m15136	AO070285000048	0	-94	-80	-81	-67	-81	-67	ATGrGAbTyyCATGA	ATGAGATTTCCATGA	ATGAGACTCTCATGA	ATGGGAGTTCCATGA	Mrfp*	MRFP*	MRLS*	MGVP*	bhkvdkksvA	sArkCkdksy	0	WV	0	0	0	0	0
7982	3662	an	AN7494.1	57.m05849	AO070287000022	0	-208	-173					ATGAACACGAGGACCTATATGATCAATCTGAACTAG	ATGAACACGAGGACCTATATGATCAATCTGAACTAG			MNTRTYMINLN*	MNTRTYMINLN*			GCCTTTGACG	AGGTTCCAGA	0	R	0	0	0	0	0
7983	3662	an	AN7494.1	57.m05849	AO070287000022	0	-190	-173					ATGATCAATCTGAACTAG	ATGATCAATCTGAACTAG			MINLN*	MINLN*			GAGGACCTAT	AGGTTCCAGA	0	R	0	0	0	0	0
7984	3662	an	AN7494.1	57.m05849	AO070287000022	0	-151	-125					ATGAGCGGCGGCAGTTTAGCGCGGTAG	ATGAGCGGCGGCAGTTTAGCGCGGTAG			MSGGSLAR*	MSGGSLAR*			TTGTTCTGCG	ACGCATCTAG	0	R	0	0	0	0	0
7986	3663	af	AN7479.1	57.m05859	AO070287000036	0			-126	-97			ATGACTCACCCGAAGGAGGATGGTGATTGA		ATGACTCACCCGAAGGAGGATGGTGATTGA		MTHPKEDGD*		MTHPKEDGD*		GTTGCATTTC	GCTGGCATGA	0	J	FG08865.1	MG08897.1	0	0	0
7987	3663	af	AN7479.1	57.m05859	AO070287000036	0			-107	-87			ATGGTGATTGAGCTGGCATGA		ATGGTGATTGAGCTGGCATGA		MVIELA*		MVIELA*		CCGAAGGAGG	TCCCACGAAC	0	J	FG08865.1	MG08897.1	0	0	0
7985	3663	an	AN7479.1	57.m05859	AO070287000036	0	-136	-104					ATGCTAATTCGTGTGACTCAGACCCTAGATTGA	ATGCTAATTCGTGTGACTCAGACCCTAGATTGA			MLIRVTQTLD*	MLIRVTQTLD*			GTTCTCAGAA	CTCACAATCT	0	J	FG08865.1	MG08897.1	0	0	0
7990	3665	af	AN4975.1	59.m08878	AO070288000042	0			-144	-13			ATGGAGTTCTCCGCATCCCGCATAAGAGGGGTGACTCTCCCAGCTGTGTATATCTTCCCCTCTGGCTTTCTTGCGATCTTCTTCAATCCATTGGTCAACTGGGATAGAGAGATACTGCAGCGAAGACCTTGA		ATGGAGTTCTCCGCATCCCGCATAAGAGGGGTGACTCTCCCAGCTGTGTATATCTTCCCCTCTGGCTTTCTTGCGATCTTCTTCAATCCATTGGTCAACTGGGATAGAGAGATACTGCAGCGAAGACCTTGA		MEFSASRIRGVTLPAVYIFPSGFLAIFFNPLVNWDREILQRRP*		MEFSASRIRGVTLPAVYIFPSGFLAIFFNPLVNWDREILQRRP*		GCGACTAGTT	TTTGAGGAAG	0	R	FG08428.1	0	0	0	0
7988	3665	an	AN4975.1	59.m08878	AO070288000042	0	-249	-46					ATGAGCTCGAAAGGGCAAGTGGTCGCAGCGGGCCGCCCGATGCCGGAAAGCGAATTGCAGATCGGCTTATCTTCGGCCACTTTTTCTTGGAGATCAGTCCATATCTTGGGGAAGAGACAGCTGGATTCTCTTTCAGCTCCCCAATTCGCATTCTGTACCCTTCAGAGCAAAAACCAGCAAGGAAAGAAAGCAGCTCAGTGTTAA	ATGAGCTCGAAAGGGCAAGTGGTCGCAGCGGGCCGCCCGATGCCGGAAAGCGAATTGCAGATCGGCTTATCTTCGGCCACTTTTTCTTGGAGATCAGTCCATATCTTGGGGAAGAGACAGCTGGATTCTCTTTCAGCTCCCCAATTCGCATTCTGTACCCTTCAGAGCAAAAACCAGCAAGGAAAGAAAGCAGCTCAGTGTTAA			MSSKGQVVAAGRPMPESELQIGLSSATFSWRSVHILGKRQLDSLSAPQFAFCTLQSKNQQGKKAAQC*	MSSKGQVVAAGRPMPESELQIGLSSATFSWRSVHILGKRQLDSLSAPQFAFCTLQSKNQQGKKAAQC*			TGCGAAAGCG	AGAACACTGC	0	R	FG08428.1	0	0	0	0
7989	3665	an	AN4975.1	59.m08878	AO070288000042	0	-210	-46					ATGCCGGAAAGCGAATTGCAGATCGGCTTATCTTCGGCCACTTTTTCTTGGAGATCAGTCCATATCTTGGGGAAGAGACAGCTGGATTCTCTTTCAGCTCCCCAATTCGCATTCTGTACCCTTCAGAGCAAAAACCAGCAAGGAAAGAAAGCAGCTCAGTGTTAA	ATGCCGGAAAGCGAATTGCAGATCGGCTTATCTTCGGCCACTTTTTCTTGGAGATCAGTCCATATCTTGGGGAAGAGACAGCTGGATTCTCTTTCAGCTCCCCAATTCGCATTCTGTACCCTTCAGAGCAAAAACCAGCAAGGAAAGAAAGCAGCTCAGTGTTAA			MPESELQIGLSSATFSWRSVHILGKRQLDSLSAPQFAFCTLQSKNQQGKKAAQC*	MPESELQIGLSSATFSWRSVHILGKRQLDSLSAPQFAFCTLQSKNQQGKKAAQC*			GGGCCGCCCG	AGAACACTGC	0	R	FG08428.1	0	0	0	0
7991	3665	ao	AN4975.1	59.m08878	AO070288000042	0					-137	-117	ATGGAGCCACTATTTTTTTAA			ATGGAGCCACTATTTTTTTAA	MEPLFF*			MEPLFF*	CGCTCCGAAC	AGGTTCCCCA	0	R	FG08428.1	0	0	0	0
7992	3667	af	AN1706.1	58.m07796	AO070305000044	0			-189	-88			ATGGATTGTGCTCCTTGCTTTGTCTCGATTGCTTGCAATTTCCTCGACCAGATGTCTTCTGCTGCCCAATGTCGGATCTGTGAGAGTATCTGGGCTTCCTGA		ATGGATTGTGCTCCTTGCTTTGTCTCGATTGCTTGCAATTTCCTCGACCAGATGTCTTCTGCTGCCCAATGTCGGATCTGTGAGAGTATCTGGGCTTCCTGA		MDCAPCFVSIACNFLDQMSSAAQCRICESIWAS*		MDCAPCFVSIACNFLDQMSSAAQCRICESIWAS*		CTTGGCGTTG	CGCTGGCAAC	0	O	0	0	0	0	0
7993	3667	af	AN1706.1	58.m07796	AO070305000044	0			-138	-88			ATGTCTTCTGCTGCCCAATGTCGGATCTGTGAGAGTATCTGGGCTTCCTGA		ATGTCTTCTGCTGCCCAATGTCGGATCTGTGAGAGTATCTGGGCTTCCTGA		MSSAAQCRICESIWAS*		MSSAAQCRICESIWAS*		CCTCGACCAG	CGCTGGCAAC	0	O	0	0	0	0	0
7994	3667	af	AN1706.1	58.m07796	AO070305000044	0			-121	-107			ATGTCGGATCTGTGA		ATGTCGGATCTGTGA		MSDL*		MSDL*		CTGCTGCCCA	GAGTATCTGG	0	O	0	0	0	0	0
7996	3667	ao	AN1706.1	58.m07796	AO070305000044	0					-98	-39	ATGGTCGCTCCTTTGTTGTGGATCTGTTCGAATTCGGGCTTATCCTCGGTCGTCGCTTGA			ATGGTCGCTCCTTTGTTGTGGATCTGTTCGAATTCGGGCTTATCCTCGGTCGTCGCTTGA	MVAPLLWICSNSGLSSVVA*			MVAPLLWICSNSGLSSVVA*	GCTATCGTTT	ACAGGGATCG	0	O	0	0	0	0	0
7999	3669	af	AN1476.1	55.m02978	AO070306000099	0			-85	-53			ATGAGTTGGGGGGGGATCACGGAAAGATCATAA		ATGAGTTGGGGGGGGATCACGGAAAGATCATAA		MSWGGITERS*		MSWGGITERS*		CTGAAGATTG	TTTCATATGA	0	R	0	0	0	0	0
7997	3669	an	AN1476.1	55.m02978	AO070306000099	0	-118	-62					ATGTGGAGCCAGCGTTCTTACTGCATCAACATCAAAGAGATAGCTTTGGACCTTTGA	ATGTGGAGCCAGCGTTCTTACTGCATCAACATCAAAGAGATAGCTTTGGACCTTTGA			MWSQRSYCINIKEIALDL*	MWSQRSYCINIKEIALDL*			CGTTGTTGCG	ACCTATCTGT	0	R	0	0	0	0	0
8002	3673	af	AN0118.1	71.m15397	AO070311000095	0			-224	-213			ATGATCATCTAA		ATGATCATCTAA		MII*		MII*		CAAAAGGGTC	CTGATTCCTG	0	Z	0	0	0	0	0
8003	3673	ao	AN0118.1	71.m15397	AO070311000095	0					-209	-198	ATGAACTCTTAA			ATGAACTCTTAA	MNS*			MNS*	AGAACAGAGC	CTACCACTAC	0	Z	0	0	0	0	0
8005	3674	af	AN8145.1	71.m15392	AO070311000100	0			-167	-129			ATGATCTCCAACATGGTATCCACCCTGATATCATCCTGA		ATGATCTCCAACATGGTATCCACCCTGATATCATCCTGA		MISNMVSTLISS*		MISNMVSTLISS*		TGTCATTGTC	TGGCGCTGTG	0	S	0	0	0	YML079W	0
8006	3674	af	AN8145.1	71.m15392	AO070311000100	0			-155	-129			ATGGTATCCACCCTGATATCATCCTGA		ATGGTATCCACCCTGATATCATCCTGA		MVSTLISS*		MVSTLISS*		GATCTCCAAC	TGGCGCTGTG	0	S	0	0	0	YML079W	0
8007	3674	af	AN8145.1	71.m15392	AO070311000100	0			-129	-76			ATGGCGCTGTGTGGCTCCGACATGATACAATTTTATCTTGTATCTACTCGGTAG		ATGGCGCTGTGTGGCTCCGACATGATACAATTTTATCTTGTATCTACTCGGTAG		MALCGSDMIQFYLVSTR*		MALCGSDMIQFYLVSTR*		TATCATCCTG	AAACGAACAA	0	S	0	0	0	YML079W	0
8008	3674	af	AN8145.1	71.m15392	AO070311000100	0			-108	-76			ATGATACAATTTTATCTTGTATCTACTCGGTAG		ATGATACAATTTTATCTTGTATCTACTCGGTAG		MIQFYLVSTR*		MIQFYLVSTR*		TGGCTCCGAC	AAACGAACAA	0	S	0	0	0	YML079W	0
8004	3674	an	AN8145.1	71.m15392	AO070311000100	0	-205	-164					ATGGGATCGCCCGTCAGATCAGTCTGGCCCAAACACACATAA	ATGGGATCGCCCGTCAGATCAGTCTGGCCCAAACACACATAA			MGSPVRSVWPKHT*	MGSPVRSVWPKHT*			ATGTCAAGTG	GAGGAGATCA	0	S	0	0	0	YML079W	0

8009	3674	ao	AN8145.1	71.m15392	AO070311000100	0					-206	-177	ATGATTCCAAGATGCAATGTAGAACTGTGA			ATGATTCCAAGATGCAATGTAGAACTGTGA	MIPRCNVEL*			MIPRCNVEL*	CGCTATATAC	TCCCTCATGA	0	S	0	0	0	YML079W	0
8010	3674	ao	AN8145.1	71.m15392	AO070311000100	0					-195	-157	ATGCAATGTAGAACTGTGATCCCTCATGAATTTGGCTGA			ATGCAATGTAGAACTGTGATCCCTCATGAATTTGGCTGA	MQCRTVIPHEFG*			MQCRTVIPHEFG*	TGATTCCAAG	CTTCCTGTAT	0	S	0	0	0	YML079W	0
8011	3674	ao	AN8145.1	71.m15392	AO070311000100	0					-170	-126	ATGAATTTGGCTGACTTCCTGTATCCTGATAAGCTCCATGAGTGA			ATGAATTTGGCTGACTTCCTGTATCCTGATAAGCTCCATGAGTGA	MNLADFLYPDKLHE*			MNLADFLYPDKLHE*	GTGATCCCTC	GGTCATCGGG	0	S	0	0	0	YML079W	0
8012	3674	ao	AN8145.1	71.m15392	AO070311000100	0					-133	-65	ATGAGTGAGGTCATCGGGACATTTATAAGCATGATTTATAGACGTCTGGGCGAGTTCCGTCTTACATAG			ATGAGTGAGGTCATCGGGACATTTATAAGCATGATTTATAGACGTCTGGGCGAGTTCCGTCTTACATAG	MSEVIGTFISMIYRRLGEFRLT*			MSEVIGTFISMIYRRLGEFRLT*	GATAAGCTCC	TATGCTCCAA	0	S	0	0	0	YML079W	0
8016	3675	af	AN1007.1	70.m15225	AO070312000026	0			-206	-171			ATGGGCGGATGCAATCGTAGCAGGGTTCGCCGATGA		ATGGGCGGATGCAATCGTAGCAGGGTTCGCCGATGA		MGGCNRSRVRR*		MGGCNRSRVRR*		AGGCTCGAAC	CAATAAATTA	0	C	0	0	0	0	0
8017	3675	af	AN1007.1	70.m15225	AO070312000026	0			-198	-187			ATGCAATCGTAG		ATGCAATCGTAG		MQS*		MQS*		ACATGGGCGG	CAGGGTTCGC	0	C	0	0	0	0	0
8018	3675	af	AN1007.1	70.m15225	AO070312000026	0			-174	-157			ATGACAATAAATTATTAG		ATGACAATAAATTATTAG		MTINY*		MTINY*		GGGTTCGCCG	CAGAAATAAA	0	C	0	0	0	0	0
8019	3675	af	AN1007.1	70.m15225	AO070312000026	0			-146	-84			ATGCAACTGACTGGTTGCGTTTCGTCCATGCCAACTCAACGAAGAGCTGTAGATTGTATATGA		ATGCAACTGACTGGTTGCGTTTCGTCCATGCCAACTCAACGAAGAGCTGTAGATTGTATATGA		MQLTGCVSSMPTQRRAVDCI*		MQLTGCVSSMPTQRRAVDCI*		CAGAAATAAA	GCAGAGAGGT	0	C	0	0	0	0	0
8020	3675	af	AN1007.1	70.m15225	AO070312000026	0			-119	-84			ATGCCAACTCAACGAAGAGCTGTAGATTGTATATGA		ATGCCAACTCAACGAAGAGCTGTAGATTGTATATGA		MPTQRRAVDCI*		MPTQRRAVDCI*		CGTTTCGTCC	GCAGAGAGGT	0	C	0	0	0	0	0
8021	3675	af	AN1007.1	70.m15225	AO070312000026	0			-87	-13			ATGAGCAGAGAGGTCCTCAGCCGTCCCCTAAAAGAGTTCATTCTGGTAATGAGCTGTGGTCAATACTGGCGTTGA		ATGAGCAGAGAGGTCCTCAGCCGTCCCCTAAAAGAGTTCATTCTGGTAATGAGCTGTGGTCAATACTGGCGTTGA		MSREVLSRPLKEFILVMSCGQYWR*		MSREVLSRPLKEFILVMSCGQYWR*		TAGATTGTAT	GACTTCGTCA	0	C	0	0	0	0	0
8015	3675	an	AN1007.1	70.m15225	AO070312000026	0	-152	-117					ATGCCACGGAGATACAATCACCAAGGCGTTTGGTGA	ATGCCACGGAGATACAATCACCAAGGCGTTTGGTGA			MPRRYNHQGVW*	MPRRYNHQGVW*			TCATGCTCCG	CTCGTTGTGC	0	C	0	0	0	0	0
8023	3675	ao	AN1007.1	70.m15225	AO070312000026	0					-169	-74	ATGGTGTCCACGGAGATGAGAGGCCCGATCCTGGATCTTGGCACCAGTAGGGTCTTGCCATATCGGATGATAGATCATGGGGGACATACTCCTTGA			ATGGTGTCCACGGAGATGAGAGGCCCGATCCTGGATCTTGGCACCAGTAGGGTCTTGCCATATCGGATGATAGATCATGGGGGACATACTCCTTGA	MVSTEMRGPILDLGTSRVLPYRMIDHGGHTP*			MVSTEMRGPILDLGTSRVLPYRMIDHGGHTP*	CCACGACCTC	TAAATAAAAA	0	C	0	0	0	0	0
8024	3675	ao	AN1007.1	70.m15225	AO070312000026	0					-154	-74	ATGAGAGGCCCGATCCTGGATCTTGGCACCAGTAGGGTCTTGCCATATCGGATGATAGATCATGGGGGACATACTCCTTGA			ATGAGAGGCCCGATCCTGGATCTTGGCACCAGTAGGGTCTTGCCATATCGGATGATAGATCATGGGGGACATACTCCTTGA	MRGPILDLGTSRVLPYRMIDHGGHTP*			MRGPILDLGTSRVLPYRMIDHGGHTP*	GTCCACGGAG	TAAATAAAAA	0	C	0	0	0	0	0
8025	3675	ao	AN1007.1	70.m15225	AO070312000026	0					-103	-74	ATGATAGATCATGGGGGACATACTCCTTGA			ATGATAGATCATGGGGGACATACTCCTTGA	MIDHGGHTP*			MIDHGGHTP*	GCCATATCGG	TAAATAAAAA	0	C	0	0	0	0	0
8026	3675	ao	AN1007.1	70.m15225	AO070312000026	0					-93	-67	ATGGGGGACATACTCCTTGATAAATAA			ATGGGGGACATACTCCTTGATAAATAA	MGDILLDK*			MGDILLDK*	ATGATAGATC	AAACGTCCGC	0	C	0	0	0	0	0
8028	3677	af	AN6853.1	71.m15279	AO070314000087	0			-143	-90			ATGAGGATTGACGAAACGACGAAAAAGCAAAGAAGAAAAGTTCTGATCCTGTGA		ATGAGGATTGACGAAACGACGAAAAAGCAAAGAAGAAAAGTTCTGATCCTGTGA		MRIDETTKKQRRKVLIL*		MRIDETTKKQRRKVLIL*		GTCGATCTCG	CATAAGTTCA	0	I	FG05890.1	0	0	0	0
8027	3677	an	AN6853.1	71.m15279	AO070314000087	0	-229	-164					ATGTTCACTAACAATGTAAGCTGTCCTGACGATCATCGCAACAAAACCCCCAATCAAACAAGCTAA	ATGTTCACTAACAATGTAAGCTGTCCTGACGATCATCGCAACAAAACCCCCAATCAAACAAGCTAA			MFTNNVSCPDDHRNKTPNQTS*	MFTNNVSCPDDHRNKTPNQTS*			CATTACGCCG	GCTTCGGAAG	0	I	FG05890.1	0	0	0	0
8030	3677	ao	AN6853.1	71.m15279	AO070314000087	0					-216	-40	ATGATTATTACTGTGTATGTCGAACGATCATCCTGTGGGCCTGTCGATCAACAGAGCCTACTCAGCGCTGAAACTTGCGCGGAAAAGAACAAAACTCCCAGGGGAGCTGCCATTGTCTCCGGTCTATATTATCCGAGCCATTGCCCCCTGAATTACAGCCTAGAGTACTTCCCATAG			ATGATTATTACTGTGTATGTCGAACGATCATCCTGTGGGCCTGTCGATCAACAGAGCCTACTCAGCGCTGAAACTTGCGCGGAAAAGAACAAAACTCCCAGGGGAGCTGCCATTGTCTCCGGTCTATATTATCCGAGCCATTGCCCCCTGAATTACAGCCTAGAGTACTTCCCATAG	MIITVYYVERSSCGPVDQQSLLSAETCAEKNKTPRGAAIVSGLYYPSHCPLNYSLEYFP*			MIITVYYVERSSCGPVDQQSLLSAETCAEKNKTPRGAAIVSGLYYPSHCPLNYSLEYFP*	TACTCCGTCT	ATTTGAACTT	0	I	FG05890.1	0	0	0	0
8031	3677	ao	AN6853.1	71.m15279	AO070314000087	0					-200	-66	ATGTCGAACGATCATCCTGTGGGCCTGTCGATCAACAGAGCCTACTCAGCGCTGAAACTTGCGCGGAAAAGAACAAAACTCCCAGGGGAGCTGCCATTGTCTCCGGTCTATATTATCCGAGCCATTGCCCCCTGA			ATGTCGAACGATCATCCTGTGGGCCTGTCGATCAACAGAGCCTACTCAGCGCTGAAACTTGCGCGGAAAAGAACAAAACTCCCAGGGGAGCTGCCATTGTCTCCGGTCTATATTATCCGAGCCATTGCCCCCTGA	MSNDHPVGLSINRAYSALKLARKRTKLPGELPLSPVYIIRAIAP*			MSNDHPVGLSINRAYSALKLARKRTKLPGELPLSPVYIIRAIAP*	ATTACTGTGT	ATTACAGCCT	0	I	FG05890.1	0	0	0	0
8032	3678	af	AN0043.1	71.m15318	AO070314000122	0			-203	-162			ATGGGCGGCTTCAAATTGTCACCTTGTCGCCCATGCGCTTAG		ATGGGCGGCTTCAAATTGTCACCTTGTCGCCCATGCGCTTAG		MGGFKLSPCRPCA*		MGGFKLSPCRPCA*		CAATAAATTT	CAGTGCATCC	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8033	3678	af	AN0043.1	71.m15318	AO070314000122	0			-171	-85			ATGCGCTTAGCAGTGCATCCATATAGATCATTTTCCTTTTTCTCGGTATGCTTAGAGCTCAGAGATTTGGTGATTTTGGTCTGCTGA		ATGCGCTTAGCAGTGCATCCATATAGATCATTTTCCTTTTTCTCGGTATGCTTAGAGCTCAGAGATTTGGTGATTTTGGTCTGCTGA		MRLAVHPYRSFSFFSVCLELRDLVILVC*		MRLAVHPYRSFSFFSVCLELRDLVILVC*		CTTGTCGCCC	CAAGGTGTCT	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8034	3678	af	AN0043.1	71.m15318	AO070314000122	0			-124	-38			ATGCTTAGAGCTCAGAGATTTGGTGATTTTGGTCTGCTGACAAGGTGTCTAATAGATCCGGCTATGTGCATGCCAGCGATCCTCTGA		ATGCTTAGAGCTCAGAGATTTGGTGATTTTGGTCTGCTGACAAGGTGTCTAATAGATCCGGCTATGTGCATGCCAGCGATCCTCTGA		MLRAQRFGDFGLLTRCLIDPAMCMPAIL*		MLRAQRFGDFGLLTRCLIDPAMCMPAIL*		TTTTCTCGGT	AGCAGAAACG	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8035	3678	af	AN0043.1	71.m15318	AO070314000122	0			-61	-38			ATGTGCATGCCAGCGATCCTCTGA		ATGTGCATGCCAGCGATCCTCTGA		MCMPAIL*		MCMPAIL*		AGATCCGGCT	AGCAGAAACG	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8037	3678	ao	AN0043.1	71.m15318	AO070314000122	0					-184	-143	ATGTATGTGCTATTACCTCTTATCCTTCTATTGTCATTTTAG			ATGTATGTGCTATTACCTCTTATCCTTCTATTGTCATTTTAG	MYVLLPLILLLSF*			MYVLLPLILLLSF*	GGTTAGGGAA	CTAATTGTTT	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8038	3678	ao	AN0043.1	71.m15318	AO070314000122	0					-180	-139	ATGTGCTATTACCTCTTATCCTTCTATTGTCATTTTAGCTAA			ATGTGCTATTACCTCTTATCCTTCTATTGTCATTTTAGCTAA	MCYYLLSFYCHFS*			MCYYLLSFYCHFS*	AGGGAAATGT	TTGTTTGACG	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8039	3678	ao	AN0043.1	71.m15318	AO070314000122	0					-93	-61	ATGCTATTTCATCCTCTCTCCGGGGTTTTCTAG			ATGCTATTTCATCCTCTCTCCGGGGTTTTCTAG	MLFHPLSGVF*			MLFHPLSGVF*	CGTACCCGCA	TTCGACCGCA	0	I	FG02725.1	MG05031.1	NCU09517.1	0	0
8040	3679	af	AN8672.1	62.m03398	AO070315000089	0			-79	-11			ATGCTCTCTTTCCGCCGTCCTAATACAACACGGTCACCTCCGGTTTATGCCCTTCTCACAAGGGCTTGA		ATGCTCTCTTTCCGCCGTCCTAATACAACACGGTCACCTCCGGTTTATGCCCTTCTCACAAGGGCTTGA		MLSFRRPNTTRSPPVYALLTRA*		MLSFRRPNTTRSPPVYALLTRA*		ATTGGAGCGG	AGCCGCGTAA	0	R	0	0	0	0	0
8042	3679	ao	AN8672.1	62.m03398	AO070315000089	0					-75	-52	ATGCTCGCCCTCCACCTTTTTTAG			ATGCTCGCCCTCCACCTTTTTTAG	MLALHLF*			MLALHLF*	CTTGGAGCGG	TACATAACGG	0	R	0	0	0	0	0
8044	3680	af	AN4581.1	57.m05499	AO070316000164	0			-251	-237			ATGCAGTCTCAATGA		ATGCAGTCTCAATGA		MQSQ*		MQSQ*		TAAGTATCGG	GATTTTGCCT	0	T	0	0	0	0	0
8045	3680	af	AN4581.1	57.m05499	AO070316000164	0			-240	-106			ATGAGATTTTGCCTATCAGTATCTCTCCCCAGCTGCCCAATGTCTCGCTGCGCTCTCGACCTTCGTGCTACACAGCCTACGCTGTCATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGA		ATGAGATTTTGCCTATCAGTATCTCTCCCCAGCTGCCCAATGTCTCGCTGCGCTCTCGACCTTCGTGCTACACAGCCTACGCTGTCATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGA		MRFCLSVSLPSCPMSRCALDLRATQPTLSWWGDKSPQPCPHRLC*		MRFCLSVSLPSCPMSRCALDLRATQPTLSWWGDKSPQPCPHRLC*		TGCAGTCTCA	GTGCCGCCTC	0	T	0	0	0	0	0
8046	3680	af	AN4581.1	57.m05499	AO070316000164	0			-201	-106			ATGTCTCGCTGCGCTCTCGACCTTCGTGCTACACAGCCTACGCTGTCATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGA		ATGTCTCGCTGCGCTCTCGACCTTCGTGCTACACAGCCTACGCTGTCATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGA		MSRCALDLRATQPTLSWWGDKSPQPCPHRLC*		MSRCALDLRATQPTLSWWGDKSPQPCPHRLC*		CAGCTGCCCA	GTGCCGCCTC	0	T	0	0	0	0	0
8047	3680	af	AN4581.1	57.m05499	AO070316000164	0			-154	-65			ATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGAGTGCCGCCTCCGCTCCGCAACTTTTTTTTCCGACGGCATAA		ATGGTGGGGAGACAAATCTCCGCAACCTTGCCCACACCGCCTTTGCTGAGTGCCGCCTCCGCTCCGCAACTTTTTTTTCCGACGGCATAA		MVGRQISATLPTPPLLSAASAPQLFFPTA*		MVGRQISATLPTPPLLSAASAPQLFFPTA*		CTACGCTGTC	AAATTACCAG	0	T	0	0	0	0	0
8050	3683	af	AN7993.1	53.m03854	AO070322000053	0			-246	-196			ATGAAGCCCCGTATCATTGCTTGCTGGTATCTGGGCAACGTTGCGGTCTGA		ATGAAGCCCCGTATCATTGCTTGCTGGTATCTGGGCAACGTTGCGGTCTGA		MKPRIIACWYLGNVAV*		MKPRIIACWYLGNVAV*		TACCCAAAGA	TTTCCTTGTG	0	U	FG06778.1	0	NCU01172.1	0	0
8051	3683	ao	AN7993.1	53.m03854	AO070322000053	0					-252	-178	ATGCTGAGGTCCCGAAAGCACGCTCCCCAAGGTTGGATTACTTGTGCTTGCGCAGTTGGTGACGTTGCATGTTAA			ATGCTGAGGTCCCGAAAGCACGCTCCCCAAGGTTGGATTACTTGTGCTTGCGCAGTTGGTGACGTTGCATGTTAA	MLRSRKHAPQGWITCACAVGDVAC*			MLRSRKHAPQGWITCACAVGDVAC*	GCCGGCTGTC	GCGACTCCTG	0	U	FG06778.1	0	NCU01172.1	0	0
8052	3683	ao	AN7993.1	53.m03854	AO070322000053	0					-184	-59	ATGTTAAGCGACTCCTGTTTGAAGTCTCGCTTGGTTACCAAAGCTGTGGCAGCGGGAACTCATTGGAGGAACGCTTGCTCTCGGTCCCACCTGGACTATTCTACAGTTGTCCTCTTGTCATGTTGA			ATGTTAAGCGACTCCTGTTTGAAGTCTCGCTTGGTTACCAAAGCTGTGGCAGCGGGAACTCATTGGAGGAACGCTTGCTCTCGGTCCCACCTGGACTATTCTACAGTTGTCCTCTTGTCATGTTGA	MLSDSCLKSRLVTKAVAAGTHWRNACSRSHLDYSTVVLLSC*			MLSDSCLKSRLVTKAVAAGTHWRNACSRSHLDYSTVVLLSC*	GTGACGTTGC	GATAACGACG	0	U	FG06778.1	0	NCU01172.1	0	0
8049	3683	conserved	AN7993.1	53.m03854	AO070322000053	0	-57	-46	-63	-52	-65	-54	ATGyTrAGdTrr	ATGCTGAGGTGA	ATGTTAAGTTAG	ATGTTGAGATAA	MLr*	MLR*	MLS*	MLR*	TsCbCkTGTC	hGwsrhybws	0	U	FG06778.1	0	NCU01172.1	0	0
8074	3686	ao	AN7729.1	71.m15765	AO070325000156	0					-66	-34	ATGACTCCCTTTTCCTTCCTTCTTGTGGGTTGA			ATGACTCCCTTTTCCTTCCTTCTTGTGGGTTGA	MTPFSFLLVG*			MTPFSFLLVG*	GGGAGATTTT	AAGGGATAGG	0	Q	0	0	0	YDR135C	0
8076	3687	af	AN8637.1	62.m03219	AO070326000073	0			-244	-44			ATGATCGTGATCACTGGATCCAGCCGAGGCCGACTGTGCCAGGGTGACGTTGACGGTCCGCCAACGTCAGAACGTCACAATAACGTGCGTCACAGCTCTGGGCATACCAAAGAGCACTTATTACACACCATCGAAGCCAGCAGAGATGTTGAAGAGACGTTCTTGTCAAGTGGGCGCTGTCAGTTCTTCACAGATCTTTAA		ATGATCGTGATCACTGGATCCAGCCGAGGCCGACTGTGCCAGGGTGACGTTGACGGTCCGCCAACGTCAGAACGTCACAATAACGTGCGTCACAGCTCTGGGCATACCAAAGAGCACTTATTACACACCATCGAAGCCAGCAGAGATGTTGAAGAGACGTTCTTGTCAAGTGGGCGCTGTCAGTTCTTCACAGATCTTTAA		MIVITGSSRGRLCQGDVDGPPTSERHNNVRHSSGHTKEHLLHTIEASRDVEETFLSSGRCQFFTDL*		MIVITGSSRGRLCQGDVDGPPTSERHNNVRHSSGHTKEHLLHTIEASRDVEETFLSSGRCQFFTDL*		AGATCGCTGG	CTTAAATTTG	0	P	0	MG10061.1	NCU08791.1	0	0
8077	3687	af	AN8637.1	62.m03219	AO070326000073	0			-99	-22			ATGTTGAAGAGACGTTCTTGTCAAGTGGGCGCTGTCAGTTCTTCACAGATCTTTAACTTAAATTTGATATTACCGTGA		ATGTTGAAGAGACGTTCTTGTCAAGTGGGCGCTGTCAGTTCTTCACAGATCTTTAACTTAAATTTGATATTACCGTGA		MLKRRSCQVGAVSSSQIFNLNLILP*		MLKRRSCQVGAVSSSQIFNLNLILP*		GCCAGCAGAG	TCGTCAATCC	0	P	0	MG10061.1	NCU08791.1	0	0
8075	3687	an	AN8637.1	62.m03219	AO070326000073	0	-154	-110					ATGTCACGACAAGCCATCCGTAGATCCTGCAACAACAGGATATAA	ATGTCACGACAAGCCATCCGTAGATCCTGCAACAACAGGATATAA			MSRQAIRRSCNNRI*	MSRQAIRRSCNNRI*			TAGGGCTGTG	AGGTCGCCAG	0	P	0	MG10061.1	NCU08791.1	0	0
8078	3687	ao	AN8637.1	62.m03219	AO070326000073	0					-232	-221	ATGTCAACGTGA			ATGTCAACGTGA	MST*			MST*	AACCAGTTCG	CGTTCATCAA	0	P	0	MG10061.1	NCU08791.1	0	0
8079	3687	ao	AN8637.1	62.m03219	AO070326000073	0					-103	-80	ATGCAAGTAATGACCGTTTCATGA			ATGCAAGTAATGACCGTTTCATGA	MQVMTVS*			MQVMTVS*	TTCTTTTCTC	ACATAGCCTC	0	P	0	MG10061.1	NCU08791.1	0	0
8080	3687	ao	AN8637.1	62.m03219	AO070326000073	0					-94	-80	ATGACCGTTTCATGA			ATGACCGTTTCATGA	MTVS*			MTVS*	CATGCAAGTA	ACATAGCCTC	0	P	0	MG10061.1	NCU08791.1	0	0
8081	3687	ao	AN8637.1	62.m03219	AO070326000073	0					-83	-57	ATGAACATAGCCTCGATCCCACCTTAA			ATGAACATAGCCTCGATCCCACCTTAA	MNIASIPP*			MNIASIPP*	TGACCGTTTC	TCTATCTCCG	0	P	0	MG10061.1	NCU08791.1	0	0
8084	3688	af	AN6623.1	62.m03222	AO070326000077	0			-207	-76			ATGAGCCGCTTTCTGGACGGCCTTATTCCTTCCCAATCCGGCCGAGCGAGACCCAATATTTATCTCCGCACTTTGAACTTTCTCGAGACCATTGAGCAGCATAGAGATTGGATTATCAGTCGGTCTGCCTAG		ATGAGCCGCTTTCTGGACGGCCTTATTCCTTCCCAATCCGGCCGAGCGAGACCCAATATTTATCTCCGCACTTTGAACTTTCTCGAGACCATTGAGCAGCATAGAGATTGGATTATCAGTCGGTCTGCCTAG		MSRFLDGLIPSQSGRARPNIYLRTLNFLETIEQHRDWIISRSA*		MSRFLDGLIPSQSGRARPNIYLRTLNFLETIEQHRDWIISRSA*		TTGGAAGTAC	TACAAGAAGT	0	R	0	0	0	0	0
8082	3688	an	AN6623.1	62.m03222	AO070326000077	0	-194	-168					ATGATTAAAACCGACAATGAGGATTGA	ATGATTAAAACCGACAATGAGGATTGA			MIKTDNED*	MIKTDNED*			TCTGTCTTCT	ATACGACATT	0	R	0	0	0	0	0

8083	3688	an	AN6623.1	62.m03222	AO070326000077	0	-178	-140					ATGAGGATTGAATACGACATTATAACCAACCATTTATAA	ATGAGGATTGAATACGACATTATAACCAACCATTTATAA			MRIEYDIITNHL*	MRIEYDIITNHL*			AAAACCGACA	CGCAGTTTTC	0	R	0	0	0	0	0
8087	3689	af	AN2772.1	59.m09271	AO070327000014	0			-192	-175			ATGATCACCAAAAGTTGA		ATGATCACCAAAAGTTGA		MITKS*		MITKS*		GAAAATACTC	TCCTGCCGCG	0	DO	FG06074.1	MG03314.1	0	0	0
8088	3689	af	AN2772.1	59.m09271	AO070327000014	0			-71				ATGGATATGATCCCAATCCTGGCTCCTCTTGCCAGAGAAATTTTGAGTTTACTCGCAATTCCGCGTCGATAA		ATGGATATGATCCCAATCCTGGCTCCTCTTGCCAGAGAAATTTTGAGTTTACTCGCAATTCCGCGTCGATAA		MDMIPILAPLAREILSLLAIPRR*		MDMIPILAPLAREILSLLAIPRR*		TGGATTGACA	TGGCGTGCGT	0	DO	FG06074.1	MG03314.1	0	0	0
8089	3689	af	AN2772.1	59.m09271	AO070327000014	0			-65				ATGATCCCAATCCTGGCTCCTCTTGCCAGAGAAATTTTGAGTTTACTCGCAATTCCGCGTCGATAA		ATGATCCCAATCCTGGCTCCTCTTGCCAGAGAAATTTTGAGTTTACTCGCAATTCCGCGTCGATAA		MIPILAPLAREILSLLAIPRR*		MIPILAPLAREILSLLAIPRR*		GACAATGGAT	TGGCGTGCGT	0	DO	FG06074.1	MG03314.1	0	0	0
8085	3689	an	AN2772.1	59.m09271	AO070327000014	0	-252	-211					ATGCCGCCGAGCGTCTTCTGTATTTACTACGGACTTCAGTGA	ATGCCGCCGAGCGTCTTCTGTATTTACTACGGACTTCAGTGA			MPPSVFCIYYGLQ*	MPPSVFCIYYGLQ*			AGAAAGAAAA	CCGCGTCCAC	0	DO	FG06074.1	MG03314.1	0	0	0
8090	3689	ao	AN2772.1	59.m09271	AO070327000014	0					-78	-34	ATGGGTAATGAACATGTTCTCGCTCCTGGCTGCCATTGCCAGTGA			ATGGGTAATGAACATGTTCTCGCTCCTGGCTGCCATTGCCAGTGA	MGNEHVLAPGCHCQ*			MGNEHVLAPGCHCQ*	GACACTGCTG	TTCAACCACG	0	DO	FG06074.1	MG03314.1	0	0	0
8092	3690	af	AN5592.1	58.m07516	AO070328000011	0			-135	-58			ATGATCGACATTATTCCCTTTGGCCGACGATTTGCATCTCTTTCGACCTCCTTCCTTCGATCTGCTGCGCGGATCTGA		ATGATCGACATTATTCCCTTTGGCCGACGATTTGCATCTCTTTCGACCTCCTTCCTTCGATCTGCTGCGCGGATCTGA		MIDIIPFGRRFASLSTSFLRSAARI*		MIDIIPFGRRFASLSTSFLRSAARI*		CTCGTGATCC	TACGACTCAC	0	T	FG10511.1	0	0	0	0
8091	3690	an	AN5592.1	58.m07516	AO070328000011	0	-181	-89					ATGCTTGACTTGACGACAACTGTCGTACAACCTCCGCTGGCCGCTACTACTCCATCCTTTTCTGTCCTTTCTTCGACTGCTGCGCAGATTTGA	ATGCTTGACTTGACGACAACTGTCGTACAACCTCCGCTGGCCGCTACTACTCCATCCTTTTCTGTCCTTTCTTCGACTGCTGCGCAGATTTGA			MLDLTTTVVQPPLAATTPSFSVLSSTAAQI*	MLDLTTTVVQPPLAATTPSFSVLSSTAAQI*			TCAGTAATCC	ACCTCCCATA	0	T	FG10511.1	0	0	0	0
8093	3690	ao	AN5592.1	58.m07516	AO070328000011	0					-143	-81	ATGCTCGACGTGATTCTTGTACAACCACATCTATCGTCGCTATCCACTCACTCCCTTTGTTAG			ATGCTCGACGTGATTCTTGTACAACCACATCTATCGTCGCTATCCACTCACTCCCTTTGTTAG	MLDVILVQPHLSSLSTHSLC*			MLDVILVQPHLSSLSTHSLC*	TCTGTAATCC	TCTGCTGCGC	0	T	FG10511.1	0	0	0	0
8094	3691	af	AN5568.1	58.m07492	AO070328000040	0			-180	-166			ATGAGAACTAATTAG		ATGAGAACTAATTAG		MRTN*		MRTN*		GGGGGAAAAA	CTAAGAGAAA	0		0	0	0	0	0
8096	3693	an	AN0465.1	54.m06603	AO070328000172	0	-269	-96					ATGGAGCATTACGACAGGGGAGCAGAGGCAGAACTCTCGATGTTGCTACTTTTTTTGCTTGGAACAACTTCCTTGAAAGATTCTTTTCTGAATGCGGCTGGGAAACTGCGAATTGGATATCCAGCGAAAGGTTACCGACAGACTCACGGCCATCGATACCACTCAGCGGGATAG	ATGGAGCATTACGACAGGGGAGCAGAGGCAGAACTCTCGATGTTGCTACTTTTTTTGCTTGGAACAACTTCCTTGAAAGATTCTTTTCTGAATGCGGCTGGGAAACTGCGAATTGGATATCCAGCGAAAGGTTACCGACAGACTCACGGCCATCGATACCACTCAGCGGGATAG			MEHYDRGAEAELSMLLLFLLGTTSLKDSFLNAAGKLRIGYPAKGYRQTHGHRYHSAG*	MEHYDRGAEAELSMLLLFLLGTTSLKDSFLNAAGKLRIGYPAKGYRQTHGHRYHSAG*			ACAAGAGGGA	AATTGAAGGC	0	J	0	0	0	0	0
8097	3693	an	AN0465.1	54.m06603	AO070328000172	0	-230	-96					ATGTTGCTACTTTTTTTGCTTGGAACAACTTCCTTGAAAGATTCTTTTCTGAATGCGGCTGGGAAACTGCGAATTGGATATCCAGCGAAAGGTTACCGACAGACTCACGGCCATCGATACCACTCAGCGGGATAG	ATGTTGCTACTTTTTTTGCTTGGAACAACTTCCTTGAAAGATTCTTTTCTGAATGCGGCTGGGAAACTGCGAATTGGATATCCAGCGAAAGGTTACCGACAGACTCACGGCCATCGATACCACTCAGCGGGATAG			MLLLFLLGTTSLKDSFLNAAGKLRIGYPAKGYRQTHGHRYHSAG*	MLLLFLLGTTSLKDSFLNAAGKLRIGYPAKGYRQTHGHRYHSAG*			AGAACTCTCG	AATTGAAGGC	0	J	0	0	0	0	0
8098	3693	an	AN0465.1	54.m06603	AO070328000172	0	-72	-40					ATGATCAGCTTCGCTTGTTTCGACTCGTGCTAA	ATGATCAGCTTCGCTTGTTTCGACTCGTGCTAA			MISFACFDSC*	MISFACFDSC*			CGGACATTAG	TCAATTATCC	0	J	0	0	0	0	0
8099	3694	ao	AN4779.1	59.m09204	AO070329000071	0					-95	-66	ATGAAAGTTGCCTTTTCTCTGTTCTGCTAG			ATGAAAGTTGCCTTTTCTCTGTTCTGCTAG	MKVAFSLFC*			MKVAFSLFC*	GTTCTGTTTT	AAGCATTTAT	0	S	0	0	0	0	0
8100	3695	af	AN9486.1	59.m09213	AO070329000083	0			-216	-130			ATGCTTAAGTTCTTTGTGCCGGAATGTGGAAGCCTCAGGCAACCCTCTGAAAGGCGATTAATCAAGATGAGTCAGCGCCGGAGGTAA		ATGCTTAAGTTCTTTGTGCCGGAATGTGGAAGCCTCAGGCAACCCTCTGAAAGGCGATTAATCAAGATGAGTCAGCGCCGGAGGTAA		MLKFFVPECGSLRQPSERRLIKMSQRRR*		MLKFFVPECGSLRQPSERRLIKMSQRRR*		ATCCTACTCC	TCGTTGAGTC	0	H	0	0	0	YOR196C	0
8101	3695	af	AN9486.1	59.m09213	AO070329000083	0			-193	-167			ATGTGGAAGCCTCAGGCAACCCTCTGA		ATGTGGAAGCCTCAGGCAACCCTCTGA		MWKPQATL*		MWKPQATL*		TTGTGCCGGA	AAGGCGATTA	0	H	0	0	0	YOR196C	0
8102	3695	af	AN9486.1	59.m09213	AO070329000083	0			-150	-130			ATGAGTCAGCGCCGGAGGTAA		ATGAGTCAGCGCCGGAGGTAA		MSQRRR*		MSQRRR*		ATTAATCAAG	TCGTTGAGTC	0	H	0	0	0	YOR196C	0
8104	3695	ao	AN9486.1	59.m09213	AO070329000083	0					-210	-196	ATGAACGAATCATAA			ATGAACGAATCATAA	MNES*			MNES*	GAAGAACCTG	TTTTCGTATT	0	H	0	0	0	YOR196C	0
8105	3695	ao	AN9486.1	59.m09213	AO070329000083	0					-164	-138	ATGCCATCATTTAGGGCAAATATTTGA			ATGCCATCATTTAGGGCAAATATTTGA	MPSFRANI*			MPSFRANI*	CTAGTAGTTC	AGGTGCTCGA	0	H	0	0	0	YOR196C	0
8106	3695	ao	AN9486.1	59.m09213	AO070329000083	0					-114	-91	ATGAGGTTAAGACACGCTGAGTAA			ATGAGGTTAAGACACGCTGAGTAA	MRLRHAE*			MRLRHAE*	TCTAAGCCGA	TGGCAGCGGA	0	H	0	0	0	YOR196C	0
8107	3695	ao	AN9486.1	59.m09213	AO070329000083	0					-91	-8	ATGGCAGCGGACTTCCTTATCATGTCGGAGCTTCGCTCATCTTTCCCGCGGAATTCAACTTTCGCAACTTTGCAAGTTGAATAG			ATGGCAGCGGACTTCCTTATCATGTCGGAGCTTCGCTCATCTTTCCCGCGGAATTCAACTTTCGCAACTTTGCAAGTTGAATAG	MAADFLIMSELRSSFPRNSTFATLQVE*			MAADFLIMSELRSSFPRNSTFATLQVE*	ACGCTGAGTA	CATCAATATG	0	H	0	0	0	YOR196C	0
8108	3695	ao	AN9486.1	59.m09213	AO070329000083	0					-70	-8	ATGTCGGAGCTTCGCTCATCTTTCCCGCGGAATTCAACTTTCGCAACTTTGCAAGTTGAATAG			ATGTCGGAGCTTCGCTCATCTTTCCCGCGGAATTCAACTTTCGCAACTTTGCAAGTTGAATAG	MSELRSSFPRNSTFATLQVE*			MSELRSSFPRNSTFATLQVE*	CTTCCTTATC	CATCAATATG	0	H	0	0	0	YOR196C	0
8109	3697	an	AN3307.1	52.m03703	AO070330000183	0	-128	-108					ATGTGGGCGTCAATATTATAG	ATGTGGGCGTCAATATTATAG			MWASIL*	MWASIL*			GACGGAGTTC	ACTCTTAATT	0	G	0	0	0	0	0
8110	3697	ao	AN3307.1	52.m03703	AO070330000183	0					-92	-81	ATGATTGCATGA			ATGATTGCATGA	MIA*			MIA*	TTGCGCATAT	TAGCGGATTA	0	G	0	0	0	0	0
8111	3697	ao	AN3307.1	52.m03703	AO070330000183	0					-84	-31	ATGATAGCGGATTACCGATTATTGCTTGCATCTTTTGGTTTGTCGCCAACTTGA			ATGATAGCGGATTACCGATTATTGCTTGCATCTTTTGGTTTGTCGCCAACTTGA	MIADYRLLLASFGLSPT*			MIADYRLLLASFGLSPT*	ATATGATTGC	CTACCGGGCG	0	G	0	0	0	0	0
8115	3698	af	AN1238.1	70.m14980	AO070331000252	0			-243	-223			ATGCAATTTGAGTCAAAATGA		ATGCAATTTGAGTCAAAATGA		MQFESK*		MQFESK*		GCACCTAACT	TCGTTCTGTT	0		0	0	0	0	0
8113	3698	an	AN1238.1	70.m14980	AO070331000252	0	-166	-137					ATGCTGGGATGCCAAGATTTTGTTTTTTGA	ATGCTGGGATGCCAAGATTTTGTTTTTTGA			MLGCQDFVF*	MLGCQDFVF*			TAGGCGGTGG	GTTGCGGAAG	0		0	0	0	0	0
8114	3698	an	AN1238.1	70.m14980	AO070331000252	0	-158	-114					ATGCCAAGATTTTGTTTTTTGAGTTGCGGAAGAGCTTCAACTTAG	ATGCCAAGATTTTGTTTTTTGAGTTGCGGAAGAGCTTCAACTTAG			MPRFCFLSCGRAST*	MPRFCFLSCGRAST*			GGATGCTGGG	CTTTCTGCCC	0		0	0	0	0	0
8116	3698	ao	AN1238.1	70.m14980	AO070331000252	0					-258	-247	ATGGTCTTCTAA			ATGGTCTTCTAA	MVF*			MVF*	CAAAGAACGT	TAATATCTAT	0		0	0	0	0	0
8117	3698	ao	AN1238.1	70.m14980	AO070331000252	0					-174	-28	ATGCGCGTTGCTAAGGCTGGCGCCAAGACCGTGTTTTTTCTGAACAGAGCTTCGGAGCTTCCCTCTTCCAACTCCACAGGCTGCGACATTCCACGTACTTGCGACAATCGGCCATGGAGACTTGAAGTGACCAATTTTACAAATTAG			ATGCGCGTTGCTAAGGCTGGCGCCAAGACCGTGTTTTTTCTGAACAGAGCTTCGGAGCTTCCCTCTTCCAACTCCACAGGCTGCGACATTCCACGTACTTGCGACAATCGGCCATGGAGACTTGAAGTGACCAATTTTACAAATTAG	MRVAKAGAKTVFFLNRASELPSSNSTGCDIPRTCDNRPWRLEVTNFTN*			MRVAKAGAKTVFFLNRASELPSSNSTGCDIPRTCDNRPWRLEVTNFTN*	CGGTGGATAA	TGGAAGGTGG	0		0	0	0	0	0
8112	3698	conserved	AN1238.1	70.m14980	AO070331000252	0	-56	-45	-59	-48	-61	-50	ATGGrGvhyTrA	ATGGGGCACTGA	ATGGAGGTTTAA	ATGGAGACTTGA	Mgh*	MGH*	MEV*	MET*	vvwwysGGCy	rvTsAmmAwT	0		0	0	0	0	0
8120	3700	ao	AN3056.1	59.m08955	AO070337000018	0					-245	-207	ATGGGGGTTGATATCGACACTAATCCACAACCGGACTAG			ATGGGGGTTGATATCGACACTAATCCACAACCGGACTAG	MGVDIDTNPQPD*			MGVDIDTNPQPD*	ACAGAGCGGT	TGTATCGTGA	0	R	0	0	0	YOL022C	0
8123	3701	an	AN2965.1	59.m09050	AO070337000162	0	-180	-124					ATGTCCACGACCTTCCTGTTATCCTTCTTCCTTACAGTTGTCCGGAGACGCATCTGA	ATGTCCACGACCTTCCTGTTATCCTTCTTCCTTACAGTTGTCCGGAGACGCATCTGA			MSTTFLLSFFLTVVRRRI*	MSTTFLLSFFLTVVRRRI*			ACGCCCTCGA	TTCGCCCGTT	0	DO	0	MG06892.1	0	0	0
8124	3704	af	AN2877.1	59.m08718	AO070338000146	0			-270	-220			ATGGCCATGACGTCGCAGCCGACTCCCCTCTTGGCAGTCTTTGTGTTGTAA		ATGGCCATGACGTCGCAGCCGACTCCCCTCTTGGCAGTCTTTGTGTTGTAA		MAMTSQPTPLLAVFVL*		MAMTSQPTPLLAVFVL*		AGTTACGGAA	CTTATGCCCT	0	T	0	0	0	0	0
8125	3704	af	AN2877.1	59.m08718	AO070338000146	0			-264	-220			ATGACGTCGCAGCCGACTCCCCTCTTGGCAGTCTTTGTGTTGTAA		ATGACGTCGCAGCCGACTCCCCTCTTGGCAGTCTTTGTGTTGTAA		MTSQPTPLLAVFVL*		MTSQPTPLLAVFVL*		GGAAATGGCC	CTTATGCCCT	0	T	0	0	0	0	0
8126	3704	af	AN2877.1	59.m08718	AO070338000146	0			-216	-184			ATGCCCTCTGAAACTCGCCCGGCAAGCAATTAA		ATGCCCTCTGAAACTCGCCCGGCAAGCAATTAA		MPSETRPASN*		MPSETRPASN*		GTTGTAACTT	TTAGTTCCTT	0	T	0	0	0	0	0
8127	3704	af	AN2877.1	59.m08718	AO070338000146	0			-144	-82			ATGCTGAAGAATTCTCTCTTCCTTCTTTATCTCCACTCCAGCTTACTTCTTCTTAGTTTCTAA		ATGCTGAAGAATTCTCTCTTCCTTCTTTATCTCCACTCCAGCTTACTTCTTCTTAGTTTCTAA		MLKNSLFLLYLHSSLLLLSF*		MLKNSLFLLYLHSSLLLLSF*		TGGGGGGCTA	GTAATCTTTC	0	T	0	0	0	0	0
8131	3705	af	AN2738.1	54.m06679	AO070338000220	0			-235	-200			ATGATTGTTTTGCCAAGTTACCTTATTGACCTGTAA		ATGATTGTTTTGCCAAGTTACCTTATTGACCTGTAA		MIVLPSYLIDL*		MIVLPSYLIDL*		GTTATTGCTG	GTAGCGTTGA	0	U	0	MG01245.1	0	0	0
8132	3705	af	AN2738.1	54.m06679	AO070338000220	0			-190	-167			ATGCATCGTGTGCCGTTTGATTGA		ATGCATCGTGTGCCGTTTGATTGA		MHRVPFD*		MHRVPFD*		AGTAGCGTTG	CATGCCGCGA	0	U	0	MG01245.1	0	0	0
8133	3705	af	AN2738.1	54.m06679	AO070338000220	0			-165	-124			ATGCCGCGATTCCTGCGTTATTTACCAATTGAGCTTCATTGA		ATGCCGCGATTCCTGCGTTATTTACCAATTGAGCTTCATTGA		MPRFLRYLPIELH*		MPRFLRYLPIELH*		TTTGATTGAC	CATTGAATAC	0	U	0	MG01245.1	0	0	0
8128	3705	an	AN2738.1	54.m06679	AO070338000220	0	-180	-61					ATGCTGGAGGACCCGTGTAGATCGTTCAATGGCTTCGTAGTTCGCTGCTGCTACCGACACTTTCGAGATCACTTCAGACTGATAACTCTCCTTCTCTTTAGGAGTTATACTACAGCCTAG	ATGCTGGAGGACCCGTGTAGATCGTTCAATGGCTTCGTAGTTCGCTGCTGCTACCGACACTTTCGAGATCACTTCAGACTGATAACTCTCCTTCTCTTTAGGAGTTATACTACAGCCTAG			MLEDPCRSFNGFVVRCCYRHFRDHFRLITLLLFRSYTTA*	MLEDPCRSFNGFVVRCCYRHFRDHFRLITLLLFRSYTTA*			TCTCCGTGAC	CCGGTCTAGG	0	U	0	MG01245.1	0	0	0
8129	3705	an	AN2738.1	54.m06679	AO070338000220	0	-152	-141					ATGGCTTCGTAG	ATGGCTTCGTAG			MAS*	MAS*			AGATCGTTCA	TTCGCTGCTG	0	U	0	MG01245.1	0	0	0
8135	3707	af	AN5991.1	72.m19149	AO070340000286	0			-206	-3			ATGGGGCGGAACGGAAAATGTCTCGGTCCGAAATACATCAGGCGGGCCGACTCGGCGAACGGCGCTGGCGGGCATTTGATTTGCGGAGTCAATGAAGTCCGGGGGATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGACCCCTTTGAACAGCAGGGTTTTGAGTAACAGCGCCTGA		ATGGGGCGGAACGGAAAATGTCTCGGTCCGAAATACATCAGGCGGGCCGACTCGGCGAACGGCGCTGGCGGGCATTTGATTTGCGGAGTCAATGAAGTCCGGGGGATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGACCCCTTTGAACAGCAGGGTTTTGAGTAACAGCGCCTGA		MGRNGKCLGPKYIRRADSANGAGGHLICGVNEVRGMLSVGCRCFTSSRQRETTFLTPLNSRVLSNSA*		MGRNGKCLGPKYIRRADSANGAGGHLICGVNEVRGMLSVGCRCFTSSRQRETTFLTPLNSRVLSNSA*		GTAAGACCTT	AGATGGCGCC	0	O	0	MG09299.1	NCU08118.1	0	0
8136	3707	af	AN5991.1	72.m19149	AO070340000286	0			-189	-112			ATGTCTCGGTCCGAAATACATCAGGCGGGCCGACTCGGCGAACGGCGCTGGCGGGCATTTGATTTGCGGAGTCAATGA		ATGTCTCGGTCCGAAATACATCAGGCGGGCCGACTCGGCGAACGGCGCTGGCGGGCATTTGATTTGCGGAGTCAATGA		MSRSEIHQAGRLGERRWRAFDLRSQ*		MSRSEIHQAGRLGERRWRAFDLRSQ*		GGAACGGAAA	AGTCCGGGGG	0	O	0	MG09299.1	NCU08118.1	0	0
8137	3707	af	AN5991.1	72.m19149	AO070340000286	0			-115	-41			ATGAAGTCCGGGGGATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGA		ATGAAGTCCGGGGGATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGA		MKSGGCYLSVVDASLPPDNVKLLS*		MKSGGCYLSVVDASLPPDNVKLLS*		TGCGGAGTCA	CCCCTTTGAA	0	O	0	MG09299.1	NCU08118.1	0	0
8138	3707	af	AN5991.1	72.m19149	AO070340000286	0			-101	-3			ATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGACCCCTTTGAACAGCAGGGTTTTGAGTAACAGCGCCTGA		ATGCTATCTGTCGGTTGTCGATGCTTCACTTCCTCCAGACAACGTGAAACTACTTTCCTGACCCCTTTGAACAGCAGGGTTTTGAGTAACAGCGCCTGA		MLSVGCRCFTSSRQRETTFLTPLNSRVLSNSA*		MLSVGCRCFTSSRQRETTFLTPLNSRVLSNSA*		AGTCCGGGGG	AGATGGCGCC	0	O	0	MG09299.1	NCU08118.1	0	0
8139	3707	af	AN5991.1	72.m19149	AO070340000286	0			-81	-55			ATGCTTCACTTCCTCCAGACAACGTGA		ATGCTTCACTTCCTCCAGACAACGTGA		MLHFLQTT*		MLHFLQTT*		TCGGTTGTCG	AACTACTTTC	0	O	0	MG09299.1	NCU08118.1	0	0
8140	3707	ao	AN5991.1	72.m19149	AO070340000286	0					-191	-33	ATGCACGTGTATCGGAGCGGATTAAGTCTCGGTCCGAGATCTATGGGCCGGCCGGCTCGGCGAACGGCGCATGGCGGGCGCTTGATTGCGGAGTCGATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA			ATGCACGTGTATCGGAGCGGATTAAGTCTCGGTCCGAGATCTATGGGCCGGCCGGCTCGGCGAACGGCGCATGGCGGGCGCTTGATTGCGGAGTCGATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA	MHVYRSGLSLGPRSMGRPARRTAHGGRLIAESMSGDILSCGLLSSSRALRCF*			MHVYRSGLSLGPRSMGRPARRTAHGGRLIAESMSGDILSCGLLSSSRALRCF*	CTAGTATTTT	ACAGAACACA	0	O	0	MG09299.1	NCU08118.1	0	0
8141	3707	ao	AN5991.1	72.m19149	AO070340000286	0					-149	-33	ATGGGCCGGCCGGCTCGGCGAACGGCGCATGGCGGGCGCTTGATTGCGGAGTCGATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA			ATGGGCCGGCCGGCTCGGCGAACGGCGCATGGCGGGCGCTTGATTGCGGAGTCGATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA	MGRPARRTAHGGRLIAESMSGDILSCGLLSSSRALRCF*			MGRPARRTAHGGRLIAESMSGDILSCGLLSSSRALRCF*	TCCGAGATCT	ACAGAACACA	0	O	0	MG09299.1	NCU08118.1	0	0
8142	3707	ao	AN5991.1	72.m19149	AO070340000286	0					-121	-107	ATGGCGGGCGCTTGA			ATGGCGGGCGCTTGA	MAGA*			MAGA*	CGAACGGCGC	TTGCGGAGTC	0	O	0	MG09299.1	NCU08118.1	0	0
8143	3707	ao	AN5991.1	72.m19149	AO070340000286	0					-95	-33	ATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA			ATGTCCGGGGACATCTTGAGCTGCGGTCTTCTCTCTTCTTCAAGAGCTCTCCGCTGCTTCTAA	MSGDILSCGLLSSSRALRCF*			MSGDILSCGLLSSSRALRCF*	TGCGGAGTCG	ACAGAACACA	0	O	0	MG09299.1	NCU08118.1	0	0

8146	3709	af	AN2065.1	57.m05763	AO070341000211	0			-127	-5			ATGATGTCTTGTTCACCCTGCTTCCGGATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		ATGATGTCTTGTTCACCCTGCTTCCGGATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		MMSCSPCFRMGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		MMSCSPCFRMGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		CCTCCACCGA	GGCCATGGAG	0	L	0	0	0	0	0
8147	3709	af	AN2065.1	57.m05763	AO070341000211	0			-124	-5			ATGTCTTGTTCACCCTGCTTCCGGATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		ATGTCTTGTTCACCCTGCTTCCGGATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		MSCSPCFRMGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		MSCSPCFRMGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		CCACCGAATG	GGCCATGGAG	0	L	0	0	0	0	0
8148	3709	af	AN2065.1	57.m05763	AO070341000211	0			-100	-5			ATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		ATGGGCAAAATCATATCGTTCTCTAAAACCACGAGCGTTCTTTCTTTGTCGGCACACTTAAATCTGTTACCGAGTCTATCCCGTTTGGGATGCTGA		MGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		MGKIISFSKTTSVLSLSAHLNLLPSLSRLGC*		CTGCTTCCGG	GGCCATGGAG	0	L	0	0	0	0	0
8144	3709	an	AN2065.1	57.m05763	AO070341000211	0	-125	-75					ATGCCTGCTTTTGCCCGACTTTCGCATTGGCAGAGTCAGGCCACTCTCTAA	ATGCCTGCTTTTGCCCGACTTTCGCATTGGCAGAGTCAGGCCACTCTCTAA			MPAFARLSHWQSQATL*	MPAFARLSHWQSQATL*			CCACTTAACG	ACAGTTACAC	0	L	0	0	0	0	0
8149	3709	ao	AN2065.1	57.m05763	AO070341000211	0					-126	-76	ATGCCCGATTTCGCTCTCTTTCCGAATGGACAGGACCGTTTCAGTCTTTAG			ATGCCCGATTTCGCTCTCTTTCCGAATGGACAGGACCGTTTCAGTCTTTAG	MPDFALFPNGQDRFSL*			MPDFALFPNGQDRFSL*	ACGCCGAACA	GAATAACCAC	0	L	0	0	0	0	0
8150	3709	ao	AN2065.1	57.m05763	AO070341000211	0					-101	-51	ATGGACAGGACCGTTTCAGTCTTTAGGAATAACCACGTCGCCTGCATCTGA			ATGGACAGGACCGTTTCAGTCTTTAGGAATAACCACGTCGCCTGCATCTGA	MDRTVSVFRNNHVACI*			MDRTVSVFRNNHVACI*	CTCTTTCCGA	TTTAAAGATA	0	L	0	0	0	0	0
8154	3710	af	AN5519.1	69.m15725	AO070341000374	0			-235	-224			ATGAGAAAGTGA		ATGAGAAAGTGA		MRK*		MRK*		ATGCCGTTGA	TCCGGGCGGA	0	U	FG06007.1	0	0	YJL024C	0
8155	3710	af	AN5519.1	69.m15725	AO070341000374	0			-212	-192			ATGCAAAGGGGTCTCCGCTGA		ATGCAAAGGGGTCTCCGCTGA		MQRGLR*		MQRGLR*		CCGGGCGGAG	TACGGCCCCG	0	U	FG06007.1	0	0	YJL024C	0
8156	3710	af	AN5519.1	69.m15725	AO070341000374	0			-118	-20			ATGCTGGTCACCAATCCGGACAGATTCGGCTATTCTGCGAATATAATAGTAGCCATTCACACTGTTCTGGTTTCTCATACCCGAGGAAGGCGAAAATAG		ATGCTGGTCACCAATCCGGACAGATTCGGCTATTCTGCGAATATAATAGTAGCCATTCACACTGTTCTGGTTTCTCATACCCGAGGAAGGCGAAAATAG		MLVTNPDRFGYSANIIVAIHTVLVSHTRGRRK*		MLVTNPDRFGYSANIIVAIHTVLVSHTRGRRK*		CGTCAGTTCT	CTTTCGAATT	0	U	FG06007.1	0	0	YJL024C	0
8151	3710	an	AN5519.1	69.m15725	AO070341000374	0	-202	-128					ATGTCAGCCGAGATAAATAAGGGACGGCCATATAGGCATGTTGCCCGAGATCTCCGCGATAAGCTCCGTCGATGA	ATGTCAGCCGAGATAAATAAGGGACGGCCATATAGGCATGTTGCCCGAGATCTCCGCGATAAGCTCCGTCGATGA			MSAEINKGRPYRHVARDLRDKLRR*	MSAEINKGRPYRHVARDLRDKLRR*			CTAAAGAGGA	TGCATGTTCC	0	U	FG06007.1	0	0	YJL024C	0
8152	3710	an	AN5519.1	69.m15725	AO070341000374	0	-131	-60					ATGATGCATGTTCCATTTCTTTCGCAGCCTGCGCGTTTCCCTTTGCGACTTTATTGTCGTCAGCTTGCTTAG	ATGATGCATGTTCCATTTCTTTCGCAGCCTGCGCGTTTCCCTTTGCGACTTTATTGTCGTCAGCTTGCTTAG			MMHVPFLSQPARFPLRLYCRQLA*	MMHVPFLSQPARFPLRLYCRQLA*			AGCTCCGTCG	TCTATCAGTC	0	U	FG06007.1	0	0	YJL024C	0
8153	3710	an	AN5519.1	69.m15725	AO070341000374	0	-128	-60					ATGCATGTTCCATTTCTTTCGCAGCCTGCGCGTTTCCCTTTGCGACTTTATTGTCGTCAGCTTGCTTAG	ATGCATGTTCCATTTCTTTCGCAGCCTGCGCGTTTCCCTTTGCGACTTTATTGTCGTCAGCTTGCTTAG			MHVPFLSQPARFPLRLYCRQLA*	MHVPFLSQPARFPLRLYCRQLA*			TCCGTCGATG	TCTATCAGTC	0	U	FG06007.1	0	0	YJL024C	0
8157	3710	ao	AN5519.1	69.m15725	AO070341000374	0					-150	-10	ATGCCGCCCCGCGGATTCAGGCCGATAAGAGAGCTTACAATAGCTTCAACTGCTATCACAACTTCATTTTTCGGTCGCTTTCGGATTTCAATATTCTCTTTATTTTTCTGTACAGTTGAATACGGATACACTATTTTATAG			ATGCCGCCCCGCGGATTCAGGCCGATAAGAGAGCTTACAATAGCTTCAACTGCTATCACAACTTCATTTTTCGGTCGCTTTCGGATTTCAATATTCTCTTTATTTTTCTGTACAGTTGAATACGGATACACTATTTTATAG	MPPRGFRPIRELTIASTAITTSFFGRFRISIFSLFFCTVEYGYTIL*			MPPRGFRPIRELTIASTAITTSFFGRFRISIFSLFFCTVEYGYTIL*	TTTTGCCGAC	AACGGCAAAA	0	U	FG06007.1	0	0	YJL024C	0
8158	3711	ao	AN5482.1	69.m15746	AO070341000403	0					-251	-219	ATGTGTGCCTTAGGCTTTTGTCACGTGGCTTAA			ATGTGTGCCTTAGGCTTTTGTCACGTGGCTTAA	MCALGFCHVA*			MCALGFCHVA*	CCTGCGGGGC	AACTTGGTGA	0	U	0	MG09952.1	0	0	0
8160	3713	af	AN1306.1	71.m15535	AO070342000436	0			-189	-169			ATGACTTTACCTATAAGCTGA		ATGACTTTACCTATAAGCTGA		MTLPIS*		MTLPIS*		CGTATTTTAC	CATCGGACCA	0	Z	0	0	0	0	0
8161	3713	af	AN1306.1	71.m15535	AO070342000436	0			-125	-21			ATGGAGATCTCCACTATCACTGCAGATCATCCTCTCCCTCGCTCACTCCTCGGCCCTAACCCAACCACCCGTCCACATAGTTTCTTTCCTCTTCTCAATTTCTAA		ATGGAGATCTCCACTATCACTGCAGATCATCCTCTCCCTCGCTCACTCCTCGGCCCTAACCCAACCACCCGTCCACATAGTTTCTTTCCTCTTCTCAATTTCTAA		MEISTITADHPLPRSLLGPNPTTRPHSFFPLLNF*		MEISTITADHPLPRSLLGPNPTTRPHSFFPLLNF*		ACTATTTTTA	CTACATTCCT	0	Z	0	0	0	0	0
8159	3713	an	AN1306.1	71.m15535	AO070342000436	0	-166	-128					ATGTTTCCCCACCGGTCCCCGCCACACCAGAACCCCTGA	ATGTTTCCCCACCGGTCCCCGCCACACCAGAACCCCTGA			MFPHRSPPHQNP*	MFPHRSPPHQNP*			TACAATATCA	CCCATTGCAG	0	Z	0	0	0	0	0
8162	3713	ao	AN1306.1	71.m15535	AO070342000436	0					-246	-163	ATGGCCAGAAAGATACAAAGACTACCCAGGTACCCAGGACCTAAGCCCAACTGCACCAAAGCTCAAAGGCTTGGATCTGTATGA			ATGGCCAGAAAGATACAAAGACTACCCAGGTACCCAGGACCTAAGCCCAACTGCACCAAAGCTCAAAGGCTTGGATCTGTATGA	MARKIQRLPRYPGPKPNCTKAQRLGSV*			MARKIQRLPRYPGPKPNCTKAQRLGSV*	CCTGTGCGAT	CCCCTCCTAC	0	Z	0	0	0	0	0
8164	3716	af	AN1061.1	70.m15172	AO070218000005	0			-218	-171			ATGTTATCTTCGTGTCTTGCCTTCAAATATCCACTGATTCCCCCTTGA		ATGTTATCTTCGTGTCTTGCCTTCAAATATCCACTGATTCCCCCTTGA		MLSSCLAFKYPLIPP*		MLSSCLAFKYPLIPP*		CTTAGCGGAG	CTAGTTCGTC	0	E	0	MG01385.1	0	0	0
8165	3716	ao	AN1061.1	70.m15172	AO070218000005	0					-214	-134	ATGCAAGCCTGTCATGGATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGA			ATGCAAGCCTGTCATGGATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGA	MQACHGCYTDHYLYASAPRSEPGLDS*			MQACHGCYTDHYLYASAPRSEPGLDS*	ACTCTTGGTG	GGTAGCAGTG	0	E	0	MG01385.1	0	0	0
8166	3716	ao	AN1061.1	70.m15172	AO070218000005	0					-201	-79	ATGGATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGAGGTAGCAGTGCTAGTAGGAGCTGGTCTGACTACTAACCTACTGTCTTATCTATAA			ATGGATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGAGGTAGCAGTGCTAGTAGGAGCTGGTCTGACTACTAACCTACTGTCTTATCTATAA	MDAIRTTTYMPPLPGPSLAWIVEVAVLVGAGLTTNLLSYL*			MDAIRTTTYMPPLPGPSLAWIVEVAVLVGAGLTTNLLSYL*	CAAGCCTGTC	CCCTATTGAC	0	E	0	MG01385.1	0	0	0
8167	3716	ao	AN1061.1	70.m15172	AO070218000005	0					-197	-138	ATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAG			ATGCTATACGGACCACTACTTATATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAG	MLYGPLLICLRSPVRAWPG*			MLYGPLLICLRSPVRAWPG*	CCTGTCATGG	TTGAGGTAGC	0	E	0	MG01385.1	0	0	0
8168	3716	ao	AN1061.1	70.m15172	AO070218000005	0					-174	-79	ATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGAGGTAGCAGTGCTAGTAGGAGCTGGTCTGACTACTAACCTACTGTCTTATCTATAA			ATGCCTCCGCTCCCCGGTCCGAGCCTGGCCTGGATAGTTGAGGTAGCAGTGCTAGTAGGAGCTGGTCTGACTACTAACCTACTGTCTTATCTATAA	MPPLPGPSLAWIVEVAVLVGAGLTTNLLSYL*			MPPLPGPSLAWIVEVAVLVGAGLTTNLLSYL*	CACTACTTAT	CCCTATTGAC	0	E	0	MG01385.1	0	0	0
8174	3717	af	AN6334.1	72.m19451	AO070236000027	0			-271	-245			ATGACCGGACCGGAGTGGGTCCGATAA		ATGACCGGACCGGAGTGGGTCCGATAA		MTGPEWVR*		MTGPEWVR*		CGCCCTGTGC	CGGCATAGTC	0	J	0	0	0	0	0
8175	3717	af	AN6334.1	72.m19451	AO070236000027	0			-232	-167			ATGACTATTATTCTGCCTCAGGCAATAAGGCTACAGCTCTTGAGCAAAAAAATCTTTTTTTGATTGA		ATGACTATTATTCTGCCTCAGGCAATAAGGCTACAGCTCTTGAGCAAAAAAATCTTTTTTTGATTGA		MTIILPQAIRLQLLSKKSFFD*		MTIILPQAIRLQLLSKKSFFD*		GCATAGTCAG	TATCGGCGGG	0	J	0	0	0	0	0
8170	3717	an	AN6334.1	72.m19451	AO070236000027	0	-212	-171					ATGATTAATCTTATCGATAAGCATTTATGCCTTAGGCTATGA	ATGATTAATCTTATCGATAAGCATTTATGCCTTAGGCTATGA			MINLIDKHLCLRL*	MINLIDKHLCLRL*			TGGTTAGCGT	GGAAAATTCA	0	J	0	0	0	0	0
8171	3717	an	AN6334.1	72.m19451	AO070236000027	0	-174	-46					ATGAGGAAAATTCATTCGGCGCTAAGAACCTCCGCCCCGAGAGAAAAAAGGCAAGATGGGTTTATGTTGAGCTTGTTTGACGGAGAAAGAGAGCAGTTCATTTCAACGCTTTCTTCAGTCACCCAGTGA	ATGAGGAAAATTCATTCGGCGCTAAGAACCTCCGCCCCGAGAGAAAAAAGGCAAGATGGGTTTATGTTGAGCTTGTTTGACGGAGAAAGAGAGCAGTTCATTTCAACGCTTTCTTCAGTCACCCAGTGA			MRKIHSALRTSAPREKRQDGFMLSLFDGEREQFISTLSSVTQ*	MRKIHSALRTSAPREKRQDGFMLSLFDGEREQFISTLSSVTQ*			GCCTTAGGCT	GGAAGATACA	0	J	0	0	0	0	0
8172	3717	an	AN6334.1	72.m19451	AO070236000027	0	-119	-105					ATGGGTTTATGTTGA	ATGGGTTTATGTTGA			MGLC*	MGLC*			AAAAGGCAAG	GCTTGTTTGA	0	J	0	0	0	0	0
8173	3717	an	AN6334.1	72.m19451	AO070236000027	0	-111	-46					ATGTTGAGCTTGTTTGACGGAGAAAGAGAGCAGTTCATTTCAACGCTTTCTTCAGTCACCCAGTGA	ATGTTGAGCTTGTTTGACGGAGAAAGAGAGCAGTTCATTTCAACGCTTTCTTCAGTCACCCAGTGA			MLSLFDGEREQFISTLSSVTQ*	MLSLFDGEREQFISTLSSVTQ*			AGATGGGTTT	GGAAGATACA	0	J	0	0	0	0	0
8176	3717	ao	AN6334.1	72.m19451	AO070236000027	0					-128	-96	ATGGAGATAATAATTTTGGACCAAGCTACCTAA			ATGGAGATAATAATTTTGGACCAAGCTACCTAA	MEIIILDQAT*			MEIIILDQAT*	AGAAAAGAAA	AGCTGCTCAC	0	J	0	0	0	0	0
8177	3721	an	AN9399.1	52.m04025	AO070274000017	0	-229	-92					ATGCACCAATCTGCTTCGCAGTCATTGGCAGTTCACCTTCAGCTTCCGGTTTCTCTCTGTGTCTCCCCGTTAGGGATCCCAGCGACATCCTCATCAGCTGCCAGTCAAACGCTCCGTTCTGCTAGAATCGCGTGCTAG	ATGCACCAATCTGCTTCGCAGTCATTGGCAGTTCACCTTCAGCTTCCGGTTTCTCTCTGTGTCTCCCCGTTAGGGATCCCAGCGACATCCTCATCAGCTGCCAGTCAAACGCTCCGTTCTGCTAGAATCGCGTGCTAG			MHQSASQSLAVHLQLPVSLCVSPLGIPATSSSAASQTLRSARIAC*	MHQSASQSLAVHLQLPVSLCVSPLGIPATSSSAASQTLRSARIAC*			GCTGTGATAG	AATAAGTACA	0	BK	0	0	0	YLR015W	0
8178	3721	ao	AN9399.1	52.m04025	AO070274000017	0					-252	-214	ATGCCAGCGTTTTTACTATCGATGCTTGTCTCCATTTAA			ATGCCAGCGTTTTTACTATCGATGCTTGTCTCCATTTAA	MPAFLLSMLVSI*			MPAFLLSMLVSI*	TTGTTCTGGA	CCAAGGGGAA	0	BK	0	0	0	YLR015W	0
8179	3721	ao	AN9399.1	52.m04025	AO070274000017	0					-231	-214	ATGCTTGTCTCCATTTAA			ATGCTTGTCTCCATTTAA	MLVSI*			MLVSI*	TTTACTATCG	CCAAGGGGAA	0	BK	0	0	0	YLR015W	0
8180	3721	ao	AN9399.1	52.m04025	AO070274000017	0					-93	-61	ATGGTCTTACACGGTAGGAGCCGGGACCATTGA			ATGGTCTTACACGGTAGGAGCCGGGACCATTGA	MVLHGRSRDH*			MVLHGRSRDH*	CAGCAAGCCC	AACATCTTTT	0	BK	0	0	0	YLR015W	0
8181	3722	af	AN9482.1	71.m15630	AO070276000024	0			-287	-180			ATGGTTTCCATTGGCGCTGTGCTACTATCAGAATCAGATACGCTAATTCATATGTTTCATTCGACGTCGCATCGTCGGCCTCTCTTGCGTCCACGTCCACGCAGGTGA		ATGGTTTCCATTGGCGCTGTGCTACTATCAGAATCAGATACGCTAATTCATATGTTTCATTCGACGTCGCATCGTCGGCCTCTCTTGCGTCCACGTCCACGCAGGTGA		MVSIGAVLLSESDTLIHMFHSTSHRRPLLRPRPRR*		MVSIGAVLLSESDTLIHMFHSTSHRRPLLRPRPRR*		ATGATCTTGA	CTACTTGGGA	0		0	0	0	0	0
8182	3722	af	AN9482.1	71.m15630	AO070276000024	0			-236	-180			ATGTTTCATTCGACGTCGCATCGTCGGCCTCTCTTGCGTCCACGTCCACGCAGGTGA		ATGTTTCATTCGACGTCGCATCGTCGGCCTCTCTTGCGTCCACGTCCACGCAGGTGA		MFHSTSHRRPLLRPRPRR*		MFHSTSHRRPLLRPRPRR*		GCTAATTCAT	CTACTTGGGA	0		0	0	0	0	0
8183	3722	af	AN9482.1	71.m15630	AO070276000024	0			-143	-21			ATGGTCCCTGAAGTGCGGGGACATCCGTCTGTCGGTTCATCCTCCTTGGACTTCCCCACGCCCACGTTATTTTGCCCATCTAGACTCCAACACGTCTTGCTTGCTATCTCGTTCCGCTCCTAG		ATGGTCCCTGAAGTGCGGGGACATCCGTCTGTCGGTTCATCCTCCTTGGACTTCCCCACGCCCACGTTATTTTGCCCATCTAGACTCCAACACGTCTTGCTTGCTATCTCGTTCCGCTCCTAG		MVPEVRGHPSVGSSSLDFPTPTLFCPSRLQHVLLAISFRS*		MVPEVRGHPSVGSSSLDFPTPTLFCPSRLQHVLLAISFRS*		TACTACTGCA	AGAACTAGAT	0		0	0	0	0	0
8184	3722	ao	AN9482.1	71.m15630	AO070276000024	0					-222	-139	ATGTATTACAGTACGGAGTATGTACCCTGTGTTTGTCGTATTAAAAGGTACCGATGGCGTCACGCGGGTTTCCCCCCTCAATGA			ATGTATTACAGTACGGAGTATGTACCCTGTGTTTGTCGTATTAAAAGGTACCGATGGCGTCACGCGGGTTTCCCCCCTCAATGA	MYYSTEYVPCVCRIKRYRWRHAGFPPQ*			MYYSTEYVPCVCRIKRYRWRHAGFPPQ*	CGCACAAGTT	ATCCGGAGTA	0		0	0	0	0	0
8185	3722	ao	AN9482.1	71.m15630	AO070276000024	0					-203	-126	ATGTACCCTGTGTTTGTCGTATTAAAAGGTACCGATGGCGTCACGCGGGTTTCCCCCCTCAATGAATCCGGAGTATAA			ATGTACCCTGTGTTTGTCGTATTAAAAGGTACCGATGGCGTCACGCGGGTTTCCCCCCTCAATGAATCCGGAGTATAA	MYPVFVVLKGTDGVTRVSPLNESGV*			MYPVFVVLKGTDGVTRVSPLNESGV*	AGTACGGAGT	CCTCCCATGA	0		0	0	0	0	0
8186	3722	ao	AN9482.1	71.m15630	AO070276000024	0					-169	-116	ATGGCGTCACGCGGGTTTCCCCCCTCAATGAATCCGGAGTATAACCTCCCATGA			ATGGCGTCACGCGGGTTTCCCCCCTCAATGAATCCGGAGTATAACCTCCCATGA	MASRGFPPSMNPEYNLP*			MASRGFPPSMNPEYNLP*	AAAGGTACCG	TCTTGAACAA	0		0	0	0	0	0
8187	3722	ao	AN9482.1	71.m15630	AO070276000024	0					-142	-116	ATGAATCCGGAGTATAACCTCCCATGA			ATGAATCCGGAGTATAACCTCCCATGA	MNPEYNLP*			MNPEYNLP*	TCCCCCCTCA	TCTTGAACAA	0		0	0	0	0	0
8188	3722	ao	AN9482.1	71.m15630	AO070276000024	0					-119		ATGATCTTGAACAACAACTACAACAACCCCATTTTCACTCTCAGATCGTCGTCTGACCTAGCTATTTTACTTTGGCTAATTTTCTCCCGAGTTAGCTTTCTCTCAGTTACTTACCAGTAA			ATGATCTTGAACAACAACTACAACAACCCCATTTTCACTCTCAGATCGTCGTCTGACCTAGCTATTTTACTTTGGCTAATTTTCTCCCGAGTTAGCTTTCTCTCAGTTACTTACCAGTAA	MILNNNYNNPIFTLRSSSDLAILLWLIFSRVSFLSVTYQ*			MILNNNYNNPIFTLRSSSDLAILLWLIFSRVSFLSVTYQ*	ATAACCTCCC	TGTATGAATC	0		0	0	0	0	0
8190	3723	an	AN2130.1	72.m19711	AO070278000033	0	-76	-17					ATGCAGCAGCCCCTGATTGCTCAAATCACTCTTTTTTTATTATTCGCCCGCGTTCGTTAA	ATGCAGCAGCCCCTGATTGCTCAAATCACTCTTTTTTTATTATTCGCCCGCGTTCGTTAA			MQQPLIAQITLFLLFARVR*	MQQPLIAQITLFLLFARVR*			GCCGCAAGGG	TTGCTGCGGC	0	T	0	0	0	0	0
8191	3723	ao	AN2130.1	72.m19711	AO070278000033	0					-96	-22	ATGAGACGTAGCGTACTGATTACCAGTTTATCTTGGCTCCCTCCCCCGCCCCCTACCGTCTCCCATTTTATCTAG			ATGAGACGTAGCGTACTGATTACCAGTTTATCTTGGCTCCCTCCCCCGCCCCCTACCGTCTCCCATTTTATCTAG	MRRSVLITSLSWLPPPPPTVSHFI*			MRRSVLITSLSWLPPPPPTVSHFI*	CGTTTGTCGC	TAACTACCAA	0	T	0	0	0	0	0

8189	3723	conserved	AN2130.1	72.m19711	AO070278000033	0	-121	-101	-111	-91	-138	-118	ATGAsCAACGCCyTTskyTrA	ATGAGCAACGCCCTTCGTTGA	ATGAGCAACGCCTTTGTCTGA	ATGACCAACGCCTTTCGTTAA	MsNAlr*	MSNALR*	MSNAFV*	MTNAFR*	CkryCTmGwC	ryyskyymrb	0	T	0	0	0	0	0
8195	3724	af	AN9297.1	52.m03971	AO070279000023	0			-266	-237			ATGCTTGATGGGAGAGGAATCTATCTCTGA		ATGCTTGATGGGAGAGGAATCTATCTCTGA		MLDGRGIYL*		MLDGRGIYL*		CAGCTGCGAC	CAAGCCCTTC	0	S	0	0	0	0	0
8196	3724	af	AN9297.1	52.m03971	AO070279000023	0			-259	-224			ATGGGAGAGGAATCTATCTCTGACAAGCCCTTCTAG		ATGGGAGAGGAATCTATCTCTGACAAGCCCTTCTAG		MGEESISDKPF*		MGEESISDKPF*		GACATGCTTG	TCATATGATG	0	S	0	0	0	0	0
8197	3724	af	AN9297.1	52.m03971	AO070279000023	0			-219	-169			ATGATGGTAGTACATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAG		ATGATGGTAGTACATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAG		MMVVHGSRPNISPPAT*		MMVVHGSRPNISPPAT*		TTCTAGTCAT	ATCAGCGCTG	0	S	0	0	0	0	0
8198	3724	af	AN9297.1	52.m03971	AO070279000023	0			-216	-169			ATGGTAGTACATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAG		ATGGTAGTACATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAG		MVVHGSRPNISPPAT*		MVVHGSRPNISPPAT*		TAGTCATATG	ATCAGCGCTG	0	S	0	0	0	0	0
8199	3724	af	AN9297.1	52.m03971	AO070279000023	0			-206	-156			ATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAGATCAGCGCTGTAG		ATGGCTCCCGGCCGAATATCAGCCCACCCGCAACCTAGATCAGCGCTGTAG		MAPGRISAHPQPRSAL*		MAPGRISAHPQPRSAL*		ATGGTAGTAC	AAGCCAAGGT	0	S	0	0	0	0	0
8192	3724	an	AN9297.1	52.m03971	AO070279000023	0	-181	-89					ATGATCTCGAAAAAAAACATGGCGATTGCTGTCAGCCCATCCGGCGACCATAAGCATATGCAAAGACCATTTGTAGACGCCCATATAAATTGA	ATGATCTCGAAAAAAAACATGGCGATTGCTGTCAGCCCATCCGGCGACCATAAGCATATGCAAAGACCATTTGTAGACGCCCATATAAATTGA			MISKKNMAIAVSPSGDHKHMQRPFVDAHIN*	MISKKNMAIAVSPSGDHKHMQRPFVDAHIN*			GATTCCAACC	ACAGTGTCAA	0	S	0	0	0	0	0
8193	3724	an	AN9297.1	52.m03971	AO070279000023	0	-163	-89					ATGGCGATTGCTGTCAGCCCATCCGGCGACCATAAGCATATGCAAAGACCATTTGTAGACGCCCATATAAATTGA	ATGGCGATTGCTGTCAGCCCATCCGGCGACCATAAGCATATGCAAAGACCATTTGTAGACGCCCATATAAATTGA			MAIAVSPSGDHKHMQRPFVDAHIN*	MAIAVSPSGDHKHMQRPFVDAHIN*			GAAAAAAAAC	ACAGTGTCAA	0	S	0	0	0	0	0
8194	3724	an	AN9297.1	52.m03971	AO070279000023	0	-124	-89					ATGCAAAGACCATTTGTAGACGCCCATATAAATTGA	ATGCAAAGACCATTTGTAGACGCCCATATAAATTGA			MQRPFVDAHIN*	MQRPFVDAHIN*			CCATAAGCAT	ACAGTGTCAA	0	S	0	0	0	0	0
8200	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-234	-166	ATGTCTGGCCAGATACTATATGATAAACCCCAACATCCACCAGGAGCTACTCAGCCCAATTTGTCCTAG			ATGTCTGGCCAGATACTATATGATAAACCCCAACATCCACCAGGAGCTACTCAGCCCAATTTGTCCTAG	MSGQILYDKPQHPPGATQPNLS*			MSGQILYDKPQHPPGATQPNLS*	TAGTCGAGAC	CCTACTATGT	0	S	0	0	0	0	0
8201	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-215	-147	ATGATAAACCCCAACATCCACCAGGAGCTACTCAGCCCAATTTGTCCTAGCCTACTATGTCACAGTTAA			ATGATAAACCCCAACATCCACCAGGAGCTACTCAGCCCAATTTGTCCTAGCCTACTATGTCACAGTTAA	MINPNIHQELLSPICPSLLCHS*			MINPNIHQELLSPICPSLLCHS*	CAGATACTAT	TGTATGCTTT	0	S	0	0	0	0	0
8202	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-159	-115	ATGTCACAGTTAATGTATGCTTTCTCAGTCCTAGCTGTCATATGA			ATGTCACAGTTAATGTATGCTTTCTCAGTCCTAGCTGTCATATGA	MSQLMYAFSVLAVI*			MSQLMYAFSVLAVI*	CTAGCCTACT	TAACTCTCAG	0	S	0	0	0	0	0
8203	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-147	-115	ATGTATGCTTTCTCAGTCCTAGCTGTCATATGA			ATGTATGCTTTCTCAGTCCTAGCTGTCATATGA	MYAFSVLAVI*			MYAFSVLAVI*	GTCACAGTTA	TAACTCTCAG	0	S	0	0	0	0	0
8204	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-143	-126	ATGCTTTCTCAGTCCTAG			ATGCTTTCTCAGTCCTAG	MLSQS*			MLSQS*	CAGTTAATGT	CTGTCATATG	0	S	0	0	0	0	0
8205	3724	ao	AN9297.1	52.m03971	AO070279000023	0					-118	-95	ATGATAACTCTCAGTGGTATTTAG			ATGATAACTCTCAGTGGTATTTAG	MITLSGI*			MITLSGI*	TAGCTGTCAT	AATCAGGGCC	0	S	0	0	0	0	0
8207	3725	ao	AN4971.1	59.m08874	AO070288000037	0					-99	-16	ATGGCTAGACATGCGCTACAGAACGTCCGTCCGCCGGTCACATCGAAATTTGGATTCCCTCCGCCCGCAGGTCTCGTCCGATAG			ATGGCTAGACATGCGCTACAGAACGTCCGTCCGCCGGTCACATCGAAATTTGGATTCCCTCCGCCCGCAGGTCTCGTCCGATAG	MARHALQNVRPPVTSKFGFPPPAGLVR*			MARHALQNVRPPVTSKFGFPPPAGLVR*	TATCAGTTGA	ATCCTCCGTC	0	TV	0	0	0	0	0
8206	3725	conserved	AN4971.1	59.m08874	AO070288000037	0	-106	-83	-112	-89	-115	-92	ATGyrGTrTyrryTsArTkryTAG	ATGCAGTGTCAACTCAATTATTAG	ATGTGGTATTGGTTGAGTGATTAG	ATGCGGTATCAGTTGAATGGCTAG	MqcqLny*	MQCQLNY*	MWYWLSD*	MRYQLNG*	yysyhbrGvr	AyATGCGCwr	0	TV	0	0	0	0	0
8210	3726	af	AN7630.1	71.m15820	AO070294000040	0			-240	-229			ATGAATTTCTAA		ATGAATTTCTAA		MNF*		MNF*		CGGGGAGAAA	GCGGTGTGTT	0	S	FG09544.1	0	NCU02477.1	0	0
8211	3726	af	AN7630.1	71.m15820	AO070294000040	0			-212	-144			ATGGAACAGATACTGATTGATCAGCAGGAGGAAAAAAAACATTCAGAGCTTTTCTGTATAAGGATTTGA		ATGGAACAGATACTGATTGATCAGCAGGAGGAAAAAAAACATTCAGAGCTTTTCTGTATAAGGATTTGA		MEQILIDQQEEKKHSELFCIRI*		MEQILIDQQEEKKHSELFCIRI*		TGTTGAACTT	AGGACCTTGT	0	S	FG09544.1	0	NCU02477.1	0	0
8208	3726	an	AN7630.1	71.m15820	AO070294000040	0	-114	-103					ATGAATTTCTAA	ATGAATTTCTAA			MNF*	MNF*			CGGGGAAGAA	GCGGGGTGAT	0	S	FG09544.1	0	NCU02477.1	0	0
8209	3726	an	AN7630.1	71.m15820	AO070294000040	0	-94	-53					ATGAAATTTCCAGCTACTTTATATTTCTGTTTTCTTTCATAG	ATGAAATTTCCAGCTACTTTATATTTCTGTTTTCTTTCATAG			MKFPATLYFCFLS*	MKFPATLYFCFLS*			AAGCGGGGTG	CATTCTAAGC	0	S	FG09544.1	0	NCU02477.1	0	0
8212	3729	af	AN1624.1	58.m07694	AO070299000090	0			-199	-62			ATGGAAGTATTTATGTCCTTGATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		ATGGAAGTATTTATGTCCTTGATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		MEVFMSLMGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		MEVFMSLMGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		AAAATTCGGC	CCTACCTTCT	0	C	0	MG00892.1	NCU02250.1	0	0
8213	3729	af	AN1624.1	58.m07694	AO070299000090	0			-187	-62			ATGTCCTTGATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		ATGTCCTTGATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		MSLMGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		MSLMGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		GGAAGTATTT	CCTACCTTCT	0	C	0	MG00892.1	NCU02250.1	0	0
8214	3729	af	AN1624.1	58.m07694	AO070299000090	0			-178	-62			ATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		ATGGGTCTCTGGGTCATCCTGCCCTCCCGCCTTTTTTCTTACCCCCCAAAAGCTCTCCCAGCTCTCCTTTTTCCTTCCTCTCCTCTTTTTTCTTTCCTTTCCTTCCACACACTCTAA		MGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		MGLWVILPSRLFSYPPKALPALLFPSSPLFSFLSFHTL*		TATGTCCTTG	CCTACCTTCT	0	C	0	MG00892.1	NCU02250.1	0	0
8215	3729	ao	AN1624.1	58.m07694	AO070299000090	0					-126	-76	ATGTCCCGGAAAGCCTCTGTTGTCAACTTCTCCAGCTTTTTTCCCTCCTAA			ATGTCCCGGAAAGCCTCTGTTGTCAACTTCTCCAGCTTTTTTCCCTCCTAA	MSRKASVVNFSSFFPS*			MSRKASVVNFSSFFPS*	GAGAGTATTT	AAAGTTCTGT	0	C	0	MG00892.1	NCU02250.1	0	0
8217	3731	af	AN1992.1	58.m07602	AO070301000083	0			-202	-179			ATGTTGGCGCCAAGTGCGCGCTAA		ATGTTGGCGCCAAGTGCGCGCTAA		MLAPSAR*		MLAPSAR*		CTGGCTTTTT	GCCTTACCGA	0	A	0	0	0	0	0
8218	3731	af	AN1992.1	58.m07602	AO070301000083	0			-143	-120			ATGGAACTGACGGCCTGTGGTTGA		ATGGAACTGACGGCCTGTGGTTGA		MELTACG*		MELTACG*		TGTAATAGCA	AGGTCAGAGG	0	A	0	0	0	0	0
8219	3731	af	AN1992.1	58.m07602	AO070301000083	0			-80	-60			ATGCCAGTCTACGAGACCTGA		ATGCCAGTCTACGAGACCTGA		MPVYET*		MPVYET*		CCGACTATCG	TATCGTCAAC	0	A	0	0	0	0	0
8216	3731	an	AN1992.1	58.m07602	AO070301000083	0	-76	-65					ATGTTCTTTTAA	ATGTTCTTTTAA			MFF*	MFF*			CGTCGCCGAC	CATAGCGGCC	0	A	0	0	0	0	0
8222	3732	af	AN3115.1	59.m08622	AO070303000034	0			-240	-199			ATGGGACTTCTGGGAGGACCATGCCTGTTGGAAGAGCAGTAA		ATGGGACTTCTGGGAGGACCATGCCTGTTGGAAGAGCAGTAA		MGLLGGPCLLEEQ*		MGLLGGPCLLEEQ*		GAATGGTTTA	AGCTCCGCGC	0	R	0	0	0	0	0
8223	3732	af	AN3115.1	59.m08622	AO070303000034	0			-220	-161			ATGCCTGTTGGAAGAGCAGTAAAGCTCCGCGCTGTGCGCGCCCGAGCTCCCGGGTTGTAG		ATGCCTGTTGGAAGAGCAGTAAAGCTCCGCGCTGTGCGCGCCCGAGCTCCCGGGTTGTAG		MPVGRAVKLRAVRARAPGL*		MPVGRAVKLRAVRARAPGL*		TGGGAGGACC	CAGGTATGTC	0	R	0	0	0	0	0
8224	3732	af	AN3115.1	59.m08622	AO070303000034	0			-120	-85			ATGCCCCCCCTATCTTGCGTCGTGTGGCATACATAA		ATGCCCCCCCTATCTTGCGTCGTGTGGCATACATAA		MPPLSCVVWHT*		MPPLSCVVWHT*		TCATCCACTC	ATACTTCCTA	0	R	0	0	0	0	0
8220	3732	an	AN3115.1	59.m08622	AO070303000034	0	-139	-128					ATGTTTGCTTGA	ATGTTTGCTTGA			MFA*	MFA*			TATAAGCCCT	TAAATAGGCA	0	R	0	0	0	0	0
8221	3732	an	AN3115.1	59.m08622	AO070303000034	0	-99	-49					ATGTTACACTCTTCGGTTTATTTTGATTCACGGCCGATCAGGAACCTCTGA	ATGTTACACTCTTCGGTTTATTTTGATTCACGGCCGATCAGGAACCTCTGA			MLHSSVYFDSRPIRNL*	MLHSSVYFDSRPIRNL*			AGCCGTGCAC	AGTGCCCATT	0	R	0	0	0	0	0
8225	3732	ao	AN3115.1	59.m08622	AO070303000034	0					-243	-232	ATGGACTTTTGA			ATGGACTTTTGA	MDF*			MDF*	AAAGGTTAGT	TATTGAGAAT	0	R	0	0	0	0	0
8226	3732	ao	AN3115.1	59.m08622	AO070303000034	0					-162	-106	ATGCGCTTGGATCCACTTCAGACTACATGGAGCTCACTGTGTTTGCATGCTGATTGA			ATGCGCTTGGATCCACTTCAGACTACATGGAGCTCACTGTGTTTGCATGCTGATTGA	MRLDPLQTTWSSLCLHAD*			MRLDPLQTTWSSLCLHAD*	CACCAATAGC	CAAACTGAAG	0	R	0	0	0	0	0
8227	3732	ao	AN3115.1	59.m08622	AO070303000034	0					-136	-110	ATGGAGCTCACTGTGTTTGCATGCTGA			ATGGAGCTCACTGTGTTTGCATGCTGA	MELTVFAC*			MELTVFAC*	TTCAGACTAC	TTGACAAACT	0	R	0	0	0	0	0
8228	3732	ao	AN3115.1	59.m08622	AO070303000034	0					-116	-75	ATGCTGATTGACAAACTGAAGCATACTAATTTCTCTATATAA			ATGCTGATTGACAAACTGAAGCATACTAATTTCTCTATATAA	MLIDKLKHTNFSI*			MLIDKLKHTNFSI*	CTGTGTTTGC	AGTCCTTCGG	0	R	0	0	0	0	0
8233	3736	af	AN5687.1	65.m07413	AO070309000102	0			-150	-79			ATGGGCAACCGCCAAGAAAAAACAACTAGATGCGTCCTGCGTCTAGAACTACCTTACCATAGACTACCTTAG		ATGGGCAACCGCCAAGAAAAAACAACTAGATGCGTCCTGCGTCTAGAACTACCTTACCATAGACTACCTTAG		MGNRQEKTTRCVLRLELPYHRLP*		MGNRQEKTTRCVLRLELPYHRLP*		TCTCGTCTCC	CTAGCGACTG	0		0	0	0	0	0
8234	3736	af	AN5687.1	65.m07413	AO070309000102	0			-121	-89			ATGCGTCCTGCGTCTAGAACTACCTTACCATAG		ATGCGTCCTGCGTCTAGAACTACCTTACCATAG		MRPASRTTLP*		MRPASRTTLP*		AAACAACTAG	ACTACCTTAG	0		0	0	0	0	0
8236	3737	an	AN5690.1	65.m07415	AO070309000105	0	-268	-248					ATGTGCTTGTCGTCAACTTAG	ATGTGCTTGTCGTCAACTTAG			MCLSST*	MCLSST*			GCTCAAGTTC	GCGCGACCCC	0	Q	0	0	0	0	0
8237	3737	an	AN5690.1	65.m07415	AO070309000105	0	-234	-145					ATGGCGCTAGCCGTGACCTTCCCTAATAGGCAGGTCCATCCAGATCTATCTCGATCTCTTCTTTATCTCCAAAACAGATGGCAAAGATGA	ATGGCGCTAGCCGTGACCTTCCCTAATAGGCAGGTCCATCCAGATCTATCTCGATCTCTTCTTTATCTCCAAAACAGATGGCAAAGATGA			MALAVTFPNRQVHPDLSRSLLYLQNRWQR*	MALAVTFPNRQVHPDLSRSLLYLQNRWQR*			CGACCCCACA	CAGCTATATA	0	Q	0	0	0	0	0
8238	3737	an	AN5690.1	65.m07415	AO070309000105	0	-157	-134					ATGGCAAAGATGACAGCTATATAA	ATGGCAAAGATGACAGCTATATAA			MAKMTAI*	MAKMTAI*			TCCAAAACAG	GTCACTGTCT	0	Q	0	0	0	0	0
8239	3737	an	AN5690.1	65.m07415	AO070309000105	0	-148	-134					ATGACAGCTATATAA	ATGACAGCTATATAA			MTAI*	MTAI*			GATGGCAAAG	GTCACTGTCT	0	Q	0	0	0	0	0
8240	3737	ao	AN5690.1	65.m07415	AO070309000105	0					-131	-84	ATGCTACTCCATCTTCTACTTCAAACCTTTCTAACATTTACCCCCTAA			ATGCTACTCCATCTTCTACTTCAAACCTTTCTAACATTTACCCCCTAA	MLLHLLLQTFLTFTP*			MLLHLLLQTFLTFTP*	CTCCCTGTAA	GACATTCGTT	0	Q	0	0	0	0	0
8242	3738	af	AN9413.1	53.m03669	AO070310000006	0			-148	-71			ATGATGCCCCAATTGGCTTCCGACTCTGTGTTAGCGAGGGAGATTTCTGAGCCCGCTCCCCGGATTCGCCTGTCCTAA		ATGATGCCCCAATTGGCTTCCGACTCTGTGTTAGCGAGGGAGATTTCTGAGCCCGCTCCCCGGATTCGCCTGTCCTAA		MMPQLASDSVLAREISEPAPRIRLS*		MMPQLASDSVLAREISEPAPRIRLS*		GGAGAACGGG	GTTGGTCCAA	0		0	0	0	0	0
8243	3738	af	AN9413.1	53.m03669	AO070310000006	0			-145	-71			ATGCCCCAATTGGCTTCCGACTCTGTGTTAGCGAGGGAGATTTCTGAGCCCGCTCCCCGGATTCGCCTGTCCTAA		ATGCCCCAATTGGCTTCCGACTCTGTGTTAGCGAGGGAGATTTCTGAGCCCGCTCCCCGGATTCGCCTGTCCTAA		MPQLASDSVLAREISEPAPRIRLS*		MPQLASDSVLAREISEPAPRIRLS*		GAACGGGATG	GTTGGTCCAA	0		0	0	0	0	0
8241	3738	an	AN9413.1	53.m03669	AO070310000006	0	-124	-62					ATGACGTTCTATCTTTACCGACGCCCCCTACGAGTACCCAAGCATTTGAGGCAGATAACCTAG	ATGACGTTCTATCTTTACCGACGCCCCCTACGAGTACCCAAGCATTTGAGGCAGATAACCTAG			MTFYLYRRPLRVPKHLRQIT*	MTFYLYRRPLRVPKHLRQIT*			GCAGCACGGC	ATCCCCCCAA	0		0	0	0	0	0
8245	3738	ao	AN9413.1	53.m03669	AO070310000006	0					-115	-62	ATGACGTTCCTTTTCGTTATCGTCTCAGTAGGTTTCAACGCCGGTGATATATGA			ATGACGTTCCTTTTCGTTATCGTCTCAGTAGGTTTCAACGCCGGTGATATATGA	MTFLFVIVSVGFNAGDI*			MTFLFVIVSVGFNAGDI*	TTCACACGGA	ACCTACCCCT	0		0	0	0	0	0
8246	3740	af	AN8210.1	53.m03766	AO070310000105	0			-242	-204			ATGCAGACTTTGGAAATTCCCTTGTATGTGTTCCAATAA		ATGCAGACTTTGGAAATTCCCTTGTATGTGTTCCAATAA		MQTLEIPLYVFQ*		MQTLEIPLYVFQ*		TCTTCCTACC	TATCCTCTCC	0	D	0	0	0	0	0
8247	3740	af	AN8210.1	53.m03766	AO070310000105	0			-217	-119			ATGTGTTCCAATAATATCCTCTCCTTTGTTGCTACTGGCTCGAGCCACGGTACGTCTTTTCCAACCCTTCGTCCAGAGTACTCGTTGGTTTCCTCATAA		ATGTGTTCCAATAATATCCTCTCCTTTGTTGCTACTGGCTCGAGCCACGGTACGTCTTTTCCAACCCTTCGTCCAGAGTACTCGTTGGTTTCCTCATAA		MCSNNILSFVATGSSHGTSFPTLRPEYSLVSS*		MCSNNILSFVATGSSHGTSFPTLRPEYSLVSS*		ATTCCCTTGT	GTGTTGTGCA	0	D	0	0	0	0	0
8248	3741	an	AN0112.1	71.m15387	AO070311000096	0	-225	-202					ATGTGTTCGGTAATTGCTGAGTAA	ATGTGTTCGGTAATTGCTGAGTAA			MCSVIAE*	MCSVIAE*			TTATTGGTGT	TAGTAACGGC	0	U	0	0	0	0	0
8251	3742	af	AN1005.1	70.m15223	AO070312000029	0			-203	-183			ATGGGAGTCCTGTCTGATTAA		ATGGGAGTCCTGTCTGATTAA		MGVLSD*		MGVLSD*		AATCTGGATA	TTCAGATCAG	0	Z	FG09793.1	0	NCU05282.1	0	0
8252	3742	af	AN1005.1	70.m15223	AO070312000029	0			-170	-135			ATGACGATGCGCGCAACAGCGCCTCGGATTCCCTAA		ATGACGATGCGCGCAACAGCGCCTCGGATTCCCTAA		MTMRATAPRIP*		MTMRATAPRIP*		CAGATCAGGT	CAAACGGTGG	0	Z	FG09793.1	0	NCU05282.1	0	0
8253	3742	af	AN1005.1	70.m15223	AO070312000029	0			-164	-135			ATGCGCGCAACAGCGCCTCGGATTCCCTAA		ATGCGCGCAACAGCGCCTCGGATTCCCTAA		MRATAPRIP*		MRATAPRIP*		AGGTATGACG	CAAACGGTGG	0	Z	FG09793.1	0	NCU05282.1	0	0
8250	3742	an	AN1005.1	70.m15223	AO070312000029	0	-170	-150					ATGATCGAGCGCCGCAAATGA	ATGATCGAGCGCCGCAAATGA			MIERRK*	MIERRK*			AACTGCTTCG	GGAGTATCGG	0	Z	FG09793.1	0	NCU05282.1	0	0
8255	3742	ao	AN1005.1	70.m15223	AO070312000029	0					-231	-211	ATGGGATCCTCTGTACTGTAA			ATGGGATCCTCTGTACTGTAA	MGSSVL*			MGSSVL*	TCAGTGACGA	CGCGACACAC	0	Z	FG09793.1	0	NCU05282.1	0	0
8257	3744	af	AN0039.1	71.m15314	AO070314000117	0			-92	-75			ATGGCCTCAACCTGCTGA		ATGGCCTCAACCTGCTGA		MASTC*		MASTC*		CCGCGTCCTC	GTGCTCCTTG	0	S	0	0	0	YNL011C	0
8256	3744	an	AN0039.1	71.m15314	AO070314000117	0	-159	-130					ATGGTCCTTATCGTGTACTCGCCTCTCTGA	ATGGTCCTTATCGTGTACTCGCCTCTCTGA			MVLIVYSPL*	MVLIVYSPL*			TCCTAGCTGA	GAATATATAT	0	S	0	0	0	YNL011C	0
8258	3744	ao	AN0039.1	71.m15314	AO070314000117	0					-228	-172	ATGATCAATCAAGGAACTAAAAACCCTACGGAGTCTTGGCTAATGACATCTTGCTAG			ATGATCAATCAAGGAACTAAAAACCCTACGGAGTCTTGGCTAATGACATCTTGCTAG	MINQGTKNPTESWLMTSC*			MINQGTKNPTESWLMTSC*	TCCTTTGTCC	GTTACGAAAT	0	S	0	0	0	YNL011C	0
8259	3744	ao	AN0039.1	71.m15314	AO070314000117	0					-186	-172	ATGACATCTTGCTAG			ATGACATCTTGCTAG	MTSC*			MTSC*	GTCTTGGCTA	GTTACGAAAT	0	S	0	0	0	YNL011C	0

8260	3744	ao	AN0039.1	71.m15314	AO070314000117	0					-163	-95	ATGGTATTTATAGAATCCGTGGCCTTAAAATATGAAAATAGATATAACGTCCAGACCTCAGGTTTATAA			ATGGTATTTATAGAATCCGTGGCCTTAAAATATGAAAATAGATATAACGTCCAGACCTCAGGTTTATAA	MVFIESVALKYENRYNVQTSGL*			MVFIESVALKYENRYNVQTSGL*	AGGTTACGAA	GTGACCGTGC	0	S	0	0	0	YNL011C	0
8261	3744	ao	AN0039.1	71.m15314	AO070314000117	0					-132	-91	ATGAAAATAGATATAACGTCCAGACCTCAGGTTTATAAGTGA			ATGAAAATAGATATAACGTCCAGACCTCAGGTTTATAAGTGA	MKIDITSRPQVYK*			MKIDITSRPQVYK*	GCCTTAAAAT	CCGTGCCTGC	0	S	0	0	0	YNL011C	0
8264	3746	af	AN8704.1	62.m03491	AO070315000132	0			-291	-136			ATGAACTACATTACGATCACAGAGGAAGAGCCAACAGATAACAATTCCCTTGCAATGATTCCCTTCTTTGATGATATCGTAGTTACCATAGAGGTATTGGAAGTCCGAAGTTGTAAGGCCACCCAAGGGCAGACGAGGTCACGTGTCGCACTTTAG		ATGAACTACATTACGATCACAGAGGAAGAGCCAACAGATAACAATTCCCTTGCAATGATTCCCTTCTTTGATGATATCGTAGTTACCATAGAGGTATTGGAAGTCCGAAGTTGTAAGGCCACCCAAGGGCAGACGAGGTCACGTGTCGCACTTTAG		MNYITITEEEPTDNNSLAMIPFFDDIVVTIEVLEVRSCKATQGQTRSRVAL*		MNYITITEEEPTDNNSLAMIPFFDDIVVTIEVLEVRSCKATQGQTRSRVAL*		AAAAAAAATT	CGAGGCCTTC	0	J	0	0	0	0	0
8265	3746	af	AN8704.1	62.m03491	AO070315000132	0			-237	-136			ATGATTCCCTTCTTTGATGATATCGTAGTTACCATAGAGGTATTGGAAGTCCGAAGTTGTAAGGCCACCCAAGGGCAGACGAGGTCACGTGTCGCACTTTAG		ATGATTCCCTTCTTTGATGATATCGTAGTTACCATAGAGGTATTGGAAGTCCGAAGTTGTAAGGCCACCCAAGGGCAGACGAGGTCACGTGTCGCACTTTAG		MIPFFDDIVVTIEVLEVRSCKATQGQTRSRVAL*		MIPFFDDIVVTIEVLEVRSCKATQGQTRSRVAL*		TTCCCTTGCA	CGAGGCCTTC	0	J	0	0	0	0	0
8266	3746	af	AN8704.1	62.m03491	AO070315000132	0			-221	-210			ATGATATCGTAG		ATGATATCGTAG		MIS*		MIS*		CCCTTCTTTG	TTACCATAGA	0	J	0	0	0	0	0
8262	3746	an	AN8704.1	62.m03491	AO070315000132	0	-217	-176					ATGCATAGGCATATAGAGCTATCTCAGCGACTTACTTCGTAG	ATGCATAGGCATATAGAGCTATCTCAGCGACTTACTTCGTAG			MHRHIELSQRLTS*	MHRHIELSQRLTS*			GCAGATTCAA	ATGAAGGGTC	0	J	0	0	0	0	0
8263	3746	an	AN8704.1	62.m03491	AO070315000132	0	-175	-134					ATGAAGGGTCAAGGGCAGAGCGGGGTCACGTGGTCCGCTTAG	ATGAAGGGTCAAGGGCAGAGCGGGGTCACGTGGTCCGCTTAG			MKGQGQSGVTWSA*	MKGQGQSGVTWSA*			TACTTCGTAG	CGAGCTCCGC	0	J	0	0	0	0	0
8267	3746	ao	AN8704.1	62.m03491	AO070315000132	0					-187	-170	ATGTCTCATAGAAGTTGA			ATGTCTCATAGAAGTTGA	MSHRS*			MSHRS*	GTCACCCCAG	AGTTGCAAAC	0	J	0	0	0	0	0
8268	3748	an	AN0984.1	70.m15624	AO070318000164	0	-197	-165					ATGAGTCTTAGAATTATTAATAAATGTTTGTAG	ATGAGTCTTAGAATTATTAATAAATGTTTGTAG			MSLRIINKCL*	MSLRIINKCL*			ACCCATAAGA	TAAAAGAAGG	0	S	0	0	0	YOR243C	0
8269	3748	an	AN0984.1	70.m15624	AO070318000164	0	-174	-127					ATGTTTGTAGTAAAAGAAGGGAGAGCGCTTACATCAATGAGGTTCTGA	ATGTTTGTAGTAAAAGAAGGGAGAGCGCTTACATCAATGAGGTTCTGA			MFVVKEGRALTSMRF*	MFVVKEGRALTSMRF*			TTATTAATAA	GCATACTCCC	0	S	0	0	0	YOR243C	0
8270	3748	an	AN0984.1	70.m15624	AO070318000164	0	-138	-127					ATGAGGTTCTGA	ATGAGGTTCTGA			MRF*	MRF*			GCTTACATCA	GCATACTCCC	0	S	0	0	0	YOR243C	0
8271	3748	ao	AN0984.1	70.m15624	AO070318000164	0					-157	-131	ATGTACTGTTCTTTATCAGAGACGTAG			ATGTACTGTTCTTTATCAGAGACGTAG	MYCSLSET*			MYCSLSET*	AATCCGCCCC	GGCTAGGGCT	0	S	0	0	0	YOR243C	0
8275	3752	af	AN5535.1	58.m07481	AO070328000056	0			-233	-204			ATGTTTCTCTTGAGATTAAGAAAAAAATAG		ATGTTTCTCTTGAGATTAAGAAAAAAATAG		MFLLRLRKK*		MFLLRLRKK*		ACAATAAAGA	CTAGCTTGAT	0	S	0	MG00102.1	NCU04505.1	0	0
8276	3752	af	AN5535.1	58.m07481	AO070328000056	0			-195	-184			ATGGAGACGTGA		ATGGAGACGTGA		MET*		MET*		AGCTAGCTTG	ACATGTAAGT	0	S	0	MG00102.1	NCU04505.1	0	0
8277	3752	af	AN5535.1	58.m07481	AO070328000056	0			-168	-97			ATGTGGTTCGAAACAGAAATTCTTTTTGTCGCGGGGGATTCGAGGAGATCTGCTTGCGGGTGGAGCCCGTAG		ATGTGGTTCGAAACAGAAATTCTTTTTGTCGCGGGGGATTCGAGGAGATCTGCTTGCGGGTGGAGCCCGTAG		MWFETEILFVAGDSRRSACGWSP*		MWFETEILFVAGDSRRSACGWSP*		TAAGTCAATA	TCTGGACCGC	0	S	0	MG00102.1	NCU04505.1	0	0
8272	3752	an	AN5535.1	58.m07481	AO070328000056	0	-119	-72					ATGATAAAATGTCGACAGAAAATGAGGGGGAATTGCCAAAGGCGGTGA	ATGATAAAATGTCGACAGAAAATGAGGGGGAATTGCCAAAGGCGGTGA			MIKCRQKMRGNCQRR*	MIKCRQKMRGNCQRR*			AGTACGCTTG	GCGAGAAGGT	0	S	0	MG00102.1	NCU04505.1	0	0
8273	3752	an	AN5535.1	58.m07481	AO070328000056	0	-111	-4					ATGTCGACAGAAAATGAGGGGGAATTGCCAAAGGCGGTGAGCGAGAAGGTCTCGACCGTTTTTCGACGTCATTGCTTGCTTTCTCACTTCAAATGTCTTAACAATTGA	ATGTCGACAGAAAATGAGGGGGAATTGCCAAAGGCGGTGAGCGAGAAGGTCTCGACCGTTTTTCGACGTCATTGCTTGCTTTCTCACTTCAAATGTCTTAACAATTGA			MSTENEGELPKAVSEKVSTVFRRHCLLSHFKCLNN*	MSTENEGELPKAVSEKVSTVFRRHCLLSHFKCLNN*			TGATGATAAA	AAAATGACGC	0	S	0	MG00102.1	NCU04505.1	0	0
8274	3752	an	AN5535.1	58.m07481	AO070328000056	0	-98	-72					ATGAGGGGGAATTGCCAAAGGCGGTGA	ATGAGGGGGAATTGCCAAAGGCGGTGA			MRGNCQRR*	MRGNCQRR*			TCGACAGAAA	GCGAGAAGGT	0	S	0	MG00102.1	NCU04505.1	0	0
8279	3752	ao	AN5535.1	58.m07481	AO070328000056	0					-250	-182	ATGTATCACCGGGGTGAAACACGGGAGAATAAGAGTTGTGTGGTGGTCGAGGATAAGAAAATCAAATAA			ATGTATCACCGGGGTGAAACACGGGAGAATAAGAGTTGTGTGGTGGTCGAGGATAAGAAAATCAAATAA	MYHRGETRENKSCVVVEDKKIK*			MYHRGETRENKSCVVVEDKKIK*	ATCCTCTAGT	TTTCTTCCAG	0	S	0	MG00102.1	NCU04505.1	0	0
8284	3753	af	AN3642.1	58.m07459	AO070328000088	0			-103	-74			ATGGCAATTGTGGGATCCTATCTGATTTGA		ATGGCAATTGTGGGATCCTATCTGATTTGA		MAIVGSYLI*		MAIVGSYLI*		GCTAAGCGGC	TTGCAAGGAC	0	U	0	0	0	0	0
8280	3753	an	AN3642.1	58.m07459	AO070328000088	0	-272	-213					ATGCATGGAGCGGTATATCCTGAGAGCAAGCTTATCGAAGTGGGAAGTGCGAAGGTGTAG	ATGCATGGAGCGGTATATCCTGAGAGCAAGCTTATCGAAGTGGGAAGTGCGAAGGTGTAG			MHGAVYPESKLIEVGSAKV*	MHGAVYPESKLIEVGSAKV*			GCTTTGGATT	CGCGGCAGCA	0	U	0	0	0	0	0
8281	3753	an	AN3642.1	58.m07459	AO070328000088	0	-268	-155					ATGGAGCGGTATATCCTGAGAGCAAGCTTATCGAAGTGGGAAGTGCGAAGGTGTAGCGCGGCAGCAATGTTCCTGTTGTCGTTGAGCGACGCCTTATGTAATCAGAGTACCTAG	ATGGAGCGGTATATCCTGAGAGCAAGCTTATCGAAGTGGGAAGTGCGAAGGTGTAGCGCGGCAGCAATGTTCCTGTTGTCGTTGAGCGACGCCTTATGTAATCAGAGTACCTAG			MERYILRASLSKWEVRRCSAAAMFLLSLSDALCNQST*	MERYILRASLSKWEVRRCSAAAMFLLSLSDALCNQST*			TGGATTATGC	TTATGCCACC	0	U	0	0	0	0	0
8282	3753	an	AN3642.1	58.m07459	AO070328000088	0	-202	-155					ATGTTCCTGTTGTCGTTGAGCGACGCCTTATGTAATCAGAGTACCTAG	ATGTTCCTGTTGTCGTTGAGCGACGCCTTATGTAATCAGAGTACCTAG			MFLLSLSDALCNQST*	MFLLSLSDALCNQST*			CGCGGCAGCA	TTATGCCACC	0	U	0	0	0	0	0
8283	3753	an	AN3642.1	58.m07459	AO070328000088	0	-133	-86					ATGCGAGGTGCCATCAACCCAGCTGGAAGCTCAACGGAGCTCAACTAG	ATGCGAGGTGCCATCAACCCAGCTGGAAGCTCAACGGAGCTCAACTAG			MRGAINPAGSSTELN*	MRGAINPAGSSTELN*			CCAGGCAGTA	TCACCCTTTG	0	U	0	0	0	0	0
8285	3753	ao	AN3642.1	58.m07459	AO070328000088	0					-127	-92	ATGGCCATACTTGGAATATCCAATTCTAACTGGTGA			ATGGCCATACTTGGAATATCCAATTCTAACTGGTGA	MAILGISNSNW*			MAILGISNSNW*	GTCCGCGACA	CCGTAACGAC	0	U	0	0	0	0	0
8288	3754	af	AN4028.1	54.m06555	AO070328000115	0			-137	-96			ATGATTGTCATCACTGAATGCTCCTCTTTCACGGATGGGTAA		ATGATTGTCATCACTGAATGCTCCTCTTTCACGGATGGGTAA		MIVITECSSFTDG*		MIVITECSSFTDG*		TCGACCTCCA	TACTGCGTGG	0	S	0	0	0	0	0
8289	3754	af	AN4028.1	54.m06555	AO070328000115	0			-120	-4			ATGCTCCTCTTTCACGGATGGGTAATACTGCGTGGTTCGAGTTGGAATACACAGGAGGCTTCACCTTCGGCGAGTCTAGGAAACCGGCGAGCCCGCTTTGGCACGAAATATCCATGA		ATGCTCCTCTTTCACGGATGGGTAATACTGCGTGGTTCGAGTTGGAATACACAGGAGGCTTCACCTTCGGCGAGTCTAGGAAACCGGCGAGCCCGCTTTGGCACGAAATATCCATGA		MLLFHGWVILRGSSWNTQEASPSASLGNRRARFGTKYP*		MLLFHGWVILRGSSWNTQEASPSASLGNRRARFGTKYP*		TCATCACTGA	AGAATGACCT	0	S	0	0	0	0	0
8286	3754	an	AN4028.1	54.m06555	AO070328000115	0	-111	-4					ATGGGTCATATGATACGTCTCTTTCTCGGAAGTCAGACGGGGGTACCAATTGGGAAAAACAAAAGATTAGAGCAACCTAGAAGACTGCATCTCGATTTCTCTCGATGA	ATGGGTCATATGATACGTCTCTTTCTCGGAAGTCAGACGGGGGTACCAATTGGGAAAAACAAAAGATTAGAGCAACCTAGAAGACTGCATCTCGATTTCTCTCGATGA			MGHMIRLFLGSQTGVPIGKNKRLEQPRRLHLDFSR*	MGHMIRLFLGSQTGVPIGKNKRLEQPRRLHLDFSR*			GTTTGCGCGG	AGAATGAGCT	0	S	0	0	0	0	0
8287	3754	an	AN4028.1	54.m06555	AO070328000115	0	-102	-4					ATGATACGTCTCTTTCTCGGAAGTCAGACGGGGGTACCAATTGGGAAAAACAAAAGATTAGAGCAACCTAGAAGACTGCATCTCGATTTCTCTCGATGA	ATGATACGTCTCTTTCTCGGAAGTCAGACGGGGGTACCAATTGGGAAAAACAAAAGATTAGAGCAACCTAGAAGACTGCATCTCGATTTCTCTCGATGA			MIRLFLGSQTGVPIGKNKRLEQPRRLHLDFSR*	MIRLFLGSQTGVPIGKNKRLEQPRRLHLDFSR*			GATGGGTCAT	AGAATGAGCT	0	S	0	0	0	0	0
8290	3754	ao	AN4028.1	54.m06555	AO070328000115	0					-111	-64	ATGGGTCATCTTATGCGTGGTTTATGCGGGAATCTTCACGGTGGTTAA			ATGGGTCATCTTATGCGTGGTTTATGCGGGAATCTTCACGGTGGTTAA	MGHLMRGLCGNLHGG*			MGHLMRGLCGNLHGG*	GTTCGCGCGC	AGGGTGACAA	0	S	0	0	0	0	0
8291	3754	ao	AN4028.1	54.m06555	AO070328000115	0					-99	-64	ATGCGTGGTTTATGCGGGAATCTTCACGGTGGTTAA			ATGCGTGGTTTATGCGGGAATCTTCACGGTGGTTAA	MRGLCGNLHGG*			MRGLCGNLHGG*	GGGTCATCTT	AGGGTGACAA	0	S	0	0	0	0	0
8292	3754	ao	AN4028.1	54.m06555	AO070328000115	0					-88	-38	ATGCGGGAATCTTCACGGTGGTTAAAGGGTGACAAGAAAGGATCTGGTTGA			ATGCGGGAATCTTCACGGTGGTTAAAGGGTGACAAGAAAGGATCTGGTTGA	MRESSRWLKGDKKGSG*			MRESSRWLKGDKKGSG*	TGCGTGGTTT	TTTGAAACGG	0	S	0	0	0	0	0
8294	3755	af	AN3305.1	71.m15151	AO070329000026	0			-185	-150			ATGAGACAATTGCATTTGTGTGAAATCCTGCTCTAG		ATGAGACAATTGCATTTGTGTGAAATCCTGCTCTAG		MRQLHLCEILL*		MRQLHLCEILL*		ATTGTCCTAC	CGACATCTGA	0	Q	0	MG07443.1	NCU01107.1	0	0
8295	3755	af	AN3305.1	71.m15151	AO070329000026	0			-115	-92			ATGACGCTCAGCCAGTCCGACTAA		ATGACGCTCAGCCAGTCCGACTAA		MTLSQSD*		MTLSQSD*		TGATATCATC	TATAACCACC	0	Q	0	MG07443.1	NCU01107.1	0	0
8293	3755	an	AN3305.1	71.m15151	AO070329000026	0	-203	-162					ATGGTCAAGTTTCCACGTAAACATGACATCACGCCTGGCTAG	ATGGTCAAGTTTCCACGTAAACATGACATCACGCCTGGCTAG			MVKFPRKHDITPG*	MVKFPRKHDITPG*			GTGCAATATA	GTCGGCAACC	0	Q	0	MG07443.1	NCU01107.1	0	0
8296	3755	ao	AN3305.1	71.m15151	AO070329000026	0					-124	-110	ATGACATCAACTTGA			ATGACATCAACTTGA	MTST*			MTST*	GCGTCATAGG	GCACATAGGG	0	Q	0	MG07443.1	NCU01107.1	0	0
8299	3757	af	AN1136.1	70.m15101	AO070331000127	0			-153	-16			ATGCTTGCCATGCCAAAATACCCGGGGCGGTTACTCACGGGTTTCTGTGAGCCTGACATCCCAGTTCCGTTGGCTTGCGATCTCTCTTCACTCATCCGTCTACCCTCCCAATCTGCATACACAATTCATACTTCATAG		ATGCTTGCCATGCCAAAATACCCGGGGCGGTTACTCACGGGTTTCTGTGAGCCTGACATCCCAGTTCCGTTGGCTTGCGATCTCTCTTCACTCATCCGTCTACCCTCCCAATCTGCATACACAATTCATACTTCATAG		MLAMPKYPGRLLTGFCEPDIPVPLACDLSSLIRLPSQSAYTIHTS*		MLAMPKYPGRLLTGFCEPDIPVPLACDLSSLIRLPSQSAYTIHTS*		CCGTAGTAGG	AAGAGCTTCA	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8300	3757	af	AN1136.1	70.m15101	AO070331000127	0			-144	-16			ATGCCAAAATACCCGGGGCGGTTACTCACGGGTTTCTGTGAGCCTGACATCCCAGTTCCGTTGGCTTGCGATCTCTCTTCACTCATCCGTCTACCCTCCCAATCTGCATACACAATTCATACTTCATAG		ATGCCAAAATACCCGGGGCGGTTACTCACGGGTTTCTGTGAGCCTGACATCCCAGTTCCGTTGGCTTGCGATCTCTCTTCACTCATCCGTCTACCCTCCCAATCTGCATACACAATTCATACTTCATAG		MPKYPGRLLTGFCEPDIPVPLACDLSSLIRLPSQSAYTIHTS*		MPKYPGRLLTGFCEPDIPVPLACDLSSLIRLPSQSAYTIHTS*		GATGCTTGCC	AAGAGCTTCA	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8297	3757	an	AN1136.1	70.m15101	AO070331000127	0	-110	-72					ATGATCTCCACTCCACCTCATCATGAACCTCCCTCTTGA	ATGATCTCCACTCCACCTCATCATGAACCTCCCTCTTGA			MISTPPHHEPPS*	MISTPPHHEPPS*			GGCCTGCTGG	CTCTTTCCCC	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8298	3757	an	AN1136.1	70.m15101	AO070331000127	0	-88	-23					ATGAACCTCCCTCTTGACTCTTTCCCCTCTCTCTTCCACTCCTCCTCCCCTTCCTCCTCACCATAA	ATGAACCTCCCTCTTGACTCTTTCCCCTCTCTCTTCCACTCCTCCTCCCCTTCCTCCTCACCATAA			MNLPLDSFPSLFHSSSPSSP*	MNLPLDSFPSLFHSSSPSSP*			CCACCTCATC	TAGAATACAC	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8301	3757	ao	AN1136.1	70.m15101	AO070331000127	0					-275	-162	ATGCATGTACCCCATCCAGATAGCCACCCACGTGAGGAGTCAAGCAATGTGGAGCCCGTCGATAGTCAATTTTATCGGTTACTCACGGTCGCTGGAGATAACCTGCACTCATAA			ATGCATGTACCCCATCCAGATAGCCACCCACGTGAGGAGTCAAGCAATGTGGAGCCCGTCGATAGTCAATTTTATCGGTTACTCACGGTCGCTGGAGATAACCTGCACTCATAA	MHVPHPDSHPREESSNVEPVDSQFYRLLTVAGDNLHS*			MHVPHPDSHPREESSNVEPVDSQFYRLLTVAGDNLHS*	TGGTAGGTTC	ACCTCGACTG	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8302	3757	ao	AN1136.1	70.m15101	AO070331000127	0					-147	-127	ATGAGGAGTCTGTCATCTTGA			ATGAGGAGTCTGTCATCTTGA	MRSLSS*			MRSLSS*	CGACTGGTCC	ATATTCTACG	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8303	3757	ao	AN1136.1	70.m15101	AO070331000127	0					-110	-42	ATGTTTCAAGAGTACATGCTCAAGAGAACACAACCAAACCAGAAGCTTGAAGCACAGCCCTCACGATAG			ATGTTTCAAGAGTACATGCTCAAGAGAACACAACCAAACCAGAAGCTTGAAGCACAGCCCTCACGATAG	MFQEYMLKRTQPNQKLEAQPSR*			MFQEYMLKRTQPNQKLEAQPSR*	TACGTCGTCC	CCATTTGAAA	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8304	3757	ao	AN1136.1	70.m15101	AO070331000127	0					-95	-42	ATGCTCAAGAGAACACAACCAAACCAGAAGCTTGAAGCACAGCCCTCACGATAG			ATGCTCAAGAGAACACAACCAAACCAGAAGCTTGAAGCACAGCCCTCACGATAG	MLKRTQPNQKLEAQPSR*			MLKRTQPNQKLEAQPSR*	TCAAGAGTAC	CCATTTGAAA	0	G	FG05701.1	0	NCU06022.1	YDR287W	0
8306	3759	af	AN0013.1	69.m15595	AO070333000040	0			-211	-173			ATGCTTTGGTCTCCAGAATGCGGGGTTGATACCGGCTGA		ATGCTTTGGTCTCCAGAATGCGGGGTTGATACCGGCTGA		MLWSPECGVDTG*		MLWSPECGVDTG*		TTATTTCCCC	ATGGACCTGT	0	R	0	0	0	0	0
8307	3759	af	AN0013.1	69.m15595	AO070333000040	0			-194	-183			ATGCGGGGTTGA		ATGCGGGGTTGA		MRG*		MRG*		GGTCTCCAGA	TACCGGCTGA	0	R	0	0	0	0	0
8308	3759	af	AN0013.1	69.m15595	AO070333000040	0			-172	-26			ATGGACCTGTATAACCGGTCAGTTGATGGGAGTCTTGGACAGAGTTGTTATGGTGCTCCTGATGCTATAGAAAGGGCCATGTTCAGGTTTCTCGAGTCTGGCTACTCTTCCTCCACACAGTTGACTGTGTCTGTTAACCGCACTTGA		ATGGACCTGTATAACCGGTCAGTTGATGGGAGTCTTGGACAGAGTTGTTATGGTGCTCCTGATGCTATAGAAAGGGCCATGTTCAGGTTTCTCGAGTCTGGCTACTCTTCCTCCACACAGTTGACTGTGTCTGTTAACCGCACTTGA		MDLYNRSVDGSLGQSCYGAPDAIERAMFRFLESGYSSSTQLTVSVNRT*		MDLYNRSVDGSLGQSCYGAPDAIERAMFRFLESGYSSSTQLTVSVNRT*		TACCGGCTGA	ACGGGAAAGA	0	R	0	0	0	0	0
8309	3759	af	AN0013.1	69.m15595	AO070333000040	0			-147	-103			ATGGGAGTCTTGGACAGAGTTGTTATGGTGCTCCTGATGCTATAG		ATGGGAGTCTTGGACAGAGTTGTTATGGTGCTCCTGATGCTATAG		MGVLDRVVMVLLML*		MGVLDRVVMVLLML*		CGGTCAGTTG	AAAGGGCCAT	0	R	0	0	0	0	0
8310	3759	af	AN0013.1	69.m15595	AO070333000040	0			-123	-103			ATGGTGCTCCTGATGCTATAG		ATGGTGCTCCTGATGCTATAG		MVLLML*		MVLLML*		CAGAGTTGTT	AAAGGGCCAT	0	R	0	0	0	0	0

8311	3759	af	AN0013.1	69.m15595	AO070333000040	0			-94	-26			ATGTTCAGGTTTCTCGAGTCTGGCTACTCTTCCTCCACACAGTTGACTGTGTCTGTTAACCGCACTTGA		ATGTTCAGGTTTCTCGAGTCTGGCTACTCTTCCTCCACACAGTTGACTGTGTCTGTTAACCGCACTTGA		MFRFLESGYSSSTQLTVSVNRT*		MFRFLESGYSSSTQLTVSVNRT*		AGAAAGGGCC	ACGGGAAAGA	0	R	0	0	0	0	0
8305	3759	an	AN0013.1	69.m15595	AO070333000040	0	-140	-117					ATGCTCCCCGCGCTGTGTATATAG	ATGCTCCCCGCGCTGTGTATATAG			MLPALCI*	MLPALCI*			TATAGCCTAA	GTTGTTCAAT	0	R	0	0	0	0	0
8312	3759	ao	AN0013.1	69.m15595	AO070333000040	0					-256	-236	ATGCCAACACTGAATGGGTGA			ATGCCAACACTGAATGGGTGA	MPTLNG*			MPTLNG*	AGCTCAACTA	CAACATCTCG	0	R	0	0	0	0	0
8313	3759	ao	AN0013.1	69.m15595	AO070333000040	0					-243	-151	ATGGGTGACAACATCTCGTGGGAAGCCCGGTTGGGGACAATGGAACCGGGAGTCCACCCAGCCGCCATCTGTACGAAGGATTGTGGTTGTTAA			ATGGGTGACAACATCTCGTGGGAAGCCCGGTTGGGGACAATGGAACCGGGAGTCCACCCAGCCGCCATCTGTACGAAGGATTGTGGTTGTTAA	MGDNISWEARLGTMEPGVHPAAICTKDCGC*			MGDNISWEARLGTMEPGVHPAAICTKDCGC*	CCAACACTGA	GCTCATTTCT	0	R	0	0	0	0	0
8314	3759	ao	AN0013.1	69.m15595	AO070333000040	0					-204	-151	ATGGAACCGGGAGTCCACCCAGCCGCCATCTGTACGAAGGATTGTGGTTGTTAA			ATGGAACCGGGAGTCCACCCAGCCGCCATCTGTACGAAGGATTGTGGTTGTTAA	MEPGVHPAAICTKDCGC*			MEPGVHPAAICTKDCGC*	GTTGGGGACA	GCTCATTTCT	0	R	0	0	0	0	0
8317	3762	af	AN2927.1	59.m09068	AO070337000182	0			-258	-205			ATGATGAGTATTTGTTGCTCTCTGATCGCCCCGGCAACGAACATTGTCAGGTGA		ATGATGAGTATTTGTTGCTCTCTGATCGCCCCGGCAACGAACATTGTCAGGTGA		MMSICCSLIAPATNIVR*		MMSICCSLIAPATNIVR*		CATCCATTTC	CTTTCCTCCG	0	D	0	0	0	0	0
8318	3762	af	AN2927.1	59.m09068	AO070337000182	0			-255	-205			ATGAGTATTTGTTGCTCTCTGATCGCCCCGGCAACGAACATTGTCAGGTGA		ATGAGTATTTGTTGCTCTCTGATCGCCCCGGCAACGAACATTGTCAGGTGA		MSICCSLIAPATNIVR*		MSICCSLIAPATNIVR*		CCATTTCATG	CTTTCCTCCG	0	D	0	0	0	0	0
8319	3762	af	AN2927.1	59.m09068	AO070337000182	0			-176	-21			ATGTTTGTCATGATCCAGGAACCAGAACAACAGCATCAACTCCGGCAGACGACACAACAAACACGATACGACACGCCCCCGCCATTGGGGCATCCGATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		ATGTTTGTCATGATCCAGGAACCAGAACAACAGCATCAACTCCGGCAGACGACACAACAAACACGATACGACACGCCCCCGCCATTGGGGCATCCGATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		MFVMIQEPEQQHQLRQTTQQTRYDTPPPLGHPMIFGNLGRAHWLTRPCRIY*		MFVMIQEPEQQHQLRQTTQQTRYDTPPPLGHPMIFGNLGRAHWLTRPCRIY*		GCCACCCGTG	TTGGGCTGAG	0	D	0	0	0	0	0
8320	3762	af	AN2927.1	59.m09068	AO070337000182	0			-167	-21			ATGATCCAGGAACCAGAACAACAGCATCAACTCCGGCAGACGACACAACAAACACGATACGACACGCCCCCGCCATTGGGGCATCCGATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		ATGATCCAGGAACCAGAACAACAGCATCAACTCCGGCAGACGACACAACAAACACGATACGACACGCCCCCGCCATTGGGGCATCCGATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		MIQEPEQQHQLRQTTQQTRYDTPPPLGHPMIFGNLGRAHWLTRPCRIY*		MIQEPEQQHQLRQTTQQTRYDTPPPLGHPMIFGNLGRAHWLTRPCRIY*		GATGTTTGTC	TTGGGCTGAG	0	D	0	0	0	0	0
8321	3762	af	AN2927.1	59.m09068	AO070337000182	0			-80	-21			ATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		ATGATTTTTGGGAATTTGGGACGGGCGCATTGGTTGACACGTCCATGTAGGATTTATTGA		MIFGNLGRAHWLTRPCRIY*		MIFGNLGRAHWLTRPCRIY*		GGGGCATCCG	TTGGGCTGAG	0	D	0	0	0	0	0
8315	3762	an	AN2927.1	59.m09068	AO070337000182	0	-236	-183					ATGCTTTGTTTACATCATACGATTGCCCCTCGCAACCATCACGTGTGGGGCTAG	ATGCTTTGTTTACATCATACGATTGCCCCTCGCAACCATCACGTGTGGGGCTAG			MLCLHHTIAPRNHHVWG*	MLCLHHTIAPRNHHVWG*			TTGCTCAAAA	TCCCAACCAG	0	D	0	0	0	0	0
8322	3762	ao	AN2927.1	59.m09068	AO070337000182	0					-236	-174	ATGAACGCCATGCTTTGTTGTCATCACACCATTGCCGTGGCAACAACCAATCACGTGATATGA			ATGAACGCCATGCTTTGTTGTCATCACACCATTGCCGTGGCAACAACCAATCACGTGATATGA	MNAMLCCHHTIAVATTNHVI*			MNAMLCCHHTIAVATTNHVI*	ACTGCAGCAA	TATCCGCTCC	0	D	0	0	0	0	0
8323	3762	ao	AN2927.1	59.m09068	AO070337000182	0					-227	-174	ATGCTTTGTTGTCATCACACCATTGCCGTGGCAACAACCAATCACGTGATATGA			ATGCTTTGTTGTCATCACACCATTGCCGTGGCAACAACCAATCACGTGATATGA	MLCCHHTIAVATTNHVI*			MLCCHHTIAVATTNHVI*	AATGAACGCC	TATCCGCTCC	0	D	0	0	0	0	0
8324	3762	ao	AN2927.1	59.m09068	AO070337000182	0					-177	-127	ATGATATCCGCTCCCAGCCTCCCCGTAACGTTGTTTCTTCGAGTACGTTGA			ATGATATCCGCTCCCAGCCTCCCCGTAACGTTGTTTCTTCGAGTACGTTGA	MISAPSLPVTLFLRVR*			MISAPSLPVTLFLRVR*	ATCACGTGAT	TCCCGACCGG	0	D	0	0	0	0	0
8327	3763	af	AN3797.1	57.m05686	AO070337000231	0			-236	-132			ATGATACCCACTTTGTTCGCGAAGAAATACTTCAAAAATATGTTCTCAGGGGTATTATTAAGATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAG		ATGATACCCACTTTGTTCGCGAAGAAATACTTCAAAAATATGTTCTCAGGGGTATTATTAAGATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAG		MIPTLFAKKYFKNMFSGVLLRCHQLFRCISQCHS*		MIPTLFAKKYFKNMFSGVLLRCHQLFRCISQCHS*		TTCCAAAGTT	AACCAACAGA	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8328	3763	af	AN3797.1	57.m05686	AO070337000231	0			-197	-132			ATGTTCTCAGGGGTATTATTAAGATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAG		ATGTTCTCAGGGGTATTATTAAGATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAG		MFSGVLLRCHQLFRCISQCHS*		MFSGVLLRCHQLFRCISQCHS*		CTTCAAAAAT	AACCAACAGA	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8329	3763	af	AN3797.1	57.m05686	AO070337000231	0			-174	-46			ATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAGAACCAACAGACTCCTGTGTTTGCCATTTTGCACATAATAGGTCACATGATTTCGTGTCGCAGCGTGTCGACGCCTGTCGGGGATGA		ATGTCATCAACTATTTCGTTGTATATCGCAATGTCACTCGTAGAACCAACAGACTCCTGTGTTTGCCATTTTGCACATAATAGGTCACATGATTTCGTGTCGCAGCGTGTCGACGCCTGTCGGGGATGA		MSSTISLYIAMSLVEPTDSCVCHFAHNRSHDFVSQRVDACRG*		MSSTISLYIAMSLVEPTDSCVCHFAHNRSHDFVSQRVDACRG*		TATTATTAAG	AGTGCATGTA	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8330	3763	af	AN3797.1	57.m05686	AO070337000231	0			-144	-46			ATGTCACTCGTAGAACCAACAGACTCCTGTGTTTGCCATTTTGCACATAATAGGTCACATGATTTCGTGTCGCAGCGTGTCGACGCCTGTCGGGGATGA		ATGTCACTCGTAGAACCAACAGACTCCTGTGTTTGCCATTTTGCACATAATAGGTCACATGATTTCGTGTCGCAGCGTGTCGACGCCTGTCGGGGATGA		MSLVEPTDSCVCHFAHNRSHDFVSQRVDACRG*		MSLVEPTDSCVCHFAHNRSHDFVSQRVDACRG*		GTATATCGCA	AGTGCATGTA	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8326	3763	an	AN3797.1	57.m05686	AO070337000231	0	-88	-68					ATGAATCACGTGACTTCGTGA	ATGAATCACGTGACTTCGTGA			MNHVTS*	MNHVTS*			AAAGTGTAAG	TATAGCGCGT	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8332	3763	ao	AN3797.1	57.m05686	AO070337000231	0					-85	-71	ATGACCACGCGATAA			ATGACCACGCGATAA	MTTR*			MTTR*	ATCCAATCAC	GAGCGCGTCA	0	L	FG08405.1	MG00630.1	NCU04733.1	0	0
8335	3765	af	AN0244.1	54.m06697	AO070338000236	0			-246	-223			ATGGAGTTTGCGGTCTACCATTGA		ATGGAGTTTGCGGTCTACCATTGA		MEFAVYH*		MEFAVYH*		ATAGGTATAC	TACCAACATC	0	U	0	0	0	0	0
8334	3765	an	AN0244.1	54.m06697	AO070338000236	0	-240	-28					ATGCGATCATTCTTTTGGGCGCCGGCGGACCTTCTTCATCTGACATTGTCGCCTTGCTTTAGAACTAGGCACCGCTCTTTACTCGACATTAACCGCCCGACTTCTCTCAGAGAACCGCCCGTCCCCGGTCTACAGTCCATTCGAGCTCAAAGCTCAAGATACGCCTCCGGCGCCAGCGCATCTTCCCTTCCGCCTTGCTGCGCACGCACTTGA	ATGCGATCATTCTTTTGGGCGCCGGCGGACCTTCTTCATCTGACATTGTCGCCTTGCTTTAGAACTAGGCACCGCTCTTTACTCGACATTAACCGCCCGACTTCTCTCAGAGAACCGCCCGTCCCCGGTCTACAGTCCATTCGAGCTCAAAGCTCAAGATACGCCTCCGGCGCCAGCGCATCTTCCCTTCCGCCTTGCTGCGCACGCACTTGA			MRSFFWAPADLLHLTLSPCFRTRHRSLLDINRPTSLREPPVPGLQSIRAQSSRYASGASASSLPPCCART*	MRSFFWAPADLLHLTLSPCFRTRHRSLLDINRPTSLREPPVPGLQSIRAQSSRYASGASASSLPPCCART*			TCTCGCTTAG	AGAAATGAAC	0	U	0	0	0	0	0
8337	3768	af	AN2088.1	57.m05790	AO070341000246	0			-282	-187			ATGAGGATGGATCAAGAAGCGCCCTCCAGATGTAGCAATGAAGAGATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		ATGAGGATGGATCAAGAAGCGCCCTCCAGATGTAGCAATGAAGAGATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		MRMDQEAPSRCSNEEMMLQEEVKQAGGTGSG*		MRMDQEAPSRCSNEEMMLQEEVKQAGGTGSG*		TTAGATAGAG	GCTAGATAGG	0	S	FG01054.1	0	0	0	0
8338	3768	af	AN2088.1	57.m05790	AO070341000246	0			-276	-187			ATGGATCAAGAAGCGCCCTCCAGATGTAGCAATGAAGAGATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		ATGGATCAAGAAGCGCCCTCCAGATGTAGCAATGAAGAGATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		MDQEAPSRCSNEEMMLQEEVKQAGGTGSG*		MDQEAPSRCSNEEMMLQEEVKQAGGTGSG*		AGAGATGAGG	GCTAGATAGG	0	S	FG01054.1	0	0	0	0
8339	3768	af	AN2088.1	57.m05790	AO070341000246	0			-245	-234			ATGAAGAGATGA		ATGAAGAGATGA		MKR*		MKR*		AGATGTAGCA	TGTTGCAAGA	0	S	FG01054.1	0	0	0	0
8340	3768	af	AN2088.1	57.m05790	AO070341000246	0			-237	-187			ATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		ATGATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		MMLQEEVKQAGGTGSG*		MMLQEEVKQAGGTGSG*		CAATGAAGAG	GCTAGATAGG	0	S	FG01054.1	0	0	0	0
8341	3768	af	AN2088.1	57.m05790	AO070341000246	0			-234	-187			ATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		ATGTTGCAAGAAGAGGTGAAACAAGCTGGCGGCACGGGATCAGGCTAG		MLQEEVKQAGGTGSG*		MLQEEVKQAGGTGSG*		TGAAGAGATG	GCTAGATAGG	0	S	FG01054.1	0	0	0	0
8342	3768	af	AN2088.1	57.m05790	AO070341000246	0			-133	-119			ATGGATGACAATTAA		ATGGATGACAATTAA		MDDN*		MDDN*		GCATCGTGAT	CATCATAAAC	0	S	FG01054.1	0	0	0	0
8343	3768	af	AN2088.1	57.m05790	AO070341000246	0			-129	-73			ATGACAATTAACATCATAAACACTCTTCGTTCAGTTGCTGTGACTCCTGACGCGTAA		ATGACAATTAACATCATAAACACTCTTCGTTCAGTTGCTGTGACTCCTGACGCGTAA		MTINIINTLRSVAVTPDA*		MTINIINTLRSVAVTPDA*		CGTGATATGG	GGGGATCTGG	0	S	FG01054.1	0	0	0	0
8344	3768	ao	AN2088.1	57.m05790	AO070341000246	0					-291	-280	ATGTCGCGGTGA			ATGTCGCGGTGA	MSR*			MSR*	GGAAGTCGCG	AGAGATGAGG	0	S	FG01054.1	0	0	0	0
8345	3768	ao	AN2088.1	57.m05790	AO070341000246	0					-275	-255	ATGAGGTTAAGGTGTGATTGA			ATGAGGTTAAGGTGTGATTGA	MRLRCD*			MRLRCD*	CGGTGAAGAG	GGCGAAACGG	0	S	FG01054.1	0	0	0	0
8346	3770	af	AN3730.1	69.m15387	AO070342000284	0			-218	-186			ATGTTATTTGTTGATACCACTGCCGTTCGTTGA		ATGTTATTTGTTGATACCACTGCCGTTCGTTGA		MLFVDTTAVR*		MLFVDTTAVR*		TCTTTCCTTC	AATCTTCTTC	0		0	0	0	0	0
8347	3770	ao	AN3730.1	69.m15387	AO070342000284	0					-185	-54	ATGGTCCCTCGCTTGCTGTCTTTTCTAAGCATTAATATCTTGGTTTCAAATATCTATTCCCGTCATTCATTATTCAAACTATTCATCTTTGGCCTTGGTAGTACAAGTGGAATTCTATCTCCAAACTTTTGA			ATGGTCCCTCGCTTGCTGTCTTTTCTAAGCATTAATATCTTGGTTTCAAATATCTATTCCCGTCATTCATTATTCAAACTATTCATCTTTGGCCTTGGTAGTACAAGTGGAATTCTATCTCCAAACTTTTGA	MVPRLLSFLSINILVSNIYSRHSLFKLFIFGLGSTSGILSPNF*			MVPRLLSFLSINILVSNIYSRHSLFKLFIFGLGSTSGILSPNF*	TTCCTTGTCC	GTGTCTGGCA	0		0	0	0	0	0
8349	3773	af	AN2147.1	72.m19694	AO070343000196	0			-169	-74			ATGGGGTTGTACTTGATACGGAAGGCGGTCTGCCGACATAGATCCAGAAATTTTTTGTATCCGCTATTTTTTTGTGAACCGGTTCCGATTAGCTAG		ATGGGGTTGTACTTGATACGGAAGGCGGTCTGCCGACATAGATCCAGAAATTTTTTGTATCCGCTATTTTTTTGTGAACCGGTTCCGATTAGCTAG		MGLYLIRKAVCRHRSRNFLYPLFFCEPVPIS*		MGLYLIRKAVCRHRSRNFLYPLFFCEPVPIS*		AATTAAAGTG	CTGGTCTGAA	0	A	0	0	0	0	0
8348	3773	an	AN2147.1	72.m19694	AO070343000196	0	-178	-164					ATGGGTAGGCGGTGA	ATGGGTAGGCGGTGA			MGRR*	MGRR*			AATTTCCAGC	GACTTTCACT	0	A	0	0	0	0	0
8352	3774	af	AN7609.1	72.m19650	AO070343000267	0			-123	-97			ATGAATCCGCGCTTTACTTGCCATTAA		ATGAATCCGCGCTTTACTTGCCATTAA		MNPRFTCH*		MNPRFTCH*		CCCGTTTCCA	TCATATACTC	0	KL	0	0	0	0	0
8350	3774	an	AN7609.1	72.m19650	AO070343000267	0	-209	-168					ATGTTGGGAAAGGCTGCAGGGCGTCTTGTCAGTCTGGATTGA	ATGTTGGGAAAGGCTGCAGGGCGTCTTGTCAGTCTGGATTGA			MLGKAAGRLVSLD*	MLGKAAGRLVSLD*			GCCAGTGCGC	CAATATCCCA	0	KL	0	0	0	0	0
8351	3774	an	AN7609.1	72.m19650	AO070343000267	0	-92	-42					ATGCTTTACTTTCTTGCCTCCGCTTTATCTCCATTTATCTCTTATTTTTAA	ATGCTTTACTTTCTTGCCTCCGCTTTATCTCCATTTATCTCTTATTTTTAA			MLYFLASALSPFISYF*	MLYFLASALSPFISYF*			TCGCATATAA	TCGTGACTGT	0	KL	0	0	0	0	0
8353	3774	ao	AN7609.1	72.m19650	AO070343000267	0					-112	-92	ATGAATTTTGTTCTTGCATAA			ATGAATTTTGTTCTTGCATAA	MNFVLA*			MNFVLA*	TCGCATACTA	TTTTTGCCTT	0	KL	0	0	0	0	0
8355	3775	af	AN3778.1	72.m19643	AO070343000274	0			-222	-118			ATGGACAATCAATGGGGGATTCCCTATCGTCCATTTGTTCGTACTTCCGCGGAGCGCGGTCCTTCTATCACGAAGTCGACTGTGAAACCGCTCCCCGCTATCTGA		ATGGACAATCAATGGGGGATTCCCTATCGTCCATTTGTTCGTACTTCCGCGGAGCGCGGTCCTTCTATCACGAAGTCGACTGTGAAACCGCTCCCCGCTATCTGA		MDNQWGIPYRPFVRTSAERGPSITKSTVKPLPAI*		MDNQWGIPYRPFVRTSAERGPSITKSTVKPLPAI*		CTTTGTAAAT	AGCTTTGTGA	0	H	FG05299.1	MG06109.1	NCU09746.1	0	0
8356	3775	af	AN3778.1	72.m19643	AO070343000274	0			-211	-62			ATGGGGGATTCCCTATCGTCCATTTGTTCGTACTTCCGCGGAGCGCGGTCCTTCTATCACGAAGTCGACTGTGAAACCGCTCCCCGCTATCTGAAGCTTTGTGATATATCTCCGATCCCGCTTATCGAGCTACCTTCCTTAAGAGCGTAA		ATGGGGGATTCCCTATCGTCCATTTGTTCGTACTTCCGCGGAGCGCGGTCCTTCTATCACGAAGTCGACTGTGAAACCGCTCCCCGCTATCTGAAGCTTTGTGATATATCTCCGATCCCGCTTATCGAGCTACCTTCCTTAAGAGCGTAA		MGDSLSSICSYFRGARSFYHEVDCETAPRYLKLCDISPIPLIELPSLRA*		MGDSLSSICSYFRGARSFYHEVDCETAPRYLKLCDISPIPLIELPSLRA*		TGGACAATCA	CGGATCCCCG	0	H	FG05299.1	MG06109.1	NCU09746.1	0	0
8354	3775	an	AN3778.1	72.m19643	AO070343000274	0	-168	-112					ATGGATGTTTTTCGTGATGGTTGTCGAGGAAAGAACTTACAGAAATTTTGTGCCTGA	ATGGATGTTTTTCGTGATGGTTGTCGAGGAAAGAACTTACAGAAATTTTGTGCCTGA			MDVFRDGCRGKNLQKFCA*	MDVFRDGCRGKNLQKFCA*			CGGTCCGTTA	GGTGTCAATG	0	H	FG05299.1	MG06109.1	NCU09746.1	0	0
8357	3775	ao	AN3778.1	72.m19643	AO070343000274	0					-218	-147	ATGTATAGCATTGATTTAAATTTCACATTGTTGTATTTAAGGGTTTATAGGAAATTAGCGATCGTTATATAA			ATGTATAGCATTGATTTAAATTTCACATTGTTGTATTTAAGGGTTTATAGGAAATTAGCGATCGTTATATAA	MYSIDLNFTLLYLRVYRKLAIVI*			MYSIDLNFTLLYLRVYRKLAIVI*	GCGCACTCTT	TTGACATTGA	0	H	FG05299.1	MG06109.1	NCU09746.1	0	0
8358	3778	an	AN5449.1	69.m15483	AO070239000028	0	-175	-164					ATGATCTTGTGA	ATGATCTTGTGA			MIL*	MIL*			TCCTGGATCC	CATTGGATGT	0	P	0	0	0	0	0
8359	3781	af	AN4617.1	57.m05535	AO070267000034	0			-152	-93			ATGTCACGTGCTGATAGTCTGATAATGCGGGCATTCTTTCGCATGAATTTCATGTTCTAG		ATGTCACGTGCTGATAGTCTGATAATGCGGGCATTCTTTCGCATGAATTTCATGTTCTAG		MSRADSLIMRAFFRMNFMF*		MSRADSLIMRAFFRMNFMF*		CAAGGCTGTA	TTCAAGTCAT	0	J	0	0	0	0	0
8360	3781	af	AN4617.1	57.m05535	AO070267000034	0			-128	-93			ATGCGGGCATTCTTTCGCATGAATTTCATGTTCTAG		ATGCGGGCATTCTTTCGCATGAATTTCATGTTCTAG		MRAFFRMNFMF*		MRAFFRMNFMF*		TAGTCTGATA	TTCAAGTCAT	0	J	0	0	0	0	0
8361	3781	af	AN4617.1	57.m05535	AO070267000034	0			-110	-93			ATGAATTTCATGTTCTAG		ATGAATTTCATGTTCTAG		MNFMF*		MNFMF*		ATTCTTTCGC	TTCAAGTCAT	0	J	0	0	0	0	0
8362	3781	ao	AN4617.1	57.m05535	AO070267000034	0					-241	-170	ATGGTTAATATAGATCTTAAAGTTATATTACTGAGTTATCTATACGTAACCACCAGTACTACCATTGCCTAG			ATGGTTAATATAGATCTTAAAGTTATATTACTGAGTTATCTATACGTAACCACCAGTACTACCATTGCCTAG	MVNIDLKVILLSYLYVTTSTTIA*			MVNIDLKVILLSYLYVTTSTTIA*	GCTCTCAAGC	TCCACTGATA	0	J	0	0	0	0	0
8363	3781	ao	AN4617.1	57.m05535	AO070267000034	0					-157	-131	ATGGCGCAGAAACAATCTCTCACGTGA			ATGGCGCAGAAACAATCTCTCACGTGA	MAQKQSLT*			MAQKQSLT*	CACTGATATA	AGATAGCCGA	0	J	0	0	0	0	0
8367	3782	af	AN8836.1	71.m15967	AO070271000042	0			-70	-14			ATGCAGTGCATATCCTTCTTGGGGTTTGATTGGTCTCAATTCCAGAACTTTGACTGA		ATGCAGTGCATATCCTTCTTGGGGTTTGATTGGTCTCAATTCCAGAACTTTGACTGA		MQCISFLGFDWSQFQNFD*		MQCISFLGFDWSQFQNFD*		TCATCTGACC	CCTCTGTCGC	0	T	0	0	0	0	0
8364	3782	an	AN8836.1	71.m15967	AO070271000042	0	-116	-105					ATGTCAGCATAA	ATGTCAGCATAA			MSA*	MSA*			TACGAAAAGT	GTCCCACGTT	0	T	0	0	0	0	0
8368	3782	ao	AN8836.1	71.m15967	AO070271000042	0					-149	-105	ATGGAAAGTAAGCCGGTGTTGCTTTTCTTTATCACTACTGCCTAG			ATGGAAAGTAAGCCGGTGTTGCTTTTCTTTATCACTACTGCCTAG	MESKPVLLFFITTA*			MESKPVLLFFITTA*	ATCTCAACTT	CAGTCATTTG	0	T	0	0	0	0	0

8369	3782	ao	AN8836.1	71.m15967	AO070271000042	0					-71	-24	ATGGCTTTGTCCCTATTCTTACATCCAAAGGGGTACTGGGACCTTTGA			ATGGCTTTGTCCCTATTCTTACATCCAAAGGGGTACTGGGACCTTTGA	MALSLFLHPKGYWDL*			MALSLFLHPKGYWDL*	GTGTATACTG	AAGGTAACTG	0	T	0	0	0	0	0
8371	3784	af	AN4265.1	65.m07442	AO070277000020	0			-120	-103			ATGAAGCACAGCTTTTGA		ATGAAGCACAGCTTTTGA		MKHSF*		MKHSF*		ACATCAAAAA	GATTGCTATT	0	BD	0	MG01639.1	NCU02828.1	0	0
8370	3784	an	AN4265.1	65.m07442	AO070277000020	0	-161	-135					ATGCTCTCAAGGCAAGATTGCCGCTGA	ATGCTCTCAAGGCAAGATTGCCGCTGA			MLSRQDCR*	MLSRQDCR*			CCCCAAAACC	TATATCGCGC	0	BD	0	MG01639.1	NCU02828.1	0	0
8372	3784	ao	AN4265.1	65.m07442	AO070277000020	0					-230	-114	ATGTTTTTGTTGACTCGCATTTGTTTGTTCTGGTCGGCCAAAGAGAGAAACTTTGCTGTATTTCCGCACATCGTGACGGGATTCAGTACGCAGCAGGTTATCATCTACAGAGGATGA			ATGTTTTTGTTGACTCGCATTTGTTTGTTCTGGTCGGCCAAAGAGAGAAACTTTGCTGTATTTCCGCACATCGTGACGGGATTCAGTACGCAGCAGGTTATCATCTACAGAGGATGA	MFLLTRICLFWSAKERNFAVFPHIVTGFSTQQVIIYRG*			MFLLTRICLFWSAKERNFAVFPHIVTGFSTQQVIIYRG*	AGTATGGCGT	GTATCTTAAA	0	BD	0	MG01639.1	NCU02828.1	0	0
8373	3784	ao	AN4265.1	65.m07442	AO070277000020	0					-117	-79	ATGAGTATCTTAAACTGTGGCTGCTTCATTGTCACTTAA			ATGAGTATCTTAAACTGTGGCTGCTTCATTGTCACTTAA	MSILNCGCFIVT*			MSILNCGCFIVT*	TCTACAGAGG	TTATCATTTT	0	BD	0	MG01639.1	NCU02828.1	0	0
8375	3785	af	AN7550.1	72.m19567	AO070277000047	0			-237	-220			ATGTTTGGGAAGTGTTGA		ATGTTTGGGAAGTGTTGA		MFGKC*		MFGKC*		CTCGATATCA	TCGATGGAGA	0	R	0	0	0	0	0
8376	3785	af	AN7550.1	72.m19567	AO070277000047	0			-216	-169			ATGGAGATAAACAGTGGAGAGATGGGTAAAGGCGCTAATCTGTATTAG		ATGGAGATAAACAGTGGAGAGATGGGTAAAGGCGCTAATCTGTATTAG		MEINSGEMGKGANLY*		MEINSGEMGKGANLY*		GTGTTGATCG	GTAAGGCAAG	0	R	0	0	0	0	0
8377	3785	af	AN7550.1	72.m19567	AO070277000047	0			-195	-169			ATGGGTAAAGGCGCTAATCTGTATTAG		ATGGGTAAAGGCGCTAATCTGTATTAG		MGKGANLY*		MGKGANLY*		CAGTGGAGAG	GTAAGGCAAG	0	R	0	0	0	0	0
8378	3785	af	AN7550.1	72.m19567	AO070277000047	0			-135	-118			ATGGAGGAAGCCACTTGA		ATGGAGGAAGCCACTTGA		MEEAT*		MEEAT*		CGACATTATC	GGCGATGATT	0	R	0	0	0	0	0
8379	3785	af	AN7550.1	72.m19567	AO070277000047	0			-113	-63			ATGATTATCATCTATGGAGTACGGAGTATGCTGGTTGCCATCAACACTTGA		ATGATTATCATCTATGGAGTACGGAGTATGCTGGTTGCCATCAACACTTGA		MIIIYGVRSMLVAINT*		MIIIYGVRSMLVAINT*		ACTTGAGGCG	ATCCTCATTT	0	R	0	0	0	0	0
8380	3785	af	AN7550.1	72.m19567	AO070277000047	0			-86	-63			ATGCTGGTTGCCATCAACACTTGA		ATGCTGGTTGCCATCAACACTTGA		MLVAINT*		MLVAINT*		AGTACGGAGT	ATCCTCATTT	0	R	0	0	0	0	0
8374	3785	an	AN7550.1	72.m19567	AO070277000047	0	-174	-151					ATGGTTCAAAGTATACCCTGTTGA	ATGGTTCAAAGTATACCCTGTTGA			MVQSIPC*	MVQSIPC*			CACTTTGTGT	TTGAAGGAAT	0	R	0	0	0	0	0
8381	3786	an	AN0623.1	70.m15662	AO070280000074	0	-177	-49					ATGATCTACACTGCCTGCAGCCGTATATCAATTTTCCCTTCCTCCCACTTCGCTGGCTCCTCTCCCACAGGATTTTTCTATTTGCGAGGGGATCGCATTTCTATTCTTCTGCCCACTCTCGTTGGTTGA	ATGATCTACACTGCCTGCAGCCGTATATCAATTTTCCCTTCCTCCCACTTCGCTGGCTCCTCTCCCACAGGATTTTTCTATTTGCGAGGGGATCGCATTTCTATTCTTCTGCCCACTCTCGTTGGTTGA			MIYTACSRISIFPSSHFAGSSPTGFFYLRGDRISILLPTLVG*	MIYTACSRISIFPSSHFAGSSPTGFFYLRGDRISILLPTLVG*			CGCCCTGTTG	TTATCCTTAC	0	E	0	0	NCU08977.1	0	0
8382	3786	ao	AN0623.1	70.m15662	AO070280000074	0					-177	-157	ATGGCACGGAAGGCGCAGTGA			ATGGCACGGAAGGCGCAGTGA	MARKAQ*			MARKAQ*	GGTGAATCTT	CGCGGACCTG	0	E	0	0	NCU08977.1	0	0
8385	3790	af	AN8879.1	56.m02290	AO070293000008	0			-231	-97			ATGTATATGAAGGTGACGTGGATCACAGGGGCTGAACGAAAAGGGTCAGATAGAAGAAAATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGACTTGATTTAA		ATGTATATGAAGGTGACGTGGATCACAGGGGCTGAACGAAAAGGGTCAGATAGAAGAAAATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGACTTGATTTAA		MYMKVTWITGAERKGSDRRKCHVFSEVYLWLTLSSFTTITYDLI*		MYMKVTWITGAERKGSDRRKCHVFSEVYLWLTLSSFTTITYDLI*		TTGTGTCCTT	TGCTACCGCC	0	U	0	0	NCU09313.1	0	0
8386	3790	af	AN8879.1	56.m02290	AO070293000008	0			-225	-97			ATGAAGGTGACGTGGATCACAGGGGCTGAACGAAAAGGGTCAGATAGAAGAAAATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGACTTGATTTAA		ATGAAGGTGACGTGGATCACAGGGGCTGAACGAAAAGGGTCAGATAGAAGAAAATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGACTTGATTTAA		MKVTWITGAERKGSDRRKCHVFSEVYLWLTLSSFTTITYDLI*		MKVTWITGAERKGSDRRKCHVFSEVYLWLTLSSFTTITYDLI*		CCTTATGTAT	TGCTACCGCC	0	U	0	0	NCU09313.1	0	0
8387	3790	af	AN8879.1	56.m02290	AO070293000008	0			-172	-107			ATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGA		ATGCCATGTTTTTTCGGAAGTTTACCTTTGGCTGACTTTGTCATCTTTCACAACCATAACTTATGA		MPCFFGSLPLADFVIFHNHNL*		MPCFFGSLPLADFVIFHNHNL*		ATAGAAGAAA	CTTGATTTAA	0	U	0	0	NCU09313.1	0	0
8388	3790	af	AN8879.1	56.m02290	AO070293000008	0			-167	-138			ATGTTTTTTCGGAAGTTTACCTTTGGCTGA		ATGTTTTTTCGGAAGTTTACCTTTGGCTGA		MFFRKFTFG*		MFFRKFTFG*		AGAAAATGCC	CTTTGTCATC	0	U	0	0	NCU09313.1	0	0
8389	3790	af	AN8879.1	56.m02290	AO070293000008	0			-97	-71			ATGCTACCGCCAATTGATCTGATCTGA		ATGCTACCGCCAATTGATCTGATCTGA		MLPPIDLI*		MLPPIDLI*		ACTTGATTTA	TGGTCAATCG	0	U	0	0	NCU09313.1	0	0
8390	3790	af	AN8879.1	56.m02290	AO070293000008	0			-71	-3			ATGGTCAATCGCAACTCGTTATCTGCGGCCTTGCTGTTCCCTGTCGACGAGGATCACCCTATGTCGTGA		ATGGTCAATCGCAACTCGTTATCTGCGGCCTTGCTGTTCCCTGTCGACGAGGATCACCCTATGTCGTGA		MVNRNSLSAALLFPVDEDHPMS*		MVNRNSLSAALLFPVDEDHPMS*		ATCTGATCTG	AGATGTCGGA	0	U	0	0	NCU09313.1	0	0
8383	3790	an	AN8879.1	56.m02290	AO070293000008	0	-207	-76					ATGGAAGCGGCCCCACATCAGCTTGGAGCCTCGAACCGCGCGGTTTCTGGCCGGTGGTCAAACATCCTGATGGCGACCTCGTCACCTGGAGCTCGACCTTCCACCTTCACAGCCTACAACAATAACTATTGA	ATGGAAGCGGCCCCACATCAGCTTGGAGCCTCGAACCGCGCGGTTTCTGGCCGGTGGTCAAACATCCTGATGGCGACCTCGTCACCTGGAGCTCGACCTTCCACCTTCACAGCCTACAACAATAACTATTGA			MEAAPHQLGASNRAVSGRWSNILMATSSPGARPSTFTAYNNNY*	MEAAPHQLGASNRAVSGRWSNILMATSSPGARPSTFTAYNNNY*			CATTCTTTAC	GTTTTTTTGC	0	U	0	0	NCU09313.1	0	0
8384	3790	an	AN8879.1	56.m02290	AO070293000008	0	-138	-76					ATGGCGACCTCGTCACCTGGAGCTCGACCTTCCACCTTCACAGCCTACAACAATAACTATTGA	ATGGCGACCTCGTCACCTGGAGCTCGACCTTCCACCTTCACAGCCTACAACAATAACTATTGA			MATSSPGARPSTFTAYNNNY*	MATSSPGARPSTFTAYNNNY*			AAACATCCTG	GTTTTTTTGC	0	U	0	0	NCU09313.1	0	0
8391	3790	ao	AN8879.1	56.m02290	AO070293000008	0					-259	-197	ATGGTGTACTATACGGAAGGGAAACACAATTACGCAATCGAACTGCTCGGCACTCCATACTAA			ATGGTGTACTATACGGAAGGGAAACACAATTACGCAATCGAACTGCTCGGCACTCCATACTAA	MVYYTEGKHNYAIELLGTPY*			MVYYTEGKHNYAIELLGTPY*	CCCTGTTATT	TACGACTCCG	0	U	0	0	NCU09313.1	0	0
8392	3790	ao	AN8879.1	56.m02290	AO070293000008	0					-100	-68	ATGCGAACATATATCTTACTCTGCCGCATATAA			ATGCGAACATATATCTTACTCTGCCGCATATAA	MRTYILLCRI*			MRTYILLCRI*	ACGATTCTAC	GCATCGTAAT	0	U	0	0	NCU09313.1	0	0
8396	3791	af	AN2266.1	71.m15910	AO070295000038	0			-222	-190			ATGAACTTTTGTACAGAACCCTTGAGCATATAA		ATGAACTTTTGTACAGAACCCTTGAGCATATAA		MNFCTEPLSI*		MNFCTEPLSI*		AGTTGGGTTC	GTTTCTGCCT	0	U	0	0	0	0	0
8394	3791	an	AN2266.1	71.m15910	AO070295000038	0	-225	-148					ATGGCTCGTGGTGGGACGAGTTACATAACTAAGCAGTGCTGCCTTGCGATCTGCCCCAGGCCTCAACAACTAGTCTAG	ATGGCTCGTGGTGGGACGAGTTACATAACTAAGCAGTGCTGCCTTGCGATCTGCCCCAGGCCTCAACAACTAGTCTAG			MARGGTSYITKQCCLAICPRPQQLV*	MARGGTSYITKQCCLAICPRPQQLV*			TGGAGCTTGG	CCAATCGACT	0	U	0	0	0	0	0
8395	3791	an	AN2266.1	71.m15910	AO070295000038	0	-66	-31					ATGCTGCTACCCGGTCGTTTTATATATTCGGTATGA	ATGCTGCTACCCGGTCGTTTTATATATTCGGTATGA			MLLPGRFIYSV*	MLLPGRFIYSV*			TTGGCTGTCC	TATAGGCTAT	0	U	0	0	0	0	0
8397	3791	ao	AN2266.1	71.m15910	AO070295000038	0					-172	-26	ATGCCTCAGGCAAGAAGAATCATGCCAAGGCATCAACAGCTGTCTAGCTTCCCCATCCCGCCCTATCGGTATCAATCGGTCAGTCGACAGCTTGACACAAGCTCCTCTAGCAACTCCTCAACCCTCGGGGAACCCGCTATGATATAG			ATGCCTCAGGCAAGAAGAATCATGCCAAGGCATCAACAGCTGTCTAGCTTCCCCATCCCGCCCTATCGGTATCAATCGGTCAGTCGACAGCTTGACACAAGCTCCTCTAGCAACTCCTCAACCCTCGGGGAACCCGCTATGATATAG	MPQARRIMPRHQQLSSFPIPPYRYQSVSRQLDTSSSSNSSTLGEPAMI*			MPQARRIMPRHQQLSSFPIPPYRYQSVSRQLDTSSSSNSSTLGEPAMI*	AGAATAGTGT	TGCCTTTTGT	0	U	0	0	0	0	0
8398	3791	ao	AN2266.1	71.m15910	AO070295000038	0					-151	-26	ATGCCAAGGCATCAACAGCTGTCTAGCTTCCCCATCCCGCCCTATCGGTATCAATCGGTCAGTCGACAGCTTGACACAAGCTCCTCTAGCAACTCCTCAACCCTCGGGGAACCCGCTATGATATAG			ATGCCAAGGCATCAACAGCTGTCTAGCTTCCCCATCCCGCCCTATCGGTATCAATCGGTCAGTCGACAGCTTGACACAAGCTCCTCTAGCAACTCCTCAACCCTCGGGGAACCCGCTATGATATAG	MPRHQQLSSFPIPPYRYQSVSRQLDTSSSSNSSTLGEPAMI*			MPRHQQLSSFPIPPYRYQSVSRQLDTSSSSNSSTLGEPAMI*	AAGAAGAATC	TGCCTTTTGT	0	U	0	0	0	0	0
8399	3792	ao	AN7260.1	72.m19789	AO070297000018	0					-190	-122	ATGACTGATGGGGGGTTGTTCGCAGTCGAAGAAAAGCTCCGCGGACAAAAAAATCCAAAAAAAGTCTAA			ATGACTGATGGGGGGTTGTTCGCAGTCGAAGAAAAGCTCCGCGGACAAAAAAATCCAAAAAAAGTCTAA	MTDGGLFAVEEKLRGQKNPKKV*			MTDGGLFAVEEKLRGQKNPKKV*	CGCATTTTGA	GGTGGAGAGC	0	JU	FG05465.1	0	0	YLR002C	0
8403	3794	af	AN8389.1	59.m08445	AO070300000072	0			-149	-96			ATGATCCACCAGGGTCGTGTTTCCCACTTCGACTTGGTCCTCGGCAACAAGTAG		ATGATCCACCAGGGTCGTGTTTCCCACTTCGACTTGGTCCTCGGCAACAAGTAG		MIHQGRVSHFDLVLGNK*		MIHQGRVSHFDLVLGNK*		GTGGACGCAG	AGAATCTTCG	0		0	0	0	0	0
8400	3794	an	AN8389.1	59.m08445	AO070300000072	0	-248	-213					ATGGTGCACAGAACGCTTATTATATGGAGTCTGTGA	ATGGTGCACAGAACGCTTATTATATGGAGTCTGTGA			MVHRTLIIWSL*	MVHRTLIIWSL*			TGTAAACAAG	CCCTACGAGA	0		0	0	0	0	0
8401	3794	an	AN8389.1	59.m08445	AO070300000072	0	-225	-172					ATGGAGTCTGTGACCCTACGAGAGAGCATGCCTAGGCTTACAGGCCGGACTTAG	ATGGAGTCTGTGACCCTACGAGAGAGCATGCCTAGGCTTACAGGCCGGACTTAG			MESVTLRESMPRLTGRT*	MESVTLRESMPRLTGRT*			CGCTTATTAT	TTTATCTATT	0		0	0	0	0	0
8402	3794	an	AN8389.1	59.m08445	AO070300000072	0	-198	-172					ATGCCTAGGCTTACAGGCCGGACTTAG	ATGCCTAGGCTTACAGGCCGGACTTAG			MPRLTGRT*	MPRLTGRT*			ACGAGAGAGC	TTTATCTATT	0		0	0	0	0	0
8405	3794	ao	AN8389.1	59.m08445	AO070300000072	0					-147	-79	ATGACGGCCCATTATTGGCGGGTTTGCTGGATTGCTGGCATTAAATGTTATCTTCTAAGTCTGCCATGA			ATGACGGCCCATTATTGGCGGGTTTGCTGGATTGCTGGCATTAAATGTTATCTTCTAAGTCTGCCATGA	MTAHYWRVCWIAGIKCYLLSLP*			MTAHYWRVCWIAGIKCYLLSLP*	CACGTGTGAG	CTACTCCGAT	0		0	0	0	0	0
8406	3794	ao	AN8389.1	59.m08445	AO070300000072	0					-103	-59	ATGTTATCTTCTAAGTCTGCCATGACTACTCCGATTAACTCATAA			ATGTTATCTTCTAAGTCTGCCATGACTACTCCGATTAACTCATAA	MLSSKSAMTTPINS*			MLSSKSAMTTPINS*	CTGGCATTAA	ATAAACCCAC	0		0	0	0	0	0
8407	3794	ao	AN8389.1	59.m08445	AO070300000072	0					-82	-59	ATGACTACTCCGATTAACTCATAA			ATGACTACTCCGATTAACTCATAA	MTTPINS*			MTTPINS*	TAAGTCTGCC	ATAAACCCAC	0		0	0	0	0	0
8410	3798	af	AN1708.1	58.m07794	AO070305000041	0			-208	-98			ATGAGTGTCCATACCGATACCACCACTAAACGCGTCGACGCGCTACGTGACGCCTCCTTATCGGACAAGCCGACATTTTCCCGTCCTGGGAACCTCTCTCAACACTTGTAG		ATGAGTGTCCATACCGATACCACCACTAAACGCGTCGACGCGCTACGTGACGCCTCCTTATCGGACAAGCCGACATTTTCCCGTCCTGGGAACCTCTCTCAACACTTGTAG		MSVHTDTTKRVDALRDASLSDKPTFSRPGNLSQHL*		MSVHTDTTKRVDALRDASLSDKPTFSRPGNLSQHL*		CCAAGAAGTG	TGTGTTTCCA	0	L	0	0	0	0	0
8411	3798	af	AN1708.1	58.m07794	AO070305000041	0			-61	-41			ATGGATTATACATCTTCTTAA		ATGGATTATACATCTTCTTAA		MDYTSS*		MDYTSS*		CATCCTCAGT	TTATCACATT	0	L	0	0	0	0	0
8408	3798	an	AN1708.1	58.m07794	AO070305000041	0	-221	-177					ATGTCTGCTTGGTGCCTGAGTATTAAGGTATCAAGAAGCCACTAA	ATGTCTGCTTGGTGCCTGAGTATTAAGGTATCAAGAAGCCACTAA			MSAWCLSIKVSRSH*	MSAWCLSIKVSRSH*			ATTAGAGCCG	ACGCGTCGAC	0	L	0	0	0	0	0
8412	3798	ao	AN1708.1	58.m07794	AO070305000041	0					-234	-211	ATGCCTGAGGCGTGGACGGAATGA			ATGCCTGAGGCGTGGACGGAATGA	MPEAWTE*			MPEAWTE*	ACTTCCCTTG	AGGCCGGAAA	0	L	0	0	0	0	0
8413	3798	ao	AN1708.1	58.m07794	AO070305000041	0					-214	-158	ATGAAGGCCGGAAAACCACTAAACGCGTCGACGCGCGACGCCCTTCCGACGATTTGA			ATGAAGGCCGGAAAACCACTAAACGCGTCGACGCGCGACGCCCTTCCGACGATTTGA	MKAGKPLNASTRDALPTI*			MKAGKPLNASTRDALPTI*	CGTGGACGGA	TAGATCGACT	0	L	0	0	0	0	0
8418	3800	af	AN4510.1	57.m05618	AO070311000065	0			-205	-188			ATGTCGCGCCACTACTGA		ATGTCGCGCCACTACTGA		MSRHY*		MSRHY*		ACGACCTCAT	CGCCCGTCCT	0	R	0	0	0	0	0
8416	3800	an	AN4510.1	57.m05618	AO070311000065	0	-195	-178					ATGTTTGCTCCCTACTGA	ATGTTTGCTCCCTACTGA			MFAPY*	MFAPY*			GGCTATTCAA	CCCCTCCCCG	0	R	0	0	0	0	0
8417	3800	an	AN4510.1	57.m05618	AO070311000065	0	-81	-55					ATGCTACTGCTCGGAGCGTACAGCTGA	ATGCTACTGCTCGGAGCGTACAGCTGA			MLLLGAYS*	MLLLGAYS*			GGCGAACTCT	ATATCTGTGT	0	R	0	0	0	0	0
8419	3800	ao	AN4510.1	57.m05618	AO070311000065	0					-179	-168	ATGCCATTCTGA			ATGCCATTCTGA	MPF*			MPF*	TGGACCGAAG	AGCTCTCCCG	0	R	0	0	0	0	0
8420	3800	ao	AN4510.1	57.m05618	AO070311000065	0					-87	-31	ATGCTACCTCTGGAAACTTCCGAACCTCTCCATCTCTCCATTCCCTATCCTGTTTGA			ATGCTACCTCTGGAAACTTCCGAACCTCTCCATCTCTCCATTCCCTATCCTGTTTGA	MLPLETSEPLHLSIPYPV*			MLPLETSEPLHLSIPYPV*	AATACACTAT	CGCTTCTTAG	0	R	0	0	0	0	0
8422	3802	af	AN0111.1	71.m15386	AO070311000109	0			-271	-209			ATGATACGCAGCGCGATAGAGGAAGAAGCTTGGGCCACTTCTGCCCGCCTGGCTGCGGCATGA		ATGATACGCAGCGCGATAGAGGAAGAAGCTTGGGCCACTTCTGCCCGCCTGGCTGCGGCATGA		MIRSAIEEEAWATSARLAA*		MIRSAIEEEAWATSARLAA*		CATTGGCACG	CAGAAGGTCA	0	A	0	0	0	0	0
8423	3802	af	AN0111.1	71.m15386	AO070311000109	0			-212	-162			ATGACAGAAGGTCACGTGCTCATGTCCAACTTCACGTTCTGCGGCGCTTGA		ATGACAGAAGGTCACGTGCTCATGTCCAACTTCACGTTCTGCGGCGCTTGA		MTEGHVLMSNFTFCGA*		MTEGHVLMSNFTFCGA*		TGGCTGCGGC	TCTTTGCTGG	0	A	0	0	0	0	0
8424	3802	af	AN0111.1	71.m15386	AO070311000109	0			-191	-162			ATGTCCAACTTCACGTTCTGCGGCGCTTGA		ATGTCCAACTTCACGTTCTGCGGCGCTTGA		MSNFTFCGA*		MSNFTFCGA*		TCACGTGCTC	TCTTTGCTGG	0	A	0	0	0	0	0
8425	3802	af	AN0111.1	71.m15386	AO070311000109	0			-115	-95			ATGCGATCCTCCCTTTTCTGA		ATGCGATCCTCCCTTTTCTGA		MRSSLF*		MRSSLF*		TCTCCAGTTC	CCCTGTGTGG	0	A	0	0	0	0	0
8421	3802	an	AN0111.1	71.m15386	AO070311000109	0	-116	-84					ATGCCATCACGTTTCCTCGCGAATACGTGCTGA	ATGCCATCACGTTTCCTCGCGAATACGTGCTGA			MPSRFLANTC*	MPSRFLANTC*			TTTCCCGCTC	CCGTGTGAGT	0	A	0	0	0	0	0
8426	3802	ao	AN0111.1	71.m15386	AO070311000109	0					-240	-76	ATGGAGGAGGAGCTTGGACCACCTGCGGCCCGCATGATAGCAGGTCACGTGGAACCTGCACAACTTCATCTCTGCAGTCTCTCAGGCGGCTATCATCCAACGCGACGAGAAAGCTCTCCAATTCATGCTACACCCCTTTCTTCGGACTCTGTGTTGACCGTGTGA			ATGGAGGAGGAGCTTGGACCACCTGCGGCCCGCATGATAGCAGGTCACGTGGAACCTGCACAACTTCATCTCTGCAGTCTCTCAGGCGGCTATCATCCAACGCGACGAGAAAGCTCTCCAATTCATGCTACACCCCTTTCTTCGGACTCTGTGTTGACCGTGTGA	MEEELGPPAARMIAGHVEPAQLHLCSLSGGYHPTRRESSPIHATPLSSDSVLTV*			MEEELGPPAARMIAGHVEPAQLHLCSLSGGYHPTRRESSPIHATPLSSDSVLTV*	ATAGGCGATA	GCCGATCCCG	0	A	0	0	0	0	0

8427	3802	ao	AN0111.1	71.m15386	AO070311000109	0					-207	-76	ATGATAGCAGGTCACGTGGAACCTGCACAACTTCATCTCTGCAGTCTCTCAGGCGGCTATCATCCAACGCGACGAGAAAGCTCTCCAATTCATGCTACACCCCTTTCTTCGGACTCTGTGTTGACCGTGTGA			ATGATAGCAGGTCACGTGGAACCTGCACAACTTCATCTCTGCAGTCTCTCAGGCGGCTATCATCCAACGCGACGAGAAAGCTCTCCAATTCATGCTACACCCCTTTCTTCGGACTCTGTGTTGACCGTGTGA	MIAGHVEPAQLHLCSLSGGYHPTRRESSPIHATPLSSDSVLTV*			MIAGHVEPAQLHLCSLSGGYHPTRRESSPIHATPLSSDSVLTV*	TGCGGCCCGC	GCCGATCCCG	0	A	0	0	0	0	0
8428	3802	ao	AN0111.1	71.m15386	AO070311000109	0					-116	-84	ATGCTACACCCCTTTCTTCGGACTCTGTGTTGA			ATGCTACACCCCTTTCTTCGGACTCTGTGTTGA	MLHPFLRTLC*			MLHPFLRTLC*	TCTCCAATTC	CCGTGTGAGC	0	A	0	0	0	0	0
8429	3804	af	AN0330.1	53.m03956	AO070312000077	0			-268	-251			ATGGATATCAGCCAATAG		ATGGATATCAGCCAATAG		MDISQ*		MDISQ*		CCTTTTCGGC	CGGTTAGAAA	0	CR	0	0	0	0	0
8430	3804	af	AN0330.1	53.m03956	AO070312000077	0			-67	-8			ATGTCTTCTCCTCTCTCACTTCACGATTCACGTCCGCATCTGTGCAACCGGACTACCTGA		ATGTCTTCTCCTCTCTCACTTCACGATTCACGTCCGCATCTGTGCAACCGGACTACCTGA		MSSPLSLHDSRPHLCNRTT*		MSSPLSLHDSRPHLCNRTT*		CAACGCCATC	AAACAACATG	0	CR	0	0	0	0	0
8431	3804	ao	AN0330.1	53.m03956	AO070312000077	0					-238	-194	ATGGCTGTAGAGCTCTGGAGAGCGCTGGCCAATGGAAAGCCGTAA			ATGGCTGTAGAGCTCTGGAGAGCGCTGGCCAATGGAAAGCCGTAA	MAVELWRALANGKP*			MAVELWRALANGKP*	GAACCAACCA	AAGGGGTATC	0	CR	0	0	0	0	0
8432	3804	ao	AN0330.1	53.m03956	AO070312000077	0					-207	-22	ATGGAAAGCCGTAAAAGGGGTATCGGCCTCGGCACCGGATCCGAGCATTTGTCAGCCGTGATTTTCTGGCATCCAAAGAGATTCCATGCAATTCATTCACCATATCGAAAATCTATAAATCGCTATGGGTTTACCCACGATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAA			ATGGAAAGCCGTAAAAGGGGTATCGGCCTCGGCACCGGATCCGAGCATTTGTCAGCCGTGATTTTCTGGCATCCAAAGAGATTCCATGCAATTCATTCACCATATCGAAAATCTATAAATCGCTATGGGTTTACCCACGATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAA	MESRKRGIGLGTGSEHLSAVIFWHPKRFHAIHSPYRKSINRYGFTHDGHYPAGHTIPVLPS*			MESRKRGIGLGTGSEHLSAVIFWHPKRFHAIHSPYRKSINRYGFTHDGHYPAGHTIPVLPS*	GCGCTGGCCA	TCATAAACCA	0	CR	0	0	0	0	0
8433	3804	ao	AN0330.1	53.m03956	AO070312000077	0					-122	-90	ATGCAATTCATTCACCATATCGAAAATCTATAA			ATGCAATTCATTCACCATATCGAAAATCTATAA	MQFIHHIENL*			MQFIHHIENL*	AAGAGATTCC	ATCGCTATGG	0	CR	0	0	0	0	0
8434	3804	ao	AN0330.1	53.m03956	AO070312000077	0					-83	-6	ATGGGTTTACCCACGATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAATCATAAACCAAGATAG			ATGGGTTTACCCACGATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAATCATAAACCAAGATAG	MGLPTMAIIQQGTPFPFSPHNHKPR*			MGLPTMAIIQQGTPFPFSPHNHKPR*	ATAAATCGCT	TCACAATGGG	0	CR	0	0	0	0	0
8435	3804	ao	AN0330.1	53.m03956	AO070312000077	0					-68	-6	ATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAATCATAAACCAAGATAG			ATGGCCATTATCCAGCAGGGCACACCATTCCCGTTCTCCCCTCATAATCATAAACCAAGATAG	MAIIQQGTPFPFSPHNHKPR*			MAIIQQGTPFPFSPHNHKPR*	TTTACCCACG	TCACAATGGG	0	CR	0	0	0	0	0
8436	3808	an	AN3907.1	69.m15658	AO070324000091	0	-176	-120					ATGATATTGCCTCTGCTTCACTTAACGTCCTGTCTCTCGAGCCTGCGCCGCTCCTAA	ATGATATTGCCTCTGCTTCACTTAACGTCCTGTCTCTCGAGCCTGCGCCGCTCCTAA			MILPLLHLTSCLSSLRRS*	MILPLLHLTSCLSSLRRS*			TTTCCCGGCA	ACTCCATGCT	0	K	FG09338.1	0	0	YGR274C	YGR274C
8437	3808	an	AN3907.1	69.m15658	AO070324000091	0	-114	-31					ATGCTCGCATCTTCTCTATCCGTCGCGTCAACTACAATAAAATTCCCCTTTTTGCGTCTACCCAGGCGTACGCTATTTCTTTGA	ATGCTCGCATCTTCTCTATCCGTCGCGTCAACTACAATAAAATTCCCCTTTTTGCGTCTACCCAGGCGTACGCTATTTCTTTGA			MLASSLSVASTTIKFPFLRLPRRTLFL*	MLASSLSVASTTIKFPFLRLPRRTLFL*			CCTAAACTCC	ACGTTTCGTC	0	K	FG09338.1	0	0	YGR274C	YGR274C
8438	3808	ao	AN3907.1	69.m15658	AO070324000091	0					-120	-103	ATGTGCGCTCCTTCATAA			ATGTGCGCTCCTTCATAA	MCAPS*			MCAPS*	ACCGTTCTCG	CGTCCAGTTG	0	K	FG09338.1	0	0	YGR274C	YGR274C
8451	3811	af	AN5600.1	58.m07524	AO070328000004	0			-267	-217			ATGGACACAGCCCTACGAATTAAGACCTTCTTTCTTCATATCATAATTAG		ATGGACACAGCCCTACGAATTAAGACCTTCTTTCTTCATATCATAATTAG		MDTALRIKTFFLSYHN*		MDTALRIKTFFLSYHN*		GTGTAGCCTG	TCGGTGGAGT	0	I	0	0	0	0	0
8449	3811	an	AN5600.1	58.m07524	AO070328000004	0	-481	-413					ATGTATTCCTGCCTCCCGCGCATTTCTCTATCCGCACCAGATCGACAAAGAGAACAGGAAACACTGTAG	ATGTATTCCTGCCTCCCGCGCATTTCTCTATCCGCACCAGATCGACAAAGAGAACAGGAAACACTGTAG			MYSCLPRISLSAPDRQREQETL*	MYSCLPRISLSAPDRQREQETL*			TCTTTCAGGT	CCTGCTTGCC	0	I	0	0	0	0	0
8450	3811	an	AN5600.1	58.m07524	AO070328000004	0	-376	-362					ATGATTTCCTGCTGA	ATGATTTCCTGCTGA			MISC*	MISC*			CGACCCTCAA	CGTTTCCTGG	0	I	0	0	0	0	0
8452	3811	ao	AN5600.1	58.m07524	AO070328000004	0					-237	-190	ATGAACACAGCCCTACAACAGAGGATCTCCATCTCGCGCCGTCTCTAG			ATGAACACAGCCCTACAACAGAGGATCTCCATCTCGCGCCGTCTCTAG	MNTALQQRISISRRL*			MNTALQQRISISRRL*	GTGTAGCCTG	TCAACCGGTG	0	I	0	0	0	0	0
8453	3812	af	AN5536.1	58.m07482	AO070328000055	0			-219	-121			ATGACGTCTGGGCGGTCCAGACTACGGGCTCCACCCGCAAGCAGATCTCCTCGAATCCCCCGCGACAAAAGAATTTCTGTTTCGAACCACATTATTGA		ATGACGTCTGGGCGGTCCAGACTACGGGCTCCACCCGCAAGCAGATCTCCTCGAATCCCCCGCGACAAAAGAATTTCTGTTTCGAACCACATTATTGA		MTSGRSRLRAPPASRSPRIPRDKKNFCFEPHY*		MTSGRSRLRAPPASRSPRIPRDKKNFCFEPHY*		AAATACTAGG	CTTACATGTT	0	L	0	0	NCU04507.1	0	0
8454	3812	af	AN5536.1	58.m07482	AO070328000055	0			-115	-92			ATGTTCACGTCTCCATCAAGCTAG		ATGTTCACGTCTCCATCAAGCTAG		MFTSPSS*		MFTSPSS*		ATTGACTTAC	CTATTTTTTT	0	L	0	0	NCU04507.1	0	0
8455	3812	ao	AN5536.1	58.m07482	AO070328000055	0					-227	-144	ATGACGTCTGGCCGGCCTTTTGGACTCCACCCCGAGCAGATCCTCAAAAAAGTACTCCCCGCGCGACTGGAAGAAATTATTTGA			ATGACGTCTGGCCGGCCTTTTGGACTCCACCCCGAGCAGATCCTCAAAAAAGTACTCCCCGCGCGACTGGAAGAAATTATTTGA	MTSGRPFGLHPEQILKKVLPARLEEII*			MTSGRPFGLHPEQILKKVLPARLEEII*	AAAGGCGCTA	TTTTCTTATC	0	L	0	0	NCU04507.1	0	0
8456	3814	an	AN4038.1	54.m06572	AO070328000136	0	-63	-34					ATGTTCAGTTCTTTCAAACTACACGGATAA	ATGTTCAGTTCTTTCAAACTACACGGATAA			MFSSFKLHG*	MFSSFKLHG*			AGTGATTTTC	CGCCTTGCTA	0	J	0	0	0	0	0
8457	3816	af	AN4859.1	59.m09466	AO070329000143	0			-182	-159			ATGCAAATCCCCCCCAAATATTAA		ATGCAAATCCCCCCCAAATATTAA		MQIPPKY*		MQIPPKY*		TGCTGCTTCC	AGGATACATT	0	P	0	0	0	0	0
8460	3820	af	AN1513.1	55.m03253	AO070334000232	0			-244	-215			ATGGAACAGCGGGTATTCCAGAAAATATAA		ATGGAACAGCGGGTATTCCAGAAAATATAA		MEQRVFQKI*		MEQRVFQKI*		CCATAGGACG	TTCAACCGTA	0	E	0	0	0	YGR012W	YGR012W
8461	3820	af	AN1513.1	55.m03253	AO070334000232	0			-187	-158			ATGCCCGATAATGACGATAATGAAGGATGA		ATGCCCGATAATGACGATAATGAAGGATGA		MPDNDDNEG*		MPDNDDNEG*		GCTGACAGAA	TGGATGGGGG	0	E	0	0	0	YGR012W	YGR012W
8462	3820	af	AN1513.1	55.m03253	AO070334000232	0			-177	-64			ATGACGATAATGAAGGATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAGATAG		ATGACGATAATGAAGGATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAGATAG		MTIMKDDGWGLAEEFLKWPELSLRLSTLTSLAWMRSR*		MTIMKDDGWGLAEEFLKWPELSLRLSTLTSLAWMRSR*		ATGCCCGATA	TTGCTCTTTT	0	E	0	0	0	YGR012W	YGR012W
8463	3820	af	AN1513.1	55.m03253	AO070334000232	0			-168	-64			ATGAAGGATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAGATAG		ATGAAGGATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAGATAG		MKDDGWGLAEEFLKWPELSLRLSTLTSLAWMRSR*		MKDDGWGLAEEFLKWPELSLRLSTLTSLAWMRSR*		AATGACGATA	TTGCTCTTTT	0	E	0	0	0	YGR012W	YGR012W
8464	3820	af	AN1513.1	55.m03253	AO070334000232	0			-161	-93			ATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAA		ATGATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAA		MMDGGWRRSSSSGPSFLSDFLH*		MMDGGWRRSSSSGPSFLSDFLH*		ATAATGAAGG	CCTCTCTCGC	0	E	0	0	0	YGR012W	YGR012W
8465	3820	af	AN1513.1	55.m03253	AO070334000232	0			-158	-93			ATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAA		ATGGATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAA		MDGGWRRSSSSGPSFLSDFLH*		MDGGWRRSSSSGPSFLSDFLH*		ATGAAGGATG	CCTCTCTCGC	0	E	0	0	0	YGR012W	YGR012W
8466	3820	af	AN1513.1	55.m03253	AO070334000232	0			-154	-68			ATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAG		ATGGGGGCTGGCGGAGGAGTTCCTCAAGTGGCCCGAGCTTTCTCTCCGACTTTCTACACTAACCTCTCTCGCTTGGATGCGATCTAG		MGAGGGVPQVARAFSPTFYTNLSRLDAI*		MGAGGGVPQVARAFSPTFYTNLSRLDAI*		AGGATGATGG	ATAGTTGCTC	0	E	0	0	0	YGR012W	YGR012W
8467	3820	af	AN1513.1	55.m03253	AO070334000232	0			-78	-64			ATGCGATCTAGATAG		ATGCGATCTAGATAG		MRSR*		MRSR*		TCTCGCTTGG	TTGCTCTTTT	0	E	0	0	0	YGR012W	YGR012W
8458	3820	an	AN1513.1	55.m03253	AO070334000232	0	-160	-77					ATGAGAAGTGGAATCTCGATCAGATGCGGGCGGAGATTGGCAGGCGGCCCGAGCTTTTACTTCGTTAACGTATCTCCAGCTTGA	ATGAGAAGTGGAATCTCGATCAGATGCGGGCGGAGATTGGCAGGCGGCCCGAGCTTTTACTTCGTTAACGTATCTCCAGCTTGA			MRSGISIRCGRRLAGGPSFYFVNVSPA*	MRSGISIRCGRRLAGGPSFYFVNVSPA*			TAGCTGGATA	CCTCCAATGA	0	E	0	0	0	YGR012W	YGR012W
8459	3820	an	AN1513.1	55.m03253	AO070334000232	0	-137	-93					ATGCGGGCGGAGATTGGCAGGCGGCCCGAGCTTTTACTTCGTTAA	ATGCGGGCGGAGATTGGCAGGCGGCCCGAGCTTTTACTTCGTTAA			MRAEIGRRPELLLR*	MRAEIGRRPELLLR*			TCTCGATCAG	CGTATCTCCA	0	E	0	0	0	YGR012W	YGR012W
8468	3821	an	AN3063.1	59.m08951	AO070337000010	0	-89	-72					ATGGTAATTTTAGCTTGA	ATGGTAATTTTAGCTTGA			MVILA*	MVILA*			GTCATACCGA	CTTTTTTAGT	0	K	0	0	NCU02401.1	0	0
8473	3822	af	AN4883.1	59.m08777	AO070338000077	0			-188	-57			ATGTTGTCTGTAAATCGTCATTCATTCCAGCGCCAGGTGTTGCGATCGATTAACGCCAACTCCGCCTTACGATCAGTTCAACTTCCGATGACTCAACATCTCCTTTATCCATTTAGACATCATGTAGTTTAG		ATGTTGTCTGTAAATCGTCATTCATTCCAGCGCCAGGTGTTGCGATCGATTAACGCCAACTCCGCCTTACGATCAGTTCAACTTCCGATGACTCAACATCTCCTTTATCCATTTAGACATCATGTAGTTTAG		MLSVNRHSFQRQVLRSINANSALRSVQLPMTQHLLYPFRHHVV*		MLSVNRHSFQRQVLRSINANSALRSVQLPMTQHLLYPFRHHVV*		GGTGGTGGGG	ATCTGAGGAC	0	L	0	MG03854.1	0	0	0
8474	3822	af	AN4883.1	59.m08777	AO070338000077	0			-101	-57			ATGACTCAACATCTCCTTTATCCATTTAGACATCATGTAGTTTAG		ATGACTCAACATCTCCTTTATCCATTTAGACATCATGTAGTTTAG		MTQHLLYPFRHHVV*		MTQHLLYPFRHHVV*		TCAACTTCCG	ATCTGAGGAC	0	L	0	MG03854.1	0	0	0
8470	3822	an	AN4883.1	59.m08777	AO070338000077	0	-177	-88					ATGGTGTCGTCGCGAATGATCATCGCCGCAGCAGCTCCCCTCCGCTCGGGGTCGGAGCTCTTGGAACTTCCCCAAACCAATCAACCATAA	ATGGTGTCGTCGCGAATGATCATCGCCGCAGCAGCTCCCCTCCGCTCGGGGTCGGAGCTCTTGGAACTTCCCCAAACCAATCAACCATAA			MVSSRMIIAAAAPLRSGSELLELPQTNQP*	MVSSRMIIAAAAPLRSGSELLELPQTNQP*			ACAGCGAACG	TTCAGCAACT	0	L	0	MG03854.1	0	0	0
8471	3822	an	AN4883.1	59.m08777	AO070338000077	0	-162	-88					ATGATCATCGCCGCAGCAGCTCCCCTCCGCTCGGGGTCGGAGCTCTTGGAACTTCCCCAAACCAATCAACCATAA	ATGATCATCGCCGCAGCAGCTCCCCTCCGCTCGGGGTCGGAGCTCTTGGAACTTCCCCAAACCAATCAACCATAA			MIIAAAAPLRSGSELLELPQTNQP*	MIIAAAAPLRSGSELLELPQTNQP*			GTCGTCGCGA	TTCAGCAACT	0	L	0	MG03854.1	0	0	0
8472	3822	an	AN4883.1	59.m08777	AO070338000077	0	-66	-10					ATGAAACTCATAATAGGCACCAACCCAGCTAATTTTATATTATCGCTACCTACGTGA	ATGAAACTCATAATAGGCACCAACCCAGCTAATTTTATATTATCGCTACCTACGTGA			MKLIIGTNPANFILSLPT*	MKLIIGTNPANFILSLPT*			GCTCGACGTC	CGGTTCAATA	0	L	0	MG03854.1	0	0	0
8475	3822	ao	AN4883.1	59.m08777	AO070338000077	0					-209	-153	ATGAAATGTAAGGTGTCGCGAACAATGACAACTCCGCCTCCGGACGAATTAAATTGA			ATGAAATGTAAGGTGTCGCGAACAATGACAACTCCGCCTCCGGACGAATTAAATTGA	MKCKVSRTMTTPPPDELN*			MKCKVSRTMTTPPPDELN*	GGAGAGGGGA	ATTGCGGGAA	0	L	0	MG03854.1	0	0	0
8476	3822	ao	AN4883.1	59.m08777	AO070338000077	0					-185	-153	ATGACAACTCCGCCTCCGGACGAATTAAATTGA			ATGACAACTCCGCCTCCGGACGAATTAAATTGA	MTTPPPDELN*			MTTPPPDELN*	GTCGCGAACA	ATTGCGGGAA	0	L	0	MG03854.1	0	0	0
8477	3823	af	AN2904.1	59.m08755	AO070338000101	0			-272	-204			ATGAATCAAGAACTCGATAGAATTGGATTCGGCAGCTCTCTGGCGGCGCCAAGCTACATAATCACGTGA		ATGAATCAAGAACTCGATAGAATTGGATTCGGCAGCTCTCTGGCGGCGCCAAGCTACATAATCACGTGA		MNQELDRIGFGSSLAAPSYIIT*		MNQELDRIGFGSSLAAPSYIIT*		ACGCAAGAAG	CTGAAACTTA	0	O	0	MG00908.1	NCU02260.1	0	0
8478	3823	ao	AN2904.1	59.m08755	AO070338000101	0					-139	-92	ATGATCAAAGCAAAAGCTCCGATTCCCTCAACACTACCTCGCCGTTAG			ATGATCAAAGCAAAAGCTCCGATTCCCTCAACACTACCTCGCCGTTAG	MIKAKAPIPSTLPRR*			MIKAKAPIPSTLPRR*	CAGTTTGGTT	ATCTCTCGCT	0	O	0	MG00908.1	NCU02260.1	0	0
8479	3826	af	AN2068.1	57.m05768	AO070341000217	0			-158	-99			ATGCTCAATGTTCCTGTATTGGCTGTAATGGCTTCTTCCCAGATGGAGATCACATACTAA		ATGCTCAATGTTCCTGTATTGGCTGTAATGGCTTCTTCCCAGATGGAGATCACATACTAA		MLNVPVLAVMASSQMEITY*		MLNVPVLAVMASSQMEITY*		TTGCTCTGGT	TCTATGCCCT	0	I	0	0	0	0	0
8480	3826	af	AN2068.1	57.m05768	AO070341000217	0			-151	-131			ATGTTCCTGTATTGGCTGTAA		ATGTTCCTGTATTGGCTGTAA		MFLYWL*		MFLYWL*		GGTATGCTCA	TGGCTTCTTC	0	I	0	0	0	0	0
8481	3826	af	AN2068.1	57.m05768	AO070341000217	0			-131	-99			ATGGCTTCTTCCCAGATGGAGATCACATACTAA		ATGGCTTCTTCCCAGATGGAGATCACATACTAA		MASSQMEITY*		MASSQMEITY*		ATTGGCTGTA	TCTATGCCCT	0	I	0	0	0	0	0
8482	3826	af	AN2068.1	57.m05768	AO070341000217	0			-116	-99			ATGGAGATCACATACTAA		ATGGAGATCACATACTAA		MEITY*		MEITY*		TTCTTCCCAG	TCTATGCCCT	0	I	0	0	0	0	0
8483	3826	ao	AN2068.1	57.m05768	AO070341000217	0					-151	-107	ATGAGTGACTGGCAGCCTAATATATCTCAAGCTCGAATCAATTGA			ATGAGTGACTGGCAGCCTAATATATCTCAAGCTCGAATCAATTGA	MSDWQPNISQARIN*			MSDWQPNISQARIN*	GGTTCCGGGT	CGAAATAGTG	0	I	0	0	0	0	0
8486	3827	af	AN5492.1	69.m15459	AO070341000393	0			-242	-69			ATGACAAAAACAGCATCAGGCCTTACATTGGCTGTGATGGCTGGGGTCCAGAGTGGGGAATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAATTTTCTGTTGATCGTATCTCTGTTTACCTTAGTTCTTGTTGGATTTTATCAGTCTAGATAG		ATGACAAAAACAGCATCAGGCCTTACATTGGCTGTGATGGCTGGGGTCCAGAGTGGGGAATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAATTTTCTGTTGATCGTATCTCTGTTTACCTTAGTTCTTGTTGGATTTTATCAGTCTAGATAG		MTKTASGLTLAVMAGVQSGECYRSPSSCASHAAISIVNFLLIVSLFTLVLVGFYQSR*		MTKTASGLTLAVMAGVQSGECYRSPSSCASHAAISIVNFLLIVSLFTLVLVGFYQSR*		TCATGAAGTG	TCCTGGACTC	0	F	0	0	0	0	0
8487	3827	af	AN5492.1	69.m15459	AO070341000393	0			-206	-69			ATGGCTGGGGTCCAGAGTGGGGAATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAATTTTCTGTTGATCGTATCTCTGTTTACCTTAGTTCTTGTTGGATTTTATCAGTCTAGATAG		ATGGCTGGGGTCCAGAGTGGGGAATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAATTTTCTGTTGATCGTATCTCTGTTTACCTTAGTTCTTGTTGGATTTTATCAGTCTAGATAG		MAGVQSGECYRSPSSCASHAAISIVNFLLIVSLFTLVLVGFYQSR*		MAGVQSGECYRSPSSCASHAAISIVNFLLIVSLFTLVLVGFYQSR*		ATTGGCTGTG	TCCTGGACTC	0	F	0	0	0	0	0
8488	3827	af	AN5492.1	69.m15459	AO070341000393	0			-183	-130			ATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAA		ATGCTATCGATCCCCGAGCTCCTGCGCCTCACATGCTGCGATCAGCATTGTTAA		MLSIPELLRLTCCDQHC*		MLSIPELLRLTCCDQHC*		AGAGTGGGGA	TTTTCTGTTG	0	F	0	0	0	0	0
8489	3827	af	AN5492.1	69.m15459	AO070341000393	0			-151	-119			ATGCTGCGATCAGCATTGTTAATTTTCTGTTGA		ATGCTGCGATCAGCATTGTTAATTTTCTGTTGA		MLRSALLIFC*		MLRSALLIFC*		TGCGCCTCAC	TCGTATCTCT	0	F	0	0	0	0	0

8484	3827	an	AN5492.1	69.m15459	AO070341000393	0	-198	-160					ATGTGCTATGCCCGGAAACAGCGATCGCGTCGGGTGTAA	ATGTGCTATGCCCGGAAACAGCGATCGCGTCGGGTGTAA			MCYARKQRSRRV*	MCYARKQRSRRV*			AAAAAAAAAA	TAACCCCTCA	0	F	0	0	0	0	0
8485	3827	an	AN5492.1	69.m15459	AO070341000393	0	-191	-39					ATGCCCGGAAACAGCGATCGCGTCGGGTGTAATAACCCCTCACGGCCTGCCAAGACCGGGTCTCCCGCCTCTACCTCTTTGGAGTTTCCCCGAAGCCTGGGCCTCCCGGCGTATGCCCCCAAACGGTCTTACTTCCGACCACCTGATCGCTAG	ATGCCCGGAAACAGCGATCGCGTCGGGTGTAATAACCCCTCACGGCCTGCCAAGACCGGGTCTCCCGCCTCTACCTCTTTGGAGTTTCCCCGAAGCCTGGGCCTCCCGGCGTATGCCCCCAAACGGTCTTACTTCCGACCACCTGATCGCTAG			MPGNSDRVGCNNPSRPAKTGSPASTSLEFPRSLGLPAYAPKRSYFRPPDR*	MPGNSDRVGCNNPSRPAKTGSPASTSLEFPRSLGLPAYAPKRSYFRPPDR*			AAAATGTGCT	GATAATCCCC	0	F	0	0	0	0	0
8490	3827	ao	AN5492.1	69.m15459	AO070341000393	0					-111	-79	ATGGCCCACCATACCTCAAGCGGGGAACCCTGA			ATGGCCCACCATACCTCAAGCGGGGAACCCTGA	MAHHTSSGEP*			MAHHTSSGEP*	GCAAACAAAC	CCATGTCAAT	0	F	0	0	0	0	0
8493	3828	af	AN3734.1	69.m15381	AO070342000274	0			-108	-94			ATGGCCCGCAACTGA		ATGGCCCGCAACTGA		MARN*		MARN*		TGCTTCTCGA	TCTCTCGGCT	0	R	0	0	0	0	0
8491	3828	an	AN3734.1	69.m15381	AO070342000274	0	-108	-94					ATGACGGCCATCTGA	ATGACGGCCATCTGA			MTAI*	MTAI*			ACATCGTTTG	GAATGATTCT	0	R	0	0	0	0	0
8492	3828	an	AN3734.1	69.m15381	AO070342000274	0	-91	-38					ATGATTCTGGCTTTGAGGCCGCAAACATATATCTATACTGTCTTGTTATGCTGA	ATGATTCTGGCTTTGAGGCCGCAAACATATATCTATACTGTCTTGTTATGCTGA			MILALRPQTYIYTVLLC*	MILALRPQTYIYTVLLC*			CCATCTGAGA	TGATAGGAAG	0	R	0	0	0	0	0
8494	3828	ao	AN3734.1	69.m15381	AO070342000274	0					-117	-103	ATGAATGGTCCTTAG			ATGAATGGTCCTTAG	MNGP*			MNGP*	ATCTGCCTCG	CTGACGCTTG	0	R	0	0	0	0	0
8495	3828	ao	AN3734.1	69.m15381	AO070342000274	0					-113	-99	ATGGTCCTTAGCTGA			ATGGTCCTTAGCTGA	MVLS*			MVLS*	GCCTCGATGA	CGCTTGTATT	0	R	0	0	0	0	0
8496	3828	ao	AN3734.1	69.m15381	AO070342000274	0					-71	-39	ATGATGCACTGCTGTTTAGGCAGCTCATACTGA			ATGATGCACTGCTGTTTAGGCAGCTCATACTGA	MMHCCLGSSY*			MMHCCLGSSY*	AAGGGCGGCT	TGTGATTCGG	0	R	0	0	0	0	0
8497	3828	ao	AN3734.1	69.m15381	AO070342000274	0					-68	-39	ATGCACTGCTGTTTAGGCAGCTCATACTGA			ATGCACTGCTGTTTAGGCAGCTCATACTGA	MHCCLGSSY*			MHCCLGSSY*	GGCGGCTATG	TGTGATTCGG	0	R	0	0	0	0	0
8498	3829	af	AN2151.1	72.m19690	AO070343000200	0			-223	-209			ATGTCTACTCTGTAA		ATGTCTACTCTGTAA		MSTL*		MSTL*		TGAAGCAATC	TGATACGATC	0	A	0	0	0	0	0
8499	3829	af	AN2151.1	72.m19690	AO070343000200	0			-209	-183			ATGATACGATCTTTTGCGACAGTCTAA		ATGATACGATCTTTTGCGACAGTCTAA		MIRSFATV*		MIRSFATV*		CTACTCTGTA	TCACTCTTCC	0	A	0	0	0	0	0
8500	3829	ao	AN2151.1	72.m19690	AO070343000200	0					-102	-40	ATGCTTTTCTACCGAGTGCGCCTGACTCGATTACCGGAGAGCATTGTTGCAATTTGGAATTGA			ATGCTTTTCTACCGAGTGCGCCTGACTCGATTACCGGAGAGCATTGTTGCAATTTGGAATTGA	MLFYRVRLTRLPESIVAIWN*			MLFYRVRLTRLPESIVAIWN*	TCTCTAGTGT	GCAGACCTTA	0	A	0	0	0	0	0
8501	3831	af	AN0649.1	70.m15253	AO070343000578	0			-129	-94			ATGGTCTTTTGCGTCTTTGTCTCTACGTATATATAG		ATGGTCTTTTGCGTCTTTGTCTCTACGTATATATAG		MVFCVFVSTYI*		MVFCVFVSTYI*		CAGTGAATGA	TTTTCTGCTT	0	I	0	0	0	0	0
8502	3831	ao	AN0649.1	70.m15253	AO070343000578	0					-145	-74	ATGACTTGCTCTCGCTCTCGCTCTCCTCAAAGTTTATATCGTTACTTCTTATTCATTTTTACCTTTTGTTGA			ATGACTTGCTCTCGCTCTCGCTCTCCTCAAAGTTTATATCGTTACTTCTTATTCATTTTTACCTTTTGTTGA	MTCSRSRSPQSLYRYFLFIFTFC*			MTCSRSRSPQSLYRYFLFIFTFC*	AATTCTATAT	ACTTGATTGG	0	I	0	0	0	0	0
8503	3836	ao	AN1254.1	70.m14968	AO070223000015	0					-191	-171	ATGTTGTGGGCGGTATTTTGA			ATGTTGTGGGCGGTATTTTGA	MLWAVF*			MLWAVF*	AGGGACGAAA	CCACGATAGC	0	R	0	0	0	0	0
8504	3836	ao	AN1254.1	70.m14968	AO070223000015	0					-101	-63	ATGGATGCTTTGTTCCGTCGCAAAACCACCCGGTGTTAG			ATGGATGCTTTGTTCCGTCGCAAAACCACCCGGTGTTAG	MDALFRRKTTRC*			MDALFRRKTTRC*	CCATTGACTG	TCCCTGTCGA	0	R	0	0	0	0	0
8506	3837	af	AN5909.1	72.m19222	AO070245000003	0			-92	-69			ATGTGTCGATCTTTGACGATATGA		ATGTGTCGATCTTTGACGATATGA		MCRSLTI*		MCRSLTI*		CGGATCTACC	CTCCACTGAC	0	F	FG09678.1	0	0	0	0
8507	3837	af	AN5909.1	72.m19222	AO070245000003	0			-72	-16			ATGACTCCACTGACTGCCTTTAGAAGTAGTCAAGTTGGGCTGATCAAGCACCCCTGA		ATGACTCCACTGACTGCCTTTAGAAGTAGTCAAGTTGGGCTGATCAAGCACCCCTGA		MTPLTAFRSSQVGLIKHP*		MTPLTAFRSSQVGLIKHP*		CTTTGACGAT	CAAGGCAGAC	0	F	FG09678.1	0	0	0	0
8505	3837	an	AN5909.1	72.m19222	AO070245000003	0	-83	-69					ATGTGGTCTACATAG	ATGTGGTCTACATAG			MWST*	MWST*			TTGCTAAAAT	GTCTACAAAC	0	F	FG09678.1	0	0	0	0
8508	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-219	-88	ATGTGGTACGATGCTCTAGGTTATGGAAGACCTGGATATAGAAACAGATTTAAGTCCTATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAA			ATGTGGTACGATGCTCTAGGTTATGGAAGACCTGGATATAGAAACAGATTTAAGTCCTATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAA	MWYDALGYGRPGYRNRFKSYVMSSRCYLSFPINASNLCRWAHS*			MWYDALGYGRPGYRNRFKSYVMSSRCYLSFPINASNLCRWAHS*	TCGTCGGTTC	CATGGAGCCG	0	F	FG09678.1	0	0	0	0
8509	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-197	-33	ATGGAAGACCTGGATATAGAAACAGATTTAAGTCCTATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA			ATGGAAGACCTGGATATAGAAACAGATTTAAGTCCTATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA	MEDLDIETDLSPMSCRVGAICLFLSMLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*			MEDLDIETDLSPMSCRVGAICLFLSMLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*	GCTCTAGGTT	TTGGATTGTC	0	F	FG09678.1	0	0	0	0
8510	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-161	-33	ATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA			ATGTCATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA	MSCRVGAICLFLSMLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*			MSCRVGAICLFLSMLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*	TTTAAGTCCT	TTGGATTGTC	0	F	FG09678.1	0	0	0	0
8511	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-156	-88	ATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAA			ATGTCGAGTCGGTGCTATCTGTCTTTTCCTATCAATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAA	MSSRCYLSFPINASNLCRWAHS*			MSSRCYLSFPINASNLCRWAHS*	GTCCTATGTC	CATGGAGCCG	0	F	FG09678.1	0	0	0	0
8512	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-122	-33	ATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA			ATGCTTCAAATCTATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA	MLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*			MLQIYVVGRIPNMEPLTIRRSNKNQRSCQ*	TTTCCTATCA	TTGGATTGTC	0	F	FG09678.1	0	0	0	0
8513	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-109	-74	ATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAA			ATGTCGTTGGGCGCATTCCTAACATGGAGCCGCTAA	MSLGAFLTWSR*			MSLGAFLTWSR*	CTTCAAATCT	CCATTCGTAG	0	F	FG09678.1	0	0	0	0
8514	3837	ao	AN5909.1	72.m19222	AO070245000003	0					-86	-33	ATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA			ATGGAGCCGCTAACCATTCGTAGGTCAAATAAAAACCAAAGATCTTGTCAATAA	MEPLTIRRSNKNQRSCQ*			MEPLTIRRSNKNQRSCQ*	CATTCCTAAC	TTGGATTGTC	0	F	FG09678.1	0	0	0	0
8516	3838	af	AN8743.1	62.m03337	AO070250000032	0			-125	-39			ATGCGTCCACGGCTCGTGTCAGCCCTGATTGATTGTCGCATTACGTCGCGAAACTGCCATGATCTCGGTCCGCTTTGCAATAAATAA		ATGCGTCCACGGCTCGTGTCAGCCCTGATTGATTGTCGCATTACGTCGCGAAACTGCCATGATCTCGGTCCGCTTTGCAATAAATAA		MRPRLVSALIDCRITSRNCHDLGPLCNK*		MRPRLVSALIDCRITSRNCHDLGPLCNK*		ACTTGGCAAC	ACCTACATTA	0	IOT	0	0	0	0	0
8515	3838	an	AN8743.1	62.m03337	AO070250000032	0	-77	-45					ATGGCTCAAAGAAACCTTCCCGGGAAACGCTGA	ATGGCTCAAAGAAACCTTCCCGGGAAACGCTGA			MAQRNLPGKR*	MAQRNLPGKR*			TCTTCACCGT	CCGTCCGGCG	0	IOT	0	0	0	0	0
8520	3839	af	AN5815.1	72.m18944	AO070260000032	0			-206	-180			ATGTGTCGAAGGAGCATAACTAGATAA		ATGTGTCGAAGGAGCATAACTAGATAA		MCRRSITR*		MCRRSITR*		TGCTGTGGTG	ACAAGTGGAT	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8521	3839	af	AN5815.1	72.m18944	AO070260000032	0			-168	-85			ATGGAATGTTACTCTTCTCTTTCCCAGAGGGCTCTCGACTTCTATCTACTATTTGACACTCCAAGTTTTCCACCATCAATGTAA		ATGGAATGTTACTCTTCTCTTTCCCAGAGGGCTCTCGACTTCTATCTACTATTTGACACTCCAAGTTTTCCACCATCAATGTAA		MECYSSLSQRALDFYLLFDTPSFPPSM*		MECYSSLSQRALDFYLLFDTPSFPPSM*		CAAGTGGATC	TTATGATTGC	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8522	3839	af	AN5815.1	72.m18944	AO070260000032	0			-163	-113			ATGTTACTCTTCTCTTTCCCAGAGGGCTCTCGACTTCTATCTACTATTTGA		ATGTTACTCTTCTCTTTCCCAGAGGGCTCTCGACTTCTATCTACTATTTGA		MLLFSFPEGSRLLSTI*		MLLFSFPEGSRLLSTI*		GGATCATGGA	CACTCCAAGT	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8523	3839	af	AN5815.1	72.m18944	AO070260000032	0			-82	-71			ATGATTGCATAA		ATGATTGCATAA		MIA*		MIA*		CAATGTAATT	ACCAATAGAG	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8518	3839	an	AN5815.1	72.m18944	AO070260000032	0	-103	-89					ATGGACACTCAATAA	ATGGACACTCAATAA			MDTQ*	MDTQ*			ATACTCCTAT	TGCTTGCTTA	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8519	3839	an	AN5815.1	72.m18944	AO070260000032	0	-89	-78					ATGCTTGCTTAA	ATGCTTGCTTAA			MLA*	MLA*			ACACTCAATA	AAGAGAACCA	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8524	3839	ao	AN5815.1	72.m18944	AO070260000032	0					-106	-95	ATGTCTATGTAA			ATGTCTATGTAA	MSM*			MSM*	AACCTAGATA	ACTACACAAG	0	D	FG06959.1	MG00479.1	0	YPL209C	0
8528	3840	af	AN4389.1	58.m07935	AO070261000034	0			-149	-66			ATGACTTATCGGACTCTGGATAAATGTACTCAGCACCGAAAGCCGTACCAGCAAGCGAACATCGAAAAGATATCAACTCTTTAG		ATGACTTATCGGACTCTGGATAAATGTACTCAGCACCGAAAGCCGTACCAGCAAGCGAACATCGAAAAGATATCAACTCTTTAG		MTYRTLDKCTQHRKPYQQANIEKISTL*		MTYRTLDKCTQHRKPYQQANIEKISTL*		CTCGGAGCGG	GGGGATAGAA	0	L	0	0	0	0	0
8529	3840	af	AN4389.1	58.m07935	AO070261000034	0			-126	-58			ATGTACTCAGCACCGAAAGCCGTACCAGCAAGCGAACATCGAAAAGATATCAACTCTTTAGGGGGATAG		ATGTACTCAGCACCGAAAGCCGTACCAGCAAGCGAACATCGAAAAGATATCAACTCTTTAGGGGGATAG		MYSAPKAVPASEHRKDINSLGG*		MYSAPKAVPASEHRKDINSLGG*		CTCTGGATAA	AAGGGACAAG	0	L	0	0	0	0	0
8525	3840	an	AN4389.1	58.m07935	AO070261000034	0	-277	-158					ATGCAACCGCAACCGCCAACTTTAAATCGAGCTTCAGGGTCAGCAATGCCCTCTATACATCGACCGCACCAAGCGTTCAGAGTTGCGATTTGCAAAAGGAATACGAGTCCGCTTTCGTAA	ATGCAACCGCAACCGCCAACTTTAAATCGAGCTTCAGGGTCAGCAATGCCCTCTATACATCGACCGCACCAAGCGTTCAGAGTTGCGATTTGCAAAAGGAATACGAGTCCGCTTTCGTAA			MQPQPPTLNRASGSAMPSIHRPHQAFRVAICKRNTSPLS*	MQPQPPTLNRASGSAMPSIHRPHQAFRVAICKRNTSPLS*			AATCTGGTAG	GGATGACAGC	0	L	0	0	0	0	0
8526	3840	an	AN4389.1	58.m07935	AO070261000034	0	-232	-158					ATGCCCTCTATACATCGACCGCACCAAGCGTTCAGAGTTGCGATTTGCAAAAGGAATACGAGTCCGCTTTCGTAA	ATGCCCTCTATACATCGACCGCACCAAGCGTTCAGAGTTGCGATTTGCAAAAGGAATACGAGTCCGCTTTCGTAA			MPSIHRPHQAFRVAICKRNTSPLS*	MPSIHRPHQAFRVAICKRNTSPLS*			AGGGTCAGCA	GGATGACAGC	0	L	0	0	0	0	0
8527	3840	an	AN4389.1	58.m07935	AO070261000034	0	-155	-135					ATGACAGCGAAAAGCCGCTGA	ATGACAGCGAAAAGCCGCTGA			MTAKSR*	MTAKSR*			TTTCGTAAGG	CTCCGCACCC	0	L	0	0	0	0	0
8530	3840	ao	AN4389.1	58.m07935	AO070261000034	0					-154	-128	ATGACATATCCCGAGCTCTCATTGTGA			ATGACATATCCCGAGCTCTCATTGTGA	MTYPELSL*			MTYPELSL*	CCCGTGATTG	CATCCACTAA	0	L	0	0	0	0	0
8531	3841	af	AN3430.1	59.m09287	AO070265000004	0			-217	-203			ATGGCATGTTCGTAG		ATGGCATGTTCGTAG		MACS*		MACS*		ATTCAACGTA	CCAATAGAAT	0		0	0	0	0	0
8532	3841	af	AN3430.1	59.m09287	AO070265000004	0			-212	-171			ATGTTCGTAGCCAATAGAATTACTGTCAATAATGATGATTGA		ATGTTCGTAGCCAATAGAATTACTGTCAATAATGATGATTGA		MFVANRITVNNDD*		MFVANRITVNNDD*		ACGTAATGGC	TGCCTTGCAG	0		0	0	0	0	0
8533	3841	af	AN3430.1	59.m09287	AO070265000004	0			-181	-128			ATGATGATTGATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGA		ATGATGATTGATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGA		MMIDALQPWRRGQDSAA*		MMIDALQPWRRGQDSAA*		ACTGTCAATA	GGCACCTAAT	0		0	0	0	0	0
8534	3841	af	AN3430.1	59.m09287	AO070265000004	0			-178	-128			ATGATTGATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGA		ATGATTGATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGA		MIDALQPWRRGQDSAA*		MIDALQPWRRGQDSAA*		GTCAATAATG	GGCACCTAAT	0		0	0	0	0	0
8535	3841	af	AN3430.1	59.m09287	AO070265000004	0			-171	-13			ATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGAGGCACCTAATTATTTCCATGTGTCAACATTCGGACCATCACCGTCAGCAGCATCTCAAACACGCCAACGCTTCGCCACTTTCTTCCTCAATCTTGCCGATATGTCTGTGGTCTGA		ATGCCTTGCAGCCGTGGCGCCGGGGGCAAGATTCTGCTGCCTGAGGCACCTAATTATTTCCATGTGTCAACATTCGGACCATCACCGTCAGCAGCATCTCAAACACGCCAACGCTTCGCCACTTTCTTCCTCAATCTTGCCGATATGTCTGTGGTCTGA		MPCSRGAGGKILLPEAPNYFHVSTFGPSPSAASQTRQRFATFFLNLADMSVV*		MPCSRGAGGKILLPEAPNYFHVSTFGPSPSAASQTRQRFATFFLNLADMSVV*		ATGATGATTG	GGTGCTTTAA	0		0	0	0	0	0
8536	3841	af	AN3430.1	59.m09287	AO070265000004	0			-110	-3			ATGTGTCAACATTCGGACCATCACCGTCAGCAGCATCTCAAACACGCCAACGCTTCGCCACTTTCTTCCTCAATCTTGCCGATATGTCTGTGGTCTGAGGTGCTTTAA		ATGTGTCAACATTCGGACCATCACCGTCAGCAGCATCTCAAACACGCCAACGCTTCGCCACTTTCTTCCTCAATCTTGCCGATATGTCTGTGGTCTGAGGTGCTTTAA		MCQHSDHHRQQHLKHANASPLSSSILPICLWSEVL*		MCQHSDHHRQQHLKHANASPLSSSILPICLWSEVL*		AATTATTTCC	CCATGCCATC	0		0	0	0	0	0
8538	3841	ao	AN3430.1	59.m09287	AO070265000004	0					-215	-147	ATGTCACGATTGCATCGAATGCCCAAGGGAATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA			ATGTCACGATTGCATCGAATGCCCAAGGGAATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA	MSRLHRMPKGMKHGSVRDQNSK*			MSRLHRMPKGMKHGSVRDQNSK*	CTGTTGACTA	CATGACTCCC	0		0	0	0	0	0
8539	3841	ao	AN3430.1	59.m09287	AO070265000004	0					-197	-147	ATGCCCAAGGGAATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA			ATGCCCAAGGGAATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA	MPKGMKHGSVRDQNSK*			MPKGMKHGSVRDQNSK*	ATTGCATCGA	CATGACTCCC	0		0	0	0	0	0
8540	3841	ao	AN3430.1	59.m09287	AO070265000004	0					-185	-147	ATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA			ATGAAGCATGGTTCCGTTCGTGACCAAAATAGTAAGTAA	MKHGSVRDQNSK*			MKHGSVRDQNSK*	GCCCAAGGGA	CATGACTCCC	0		0	0	0	0	0
8541	3841	ao	AN3430.1	59.m09287	AO070265000004	0					-178	-122	ATGGTTCCGTTCGTGACCAAAATAGTAAGTAACATGACTCCCTGCCTCGGCGCCTGA			ATGGTTCCGTTCGTGACCAAAATAGTAAGTAACATGACTCCCTGCCTCGGCGCCTGA	MVPFVTKIVSNMTPCLGA*			MVPFVTKIVSNMTPCLGA*	GGAATGAAGC	GCGGCTTTTT	0		0	0	0	0	0
8542	3841	ao	AN3430.1	59.m09287	AO070265000004	0					-145	-122	ATGACTCCCTGCCTCGGCGCCTGA			ATGACTCCCTGCCTCGGCGCCTGA	MTPCLGA*			MTPCLGA*	AGTAAGTAAC	GCGGCTTTTT	0		0	0	0	0	0

8549	3842	af	AN5267.1	72.m19543	AO070275000042	0			-195	-88			ATGGAAAGACAGGCCTGGTCAACATTAGCCGGGAGGTTAAATCATCTGAATCGGACGATCAAAGGCATAAATACCAGGCACAATTGTCATCGAGACATTGCTTCGTAG		ATGGAAAGACAGGCCTGGTCAACATTAGCCGGGAGGTTAAATCATCTGAATCGGACGATCAAAGGCATAAATACCAGGCACAATTGTCATCGAGACATTGCTTCGTAG		MERQAWSTLAGRLNHLNRTIKGINTRHNCHRDIAS*		MERQAWSTLAGRLNHLNRTIKGINTRHNCHRDIAS*		CTCTTCAGCA	GACTCTCAGC	0	Q	0	0	0	0	0
8543	3842	an	AN5267.1	72.m19543	AO070275000042	0	-231	-121					ATGATGAAGATCGTACATATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA	ATGATGAAGATCGTACATATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA			MMKIVHMEGVSSIRPSMQGSVANLAMICAGILAVNS*	MMKIVHMEGVSSIRPSMQGSVANLAMICAGILAVNS*			CACTGGAAAA	CCGCAATATA	0	Q	0	0	0	0	0
8544	3842	an	AN5267.1	72.m19543	AO070275000042	0	-228	-121					ATGAAGATCGTACATATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA	ATGAAGATCGTACATATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA			MKIVHMEGVSSIRPSMQGSVANLAMICAGILAVNS*	MKIVHMEGVSSIRPSMQGSVANLAMICAGILAVNS*			TGGAAAAATG	CCGCAATATA	0	Q	0	0	0	0	0
8545	3842	an	AN5267.1	72.m19543	AO070275000042	0	-213	-121					ATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA	ATGGAGGGCGTCTCGTCAATCAGACCCTCCATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA			MEGVSSIRPSMQGSVANLAMICAGILAVNS*	MEGVSSIRPSMQGSVANLAMICAGILAVNS*			GATCGTACAT	CCGCAATATA	0	Q	0	0	0	0	0
8546	3842	an	AN5267.1	72.m19543	AO070275000042	0	-183	-121					ATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA	ATGCAGGGCTCCGTTGCTAACCTAGCAATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA			MQGSVANLAMICAGILAVNS*	MQGSVANLAMICAGILAVNS*			CAGACCCTCC	CCGCAATATA	0	Q	0	0	0	0	0
8547	3842	an	AN5267.1	72.m19543	AO070275000042	0	-156	-121					ATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA	ATGATCTGCGCGGGAATCCTGGCGGTTAACTCTTGA			MICAGILAVNS*	MICAGILAVNS*			TAACCTAGCA	CCGCAATATA	0	Q	0	0	0	0	0
8548	3842	an	AN5267.1	72.m19543	AO070275000042	0	-93	-55					ATGGGACTGCTGATACTTCTCAACTTACCAGTGCCTTGA	ATGGGACTGCTGATACTTCTCAACTTACCAGTGCCTTGA			MGLLILLNLPVP*	MGLLILLNLPVP*			AATATCTGCC	CATTTTACCT	0	Q	0	0	0	0	0
8550	3842	ao	AN5267.1	72.m19543	AO070275000042	0					-169	-68	ATGTCAGGGGTCAAATCATCCATGAATGTTGCAGCGTACATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA			ATGTCAGGGGTCAAATCATCCATGAATGTTGCAGCGTACATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA	MSGVKSSMNVAAYMYTAKAINSSMSFSRVSVAQ*			MSGVKSSMNVAAYMYTAKAINSSMSFSRVSVAQ*	TCGAGGAATC	GTATCATTAC	0	Q	0	0	0	0	0
8551	3842	ao	AN5267.1	72.m19543	AO070275000042	0					-148	-68	ATGAATGTTGCAGCGTACATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA			ATGAATGTTGCAGCGTACATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA	MNVAAYMYTAKAINSSMSFSRVSVAQ*			MNVAAYMYTAKAINSSMSFSRVSVAQ*	CAAATCATCC	GTATCATTAC	0	Q	0	0	0	0	0
8552	3842	ao	AN5267.1	72.m19543	AO070275000042	0					-144	-109	ATGTTGCAGCGTACATGTACACGGCAAAAGCTATAA			ATGTTGCAGCGTACATGTACACGGCAAAAGCTATAA	MLQRTCTRQKL*			MLQRTCTRQKL*	TCATCCATGA	ATTCCAGCAT	0	Q	0	0	0	0	0
8553	3842	ao	AN5267.1	72.m19543	AO070275000042	0					-130	-68	ATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA			ATGTACACGGCAAAAGCTATAAATTCCAGCATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA	MYTAKAINSSMSFSRVSVAQ*			MYTAKAINSSMSFSRVSVAQ*	TGCAGCGTAC	GTATCATTAC	0	Q	0	0	0	0	0
8554	3842	ao	AN5267.1	72.m19543	AO070275000042	0					-100	-68	ATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA			ATGAGCTTTTCGAGAGTGTCAGTTGCTCAGTGA	MSFSRVSVAQ*			MSFSRVSVAQ*	AAATTCCAGC	GTATCATTAC	0	Q	0	0	0	0	0
8555	3845	af	AN8794.1	71.m15601	AO070276000069	0			-246	-193			ATGCACCGAGGAAGTTGGGATAGCATTGGGTGGTTTGAACTGAAGATCCGATAA		ATGCACCGAGGAAGTTGGGATAGCATTGGGTGGTTTGAACTGAAGATCCGATAA		MHRGSWDSIGWFELKIR*		MHRGSWDSIGWFELKIR*		AGCAAGACGA	CTCTTTACTG	0		FG09009.1	0	0	0	0
8556	3845	ao	AN8794.1	71.m15601	AO070276000069	0					-234	-208	ATGAGTATTCCGTCAAGGAATCAATAG			ATGAGTATTCCGTCAAGGAATCAATAG	MSIPSRNQ*			MSIPSRNQ*	ACAAAACTAA	TATTTGCTGT	0		FG09009.1	0	0	0	0
8557	3846	af	AN0583.1	69.m15265	AO070280000005	0			-171	-130			ATGCAAAGGGTTCTGTGTTCTATTTTGCGTCTTGCAACTTGA		ATGCAAAGGGTTCTGTGTTCTATTTTGCGTCTTGCAACTTGA		MQRVLCSILRLAT*		MQRVLCSILRLAT*		AAGTAATTGG	TGGAATTCGA	0	A	0	MG04179.1	0	0	0
8558	3846	af	AN0583.1	69.m15265	AO070280000005	0			-130	-113			ATGGAATTCGAAGCCTGA		ATGGAATTCGAAGCCTGA		MEFEA*		MEFEA*		TTGCAACTTG	GCTGTCCTGA	0	A	0	MG04179.1	0	0	0
8559	3846	ao	AN0583.1	69.m15265	AO070280000005	0					-233	-171	ATGATCGATAAGAAGTCAATTATTGGACGAGGAGAGGAGCATTGTCTTTTCTCGTCATTTTAA			ATGATCGATAAGAAGTCAATTATTGGACGAGGAGAGGAGCATTGTCTTTTCTCGTCATTTTAA	MIDKKSIIGRGEEHCLFSSF*			MIDKKSIIGRGEEHCLFSSF*	AAAAAAGTTG	ATCGCTTTTC	0	A	0	MG04179.1	0	0	0
8560	3846	ao	AN0583.1	69.m15265	AO070280000005	0					-104	-63	ATGAAGTTTTCTACGCCAGCAATTTGGTCCCTTTCTCAGTGA			ATGAAGTTTTCTACGCCAGCAATTTGGTCCCTTTCTCAGTGA	MKFSTPAIWSLSQ*			MKFSTPAIWSLSQ*	GTTTTGTTTG	ACCTTTTTTT	0	A	0	MG04179.1	0	0	0
8565	3850	af	AN8218.1	53.m03752	AO070310000090	0			-181	-83			ATGGATGCACGATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAAGTATCTTGGATCGTGCTTCTGGCCCTGCCTGCTGAGATCACCTATTTAA		ATGGATGCACGATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAAGTATCTTGGATCGTGCTTCTGGCCCTGCCTGCTGAGATCACCTATTTAA		MDARCRRVDCDPDHLLKYLGSCFWPCLLRSPI*		MDARCRRVDCDPDHLLKYLGSCFWPCLLRSPI*		AAAGAAAAGG	GCGGTCCTTG	0	O	0	0	0	0	0
8566	3850	af	AN8218.1	53.m03752	AO070310000090	0			-177	-97			ATGCACGATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAAGTATCTTGGATCGTGCTTCTGGCCCTGCCTGCTGA		ATGCACGATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAAGTATCTTGGATCGTGCTTCTGGCCCTGCCTGCTGA		MHDVVVSIAIPTTYLSILDRASGPAC*		MHDVVVSIAIPTTYLSILDRASGPAC*		AAAAGGATGG	GATCACCTAT	0	O	0	0	0	0	0
8567	3850	af	AN8218.1	53.m03752	AO070310000090	0			-170	-132			ATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAA		ATGTCGTCGTGTCGATTGCGATCCCGACCACCTACTTAA		MSSCRLRSRPPT*		MSSCRLRSRPPT*		TGGATGCACG	GTATCTTGGA	0	O	0	0	0	0	0
8561	3850	an	AN8218.1	53.m03752	AO070310000090	0	-220	-77					ATGAACTATTGGGCCGATCATCATCATGATTCAATCTTGCAGCTGCTTACCCGTGGCTGGCTGATGCCTTCTCGTCTAGCGCACTGGCTTGGGAAGCAAATACCTTCCGAATACATAAATATCCCCCTCCTTCGTTATCTGTAA	ATGAACTATTGGGCCGATCATCATCATGATTCAATCTTGCAGCTGCTTACCCGTGGCTGGCTGATGCCTTCTCGTCTAGCGCACTGGCTTGGGAAGCAAATACCTTCCGAATACATAAATATCCCCCTCCTTCGTTATCTGTAA			MNYWADHHHDSILQLLTRGWLMPSRLAHWLGKQIPSEYINIPLLRYL*	MNYWADHHHDSILQLLTRGWLMPSRLAHWLGKQIPSEYINIPLLRYL*			TGCAATCCGC	TGAAGCAGCG	0	O	0	0	0	0	0
8562	3850	an	AN8218.1	53.m03752	AO070310000090	0	-195	-157					ATGATTCAATCTTGCAGCTGCTTACCCGTGGCTGGCTGA	ATGATTCAATCTTGCAGCTGCTTACCCGTGGCTGGCTGA			MIQSCSCLPVAG*	MIQSCSCLPVAG*			GATCATCATC	TGCCTTCTCG	0	O	0	0	0	0	0
8563	3850	an	AN8218.1	53.m03752	AO070310000090	0	-157	-77					ATGCCTTCTCGTCTAGCGCACTGGCTTGGGAAGCAAATACCTTCCGAATACATAAATATCCCCCTCCTTCGTTATCTGTAA	ATGCCTTCTCGTCTAGCGCACTGGCTTGGGAAGCAAATACCTTCCGAATACATAAATATCCCCCTCCTTCGTTATCTGTAA			MPSRLAHWLGKQIPSEYINIPLLRYL*	MPSRLAHWLGKQIPSEYINIPLLRYL*			TGGCTGGCTG	TGAAGCAGCG	0	O	0	0	0	0	0
8564	3850	an	AN8218.1	53.m03752	AO070310000090	0	-77	-15					ATGAAGCAGCGAGCAGCCAGCCTTCAGCCAGTCCAATCGCGCTATAGTGCAGGGTACCTGTAG	ATGAAGCAGCGAGCAGCCAGCCTTCAGCCAGTCCAATCGCGCTATAGTGCAGGGTACCTGTAG			MKQRAASLQPVQSRYSAGYL*	MKQRAASLQPVQSRYSAGYL*			GTTATCTGTA	TGGTTCAGTT	0	O	0	0	0	0	0
8568	3850	ao	AN8218.1	53.m03752	AO070310000090	0					-153	-103	ATGCAATGCTTGATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGA			ATGCAATGCTTGATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGA	MQCLMIFLSWPVGMRC*			MQCLMIFLSWPVGMRC*	TCTTGGCAGC	ATCCTGCTCA	0	O	0	0	0	0	0
8569	3850	ao	AN8218.1	53.m03752	AO070310000090	0					-148	-68	ATGCTTGATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGAATCCTGCTCAGATGCTATGCTTTGACAATATTTAA			ATGCTTGATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGAATCCTGCTCAGATGCTATGCTTTGACAATATTTAA	MLDDLSQLASGHALLNPAQMLCFDNI*			MLDDLSQLASGHALLNPAQMLCFDNI*	GCAGCATGCA	ACCATTCATG	0	O	0	0	0	0	0
8570	3850	ao	AN8218.1	53.m03752	AO070310000090	0					-141	-103	ATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGA			ATGATCTTTCTCAGCTGGCCAGTGGGCATGCGCTGCTGA	MIFLSWPVGMRC*			MIFLSWPVGMRC*	GCAATGCTTG	ATCCTGCTCA	0	O	0	0	0	0	0
8571	3850	ao	AN8218.1	53.m03752	AO070310000090	0					-114	-103	ATGCGCTGCTGA			ATGCGCTGCTGA	MRC*			MRC*	GCCAGTGGGC	ATCCTGCTCA	0	O	0	0	0	0	0
8572	3850	ao	AN8218.1	53.m03752	AO070310000090	0					-91	-68	ATGCTATGCTTTGACAATATTTAA			ATGCTATGCTTTGACAATATTTAA	MLCFDNI*			MLCFDNI*	TCCTGCTCAG	ACCATTCATG	0	O	0	0	0	0	0
8575	3851	af	AN3811.1	57.m05671	AO070311000008	0			-260	-192			ATGAATCAAAAGCGCTCAGTGAAGTTGATAGGATATGATCTAGGTTTTTCCAACCCAAATGACGTATGA		ATGAATCAAAAGCGCTCAGTGAAGTTGATAGGATATGATCTAGGTTTTTCCAACCCAAATGACGTATGA		MNQKRSVKLIGYDLGFSNPNDV*		MNQKRSVKLIGYDLGFSNPNDV*		TTGAGCGAAA	GGAATTGCGA	0	KL	0	0	0	0	0
8576	3851	af	AN3811.1	57.m05671	AO070311000008	0			-195	-85			ATGAGGAATTGCGAGGGCAGACGAAGGCGACAGACGGCGAAGGTCGAAGTGGGAGCGGACAAATTCAGTTTGCGGCCAACAGCTCTTTTCCTAGTCGGGAAATCCGCCTGA		ATGAGGAATTGCGAGGGCAGACGAAGGCGACAGACGGCGAAGGTCGAAGTGGGAGCGGACAAATTCAGTTTGCGGCCAACAGCTCTTTTCCTAGTCGGGAAATCCGCCTGA		MRNCEGRRRRQTAKVEVGADKFSLRPTALFLVGKSA*		MRNCEGRRRRQTAKVEVGADKFSLRPTALFLVGKSA*		CAAATGACGT	TAAGTATCCA	0	KL	0	0	0	0	0
8573	3851	an	AN3811.1	57.m05671	AO070311000008	0	-250	-158					ATGTGTATATATCCAGTAAAAAGAAGTTTAACAGGCACAGTACCAAATTATGCTGCAAGTTGTTCGACCGCAGGAGTGAAGTCCAAAGGGTGA	ATGTGTATATATCCAGTAAAAAGAAGTTTAACAGGCACAGTACCAAATTATGCTGCAAGTTGTTCGACCGCAGGAGTGAAGTCCAAAGGGTGA			MCIYPVKRSLTGTVPNYAASCSTAGVKSKG*	MCIYPVKRSLTGTVPNYAASCSTAGVKSKG*			CCGTGAAATA	GAGGAAGCCA	0	KL	0	0	0	0	0
8574	3851	an	AN3811.1	57.m05671	AO070311000008	0	-201	-172					ATGCTGCAAGTTGTTCGACCGCAGGAGTGA	ATGCTGCAAGTTGTTCGACCGCAGGAGTGA			MLQVVRPQE*	MLQVVRPQE*			GTACCAAATT	AGTCCAAAGG	0	KL	0	0	0	0	0
8577	3851	ao	AN3811.1	57.m05671	AO070311000008	0					-198	-94	ATGGCTGGTTTTAGCAGAAGAGACGATAACGGCGGCGGGGAATTTGGATCGGCGACAAAAATCAATTTGAAAGAATTGAGCTCCTTTCCCGATTGGGTAATATAG			ATGGCTGGTTTTAGCAGAAGAGACGATAACGGCGGCGGGGAATTTGGATCGGCGACAAAAATCAATTTGAAAGAATTGAGCTCCTTTCCCGATTGGGTAATATAG	MAGFSRRDDNGGGEFGSATKINLKELSSFPDWVI*			MAGFSRRDDNGGGEFGSATKINLKELSSFPDWVI*	AAAAGGCACA	ATCCTCCGCC	0	KL	0	0	0	0	0
8580	3853	af	AN2555.1	57.m05650	AO070319000164	0			-191	-171			ATGTCTCCCGGCTTCTGGTGA		ATGTCTCCCGGCTTCTGGTGA		MSPGFW*		MSPGFW*		TGGACTTTCC	TAGGCTAAAA	0	OE	0	0	0	0	0
8581	3853	af	AN2555.1	57.m05650	AO070319000164	0			-119	-102			ATGGCTATCGTCATATAA		ATGGCTATCGTCATATAA		MAIVI*		MAIVI*		CGTGGCAGAC	ATGCAGCCAA	0	OE	0	0	0	0	0
8582	3853	af	AN2555.1	57.m05650	AO070319000164	0			-101	-27			ATGCAGCCAATTCTCCTCGGCGTAATTGGGACTGATCTTCACCCGTACCTGCAAGCCTCAGTTTCCCGTCTTTGA		ATGCAGCCAATTCTCCTCGGCGTAATTGGGACTGATCTTCACCCGTACCTGCAAGCCTCAGTTTCCCGTCTTTGA		MQPILLGVIGTDLHPYLQASVSRL*		MQPILLGVIGTDLHPYLQASVSRL*		CGTCATATAA	TTTCCCCTTT	0	OE	0	0	0	0	0
8578	3853	an	AN2555.1	57.m05650	AO070319000164	0	-127	-80					ATGCGTTTCTCCACTGTTGCACCGCTTATAAACGACTGTTCCCCTTGA	ATGCGTTTCTCCACTGTTGCACCGCTTATAAACGACTGTTCCCCTTGA			MRFSTVAPLINDCSP*	MRFSTVAPLINDCSP*			CTCTTCTACC	TCTGGTGATG	0	OE	0	0	0	0	0
8579	3853	an	AN2555.1	57.m05650	AO070319000164	0	-72	-52					ATGGGAAGGAATAAGAATTAA	ATGGGAAGGAATAAGAATTAA			MGRNKN*	MGRNKN*			TGATCTGGTG	CTTTCCGCTC	0	OE	0	0	0	0	0
8583	3853	ao	AN2555.1	57.m05650	AO070319000164	0					-172	-149	ATGGAGCGGCCCACAAGCTGGTAG			ATGGAGCGGCCCACAAGCTGGTAG	MERPTSW*			MERPTSW*	GAACAGTTCC	AATACCTCCG	0	OE	0	0	0	0	0
8584	3853	ao	AN2555.1	57.m05650	AO070319000164	0					-95	-21	ATGCAGGCCGTGGGCTCATCCCGTTCCATTGTCTATAAAGGCCCGCGCACCCCGACGGGAAAAGCCTTTCTCTGA			ATGCAGGCCGTGGGCTCATCCCGTTCCATTGTCTATAAAGGCCCGCGCACCCCGACGGGAAAAGCCTTTCTCTGA	MQAVGSSRSIVYKGPRTPTGKAFL*			MQAVGSSRSIVYKGPRTPTGKAFL*	CTCTACCGTC	TTTAATCACG	0	OE	0	0	0	0	0
8588	3856	an	AN5722.1	54.m06842	AO070324000128	0	-124	-98					ATGCTGGCCTTGATGCCTGGGGCATAA	ATGCTGGCCTTGATGCCTGGGGCATAA			MLALMPGA*	MLALMPGA*			CGTTGCGGTG	TTTGCCGACA	0	T	0	0	0	0	0
8589	3856	an	AN5722.1	54.m06842	AO070324000128	0	-112	-98					ATGCCTGGGGCATAA	ATGCCTGGGGCATAA			MPGA*	MPGA*			GCTGGCCTTG	TTTGCCGACA	0	T	0	0	0	0	0
8590	3856	ao	AN5722.1	54.m06842	AO070324000128	0					-134	-87	ATGGCTGGGGTCCGATTAAACCCCGAAAGGTCTCCGCCATTAGACTAG			ATGGCTGGGGTCCGATTAAACCCCGAAAGGTCTCCGCCATTAGACTAG	MAGVRLNPERSPPLD*			MAGVRLNPERSPPLD*	ATAAGCCGTC	TAAATAGCTG	0	T	0	0	0	0	0
8591	3857	an	AN6596.1	62.m03202	AO070326000045	0	-177	-166					ATGGCGAGTTAG	ATGGCGAGTTAG			MAS*	MAS*			TAGATCGTCC	TTCGTGGTTG	0		0	0	0	0	0
8592	3857	an	AN6596.1	62.m03202	AO070326000045	0	-137	-111					ATGAGTCATCATAGCTCCCTTAATTAG	ATGAGTCATCATAGCTCCCTTAATTAG			MSHHSSLN*	MSHHSSLN*			CCTGCATTTG	GTTAGTCTAG	0		0	0	0	0	0
8593	3857	ao	AN6596.1	62.m03202	AO070326000045	0					-201	-184	ATGACCTACTCTCGGTAG			ATGACCTACTCTCGGTAG	MTYSR*			MTYSR*	AGACTAAAAC	GCGGTGTACC	0		0	0	0	0	0
8594	3857	ao	AN6596.1	62.m03202	AO070326000045	0					-133	-26	ATGCCCCCGTATTCCTGCCACGTGCTGCCTCAGGCATATGCCATAAGCGTCATTATTGTCTGTGAAGCAACACGAAGTTGCGGCATTCCGCTCCGTCGGCCACTCTAG			ATGCCCCCGTATTCCTGCCACGTGCTGCCTCAGGCATATGCCATAAGCGTCATTATTGTCTGTGAAGCAACACGAAGTTGCGGCATTCCGCTCCGTCGGCCACTCTAG	MPPYSCHVLPQAYAISVIIVCEATRSCGIPLRRPL*			MPPYSCHVLPQAYAISVIIVCEATRSCGIPLRRPL*	CGTACATTGC	GCTTCGACCT	0		0	0	0	0	0
8597	3858	af	AN6614.1	62.m03213	AO070326000063	0			-124	-113			ATGCGGGCCTGA		ATGCGGGCCTGA		MRA*		MRA*		TACAATAACA	AATGCCACTT	0	P	FG05149.1	0	0	0	0
8598	3858	af	AN6614.1	62.m03213	AO070326000063	0			-111	-85			ATGCCACTTACCGTGATAGGATCCTGA		ATGCCACTTACCGTGATAGGATCCTGA		MPLTVIGS*		MPLTVIGS*		CGGGCCTGAA	ATTAAATATA	0	P	FG05149.1	0	0	0	0
8595	3858	an	AN6614.1	62.m03213	AO070326000063	0	-159	-121					ATGGTCCTATCGGGACACCCTGGAAGCAACGCAAAATAA	ATGGTCCTATCGGGACACCCTGGAAGCAACGCAAAATAA			MVLSGHPGSNAK*	MVLSGHPGSNAK*			CAACCATAAG	ACACACTAAG	0	P	FG05149.1	0	0	0	0
8596	3858	an	AN6614.1	62.m03213	AO070326000063	0	-104	-21					ATGACAGCTTTCCTTGTGGCACTGGAGCCTACGGACTGCTCCCGCACACCGGAATACAAATTTGATCCCGTGCTTTTTAAGTGA	ATGACAGCTTTCCTTGTGGCACTGGAGCCTACGGACTGCTCCCGCACACCGGAATACAAATTTGATCCCGTGCTTTTTAAGTGA			MTAFLVALEPTDCSRTPEYKFDPVLFK*	MTAFLVALEPTDCSRTPEYKFDPVLFK*			TAAGCGGGAC	GTCGACTGAC	0	P	FG05149.1	0	0	0	0

8599	3858	ao	AN6614.1	62.m03213	AO070326000063	0					-126	-88	ATGGTCCTGCTGAAAAGTCTTGGATGCAACTCGACGTGA			ATGGTCCTGCTGAAAAGTCTTGGATGCAACTCGACGTGA	MVLLKSLGCNST*			MVLLKSLGCNST*	CGCATCAACA	CATGATATCA	0	P	FG05149.1	0	0	0	0
8600	3858	ao	AN6614.1	62.m03213	AO070326000063	0					-103	-83	ATGCAACTCGACGTGACATGA			ATGCAACTCGACGTGACATGA	MQLDVT*			MQLDVT*	AAAGTCTTGG	TATCATTTGC	0	P	FG05149.1	0	0	0	0
8601	3858	ao	AN6614.1	62.m03213	AO070326000063	0					-86	-57	ATGATATCATTTGCTAGTGCAGGAGCTTGA			ATGATATCATTTGCTAGTGCAGGAGCTTGA	MISFASAGA*			MISFASAGA*	TCGACGTGAC	GGACTGCTCC	0	P	FG05149.1	0	0	0	0
8603	3859	af	AN3425.1	59.m09279	AO070327000006	0			-178	-125			ATGTCCATCGTCTTTGTGAAAACATTCTTTCTGCCGACACTCTCCATACCCTAG		ATGTCCATCGTCTTTGTGAAAACATTCTTTCTGCCGACACTCTCCATACCCTAG		MSIVFVKTFFLPTLSIP*		MSIVFVKTFFLPTLSIP*		CAGTCTTATC	TATTGAGATA	0	Z	0	0	NCU04256.1	0	0
8602	3859	an	AN3425.1	59.m09279	AO070327000006	0	-212	-141					ATGTCATTTGTCTCTCAAACTACCAGTCTCTTTGCATCACACTCGATACCGTTTGATAGTCGGACTCGATAA	ATGTCATTTGTCTCTCAAACTACCAGTCTCTTTGCATCACACTCGATACCGTTTGATAGTCGGACTCGATAA			MSFVSQTTSLFASHSIPFDSRTR*	MSFVSQTTSLFASHSIPFDSRTR*			TGAGATTACC	CTGCACTATC	0	Z	0	0	NCU04256.1	0	0
8604	3859	ao	AN3425.1	59.m09279	AO070327000006	0					-222	-163	ATGAACTTTGTCTCCGAGAAATTATTCCTATTGTCAACTATTTCCATACCTCTCGCATAG			ATGAACTTTGTCTCCGAGAAATTATTCCTATTGTCAACTATTTCCATACCTCTCGCATAG	MNFVSEKLFLLSTISIPLA*			MNFVSEKLFLLSTISIPLA*	GTGTTATACC	CCCTACTTTG	0	Z	0	0	NCU04256.1	0	0
8609	3860	af	AN2348.1	59.m09458	AO070327000141	0			-240	-13			ATGGTCAGAAAGACCATGACCTACAATGCCTTGACGAATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAACCAAAATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		ATGGTCAGAAAGACCATGACCTACAATGCCTTGACGAATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAACCAAAATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		MVRKTMTYNALTNDGSSRPLFPEELTKMPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		MVRKTMTYNALTNDGSSRPLFPEELTKMPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		GGATAGCATC	TTCCGACCAA	0	M	0	0	0	0	0
8610	3860	af	AN2348.1	59.m09458	AO070327000141	0			-225	-13			ATGACCTACAATGCCTTGACGAATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAACCAAAATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		ATGACCTACAATGCCTTGACGAATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAACCAAAATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		MTYNALTNDGSSRPLFPEELTKMPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		MTYNALTNDGSSRPLFPEELTKMPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		CAGAAAGACC	TTCCGACCAA	0	M	0	0	0	0	0
8611	3860	af	AN2348.1	59.m09458	AO070327000141	0			-203	-165			ATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAA		ATGATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAA		MMGHLDHYSPKS*		MMGHLDHYSPKS*		GCCTTGACGA	CCAAAATGCC	0	M	0	0	0	0	0
8612	3860	af	AN2348.1	59.m09458	AO070327000141	0			-200	-165			ATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAA		ATGGGTCATCTCGACCATTATTCCCCGAAGAGCTAA		MGHLDHYSPKS*		MGHLDHYSPKS*		TTGACGAATG	CCAAAATGCC	0	M	0	0	0	0	0
8613	3860	af	AN2348.1	59.m09458	AO070327000141	0			-159	-13			ATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		ATGCCGGGACCAGTCGAACTCGCATGGCATGATCCTTCAGTCGGGCACAGCCAACGTATAAAAGACCTGTCCACTCGATGTCTCACAATCGATATCGATCTGTCCTGGCGTGTTCATCAATTCCACAGGGCCAAACATTATTCATAG		MPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		MPGPVELAWHDPSVGHSQRIKDLSTRCLTIDIDLSWRVHQFHRAKHYS*		GCTAACCAAA	TTCCGACCAA	0	M	0	0	0	0	0
8614	3860	af	AN2348.1	59.m09458	AO070327000141	0			-131	-99			ATGATCCTTCAGTCGGGCACAGCCAACGTATAA		ATGATCCTTCAGTCGGGCACAGCCAACGTATAA		MILQSGTANV*		MILQSGTANV*		CTCGCATGGC	AAGACCTGTC	0	M	0	0	0	0	0
8605	3860	an	AN2348.1	59.m09458	AO070327000141	0	-198	-7					ATGGCCCAGTATACTTCAGTCTGCATACGCAAAACCAAAATAAACAACCAATCAGGACTCGGCAAGAATGCACCCTGCAGGACTAGTTGCAGTGGGGGCGATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGAGCCACCACCGTCTCAGAGAGTCAAAGCGGCTATTTTCCATGTGA	ATGGCCCAGTATACTTCAGTCTGCATACGCAAAACCAAAATAAACAACCAATCAGGACTCGGCAAGAATGCACCCTGCAGGACTAGTTGCAGTGGGGGCGATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGAGCCACCACCGTCTCAGAGAGTCAAAGCGGCTATTTTCCATGTGA			MAQYTSVCIRKTKINNQSGLGKNAPCRTSCSGGDGDTEPPMLTISFLPLSHHRLRESKRLFSM*	MAQYTSVCIRKTKINNQSGLGKNAPCRTSCSGGDGDTEPPMLTISFLPLSHHRLRESKRLFSM*			GGTTAGCAAA	TGCAGGATGG	0	M	0	0	0	0	0
8606	3860	an	AN2348.1	59.m09458	AO070327000141	0	-131	-51					ATGCACCCTGCAGGACTAGTTGCAGTGGGGGCGATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGA	ATGCACCCTGCAGGACTAGTTGCAGTGGGGGCGATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGA			MHPAGLVAVGAMEIRSPLCSPSPSCR*	MHPAGLVAVGAMEIRSPLCSPSPSCR*			CTCGGCAAGA	GCCACCACCG	0	M	0	0	0	0	0
8607	3860	an	AN2348.1	59.m09458	AO070327000141	0	-98	-51					ATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGA	ATGGAGATACGGAGCCCCCTATGCTCACCATCTCCTTCTTGCCGCTGA			MEIRSPLCSPSPSCR*	MEIRSPLCSPSPSCR*			AGTGGGGGCG	GCCACCACCG	0	M	0	0	0	0	0
8608	3860	an	AN2348.1	59.m09458	AO070327000141	0	-78	-7					ATGCTCACCATCTCCTTCTTGCCGCTGAGCCACCACCGTCTCAGAGAGTCAAAGCGGCTATTTTCCATGTGA	ATGCTCACCATCTCCTTCTTGCCGCTGAGCCACCACCGTCTCAGAGAGTCAAAGCGGCTATTTTCCATGTGA			MLTISFLPLSHHRLRESKRLFSM*	MLTISFLPLSHHRLRESKRLFSM*			GGAGCCCCCT	TGCAGGATGG	0	M	0	0	0	0	0
8615	3860	ao	AN2348.1	59.m09458	AO070327000141	0					-253	-233	ATGCCGCCGCTTACAGCCTGA			ATGCCGCCGCTTACAGCCTGA	MPPLTA*			MPPLTA*	AAGCTCTAAT	CATTTGACTT	0	M	0	0	0	0	0
8616	3860	ao	AN2348.1	59.m09458	AO070327000141	0					-213	-187	ATGAGAGGGTTGATAAGCATCAGGTGA			ATGAGAGGGTTGATAAGCATCAGGTGA	MRGLISIR*			MRGLISIR*	TGAAGAGCGT	CGCCCTGGCC	0	M	0	0	0	0	0
8617	3860	ao	AN2348.1	59.m09458	AO070327000141	0					-174	-103	ATGACGGGTCGGGATGACCCGGTGATCGTCTTGTACACAGCACATTTATACTACGGTGGAGAGCTGAGATAA			ATGACGGGTCGGGATGACCCGGTGATCGTCTTGTACACAGCACATTTATACTACGGTGGAGAGCTGAGATAA	MTGRDDPVIVLYTAHLYYGGELR*			MTGRDDPVIVLYTAHLYYGGELR*	CCCTGGCCCC	ATAAAGCTGC	0	M	0	0	0	0	0
8618	3860	ao	AN2348.1	59.m09458	AO070327000141	0					-161	-150	ATGACCCGGTGA			ATGACCCGGTGA	MTR*			MTR*	ACGGGTCGGG	TCGTCTTGTA	0	M	0	0	0	0	0
8620	3862	af	AN0460.1	54.m06609	AO070328000178	0			-227	-216			ATGGAAACATAA		ATGGAAACATAA		MET*		MET*		TTTGATCGCT	TGATGAGACA	0		0	0	0	0	0
8621	3862	af	AN0460.1	54.m06609	AO070328000178	0			-216	-151			ATGATGAGACATCCTTTAACAGTATATAGGCAATTTTCTTTGACGACGGTTCAATACACACTATAA		ATGATGAGACATCCTTTAACAGTATATAGGCAATTTTCTTTGACGACGGTTCAATACACACTATAA		MMRHPLTVYRQFSLTTVQYTL*		MMRHPLTVYRQFSLTTVQYTL*		TGGAAACATA	GTATGCTTTT	0		0	0	0	0	0
8622	3862	af	AN0460.1	54.m06609	AO070328000178	0			-213	-151			ATGAGACATCCTTTAACAGTATATAGGCAATTTTCTTTGACGACGGTTCAATACACACTATAA		ATGAGACATCCTTTAACAGTATATAGGCAATTTTCTTTGACGACGGTTCAATACACACTATAA		MRHPLTVYRQFSLTTVQYTL*		MRHPLTVYRQFSLTTVQYTL*		AAACATAATG	GTATGCTTTT	0		0	0	0	0	0
8623	3862	af	AN0460.1	54.m06609	AO070328000178	0			-148	-104			ATGCTTTTTTCGGCTAATATCTCAAACATCCGGAATCCTCTATGA		ATGCTTTTTTCGGCTAATATCTCAAACATCCGGAATCCTCTATGA		MLFSANISNIRNPL*		MLFSANISNIRNPL*		CACTATAAGT	GCAAGATGTG	0		0	0	0	0	0
8624	3862	af	AN0460.1	54.m06609	AO070328000178	0			-107	-90			ATGAGCAAGATGTGCTAA		ATGAGCAAGATGTGCTAA		MSKMC*		MSKMC*		GGAATCCTCT	AAATCTCTGA	0		0	0	0	0	0
8619	3862	an	AN0460.1	54.m06609	AO070328000178	0	-160	-89					ATGTTGCCGTTCTATAACTATTGTGTTGCCTTTACTCATCATAAGGCTGGCCCACTTGTGCGGGCATTATAA	ATGTTGCCGTTCTATAACTATTGTGTTGCCTTTACTCATCATAAGGCTGGCCCACTTGTGCGGGCATTATAA			MLPFYNYCVAFTHHKAGPLVRAL*	MLPFYNYCVAFTHHKAGPLVRAL*			CTCAGACCTG	CCTGGATTTT	0		0	0	0	0	0
8625	3862	ao	AN0460.1	54.m06609	AO070328000178	0					-144	-124	ATGATGTCGCTAATGCTTTAG			ATGATGTCGCTAATGCTTTAG	MMSLML*			MMSLML*	CAGACGAATT	ACTGGAGTAC	0		0	0	0	0	0
8626	3862	ao	AN0460.1	54.m06609	AO070328000178	0					-141	-124	ATGTCGCTAATGCTTTAG			ATGTCGCTAATGCTTTAG	MSLML*			MSLML*	ACGAATTATG	ACTGGAGTAC	0		0	0	0	0	0
8627	3862	ao	AN0460.1	54.m06609	AO070328000178	0					-72	-46	ATGTACTTTCAGGGTAACCGCCACTAG			ATGTACTTTCAGGGTAACCGCCACTAG	MYFQGNRH*			MYFQGNRH*	TCGGATACTC	ACCTTTTAGC	0		0	0	0	0	0
8634	3864	af	AN8070.1	53.m03921	AO070330000027	0			-136	-113			ATGACCATGTCACCAACAGTATAG		ATGACCATGTCACCAACAGTATAG		MTMSPTV*		MTMSPTV*		GAAGTGCAAG	AGATTGAGCG	0	S	0	0	0	0	0
8635	3864	af	AN8070.1	53.m03921	AO070330000027	0			-130	-113			ATGTCACCAACAGTATAG		ATGTCACCAACAGTATAG		MSPTV*		MSPTV*		CAAGATGACC	AGATTGAGCG	0	S	0	0	0	0	0
8628	3864	an	AN8070.1	53.m03921	AO070330000027	0	-274	-161					ATGCAGCATCATGGACGCATTCCTTTGGCAGCGAAGCCATTAGCTGCAAGTGCCATGAACATTATTGGTTTAACAAGAACGTCTAACAAGCTGATGCTCGTCAGAACACGGTAA	ATGCAGCATCATGGACGCATTCCTTTGGCAGCGAAGCCATTAGCTGCAAGTGCCATGAACATTATTGGTTTAACAAGAACGTCTAACAAGCTGATGCTCGTCAGAACACGGTAA			MQHHGRIPLAAKPLAASAMNIIGLTRTSNKLMLVRTR*	MQHHGRIPLAAKPLAASAMNIIGLTRTSNKLMLVRTR*			ACCAGGAGCA	GGTTGGATGT	0	S	0	0	0	0	0
8629	3864	an	AN8070.1	53.m03921	AO070330000027	0	-264	-232					ATGGACGCATTCCTTTGGCAGCGAAGCCATTAG	ATGGACGCATTCCTTTGGCAGCGAAGCCATTAG			MDAFLWQRSH*	MDAFLWQRSH*			ATGCAGCATC	CTGCAAGTGC	0	S	0	0	0	0	0
8630	3864	an	AN8070.1	53.m03921	AO070330000027	0	-220	-161					ATGAACATTATTGGTTTAACAAGAACGTCTAACAAGCTGATGCTCGTCAGAACACGGTAA	ATGAACATTATTGGTTTAACAAGAACGTCTAACAAGCTGATGCTCGTCAGAACACGGTAA			MNIIGLTRTSNKLMLVRTR*	MNIIGLTRTSNKLMLVRTR*			TGCAAGTGCC	GGTTGGATGT	0	S	0	0	0	0	0
8631	3864	an	AN8070.1	53.m03921	AO070330000027	0	-181	-161					ATGCTCGTCAGAACACGGTAA	ATGCTCGTCAGAACACGGTAA			MLVRTR*	MLVRTR*			TAACAAGCTG	GGTTGGATGT	0	S	0	0	0	0	0
8632	3864	an	AN8070.1	53.m03921	AO070330000027	0	-154	-140					ATGTTGAGGACATGA	ATGTTGAGGACATGA			MLRT*	MLRT*			GTAAGGTTGG	GAAGTGATAC	0	S	0	0	0	0	0
8633	3864	an	AN8070.1	53.m03921	AO070330000027	0	-143	-102					ATGAGAAGTGATACTCGAGGCGGTGACAGCCGGCAGTTCTAG	ATGAGAAGTGATACTCGAGGCGGTGACAGCCGGCAGTTCTAG			MRSDTRGGDSRQF*	MRSDTRGGDSRQF*			TGTTGAGGAC	AAGAGTGGCC	0	S	0	0	0	0	0
8636	3864	ao	AN8070.1	53.m03921	AO070330000027	0					-102	-85	ATGATAGGCGGTGGATAA			ATGATAGGCGGTGGATAA	MIGGG*			MIGGG*	ACGCCGAGGG	TGGCAGTATA	0	S	0	0	0	0	0
8637	3864	ao	AN8070.1	53.m03921	AO070330000027	0					-85	-62	ATGGCAGTATACAATGACCGATAG			ATGGCAGTATACAATGACCGATAG	MAVYNDR*			MAVYNDR*	GCGGTGGATA	CGACTGCGAC	0	S	0	0	0	0	0
8642	3865	af	AN1132.1	70.m15104	AO070331000124	0			-148	-107			ATGTTTGCCATATCAATCAATACATTGGTTCTTTCTTCCTGA		ATGTTTGCCATATCAATCAATACATTGGTTCTTTCTTCCTGA		MFAISINTLVLSS*		MFAISINTLVLSS*		AACTTTATTG	CCCCTTCACA	0	E	0	0	0	0	0
8643	3865	af	AN1132.1	70.m15104	AO070331000124	0			-63	-31			ATGTGCAGCTTTCGAGTCTCCGGTTGTTCATGA		ATGTGCAGCTTTCGAGTCTCCGGTTGTTCATGA		MCSFRVSGCS*		MCSFRVSGCS*		TTCTTTCAAC	GCTTTAAGTC	0	E	0	0	0	0	0
8638	3865	an	AN1132.1	70.m15104	AO070331000124	0	-86	-15					ATGTTTCATGCGTTCTCTTCACAATATATAACATGTCAGCCTAACATGATTTCCACCTTTGCTGTGGTATAA	ATGTTTCATGCGTTCTCTTCACAATATATAACATGTCAGCCTAACATGATTTCCACCTTTGCTGTGGTATAA			MFHAFSSQYITCQPNMISTFAVV*	MFHAFSSQYITCQPNMISTFAVV*			TCCACCTCTG	TCCGTCGTCT	0	E	0	0	0	0	0
8639	3865	an	AN1132.1	70.m15104	AO070331000124	0	-79	-56					ATGCGTTCTCTTCACAATATATAA	ATGCGTTCTCTTCACAATATATAA			MRSLHNI*	MRSLHNI*			CTGATGTTTC	CATGTCAGCC	0	E	0	0	0	0	0
8644	3865	ao	AN1132.1	70.m15104	AO070331000124	0					-188	-159	ATGCCGTCACCCGGTCATTCTAGCTTTTGA			ATGCCGTCACCCGGTCATTCTAGCTTTTGA	MPSPGHSSF*			MPSPGHSSF*	AGACTCACTC	CAGTGAATTC	0	E	0	0	0	0	0
8645	3865	ao	AN1132.1	70.m15104	AO070331000124	0					-89	-57	ATGTCTCCATCTCGTTACCCACGCCGCGCATAA			ATGTCTCCATCTCGTTACCCACGCCGCGCATAA	MSPSRYPRRA*			MSPSRYPRRA*	TCCTTGTTCA	TCCAGGAATG	0	E	0	0	0	0	0
8650	3866	af	AN9130.1	66.m04599	AO070332000125	0			-225	-73			ATGCCATCCTATTCCAGTTGGACGAATCCAATATACTTGGCACCTGCATCTTTCCTTTCCGACATACCCGAAGGACGCCTCTCTGCATGGTCAGGCACAGTCAGGTCAGATTTGTCGTTCCTTGATTACCAGCTTCCCGGGGGGGGGGGGTTAA		ATGCCATCCTATTCCAGTTGGACGAATCCAATATACTTGGCACCTGCATCTTTCCTTTCCGACATACCCGAAGGACGCCTCTCTGCATGGTCAGGCACAGTCAGGTCAGATTTGTCGTTCCTTGATTACCAGCTTCCCGGGGGGGGGGGGTTAA		MPSYSSWTNPIYLAPASFLSDIPEGRLSAWSGTVRSDLSFLDYQLPGGGG*		MPSYSSWTNPIYLAPASFLSDIPEGRLSAWSGTVRSDLSFLDYQLPGGGG*		CTGTTGGCGA	AACAAACCCG	0	I	0	0	0	0	0
8651	3866	af	AN9130.1	66.m04599	AO070332000125	0			-139	-101			ATGGTCAGGCACAGTCAGGTCAGATTTGTCGTTCCTTGA		ATGGTCAGGCACAGTCAGGTCAGATTTGTCGTTCCTTGA		MVRHSQVRFVVP*		MVRHSQVRFVVP*		GCCTCTCTGC	TTACCAGCTT	0	I	0	0	0	0	0
8647	3866	an	AN9130.1	66.m04599	AO070332000125	0	-149	-96					ATGCAGGCTTCTGCGACTGTTGTTATTATTATGACTATGATTATTATTATTTAA	ATGCAGGCTTCTGCGACTGTTGTTATTATTATGACTATGATTATTATTATTTAA			MQASATVVIIMTMIIII*	MQASATVVIIMTMIIII*			CTGACGAGCC	ACATCGGCAA	0	I	0	0	0	0	0
8648	3866	an	AN9130.1	66.m04599	AO070332000125	0	-119	-96					ATGACTATGATTATTATTATTTAA	ATGACTATGATTATTATTATTTAA			MTMIIII*	MTMIIII*			TGTTATTATT	ACATCGGCAA	0	I	0	0	0	0	0
8649	3866	an	AN9130.1	66.m04599	AO070332000125	0	-113	-96					ATGATTATTATTATTTAA	ATGATTATTATTATTTAA			MIIII*	MIIII*			TATTATGACT	ACATCGGCAA	0	I	0	0	0	0	0
8653	3869	af	AN1520.1	55.m03039	AO070334000238	0			-210	-199			ATGCGCAAGTGA		ATGCGCAAGTGA		MRK*		MRK*		TTGTTGTTGA	ACCATTGATT	0	Y	0	0	0	0	0
8654	3869	ao	AN1520.1	55.m03039	AO070334000238	0					-193	-170	ATGTTGTTGTTGTTGTTGTTGTGA			ATGTTGTTGTTGTTGTTGTTGTGA	MLLLLLL*			MLLLLLL*	ATTCCTGTTG	GCCGTAGGCA	0	Y	0	0	0	0	0
8657	3871	af	AN1038.1	70.m15196	AO070336000073	0			-242	-228			ATGCGATGGCCATAA		ATGCGATGGCCATAA		MRWP*		MRWP*		GTCATCTAAA	GGGTGTCTTG	0	R	0	0	0	0	0
8658	3871	af	AN1038.1	70.m15196	AO070336000073	0			-237	-118			ATGGCCATAAGGGTGTCTTGTCTTCGTATGAACAATGCCAAGAGATGTAGCTACCTAGTATGCGGAGAGACTCGACCGCCTTCCTGCCAGAGGACCAGACATCTGGATATTGTCTCCTGA		ATGGCCATAAGGGTGTCTTGTCTTCGTATGAACAATGCCAAGAGATGTAGCTACCTAGTATGCGGAGAGACTCGACCGCCTTCCTGCCAGAGGACCAGACATCTGGATATTGTCTCCTGA		MAIRVSCLRMNNAKRCSYLVCGETRPPSCQRTRHLDIVS*		MAIRVSCLRMNNAKRCSYLVCGETRPPSCQRTRHLDIVS*		CTAAAATGCG	ATGAAGCAGA	0	R	0	0	0	0	0
8659	3871	af	AN1038.1	70.m15196	AO070336000073	0			-210	-118			ATGAACAATGCCAAGAGATGTAGCTACCTAGTATGCGGAGAGACTCGACCGCCTTCCTGCCAGAGGACCAGACATCTGGATATTGTCTCCTGA		ATGAACAATGCCAAGAGATGTAGCTACCTAGTATGCGGAGAGACTCGACCGCCTTCCTGCCAGAGGACCAGACATCTGGATATTGTCTCCTGA		MNNAKRCSYLVCGETRPPSCQRTRHLDIVS*		MNNAKRCSYLVCGETRPPSCQRTRHLDIVS*		TTGTCTTCGT	ATGAAGCAGA	0	R	0	0	0	0	0
8660	3871	af	AN1038.1	70.m15196	AO070336000073	0			-203	-180			ATGCCAAGAGATGTAGCTACCTAG		ATGCCAAGAGATGTAGCTACCTAG		MPRDVAT*		MPRDVAT*		CGTATGAACA	TATGCGGAGA	0	R	0	0	0	0	0

8661	3871	af	AN1038.1	70.m15196	AO070336000073	0			-117	-76			ATGAAGCAGACGCCTGTGCTAAGGTACCTACCTTGCCGCTGA		ATGAAGCAGACGCCTGTGCTAAGGTACCTACCTTGCCGCTGA		MKQTPVLRYLPCR*		MKQTPVLRYLPCR*		TGTCTCCTGA	TTGTTGAAAT	0	R	0	0	0	0	0
8655	3871	an	AN1038.1	70.m15196	AO070336000073	0	-130	-17					ATGTCGTCGATTGCCTCTACCTCTCACCATTCCATTATTGCTCGTAGGAGTAGAGGCTATTGTAACCCGACTGCCGACCGGAATGCTCCTCGCGCGCAGACAGCTTCCCCCTGA	ATGTCGTCGATTGCCTCTACCTCTCACCATTCCATTATTGCTCGTAGGAGTAGAGGCTATTGTAACCCGACTGCCGACCGGAATGCTCCTCGCGCGCAGACAGCTTCCCCCTGA			MSSIASTSHHSIIARRSRGYCNPTADRNAPRAQTASP*	MSSIASTSHHSIIARRSRGYCNPTADRNAPRAQTASP*			GCCGTTACGG	ATAGTGCGCG	0	R	0	0	0	0	0
8663	3871	ao	AN1038.1	70.m15196	AO070336000073	0					-249	-208	ATGCTGTTTATTTTGCGTATAGATATAAATAAGTGTATATAA			ATGCTGTTTATTTTGCGTATAGATATAAATAAGTGTATATAA	MLFILRIDINKCI*			MLFILRIDINKCI*	CGAGTTTGTC	AGACCACCGT	0	R	0	0	0	0	0
8665	3872	af	AN3040.1	59.m08977	AO070337000054	0			-81	-34			ATGACTGAACAAATTGATATCTATTGTAGATATCCGTCATCGCGATAA		ATGACTGAACAAATTGATATCTATTGTAGATATCCGTCATCGCGATAA		MTEQIDIYCRYPSSR*		MTEQIDIYCRYPSSR*		AAGAAGGACT	GATCTGATAG	0	Z	0	0	0	0	0
8666	3872	ao	AN3040.1	59.m08977	AO070337000054	0					-282	-199	ATGGTATGGATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAGACCCGAAACACGTTACGTCATAAAACACCGCGTTAATTGA			ATGGTATGGATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAGACCCGAAACACGTTACGTCATAAAACACCGCGTTAATTGA	MVWMSKLQRRESRSRPETRYVIKHRVN*			MVWMSKLQRRESRSRPETRYVIKHRVN*	AATGATAATG	TTTCGCGCAC	0	Z	0	0	0	0	0
8667	3872	ao	AN3040.1	59.m08977	AO070337000054	0					-277	-239	ATGGATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAG			ATGGATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAG	MDVKTAKKRIQK*			MDVKTAKKRIQK*	TAATGATGGT	ACCCGAAACA	0	Z	0	0	0	0	0
8668	3872	ao	AN3040.1	59.m08977	AO070337000054	0					-273	-199	ATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAGACCCGAAACACGTTACGTCATAAAACACCGCGTTAATTGA			ATGTCAAAACTGCAAAGAAGAGAATCCAGAAGTAGACCCGAAACACGTTACGTCATAAAACACCGCGTTAATTGA	MSKLQRRESRSRPETRYVIKHRVN*			MSKLQRRESRSRPETRYVIKHRVN*	GATGGTATGG	TTTCGCGCAC	0	Z	0	0	0	0	0
8670	3877	af	AN4894.1	59.m08792	AO070338000062	0			-111	-55			ATGTCTTTTTTTCCCCGTCAACCCCCGCTGTTCTTTCCCTACTGGCCCTGTTCCTAA		ATGTCTTTTTTTCCCCGTCAACCCCCGCTGTTCTTTCCCTACTGGCCCTGTTCCTAA		MSFFPRQPPLFFPYWPCS*		MSFFPRQPPLFFPYWPCS*		CTTTCTCTCT	ACGTGGAGAA	0	BK	0	0	0	0	0
8669	3877	an	AN4894.1	59.m08792	AO070338000062	0	-111	-61					ATGTATTTTTTCATCGTTCAAACCCGCTCGTTGTTGCCTACCCGAATCTGA	ATGTATTTTTTCATCGTTCAAACCCGCTCGTTGTTGCCTACCCGAATCTGA			MYFFIVQTRSLLPTRI*	MYFFIVQTRSLLPTRI*			CTTTATCTCT	TTATAACCGT	0	BK	0	0	0	0	0
8671	3877	ao	AN4894.1	59.m08792	AO070338000062	0					-111	-61	ATGTTTTTTTCAGCCACTCAAGCCGCCCTGTTGCTACCTCTCCGCACCTGA			ATGTTTTTTTCAGCCACTCAAGCCGCCCTGTTGCTACCTCTCCGCACCTGA	MFFSATQAALLLPLRT*			MFFSATQAALLLPLRT*	GTTTGTCTCT	ATTTAACCGT	0	BK	0	0	0	0	0
8672	3879	conserved	AN5057.1	59.m08669	AO070338000201	0	-181	-170	-210	-199	-185	-174	ATGATTGTTTAG	ATGATTGTTTAG	ATGATTGTTTAG	ATGATTGTTTAG	MIV*	MIV*	MIV*	MIV*	svdyCvrAys	vTyrswkhhh	0	V	0	0	0	YFR028C	0
8676	3880	af	AN0407.1	54.m06667	AO070338000247	0			-250	-152			ATGAATGTGGAAGCTGTGGACAGAACTCTACTTGACTACGTTGGATACATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGA		ATGAATGTGGAAGCTGTGGACAGAACTCTACTTGACTACGTTGGATACATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGA		MNVEAVDRTLLDYVGYMPSDTSSIAIGLLYSW*		MNVEAVDRTLLDYVGYMPSDTSSIAIGLLYSW*		CGCGCCTTGA	TACATTTGTA	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8677	3880	af	AN0407.1	54.m06667	AO070338000247	0			-246	-124			ATGTGGAAGCTGTGGACAGAACTCTACTTGACTACGTTGGATACATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGATACATTTGTACTCTGTATGCCTCTGTGA		ATGTGGAAGCTGTGGACAGAACTCTACTTGACTACGTTGGATACATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGATACATTTGTACTCTGTATGCCTCTGTGA		MWKLWTELYLTTLDTCHLIHPASQLGCSTLGDTFVLCMPL*		MWKLWTELYLTTLDTCHLIHPASQLGCSTLGDTFVLCMPL*		CCTTGAATGA	ATCTGCACCT	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8678	3880	af	AN0407.1	54.m06667	AO070338000247	0			-202	-152			ATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGA		ATGCCATCTGATACATCCAGCATCGCAATTGGGTTGCTCTACTCTTGGTGA		MPSDTSSIAIGLLYSW*		MPSDTSSIAIGLLYSW*		CGTTGGATAC	TACATTTGTA	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8679	3880	af	AN0407.1	54.m06667	AO070338000247	0			-135	-124			ATGCCTCTGTGA		ATGCCTCTGTGA		MPL*		MPL*		TGTACTCTGT	ATCTGCACCT	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8680	3880	af	AN0407.1	54.m06667	AO070338000247	0			-76	-23			ATGGACGGCGATTCATTTGGTTTTCTCTACAACGTCATAGACCCAGGTGGATAG		ATGGACGGCGATTCATTTGGTTTTCTCTACAACGTCATAGACCCAGGTGGATAG		MDGDSFGFLYNVIDPGG*		MDGDSFGFLYNVIDPGG*		TCCCGCGTTC	TTCAAAATTG	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8673	3880	an	AN0407.1	54.m06667	AO070338000247	0	-89	-72					ATGATCCCGGGATTCTAG	ATGATCCCGGGATTCTAG			MIPGF*	MIPGF*			ACTCAGTATT	CCACCAAAGT	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8681	3880	ao	AN0407.1	54.m06667	AO070338000247	0					-262	-209	ATGAGAGTGGACTCAAAATCAGCTATGATCGGCCCTCGTCCTCGGCATCTTTAA			ATGAGAGTGGACTCAAAATCAGCTATGATCGGCCCTCGTCCTCGGCATCTTTAA	MRVDSKSAMIGPRPRHL*			MRVDSKSAMIGPRPRHL*	ACACGCACGA	GTTCCACGCC	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8682	3880	ao	AN0407.1	54.m06667	AO070338000247	0					-238	-209	ATGATCGGCCCTCGTCCTCGGCATCTTTAA			ATGATCGGCCCTCGTCCTCGGCATCTTTAA	MIGPRPRHL*			MIGPRPRHL*	AAAATCAGCT	GTTCCACGCC	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8683	3880	ao	AN0407.1	54.m06667	AO070338000247	0					-75	-22	ATGGGCAATTGGCCTCAAAAAGCGTTAAGCAAGACAAGAGACCCTGGTGGATAG			ATGGGCAATTGGCCTCAAAAAGCGTTAAGCAAGACAAGAGACCCTGGTGGATAG	MGNWPQKALSKTRDPGG*			MGNWPQKALSKTRDPGG*	TTTTTTTTTT	CCGAAGACCC	0	K	FG05376.1	0	NCU00310.1	YGR047C	0
8686	3882	af	AN6685.1	65.m07296	AO070339000093	0			-159	-136			ATGATTTTGGGTGGAGGAATTTGA		ATGATTTTGGGTGGAGGAATTTGA		MILGGGI*		MILGGGI*		AGCCTCCTGT	GCCCATTATA	0	U	0	0	0	0	0
8684	3882	an	AN6685.1	65.m07296	AO070339000093	0	-80	-69					ATGCCTCTCTGA	ATGCCTCTCTGA			MPL*	MPL*			TATCCTTCCT	ATGCCCTGTG	0	U	0	0	0	0	0
8685	3882	an	AN6685.1	65.m07296	AO070339000093	0	-68	-27					ATGCCCTGTGCGATTATATCCTCGCTGGAACTCCCCTTATAG	ATGCCCTGTGCGATTATATCCTCGCTGGAACTCCCCTTATAG			MPCAIISSLELPL*	MPCAIISSLELPL*			GCCTCTCTGA	AAGGACTGTC	0	U	0	0	0	0	0
8687	3882	ao	AN6685.1	65.m07296	AO070339000093	0					-229	-173	ATGTTTTTGGTTTTTCGGTGTTCTCAGACCACATTCCTTTCTCGACTCCTTTTCTAG			ATGTTTTTGGTTTTTCGGTGTTCTCAGACCACATTCCTTTCTCGACTCCTTTTCTAG	MFLVFRCSQTTFLSRLLF*			MFLVFRCSQTTFLSRLLF*	TGTTTTCTTG	CATTATTCGC	0	U	0	0	0	0	0
8688	3885	af	AN2077.1	57.m05776	AO070341000230	0			-229	-71			ATGCCATCGAGACCCGACGGAGTTTGGCTCGGGCCGCCTCGCCCAATCAAGTGTAAGCTGCATCCGCATTGTCATTGTCACGTGCCCGCTCAGCTATCAATTGTCTCCACCCAAACTTTTTTTCTTTTATCAGAGAGCGATATCTTTGGAGAGCGGTAA		ATGCCATCGAGACCCGACGGAGTTTGGCTCGGGCCGCCTCGCCCAATCAAGTGTAAGCTGCATCCGCATTGTCATTGTCACGTGCCCGCTCAGCTATCAATTGTCTCCACCCAAACTTTTTTTCTTTTATCAGAGAGCGATATCTTTGGAGAGCGGTAA		MPSRPDGVWLGPPRPIKCKLHPHCHCHVPAQLSIVSTQTFFLLSESDIFGER*		MPSRPDGVWLGPPRPIKCKLHPHCHCHVPAQLSIVSTQTFFLLSESDIFGER*		GCTCCGTTCG	CAATTTTCGC	0	R	FG08439.1	0	0	0	0
8689	3886	ao	AN3692.1	69.m15406	AO070341000323	0					-210	-157	ATGTTCAAAATAGGGTATCCAATCAAATGGAGGCGATCGATCAGAGCCAAATAA			ATGTTCAAAATAGGGTATCCAATCAAATGGAGGCGATCGATCAGAGCCAAATAA	MFKIGYPIKWRRSIRAK*			MFKIGYPIKWRRSIRAK*	CCCCGGGCGG	CGCACCAAAC	0	S	FG00333.1	0	0	0	0
8690	3886	ao	AN3692.1	69.m15406	AO070341000323	0					-184	-125	ATGGAGGCGATCGATCAGAGCCAAATAACGCACCAAACCAAAGGCGGAAGTGCTGCTTAG			ATGGAGGCGATCGATCAGAGCCAAATAACGCACCAAACCAAAGGCGGAAGTGCTGCTTAG	MEAIDQSQITHQTKGGSAA*			MEAIDQSQITHQTKGGSAA*	ATCCAATCAA	CCCGAAATCC	0	S	FG00333.1	0	0	0	0
8693	3889	af	AN3082.1	59.m08916	AO070224000004	0			-234	-184			ATGACCATCGAGGAACGTATCGCATATTATTGTCTTCATTACCACACCTAA		ATGACCATCGAGGAACGTATCGCATATTATTGTCTTCATTACCACACCTAA		MTIEERIAYYCLHYHT*		MTIEERIAYYCLHYHT*		CGAGCATGAA	CAGCTCTCAT	0	A	0	0	0	0	0
8694	3889	af	AN3082.1	59.m08916	AO070224000004	0			-145	-125			ATGATAAGTGATATGATTTGA		ATGATAAGTGATATGATTTGA		MISDMI*		MISDMI*		TTATCTGGCT	TATTCTATAC	0	A	0	0	0	0	0
8695	3889	af	AN3082.1	59.m08916	AO070224000004	0			-100	-80			ATGGGCGGATCATTGAATTGA		ATGGGCGGATCATTGAATTGA		MGGSLN*		MGGSLN*		ATTACTCTCT	GAGTTCTCCC	0	A	0	0	0	0	0
8691	3889	an	AN3082.1	59.m08916	AO070224000004	0	-163	-137					ATGGTCATTTTTTACGTTCTGTGCTGA	ATGGTCATTTTTTACGTTCTGTGCTGA			MVIFYVLC*	MVIFYVLC*			ACTGTCATTC	GCATGGTATG	0	A	0	0	0	0	0
8692	3889	an	AN3082.1	59.m08916	AO070224000004	0	-134	-117					ATGGTATGCACTAAATAG	ATGGTATGCACTAAATAG			MVCTK*	MVCTK*			TGTGCTGAGC	ACATATATTG	0	A	0	0	0	0	0
8696	3889	ao	AN3082.1	59.m08916	AO070224000004	0					-241	-122	ATGCTTCCCCGGAACTCTCCAATCACCTCAATAACACGATTCCTCCTCAATGCCTTGAGTTTGAATCCATTTCTAAGTGAGAAGAGACGTGATGTTATGATTGAAGTCTATTGGTCTTAA			ATGCTTCCCCGGAACTCTCCAATCACCTCAATAACACGATTCCTCCTCAATGCCTTGAGTTTGAATCCATTTCTAAGTGAGAAGAGACGTGATGTTATGATTGAAGTCTATTGGTCTTAA	MLPRNSPITSITRFLLNALSLNPFLSEKRRDVMIEVYWS*			MLPRNSPITSITRFLLNALSLNPFLSEKRRDVMIEVYWS*	CAGATCCGCG	CCGTTCTTGT	0	A	0	0	0	0	0
8697	3889	ao	AN3082.1	59.m08916	AO070224000004	0					-145	-122	ATGATTGAAGTCTATTGGTCTTAA			ATGATTGAAGTCTATTGGTCTTAA	MIEVYWS*			MIEVYWS*	ACGTGATGTT	CCGTTCTTGT	0	A	0	0	0	0	0
8698	3889	ao	AN3082.1	59.m08916	AO070224000004	0					-101	-72	ATGACTAGATTGGAAGCGCTGCAACACTAA			ATGACTAGATTGGAAGCGCTGCAACACTAA	MTRLEALQH*			MTRLEALQH*	ATTTGAATTG	GTGTCCGAGA	0	A	0	0	0	0	0
8704	3890	af	AN7439.1	57.m05910	AO070229000005	0			-280	-254			ATGGACCTCTACGGAGTACCTACATAG		ATGGACCTCTACGGAGTACCTACATAG		MDLYGVPT*		MDLYGVPT*		GAAAGGTCAA	TGTTTCAAAT	0	L	0	0	0	YPR175W	0
8705	3890	af	AN7439.1	57.m05910	AO070229000005	0			-188	-102			ATGATCGCTCTAACCCAGCATCTTGTTTACCTTTTCAGAGAACCCGACTTCTGTCATGACAATAGCAGTGAAACTCACAGAGCATGA		ATGATCGCTCTAACCCAGCATCTTGTTTACCTTTTCAGAGAACCCGACTTCTGTCATGACAATAGCAGTGAAACTCACAGAGCATGA		MIALTQHLVYLFREPDFCHDNSSETHRA*		MIALTQHLVYLFREPDFCHDNSSETHRA*		TGGATAACCC	CTTATAGCCC	0	L	0	0	0	YPR175W	0
8706	3890	af	AN7439.1	57.m05910	AO070229000005	0			-133	-95			ATGACAATAGCAGTGAAACTCACAGAGCATGACTTATAG		ATGACAATAGCAGTGAAACTCACAGAGCATGACTTATAG		MTIAVKLTEHDL*		MTIAVKLTEHDL*		GACTTCTGTC	CCCGCTCATC	0	L	0	0	0	YPR175W	0
8707	3890	af	AN7439.1	57.m05910	AO070229000005	0			-105	-37			ATGACTTATAGCCCGCTCATCGTCCTTGAAGCTACGTTCATTTGGTCCTCAGTCCTGACACATCTCTGA		ATGACTTATAGCCCGCTCATCGTCCTTGAAGCTACGTTCATTTGGTCCTCAGTCCTGACACATCTCTGA		MTYSPLIVLEATFIWSSVLTHL*		MTYSPLIVLEATFIWSSVLTHL*		CTCACAGAGC	AGAGACTAAG	0	L	0	0	0	YPR175W	0
8699	3890	an	AN7439.1	57.m05910	AO070229000005	0	-221	-57					ATGAAACATGGGATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAAACACACATATATTCTGTGAGTTAGGCATAGCATTGTTTTCCTTCGCGCAAACGCCCGTTTCCCGCAAGCTAATGAGTTCTAAGTGA	ATGAAACATGGGATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAAACACACATATATTCTGTGAGTTAGGCATAGCATTGTTTTCCTTCGCGCAAACGCCCGTTTCCCGCAAGCTAATGAGTTCTAAGTGA			MKHGMLSTHLLWSLCNKSCENSIIFLNTHIFCELGIALFSFAQTPVSRKLMSSK*	MKHGMLSTHLLWSLCNKSCENSIIFLNTHIFCELGIALFSFAQTPVSRKLMSSK*			TTATGGTACA	ACAACTTCTA	0	L	0	0	0	YPR175W	0
8700	3890	an	AN7439.1	57.m05910	AO070229000005	0	-214	-143					ATGGGATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAA	ATGGGATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAA			MGCSAPTSYGLYAINRVRTQSSF*	MGCSAPTSYGLYAINRVRTQSSF*			ACAATGAAAC	ACACACATAT	0	L	0	0	0	YPR175W	0
8701	3890	an	AN7439.1	57.m05910	AO070229000005	0	-209	-57					ATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAAACACACATATATTCTGTGAGTTAGGCATAGCATTGTTTTCCTTCGCGCAAACGCCCGTTTCCCGCAAGCTAATGAGTTCTAAGTGA	ATGCTCAGCACCCACCTCTTATGGTCTTTATGCAATAAATCGTGTGAGAACTCAATCATCTTTTTAAACACACATATATTCTGTGAGTTAGGCATAGCATTGTTTTCCTTCGCGCAAACGCCCGTTTCCCGCAAGCTAATGAGTTCTAAGTGA			MLSTHLLWSLCNKSCENSIIFLNTHIFCELGIALFSFAQTPVSRKLMSSK*	MLSTHLLWSLCNKSCENSIIFLNTHIFCELGIALFSFAQTPVSRKLMSSK*			GAAACATGGG	ACAACTTCTA	0	L	0	0	0	YPR175W	0
8702	3890	an	AN7439.1	57.m05910	AO070229000005	0	-189	-172					ATGGTCTTTATGCAATAA	ATGGTCTTTATGCAATAA			MVFMQ*	MVFMQ*			CCCACCTCTT	ATCGTGTGAG	0	L	0	0	0	YPR175W	0
8703	3890	an	AN7439.1	57.m05910	AO070229000005	0	-71	-57					ATGAGTTCTAAGTGA	ATGAGTTCTAAGTGA			MSSK*	MSSK*			CCGCAAGCTA	ACAACTTCTA	0	L	0	0	0	YPR175W	0
8710	3892	af	AN1421.1	55.m02935	AO070232000017	0			-152	-120			ATGATTTTAGGAGAGCCTGTTCAATGCTATTGA		ATGATTTTAGGAGAGCCTGTTCAATGCTATTGA		MILGEPVQCY*		MILGEPVQCY*		TTTGCACTCA	TCTTGTCTCT	0	K	0	0	0	0	0
8711	3892	af	AN1421.1	55.m02935	AO070232000017	0			-129	-100			ATGCTATTGATCTTGTCTCTATTGTGTTGA		ATGCTATTGATCTTGTCTCTATTGTGTTGA		MLLILSLLC*		MLLILSLLC*		AGCCTGTTCA	TTCCAGAGAC	0	K	0	0	0	0	0
8712	3892	af	AN1421.1	55.m02935	AO070232000017	0			-66	-52			ATGCAGCTCTCTTAA		ATGCAGCTCTCTTAA		MQLS*		MQLS*		ATCCAACCAA	AAATCTCAGT	0	K	0	0	0	0	0
8708	3892	an	AN1421.1	55.m02935	AO070232000017	0	-180	-136					ATGGCGTTACAACGCAATTGGATGATCAATCACTTTTATTTATAG	ATGGCGTTACAACGCAATTGGATGATCAATCACTTTTATTTATAG			MALQRNWMINHFYL*	MALQRNWMINHFYL*			GGCCGATTAT	CTTATCCTAA	0	K	0	0	0	0	0
8709	3892	an	AN1421.1	55.m02935	AO070232000017	0	-159	-136					ATGATCAATCACTTTTATTTATAG	ATGATCAATCACTTTTATTTATAG			MINHFYL*	MINHFYL*			ACGCAATTGG	CTTATCCTAA	0	K	0	0	0	0	0
8713	3892	ao	AN1421.1	55.m02935	AO070232000017	0					-237	-187	ATGCCTCTCTCACTAATTGAGGGTCGGTCTGTTTATTTCGTTTCAATATAG			ATGCCTCTCTCACTAATTGAGGGTCGGTCTGTTTATTTCGTTTCAATATAG	MPLSLIEGRSVYFVSI*			MPLSLIEGRSVYFVSI*	TCCTTTACAC	AATGCGACAG	0	K	0	0	0	0	0
8714	3892	ao	AN1421.1	55.m02935	AO070232000017	0					-185	-156	ATGCGACAGAATCTTAGCCATTTTTTCTGA			ATGCGACAGAATCTTAGCCATTTTTTCTGA	MRQNLSHFF*			MRQNLSHFF*	TCAATATAGA	CCTAGAGCTA	0	K	0	0	0	0	0
8718	3893	af	AN5198.1	69.m14897	AO070237000028	0			-175	-149			ATGTTGAATGCGATTGCTCCATTTTGA		ATGTTGAATGCGATTGCTCCATTTTGA		MLNAIAPF*		MLNAIAPF*		AAAACCAATC	CGCTTAATTT	0	R	0	0	0	0	0
8719	3893	af	AN5198.1	69.m14897	AO070237000028	0			-168	-142			ATGCGATTGCTCCATTTTGACGCTTAA		ATGCGATTGCTCCATTTTGACGCTTAA		MRLLHFDA*		MRLLHFDA*		ATCATGTTGA	TTTGTCATCG	0	R	0	0	0	0	0
8720	3893	af	AN5198.1	69.m14897	AO070237000028	0			-118	-53			ATGTCTTATCATCACGTGATTTACTTTTCGTGTTCAACTCGCTCATCATGTACTCGCCCTTTTTGA		ATGTCTTATCATCACGTGATTTACTTTTCGTGTTCAACTCGCTCATCATGTACTCGCCCTTTTTGA		MSYHHVIYFSCSTRSSCTRPF*		MSYHHVIYFSCSTRSSCTRPF*		GTCAGTGGGG	CCTGCGTCGT	0	R	0	0	0	0	0
8716	3893	an	AN5198.1	69.m14897	AO070237000028	0	-70	-2					ATGTCGAGGCATCCATTCGTCTTCTCTTTTCAGTTGATGGAGGTGCTAGGTGATCCGACTCGCTTGTAG	ATGTCGAGGCATCCATTCGTCTTCTCTTTTCAGTTGATGGAGGTGCTAGGTGATCCGACTCGCTTGTAG			MSRHPFVFSFQLMEVLGDPTRL*	MSRHPFVFSFQLMEVLGDPTRL*			ATAGTTGGAG	CATGTCGTCA	0	R	0	0	0	0	0
8721	3893	ao	AN5198.1	69.m14897	AO070237000028	0					-192	-181	ATGATCCAATGA			ATGATCCAATGA	MIQ*			MIQ*	CGAGAGCCGA	AAATGTACCC	0	R	0	0	0	0	0

8722	3893	ao	AN5198.1	69.m14897	AO070237000028	0					-184	-152	ATGAAAATGTACCCTTTGCGATATAATTTGTAA			ATGAAAATGTACCCTTTGCGATATAATTTGTAA	MKMYPLRYNL*			MKMYPLRYNL*	GAATGATCCA	GCCCAGTGGG	0	R	0	0	0	0	0
8723	3893	ao	AN5198.1	69.m14897	AO070237000028	0					-178	-152	ATGTACCCTTTGCGATATAATTTGTAA			ATGTACCCTTTGCGATATAATTTGTAA	MYPLRYNL*			MYPLRYNL*	TCCAATGAAA	GCCCAGTGGG	0	R	0	0	0	0	0
8727	3894	af	AN3163.1	59.m08551	AO070256000032	0			-254	-192			ATGAGAGCTACCTCTTGTTATTTAACCCCGCAAACATCCCCATCTTCCTTTACTGCACAATAA		ATGAGAGCTACCTCTTGTTATTTAACCCCGCAAACATCCCCATCTTCCTTTACTGCACAATAA		MRATSCYLTPQTSPSSFTAQ*		MRATSCYLTPQTSPSSFTAQ*		TGCACGCGAA	GTCCAAGTCT	0	O	0	MG02410.1	NCU03388.1	0	0
8724	3894	an	AN3163.1	59.m08551	AO070256000032	0	-245	-96					ATGCTAACCAATGCGAAAGCTGGCTACCCCAGATTAGTGCACTGCCCAGGGCAGATTGGCCCACCCGGGCGACACCTATGGCCGTCTTTCCCGACCGTGGTCGGGTGGTCAACAGGTGACGTCCTTGAGCCTGCGGACTGCGCTACTTAA	ATGCTAACCAATGCGAAAGCTGGCTACCCCAGATTAGTGCACTGCCCAGGGCAGATTGGCCCACCCGGGCGACACCTATGGCCGTCTTTCCCGACCGTGGTCGGGTGGTCAACAGGTGACGTCCTTGAGCCTGCGGACTGCGCTACTTAA			MLTNAKAGYPRLVHCPGQIGPPGRHLWPSFPTVVGWSTGDVLEPADCAT*	MLTNAKAGYPRLVHCPGQIGPPGRHLWPSFPTVVGWSTGDVLEPADCAT*			GACCTCCTCC	ATACCATTCC	0	O	0	MG02410.1	NCU03388.1	0	0
8725	3894	an	AN3163.1	59.m08551	AO070256000032	0	-235	-209					ATGCGAAAGCTGGCTACCCCAGATTAG	ATGCGAAAGCTGGCTACCCCAGATTAG			MRKLATPD*	MRKLATPD*			ATGCTAACCA	TGCACTGCCC	0	O	0	MG02410.1	NCU03388.1	0	0
8726	3894	an	AN3163.1	59.m08551	AO070256000032	0	-168	-127					ATGGCCGTCTTTCCCGACCGTGGTCGGGTGGTCAACAGGTGA	ATGGCCGTCTTTCCCGACCGTGGTCGGGTGGTCAACAGGTGA			MAVFPDRGRVVNR*	MAVFPDRGRVVNR*			GGCGACACCT	CGTCCTTGAG	0	O	0	MG02410.1	NCU03388.1	0	0
8728	3894	ao	AN3163.1	59.m08551	AO070256000032	0					-230	-213	ATGCATGGTGAGAAGTAA			ATGCATGGTGAGAAGTAA	MHGEK*			MHGEK*	TAACTAGCTC	CATCCCAAAT	0	O	0	MG02410.1	NCU03388.1	0	0
8729	3894	ao	AN3163.1	59.m08551	AO070256000032	0					-226	-188	ATGGTGAGAAGTAACATCCCAAATCAATTTGTTATTTAA			ATGGTGAGAAGTAACATCCCAAATCAATTTGTTATTTAA	MVRSNIPNQFVI*			MVRSNIPNQFVI*	TAGCTCATGC	TCCGTTCATC	0	O	0	MG02410.1	NCU03388.1	0	0
8733	3901	af	AN1085.1	70.m15159	AO070285000085	0			-231	-22			ATGGTCATTTACATCATCTGCAGTCGCTCATCCCACAAGCAACATTGCTCTGGTTACCACTCGCCACGGTCTCCGCATCTTGACGATTCCCCAACCGCTGCTCAGTGGTACTCTGTTCGCACCTTTTTGGTTTTCGCAACAACGAAAAACTCGACATTGTCTAAGGAATTGACAGCGTCTCCGTCATATTCCTTATCTCCCAACGGCTGA		ATGGTCATTTACATCATCTGCAGTCGCTCATCCCACAAGCAACATTGCTCTGGTTACCACTCGCCACGGTCTCCGCATCTTGACGATTCCCCAACCGCTGCTCAGTGGTACTCTGTTCGCACCTTTTTGGTTTTCGCAACAACGAAAAACTCGACATTGTCTAAGGAATTGACAGCGTCTCCGTCATATTCCTTATCTCCCAACGGCTGA		MVIYIICSRSSHKQHCSGYHSPRSPHLDDSPTAAQWYSVRTFLVFATTKNSTLSKELTASPSYSLSPNG*		MVIYIICSRSSHKQHCSGYHSPRSPHLDDSPTAAQWYSVRTFLVFATTKNSTLSKELTASPSYSLSPNG*		ATTTCCTTGT	CTTCGTAAAA	0	R	FG00833.1	0	0	0	0
8732	3901	an	AN1085.1	70.m15159	AO070285000085	0	-206	-165					ATGAACTTTCGGTCTCCTTACAGCCGATCGGCCCTGCGTTAA	ATGAACTTTCGGTCTCCTTACAGCCGATCGGCCCTGCGTTAA			MNFRSPYSRSALR*	MNFRSPYSRSALR*			TTCTTTGCAC	GCTTCCTAAG	0	R	FG00833.1	0	0	0	0
8738	3902	af	AN4951.1	59.m08856	AO070288000003	0			-217	-191			ATGGTCTCTTTTCTCTACATGGACTAA		ATGGTCTCTTTTCTCTACATGGACTAA		MVSFLYMD*		MVSFLYMD*		TTATTCTGCG	TTAAGTGATC	0	U	0	0	NCU06284.1	0	0
8734	3902	an	AN4951.1	59.m08856	AO070288000003	0	-252	-208					ATGCCAGTTCCACCACTCCAGCACCGTTCAACTCCAACTCCCTGA	ATGCCAGTTCCACCACTCCAGCACCGTTCAACTCCAACTCCCTGA			MPVPPLQHRSTPTP*	MPVPPLQHRSTPTP*			CAACGGCATT	TTAATGAATG	0	U	0	0	NCU06284.1	0	0
8735	3902	an	AN4951.1	59.m08856	AO070288000003	0	-204	-169					ATGAATGAACTTCACTCTCTGTTCTATGGAATCTGA	ATGAATGAACTTCACTCTCTGTTCTATGGAATCTGA			MNELHSLFYGI*	MNELHSLFYGI*			TCCCTGATTA	AAGCAGTCAA	0	U	0	0	NCU06284.1	0	0
8736	3902	an	AN4951.1	59.m08856	AO070288000003	0	-200	-69					ATGAACTTCACTCTCTGTTCTATGGAATCTGAAAGCAGTCAAATCTCTTCCGTTCCAGTGTTTTCCCTCCGATATTATCATAGTTTCATCTCTCCCCTCCCTTTTGAGCCATTCCAGCTGCTTACCGCCTAA	ATGAACTTCACTCTCTGTTCTATGGAATCTGAAAGCAGTCAAATCTCTTCCGTTCCAGTGTTTTCCCTCCGATATTATCATAGTTTCATCTCTCCCCTCCCTTTTGAGCCATTCCAGCTGCTTACCGCCTAA			MNFTLCSMESESSQISSVPVFSLRYYHSFISPLPFEPFQLLTA*	MNFTLCSMESESSQISSVPVFSLRYYHSFISPLPFEPFQLLTA*			TGATTAATGA	ACCCAAGCCG	0	U	0	0	NCU06284.1	0	0
8739	3902	ao	AN4951.1	59.m08856	AO070288000003	0					-223	-182	ATGTCAATCCACTGCGCCTCTTCTTCTGCTGTTGTTGATTAA			ATGTCAATCCACTGCGCCTCTTCTTCTGCTGTTGTTGATTAA	MSIHCASSSAVVD*			MSIHCASSSAVVD*	ATGTGATCGC	TCTTTCCTCC	0	U	0	0	NCU06284.1	0	0
8744	3903	af	AN5617.1	58.m07541	AO070301000017	0			-209	-186			ATGTGCGTCATTTCAAGAAACTAG		ATGTGCGTCATTTCAAGAAACTAG		MCVISRN*		MCVISRN*		AAGGTTGTAA	GATTACTAAA	0	L	0	0	0	0	0
8745	3903	af	AN5617.1	58.m07541	AO070301000017	0			-77	-48			ATGGTCCCTCCACGAAATTTGTCTGATTGA		ATGGTCCCTCCACGAAATTTGTCTGATTGA		MVPPRNLSD*		MVPPRNLSD*		TTCATCCTTC	TCACCAATTC	0	L	0	0	0	0	0
8741	3903	an	AN5617.1	58.m07541	AO070301000017	0	-166	-146					ATGCGAGCCTACAGGACGTGA	ATGCGAGCCTACAGGACGTGA			MRAYRT*	MRAYRT*			TAAGGCACCA	CTAAGCTATC	0	L	0	0	0	0	0
8742	3903	an	AN5617.1	58.m07541	AO070301000017	0	-91	-5					ATGTCTTCAACGATTTCATTCAAGATACTCATGAATCTGTCATCCCAGTGCCCTGGTCTGGCACACAGGTCAGCTGTCGGTGATTGA	ATGTCTTCAACGATTTCATTCAAGATACTCATGAATCTGTCATCCCAGTGCCCTGGTCTGGCACACAGGTCAGCTGTCGGTGATTGA			MSSTISFKILMNLSSQCPGLAHRSAVGD*	MSSTISFKILMNLSSQCPGLAHRSAVGD*			ATCAACTCCG	AACCATGGTA	0	L	0	0	0	0	0
8743	3903	an	AN5617.1	58.m07541	AO070301000017	0	-61	-5					ATGAATCTGTCATCCCAGTGCCCTGGTCTGGCACACAGGTCAGCTGTCGGTGATTGA	ATGAATCTGTCATCCCAGTGCCCTGGTCTGGCACACAGGTCAGCTGTCGGTGATTGA			MNLSSQCPGLAHRSAVGD*	MNLSSQCPGLAHRSAVGD*			CAAGATACTC	AACCATGGTA	0	L	0	0	0	0	0
8746	3903	ao	AN5617.1	58.m07541	AO070301000017	0					-63	-46	ATGATCGCATTGCTCTGA			ATGATCGCATTGCTCTGA	MIALL*			MIALL*	TTGATCGAAG	CTCCCAACAA	0	L	0	0	0	0	0
8751	3904	af	AN6263.1	72.m19394	AO070304000026	0			-82	-50			ATGCGGACGTTTGCGATTTGCAACTCAGCATAA		ATGCGGACGTTTGCGATTTGCAACTCAGCATAA		MRTFAICNSA*		MRTFAICNSA*		GAATTGGTTG	CCCCATCCTC	0	O	0	0	0	0	0
8747	3904	an	AN6263.1	72.m19394	AO070304000026	0	-183	-166					ATGTACATTGCACACTGA	ATGTACATTGCACACTGA			MYIAH*	MYIAH*			AGGAAAAGCT	TGAGAAATCA	0	O	0	0	0	0	0
8748	3904	an	AN6263.1	72.m19394	AO070304000026	0	-166	-113					ATGAGAAATCACGTGGTTGCTGACAAAGAACAAACTGGGCTTCCATGGGCTTAA	ATGAGAAATCACGTGGTTGCTGACAAAGAACAAACTGGGCTTCCATGGGCTTAA			MRNHVVADKEQTGLPWA*	MRNHVVADKEQTGLPWA*			TTGCACACTG	GATAAAAAAG	0	O	0	0	0	0	0
8749	3904	an	AN6263.1	72.m19394	AO070304000026	0	-122	-108					ATGGGCTTAAGATAA	ATGGGCTTAAGATAA			MGLR*	MGLR*			CTGGGCTTCC	AAAAGTTCCG	0	O	0	0	0	0	0
8750	3904	an	AN6263.1	72.m19394	AO070304000026	0	-72	-25					ATGCAGACGTTTGTTTCGTGCAGCATCAGCAGCCTCACTATTCTCTGA	ATGCAGACGTTTGTTTCGTGCAGCATCAGCAGCCTCACTATTCTCTGA			MQTFVSCSISSLTIL*	MQTFVSCSISSLTIL*			TTGACATCTG	TTCCGGCGGC	0	O	0	0	0	0	0
8752	3904	ao	AN6263.1	72.m19394	AO070304000026	0					-198	-181	ATGACTAAGCAGCAATAA			ATGACTAAGCAGCAATAA	MTKQQ*			MTKQQ*	TAGGGCTGCA	GTGCCGAAAA	0	O	0	0	0	0	0
8753	3904	ao	AN6263.1	72.m19394	AO070304000026	0					-156	-37	ATGATATCAAACTCCGGCGACCGCCCGAAAGGAGCAGTTATTGAACTGTTGTTTCCACCGACAACTCGACTGATACAACTACTCGCTGCCTGCGGTCGAAGCAGATCCAGCATTCATTAA			ATGATATCAAACTCCGGCGACCGCCCGAAAGGAGCAGTTATTGAACTGTTGTTTCCACCGACAACTCGACTGATACAACTACTCGCTGCCTGCGGTCGAAGCAGATCCAGCATTCATTAA	MISNSGDRPKGAVIELLFPPTTRLIQLLAACGRSRSSIH*			MISNSGDRPKGAVIELLFPPTTRLIQLLAACGRSRSSIH*	TACAGATCAC	ATCCAGTGGC	0	O	0	0	0	0	0
8758	3909	af	AN0357.1	54.m06397	AO070318000033	0			-280	-263			ATGGTATTGCTCTCTTGA		ATGGTATTGCTCTCTTGA		MVLLS*		MVLLS*		CTAAATGGCT	TCACTGAAAT	0	C	0	0	0	0	0
8757	3909	an	AN0357.1	54.m06397	AO070318000033	0	-249	-229					ATGCGATTGTTTTTCATATAA	ATGCGATTGTTTTTCATATAA			MRLFFI*	MRLFFI*			TTCTGGTGTC	GACTCGCTTT	0	C	0	0	0	0	0
8759	3909	ao	AN0357.1	54.m06397	AO070318000033	0					-272	-207	ATGTGGCTGCTGATTTATGGATCGAATTTTGTTGTTCCGAAAAGTCGCGGTTTTCACCGAAGGTAG			ATGTGGCTGCTGATTTATGGATCGAATTTTGTTGTTCCGAAAAGTCGCGGTTTTCACCGAAGGTAG	MWLLIYGSNFVVPKSRGFHRR*			MWLLIYGSNFVVPKSRGFHRR*	GGCTGTCATC	TTAGAGCCGT	0	C	0	0	0	0	0
8760	3909	ao	AN0357.1	54.m06397	AO070318000033	0					-256	-203	ATGGATCGAATTTTGTTGTTCCGAAAAGTCGCGGTTTTCACCGAAGGTAGTTAG			ATGGATCGAATTTTGTTGTTCCGAAAAGTCGCGGTTTTCACCGAAGGTAGTTAG	MDRILLFRKVAVFTEGS*			MDRILLFRKVAVFTEGS*	CTGCTGATTT	AGCCGTGGTG	0	C	0	0	0	0	0
8762	3910	af	AN0892.1	70.m15489	AO070320000063	0			-293	-222			ATGCTCACCAGTCCTTTGCATATGTTTCTTGCTCTCGGTCGTTCTCTTTTTTCTCCTTCTCCGGGCCGGTAG		ATGCTCACCAGTCCTTTGCATATGTTTCTTGCTCTCGGTCGTTCTCTTTTTTCTCCTTCTCCGGGCCGGTAG		MLTSPLHMFLALGRSLFSPSPGR*		MLTSPLHMFLALGRSLFSPSPGR*		GTTCACTTCC	TCTTTCCCTT	0	O	0	0	0	0	0
8763	3910	af	AN0892.1	70.m15489	AO070320000063	0			-272	-222			ATGTTTCTTGCTCTCGGTCGTTCTCTTTTTTCTCCTTCTCCGGGCCGGTAG		ATGTTTCTTGCTCTCGGTCGTTCTCTTTTTTCTCCTTCTCCGGGCCGGTAG		MFLALGRSLFSPSPGR*		MFLALGRSLFSPSPGR*		TCCTTTGCAT	TCTTTCCCTT	0	O	0	0	0	0	0
8764	3910	af	AN0892.1	70.m15489	AO070320000063	0			-105	-76			ATGTCATGTGCAATACGACTGGACTTTTGA		ATGTCATGTGCAATACGACTGGACTTTTGA		MSCAIRLDF*		MSCAIRLDF*		GTTACGGTTT	CCGACACGGC	0	O	0	0	0	0	0
8765	3910	af	AN0892.1	70.m15489	AO070320000063	0			-100	-32			ATGTGCAATACGACTGGACTTTTGACCGACACGGCTAGAACCCGCTCATTTGGCAATACGCAATATTGA		ATGTGCAATACGACTGGACTTTTGACCGACACGGCTAGAACCCGCTCATTTGGCAATACGCAATATTGA		MCNTTGLLTDTARTRSFGNTQY*		MCNTTGLLTDTARTRSFGNTQY*		GGTTTATGTC	AGGCCGTTGA	0	O	0	0	0	0	0
8761	3910	an	AN0892.1	70.m15489	AO070320000063	0	-104	-24					ATGTACAGCAGGAGTAGACAAATACCAGGCTACAGTGGCATACGCTCTTTAATAGTCACCGAGACATTGATTGCTCCTTAG	ATGTACAGCAGGAGTAGACAAATACCAGGCTACAGTGGCATACGCTCTTTAATAGTCACCGAGACATTGATTGCTCCTTAG			MYSRSRQIPGYSGIRSLIVTETLIAP*	MYSRSRQIPGYSGIRSLIVTETLIAP*			TTGTCAGGTC	CTGGCCGGTC	0	O	0	0	0	0	0
8768	3912	af	AN1733.1	69.m15036	AO070324000063	0			-277	-248			ATGCAGCACTTCATGAGGGGAACAAAGTAA		ATGCAGCACTTCATGAGGGGAACAAAGTAA		MQHFMRGTK*		MQHFMRGTK*		ACCAGTGATT	AGAATTTGGA	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8769	3912	af	AN1733.1	69.m15036	AO070324000063	0			-265	-248			ATGAGGGGAACAAAGTAA		ATGAGGGGAACAAAGTAA		MRGTK*		MRGTK*		GCAGCACTTC	AGAATTTGGA	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8770	3912	af	AN1733.1	69.m15036	AO070324000063	0			-227	-192			ATGTCACAGGAATGTATGGTAATAAATGCTGACTGA		ATGTCACAGGAATGTATGGTAATAAATGCTGACTGA		MSQECMVINAD*		MSQECMVINAD*		GAACGGATCC	TTTTCTTCTT	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8771	3912	af	AN1733.1	69.m15036	AO070324000063	0			-216	-196			ATGTATGGTAATAAATGCTGA		ATGTATGGTAATAAATGCTGA		MYGNKC*		MYGNKC*		TGTCACAGGA	CTGATTTTCT	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8772	3912	af	AN1733.1	69.m15036	AO070324000063	0			-212	-192			ATGGTAATAAATGCTGACTGA		ATGGTAATAAATGCTGACTGA		MVINAD*		MVINAD*		ACAGGAATGT	TTTTCTTCTT	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8773	3912	af	AN1733.1	69.m15036	AO070324000063	0			-202	-173			ATGCTGACTGATTTTCTTCTTCATCTCTGA		ATGCTGACTGATTTTCTTCTTCATCTCTGA		MLTDFLLHL*		MLTDFLLHL*		ATGGTAATAA	CTGGCTCATT	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8767	3912	an	AN1733.1	69.m15036	AO070324000063	0	-114	-22					ATGCATACACCGTGTTTGCTCTCCCTTCCTCCTCATTTCCCCTCCTCATCTTCTTCCTCTTCTTCTCTCCTCTCTTCGTTCGCTCCACTTTGA	ATGCATACACCGTGTTTGCTCTCCCTTCCTCCTCATTTCCCCTCCTCATCTTCTTCCTCTTCTTCTCTCCTCTCTTCGTTCGCTCCACTTTGA			MHTPCLLSLPPHFPSSSSSSSSLLSSFAPL*	MHTPCLLSLPPHFPSSSSSSSSLLSSFAPL*			ACTTGCATAC	ACTGCGAAGT	0	E	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
8775	3918	af	AN5443.1	69.m15491	AO070333000106	0			-212	-39			ATGTTGGGTCACCTGCCGCTGAGTCACGCGGGCGGCACGAGACCAGCGTCATCGCAAATTATCAGGTACATTGGGGATAGTCACAATTTTGGGAGGGGCTGCACGACTTTTTTCCATCACGGAACAGCCCCATCTATTTTGATCTCATACGTTAAAATACTGTTTAGATTTTGA		ATGTTGGGTCACCTGCCGCTGAGTCACGCGGGCGGCACGAGACCAGCGTCATCGCAAATTATCAGGTACATTGGGGATAGTCACAATTTTGGGAGGGGCTGCACGACTTTTTTCCATCACGGAACAGCCCCATCTATTTTGATCTCATACGTTAAAATACTGTTTAGATTTTGA		MLGHLPLSHAGGTRPASSQIIRYIGDSHNFGRGCTTFFHHGTAPSILISYVKILFRF*		MLGHLPLSHAGGTRPASSQIIRYIGDSHNFGRGCTTFFHHGTAPSILISYVKILFRF*		AACCAGTCAC	GTTCAGAGAG	0	J	FG06894.1	0	0	0	0
8774	3918	an	AN5443.1	69.m15491	AO070333000106	0	-154	-41					ATGGGTCCCGTACCATGTGACGTCGGTTATCGATACTGGCACGAATTTATTATCCTCAGCACGAAGAGTTATTATTTATTGTCTCGCCTGTCGCACGCATCCCATCATACTTAA	ATGGGTCCCGTACCATGTGACGTCGGTTATCGATACTGGCACGAATTTATTATCCTCAGCACGAAGAGTTATTATTTATTGTCTCGCCTGTCGCACGCATCCCATCATACTTAA			MGPVPCDVGYRYWHEFIILSTKSYYLLSRLSHASHHT*	MGPVPCDVGYRYWHEFIILSTKSYYLLSRLSHASHHT*			CAGCTGCGGG	TTTATTACGG	0	J	FG06894.1	0	0	0	0
8776	3918	ao	AN5443.1	69.m15491	AO070333000106	0					-141	-130	ATGTTGACCTAA			ATGTTGACCTAA	MLT*			MLT*	TCCTGGGAAA	TTTCTTCACG	0	J	FG06894.1	0	0	0	0
8777	3920	af	AN2967.1	59.m09040	AO070337000149	0			-246	-181			ATGAACGGAAGACTCCGAAGTAGCAATGGAGATCAAATGAAGCTTATCAGTTTTATCTTCACGTGA		ATGAACGGAAGACTCCGAAGTAGCAATGGAGATCAAATGAAGCTTATCAGTTTTATCTTCACGTGA		MNGRLRSSNGDQMKLISFIFT*		MNGRLRSSNGDQMKLISFIFT*		ATATCCGTCT	CTTCCACTTT	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8778	3920	af	AN2967.1	59.m09040	AO070337000149	0			-221	-207			ATGGAGATCAAATGA		ATGGAGATCAAATGA		MEIK*		MEIK*		CGAAGTAGCA	AGCTTATCAG	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8779	3920	af	AN2967.1	59.m09040	AO070337000149	0			-210	-181			ATGAAGCTTATCAGTTTTATCTTCACGTGA		ATGAAGCTTATCAGTTTTATCTTCACGTGA		MKLISFIFT*		MKLISFIFT*		TGGAGATCAA	CTTCCACTTT	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8780	3920	af	AN2967.1	59.m09040	AO070337000149	0			-151	-104			ATGTCTGTCGCCATCCACTTTGTAGGTCGTCGATTTACATTTCTGTAA		ATGTCTGTCGCCATCCACTTTGTAGGTCGTCGATTTACATTTCTGTAA		MSVAIHFVGRRFTFL*		MSVAIHFVGRRFTFL*		CACCTTTTCA	GACAACTTTA	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8782	3920	ao	AN2967.1	59.m09040	AO070337000149	0					-251	-177	ATGCAATACCCGTCACAATACCCGAGCGAAAAGAATGCGAAGGAAAATTTTAACTTATCGTCTATCTTCACGTGA			ATGCAATACCCGTCACAATACCCGAGCGAAAAGAATGCGAAGGAAAATTTTAACTTATCGTCTATCTTCACGTGA	MQYPSQYPSEKNAKENFNLSSIFT*			MQYPSQYPSEKNAKENFNLSSIFT*	GCCCGGTAAT	TATAGACTTT	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0

8783	3920	ao	AN2967.1	59.m09040	AO070337000149	0					-217	-92	ATGCGAAGGAAAATTTTAACTTATCGTCTATCTTCACGTGATATAGACTTTTTCCCTCCGCCTTCCAAGGATAATGAACTACTCCATGACTTAACTATACGAACGCCCACGAAGTCGATTTCTTGA			ATGCGAAGGAAAATTTTAACTTATCGTCTATCTTCACGTGATATAGACTTTTTCCCTCCGCCTTCCAAGGATAATGAACTACTCCATGACTTAACTATACGAACGCCCACGAAGTCGATTTCTTGA	MRRKILTYRLSSRDIDFFPPPSKDNELLHDLTIRTPTKSIS*			MRRKILTYRLSSRDIDFFPPPSKDNELLHDLTIRTPTKSIS*	AGCGAAAAGA	CCGTCTGAGT	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8784	3920	ao	AN2967.1	59.m09040	AO070337000149	0					-144	-124	ATGAACTACTCCATGACTTAA			ATGAACTACTCCATGACTTAA	MNYSMT*			MNYSMT*	TCCAAGGATA	CTATACGAAC	0	J	FG06863.1	MG01648.1	NCU00950.1	YNR015W	0
8789	3921	af	AN4876.1	59.m08772	AO070338000084	0			-165	-10			ATGTGTTTCGACCCATCCAACCGGCATTCAACGGCGATTTGGGCTAGGTGCTTAGTCATCAGCTATCCCCGAGTTACCCCAGGTCCACCAACTGCTCGTCATGACTCGATCCCCCCACCCGTGGTGATCCTTCAATTGCTCCAGGTACGGAAATAG		ATGTGTTTCGACCCATCCAACCGGCATTCAACGGCGATTTGGGCTAGGTGCTTAGTCATCAGCTATCCCCGAGTTACCCCAGGTCCACCAACTGCTCGTCATGACTCGATCCCCCCACCCGTGGTGATCCTTCAATTGCTCCAGGTACGGAAATAG		MCFDPSNRHSTAIWARCLVISYPRVTPGPPTARHDSIPPPVVILQLLQVRK*		MCFDPSNRHSTAIWARCLVISYPRVTPGPPTARHDSIPPPVVILQLLQVRK*		TTTGCAAAGA	GCATTCGCCA	0	U	0	MG03313.1	0	0	0
8790	3921	af	AN4876.1	59.m08772	AO070338000084	0			-65	-39			ATGACTCGATCCCCCCACCCGTGGTGA		ATGACTCGATCCCCCCACCCGTGGTGA		MTRSPHPW*		MTRSPHPW*		ACTGCTCGTC	TCCTTCAATT	0	U	0	MG03313.1	0	0	0
8785	3921	an	AN4876.1	59.m08772	AO070338000084	0	-216	-115					ATGGTCTATCGTGACCAAACCAGGATTGCGAGGAACGATAATATGATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG	ATGGTCTATCGTGACCAAACCAGGATTGCGAGGAACGATAATATGATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG			MVYRDQTRIARNDNMMRTTLLEAFCKSGVTDVA*	MVYRDQTRIARNDNMMRTTLLEAFCKSGVTDVA*			CCTGCAAAAC	TCATCTCATG	0	U	0	MG03313.1	0	0	0
8786	3921	an	AN4876.1	59.m08772	AO070338000084	0	-174	-115					ATGATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG	ATGATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG			MMRTTLLEAFCKSGVTDVA*	MMRTTLLEAFCKSGVTDVA*			GAACGATAAT	TCATCTCATG	0	U	0	MG03313.1	0	0	0
8787	3921	an	AN4876.1	59.m08772	AO070338000084	0	-171	-115					ATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG	ATGCGAACTACTCTTCTAGAAGCTTTCTGCAAAAGCGGCGTGACGGATGTTGCTTAG			MRTTLLEAFCKSGVTDVA*	MRTTLLEAFCKSGVTDVA*			CGATAATATG	TCATCTCATG	0	U	0	MG03313.1	0	0	0
8788	3921	an	AN4876.1	59.m08772	AO070338000084	0	-93	-52					ATGGGAGTTACCCCAGGTACAGCTCCTTCGCCGATGTCATGA	ATGGGAGTTACCCCAGGTACAGCTCCTTCGCCGATGTCATGA			MGVTPGTAPSPMS*	MGVTPGTAPSPMS*			CGCGGTTAGC	GCTCCCCGTC	0	U	0	MG03313.1	0	0	0
8791	3921	ao	AN4876.1	59.m08772	AO070338000084	0					-234	-211	ATGACAAACACGGTCGGCCGTTGA			ATGACAAACACGGTCGGCCGTTGA	MTNTVGR*			MTNTVGR*	TTCTAGTGCC	AGATCTGAAA	0	U	0	MG03313.1	0	0	0
8792	3921	ao	AN4876.1	59.m08772	AO070338000084	0					-62	-30	ATGCTTTCTTGCATCGGTGACACTCCAGCATAG			ATGCTTTCTTGCATCGGTGACACTCCAGCATAG	MLSCIGDTPA*			MLSCIGDTPA*	CATCCCGGAC	CTCCATCAGG	0	U	0	MG03313.1	0	0	0
8796	3923	af	AN0432.1	54.m06625	AO070338000285	0			-230	-123			ATGGACACAAATACCTTACCGTCAGGAACGGGTATTGCGTCATACGGACCAGTTAGTAAGACGGACAGTTTGGGATCCGAACAGCGAGAACCACTCCGTACCTACTAA		ATGGACACAAATACCTTACCGTCAGGAACGGGTATTGCGTCATACGGACCAGTTAGTAAGACGGACAGTTTGGGATCCGAACAGCGAGAACCACTCCGTACCTACTAA		MDTNTLPSGTGIASYGPVSKTDSLGSEQREPLRTY*		MDTNTLPSGTGIASYGPVSKTDSLGSEQREPLRTY*		TTGATTAGTC	CTCCGTCGGT	0	HC	FG00926.1	MG03708.1	NCU03112.1	0	0
8793	3923	an	AN0432.1	54.m06625	AO070338000285	0	-193	-179					ATGCCCGACAAATGA	ATGCCCGACAAATGA			MPDK*	MPDK*			GAGCCCTGAT	TTGATTGATA	0	HC	FG00926.1	MG03708.1	NCU03112.1	0	0
8794	3923	an	AN0432.1	54.m06625	AO070338000285	0	-182	-171					ATGATTGATTGA	ATGATTGATTGA			MID*	MID*			TGCCCGACAA	TAATCGCGTG	0	HC	FG00926.1	MG03708.1	NCU03112.1	0	0
8795	3923	an	AN0432.1	54.m06625	AO070338000285	0	-129	-31					ATGTACGGAGTAGCGTCGGCGTTTTCGGGTCCCGCTTTTCGAAGCTCCTTCCAACAGACATCTTCGGCCGGACTTCTGACACAACCTAACGCCCATTGA	ATGTACGGAGTAGCGTCGGCGTTTTCGGGTCCCGCTTTTCGAAGCTCCTTCCAACAGACATCTTCGGCCGGACTTCTGACACAACCTAACGCCCATTGA			MYGVASAFSGPAFRSSFQQTSSAGLLTQPNAH*	MYGVASAFSGPAFRSSFQQTSSAGLLTQPNAH*			GTATTACGTC	CATTCCAGTC	0	HC	FG00926.1	MG03708.1	NCU03112.1	0	0
8797	3923	ao	AN0432.1	54.m06625	AO070338000285	0					-144	-61	ATGTGGAATCGGCGAGGTCGGAGGGCGGGTCCCGAAAACGAAAAGAGCTCAATTAAGGTACTTAGTCTCCAGCCGCCTTTCTAA			ATGTGGAATCGGCGAGGTCGGAGGGCGGGTCCCGAAAACGAAAAGAGCTCAATTAAGGTACTTAGTCTCCAGCCGCCTTTCTAA	MWNRRGRRAGPENEKSSIKVLSLQPPF*			MWNRRGRRAGPENEKSSIKVLSLQPPF*	GCATTGCGTC	TCTTCTCGCT	0	HC	FG00926.1	MG03708.1	NCU03112.1	0	0
8800	3924	af	AN1560.1	55.m03076	AO070339000293	0			-226	-206			ATGACCCGGTTCCAGTACTGA		ATGACCCGGTTCCAGTACTGA		MTRFQY*		MTRFQY*		GAGACATTGG	CCGTTTCAAG	0	D	0	0	0	0	0
8801	3924	af	AN1560.1	55.m03076	AO070339000293	0			-112	-65			ATGACTACGACAAATATTTCGTCTCACCTTGCCTGGTCACACGATTGA		ATGACTACGACAAATATTTCGTCTCACCTTGCCTGGTCACACGATTGA		MTTTNISSHLAWSHD*		MTTTNISSHLAWSHD*		TGTTACTTTT	TCTCCAATGC	0	D	0	0	0	0	0
8798	3924	an	AN1560.1	55.m03076	AO070339000293	0	-175	-143					ATGTTCATATACCCCCTCTGCTTTTGCGATTGA	ATGTTCATATACCCCCTCTGCTTTTGCGATTGA			MFIYPLCFCD*	MFIYPLCFCD*			TCGGCAGTCC	CTGTTCCTAT	0	D	0	0	0	0	0
8799	3924	an	AN1560.1	55.m03076	AO070339000293	0	-107	-93					ATGCATATACAATAG	ATGCATATACAATAG			MHIQ*	MHIQ*			CTACGCCTGC	CCGCCCGCAT	0	D	0	0	0	0	0
8804	3924	ao	AN1560.1	55.m03076	AO070339000293	0					-242	-174	ATGCGCTGTCCGATGAGAATCTTATTTCACTATTTCTTAACTCCCTCGGGGTATACTGATGAAGCATAG			ATGCGCTGTCCGATGAGAATCTTATTTCACTATTTCTTAACTCCCTCGGGGTATACTGATGAAGCATAG	MRCPMRILFHYFLTPSGYTDEA*			MRCPMRILFHYFLTPSGYTDEA*	CATGTAATCA	GCACTATCAC	0	D	0	0	0	0	0
8805	3924	ao	AN1560.1	55.m03076	AO070339000293	0					-230	-174	ATGAGAATCTTATTTCACTATTTCTTAACTCCCTCGGGGTATACTGATGAAGCATAG			ATGAGAATCTTATTTCACTATTTCTTAACTCCCTCGGGGTATACTGATGAAGCATAG	MRILFHYFLTPSGYTDEA*			MRILFHYFLTPSGYTDEA*	GCGCTGTCCG	GCACTATCAC	0	D	0	0	0	0	0
8806	3924	ao	AN1560.1	55.m03076	AO070339000293	0					-184	-125	ATGAAGCATAGGCACTATCACGCCAGTATACCCCTTCCGCGCTTGAGTTTTTGTAATTGA			ATGAAGCATAGGCACTATCACGCCAGTATACCCCTTCCGCGCTTGAGTTTTTGTAATTGA	MKHRHYHASIPLPRLSFCN*			MKHRHYHASIPLPRLSFCN*	GGGTATACTG	TGAACGTTAC	0	D	0	0	0	0	0
8807	3924	ao	AN1560.1	55.m03076	AO070339000293	0					-125	-48	ATGAACGTTACGACTGCCCTGCCTGAATCTAACCCGTCTCTCTGCCCTTGCGCAATTGGTCTCGACCACCATTATTGA			ATGAACGTTACGACTGCCCTGCCTGAATCTAACCCGTCTCTCTGCCCTTGCGCAATTGGTCTCGACCACCATTATTGA	MNVTTALPESNPSLCPCAIGLDHHY*			MNVTTALPESNPSLCPCAIGLDHHY*	TTTGTAATTG	TACCCACCAA	0	D	0	0	0	0	0
8809	3929	af	AN0689.1	70.m15292	AO070343000524	0			-162	-118			ATGCGAGGCAACTATCTCGCCTTCAGTACCTGGATCGTCGCCTAA		ATGCGAGGCAACTATCTCGCCTTCAGTACCTGGATCGTCGCCTAA		MRGNYLAFSTWIVA*		MRGNYLAFSTWIVA*		AACACCTCGA	CCTTACGGAG	0		0	0	0	0	0
8808	3929	an	AN0689.1	70.m15292	AO070343000524	0	-140	-114					ATGGGTATCTCGATTCACTGCCCCTGA	ATGGGTATCTCGATTCACTGCCCCTGA			MGISIHCP*	MGISIHCP*			AAACTTATAC	ATATATACTC	0		0	0	0	0	0
8812	3933	af	AN5886.1	72.m19244	AO070245000021	0			-242	-132			ATGTCGGATCCGCCCCTCATCGTCTCTGAGCGACATCGCGACCCCCCATCCCCAATAAAATGTTGCAGCTCCTCCTTGAGATTGCATCAGCATCATAATTGTCATCATTAG		ATGTCGGATCCGCCCCTCATCGTCTCTGAGCGACATCGCGACCCCCCATCCCCAATAAAATGTTGCAGCTCCTCCTTGAGATTGCATCAGCATCATAATTGTCATCATTAG		MSDPPLIVSERHRDPPSPIKCCSSSLRLHQHHNCHH*		MSDPPLIVSERHRDPPSPIKCCSSSLRLHQHHNCHH*		GACCGGACCG	TATCTCCAAG	0	E	0	0	0	0	0
8813	3933	af	AN5886.1	72.m19244	AO070245000021	0			-183	-145			ATGTTGCAGCTCCTCCTTGAGATTGCATCAGCATCATAA		ATGTTGCAGCTCCTCCTTGAGATTGCATCAGCATCATAA		MLQLLLEIASAS*		MLQLLLEIASAS*		CCCCAATAAA	TTGTCATCAT	0	E	0	0	0	0	0
8810	3933	an	AN5886.1	72.m19244	AO070245000021	0	-181	-41					ATGCTGTGGCCAGCGACATCGCGATCCATAAGAGTTCTTATAATGCTGAAGAGCTTTCTGTCTGTCTCAAGCATCTCATACCTGACTATTCGTTCTTTCCGGAGACACTTGCTCTTCTCCTTCTGCGCCATCCCCACTTAA	ATGCTGTGGCCAGCGACATCGCGATCCATAAGAGTTCTTATAATGCTGAAGAGCTTTCTGTCTGTCTCAAGCATCTCATACCTGACTATTCGTTCTTTCCGGAGACACTTGCTCTTCTCCTTCTGCGCCATCCCCACTTAA			MLWPATSRSIRVLIMLKSFLSVSSISYLTIRSFRRHLLFSFCAIPT*	MLWPATSRSIRVLIMLKSFLSVSSISYLTIRSFRRHLLFSFCAIPT*			GAGCCCCTCG	TTGGATTCCC	0	E	0	0	0	0	0
8811	3933	an	AN5886.1	72.m19244	AO070245000021	0	-139	-41					ATGCTGAAGAGCTTTCTGTCTGTCTCAAGCATCTCATACCTGACTATTCGTTCTTTCCGGAGACACTTGCTCTTCTCCTTCTGCGCCATCCCCACTTAA	ATGCTGAAGAGCTTTCTGTCTGTCTCAAGCATCTCATACCTGACTATTCGTTCTTTCCGGAGACACTTGCTCTTCTCCTTCTGCGCCATCCCCACTTAA			MLKSFLSVSSISYLTIRSFRRHLLFSFCAIPT*	MLKSFLSVSSISYLTIRSFRRHLLFSFCAIPT*			AGTTCTTATA	TTGGATTCCC	0	E	0	0	0	0	0
8814	3933	ao	AN5886.1	72.m19244	AO070245000021	0					-209	-171	ATGCCCCTCGATGGTCGCGCTGCGACATCGCGGTCTTAA			ATGCCCCTCGATGGTCGCGCTGCGACATCGCGGTCTTAA	MPLDGRAATSRS*			MPLDGRAATSRS*	GAGATCGGGG	AGAGGGTTAA	0	E	0	0	0	0	0
8815	3933	ao	AN5886.1	72.m19244	AO070245000021	0					-199	-161	ATGGTCGCGCTGCGACATCGCGGTCTTAAAGAGGGTTAA			ATGGTCGCGCTGCGACATCGCGGTCTTAAAGAGGGTTAA	MVALRHRGLKEG*			MVALRHRGLKEG*	ATGCCCCTCG	AATGTTCCCC	0	E	0	0	0	0	0
8816	3933	ao	AN5886.1	72.m19244	AO070245000021	0					-159	-76	ATGTTCCCCAAGGTATCTCTGTACTCGTCCAGATTCCCCAGATATAATTTCTTCACAACCGTTGGCGAAGACGCAAACAGTTGA			ATGTTCCCCAAGGTATCTCTGTACTCGTCCAGATTCCCCAGATATAATTTCTTCACAACCGTTGGCGAAGACGCAAACAGTTGA	MFPKVSLYSSRFPRYNFFTTVGEDANS*			MFPKVSLYSSRFPRYNFFTTVGEDANS*	GAGGGTTAAA	GTCTGTGTCT	0	E	0	0	0	0	0
8817	3935	af	AN3181.1	59.m08573	AO070256000007	0			-199	-113			ATGCTGAAAATCCCGCTGATACCTGCAAGGAGAATCATTATGCATGGCTGCGGAGTAGTGTTACAGGTCATCATTCTAATAGTCTAG		ATGCTGAAAATCCCGCTGATACCTGCAAGGAGAATCATTATGCATGGCTGCGGAGTAGTGTTACAGGTCATCATTCTAATAGTCTAG		MLKIPLIPARRIIMHGCGVVLQVIILIV*		MLKIPLIPARRIIMHGCGVVLQVIILIV*		GATATACTGG	ACTTCCTACA	0	T	0	0	0	0	0
8818	3935	af	AN3181.1	59.m08573	AO070256000007	0			-160	-113			ATGCATGGCTGCGGAGTAGTGTTACAGGTCATCATTCTAATAGTCTAG		ATGCATGGCTGCGGAGTAGTGTTACAGGTCATCATTCTAATAGTCTAG		MHGCGVVLQVIILIV*		MHGCGVVLQVIILIV*		GAGAATCATT	ACTTCCTACA	0	T	0	0	0	0	0
8819	3935	af	AN3181.1	59.m08573	AO070256000007	0			-156	-142			ATGGCTGCGGAGTAG		ATGGCTGCGGAGTAG		MAAE*		MAAE*		ATCATTATGC	TGTTACAGGT	0	T	0	0	0	0	0
8820	3935	ao	AN3181.1	59.m08573	AO070256000007	0					-241	-218	ATGGTGATGATCTCGTCCTTCTGA			ATGGTGATGATCTCGTCCTTCTGA	MVMISSF*			MVMISSF*	GTGTCCACTA	CGAGGAACCA	0	T	0	0	0	0	0
8821	3935	ao	AN3181.1	59.m08573	AO070256000007	0					-235	-218	ATGATCTCGTCCTTCTGA			ATGATCTCGTCCTTCTGA	MISSF*			MISSF*	ACTAATGGTG	CGAGGAACCA	0	T	0	0	0	0	0
8822	3935	ao	AN3181.1	59.m08573	AO070256000007	0					-151	-137	ATGACAGTCACTTAG			ATGACAGTCACTTAG	MTVT*			MTVT*	AATCTCTTAT	TGGCGTACAC	0	T	0	0	0	0	0
8827	3936	af	AN2508.1	59.m08476	AO070263000056	0			-242	-201			ATGATACATCGGACAATAGGTAGGTCCGTAGAAGATGGCTGA		ATGATACATCGGACAATAGGTAGGTCCGTAGAAGATGGCTGA		MIHRTIGRSVEDG*		MIHRTIGRSVEDG*		CTATCCACAA	TATGCCGGTG	0	E	FG10049.1	0	0	0	0
8828	3936	af	AN2508.1	59.m08476	AO070263000056	0			-208	-119			ATGGCTGATATGCCGGTGAAAAATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAGCGGCAATGATATAA		ATGGCTGATATGCCGGTGAAAAATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAGCGGCAATGATATAA		MADMPVKNDQENSRSYLLAPLRSGLAAMI*		MADMPVKNDQENSRSYLLAPLRSGLAAMI*		TCCGTAGAAG	CCGGATCCAA	0	E	FG10049.1	0	0	0	0
8829	3936	af	AN2508.1	59.m08476	AO070263000056	0			-199	-119			ATGCCGGTGAAAAATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAGCGGCAATGATATAA		ATGCCGGTGAAAAATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAGCGGCAATGATATAA		MPVKNDQENSRSYLLAPLRSGLAAMI*		MPVKNDQENSRSYLLAPLRSGLAAMI*		GATGGCTGAT	CCGGATCCAA	0	E	FG10049.1	0	0	0	0
8830	3936	af	AN2508.1	59.m08476	AO070263000056	0			-186	-133			ATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAG		ATGACCAAGAGAATTCTCGGAGCTATCTGCTTGCTCCGCTCCGATCGGGCTTAG		MTKRILGAICLLRSDRA*		MTKRILGAICLLRSDRA*		CCGGTGAAAA	CGGCAATGAT	0	E	FG10049.1	0	0	0	0
8823	3936	an	AN2508.1	59.m08476	AO070263000056	0	-252	-223					ATGCCGACGTTAGACCTTAGATATAGATGA	ATGCCGACGTTAGACCTTAGATATAGATGA			MPTLDLRYR*	MPTLDLRYR*			ACAAATTTAC	AGTGAGGTGA	0	E	FG10049.1	0	0	0	0
8824	3936	an	AN2508.1	59.m08476	AO070263000056	0	-211	-146					ATGGGAATGCCAGAGATTGGGCTATACTGGAAGTCCGGGGTTCGGGGTCGGGGTCGGACATACTGA	ATGGGAATGCCAGAGATTGGGCTATACTGGAAGTCCGGGGTTCGGGGTCGGGGTCGGACATACTGA			MGMPEIGLYWKSGVRGRGRTY*	MGMPEIGLYWKSGVRGRGRTY*			GTGAGGTGAA	TCGGGGGTAG	0	E	FG10049.1	0	0	0	0
8825	3936	an	AN2508.1	59.m08476	AO070263000056	0	-205	-146					ATGCCAGAGATTGGGCTATACTGGAAGTCCGGGGTTCGGGGTCGGGGTCGGACATACTGA	ATGCCAGAGATTGGGCTATACTGGAAGTCCGGGGTTCGGGGTCGGGGTCGGACATACTGA			MPEIGLYWKSGVRGRGRTY*	MPEIGLYWKSGVRGRGRTY*			TGAAATGGGA	TCGGGGGTAG	0	E	FG10049.1	0	0	0	0
8832	3936	ao	AN2508.1	59.m08476	AO070263000056	0					-183	-124	ATGCCAGTTCCCAAAGGGGAAAGCACCTTCGGACTATCTGATAAATCCGATCGGGCTTAG			ATGCCAGTTCCCAAAGGGGAAAGCACCTTCGGACTATCTGATAAATCCGATCGGGCTTAG	MPVPKGESTFGLSDKSDRA*			MPVPKGESTFGLSDKSDRA*	CGAAAGCCCG	TGGGCTCGGC	0	E	FG10049.1	0	0	0	0
8835	3937	af	AN3455.1	59.m09317	AO070265000031	0			-225	-211			ATGGTGCTTATCTAA		ATGGTGCTTATCTAA		MVLI*		MVLI*		TACTGAAGAT	ACAAAGTAAG	0	S	0	0	0	0	0
8836	3937	af	AN3455.1	59.m09317	AO070265000031	0			-197	-174			ATGGCTTCAGAAAATTTATCTTAA		ATGGCTTCAGAAAATTTATCTTAA		MASENLS*		MASENLS*		AAGTAAGGAA	GAAATTTGCT	0	S	0	0	0	0	0
8837	3937	af	AN3455.1	59.m09317	AO070265000031	0			-92	-81			ATGATTTTCTAA		ATGATTTTCTAA		MIF*		MIF*		TTGGGCTGTT	GTGTATTATT	0	S	0	0	0	0	0
8833	3937	an	AN3455.1	59.m09317	AO070265000031	0	-167	-144					ATGCTGTGGCGCTCCGGCCAATAA	ATGCTGTGGCGCTCCGGCCAATAA			MLWRSGQ*	MLWRSGQ*			GCGGCCTTGG	CACGTGATCT	0	S	0	0	0	0	0
8834	3937	an	AN3455.1	59.m09317	AO070265000031	0	-79	-59					ATGGAGACTTTCAAGTTCTGA	ATGGAGACTTTCAAGTTCTGA			METFKF*	METFKF*			AAAAGTTTCG	CTTGGAGCAG	0	S	0	0	0	0	0
8838	3939	af	AN4439.1	58.m07886	AO070273000015	0			-252	-172			ATGAGTGCTGCTACCTTCAATATCTGCCGTCGTTGTGCCGTGGGCTGCGCATTCTGGAACTGCAGCCGCCCGCCTTCTTAA		ATGAGTGCTGCTACCTTCAATATCTGCCGTCGTTGTGCCGTGGGCTGCGCATTCTGGAACTGCAGCCGCCCGCCTTCTTAA		MSAATFNICRRCAVGCAFWNCSRPPS*		MSAATFNICRRCAVGCAFWNCSRPPS*		GAAAGAGAGC	CCTTGGATGA	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8839	3939	af	AN4439.1	58.m07886	AO070273000015	0			-165	-70			ATGATTTATCAGAATGACCCCACCAGTGGATGCCAGTCAGCCGCCTCTGACGTGACAGCATCAAGCGTTATTTGGATGGCTGTTACCTTAGCTTAA		ATGATTTATCAGAATGACCCCACCAGTGGATGCCAGTCAGCCGCCTCTGACGTGACAGCATCAAGCGTTATTTGGATGGCTGTTACCTTAGCTTAA		MIYQNDPTSGCQSAASDVTASSVIWMAVTLA*		MIYQNDPTSGCQSAASDVTASSVIWMAVTLA*		TTAACCTTGG	CAGCCCTTTC	0		FG01611.1	MG06214.1	NCU08736.1	0	0

8840	3939	af	AN4439.1	58.m07886	AO070273000015	0			-152	-111			ATGACCCCACCAGTGGATGCCAGTCAGCCGCCTCTGACGTGA		ATGACCCCACCAGTGGATGCCAGTCAGCCGCCTCTGACGTGA		MTPPVDASQPPLT*		MTPPVDASQPPLT*		ATTTATCAGA	CAGCATCAAG	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8841	3939	af	AN4439.1	58.m07886	AO070273000015	0			-136	-116			ATGCCAGTCAGCCGCCTCTGA		ATGCCAGTCAGCCGCCTCTGA		MPVSRL*		MPVSRL*		CCACCAGTGG	CGTGACAGCA	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8842	3939	af	AN4439.1	58.m07886	AO070273000015	0			-90	-70			ATGGCTGTTACCTTAGCTTAA		ATGGCTGTTACCTTAGCTTAA		MAVTLA*		MAVTLA*		CGTTATTTGG	CAGCCCTTTC	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8843	3939	ao	AN4439.1	58.m07886	AO070273000015	0					-231	-34	ATGAACAACTCCGTTGTTTGGGGCTGTCTTTGTATGATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA			ATGAACAACTCCGTTGTTTGGGGCTGTCTTTGTATGATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA	MNNSVVWGCLCMMQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*			MNNSVVWGCLCMMQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*	ATATAAAGTT	ACAGTCTGTT	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8844	3939	ao	AN4439.1	58.m07886	AO070273000015	0					-198	-34	ATGATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA			ATGATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA	MMQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*			MMQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*	CTGTCTTTGT	ACAGTCTGTT	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8845	3939	ao	AN4439.1	58.m07886	AO070273000015	0					-195	-34	ATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA			ATGCAATTCTCTGCAGCCACCCGCGGGGGAGAATCCACCGGGCGCCAGCCTTCGGGACTTCTCTCAACCTTCCATTCCATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA	MQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*			MQFSAATRGGESTGRQPSGLLSTFHSMDSTFSTFRKLLAVSDVPDKKALVTTL*	TCTTTGTATG	ACAGTCTGTT	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8846	3939	ao	AN4439.1	58.m07886	AO070273000015	0					-117	-34	ATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA			ATGGATTCAACTTTCTCCACTTTCAGAAAGCTCTTGGCCGTGTCTGACGTCCCCGACAAGAAGGCCCTTGTTACCACACTTTAA	MDSTFSTFRKLLAVSDVPDKKALVTTL*			MDSTFSTFRKLLAVSDVPDKKALVTTL*	CTTCCATTCC	ACAGTCTGTT	0		FG01611.1	MG06214.1	NCU08736.1	0	0
8847	3943	an	AN4728.1	71.m15638	AO070284000080	0	-126	-25					ATGAAGATGAGCAAAGCCCCAGGGCTCGGCGTCGGAGTTCCCCAAGTTCTCCACTACGTTACCTTTATCTTCCTCGCCCTCGCAACCATCAACACCCAATGA	ATGAAGATGAGCAAAGCCCCAGGGCTCGGCGTCGGAGTTCCCCAAGTTCTCCACTACGTTACCTTTATCTTCCTCGCCCTCGCAACCATCAACACCCAATGA			MKMSKAPGLGVGVPQVLHYVTFIFLALATINTQ*	MKMSKAPGLGVGVPQVLHYVTFIFLALATINTQ*			AATCTAGTAG	CCCCTCCACG	0	S	FG00261.1	MG02867.1	0	0	0
8848	3943	an	AN4728.1	71.m15638	AO070284000080	0	-120	-25					ATGAGCAAAGCCCCAGGGCTCGGCGTCGGAGTTCCCCAAGTTCTCCACTACGTTACCTTTATCTTCCTCGCCCTCGCAACCATCAACACCCAATGA	ATGAGCAAAGCCCCAGGGCTCGGCGTCGGAGTTCCCCAAGTTCTCCACTACGTTACCTTTATCTTCCTCGCCCTCGCAACCATCAACACCCAATGA			MSKAPGLGVGVPQVLHYVTFIFLALATINTQ*	MSKAPGLGVGVPQVLHYVTFIFLALATINTQ*			GTAGATGAAG	CCCCTCCACG	0	S	FG00261.1	MG02867.1	0	0	0
8851	3944	af	AN1102.1	70.m15130	AO070285000036	0			-359	-288			ATGCCCCTTTCACCCCGCCGAATTTCCATCAAACCATCAACAATTGCTCATCTACATCTTCTGAAACATTGA		ATGCCCCTTTCACCCCGCCGAATTTCCATCAAACCATCAACAATTGCTCATCTACATCTTCTGAAACATTGA		MPLSPRRISIKPSTIAHLHLLKH*		MPLSPRRISIKPSTIAHLHLLKH*		TCCTCCGTCG	AACCTGGCCA	0	O	0	0	NCU00447.1	0	0
8852	3944	ao	AN1102.1	70.m15130	AO070285000036	0					-331	-236	ATGCCGCCCTCGAGTCTTGGTCTTCTTTTCGTTTCTCCCTCGCATCTGTTGGCTATTTGCACGAGTGTTTCGCACACTGGTCTGGATTGTGGCTGA			ATGCCGCCCTCGAGTCTTGGTCTTCTTTTCGTTTCTCCCTCGCATCTGTTGGCTATTTGCACGAGTGTTTCGCACACTGGTCTGGATTGTGGCTGA	MPPSSLGLLFVSPSHLLAICTSVSHTGLDCG*			MPPSSLGLLFVSPSHLLAICTSVSHTGLDCG*	CTGTCTGTGT	CTGCTTTCCT	0	O	0	0	NCU00447.1	0	0
8854	3945	af	AN7784.1	71.m15815	AO070286000028	0			-221	-198			ATGCTGCGACTGCTTATAAGATGA		ATGCTGCGACTGCTTATAAGATGA		MLRLLIR*		MLRLLIR*		GTATTCGAGC	TTCACACCTA	0	R	0	0	0	0	0
8855	3945	af	AN7784.1	71.m15815	AO070286000028	0			-201	-139			ATGATTCACACCTACTATATGATCCAGCGTGGATTTTCATCCAAAATCTCTACCCGAGTCTGA		ATGATTCACACCTACTATATGATCCAGCGTGGATTTTCATCCAAAATCTCTACCCGAGTCTGA		MIHTYYMIQRGFSSKISTRV*		MIHTYYMIQRGFSSKISTRV*		TGCTTATAAG	CCTGCCGTCT	0	R	0	0	0	0	0
8856	3945	af	AN7784.1	71.m15815	AO070286000028	0			-183	-139			ATGATCCAGCGTGGATTTTCATCCAAAATCTCTACCCGAGTCTGA		ATGATCCAGCGTGGATTTTCATCCAAAATCTCTACCCGAGTCTGA		MIQRGFSSKISTRV*		MIQRGFSSKISTRV*		CACCTACTAT	CCTGCCGTCT	0	R	0	0	0	0	0
8853	3945	an	AN7784.1	71.m15815	AO070286000028	0	-199	-188					ATGTTGCGCTGA	ATGTTGCGCTGA			MLR*	MLR*			CGGTATAATC	ACTATACAAT	0	R	0	0	0	0	0
8857	3945	ao	AN7784.1	71.m15815	AO070286000028	0					-231	-208	ATGTTGCGCCTGTCTTTACGATGA			ATGTTGCGCCTGTCTTTACGATGA	MLRLSLR*			MLRLSLR*	CCTTGGAAGG	GCCTTGATTT	0	R	0	0	0	0	0
8858	3945	ao	AN7784.1	71.m15815	AO070286000028	0					-211	-152	ATGAGCCTTGATTTACCATTCTCACACTTCCATCCAAGGGCGTGCTTCTATATCTACTGA			ATGAGCCTTGATTTACCATTCTCACACTTCCATCCAAGGGCGTGCTTCTATATCTACTGA	MSLDLPFSHFHPRACFYIY*			MSLDLPFSHFHPRACFYIY*	TGTCTTTACG	TCGCCCCGAG	0	R	0	0	0	0	0
8862	3947	af	AN4954.1	59.m08859	AO070288000007	0			-234	-124			ATGGCATTTGTTGCAGCAGATATGATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		ATGGCATTTGTTGCAGCAGATATGATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		MAFVAADMMNCEVFNQFNIMALSHIIHQDGINLGRR*		MAFVAADMMNCEVFNQFNIMALSHIIHQDGINLGRR*		AGGCACCTCA	ATAACAGTAG	0		0	0	0	0	0
8863	3947	af	AN4954.1	59.m08859	AO070288000007	0			-213	-124			ATGATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		ATGATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		MMNCEVFNQFNIMALSHIIHQDGINLGRR*		MMNCEVFNQFNIMALSHIIHQDGINLGRR*		TGCAGCAGAT	ATAACAGTAG	0		0	0	0	0	0
8864	3947	af	AN4954.1	59.m08859	AO070288000007	0			-210	-124			ATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		ATGAACTGTGAAGTATTCAATCAATTCAATATAATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		MNCEVFNQFNIMALSHIIHQDGINLGRR*		MNCEVFNQFNIMALSHIIHQDGINLGRR*		AGCAGATATG	ATAACAGTAG	0		0	0	0	0	0
8865	3947	af	AN4954.1	59.m08859	AO070288000007	0			-177	-124			ATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		ATGGCATTAAGTCATATTATACACCAAGATGGAATCAATCTCGGCCGTAGATAG		MALSHIIHQDGINLGRR*		MALSHIIHQDGINLGRR*		ATTCAATATA	ATAACAGTAG	0		0	0	0	0	0
8866	3947	af	AN4954.1	59.m08859	AO070288000007	0			-149	-120			ATGGAATCAATCTCGGCCGTAGATAGATAA		ATGGAATCAATCTCGGCCGTAGATAGATAA		MESISAVDR*		MESISAVDR*		ATACACCAAG	CAGTAGCTGT	0		0	0	0	0	0
8859	3947	an	AN4954.1	59.m08859	AO070288000007	0	-202	-128					ATGTACGCCGCATGGAGGGCATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAACTTAGCGCGCGCTTAA	ATGTACGCCGCATGGAGGGCATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAACTTAGCGCGCGCTTAA			MYAAWRAWSAHSTVSSAALNLARA*	MYAAWRAWSAHSTVSSAALNLARA*			CCCATTCACA	GGAGTCACTC	0		0	0	0	0	0
8860	3947	an	AN4954.1	59.m08859	AO070288000007	0	-191	-144					ATGGAGGGCATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAA	ATGGAGGGCATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAA			MEGMECSFHSIQCGA*	MEGMECSFHSIQCGA*			TGTACGCCGC	CTTAGCGCGC	0		0	0	0	0	0
8861	3947	an	AN4954.1	59.m08859	AO070288000007	0	-182	-144					ATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAA	ATGGAGTGCTCATTCCACAGTATCCAGTGCGGCGCTTAA			MECSFHSIQCGA*	MECSFHSIQCGA*			CATGGAGGGC	CTTAGCGCGC	0		0	0	0	0	0
8868	3954	af	AN0124.1	71.m15405	AO070311000088	0			-262	-224			ATGAAAAGAAATGCTTTGATTTCGTCGATACGTATTTAA		ATGAAAAGAAATGCTTTGATTTCGTCGATACGTATTTAA		MKRNALISSIRI*		MKRNALISSIRI*		TGTGCCACCA	AGACCTTTGG	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8869	3954	af	AN0124.1	71.m15405	AO070311000088	0			-152	-108			ATGCGCTCGAATAGGAAAGTAGGGCATAGGGTTTCACACATGTAA		ATGCGCTCGAATAGGAAAGTAGGGCATAGGGTTTCACACATGTAA		MRSNRKVGHRVSHM*		MRSNRKVGHRVSHM*		ATACCCAAAG	CTTTTTTCCG	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8867	3954	an	AN0124.1	71.m15405	AO070311000088	0	-186	-175					ATGATACATTGA	ATGATACATTGA			MIH*	MIH*			GTCCTTGTAC	TTGGCAATTC	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8870	3954	ao	AN0124.1	71.m15405	AO070311000088	0					-197	-183	ATGGGCAAATTGTAG			ATGGGCAAATTGTAG	MGKL*			MGKL*	CAGAATCTGG	CTCAAAGCCC	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8871	3954	ao	AN0124.1	71.m15405	AO070311000088	0					-106	-23	ATGTCACTTTTTCTCCATCATGTCCGCGGCATCTCTCAGTATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAATGCCCTAG			ATGTCACTTTTTCTCCATCATGTCCGCGGCATCTCTCAGTATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAATGCCCTAG	MSLFLHHVRGISQYAVCGSRRSLVLMP*			MSLFLHHVRGISQYAVCGSRRSLVLMP*	CAAGGGGGGG	GCTTCGGTGA	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8872	3954	ao	AN0124.1	71.m15405	AO070311000088	0					-87	-31	ATGTCCGCGGCATCTCTCAGTATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAA			ATGTCCGCGGCATCTCTCAGTATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAA	MSAASLSMQSAVLEGHWF*			MSAASLSMQSAVLEGHWF*	TTTCTCCATC	TGCCCTAGGC	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8873	3954	ao	AN0124.1	71.m15405	AO070311000088	0					-66	-31	ATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAA			ATGCAGTCTGCGGTTCTAGAAGGTCACTGGTTCTAA	MQSAVLEGHWF*			MQSAVLEGHWF*	ATCTCTCAGT	TGCCCTAGGC	0	TR	FG09784.1	MG07119.1	NCU07722.1	0	0
8876	3958	af	AN0190.1	71.m15460	AO070321000053	0			-260	-135			ATGGTAAGTCAAACGCCTTTTTTCTTTGTCTTTCATGTACCCTCACATGATTATACAACTACTATAATCTGTCAATCCCCTGAAGCTCATTTATTTATCTCAAAAATTTCGAGCACATGTGATTGA		ATGGTAAGTCAAACGCCTTTTTTCTTTGTCTTTCATGTACCCTCACATGATTATACAACTACTATAATCTGTCAATCCCCTGAAGCTCATTTATTTATCTCAAAAATTTCGAGCACATGTGATTGA		MVSQTPFFFVFHVPSHDYTTTIICQSPEAHLFISKISSTCD*		MVSQTPFFFVFHVPSHDYTTTIICQSPEAHLFISKISSTCD*		AATTCGTCTG	GAAACGTATC	0	J	0	0	0	0	0
8877	3958	af	AN0190.1	71.m15460	AO070321000053	0			-226	-194			ATGTACCCTCACATGATTATACAACTACTATAA		ATGTACCCTCACATGATTATACAACTACTATAA		MYPHMIIQLL*		MYPHMIIQLL*		TTTGTCTTTC	TCTGTCAATC	0	J	0	0	0	0	0
8875	3958	an	AN0190.1	71.m15460	AO070321000053	0	-235	-122					ATGGTAAGTTCGAATCAGCATTATTTCGCGCACAGATCAAATGATTATATACCTACTATAATCTGTCAATCCCCTGAAGCTCGCTATATAATCTCATCAAAGAGCACAACGTGA	ATGGTAAGTTCGAATCAGCATTATTTCGCGCACAGATCAAATGATTATATACCTACTATAATCTGTCAATCCCCTGAAGCTCGCTATATAATCTCATCAAAGAGCACAACGTGA			MVSSNQHYFAHRSNDYIPTIICQSPEARYIISSKSTT*	MVSSNQHYFAHRSNDYIPTIICQSPEARYIISSKSTT*			TTCGTTCTTG	TTGAGAAACG	0	J	0	0	0	0	0
8878	3958	ao	AN0190.1	71.m15460	AO070321000053	0					-260	-195	ATGGTAAGTTACTATCTCTACTTTCTTAATATTGCCTGTCTTTGCATGATTATACAAATACTATAA			ATGGTAAGTTACTATCTCTACTTTCTTAATATTGCCTGTCTTTGCATGATTATACAAATACTATAA	MVSYYLYFLNIACLCMIIQIL*			MVSYYLYFLNIACLCMIIQIL*	ATCTCTTCTG	TCTGTCAATC	0	J	0	0	0	0	0
8879	3958	ao	AN0190.1	71.m15460	AO070321000053	0					-134	-120	ATGTATCGAAAATGA			ATGTATCGAAAATGA	MYRK*			MYRK*	TGATTGAGAA	TTTGCATTCT	0	J	0	0	0	0	0
8880	3958	ao	AN0190.1	71.m15460	AO070321000053	0					-123	-67	ATGATTTGCATTCTTAATTTCCCATGTGGATCTTGCATGTCTTGGGCTGAGCAATAA			ATGATTTGCATTCTTAATTTCCCATGTGGATCTTGCATGTCTTGGGCTGAGCAATAA	MICILNFPCGSCMSWAEQ*			MICILNFPCGSCMSWAEQ*	TGTATCGAAA	GCTAACATTA	0	J	0	0	0	0	0
8881	3958	ao	AN0190.1	71.m15460	AO070321000053	0					-100	-74	ATGTGGATCTTGCATGTCTTGGGCTGA			ATGTGGATCTTGCATGTCTTGGGCTGA	MWILHVLG*			MWILHVLG*	TTAATTTCCC	GCAATAAGCT	0	J	0	0	0	0	0
8882	3958	ao	AN0190.1	71.m15460	AO070321000053	0					-87	-67	ATGTCTTGGGCTGAGCAATAA			ATGTCTTGGGCTGAGCAATAA	MSWAEQ*			MSWAEQ*	TGGATCTTGC	GCTAACATTA	0	J	0	0	0	0	0
8874	3958	conserved	AN0190.1	71.m15460	AO070321000053	0	-195	-175	-214	-194	-215	-195	ATGATTATAyAmmTACTATAA	ATGATTATATACCTACTATAA	ATGATTATACAACTACTATAA	ATGATTATACAAATACTATAA	MIIylL*	MIIYLL*	MIIQLL*	MIIQIL*	swvhshTyrm	TCTGTCAATC	0	J	0	0	0	0	0
8886	3960	af	AN6630.1	62.m03226	AO070326000082	0			-192	-10			ATGTTTATATTGATTTTACGGGTTCCAAATTCATCTCTGGGCCCAATTTCGAAATTCCTGCGCTTTTGGTGGAGATTTCAGTGTTTCGTGGGGCATTTTCCAACCTTTATATTTGAACCGCCAGACGGTGCTCCAGTTCGAATCGCTAACTGTCAATTTAACAGCCCTTCTAGGCTCGTTTAG		ATGTTTATATTGATTTTACGGGTTCCAAATTCATCTCTGGGCCCAATTTCGAAATTCCTGCGCTTTTGGTGGAGATTTCAGTGTTTCGTGGGGCATTTTCCAACCTTTATATTTGAACCGCCAGACGGTGCTCCAGTTCGAATCGCTAACTGTCAATTTAACAGCCCTTCTAGGCTCGTTTAG		MFILILRVPNSSLGPISKFLRFWWRFQCFVGHFPTFIFEPPDGAPVRIANCQFNSPSRLV*		MFILILRVPNSSLGPISKFLRFWWRFQCFVGHFPTFIFEPPDGAPVRIANCQFNSPSRLV*		TGAACTAGGT	ACCGCAAAAA	0	K	0	0	0	YHR193C	0
8883	3960	an	AN6630.1	62.m03226	AO070326000082	0	-194	-183					ATGTTCAACTGA	ATGTTCAACTGA			MFN*	MFN*			ACTCGCAGGT	ATTGTGCGAC	0	K	0	0	0	YHR193C	0
8884	3960	an	AN6630.1	62.m03226	AO070326000082	0	-165	-139					ATGGATTTTCCAAATCGGACGTGGTGA	ATGGATTTTCCAAATCGGACGTGGTGA			MDFPNRTW*	MDFPNRTW*			GACCGCGAAA	TAATCCCGCG	0	K	0	0	0	YHR193C	0
8888	3963	an	AN5576.1	58.m07503	AO070328000028	0	-282	-265					ATGGTTGTAGTTGGCTGA	ATGGTTGTAGTTGGCTGA			MVVVG*	MVVVG*			TCGACCGTTT	TAGTCGGAAC	0		0	0	0	0	0
8889	3963	an	AN5576.1	58.m07503	AO070328000028	0	-220	-206					ATGGATGAAAAATAA	ATGGATGAAAAATAA			MDEK*	MDEK*			TCGACCTTGA	AAGTCGTGAT	0		0	0	0	0	0
8890	3963	an	AN5576.1	58.m07503	AO070328000028	0	-216	-148					ATGAAAAATAAAAGTCGTGATGGACATATCCATTATATCCTACTTATACAGAATTCTACAAGGATCTGA	ATGAAAAATAAAAGTCGTGATGGACATATCCATTATATCCTACTTATACAGAATTCTACAAGGATCTGA			MKNKSRDGHIHYILLIQNSTRI*	MKNKSRDGHIHYILLIQNSTRI*			CCTTGAATGG	CGTCCTTGAC	0		0	0	0	0	0

8891	3963	an	AN5576.1	58.m07503	AO070328000028	0	-197	-81					ATGGACATATCCATTATATCCTACTTATACAGAATTCTACAAGGATCTGACGTCCTTGACGCTGGGGTGTCGACCGTCAGCAGTGCTCCCACGTCATTGCCGCAATTTCCTTTTTAG	ATGGACATATCCATTATATCCTACTTATACAGAATTCTACAAGGATCTGACGTCCTTGACGCTGGGGTGTCGACCGTCAGCAGTGCTCCCACGTCATTGCCGCAATTTCCTTTTTAG			MDISIISYLYRILQGSDVLDAGVSTVSSAPTSLPQFPF*	MDISIISYLYRILQGSDVLDAGVSTVSSAPTSLPQFPF*			AAAAGTCGTG	GCTGGTCATC	0		0	0	0	0	0
8892	3964	ao	AN5569.1	58.m07493	AO070328000037	0					-238	-200	ATGCGGTCACGTGTCGATGCGGTCATGGTCAAGGCTTAA			ATGCGGTCACGTGTCGATGCGGTCATGGTCAAGGCTTAA	MRSRVDAVMVKA*			MRSRVDAVMVKA*	GAAGGCGGAG	CTGAACTCGT	0	KL	0	0	0	0	0
8893	3964	ao	AN5569.1	58.m07493	AO070328000037	0					-222	-196	ATGCGGTCATGGTCAAGGCTTAACTGA			ATGCGGTCATGGTCAAGGCTTAACTGA	MRSWSRLN*			MRSWSRLN*	TCACGTGTCG	ACTCGTTGCG	0	KL	0	0	0	0	0
8894	3964	ao	AN5569.1	58.m07493	AO070328000037	0					-214	-200	ATGGTCAAGGCTTAA			ATGGTCAAGGCTTAA	MVKA*			MVKA*	CGATGCGGTC	CTGAACTCGT	0	KL	0	0	0	0	0
8897	3965	af	AN3628.1	58.m07473	AO070328000066	0			-140	-117			ATGAGGCTAAGAAGAATACTATAA		ATGAGGCTAAGAAGAATACTATAA		MRLRRIL*		MRLRRIL*		GATATTGTTT	GTGCTCGTCA	0	B	0	0	0	0	0
8895	3965	an	AN3628.1	58.m07473	AO070328000066	0	-193	-167					ATGGGTCTAGGCTGTCGAGCGCAGTGA	ATGGGTCTAGGCTGTCGAGCGCAGTGA			MGLGCRAQ*	MGLGCRAQ*			AAGAAGCAGC	ATGGACATTG	0	B	0	0	0	0	0
8896	3965	an	AN3628.1	58.m07473	AO070328000066	0	-166	-128					ATGGACATTGTAGGCGGGATCGTTGACTGCTGGCGCTGA	ATGGACATTGTAGGCGGGATCGTTGACTGCTGGCGCTGA			MDIVGGIVDCWR*	MDIVGGIVDCWR*			AGCGCAGTGA	GGTCGAGCTT	0	B	0	0	0	0	0
8900	3969	af	AN0409.1	54.m07007	AO070338000252	0			-208	-179			ATGTGGATGGTCATAGGAAATCAGGGTTGA		ATGTGGATGGTCATAGGAAATCAGGGTTGA		MWMVIGNQG*		MWMVIGNQG*		ACCTCGGAGG	ATCGTTGCTA	0	TZ	0	0	0	0	0
8901	3969	af	AN0409.1	54.m07007	AO070338000252	0			-202	-179			ATGGTCATAGGAAATCAGGGTTGA		ATGGTCATAGGAAATCAGGGTTGA		MVIGNQG*		MVIGNQG*		GAGGATGTGG	ATCGTTGCTA	0	TZ	0	0	0	0	0
8902	3969	af	AN0409.1	54.m07007	AO070338000252	0			-101	-63			ATGTCGACTCCTGTCTTTCGCCTTACGAGTATCTCCTGA		ATGTCGACTCCTGTCTTTCGCCTTACGAGTATCTCCTGA		MSTPVFRLTSIS*		MSTPVFRLTSIS*		TGTCAGCAAG	GTGTCCTTCA	0	TZ	0	0	0	0	0
8898	3969	an	AN0409.1	54.m07007	AO070338000252	0	-165	-64					ATGATACTGACGTTCTTTTCGTTTAGTTTATTCCGCGTCCCTTTTGCTCCGCTGTCGTCCACCAGCAAGATGTCGACCTGTTTTTACCCTACGAGAGCTTGA	ATGATACTGACGTTCTTTTCGTTTAGTTTATTCCGCGTCCCTTTTGCTCCGCTGTCGTCCACCAGCAAGATGTCGACCTGTTTTTACCCTACGAGAGCTTGA			MILTFFSFSLFRVPFAPLSSTSKMSTCFYPTRA*	MILTFFSFSLFRVPFAPLSSTSKMSTCFYPTRA*			CCAAGGGAAA	GCGTTGTTCT	0	TZ	0	0	0	0	0
8899	3969	an	AN0409.1	54.m07007	AO070338000252	0	-96	-64					ATGTCGACCTGTTTTTACCCTACGAGAGCTTGA	ATGTCGACCTGTTTTTACCCTACGAGAGCTTGA			MSTCFYPTRA*	MSTCFYPTRA*			CACCAGCAAG	GCGTTGTTCT	0	TZ	0	0	0	0	0
8903	3969	ao	AN0409.1	54.m07007	AO070338000252	0					-100	-62	ATGTCGACTTCTGTTTTGAACACTGCGAGTAGTTGTTGA			ATGTCGACTTCTGTTTTGAACACTGCGAGTAGTTGTTGA	MSTSVLNTASSC*			MSTSVLNTASSC*	TGTCAGCAAA	GCGCTCCTCT	0	TZ	0	0	0	0	0
8908	3973	af	AN2150.1	72.m19691	AO070343000199	0			-244	-155			ATGGCCGAGCTTCCACTGCTGGAGATCTCGTTCTGCTACCCACTCTCAGTTGGTCTCCCGCTAAAAGTTCTGCCGGTCCGGAGGCGGTGA		ATGGCCGAGCTTCCACTGCTGGAGATCTCGTTCTGCTACCCACTCTCAGTTGGTCTCCCGCTAAAAGTTCTGCCGGTCCGGAGGCGGTGA		MAELPLLEISFCYPLSVGLPLKVLPVRRR*		MAELPLLEISFCYPLSVGLPLKVLPVRRR*		TTGTGACGAG	ATGTTTTCGA	0	J	0	MG10357.1	0	0	0
8909	3973	af	AN2150.1	72.m19691	AO070343000199	0			-154	-107			ATGTTTTCGAAGATGCATCCCACTTTGGCGAGGGGAATGCGGCCCTGA		ATGTTTTCGAAGATGCATCCCACTTTGGCGAGGGGAATGCGGCCCTGA		MFSKMHPTLARGMRP*		MFSKMHPTLARGMRP*		GAGGCGGTGA	ATTTGCTCCC	0	J	0	MG10357.1	0	0	0
8910	3973	af	AN2150.1	72.m19691	AO070343000199	0			-142	-107			ATGCATCCCACTTTGGCGAGGGGAATGCGGCCCTGA		ATGCATCCCACTTTGGCGAGGGGAATGCGGCCCTGA		MHPTLARGMRP*		MHPTLARGMRP*		GTTTTCGAAG	ATTTGCTCCC	0	J	0	MG10357.1	0	0	0
8911	3973	af	AN2150.1	72.m19691	AO070343000199	0			-118	-107			ATGCGGCCCTGA		ATGCGGCCCTGA		MRP*		MRP*		GGCGAGGGGA	ATTTGCTCCC	0	J	0	MG10357.1	0	0	0
8904	3973	an	AN2150.1	72.m19691	AO070343000199	0	-227	-162					ATGCTGTGTGAGCGAATGTCAAGCTCCGACAGCTGCTTTTCTGGGGGGTTGAATGGCTGCGCTAA	ATGCTGTGTGAGCGAATGTCAAGCTCCGACAGCTGCTTTTCTGGGGGGTTGAATGGCTGCGCTAA			MLCERMSSSDSCFSGGLNGLR*	MLCERMSSSDSCFSGGLNGLR*			GTTTATACGT	GCAAAAGATT	0	J	0	MG10357.1	0	0	0
8905	3973	an	AN2150.1	72.m19691	AO070343000199	0	-212	-162					ATGTCAAGCTCCGACAGCTGCTTTTCTGGGGGGTTGAATGGGCTGCGCTAA	ATGTCAAGCTCCGACAGCTGCTTTTCTGGGGGGTTGAATGGGCTGCGCTAA			MSSSDSCFSGGLNGLR*	MSSSDSCFSGGLNGLR*			GTGTGAGCGA	GCAAAAGATT	0	J	0	MG10357.1	0	0	0
8906	3973	an	AN2150.1	72.m19691	AO070343000199	0	-175	-134					ATGGGCTGCGCTAAGCAAAAGATTCTGCCAGGCGGGCGGTGA	ATGGGCTGCGCTAAGCAAAAGATTCTGCCAGGCGGGCGGTGA			MGCAKQKILPGGR*	MGCAKQKILPGGR*			GGGGGGTTGA	CAATATTTCG	0	J	0	MG10357.1	0	0	0
8907	3973	an	AN2150.1	72.m19691	AO070343000199	0	-99	-52					ATGAGTCAAATCCTCCACGAGACCCCGGACTGCCTTTCCTTTCTTTAG	ATGAGTCAAATCCTCCACGAGACCCCGGACTGCCTTTCCTTTCTTTAG			MSQILHETPDCLSFL*	MSQILHETPDCLSFL*			TTCCCCCTCA	AATTCACGTT	0	J	0	MG10357.1	0	0	0
8913	3975	af	AN6503.1	62.m03091	AO070222000019	0			-120	-76			ATGGGATTCTTGGATCCCCACCGTCCTTCTGTCAGCAGAAACTGA		ATGGGATTCTTGGATCCCCACCGTCCTTCTGTCAGCAGAAACTGA		MGFLDPHRPSVSRN*		MGFLDPHRPSVSRN*		GGAGACCTCT	GAGAGATAGA	0	R	0	0	0	0	0
8912	3975	an	AN6503.1	62.m03091	AO070222000019	0	-162	-133					ATGTACTCCAGGTCACAACAAGGTAGCTGA	ATGTACTCCAGGTCACAACAAGGTAGCTGA			MYSRSQQGS*	MYSRSQQGS*			CCAGCTTAAG	TATCAACGCA	0	R	0	0	0	0	0
8914	3975	ao	AN6503.1	62.m03091	AO070222000019	0					-117	-70	ATGAACGTGAGAGCTGACATGGAGACAGCGAGGACAAGAGACGAGTAG			ATGAACGTGAGAGCTGACATGGAGACAGCGAGGACAAGAGACGAGTAG	MNVRADMETARTRDE*			MNVRADMETARTRDE*	GTTGTCACAT	ATAGCAAAGA	0	R	0	0	0	0	0
8915	3975	ao	AN6503.1	62.m03091	AO070222000019	0					-99	-70	ATGGAGACAGCGAGGACAAGAGACGAGTAG			ATGGAGACAGCGAGGACAAGAGACGAGTAG	METARTRDE*			METARTRDE*	GAGAGCTGAC	ATAGCAAAGA	0	R	0	0	0	0	0
8920	3978	af	AN3168.1	59.m08557	AO070256000022	0			-101	-90			ATGCTTACATAA		ATGCTTACATAA		MLT*		MLT*		GTGGCCGTGA	TGCAGCGGGA	0	C	FG10907.1	MG07007.1	0	0	0
8921	3978	af	AN3168.1	59.m08557	AO070256000022	0			-90	-28			ATGCAGCGGGAGGTGTGGCAGAGAAACAGCTCCAGGTGTTGGTCTGCGGAGAGGCTCAGGTAA		ATGCAGCGGGAGGTGTGGCAGAGAAACAGCTCCAGGTGTTGGTCTGCGGAGAGGCTCAGGTAA		MQREVWQRNSSRCWSAERLR*		MQREVWQRNSSRCWSAERLR*		TGCTTACATA	CCTCGGGGTA	0	C	FG10907.1	MG07007.1	0	0	0
8917	3978	an	AN3168.1	59.m08557	AO070256000022	0	-93	-10					ATGGCTTACGTAAAACTGGCCGGCCAAAGAACAGCAGCACCTGGAGCTCTCCATGTCGATGCGGAGAGCCGTCTGATCTGCTAG	ATGGCTTACGTAAAACTGGCCGGCCAAAGAACAGCAGCACCTGGAGCTCTCCATGTCGATGCGGAGAGCCGTCTGATCTGCTAG			MAYVKLAGQRTAAPGALHVDAESRLIC*	MAYVKLAGQRTAAPGALHVDAESRLIC*			AGGCGGTGTA	AGTCACACAA	0	C	FG10907.1	MG07007.1	0	0	0
8922	3978	ao	AN3168.1	59.m08557	AO070256000022	0					-160	-95	ATGAAAAAAGCGAGAGCGATCCGAGTGGCTGAGTGGCTGGTGGGTGCGGCGGTGCGTCTTACGTAA			ATGAAAAAAGCGAGAGCGATCCGAGTGGCTGAGTGGCTGGTGGGTGCGGCGGTGCGTCTTACGTAA	MKKARAIRVAEWLVGAAVRLT*			MKKARAIRVAEWLVGAAVRLT*	AAGTAAAAAA	CGCGGGAAGC	0	C	FG10907.1	MG07007.1	0	0	0
8923	3979	af	AN4592.1	57.m05515	AO070267000008	0			-73	-38			ATGCTGGAGTCTATCCAGATCCGTACTCACTCCTGA		ATGCTGGAGTCTATCCAGATCCGTACTCACTCCTGA		MLESIQIRTHS*		MLESIQIRTHS*		AGACAAGGCG	GCTCGAGTCT	0	I	0	0	0	0	0
8924	3979	ao	AN4592.1	57.m05515	AO070267000008	0					-63	-28	ATGTTGACCCGAACCGCTTTACTCTACCGCGACTGA			ATGTTGACCCGAACCGCTTTACTCTACCGCGACTGA	MLTRTALLYRD*			MLTRTALLYRD*	AGGTCGTACG	GCTGGATACG	0	I	0	0	0	0	0
8926	3982	af	AN0585.1	69.m15264	AO070280000007	0			-284	-267			ATGATCGACACACCCTAG		ATGATCGACACACCCTAG		MIDTP*		MIDTP*		GCATAATTCA	TTTATGACTT	0	TZ	0	0	0	0	0
8927	3982	af	AN0585.1	69.m15264	AO070280000007	0			-263	-198			ATGACTTATCCAATCGCAGATATTGTACTGACTGATTATAAGCTCCTCCGGTCCATGGACTTGTAA		ATGACTTATCCAATCGCAGATATTGTACTGACTGATTATAAGCTCCTCCGGTCCATGGACTTGTAA		MTYPIADIVLTDYKLLRSMDL*		MTYPIADIVLTDYKLLRSMDL*		ACCCTAGTTT	GCGTGAGAAT	0	TZ	0	0	0	0	0
8928	3982	af	AN0585.1	69.m15264	AO070280000007	0			-209	-198			ATGGACTTGTAA		ATGGACTTGTAA		MDL*		MDL*		CCTCCGGTCC	GCGTGAGAAT	0	TZ	0	0	0	0	0
8929	3982	af	AN0585.1	69.m15264	AO070280000007	0			-182	-165			ATGACGACCGGTGATTGA		ATGACGACCGGTGATTGA		MTTGD*		MTTGD*		AGAATCTCAG	GAAGAAAGAA	0	TZ	0	0	0	0	0
8930	3982	af	AN0585.1	69.m15264	AO070280000007	0			-108	-52			ATGCCAGATATGCTGCCTATTTCAACATCAGATCTAGTTTGTTTTCTGTTCCTTTGA		ATGCCAGATATGCTGCCTATTTCAACATCAGATCTAGTTTGTTTTCTGTTCCTTTGA		MPDMLPISTSDLVCFLFL*		MPDMLPISTSDLVCFLFL*		CCTTCTCTCC	ACCCTTCCAG	0	TZ	0	0	0	0	0
8931	3982	af	AN0585.1	69.m15264	AO070280000007	0			-99	-52			ATGCTGCCTATTTCAACATCAGATCTAGTTTGTTTTCTGTTCCTTTGA		ATGCTGCCTATTTCAACATCAGATCTAGTTTGTTTTCTGTTCCTTTGA		MLPISTSDLVCFLFL*		MLPISTSDLVCFLFL*		CATGCCAGAT	ACCCTTCCAG	0	TZ	0	0	0	0	0
8925	3982	an	AN0585.1	69.m15264	AO070280000007	0	-75	-25					ATGCCCGCCAACCGAGGGTCTTTGAGTGCCGGATATGCTGCCCTTTTCTAA	ATGCCCGCCAACCGAGGGTCTTTGAGTGCCGGATATGCTGCCCTTTTCTAA			MPANRGSLSAGYAALF*	MPANRGSLSAGYAALF*			CTGGTCAACT	ACCAACTCAC	0	TZ	0	0	0	0	0
8932	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-232	-203	ATGACTCCTCCAATAATGATCCTGGGCTGA			ATGACTCCTCCAATAATGATCCTGGGCTGA	MTPPIMILG*			MTPPIMILG*	GTCCTAATTT	CTTGATTATA	0	TZ	0	0	0	0	0
8933	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-217	-203	ATGATCCTGGGCTGA			ATGATCCTGGGCTGA	MILG*			MILG*	TCCTCCAATA	CTTGATTATA	0	TZ	0	0	0	0	0
8934	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-168	-136	ATGCGTGGAGTTTCAATAATGACTGCCGATTGA			ATGCGTGGAGTTTCAATAATGACTGCCGATTGA	MRGVSIMTAD*			MRGVSIMTAD*	TCTGACTGCA	ACAGGAAACT	0	TZ	0	0	0	0	0
8935	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-150	-136	ATGACTGCCGATTGA			ATGACTGCCGATTGA	MTAD*			MTAD*	AGTTTCAATA	ACAGGAAACT	0	TZ	0	0	0	0	0
8936	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-85	-38	ATGCTGCCCATGTCAATATCGACTACAACCCTCTTCCCGTTCTTGTAA			ATGCTGCCCATGTCAATATCGACTACAACCCTCTTCCCGTTCTTGTAA	MLPMSISTTTLFPFL*			MLPMSISTTTLFPFL*	GTACCGGAAT	TTCGCGTCCC	0	TZ	0	0	0	0	0
8937	3982	ao	AN0585.1	69.m15264	AO070280000007	0					-76	-38	ATGTCAATATCGACTACAACCCTCTTCCCGTTCTTGTAA			ATGTCAATATCGACTACAACCCTCTTCCCGTTCTTGTAA	MSISTTTLFPFL*			MSISTTTLFPFL*	TATGCTGCCC	TTCGCGTCCC	0	TZ	0	0	0	0	0
8939	3983	af	AN5116.1	54.m06907	AO070291000063	0			-167	-111			ATGATTCTCATGGCGTTTTATCTTCGCGTTGCCTGCAATTCGCCTGCCACCATGTGA		ATGATTCTCATGGCGTTTTATCTTCGCGTTGCCTGCAATTCGCCTGCCACCATGTGA		MILMAFYLRVACNSPATM*		MILMAFYLRVACNSPATM*		ACAAGACTTT	CTGATAGGCG	0	O	0	MG08570.1	0	0	0
8940	3983	af	AN5116.1	54.m06907	AO070291000063	0			-158	-111			ATGGCGTTTTATCTTCGCGTTGCCTGCAATTCGCCTGCCACCATGTGA		ATGGCGTTTTATCTTCGCGTTGCCTGCAATTCGCCTGCCACCATGTGA		MAFYLRVACNSPATM*		MAFYLRVACNSPATM*		TATGATTCTC	CTGATAGGCG	0	O	0	MG08570.1	0	0	0
8941	3983	af	AN5116.1	54.m06907	AO070291000063	0			-95	-66			ATGACTTCAATTGGGATTCCTTCATTGTGA		ATGACTTCAATTGGGATTCCTTCATTGTGA		MTSIGIPSL*		MTSIGIPSL*		AGGCGTGTAC	ATAGTATATA	0	O	0	MG08570.1	0	0	0
8938	3983	an	AN5116.1	54.m06907	AO070291000063	0	-243	-157					ATGTGCTTCCACTGGCTCCCCGCACCTCACAACTGCCATATCATTCCATCTGTTTCCATTACTCTTTCCTGTATTCCTACAAACTGA	ATGTGCTTCCACTGGCTCCCCGCACCTCACAACTGCCATATCATTCCATCTGTTTCCATTACTCTTTCCTGTATTCCTACAAACTGA			MCFHWLPAPHNCHIIPSVSITLSCIPTN*	MCFHWLPAPHNCHIIPSVSITLSCIPTN*			GGAATTCGAG	CCGCGGTCCA	0	O	0	MG08570.1	0	0	0
8942	3983	ao	AN5116.1	54.m06907	AO070291000063	0					-110	-3	ATGAAGTCTTACCTGATGACTGGGCTCCCCCACGTCGAAAAAGTAGAGCAACTCATTTGCTCACCTAGAACCACTTTTTCTCGATTGAAGGGCACGCATTCCAAGTGA			ATGAAGTCTTACCTGATGACTGGGCTCCCCCACGTCGAAAAAGTAGAGCAACTCATTTGCTCACCTAGAACCACTTTTTCTCGATTGAAGGGCACGCATTCCAAGTGA	MKSYLMTGLPHVEKVEQLICSPRTTFSRLKGTHSK*			MKSYLMTGLPHVEKVEQLICSPRTTFSRLKGTHSK*	ACACTTGCAC	CTATGTCATT	0	O	0	MG08570.1	0	0	0
8943	3983	ao	AN5116.1	54.m06907	AO070291000063	0					-95	-3	ATGACTGGGCTCCCCCACGTCGAAAAAGTAGAGCAACTCATTTGCTCACCTAGAACCACTTTTTCTCGATTGAAGGGCACGCATTCCAAGTGA			ATGACTGGGCTCCCCCACGTCGAAAAAGTAGAGCAACTCATTTGCTCACCTAGAACCACTTTTTCTCGATTGAAGGGCACGCATTCCAAGTGA	MTGLPHVEKVEQLICSPRTTFSRLKGTHSK*			MTGLPHVEKVEQLICSPRTTFSRLKGTHSK*	GTCTTACCTG	CTATGTCATT	0	O	0	MG08570.1	0	0	0
8944	3985	ao	AN2055.1	58.m07643	AO070292000025	0					-98	-78	ATGTTATCGATTACCTTTTAA			ATGTTATCGATTACCTTTTAA	MLSITF*			MLSITF*	CTTTTTCCCC	TTTTTCTTGT	0		0	MG05176.1	0	0	0
8946	3988	af	AN9163.1	55.m03303	AO070296000059	0			-264	-235			ATGCTTGAGACCATTACCTCCTGCTGGTAG		ATGCTTGAGACCATTACCTCCTGCTGGTAG		MLETITSCW*		MLETITSCW*		TCTATAATCC	ATCATTGGTC	0		0	0	0	0	0
8947	3988	af	AN9163.1	55.m03303	AO070296000059	0			-214	-161			ATGATTATTTCAAGACTATTAACCACTAAAGACTGGGGCACAATGTTAAAATGA		ATGATTATTTCAAGACTATTAACCACTAAAGACTGGGGCACAATGTTAAAATGA		MIISRLLTTKDWGTMLK*		MIISRLLTTKDWGTMLK*		AAACTATATA	TGATGCTATA	0		0	0	0	0	0
8948	3988	af	AN9163.1	55.m03303	AO070296000059	0			-172	-161			ATGTTAAAATGA		ATGTTAAAATGA		MLK*		MLK*		CTGGGGCACA	TGATGCTATA	0		0	0	0	0	0
8949	3988	af	AN9163.1	55.m03303	AO070296000059	0			-164	-150			ATGATGATGCTATAA		ATGATGATGCTATAA		MMML*		MMML*		CAATGTTAAA	TTCGCATTCT	0		0	0	0	0	0
8950	3988	af	AN9163.1	55.m03303	AO070296000059	0			-161	-150			ATGATGCTATAA		ATGATGCTATAA		MML*		MML*		TGTTAAAATG	TTCGCATTCT	0		0	0	0	0	0
8945	3988	an	AN9163.1	55.m03303	AO070296000059	0	-132	-52					ATGACGTCACCATCTCTCAGCTTCCAAGTTTCAATTGATGTCTATTATGTTAAATCACCCCCTGCTCACAAACTATCCTAA	ATGACGTCACCATCTCTCAGCTTCCAAGTTTCAATTGATGTCTATTATGTTAAATCACCCCCTGCTCACAAACTATCCTAA			MTSPSLSFQVSIDVYYVKSPPAHKLS*	MTSPSLSFQVSIDVYYVKSPPAHKLS*			TAATTATGCC	AGTTTCTCAA	0		0	0	0	0	0
8951	3989	af	AN1630.1	58.m07716	AO070299000035	0			-244	-113			ATGAGGGGATATCTCTTATGCAATGGCAAGAGCTGCTGCACTTTATTAGTAGCCAGTTATCCCTGCCCTCTTCCTCATTCCTTCTTATCCTTCCCTCTCCCTTTGTCAGATTCTCACTCTGTTTCTTCGTAA		ATGAGGGGATATCTCTTATGCAATGGCAAGAGCTGCTGCACTTTATTAGTAGCCAGTTATCCCTGCCCTCTTCCTCATTCCTTCTTATCCTTCCCTCTCCCTTTGTCAGATTCTCACTCTGTTTCTTCGTAA		MRGYLLCNGKSCCTLLVASYPCPLPHSFLSFPLPLSDSHSVSS*		MRGYLLCNGKSCCTLLVASYPCPLPHSFLSFPLPLSDSHSVSS*		CAGCAGAAGG	ATCGACTTTT	0	P	0	0	0	0	0
8952	3989	af	AN1630.1	58.m07716	AO070299000035	0			-222	-196			ATGGCAAGAGCTGCTGCACTTTATTAG		ATGGCAAGAGCTGCTGCACTTTATTAG		MARAAALY*		MARAAALY*		CTCTTATGCA	TAGCCAGTTA	0	P	0	0	0	0	0
8956	3991	af	AN6239.1	52.m04100	AO070302000122	0			-182	-3			ATGAGGCACCGAGACAAGCTTGAACCTGCAGTGCCGATCTCGGCCATTTATCAGATTGGACGAGGGGCATGGCACCAATGCATTTCTGGATGCGATTTCTGCTATTCCCTGCAGATTTTCTTTTTCCGTCCCAGCTTCAACCACAATCAAAACGACCAATTGCTGCTCTATACACATTGA		ATGAGGCACCGAGACAAGCTTGAACCTGCAGTGCCGATCTCGGCCATTTATCAGATTGGACGAGGGGCATGGCACCAATGCATTTCTGGATGCGATTTCTGCTATTCCCTGCAGATTTTCTTTTTCCGTCCCAGCTTCAACCACAATCAAAACGACCAATTGCTGCTCTATACACATTGA		MRHRDKLEPAVPISAIYQIGRGAWHQCISGCDFCYSLQIFFFRPSFNHNQNDQLLLYTH*		MRHRDKLEPAVPISAIYQIGRGAWHQCISGCDFCYSLQIFFFRPSFNHNQNDQLLLYTH*		GCAGCAGCAC	ATATGTACTC	0	R	0	0	0	0	0
8953	3991	an	AN6239.1	52.m04100	AO070302000122	0	-212	-189					ATGCGAATTCCCACTCTTGACTAA	ATGCGAATTCCCACTCTTGACTAA			MRIPTLD*	MRIPTLD*			ATTCAAAGAG	AAAGCTGAAA	0	R	0	0	0	0	0
8954	3991	an	AN6239.1	52.m04100	AO070302000122	0	-113	-84					ATGATGAAATTGCAAGCAGTGCTGTGCTGA	ATGATGAAATTGCAAGCAGTGCTGTGCTGA			MMKLQAVLC*	MMKLQAVLC*			ACCTAGCCAC	TAACACCAAA	0	R	0	0	0	0	0
8955	3991	an	AN6239.1	52.m04100	AO070302000122	0	-110	-84					ATGAAATTGCAAGCAGTGCTGTGCTGA	ATGAAATTGCAAGCAGTGCTGTGCTGA			MKLQAVLC*	MKLQAVLC*			TAGCCACATG	TAACACCAAA	0	R	0	0	0	0	0

8957	3991	ao	AN6239.1	52.m04100	AO070302000122	0					-229	-68	ATGGAGATATCCACAGCATCCCAACGCCGACGAAAAGCGCAACCAAAGGCACATGAATCCGATCTCGGATATTCCACACTCCTGCAGAAAATGAACCGTTGCAACGAACTTCTTGACTCAATCCTAGTTCACGAAAGTCACACACGAACTACTACTTACTAG			ATGGAGATATCCACAGCATCCCAACGCCGACGAAAAGCGCAACCAAAGGCACATGAATCCGATCTCGGATATTCCACACTCCTGCAGAAAATGAACCGTTGCAACGAACTTCTTGACTCAATCCTAGTTCACGAAAGTCACACACGAACTACTACTTACTAG	MEISTASQRRRKAQPKAHESDLGYSTLLQKMNRCNELLDSILVHESHTRTTTY*			MEISTASQRRRKAQPKAHESDLGYSTLLQKMNRCNELLDSILVHESHTRTTTY*	CCACCTTCTC	TTTTGACAAG	0	R	0	0	0	0	0
8958	3991	ao	AN6239.1	52.m04100	AO070302000122	0					-177	-136	ATGAATCCGATCTCGGATATTCCACACTCCTGCAGAAAATGA			ATGAATCCGATCTCGGATATTCCACACTCCTGCAGAAAATGA	MNPISDIPHSCRK*			MNPISDIPHSCRK*	CCAAAGGCAC	ACCGTTGCAA	0	R	0	0	0	0	0
8959	3991	ao	AN6239.1	52.m04100	AO070302000122	0					-139	-68	ATGAACCGTTGCAACGAACTTCTTGACTCAATCCTAGTTCACGAAAGTCACACACGAACTACTACTTACTAG			ATGAACCGTTGCAACGAACTTCTTGACTCAATCCTAGTTCACGAAAGTCACACACGAACTACTACTTACTAG	MNRCNELLDSILVHESHTRTTTY*			MNRCNELLDSILVHESHTRTTTY*	CCTGCAGAAA	TTTTGACAAG	0	R	0	0	0	0	0
8963	3995	ao	AN1461.1	55.m03257	AO070306000077	0					-255	-193	ATGTTGCTCTGCTTCCAACTGCAGCGAGGGCTTTCCCTCCAGAATTCATATCCTCCCATATAG			ATGTTGCTCTGCTTCCAACTGCAGCGAGGGCTTTCCCTCCAGAATTCATATCCTCCCATATAG	MLLCFQLQRGLSLQNSYPPI*			MLLCFQLQRGLSLQNSYPPI*	CACAGCTGTC	TACCATGATG	0	R	0	0	0	0	0
8967	3997	af	AN3749.1	65.m07385	AO070309000073	0			-213	-187			ATGATTTACGCAATCCAGAAGTCTTGA		ATGATTTACGCAATCCAGAAGTCTTGA		MIYAIQKS*		MIYAIQKS*		ATTACCTGGG	ATCAGGCTGG	0	L	FG07112.1	MG09306.1	0	0	0
8968	3997	af	AN3749.1	65.m07385	AO070309000073	0			-169	-2			ATGAATACCGAGATTTTCAGTAAGGTGCACACTGGTACCTCTCGCTCAAAAGAAATCGGAAGAGTCATCGCCACTTCTACACTTGCGATGCCAAACCCCACGCCTCTCCTGATCCCGCTTCGTGTTGAACAGTTGACTCAGGAGTCCACAGCGACTCCCGCGAGGTAA		ATGAATACCGAGATTTTCAGTAAGGTGCACACTGGTACCTCTCGCTCAAAAGAAATCGGAAGAGTCATCGCCACTTCTACACTTGCGATGCCAAACCCCACGCCTCTCCTGATCCCGCTTCGTGTTGAACAGTTGACTCAGGAGTCCACAGCGACTCCCGCGAGGTAA		MNTEIFSKVHTGTSRSKEIGRVIATSTLAMPNPTPLLIPLRVEQLTQESTATPAR*		MNTEIFSKVHTGTSRSKEIGRVIATSTLAMPNPTPLLIPLRVEQLTQESTATPAR*		TGGTTAATAA	AATGACACTA	0	L	FG07112.1	MG09306.1	0	0	0
8969	3997	af	AN3749.1	65.m07385	AO070309000073	0			-82	-2			ATGCCAAACCCCACGCCTCTCCTGATCCCGCTTCGTGTTGAACAGTTGACTCAGGAGTCCACAGCGACTCCCGCGAGGTAA		ATGCCAAACCCCACGCCTCTCCTGATCCCGCTTCGTGTTGAACAGTTGACTCAGGAGTCCACAGCGACTCCCGCGAGGTAA		MPNPTPLLIPLRVEQLTQESTATPAR*		MPNPTPLLIPLRVEQLTQESTATPAR*		TACACTTGCG	AATGACACTA	0	L	FG07112.1	MG09306.1	0	0	0
8966	3997	an	AN3749.1	65.m07385	AO070309000073	0	-128	-96					ATGACGGCAATATTGCGGCCCCTGGAGCGTTAA	ATGACGGCAATATTGCGGCCCCTGGAGCGTTAA			MTAILRPLER*	MTAILRPLER*			CCGCAGTATA	AAGGCTTGCA	0	L	FG07112.1	MG09306.1	0	0	0
8970	3997	ao	AN3749.1	65.m07385	AO070309000073	0					-248	-216	ATGCGGGGCTGTCAACCGCTAATGGCCGCATGA			ATGCGGGGCTGTCAACCGCTAATGGCCGCATGA	MRGCQPLMAA*			MRGCQPLMAA*	CGTTAATACT	TATCCTGGTA	0	L	FG07112.1	MG09306.1	0	0	0
8971	3997	ao	AN3749.1	65.m07385	AO070309000073	0					-227	-216	ATGGCCGCATGA			ATGGCCGCATGA	MAA*			MAA*	TCAACCGCTA	TATCCTGGTA	0	L	FG07112.1	MG09306.1	0	0	0
8972	3997	ao	AN3749.1	65.m07385	AO070309000073	0					-219	-187	ATGATATCCTGGTATCCAATACTTGTTTACTAA			ATGATATCCTGGTATCCAATACTTGTTTACTAA	MISWYPILVY*			MISWYPILVY*	TAATGGCCGC	ACCTATTTCG	0	L	FG07112.1	MG09306.1	0	0	0
8973	3997	ao	AN3749.1	65.m07385	AO070309000073	0					-175	-56	ATGCTTTTTACGAAAACCTATTGCCGAGAGCTTCCTTTGCCACCTCTTCCTTGGCCGCTGATCCATTACTACGTTTCGCCCATCTCGTTGTATCTTATTTCTTCTTGGAGTATCACGTAA			ATGCTTTTTACGAAAACCTATTGCCGAGAGCTTCCTTTGCCACCTCTTCCTTGGCCGCTGATCCATTACTACGTTTCGCCCATCTCGTTGTATCTTATTTCTTCTTGGAGTATCACGTAA	MLFTKTYCRELPLPPLPWPLIHYYVSPISLYLISSWSIT*			MLFTKTYCRELPLPPLPWPLIHYYVSPISLYLISSWSIT*	CCTATTTCGA	TAGAGCGCCT	0	L	FG07112.1	MG09306.1	0	0	0
8975	3998	af	AN8214.1	53.m03759	AO070310000098	0			-193	-110			ATGCGTGTGGTACAAAAAGCGGTGGGAAAACAAAGCAAACTGTGGTGTCTACAGAGTAAGTCTAGTGGATTTATCAATTGCTAG		ATGCGTGTGGTACAAAAAGCGGTGGGAAAACAAAGCAAACTGTGGTGTCTACAGAGTAAGTCTAGTGGATTTATCAATTGCTAG		MRVVQKAVGKQSKLWCLQSKSSGFINC*		MRVVQKAVGKQSKLWCLQSKSSGFINC*		AATTGGGCTG	CATTTACTAG	0	A	0	MG07477.1	0	0	0
8976	3998	ao	AN8214.1	53.m03759	AO070310000098	0					-271	-176	ATGAAAGTAACCTTTGGAGTTGGAGAAGATTTAAAGTATCCCTTCAAAAAAATAAAATACAATCTTCCTGTCCGATCATATGCAACGAGACGGTAA			ATGAAAGTAACCTTTGGAGTTGGAGAAGATTTAAAGTATCCCTTCAAAAAAATAAAATACAATCTTCCTGTCCGATCATATGCAACGAGACGGTAA	MKVTFGVGEDLKYPFKKIKYNLPVRSYATRR*			MKVTFGVGEDLKYPFKKIKYNLPVRSYATRR*	ATAGTTGAAT	GAGGAAGAAC	0	A	0	MG07477.1	0	0	0
8977	3998	ao	AN8214.1	53.m03759	AO070310000098	0					-192	-163	ATGCAACGAGACGGTAAGAGGAAGAACTGA			ATGCAACGAGACGGTAAGAGGAAGAACTGA	MQRDGKRKN*			MQRDGKRKN*	GTCCGATCAT	CAATGCGGAG	0	A	0	MG07477.1	0	0	0
8981	4003	af	AN0910.1	70.m15519	AO070320000091	0			-127	-32			ATGCATACAACTTGGCTGACAACAAATCGATCTCATCTCATCTCAGTCTGCTTGTACAGGACACCACATACATCATCCCCATATCTTCTCCCGTAA		ATGCATACAACTTGGCTGACAACAAATCGATCTCATCTCATCTCAGTCTGCTTGTACAGGACACCACATACATCATCCCCATATCTTCTCCCGTAA		MHTTWLTTNRSHLISVCLYRTPHTSSPYLLP*		MHTTWLTTNRSHLISVCLYRTPHTSSPYLLP*		GAAATAGTTG	GGGATGATGT	0	I	0	0	0	0	0
8978	4003	an	AN0910.1	70.m15519	AO070320000091	0	-95	-78					ATGAGTCTATCCTACTGA	ATGAGTCTATCCTACTGA			MSLSY*	MSLSY*			ACCTGTTCAC	AAATCCCGCG	0	I	0	0	0	0	0
8984	4003	ao	AN0910.1	70.m15519	AO070320000091	0					-135	-115	ATGCAAAAGCACGAGATTTGA			ATGCAAAAGCACGAGATTTGA	MQKHEI*			MQKHEI*	CTGCAGCATG	GGGGGAAAGA	0	I	0	0	0	0	0
8989	4004	af	AN3537.1	57.m05323	AO070321000015	0			-238	-191			ATGAAATGGGTTGGGTGGGACCGCGTTACATTTGAAGCCCTAAGTTGA		ATGAAATGGGTTGGGTGGGACCGCGTTACATTTGAAGCCCTAAGTTGA		MKWVGWDRVTFEALS*		MKWVGWDRVTFEALS*		GGAAACCTGG	TGGTGTCATG	0	Q	0	0	0	0	0
8990	4004	af	AN3537.1	57.m05323	AO070321000015	0			-233	-204			ATGGGTTGGGTGGGACCGCGTTACATTTGA		ATGGGTTGGGTGGGACCGCGTTACATTTGA		MGWVGPRYI*		MGWVGPRYI*		CCTGGATGAA	AGCCCTAAGT	0	Q	0	0	0	0	0
8991	4004	af	AN3537.1	57.m05323	AO070321000015	0			-191	-132			ATGGTGTCATGTTCCGGGTGCAGAAGTATTCCTATACTTTTCCTCCCACTACAAAGCTAG		ATGGTGTCATGTTCCGGGTGCAGAAGTATTCCTATACTTTTCCTCCCACTACAAAGCTAG		MVSCSGCRSIPILFLPLQS*		MVSCSGCRSIPILFLPLQS*		CCCTAAGTTG	GTGCTGTTGA	0	Q	0	0	0	0	0
8985	4004	an	AN3537.1	57.m05323	AO070321000015	0	-262	-245					ATGGGTTGTGAAACCTGA	ATGGGTTGTGAAACCTGA			MGCET*	MGCET*			CGATAGTGAA	GTCGTCGGTA	0	Q	0	0	0	0	0
8986	4004	an	AN3537.1	57.m05323	AO070321000015	0	-189	-67					ATGTGTCATGACCCCGATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAGAGGGTCGAGTGCCATCGTCTGAGAACTGTGTTCTCCAAATGTCATAA	ATGTGTCATGACCCCGATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAGAGGGTCGAGTGCCATCGTCTGAGAACTGTGTTCTCCAAATGTCATAA			MCHDPDAEVVRKRFPAHRERYQSLLEGRVPSSENCVLQMS*	MCHDPDAEVVRKRFPAHRERYQSLLEGRVPSSENCVLQMS*			GCCTGAGTGG	TTTTCTGCTG	0	Q	0	0	0	0	0
8987	4004	an	AN3537.1	57.m05323	AO070321000015	0	-182	-114					ATGACCCCGATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAG	ATGACCCCGATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAG			MTPMQKLFGNDSQRIESAINHY*	MTPMQKLFGNDSQRIESAINHY*			TGGATGTGTC	AGGGTCGAGT	0	Q	0	0	0	0	0
8988	4004	an	AN3537.1	57.m05323	AO070321000015	0	-173	-114					ATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAG	ATGCAGAAGTTGTTCGGAAACGATTCCCAGCGCATAGAGAGCGCTATCAATCATTATTAG			MQKLFGNDSQRIESAINHY*	MQKLFGNDSQRIESAINHY*			CATGACCCCG	AGGGTCGAGT	0	Q	0	0	0	0	0
8992	4004	ao	AN3537.1	57.m05323	AO070321000015	0					-264	-235	ATGACTCCAAATTCAATTAGTGGGGCGTAA			ATGACTCCAAATTCAATTAGTGGGGCGTAA	MTPNSISGA*			MTPNSISGA*	AGCAATCTCC	TTTATCTACA	0	Q	0	0	0	0	0
8993	4004	ao	AN3537.1	57.m05323	AO070321000015	0					-199	-182	ATGCCCCACGTTCAATAA			ATGCCCCACGTTCAATAA	MPHVQ*			MPHVQ*	TACCCAGAAA	CGAAATACCT	0	Q	0	0	0	0	0
8994	4004	ao	AN3537.1	57.m05323	AO070321000015	0					-165	-151	ATGGAACTCCACTAG			ATGGAACTCCACTAG	MELH*			MELH*	ACCTATACAC	TTTCTTCCGC	0	Q	0	0	0	0	0
8995	4004	ao	AN3537.1	57.m05323	AO070321000015	0					-71	-42	ATGGTTGAATTGCCTGTCTGCTCCCGATAA			ATGGTTGAATTGCCTGTCTGCTCCCGATAA	MVELPVCSR*			MVELPVCSR*	CCATAGTTCC	CGTCTACATC	0	Q	0	0	0	0	0
8996	4005	af	AN0204.1	71.m15469	AO070321000040	0			-201	-190			ATGTACAAGTAG		ATGTACAAGTAG		MYK*		MYK*		TATATAATTT	ACGGCAACAT	0	A	0	0	NCU06520.1	0	0
8997	4006	ao	AN1778.1	69.m15077	AO070324000018	0					-252	-235	ATGATACGCCATACATAG			ATGATACGCCATACATAG	MIRHT*			MIRHT*	TAGTACATAC	AGTGGAGGCA	0	H	FG09312.1	MG00599.1	0	0	0
9001	4008	an	AN7723.1	71.m15750	AO070325000138	0	-209	-192					ATGGAAGTCGCGTTCTAG	ATGGAAGTCGCGTTCTAG			MEVAF*	MEVAF*			CTAACTAGAA	GCGCGCGCAA	0	L	FG06122.1	0	NCU01370.1	0	0
9003	4008	ao	AN7723.1	71.m15750	AO070325000138	0					-186	-142	ATGAACCGCGTTGGAGGCGCGCCGAGAAAAAGCCACGAGGGATAA			ATGAACCGCGTTGGAGGCGCGCCGAGAAAAAGCCACGAGGGATAA	MNRVGGAPRKSHEG*			MNRVGGAPRKSHEG*	TCCTCAATCA	AGGACTAGAG	0	L	FG06122.1	0	NCU01370.1	0	0
9005	4009	af	AN3427.1	59.m09282	AO070327000003	0			-140	-63			ATGCGCTTGGGTTACCTTGGCCAGTCAAAACAAGCTCCTATTCTGAATTGCTATTTTACGGCCTCATTAATCTATTAA		ATGCGCTTGGGTTACCTTGGCCAGTCAAAACAAGCTCCTATTCTGAATTGCTATTTTACGGCCTCATTAATCTATTAA		MRLGYLGQSKQAPILNCYFTASLIY*		MRLGYLGQSKQAPILNCYFTASLIY*		CAATAGTTGA	TGAAGTGGGC	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9006	4009	af	AN3427.1	59.m09282	AO070327000003	0			-63	-43			ATGAAGTGGGCCATTTTCTAA		ATGAAGTGGGCCATTTTCTAA		MKWAIF*		MKWAIF*		TAATCTATTA	CGACGATTTT	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9007	4009	ao	AN3427.1	59.m09282	AO070327000003	0					-245	-225	ATGGGACCAAATGCCAAATGA			ATGGGACCAAATGCCAAATGA	MGPNAK*			MGPNAK*	AGAGGCCCTT	TTGAAGGGTG	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9008	4009	ao	AN3427.1	59.m09282	AO070327000003	0					-235	-221	ATGCCAAATGATTGA			ATGCCAAATGATTGA	MPND*			MPND*	ATGGGACCAA	AGGGTGATCC	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9009	4009	ao	AN3427.1	59.m09282	AO070327000003	0					-228	-214	ATGATTGAAGGGTGA			ATGATTGAAGGGTGA	MIEG*			MIEG*	CAAATGCCAA	TCCGGGCGGA	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9010	4009	ao	AN3427.1	59.m09282	AO070327000003	0					-203	-150	ATGTTTCTGCCCGTCAAAAGAGGGAAAGGAAAAAGAAAAAAAAATAGAAATTTAG			ATGTTTCTGCCCGTCAAAAGAGGGAAAGGAAAAAGAAAAAAAAATAGAAATTTAG	MFLPVKRGKGKRKKIEI*			MFLPVKRGKGKRKKIEI*	TCCGGGCGGA	TTTCCCTCGA	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9011	4009	ao	AN3427.1	59.m09282	AO070327000003	0					-137	-78	ATGAGCGGTACTAGTAGATCGTGCCACAATCTGACCGAGTGCTTGTTACATTACTACTGA			ATGAGCGGTACTAGTAGATCGTGCCACAATCTGACCGAGTGCTTGTTACATTACTACTGA	MSGTSRSCHNLTECLLHYY*			MSGTSRSCHNLTECLLHYY*	TCCCTCGACA	TCATCGTCCT	0	K	FG10156.1	0	NCU04273.1	YNL175C	YNL175C
9017	4010	af	AN9038.1	59.m08392	AO070330000171	0			-246	-181			ATGAAATGCGTCAAAACAGGCCTCGTGGAGTCCCATCCCTGTTTATGGGCTGTTTATGGTGTCTAA		ATGAAATGCGTCAAAACAGGCCTCGTGGAGTCCCATCCCTGTTTATGGGCTGTTTATGGTGTCTAA		MKCVKTGLVESHPCLWAVYGV*		MKCVKTGLVESHPCLWAVYGV*		CTCCGCGGCA	CCAAACAGGA	0	H	FG05299.1	0	0	0	0
9018	4010	af	AN9038.1	59.m08392	AO070330000171	0			-241	-86			ATGCGTCAAAACAGGCCTCGTGGAGTCCCATCCCTGTTTATGGGCTGTTTATGGTGTCTAACCAAACAGGATAGTACTATTGTATGTGCACTAACGATTGTCATTGAGGTTTATCGGAGGTTTGGTAGACTCGTGAGTAAGAAATCTCCCCCATGA		ATGCGTCAAAACAGGCCTCGTGGAGTCCCATCCCTGTTTATGGGCTGTTTATGGTGTCTAACCAAACAGGATAGTACTATTGTATGTGCACTAACGATTGTCATTGAGGTTTATCGGAGGTTTGGTAGACTCGTGAGTAAGAAATCTCCCCCATGA		MRQNRPRGVPSLFMGCLWCLTKQDSTIVCALTIVIEVYRRFGRLVSKKSPP*		MRQNRPRGVPSLFMGCLWCLTKQDSTIVCALTIVIEVYRRFGRLVSKKSPP*		CGGCAATGAA	TCTTACAAAC	0	H	FG05299.1	0	0	0	0
9019	4010	af	AN9038.1	59.m08392	AO070330000171	0			-202	-86			ATGGGCTGTTTATGGTGTCTAACCAAACAGGATAGTACTATTGTATGTGCACTAACGATTGTCATTGAGGTTTATCGGAGGTTTGGTAGACTCGTGAGTAAGAAATCTCCCCCATGA		ATGGGCTGTTTATGGTGTCTAACCAAACAGGATAGTACTATTGTATGTGCACTAACGATTGTCATTGAGGTTTATCGGAGGTTTGGTAGACTCGTGAGTAAGAAATCTCCCCCATGA		MGCLWCLTKQDSTIVCALTIVIEVYRRFGRLVSKKSPP*		MGCLWCLTKQDSTIVCALTIVIEVYRRFGRLVSKKSPP*		ATCCCTGTTT	TCTTACAAAC	0	H	FG05299.1	0	0	0	0
9020	4010	af	AN9038.1	59.m08392	AO070330000171	0			-191	-168			ATGGTGTCTAACCAAACAGGATAG		ATGGTGTCTAACCAAACAGGATAG		MVSNQTG*		MVSNQTG*		TGGGCTGTTT	TACTATTGTA	0	H	FG05299.1	0	0	0	0
9021	4010	af	AN9038.1	59.m08392	AO070330000171	0			-158	-135			ATGTGCACTAACGATTGTCATTGA		ATGTGCACTAACGATTGTCATTGA		MCTNDCH*		MCTNDCH*		GTACTATTGT	GGTTTATCGG	0	H	FG05299.1	0	0	0	0
9012	4010	an	AN9038.1	59.m08392	AO070330000171	0	-148	-77					ATGAATGGAGGTGTTCGTATTGGCTCTAATGACCTCATTATGATGCGCGCGGGGATTCCCAGATATTTTTGA	ATGAATGGAGGTGTTCGTATTGGCTCTAATGACCTCATTATGATGCGCGCGGGGATTCCCAGATATTTTTGA			MNGGVRIGSNDLIMMRAGIPRYF*	MNGGVRIGSNDLIMMRAGIPRYF*			GTTACAAATC	AGCTGCCAAG	0	H	FG05299.1	0	0	0	0
9013	4010	an	AN9038.1	59.m08392	AO070330000171	0	-144	-106					ATGGAGGTGTTCGTATTGGCTCTAATGACCTCATTATGA	ATGGAGGTGTTCGTATTGGCTCTAATGACCTCATTATGA			MEVFVLALMTSL*	MEVFVLALMTSL*			CAAATCATGA	TGCGCGCGGG	0	H	FG05299.1	0	0	0	0
9014	4010	an	AN9038.1	59.m08392	AO070330000171	0	-120	-106					ATGACCTCATTATGA	ATGACCTCATTATGA			MTSL*	MTSL*			ATTGGCTCTA	TGCGCGCGGG	0	H	FG05299.1	0	0	0	0
9015	4010	an	AN9038.1	59.m08392	AO070330000171	0	-109	-77					ATGATGCGCGCGGGGATTCCCAGATATTTTTGA	ATGATGCGCGCGGGGATTCCCAGATATTTTTGA			MMRAGIPRYF*	MMRAGIPRYF*			TGACCTCATT	AGCTGCCAAG	0	H	FG05299.1	0	0	0	0
9016	4010	an	AN9038.1	59.m08392	AO070330000171	0	-106	-77					ATGCGCGCGGGGATTCCCAGATATTTTTGA	ATGCGCGCGGGGATTCCCAGATATTTTTGA			MRAGIPRYF*	MRAGIPRYF*			CCTCATTATG	AGCTGCCAAG	0	H	FG05299.1	0	0	0	0
9024	4010	ao	AN9038.1	59.m08392	AO070330000171	0					-208	-191	ATGGGTTATAGTCGCTAG			ATGGGTTATAGTCGCTAG	MGYSR*			MGYSR*	GAAGAGGTAT	TTGACGCGCG	0	H	FG05299.1	0	0	0	0
9025	4010	ao	AN9038.1	59.m08392	AO070330000171	0					-140	-111	ATGGCGCAAAGGAAAAGGTACCAAAGATGA			ATGGCGCAAAGGAAAAGGTACCAAAGATGA	MAQRKRYQR*			MAQRKRYQR*	AATCAAGTAT	CGCCAATATT	0	H	FG05299.1	0	0	0	0
9026	4010	ao	AN9038.1	59.m08392	AO070330000171	0					-114	-97	ATGACGCCAATATTATGA			ATGACGCCAATATTATGA	MTPIL*			MTPIL*	GGTACCAAAG	AATTAGGTTT	0	H	FG05299.1	0	0	0	0

9027	4010	ao	AN9038.1	59.m08392	AO070330000171	0					-100	-38	ATGAAATTAGGGTTACGACGACCACAATCCTTTATTCATATTTCTACGCCAACAACAGACTGA			ATGAAATTAGGGTTACGACGACCACAATCCTTTATTCATATTTCTACGCCAACAACAGACTGA	MKLGLRRPQSFIHISTPTTD*			MKLGLRRPQSFIHISTPTTD*	CGCCAATATT	ACATAATAAA	0	H	FG05299.1	0	0	0	0
9029	4011	af	AN2879.1	53.m04051	AO070330000208	0			-111	-61			ATGCTGAACCCCGCCTTGACTCGCATGTGTAAAGGCCTGTACTTACTATGA		ATGCTGAACCCCGCCTTGACTCGCATGTGTAAAGGCCTGTACTTACTATGA		MLNPALTRMCKGLYLL*		MLNPALTRMCKGLYLL*		AGTGCTATCA	CCGCCGCAAC	0	JIT	0	0	0	0	0
9030	4011	af	AN2879.1	53.m04051	AO070330000208	0			-87	-61			ATGTGTAAAGGCCTGTACTTACTATGA		ATGTGTAAAGGCCTGTACTTACTATGA		MCKGLYLL*		MCKGLYLL*		CTTGACTCGC	CCGCCGCAAC	0	JIT	0	0	0	0	0
9031	4011	af	AN2879.1	53.m04051	AO070330000208	0			-64	-44			ATGACCGCCGCAACTATTTAA		ATGACCGCCGCAACTATTTAA		MTAATI*		MTAATI*		TGTACTTACT	GGCAGTCGAG	0	JIT	0	0	0	0	0
9028	4011	an	AN2879.1	53.m04051	AO070330000208	0	-263	-117					ATGGCGAGCCGGCGGTTTGGCCGGCGTATACGTTGGCCTTCCCCACGCTACCTCCTTAGCTTCGATAAGCACAGGTGGACACAGGCTCACTTGGAGTTGCTTCCCATCTTCCAACGTACAAATAACTTGAAAAGCACAATAGATTAA	ATGGCGAGCCGGCGGTTTGGCCGGCGTATACGTTGGCCTTCCCCACGCTACCTCCTTAGCTTCGATAAGCACAGGTGGACACAGGCTCACTTGGAGTTGCTTCCCATCTTCCAACGTACAAATAACTTGAAAAGCACAATAGATTAA			MASRRFGRRIRWPSPRYLLSFDKHRWTQAHLELLPIFQRTNNLKSTID*	MASRRFGRRIRWPSPRYLLSFDKHRWTQAHLELLPIFQRTNNLKSTID*			TTCAGGAACG	TAATAGACAC	0	JIT	0	0	0	0	0
9033	4011	ao	AN2879.1	53.m04051	AO070330000208	0					-146	-78	ATGCGGAAGGTAGACGCGCTTCGGCCGGTAAAGGATTGTTGGAGGTTCTCCTCACGCGGAGCAACTTAG			ATGCGGAAGGTAGACGCGCTTCGGCCGGTAAAGGATTGTTGGAGGTTCTCCTCACGCGGAGCAACTTAG	MRKVDALRPVKDCWRFSSRGAT*			MRKVDALRPVKDCWRFSSRGAT*	AACCATCCCA	CACTGAGGCC	0	JIT	0	0	0	0	0
9034	4012	af	AN1191.1	70.m15030	AO070331000192	0			-114	-13			ATGCGACTTCCCCACTTCGGGACGAACACTGACAAGTCATATCAATCTCAGGAACCCCAGCAACTCAACAGCAGTCTCTTCATTCTCTTGTCTAAAGTCTGA		ATGCGACTTCCCCACTTCGGGACGAACACTGACAAGTCATATCAATCTCAGGAACCCCAGCAACTCAACAGCAGTCTCTTCATTCTCTTGTCTAAAGTCTGA		MRLPHFGTNTDKSYQSQEPQQLNSSLFILLSKV*		MRLPHFGTNTDKSYQSQEPQQLNSSLFILLSKV*		TTCACCTTGT	TTACCCGTCA	0	O	0	MG05737.1	0	YDR510W	0
9037	4016	af	AN4921.1	59.m08824	AO070338000022	0			-94	-20			ATGGCACTTCCCTTGCATTGCTTATCTTGTCACAAGCAGCATCGCCTCACCAACATTCATCTACTTATACACTAA		ATGGCACTTCCCTTGCATTGCTTATCTTGTCACAAGCAGCATCGCCTCACCAACATTCATCTACTTATACACTAA		MALPLHCLSCHKQHRLTNIHLLIH*		MALPLHCLSCHKQHRLTNIHLLIH*		AGCCAGCACC	CACAAACCAA	0		0	0	0	0	0
9036	4016	an	AN4921.1	59.m08824	AO070338000022	0	-231	-154					ATGATCGAGTACCTTGGGGACTCAAGTACCCTGAGGAACATCCACAGGGTGCACGAGACCAGTGCCTATCAGTCTTGA	ATGATCGAGTACCTTGGGGACTCAAGTACCCTGAGGAACATCCACAGGGTGCACGAGACCAGTGCCTATCAGTCTTGA			MIEYLGDSSTLRNIHRVHETSAYQS*	MIEYLGDSSTLRNIHRVHETSAYQS*			AAAGGGAGTA	ATCCCCTATA	0		0	0	0	0	0
9038	4016	ao	AN4921.1	59.m08824	AO070338000022	0					-223	-101	ATGACCAAACCATCATGTTTTTTGCCATTATTGGCTTTAAAGGACCTTGGGATCCAAGTACCCCGGAGGCCATCATTTACCACCAACAGATTTATAGAAGCTGTACGGAACTATCTCATGTAA			ATGACCAAACCATCATGTTTTTTGCCATTATTGGCTTTAAAGGACCTTGGGATCCAAGTACCCCGGAGGCCATCATTTACCACCAACAGATTTATAGAAGCTGTACGGAACTATCTCATGTAA	MTKPSCFLPLLALKDLGIQVPRRPSFTTNRFIEAVRNYLM*			MTKPSCFLPLLALKDLGIQVPRRPSFTTNRFIEAVRNYLM*	GACGCAGATC	CTGCTAGTTC	0		0	0	0	0	0
9039	4016	ao	AN4921.1	59.m08824	AO070338000022	0					-209	-36	ATGTTTTTTGCCATTATTGGCTTTAAAGGACCTTGGGATCCAAGTACCCCGGAGGCCATCATTTACCACCAACAGATTTATAGAAGCTGTACGGAACTATCTCATGTAACTGCTAGTTCAAAGAAAACTTTTGCTCTTCTGAGTATACCTAAATCCTCGGGTGACAACCCCTGA			ATGTTTTTTGCCATTATTGGCTTTAAAGGACCTTGGGATCCAAGTACCCCGGAGGCCATCATTTACCACCAACAGATTTATAGAAGCTGTACGGAACTATCTCATGTAACTGCTAGTTCAAAGAAAACTTTTGCTCTTCTGAGTATACCTAAATCCTCGGGTGACAACCCCTGA	MFFAIIGFKGPWDPSTPEAIIYHQQIYRSCTELSHVTASSKKTFALLSIPKSSGDNP*			MFFAIIGFKGPWDPSTPEAIIYHQQIYRSCTELSHVTASSKKTFALLSIPKSSGDNP*	CCAAACCATC	ACAACCCTAA	0		0	0	0	0	0
9041	4017	af	AN6726.1	65.m07244	AO070339000170	0			-261	-154			ATGAGGAACCTCAGGCAACAACTGCACTTACCTGCTCGCGTAAGCCAGTTCTGGCATTTGTATCGTCACCGCCCCAGACATGGCTTGGCGCTGGGCAGATGGACCTAA		ATGAGGAACCTCAGGCAACAACTGCACTTACCTGCTCGCGTAAGCCAGTTCTGGCATTTGTATCGTCACCGCCCCAGACATGGCTTGGCGCTGGGCAGATGGACCTAA		MRNLRQQLHLPARVSQFWHLYRHRPRHGLALGRWT*		MRNLRQQLHLPARVSQFWHLYRHRPRHGLALGRWT*		GCTTCGAGAC	GCTGTGCTGC	0	O	0	0	0	0	0
9042	4017	af	AN6726.1	65.m07244	AO070339000170	0			-182	-48			ATGGCTTGGCGCTGGGCAGATGGACCTAAGCTGTGCTGCGTCAACACCTTGTCGCCTGTTGCTTGGAGGAGGAGAGCTTCACTTGAACTTCAACAATTTCATTTTGTCTTCATATTATCTTCCCCATCTTTTTGA		ATGGCTTGGCGCTGGGCAGATGGACCTAAGCTGTGCTGCGTCAACACCTTGTCGCCTGTTGCTTGGAGGAGGAGAGCTTCACTTGAACTTCAACAATTTCATTTTGTCTTCATATTATCTTCCCCATCTTTTTGA		MAWRWADGPKLCCVNTLSPVAWRRRASLELQQFHFVFILSSPSF*		MAWRWADGPKLCCVNTLSPVAWRRRASLELQQFHFVFILSSPSF*		CGCCCCAGAC	TAGCTCTATA	0	O	0	0	0	0	0
9040	4017	an	AN6726.1	65.m07244	AO070339000170	0	-196	-137					ATGGAGGAGCTCCGATTTACTGCCACCGCCTTCCGACTTTGGACTGGTAAACTGATGTGA	ATGGAGGAGCTCCGATTTACTGCCACCGCCTTCCGACTTTGGACTGGTAAACTGATGTGA			MEELRFTATAFRLWTGKLM*	MEELRFTATAFRLWTGKLM*			GCGAGTGGAG	GCTGAAGGCT	0	O	0	0	0	0	0
9043	4017	ao	AN6726.1	65.m07244	AO070339000170	0					-241	-200	ATGGAAACGGCGCTAAGTGCTCGCCTAGCGTCACCGCCTTAG			ATGGAAACGGCGCTAAGTGCTCGCCTAGCGTCACCGCCTTAG	METALSARLASPP*			METALSARLASPP*	AGAGAAGCTG	GCGCGGCTTG	0	O	0	0	0	0	0
9044	4018	an	AN4188.1	54.m06746	AO070342000109	0	-166	-122					ATGGCGGGGAACTGTAGGGAGAGGGTGGAGGAGCGGATGCGATGA	ATGGCGGGGAACTGTAGGGAGAGGGTGGAGGAGCGGATGCGATGA			MAGNCRERVEERMR*	MAGNCRERVEERMR*			GAGGGGAAAG	GGTTCTGCGC	0		0	0	0	0	0
9052	4021	af	AN1020.1	70.m15238	AO070343000595	0			-84	-49			ATGATCGTGGTCTGCAAAGGTAATTGTTCAGCATAA		ATGATCGTGGTCTGCAAAGGTAATTGTTCAGCATAA		MIVVCKGNCSA*		MIVVCKGNCSA*		TATTCTTGCG	CTGTCATCTA	0	S	0	0	0	0	0
9045	4021	an	AN1020.1	70.m15238	AO070343000595	0	-261	-232					ATGATAGATTCGATGACAGTGACACCTTAG	ATGATAGATTCGATGACAGTGACACCTTAG			MIDSMTVTP*	MIDSMTVTP*			AAGAGATAAG	CTATGGTTGG	0	S	0	0	0	0	0
9046	4021	an	AN1020.1	70.m15238	AO070343000595	0	-249	-232					ATGACAGTGACACCTTAG	ATGACAGTGACACCTTAG			MTVTP*	MTVTP*			GATAGATTCG	CTATGGTTGG	0	S	0	0	0	0	0
9047	4021	an	AN1020.1	70.m15238	AO070343000595	0	-229	-191					ATGGTTGGAACGCATATCTTTAGAACGGTACTTGCATGA	ATGGTTGGAACGCATATCTTTAGAACGGTACTTGCATGA			MVGTHIFRTVLA*	MVGTHIFRTVLA*			CACCTTAGCT	TACTTTTTTG	0	S	0	0	0	0	0
9048	4021	an	AN1020.1	70.m15238	AO070343000595	0	-194	-174					ATGATACTTTTTTGGAACTAG	ATGATACTTTTTTGGAACTAG			MILFWN*	MILFWN*			CGGTACTTGC	ATGGAGAGCT	0	S	0	0	0	0	0
9049	4021	an	AN1020.1	70.m15238	AO070343000595	0	-173	-162					ATGGAGAGCTAG	ATGGAGAGCTAG			MES*	MES*			TTGGAACTAG	CTTTGGAAGG	0	S	0	0	0	0	0
9050	4021	an	AN1020.1	70.m15238	AO070343000595	0	-150	-91					ATGAGGCTCTTTCAAAGCAACCTTGGATATGGAGTATACTCCAGAGTAAAAACCCTATGA	ATGAGGCTCTTTCAAAGCAACCTTGGATATGGAGTATACTCCAGAGTAAAAACCCTATGA			MRLFQSNLGYGVYSRVKTL*	MRLFQSNLGYGVYSRVKTL*			TTTGGAAGGG	CGTAACGTGA	0	S	0	0	0	0	0
9051	4021	an	AN1020.1	70.m15238	AO070343000595	0	-122	-102					ATGGAGTATACTCCAGAGTAA	ATGGAGTATACTCCAGAGTAA			MEYTPE*	MEYTPE*			AACCTTGGAT	AAACCCTATG	0	S	0	0	0	0	0
9053	4021	ao	AN1020.1	70.m15238	AO070343000595	0					-134	-30	ATGGCGACTTTCCATTTTTGGAAACCCTCAAACCCTTACTTGGCTGAAGAAAGAACGACACCTGAGATCCTCACCCGCTTGCATGCAGCAAACAACACTGCCTGA			ATGGCGACTTTCCATTTTTGGAAACCCTCAAACCCTTACTTGGCTGAAGAAAGAACGACACCTGAGATCCTCACCCGCTTGCATGCAGCAAACAACACTGCCTGA	MATFHFWKPSNPYLAEERTTPEILTRLHAANNTA*			MATFHFWKPSNPYLAEERTTPEILTRLHAANNTA*	AAATGACGTC	AAACTATCCA	0	S	0	0	0	0	0
9054	4022	af	AN2008.1	58.m07617	AO070179000004	0			-167	-150			ATGGACTGTCCTCTTTGA		ATGGACTGTCCTCTTTGA		MDCPL*		MDCPL*		AGTACATAAC	TCCCTTGCTT	0	R	0	0	0	YHR100C	0
9055	4024	an	AN4402.1	58.m07924	AO070261000046	0	-249	-232					ATGCCCCAGGCGTTTTAA	ATGCCCCAGGCGTTTTAA			MPQAF*	MPQAF*			GTAATATCGG	GGCACCGTCG	0	P	0	0	0	0	0
9056	4026	an	AN0600.1	69.m15248	AO070280000025	0	-189	-169					ATGGAATTTTGCTGCCTTTGA	ATGGAATTTTGCTGCCTTTGA			MEFCCL*	MEFCCL*			GACAATCATT	TCCGTTACGC	0		0	0	0	0	0
9057	4026	an	AN0600.1	69.m15248	AO070280000025	0	-98	-51					ATGTTGTTACCAATATTTATAAGGACTCATACAAATCGCGCCCCCTAG	ATGTTGTTACCAATATTTATAAGGACTCATACAAATCGCGCCCCCTAG			MLLPIFIRTHTNRAP*	MLLPIFIRTHTNRAP*			AATCTTTTTA	CGCCATCACT	0		0	0	0	0	0
9058	4026	ao	AN0600.1	69.m15248	AO070280000025	0					-257	-135	ATGACCCCTGGGACCCAACCTTTTCATTCAACAATGCTGCCTGGGACTGCGTACAAGTGCAAACCTTTTCCACTCTTCAGCCTTATAATACCTCTTTGTCGTGAAACTTCTGTTGAAATTTAG			ATGACCCCTGGGACCCAACCTTTTCATTCAACAATGCTGCCTGGGACTGCGTACAAGTGCAAACCTTTTCCACTCTTCAGCCTTATAATACCTCTTTGTCGTGAAACTTCTGTTGAAATTTAG	MTPGTQPFHSTMLPGTAYKCKPFPLFSLIIPLCRETSVEI*			MTPGTQPFHSTMLPGTAYKCKPFPLFSLIIPLCRETSVEI*	CTGCGACACC	CTCTTAGCTT	0		0	0	0	0	0
9059	4026	ao	AN0600.1	69.m15248	AO070280000025	0					-224	-135	ATGCTGCCTGGGACTGCGTACAAGTGCAAACCTTTTCCACTCTTCAGCCTTATAATACCTCTTTGTCGTGAAACTTCTGTTGAAATTTAG			ATGCTGCCTGGGACTGCGTACAAGTGCAAACCTTTTCCACTCTTCAGCCTTATAATACCTCTTTGTCGTGAAACTTCTGTTGAAATTTAG	MLPGTAYKCKPFPLFSLIIPLCRETSVEI*			MLPGTAYKCKPFPLFSLIIPLCRETSVEI*	TCATTCAACA	CTCTTAGCTT	0		0	0	0	0	0
9061	4027	ao	AN4984.1	59.m08886	AO070288000052	0					-530	-450	ATGGTTCGTATCTGCATTTCAATTTTCTGTGTTGCCCTGATTAGCGAAGGTCTATTTTACCATTGTGGTATAATATACTGA			ATGGTTCGTATCTGCATTTCAATTTTCTGTGTTGCCCTGATTAGCGAAGGTCTATTTTACCATTGTGGTATAATATACTGA	MVRICISIFCVALISEGLFYHCGIIY*			MVRICISIFCVALISEGLFYHCGIIY*	AGACGTGTAG	CGGGACTCTC	0	R	0	0	0	0	0
9062	4029	af	AN2050.1	58.m07638	AO070292000017	0			-128	-81			ATGCACACCTCCTCAAATCGCCAGCTGGAGCATTGCATTCAACCTTAA		ATGCACACCTCCTCAAATCGCCAGCTGGAGCATTGCATTCAACCTTAA		MHTSSNRQLEHCIQP*		MHTSSNRQLEHCIQP*		ATCAACACTC	TCTCATTTCC	0	U	0	0	0	0	0
9064	4030	af	AN2218.1	71.m15851	AO070294000007	0			-234	-169			ATGAGTGATTGTGTATTACTGAAATCGAGCATCGTTTCATCAGATCGGTTTCTTTCAACGTCCTAA		ATGAGTGATTGTGTATTACTGAAATCGAGCATCGTTTCATCAGATCGGTTTCTTTCAACGTCCTAA		MSDCVLLKSSIVSSDRFLSTS*		MSDCVLLKSSIVSSDRFLSTS*		TTTTACCAGC	CTGCACCCAT	0	S	0	0	0	0	0
9063	4030	an	AN2218.1	71.m15851	AO070294000007	0	-179	-147					ATGATCACTCTTTTAAACTCGTTCAACGTATAA	ATGATCACTCTTTTAAACTCGTTCAACGTATAA			MITLLNSFNV*	MITLLNSFNV*			CCTCTTCAGC	TTACACCGCG	0	S	0	0	0	0	0
9065	4030	ao	AN2218.1	71.m15851	AO070294000007	0					-254	-222	ATGAACACTCGTCCAGGGTCAAAGTTGAACTGA			ATGAACACTCGTCCAGGGTCAAAGTTGAACTGA	MNTRPGSKLN*			MNTRPGSKLN*	CCTTAACAGC	ACCCTGAAAG	0	S	0	0	0	0	0
9071	4033	af	AN3387.1	72.m19372	AO070304000008	0			-101	-21			ATGCTAGGAACCAGGAACCTACTTGCCGAACTCCATCAGTCTGGCGTCTTTCTCAACGACCGCATCACCAACCGGCCTTGA		ATGCTAGGAACCAGGAACCTACTTGCCGAACTCCATCAGTCTGGCGTCTTTCTCAACGACCGCATCACCAACCGGCCTTGA		MLGTRNLLAELHQSGVFLNDRITNRP*		MLGTRNLLAELHQSGVFLNDRITNRP*		GGTACCTGTC	ACGGGCGATG	0		0	0	0	0	0
9066	4033	an	AN3387.1	72.m19372	AO070304000008	0	-261	-133					ATGCAAGGAGGAGTGTCACTGACAGGGTCTTGGACGATATTAAGCTTTCGCCAATGCCCCACGATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGA	ATGCAAGGAGGAGTGTCACTGACAGGGTCTTGGACGATATTAAGCTTTCGCCAATGCCCCACGATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGA			MQGGVSLTGSWTILSFRQCPTMAAKSVQSGHAVPGSRMQACR*	MQGGVSLTGSWTILSFRQCPTMAAKSVQSGHAVPGSRMQACR*			CGCCGGACTA	TCAGGTGTAT	0		0	0	0	0	0
9067	4033	an	AN3387.1	72.m19372	AO070304000008	0	-208	-104					ATGCCCCACGATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGATCAGGTGTATTTTCTTTTTTAAGTACTGA	ATGCCCCACGATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGATCAGGTGTATTTTCTTTTTTAAGTACTGA			MPHDGGEKRAKWPRRTRFQNAGLPVIRCIFFFKY*	MPHDGGEKRAKWPRRTRFQNAGLPVIRCIFFFKY*			GCTTTCGCCA	GAATACGCCA	0		0	0	0	0	0
9068	4033	an	AN3387.1	72.m19372	AO070304000008	0	-198	-133					ATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGA	ATGGCGGCGAAAAGCGTGCAAAGTGGCCACGCCGTACCCGGTTCCAGAATGCAGGCTTGCCGGTGA			MAAKSVQSGHAVPGSRMQACR*	MAAKSVQSGHAVPGSRMQACR*			ATGCCCCACG	TCAGGTGTAT	0		0	0	0	0	0
9069	4033	an	AN3387.1	72.m19372	AO070304000008	0	-150	-133					ATGCAGGCTTGCCGGTGA	ATGCAGGCTTGCCGGTGA			MQACR*	MQACR*			CGGTTCCAGA	TCAGGTGTAT	0		0	0	0	0	0
9070	4033	an	AN3387.1	72.m19372	AO070304000008	0	-94	-62					ATGCACTGGCCGTTTCACCAGGGACGGGATTGA	ATGCACTGGCCGTTTCACCAGGGACGGGATTGA			MHWPFHQGRD*	MHWPFHQGRD*			AGAATACGCC	CTTGCCGCCG	0		0	0	0	0	0
9072	4033	ao	AN3387.1	72.m19372	AO070304000008	0					-174	-64	ATGAGGAGCTTAGCCGGGACAACAAAATGTTCTAAATTCTGGGTCAGGAACCGTCCCCAAACCTCAATGATAAGCGGTTATATACCCTCATTCTTTCCCAGGGACTTCTAG			ATGAGGAGCTTAGCCGGGACAACAAAATGTTCTAAATTCTGGGTCAGGAACCGTCCCCAAACCTCAATGATAAGCGGTTATATACCCTCATTCTTTCCCAGGGACTTCTAG	MRSLAGTTKCSKFWVRNRPQTSMISGYIPSFFPRDF*			MRSLAGTTKCSKFWVRNRPQTSMISGYIPSFFPRDF*	AAAGCTTTTG	GCGCGGATAC	0		0	0	0	0	0
9073	4033	ao	AN3387.1	72.m19372	AO070304000008	0					-108	-64	ATGATAAGCGGTTATATACCCTCATTCTTTCCCAGGGACTTCTAG			ATGATAAGCGGTTATATACCCTCATTCTTTCCCAGGGACTTCTAG	MISGYIPSFFPRDF*			MISGYIPSFFPRDF*	CCAAACCTCA	GCGCGGATAC	0		0	0	0	0	0
9075	4034	af	AN6257.1	72.m19399	AO070304000031	0			-84	-58			ATGATTGTCATCGTCAGACGGTTCTGA		ATGATTGTCATCGTCAGACGGTTCTGA		MIVIVRRF*		MIVIVRRF*		TTGTCGTTTA	GTCTGATCCT	0	U	0	0	0	0	0
9074	4034	an	AN6257.1	72.m19399	AO070304000031	0	-158	-135					ATGCACCCCTCGGCTCTCGATTAG	ATGCACCCCTCGGCTCTCGATTAG			MHPSALD*	MHPSALD*			TCTTCCGTCC	AGGGGAAAGT	0	U	0	0	0	0	0
9076	4034	ao	AN6257.1	72.m19399	AO070304000031	0					-86	-42	ATGATAGTTGCTGCCAGACCGTTCCTTAGTCTGGTTATCTCCTAA			ATGATAGTTGCTGCCAGACCGTTCCTTAGTCTGGTTATCTCCTAA	MIVAARPFLSLVIS*			MIVAARPFLSLVIS*	TTCTTGTTTC	TCTATAGTAC	0	U	0	0	0	0	0

9082	4035	af	AN6248.1	72.m19405	AO070304000104	0			-222	-46			ATGATCGTCTGTCTCATGAATCTCTTCTTTCCATCGGCCCGAAGATCCCCTGCCATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		ATGATCGTCTGTCTCATGAATCTCTTCTTTCCATCGGCCCGAAGATCCCCTGCCATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		MIVCLMNLFFPSARRSPAMTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		MIVCLMNLFFPSARRSPAMTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		ATTAGTGATA	AAGCTCCATA	0	O	FG00305.1	0	NCU01516.1	0	0
9083	4035	af	AN6248.1	72.m19405	AO070304000104	0			-207	-46			ATGAATCTCTTCTTTCCATCGGCCCGAAGATCCCCTGCCATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		ATGAATCTCTTCTTTCCATCGGCCCGAAGATCCCCTGCCATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		MNLFFPSARRSPAMTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		MNLFFPSARRSPAMTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		CGTCTGTCTC	AAGCTCCATA	0	O	FG00305.1	0	NCU01516.1	0	0
9084	4035	af	AN6248.1	72.m19405	AO070304000104	0			-168	-46			ATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		ATGACCCAACACGGTAAGCGGTCAGGTGATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		MTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		MTQHGKRSGDAMPCSFESSIFLAGKELALPQLHTPCSFPL*		ATCCCCTGCC	AAGCTCCATA	0	O	FG00305.1	0	NCU01516.1	0	0
9085	4035	af	AN6248.1	72.m19405	AO070304000104	0			-140	-18			ATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAAAAGCTCCATATTCCTTTTTCATCTCTAA		ATGCCATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAAAAGCTCCATATTCCTTTTTCATCTCTAA		MPCPVASKVPFFWRAKNWLYHSFTLLALSPFKSSIFLFHL*		MPCPVASKVPFFWRAKNWLYHSFTLLALSPFKSSIFLFHL*		CGGTCAGGTG	AATATCCCTC	0	O	FG00305.1	0	NCU01516.1	0	0
9086	4035	af	AN6248.1	72.m19405	AO070304000104	0			-135	-46			ATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		ATGCCCTGTAGCTTCGAAAGTTCCATTTTTCTGGCGGGCAAAGAACTGGCTCTACCACAGCTTCACACTCCTTGCTCTTTCCCCCTTTAA		MPCSFESSIFLAGKELALPQLHTPCSFPL*		MPCSFESSIFLAGKELALPQLHTPCSFPL*		AGGTGATGCC	AAGCTCCATA	0	O	FG00305.1	0	NCU01516.1	0	0
9077	4035	an	AN6248.1	72.m19405	AO070304000104	0	-201	-166					ATGGTTTCCACAATTACTTGGGACATCAAAGTATGA	ATGGTTTCCACAATTACTTGGGACATCAAAGTATGA			MVSTITWDIKV*	MVSTITWDIKV*			GACCTCGGGT	TACGCGTCGC	0	O	FG00305.1	0	NCU01516.1	0	0
9078	4035	an	AN6248.1	72.m19405	AO070304000104	0	-169	-143					ATGATACGCGTCGCATCTCATGTATAG	ATGATACGCGTCGCATCTCATGTATAG			MIRVASHV*	MIRVASHV*			ACATCAAAGT	TTCGGTGGGA	0	O	FG00305.1	0	NCU01516.1	0	0
9079	4035	an	AN6248.1	72.m19405	AO070304000104	0	-150	-106					ATGTATAGTTCGGTGGGATGTTTTTCCTTCGGCGCGGTCAGGTGA	ATGTATAGTTCGGTGGGATGTTTTTCCTTCGGCGCGGTCAGGTGA			MYSSVGCFSFGAVR*	MYSSVGCFSFGAVR*			GTCGCATCTC	CGTCGAAGCT	0	O	FG00305.1	0	NCU01516.1	0	0
9080	4035	an	AN6248.1	72.m19405	AO070304000104	0	-133	-77					ATGTTTTTCCTTCGGCGCGGTCAGGTGACGTCGAAGCTTTCATATTTTCTGCTGTAA	ATGTTTTTCCTTCGGCGCGGTCAGGTGACGTCGAAGCTTTCATATTTTCTGCTGTAA			MFFLRRGQVTSKLSYFLL*	MFFLRRGQVTSKLSYFLL*			GTTCGGTGGG	TGCCGAGTGT	0	O	FG00305.1	0	NCU01516.1	0	0
9081	4035	an	AN6248.1	72.m19405	AO070304000104	0	-77	-24					ATGCCGAGTGTCTCATTAGCACCAACCCTGTTCCTCTACCTTCAATCATTATAA	ATGCCGAGTGTCTCATTAGCACCAACCCTGTTCCTCTACCTTCAATCATTATAA			MPSVSLAPTLFLYLQSL*	MPSVSLAPTLFLYLQSL*			TTCTGCTGTA	TCTCCAAATC	0	O	FG00305.1	0	NCU01516.1	0	0
9087	4035	ao	AN6248.1	72.m19405	AO070304000104	0					-119	-96	ATGCCGAAATATCTGTTTTTCTAG			ATGCCGAAATATCTGTTTTTCTAG	MPKYLFF*			MPKYLFF*	CAGGTGATTT	CGATATCGCT	0	O	FG00305.1	0	NCU01516.1	0	0
9091	4036	af	AN3815.1	57.m05667	AO070311000013	0			-153	-79			ATGGCCTTCTTCGCCGCAGTCATCAGTAGAACACCCGAATTAATGATCACATTCTGCACTTTGTCTCGTGTGTGA		ATGGCCTTCTTCGCCGCAGTCATCAGTAGAACACCCGAATTAATGATCACATTCTGCACTTTGTCTCGTGTGTGA		MAFFAAVISRTPELMITFCTLSRV*		MAFFAAVISRTPELMITFCTLSRV*		CCCCTTGTCG	AGCTCCGATC	0	Z	0	0	0	0	0
9092	4036	af	AN3815.1	57.m05667	AO070311000013	0			-111	-79			ATGATCACATTCTGCACTTTGTCTCGTGTGTGA		ATGATCACATTCTGCACTTTGTCTCGTGTGTGA		MITFCTLSRV*		MITFCTLSRV*		ACCCGAATTA	AGCTCCGATC	0	Z	0	0	0	0	0
9088	4036	an	AN3815.1	57.m05667	AO070311000013	0	-143	-114					ATGCCATCGCTTCGAATTGGATGTATATGA	ATGCCATCGCTTCGAATTGGATGTATATGA			MPSLRIGCI*	MPSLRIGCI*			TTCCCTTCTC	GTAAATACGC	0	Z	0	0	0	0	0
9089	4036	an	AN3815.1	57.m05667	AO070311000013	0	-123	-70					ATGTATATGAGTAAATACGCGATCTATTGGTGGATTGGAACGACACTTTTCTAG	ATGTATATGAGTAAATACGCGATCTATTGGTGGATTGGAACGACACTTTTCTAG			MYMSKYAIYWWIGTTLF*	MYMSKYAIYWWIGTTLF*			TTCGAATTGG	CAGCAGCTTT	0	Z	0	0	0	0	0
9090	4036	an	AN3815.1	57.m05667	AO070311000013	0	-117	-70					ATGAGTAAATACGCGATCTATTGGTGGATTGGAACGACACTTTTCTAG	ATGAGTAAATACGCGATCTATTGGTGGATTGGAACGACACTTTTCTAG			MSKYAIYWWIGTTLF*	MSKYAIYWWIGTTLF*			TTGGATGTAT	CAGCAGCTTT	0	Z	0	0	0	0	0
9093	4036	ao	AN3815.1	57.m05667	AO070311000013	0					-116	-81	ATGCATATCTGCAGGACCGCTATACTAAGGAGGTGA			ATGCATATCTGCAGGACCGCTATACTAAGGAGGTGA	MHICRTAILRR*			MHICRTAILRR*	GAGATCTCGA	AGGGTTGCCC	0	Z	0	0	0	0	0
9096	4037	af	AN2693.1	71.m15180	AO070313000094	0			-220	-128			ATGTATGGGGTAATTCGTAGTGATTCATTGTCCAAGCTCGGACGCAGTATGCCTGAGGCACCCAGGCAATCTGTTATCGATAAGCTCCTTTGA		ATGTATGGGGTAATTCGTAGTGATTCATTGTCCAAGCTCGGACGCAGTATGCCTGAGGCACCCAGGCAATCTGTTATCGATAAGCTCCTTTGA		MYGVIRSDSLSKLGRSMPEAPRQSVIDKLL*		MYGVIRSDSLSKLGRSMPEAPRQSVIDKLL*		TTTACATTAG	TTCCCCCGAA	0	R	0	0	0	0	0
9097	4037	af	AN2693.1	71.m15180	AO070313000094	0			-172	-128			ATGCCTGAGGCACCCAGGCAATCTGTTATCGATAAGCTCCTTTGA		ATGCCTGAGGCACCCAGGCAATCTGTTATCGATAAGCTCCTTTGA		MPEAPRQSVIDKLL*		MPEAPRQSVIDKLL*		CGGACGCAGT	TTCCCCCGAA	0	R	0	0	0	0	0
9098	4037	af	AN2693.1	71.m15180	AO070313000094	0			-106	-14			ATGGGTTGTCTGCGCAGTCTGCCCTCAACATCTACTCCTATTAGGACGATATCATTAGTTCTATCATCTATCCTTACTGTCAGTTATCCTTAG		ATGGGTTGTCTGCGCAGTCTGCCCTCAACATCTACTCCTATTAGGACGATATCATTAGTTCTATCATCTATCCTTACTGTCAGTTATCCTTAG		MGCLRSLPSTSTPIRTISLVLSSILTVSYP*		MGCLRSLPSTSTPIRTISLVLSSILTVSYP*		CTTTTTCCTC	CTTCTACATC	0	R	0	0	0	0	0
9094	4037	an	AN2693.1	71.m15180	AO070313000094	0	-263	-180					ATGGTTGGAGATTGGAAGAATCTGGGCAGCTATGACAACATCTTGCAGCCTGAGGCAGAAGGCAGATATCACAGAGCGCTGTAA	ATGGTTGGAGATTGGAAGAATCTGGGCAGCTATGACAACATCTTGCAGCCTGAGGCAGAAGGCAGATATCACAGAGCGCTGTAA			MVGDWKNLGSYDNILQPEAEGRYHRAL*	MVGDWKNLGSYDNILQPEAEGRYHRAL*			TCAGCCCACG	GGCATCAAGG	0	R	0	0	0	0	0
9095	4037	an	AN2693.1	71.m15180	AO070313000094	0	-232	-104					ATGACAACATCTTGCAGCCTGAGGCAGAAGGCAGATATCACAGAGCGCTGTAAGGCATCAAGGCAAACACAGTTGCTATCGATAAGAGTCGCTTTTTTCGTTCTCCAGCTTTGTCCAGGTTGGAGTTAA	ATGACAACATCTTGCAGCCTGAGGCAGAAGGCAGATATCACAGAGCGCTGTAAGGCATCAAGGCAAACACAGTTGCTATCGATAAGAGTCGCTTTTTTCGTTCTCCAGCTTTGTCCAGGTTGGAGTTAA			MTTSCSLRQKADITERCKASRQTQLLSIRVAFFVLQLCPGWS*	MTTSCSLRQKADITERCKASRQTQLLSIRVAFFVLQLCPGWS*			CTGGGCAGCT	ACAACATCTC	0	R	0	0	0	0	0
9099	4037	ao	AN2693.1	71.m15180	AO070313000094	0					-191	-102	ATGAACCTCCTTATCGATAAGCTAAATGTATCCAGATTCCAGACTTTTTTTTCCTCCGCTCCACTTCTCATATCTCACATTATATCATAA			ATGAACCTCCTTATCGATAAGCTAAATGTATCCAGATTCCAGACTTTTTTTTCCTCCGCTCCACTTCTCATATCTCACATTATATCATAA	MNLLIDKLNVSRFQTFFSSAPLLISHIIS*			MNLLIDKLNVSRFQTFFSSAPLLISHIIS*	TAAGGCATAA	CATGACCTGT	0	R	0	0	0	0	0
9100	4037	ao	AN2693.1	71.m15180	AO070313000094	0					-166	-74	ATGTATCCAGATTCCAGACTTTTTTTTCCTCCGCTCCACTTCTCATATCTCACATTATATCATAACATGACCTGTCCCCATATCCATACTTGA			ATGTATCCAGATTCCAGACTTTTTTTTCCTCCGCTCCACTTCTCATATCTCACATTATATCATAACATGACCTGTCCCCATATCCATACTTGA	MYPDSRLFFPPLHFSYLTLYHNMTCPHIHT*			MYPDSRLFFPPLHFSYLTLYHNMTCPHIHT*	GATAAGCTAA	TATTTTACCC	0	R	0	0	0	0	0
9101	4037	ao	AN2693.1	71.m15180	AO070313000094	0					-100	-74	ATGACCTGTCCCCATATCCATACTTGA			ATGACCTGTCCCCATATCCATACTTGA	MTCPHIHT*			MTCPHIHT*	ATATCATAAC	TATTTTACCC	0	R	0	0	0	0	0
9105	4038	af	AN6843.1	71.m15300	AO070314000096	0			-189	-100			ATGGCTGGAATTGACGCTCTTCGAGCTCTCAGATGGCTTTCGCGAAGCTCAAGTGGCCTGTTGACAGGCGCTGAAGCCACAACGGTATAA		ATGGCTGGAATTGACGCTCTTCGAGCTCTCAGATGGCTTTCGCGAAGCTCAAGTGGCCTGTTGACAGGCGCTGAAGCCACAACGGTATAA		MAGIDALRALRWLSRSSSGLLTGAEATTV*		MAGIDALRALRWLSRSSSGLLTGAEATTV*		AAACTGCAAA	CTTGTGTCTT	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9103	4038	an	AN6843.1	71.m15300	AO070314000096	0	-310	-188					ATGGCGGGGAGCAGCGCTTTCGGCACTTTCAGATGGCTGTCTCGCAGCTCAAGGGGTCTTCTTTCTGGAACTGAAGCCACCACGGTTGGTTCACCCATCTACACCTCAAGGAATGCGAATTGA	ATGGCGGGGAGCAGCGCTTTCGGCACTTTCAGATGGCTGTCTCGCAGCTCAAGGGGTCTTCTTTCTGGAACTGAAGCCACCACGGTTGGTTCACCCATCTACACCTCAAGGAATGCGAATTGA			MAGSSAFGTFRWLSRSRGLLSGTEATTVGSPIYTSRNAN*	MAGSSAFGTFRWLSRSSRGLLSGTEATTVGSPIYTSRNAN*			AGTCATAGCA	CATCCCGTAG	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9104	4038	an	AN6843.1	71.m15300	AO070314000096	0	-198	-178					ATGCGAATTGACATCCCGTAG	ATGCGAATTGACATCCCGTAG			MRIDIP*	MRIDIP*			ACCTCAAGGA	CAGCGATGCC	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9106	4038	ao	AN6843.1	71.m15300	AO070314000096	0					-198	-67	ATGCCTGGAGGTGACGCTCTTCGTGCCTTAAGATGGCTCTCCCGAAGCACTGGTGGGTTGCTCTCGGGGTCTGAGACCACTACAGTATGTGCTGTCGTTTTCTTTATGTTCCCGGTTGCAACACAATTATAA			ATGCCTGGAGGTGACGCTCTTCGTGCCTTAAGATGGCTCTCCCGAAGCACTGGTGGGTTGCTCTCGGGGTCTGAGACCACTACAGTATGTGCTGTCGTTTTCTTTATGTTCCCGGTTGCAACACAATTATAA	MPGGDALRALRWLSRSTGGLLSGSETTVCAVVFFMFPVATQL*			MPGGDALRALRWLSRSTGGLLSGSETTVCAVVFFMFPVATQL*	TGACAACACA	CATCAACTCT	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9107	4038	ao	AN6843.1	71.m15300	AO070314000096	0					-93	-67	ATGTTCCCGGTTGCAACACAATTATAA			ATGTTCCCGGTTGCAACACAATTATAA	MFPVATQL*			MFPVATQL*	CGTTTTCTTT	CATCAACTCT	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
9110	4040	af	AN0211.1	71.m15474	AO070321000033	0			-181	-167			ATGCGGCTTCAATAA		ATGCGGCTTCAATAA		MRLQ*		MRLQ*		TCTTGAGGTA	TTCAGCCATG	0	A	0	0	0	0	0
9108	4040	an	AN0211.1	71.m15474	AO070321000033	0	-174	-22					ATGTCTCACCGCCGGGCAGAATTCTCTCTGAGCTCTCCAGAAATCGACGCGAAGTTCATTCTGCCGTTCACATTACCACGATTGCACTTTATAATTCTTTATCATCCCTCGAGATTCACTCTTTTCAATTCAACCGCCTTGCTCCGTTTATGA	ATGTCTCACCGCCGGGCAGAATTCTCTCTGAGCTCTCCAGAAATCGACGCGAAGTTCATTCTGCCGTTCACATTACCACGATTGCACTTTATAATTCTTTATCATCCCTCGAGATTCACTCTTTTCAATTCAACCGCCTTGCTCCGTTTATGA			MSHRRAEFSLSSPEIDAKFILPFTLPRLHFIILYHPSRFTLFNSTALLRL*	MSHRRAEFSLSSPEIDAKFILPFTLPRLHFIILYHPSRFTLFNSTALLRL*			ACAGGACCTG	ACCGCTCATA	0	A	0	0	0	0	0
9112	4040	ao	AN0211.1	71.m15474	AO070321000033	0					-268	-83	ATGGTCCATAGAGTATGTGATCACGTGCATGTGTGCTGGTTCGTCAGCTCACCGCCCTGGCAAAATCCTTTGCGGTACCGCTTCGATAATTTGGTATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGATCTTTTCATTGTCAATTTACTGTCCTTTGGGCGTGATCTGTCGAGACTCTGA			ATGGTCCATAGAGTATGTGATCACGTGCATGTGTGCTGGTTCGTCAGCTCACCGCCCTGGCAAAATCCTTTGCGGTACCGCTTCGATAATTTGGTATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGATCTTTTCATTGTCAATTTACTGTCCTTTGGGCGTGATCTGTCGAGACTCTGA	MVHRVCDHVHVCWFVSSPPWQNPLRYRFDNLVCVKELWLLSAYFDLFIVNLLSFGRDLSRL*			MVHRVCDHVHVCWFVSSPPWQNPLRYRFDNLVCVKELWLLSAYFDLFIVNLLSFGRDLSRL*	TTAGTCGTCA	ATTCTGTATT	0	A	0	0	0	0	0
9113	4040	ao	AN0211.1	71.m15474	AO070321000033	0					-240	-46	ATGTGTGCTGGTTCGTCAGCTCACCGCCCTGGCAAAATCCTTTGCGGTACCGCTTCGATAATTTGGTATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGATCTTTTCATTGTCAATTTACTGTCCTTTGGGCGTGATCTGTCGAGACTCTGAATTCTGTATTAATCGTACTCTTTGCTGCTTCCCATAA			ATGTGTGCTGGTTCGTCAGCTCACCGCCCTGGCAAAATCCTTTGCGGTACCGCTTCGATAATTTGGTATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGATCTTTTCATTGTCAATTTACTGTCCTTTGGGCGTGATCTGTCGAGACTCTGAATTCTGTATTAATCGTACTCTTTGCTGCTTCCCATAA	MCAGSSAHRPGKILCGTASIIWYASRSSGCSPHTLIFSLSIYCPLGVICRDSEFCINRTLCCFP*			MCAGSSAHRPGKILCGTASIIWYASRSSGCSPHTLIFSLSIYCPLGVICRDSEFCINRTLCCFP*	GATCACGTGC	TTGCATGATA	0	A	0	0	0	0	0
9114	4040	ao	AN0211.1	71.m15474	AO070321000033	0					-173	-135	ATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGA			ATGCGTCAAGGAGCTCTGGCTGCTCTCCGCATACTTTGA	MRQGALAALRIL*			MRQGALAALRIL*	ATAATTTGGT	TCTTTTCATT	0	A	0	0	0	0	0
9115	4041	af	AN4726.1	71.m15495	AO070323000058	0			-214	-203			ATGGTGCTGTGA		ATGGTGCTGTGA		MVL*		MVL*		TGTCATTGAA	CTCGTGAGGG	0	Q	0	MG07443.1	0	0	0
9116	4041	af	AN4726.1	71.m15495	AO070323000058	0			-188	-81			ATGTTGGTAATCTTAAGATGGTGGTGGTGGCGGGAGATCGGCCGCTATCTGACTTCTGACGCAGCTCCGGCTGCTCTTTTGAGTGTTTCAGCGGGATTGCATTCCTGA		ATGTTGGTAATCTTAAGATGGTGGTGGTGGCGGGAGATCGGCCGCTATCTGACTTCTGACGCAGCTCCGGCTGCTCTTTTGAGTGTTTCAGCGGGATTGCATTCCTGA		MLVILRWWWWREIGRYLTSDAAPAALLSVSAGLHS*		MLVILRWWWWREIGRYLTSDAAPAALLSVSAGLHS*		TGAGGGGAAA	ACCTGTTCAC	0	Q	0	MG07443.1	0	0	0
9117	4041	af	AN4726.1	71.m15495	AO070323000058	0			-171	-130			ATGGTGGTGGTGGCGGGAGATCGGCCGCTATCTGACTTCTGA		ATGGTGGTGGTGGCGGGAGATCGGCCGCTATCTGACTTCTGA		MVVVAGDRPLSDF*		MVVVAGDRPLSDF*		TAATCTTAAG	CGCAGCTCCG	0	Q	0	MG07443.1	0	0	0
9118	4041	ao	AN4726.1	71.m15495	AO070323000058	0					-248	-225	ATGTGTTTCATTTCAATGATTTAG			ATGTGTTTCATTTCAATGATTTAG	MCFISMI*			MCFISMI*	TAGGAGGTCA	TGGTTTGCGG	0	Q	0	MG07443.1	0	0	0
9119	4041	ao	AN4726.1	71.m15495	AO070323000058	0					-156	-73	ATGGCGGTAGACTGGGCGGTGAGCTTATTTGTGGTCTGGGCCCTGCATTTGATCCTATGTTTAGTAGCAGCTTTCTGTCCATAA			ATGGCGGTAGACTGGGCGGTGAGCTTATTTGTGGTCTGGGCCCTGCATTTGATCCTATGTTTAGTAGCAGCTTTCTGTCCATAA	MAVDWAVSLFVVWALHLILCLVAAFCP*			MAVDWAVSLFVVWALHLILCLVAAFCP*	GACGAAGCAG	TTGGATTGTT	0	Q	0	MG07443.1	0	0	0
9123	4046	af	AN3648.1	58.m07451	AO070328000096	0			-250	-137			ATGCTGACTGGAGAGCTTCTGCAGGTCGACAATAGCTACAGTATATCTCCTTTCTTTTTCCTCCGCTCTCCTACGTACTTCTTCCTCTTCTTTTCAGCATCATGCCTCCGGTAA		ATGCTGACTGGAGAGCTTCTGCAGGTCGACAATAGCTACAGTATATCTCCTTTCTTTTTCCTCCGCTCTCCTACGTACTTCTTCCTCTTCTTTTCAGCATCATGCCTCCGGTAA		MLTGELLQVDNSYSISPFFFLRSPTYFFLFFSASCLR*		MLTGELLQVDNSYSISPFFFLRSPTYFFLFFSASCLR*		ATCTCCTGGA	GTTCTCCCCA	0	D	0	MG05646.1	0	0	0

9124	4046	af	AN3648.1	58.m07451	AO070328000096	0			-149	-111			ATGCCTCCGGTAAGTTCTCCCCATGAGAGACACGCGTAA		ATGCCTCCGGTAAGTTCTCCCCATGAGAGACACGCGTAA		MPPVSSPHERHA*		MPPVSSPHERHA*		TTTCAGCATC	TACTTCTACG	0	D	0	MG05646.1	0	0	0
9120	4046	an	AN3648.1	58.m07451	AO070328000096	0	-239	-120					ATGCTGACTGAAGTCCAGCGACGTGCACAGTTACTGAACCAAGACATTATCTTAAATCTTGCTATAATCTGTCGAGGGCTTTTCCTGCTCCTCGCGCTCTCTTCGCTATGCCTCCGGTAA	ATGCTGACTGAAGTCCAGCGACGTGCACAGTTACTGAACCAAGACATTATCTTAAATCTTGCTATAATCTGTCGAGGGCTTTTCCTGCTCCTCGCGCTCTCTTCGCTATGCCTCCGGTAA			MLTEVQRRAQLLNQDIILNLAIICRGLFLLLALSSLCLR*	MLTEVQRRAQLLNQDIILNLAIICRGLFLLLALSSLCLR*			ACCGTAGGGA	GGTTCCTCTG	0	D	0	MG05646.1	0	0	0
9121	4046	an	AN3648.1	58.m07451	AO070328000096	0	-132	-103					ATGCCTCCGGTAAGGTTCCTCTGGATTTGA	ATGCCTCCGGTAAGGTTCCTCTGGATTTGA			MPPVRFLWI*	MPPVRFLWI*			TCTCTTCGCT	CGCGTTACAA	0	D	0	MG05646.1	0	0	0
9122	4046	an	AN3648.1	58.m07451	AO070328000096	0	-93	-28					ATGAGTCACAACTGCTTCACCCTGGCGACGCGACTTCCTGTGGCTAACACATTGATTTCTGCTTAG	ATGAGTCACAACTGCTTCACCCTGGCGACGCGACTTCCTGTGGCTAACACATTGATTTCTGCTTAG			MSHNCFTLATRLPVANTLISA*	MSHNCFTLATRLPVANTLISA*			ACGCGTTACA	GCTCGAAACC	0	D	0	MG05646.1	0	0	0
9125	4046	ao	AN3648.1	58.m07451	AO070328000096	0					-249	-214	ATGCTGACGAGACGACAAGGACAGGAACCGCAGTAA			ATGCTGACGAGACGACAAGGACAGGAACCGCAGTAA	MLTRRQGQEPQ*			MLTRRQGQEPQ*	CTTCATTGGA	CCATAATCAA	0	D	0	MG05646.1	0	0	0
9126	4046	ao	AN3648.1	58.m07451	AO070328000096	0					-147	-115	ATGCCTACGGTAAGCTTTTCACAACTCCTATGA			ATGCCTACGGTAAGCTTTTCACAACTCCTATGA	MPTVSFSQLL*			MPTVSFSQLL*	TTCCCTCACA	CGCATTGATT	0	D	0	MG05646.1	0	0	0
9127	4046	ao	AN3648.1	58.m07451	AO070328000096	0					-118	-107	ATGACGCATTGA			ATGACGCATTGA	MTH*			MTH*	CACAACTCCT	TTCTTACCAG	0	D	0	MG05646.1	0	0	0
9129	4048	af	AN0475.1	54.m06595	AO070328000165	0			-253	-215			ATGCAGCCGTCGAGGATGTGGCCGTTGTTGGGGTTGTGA		ATGCAGCCGTCGAGGATGTGGCCGTTGTTGGGGTTGTGA		MQPSRMWPLLGL*		MQPSRMWPLLGL*		AGTGCGATAA	AAAGGTCGTG	0	S	0	0	0	YML093W	0
9130	4048	af	AN0475.1	54.m06595	AO070328000165	0			-238	-215			ATGTGGCCGTTGTTGGGGTTGTGA		ATGTGGCCGTTGTTGGGGTTGTGA		MWPLLGL*		MWPLLGL*		GCCGTCGAGG	AAAGGTCGTG	0	S	0	0	0	YML093W	0
9128	4048	an	AN0475.1	54.m06595	AO070328000165	0	-185	-105					ATGCGGAGATCGAAGTCAGTTGGCGGTCGGTCAAGCTCTCCGCCTTGCCAAGAAATTATTTTTTTCTGCCGCCATCGATAA	ATGCGGAGATCGAAGTCAGTTGGCGGTCGGTCAAGCTCTCCGCCTTGCCAAGAAATTATTTTTTTCTGCCGCCATCGATAA			MRRSKSVGGRSSSPPCQEIIFFCRHR*	MRRSKSVGGRSSSPPCQEIIFFCRHR*			ATCGACGGAG	GCAAAATTGT	0	S	0	0	0	YML093W	0
9131	4048	ao	AN0475.1	54.m06595	AO070328000165	0					-248	-207	ATGTCGGAGTCGGAGGAAGGATTTGAAAGTCGGCGGCGCTAA			ATGTCGGAGTCGGAGGAAGGATTTGAAAGTCGGCGGCGCTAA	MSESEEGFESRRR*			MSESEEGFESRRR*	AATAATACCA	GACCAACTTA	0	S	0	0	0	YML093W	0
9132	4048	ao	AN0475.1	54.m06595	AO070328000165	0					-70	-14	ATGATTAAGATCGTGAATATATTCTTTATACGATCTTGCCTCTTAGCGTTTATATAA			ATGATTAAGATCGTGAATATATTCTTTATACGATCTTGCCTCTTAGCGTTTATATAA	MIKIVNIFFIRSCLLAFI*			MIKIVNIFFIRSCLLAFI*	TTTCAGGGCT	AGGTCCCGCA	0	S	0	0	0	YML093W	0
9133	4049	af	AN4862.1	59.m09109	AO070329000148	0			-194	-114			ATGATACCGGAGGATTTTCTCTTTCCCCTCCACATTTGTACTGTGAATAGTATCACCACCTGCAATCTCTCTGACTATTGA		ATGATACCGGAGGATTTTCTCTTTCCCCTCCACATTTGTACTGTGAATAGTATCACCACCTGCAATCTCTCTGACTATTGA		MIPEDFLFPLHICTVNSITTCNLSDY*		MIPEDFLFPLHICTVNSITTCNLSDY*		AATAATTATA	AATATTTAGT	0	AYT	FG00562.1	MG01248.1	NCU03207.1	0	0
9134	4049	ao	AN4862.1	59.m09109	AO070329000148	0					-247	-182	ATGGATCGGATTGGGTTTAGCGTGAGATTTGGGTTCTTCATTGCAGGTGCATATCATCCCGCTTGA			ATGGATCGGATTGGGTTTAGCGTGAGATTTGGGTTCTTCATTGCAGGTGCATATCATCCCGCTTGA	MDRIGFSVRFGFFIAGAYHPA*			MDRIGFSVRFGFFIAGAYHPA*	AAGTTTTGTT	CCTATTGAAG	0	AYT	FG00562.1	MG01248.1	NCU03207.1	0	0
9137	4051	af	AN9112.1	66.m04571	AO070332000162	0			-140	-69			ATGGCGGTGTTTACTTTCTTCCCCTTTTGGAATAATCCCTGCTGCATGGAAAATAACGGTCGTCGACAATAA		ATGGCGGTGTTTACTTTCTTCCCCTTTTGGAATAATCCCTGCTGCATGGAAAATAACGGTCGTCGACAATAA		MAVFTFFPFWNNPCCMENNGRRQ*		MAVFTFFPFWNNPCCMENNGRRQ*		AGCCCCAGCA	TAATCTCTCA	0	Q	0	0	0	0	0
9138	4051	af	AN9112.1	66.m04571	AO070332000162	0			-95	-69			ATGGAAAATAACGGTCGTCGACAATAA		ATGGAAAATAACGGTCGTCGACAATAA		MENNGRRQ*		MENNGRRQ*		TCCCTGCTGC	TAATCTCTCA	0	Q	0	0	0	0	0
9135	4051	an	AN9112.1	66.m04571	AO070332000162	0	-182	-93					ATGAGCGACGCCACAGAACGGGCGGGGCCGGCGTCTTTGGTCTGTCTCGCTTCCCCAACAGTCCACAATGTTTACATTCTTCCCCTTTAG	ATGAGCGACGCCACAGAACGGGCGGGGCCGGCGTCTTTGGTCTGTCTCGCTTCCCCAACAGTCCACAATGTTTACATTCTTCCCCTTTAG			MSDATERAGPASLVCLASPTVHNVYILPL*	MSDATERAGPASLVCLASPTVHNVYILPL*			GGCAACCGAC	GAGTTTTGAC	0	Q	0	0	0	0	0
9136	4051	an	AN9112.1	66.m04571	AO070332000162	0	-115	-44					ATGTTTACATTCTTCCCCTTTAGGAGTTTTGACTTGACTGAACCTCATCCGAGGACATCACCTCGGTTTTAA	ATGTTTACATTCTTCCCCTTTAGGAGTTTTGACTTGACTGAACCTCATCCGAGGACATCACCTCGGTTTTAA			MFTFFPFRSFDLTEPHPRTSPRF*	MFTFFPFRSFDLTEPHPRTSPRF*			ACAGTCCACA	AACTACATTA	0	Q	0	0	0	0	0
9139	4051	ao	AN9112.1	66.m04571	AO070332000162	0					-189	-106	ATGCGACTGCGCCTTTGGTGCATCCGGCCCACCGCGGAAAAGGCGGTGTTTACATTCTTCCCCATTCGGAATCCCTGCAAGTGA			ATGCGACTGCGCCTTTGGTGCATCCGGCCCACCGCGGAAAAGGCGGTGTTTACATTCTTCCCCATTCGGAATCCCTGCAAGTGA	MRLRLWCIRPTAEKAVFTFFPIRNPCK*			MRLRLWCIRPTAEKAVFTFFPIRNPCK*	GGCGACGATC	AAATAACGGC	0	Q	0	0	0	0	0
9142	4052	af	AN4926.1	59.m08828	AO070338000017	0			-131	-15			ATGGAGGAGCTGGTCTCATCCGACCTCGAGATAAGCAGTCATTCAACTTTCCGGACCGAGAGCAATGTCCACAGTCCTCGGACGATACCTCCTCGTGGATCTATAGTACAGGATTGA		ATGGAGGAGCTGGTCTCATCCGACCTCGAGATAAGCAGTCATTCAACTTTCCGGACCGAGAGCAATGTCCACAGTCCTCGGACGATACCTCCTCGTGGATCTATAGTACAGGATTGA		MEELVSSDLEISSHSTFRTESNVHSPRTIPPRGSIVQD*		MEELVSSDLEISSHSTFRTESNVHSPRTIPPRGSIVQD*		TTTCTCTTAC	ATATATACCC	0		0	0	0	0	0
9143	4052	af	AN4926.1	59.m08828	AO070338000017	0			-67	-26			ATGTCCACAGTCCTCGGACGATACCTCCTCGTGGATCTATAG		ATGTCCACAGTCCTCGGACGATACCTCCTCGTGGATCTATAG		MSTVLGRYLLVDL*		MSTVLGRYLLVDL*		ACCGAGAGCA	TACAGGATTG	0		0	0	0	0	0
9140	4052	an	AN4926.1	59.m08828	AO070338000017	0	-183	-148					ATGGTTTCCGACGGTGCACGCCTGCATATGCCATAA	ATGGTTTCCGACGGTGCACGCCTGCATATGCCATAA			MVSDGARLHMP*	MVSDGARLHMP*			TAGCGTTTCA	CTTGTCTGTC	0		0	0	0	0	0
9141	4052	an	AN4926.1	59.m08828	AO070338000017	0	-123	-61					ATGGAGGAGTTGGTTCTGTCGAAGTCAGCAACAGCTACTGTCCACCCCCGGCCGGGGGGGTGA	ATGGAGGAGTTGGTTCTGTCGAAGTCAGCAACAGCTACTGTCCACCCCCGGCCGGGGGGGTGA			MEELVLSKSATATVHPRPGG*	MEELVLSKSATATVHPRPGG*			AACACTTTAC	GCTACACCTC	0		0	0	0	0	0
9144	4052	ao	AN4926.1	59.m08828	AO070338000017	0					-184	-149	ATGCAATTCATGGGCGCCCTCTCGTACATGCTCTGA			ATGCAATTCATGGGCGCCCTCTCGTACATGCTCTGA	MQFMGALSYML*			MQFMGALSYML*	GCCATATTCG	TACCCTTCGA	0		0	0	0	0	0
9145	4052	ao	AN4926.1	59.m08828	AO070338000017	0					-175	-149	ATGGGCGCCCTCTCGTACATGCTCTGA			ATGGGCGCCCTCTCGTACATGCTCTGA	MGALSYML*			MGALSYML*	GATGCAATTC	TACCCTTCGA	0		0	0	0	0	0
9146	4052	ao	AN4926.1	59.m08828	AO070338000017	0					-122	-3	ATGGAGGAGCTGGTCTCCCTCGCTAACAGCAATTACGATCCGCTCCCGGTTGGGGGAGATGTGCATCTTTCCAGGACTCTCCCTTGTCTTGGACCTATAGTCACCATTGGTTACTTTTGA			ATGGAGGAGCTGGTCTCCCTCGCTAACAGCAATTACGATCCGCTCCCGGTTGGGGGAGATGTGCATCTTTCCAGGACTCTCCCTTGTCTTGGACCTATAGTCACCATTGGTTACTTTTGA	MEELVSLANSNYDPLPVGGDVHLSRTLPCLGPIVTIGYF*			MEELVSLANSNYDPLPVGGDVHLSRTLPCLGPIVTIGYF*	CCTATAGTAT	CCATGTCTCC	0		0	0	0	0	0
9147	4052	ao	AN4926.1	59.m08828	AO070338000017	0					-64	-23	ATGTGCATCTTTCCAGGACTCTCCCTTGTCTTGGACCTATAG			ATGTGCATCTTTCCAGGACTCTCCCTTGTCTTGGACCTATAG	MCIFPGLSLVLDL*			MCIFPGLSLVLDL*	GTTGGGGGAG	TCACCATTGG	0		0	0	0	0	0
9148	4055	an	AN4102.1	54.m06742	AO070342000101	0	-106	-83					ATGGGCTGGAGCCTGTGCTTATAA	ATGGGCTGGAGCCTGTGCTTATAA			MGWSLCL*	MGWSLCL*			ATATGTTGAC	CCTCCTTGCT	0	G	0	MG09272.1	0	0	0
9149	4055	ao	AN4102.1	54.m06742	AO070342000101	0					-191	-177	ATGTGTGGTACTTAA			ATGTGTGGTACTTAA	MCGT*			MCGT*	GGAATACATC	CCTTCCCATC	0	G	0	MG09272.1	0	0	0
9150	4055	ao	AN4102.1	54.m06742	AO070342000101	0					-136	-59	ATGCCGGTTCTTATTTATATCACCTTTCTCCCCTCCACTGTTGGTGAATTTCCCTCATTCAACAATCACTCTTTGTGA			ATGCCGGTTCTTATTTATATCACCTTTCTCCCCTCCACTGTTGGTGAATTTCCCTCATTCAACAATCACTCTTTGTGA	MPVLIYITFLPSTVGEFPSFNNHSL*			MPVLIYITFLPSTVGEFPSFNNHSL*	CCTCGTTACC	GCACTGTGTG	0	G	0	MG09272.1	0	0	0
9151	4056	af	AN1934.1	58.m08870	AO070342000199	0			-196	-125			ATGGTCGCATTGGCAAATCACGATGTTGACGTACATCAAGATATAGAAAATCGGCCGCCACCTTCATATTAG		ATGGTCGCATTGGCAAATCACGATGTTGACGTACATCAAGATATAGAAAATCGGCCGCCACCTTCATATTAG		MVALANHDVDVHQDIENRPPPSY*		MVALANHDVDVHQDIENRPPPSY*		TCGCTGGTAT	ACCGTATATG	0		0	0	0	0	0
9152	4056	af	AN1934.1	58.m08870	AO070342000199	0			-174	-151			ATGTTGACGTACATCAAGATATAG		ATGTTGACGTACATCAAGATATAG		MLTYIKI*		MLTYIKI*		GCAAATCACG	AAAATCGGCC	0		0	0	0	0	0
9153	4056	af	AN1934.1	58.m08870	AO070342000199	0			-117	-64			ATGGAACGCCTCCGATCAGCGTCCCCGGTTCGCGTTCACGCGCCTAATCGATAA		ATGGAACGCCTCCGATCAGCGTCCCCGGTTCGCGTTCACGCGCCTAATCGATAA		MERLRSASPVRVHAPNR*		MERLRSASPVRVHAPNR*		TAGACCGTAT	CCAAGTTATG	0		0	0	0	0	0
9154	4056	ao	AN1934.1	58.m08870	AO070342000199	0					-255	-13	ATGGTAATATACTGTGTAGATCAAATAACGAAGATCTGTTTGATTTTTAATGTAAGCCAGGTACTTGAAACTTGGGATACAATCGGTAGATTGATATCCATATCAATTGTGAAACACAAACTACGGATCAATGACCATGACCAGGGTAATTGTTATTACACGTGGTTGTCGCATATCGATAAGAAGTCGCGACACCGCGATTCTCAGCCTTCTACAACATCACATCTCTCAACCGACAAGTAA			ATGGTAATATACTGTGTAGATCAAATAACGAAGATCTGTTTGATTTTTAATGTAAGCCAGGTACTTGAAACTTGGGATACAATCGGTAGATTGATATCCATATCAATTGTGAAACACAAACTACGGATCAATGACCATGACCAGGGTAATTGTTATTACACGTGGTTGTCGCATATCGATAAGAAGTCGCGACACCGCGATTCTCAGCCTTCTACAACATCACATCTCTCAACCGACAAGTAA	MVIYCVDQITKICLIFNVSQVLETWDTIGRLISISIVKHKLRINDHDQGNCYYTWLSHIDKKSRHRDSQPSTTSHLSTDK*			MVIYCVDQITKICLIFNVSQVLETWDTIGRLISISIVKHKLRINDHDQGNCYYTWLSHIDKKSRHRDSQPSTTSHLSTDK*	ACTTCACGCT	ACAGCTCAGT	0		0	0	0	0	0
9158	4058	af	AN7559.1	72.m19579	AO070343000399	0			-108	-16			ATGACAACGGCACAACACGATTTTAGAGGATTACTTCTTTTTTTCAAACCTCATCGGTGTTGTCGGTTCTGTGGAGTGCTCTATCTTTCCTAA		ATGACAACGGCACAACACGATTTTAGAGGATTACTTCTTTTTTTCAAACCTCATCGGTGTTGTCGGTTCTGTGGAGTGCTCTATCTTTCCTAA		MTTAQHDFRGLLLFFKPHRCCRFCGVLYLS*		MTTAQHDFRGLLLFFKPHRCCRFCGVLYLS*		CTCTCTCATC	TTATACATCG	0	K	0	0	0	0	0
9155	4058	an	AN7559.1	72.m19579	AO070343000399	0	-158	-39					ATGAATGTTAAGGTGAAGAAGAAAGCGGACTGGGACTGCGCTCCCTCTTGGCCTCGGCCGCCTTGCCCGACTTCTCTTCCAACACCTCTCACCTCACCATCACGTCTTTCTCATACATGA	ATGAATGTTAAGGTGAAGAAGAAAGCGGACTGGGACTGCGCTCCCTCTTGGCCTCGGCCGCCTTGCCCGACTTCTCTTCCAACACCTCTCACCTCACCATCACGTCTTTCTCATACATGA			MNVKVKKKADWDCAPSWPRPPCPTSLPTPLTSPSRLSHT*	MNVKVKKKADWDCAPSWPRPPCPTSLPTPLTSPSRLSHT*			GTTGGTGGTG	CCCACGATTG	0	K	0	0	0	0	0
9156	4058	an	AN7559.1	72.m19579	AO070343000399	0	-154	-143					ATGTTAAGGTGA	ATGTTAAGGTGA			MLR*	MLR*			GTGGTGATGA	AGAAGAAAGC	0	K	0	0	0	0	0
9159	4063	an	AN4386.1	58.m08970	AO070261000031	0	-239	-192					ATGCGACGGCATCGGCAGCGGCGAGACTCGGACTGGAGGCGAACATAA	ATGCGACGGCATCGGCAGCGGCGAGACTCGGACTGGAGGCGAACATAA			MRRHRQRRDSDWRRT*	MRRHRQRRDSDWRRT*			GTAAATCCAC	TGCCACGATC	0	R	FG09938.1	MG00957.1	NCU04259.1	YLR253W	0
9160	4063	an	AN4386.1	58.m08970	AO070261000031	0	-192	-31					ATGCCACGATCAGCATCGCAACGGCCACGCGGCAATTTTTGTCTCCTCCGCCATCCGCTATCTCTCCTTCCCTTCAGAACTACCTCATCTACACCTCCATCTTTCGCCCAATGGCCTTGGGGTACGGATGAACACTTCACCCGACAGACTTTTCTCCCTTGA	ATGCCACGATCAGCATCGCAACGGCCACGCGGCAATTTTTGTCTCCTCCGCCATCCGCTATCTCTCCTTCCCTTCAGAACTACCTCATCTACACCTCCATCTTTCGCCCAATGGCCTTGGGGTACGGATGAACACTTCACCCGACAGACTTTTCTCCCTTGA			MPRSASQRPRGNFCLLRHPLSLLPFRTTSSTPPSFAQWPWGTDEHFTRQTFLP*	MPRSASQRPRGNFCLLRHPLSLLPFRTTSSTPPSFAQWPWGTDEHFTRQTFLP*			GGCGAACATA	CTCGTGGCTG	0	R	FG09938.1	MG00957.1	NCU04259.1	YLR253W	0
9161	4063	an	AN4386.1	58.m08970	AO070261000031	0	-82	-62					ATGGCCTTGGGGTACGGATGA	ATGGCCTTGGGGTACGGATGA			MALGYG*	MALGYG*			CTTTCGCCCA	ACACTTCACC	0	R	FG09938.1	MG00957.1	NCU04259.1	YLR253W	0
9165	4065	af	AN6520.1	62.m03108	AO070270000018	0			-229	-170			ATGTTAATACACCAGCAGCAAGAGATTCGGAGTTGCTCTAGTGCTGAGAGTGGTAGATGA		ATGTTAATACACCAGCAGCAAGAGATTCGGAGTTGCTCTAGTGCTGAGAGTGGTAGATGA		MLIHQQQEIRSCSSAESGR*		MLIHQQQEIRSCSSAESGR*		ACGATATCAT	GGAAAAACGA	0	HC	FG00926.1	0	NCU03112.1	0	0
9166	4065	af	AN6520.1	62.m03108	AO070270000018	0			-173	-129			ATGAGGAAAAACGAAGACGATCATCGACAAGGGGTTCTTCATTGA		ATGAGGAAAAACGAAGACGATCATCGACAAGGGGTTCTTCATTGA		MRKNEDDHRQGVLH*		MRKNEDDHRQGVLH*		AGAGTGGTAG	TACCCGATTG	0	HC	FG00926.1	0	NCU03112.1	0	0
9163	4065	an	AN6520.1	62.m03108	AO070270000018	0	-249	-49					ATGAGGGAAGTCCGAAATCCTAGGGAAGAAGGGCGACAGGCTAATCTTGCCTTCTGGCTGGCACAAGTAAACGGAGCTCGAGCGCTTGAGGATCGTCATTCGTGCCCAATTCGGACTAGTGCTTCACCCTTGCAAAAAAGACCAGGGGCGGCTATGTGCGGAGTTCCAGAGACCGCGATATCTTCTACTTTGAGATTTTAG	ATGAGGGAAGTCCGAAATCCTAGGGAAGAAGGGCGACAGGCTAATCTTGCCTTCTGGCTGGCACAAGTAAACGGAGCTCGAGCGCTTGAGGATCGTCATTCGTGCCCAATTCGGACTAGTGCTTCACCCTTGCAAAAAAGACCAGGGGCGGCTATGTGCGGAGTTCCAGAGACCGCGATATCTTCTACTTTGAGATTTTAG			MREVRNPREEGRQANLAFWLAQVNGARALEDRHSCPIRTSASPLQKRPGAAMCGVPETAISSTLRF*	MREVRNPREEGRQANLAFWLAQVNGARALEDRHSCPIRTSASPLQKRPGAAMCGVPETAISSTLRF*			AATAACATAA	ACCGTCCCAT	0	HC	FG00926.1	0	NCU03112.1	0	0
9164	4065	an	AN6520.1	62.m03108	AO070270000018	0	-96	-49					ATGTGCGGAGTTCCAGAGACCGCGATATCTTCTACTTTGAGATTTTAG	ATGTGCGGAGTTCCAGAGACCGCGATATCTTCTACTTTGAGATTTTAG			MCGVPETAISSTLRF*	MCGVPETAISSTLRF*			AGGGGCGGCT	ACCGTCCCAT	0	HC	FG00926.1	0	NCU03112.1	0	0
9167	4065	ao	AN6520.1	62.m03108	AO070270000018	0					-212	-129	ATGAAGACAGAAGTAACCGCAAGATATTCTCGTCTTTTGGCTGAAAGAAACAGGGAGAGAAAAAGACCAGCTCCAATGCTGTAG			ATGAAGACAGAAGTAACCGCAAGATATTCTCGTCTTTTGGCTGAAAGAAACAGGGAGAGAAAAAGACCAGCTCCAATGCTGTAG	MKTEVTARYSRLLAERNRERKRPAPML*			MKTEVTARYSRLLAERNRERKRPAPML*	GCCCCTCTGT	AAGAAATGCA	0	HC	FG00926.1	0	NCU03112.1	0	0
9168	4067	an	AN0589.1	69.m15260	AO070280000011	0	-195	-184					ATGTTTCGTTAG	ATGTTTCGTTAG			MFR*	MFR*			CAAAGACAAA	CTCGTCAACA	0	A	0	MG08049.1	NCU04439.1	0	0

9169	4067	an	AN0589.1	69.m15260	AO070280000011	0	-150	-112					ATGAGGCTATCGCGATCCTTATCGGTGCTGACTAAGTAA	ATGAGGCTATCGCGATCCTTATCGGTGCTGACTAAGTAA			MRLSRSLSVLTK*	MRLSRSLSVLTK*			ACTGCGACGC	GTTCCCGCCC	0	A	0	MG08049.1	NCU04439.1	0	0
9170	4067	ao	AN0589.1	69.m15260	AO070280000011	0					-232	-200	ATGCTACTGATAAAAGCTCCGCATGGAGAATAG			ATGCTACTGATAAAAGCTCCGCATGGAGAATAG	MLLIKAPHGE*			MLLIKAPHGE*	ACAGATTCGG	AGATGGTCGC	0	A	0	MG08049.1	NCU04439.1	0	0
9171	4067	ao	AN0589.1	69.m15260	AO070280000011	0					-210	-178	ATGGAGAATAGAGATGGTCGCATGTCTCCATAA			ATGGAGAATAGAGATGGTCGCATGTCTCCATAA	MENRDGRMSP*			MENRDGRMSP*	AAAGCTCCGC	CCATCGATAA	0	A	0	MG08049.1	NCU04439.1	0	0
9172	4067	ao	AN0589.1	69.m15260	AO070280000011	0					-197	-168	ATGGTCGCATGTCTCCATAACCATCGATAA			ATGGTCGCATGTCTCCATAACCATCGATAA	MVACLHNHR*			MVACLHNHR*	GAGAATAGAG	GCCTTCATCT	0	A	0	MG08049.1	NCU04439.1	0	0
9173	4067	ao	AN0589.1	69.m15260	AO070280000011	0					-189	-178	ATGTCTCCATAA			ATGTCTCCATAA	MSP*			MSP*	AGATGGTCGC	CCATCGATAA	0	A	0	MG08049.1	NCU04439.1	0	0
9176	4068	af	AN2525.1	59.m08455	AO070286000098	0			-132	-16			ATGACTCAAATCGGGCTCATCTCCGATGAAGAGCTCCGCCTTCCGTATACACCATCTTTTTCCTGCCTCATGAGAATTCACGTCCTTCCTTTTTCGTTATCGAACCAATACATCTAG		ATGACTCAAATCGGGCTCATCTCCGATGAAGAGCTCCGCCTTCCGTATACACCATCTTTTTCCTGCCTCATGAGAATTCACGTCCTTCCTTTTTCGTTATCGAACCAATACATCTAG		MTQIGLISDEELRLPYTPSFSCLMRIHVLPFSLSNQYI*		MTQIGLISDEELRLPYTPSFSCLMRIHVLPFSLSNQYI*		TCCGTAGCCG	AGCCCCAAAT	0	TE	FG10119.1	MG09501.1	0	0	0
9177	4068	af	AN2525.1	59.m08455	AO070286000098	0			-107	-60			ATGAAGAGCTCCGCCTTCCGTATACACCATCTTTTTCCTGCCTCATGA		ATGAAGAGCTCCGCCTTCCGTATACACCATCTTTTTCCTGCCTCATGA		MKSSAFRIHHLFPAS*		MKSSAFRIHHLFPAS*		CTCATCTCCG	GAATTCACGT	0	TE	FG10119.1	MG09501.1	0	0	0
9178	4068	af	AN2525.1	59.m08455	AO070286000098	0			-63	-16			ATGAGAATTCACGTCCTTCCTTTTTCGTTATCGAACCAATACATCTAG		ATGAGAATTCACGTCCTTCCTTTTTCGTTATCGAACCAATACATCTAG		MRIHVLPFSLSNQYI*		MRIHVLPFSLSNQYI*		TTCCTGCCTC	AGCCCCAAAT	0	TE	FG10119.1	MG09501.1	0	0	0
9174	4068	an	AN2525.1	59.m08455	AO070286000098	0	-158	-78					ATGACTCACATATTCCGACTTCGCAATATTCCGCCGGGATGGCTCGCGACTCCAAATAGATCACTCTCCAACTCCGCATAA	ATGACTCACATATTCCGACTTCGCAATATTCCGCCGGGATGGCTCGCGACTCCAAATAGATCACTCTCCAACTCCGCATAA			MTHIFRLRNIPPGWLATPNRSLSNSA*	MTHIFRLRNIPPGWLATPNRSLSNSA*			CGAAGCGCCC	CCCCACCAGG	0	TE	FG10119.1	MG09501.1	0	0	0
9175	4068	an	AN2525.1	59.m08455	AO070286000098	0	-120	-100					ATGGCTCGCGACTCCAAATAG	ATGGCTCGCGACTCCAAATAG			MARDSK*	MARDSK*			TTCCGCCGGG	ATCACTCTCC	0	TE	FG10119.1	MG09501.1	0	0	0
9189	4072	af	AN2312.1	71.m15515	AO070323000042	0			-289	-263			ATGTCCCACCAGAGATCCGAAGCCTGA		ATGTCCCACCAGAGATCCGAAGCCTGA		MSHQRSEA*		MSHQRSEA*		CACCAGGCTC	AAATTATGGC	0	R	0	0	0	0	0
9190	4072	af	AN2312.1	71.m15515	AO070323000042	0			-257	-231			ATGGCAGTGTCCCTCAAAATCAAGTGA		ATGGCAGTGTCCCTCAAAATCAAGTGA		MAVSLKIK*		MAVSLKIK*		CCTGAAAATT	CATGGACCGA	0	R	0	0	0	0	0
9192	4074	ao	AN6578.1	62.m03158	AO070326000025	0					-152	-105	ATGCTATCCTCCTTTCTGCGGGTTGGGAGTGACTACTTTGTTGAATAA			ATGCTATCCTCCTTTCTGCGGGTTGGGAGTGACTACTTTGTTGAATAA	MLSSFLRVGSDYFVE*			MLSSFLRVGSDYFVE*	GGTCTTGTGT	CCATTTAGCC	0	TG	0	0	0	0	0
9194	4076	ao	AN1168.1	70.m15052	AO070331000162	0					-247	-230	ATGAGGACCTGCGATTGA			ATGAGGACCTGCGATTGA	MRTCD*			MRTCD*	CGTTACGCTG	TTGGGTTTTA	0	PT	FG01364.1	0	0	YGR217W	YGR217W
9197	4078	af	AN8717.1	66.m04554	AO070335000284	0			-211	-194			ATGTGTGGTGTGTGGTAG		ATGTGTGGTGTGTGGTAG		MCGVW*		MCGVW*		TGATGGACTA	ATGGACAGTA	0	BD	0	0	0	0	0
9198	4078	af	AN8717.1	66.m04554	AO070335000284	0			-193	-92			ATGGACAGTAGTACAGTAAAACCTCGTTATAACGAGTCTCGATATAACGAGAACCTCGATATAACGAGCGCAACCCCTTGCCTCAATTATTTTCCCATGTAA		ATGGACAGTAGTACAGTAAAACCTCGTTATAACGAGTCTCGATATAACGAGAACCTCGATATAACGAGCGCAACCCCTTGCCTCAATTATTTTCCCATGTAA		MDSSTVKPRYNESRYNENLDITSATPCLNYFPM*		MDSSTVKPRYNESRYNENLDITSATPCLNYFPM*		TGTGTGGTAG	ATAACGAGAT	0	BD	0	0	0	0	0
9195	4078	an	AN8717.1	66.m04554	AO070335000284	0	-249	-217					ATGAGTATTTTGAGTGTGGTTGTGGATCGATAG	ATGAGTATTTTGAGTGTGGTTGTGGATCGATAG			MSILSVVVDR*	MSILSVVVDR*			TTGCTCCCGC	AAATTTGCGG	0	BD	0	0	0	0	0
9196	4078	an	AN8717.1	66.m04554	AO070335000284	0	-123	-40					ATGAATTCCATCCCATATAAATTTACCTCGCTTTACTATGTAACCCCGATCCCCGATATATCGACAAGCATATCGTCTATTTGA	ATGAATTCCATCCCATATAAATTTACCTCGCTTTACTATGTAACCCCGATCCCCGATATATCGACAAGCATATCGTCTATTTGA			MNSIPYKFTSLYYVTPIPDISTSISSI*	MNSIPYKFTSLYYVTPIPDISTSISSI*			TCATCTCGGG	AAAGCTCGTC	0	BD	0	0	0	0	0
9199	4078	ao	AN8717.1	66.m04554	AO070335000284	0					-164	-138	ATGTCTGTTATAAGCATATTGGTCTGA			ATGTCTGTTATAAGCATATTGGTCTGA	MSVISILV*			MSVISILV*	TATAAGCAAC	TGGTAAAGTT	0	BD	0	0	0	0	0
9200	4078	ao	AN8717.1	66.m04554	AO070335000284	0					-138	-112	ATGGTAAAGTTGGCTCCGTGTCCTTAA			ATGGTAAAGTTGGCTCCGTGTCCTTAA	MVKLAPCP*			MVKLAPCP*	TATTGGTCTG	AAATTTTATT	0	BD	0	0	0	0	0
9201	4079	af	AN4901.1	59.m08801	AO070338000047	0			-197	-186			ATGTGGAGTTGA		ATGTGGAGTTGA		MWS*		MWS*		CGTCCGTCCC	ATCAATCTGC	0		0	0	0	0	0
9203	4079	ao	AN4901.1	59.m08801	AO070338000047	0					-196	-20	ATGGTAGAGAATCTCTTACGCCAGGTAATTAGGATTGGAGTAGATCATTACTGTTTGGGATCTTCTCCGACACCATTGCATCACGGGGTTTGCACGTGGTCGGTGCCTGCATACCTCTCACATCCCCTCTTTTGCTTCTGTGTTATTTTCTTTCTTTCGCTCACCTATCACTCGTGA			ATGGTAGAGAATCTCTTACGCCAGGTAATTAGGATTGGAGTAGATCATTACTGTTTGGGATCTTCTCCGACACCATTGCATCACGGGGTTTGCACGTGGTCGGTGCCTGCATACCTCTCACATCCCCTCTTTTGCTTCTGTGTTATTTTCTTTCTTTCGCTCACCTATCACTCGTGA	MVENLLRQVIRIGVDHYCLGSSPTPLHHGVCTWSVPAYLSHPLFCFCVIFFLSLTYHS*			MVENLLRQVIRIGVDHYCLGSSPTPLHHGVCTWSVPAYLSHPLFCFCVIFFLSLTYHS*	TAAAGTATTC	TCAATCCGAC	0		0	0	0	0	0
9206	4082	af	AN6085.1	72.m19075	AO070340000136	0			-249	-43			ATGAAAAATAAGTATAGAGAACTGAGTATGGAGTACCAAGTGGATCAAATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		ATGAAAAATAAGTATAGAGAACTGAGTATGGAGTACCAAGTGGATCAAATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		MKNKYRELSMEYQVDQMNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		MKNKYRELSMEYQVDQMNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		ACTTTGTTTC	TATTTTCTTT	0	A	0	0	0	YKL078W	0
9207	4082	af	AN6085.1	72.m19075	AO070340000136	0			-222	-43			ATGGAGTACCAAGTGGATCAAATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		ATGGAGTACCAAGTGGATCAAATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		MEYQVDQMNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		MEYQVDQMNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		AGAACTGAGT	TATTTTCTTT	0	A	0	0	0	YKL078W	0
9208	4082	af	AN6085.1	72.m19075	AO070340000136	0			-201	-43			ATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		ATGAACTGGTATACGCCAGGTAGCTGGCTTATCGATAAGGCTCTCCCGCAGAAAAATTTCGGGAACTCCACCGATCACCTCCATGCACGGGACTTGATAATCATTAGACTGCGATTGTTGTGCTTGTTCTCAATAGACAGGTACTCTGTTAACTATTAA		MNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		MNWYTPGSWLIDKALPQKNFGNSTDHLHARDLIIIRLRLLCLFSIDRYSVNY*		AGTGGATCAA	TATTTTCTTT	0	A	0	0	0	YKL078W	0
9209	4082	af	AN6085.1	72.m19075	AO070340000136	0			-119	-105			ATGCACGGGACTTGA		ATGCACGGGACTTGA		MHGT*		MHGT*		GATCACCTCC	TAATCATTAG	0	A	0	0	0	YKL078W	0
9204	4082	an	AN6085.1	72.m19075	AO070340000136	0	-174	-31					ATGCCAAGACCAGTTTATGATAAGATAACCTTCCACCCAGAATTTTTCTGGGGATCAGGATCCGAAATCGTCAAAGTCAAAAAGATAACAGGCAAGGAGACAACTGCTCGAGCAATAACTCACAGACTCATCTTAGAGATATAG	ATGCCAAGACCAGTTTATGATAAGATAACCTTCCACCCAGAATTTTTCTGGGGATCAGGATCCGAAATCGTCAAAGTCAAAAAGATAACAGGCAAGGAGACAACTGCTCGAGCAATAACTCACAGACTCATCTTAGAGATATAG			MPRPVYDKITFHPEFFWGSGSEIVKVKKITGKETTARAITHRLILEI*	MPRPVYDKITFHPEFFWGSGSEIVKVKKITGKETTARAITHRLILEI*			CTGGGGCGGG	CAGATACAAC	0	A	0	0	0	YKL078W	0
9205	4082	an	AN6085.1	72.m19075	AO070340000136	0	-158	-147					ATGATAAGATAA	ATGATAAGATAA			MIR*	MIR*			AGACCAGTTT	CCTTCCACCC	0	A	0	0	0	YKL078W	0
9210	4082	ao	AN6085.1	72.m19075	AO070340000136	0					-229	-167	ATGTATAGTCGAACTGTTAAATCAGTCTCCGCGCCAAGCGTCTTATCGATAAGCTTCACTTAA			ATGTATAGTCGAACTGTTAAATCAGTCTCCGCGCCAAGCGTCTTATCGATAAGCTTCACTTAA	MYSRTVKSVSAPSVLSISFT*			MYSRTVKSVSAPSVLSISFT*	CGACTGCAGT	AAAATTTCGG	0	A	0	0	0	YKL078W	0
9211	4082	ao	AN6085.1	72.m19075	AO070340000136	0					-111	-97	ATGATGAACACCTAA			ATGATGAACACCTAA	MMNT*			MMNT*	GCGATACGAC	TTAGACTAAC	0	A	0	0	0	YKL078W	0
9212	4082	ao	AN6085.1	72.m19075	AO070340000136	0					-108	-97	ATGAACACCTAA			ATGAACACCTAA	MNT*			MNT*	ATACGACATG	TTAGACTAAC	0	A	0	0	0	YKL078W	0
9216	4083	af	AN5732.1	54.m06851	AO070341000028	0			-282	-262			ATGTGTCAGCCCTTAGTTTGA		ATGTGTCAGCCCTTAGTTTGA		MCQPLV*		MCQPLV*		AATCTGACAG	GGTCGCAAAA	0	H	FG01642.1	0	NCU05421.1	0	0
9217	4083	af	AN5732.1	54.m06851	AO070341000028	0			-248	-123			ATGAAGTGGGACTTTTTAACAACAGTCATCGATGTTGCTTATCTGGGTTTAGTGCGCCGGCGATCGGAGATATCTTTCATCAACAAGATCTTACATTACAGTACCCAGCATCTATTTTTCACCTGA		ATGAAGTGGGACTTTTTAACAACAGTCATCGATGTTGCTTATCTGGGTTTAGTGCGCCGGCGATCGGAGATATCTTTCATCAACAAGATCTTACATTACAGTACCCAGCATCTATTTTTCACCTGA		MKWDFLTTVIDVAYLGLVRRRSEISFINKILHYSTQHLFFT*		MKWDFLTTVIDVAYLGLVRRRSEISFINKILHYSTQHLFFT*		CGCAAAAGAG	GGCTCGGAGA	0	H	FG01642.1	0	NCU05421.1	0	0
9218	4083	af	AN5732.1	54.m06851	AO070341000028	0			-217	-197			ATGTTGCTTATCTGGGTTTAG		ATGTTGCTTATCTGGGTTTAG		MLLIWV*		MLLIWV*		ACAGTCATCG	TGCGCCGGCG	0	H	FG01642.1	0	NCU05421.1	0	0
9213	4083	an	AN5732.1	54.m06851	AO070341000028	0	-190	-47					ATGATGCTCAAGAGTGACTCGAGATCGGGAATATTTTCGGTGACTACTGATACTCGTTTCGGCTTAGCGCCCGCGATCGGAGCTCTGCATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGATAAGAAAATCAAGATAA	ATGATGCTCAAGAGTGACTCGAGATCGGGAATATTTTCGGTGACTACTGATACTCGTTTCGGCTTAGCGCCCGCGATCGGAGCTCTGCATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGATAAGAAAATCAAGATAA			MMLKSDSRSGIFSVTTDTRFGLAPAIGALHGYRSFQADGGHVIRKSR*	MMLKSDSRSGIFSVTTDTRFGLAPAIGALHGYRSFQADGGHVIRKSR*			GGAACAACTT	TAATTGACAG	0	H	FG01642.1	0	NCU05421.1	0	0
9214	4083	an	AN5732.1	54.m06851	AO070341000028	0	-187	-47					ATGCTCAAGAGTGACTCGAGATCGGGAATATTTTCGGTGACTACTGATACTCGTTTCGGCTTAGCGCCCGCGATCGGAGCTCTGCATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGATAAGAAAATCAAGATAA	ATGCTCAAGAGTGACTCGAGATCGGGAATATTTTCGGTGACTACTGATACTCGTTTCGGCTTAGCGCCCGCGATCGGAGCTCTGCATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGATAAGAAAATCAAGATAA			MLKSDSRSGIFSVTTDTRFGLAPAIGALHGYRSFQADGGHVIRKSR*	MLKSDSRSGIFSVTTDTRFGLAPAIGALHGYRSFQADGGHVIRKSR*			ACAACTTATG	TAATTGACAG	0	H	FG01642.1	0	NCU05421.1	0	0
9215	4083	an	AN5732.1	54.m06851	AO070341000028	0	-102	-64					ATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGA	ATGGATACCGGAGCTTTCAGGCTGACGGCGGACATGTGA			MDTGAFRLTADM*	MDTGAFRLTADM*			GGAGCTCTGC	TAAGAAAATC	0	H	FG01642.1	0	NCU05421.1	0	0
9219	4083	ao	AN5732.1	54.m06851	AO070341000028	0					-201	-184	ATGATGAAAATAAGGTGA			ATGATGAAAATAAGGTGA	MMKIR*			MMKIR*	CAACGATTGC	GAAATATGGC	0	H	FG01642.1	0	NCU05421.1	0	0
9220	4083	ao	AN5732.1	54.m06851	AO070341000028	0					-198	-184	ATGAAAATAAGGTGA			ATGAAAATAAGGTGA	MKIR*			MKIR*	CGATTGCATG	GAAATATGGC	0	H	FG01642.1	0	NCU05421.1	0	0
9221	4083	ao	AN5732.1	54.m06851	AO070341000028	0					-178	-161	ATGGCATCTTTTCACTGA			ATGGCATCTTTTCACTGA	MASFH*			MASFH*	GGTGAGAAAT	CCCGATCTGG	0	H	FG01642.1	0	NCU05421.1	0	0
9222	4083	ao	AN5732.1	54.m06851	AO070341000028	0					-108	-94	ATGATGGGGCGGTGA			ATGATGGGGCGGTGA	MMGR*			MMGR*	TGAGTCACCA	ACGGACACTG	0	H	FG01642.1	0	NCU05421.1	0	0
9223	4083	ao	AN5732.1	54.m06851	AO070341000028	0					-105	-94	ATGGGGCGGTGA			ATGGGGCGGTGA	MGR*			MGR*	GTCACCAATG	ACGGACACTG	0	H	FG01642.1	0	NCU05421.1	0	0
9232	4086	af	AN7781.1	57.m05368	AO070343000355	0			-221	-126			ATGCTTAAGGAGATGCAAGCTGTTATCAGGGCATATACCGAACGACTAGAAAGCTCTACTAACTTTCCTACCATGGTAAAGATACACAGTTGCTAA		ATGCTTAAGGAGATGCAAGCTGTTATCAGGGCATATACCGAACGACTAGAAAGCTCTACTAACTTTCCTACCATGGTAAAGATACACAGTTGCTAA		MLKEMQAVIRAYTERLESSTNFPTMVKIHSC*		MLKEMQAVIRAYTERLESSTNFPTMVKIHSC*		ATATCCTGCC	CTAGATGCAA	0		0	0	0	0	0
9233	4086	af	AN7781.1	57.m05368	AO070343000355	0			-209	-126			ATGCAAGCTGTTATCAGGGCATATACCGAACGACTAGAAAGCTCTACTAACTTTCCTACCATGGTAAAGATACACAGTTGCTAA		ATGCAAGCTGTTATCAGGGCATATACCGAACGACTAGAAAGCTCTACTAACTTTCCTACCATGGTAAAGATACACAGTTGCTAA		MQAVIRAYTERLESSTNFPTMVKIHSC*		MQAVIRAYTERLESSTNFPTMVKIHSC*		GCTTAAGGAG	CTAGATGCAA	0		0	0	0	0	0
9234	4086	af	AN7781.1	57.m05368	AO070343000355	0			-149	-126			ATGGTAAAGATACACAGTTGCTAA		ATGGTAAAGATACACAGTTGCTAA		MVKIHSC*		MVKIHSC*		CTTTCCTACC	CTAGATGCAA	0		0	0	0	0	0
9235	4086	af	AN7781.1	57.m05368	AO070343000355	0			-69	-28			ATGCTGGGGCAGGTTTGTCTCTCAAATTGTATTGTCAGTTGA		ATGCTGGGGCAGGTTTGTCTCTCAAATTGTATTGTCAGTTGA		MLGQVCLSNCIVS*		MLGQVCLSNCIVS*		ACTTTGAGTA	AAGCTGGTAC	0		0	0	0	0	0
9224	4086	an	AN7781.1	57.m05368	AO070343000355	0	-239	-180					ATGACGGATAAAACGCCATTCATGTTCACAGCGCGCCAAGATCCCGCAGGAGAAGGCTGA	ATGACGGATAAAACGCCATTCATGTTCACAGCGCGCCAAGATCCCGCAGGAGAAGGCTGA			MTDKTPFMFTARQDPAGEG*	MTDKTPFMFTARQDPAGEG*			TGCAACCTGC	AGCTCAAGCT	0		0	0	0	0	0
9225	4086	an	AN7781.1	57.m05368	AO070343000355	0	-218	-180					ATGTTCACAGCGCGCCAAGATCCCGCAGGAGAAGGCTGA	ATGTTCACAGCGCGCCAAGATCCCGCAGGAGAAGGCTGA			MFTARQDPAGEG*	MFTARQDPAGEG*			AACGCCATTC	AGCTCAAGCT	0		0	0	0	0	0
9226	4086	an	AN7781.1	57.m05368	AO070343000355	0	-161	-102					ATGTGGTATGATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAA	ATGTGGTATGATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAA			MWYDGVEKDGGFLGGAGKT*	MWYDGVEKDGGFLGGAGKT*			CTCCGGTTGA	ATAGAGGCAT	0		0	0	0	0	0

9227	4086	an	AN7781.1	57.m05368	AO070343000355	0	-154	-98					ATGATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG	ATGATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG			MMGLRRMAVFWGGQERHK*	MMGLRRMAVFWGGQERHK*			TGAATGTGGT	AGGCATATCT	0		0	0	0	0	0
9228	4086	an	AN7781.1	57.m05368	AO070343000355	0	-151	-98					ATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG	ATGGGGTTGAGAAGGATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG			MGLRRMAVFWGGQERHK*	MGLRRMAVFWGGQERHK*			ATGTGGTATG	AGGCATATCT	0		0	0	0	0	0
9229	4086	an	AN7781.1	57.m05368	AO070343000355	0	-136	-98					ATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG	ATGGCGGTTTTCTGGGGGGGGCAGGAAAGACATAAATAG			MAVFWGGQERHK*	MAVFWGGQERHK*			GTTGAGAAGG	AGGCATATCT	0		0	0	0	0	0
9230	4086	an	AN7781.1	57.m05368	AO070343000355	0	-61	-23					ATGAGTTCGAATGACCAGATCCCATTTCTGCCCAATTGA	ATGAGTTCGAATGACCAGATCCCATTTCTGCCCAATTGA			MSSNDQIPFLPN*	MSSNDQIPFLPN*			AGTCTTGTGA	GCTAGACCCT	0		0	0	0	0	0
9236	4086	ao	AN7781.1	57.m05368	AO070343000355	0					-184	-131	ATGCGGAGAGATGTGGGTCTTGACCACGCAACGACGAGAAACCACTGCCTTTGA			ATGCGGAGAGATGTGGGTCTTGACCACGCAACGACGAGAAACCACTGCCTTTGA	MRRDVGLDHATTRNHCL*			MRRDVGLDHATTRNHCL*	TCAGTTCCCT	AGACCTCTCA	0		0	0	0	0	0
9237	4086	ao	AN7781.1	57.m05368	AO070343000355	0					-174	-112	ATGTGGGTCTTGACCACGCAACGACGAGAAACCACTGCCTTTGAAGACCTCTCATTTGGGTAA			ATGTGGGTCTTGACCACGCAACGACGAGAAACCACTGCCTTTGAAGACCTCTCATTTGGGTAA	MWVLTTQRRETTAFEDLSFG*			MWVLTTQRRETTAFEDLSFG*	ATGCGGAGAG	TTCTCCGGCC	0		0	0	0	0	0
9238	4086	ao	AN7781.1	57.m05368	AO070343000355	0					-100	-83	ATGTCTTGGATAGCATGA			ATGTCTTGGATAGCATGA	MSWIA*			MSWIA*	TCTCCGGCCA	GCTGGTCGAA	0		0	0	0	0	0
9239	4086	ao	AN7781.1	57.m05368	AO070343000355	0					-86	-66	ATGAGCTGGTCGAATATATAA			ATGAGCTGGTCGAATATATAA	MSWSNI*			MSWSNI*	CTTGGATAGC	ATATCCGACT	0		0	0	0	0	0
9244	4089	af	AN4216.1	54.m06773	AO070231000008	0			-237	-163			ATGACCTTGTTTAGAGGCTGCGCATGTATCTATGAATTGTCTTTCTGTACGAGTAATTTCTTTGATAGGAATTGA		ATGACCTTGTTTAGAGGCTGCGCATGTATCTATGAATTGTCTTTCTGTACGAGTAATTTCTTTGATAGGAATTGA		MTLFRGCACIYELSFCTSNFFDRN*		MTLFRGCACIYELSFCTSNFFDRN*		GGTAAACTGT	AAGATCGATA	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9245	4089	af	AN4216.1	54.m06773	AO070231000008	0			-214	-203			ATGTATCTATGA		ATGTATCTATGA		MYL*		MYL*		GAGGCTGCGC	ATTGTCTTTC	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9246	4089	af	AN4216.1	54.m06773	AO070231000008	0			-206	-120			ATGAATTGTCTTTCTGTACGAGTAATTTCTTTGATAGGAATTGAAAGATCGATAGTTCTATATGAGTTGTATGCGCATTTCAATTGA		ATGAATTGTCTTTCTGTACGAGTAATTTCTTTGATAGGAATTGAAAGATCGATAGTTCTATATGAGTTGTATGCGCATTTCAATTGA		MNCLSVRVISLIGIERSIVLYELYAHFN*		MNCLSVRVISLIGIERSIVLYELYAHFN*		GCATGTATCT	AGAGCTGTCT	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9247	4089	af	AN4216.1	54.m06773	AO070231000008	0			-145	-44			ATGAGTTGTATGCGCATTTCAATTGAAGAGCTGTCTTTCAGGGCAGTGAAGATCACGTGTATCCTTGCACTGATCTCCGCCGTCACCCCATGGCCTCGATGA		ATGAGTTGTATGCGCATTTCAATTGAAGAGCTGTCTTTCAGGGCAGTGAAGATCACGTGTATCCTTGCACTGATCTCCGCCGTCACCCCATGGCCTCGATGA		MSCMRISIEELSFRAVKITCILALISAVTPWPR*		MSCMRISIEELSFRAVKITCILALISAVTPWPR*		ATAGTTCTAT	TGCCATTCGT	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9248	4089	af	AN4216.1	54.m06773	AO070231000008	0			-136	-44			ATGCGCATTTCAATTGAAGAGCTGTCTTTCAGGGCAGTGAAGATCACGTGTATCCTTGCACTGATCTCCGCCGTCACCCCATGGCCTCGATGA		ATGCGCATTTCAATTGAAGAGCTGTCTTTCAGGGCAGTGAAGATCACGTGTATCCTTGCACTGATCTCCGCCGTCACCCCATGGCCTCGATGA		MRISIEELSFRAVKITCILALISAVTPWPR*		MRISIEELSFRAVKITCILALISAVTPWPR*		TATGAGTTGT	TGCCATTCGT	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9240	4089	an	AN4216.1	54.m06773	AO070231000008	0	-182	-162					ATGGCCATGGGTCTCTTTTAA	ATGGCCATGGGTCTCTTTTAA			MAMGLF*	MAMGLF*			CCCTCTGACC	TGACTTTGGC	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9241	4089	an	AN4216.1	54.m06773	AO070231000008	0	-176	-162					ATGGGTCTCTTTTAA	ATGGGTCTCTTTTAA			MGLF*	MGLF*			GACCATGGCC	TGACTTTGGC	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9242	4089	an	AN4216.1	54.m06773	AO070231000008	0	-162	-100					ATGACTTTGGCAGATAACAGCCACAGCCCATTGGTAACAGAAAAGCAATGGTCTATGCTTTAA	ATGACTTTGGCAGATAACAGCCACAGCCCATTGGTAACAGAAAAGCAATGGTCTATGCTTTAA			MTLADNSHSPLVTEKQWSML*	MTLADNSHSPLVTEKQWSML*			GTCTCTTTTA	AAGTAGGAGT	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9243	4089	an	AN4216.1	54.m06773	AO070231000008	0	-115	-83					ATGGTCTATGCTTTAAAAGTAGGAGTCACGTGA	ATGGTCTATGCTTTAAAAGTAGGAGTCACGTGA			MVYALKVGVT*	MVYALKVGVT*			CAGAAAAGCA	ACTGTCAGAT	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9249	4089	ao	AN4216.1	54.m06773	AO070231000008	0					-295	-227	ATGCCAATCACCATTCCATACTACGAACCATCTCAACTCACACCCCAACAACTATATCATAGTCACTAA			ATGCCAATCACCATTCCATACTACGAACCATCTCAACTCACACCCCAACAACTATATCATAGTCACTAA	MPITIPYYEPSQLTPQQLYHSH*			MPITIPYYEPSQLTPQQLYHSH*	TTTCGCTCCA	TACCCCCAAA	0		FG02096.1	MG05446.1	NCU01218.1	0	0
9252	4090	af	AN1343.1	70.m14890	AO070247000021	0			-126	-91			ATGTCATCCTCTTGTTGCCATGTCGCGAAGCCATGA		ATGTCATCCTCTTGTTGCCATGTCGCGAAGCCATGA		MSSSCCHVAKP*		MSSSCCHVAKP*		TACAAGCCGT	GGTGAAGGGG	0	K	0	0	0	0	0
9253	4090	af	AN1343.1	70.m14890	AO070247000021	0			-107	-42			ATGTCGCGAAGCCATGAGGTGAAGGGGAATCAAAAGGTCGCTGAGTTTGCCGTCGGTATCCTGTAG		ATGTCGCGAAGCCATGAGGTGAAGGGGAATCAAAAGGTCGCTGAGTTTGCCGTCGGTATCCTGTAG		MSRSHEVKGNQKVAEFAVGIL*		MSRSHEVKGNQKVAEFAVGIL*		TCTTGTTGCC	ATAACTGCGC	0	K	0	0	0	0	0
9250	4090	an	AN1343.1	70.m14890	AO070247000021	0	-127	-71					ATGGTTGCCTTGACCTGTTCGCTGTACTTTTCGCTGCCCCTCGGAATGTTCCGGTGA	ATGGTTGCCTTGACCTGTTCGCTGTACTTTTCGCTGCCCCTCGGAATGTTCCGGTGA			MVALTCSLYFSLPLGMFR*	MVALTCSLYFSLPLGMFR*			CCTGTCCCTC	TCGCTGACTT	0	K	0	0	0	0	0
9251	4090	an	AN1343.1	70.m14890	AO070247000021	0	-82	-71					ATGTTCCGGTGA	ATGTTCCGGTGA			MFR*	MFR*			GCCCCTCGGA	TCGCTGACTT	0	K	0	0	0	0	0
9254	4090	ao	AN1343.1	70.m14890	AO070247000021	0					-114	-61	ATGCTGCCTTACCTCGATCCATGTCCGATTGTTCCTACACTACACGAGTGCTAA			ATGCTGCCTTACCTCGATCCATGTCCGATTGTTCCTACACTACACGAGTGCTAA	MLPYLDPCPIVPTLHEC*			MLPYLDPCPIVPTLHEC*	TGCAATCTCA	CTAGCACGTT	0	K	0	0	0	0	0
9255	4090	ao	AN1343.1	70.m14890	AO070247000021	0					-94	-38	ATGTCCGATTGTTCCTACACTACACGAGTGCTAACTAGCACGTTCTCCCTTAGATAG			ATGTCCGATTGTTCCTACACTACACGAGTGCTAACTAGCACGTTCTCCCTTAGATAG	MSDCSYTTRVLTSTFSLR*			MSDCSYTTRVLTSTFSLR*	ACCTCGATCC	CTGCGCCAGC	0	K	0	0	0	0	0
9261	4095	af	AN8798.1	71.m15605	AO070276000062	0			-85	-50			ATGGAACGCTTGCTTCTACGTCTATCCTACTCCTAA		ATGGAACGCTTGCTTCTACGTCTATCCTACTCCTAA		MERLLLRLSYS*		MERLLLRLSYS*		AAATCAGATC	TTCCGTCCCC	0	R	0	MG04080.1	0	0	0
9256	4095	an	AN8798.1	71.m15605	AO070276000062	0	-213	-187					ATGATGCTCCAGGGGAAGAGTCATTGA	ATGATGCTCCAGGGGAAGAGTCATTGA			MMLQGKSH*	MMLQGKSH*			ATAGTCGCCC	CACAGCATCC	0	R	0	MG04080.1	0	0	0
9257	4095	an	AN8798.1	71.m15605	AO070276000062	0	-210	-187					ATGCTCCAGGGGAAGAGTCATTGA	ATGCTCCAGGGGAAGAGTCATTGA			MLQGKSH*	MLQGKSH*			GTCGCCCATG	CACAGCATCC	0	R	0	MG04080.1	0	0	0
9258	4095	an	AN8798.1	71.m15605	AO070276000062	0	-174	-112					ATGTTTATGAATTCAGTCTTTTTCATTGAAGCGACCTTTTTAATGTCACCATTTTACTTTTAG	ATGTTTATGAATTCAGTCTTTTTCATTGAAGCGACCTTTTTAATGTCACCATTTTACTTTTAG			MFMNSVFFIEATFLMSPFYF*	MFMNSVFFIEATFLMSPFYF*			CAGCATCCCA	ACTGCACATA	0	R	0	MG04080.1	0	0	0
9259	4095	an	AN8798.1	71.m15605	AO070276000062	0	-168	-112					ATGAATTCAGTCTTTTTCATTGAAGCGACCTTTTTAATGTCACCATTTTACTTTTAG	ATGAATTCAGTCTTTTTCATTGAAGCGACCTTTTTAATGTCACCATTTTACTTTTAG			MNSVFFIEATFLMSPFYF*	MNSVFFIEATFLMSPFYF*			CCCAATGTTT	ACTGCACATA	0	R	0	MG04080.1	0	0	0
9260	4095	an	AN8798.1	71.m15605	AO070276000062	0	-132	-112					ATGTCACCATTTTACTTTTAG	ATGTCACCATTTTACTTTTAG			MSPFYF*	MSPFYF*			GACCTTTTTA	ACTGCACATA	0	R	0	MG04080.1	0	0	0
9262	4095	ao	AN8798.1	71.m15605	AO070276000062	0					-213	-181	ATGCAGTGTGCCAAGTGGTCAGTTCTTGATTAA			ATGCAGTGTGCCAAGTGGTCAGTTCTTGATTAA	MQCAKWSVLD*			MQCAKWSVLD*	ATTTACTGTA	TGCTTGCTTT	0	R	0	MG04080.1	0	0	0
9263	4095	ao	AN8798.1	71.m15605	AO070276000062	0					-181	-167	ATGCTTGCTTTGTGA			ATGCTTGCTTTGTGA	MLAL*			MLAL*	TTCTTGATTA	ATATTTCCGG	0	R	0	MG04080.1	0	0	0
9264	4095	ao	AN8798.1	71.m15605	AO070276000062	0					-156	-49	ATGCTCTATACACCAGACGCTCTATCACACGAACAGGATCAGCTCACTCGATCGTTGATGGTGAGGCTAGACCATGGAACTACTTATCTCCCCCGATCTCTATCCTAA			ATGCTCTATACACCAGACGCTCTATCACACGAACAGGATCAGCTCACTCGATCGTTGATGGTGAGGCTAGACCATGGAACTACTTATCTCCCCCGATCTCTATCCTAA	MLYTPDALSHEQDQLTRSLMVRLDHGTTYLPRSLS*			MLYTPDALSHEQDQLTRSLMVRLDHGTTYLPRSLS*	ATATTTCCGG	TTCAGTCCTC	0	R	0	MG04080.1	0	0	0
9265	4095	ao	AN8798.1	71.m15605	AO070276000062	0					-99	-49	ATGGTGAGGCTAGACCATGGAACTACTTATCTCCCCCGATCTCTATCCTAA			ATGGTGAGGCTAGACCATGGAACTACTTATCTCCCCCGATCTCTATCCTAA	MVRLDHGTTYLPRSLS*			MVRLDHGTTYLPRSLS*	TCGATCGTTG	TTCAGTCCTC	0	R	0	MG04080.1	0	0	0
9266	4095	ao	AN8798.1	71.m15605	AO070276000062	0					-83	-9	ATGGAACTACTTATCTCCCCCGATCTCTATCCTAATTCAGTCCTCCCAGACACCTCCCTATTCGTACTAAATTGA			ATGGAACTACTTATCTCCCCCGATCTCTATCCTAATTCAGTCCTCCCAGACACCTCCCTATTCGTACTAAATTGA	MELLISPDLYPNSVLPDTSLFVLN*			MELLISPDLYPNSVLPDTSLFVLN*	AGGCTAGACC	CTATCGCCAT	0	R	0	MG04080.1	0	0	0
9269	4096	af	AN7549.1	72.m19566	AO070277000046	0			-164	-102			ATGCTGCCTACTTGTTTCCGCCGTGCAACATGCGCGCGGACCTACCAGGCTGCCAGCCTATAA		ATGCTGCCTACTTGTTTCCGCCGTGCAACATGCGCGCGGACCTACCAGGCTGCCAGCCTATAA		MLPTCFRRATCARTYQAASL*		MLPTCFRRATCARTYQAASL*		GCCTCGTTGG	AAGCCAGAGA	0	O	0	0	0	0	0
9270	4096	af	AN7549.1	72.m19566	AO070277000046	0			-135	-61			ATGCGCGCGGACCTACCAGGCTGCCAGCCTATAAAAGCCAGAGAAACCTATATAATGAGCGATGAAGACGGGTAG		ATGCGCGCGGACCTACCAGGCTGCCAGCCTATAAAAGCCAGAGAAACCTATATAATGAGCGATGAAGACGGGTAG		MRADLPGCQPIKARETYIMSDEDG*		MRADLPGCQPIKARETYIMSDEDG*		GCCGTGCAAC	TCTTCTTTTC	0	O	0	0	0	0	0
9271	4096	af	AN7549.1	72.m19566	AO070277000046	0			-81	-61			ATGAGCGATGAAGACGGGTAG		ATGAGCGATGAAGACGGGTAG		MSDEDG*		MSDEDG*		AACCTATATA	TCTTCTTTTC	0	O	0	0	0	0	0
9267	4096	an	AN7549.1	72.m19566	AO070277000046	0	-182	-3					ATGAGCCTCACTATAGGTATAAAGGTCCAGACCTCAGACCTCAGATTTCACACCACAATCAACCTTCAAACGAATGGGACACACTCTCATCCCTCTTTTTTCTCCTCTTATCCCCATCTTTGTCTCTACAATAATACAACCCTGAGGTCACTCGAATCCCCGTTAAGTTCGAGCAAGTAA	ATGAGCCTCACTATAGGTATAAAGGTCCAGACCTCAGACCTCAGATTTCACACCACAATCAACCTTCAAACGAATGGGACACACTCTCATCCCTCTTTTTTCTCCTCTTATCCCCATCTTTGTCTCTACAATAATACAACCCTGAGGTCACTCGAATCCCCGTTAAGTTCGAGCAAGTAA			MSLTIGIKVQTSDLRFHTTINLQTNGTHSHPSFFSSYPHLCLYNNTTLRSLESPLSSSK*	MSLTIGIKVQTSDLRFHTTINLQTNGTHSHPSFFSSYPHLCLYNNTTLRSLESPLSSSK*			GCCTGCTCAT	CAATGGCCTC	0	O	0	0	0	0	0
9268	4096	an	AN7549.1	72.m19566	AO070277000046	0	-109	-38					ATGGGACACACTCTCATCCCTCTTTTTTCTCCTCTTATCCCCATCTTTGTCTCTACAATAATACAACCCTGA	ATGGGACACACTCTCATCCCTCTTTTTTCTCCTCTTATCCCCATCTTTGTCTCTACAATAATACAACCCTGA			MGHTLIPLFSPLIPIFVSTIIQP*	MGHTLIPLFSPLIPIFVSTIIQP*			CTTCAAACGA	GGTCACTCGA	0	O	0	0	0	0	0
9272	4096	ao	AN7549.1	72.m19566	AO070277000046	0					-64	-8	ATGCCAAAACAACATACTACCTTTTCGTCTTCAGAGACCCTGATTGGGACCATATAA			ATGCCAAAACAACATACTACCTTTTCGTCTTCAGAGACCCTGATTGGGACCATATAA	MPKQHTTFSSSETLIGTI*			MPKQHTTFSSSETLIGTI*	TATACATTAC	AGCCATCATG	0	O	0	0	0	0	0
9274	4099	af	AN2262.1	71.m15903	AO070295000025	0			-173	-153			ATGTTTCTGCCCAAGGCATGA		ATGTTTCTGCCCAAGGCATGA		MFLPKA*		MFLPKA*		GGTGAGCGCG	ATCTGCCGAT	0	S	FG07195.1	0	0	YKL143W	0
9275	4099	af	AN2262.1	71.m15903	AO070295000025	0			-156	-28			ATGAATCTGCCGATAAGGGAGCACGTGACTCGATACAACCCACTATCACGAAATTTTGATTTTTCGATCTCCGGAAGAGACTTGGAAAGAGAGACAGAGACAGAGCAGATTAGACGGTCAAGATTTTAG		ATGAATCTGCCGATAAGGGAGCACGTGACTCGATACAACCCACTATCACGAAATTTTGATTTTTCGATCTCCGGAAGAGACTTGGAAAGAGAGACAGAGACAGAGCAGATTAGACGGTCAAGATTTTAG		MNLPIREHVTRYNPLSRNFDFSISGRDLERETETEQIRRSRF*		MNLPIREHVTRYNPLSRNFDFSISGRDLERETETEQIRRSRF*		TGCCCAAGGC	GACGTCGATA	0	S	FG07195.1	0	0	YKL143W	0
9273	4099	an	AN2262.1	71.m15903	AO070295000025	0	-195	-166					ATGGTATCCTCTCCTCTCGATTTAATATAG	ATGGTATCCTCTCCTCTCGATTTAATATAG			MVSSPLDLI*	MVSSPLDLI*			AGATTTTAAG	ATCCTCCGGT	0	S	FG07195.1	0	0	YKL143W	0
9277	4102	af	AN6304.1	72.m19330	AO070308000059	0			-154	-32			ATGTGCTTAGCGCATATCTTCCCTTCATCACAGCCCTCCATCCCCCTACGGTTTGGACTACTACACTGTGTCTTCACTGGGTTCAATATTTGTTGGCCGATTCCATTAGGGACACGACCGTAA		ATGTGCTTAGCGCATATCTTCCCTTCATCACAGCCCTCCATCCCCCTACGGTTTGGACTACTACACTGTGTCTTCACTGGGTTCAATATTTGTTGGCCGATTCCATTAGGGACACGACCGTAA		MCLAHIFPSSQPSIPLRFGLLHCVFTGFNICWPIPLGTRP*		MCLAHIFPSSQPSIPLRFGLLHCVFTGFNICWPIPLGTRP*		TATCTGCTCC	TCTTTGAAAC	0	T	0	0	0	0	0
9276	4102	an	AN6304.1	72.m19330	AO070308000059	0	-116	-93					ATGAGAGCACAGGACGTACGATAG	ATGAGAGCACAGGACGTACGATAG			MRAQDVR*	MRAQDVR*			TCAGTCCGCA	CCCTGTTAAA	0	T	0	0	0	0	0
9278	4102	ao	AN6304.1	72.m19330	AO070308000059	0					-119	-75	ATGCCCAGACGAACACCACCAGCGACTATACAGTGTCTACCTTAA			ATGCCCAGACGAACACCACCAGCGACTATACAGTGTCTACCTTAA	MPRRTPPATIQCLP*			MPRRTPPATIQCLP*	ACTTGGAATC	ATCCAGAATT	0	T	0	0	0	0	0
9281	4104	af	AN5685.1	65.m07411	AO070309000100	0			-252	-166			ATGATGTTGCTTCAACAGAGCCAACCTGGAGGCTTGGCCGACGAGCTCGGAAGCGGTCGAGCCAACCACCGACTAGACAAGGCTTAG		ATGATGTTGCTTCAACAGAGCCAACCTGGAGGCTTGGCCGACGAGCTCGGAAGCGGTCGAGCCAACCACCGACTAGACAAGGCTTAG		MMLLQQSQPGGLADELGSGRANHRLDKA*		MMLLQQSQPGGLADELGSGRANHRLDKA*		TAGGCTGAGG	TTCTTATCGG	0	S	0	0	0	0	0
9282	4104	af	AN5685.1	65.m07411	AO070309000100	0			-249	-166			ATGTTGCTTCAACAGAGCCAACCTGGAGGCTTGGCCGACGAGCTCGGAAGCGGTCGAGCCAACCACCGACTAGACAAGGCTTAG		ATGTTGCTTCAACAGAGCCAACCTGGAGGCTTGGCCGACGAGCTCGGAAGCGGTCGAGCCAACCACCGACTAGACAAGGCTTAG		MLLQQSQPGGLADELGSGRANHRLDKA*		MLLQQSQPGGLADELGSGRANHRLDKA*		GCTGAGGATG	TTCTTATCGG	0	S	0	0	0	0	0
9283	4104	af	AN5685.1	65.m07411	AO070309000100	0			-150	-76			ATGATCATATCAGCAACCTTTTTTTTCCTTTTTAGTCCAATCTTTTTTAAGGGTCAAAATTGTTATCAAATTTGA		ATGATCATATCAGCAACCTTTTTTTTCCTTTTTAGTCCAATCTTTTTTAAGGGTCAAAATTGTTATCAAATTTGA		MIISATFFFLFSPIFFKGQNCYQI*		MIISATFFFLFSPIFFKGQNCYQI*		ATCGGCCGCA	AATCAATTGA	0	S	0	0	0	0	0
9279	4104	an	AN5685.1	65.m07411	AO070309000100	0	-183	-13					ATGATGTTGAAATCGAAGCCAGGCTGTTGGATTGGGCGAGCTCGGAGGGCGGTCAGATCGGTGCCAGCTCCGGCGGATGCAAGATTTCGTCCACTTTTTTTCTGGCCGACAGATTCCCATACAAATTCAATCCGCCATATCGCTTATTCATTTCAGTATCTGGACCTATAA	ATGATGTTGAAATCGAAGCCAGGCTGTTGGATTGGGCGAGCTCGGAGGGCGGTCAGATCGGTGCCAGCTCCGGCGGATGCAAGATTTCGTCCACTTTTTTTCTGGCCGACAGATTCCCATACAAATTCAATCCGCCATATCGCTTATTCATTTCAGTATCTGGACCTATAA			MMLKSKPGCWIGRARRAVRSVPAPADARFRPLFFWPTDSHTNSIRHIAYSFQYLDL*	MMLKSKPGCWIGRARRAVRSVPAPADARFRPLFFWPTDSHTNSIRHIAYSFQYLDL*			CCGCTGGAGG	TCATCGATCG	0	S	0	0	0	0	0

9280	4104	an	AN5685.1	65.m07411	AO070309000100	0	-180	-13					ATGTTGAAATCGAAGCCAGGCTGTTGGATTGGGCGAGCTCGGAGGGCGGTCAGATCGGTGCCAGCTCCGGCGGATGCAAGATTTCGTCCACTTTTTTTCTGGCCGACAGATTCCCATACAAATTCAATCCGCCATATCGCTTATTCATTTCAGTATCTGGACCTATAA	ATGTTGAAATCGAAGCCAGGCTGTTGGATTGGGCGAGCTCGGAGGGCGGTCAGATCGGTGCCAGCTCCGGCGGATGCAAGATTTCGTCCACTTTTTTTCTGGCCGACAGATTCCCATACAAATTCAATCCGCCATATCGCTTATTCATTTCAGTATCTGGACCTATAA			MLKSKPGCWIGRARRAVRSVPAPADARFRPLFFWPTDSHTNSIRHIAYSFQYLDL*	MLKSKPGCWIGRARRAVRSVPAPADARFRPLFFWPTDSHTNSIRHIAYSFQYLDL*			CTGGAGGATG	TCATCGATCG	0	S	0	0	0	0	0
9284	4104	ao	AN5685.1	65.m07411	AO070309000100	0					-250	-173	ATGGTGGTTGGAGACAGGCTGGAGGATTGGCCGAACGGGGCTCGGAGGCGGTCGACCCAAATCACCGGCAAGGCTTAG			ATGGTGGTTGGAGACAGGCTGGAGGATTGGCCGAACGGGGCTCGGAGGCGGTCGACCCAAATCACCGGCAAGGCTTAG	MVVGDRLEDWPNGARRRSTQITGKA*			MVVGDRLEDWPNGARRRSTQITGKA*	CCCCGGAGGT	CTTCACTTTG	0	S	0	0	0	0	0
9285	4104	ao	AN5685.1	65.m07411	AO070309000100	0					-138	-94	ATGGCTCTTTTATATCGAAACCATATCACCGAATACGTGGGTTAA			ATGGCTCTTTTATATCGAAACCATATCACCGAATACGTGGGTTAA	MALLYRNHITEYVG*			MALLYRNHITEYVG*	GATTTTTTTT	TAACGCACTT	0	S	0	0	0	0	0
9286	4105	af	AN8248.1	53.m03717	AO070310000058	0			-208	-125			ATGAGAGAGATTTCTATATGGTCGATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAG		ATGAGAGAGATTTCTATATGGTCGATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAG		MREISIWSMEVRKENPKKAGNSDIKRS*		MREISIWSMEVRKENPKKAGNSDIKRS*		CTGACCAGGA	AGAAATCCAT	0		0	0	0	0	0
9287	4105	af	AN8248.1	53.m03717	AO070310000058	0			-191	-87			ATGGTCGATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAGAGAAATCCATCGGCGTCACTCTTCGTAGCTCCATCTAA		ATGGTCGATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAGAGAAATCCATCGGCGTCACTCTTCGTAGCTCCATCTAA		MVDGGKKRKSEKGGKFGHKAQLEKSIGVTLRSSI*		MVDGGKKRKSEKGGKFGHKAQLEKSIGVTLRSSI*		AGATTTCTAT	AATCATCTTC	0		0	0	0	0	0
9288	4105	af	AN8248.1	53.m03717	AO070310000058	0			-184	-125			ATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAG		ATGGAGGTAAGAAAAGAAAATCCGAAAAAGGCGGGAAATTCGGACATAAAGCGCAGCTAG		MEVRKENPKKAGNSDIKRS*		MEVRKENPKKAGNSDIKRS*		TATATGGTCG	AGAAATCCAT	0		0	0	0	0	0
9289	4107	an	AN4481.1	57.m05651	AO070311000027	0	-194	-117					ATGGTCTTGTCTCGAGCGATTTGGTTTCTTTCACCACATTATTCAAGAACATCCCCTGCTGCTCTTCAAGAGAGTTGA	ATGGTCTTGTCTCGAGCGATTTGGTTTCTTTCACCACATTATTCAAGAACATCCCCTGCTGCTCTTCAAGAGAGTTGA			MVLSRAIWFLSPHYSRTSPAALQES*	MVLSRAIWFLSPHYSRTSPAALQES*			GTCAAAGATC	CCCAAGGAAG	0	G	0	0	0	0	0
9290	4109	af	AN3145.1	59.m08506	AO070312000163	0			-282	-127			ATGCTAACACGTTATAGGTGTCGACTGGCTCTTTTTCGAACAAAATCCTTTCACGAGCAACGCTTTCCTCACACTCCGTCAATCCTTCCAGGAATCTCGCAGTGCTGTCTGATTATTTCCGTCCCGCGTGCCCTCAGCATCATACTAATAACGTAA		ATGCTAACACGTTATAGGTGTCGACTGGCTCTTTTTCGAACAAAATCCTTTCACGAGCAACGCTTTCCTCACACTCCGTCAATCCTTCCAGGAATCTCGCAGTGCTGTCTGATTATTTCCGTCCCGCGTGCCCTCAGCATCATACTAATAACGTAA		MLTRYRCRLALFRTKSFHEQRFPHTPSILPGISQCCLIISVPRALSIILIT*		MLTRYRCRLALFRTKSFHEQRFPHTPSILPGISQCCLIISVPRALSIILIT*		GAATTTGCTA	TTCCTCGAAC	0	A	0	0	0	0	0
9308	4112	af	AN8691.1	62.m03474	AO070315000112	0			-143	-132			ATGACGCGCTAA		ATGACGCGCTAA		MTR*		MTR*		TTCGGCCGGG	AGCCCCCGAA	0	A	0	0	0	YNL221C	0
9307	4112	an	AN8691.1	62.m03474	AO070315000112	0	-91	-80					ATGGAGCTCTAA	ATGGAGCTCTAA			MEL*	MEL*			CAATTTCCCA	GTTTCACTCT	0	A	0	0	0	YNL221C	0
9309	4112	ao	AN8691.1	62.m03474	AO070315000112	0					-122	-111	ATGGAATTTTAA			ATGGAATTTTAA	MEF*			MEF*	GCTTTCCTAT	TTCCAGACCA	0	A	0	0	0	YNL221C	0
9310	4112	ao	AN8691.1	62.m03474	AO070315000112	0					-94	-83	ATGCCACTATAA			ATGCCACTATAA	MPL*			MPL*	ACCACATTTA	TTCACCAGCC	0	A	0	0	0	YNL221C	0
9311	4113	an	AN8724.1	62.m03342	AO070315000152	0	-256	-203					ATGCTTCCCCGCTACCCCTCCGTTGTCGAAGGGTCCTCTATTTCTCTTGCCTAG	ATGCTTCCCCGCTACCCCTCCGTTGTCGAAGGGTCCTCTATTTCTCTTGCCTAG			MLPRYPSVVEGSSISLA*	MLPRYPSVVEGSSISLA*			GCAGGTCTCT	GTTGGAGTAC	0	TV	0	0	0	0	0
9312	4113	ao	AN8724.1	62.m03342	AO070315000152	0					-162	-118	ATGAGAGCTTACATTCCATGTCTGACAAAAGTGGAGCTTCAATAG			ATGAGAGCTTACATTCCATGTCTGACAAAAGTGGAGCTTCAATAG	MRAYIPCLTKVELQ*			MRAYIPCLTKVELQ*	ACGAGAAACG	TTCGATAAAA	0	TV	0	0	0	0	0
9313	4113	ao	AN8724.1	62.m03342	AO070315000152	0					-145	-110	ATGTCTGACAAAAGTGGAGCTTCAATAGTTCGATAA			ATGTCTGACAAAAGTGGAGCTTCAATAGTTCGATAA	MSDKSGASIVR*			MSDKSGASIVR*	CTTACATTCC	AAATTAATGT	0	TV	0	0	0	0	0
9314	4113	ao	AN8724.1	62.m03342	AO070315000152	0					-103	-83	ATGTCCCATTCACGCGCCTAG			ATGTCCCATTCACGCGCCTAG	MSHSRA*			MSHSRA*	ATAAAAATTA	TTCACTACAA	0	TV	0	0	0	0	0
9316	4114	af	AN0632.1	70.m15650	AO070318000122	0			-208	-35			ATGTTGGTGGTTGAGGTGTTTGCCTTTGTCACGAGAGTGAGAGCTATCCGGCGGAGGAAAGAAGCTCGCCCCGGCGAATGTGGCCGCTTGCACCGCCGTTGCTTCAAGATCATTTCTACTATCTCCCACAACTCTCATTATACGCGCATGTCTTGGTTACTCTTAGCATCCTAG		ATGTTGGTGGTTGAGGTGTTTGCCTTTGTCACGAGAGTGAGAGCTATCCGGCGGAGGAAAGAAGCTCGCCCCGGCGAATGTGGCCGCTTGCACCGCCGTTGCTTCAAGATCATTTCTACTATCTCCCACAACTCTCATTATACGCGCATGTCTTGGTTACTCTTAGCATCCTAG		MLVVEVFAFVTRVRAIRRRKEARPGECGRLHRRCFKIISTISHNSHYTRMSWLLLAS*		MLVVEVFAFVTRVRAIRRRKEARPGECGRLHRRCFKIISTISHNSHYTRMSWLLLAS*		CGGGCTGGCG	TTAGCGACTG	0	A	0	0	0	0	0
9317	4114	af	AN0632.1	70.m15650	AO070318000122	0			-61	-35			ATGTCTTGGTTACTCTTAGCATCCTAG		ATGTCTTGGTTACTCTTAGCATCCTAG		MSWLLLAS*		MSWLLLAS*		TTATACGCGC	TTAGCGACTG	0	A	0	0	0	0	0
9315	4114	an	AN0632.1	70.m15650	AO070318000122	0	-172	-146					ATGAAATCGAGGTTAATTACGACCTAG	ATGAAATCGAGGTTAATTACGACCTAG			MKSRLITT*	MKSRLITT*			GAAGCGGTAG	CTCTTCTCGA	0	A	0	0	0	0	0
9318	4114	ao	AN0632.1	70.m15650	AO070318000122	0					-254	-228	ATGTTCAGCGGAAGTTGTTGCGGTTGA			ATGTTCAGCGGAAGTTGTTGCGGTTGA	MFSGSCCG*			MFSGSCCG*	GAGGGATTGA	AATTAAATGG	0	A	0	0	0	0	0
9319	4114	ao	AN0632.1	70.m15650	AO070318000122	0					-221	-162	ATGGAGAGCTCCGGTTTTGTCACGAGTTTAAGCTCGACCGCCGAGGAGCTTCTAGTCTAG			ATGGAGAGCTCCGGTTTTGTCACGAGTTTAAGCTCGACCGCCGAGGAGCTTCTAGTCTAG	MESSGFVTSLSSTAEELLV*			MESSGFVTSLSSTAEELLV*	TTGAAATTAA	TCCGCCCTCT	0	A	0	0	0	0	0
9320	4115	ao	AN0140.1	71.m15423	AO070321000112	0					-262	-245	ATGGGCATACGTATGTGA			ATGGGCATACGTATGTGA	MGIRM*			MGIRM*	ACCTAAAACA	CTTAAGGTAC	0	Z	FG10856.1	MG03879.1	NCU01756.1	YJR065C	YJR065C
9323	4116	af	AN1751.1	69.m15052	AO070324000042	0			-199	-170			ATGGAAGCGGTGATGATCTTTTTTACTTGA		ATGGAAGCGGTGATGATCTTTTTTACTTGA		MEAVMIFFT*		MEAVMIFFT*		ACGCAAATCA	GATGAAAAAA	0	DR	0	MG00559.1	NCU04040.1	0	0
9324	4116	af	AN1751.1	69.m15052	AO070324000042	0			-187	-170			ATGATCTTTTTTACTTGA		ATGATCTTTTTTACTTGA		MIFFT*		MIFFT*		GGAAGCGGTG	GATGAAAAAA	0	DR	0	MG00559.1	NCU04040.1	0	0
9325	4116	af	AN1751.1	69.m15052	AO070324000042	0			-168	-4			ATGAAAAAAAGCGGCAGAAAAGAGGCCCGCCTTTTTACGCATTTTAATCTTATCGCTTCATCTCCCCACATTGAATTTCTACCAGAGATCCAACTGGACGGCAATTTATACATCTACACTGCCTTACAATCCCAGTACTTGCGAGGGATTGTTATCAGTTCCTGA		ATGAAAAAAAGCGGCAGAAAAGAGGCCCGCCTTTTTACGCATTTTAATCTTATCGCTTCATCTCCCCACATTGAATTTCTACCAGAGATCCAACTGGACGGCAATTTATACATCTACACTGCCTTACAATCCCAGTACTTGCGAGGGATTGTTATCAGTTCCTGA		MKKSGRKEARLFTHFNLIASSPHIEFLPEIQLDGNLYIYTALQSQYLRGIVISS*		MKKSGRKEARLFTHFNLIASSPHIEFLPEIQLDGNLYIYTALQSQYLRGIVISS*		TTTACTTGAG	AAAATGGGGA	0	DR	0	MG00559.1	NCU04040.1	0	0
9321	4116	an	AN1751.1	69.m15052	AO070324000042	0	-226	-200					ATGAGAAATTTATTGAGTCAAAGTTGA	ATGAGAAATTTATTGAGTCAAAGTTGA			MRNLLSQS*	MRNLLSQS*			CCCATATTAT	TCAGTGCAGT	0	DR	0	MG00559.1	NCU04040.1	0	0
9322	4116	an	AN1751.1	69.m15052	AO070324000042	0	-189	-10					ATGTTATTCCTTCGGCGAGTTCGATTTTTGGAGCAGAAAAAAAGGCGGCAGAACAATCCCACCGCCTTCTATTTCTTAGTTCCAATCTTATCGCCAGCCCCACGCACCAAAAGAAATCGCAATTGTCCCCTCAGACCCCTCCTCTATTCCTTTTTGTCGCCCATTGGGAATCGAAGATAG	ATGTTATTCCTTCGGCGAGTTCGATTTTTGGAGCAGAAAAAAAGGCGGCAGAACAATCCCACCGCCTTCTATTTCTTAGTTCCAATCTTATCGCCAGCCCCACGCACCAAAAGAAATCGCAATTGTCCCCTCAGACCCCTCCTCTATTCCTTTTTGTCGCCCATTGGGAATCGAAGATAG			MLFLRRVRFLEQKKRRQNNPTAFYFLVPILSPAPRTKRNRNCPLRPLLYSFLSPIGNRR*	MLFLRRVRFLEQKKRRQNNPTAFYFLVPILSPAPRTKRNRNCPLRPLLYSFLSPIGNRR*			TCAGTGCAGT	ACAGTCGCCA	0	DR	0	MG00559.1	NCU04040.1	0	0
9326	4116	ao	AN1751.1	69.m15052	AO070324000042	0					-210	-181	ATGAGGATATATGTTGTTTCTGGTTTTTGA			ATGAGGATATATGTTGTTTCTGGTTTTTGA	MRIYVVSGF*			MRIYVVSGF*	GGAAGCAATT	AGAATTATTT	0	DR	0	MG00559.1	NCU04040.1	0	0
9328	4117	af	AN6597.1	62.m03201	AO070326000046	0			-99	-28			ATGTCCCTCTTGCCAACTTCCTACAAATGTACGCAACCCACTACGGCTTCAATATTTTGCTCTCTCGAATGA		ATGTCCCTCTTGCCAACTTCCTACAAATGTACGCAACCCACTACGGCTTCAATATTTTGCTCTCTCGAATGA		MSLLPTSYKCTQPTTASIFCSLE*		MSLLPTSYKCTQPTTASIFCSLE*		GAAAGCTAGG	TCTTGCGGTA	0	R	0	0	0	0	0
9329	4117	af	AN6597.1	62.m03201	AO070326000046	0			-73	-17			ATGTACGCAACCCACTACGGCTTCAATATTTTGCTCTCTCGAATGATCTTGCGGTAG		ATGTACGCAACCCACTACGGCTTCAATATTTTGCTCTCTCGAATGATCTTGCGGTAG		MYATHYGFNILLSRMILR*		MYATHYGFNILLSRMILR*		CTTCCTACAA	CCCCAACTCT	0	R	0	0	0	0	0
9327	4117	an	AN6597.1	62.m03201	AO070326000046	0	-126	-79					ATGACCGACCGCTCTGGGCTCGAGCTTCATTCGGCCAACCTCGACTGA	ATGACCGACCGCTCTGGGCTCGAGCTTCATTCGGCCAACCTCGACTGA			MTDRSGLELHSANLD*	MTDRSGLELHSANLD*			CGCGGGAAAA	CTCAATTGCC	0	R	0	0	0	0	0
9331	4117	ao	AN6597.1	62.m03201	AO070326000046	0					-241	-212	ATGCGATGCGGTAAGCAGCAGATACCTTAA			ATGCGATGCGGTAAGCAGCAGATACCTTAA	MRCGKQQIP*			MRCGKQQIP*	ACTCCGTAAT	TGACGATAAG	0	R	0	0	0	0	0
9332	4117	ao	AN6597.1	62.m03201	AO070326000046	0					-212	-75	ATGACGATAAGATGCGGCTGTGATACGCTAATCCCAGCCAGGTATAGTGGTTTCCGCGGGGGACTCTCACCGCTCACGTCACGTTTCCGGGTACTGCATCAGTTGGCCGCGGGAAAACGGAATGCTTCTGGTGACTGA			ATGACGATAAGATGCGGCTGTGATACGCTAATCCCAGCCAGGTATAGTGGTTTCCGCGGGGGACTCTCACCGCTCACGTCACGTTTCCGGGTACTGCATCAGTTGGCCGCGGGAAAACGGAATGCTTCTGGTGACTGA	MTIRCGCDTLIPARYSGFRGGLSPLTSRFRVLHQLAAGKRNASGD*			MTIRCGCDTLIPARYSGFRGGLSPLTSRFRVLHQLAAGKRNASGD*	AGATACCTTA	TTCATCCGCC	0	R	0	0	0	0	0
9333	4117	ao	AN6597.1	62.m03201	AO070326000046	0					-201	-190	ATGCGGCTGTGA			ATGCGGCTGTGA	MRL*			MRL*	TGACGATAAG	TACGCTAATC	0	R	0	0	0	0	0
9336	4118	af	AN4776.1	59.m09207	AO070329000076	0			-110	-39			ATGTCAAGCATTCAGCTTCACTCTCGCATAGATGGACAGCTTATAGAATATCTGCATAAATCTCTTTTCTAA		ATGTCAAGCATTCAGCTTCACTCTCGCATAGATGGACAGCTTATAGAATATCTGCATAAATCTCTTTTCTAA		MSSIQLHSRIDGQLIEYLHKSLF*		MSSIQLHSRIDGQLIEYLHKSLF*		GGGCCAGGAC	TCGTGACAAC	0	E	0	0	0	0	0
9337	4118	af	AN4776.1	59.m09207	AO070329000076	0			-79	-65			ATGGACAGCTTATAG		ATGGACAGCTTATAG		MDSL*		MDSL*		TCTCGCATAG	AATATCTGCA	0	E	0	0	0	0	0
9335	4118	an	AN4776.1	59.m09207	AO070329000076	0	-176	-102					ATGTGTGGTCTTCGCCACAAACCACGAACGTTATCTTATCAGCATAAAATTGTACTATCTCTTCCGCTGCGTTGA	ATGTGTGGTCTTCGCCACAAACCACGAACGTTATCTTATCAGCATAAAATTGTACTATCTCTTCCGCTGCGTTGA			MCGLRHKPRTLSYQHKIVLSLPLR*	MCGLRHKPRTLSYQHKIVLSLPLR*			TTAGACTGGT	CTCCAAGCCC	0	E	0	0	0	0	0
9338	4118	ao	AN4776.1	59.m09207	AO070329000076	0					-302	-282	ATGCGTAGAAGAATACTATAG			ATGCGTAGAAGAATACTATAG	MRRRIL*			MRRRIL*	TGTTGAAGGT	CCAGGATGAG	0	E	0	0	0	0	0
9339	4118	ao	AN4776.1	59.m09207	AO070329000076	0					-276	-130	ATGAGACTCCAATTGAGTTCCACATCCTGCACTGCAGTGCCAAACTGGTCTGTTTCTATACTTACGATGCCCTATAGAGGGGAAACGAATAATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAA			ATGAGACTCCAATTGAGTTCCACATCCTGCACTGCAGTGCCAAACTGGTCTGTTTCTATACTTACGATGCCCTATAGAGGGGAAACGAATAATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAA	MRLQLSSTSCTAVPNWSVSILTMPYRGETNNATLSRLSYLIGSTIQFN*			MRLQLSSTSCTAVPNWSVSILTMPYRGETNNATLSRLSYLIGSTIQFN*	TATAGCCAGG	ACCGTACTAA	0	E	0	0	0	0	0
9340	4118	ao	AN4776.1	59.m09207	AO070329000076	0					-210	-130	ATGCCCTATAGAGGGGAAACGAATAATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAA			ATGCCCTATAGAGGGGAAACGAATAATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAA	MPYRGETNNATLSRLSYLIGSTIQFN*			MPYRGETNNATLSRLSYLIGSTIQFN*	TATACTTACG	ACCGTACTAA	0	E	0	0	0	0	0
9341	4118	ao	AN4776.1	59.m09207	AO070329000076	0					-185	-120	ATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAAACCGTACTAA			ATGCCACTCTTTCCCGCCTTTCTTATCTTATCGGCTCTACAATTCAATTCAACTAAACCGTACTAA	MPLFPAFLILSALQFNSTKPY*			MPLFPAFLILSALQFNSTKPY*	GAAACGAATA	GTCTCCGATC	0	E	0	0	0	0	0
9344	4119	af	AN1121.1	70.m15111	AO070331000113	0			-182	-138			ATGGCAGCCTTTGGAGGAAGTAGGTACGTCAGGCAGCTGAGTTAG		ATGGCAGCCTTTGGAGGAAGTAGGTACGTCAGGCAGCTGAGTTAG		MAAFGGSRYVRQLS*		MAAFGGSRYVRQLS*		ATCTTCGGCG	TGAAGAACGG	0		0	0	0	0	0
9345	4119	af	AN1121.1	70.m15111	AO070331000113	0			-75	-25			ATGGTCAGGTCTACCAACTCCATCAAAAAGACAGAGCAGACTCAGTCTTGA		ATGGTCAGGTCTACCAACTCCATCAAAAAGACAGAGCAGACTCAGTCTTGA		MVRSTNSIKKTEQTQS*		MVRSTNSIKKTEQTQS*		CCGCTTTTTC	CCCCGCGAAC	0		0	0	0	0	0
9342	4119	an	AN1121.1	70.m15111	AO070331000113	0	-160	-146					ATGTTAAGGAGATGA	ATGTTAAGGAGATGA			MLRR*	MLRR*			ATAGTTGAGG	CGACGGAGGC	0		0	0	0	0	0
9343	4119	an	AN1121.1	70.m15111	AO070331000113	0	-149	-132					ATGACGACGGAGGCCTAG	ATGACGACGGAGGCCTAG			MTTEA*	MTTEA*			TGTTAAGGAG	AGTGGGTGGC	0		0	0	0	0	0
9346	4119	ao	AN1121.1	70.m15111	AO070331000113	0					-231	-181	ATGACGTCCGTTGGAATGGGGAGAAGAAGGAGTGGTGTCGATGTAGCCTGA			ATGACGTCCGTTGGAATGGGGAGAAGAAGGAGTGGTGTCGATGTAGCCTGA	MTSVGMGRRRSGVDVA*			MTSVGMGRRRSGVDVA*	AGGGAGAAAG	TGGAGCAAAG	0		0	0	0	0	0
9347	4119	ao	AN1121.1	70.m15111	AO070331000113	0					-216	-181	ATGGGGAGAAGAAGGAGTGGTGTCGATGTAGCCTGA			ATGGGGAGAAGAAGGAGTGGTGTCGATGTAGCCTGA	MGRRRSGVDVA*			MGRRRSGVDVA*	GTCCGTTGGA	TGGAGCAAAG	0		0	0	0	0	0

9348	4119	ao	AN1121.1	70.m15111	AO070331000113	0					-181	-2	ATGGAGCAAAGCGAATGGGATCAGTTAAGTTGCCCAATAGTGGAGAGTCCGTCCGGAGTTAGTGGCGGTGCTGCGGCGGCAGTAAGACTCCGCCTTGTGTCGCAAATGGCATATTGCCTGTCCTCGTATCCGTACTCAATACCCTGGAAAGCAACGCCAAAAAGTACTTTCACTGCTTAA			ATGGAGCAAAGCGAATGGGATCAGTTAAGTTGCCCAATAGTGGAGAGTCCGTCCGGAGTTAGTGGCGGTGCTGCGGCGGCAGTAAGACTCCGCCTTGTGTCGCAAATGGCATATTGCCTGTCCTCGTATCCGTACTCAATACCCTGGAAAGCAACGCCAAAAAGTACTTTCACTGCTTAA	MEQSEWDQLSCPIVESPSGVSGGAAAAVRLRLVSQMAYCLSSYPYSIPWKATPKSTFTA*			MEQSEWDQLSCPIVESPSGVSGGAAAAVRLRLVSQMAYCLSSYPYSIPWKATPKSTFTA*	ATGTAGCCTG	CATGAAAGGC	0		0	0	0	0	0
9349	4119	ao	AN1121.1	70.m15111	AO070331000113	0					-167	-120	ATGGGATCAGTTAAGTTGCCCAATAGTGGAGAGTCCGTCCGGAGTTAG			ATGGGATCAGTTAAGTTGCCCAATAGTGGAGAGTCCGTCCGGAGTTAG	MGSVKLPNSGESVRS*			MGSVKLPNSGESVRS*	AGCAAAGCGA	TGGCGGTGCT	0		0	0	0	0	0
9350	4119	ao	AN1121.1	70.m15111	AO070331000113	0					-76	-2	ATGGCATATTGCCTGTCCTCGTATCCGTACTCAATACCCTGGAAAGCAACGCCAAAAAGTACTTTCACTGCTTAA			ATGGCATATTGCCTGTCCTCGTATCCGTACTCAATACCCTGGAAAGCAACGCCAAAAAGTACTTTCACTGCTTAA	MAYCLSSYPYSIPWKATPKSTFTA*			MAYCLSSYPYSIPWKATPKSTFTA*	TGTGTCGCAA	CATGAAAGGC	0		0	0	0	0	0
9351	4120	an	AN1134.1	70.m15103	AO070331000125	0	-253	-227					ATGATCGCTTTTATCCATATGATCTAA	ATGATCGCTTTTATCCATATGATCTAA			MIAFIHMI*	MIAFIHMI*			CTCCCACAAC	TTCAATTACT	0		0	0	0	0	0
9352	4120	an	AN1134.1	70.m15103	AO070331000125	0	-214	-200					ATGCATGGTATCTGA	ATGCATGGTATCTGA			MHGI*	MHGI*			CAATTACTTC	CTTGGACGAG	0		0	0	0	0	0
9353	4120	an	AN1134.1	70.m15103	AO070331000125	0	-210	-187					ATGGTATCTGACTTGGACGAGTAA	ATGGTATCTGACTTGGACGAGTAA			MVSDLDE*	MVSDLDE*			TACTTCATGC	GGATTTTAAT	0		0	0	0	0	0
9354	4120	ao	AN1134.1	70.m15103	AO070331000125	0					-76	-50	ATGATACATCTCGGTTGCAACATCTGA			ATGATACATCTCGGTTGCAACATCTGA	MIHLGCNI*			MIHLGCNI*	CTGCCGGCAA	CGATGGACAT	0		0	0	0	0	0
9358	4121	af	AN1041.1	70.m15198	AO070336000075	0			-200	-105			ATGGAGGACAGCTTTCTTCTGTTCTTCCCATCAGCATTCCTTTCTCACGGTCTCAGCACCTTCCATTCTCTCATTCTGTTCTATCGGCTTCATTGA		ATGGAGGACAGCTTTCTTCTGTTCTTCCCATCAGCATTCCTTTCTCACGGTCTCAGCACCTTCCATTCTCTCATTCTGTTCTATCGGCTTCATTGA		MEDSFLLFFPSAFLSHGLSTFHSLILFYRLH*		MEDSFLLFFPSAFLSHGLSTFHSLILFYRLH*		CTTCGTCACG	CTGAAGTCCT	0	PT	0	0	0	0	0
9355	4121	an	AN1041.1	70.m15198	AO070336000075	0	-237	-217					ATGGGACATGGATGTATATAA	ATGGGACATGGATGTATATAA			MGHGCI*	MGHGCI*			TTGTGGGCAG	AGGCGTTCAA	0	PT	0	0	0	0	0
9356	4121	an	AN1041.1	70.m15198	AO070336000075	0	-230	-192					ATGGATGTATATAAAGGCGTTCAACCTCGACGACAGTAA	ATGGATGTATATAAAGGCGTTCAACCTCGACGACAGTAA			MDVYKGVQPRRQ*	MDVYKGVQPRRQ*			CAGATGGGAC	AGGCTCTTCT	0	PT	0	0	0	0	0
9357	4121	an	AN1041.1	70.m15198	AO070336000075	0	-226	-98					ATGTATATAAAGGCGTTCAACCTCGACGACAGTAAAGGCTCTTCTCTTCTTTCTACCACCAACCCTTGCATTCTTTTCACCAGGATCAACGATCCATTCGTTCTCTTACTTTCCCACTTCATTGATTGA	ATGTATATAAAGGCGTTCAACCTCGACGACAGTAAAGGCTCTTCTCTTCTTTCTACCACCAACCCTTGCATTCTTTTCACCAGGATCAACGATCCATTCGTTCTCTTACTTTCCCACTTCATTGATTGA			MYIKAFNLDDSKGSSLLSTTNPCILFTRINDPFVLLLSHFID*	MYIKAFNLDDSKGSSLLSTTNPCILFTRINDPFVLLLSHFID*			TGGGACATGG	AGTCTGGACA	0	PT	0	0	0	0	0
9359	4121	ao	AN1041.1	70.m15198	AO070336000075	0					-201	-136	ATGATGGATAACGCATTCTTCTCTTCCTCATCAGCTTTACATTCCTTTCTTTCTTTAGGGTCTTAG			ATGATGGATAACGCATTCTTCTCTTCCTCATCAGCTTTACATTCCTTTCTTTCTTTAGGGTCTTAG	MMDNAFFSSSSALHSFLSLGS*			MMDNAFFSSSSALHSFLSLGS*	TCATTTCGCG	AACCTGCCGT	0	PT	0	0	0	0	0
9360	4121	ao	AN1041.1	70.m15198	AO070336000075	0					-198	-136	ATGGATAACGCATTCTTCTCTTCCTCATCAGCTTTACATTCCTTTCTTTCTTTAGGGTCTTAG			ATGGATAACGCATTCTTCTCTTCCTCATCAGCTTTACATTCCTTTCTTTCTTTAGGGTCTTAG	MDNAFFSSSSALHSFLSLGS*			MDNAFFSSSSALHSFLSLGS*	TTTCGCGATG	AACCTGCCGT	0	PT	0	0	0	0	0
9361	4122	af	AN3018.1	59.m08991	AO070337000096	0			-111	-37			ATGCCCTCATCGTCGGTCTGTAAACACATTCTGCGAGAAAAGCTGGAAAAAACTTGTATGGGCGTTCAGAAGTAG		ATGCCCTCATCGTCGGTCTGTAAACACATTCTGCGAGAAAAGCTGGAAAAAACTTGTATGGGCGTTCAGAAGTAG		MPSSSVCKHILREKLEKTCMGVQK*		MPSSSVCKHILREKLEKTCMGVQK*		GCCCACACTT	CAAAATTAAA	0	E	0	MG03562.1	0	0	0
9366	4123	af	AN4943.1	59.m08847	AO070338000001	0			-196	-98			ATGAGAGTAATTGTTGTTGAGATCGTATCGCACTGCATCAGACTCACGCTGTCTCTGTTCTGCCTCAGGCTGCAACGATCTCCGCCTCCGCTCTGGTAG		ATGAGAGTAATTGTTGTTGAGATCGTATCGCACTGCATCAGACTCACGCTGTCTCTGTTCTGCCTCAGGCTGCAACGATCTCCGCCTCCGCTCTGGTAG		MRVIVVEIVSHCIRLTLSLFCLRLQRSPPPLW*		MRVIVVEIVSHCIRLTLSLFCLRLQRSPPPLW*		GGTGCTGTTC	CCTCTTGATT	0	R	0	0	NCU04772.1	0	0
9363	4123	an	AN4943.1	59.m08847	AO070338000001	0	-254	-240					ATGATAAAGCAGTAG	ATGATAAAGCAGTAG			MIKQ*	MIKQ*			CCTCGATAGG	CCAGTCGCAG	0	R	0	0	NCU04772.1	0	0
9364	4123	an	AN4943.1	59.m08847	AO070338000001	0	-226	-167					ATGTGTTGGTTAATAGGCGAGGTCACTGGTTTCCGCAGGATGCACCAAATTTTGGCCTGA	ATGTGTTGGTTAATAGGCGAGGTCACTGGTTTCCGCAGGATGCACCAAATTTTGGCCTGA			MCWLIGEVTGFRRMHQILA*	MCWLIGEVTGFRRMHQILA*			GTCGCAGGCA	GCCCCAAGGC	0	R	0	0	NCU04772.1	0	0
9365	4123	an	AN4943.1	59.m08847	AO070338000001	0	-187	-167					ATGCACCAAATTTTGGCCTGA	ATGCACCAAATTTTGGCCTGA			MHQILA*	MHQILA*			TTTCCGCAGG	GCCCCAAGGC	0	R	0	0	NCU04772.1	0	0
9367	4123	ao	AN4943.1	59.m08847	AO070338000001	0					-180	-166	ATGGATAAACCATAA			ATGGATAAACCATAA	MDKP*			MDKP*	TTGACGAGCA	GACAAGCACC	0	R	0	0	NCU04772.1	0	0
9371	4127	af	AN3658.1	58.m07442	AO070342000030	0			-168	-85			ATGCTGTTCCTGATCACCTCTGTTTCTCTCTTCCCCAGATTACTCATGGGGTCCAGGTTCGGATTCTACTTACTGTGCTCCTAA		ATGCTGTTCCTGATCACCTCTGTTTCTCTCTTCCCCAGATTACTCATGGGGTCCAGGTTCGGATTCTACTTACTGTGCTCCTAA		MLFLITSVSLFPRLLMGSRFGFYLLCS*		MLFLITSVSLFPRLLMGSRFGFYLLCS*		AAAATTGGTC	TATGTACAAT	0	G	0	0	0	YKL221W	0
9372	4127	af	AN3658.1	58.m07442	AO070342000030	0			-123	-85			ATGGGGTCCAGGTTCGGATTCTACTTACTGTGCTCCTAA		ATGGGGTCCAGGTTCGGATTCTACTTACTGTGCTCCTAA		MGSRFGFYLLCS*		MGSRFGFYLLCS*		CAGATTACTC	TATGTACAAT	0	G	0	0	0	YKL221W	0
9373	4127	af	AN3658.1	58.m07442	AO070342000030	0			-83	-72			ATGTACAATTGA		ATGTACAATTGA		MYN*		MYN*		TGCTCCTAAT	GTCGTGGGGA	0	G	0	0	0	YKL221W	0
9368	4127	an	AN3658.1	58.m07442	AO070342000030	0	-177	-163					ATGGAGTTGCTGTAG	ATGGAGTTGCTGTAG			MELL*	MELL*			TCCACGTCTC	GTATATATGC	0	G	0	0	0	YKL221W	0
9369	4127	an	AN3658.1	58.m07442	AO070342000030	0	-156	-118					ATGCCTATGCGCAGTTCAGCCTCTCTCTTGCTGTTATAG	ATGCCTATGCGCAGTTCAGCCTCTCTCTTGCTGTTATAG			MPMRSSASLLLL*	MPMRSSASLLLL*			GTAGGTATAT	AGTCCCTTAT	0	G	0	0	0	YKL221W	0
9370	4127	an	AN3658.1	58.m07442	AO070342000030	0	-150	-118					ATGCGCAGTTCAGCCTCTCTCTTGCTGTTATAG	ATGCGCAGTTCAGCCTCTCTCTTGCTGTTATAG			MRSSASLLLL*	MRSSASLLLL*			ATATATGCCT	AGTCCCTTAT	0	G	0	0	0	YKL221W	0
9374	4127	ao	AN3658.1	58.m07442	AO070342000030	0					-159	-148	ATGTTCCCTTAG			ATGTTCCCTTAG	MFP*			MFP*	TTATTAGTTC	TTTCTTGGAC	0	G	0	0	0	YKL221W	0
9375	4127	ao	AN3658.1	58.m07442	AO070342000030	0					-88	-59	ATGAGCATAGTTATGTCCTCTCATGTATAG			ATGAGCATAGTTATGTCCTCTCATGTATAG	MSIVMSSHV*			MSIVMSSHV*	CTATTCTTTC	TAAGCGGAGG	0	G	0	0	0	YKL221W	0
9376	4127	ao	AN3658.1	58.m07442	AO070342000030	0					-76	-59	ATGTCCTCTCATGTATAG			ATGTCCTCTCATGTATAG	MSSHV*			MSSHV*	GAGCATAGTT	TAAGCGGAGG	0	G	0	0	0	YKL221W	0
9377	4127	ao	AN3658.1	58.m07442	AO070342000030	0					-66	-1	ATGTATAGTAAGCGGAGGGAGAGACGCAAAATCACACATTACTTTTATCTATTTTTCGTCGCATGA			ATGTATAGTAAGCGGAGGGAGAGACGCAAAATCACACATTACTTTTATCTATTTTTCGTCGCATGA	MYSKRRERRKITHYFYLFFVA*			MYSKRRERRKITHYFYLFFVA*	ATGTCCTCTC	ATGGCAGACA	0	G	0	0	0	YKL221W	0
9381	4128	af	AN2148.1	72.m19693	AO070343000197	0			-112	-89			ATGCCGCAGTTTTGCACCGTTTAG		ATGCCGCAGTTTTGCACCGTTTAG		MPQFCTV*		MPQFCTV*		CAGCTCCACC	CCAATTCTTC	0	S	0	0	0	0	0
9378	4128	an	AN2148.1	72.m19693	AO070343000197	0	-201	-76					ATGCTGGAAATTTCGCGTCAGACACAAGCACGTCCACGTCCACGTCGCGAGCAGGAAACGAGTCTCGCGAATGTTGCTTGGTGGATTCTCAGCTCCACCATGCCTCGATTCTCCTCTTTTGCCTAA	ATGCTGGAAATTTCGCGTCAGACACAAGCACGTCCACGTCCACGTCGCGAGCAGGAAACGAGTCTCGCGAATGTTGCTTGGTGGATTCTCAGCTCCACCATGCCTCGATTCTCCTCTTTTGCCTAA			MLEISRQTQARPRPRREQETSLANVAWWILSSTMPRFSSFA*	MLEISRQTQARPRPRREQETSLANVAWWILSSTMPRFSSFA*			CCGCCTACCC	GCTCCCCTCC	0	S	0	0	0	0	0
9379	4128	an	AN2148.1	72.m19693	AO070343000197	0	-102	-76					ATGCCTCGATTCTCCTCTTTTGCCTAA	ATGCCTCGATTCTCCTCTTTTGCCTAA			MPRFSSFA*	MPRFSSFA*			CAGCTCCACC	GCTCCCCTCC	0	S	0	0	0	0	0
9383	4128	ao	AN2148.1	72.m19693	AO070343000197	0					-221	-198	ATGCCTCACCGCCTGCCACAATAA			ATGCCTCACCGCCTGCCACAATAA	MPHRLPQ*			MPHRLPQ*	CCTTAATTGA	GCGACTCGCG	0	S	0	0	0	0	0
9384	4128	ao	AN2148.1	72.m19693	AO070343000197	0					-96	-73	ATGCGTCTGTCTTCTGCCACTTAG			ATGCGTCTGTCTTCTGCCACTTAG	MRLSSAT*			MRLSSAT*	GAGCTCCACT	CCCCAACATC	0	S	0	0	0	0	0
9390	4130	af	AN5902.1	72.m19228	AO070248000040	0			-291	-280			ATGGGCCGATGA		ATGGGCCGATGA		MGR*		MGR*		CAGGGAGAAT	AATATTGATG	0	OKIT	0	0	0	0	0
9391	4130	af	AN5902.1	72.m19228	AO070248000040	0			-283	-272			ATGAAATATTGA		ATGAAATATTGA		MKY*		MKY*		ATATGGGCCG	TGAGCAAGGC	0	OKIT	0	0	0	0	0
9392	4130	af	AN5902.1	72.m19228	AO070248000040	0			-272	-225			ATGAGCAAGGCCCCTCTGAGAGTGAATTATCGCATCAAATCTCTTTAG		ATGAGCAAGGCCCCTCTGAGAGTGAATTATCGCATCAAATCTCTTTAG		MSKAPLRVNYRIKSL*		MSKAPLRVNYRIKSL*		TGAAATATTG	AATTAGGGAA	0	OKIT	0	0	0	0	0
9393	4130	af	AN5902.1	72.m19228	AO070248000040	0			-214	-197			ATGTATTCTATCCAGTGA		ATGTATTCTATCCAGTGA		MYSIQ*		MYSIQ*		AATTAGGGAA	TGCATACACT	0	OKIT	0	0	0	0	0
9394	4130	af	AN5902.1	72.m19228	AO070248000040	0			-197	-183			ATGCATACACTTTAG		ATGCATACACTTTAG		MHTL*		MHTL*		CTATCCAGTG	TTCTTTCATC	0	OKIT	0	0	0	0	0
9395	4130	af	AN5902.1	72.m19228	AO070248000040	0			-146	-96			ATGTTTGAACCGTTTGCAATTGAATTATTTACTGGAGCTTGGATAGCTTAA		ATGTTTGAACCGTTTGCAATTGAATTATTTACTGGAGCTTGGATAGCTTAA		MFEPFAIELFTGAWIA*		MFEPFAIELFTGAWIA*		TGTCAAGGTG	GCTCCATCCA	0	OKIT	0	0	0	0	0
9386	4130	an	AN5902.1	72.m19228	AO070248000040	0	-221	-177					ATGAAAAGATTAGACTCAGGGCCAGTGATACATGACTTCGCTTGA	ATGAAAAGATTAGACTCAGGGCCAGTGATACATGACTTCGCTTGA			MKRLDSGPVIHDFA*	MKRLDSGPVIHDFA*			GAGAAATCGG	CTTAATTCAC	0	OKIT	0	0	0	0	0
9387	4130	an	AN5902.1	72.m19228	AO070248000040	0	-190	-161					ATGACTTCGCTTGACTTAATTCACGTATAG	ATGACTTCGCTTGACTTAATTCACGTATAG			MTSLDLIHV*	MTSLDLIHV*			CCAGTGATAC	CTGTAGTTGC	0	OKIT	0	0	0	0	0
9388	4130	an	AN5902.1	72.m19228	AO070248000040	0	-127	-77					ATGTCGAAGTACGGTTTGTACTGTTTGCAAGCGGTACCATACCGTCGCTAG	ATGTCGAAGTACGGTTTGTACTGTTTGCAAGCGGTACCATACCGTCGCTAG			MSKYGLYCLQAVPYRR*	MSKYGLYCLQAVPYRR*			GGTAGCTGAA	CAGAAGCAAC	0	OKIT	0	0	0	0	0
9396	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-255	-241	ATGCGCAAAACCTAG			ATGCGCAAAACCTAG	MRKT*			MRKT*	GCTTATCGTG	CGACAGTCGT	0	OKIT	0	0	0	0	0
9397	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-216	-175	ATGTTCAGTAAAGGAGGCAACGATGGTCGTCGCAGCGTCTAG			ATGTTCAGTAAAGGAGGCAACGATGGTCGTCGCAGCGTCTAG	MFSKGGNDGRRSV*			MFSKGGNDGRRSV*	ATCATTTAAA	ACCATACATA	0	OKIT	0	0	0	0	0
9398	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-194	-150	ATGGTCGTCGCAGCGTCTAGACCATACATAAAGCTGGGGATATAG			ATGGTCGTCGCAGCGTCTAGACCATACATAAAGCTGGGGATATAG	MVVAASRPYIKLGI*			MVVAASRPYIKLGI*	GGAGGCAACG	AATCGCCCAA	0	OKIT	0	0	0	0	0
9399	4130	ao	AN5902.1	72.m19228	AO070248000040	0					-107	-63	ATGTTTCTCCGCGGTCATTTTAATTTACAGAGTAGTTGTCACTGA			ATGTTTCTCCGCGGTCATTTTAATTTACAGAGTAGTTGTCACTGA	MFLRGHFNLQSSCH*			MFLRGHFNLQSSCH*	TGCAGATTTA	CTCCATGATT	0	OKIT	0	0	0	0	0
9405	4132	af	AN7652.1	57.m05411	AO070268000009	0			-274	-200			ATGGGCAATGTATATAATTGTACATGTACAACAATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGA		ATGGGCAATGTATATAATTGTACATGTACAACAATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGA		MGNVYNCTCTTMTRATSQVLVART*		MGNVYNCTCTTMTRATSQVLVART*		TATGTGAAGG	CAAGACACCA	0	L	0	0	0	0	0
9406	4132	af	AN7652.1	57.m05411	AO070268000009	0			-267	-238			ATGTATATAATTGTACATGTACAACAATGA		ATGTATATAATTGTACATGTACAACAATGA		MYIIVHVQQ*		MYIIVHVQQ*		AGGATGGGCA	CTCGAGCCAC	0	L	0	0	0	0	0
9407	4132	af	AN7652.1	57.m05411	AO070268000009	0			-251	-126			ATGTACAACAATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGACAAGACACCAGCTACGGACATATCTTGATCTTATCTCCGACCACTTTCAAAGATCCCAAAGCCAAGTCAGTTGA		ATGTACAACAATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGACAAGACACCAGCTACGGACATATCTTGATCTTATCTCCGACCACTTTCAAAGATCCCAAAGCCAAGTCAGTTGA		MYNNDSSHIPSVGCTHVTRHQLRTYLDLISDHFQRSQSQVS*		MYNNDSSHIPSVGCTHVTRHQLRTYLDLISDHFQRSQSQVS*		ATAATTGTAC	TACCTCTCTA	0	L	0	0	0	0	0
9408	4132	af	AN7652.1	57.m05411	AO070268000009	0			-241	-200			ATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGA		ATGACTCGAGCCACATCCCAAGTGTTGGTTGCACGCACGTGA		MTRATSQVLVART*		MTRATSQVLVART*		ATGTACAACA	CAAGACACCA	0	L	0	0	0	0	0
9402	4132	an	AN7652.1	57.m05411	AO070268000009	0	-187	-104					ATGAAGTCACTGAACGGAGTTAAGCTATTTTCTCTCCCCGCACGAGCTTGCAGAGCTGCACAGCTCCCTCTTCAAGCCAAATGA	ATGAAGTCACTGAACGGAGTTAAGCTATTTTCTCTCCCCGCACGAGCTTGCAGAGCTGCACAGCTCCCTCTTCAAGCCAAATGA			MKSLNGVKLFSLPARACRAAQLPLQAK*	MKSLNGVKLFSLPARACRAAQLPLQAK*			TAAACTAGTT	TTCAACGACC	0	L	0	0	0	0	0
9403	4132	an	AN7652.1	57.m05411	AO070268000009	0	-107	-90					ATGATTCAACGACCGTAA	ATGATTCAACGACCGTAA			MIQRP*	MIQRP*			TTCAAGCCAA	ACCTTACCCA	0	L	0	0	0	0	0
9409	4132	ao	AN7652.1	57.m05411	AO070268000009	0					-209	-186	ATGACTAAGCAGACCGAGTTATGA			ATGACTAAGCAGACCGAGTTATGA	MTKQTEL*			MTKQTEL*	TTGTAAACAC	AATCATCCCC	0	L	0	0	0	0	0
9410	4132	ao	AN7652.1	57.m05411	AO070268000009	0					-189	-166	ATGAAATCATCCCCGCGGACATAA			ATGAAATCATCCCCGCGGACATAA	MKSSPRT*			MKSSPRT*	AGACCGAGTT	AACCCCACTC	0	L	0	0	0	0	0
9416	4133	af	AN7664.1	57.m05434	AO070268000037	0			-226	-122			ATGATGGAAGCATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGACTGGTATAACTTAGGACAATCCCCGCACCTCTATACGTAA		ATGATGGAAGCATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGACTGGTATAACTTAGGACAATCCCCGCACCTCTATACGTAA		MMEAWQPLTFIRSTPGLHPYDDWYNLGQSPHLYT*		MMEAWQPLTFIRSTPGLHPYDDWYNLGQSPHLYT*		CATGCAGGGG	CCTAACATTC	0	P	0	0	0	0	0
9417	4133	af	AN7664.1	57.m05434	AO070268000037	0			-223	-122			ATGGAAGCATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGACTGGTATAACTTAGGACAATCCCCGCACCTCTATACGTAA		ATGGAAGCATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGACTGGTATAACTTAGGACAATCCCCGCACCTCTATACGTAA		MEAWQPLTFIRSTPGLHPYDDWYNLGQSPHLYT*		MEAWQPLTFIRSTPGLHPYDDWYNLGQSPHLYT*		GCAGGGGATG	CCTAACATTC	0	P	0	0	0	0	0
9418	4133	af	AN7664.1	57.m05434	AO070268000037	0			-215	-162			ATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGA		ATGGCAACCCCTCACGTTTATCAGGTCAACACCTGGGCTTCATCCATACGATGA		MATPHVYQVNTWASSIR*		MATPHVYQVNTWASSIR*		TGATGGAAGC	CTGGTATAAC	0	P	0	0	0	0	0
9419	4133	af	AN7664.1	57.m05434	AO070268000037	0			-165	-148			ATGACTGGTATAACTTAG		ATGACTGGTATAACTTAG		MTGIT*		MTGIT*		CATCCATACG	GACAATCCCC	0	P	0	0	0	0	0

9413	4133	an	AN7664.1	57.m05434	AO070268000037	0	-231	-130					ATGAATGGTGCAGCCATGACAACCCCTCATGCCGTGATTCTTGGTCGCGGCCATCCCCCACCCCAGACGGATCCCCTGTCGGCCTATATAAAGTACGTTTAG	ATGAATGGTGCAGCCATGACAACCCCTCATGCCGTGATTCTTGGTCGCGGCCATCCCCCACCCCAGACGGATCCCCTGTCGGCCTATATAAAGTACGTTTAG			MNGAAMTTPHAVILGRGHPPPQTDPLSAYIKYV*	MNGAAMTTPHAVILGRGHPPPQTDPLSAYIKYV*			GGCACGTATC	AGGACACTCA	0	P	0	0	0	0	0
9414	4133	an	AN7664.1	57.m05434	AO070268000037	0	-227	-213					ATGGTGCAGCCATGA	ATGGTGCAGCCATGA			MVQP*	MVQP*			CGTATCATGA	CAACCCCTCA	0	P	0	0	0	0	0
9415	4133	an	AN7664.1	57.m05434	AO070268000037	0	-216	-130					ATGACAACCCCTCATGCCGTGATTCTTGGTCGCGGCCATCCCCCACCCCAGACGGATCCCCTGTCGGCCTATATAAAGTACGTTTAG	ATGACAACCCCTCATGCCGTGATTCTTGGTCGCGGCCATCCCCCACCCCAGACGGATCCCCTGTCGGCCTATATAAAGTACGTTTAG			MTTPHAVILGRGHPPPQTDPLSAYIKYV*	MTTPHAVILGRGHPPPQTDPLSAYIKYV*			TGGTGCAGCC	AGGACACTCA	0	P	0	0	0	0	0
9420	4133	ao	AN7664.1	57.m05434	AO070268000037	0					-232	-113	ATGGCAACCCCTCACTGCCCTTCGCCTCGTACCTTGCCTCTCCCGCGGCTAGAGCTGGAGTATAAGTGGCTCTCTCGATATCCCTGGAATCTGTCTGGATTGGATCGTTATTCACTTTGA			ATGGCAACCCCTCACTGCCCTTCGCCTCGTACCTTGCCTCTCCCGCGGCTAGAGCTGGAGTATAAGTGGCTCTCTCGATATCCCTGGAATCTGTCTGGATTGGATCGTTATTCACTTTGA	MATPHCPSPRTLPLPRLELEYKWLSRYPWNLSGLDRYSL*			MATPHCPSPRTLPLPRLELEYKWLSRYPWNLSGLDRYSL*	CAGGAGCGCA	TCGTTCCTCT	0	P	0	0	0	0	0
9421	4135	af	AN6345.1	72.m19510	AO070275000008	0			-85	-62			ATGGCCGCAGTGCGTTCTCAGTAG		ATGGCCGCAGTGCGTTCTCAGTAG		MAAVRSQ*		MAAVRSQ*		ACCCCGAGCA	CTCCGCTTTT	0	I	FG02055.1	0	0	0	0
9425	4136	af	AN3368.1	66.m04636	AO070281000024	0			-210	-19			ATGTGCTCATACTACGAACTCATGGAGACGTTGAGATGCTACAGTAAATATGGGGTGCTGACTCTAAATTCGCGGCTTCCCCCGCCAATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		ATGTGCTCATACTACGAACTCATGGAGACGTTGAGATGCTACAGTAAATATGGGGTGCTGACTCTAAATTCGCGGCTTCCCCCGCCAATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		MCSYYELMETLRCYSKYGVLTLNSRLPPPMEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		MCSYYELMETLRCYSKYGVLTLNSRLPPPMEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		TCTCCGTGTT	TTACCCAGAA	0	G	0	0	0	0	0
9426	4136	af	AN3368.1	66.m04636	AO070281000024	0			-189	-19			ATGGAGACGTTGAGATGCTACAGTAAATATGGGGTGCTGACTCTAAATTCGCGGCTTCCCCCGCCAATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		ATGGAGACGTTGAGATGCTACAGTAAATATGGGGTGCTGACTCTAAATTCGCGGCTTCCCCCGCCAATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		METLRCYSKYGVLTLNSRLPPPMEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		METLRCYSKYGVLTLNSRLPPPMEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		CTACGAACTC	TTACCCAGAA	0	G	0	0	0	0	0
9427	4136	af	AN3368.1	66.m04636	AO070281000024	0			-175	-164			ATGCTACAGTAA		ATGCTACAGTAA		MLQ*		MLQ*		AGACGTTGAG	ATATGGGGTG	0	G	0	0	0	0	0
9428	4136	af	AN3368.1	66.m04636	AO070281000024	0			-161	-150			ATGGGGTGCTGA		ATGGGGTGCTGA		MGC*		MGC*		TACAGTAAAT	CTCTAAATTC	0	G	0	0	0	0	0
9429	4136	af	AN3368.1	66.m04636	AO070281000024	0			-123	-19			ATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		ATGGAGGAATGGGGAATCAGAAGATTTCATCCATTCCTTCTCAGTCGTGGCCGGATTCTCCTGAACATCATCAAGTATCCGTTCCGGTTTTCGCGACAGCTCTAG		MEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		MEEWGIRRFHPFLLSRGRILLNIIKYPFRFSRQL*		TCCCCCGCCA	TTACCCAGAA	0	G	0	0	0	0	0
9424	4136	an	AN3368.1	66.m04636	AO070281000024	0	-107	-87					ATGGCAGCCGTCGGCAGTTAA	ATGGCAGCCGTCGGCAGTTAA			MAAVGS*	MAAVGS*			CACAGGATAA	GAATGTTTTG	0	G	0	0	0	0	0
9430	4136	ao	AN3368.1	66.m04636	AO070281000024	0					-241	-200	ATGGCTCAAAGAGGAAATCCCAGCACGTGGGGTGCGGAGTGA			ATGGCTCAAAGAGGAAATCCCAGCACGTGGGGTGCGGAGTGA	MAQRGNPSTWGAE*			MAQRGNPSTWGAE*	TCCGTCCAGA	CACTCCGCAT	0	G	0	0	0	0	0
9431	4136	ao	AN3368.1	66.m04636	AO070281000024	0					-164	-48	ATGAGAATCTGCGCCTTACAACGATCCTTTCAACATGGGGAGCCGGCATCTAAAATCCGGGGAATTTCCACTTTCTGGGGTTCAATGAACACAAGTTTTCTCTGCCCTCTGCTGTGA			ATGAGAATCTGCGCCTTACAACGATCCTTTCAACATGGGGAGCCGGCATCTAAAATCCGGGGAATTTCCACTTTCTGGGGTTCAATGAACACAAGTTTTCTCTGCCCTCTGCTGTGA	MRICALQRSFQHGEPASKIRGISTFWGSMNTSFLCPLL*			MRICALQRSFQHGEPASKIRGISTFWGSMNTSFLCPLL*	GCATACACTT	AGTGTCCGAG	0	G	0	0	0	0	0
9432	4136	ao	AN3368.1	66.m04636	AO070281000024	0					-130	-77	ATGGGGAGCCGGCATCTAAAATCCGGGGAATTTCCACTTTCTGGGGTTCAATGA			ATGGGGAGCCGGCATCTAAAATCCGGGGAATTTCCACTTTCTGGGGTTCAATGA	MGSRHLKSGEFPLSGVQ*			MGSRHLKSGEFPLSGVQ*	TCCTTTCAAC	ACACAAGTTT	0	G	0	0	0	0	0
9433	4136	ao	AN3368.1	66.m04636	AO070281000024	0					-80	-48	ATGAACACAAGTTTTCTCTGCCCTCTGCTGTGA			ATGAACACAAGTTTTCTCTGCCCTCTGCTGTGA	MNTSFLCPLL*			MNTSFLCPLL*	CTGGGGTTCA	AGTGTCCGAG	0	G	0	0	0	0	0
9435	4137	af	AN0233.1	69.m15589	AO070283000035	0			-192	-100			ATGCCTTTCCATCAAGGAGCATCTCAGACCAGGACCTCGGTCAGAGCTATCAACAGGGTCGTCGCGGCCCATCACCAGTCCGCCCTGGCGTAA		ATGCCTTTCCATCAAGGAGCATCTCAGACCAGGACCTCGGTCAGAGCTATCAACAGGGTCGTCGCGGCCCATCACCAGTCCGCCCTGGCGTAA		MPFHQGASQTRTSVRAINRVVAAHHQSALA*		MPFHQGASQTRTSVRAINRVVAAHHQSALA*		GGGTTGCAGG	GCCATCTCCC	0	R	FG05720.1	0	NCU05853.1	0	0
9434	4137	an	AN0233.1	69.m15589	AO070283000035	0	-178	-143					ATGCAGTGCGCATTCCTAGGCATTTTTGGAGATTAA	ATGCAGTGCGCATTCCTAGGCATTTTTGGAGATTAA			MQCAFLGIFGD*	MQCAFLGIFGD*			TGTTGCGCCA	CCATGTCGGT	0	R	FG05720.1	0	NCU05853.1	0	0
9437	4138	af	AN7504.1	57.m05835	AO070287000007	0			-190	-164			ATGTTGGGGAACGGCAGCTCAGTCTAG		ATGTTGGGGAACGGCAGCTCAGTCTAG		MLGNGSSV*		MLGNGSSV*		GTAGGGTTGG	GTTATCAGTC	0		0	MG04163.1	0	0	0
9436	4138	an	AN7504.1	57.m05835	AO070287000007	0	-213	-190					ATGGGGAACTACGGCTCAGTTTAG	ATGGGGAACTACGGCTCAGTTTAG			MGNYGSV*	MGNYGSV*			AGATTGAGTG	TCTGGCTGTG	0		0	MG04163.1	0	0	0
9438	4138	ao	AN7504.1	57.m05835	AO070287000007	0					-169	-140	ATGGGGAACTGCAGTTCCAAGATAGTTTAG			ATGGGGAACTGCAGTTCCAAGATAGTTTAG	MGNCSSKIV*			MGNCSSKIV*	TGATTGAATC	CTGTCTGGCT	0		0	MG04163.1	0	0	0
9440	4142	af	AN8026.1	52.m03630	AO070319000174	0			-98	-78			ATGGGGTACGTTCAGGTATAA		ATGGGGTACGTTCAGGTATAA		MGYVQV*		MGYVQV*		CCAAACCCCC	AAATGTCAAA	0	E	0	0	0	0	0
9441	4142	af	AN8026.1	52.m03630	AO070319000174	0			-75	-43			ATGTCAAACGATCTGTCCCTCGGCCATCGTTGA		ATGTCAAACGATCTGTCCCTCGGCCATCGTTGA		MSNDLSLGHR*		MSNDLSLGHR*		AGGTATAAAA	TTTTTCTTTA	0	E	0	0	0	0	0
9439	4142	an	AN8026.1	52.m03630	AO070319000174	0	-123	-100					ATGGGGCTTGCCCAGATACCCTAG	ATGGGGCTTGCCCAGATACCCTAG			MGLAQIP*	MGLAQIP*			TGGGAAATAT	TGTTACCCGG	0	E	0	0	0	0	0
9442	4142	ao	AN8026.1	52.m03630	AO070319000174	0					-186	-85	ATGATGGCGCCAGTGGCAAGTTATTCCCGCAATCTGTCGTGGTATTTACTTCGTGCCGTAATTGGACGCTTGATCAAGGACGGCTTGAGACAAGTGATATAA			ATGATGGCGCCAGTGGCAAGTTATTCCCGCAATCTGTCGTGGTATTTACTTCGTGCCGTAATTGGACGCTTGATCAAGGACGGCTTGAGACAAGTGATATAA	MMAPVASYSRNLSWYLLRAVIGRLIKDGLRQVI*			MMAPVASYSRNLSWYLLRAVIGRLIKDGLRQVI*	CCTGGGATGG	ATACATCCAA	0	E	0	0	0	0	0
9443	4142	ao	AN8026.1	52.m03630	AO070319000174	0					-183	-85	ATGGCGCCAGTGGCAAGTTATTCCCGCAATCTGTCGTGGTATTTACTTCGTGCCGTAATTGGACGCTTGATCAAGGACGGCTTGAGACAAGTGATATAA			ATGGCGCCAGTGGCAAGTTATTCCCGCAATCTGTCGTGGTATTTACTTCGTGCCGTAATTGGACGCTTGATCAAGGACGGCTTGAGACAAGTGATATAA	MAPVASYSRNLSWYLLRAVIGRLIKDGLRQVI*			MAPVASYSRNLSWYLLRAVIGRLIKDGLRQVI*	GGGATGGATG	ATACATCCAA	0	E	0	0	0	0	0
9446	4143	af	AN0855.1	70.m15454	AO070320000002	0			-225	-151			ATGCAGAAGGCGCCTAACGCAGATAGTGTACAGCGGCTTCTCCATACAGCTGGGAAGTCATCCGAAGCCGATTAA		ATGCAGAAGGCGCCTAACGCAGATAGTGTACAGCGGCTTCTCCATACAGCTGGGAAGTCATCCGAAGCCGATTAA		MQKAPNADSVQRLLHTAGKSSEAD*		MQKAPNADSVQRLLHTAGKSSEAD*		GCTGCTACTC	TGGTCCAATA	0	L	0	0	0	0	0
9447	4143	af	AN0855.1	70.m15454	AO070320000002	0			-151	-104			ATGGTCCAATATCTCTCGATATGGATATGCAAAATAACACTCACGTGA		ATGGTCCAATATCTCTCGATATGGATATGCAAAATAACACTCACGTGA		MVQYLSIWICKITLT*		MVQYLSIWICKITLT*		AAGCCGATTA	CCACGCGCTC	0	L	0	0	0	0	0
9444	4143	an	AN0855.1	70.m15454	AO070320000002	0	-161	-72					ATGAGATTCATCAATTATCCAGTATTTAGCAGGAAAATCGTATGCATACGAAATTGGAGTCACGTGAACACGCGTTCCCATGGCGCCTGA	ATGAGATTCATCAATTATCCAGTATTTAGCAGGAAAATCGTATGCATACGAAATTGGAGTCACGTGAACACGCGTTCCCATGGCGCCTGA			MRFINYPVFSRKIVCIRNWSHVNTRSHGA*	MRFINYPVFSRKIVCIRNWSHVNTRSHGA*			CTGACTCTTA	CGCGAGTCTC	0	L	0	0	0	0	0
9445	4143	an	AN0855.1	70.m15454	AO070320000002	0	-120	-52					ATGCATACGAAATTGGAGTCACGTGAACACGCGTTCCCATGGCGCCTGACGCGAGTCTCTTCCACTTGA	ATGCATACGAAATTGGAGTCACGTGAACACGCGTTCCCATGGCGCCTGACGCGAGTCTCTTCCACTTGA			MHTKLESREHAFPWRLTRVSST*	MHTKLESREHAFPWRLTRVSST*			GGAAAATCGT	ACTTTCAACA	0	L	0	0	0	0	0
9448	4143	ao	AN0855.1	70.m15454	AO070320000002	0					-228	-205	ATGTTTATTACCTATCAAAATTAA			ATGTTTATTACCTATCAAAATTAA	MFITYQN*			MFITYQN*	GCAAACCAGG	GATTCCTACA	0	L	0	0	0	0	0
9449	4143	ao	AN0855.1	70.m15454	AO070320000002	0					-162	-103	ATGGAAATTACTGTATTTAACTATACTTACTTGTTCTGGCAATACTCAACCTCAACCTAG			ATGGAAATTACTGTATTTAACTATACTTACTTGTTCTGGCAATACTCAACCTCAACCTAG	MEITVFNYTYLFWQYSTST*			MEITVFNYTYLFWQYSTST*	TCGGTGCAGA	ATCATGTGAT	0	L	0	0	0	0	0
9452	4144	af	AN4557.1	57.m05569	AO070321000171	0			-228	-91			ATGAGTCAGCAAACCAGCGGAACTGCGAAAAATCCCAGGCCGACGGAAGGTGTCAAGGGCCGGCGGCGAACTGCGTCCGCAAGAGCTCCTCTCAGGCCCGAACAAACATCTACCTATCCTCTTTTTTATCTCATCTAG		ATGAGTCAGCAAACCAGCGGAACTGCGAAAAATCCCAGGCCGACGGAAGGTGTCAAGGGCCGGCGGCGAACTGCGTCCGCAAGAGCTCCTCTCAGGCCCGAACAAACATCTACCTATCCTCTTTTTTATCTCATCTAG		MSQQTSGTAKNPRPTEGVKGRRRTASARAPLRPEQTSTYPLFYLI*		MSQQTSGTAKNPRPTEGVKGRRRTASARAPLRPEQTSTYPLFYLI*		GTTGCGACTG	AGCCTCTATG	0	O	0	0	0	0	0
9450	4144	an	AN4557.1	57.m05569	AO070321000171	0	-234	-130					ATGACTCAGCCGGAACGGCGAAAAAACCAGGTCCGATCCAACCTCCCGAAGGCGGGCGACGACAGACAAGTTCACCAACTGACCTTAACAATTCCAACTGAGTGA	ATGACTCAGCCGGAACGGCGAAAAAACCAGGTCCGATCCAACCTCCCGAAGGCGGGCGACGACAGACAAGTTCACCAACTGACCTTAACAATTCCAACTGAGTGA			MTQPERRKNQVRSNLPKAGDDRQVHQLTLTIPTE*	MTQPERRKNQVRSNLPKAGDDRQVHQLTLTIPTE*			GGCAGACTGG	CACGTATTCA	0	O	0	0	0	0	0
9454	4144	ao	AN4557.1	57.m05569	AO070321000171	0					-241	-170	ATGACTCAGCTACCGGGGCGGAACTACGAAAAAACCCAAAGTCCGACAAAAGGCGGCGGGAACTCAACTTAG			ATGACTCAGCTACCGGGGCGGAACTACGAAAAAACCCAAAGTCCGACAAAAGGCGGCGGGAACTCAACTTAG	MTQLPGRNYEKTQSPTKGGGNST*			MTQLPGRNYEKTQSPTKGGGNST*	CCGTAACCCG	TAACTCAACG	0	O	0	0	0	0	0
9457	4146	af	AN6594.1	62.m03203	AO070326000044	0			-147	-109			ATGGTAAGTATCTGCTTGAAGGGCGGCCGGCCCCGCTGA		ATGGTAAGTATCTGCTTGAAGGGCGGCCGGCCCCGCTGA		MVSICLKGGRPR*		MVSICLKGGRPR*		TAATCCACAA	GTCACTAAAA	0	S	0	0	0	0	0
9458	4146	af	AN6594.1	62.m03203	AO070326000044	0			-87	-76			ATGGATAAATAA		ATGGATAAATAA		MDK*		MDK*		ACTCATAGAT	TCGAGGATCT	0	S	0	0	0	0	0
9456	4146	an	AN6594.1	62.m03203	AO070326000044	0	-145	-122					ATGGCCCATCTTATCGCCGCGTAA	ATGGCCCATCTTATCGCCGCGTAA			MAHLIAA*	MAHLIAA*			TAGATCCACA	AAGCGGCATC	0	S	0	0	0	0	0
9459	4146	ao	AN6594.1	62.m03203	AO070326000044	0					-159	-115	ATGTTCTGTCATATCGGTATTGACTATACTGTAAGAGGCAAGTAA			ATGTTCTGTCATATCGGTATTGACTATACTGTAAGAGGCAAGTAA	MFCHIGIDYTVRGK*			MFCHIGIDYTVRGK*	GGATCTGTAA	TTTGACTCAT	0	S	0	0	0	0	0
9463	4149	af	AN1200.1	70.m15019	AO070331000206	0			-237	-52			ATGTCACATTATATAATCATACTATCATGTAATTTTCTATATTTGCAACTGATACTGCAGACCTTACTCCATAGGCATGGTCCAAGCGGCCGGCATCTCGGGGACCGCGAAACTATTCTCCGGCGGCCAACAGCATCTCCGCAGCAAAGTTTCGTCTTCCAGCGGCAGAAAAAAAAAGTTGGATGA		ATGTCACATTATATAATCATACTATCATGTAATTTTCTATATTTGCAACTGATACTGCAGACCTTACTCCATAGGCATGGTCCAAGCGGCCGGCATCTCGGGGACCGCGAAACTATTCTCCGGCGGCCAACAGCATCTCCGCAGCAAAGTTTCGTCTTCCAGCGGCAGAAAAAAAAAGTTGGATGA		MSHYIIILSCNFLYLQLILQTLLHRHGPSGRHLGDRETILRRPTASPQQSFVFQRQKKKVG*		MSHYIIILSCNFLYLQLILQTLLHRHGPSGRHLGDRETILRRPTASPQQSFVFQRQKKKVG*		ACAACAGTCA	TCGAAGTCAA	0	JK	0	0	0	0	0
9461	4149	an	AN1200.1	70.m15019	AO070331000206	0	-197	-171					ATGCTTGTTACTCTTCGTTTAGCTTAG	ATGCTTGTTACTCTTCGTTTAGCTTAG			MLVTLRLA*	MLVTLRLA*			GCCTGAACAG	TTATTGAACT	0	JK	0	0	0	0	0
9462	4149	an	AN1200.1	70.m15019	AO070331000206	0	-137	-102					ATGCGGTCGGCATCCGGTACCACGTTAGTCCGATAG	ATGCGGTCGGCATCCGGTACCACGTTAGTCCGATAG			MRSASGTTLVR*	MRSASGTTLVR*			GCTTCGCGAA	CCTAGGCGGA	0	JK	0	0	0	0	0
9464	4149	ao	AN1200.1	70.m15019	AO070331000206	0					-254	-201	ATGATCAGAATGATAAACAGAAGGGAACGTTTATCTCCAATATCATGGATATGA			ATGATCAGAATGATAAACAGAAGGGAACGTTTATCTCCAATATCATGGATATGA	MIRMINRRERLSPISWI*			MIRMINRRERLSPISWI*	ATAGGGAAAT	TTAGTTGGAG	0	JK	0	0	0	0	0
9465	4149	ao	AN1200.1	70.m15019	AO070331000206	0					-245	-201	ATGATAAACAGAAGGGAACGTTTATCTCCAATATCATGGATATGA			ATGATAAACAGAAGGGAACGTTTATCTCCAATATCATGGATATGA	MINRRERLSPISWI*			MINRRERLSPISWI*	TATGATCAGA	TTAGTTGGAG	0	JK	0	0	0	0	0
9466	4149	ao	AN1200.1	70.m15019	AO070331000206	0					-210	-181	ATGGATATGATTAGTTGGAGATCTAAATAA			ATGGATATGATTAGTTGGAGATCTAAATAA	MDMISWRSK*			MDMISWRSK*	CTCCAATATC	AAGGTCCGCA	0	JK	0	0	0	0	0
9467	4149	ao	AN1200.1	70.m15019	AO070331000206	0					-204	-181	ATGATTAGTTGGAGATCTAAATAA			ATGATTAGTTGGAGATCTAAATAA	MISWRSK*			MISWRSK*	TATCATGGAT	AAGGTCCGCA	0	JK	0	0	0	0	0
9470	4150	af	AN2997.1	59.m09019	AO070337000120	0			-162	-139			ATGAAATTCACTAAGAATAATTAG		ATGAAATTCACTAAGAATAATTAG		MKFTKNN*		MKFTKNN*		GAACTGTGCG	TCGACGACGC	0	JT	0	0	0	YMR146C	0
9468	4150	an	AN2997.1	59.m09019	AO070337000120	0	-217	-164					ATGCATACGGCCAATAGAGAAGGCTTGGCATTAGTCCCGCAGACTGTGCGATGA	ATGCATACGGCCAATAGAGAAGGCTTGGCATTAGTCCCGCAGACTGTGCGATGA			MHTANREGLALVPQTVR*	MHTANREGLALVPQTVR*			ACTCAGTGTC	AATTCGTGAA	0	JT	0	0	0	YMR146C	0
9469	4150	an	AN2997.1	59.m09019	AO070337000120	0	-167	-117					ATGAAATTCGTGAACTTGTCGGGTGAGGTTCAAGAAAGGCCGCCGCAATAA	ATGAAATTCGTGAACTTGTCGGGTGAGGTTCAAGAAAGGCCGCCGCAATAA			MKFVNLSGEVQERPPQ*	MKFVNLSGEVQERPPQ*			AGACTGTGCG	TCAACCCCGC	0	JT	0	0	0	YMR146C	0

9471	4150	ao	AN2997.1	59.m09019	AO070337000120	0					-162	-58	ATGAAATTCACTAGTCTGACTACGCCGACGAAGAGAGCCGCCAGCACCCCGCCAGCAGTTCCGCCTCAGAAACGATACAGTCGGTCACAGGATCCCAATCTGTGA			ATGAAATTCACTAGTCTGACTACGCCGACGAAGAGAGCCGCCAGCACCCCGCCAGCAGTTCCGCCTCAGAAACGATACAGTCGGTCACAGGATCCCAATCTGTGA	MKFTSLTTPTKRAASTPPAVPPQKRYSRSQDPNL*			MKFTSLTTPTKRAASTPPAVPPQKRYSRSQDPNL*	GGACTGTGCG	TCTAATACCT	0	JT	0	0	0	YMR146C	0
9475	4151	af	AN0248.1	54.m06701	AO070338000241	0			-194	-177			ATGGCGGAGCTGTTTTGA		ATGGCGGAGCTGTTTTGA		MAELF*		MAELF*		TGTTTGCATC	TCTCCGCCGT	0	O	0	MG06786.1	NCU00813.1	0	0
9476	4151	af	AN0248.1	54.m06701	AO070338000241	0			-163	-122			ATGCCAAGAGCTTCAGGACACCTTGCTTCAACACCCAAGTAG		ATGCCAAGAGCTTCAGGACACCTTGCTTCAACACCCAAGTAG		MPRASGHLASTPK*		MPRASGHLASTPK*		CCGCCGTCAC	ACAGCTCTAA	0	O	0	MG06786.1	NCU00813.1	0	0
9477	4151	af	AN0248.1	54.m06701	AO070338000241	0			-82	-41			ATGATACTTGGCTGGTGTGCCTTGCTACTACCTACTCTCTAG		ATGATACTTGGCTGGTGTGCCTTGCTACTACCTACTCTCTAG		MILGWCALLLPTL*		MILGWCALLLPTL*		TTGGACAATC	TCACTAATCA	0	O	0	MG06786.1	NCU00813.1	0	0
9472	4151	an	AN0248.1	54.m06701	AO070338000241	0	-172	-128					ATGCCAAGACTCACGAGCGTCAGGACTGAGGACACCTTGCTTTAA	ATGCCAAGACTCACGAGCGTCAGGACTGAGGACACCTTGCTTTAA			MPRLTSVRTEDTLL*	MPRLTSVRTEDTLL*			CAACCGTGAC	TTCCTCCAGC	0	O	0	MG06786.1	NCU00813.1	0	0
9473	4151	an	AN0248.1	54.m06701	AO070338000241	0	-74	-60					ATGTTTAATCTATGA	ATGTTTAATCTATGA			MFNL*	MFNL*			CCTCTCTGAC	CCATTGACTT	0	O	0	MG06786.1	NCU00813.1	0	0
9474	4151	an	AN0248.1	54.m06701	AO070338000241	0	-63	-19					ATGACCATTGACTTGCTCGTCCATATCGTACAATTAGCCAGGTAG	ATGACCATTGACTTGCTCGTCCATATCGTACAATTAGCCAGGTAG			MTIDLLVHIVQLAR*	MTIDLLVHIVQLAR*			TGTTTAATCT	TAATCCCACA	0	O	0	MG06786.1	NCU00813.1	0	0
9478	4151	ao	AN0248.1	54.m06701	AO070338000241	0					-218	-123	ATGGGCGGAGCGGAAGCTTCCCCGGTCACATGCCAAGAGCGCGTCTTTAGGACACATTGCTTCATTGCTTTTCTTTCAACCTCTGCCCAACCATAA			ATGGGCGGAGCGGAAGCTTCCCCGGTCACATGCCAAGAGCGCGTCTTTAGGACACATTGCTTCATTGCTTTTCTTTCAACCTCTGCCCAACCATAA	MGGAEASPVTCQERVFRTHCFIAFLSTSAQP*			MGGAEASPVTCQERVFRTHCFIAFLSTSAQP*	AAGGGTATTT	ATACGGTTTC	0	O	0	MG06786.1	NCU00813.1	0	0
9479	4151	ao	AN0248.1	54.m06701	AO070338000241	0					-189	-169	ATGCCAAGAGCGCGTCTTTAG			ATGCCAAGAGCGCGTCTTTAG	MPRARL*			MPRARL*	CCCCGGTCAC	GACACATTGC	0	O	0	MG06786.1	NCU00813.1	0	0
9502	4156	af	AN1876.1	57.m05742	AO070341000183	0			-64	-50			ATGTCGCTGCAGTAG		ATGTCGCTGCAGTAG		MSLQ*		MSLQ*		CGCCTTAAAT	CCCGTGCTAC	0	S	0	0	0	0	0
9501	4156	an	AN1876.1	57.m05742	AO070341000183	0	-75	-52					ATGTCCCTCGACTCCTCCGTCTGA	ATGTCCCTCGACTCCTCCGTCTGA			MSLDSSV*	MSLDSSV*			CTCCAACAGA	ACCCGCCCGC	0	S	0	0	0	0	0
9503	4156	ao	AN1876.1	57.m05742	AO070341000183	0					-106	-59	ATGGTCCAATTGCCCGAACTGCGCCGTCGAAATATGTCCCTCCAGTAG			ATGGTCCAATTGCCCGAACTGCGCCGTCGAAATATGTCCCTCCAGTAG	MVQLPELRRRNMSLQ*			MVQLPELRRRNMSLQ*	TCTTCAACGC	TCCTCCTTCG	0	S	0	0	0	0	0
9504	4156	ao	AN1876.1	57.m05742	AO070341000183	0					-73	-59	ATGTCCCTCCAGTAG			ATGTCCCTCCAGTAG	MSLQ*			MSLQ*	CCGTCGAAAT	TCCTCCTTCG	0	S	0	0	0	0	0
9511	4158	af	AN0828.1	70.m15429	AO070255000017	0			-174	-145			ATGTCCATAGGCACATGTGAACCGCGGTAA		ATGTCCATAGGCACATGTGAACCGCGGTAA		MSIGTCEPR*		MSIGTCEPR*		TAAGAGTACG	GTCAACTACG	0	J	0	0	0	0	0
9512	4158	af	AN0828.1	70.m15429	AO070255000017	0			-81	-31			ATGACACTCCCCAAACACTACTTACCCTTTACTGTCGATCCTTCACTTTAG		ATGACACTCCCCAAACACTACTTACCCTTTACTGTCGATCCTTCACTTTAG		MTLPKHYLPFTVDPSL*		MTLPKHYLPFTVDPSL*		GAGCTTAAAT	TAAAAGGGGA	0	J	0	0	0	0	0
9505	4158	an	AN0828.1	70.m15429	AO070255000017	0	-218	-201					ATGATAATCGCATGCTGA	ATGATAATCGCATGCTGA			MIIAC*	MIIAC*			ATCTGAGACC	TTACCCAGAA	0	J	0	0	0	0	0
9506	4158	an	AN0828.1	70.m15429	AO070255000017	0	-207	-94					ATGCTGATTACCCAGAAAGAAGAGATGGCGCAGAATAGACTCATCGATGCCGATGGCGGAGAACAAGAACGAAGAGTGACCAAGAATCACATGCAAAAAGATTGGGCAGCCTGA	ATGCTGATTACCCAGAAAGAAGAGATGGCGCAGAATAGACTCATCGATGCCGATGGCGGAGAACAAGAACGAAGAGTGACCAAGAATCACATGCAAAAAGATTGGGCAGCCTGA			MLITQKEEMAQNRLIDADGGEQERRVTKNHMQKDWAA*	MLITQKEEMAQNRLIDADGGEQERRVTKNHMQKDWAA*			TGATAATCGC	GCTCGGTACG	0	J	0	0	0	0	0
9507	4158	an	AN0828.1	70.m15429	AO070255000017	0	-183	-94					ATGGCGCAGAATAGACTCATCGATGCCGATGGCGGAGAACAAGAACGAAGAGTGACCAAGAATCACATGCAAAAAGATTGGGCAGCCTGA	ATGGCGCAGAATAGACTCATCGATGCCGATGGCGGAGAACAAGAACGAAGAGTGACCAAGAATCACATGCAAAAAGATTGGGCAGCCTGA			MAQNRLIDADGGEQERRVTKNHMQKDWAA*	MAQNRLIDADGGEQERRVTKNHMQKDWAA*			GAAAGAAGAG	GCTCGGTACG	0	J	0	0	0	0	0
9508	4158	an	AN0828.1	70.m15429	AO070255000017	0	-161	-129					ATGCCGATGGCGGAGAACAAGAACGAAGAGTGA	ATGCCGATGGCGGAGAACAAGAACGAAGAGTGA			MPMAENKNEE*	MPMAENKNEE*			AGACTCATCG	CCAAGAATCA	0	J	0	0	0	0	0
9509	4158	an	AN0828.1	70.m15429	AO070255000017	0	-155	-129					ATGGCGGAGAACAAGAACGAAGAGTGA	ATGGCGGAGAACAAGAACGAAGAGTGA			MAENKNEE*	MAENKNEE*			ATCGATGCCG	CCAAGAATCA	0	J	0	0	0	0	0
9510	4158	an	AN0828.1	70.m15429	AO070255000017	0	-117	-94					ATGCAAAAAGATTGGGCAGCCTGA	ATGCAAAAAGATTGGGCAGCCTGA			MQKDWAA*	MQKDWAA*			CAAGAATCAC	GCTCGGTACG	0	J	0	0	0	0	0
9513	4158	ao	AN0828.1	70.m15429	AO070255000017	0					-239	-186	ATGTGTAGAATAATAATGGACATATGTACAGTACGAACTTTAAAGTATAAATAA			ATGTGTAGAATAATAATGGACATATGTACAGTACGAACTTTAAAGTATAAATAA	MCRIIMDICTVRTLKYK*			MCRIIMDICTVRTLKYK*	TATCTAATAA	ATGCATCAAT	0	J	0	0	0	0	0
9514	4158	ao	AN0828.1	70.m15429	AO070255000017	0					-224	-186	ATGGACATATGTACAGTACGAACTTTAAAGTATAAATAA			ATGGACATATGTACAGTACGAACTTTAAAGTATAAATAA	MDICTVRTLKYK*			MDICTVRTLKYK*	TAGAATAATA	ATGCATCAAT	0	J	0	0	0	0	0
9515	4158	ao	AN0828.1	70.m15429	AO070255000017	0					-216	-190	ATGTACAGTACGAACTTTAAAGTATAA			ATGTACAGTACGAACTTTAAAGTATAA	MYSTNFKV*			MYSTNFKV*	TAATGGACAT	ATAAATGCAT	0	J	0	0	0	0	0
9516	4158	ao	AN0828.1	70.m15429	AO070255000017	0					-185	-174	ATGCATCAATAG			ATGCATCAATAG	MHQ*			MHQ*	GTATAAATAA	AGCCGATCAG	0	J	0	0	0	0	0
9517	4158	ao	AN0828.1	70.m15429	AO070255000017	0					-119	-81	ATGCTGAACCGCGGTCCATTGATTGATCAAACAAAATGA			ATGCTGAACCGCGGTCCATTGATTGATCAAACAAAATGA	MLNRGPLIDQTK*			MLNRGPLIDQTK*	GCTGGACCAC	TTTAAACCCA	0	J	0	0	0	0	0
9519	4159	af	AN3177.1	59.m08567	AO070256000013	0			-258	-241			ATGTCGATCTCTCTCTAA		ATGTCGATCTCTCTCTAA		MSISL*		MSISL*		TCAAGTGACC	ATTTCCAGAA	0	S	0	0	0	0	0
9520	4159	af	AN3177.1	59.m08567	AO070256000013	0			-228	-184			ATGCGCAGCCGCCTGTCTGCCTTGGGCCAACGTCTCACGCGATAG		ATGCGCAGCCGCCTGTCTGCCTTGGGCCAACGTCTCACGCGATAG		MRSRLSALGQRLTR*		MRSRLSALGQRLTR*		TTCCAGAAAC	ACCAACTTCC	0	S	0	0	0	0	0
9518	4159	an	AN3177.1	59.m08567	AO070256000013	0	-238	-185					ATGCGCGGCTTTGTCTCTGCCTTGTCCCTCAGCCCTCGCCAATCTTACGCCTAA	ATGCGCGGCTTTGTCTCTGCCTTGTCCCTCAGCCCTCGCCAATCTTACGCCTAA			MRGFVSALSLSPRQSYA*	MRGFVSALSLSPRQSYA*			TTTGACGGCA	CCATCGGCCC	0	S	0	0	0	0	0
9523	4160	af	AN8165.1	53.m03816	AO070266000010	0			-148	-41			ATGTTTCCCCGCAATTTCTCCATCTCCAAATCGTCGAGTCAGAAAGGAAGCCTGCCAATTGATTCGGAGTTAGTTGGAGGTCTCATAACTGCTATGCGCCATTCATAG		ATGTTTCCCCGCAATTTCTCCATCTCCAAATCGTCGAGTCAGAAAGGAAGCCTGCCAATTGATTCGGAGTTAGTTGGAGGTCTCATAACTGCTATGCGCCATTCATAG		MFPRNFSISKSSSQKGSLPIDSELVGGLITAMRHS*		MFPRNFSISKSSSQKGSLPIDSELVGGLITAMRHS*		AAAAGTTGAG	CGATCTGTAT	0	A	0	0	0	0	0
9521	4160	an	AN8165.1	53.m03816	AO070266000010	0	-153	-121					ATGCTCCAAATGTTATTGGTCGTGCTTTTCTAG	ATGCTCCAAATGTTATTGGTCGTGCTTTTCTAG			MLQMLLVVLF*	MLQMLLVVLF*			AGGCCGCTCT	AAAACCCCGT	0	A	0	0	0	0	0
9522	4160	an	AN8165.1	53.m03816	AO070266000010	0	-144	-121					ATGTTATTGGTCGTGCTTTTCTAG	ATGTTATTGGTCGTGCTTTTCTAG			MLLVVLF*	MLLVVLF*			TATGCTCCAA	AAAACCCCGT	0	A	0	0	0	0	0
9527	4161	af	AN4430.1	58.m07895	AO070273000027	0			-218	-201			ATGTTTCCGCTAGTCTAA		ATGTTTCCGCTAGTCTAA		MFPLV*		MFPLV*		GCATCCTCCC	AGAAGGTCTA	0	E	FG06282.1	MG01104.1	0	0	0
9528	4161	af	AN4430.1	58.m07895	AO070273000027	0			-114	-73			ATGCGATTTATGACTACCGACACCGATTCCCTCTCGCCCTAG		ATGCGATTTATGACTACCGACACCGATTCCCTCTCGCCCTAG		MRFMTTDTDSLSP*		MRFMTTDTDSLSP*		CGAGTATAAA	AAAAAGACTC	0	E	FG06282.1	MG01104.1	0	0	0
9529	4161	af	AN4430.1	58.m07895	AO070273000027	0			-105	-73			ATGACTACCGACACCGATTCCCTCTCGCCCTAG		ATGACTACCGACACCGATTCCCTCTCGCCCTAG		MTTDTDSLSP*		MTTDTDSLSP*		AATGCGATTT	AAAAAGACTC	0	E	FG06282.1	MG01104.1	0	0	0
9525	4161	an	AN4430.1	58.m07895	AO070273000027	0	-218	-189					ATGTATATAGAGCGCACTAGTCTACATTAG	ATGTATATAGAGCGCACTAGTCTACATTAG			MYIERTSLH*	MYIERTSLH*			TTGTGGTCAC	GCTAGCGGTA	0	E	FG06282.1	MG01104.1	0	0	0
9526	4161	an	AN4430.1	58.m07895	AO070273000027	0	-138	-94					ATGAGTCAGCTCCCCGAGGTCGGACCCGTGACCGGACCCAGATAA	ATGAGTCAGCTCCCCGAGGTCGGACCCGTGACCGGACCCAGATAA			MSQLPEVGPVTGPR*	MSQLPEVGPVTGPR*			CGGCCGGAGA	AAGGAAATGC	0	E	FG06282.1	MG01104.1	0	0	0
9530	4161	ao	AN4430.1	58.m07895	AO070273000027	0					-213	-163	ATGCTGCACTGGGACCAAAGCGGTATAGCGGTAATGCTCCGGAGTCAGTGA			ATGCTGCACTGGGACCAAAGCGGTATAGCGGTAATGCTCCGGAGTCAGTGA	MLHWDQSGIAVMLRSQ*			MLHWDQSGIAVMLRSQ*	TCAGGTGCCA	CCTTACTCCG	0	E	FG06282.1	MG01104.1	0	0	0
9531	4161	ao	AN4430.1	58.m07895	AO070273000027	0					-180	-163	ATGCTCCGGAGTCAGTGA			ATGCTCCGGAGTCAGTGA	MLRSQ*			MLRSQ*	TATAGCGGTA	CCTTACTCCG	0	E	FG06282.1	MG01104.1	0	0	0
9532	4161	ao	AN4430.1	58.m07895	AO070273000027	0					-103	-65	ATGCGATTTATGACTACAATCCCCATCCGTCAAGTGTGA			ATGCGATTTATGACTACAATCCCCATCCGTCAAGTGTGA	MRFMTTIPIRQV*			MRFMTTIPIRQV*	CGACTATAAA	AGTCACTGCC	0	E	FG06282.1	MG01104.1	0	0	0
9533	4161	ao	AN4430.1	58.m07895	AO070273000027	0					-94	-65	ATGACTACAATCCCCATCCGTCAAGTGTGA			ATGACTACAATCCCCATCCGTCAAGTGTGA	MTTIPIRQV*			MTTIPIRQV*	AATGCGATTT	AGTCACTGCC	0	E	FG06282.1	MG01104.1	0	0	0
9534	4162	an	AN7496.1	57.m05846	AO070287000019	0	-63	-4					ATGTTTCAGAAGTCCTATTGCCACACATCCCGCATTTATAGCTTCAAAACACATGTCTAA	ATGTTTCAGAAGTCCTATTGCCACACATCCCGCATTTATAGCTTCAAAACACATGTCTAA			MFQKSYCHTSRIYSFKTHV*	MFQKSYCHTSRIYSFKTHV*			TATTTCATCT	CAGATGTCGC	0	RP	0	0	0	0	0
9535	4162	ao	AN7496.1	57.m05846	AO070287000019	0					-65	-48	ATGAGTTCAACCTTATAG			ATGAGTTCAACCTTATAG	MSSTL*			MSSTL*	AAGTTTAGCC	TCGCCACTTG	0	RP	0	0	0	0	0
9537	4165	af	AN7252.1	72.m19797	AO070297000007	0			-264	-202			ATGTGGCTTACCTGCTTGGCTCAGCTGCCCTCAACACTTGCATCACCCTCCGACCTCGCTTAA		ATGTGGCTTACCTGCTTGGCTCAGCTGCCCTCAACACTTGCATCACCCTCCGACCTCGCTTAA		MWLTCLAQLPSTLASPSDLA*		MWLTCLAQLPSTLASPSDLA*		TTCCCCGTCC	TCGCAACTCT	0	T	0	0	0	0	0
9538	4165	af	AN7252.1	72.m19797	AO070297000007	0			-189	-166			ATGACCTCGACTGCGATCTTCTAA		ATGACCTCGACTGCGATCTTCTAA		MTSTAIF*		MTSTAIF*		GCAACTCTGG	AGCAGACCAA	0	T	0	0	0	0	0
9539	4165	af	AN7252.1	72.m19797	AO070297000007	0			-138	-97			ATGCACCCCGTCTTCTCACTTTGCAGTCACTCTTTACAGTAG		ATGCACCCCGTCTTCTCACTTTGCAGTCACTCTTTACAGTAG		MHPVFSLCSHSLQ*		MHPVFSLCSHSLQ*		CTCATAATCT	TGTTGCTGCA	0	T	0	0	0	0	0
9536	4165	an	AN7252.1	72.m19797	AO070297000007	0	-200	-141					ATGTGGCACACCCGCTTGGCCGATTCTCGCACACTCTTTAGCTTTCGGGTTCGACAGTGA	ATGTGGCACACCCGCTTGGCCGATTCTCGCACACTCTTTAGCTTTCGGGTTCGACAGTGA			MWHTRLADSRTLFSFRVRQ*	MWHTRLADSRTLFSFRVRQ*			CAGCCATCCC	ATGACACGAT	0	T	0	0	0	0	0
9540	4165	ao	AN7252.1	72.m19797	AO070297000007	0					-228	-169	ATGTGGCACACTCTCTTGGCTGAGACTTCTTCAGCTGCCTATTTGATCTTGATCTCCTGA			ATGTGGCACACTCTCTTGGCTGAGACTTCTTCAGCTGCCTATTTGATCTTGATCTCCTGA	MWHTLLAETSSAAYLILIS*			MWHTLLAETSSAAYLILIS*	CGTCCCGTCC	TTGCGATCGT	0	T	0	0	0	0	0
9547	4167	af	AN5674.1	65.m07400	AO070309000087	0			-212	-189			ATGTATTTGACTCTCTGTGAATGA		ATGTATTTGACTCTCTGTGAATGA		MYLTLCE*		MYLTLCE*		GGCGATTGGT	TGTATCTCCC	0	T	0	0	0	0	0
9548	4167	af	AN5674.1	65.m07400	AO070309000087	0			-192	-163			ATGATGTATCTCCCAAGGCTTTTGTGGTGA		ATGATGTATCTCCCAAGGCTTTTGTGGTGA		MMYLPRLLW*		MMYLPRLLW*		CTCTCTGTGA	AAGATGCACT	0	T	0	0	0	0	0
9549	4167	af	AN5674.1	65.m07400	AO070309000087	0			-189	-163			ATGTATCTCCCAAGGCTTTTGTGGTGA		ATGTATCTCCCAAGGCTTTTGTGGTGA		MYLPRLLW*		MYLPRLLW*		TCTGTGAATG	AAGATGCACT	0	T	0	0	0	0	0
9550	4167	af	AN5674.1	65.m07400	AO070309000087	0			-159	-25			ATGCACTTGATACAGACACTTGTTATTTCATTGTGCTCGAAATCATTCGGCAAGCGACTGATTTACACTTGTGAAGTGGCTGATCGTTGGTCATCTGTTACAGGGTCCCCCCAAGTGCTTACATCCTTCTTGTGA		ATGCACTTGATACAGACACTTGTTATTTCATTGTGCTCGAAATCATTCGGCAAGCGACTGATTTACACTTGTGAAGTGGCTGATCGTTGGTCATCTGTTACAGGGTCCCCCCAAGTGCTTACATCCTTCTTGTGA		MHLIQTLVISLCSKSFGKRLIYTCEVADRWSSVTGSPQVLTSFL*		MHLIQTLVISLCSKSFGKRLIYTCEVADRWSSVTGSPQVLTSFL*		GTGGTGAAAG	TCGGCTGCTC	0	T	0	0	0	0	0
9541	4167	an	AN5674.1	65.m07400	AO070309000087	0	-223	-173					ATGTTGTGCCTCCTCCTTACCCCACTTGTTGAGACTTACAACTATCGGTAG	ATGTTGTGCCTCCTCCTTACCCCACTTGTTGAGACTTACAACTATCGGTAG			MLCLLLTPLVETYNYR*	MLCLLLTPLVETYNYR*			GACCTCATTC	GTGAGTAAAC	0	T	0	0	0	0	0
9542	4167	an	AN5674.1	65.m07400	AO070309000087	0	-137	-63					ATGATCGCCTATTTACTACGCCCCATCAATCTGGCTATGCCTATGCTGGCAATGCAACGCACTCTCTTGTGCTAA	ATGATCGCCTATTTACTACGCCCCATCAATCTGGCTATGCCTATGCTGGCAATGCAACGCACTCTCTTGTGCTAA			MIAYLLRPINLAMPMLAMQRTLLC*	MIAYLLRPINLAMPMLAMQRTLLC*			GTCGAGGCCG	TGCAGTATTC	0	T	0	0	0	0	0
9543	4167	an	AN5674.1	65.m07400	AO070309000087	0	-101	-63					ATGCCTATGCTGGCAATGCAACGCACTCTCTTGTGCTAA	ATGCCTATGCTGGCAATGCAACGCACTCTCTTGTGCTAA			MPMLAMQRTLLC*	MPMLAMQRTLLC*			CAATCTGGCT	TGCAGTATTC	0	T	0	0	0	0	0
9544	4167	an	AN5674.1	65.m07400	AO070309000087	0	-95	-63					ATGCTGGCAATGCAACGCACTCTCTTGTGCTAA	ATGCTGGCAATGCAACGCACTCTCTTGTGCTAA			MLAMQRTLLC*	MLAMQRTLLC*			GGCTATGCCT	TGCAGTATTC	0	T	0	0	0	0	0
9545	4167	an	AN5674.1	65.m07400	AO070309000087	0	-86	-63					ATGCAACGCACTCTCTTGTGCTAA	ATGCAACGCACTCTCTTGTGCTAA			MQRTLLC*	MQRTLLC*			TATGCTGGCA	TGCAGTATTC	0	T	0	0	0	0	0
9546	4167	an	AN5674.1	65.m07400	AO070309000087	0	-63	-28					ATGCAGTATTCAGACATTGCAAGTTCTAGTGGGTGA	ATGCAGTATTCAGACATTGCAAGTTCTAGTGGGTGA			MQYSDIASSSG*	MQYSDIASSSG*			TCTTGTGCTA	TCGAGAGATA	0	T	0	0	0	0	0
9551	4167	ao	AN5674.1	65.m07400	AO070309000087	0					-240	-127	ATGTTGTTATCTTGGAACCTTTACGCTTATCATGCGTTGTCATTTTTAGTTATACTTTCTACCAAGGACTTGTTTTTTACTTACTTTCGTTCCTCCATATCTCTGTGCCTATAG			ATGTTGTTATCTTGGAACCTTTACGCTTATCATGCGTTGTCATTTTTAGTTATACTTTCTACCAAGGACTTGTTTTTTACTTACTTTCGTTCCTCCATATCTCTGTGCCTATAG	MLLSWNLYAYHALSFLVILSTKDLFFTYFRSSISLCL*			MLLSWNLYAYHALSFLVILSTKDLFFTYFRSSISLCL*	TTTGGTCGGT	CCGCTCTGCA	0	T	0	0	0	0	0
9552	4167	ao	AN5674.1	65.m07400	AO070309000087	0					-209	-192	ATGCGTTGTCATTTTTAG			ATGCGTTGTCATTTTTAG	MRCHF*			MRCHF*	TACGCTTATC	TTATACTTTC	0	T	0	0	0	0	0
9555	4173	af	AN4820.1	59.m09459	AO070327000167	0			-202	-179			ATGTACATATCTATATCAAAATAA		ATGTACATATCTATATCAAAATAA		MYISISK*		MYISISK*		TTCTAAGTCG	TACCATACTA	0	C	0	0	0	0	0
9556	4173	af	AN4820.1	59.m09459	AO070327000167	0			-166	-155			ATGTCTGCATGA		ATGTCTGCATGA		MSA*		MSA*		CCATACTACA	TAAACGGCGA	0	C	0	0	0	0	0
9557	4173	af	AN4820.1	59.m09459	AO070327000167	0			-158	-15			ATGATAAACGGCGACACAGGATCACAGCCGAGTTACTGCCGATTAGTGCGGGGTCAAATGGGTGCTGTTGGTGATAAAGTCGCACAGAGCCCCTCATCCTCATCGCTGATCTTCTCAACTCACCCTTCTTCTGCTATCAAATAG		ATGATAAACGGCGACACAGGATCACAGCCGAGTTACTGCCGATTAGTGCGGGGTCAAATGGGTGCTGTTGGTGATAAAGTCGCACAGAGCCCCTCATCCTCATCGCTGATCTTCTCAACTCACCCTTCTTCTGCTATCAAATAG		MINGDTGSQPSYCRLVRGQMGAVGDKVAQSPSSSSLIFSTHPSSAIK*		MINGDTGSQPSYCRLVRGQMGAVGDKVAQSPSSSSLIFSTHPSSAIK*		CAATGTCTGC	AGAACATGTC	0	C	0	0	0	0	0

9558	4173	af	AN4820.1	59.m09459	AO070327000167	0			-101	-15			ATGGGTGCTGTTGGTGATAAAGTCGCACAGAGCCCCTCATCCTCATCGCTGATCTTCTCAACTCACCCTTCTTCTGCTATCAAATAG		ATGGGTGCTGTTGGTGATAAAGTCGCACAGAGCCCCTCATCCTCATCGCTGATCTTCTCAACTCACCCTTCTTCTGCTATCAAATAG		MGAVGDKVAQSPSSSSLIFSTHPSSAIK*		MGAVGDKVAQSPSSSSLIFSTHPSSAIK*		GCGGGGTCAA	AGAACATGTC	0	C	0	0	0	0	0
9554	4173	an	AN4820.1	59.m09459	AO070327000167	0	-120	-13					ATGAGGGGTTGCGGGGTCAATCCCAATAACTATCCTGCCTGCGTCACTTCTTCTCGTCTCCATCTCCTTCGTCTCTACCATCTCCCTTCGAATAATTCCATCCAGTAA	ATGAGGGGTTGCGGGGTCAATCCCAATAACTATCCTGCCTGCGTCACTTCTTCTCGTCTCCATCTCCTTCGTCTCTACCATCTCCCTTCGAATAATTCCATCCAGTAA			MRGCGVNPNNYPACVTSSRLHLLRLYHLPSNNSIQ*	MRGCGVNPNNYPACVTSSRLHLLRLYHLPSNNSIQ*			TGCCGATAAG	GAGTGGCTAA	0	C	0	0	0	0	0
9559	4173	ao	AN4820.1	59.m09459	AO070327000167	0					-210	-13	ATGGGCGGGGACTTTGATATATCCTGTGACAAGTTTTCACTACCATTGCCGAGGGTAAGAAAATCCAAAGAGGGGTTGCGCTGCGGGGTTGAAAGAGCATCCCAGATGCCTATAAATTTTGATCTCCCCCTTTCTCTTCCTCCCGGTATTTATTTCTCTGTAGCGACGGAATCCACAGGGTCAACCGTACAGACATAG			ATGGGCGGGGACTTTGATATATCCTGTGACAAGTTTTCACTACCATTGCCGAGGGTAAGAAAATCCAAAGAGGGGTTGCGCTGCGGGGTTGAAAGAGCATCCCAGATGCCTATAAATTTTGATCTCCCCCTTTCTCTTCCTCCCGGTATTTATTTCTCTGTAGCGACGGAATCCACAGGGTCAACCGTACAGACATAG	MGGDFDISCDKFSLPLPRVRKSKEGLRCGVERASQMPINFDLPLSLPPGIYFSVATESTGSTVQT*			MGGDFDISCDKFSLPLPRVRKSKEGLRCGVERASQMPINFDLPLSLPPGIYFSVATESTGSTVQT*	TTCGAAAGCA	TAGTAGTTCA	0	C	0	0	0	0	0
9560	4173	ao	AN4820.1	59.m09459	AO070327000167	0					-105	-13	ATGCCTATAAATTTTGATCTCCCCCTTTCTCTTCCTCCCGGTATTTATTTCTCTGTAGCGACGGAATCCACAGGGTCAACCGTACAGACATAG			ATGCCTATAAATTTTGATCTCCCCCTTTCTCTTCCTCCCGGTATTTATTTCTCTGTAGCGACGGAATCCACAGGGTCAACCGTACAGACATAG	MPINFDLPLSLPPGIYFSVATESTGSTVQT*			MPINFDLPLSLPPGIYFSVATESTGSTVQT*	AGCATCCCAG	TAGTAGTTCA	0	C	0	0	0	0	0
9562	4174	af	AN4818.1	59.m09157	AO070327000169	0			-97	-80			ATGGATCTCAACGTTTGA		ATGGATCTCAACGTTTGA		MDLNV*		MDLNV*		GGGCCAAGAA	ATATCGGACC	0	T	0	0	0	0	0
9561	4174	an	AN4818.1	59.m09157	AO070327000169	0	-81	-70					ATGTGGTGGTAG	ATGTGGTGGTAG			MWW*	MWW*			GAATTCGACG	GAAAAAAAAA	0	T	0	0	0	0	0
9563	4174	ao	AN4818.1	59.m09157	AO070327000169	0					-89	-75	ATGGAGTGCGACTGA			ATGGAGTGCGACTGA	MECD*			MECD*	AGGACTGACG	AACCCTTAAA	0	T	0	0	0	0	0
9567	4179	af	AN1052.1	70.m15191	AO070336000059	0			-104	-90			ATGCCAACACTATAG		ATGCCAACACTATAG		MPTL*		MPTL*		AAGCGATTCG	CCGTCATCTA	0	WV	0	0	0	0	0
9570	4180	af	AN4608.1	65.m07143	AO070337000243	0			-155	-105			ATGGCCAGACTGATGAGGGCTACGTCAAGTCATGTATACCTTCAAGACTGA		ATGGCCAGACTGATGAGGGCTACGTCAAGTCATGTATACCTTCAAGACTGA		MARLMRATSSHVYLQD*		MARLMRATSSHVYLQD*		AACATTAGTC	AGATAAAAGG	0	MG	0	0	0	0	0
9571	4180	af	AN4608.1	65.m07143	AO070337000243	0			-143	-105			ATGAGGGCTACGTCAAGTCATGTATACCTTCAAGACTGA		ATGAGGGCTACGTCAAGTCATGTATACCTTCAAGACTGA		MRATSSHVYLQD*		MRATSSHVYLQD*		GGCCAGACTG	AGATAAAAGG	0	MG	0	0	0	0	0
9572	4180	af	AN4608.1	65.m07143	AO070337000243	0			-124	-89			ATGTATACCTTCAAGACTGAAGATAAAAGGACTTGA		ATGTATACCTTCAAGACTGAAGATAAAAGGACTTGA		MYTFKTEDKRT*		MYTFKTEDKRT*		ACGTCAAGTC	TTAGTAGCAG	0	MG	0	0	0	0	0
9573	4180	af	AN4608.1	65.m07143	AO070337000243	0			-73	-17			ATGACTATCAACAAGATCTTCAATTCCCAACAACTCAACTTTCATCGACTATCATAG		ATGACTATCAACAAGATCTTCAATTCCCAACAACTCAACTTTCATCGACTATCATAG		MTINKIFNSQQLNFHRLS*		MTINKIFNSQQLNFHRLS*		AGCAGGAGCC	CTATCAATTC	0	MG	0	0	0	0	0
9568	4180	an	AN4608.1	65.m07143	AO070337000243	0	-199	-107					ATGATTGGCCACTTCGGGTTTGTTGACGGGTGGCTCTCCGTTATGCGTCAGGATTCAATCCTTCAGAAGTATGTGAGTGCTAAAGGTATATAA	ATGATTGGCCACTTCGGGTTTGTTGACGGGTGGCTCTCCGTTATGCGTCAGGATTCAATCCTTCAGAAGTATGTGAGTGCTAAAGGTATATAA			MIGHFGFVDGWLSVMRQDSILQKYVSAKGI*	MIGHFGFVDGWLSVMRQDSILQKYVSAKGI*			TGAAGGATCC	GGGTGCTGGT	0	MG	0	0	0	0	0
9569	4180	an	AN4608.1	65.m07143	AO070337000243	0	-157	-107					ATGCGTCAGGATTCAATCCTTCAGAAGTATGTGAGTGCTAAAGGTATATAA	ATGCGTCAGGATTCAATCCTTCAGAAGTATGTGAGTGCTAAAGGTATATAA			MRQDSILQKYVSAKGI*	MRQDSILQKYVSAKGI*			GCTCTCCGTT	GGGTGCTGGT	0	MG	0	0	0	0	0
9574	4180	ao	AN4608.1	65.m07143	AO070337000243	0					-202	-185	ATGTTGACTGAGGGGTAA			ATGTTGACTGAGGGGTAA	MLTEG*			MLTEG*	TCTCCAGAAC	GAGATACAAT	0	MG	0	0	0	0	0
9575	4180	ao	AN4608.1	65.m07143	AO070337000243	0					-125	-96	ATGATGTTGGACCAAGATACTATTGACTAG			ATGATGTTGGACCAAGATACTATTGACTAG	MMLDQDTID*			MMLDQDTID*	GGCACAATCC	AAGCAAACAC	0	MG	0	0	0	0	0
9576	4180	ao	AN4608.1	65.m07143	AO070337000243	0					-122	-96	ATGTTGGACCAAGATACTATTGACTAG			ATGTTGGACCAAGATACTATTGACTAG	MLDQDTID*			MLDQDTID*	ACAATCCATG	AAGCAAACAC	0	MG	0	0	0	0	0
9579	4181	af	AN2899.1	59.m08749	AO070338000108	0			-61	-29			ATGTTCACGACTTCATTGAAAGTTCCAGATTGA		ATGTTCACGACTTCATTGAAAGTTCCAGATTGA		MFTTSLKVPD*		MFTTSLKVPD*		TACCTCGGGA	ATTATTCACA	0	T	0	0	0	0	0
9577	4181	an	AN2899.1	59.m08749	AO070338000108	0	-173	-87					ATGTGCCCACCTTCTCGTTCTCCCATCTACAACCTCTTATATCTTAATGTGCCCATCCCTTCGGTATCCGCGGGTTATATGGCCTAA	ATGTGCCCACCTTCTCGTTCTCCCATCTACAACCTCTTATATCTTAATGTGCCCATCCCTTCGGTATCCGCGGGTTATATGGCCTAA			MCPPSRSPIYNLLYLNVPIPSVSAGYMA*	MCPPSRSPIYNLLYLNVPIPSVSAGYMA*			CTTGCTTGAT	AACCAGTTGA	0	T	0	0	0	0	0
9578	4181	an	AN2899.1	59.m08749	AO070338000108	0	-127	-77					ATGTGCCCATCCCTTCGGTATCCGCGGGTTATATGGCCTAAAACCAGTTGA	ATGTGCCCATCCCTTCGGTATCCGCGGGTTATATGGCCTAAAACCAGTTGA			MCPSLRYPRVIWPKTS*	MCPSLRYPRVIWPKTS*			TTATATCTTA	GGAGCGCTAA	0	T	0	0	0	0	0
9580	4181	ao	AN2899.1	59.m08749	AO070338000108	0					-159	-142	ATGTCTCTCGTCTGTTAG			ATGTCTCTCGTCTGTTAG	MSLVC*			MSLVC*	CTCCCTTGTT	CCCCTCCAAA	0	T	0	0	0	0	0
9581	4181	ao	AN2899.1	59.m08749	AO070338000108	0					-104	-93	ATGACTTCATAA			ATGACTTCATAA	MTS*			MTS*	GCCTGTCCGC	ATTCGATGCT	0	T	0	0	0	0	0
9582	4181	ao	AN2899.1	59.m08749	AO070338000108	0					-87	-34	ATGCTCACGGGTTATGGTTTACAAATGAAAATTTCACCTTTTAATTCAACTTGA			ATGCTCACGGGTTATGGTTTACAAATGAAAATTTCACCTTTTAATTCAACTTGA	MLTGYGLQMKISPFNST*			MLTGYGLQMKISPFNST*	CATAAATTCG	CCAAGTCTTC	0	T	0	0	0	0	0
9583	4181	ao	AN2899.1	59.m08749	AO070338000108	0					-74	-60	ATGGTTTACAAATGA			ATGGTTTACAAATGA	MVYK*			MVYK*	CTCACGGGTT	AAATTTCACC	0	T	0	0	0	0	0
9584	4181	ao	AN2899.1	59.m08749	AO070338000108	0					-63	-34	ATGAAAATTTCACCTTTTAATTCAACTTGA			ATGAAAATTTCACCTTTTAATTCAACTTGA	MKISPFNST*			MKISPFNST*	TGGTTTACAA	CCAAGTCTTC	0	T	0	0	0	0	0
9585	4182	af	AN6017.1	72.m19936	AO070340000258	0			-169	-122			ATGTGGTGGTTTTCCTTCTCTCTCTTCCTCACCTTACCTGGTCGTTGA		ATGTGGTGGTTTTCCTTCTCTCTCTTCCTCACCTTACCTGGTCGTTGA		MWWFSFSLFLTLPGR*		MWWFSFSLFLTLPGR*		AAAGAGAAAG	GCTTGTAGAG	0	J	0	0	0	0	0
9587	4183	af	AN3946.1	69.m14975	AO070341000066	0			-174	-88			ATGAATTTGTTCAATGATCCATCCACTGACGACTTCTCGACTTCCTCAATCCCAATCCTCAATCTGACGCATCCGAACTGCGATTGA		ATGAATTTGTTCAATGATCCATCCACTGACGACTTCTCGACTTCCTCAATCCCAATCCTCAATCTGACGCATCCGAACTGCGATTGA		MNLFNDPSTDDFSTSSIPILNLTHPNCD*		MNLFNDPSTDDFSTSSIPILNLTHPNCD*		TCAACTTTCA	CGATACCGTG	0	D	0	0	0	0	0
9588	4183	af	AN3946.1	69.m14975	AO070341000066	0			-161	-108			ATGATCCATCCACTGACGACTTCTCGACTTCCTCAATCCCAATCCTCAATCTGA		ATGATCCATCCACTGACGACTTCTCGACTTCCTCAATCCCAATCCTCAATCTGA		MIHPLTTSRLPQSQSSI*		MIHPLTTSRLPQSQSSI*		AATTTGTTCA	CGCATCCGAA	0	D	0	0	0	0	0
9586	4183	an	AN3946.1	69.m14975	AO070341000066	0	-174	-109					ATGAACTCGACCATTTCAACGACCATCGACACCCACGACAGCCCTTCGGAATTCGGCCGCTCCTGA	ATGAACTCGACCATTTCAACGACCATCGACACCCACGACAGCCCTTCGGAATTCGGCCGCTCCTGA			MNSTISTTIDTHDSPSEFGRS*	MNSTISTTIDTHDSPSEFGRS*			GGAAAAGCTG	CTCTCGCTTT	0	D	0	0	0	0	0
9589	4184	af	AN7566.1	72.m19585	AO070343000409	0			-126	-106			ATGCCGAGTTCGGTTTTGTAA		ATGCCGAGTTCGGTTTTGTAA		MPSSVL*		MPSSVL*		TGACTGCTTT	TCTAGGACAG	0	L	0	0	0	YGR276C	YGR276C
9590	4184	af	AN7566.1	72.m19585	AO070343000409	0			-76	-35			ATGTCCCATATCTTAAGTGATTGCAACATACCTAGCCACTAA		ATGTCCCATATCTTAAGTGATTGCAACATACCTAGCCACTAA		MSHILSDCNIPSH*		MSHILSDCNIPSH*		AGGAACACGG	ATATCTGCTT	0	L	0	0	0	YGR276C	YGR276C
9591	4184	ao	AN7566.1	72.m19585	AO070343000409	0					-242	-150	ATGTCTGAGTCATCAGTGCACGTCGATCTACTATCGGCACGTGATACAAAAAGTCGATTGATAAATCCCGATCCGGGAGTTATCAAGCTCTAG			ATGTCTGAGTCATCAGTGCACGTCGATCTACTATCGGCACGTGATACAAAAAGTCGATTGATAAATCCCGATCCGGGAGTTATCAAGCTCTAG	MSESSVHVDLLSARDTKSRLINPDPGVIKL*			MSESSVHVDLLSARDTKSRLINPDPGVIKL*	CGTTATTGCT	AGACCGATCA	0	L	0	0	0	YGR276C	YGR276C
9595	4185	af	AN0706.1	70.m15313	AO070343000503	0			-229	-200			ATGAAGGCGGGATTTCGGCGCTATTCTTGA		ATGAAGGCGGGATTTCGGCGCTATTCTTGA		MKAGFRRYS*		MKAGFRRYS*		CTGCGATAAG	CGCGGTTCCG	0	U	0	0	0	0	0
9596	4185	af	AN0706.1	70.m15313	AO070343000503	0			-109	-86			ATGACAACGCAATTGGAATTGTGA		ATGACAACGCAATTGGAATTGTGA		MTTQLEL*		MTTQLEL*		TGTTGTGGTG	GCTTATTTTG	0	U	0	0	0	0	0
9593	4185	an	AN0706.1	70.m15313	AO070343000503	0	-241	-161					ATGCGACAGGCGAGAGTCGCCGGCCGAAGGTTGCGGCTGTCGGCGCTTCCTTTGTCGCGGTTCCGACTGGCTCTATGGTAG	ATGCGACAGGCGAGAGTCGCCGGCCGAAGGTTGCGGCTGTCGGCGCTTCCTTTGTCGCGGTTCCGACTGGCTCTATGGTAG			MRQARVAGRRLRLSALPLSRFRLALW*	MRQARVAGRRLRLSALPLSRFRLALW*			GACTCTGCGA	CGGCCACTTG	0	U	0	0	0	0	0
9594	4185	an	AN0706.1	70.m15313	AO070343000503	0	-167	-135					ATGGTAGCGGCCACTTGGCGGTGGGCTTGTTGA	ATGGTAGCGGCCACTTGGCGGTGGGCTTGTTGA			MVAATWRWAC*	MVAATWRWAC*			GACTGGCTCT	CTTGTAATGT	0	U	0	0	0	0	0
9597	4185	ao	AN0706.1	70.m15313	AO070343000503	0					-128	-105	ATGAACAACTCACCTTGTTTGTGA			ATGAACAACTCACCTTGTTTGTGA	MNNSPCL*			MNNSPCL*	TAGCTTCGGA	ACTAACCCCC	0	U	0	0	0	0	0
9592	4185	conserved	AN0706.1	70.m15313	AO070343000503	0	-63	-28	-63	-28	-63	-28	ATGymTrwhdwyTGsTAydyCybCGGCyrsCGGTGA	ATGTATATCGATTGCTACTCCTCCGGCCACCGGTGA	ATGCCTGAATATTGCTACGCCCTCGGCCGGCGGTGA	ATGCCTAATATCTGGTATATCCGCGGCTGGCGGTGA	MyidcYssGhR*	MYIDCYSSGHR*	MPEYCYALGRR*	MPNIWYIRGWR*	mrryyrTTCr	yCATGAwAyw	0	U	0	0	0	0	0
9601	4189	af	AN6443.1	58.m08930	AO070238000002	0			-193	-182			ATGGCTCACTAA		ATGGCTCACTAA		MAH*		MAH*		AACAAGTGGA	CTTGACGAAC	0	Q	0	0	0	YGR281W	0
9598	4189	an	AN6443.1	58.m08930	AO070238000002	0	-253	-230					ATGCGTTTTCACCAGAAATCCTGA	ATGCGTTTTCACCAGAAATCCTGA			MRFHQKS*	MRFHQKS*			TTTTTTGTTG	TAGTACCTGA	0	Q	0	0	0	YGR281W	0
9599	4189	an	AN6443.1	58.m08930	AO070238000002	0	-153	-16					ATGAGAAGAACGCTTAGTAATGGGCCACCCGGGTATCGGCACCCTTATCGCCGATACCACCGATGGCTCCCATCAAGACTGTCCTCTTTATCCTGTGCTCCCCCCACGGGTCGTGACTCCGTCGCAGCCTCGAGATGA	ATGAGAAGAACGCTTAGTAATGGGCCACCCGGGTATCGGCACCCTTATCGCCGATACCACCGATGGCTCCCATCAAGACTGTCCTCTTTATCCTGTGCTCCCCCCACGGGTCGTGACTCCGTCGCAGCCTCGAGATGA			MRRTLSNGPPGYRHPYRRYHRWLPSRLSSLSCAPPTGRDSVAASR*	MRRTLSNGPPGYRHPYRRYHRWLPSRLSSLSCAPPTGRDSVAASR*			GGGCTGACCA	GATCCTCTCA	0	Q	0	0	0	YGR281W	0
9600	4189	an	AN6443.1	58.m08930	AO070238000002	0	-91	-38					ATGGCTCCCATCAAGACTGTCCTCTTTATCCTGTGCTCCCCCCACGGGTCGTGA	ATGGCTCCCATCAAGACTGTCCTCTTTATCCTGTGCTCCCCCCACGGGTCGTGA			MAPIKTVLFILCSPHGS*	MAPIKTVLFILCSPHGS*			GATACCACCG	CTCCGTCGCA	0	Q	0	0	0	YGR281W	0
9604	4189	ao	AN6443.1	58.m08930	AO070238000002	0					-216	-163	ATGCATAACTTGATCCAGTGCCTCTGCCTGACAGGATTGGCTGACTACATTTAA			ATGCATAACTTGATCCAGTGCCTCTGCCTGACAGGATTGGCTGACTACATTTAA	MHNLIQCLCLTGLADYI*			MHNLIQCLCLTGLADYI*	TTACTTTACT	GGGGTTGACC	0	Q	0	0	0	YGR281W	0
9605	4189	ao	AN6443.1	58.m08930	AO070238000002	0					-118	-92	ATGAAAGTACTTATCCCCTTTACCTGA			ATGAAAGTACTTATCCCCTTTACCTGA	MKVLIPFT*			MKVLIPFT*	CAAGAATGAC	TTTGATGAAC	0	Q	0	0	0	YGR281W	0
9606	4189	ao	AN6443.1	58.m08930	AO070238000002	0					-74	-45	ATGGAAGAGAGTCTCGTGGATCATTGCTAG			ATGGAAGAGAGTCTCGTGGATCATTGCTAG	MEESLVDHC*			MEESLVDHC*	AACCTGCTGT	CTGTCTGTCG	0	Q	0	0	0	YGR281W	0
9607	4190	ao	AN1375.1	70.m15754	AO070243000005	0					-149	-138	ATGAGTCGTTGA			ATGAGTCGTTGA	MSR*			MSR*	AGTATTCCTC	AATCTTCCGA	0		0	0	0	0	0
9608	4190	ao	AN1375.1	70.m15754	AO070243000005	0					-113	-96	ATGGTATACATAACCTGA			ATGGTATACATAACCTGA	MVYIT*			MVYIT*	GATTCGCTTG	CCTCTTTTAC	0		0	0	0	0	0
9610	4193	an	AN8742.1	62.m03338	AO070250000039	0	-93	-70					ATGACCGGGATGGGAGGACAATAA	ATGACCGGGATGGGAGGACAATAA			MTGMGGQ*	MTGMGGQ*			GTCGCCCTCA	CGGATCTCGC	0	BDL	0	0	0	0	0
9611	4193	an	AN8742.1	62.m03338	AO070250000039	0	-84	-70					ATGGGAGGACAATAA	ATGGGAGGACAATAA			MGGQ*	MGGQ*			AATGACCGGG	CGGATCTCGC	0	BDL	0	0	0	0	0
9612	4193	ao	AN8742.1	62.m03338	AO070250000039	0					-174	-52	ATGACAATAAACTGCCACCCACGACCGCCTAACCAAAACACAACTAGATTGATAGATCCACGGCGCGTCGCGACCGCGCTGATCATCGCATTTAAGCCCCAAAACCACAATATTTATCCATGA			ATGACAATAAACTGCCACCCACGACCGCCTAACCAAAACACAACTAGATTGATAGATCCACGGCGCGTCGCGACCGCGCTGATCATCGCATTTAAGCCCCAAAACCACAATATTTATCCATGA	MTINCHPRPPNQNTTRLIDPRRVATALIIAFKPQNHNIYP*			MTINCHPRPPNQNTTRLIDPRRVATALIIAFKPQNHNIYP*	GAAACCCAAA	ATACCAGATG	0	BDL	0	0	0	0	0
9614	4194	af	AN2455.1	69.m15204	AO070264000021	0			-98	-78			ATGCTTTGTAATATATTGTAG		ATGCTTTGTAATATATTGTAG		MLCNIL*		MLCNIL*		TTTGGGCCCA	TCCCTCTATT	0	R	0	0	0	0	0
9616	4195	af	AN6678.1	65.m07302	AO070289000018	0			-116	-42			ATGGAACACTCGTGTCAGCGCGTCGTTGGCCATCAAATTGATACTAGTGATGCTGTCTACAGAGAGTCTCTCTAA		ATGGAACACTCGTGTCAGCGCGTCGTTGGCCATCAAATTGATACTAGTGATGCTGTCTACAGAGAGTCTCTCTAA		MEHSCQRVVGHQIDTSDAVYRESL*		MEHSCQRVVGHQIDTSDAVYRESL*		CTTTTCGTGG	GAATTTCATT	0	S	0	0	0	0	0
9615	4195	an	AN6678.1	65.m07302	AO070289000018	0	-101	-36					ATGCCCTCGGTTGGTCCGAGATATTTATATATATTGATAACGCGCGATTACCTTATTTCGCTTTAG	ATGCCCTCGGTTGGTCCGAGATATTTATATATATTGATAACGCGCGATTACCTTATTTCGCTTTAG			MPSVGPRYLYILITRDYLISL*	MPSVGPRYLYILITRDYLISL*			TGTGCCTGGA	AATCCGATCG	0	S	0	0	0	0	0
9617	4195	ao	AN6678.1	65.m07302	AO070289000018	0					-82	-59	ATGTTGGCGTTAGGTCGTAGATAA			ATGTTGGCGTTAGGTCGTAGATAA	MLALGRR*			MLALGRR*	CGCCATTTGG	GGGTTTCTTG	0	S	0	0	0	0	0
9620	4196	af	AN1150.1	72.m19355	AO070308000028	0			-231	-187			ATGCGGAGTGGCGGAGATGGCATCGAGTCATTTCTTACTGCGTGA		ATGCGGAGTGGCGGAGATGGCATCGAGTCATTTCTTACTGCGTGA		MRSGGDGIESFLTA*		MRSGGDGIESFLTA*		ACAAGTGGAA	AGTTTGCCCG	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9621	4196	af	AN1150.1	72.m19355	AO070308000028	0			-215	-57			ATGGCATCGAGTCATTTCTTACTGCGTGAAGTTTGCCCGATAAGCGGGCCGCCCGATATCGCGGCACATTTCTGGGTCCATCACAGTCACAGTCTCAGTCATCAACTTTATGACTCTGACTCTCCTTGTCTAATTCCTATATATTTATTTCTTTCTTGA		ATGGCATCGAGTCATTTCTTACTGCGTGAAGTTTGCCCGATAAGCGGGCCGCCCGATATCGCGGCACATTTCTGGGTCCATCACAGTCACAGTCTCAGTCATCAACTTTATGACTCTGACTCTCCTTGTCTAATTCCTATATATTTATTTCTTTCTTGA		MASSHFLLREVCPISGPPDIAAHFWVHHSHSLSHQLYDSDSPCLIPIYLFLS*		MASSHFLLREVCPISGPPDIAAHFWVHHSHSLSHQLYDSDSPCLIPIYLFLS*		AGTGGCGGAG	GTCAATTGCT	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9622	4196	af	AN1150.1	72.m19355	AO070308000028	0			-106	-83			ATGACTCTGACTCTCCTTGTCTAA		ATGACTCTGACTCTCCTTGTCTAA		MTLTLLV*		MTLTLLV*		CATCAACTTT	TTCCTATATA	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9618	4196	an	AN1150.1	72.m19355	AO070308000028	0	-177	-139					ATGGAAGTTGCGGAGGTGCCGAGCCGATATCGCCCATGA	ATGGAAGTTGCGGAGGTGCCGAGCCGATATCGCCCATGA			MEVAEVPSRYRP*	MEVAEVPSRYRP*			GGAGTGGCGG	ATCATCCAAC	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9619	4196	an	AN1150.1	72.m19355	AO070308000028	0	-110	-60					ATGCGGCATTTCTTCGCTTCTCACGCTATCCCCCTTCCCTCCCACTCTTGA	ATGCGGCATTTCTTCGCTTCTCACGCTATCCCCCTTCCCTCCCACTCTTGA			MRHFFASHAIPLPSHS*	MRHFFASHAIPLPSHS*			TCGTTTTTGG	ACTCGGCCGC	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0

9623	4196	ao	AN1150.1	72.m19355	AO070308000028	0					-274	-227	ATGACTTCAGAAGAGACGAGTCTGAGTCAAGTTACCTTAGGTAAATGA			ATGACTTCAGAAGAGACGAGTCTGAGTCAAGTTACCTTAGGTAAATGA	MTSEETSLSQVTLGK*			MTSEETSLSQVTLGK*	GTAGTCAAAG	ATTTAATTGC	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9624	4196	ao	AN1150.1	72.m19355	AO070308000028	0					-230	-183	ATGAATTTAATTGCGGAGCAAATCACAATACAATTTCTGATCAGATAA			ATGAATTTAATTGCGGAGCAAATCACAATACAATTTCTGATCAGATAA	MNLIAEQITIQFLIR*			MNLIAEQITIQFLIR*	CCTTAGGTAA	GCCGCTTGCT	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9625	4196	ao	AN1150.1	72.m19355	AO070308000028	0					-167	-66	ATGGGTTTCCCGATATCGCGGGATTTGTTTGACCCGTACATTTCGTCCTTTCGTTTTTCTCTCCTTTCAATGACTCACCGAATCCCTCTCTATTCTTCTTAA			ATGGGTTTCCCGATATCGCGGGATTTGTTTGACCCGTACATTTCGTCCTTTCGTTTTTCTCTCCTTTCAATGACTCACCGAATCCCTCTCTATTCTTCTTAA	MGFPISRDLFDPYISSFRFSLLSMTHRIPLYSS*			MGFPISRDLFDPYISSFRFSLLSMTHRIPLYSS*	TTGCTCATTT	ATACTCCCTT	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9626	4196	ao	AN1150.1	72.m19355	AO070308000028	0					-98	-66	ATGACTCACCGAATCCCTCTCTATTCTTCTTAA			ATGACTCACCGAATCCCTCTCTATTCTTCTTAA	MTHRIPLYSS*			MTHRIPLYSS*	TCTCCTTTCA	ATACTCCCTT	0	E	FG01573.1	MG02375.1	NCU05410.1	YOL140W	0
9627	4197	af	AN6312.1	72.m19322	AO070308000067	0			-190	-50			ATGCTGGTAAACGCTGCTTTATACCACAGAACCCATGACGATCACCCCACATTTTCTGCCGGCAGAACAATACCACCGCCTGCAACAGAAGATCTTGCTAGGATTCAGCTACCATCTTATCGCAGACTGATTACTTTTTGA		ATGCTGGTAAACGCTGCTTTATACCACAGAACCCATGACGATCACCCCACATTTTCTGCCGGCAGAACAATACCACCGCCTGCAACAGAAGATCTTGCTAGGATTCAGCTACCATCTTATCGCAGACTGATTACTTTTTGA		MLVNAALYHRTHDDHPTFSAGRTIPPPATEDLARIQLPSYRRLITF*		MLVNAALYHRTHDDHPTFSAGRTIPPPATEDLARIQLPSYRRLITF*		GCCGCTGGTC	GGCAATCGGA	0		0	0	0	0	0
9628	4197	af	AN6312.1	72.m19322	AO070308000067	0			-156	-61			ATGACGATCACCCCACATTTTCTGCCGGCAGAACAATACCACCGCCTGCAACAGAAGATCTTGCTAGGATTCAGCTACCATCTTATCGCAGACTGA		ATGACGATCACCCCACATTTTCTGCCGGCAGAACAATACCACCGCCTGCAACAGAAGATCTTGCTAGGATTCAGCTACCATCTTATCGCAGACTGA		MTITPHFLPAEQYHRLQQKILLGFSYHLIAD*		MTITPHFLPAEQYHRLQQKILLGFSYHLIAD*		CACAGAACCC	TTACTTTTTG	0		0	0	0	0	0
9629	4197	ao	AN6312.1	72.m19322	AO070308000067	0					-243	-226	ATGAATACTAGCAAATAG			ATGAATACTAGCAAATAG	MNTSK*			MNTSK*	CCCTAACAGC	ACATGCTTTC	0		0	0	0	0	0
9630	4197	ao	AN6312.1	72.m19322	AO070308000067	0					-223	-200	ATGCTTTCAGTACTTAGTGCCTAG			ATGCTTTCAGTACTTAGTGCCTAG	MLSVLSA*			MLSVLSA*	GCAAATAGAC	TACATACTAA	0		0	0	0	0	0
9631	4197	ao	AN6312.1	72.m19322	AO070308000067	0					-110	-39	ATGATAATTCCCCGACTTGTTTGCGACAACCTGAACAAGTACACAACCCTCAATTCAAGTCAAGTGTTATAA			ATGATAATTCCCCGACTTGTTTGCGACAACCTGAACAAGTACACAACCCTCAATTCAAGTCAAGTGTTATAA	MIIPRLVCDNLNKYTTLNSSQVL*			MIIPRLVCDNLNKYTTLNSSQVL*	CACCCCACCC	ACTCTCTAGC	0		0	0	0	0	0
9633	4199	ao	AN0869.1	70.m15458	AO070320000020	0					-120	-73	ATGATTGCTACCACCAGGGCCCCTCTGTTATCTATATCTCATATGTGA			ATGATTGCTACCACCAGGGCCCCTCTGTTATCTATATCTCATATGTGA	MIATTRAPLLSISHM*			MIATTRAPLLSISHM*	AATACTATTG	GCTATTGGTC	0		0	0	0	0	0
9634	4200	ao	AN0979.1	70.m15619	AO070320000183	0					-179	-126	ATGTGGTACAGGATCTCTGTTTTCTTCCTTTCTCCTCCCTCGAGTTACTCCTGA			ATGTGGTACAGGATCTCTGTTTTCTTCCTTTCTCCTCCCTCGAGTTACTCCTGA	MWYRISVFFLSPPSSYS*			MWYRISVFFLSPPSSYS*	GCTGACGGGC	CCCTATACCT	0	Y	0	0	0	0	0
9637	4201	af	AN3909.1	69.m15021	AO070324000094	0			-221	-144			ATGGAAACATACCTTCGGCCAATCACATCGTTCACCGCCTCAGGCTGCGCTATTTTCTGCCGCCATTTGCCGCCCTAG		ATGGAAACATACCTTCGGCCAATCACATCGTTCACCGCCTCAGGCTGCGCTATTTTCTGCCGCCATTTGCCGCCCTAG		METYLRPITSFTASGCAIFCRHLPP*		METYLRPITSFTASGCAIFCRHLPP*		CATCTTTTCC	AGCTTCCCGC	0	L	0	0	0	0	0
9638	4201	af	AN3909.1	69.m15021	AO070324000094	0			-124	-77			ATGACGTCGTGTCAGCCGTTCGCGTCCTCCGCCACTCAACACGAGTAG		ATGACGTCGTGTCAGCCGTTCGCGTCCTCCGCCACTCAACACGAGTAG		MTSCQPFASSATQHE*		MTSCQPFASSATQHE*		CTCTTGTCAC	ACGTTGTCTT	0	L	0	0	0	0	0
9635	4201	an	AN3909.1	69.m15021	AO070324000094	0	-213	-142					ATGTACCGCCAATTACTGCCCTTAAGATTATCACATGATTTCGTACCGTTGTCGCGTCTCCTGCATCTTTAG	ATGTACCGCCAATTACTGCCCTTAAGATTATCACATGATTTCGTACCGTTGTCGCGTCTCCTGCATCTTTAG			MYRQLLPLRLSHDFVPLSRLLHL*	MYRQLLPLRLSHDFVPLSRLLHL*			CAACGCTTTG	GCAGAAGCTC	0	L	0	0	0	0	0
9636	4201	an	AN3909.1	69.m15021	AO070324000094	0	-100	-17					ATGTCTTATTATCTCTTTCTCGAGGCTACTCCGTTACCTATATTGGCCGTCTTACTCTGTTCAGCTCCCCCGGTCATGAGGTGA	ATGTCTTATTATCTCTTTCTCGAGGCTACTCCGTTACCTATATTGGCCGTCTTACTCTGTTCAGCTCCCCCGGTCATGAGGTGA			MSYYLFLEATPLPILAVLLCSAPPVMR*	MSYYLFLEATPLPILAVLLCSAPPVMR*			CGCGAGAAAG	TCTTGCTTTG	0	L	0	0	0	0	0
9639	4201	ao	AN3909.1	69.m15021	AO070324000094	0					-136	-50	ATGACTTCGTTCCGCTCGTCACGAAGCTCAGCCGCCACCGCGTGTCTGGTCCAAAGTTCTCTCGTCGCCTTCGTTTCTTGTCCATAA			ATGACTTCGTTCCGCTCGTCACGAAGCTCAGCCGCCACCGCGTGTCTGGTCCAAAGTTCTCTCGTCGCCTTCGTTTCTTGTCCATAA	MTSFRSSRSSAATACLVQSSLVAFVSCP*			MTSFRSSRSSAATACLVQSSLVAFVSCP*	ACCGCATCAC	ATTGCTGACG	0	L	0	0	0	0	0
9644	4202	af	AN7715.1	71.m15740	AO070325000127	0			-205	-188			ATGGCATTCCACGCATGA		ATGGCATTCCACGCATGA		MAFHA*		MAFHA*		CCCCAATTTT	TGGCCATTGT	0	R	FG06214.1	0	NCU06386.1	0	0
9645	4202	af	AN7715.1	71.m15740	AO070325000127	0			-191	-141			ATGATGGCCATTGTCTGTAGCGACTTCAACGATCAATGCAAGCATTACTGA		ATGATGGCCATTGTCTGTAGCGACTTCAACGATCAATGCAAGCATTACTGA		MMAIVCSDFNDQCKHY*		MMAIVCSDFNDQCKHY*		CATTCCACGC	CCAGACAGGC	0	R	FG06214.1	0	NCU06386.1	0	0
9646	4202	af	AN7715.1	71.m15740	AO070325000127	0			-188	-141			ATGGCCATTGTCTGTAGCGACTTCAACGATCAATGCAAGCATTACTGA		ATGGCCATTGTCTGTAGCGACTTCAACGATCAATGCAAGCATTACTGA		MAIVCSDFNDQCKHY*		MAIVCSDFNDQCKHY*		TCCACGCATG	CCAGACAGGC	0	R	FG06214.1	0	NCU06386.1	0	0
9647	4202	af	AN7715.1	71.m15740	AO070325000127	0			-156	-88			ATGCAAGCATTACTGACCAGACAGGCTCCGTGTCGCATGGCCGACCAACCAGGGATCGTCTTGATCTGA		ATGCAAGCATTACTGACCAGACAGGCTCCGTGTCGCATGGCCGACCAACCAGGGATCGTCTTGATCTGA		MQALLTRQAPCRMADQPGIVLI*		MQALLTRQAPCRMADQPGIVLI*		TCAACGATCA	ATCTCCAGCT	0	R	FG06214.1	0	NCU06386.1	0	0
9648	4202	af	AN7715.1	71.m15740	AO070325000127	0			-120	-88			ATGGCCGACCAACCAGGGATCGTCTTGATCTGA		ATGGCCGACCAACCAGGGATCGTCTTGATCTGA		MADQPGIVLI*		MADQPGIVLI*		TCCGTGTCGC	ATCTCCAGCT	0	R	FG06214.1	0	NCU06386.1	0	0
9641	4202	an	AN7715.1	71.m15740	AO070325000127	0	-179	-141					ATGGTCATTGTATTCTGTGTTAAACCTCTGCCCTGTTGA	ATGGTCATTGTATTCTGTGTTAAACCTCTGCCCTGTTGA			MVIVFCVKPLPC*	MVIVFCVKPLPC*			GAAATCCATA	TTACTTTCCG	0	R	FG06214.1	0	NCU06386.1	0	0
9642	4202	an	AN7715.1	71.m15740	AO070325000127	0	-116	-81					ATGGCCGGTCAGGAGCGCGCTGTCATCATCCCATGA	ATGGCCGGTCAGGAGCGCGCTGTCATCATCCCATGA			MAGQERAVIIP*	MAGQERAVIIP*			ATCCTGTCGC	GAGCTCTATA	0	R	FG06214.1	0	NCU06386.1	0	0
9643	4202	an	AN7715.1	71.m15740	AO070325000127	0	-84	-70					ATGAGAGCTCTATAG	ATGAGAGCTCTATAG			MRAL*	MRAL*			TCATCATCCC	CTGCTCAAAC	0	R	FG06214.1	0	NCU06386.1	0	0
9649	4202	ao	AN7715.1	71.m15740	AO070325000127	0					-233	-174	ATGTCCGCTTGCTTCCCCCTCACATCGTCTTCCCATCCCATCTTGACTTCCCGTCCATGA			ATGTCCGCTTGCTTCCCCCTCACATCGTCTTCCCATCCCATCTTGACTTCCCGTCCATGA	MSACFPLTSSSHPILTSRP*			MSACFPLTSSSHPILTSRP*	TGTCGGAGAT	TGCTCTTCCG	0	R	FG06214.1	0	NCU06386.1	0	0
9650	4202	ao	AN7715.1	71.m15740	AO070325000127	0					-177	-139	ATGATGCTCTTCCGCGATCATTCTGTCCGATTTTCATGA			ATGATGCTCTTCCGCGATCATTCTGTCCGATTTTCATGA	MMLFRDHSVRFS*			MMLFRDHSVRFS*	CTTCCCGTCC	TAGTTCTTTC	0	R	FG06214.1	0	NCU06386.1	0	0
9651	4202	ao	AN7715.1	71.m15740	AO070325000127	0					-174	-139	ATGCTCTTCCGCGATCATTCTGTCCGATTTTCATGA			ATGCTCTTCCGCGATCATTCTGTCCGATTTTCATGA	MLFRDHSVRFS*			MLFRDHSVRFS*	CCCGTCCATG	TAGTTCTTTC	0	R	FG06214.1	0	NCU06386.1	0	0
9652	4202	ao	AN7715.1	71.m15740	AO070325000127	0					-142	-62	ATGATAGTTCTTTCTCCAAGACAGGCTCCGTGTCGCATGGCTGGCCAAGTCCGGATTGTCCCTGTTCAGTTGAGCGCTTGA			ATGATAGTTCTTTCTCCAAGACAGGCTCCGTGTCGCATGGCTGGCCAAGTCCGGATTGTCCCTGTTCAGTTGAGCGCTTGA	MIVLSPRQAPCRMAGQVRIVPVQLSA*			MIVLSPRQAPCRMAGQVRIVPVQLSA*	TCCGATTTTC	GCTCATACTA	0	R	FG06214.1	0	NCU06386.1	0	0
9653	4202	ao	AN7715.1	71.m15740	AO070325000127	0					-106	-62	ATGGCTGGCCAAGTCCGGATTGTCCCTGTTCAGTTGAGCGCTTGA			ATGGCTGGCCAAGTCCGGATTGTCCCTGTTCAGTTGAGCGCTTGA	MAGQVRIVPVQLSA*			MAGQVRIVPVQLSA*	TCCGTGTCGC	GCTCATACTA	0	R	FG06214.1	0	NCU06386.1	0	0
9656	4203	af	AN6561.1	62.m03148	AO070326000002	0			-238	-218			ATGGAAGAAACGGCAAAATAG		ATGGAAGAAACGGCAAAATAG		MEETAK*		MEETAK*		GCTTGTAAGG	AAAGGCGACA	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9654	4203	an	AN6561.1	62.m03148	AO070326000002	0	-231	-16					ATGTACCGGAACAGAAGAGGCGATAAGTCTAAGCGCTCGCTGCGTCCAGCAAAATCAAACATCCCCATGGCACTTACCGCCTTGATACACCGGCAGAAAACGATTCCAATTTTCGGTGCGACTTCACCGCCGACAACAATTTCAACAAGCCGATCAGTTCTCCGCCAGCAGTGCTGTGCTTGCCTTTGGTTTTATATAGTCTCGGACAAGCTCTGA	ATGTACCGGAACAGAAGAGGCGATAAGTCTAAGCGCTCGCTGCGTCCAGCAAAATCAAACATCCCCATGGCACTTACCGCCTTGATACACCGGCAGAAAACGATTCCAATTTTCGGTGCGACTTCACCGCCGACAACAATTTCAACAAGCCGATCAGTTCTCCGCCAGCAGTGCTGTGCTTGCCTTTGGTTTTATATAGTCTCGGACAAGCTCTGA			MYRNRRGDKSKRSLRPAKSNIPMALTALIHRQKTIPIFGATSPPTTISTSRSVLRQQCCACLWFYIVSDKL*	MYRNRRGDKSKRSLRPAKSNIPMALTALIHRQKTIPIFGATSPPTTISTSRSVLRQQCCACLWFYIVSDKL*			CAACAAAACA	TAGACAGACA	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9655	4203	an	AN6561.1	62.m03148	AO070326000002	0	-165	-16					ATGGCACTTACCGCCTTGATACACCGGCAGAAAACGATTCCAATTTTCGGTGCGACTTCACCGCCGACAACAATTTCAACAAGCCGATCAGTTCTCCGCCAGCAGTGCTGTGCTTGCCTTTGGTTTTATATAGTCTCGGACAAGCTCTGA	ATGGCACTTACCGCCTTGATACACCGGCAGAAAACGATTCCAATTTTCGGTGCGACTTCACCGCCGACAACAATTTCAACAAGCCGATCAGTTCTCCGCCAGCAGTGCTGTGCTTGCCTTTGGTTTTATATAGTCTCGGACAAGCTCTGA			MALTALIHRQKTIPIFGATSPPTTISTSRSVLRQQCCACLWFYIVSDKL*	MALTALIHRQKTIPIFGATSPPTTISTSRSVLRQQCCACLWFYIVSDKL*			AAACATCCCC	TAGACAGACA	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9657	4203	ao	AN6561.1	62.m03148	AO070326000002	0					-227	-93	ATGAAACTGATGGCGAAATGGAAAATCGCGACCAAACGGTCTAGATCCACCAACGAGAGCGAAGCTACTTCTCTCACCGCCTTAAACAACCAGCAGTATCGCTTCGATTTTTTGCTCCGCCTTCACCGCCATTGA			ATGAAACTGATGGCGAAATGGAAAATCGCGACCAAACGGTCTAGATCCACCAACGAGAGCGAAGCTACTTCTCTCACCGCCTTAAACAACCAGCAGTATCGCTTCGATTTTTTGCTCCGCCTTCACCGCCATTGA	MKLMAKWKIATKRSRSTNESEATSLTALNNQQYRFDFLLRLHRH*			MKLMAKWKIATKRSRSTNESEATSLTALNNQQYRFDFLLRLHRH*	CGAGAATGCG	TTGGCTTCTT	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9658	4203	ao	AN6561.1	62.m03148	AO070326000002	0					-218	-93	ATGGCGAAATGGAAAATCGCGACCAAACGGTCTAGATCCACCAACGAGAGCGAAGCTACTTCTCTCACCGCCTTAAACAACCAGCAGTATCGCTTCGATTTTTTGCTCCGCCTTCACCGCCATTGA			ATGGCGAAATGGAAAATCGCGACCAAACGGTCTAGATCCACCAACGAGAGCGAAGCTACTTCTCTCACCGCCTTAAACAACCAGCAGTATCGCTTCGATTTTTTGCTCCGCCTTCACCGCCATTGA	MAKWKIATKRSRSTNESEATSLTALNNQQYRFDFLLRLHRH*			MAKWKIATKRSRSTNESEATSLTALNNQQYRFDFLLRLHRH*	GATGAAACTG	TTGGCTTCTT	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9659	4203	ao	AN6561.1	62.m03148	AO070326000002	0					-210	-184	ATGGAAAATCGCGACCAAACGGTCTAG			ATGGAAAATCGCGACCAAACGGTCTAG	MENRDQTV*			MENRDQTV*	TGATGGCGAA	ATCCACCAAC	0	S	FG07399.1	MG06938.1	0	YOR287C	0
9663	4206	af	AN2239.1	71.m15830	AO070326000142	0			-199	-155			ATGAATTGGAGCATCTATGAGGAAGGTGCAATGGCAGGCACCTAA		ATGAATTGGAGCATCTATGAGGAAGGTGCAATGGCAGGCACCTAA		MNWSIYEEGAMAGT*		MNWSIYEEGAMAGT*		TCTCTATTCT	AAATTGCTGC	0	C	0	0	0	0	0
9664	4206	af	AN2239.1	71.m15830	AO070326000142	0			-183	-97			ATGAGGAAGGTGCAATGGCAGGCACCTAAAAATTGCTGCCTCAGGCCTCAAGCACTCGAGATGATGTCATTCCGAACTTCGGCCTAA		ATGAGGAAGGTGCAATGGCAGGCACCTAAAAATTGCTGCCTCAGGCCTCAAGCACTCGAGATGATGTCATTCCGAACTTCGGCCTAA		MRKVQWQAPKNCCLRPQALEMMSFRTSA*		MRKVQWQAPKNCCLRPQALEMMSFRTSA*		TGGAGCATCT	GGCCTTCAAC	0	C	0	0	0	0	0
9665	4206	af	AN2239.1	71.m15830	AO070326000142	0			-169	-155			ATGGCAGGCACCTAA		ATGGCAGGCACCTAA		MAGT*		MAGT*		GGAAGGTGCA	AAATTGCTGC	0	C	0	0	0	0	0
9666	4206	af	AN2239.1	71.m15830	AO070326000142	0			-123	-97			ATGATGTCATTCCGAACTTCGGCCTAA		ATGATGTCATTCCGAACTTCGGCCTAA		MMSFRTSA*		MMSFRTSA*		AGCACTCGAG	GGCCTTCAAC	0	C	0	0	0	0	0
9667	4206	af	AN2239.1	71.m15830	AO070326000142	0			-120	-97			ATGTCATTCCGAACTTCGGCCTAA		ATGTCATTCCGAACTTCGGCCTAA		MSFRTSA*		MSFRTSA*		ACTCGAGATG	GGCCTTCAAC	0	C	0	0	0	0	0
9660	4206	an	AN2239.1	71.m15830	AO070326000142	0	-225	-175					ATGCCTAGTTCTAAATCGTCTTGCCCTGTGTCTTTCAGTTATGCTAACTAA	ATGCCTAGTTCTAAATCGTCTTGCCCTGTGTCTTTCAGTTATGCTAACTAA			MPSSKSSCPVSFSYAN*	MPSSKSSCPVSFSYAN*			CCTTCACTTG	GAATCCTTAT	0	C	0	0	0	0	0
9661	4206	an	AN2239.1	71.m15830	AO070326000142	0	-185	-120					ATGCTAACTAAGAATCCTTATCTAACTGCACCTTTGCTCTACAGATTGCACAGTAAACATGGATGA	ATGCTAACTAAGAATCCTTATCTAACTGCACCTTTGCTCTACAGATTGCACAGTAAACATGGATGA			MLTKNPYLTAPLLYRLHSKHG*	MLTKNPYLTAPLLYRLHSKHG*			TCTTTCAGTT	CATCAGCGGA	0	C	0	0	0	0	0
9662	4206	an	AN2239.1	71.m15830	AO070326000142	0	-123	-61					ATGACATCAGCGGAACCCCGCAGTGCCCAAAGTGCCCGCACAAACTCTATCGTTCGATCATGA	ATGACATCAGCGGAACCCCGCAGTGCCCAAAGTGCCCGCACAAACTCTATCGTTCGATCATGA			MTSAEPRSAQSARTNSIVRS*	MTSAEPRSAQSARTNSIVRS*			GTAAACATGG	GCCGCATCAA	0	C	0	0	0	0	0
9669	4206	ao	AN2239.1	71.m15830	AO070326000142	0					-202	-185	ATGGATTATGGAGTATAG			ATGGATTATGGAGTATAG	MDYGV*			MDYGV*	GACTAGGAAG	AAACAATAGC	0	C	0	0	0	0	0
9670	4206	ao	AN2239.1	71.m15830	AO070326000142	0					-195	-148	ATGGAGTATAGAAACAATAGCATAGGTATACACATAAATAATGCATAA			ATGGAGTATAGAAACAATAGCATAGGTATACACATAAATAATGCATAA	MEYRNNSIGIHINNA*			MEYRNNSIGIHINNA*	AAGATGGATT	TTACATAATC	0	C	0	0	0	0	0
9671	4206	ao	AN2239.1	71.m15830	AO070326000142	0					-112	-92	ATGCAGCGAACTTCGGCCTGA			ATGCAGCGAACTTCGGCCTGA	MQRTSA*			MQRTSA*	AGTTCAAATA	CGTCATTCCG	0	C	0	0	0	0	0
9676	4208	af	AN9066.1	66.m04520	AO070332000218	0			-186	-169			ATGAGGAAGGCTTATTAA		ATGAGGAAGGCTTATTAA		MRKAY*		MRKAY*		GGACTGGCCA	GCTAAATGTG	0	C	FG00706.1	0	0	0	0
9677	4208	af	AN9066.1	66.m04520	AO070332000218	0			-163	-128			ATGTGCATATGCATATTTTCGTTGGAGCGGTGCTAA		ATGTGCATATGCATATTTTCGTTGGAGCGGTGCTAA		MCICIFSLERC*		MCICIFSLERC*		ATTAAGCTAA	GAAAATATCC	0	C	FG00706.1	0	0	0	0
9678	4208	af	AN9066.1	66.m04520	AO070332000218	0			-155	-111			ATGCATATTTTCGTTGGAGCGGTGCTAAGAAAATATCCGTCATGA		ATGCATATTTTCGTTGGAGCGGTGCTAAGAAAATATCCGTCATGA		MHIFVGAVLRKYPS*		MHIFVGAVLRKYPS*		AAATGTGCAT	ACGGAGTATC	0	C	FG00706.1	0	0	0	0
9679	4208	af	AN9066.1	66.m04520	AO070332000218	0			-114	-91			ATGAACGGAGTATCCCTGACCTGA		ATGAACGGAGTATCCCTGACCTGA		MNGVSLT*		MNGVSLT*		AATATCCGTC	CGGAGAAAAC	0	C	FG00706.1	0	0	0	0
9673	4208	an	AN9066.1	66.m04520	AO070332000218	0	-254	-186					ATGGCTCTGAGTTGGGAATCGTATGATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGA	ATGGCTCTGAGTTGGGAATCGTATGATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGA			MALSWESYDVLAGTFISPKRRS*	MALSWESYDVLAGTFISPKRRS*			GGTTAAAAGT	GCTCACGTGA	0	C	FG00706.1	0	0	0	0

9674	4208	an	AN9066.1	66.m04520	AO070332000218	0	-232	-176					ATGATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGAGCTCACGTGA	ATGATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGAGCTCACGTGA			MMYWLAHLFRRSAGVELT*	MMYWLAHLFRRSAGVELT*			TGGGAATCGT	TTGAAGCTAG	0	C	FG00706.1	0	0	0	0
9675	4208	an	AN9066.1	66.m04520	AO070332000218	0	-229	-176					ATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGAGCTCACGTGA	ATGTACTGGCTGGCACATTTATTTCGCCGAAGCGCAGGAGTTGAGCTCACGTGA			MYWLAHLFRRSAGVELT*	MYWLAHLFRRSAGVELT*			GAATCGTATG	TTGAAGCTAG	0	C	FG00706.1	0	0	0	0
9681	4208	ao	AN9066.1	66.m04520	AO070332000218	0					-194	-84	ATGGTCGTGCCAAGACCGCCTTGCCAGAATAAGACTAAGCTAAGTCCAGGGAAGCTATCAACTATCTATCAGTTCAAGTTGCCCACCTGGCATGCATCCGCCGGGCTATGA			ATGGTCGTGCCAAGACCGCCTTGCCAGAATAAGACTAAGCTAAGTCCAGGGAAGCTATCAACTATCTATCAGTTCAAGTTGCCCACCTGGCATGCATCCGCCGGGCTATGA	MVVPRPPCQNKTKLSPGKLSTIYQFKLPTWHASAGL*			MVVPRPPCQNKTKLSPGKLSTIYQFKLPTWHASAGL*	CGGAACTTTG	TTTGACAGAA	0	C	FG00706.1	0	0	0	0
9682	4208	ao	AN9066.1	66.m04520	AO070332000218	0					-103	-68	ATGCATCCGCCGGGCTATGATTTGACAGAACTTTGA			ATGCATCCGCCGGGCTATGATTTGACAGAACTTTGA	MHPPGYDLTEL*			MHPPGYDLTEL*	CCCACCTGGC	AATCGCTTCG	0	C	FG00706.1	0	0	0	0
9684	4209	af	AN5407.1	69.m15524	AO070333000121	0			-204	-100			ATGCTGCCGTTATTGGTAGTCTTTCGACCTCTCGTTCGGCTCATTTCTCCTTATCGCTCCTTTGATTCTGGATCAAGCCTCTGCGGGTACTCAATTTTCACATAG		ATGCTGCCGTTATTGGTAGTCTTTCGACCTCTCGTTCGGCTCATTTCTCCTTATCGCTCCTTTGATTCTGGATCAAGCCTCTGCGGGTACTCAATTTTCACATAG		MLPLLVVFRPLVRLISPYRSFDSGSSLCGYSIFT*		MLPLLVVFRPLVRLISPYRSFDSGSSLCGYSIFT*		TTTAGAAGCG	ATACTGGCTA	0	R	0	0	0	0	0
9683	4209	an	AN5407.1	69.m15524	AO070333000121	0	-146	-81					ATGCCGCTGTTTGTCGTCCAATTCCCACCGGCAGCTTCTCGACCTGATCGCGACTTCCGAATTTGA	ATGCCGCTGTTTGTCGTCCAATTCCCACCGGCAGCTTCTCGACCTGATCGCGACTTCCGAATTTGA			MPLFVVQFPPAASRPDRDFRI*	MPLFVVQFPPAASRPDRDFRI*			CCCACGAGCG	CCCCTCCAAC	0	R	0	0	0	0	0
9685	4209	ao	AN5407.1	69.m15524	AO070333000121	0					-206	-132	ATGCTGTCATTATTGACGGCCACTGCTTCGATTGATCGCCGCCACTCTTCTTATCGTGTACTCGCTCTCCGTTAG			ATGCTGTCATTATTGACGGCCACTGCTTCGATTGATCGCCGCCACTCTTCTTATCGTGTACTCGCTCTCCGTTAG	MLSLLTATASIDRRHSSYRVLALR*			MLSLLTATASIDRRHSSYRVLALR*	GCACCCAGAA	CCCCTCGTTC	0	R	0	0	0	0	0
9686	4209	ao	AN5407.1	69.m15524	AO070333000121	0					-65	-54	ATGAGTCTTTGA			ATGAGTCTTTGA	MSL*			MSL*	TCCCTGGGGA	TCTCGATAAT	0	R	0	0	0	0	0
9688	4211	af	AN5221.1	57.m05713	AO070337000257	0			-187	-137			ATGAGCGGCGACCGGGAGACGCGCTTGTTGATGTATGTTGTAGTTTGTTGA		ATGAGCGGCGACCGGGAGACGCGCTTGTTGATGTATGTTGTAGTTTGTTGA		MSGDRETRLLMYVVVC*		MSGDRETRLLMYVVVC*		AGGTGGTCAC	CGGCGTCGGA	0	RP	FG00672.1	MG03693.1	0	0	0
9689	4211	af	AN5221.1	57.m05713	AO070337000257	0			-157	-137			ATGTATGTTGTAGTTTGTTGA		ATGTATGTTGTAGTTTGTTGA		MYVVVC*		MYVVVC*		GCGCTTGTTG	CGGCGTCGGA	0	RP	FG00672.1	MG03693.1	0	0	0
9690	4211	af	AN5221.1	57.m05713	AO070337000257	0			-120	-103			ATGCTACTTTCCGTTTGA		ATGCTACTTTCCGTTTGA		MLLSV*		MLLSV*		CGGATTGATA	GAACAATCGT	0	RP	FG00672.1	MG03693.1	0	0	0
9687	4211	an	AN5221.1	57.m05713	AO070337000257	0	-150	-28					ATGACTGCCCGCCGGGGTGACGCGCTTGTTGGACTGAAGATCAAGGCGTCAATACTCAATCCATCACTAAGGCACAGACAAATTGTATGCTGCTGGGCACCGGCGGCGGACGTACTACAATAA	ATGACTGCCCGCCGGGGTGACGCGCTTGTTGGACTGAAGATCAAGGCGTCAATACTCAATCCATCACTAAGGCACAGACAAATTGTATGCTGCTGGGCACCGGCGGCGGACGTACTACAATAA			MTARRGDALVGLKIKASILNPSLRHRQIVCCWAPAADVLQ*	MTARRGDALVGLKIKASILNPSLRHRQIVCCWAPAADVLQ*			CTTAAATCAC	AATCGTCTGT	0	RP	FG00672.1	MG03693.1	0	0	0
9691	4211	ao	AN5221.1	57.m05713	AO070337000257	0					-251	-237	ATGGGCATTATGTAA			ATGGGCATTATGTAA	MGIM*			MGIM*	ACCTAATCGT	TAAATGACTA	0	RP	FG00672.1	MG03693.1	0	0	0
9692	4211	ao	AN5221.1	57.m05713	AO070337000257	0					-233	-183	ATGACTAATCGCGATAACAGAATCGTTTGTTTACATCGAGCGATCACATGA			ATGACTAATCGCGATAACAGAATCGTTTGTTTACATCGAGCGATCACATGA	MTNRDNRIVCLHRAIT*			MTNRDNRIVCLHRAIT*	TATGTAATAA	GCACCTCCCG	0	RP	FG00672.1	MG03693.1	0	0	0
9693	4211	ao	AN5221.1	57.m05713	AO070337000257	0					-186	-130	ATGAGCACCTCCCGGGAGACGCGCGACTTTTGGGGGTTGTTATACTTGTGTGGTTAA			ATGAGCACCTCCCGGGAGACGCGCGACTTTTGGGGGTTGTTATACTTGTGTGGTTAA	MSTSRETRDFWGLLYLCG*			MSTSRETRDFWGLLYLCG*	GAGCGATCAC	TGAGGGCGCA	0	RP	FG00672.1	MG03693.1	0	0	0
9694	4211	ao	AN5221.1	57.m05713	AO070337000257	0					-130	-113	ATGAGGGCGCAACGCTAA			ATGAGGGCGCAACGCTAA	MRAQR*			MRAQR*	TGTGTGGTTA	GTGGACCATG	0	RP	FG00672.1	MG03693.1	0	0	0
9695	4211	ao	AN5221.1	57.m05713	AO070337000257	0					-105	-73	ATGTTTATTATTTCAACCTTCGAGAAAAACTGA			ATGTTTATTATTTCAACCTTCGAGAAAAACTGA	MFIISTFEKN*			MFIISTFEKN*	TAAGTGGACC	GATTACAGAT	0	RP	FG00672.1	MG03693.1	0	0	0
9699	4216	af	AN4678.1	71.m15665	AO070284000022	0			-148	-44			ATGTCTTTGGAGTCGACGCGACGTGCGCGAAGAGAACCAATTTTTCCGGACCAACGCATGGTGCATCGACGACGTTACACTCACAAATTCAAGCAAAGCACTTGA		ATGTCTTTGGAGTCGACGCGACGTGCGCGAAGAGAACCAATTTTTCCGGACCAACGCATGGTGCATCGACGACGTTACACTCACAAATTCAAGCAAAGCACTTGA		MSLESTRRARREPIFPDQRMVHRRRYTHKFKQST*		MSLESTRRARREPIFPDQRMVHRRRYTHKFKQST*		TCCCGAACCC	TACATACAGA	0	L	0	MG02924.1	0	0	0
9700	4216	af	AN4678.1	71.m15665	AO070284000022	0			-91	-44			ATGGTGCATCGACGACGTTACACTCACAAATTCAAGCAAAGCACTTGA		ATGGTGCATCGACGACGTTACACTCACAAATTCAAGCAAAGCACTTGA		MVHRRRYTHKFKQST*		MVHRRRYTHKFKQST*		GGACCAACGC	TACATACAGA	0	L	0	MG02924.1	0	0	0
9696	4216	an	AN4678.1	71.m15665	AO070284000022	0	-222	-202					ATGCTGGGGTACCAGCACTAG	ATGCTGGGGTACCAGCACTAG			MLGYQH*	MLGYQH*			GGCCCGTACC	CCCGATTAGG	0	L	0	MG02924.1	0	0	0
9697	4216	an	AN4678.1	71.m15665	AO070284000022	0	-148	-131					ATGATCCGCAGAATTTAG	ATGATCCGCAGAATTTAG			MIRRI*	MIRRI*			GCAACGACAG	TAGCCATAAA	0	L	0	MG02924.1	0	0	0
9698	4216	an	AN4678.1	71.m15665	AO070284000022	0	-88	-38					ATGAGATTTAACGTCTCATATTTGCTCAAGACGTGTTACTCATCAGCATAG	ATGAGATTTAACGTCTCATATTTGCTCAAGACGTGTTACTCATCAGCATAG			MRFNVSYLLKTCYSSA*	MRFNVSYLLKTCYSSA*			ATCCGCAACT	GTATCTCCGC	0	L	0	MG02924.1	0	0	0
9701	4216	ao	AN4678.1	71.m15665	AO070284000022	0					-225	-202	ATGTCGAATCGCACGCTAACCTAA			ATGTCGAATCGCACGCTAACCTAA	MSNRTLT*			MSNRTLT*	CGTGTGGGCC	ATTAGTATTG	0	L	0	MG02924.1	0	0	0
9702	4216	ao	AN4678.1	71.m15665	AO070284000022	0					-153	-34	ATGAGTCCGAATTTAGGCGATGATCTTCATCTCGACATAGAGTATGGTTCGGACAACAGAGACTGCACGCGTTCACAAACCGGGATGCCACAGTCCCGATTTACCACGTCCCGCCATTAA			ATGAGTCCGAATTTAGGCGATGATCTTCATCTCGACATAGAGTATGGTTCGGACAACAGAGACTGCACGCGTTCACAAACCGGGATGCCACAGTCCCGATTTACCACGTCCCGCCATTAA	MSPNLGDDLHLDIEYGSDNRDCTRSQTGMPQSRFTTSRH*			MSPNLGDDLHLDIEYGSDNRDCTRSQTGMPQSRFTTSRH*	CGGTCGGCGG	AGCCAGCATG	0	L	0	MG02924.1	0	0	0
9703	4216	ao	AN4678.1	71.m15665	AO070284000022	0					-134	-114	ATGATCTTCATCTCGACATAG			ATGATCTTCATCTCGACATAG	MIFIST*			MIFIST*	AATTTAGGCG	AGTATGGTTC	0	L	0	MG02924.1	0	0	0
9704	4216	ao	AN4678.1	71.m15665	AO070284000022	0					-69	-34	ATGCCACAGTCCCGATTTACCACGTCCCGCCATTAA			ATGCCACAGTCCCGATTTACCACGTCCCGCCATTAA	MPQSRFTTSRH*			MPQSRFTTSRH*	ACAAACCGGG	AGCCAGCATG	0	L	0	MG02924.1	0	0	0
9707	4218	af	AN4996.1	59.m08898	AO070288000079	0			-142	-128			ATGCCTCAGGCATAA		ATGCCTCAGGCATAA		MPQA*		MPQA*		TTACTAATTA	ACTGGTGATA	0		0	0	0	0	0
9708	4218	af	AN4996.1	59.m08898	AO070288000079	0			-85	-14			ATGATAGAAACATCCCGCACCGCGTCCACCAGCAACAAAAGTCAACGAACAACCAACCTACAGCAGCAGTAG		ATGATAGAAACATCCCGCACCGCGTCCACCAGCAACAAAAGTCAACGAACAACCAACCTACAGCAGCAGTAG		MIETSRTASTSNKSQRTTNLQQQ*		MIETSRTASTSNKSQRTTNLQQQ*		AGAGTAAATA	CAGCATAACA	0		0	0	0	0	0
9705	4218	an	AN4996.1	59.m08898	AO070288000079	0	-192	-169					ATGCTTCCCCTTTCTAGTTTGTAG	ATGCTTCCCCTTTCTAGTTTGTAG			MLPLSSL*	MLPLSSL*			TGCCTGAGAA	CCTGATGGTT	0		0	0	0	0	0
9706	4218	an	AN4996.1	59.m08898	AO070288000079	0	-164	-114					ATGGTTCAGGCAGTAATATATTTAGGCTACAAGGCACTTAACATCCGCTAA	ATGGTTCAGGCAGTAATATATTTAGGCTACAAGGCACTTAACATCCGCTAA			MVQAVIYLGYKALNIR*	MVQAVIYLGYKALNIR*			TTGTAGCCTG	TGGCCCATCC	0		0	0	0	0	0
9709	4218	ao	AN4996.1	59.m08898	AO070288000079	0					-108	-64	ATGCGAACCCCCGAGGACGAGAAGTATCCAACGGAGAGAAGATAG			ATGCGAACCCCCGAGGACGAGAAGTATCCAACGGAGAGAAGATAG	MRTPEDEKYPTERR*			MRTPEDEKYPTERR*	GCGTTTATAC	ATCCACACAT	0		0	0	0	0	0
9711	4219	af	AN1475.1	55.m02977	AO070306000098	0			-246	-208			ATGAAAACTTATCTGCTCCTATCAAATTTCAATCAATGA		ATGAAAACTTATCTGCTCCTATCAAATTTCAATCAATGA		MKTYLLLSNFNQ*		MKTYLLLSNFNQ*		CAGGAGAGCC	TCAGTCAATG	0	ZR	0	0	0	0	0
9712	4219	af	AN1475.1	55.m02977	AO070306000098	0			-211	-197			ATGATCAGTCAATGA		ATGATCAGTCAATGA		MISQ*		MISQ*		ATTTCAATCA	TCTAAAGTGC	0	ZR	0	0	0	0	0
9710	4219	an	AN1475.1	55.m02977	AO070306000098	0	-201	-187					ATGACTGCCCGTTGA	ATGACTGCCCGTTGA			MTAR*	MTAR*			CAGCTCCAGA	TCGTTCTTAT	0	ZR	0	0	0	0	0
9713	4219	ao	AN1475.1	55.m02977	AO070306000098	0					-178	-161	ATGACTGCTGGTCTATGA			ATGACTGCTGGTCTATGA	MTAGL*			MTAGL*	TATCAACATT	TCAGTCACGC	0	ZR	0	0	0	0	0
9714	4219	ao	AN1475.1	55.m02977	AO070306000098	0					-164	-90	ATGATCAGTCACGCAGTTACCTCCGTCTTCGCAGCTTATCCCTTCCTTCGATATCGGACTTGTTTTCTACGCTGA			ATGATCAGTCACGCAGTTACCTCCGTCTTCGCAGCTTATCCCTTCCTTCGATATCGGACTTGTTTTCTACGCTGA	MISHAVTSVFAAYPFLRYRTCFLR*			MISHAVTSVFAAYPFLRYRTCFLR*	CTGCTGGTCT	GTTCCTTTCT	0	ZR	0	0	0	0	0
9715	4224	an	AN0854.1	70.m15453	AO070320000001	0	-163	-80					ATGACGTCGCCTGTTTTGCTCCAACTCATCAACGAGCAGAGCATACGGCACCAACAAAACAAACGAAAAACAATCGTCCCTTGA	ATGACGTCGCCTGTTTTGCTCCAACTCATCAACGAGCAGAGCATACGGCACCAACAAAACAAACGAAAAACAATCGTCCCTTGA			MTSPVLLQLINEQSIRHQNKRKTIVP*	MTSPVLLQLINEQSIRHQNKRKTIVP*			CCTGCTTGCA	TGTCTTCACC	0	A	0	0	0	0	0
9716	4224	an	AN0854.1	70.m15453	AO070320000001	0	-61	-29					ATGCTGTTCCGGATAAGTACTGCAAAATACTAA	ATGCTGTTCCGGATAAGTACTGCAAAATACTAA			MLFRISTAKY*	MLFRISTAKY*			CCCGGTGCGC	CAATTGCCGT	0	A	0	0	0	0	0
9718	4224	ao	AN0854.1	70.m15453	AO070320000001	0					-133	-116	ATGCTATCAACAAAATAA			ATGCTATCAACAAAATAA	MLSTK*			MLSTK*	GGTACAACAC	CCCACCCACC	0	A	0	0	0	0	0
9719	4226	ao	AN5719.1	54.m06840	AO070324000131	0					-224	-177	ATGGATTGCCTATTCGGGGCTAGCGTAAAGTCACGGGAGGGGCGGTGA			ATGGATTGCCTATTCGGGGCTAGCGTAAAGTCACGGGAGGGGCGGTGA	MDCLFGASVKSREGR*			MDCLFGASVKSREGR*	CGATGATGGC	CGCTAAGCCA	0	J	FG10368.1	0	0	0	0
9724	4228	af	AN2757.1	59.m09254	AO070327000036	0			-68	-15			ATGGTGGCAACAGTGGTACCGACGACAATGGAGGCTTTCCTGCTGCTTCTTTGA		ATGGTGGCAACAGTGGTACCGACGACAATGGAGGCTTTCCTGCTGCTTCTTTGA		MVATVVPTTMEAFLLLL*		MVATVVPTTMEAFLLLL*		TTCCCCTCAC	TTGACTTGGT	0	R	0	0	0	0	0
9721	4228	an	AN2757.1	59.m09254	AO070327000036	0	-224	-159					ATGACAGACATAGCCACCTTTCCCTTACCCAGTATGTGCTGGGAAGATAGACTATTATTGCTTTGA	ATGACAGACATAGCCACCTTTCCCTTACCCAGTATGTGCTGGGAAGATAGACTATTATTGCTTTGA			MTDIATFPLPSMCWEDRLLLL*	MTDIATFPLPSMCWEDRLLLL*			CCCAGTATTG	ATTCTTTGAT	0	R	0	0	0	0	0
9722	4228	an	AN2757.1	59.m09254	AO070327000036	0	-191	-159					ATGTGCTGGGAAGATAGACTATTATTGCTTTGA	ATGTGCTGGGAAGATAGACTATTATTGCTTTGA			MCWEDRLLLL*	MCWEDRLLLL*			CTTACCCAGT	ATTCTTTGAT	0	R	0	0	0	0	0
9720	4228	conserved	AN2757.1	59.m09254	AO070327000036	0	-63	-16	-41	-15	-41	-15	ATGsrsshkyysmTGbTssThbykwrATCCTCGCTAAAACGGGTTTGA	ATGCGGCAGCCGATGGTCGTCGCGAAATCCTCGCTAAAACGGGTTTGA	ATGGAGGCTTTCCTGCTGCTTCTTTGA	ATGGACCTTTCGATGTTGCTATTGTGA	Mrqpmvvaksslkrv*	MRQPMVVAKSSLKRV*	MEAFLLLL*	MDLSMLLL*	whhsmysAyr	TTGAmykGsy	0	R	0	0	0	0	0
9728	4231	af	AN2729.1	63.m00657	AO070330000123	0			-86	-75			ATGGAAATATAA		ATGGAAATATAA		MEI*		MEI*		CACAGCTCAG	GAAGATATCA	0	G	0	0	0	0	0
9727	4231	an	AN2729.1	63.m00657	AO070330000123	0	-132	-37					ATGAATCTTAGGCGGAGTTGGCACTCCTTTGAGCTTGGCTACTTACTCCGTTCGCTTATATTCTGCCCTTCCCCATGTGGTGTAGCAGTCCAATAG	ATGAATCTTAGGCGGAGTTGGCACTCCTTTGAGCTTGGCTACTTACTCCGTTCGCTTATATTCTGCCCTTCCCCATGTGGTGTAGCAGTCCAATAG			MNLRRSWHSFELGYLLRSLIFCPSPCGVAVQ*	MNLRRSWHSFELGYLLRSLIFCPSPCGVAVQ*			ATCTAGCTTC	ATACAGGTCT	0	G	0	0	0	0	0
9729	4231	ao	AN2729.1	63.m00657	AO070330000123	0					-199	-131	ATGTGCTTTGCAAGCTCATTGTTATGTTGTGCTATTTCCGGGCCCACAATGTCTAGTTCCACCATCTAG			ATGTGCTTTGCAAGCTCATTGTTATGTTGTGCTATTTCCGGGCCCACAATGTCTAGTTCCACCATCTAG	MCFASSLLCCAISGPTMSSSTI*			MCFASSLLCCAISGPTMSSSTI*	TGTTACATCA	TGTATCTTTT	0	G	0	0	0	0	0
9730	4231	ao	AN2729.1	63.m00657	AO070330000123	0					-176	-144	ATGTTGTGCTATTTCCGGGCCCACAATGTCTAG			ATGTTGTGCTATTTCCGGGCCCACAATGTCTAG	MLCYFRAHNV*			MLCYFRAHNV*	GCTCATTGTT	TTCCACCATC	0	G	0	0	0	0	0
9731	4231	ao	AN2729.1	63.m00657	AO070330000123	0					-151	-131	ATGTCTAGTTCCACCATCTAG			ATGTCTAGTTCCACCATCTAG	MSSSTI*			MSSSTI*	CGGGCCCACA	TGTATCTTTT	0	G	0	0	0	0	0
9732	4231	ao	AN2729.1	63.m00657	AO070330000123	0					-68	-57	ATGCAGTCCTAG			ATGCAGTCCTAG	MQS*			MQS*	TTCCCCAGAA	CCTAGATCTG	0	G	0	0	0	0	0
9735	4232	af	AN1164.1	70.m15056	AO070331000156	0			-175	-131			ATGCCTCGCCCGTATCAATTGGTATATTTGTATATAGACAAATAG		ATGCCTCGCCCGTATCAATTGGTATATTTGTATATAGACAAATAG		MPRPYQLVYLYIDK*		MPRPYQLVYLYIDK*		CGATTGGACA	AACAAACATA	0	B	0	0	0	0	0
9733	4232	an	AN1164.1	70.m15056	AO070331000156	0	-167	-96					ATGGTTACAGAACGTATTGTACCAAAACATGTGCTTCTCCCCTCTTCGAGACTAGAGCCTCGAGGGCGGTGA	ATGGTTACAGAACGTATTGTACCAAAACATGTGCTTCTCCCCTCTTCGAGACTAGAGCCTCGAGGGCGGTGA			MVTERIVPKHVLLPSSRLEPRGR*	MVTERIVPKHVLLPSSRLEPRGR*			TCTTGTATTT	AGGTCTCACC	0	B	0	0	0	0	0
9734	4232	an	AN1164.1	70.m15056	AO070331000156	0	-139	-113					ATGTGCTTCTCCCCTCTTCGAGACTAG	ATGTGCTTCTCCCCTCTTCGAGACTAG			MCFSPLRD*	MCFSPLRD*			GTACCAAAAC	AGCCTCGAGG	0	B	0	0	0	0	0
9736	4233	af	AN3107.1	59.m08630	AO070334000152	0			-118	-59			ATGTACACTGCACGCCGCTCTCTCTGGTGTCCGTCGCCTAGTGGTCTCCCAAGCGCTTGA		ATGTACACTGCACGCCGCTCTCTCTGGTGTCCGTCGCCTAGTGGTCTCCCAAGCGCTTGA		MYTARRSLWCPSPSGLPSA*		MYTARRSLWCPSPSGLPSA*		CGAATATTAA	AAGCTGAGTT	0		0	0	0	0	0
9737	4233	ao	AN3107.1	59.m08630	AO070334000152	0					-157	-143	ATGACCGAGAAATAA			ATGACCGAGAAATAA	MTEK*			MTEK*	CATTCTTCCC	TCTCCAAATT	0		0	0	0	0	0
9738	4233	ao	AN3107.1	59.m08630	AO070334000152	0					-113	-48	ATGAAGGCCCGCACACGGCGCTCTGGCGTCTTGTTACTGCGTTCTCTCGTCGCCGCCACCGTCTGA			ATGAAGGCCCGCACACGGCGCTCTGGCGTCTTGTTACTGCGTTCTCTCGTCGCCGCCACCGTCTGA	MKARTRRSGVLLLRSLVAATV*			MKARTRRSGVLLLRSLVAATV*	GTGGACTTGT	CCATGACCCC	0		0	0	0	0	0
9744	4235	af	AN2857.1	59.m08700	AO070338000165	0			-258	-166			ATGTCCAACGACGCCGCATCAATCTCTAGTCCTTGTGCTCGTTGCGCATCTTTTCCCACTGAGATTGTCGATCGCAAGCTGCTTTGGATCTGA		ATGTCCAACGACGCCGCATCAATCTCTAGTCCTTGTGCTCGTTGCGCATCTTTTCCCACTGAGATTGTCGATCGCAAGCTGCTTTGGATCTGA		MSNDAASISSPCARCASFPTEIVDRKLLWI*		MSNDAASISSPCARCASFPTEIVDRKLLWI*		CATCACGGTC	TTCGAAGCTA	0	B	0	0	0	0	0
9745	4235	af	AN2857.1	59.m08700	AO070338000165	0			-123	-94			ATGGCTGCGCGGATGGTGCCACCCACCTAG		ATGGCTGCGCGGATGGTGCCACCCACCTAG		MAARMVPPT*		MAARMVPPT*		CGCTACCTTC	CCCCCTACCA	0	B	0	0	0	0	0
9746	4235	af	AN2857.1	59.m08700	AO070338000165	0			-111	-94			ATGGTGCCACCCACCTAG		ATGGTGCCACCCACCTAG		MVPPT*		MVPPT*		GGCTGCGCGG	CCCCCTACCA	0	B	0	0	0	0	0
9742	4235	an	AN2857.1	59.m08700	AO070338000165	0	-129	-88					ATGGCTGCACCGTCGCGCATGGTGCTGCCTGCTGAGCCCTGA	ATGGCTGCACCGTCGCGCATGGTGCTGCCTGCTGAGCCCTGA			MAAPSRMVLPAEP*	MAAPSRMVLPAEP*			TTTTTCCCAT	CTACCTCTGC	0	B	0	0	0	0	0
9743	4235	an	AN2857.1	59.m08700	AO070338000165	0	-111	-88					ATGGTGCTGCCTGCTGAGCCCTGA	ATGGTGCTGCCTGCTGAGCCCTGA			MVLPAEP*	MVLPAEP*			ACCGTCGCGC	CTACCTCTGC	0	B	0	0	0	0	0

9747	4235	ao	AN2857.1	59.m08700	AO070338000165	0					-106	-74	ATGGCCTCGCCGTCACACATGGTGCCGTCATAA			ATGGCCTCGCCGTCACACATGGTGCCGTCATAA	MASPSHMVPS*			MASPSHMVPS*	ACTTCCCTCG	ACAATAACAT	0	B	0	0	0	0	0
9748	4235	ao	AN2857.1	59.m08700	AO070338000165	0					-88	-74	ATGGTGCCGTCATAA			ATGGTGCCGTCATAA	MVPS*			MVPS*	GCCGTCACAC	ACAATAACAT	0	B	0	0	0	0	0
9741	4235	conserved	AN2857.1	59.m08700	AO070338000165	0	-157	-143	-149	-135	-131	-117	ATGCdwyTssmCTGA	ATGCTTTTCCACTGA	ATGCAACTGCCCTGA	ATGCGTTTGGACTGA	Mlfh*	MLFH*	MQLP*	MRLD*	bbbwCrkyyC	dmbyyhyyyb	0	B	0	0	0	0	0
9749	4237	af	AN5996.1	72.m19144	AO070340000281	0			-221	-189			ATGGTTCAATTCTCTAATTCTTACTTTCCCTAA		ATGGTTCAATTCTCTAATTCTTACTTTCCCTAA		MVQFSNSYFP*		MVQFSNSYFP*		CGATATTTTG	CCACTTCGCT	0	J	0	0	0	0	0
9750	4239	af	AN7571.1	72.m19590	AO070343000417	0			-132	-112			ATGGCCCACATTGGTCCCTAA		ATGGCCCACATTGGTCCCTAA		MAHIGP*		MAHIGP*		TTTTATTTAT	CCATCTACTA	0	M	0	0	0	0	0
9751	4239	ao	AN7571.1	72.m19590	AO070343000417	0					-224	-123	ATGCTACTACTGCCCCTCTGCCGAAACTGTTTCAACCCTTCCAGACTCCTTGGGGTTGCCAGATACCGGGGTCTCGTCCATTCATTCTTTTGCTTCATTTAG			ATGCTACTACTGCCCCTCTGCCGAAACTGTTTCAACCCTTCCAGACTCCTTGGGGTTGCCAGATACCGGGGTCTCGTCCATTCATTCTTTTGCTTCATTTAG	MLLLPLCRNCFNPSRLLGVARYRGLVHSFFCFI*			MLLLPLCRNCFNPSRLLGVARYRGLVHSFFCFI*	ACATATTTAT	TCATTCCTTT	0	M	0	0	0	0	0
9752	4240	an	AN1408.1	55.m02915	AO070242000011	0	-275	-231					ATGGGTAAATTTACGTTTAAAATTCTTGATATTTTCAGATTCTAA	ATGGGTAAATTTACGTTTAAAATTCTTGATATTTTCAGATTCTAA			MGKFTFKILDIFRF*	MGKFTFKILDIFRF*			CAGGTACAAT	GAGAAGCCCC	0	J	0	0	0	0	0
9758	4241	af	AN5882.1	72.m19249	AO070245000026	0			-187	-89			ATGCTACGACGATCCTTCATCCTTTGCCTCAGTGTTCAACGAAATAATCGTCAAAGAGCTCTGAAGCCGACCGCACCAAAGTCATCAACAACAAGATAA		ATGCTACGACGATCCTTCATCCTTTGCCTCAGTGTTCAACGAAATAATCGTCAAAGAGCTCTGAAGCCGACCGCACCAAAGTCATCAACAACAAGATAA		MLRRSFILCLSVQRNNRQRALKPTAPKSSTTR*		MLRRSFILCLSVQRNNRQRALKPTAPKSSTTR*		GCACTTCGCC	TTGTCTCTTG	0	Y	0	0	0	0	0
9759	4241	af	AN5882.1	72.m19249	AO070245000026	0			-70	-38			ATGGGTAACTGTGGAAGGTCTACCTGGCCTTGA		ATGGGTAACTGTGGAAGGTCTACCTGGCCTTGA		MGNCGRSTWP*		MGNCGRSTWP*		TGCCCAAGGA	AGTCCAGCCG	0	Y	0	0	0	0	0
9755	4241	an	AN5882.1	72.m19249	AO070245000026	0	-192	-154					ATGTTCGCCTTTCCCACGCCTTTCGTCGCCGCGCCTTGA	ATGTTCGCCTTTCCCACGCCTTTCGTCGCCGCGCCTTGA			MFAFPTPFVAAP*	MFAFPTPFVAAP*			CGGACAAAAG	TGGTTGTTAT	0	Y	0	0	0	0	0
9756	4241	an	AN5882.1	72.m19249	AO070245000026	0	-154	-128					ATGGTTGTTATCCCAGTCCCTGGCTAA	ATGGTTGTTATCCCAGTCCCTGGCTAA			MVVIPVPG*	MVVIPVPG*			CCGCGCCTTG	AGGCAGGTCG	0	Y	0	0	0	0	0
9757	4241	an	AN5882.1	72.m19249	AO070245000026	0	-82	-47					ATGAAAAGGCTAGTTCGCCTAATTAATCGGCACTGA	ATGAAAAGGCTAGTTCGCCTAATTAATCGGCACTGA			MKRLVRLINRH*	MKRLVRLINRH*			ACTTCTACTC	CCCAGGAGCC	0	Y	0	0	0	0	0
9760	4241	ao	AN5882.1	72.m19249	AO070245000026	0					-188	-60	ATGCTCTGTCGTGTTTCAATGAGCCATCAGCTTCATTGTCGCACGGCAAACGCCTCAGAAGGCGTAGTAATCACATCCCACCTTCACATACACAAGAAAAACCACGGTTTTCTAGGAAGGAATGGGTAA			ATGCTCTGTCGTGTTTCAATGAGCCATCAGCTTCATTGTCGCACGGCAAACGCCTCAGAAGGCGTAGTAATCACATCCCACCTTCACATACACAAGAAAAACCACGGTTTTCTAGGAAGGAATGGGTAA	MLCRVSMSHQLHCRTANASEGVVITSHLHIHKKNHGFLGRNG*			MLCRVSMSHQLHCRTANASEGVVITSHLHIHKKNHGFLGRNG*	CTCTTCGCAA	GTCGAAGGGC	0	Y	0	0	0	0	0
9761	4241	ao	AN5882.1	72.m19249	AO070245000026	0					-170	-60	ATGAGCCATCAGCTTCATTGTCGCACGGCAAACGCCTCAGAAGGCGTAGTAATCACATCCCACCTTCACATACACAAGAAAAACCACGGTTTTCTAGGAAGGAATGGGTAA			ATGAGCCATCAGCTTCATTGTCGCACGGCAAACGCCTCAGAAGGCGTAGTAATCACATCCCACCTTCACATACACAAGAAAAACCACGGTTTTCTAGGAAGGAATGGGTAA	MSHQLHCRTANASEGVVITSHLHIHKKNHGFLGRNG*			MSHQLHCRTANASEGVVITSHLHIHKKNHGFLGRNG*	TCGTGTTTCA	GTCGAAGGGC	0	Y	0	0	0	0	0
9762	4241	ao	AN5882.1	72.m19249	AO070245000026	0					-67	-47	ATGGGTAAGTCGAAGGGCTGA			ATGGGTAAGTCGAAGGGCTGA	MGKSKG*			MGKSKG*	CTAGGAAGGA	ACCTGACCTA	0	Y	0	0	0	0	0
9766	4243	af	AN2460.1	69.m15675	AO070264000013	0			-179	-141			ATGAACTTATCCAGGACATTTCACAGCTGTCAACCATGA		ATGAACTTATCCAGGACATTTCACAGCTGTCAACCATGA		MNLSRTFHSCQP*		MNLSRTFHSCQP*		TGTGACCTTA	GGCACTACCA	0	A	0	0	0	0	0
9767	4243	af	AN2460.1	69.m15675	AO070264000013	0			-144	-118			ATGAGGCACTACCATACCCTGGTCTAG		ATGAGGCACTACCATACCCTGGTCTAG		MRHYHTLV*		MRHYHTLV*		GCTGTCAACC	AAGATATGAG	0	A	0	0	0	0	0
9763	4243	an	AN2460.1	69.m15675	AO070264000013	0	-189	-115					ATGAACAGAGAATTGCAGAGCAGGCTCGACAAGTCCTGGCCAACACACAGAACGCATCCGATGCTGGAGATATGA	ATGAACAGAGAATTGCAGAGCAGGCTCGACAAGTCCTGGCCAACACACAGAACGCATCCGATGCTGGAGATATGA			MNRELQSRLDKSWPTHRTHPMLEI*	MNRELQSRLDKSWPTHRTHPMLEI*			AGCTGACTGA	GGACTCGCCT	0	A	0	0	0	0	0
9764	4243	an	AN2460.1	69.m15675	AO070264000013	0	-129	-115					ATGCTGGAGATATGA	ATGCTGGAGATATGA			MLEI*	MLEI*			AACGCATCCG	GGACTCGCCT	0	A	0	0	0	0	0
9765	4243	an	AN2460.1	69.m15675	AO070264000013	0	-118	-14					ATGAGGACTCGCCTGCGAAATCATCCATCCATCCTCTTCCCTCACTTCGACCGCTGTGGCCTGCGGCAGCAGTACTGTAACCCCCAGAACACACCCCATCCATGA	ATGAGGACTCGCCTGCGAAATCATCCATCCATCCTCTTCCCTCACTTCGACCGCTGTGGCCTGCGGCAGCAGTACTGTAACCCCCAGAACACACCCCATCCATGA			MRTRLRNHPSILFPHFDRCGLRQQYCNPQNTPHP*	MRTRLRNHPSILFPHFDRCGLRQQYCNPQNTPHP*			TGCTGGAGAT	CCCCCGCCTC	0	A	0	0	0	0	0
9768	4243	ao	AN2460.1	69.m15675	AO070264000013	0					-117	-19	ATGAGGATCTTTCGGTCACACTCAGCTATCACGTCCTCCGTCGCTCAAATGCAGTCAGTGTTCGACTGCTGCTGCATTGTAAACAATCATACTCATTAA			ATGAGGATCTTTCGGTCACACTCAGCTATCACGTCCTCCGTCGCTCAAATGCAGTCAGTGTTCGACTGCTGCTGCATTGTAAACAATCATACTCATTAA	MRIFRSHSAITSSVAQMQSVFDCCCIVNNHTH*			MRIFRSHSAITSSVAQMQSVFDCCCIVNNHTH*	CGCAAAAGAT	TGATTTCATC	0	A	0	0	0	0	0
9769	4243	ao	AN2460.1	69.m15675	AO070264000013	0					-69	-19	ATGCAGTCAGTGTTCGACTGCTGCTGCATTGTAAACAATCATACTCATTAA			ATGCAGTCAGTGTTCGACTGCTGCTGCATTGTAAACAATCATACTCATTAA	MQSVFDCCCIVNNHTH*			MQSVFDCCCIVNNHTH*	CGTCGCTCAA	TGATTTCATC	0	A	0	0	0	0	0
9776	4244	af	AN0576.1	69.m15269	AO070272000056	0			-182	-141			ATGTCAGGACATGATGATCAGGGCATCTATTCAGAGAGTTAG		ATGTCAGGACATGATGATCAGGGCATCTATTCAGAGAGTTAG		MSGHDDQGIYSES*		MSGHDDQGIYSES*		CCCGACACTT	CGTACAGATC	0	T	FG05306.1	MG06100.1	0	0	0
9777	4244	af	AN0576.1	69.m15269	AO070272000056	0			-172	-95			ATGATGATCAGGGCATCTATTCAGAGAGTTAGCGTACAGATCGCTTCAATATCAATATCAACTCCATCAACGTTGTAG		ATGATGATCAGGGCATCTATTCAGAGAGTTAGCGTACAGATCGCTTCAATATCAATATCAACTCCATCAACGTTGTAG		MMIRASIQRVSVQIASISISTPSTL*		MMIRASIQRVSVQIASISISTPSTL*		ATGTCAGGAC	GCTTGTGTCT	0	T	FG05306.1	MG06100.1	0	0	0
9778	4244	af	AN0576.1	69.m15269	AO070272000056	0			-169	-95			ATGATCAGGGCATCTATTCAGAGAGTTAGCGTACAGATCGCTTCAATATCAATATCAACTCCATCAACGTTGTAG		ATGATCAGGGCATCTATTCAGAGAGTTAGCGTACAGATCGCTTCAATATCAATATCAACTCCATCAACGTTGTAG		MIRASIQRVSVQIASISISTPSTL*		MIRASIQRVSVQIASISISTPSTL*		TCAGGACATG	GCTTGTGTCT	0	T	FG05306.1	MG06100.1	0	0	0
9770	4244	an	AN0576.1	69.m15269	AO070272000056	0	-248	-21					ATGGAAGATGGCCAAAGAGATAAGCCGGCCTTCACCGCCTTTCTGCCATGTGATGTCGCGGCCACCCGTCTCTGGACCCTCTTAGGTGCCGTACGCGTCCTCTGTCCTCCAATTGTGATCTCTGATCGTACAGGTCAGGTCTCATCGGAGATAGTTCGTGGGATAATCATCTGGGTTTTCTTTAGATGCTTTCCTAAACATGATTGTTTTATGAACCTATTCTTATGA	ATGGAAGATGGCCAAAGAGATAAGCCGGCCTTCACCGCCTTTCTGCCATGTGATGTCGCGGCCACCCGTCTCTGGACCCTCTTAGGTGCCGTACGCGTCCTCTGTCCTCCAATTGTGATCTCTGATCGTACAGGTCAGGTCTCATCGGAGATAGTTCGTGGGATAATCATCTGGGTTTTCTTTAGATGCTTTCCTAAACATGATTGTTTTATGAACCTATTCTTATGA			MEDGQRDKPAFTAFLPCDVAATRLWTLLGAVRVLCPPIVISDRTGQVSSEIVRGIIIWVFFRCFPKHDCFMNLFL*	MEDGQRDKPAFTAFLPCDVAATRLWTLLGAVRVLCPPIVISDRTGQVSSEIVRGIIIWVFFRCFPKHDCFMNLFL*			AGAATATTGA	AATGAAGACG	0	T	FG05306.1	MG06100.1	0	0	0
9771	4244	an	AN0576.1	69.m15269	AO070272000056	0	-241	-164					ATGGCCAAAGAGATAAGCCGGCCTTCACCGCCTTTCTGCCATGTGATGTCGCGGCCACCCGTCTCTGGACCCTCTTAG	ATGGCCAAAGAGATAAGCCGGCCTTCACCGCCTTTCTGCCATGTGATGTCGCGGCCACCCGTCTCTGGACCCTCTTAG			MAKEISRPSPPFCHVMSRPPVSGPS*	MAKEISRPSPPFCHVMSRPPVSGPS*			TGAATGGAAG	GTGCCGTACG	0	T	FG05306.1	MG06100.1	0	0	0
9772	4244	an	AN0576.1	69.m15269	AO070272000056	0	-196	-164					ATGTCGCGGCCACCCGTCTCTGGACCCTCTTAG	ATGTCGCGGCCACCCGTCTCTGGACCCTCTTAG			MSRPPVSGPS*	MSRPPVSGPS*			CTGCCATGTG	GTGCCGTACG	0	T	FG05306.1	MG06100.1	0	0	0
9773	4244	an	AN0576.1	69.m15269	AO070272000056	0	-63	-52					ATGCTTTCCTAA	ATGCTTTCCTAA			MLS*	MLS*			TTTTCTTTAG	ACATGATTGT	0	T	FG05306.1	MG06100.1	0	0	0
9780	4244	ao	AN0576.1	69.m15269	AO070272000056	0					-190	-47	ATGTACATTACCAACGACGACACCTTTCAACGCGTCAACGTCAACTTTGCAAGGTATGACTGCCAAATACTCGTTTTTCTGTCAAGGCGATCACGTAGATTTGCTCTGTATAACACACAGATGCTTCTCCCATTCTTGCTTTGA			ATGTACATTACCAACGACGACACCTTTCAACGCGTCAACGTCAACTTTGCAAGGTATGACTGCCAAATACTCGTTTTTCTGTCAAGGCGATCACGTAGATTTGCTCTGTATAACACACAGATGCTTCTCCCATTCTTGCTTTGA	MYITNDDTFQRVNVNFARYDCQILVFLSRRSRRFALYNTQMLLPFLL*			MYITNDDTFQRVNVNFARYDCQILVFLSRRSRRFALYNTQMLLPFLL*	ATCATGTGAC	TGAGTTTCAT	0	T	FG05306.1	MG06100.1	0	0	0
9781	4244	ao	AN0576.1	69.m15269	AO070272000056	0					-135	-13	ATGACTGCCAAATACTCGTTTTTCTGTCAAGGCGATCACGTAGATTTGCTCTGTATAACACACAGATGCTTCTCCCATTCTTGCTTTGATGAGTTTCATTGCTTTCAAAGGCCTCTGGGATGA			ATGACTGCCAAATACTCGTTTTTCTGTCAAGGCGATCACGTAGATTTGCTCTGTATAACACACAGATGCTTCTCCCATTCTTGCTTTGATGAGTTTCATTGCTTTCAAAGGCCTCTGGGATGA	MTAKYSFFCQGDHVDLLCITHRCFSHSCFDEFHCFQRPLG*			MTAKYSFFCQGDHVDLLCITHRCFSHSCFDEFHCFQRPLG*	TTTGCAAGGT	AGGAACCTCA	0	T	FG05306.1	MG06100.1	0	0	0
9782	4244	ao	AN0576.1	69.m15269	AO070272000056	0					-70	-47	ATGCTTCTCCCATTCTTGCTTTGA			ATGCTTCTCCCATTCTTGCTTTGA	MLLPFLL*			MLLPFLL*	TAACACACAG	TGAGTTTCAT	0	T	FG05306.1	MG06100.1	0	0	0
9788	4246	af	AN7230.1	72.m20024	AO070290000040	0			-236	-162			ATGACCACGCCAATTTATCCAGAACGTGTACTGTCCAACGTACAGGCTCTCCCTCAGGCCGAGCCAATACCATGA		ATGACCACGCCAATTTATCCAGAACGTGTACTGTCCAACGTACAGGCTCTCCCTCAGGCCGAGCCAATACCATGA		MTTPIYPERVLSNVQALPQAEPIP*		MTTPIYPERVLSNVQALPQAEPIP*		ACGATATGAA	CAGTGATCCT	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9789	4246	af	AN7230.1	72.m20024	AO070290000040	0			-165	-85			ATGACAGTGATCCTCCGGGGCGGGTTGCATCATGGACGCCCAGACGGGGGGTTGCACATGGAATCGGTCCTGTGTATCTGA		ATGACAGTGATCCTCCGGGGCGGGTTGCATCATGGACGCCCAGACGGGGGGTTGCACATGGAATCGGTCCTGTGTATCTGA		MTVILRGGLHHGRPDGGLHMESVLCI*		MTVILRGGLHHGRPDGGLHMESVLCI*		AGCCAATACC	CCGGGTCCTG	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9790	4246	af	AN7230.1	72.m20024	AO070290000040	0			-134				ATGGACGCCCAGACGGGGGGTTGCACATGGAATCGGTCCTGTGTATCTGACCGGGTCCTGTGGTATATCTTCAGCTCGTTCGCACTCTGCTCTCGACGAGTCACATCGATCCACGACGCTGTGCTTCGCCAGTGA		ATGGACGCCCAGACGGGGGGTTGCACATGGAATCGGTCCTGTGTATCTGACCGGGTCCTGTGGTATATCTTCAGCTCGTTCGCACTCTGCTCTCGACGAGTCACATCGATCCACGACGCTGTGCTTCGCCAGTGA		MDAQTGGCTWNRSCVSDRVLWYIFSSFALCSRRVTSIHDAVLRQ*		MDAQTGGCTWNRSCVSDRVLWYIFSSFALCSRRVTSIHDAVLRQ*		GGGTTGCATC	TGAAGCTCTT	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9791	4246	af	AN7230.1	72.m20024	AO070290000040	0			-108	-85			ATGGAATCGGTCCTGTGTATCTGA		ATGGAATCGGTCCTGTGTATCTGA		MESVLCI*		MESVLCI*		GGGGTTGCAC	CCGGGTCCTG	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9783	4246	an	AN7230.1	72.m20024	AO070290000040	0	-260	-195					ATGGAAATCAAGCGGGTGCTTAAATGTGCCCGTTTCATTTGCGGTGGGTTTGTTGTTGCAGGTTGA	ATGGAAATCAAGCGGGTGCTTAAATGTGCCCGTTTCATTTGCGGTGGGTTTGTTGTTGCAGGTTGA			MEIKRVLKCARFICGGFVVAG*	MEIKRVLKCARFICGGFVVAG*			CTGGGACGAT	GGCTGCTCGG	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9784	4246	an	AN7230.1	72.m20024	AO070290000040	0	-237	-58					ATGTGCCCGTTTCATTTGCGGTGGGTTTGTTGTTGCAGGTTGAGGCTGCTCGGAATGGTCACTGCTCACCGTCGGCCAGCTATATATTCCTCCAACCCATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA	ATGTGCCCGTTTCATTTGCGGTGGGTTTGTTGTTGCAGGTTGAGGCTGCTCGGAATGGTCACTGCTCACCGTCGGCCAGCTATATATTCCTCCAACCCATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA			MCPFHLRWVCCCRLRLLGMVTAHRRPAIYSSNPCARPGMLTICNCSLPRLQFTLFCSSW*	MCPFHLRWVCCCRLRLLGMVTAHRRPAIYSSNPCARPGMLTICNCSLPRLQFTLFCSSW*			GGGTGCTTAA	CGATTGCCTC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9785	4246	an	AN7230.1	72.m20024	AO070290000040	0	-183	-58					ATGGTCACTGCTCACCGTCGGCCAGCTATATATTCCTCCAACCCATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA	ATGGTCACTGCTCACCGTCGGCCAGCTATATATTCCTCCAACCCATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA			MVTAHRRPAIYSSNPCARPGMLTICNCSLPRLQFTLFCSSW*	MVTAHRRPAIYSSNPCARPGMLTICNCSLPRLQFTLFCSSW*			GCTGCTCGGA	CGATTGCCTC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9786	4246	an	AN7230.1	72.m20024	AO070290000040	0	-139	-17					ATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGACGATTGCCTCCCTTCCTTCGTTTCTTTTACCTTCTCTTTAA	ATGCGCTCGACCAGGGATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGACGATTGCCTCCCTTCCTTCGTTTCTTTTACCTTCTCTTTAA			MRSTRDAHYLQLLFAKVAVHFVLLVLVTIASLPSFLLPSL*	MRSTRDAHYLQLLFAKVAVHFVLLVLVTIASLPSFLLPSL*			CCTCCAACCC	ACCCCCTGTC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9787	4246	an	AN7230.1	72.m20024	AO070290000040	0	-123	-58					ATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA	ATGCTCACTATCTGCAATTGCTCTTTGCCAAGGTTGCAGTTCACTTTGTTTTGCTCGTCCTGGTGA			MLTICNCSLPRLQFTLFCSSW*	MLTICNCSLPRLQFTLFCSSW*			TCGACCAGGG	CGATTGCCTC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9792	4246	ao	AN7230.1	72.m20024	AO070290000040	0					-227	-69	ATGCGAGAACGCCAGCGAGCCAAGATGCGCTACAGTATCAGCTACGACACGTTTGAGTCCGGCAATGTCCCTGCAATATGGATCCGCGGGCCGGGTGTCGAGCCATCTGTATCGGGGCATTCGTCCTGGTGTCATCCGTGGGCGCCATTGTATATCTAG			ATGCGAGAACGCCAGCGAGCCAAGATGCGCTACAGTATCAGCTACGACACGTTTGAGTCCGGCAATGTCCCTGCAATATGGATCCGCGGGCCGGGTGTCGAGCCATCTGTATCGGGGCATTCGTCCTGGTGTCATCCGTGGGCGCCATTGTATATCTAG	MRERQRAKMRYSISYDTFESGNVPAIWIRGPGVEPSVSGHSSWCHPWAPLYI*			MRERQRAKMRYSISYDTFESGNVPAIWIRGPGVEPSVSGHSSWCHPWAPLYI*	TCCAGTCAAT	GGCTCGACCC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0

9793	4246	ao	AN7230.1	72.m20024	AO070290000040	0					-203	-69	ATGCGCTACAGTATCAGCTACGACACGTTTGAGTCCGGCAATGTCCCTGCAATATGGATCCGCGGGCCGGGTGTCGAGCCATCTGTATCGGGGCATTCGTCCTGGTGTCATCCGTGGGCGCCATTGTATATCTAG			ATGCGCTACAGTATCAGCTACGACACGTTTGAGTCCGGCAATGTCCCTGCAATATGGATCCGCGGGCCGGGTGTCGAGCCATCTGTATCGGGGCATTCGTCCTGGTGTCATCCGTGGGCGCCATTGTATATCTAG	MRYSISYDTFESGNVPAIWIRGPGVEPSVSGHSSWCHPWAPLYI*			MRYSISYDTFESGNVPAIWIRGPGVEPSVSGHSSWCHPWAPLYI*	GCGAGCCAAG	GGCTCGACCC	0	E	FG09085.1	MG11036.1	NCU00206.1	0	0
9798	4248	af	AN1669.1	58.m07734	AO070299000051	0			-247	-218			ATGTTCATGTCGATGATGGCGTTAGCTTGA		ATGTTCATGTCGATGATGGCGTTAGCTTGA		MFMSMMALA*		MFMSMMALA*		GCAGAGAAAG	TAGTTGGATT	0	RP	0	0	0	0	0
9799	4248	af	AN1669.1	58.m07734	AO070299000051	0			-241	-218			ATGTCGATGATGGCGTTAGCTTGA		ATGTCGATGATGGCGTTAGCTTGA		MSMMALA*		MSMMALA*		AAAGATGTTC	TAGTTGGATT	0	RP	0	0	0	0	0
9800	4248	af	AN1669.1	58.m07734	AO070299000051	0			-235	-218			ATGATGGCGTTAGCTTGA		ATGATGGCGTTAGCTTGA		MMALA*		MMALA*		GTTCATGTCG	TAGTTGGATT	0	RP	0	0	0	0	0
9801	4248	af	AN1669.1	58.m07734	AO070299000051	0			-232	-218			ATGGCGTTAGCTTGA		ATGGCGTTAGCTTGA		MALA*		MALA*		CATGTCGATG	TAGTTGGATT	0	RP	0	0	0	0	0
9802	4248	af	AN1669.1	58.m07734	AO070299000051	0			-180	-124			ATGGTTCGCGGTTCCGTATTGCGGAACTTCTTTCGCCTTCTTTGCCTCAGCCATTAA		ATGGTTCGCGGTTCCGTATTGCGGAACTTCTTTCGCCTTCTTTGCCTCAGCCATTAA		MVRGSVLRNFFRLLCLSH*		MVRGSVLRNFFRLLCLSH*		AATCAGAAGT	AATCTGAACA	0	RP	0	0	0	0	0
9794	4248	an	AN1669.1	58.m07734	AO070299000051	0	-210	-187					ATGCAGGTATCTGACGGTCATTGA	ATGCAGGTATCTGACGGTCATTGA			MQVSDGH*	MQVSDGH*			GTTAAGAGCA	TATGTCGCGT	0	RP	0	0	0	0	0
9795	4248	an	AN1669.1	58.m07734	AO070299000051	0	-185	-75					ATGTCGCGTTACCCAATCAGATTGATGCCCCGTTGTTCCGCGCGGCGGATCTTTGCAAGTGCTTTTTGCCGCCCGCTCCCCAAAAGTTCTCTTCACTTTACTTTTGCATGA	ATGTCGCGTTACCCAATCAGATTGATGCCCCGTTGTTCCGCGCGGCGGATCTTTGCAAGTGCTTTTTGCCGCCCGCTCCCCAAAAGTTCTCTTCACTTTACTTTTGCATGA			MSRYPIRLMPRCSARRIFASAFCRPLPKSSLHFTFA*	MSRYPIRLMPRCSARRIFASAFCRPLPKSSLHFTFA*			GGTCATTGAT	AAGTCGCAAC	0	RP	0	0	0	0	0
9796	4248	an	AN1669.1	58.m07734	AO070299000051	0	-161	-75					ATGCCCCGTTGTTCCGCGCGGCGGATCTTTGCAAGTGCTTTTTGCCGCCCGCTCCCCAAAAGTTCTCTTCACTTTACTTTTGCATGA	ATGCCCCGTTGTTCCGCGCGGCGGATCTTTGCAAGTGCTTTTTGCCGCCCGCTCCCCAAAAGTTCTCTTCACTTTACTTTTGCATGA			MPRCSARRIFASAFCRPLPKSSLHFTFA*	MPRCSARRIFASAFCRPLPKSSLHFTFA*			AATCAGATTG	AAGTCGCAAC	0	RP	0	0	0	0	0
9797	4248	an	AN1669.1	58.m07734	AO070299000051	0	-78	-34					ATGAAAGTCGCAACCTTTTTCACTTCCTGGCATTCGATTGAGTGA	ATGAAAGTCGCAACCTTTTTCACTTCCTGGCATTCGATTGAGTGA			MKVATFFTSWHSIE*	MKVATFFTSWHSIE*			TTACTTTTGC	TAGCTTTCGC	0	RP	0	0	0	0	0
9805	4248	ao	AN1669.1	58.m07734	AO070299000051	0					-218	-180	ATGTCGAGACCTTTAGGTGTTTGGTTCAAATGTACCTAA			ATGTCGAGACCTTTAGGTGTTTGGTTCAAATGTACCTAA	MSRPLGVWFKCT*			MSRPLGVWFKCT*	GGTGACAGTG	ACCCAGCAGC	0	RP	0	0	0	0	0
9806	4248	ao	AN1669.1	58.m07734	AO070299000051	0					-189	-10	ATGTACCTAAACCCAGCAGCTCGCGCGGACCAATCAAAAGCTCCGGCGACCGTTCCGCGCGGCGGAACTTCCGACAATTTCTTTGCCTTGCCATTTCTCCCCACCCTTGTACTTTTTTTTCTTTGCCTCCGTTGCTTGGTGCTGGTACTTGCACATTTGCATATCATCACCCGCGACTGA			ATGTACCTAAACCCAGCAGCTCGCGCGGACCAATCAAAAGCTCCGGCGACCGTTCCGCGCGGCGGAACTTCCGACAATTTCTTTGCCTTGCCATTTCTCCCCACCCTTGTACTTTTTTTTCTTTGCCTCCGTTGCTTGGTGCTGGTACTTGCACATTTGCATATCATCACCCGCGACTGA	MYLNPAARADQSKAPATVPRGGTSDNFFALPFLPTLVLFFLCLRCLVLVLAHLHIITRD*			MYLNPAARADQSKAPATVPRGGTSDNFFALPFLPTLVLFFLCLRCLVLVLAHLHIITRD*	TTTGGTTCAA	GCTCCCACGA	0	RP	0	0	0	0	0
9807	4249	an	AN6231.1	72.m19978	AO070304000084	0	-205	-137					ATGCGCCTGCAGAGCAACGGTGACTCAAACGCAGCATTTCACCCCTTCCTTCGTCTGCCACTCCTTTAA	ATGCGCCTGCAGAGCAACGGTGACTCAAACGCAGCATTTCACCCCTTCCTTCGTCTGCCACTCCTTTAA			MRLQSNGDSNAAFHPFLRLPLL*	MRLQSNGDSNAAFHPFLRLPLL*			TGATCGCTTG	ATCGACCCGC	0	E	0	0	0	YGL026C	0
9808	4249	ao	AN6231.1	72.m19978	AO070304000084	0					-209	-186	ATGCAGAGACAAGAGGAGCCATGA			ATGCAGAGACAAGAGGAGCCATGA	MQRQEEP*			MQRQEEP*	GGCAATTTGA	CTCAAAACGC	0	E	0	0	0	YGL026C	0
9809	4249	ao	AN6231.1	72.m19978	AO070304000084	0					-189	-169	ATGACTCAAAACGCAGTGTGA			ATGACTCAAAACGCAGTGTGA	MTQNAV*			MTQNAV*	AAGAGGAGCC	CTTTGACAAG	0	E	0	0	0	YGL026C	0
9814	4250	af	AN6245.1	72.m19412	AO070304000099	0			-81	-28			ATGAGGCATCAAAACACAAAGTATATGCACCTCGCCACAAAATACCCTCTTTAA		ATGAGGCATCAAAACACAAAGTATATGCACCTCGCCACAAAATACCCTCTTTAA		MRHQNTKYMHLATKYPL*		MRHQNTKYMHLATKYPL*		TGTAGCGGAC	GACCCTCACT	0		0	0	0	0	0
9810	4250	an	AN6245.1	72.m19412	AO070304000099	0	-140	-36					ATGTGTTTGTGCCTTGATGCCTTGATGCCTTATTCCCGGCGGCAGAAGTCACATGATTATATCAACACCAAAATGTTATGCCGGCGACCAGAAGCTAGCATATAG	ATGTGTTTGTGCCTTGATGCCTTGATGCCTTATTCCCGGCGGCAGAAGTCACATGATTATATCAACACCAAAATGTTATGCCGGCGACCAGAAGCTAGCATATAG			MCLCLDALMPYSRRQKSHDYINTKMLCRRPEASI*	MCLCLDALMPYSRRQKSHDYINTKMLCRRPEASI*			ATTAGAAAAA	AGAAATCGCA	0		0	0	0	0	0
9811	4250	an	AN6245.1	72.m19412	AO070304000099	0	-116	-36					ATGCCTTATTCCCGGCGGCAGAAGTCACATGATTATATCAACACCAAAATGTTATGCCGGCGACCAGAAGCTAGCATATAG	ATGCCTTATTCCCGGCGGCAGAAGTCACATGATTATATCAACACCAAAATGTTATGCCGGCGACCAGAAGCTAGCATATAG			MPYSRRQKSHDYINTKMLCRRPEASI*	MPYSRRQKSHDYINTKMLCRRPEASI*			TGATGCCTTG	AGAAATCGCA	0		0	0	0	0	0
9812	4250	an	AN6245.1	72.m19412	AO070304000099	0	-68	-36					ATGTTATGCCGGCGACCAGAAGCTAGCATATAG	ATGTTATGCCGGCGACCAGAAGCTAGCATATAG			MLCRRPEASI*	MLCRRPEASI*			CAACACCAAA	AGAAATCGCA	0		0	0	0	0	0
9813	4250	an	AN6245.1	72.m19412	AO070304000099	0	-63	-43					ATGCCGGCGACCAGAAGCTAG	ATGCCGGCGACCAGAAGCTAG			MPATRS*	MPATRS*			CCAAAATGTT	CATATAGAGA	0		0	0	0	0	0
9816	4250	ao	AN6245.1	72.m19412	AO070304000099	0					-203	-192	ATGTCTCAATAA			ATGTCTCAATAA	MSQ*			MSQ*	ACCGCAGTGT	TACTTCTAGA	0		0	0	0	0	0
9820	4253	af	AN0054.1	71.m15327	AO070314000133	0			-200	-117			ATGCAAATGGCAAGCTATATATCACTGCGTCTCCCCATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		ATGCAAATGGCAAGCTATATATCACTGCGTCTCCCCATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		MQMASYISLRLPMEQKDSFFSSHLRQS*		MQMASYISLRLPMEQKDSFFSSHLRQS*		GAAGATTCAA	CTTCGCCGGC	0	I	0	0	0	0	0
9821	4253	af	AN0054.1	71.m15327	AO070314000133	0			-194	-117			ATGGCAAGCTATATATCACTGCGTCTCCCCATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		ATGGCAAGCTATATATCACTGCGTCTCCCCATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		MASYISLRLPMEQKDSFFSSHLRQS*		MASYISLRLPMEQKDSFFSSHLRQS*		TCAAATGCAA	CTTCGCCGGC	0	I	0	0	0	0	0
9822	4253	af	AN0054.1	71.m15327	AO070314000133	0			-164	-117			ATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		ATGGAGCAAAAGGATAGCTTTTTTTCTTCGCATCTTCGTCAGTCTTAG		MEQKDSFFSSHLRQS*		MEQKDSFFSSHLRQS*		GCGTCTCCCC	CTTCGCCGGC	0	I	0	0	0	0	0
9818	4253	an	AN0054.1	71.m15327	AO070314000133	0	-185	-123					ATGGGAGATTCCTACAGCTGCAGTATGCGAACTATTTATCACCCGGTGCTTCCCTTCGCCTGA	ATGGGAGATTCCTACAGCTGCAGTATGCGAACTATTTATCACCCGGTGCTTCCCTTCGCCTGA			MGDSYSCSMRTIYHPVLPFA*	MGDSYSCSMRTIYHPVLPFA*			TATCTATAGG	GGAGCATTCC	0	I	0	0	0	0	0
9819	4253	an	AN0054.1	71.m15327	AO070314000133	0	-161	-123					ATGCGAACTATTTATCACCCGGTGCTTCCCTTCGCCTGA	ATGCGAACTATTTATCACCCGGTGCTTCCCTTCGCCTGA			MRTIYHPVLPFA*	MRTIYHPVLPFA*			CAGCTGCAGT	GGAGCATTCC	0	I	0	0	0	0	0
9823	4253	ao	AN0054.1	71.m15327	AO070314000133	0					-236	-159	ATGCACCAGAAGGATTTGGGGGATTTTTTTTTCCCTCCTTTGTTTCCCTTTTTTCATTTGGTGAAGTCTCCAGCATGA			ATGCACCAGAAGGATTTGGGGGATTTTTTTTTCCCTCCTTTGTTTCCCTTTTTTCATTTGGTGAAGTCTCCAGCATGA	MHQKDLGDFFFPPLFPFFHLVKSPA*			MHQKDLGDFFFPPLFPFFHLVKSPA*	TTCCTCGTCC	CAAAAACATC	0	I	0	0	0	0	0
9824	4253	ao	AN0054.1	71.m15327	AO070314000133	0					-162	-4	ATGACAAAAACATCTGTTCAAGCGCGATATGACCATCCACATATTTATTACCCAGGATGCCCTCTGTCTTTTGGACTTCCTACTTTCGTCGATCCTCACTCTCCGACGAGCCCTTATTACTATTACTCTAAACTCCCCCCTTCTCTCCTCGATTACTAA			ATGACAAAAACATCTGTTCAAGCGCGATATGACCATCCACATATTTATTACCCAGGATGCCCTCTGTCTTTTGGACTTCCTACTTTCGTCGATCCTCACTCTCCGACGAGCCCTTATTACTATTACTCTAAACTCCCCCCTTCTCTCCTCGATTACTAA	MTKTSVQARYDHPHIYYPGCPLSFGLPTFVDPHSPTSPYYYYSKLPPSLLDY*			MTKTSVQARYDHPHIYYPGCPLSFGLPTFVDPHSPTSPYYYYSKLPPSLLDY*	AGTCTCCAGC	ACCATGGGTC	0	I	0	0	0	0	0
9825	4253	ao	AN0054.1	71.m15327	AO070314000133	0					-106	-32	ATGCCCTCTGTCTTTTGGACTTCCTACTTTCGTCGATCCTCACTCTCCGACGAGCCCTTATTACTATTACTCTAA			ATGCCCTCTGTCTTTTGGACTTCCTACTTTCGTCGATCCTCACTCTCCGACGAGCCCTTATTACTATTACTCTAA	MPSVFWTSYFRRSSLSDEPLLLLL*			MPSVFWTSYFRRSSLSDEPLLLLL*	ATTACCCAGG	ACTCCCCCCT	0	I	0	0	0	0	0
9829	4258	af	AN5920.1	72.m19212	AO070340000366	0			-225	-205			ATGTTTGTTGGTACCAGTTGA		ATGTTTGTTGGTACCAGTTGA		MFVGTS*		MFVGTS*		AGTTTTTAAT	TACCTTCATT	0	U	0	0	0	0	0
9826	4258	an	AN5920.1	72.m19212	AO070340000366	0	-188	-150					ATGTGGGGACAAGGCTTCGGAATGTCGGAATCTGCTTGA	ATGTGGGGACAAGGCTTCGGAATGTCGGAATCTGCTTGA			MWGQGFGMSESA*	MWGQGFGMSESA*			GGCAACGGTC	TAAAAAATGC	0	U	0	0	0	0	0
9827	4258	an	AN5920.1	72.m19212	AO070340000366	0	-167	-150					ATGTCGGAATCTGCTTGA	ATGTCGGAATCTGCTTGA			MSESA*	MSESA*			AGGCTTCGGA	TAAAAAATGC	0	U	0	0	0	0	0
9828	4258	an	AN5920.1	72.m19212	AO070340000366	0	-143	-111					ATGCTATACTTTTACTTCTGTGTCAAGATCTAA	ATGCTATACTTTTACTTCTGTGTCAAGATCTAA			MLYFYFCVKI*	MLYFYFCVKI*			TTGATAAAAA	GTTCTATCCA	0	U	0	0	0	0	0
9830	4258	ao	AN5920.1	72.m19212	AO070340000366	0					-236	-216	ATGCTTGGTCTGTACGAGTAA			ATGCTTGGTCTGTACGAGTAA	MLGLYE*			MLGLYE*	CACTAACAGT	AATTATTTCC	0	U	0	0	0	0	0
9831	4258	ao	AN5920.1	72.m19212	AO070340000366	0					-147	-112	ATGTGTTATCTATCGATTAACAGTAGCGCCAGATAA			ATGTGTTATCTATCGATTAACAGTAGCGCCAGATAA	MCYLSINSSAR*			MCYLSINSSAR*	GTGTTGGTTT	TTGCGCGCAA	0	U	0	0	0	0	0
9833	4259	af	AN5750.1	69.m14848	AO070341000007	0			-139	-104			ATGTCTCTGCAACCTACTTCCATCCTCTGCTTCTGA		ATGTCTCTGCAACCTACTTCCATCCTCTGCTTCTGA		MSLQPTSILCF*		MSLQPTSILCF*		TCGTCAGATC	ACTGCGCATC	0		0	0	0	0	0
9832	4259	an	AN5750.1	69.m14848	AO070341000007	0	-159	-142					ATGCCTTTGCTTCCCTGA	ATGCCTTTGCTTCCCTGA			MPLLP*	MPLLP*			CATCCTCGAC	ATCTTGTCTT	0		0	0	0	0	0
9834	4259	ao	AN5750.1	69.m14848	AO070341000007	0					-166	-143	ATGGACAATGCGTCTTCTTCCTAA			ATGGACAATGCGTCTTCTTCCTAA	MDNASSS*			MDNASSS*	AAGAAAACCA	TTGAACTCGA	0		0	0	0	0	0
9835	4259	ao	AN5750.1	69.m14848	AO070341000007	0					-159	-139	ATGCGTCTTCTTCCTAATTGA			ATGCGTCTTCTTCCTAATTGA	MRLLPN*			MRLLPN*	CCAATGGACA	ACTCGAACCA	0		0	0	0	0	0
9836	4260	an	AN2070.1	57.m05773	AO070341000226	0	-142	-89					ATGGTCGAATCGGCCCAGCTGTGTTACAGACTATTATTGCTAAGTGAAGGATAA	ATGGTCGAATCGGCCCAGCTGTGTTACAGACTATTATTGCTAAGTGAAGGATAA			MVESAQLCYRLLLLSEG*	MVESAQLCYRLLLLSEG*			CTGCTGTTTC	TTGCAGGAGG	0	R	0	0	0	0	0
9839	4261	af	AN4086.1	54.m06727	AO070342000079	0			-184	-107			ATGACTGCGATTATCTGCCCGACACTGGAGAACAGACAGAGCATCGGCGGAGTTACCAACGCTGTGGATCCGTGCTGA		ATGACTGCGATTATCTGCCCGACACTGGAGAACAGACAGAGCATCGGCGGAGTTACCAACGCTGTGGATCCGTGCTGA		MTAIICPTLENRQSIGGVTNAVDPC*		MTAIICPTLENRQSIGGVTNAVDPC*		TTTAAGTTCT	ATAACTTGGA	0	J	0	0	0	YLR060W	0
9837	4261	an	AN4086.1	54.m06727	AO070342000079	0	-232	-122					ATGTGGCTGTCCTCCCGCTTTTGCTCCTCAAATTTGTATGACTCCGTCCGCCGACTTGTCCTGCGACCCCGAATTGAACTCCAACTGCGGGCCGACCACAGGAAAGTATAG	ATGTGGCTGTCCTCCCGCTTTTGCTCCTCAAATTTGTATGACTCCGTCCGCCGACTTGTCCTGCGACCCCGAATTGAACTCCAACTGCGGGCCGACCACAGGAAAGTATAG			MWLSSRFCSSNLYDSVRRLVLRPRIELQLRADHRKV*	MWLSSRFCSSNLYDSVRRLVLRPRIELQLRADHRKV*			GTGGCGGTGC	CCTGTCGAAG	0	J	0	0	0	YLR060W	0
9838	4261	an	AN4086.1	54.m06727	AO070342000079	0	-195	-52					ATGACTCCGTCCGCCGACTTGTCCTGCGACCCCGAATTGAACTCCAACTGCGGGCCGACCACAGGAAAGTATAGCCTGTCGAAGCGTGGCTTATATTCCGCTGGCATAACCGATACCATAGCCGAGTTTTGGGAGAAAACTTGA	ATGACTCCGTCCGCCGACTTGTCCTGCGACCCCGAATTGAACTCCAACTGCGGGCCGACCACAGGAAAGTATAGCCTGTCGAAGCGTGGCTTATATTCCGCTGGCATAACCGATACCATAGCCGAGTTTTGGGAGAAAACTTGA			MTPSADLSCDPELNSNCGPTTGKYSLSKRGLYSAGITDTIAEFWEKT*	MTPSADLSCDPELNSNCGPTTGKYSLSKRGLYSAGITDTIAEFWEKT*			TCAAATTTGT	TCTCACACGA	0	J	0	0	0	YLR060W	0
9840	4261	ao	AN4086.1	54.m06727	AO070342000079	0					-242	-216	ATGTGGCTGGCGCAGCGCCCGCCTTGA			ATGTGGCTGGCGCAGCGCCCGCCTTGA	MWLAQRPP*			MWLAQRPP*	GTGCACGGAG	GGGTCAAGCC	0	J	0	0	0	YLR060W	0
9841	4261	ao	AN4086.1	54.m06727	AO070342000079	0					-181	-95	ATGACTCCTCCACCGGTGGCATACTTAGACTCAGCGCAATCACTGAACCCCGCACACGGACACTTTTGCCGGTTGGACTTTGGGTAA			ATGACTCCTCCACCGGTGGCATACTTAGACTCAGCGCAATCACTGAACCCCGCACACGGACACTTTTGCCGGTTGGACTTTGGGTAA	MTPPPVAYLDSAQSLNPAHGHFCRLDFG*			MTPPPVAYLDSAQSLNPAHGHFCRLDFG*	CACGGACTTT	TTCCATAGAG	0	J	0	0	0	YLR060W	0
9843	4264	ao	AN3176.1	59.m08566	AO070256000014	0					-87	-31	ATGGATGAGCGACGGAAGTTCCATCATTCGAATAATCTGTTGAGGGTAGGCTCGTAA			ATGGATGAGCGACGGAAGTTCCATCATTCGAATAATCTGTTGAGGGTAGGCTCGTAA	MDERRKFHHSNNLLRVGS*			MDERRKFHHSNNLLRVGS*	TTTAGTTTGT	GGGAGCCAAT	0	A	FG10896.1	0	NCU03380.1	0	0
9844	4264	ao	AN3176.1	59.m08566	AO070256000014	0					-83	-45	ATGAGCGACGGAAGTTCCATCATTCGAATAATCTGTTGA			ATGAGCGACGGAAGTTCCATCATTCGAATAATCTGTTGA	MSDGSSIIRIIC*			MSDGSSIIRIIC*	GTTTGTATGG	GGGTAGGCTC	0	A	FG10896.1	0	NCU03380.1	0	0
9848	4266	af	AN4986.1	59.m08889	AO070288000054	0			-127	-80			ATGCCAAGAATTATACTCCATCAGCTCTATCTGAGGAGTCTAGGCTGA		ATGCCAAGAATTATACTCCATCAGCTCTATCTGAGGAGTCTAGGCTGA		MPRIILHQLYLRSLG*		MPRIILHQLYLRSLG*		GGTTTTGTCT	TTGTCACGAT	0		0	MG02749.1	0	0	0
9846	4266	an	AN4986.1	59.m08889	AO070288000054	0	-199	-167					ATGCATGGGCCGGGACATAGCTCGGCCAAATGA	ATGCATGGGCCGGGACATAGCTCGGCCAAATGA			MHGPGHSSAK*	MHGPGHSSAK*			GAAAATCAGA	AGTTCCGTTG	0		0	MG02749.1	0	0	0
9847	4266	an	AN4986.1	59.m08889	AO070288000054	0	-170	-105					ATGAAGTTCCGTTGCTGGGATTTTCTGCCAGTTTCTCCACTCCTCTCCATCCACATACAGTACTGA	ATGAAGTTCCGTTGCTGGGATTTTCTGCCAGTTTCTCCACTCCTCTCCATCCACATACAGTACTGA			MKFRCWDFLPVSPLLSIHIQY*	MKFRCWDFLPVSPLLSIHIQY*			GCTCGGCCAA	GTTACGGAGT	0		0	MG02749.1	0	0	0
9849	4266	ao	AN4986.1	59.m08889	AO070288000054	0					-279	-238	ATGAAGCTATCACTATCAAATCTGGGGAATACATATAGATAA			ATGAAGCTATCACTATCAAATCTGGGGAATACATATAGATAA	MKLSLSNLGNTYR*			MKLSLSNLGNTYR*	ACTTTATCTC	CGATAATATA	0		0	MG02749.1	0	0	0
9856	4267	af	AN5140.1	54.m06882	AO070291000036	0			-131	-78			ATGCTGATGGATACCGGATTGTCCCTTTTCGCTTCTCTTCTTCCCTTCGTTTGA		ATGCTGATGGATACCGGATTGTCCCTTTTCGCTTCTCTTCTTCCCTTCGTTTGA		MLMDTGLSLFASLLPFV*		MLMDTGLSLFASLLPFV*		TCGGTGTCTC	TCGAGTCACT	0	R	0	0	NCU09098.1	0	0
9857	4267	af	AN5140.1	54.m06882	AO070291000036	0			-125	-78			ATGGATACCGGATTGTCCCTTTTCGCTTCTCTTCTTCCCTTCGTTTGA		ATGGATACCGGATTGTCCCTTTTCGCTTCTCTTCTTCCCTTCGTTTGA		MDTGLSLFASLLPFV*		MDTGLSLFASLLPFV*		TCTCATGCTG	TCGAGTCACT	0	R	0	0	NCU09098.1	0	0

9850	4267	an	AN5140.1	54.m06882	AO070291000036	0	-210	-175					ATGGTGGGCCTACTCCATAATATATATTCAATATGA	ATGGTGGGCCTACTCCATAATATATATTCAATATGA			MVGLLHNIYSI*	MVGLLHNIYSI*			AGCCTGGCCG	TTCGTGGGGC	0	R	0	0	NCU09098.1	0	0
9851	4267	an	AN5140.1	54.m06882	AO070291000036	0	-178	-149					ATGATTCGTGGGGCTGGGTTGAGCGAATGA	ATGATTCGTGGGGCTGGGTTGAGCGAATGA			MIRGAGLSE*	MIRGAGLSE*			TATATTCAAT	CATAATTTGT	0	R	0	0	NCU09098.1	0	0
9852	4267	an	AN5140.1	54.m06882	AO070291000036	0	-123	-7					ATGATTTGGAATGAATCAGATGGACAGCTTGCATTAATTATTCTGAACACACCATATAAATGCTGTTCTCTCTTCCTTTCCTGGACGCTGACCAGTGAACCCCTTCCTGCTTGCTAG	ATGATTTGGAATGAATCAGATGGACAGCTTGCATTAATTATTCTGAACACACCATATAAATGCTGTTCTCTCTTCCTTTCCTGGACGCTGACCAGTGAACCCCTTCCTGCTTGCTAG			MIWNESDGQLALIILNTPYKCCSLFLSWTLTSEPLPAC*	MIWNESDGQLALIILNTPYKCCSLFLSWTLTSEPLPAC*			TGGAACTTGA	CACACCATGG	0	R	0	0	NCU09098.1	0	0
9853	4267	an	AN5140.1	54.m06882	AO070291000036	0	-113	-87					ATGAATCAGATGGACAGCTTGCATTAA	ATGAATCAGATGGACAGCTTGCATTAA			MNQMDSLH*	MNQMDSLH*			ATGATTTGGA	TTATTCTGAA	0	R	0	0	NCU09098.1	0	0
9854	4267	an	AN5140.1	54.m06882	AO070291000036	0	-104	-87					ATGGACAGCTTGCATTAA	ATGGACAGCTTGCATTAA			MDSLH*	MDSLH*			AATGAATCAG	TTATTCTGAA	0	R	0	0	NCU09098.1	0	0
9855	4267	an	AN5140.1	54.m06882	AO070291000036	0	-64	-26					ATGCTGTTCTCTCTTCCTTTCCTGGACGCTGACCAGTGA	ATGCTGTTCTCTCTTCCTTTCCTGGACGCTGACCAGTGA			MLFSLPFLDADQ*	MLFSLPFLDADQ*			CACCATATAA	ACCCCTTCCT	0	R	0	0	NCU09098.1	0	0
9858	4267	ao	AN5140.1	54.m06882	AO070291000036	0					-191	-177	ATGTGGCTTACATAA			ATGTGGCTTACATAA	MWLT*			MWLT*	TTCGCCGATC	GTCGACAAAT	0	R	0	0	NCU09098.1	0	0
9859	4267	ao	AN5140.1	54.m06882	AO070291000036	0					-70	-59	ATGCTGGACTAA			ATGCTGGACTAA	MLD*			MLD*	GGAAATCTTC	TCGTTCTTTC	0	R	0	0	NCU09098.1	0	0
9860	4268	af	AN5618.1	58.m07543	AO070301000019	0			-208	-119			ATGCGACTACTTCCCAGCGCGTTTCTCCGCAGACAAAGACGAAGCAAATCCCCACAATTAAACACCACAGCATTGTCCGACTTTCCATAG		ATGCGACTACTTCCCAGCGCGTTTCTCCGCAGACAAAGACGAAGCAAATCCCCACAATTAAACACCACAGCATTGTCCGACTTTCCATAG		MRLLPSAFLRRQRRSKSPQLNTTALSDFP*		MRLLPSAFLRRQRRSKSPQLNTTALSDFP*		CGTCTGTCCA	CTTCGAAAGT	0	ZD	0	0	0	YOR257W	0
9862	4270	af	AN1720.1	58.m08961	AO070305000035	0			-242	-222			ATGCCCTTGACTTTGAGATAG		ATGCCCTTGACTTTGAGATAG		MPLTLR*		MPLTLR*		CTACGTAGTG	TTTTCGCAGA	0		0	0	0	0	0
9863	4270	af	AN1720.1	58.m08961	AO070305000035	0			-185	-12			ATGGAGATGCAGATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		ATGGAGATGCAGATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		MEMQMYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		MEMQMYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		AGACTTGTAG	TTCAAAGCAA	0		0	0	0	0	0
9864	4270	af	AN1720.1	58.m08961	AO070305000035	0			-179	-12			ATGCAGATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		ATGCAGATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		MQMYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		MQMYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		GTAGATGGAG	TTCAAAGCAA	0		0	0	0	0	0
9865	4270	af	AN1720.1	58.m08961	AO070305000035	0			-173	-12			ATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		ATGTACGGAGTAGATGTAGCCCTATGCGACGGTAGCTGTGGGGGTGCCGAATCGCCAACCTTCCAGCTATTCGGCCTACTTATTCGCTGTCTGCTGGCACCTCTCCGTCACCGTCCCAGCCGCTTTACCTCAACAGCATCGCGGCTCAGTCCGAACTTCTAA		MYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		MYGVDVALCDGSCGGAESPTFQLFGLLIRCLLAPLRHRPSRFTSTASRLSPNF*		GGAGATGCAG	TTCAAAGCAA	0		0	0	0	0	0
9866	4270	af	AN1720.1	58.m08961	AO070305000035	0			-150	-139			ATGCGACGGTAG		ATGCGACGGTAG		MRR*		MRR*		ATGTAGCCCT	CTGTGGGGGT	0		0	0	0	0	0
9861	4270	an	AN1720.1	58.m08961	AO070305000035	0	-175	-71					ATGTGGTGGGTCGCCGTGCGAAGTGTCAGACCTCAATTCCAGGCGGCTGTTTTCAACTCCCCTTCTCTTCCTCGTCACGATCTAGCCAAACCAGACACTATTTAA	ATGTGGTGGGTCGCCGTGCGAAGTGTCAGACCTCAATTCCAGGCGGCTGTTTTCAACTCCCCTTCTCTTCCTCGTCACGATCTAGCCAAACCAGACACTATTTAA			MWWVAVRSVRPQFQAAVFNSPSLPRHDLAKPDTI*	MWWVAVRSVRPQFQAAVFNSPSLPRHDLAKPDTI*			ATAGGTACGA	TCCCTCTACG	0		0	0	0	0	0
9868	4272	ao	AN8202.1	53.m03772	AO070310000115	0					-237	-214	ATGTTTGCAGCCATCACGTGGTGA			ATGTTTGCAGCCATCACGTGGTGA	MFAAITW*			MFAAITW*	AGCATTTGCC	TTGTGGATGA	0		0	0	0	0	0
9872	4276	af	AN8956.1	56.m02375	AO070319000056	0			-167	-93			ATGGTATCCCAACGCACACGAGCCGCCTTGGCGAGCACCGCATGGATCCCTACTTCTGCCGAGCTCGATATATAG		ATGGTATCCCAACGCACACGAGCCGCCTTGGCGAGCACCGCATGGATCCCTACTTCTGCCGAGCTCGATATATAG		MVSQRTRAALASTAWIPTSAELDI*		MVSQRTRAALASTAWIPTSAELDI*		CTTGTCTAGG	CACCTCTCAC	0	P	0	0	0	0	0
9873	4276	af	AN8956.1	56.m02375	AO070319000056	0			-126	-67			ATGGATCCCTACTTCTGCCGAGCTCGATATATAGCACCTCTCACTTCTCTGTGTCTGTAG		ATGGATCCCTACTTCTGCCGAGCTCGATATATAGCACCTCTCACTTCTCTGTGTCTGTAG		MDPYFCRARYIAPLTSLCL*		MDPYFCRARYIAPLTSLCL*		CGAGCACCGC	TTCCCAATCA	0	P	0	0	0	0	0
9871	4276	an	AN8956.1	56.m02375	AO070319000056	0	-184	-146					ATGAGTCCTACCGGGCGTCACTTGGCGGGCATTGCCTGA	ATGAGTCCTACCGGGCGTCACTTGGCGGGCATTGCCTGA			MSPTGRHLAGIA*	MSPTGRHLAGIA*			CAACTGCGAG	GTCTCTGCCT	0	P	0	0	0	0	0
9874	4276	ao	AN8956.1	56.m02375	AO070319000056	0					-234	-118	ATGAGATGCAGCATTCGATACCTTGGCATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAG			ATGAGATGCAGCATTCGATACCTTGGCATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAG	MRCSIRYLGMKSVSTFSPNVAVSPTIVEMGYYLILFRP*			MRCSIRYLGMKSVSTFSPNVAVSPTIVEMGYYLILFRP*	GTGTGCCGAG	AATAACAATT	0	P	0	0	0	0	0
9875	4276	ao	AN8956.1	56.m02375	AO070319000056	0					-229	-113	ATGCAGCATTCGATACCTTGGCATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAGAATAA			ATGCAGCATTCGATACCTTGGCATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAGAATAA	MQHSIPWHEVCQHVFAERSSLPDHSRDGLLLNTLPPVE*			MQHSIPWHEVCQHVFAERSSLPDHSRDGLLLNTLPPVE*	CCGAGATGAG	CAATTTTGAG	0	P	0	0	0	0	0
9876	4276	ao	AN8956.1	56.m02375	AO070319000056	0					-207	-118	ATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAG			ATGAAGTCTGTCAGCACGTTTTCGCCGAACGTAGCAGTCTCCCCGACCATAGTAGAGATGGGTTACTACTTAATACTCTTCCGCCCGTAG	MKSVSTFSPNVAVSPTIVEMGYYLILFRP*			MKSVSTFSPNVAVSPTIVEMGYYLILFRP*	ATACCTTGGC	AATAACAATT	0	P	0	0	0	0	0
9877	4276	ao	AN8956.1	56.m02375	AO070319000056	0					-150	-118	ATGGGTTACTACTTAATACTCTTCCGCCCGTAG			ATGGGTTACTACTTAATACTCTTCCGCCCGTAG	MGYYLILFRP*			MGYYLILFRP*	CATAGTAGAG	AATAACAATT	0	P	0	0	0	0	0
9878	4277	an	AN0925.1	70.m15533	AO070320000104	0	-165	-112					ATGTATACGAGCATACAGGAGACTATATACTGGTATCTTTGCTGTACTGGCTAG	ATGTATACGAGCATACAGGAGACTATATACTGGTATCTTTGCTGTACTGGCTAG			MYTSIQETIYWYLCCTG*	MYTSIQETIYWYLCCTG*			CTTCGAGATA	GTTTTTTACA	0	I	0	0	0	0	0
9879	4277	ao	AN0925.1	70.m15533	AO070320000104	0					-257	-174	ATGAAGTCAGCGAGTGGAGATCAGCTGCCCTTGTCCAAGCTAAGCTATATACCTTACATGACCTCCACTATTTTTTCCTCATGA			ATGAAGTCAGCGAGTGGAGATCAGCTGCCCTTGTCCAAGCTAAGCTATATACCTTACATGACCTCCACTATTTTTTCCTCATGA	MKSASGDQLPLSKLSYIPYMTSTIFSS*			MKSASGDQLPLSKLSYIPYMTSTIFSS*	ACCTGAACCG	CATACTCTTG	0	I	0	0	0	0	0
9880	4277	ao	AN0925.1	70.m15533	AO070320000104	0					-200	-174	ATGACCTCCACTATTTTTTCCTCATGA			ATGACCTCCACTATTTTTTCCTCATGA	MTSTIFSS*			MTSTIFSS*	TATACCTTAC	CATACTCTTG	0	I	0	0	0	0	0
9884	4279	af	AN8034.1	53.m03883	AO070322000125	0			-200	-186			ATGCTGCTTGGCTAG		ATGCTGCTTGGCTAG		MLLG*		MLLG*		CTGTCCAGTG	ACCTCTCTGC	0	A	0	0	0	0	0
9885	4279	af	AN8034.1	53.m03883	AO070322000125	0			-63	-43			ATGATCGATTCACTCCCTTAA		ATGATCGATTCACTCCCTTAA		MIDSLP*		MIDSLP*		TCATTTTGTC	GTACCACAAT	0	A	0	0	0	0	0
9883	4279	an	AN8034.1	53.m03883	AO070322000125	0	-66	-40					ATGATCTTGCCGCTATTGTCTTCTTAA	ATGATCTTGCCGCTATTGTCTTCTTAA			MILPLLSS*	MILPLLSS*			CAGGAATGCC	ATTCCTTGAA	0	A	0	0	0	0	0
9888	4282	af	AN2245.1	71.m15879	AO070326000128	0			-218	-198			ATGAAAGAATCTCCACACTGA		ATGAAAGAATCTCCACACTGA		MKESPH*		MKESPH*		AGACTGGAAA	AATAGAATGT	0	R	0	0	0	0	0
9889	4282	af	AN2245.1	71.m15879	AO070326000128	0			-191	-72			ATGTGTGTAATACAGCTTCAGAAAAGTTGTCTCGCAAAGCATATCAAAATCATCGCAGCAAAAACGGCGCCAAGACCCATCGCTTACATAATCTCATCATCGCCTCGTGATTTCACCTGA		ATGTGTGTAATACAGCTTCAGAAAAGTTGTCTCGCAAAGCATATCAAAATCATCGCAGCAAAAACGGCGCCAAGACCCATCGCTTACATAATCTCATCATCGCCTCGTGATTTCACCTGA		MCVIQLQKSCLAKHIKIIAAKTAPRPIAYIISSSPRDFT*		MCVIQLQKSCLAKHIKIIAAKTAPRPIAYIISSSPRDFT*		CTGAAATAGA	AGGCATCGCA	0	R	0	0	0	0	0
9887	4282	an	AN2245.1	71.m15879	AO070326000128	0	-108	-85					ATGCCAAGGCCTAATCTGGCTTAA	ATGCCAAGGCCTAATCTGGCTTAA			MPRPNLA*	MPRPNLA*			ATTCGTTGTG	GTAATCATCG	0	R	0	0	0	0	0
9890	4282	ao	AN2245.1	71.m15879	AO070326000128	0					-138	-106	ATGCAAGCTAGACCGCAACCGGCAAAACCATAA			ATGCAAGCTAGACCGCAACCGGCAAAACCATAA	MQARPQPAKP*			MQARPQPAKP*	TCAATACAAC	TCCGACCAGA	0	R	0	0	0	0	0
9894	4283	af	AN4751.1	59.m09234	AO070327000068	0			-245	-138			ATGATTGACGAGGGGTTTCTTATGATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		ATGATTGACGAGGGGTTTCTTATGATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		MIDEGFLMMIGRSASWITHDRSSGPVSDWLKLIDK*		MIDEGFLMMIGRSASWITHDRSSGPVSDWLKLIDK*		TAACGAATAC	CTGCTGACTC	0	R	0	0	0	0	0
9895	4283	af	AN4751.1	59.m09234	AO070327000068	0			-224	-138			ATGATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		ATGATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		MMIGRSASWITHDRSSGPVSDWLKLIDK*		MMIGRSASWITHDRSSGPVSDWLKLIDK*		GGGGTTTCTT	CTGCTGACTC	0	R	0	0	0	0	0
9896	4283	af	AN4751.1	59.m09234	AO070327000068	0			-221	-138			ATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		ATGATTGGGCGGAGCGCGTCTTGGATCACCCATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGA		MIGRSASWITHDRSSGPVSDWLKLIDK*		MIGRSASWITHDRSSGPVSDWLKLIDK*		GTTTCTTATG	CTGCTGACTC	0	R	0	0	0	0	0
9897	4283	af	AN4751.1	59.m09234	AO070327000068	0			-190	-131			ATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGACTGCTGA		ATGACAGGTCCTCCGGTCCCGTTTCTGATTGGCTTAAGCTTATCGATAAATGACTGCTGA		MTGPPVPFLIGLSLSINDC*		MTGPPVPFLIGLSLSINDC*		TGGATCACCC	CTCAGCATAA	0	R	0	0	0	0	0
9898	4283	af	AN4751.1	59.m09234	AO070327000068	0			-141	-121			ATGACTGCTGACTCAGCATAA		ATGACTGCTGACTCAGCATAA		MTADSA*		MTADSA*		TTATCGATAA	AAAGTTGTGA	0	R	0	0	0	0	0
9891	4283	an	AN4751.1	59.m09234	AO070327000068	0	-255	-241					ATGCGTGTAGGATAA	ATGCGTGTAGGATAA			MRVG*	MRVG*			AGATGAATCA	TTTCGAGACT	0	R	0	0	0	0	0
9892	4283	an	AN4751.1	59.m09234	AO070327000068	0	-205	-185					ATGCTGGTGGTAACGCGCTGA	ATGCTGGTGGTAACGCGCTGA			MLVVTR*	MLVVTR*			GCGATTGTTT	GCGTCCGTTC	0	R	0	0	0	0	0
9893	4283	an	AN4751.1	59.m09234	AO070327000068	0	-173	-135					ATGAAGCCCGCTATTTGGTTGGAGTGGGCTTATCGATAA	ATGAAGCCCGCTATTTGGTTGGAGTGGGCTTATCGATAA			MKPAIWLEWAYR*	MKPAIWLEWAYR*			CGTCCGTTCA	CAAAAGGCTT	0	R	0	0	0	0	0
9899	4283	ao	AN4751.1	59.m09234	AO070327000068	0					-219	-166	ATGTCCCAATTTCGCAAGAGGGGTTGTTGTTCTTCGGTGGAAAGCGCGTGTTGA			ATGTCCCAATTTCGCAAGAGGGGTTGTTGTTCTTCGGTGGAAAGCGCGTGTTGA	MSQFRKRGCCSSVESAC*			MSQFRKRGCCSSVESAC*	GCTGCAGCGC	TGACATGGAA	0	R	0	0	0	0	0
9900	4283	ao	AN4751.1	59.m09234	AO070327000068	0					-166	-65	ATGACATGGAAGAGTTGGAGTGTAATTGGCCGTGGCTTATCGATAAGCCGGCTGACTCAGCATAAAAAAAGTTGCTACGGATCAAGTCTTATTGATAAATGA			ATGACATGGAAGAGTTGGAGTGTAATTGGCCGTGGCTTATCGATAAGCCGGCTGACTCAGCATAAAAAAAGTTGCTACGGATCAAGTCTTATTGATAAATGA	MTWKSWSVIGRGLSISRLTQHKKSCYGSSLIDK*			MTWKSWSVIGRGLSISRLTQHKKSCYGSSLIDK*	GCGCGTGTTG	ATTCTAACCA	0	R	0	0	0	0	0
9901	4283	ao	AN4751.1	59.m09234	AO070327000068	0					-161	-102	ATGGAAGAGTTGGAGTGTAATTGGCCGTGGCTTATCGATAAGCCGGCTGACTCAGCATAA			ATGGAAGAGTTGGAGTGTAATTGGCCGTGGCTTATCGATAAGCCGGCTGACTCAGCATAA	MEELECNWPWLIDKPADSA*			MEELECNWPWLIDKPADSA*	TGTTGATGAC	AAAAAGTTGC	0	R	0	0	0	0	0
9902	4283	ao	AN4751.1	59.m09234	AO070327000068	0					-68	-51	ATGAATTCTAACCATTGA			ATGAATTCTAACCATTGA	MNSNH*			MNSNH*	TTATTGATAA	ATGTTTCTTT	0	R	0	0	0	0	0
9904	4290	an	AN7607.1	72.m19637	AO070343000280	0	-226	-128					ATGCGCCATCGCAATCAACCCACTTCCAGAAGGCTTAACTTCCAGTCTCATTGGCTGTCCTATGAAGATCAGACAAATTTCATGCAGAGCTTTGAATGA	ATGCGCCATCGCAATCAACCCACTTCCAGAAGGCTTAACTTCCAGTCTCATTGGCTGTCCTATGAAGATCAGACAAATTTCATGCAGAGCTTTGAATGA			MRHRNQPTSRRLNFQSHWLSYEDQTNFMQSFE*	MRHRNQPTSRRLNFQSHWLSYEDQTNFMQSFE*			GGAACCGCGG	ATTGTCTCCA	0		0	0	0	0	0
9905	4290	an	AN7607.1	72.m19637	AO070343000280	0	-165	-88					ATGAAGATCAGACAAATTTCATGCAGAGCTTTGAATGAATTGTCTCCAGTTGAAAGGCTGAGTTGTTCACAGTACTGA	ATGAAGATCAGACAAATTTCATGCAGAGCTTTGAATGAATTGTCTCCAGTTGAAAGGCTGAGTTGTTCACAGTACTGA			MKIRQISCRALNELSPVERLSCSQY*	MKIRQISCRALNELSPVERLSCSQY*			TGGCTGTCCT	AGACAACGCA	0		0	0	0	0	0
9906	4290	an	AN7607.1	72.m19637	AO070343000280	0	-145	-128					ATGCAGAGCTTTGAATGA	ATGCAGAGCTTTGAATGA			MQSFE*	MQSFE*			GACAAATTTC	ATTGTCTCCA	0		0	0	0	0	0
9907	4290	an	AN7607.1	72.m19637	AO070343000280	0	-131	-105					ATGAATTGTCTCCAGTTGAAAGGCTGA	ATGAATTGTCTCCAGTTGAAAGGCTGA			MNCLQLKG*	MNCLQLKG*			AGAGCTTTGA	GTTGTTCACA	0		0	0	0	0	0

9908	4290	an	AN7607.1	72.m19637	AO070343000280	0	-77	-63					ATGTTGGGTATATAG	ATGTTGGGTATATAG			MLGI*	MLGI*			AGACAACGCA	CGCCGTTCCT	0		0	0	0	0	0
9909	4290	ao	AN7607.1	72.m19637	AO070343000280	0					-231	-151	ATGATCTGCTTCGGAATCTGCTCGCTGATGCTTGGGAGGCTTAGTAGGGCTGTCGGCGAAAAATCGAAAAGGGGAATATGA			ATGATCTGCTTCGGAATCTGCTCGCTGATGCTTGGGAGGCTTAGTAGGGCTGTCGGCGAAAAATCGAAAAGGGGAATATGA	MICFGICSLMLGRLSRAVGEKSKRGI*			MICFGICSLMLGRLSRAVGEKSKRGI*	GCTCTTCCTA	GGCAAAAATC	0		0	0	0	0	0
9910	4290	ao	AN7607.1	72.m19637	AO070343000280	0					-204	-151	ATGCTTGGGAGGCTTAGTAGGGCTGTCGGCGAAAAATCGAAAAGGGGAATATGA			ATGCTTGGGAGGCTTAGTAGGGCTGTCGGCGAAAAATCGAAAAGGGGAATATGA	MLGRLSRAVGEKSKRGI*			MLGRLSRAVGEKSKRGI*	CTGCTCGCTG	GGCAAAAATC	0		0	0	0	0	0
9911	4290	ao	AN7607.1	72.m19637	AO070343000280	0					-154	-95	ATGAGGCAAAAATCAGTTCACTCTAATCTTGGCATGTTGCTGCTTGCGGTTGGTTCTTAA			ATGAGGCAAAAATCAGTTCACTCTAATCTTGGCATGTTGCTGCTTGCGGTTGGTTCTTAA	MRQKSVHSNLGMLLLAVGS*			MRQKSVHSNLGMLLLAVGS*	AAAGGGGAAT	ACCCCTTGGC	0		0	0	0	0	0
9912	4290	ao	AN7607.1	72.m19637	AO070343000280	0					-121	-95	ATGTTGCTGCTTGCGGTTGGTTCTTAA			ATGTTGCTGCTTGCGGTTGGTTCTTAA	MLLLAVGS*			MLLLAVGS*	TAATCTTGGC	ACCCCTTGGC	0		0	0	0	0	0
9915	4292	af	AN0495.1	69.m15311	AO070226000029	0			-205	-167			ATGATGCTCAATCTGGAAATGAGAGCAACCCAACCCTAA		ATGATGCTCAATCTGGAAATGAGAGCAACCCAACCCTAA		MMLNLEMRATQP*		MMLNLEMRATQP*		GATGATGACG	TCTTATCGAT	0	F	0	0	0	0	0
9916	4292	af	AN0495.1	69.m15311	AO070226000029	0			-202	-167			ATGCTCAATCTGGAAATGAGAGCAACCCAACCCTAA		ATGCTCAATCTGGAAATGAGAGCAACCCAACCCTAA		MLNLEMRATQP*		MLNLEMRATQP*		GATGACGATG	TCTTATCGAT	0	F	0	0	0	0	0
9917	4292	af	AN0495.1	69.m15311	AO070226000029	0			-187	-167			ATGAGAGCAACCCAACCCTAA		ATGAGAGCAACCCAACCCTAA		MRATQP*		MRATQP*		CAATCTGGAA	TCTTATCGAT	0	F	0	0	0	0	0
9913	4292	an	AN0495.1	69.m15311	AO070226000029	0	-214	-182					ATGTTCGCTCTTATCGATCTTATCAAGCGATGA	ATGTTCGCTCTTATCGATCTTATCAAGCGATGA			MFALIDLIKR*	MFALIDLIKR*			GTGGCCTAGA	CTCAGCAACC	0	F	0	0	0	0	0
9914	4292	an	AN0495.1	69.m15311	AO070226000029	0	-185	-147					ATGACTCAGCAACCGCAAGCAGGACAGTTCTGCACGTGA	ATGACTCAGCAACCGCAAGCAGGACAGTTCTGCACGTGA			MTQQPQAGQFCT*	MTQQPQAGQFCT*			TTATCAAGCG	CTGTTTCAAA	0	F	0	0	0	0	0
9918	4296	af	AN6538.1	62.m03135	AO070270000046	0			-252	-160			ATGGTCCCAAAAATCATGCTTTCACTATCTACCACTAGCCCGTCTTTATCTAATATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		ATGGTCCCAAAAATCATGCTTTCACTATCTACCACTAGCCCGTCTTTATCTAATATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		MVPKIMLSLSTTSPSLSNMHARDYHVVTLS*		MVPKIMLSLSTTSPSLSNMHARDYHVVTLS*		AACTAGTTTC	CTTGGTTCAT	0	S	0	0	0	0	0
9919	4296	af	AN6538.1	62.m03135	AO070270000046	0			-237	-160			ATGCTTTCACTATCTACCACTAGCCCGTCTTTATCTAATATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		ATGCTTTCACTATCTACCACTAGCCCGTCTTTATCTAATATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		MLSLSTTSPSLSNMHARDYHVVTLS*		MLSLSTTSPSLSNMHARDYHVVTLS*		CCCAAAAATC	CTTGGTTCAT	0	S	0	0	0	0	0
9920	4296	af	AN6538.1	62.m03135	AO070270000046	0			-198	-160			ATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		ATGCATGCCCGCGATTACCATGTGGTGACACTCAGCTAA		MHARDYHVVTLS*		MHARDYHVVTLS*		TTTATCTAAT	CTTGGTTCAT	0	S	0	0	0	0	0
9921	4296	af	AN6538.1	62.m03135	AO070270000046	0			-194	-171			ATGCCCGCGATTACCATGTGGTGA		ATGCCCGCGATTACCATGTGGTGA		MPAITMW*		MPAITMW*		TCTAATATGC	CACTCAGCTA	0	S	0	0	0	0	0
9922	4296	ao	AN6538.1	62.m03135	AO070270000046	0					-196	-110	ATGCCATTCCACTCTTGTCGTCCGATGATAACTAACCAATTCCCTGCCTTTTTGGGGTTTCTGCAATTTAGTGAGAAACGGCACTGA			ATGCCATTCCACTCTTGTCGTCCGATGATAACTAACCAATTCCCTGCCTTTTTGGGGTTTCTGCAATTTAGTGAGAAACGGCACTGA	MPFHSCRPMITNQFPAFLGFLQFSEKRH*			MPFHSCRPMITNQFPAFLGFLQFSEKRH*	GTATTGCAGC	GGTCGTCGAT	0	S	0	0	0	0	0
9923	4296	ao	AN6538.1	62.m03135	AO070270000046	0					-172	-110	ATGATAACTAACCAATTCCCTGCCTTTTTGGGGTTTCTGCAATTTAGTGAGAAACGGCACTGA			ATGATAACTAACCAATTCCCTGCCTTTTTGGGGTTTCTGCAATTTAGTGAGAAACGGCACTGA	MITNQFPAFLGFLQFSEKRH*			MITNQFPAFLGFLQFSEKRH*	TTGTCGTCCG	GGTCGTCGAT	0	S	0	0	0	0	0
9924	4297	af	AN3046.1	72.m19544	AO070275000043	0			-228	-208			ATGAAAACGCCTGGATTATGA		ATGAAAACGCCTGGATTATGA		MKTPGL*		MKTPGL*		AACTCGTTCG	TCTGTGGTGG	0		0	0	0	0	0
9925	4297	af	AN3046.1	72.m19544	AO070275000043	0			-211	-194			ATGATCTGTGGTGGGTGA		ATGATCTGTGGTGGGTGA		MICGG*		MICGG*		CGCCTGGATT	TAGAGACACT	0		0	0	0	0	0
9926	4297	ao	AN3046.1	72.m19544	AO070275000043	0					-191	-177	ATGATATGCGTCTAG			ATGATATGCGTCTAG	MICV*			MICV*	AGCAGAGGTT	AGCGAGAGCT	0		0	0	0	0	0
9927	4297	ao	AN3046.1	72.m19544	AO070275000043	0					-186	-139	ATGCGTCTAGAGCGAGAGCTTAAAGTCTCCCATCCAAAAGATATATAA			ATGCGTCTAGAGCGAGAGCTTAAAGTCTCCCATCCAAAAGATATATAA	MRLERELKVSHPKDI*			MRLERELKVSHPKDI*	AGGTTATGAT	GGACAAGTAA	0		0	0	0	0	0
9930	4298	af	AN3051.1	59.m09447	AO070285000008	0			-180	-94			ATGCCGCTCGGAGTTGACGCATTTGAAGGTATATATAGTAGGAGTGGTAATCAGACCATCTTTGACCATTGTCGCATGTGTTCCTAA		ATGCCGCTCGGAGTTGACGCATTTGAAGGTATATATAGTAGGAGTGGTAATCAGACCATCTTTGACCATTGTCGCATGTGTTCCTAA		MPLGVDAFEGIYSRSGNQTIFDHCRMCS*		MPLGVDAFEGIYSRSGNQTIFDHCRMCS*		TTTCGGTCTT	GATTTATTTG	0		0	0	0	0	0
9931	4298	af	AN3051.1	59.m09447	AO070285000008	0			-105	-94			ATGTGTTCCTAA		ATGTGTTCCTAA		MCS*		MCS*		CCATTGTCGC	GATTTATTTG	0		0	0	0	0	0
9932	4298	af	AN3051.1	59.m09447	AO070285000008	0			-83	-69			ATGACCGTTAGATAA		ATGACCGTTAGATAA		MTVR*		MTVR*		GATTTATTTG	GCGCCTCGCT	0		0	0	0	0	0
9928	4298	an	AN3051.1	59.m09447	AO070285000008	0	-223	-203					ATGACGAATGGGAAAAGGTGA	ATGACGAATGGGAAAAGGTGA			MTNGKR*	MTNGKR*			AACGATCAAC	TCCCCTGAGT	0		0	0	0	0	0
9929	4298	an	AN3051.1	59.m09447	AO070285000008	0	-216	-190					ATGGGAAAAGGTGATCCCCTGAGTTAG	ATGGGAAAAGGTGATCCCCTGAGTTAG			MGKGDPLS*	MGKGDPLS*			AACATGACGA	GACTAGGTAT	0		0	0	0	0	0
9934	4299	an	AN1831.1	52.m03902	AO070292000078	0	-159	-142					ATGAGCCAGCACATATAA	ATGAGCCAGCACATATAA			MSQHI*	MSQHI*			GCATACGGTT	GATTGGATAT	0	IQR	0	0	0	0	0
9935	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-213	-172	ATGTGGACATATGTGGATAAGCATCCCCAAGCAATATTATGA			ATGTGGACATATGTGGATAAGCATCCCCAAGCAATATTATGA	MWTYVDKHPQAIL*			MWTYVDKHPQAIL*	CAAAGAACTC	AACATGTACC	0	IQR	0	0	0	0	0
9936	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-203	-132	ATGTGGATAAGCATCCCCAAGCAATATTATGAAACATGTACCTCTCAATGTTTGAATCGGCCATCCTACTAG			ATGTGGATAAGCATCCCCAAGCAATATTATGAAACATGTACCTCTCAATGTTTGAATCGGCCATCCTACTAG	MWISIPKQYYETCTSQCLNRPSY*			MWISIPKQYYETCTSQCLNRPSY*	ATGTGGACAT	TTTAGTCGTG	0	IQR	0	0	0	0	0
9937	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-175	-149	ATGAAACATGTACCTCTCAATGTTTGA			ATGAAACATGTACCTCTCAATGTTTGA	MKHVPLNV*			MKHVPLNV*	AAGCAATATT	ATCGGCCATC	0	IQR	0	0	0	0	0
9938	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-168	-127	ATGTACCTCTCAATGTTTGAATCGGCCATCCTACTAGTTTAG			ATGTACCTCTCAATGTTTGAATCGGCCATCCTACTAGTTTAG	MYLSMFESAILLV*			MYLSMFESAILLV*	ATTATGAAAC	TCGTGGATAA	0	IQR	0	0	0	0	0
9939	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-156	-127	ATGTTTGAATCGGCCATCCTACTAGTTTAG			ATGTTTGAATCGGCCATCCTACTAGTTTAG	MFESAILLV*			MFESAILLV*	GTACCTCTCA	TCGTGGATAA	0	IQR	0	0	0	0	0
9940	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-99	-25	ATGATAAACATATATATGAGTCCCCCAACATTCCAATCAATCGCTCTTACTCCCCCAGACACAATAATCCCCTAA			ATGATAAACATATATATGAGTCCCCCAACATTCCAATCAATCGCTCTTACTCCCCCAGACACAATAATCCCCTAA	MINIYMSPPTFQSIALTPPDTIIP*			MINIYMSPPTFQSIALTPPDTIIP*	AAATCTCAGC	AACACAACTC	0	IQR	0	0	0	0	0
9941	4299	ao	AN1831.1	52.m03902	AO070292000078	0					-84	-25	ATGAGTCCCCCAACATTCCAATCAATCGCTCTTACTCCCCCAGACACAATAATCCCCTAA			ATGAGTCCCCCAACATTCCAATCAATCGCTCTTACTCCCCCAGACACAATAATCCCCTAA	MSPPTFQSIALTPPDTIIP*			MSPPTFQSIALTPPDTIIP*	AAACATATAT	AACACAACTC	0	IQR	0	0	0	0	0
9942	4304	an	AN8670.1	62.m03475	AO070315000087	0	-227	-207					ATGTTGGACACCTTGACTTGA	ATGTTGGACACCTTGACTTGA			MLDTLT*	MLDTLT*			AACAACGTGC	CAACAGGGGC	0	Y	0	0	0	0	0
9943	4304	ao	AN8670.1	62.m03475	AO070315000087	0					-158	-114	ATGTCTCCTGATCGGTTTGGAAAGTCTTATATGGCTGAGGTCTAG			ATGTCTCCTGATCGGTTTGGAAAGTCTTATATGGCTGAGGTCTAG	MSPDRFGKSYMAEV*			MSPDRFGKSYMAEV*	GACATTTCAT	TCGATTCCCT	0	Y	0	0	0	0	0
9944	4304	ao	AN8670.1	62.m03475	AO070315000087	0					-128	-114	ATGGCTGAGGTCTAG			ATGGCTGAGGTCTAG	MAEV*			MAEV*	AAAGTCTTAT	TCGATTCCCT	0	Y	0	0	0	0	0
9947	4306	af	AN0944.1	70.m15576	AO070320000139	0			-214	-26			ATGGTGCTGTTAGTGGATGCTCAAAAAAATCAAGGAGACCGAGCACATCCTCGCCATCTGATTGGTCCGTGCGAGAAAGAATTTCTGCATCGGGACTTTTTCTGTTCACGGAGAACCCGACAACCATCGCAACAAAGAACAGCTTTAATCAGACCAGGCGCGATCGCGTACATCGACCTATCTGCATAA		ATGGTGCTGTTAGTGGATGCTCAAAAAAATCAAGGAGACCGAGCACATCCTCGCCATCTGATTGGTCCGTGCGAGAAAGAATTTCTGCATCGGGACTTTTTCTGTTCACGGAGAACCCGACAACCATCGCAACAAAGAACAGCTTTAATCAGACCAGGCGCGATCGCGTACATCGACCTATCTGCATAA		MVLLVDAQKNQGDRAHPRHLIGPCEKEFLHRDFFCSRRTRQPSQQRTALIRPGAIAYIDLSA*		MVLLVDAQKNQGDRAHPRHLIGPCEKEFLHRDFFCSRRTRQPSQQRTALIRPGAIAYIDLSA*		GTAGTCCTCT	GCATTTACCA	0	A	0	0	0	0	0
9948	4306	af	AN0944.1	70.m15576	AO070320000139	0			-198	-154			ATGCTCAAAAAAATCAAGGAGACCGAGCACATCCTCGCCATCTGA		ATGCTCAAAAAAATCAAGGAGACCGAGCACATCCTCGCCATCTGA		MLKKIKETEHILAI*		MLKKIKETEHILAI*		CTGTTAGTGG	TTGGTCCGTG	0	A	0	0	0	0	0
9945	4306	an	AN0944.1	70.m15576	AO070320000139	0	-199	-146					ATGGCACGTTCCAGTTTGCCGTATACTGGCCGGTGTGGAATTGCGGCGACTTGA	ATGGCACGTTCCAGTTTGCCGTATACTGGCCGGTGTGGAATTGCGGCGACTTGA			MARSSLPYTGRCGIAAT*	MARSSLPYTGRCGIAAT*			CGAGACCTTC	TCGTTCCGCG	0	A	0	0	0	0	0
9946	4306	an	AN0944.1	70.m15576	AO070320000139	0	-75	-61					ATGCCAACAACTTAA	ATGCCAACAACTTAA			MPTT*	MPTT*			AAGTTTCCAA	TCAAGCCTTA	0	A	0	0	0	0	0
9949	4306	ao	AN0944.1	70.m15576	AO070320000139	0					-220	-149	ATGCTAGCAGCTTTTTTGTGGAGTCCATGTTTAAGGTACGATACCGTAACAGATGGAGAAACACAACGCTGA			ATGCTAGCAGCTTTTTTGTGGAGTCCATGTTTAAGGTACGATACCGTAACAGATGGAGAAACACAACGCTGA	MLAAFLWSPCLRYDTVTDGETQR*			MLAAFLWSPCLRYDTVTDGETQR*	AATCAATTAA	TTGGCCCGTG	0	A	0	0	0	0	0
9950	4306	ao	AN0944.1	70.m15576	AO070320000139	0					-194	-63	ATGTTTAAGGTACGATACCGTAACAGATGGAGAAACACAACGCTGATTGGCCCGTGCGGGAAAGAATTTCTGCTTTCCAACTTTTTTTTTATACCGTGTATCCAACCACCACCACACCTTTATAACCTGTAA			ATGTTTAAGGTACGATACCGTAACAGATGGAGAAACACAACGCTGATTGGCCCGTGCGGGAAAGAATTTCTGCTTTCCAACTTTTTTTTTATACCGTGTATCCAACCACCACCACACCTTTATAACCTGTAA	MFKVRYRNRWRNTTLIGPCGKEFLLSNFFFIPCIQPPHLYNL*			MFKVRYRNRWRNTTLIGPCGKEFLLSNFFFIPCIQPPHLYNL*	TGTGGAGTCC	ACCCGTCGCA	0	A	0	0	0	0	0
9951	4306	ao	AN0944.1	70.m15576	AO070320000139	0					-168	-70	ATGGAGAAACACAACGCTGATTGGCCCGTGCGGGAAAGAATTTCTGCTTTCCAACTTTTTTTTTATACCGTGTATCCAACCACCACCACACCTTTATAA			ATGGAGAAACACAACGCTGATTGGCCCGTGCGGGAAAGAATTTCTGCTTTCCAACTTTTTTTTTATACCGTGTATCCAACCACCACCACACCTTTATAA	MEKHNADWPVRERISAFQLFFYTVYPTTTPL*			MEKHNADWPVRERISAFQLFFYTVYPTTTPL*	ACCGTAACAG	CCTGTAAACC	0	A	0	0	0	0	0
9952	4307	af	AN0956.1	70.m15605	AO070320000158	0			-251	-180			ATGGCAATGGCGACTGGAATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		ATGGCAATGGCGACTGGAATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		MAMATGMMVRDKIRLALLFFRSG*		MAMATGMMVRDKIRLALLFFRSG*		ATCTGTACTC	TCGCCGCTGA	0	J	0	MG08825.1	NCU00065.1	0	0
9953	4307	af	AN0956.1	70.m15605	AO070320000158	0			-245	-180			ATGGCGACTGGAATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		ATGGCGACTGGAATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		MATGMMVRDKIRLALLFFRSG*		MATGMMVRDKIRLALLFFRSG*		ACTCATGGCA	TCGCCGCTGA	0	J	0	MG08825.1	NCU00065.1	0	0
9954	4307	af	AN0956.1	70.m15605	AO070320000158	0			-233	-180			ATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		ATGATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		MMVRDKIRLALLFFRSG*		MMVRDKIRLALLFFRSG*		GGCGACTGGA	TCGCCGCTGA	0	J	0	MG08825.1	NCU00065.1	0	0
9955	4307	af	AN0956.1	70.m15605	AO070320000158	0			-230	-180			ATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		ATGGTTAGAGATAAGATAAGACTCGCTCTGTTGTTTTTCCGTTCCGGATAA		MVRDKIRLALLFFRSG*		MVRDKIRLALLFFRSG*		GACTGGAATG	TCGCCGCTGA	0	J	0	MG08825.1	NCU00065.1	0	0
9956	4307	ao	AN0956.1	70.m15605	AO070320000158	0					-149	-117	ATGCGAATAATCCGGGGAATAATTTCAAGCTGA			ATGCGAATAATCCGGGGAATAATTTCAAGCTGA	MRIIRGIISS*			MRIIRGIISS*	GTTGCCCGCA	TAACACTCTC	0	J	0	MG08825.1	NCU00065.1	0	0
9968	4309	af	AN1773.1	69.m15063	AO070324000031	0			-238	-209			ATGCCTCTTGCTGACCGACAGAGTTTCTAG		ATGCCTCTTGCTGACCGACAGAGTTTCTAG		MPLADRQSF*		MPLADRQSF*		TGGCGCATAT	CAAACATAGT	0	R	0	0	0	0	0
9967	4309	an	AN1773.1	69.m15063	AO070324000031	0	-188	-171					ATGATCGTGTTTGGATAG	ATGATCGTGTTTGGATAG			MIVFG*	MIVFG*			GAATTTGTCG	ATAGAGCTGA	0	R	0	0	0	0	0
9970	4311	an	AN4925.1	59.m08827	AO070338000018	0	-105	-76					ATGCTAGTCGTTCCTTTCCCCAGATCATGA	ATGCTAGTCGTTCCTTTCCCCAGATCATGA			MLVVPFPRS*	MLVVPFPRS*			GAGCATGTCT	TCCCGTTGCG	0	OPR	0	0	0	0	0
9969	4311	conserved	AN4925.1	59.m08827	AO070338000018	0	-111	-76	-108	-70	-108	-70	ATGTykvysvywrTCryTCCTTTyyCmwsmwsATsATGA	ATGTCTATGCTAGTCGTTCCTTTCCCCAGATCATGA	ATGTCGCTCACTGTCGCTCCTTTCTCATCCAGATCATGA	ATGTTTGCGGCTATCACTCCTTTTTCATCCAGATCATGA	MsmlvvPFprs*	MSMLVVPFPRS*	MSLTVAPFSSRS*	MFAAITPFSSRS*	vwCwGGGAGy	TCCCGyTkms	0	OPR	0	0	0	0	0
9973	4315	af	AN5667.1	58.m07309	AO070342000259	0			-190	-167			ATGCAGATCGTCGCTGATATATAG		ATGCAGATCGTCGCTGATATATAG		MQIVADI*		MQIVADI*		ACTGCAGTCC	TCTCTTGGCG	0	S	0	0	0	0	0
9971	4315	an	AN5667.1	58.m07309	AO070342000259	0	-179	-99					ATGCCTAATGGATTACGTCTTGGCGGACTCTCCACAGCGATCCGTCTGCTCCGTTCGCGCCCACGCCTCATTCGCGGCTGA	ATGCCTAATGGATTACGTCTTGGCGGACTCTCCACAGCGATCCGTCTGCTCCGTTCGCGCCCACGCCTCATTCGCGGCTGA			MPNGLRLGGLSTAIRLLRSRPRLIRG*	MPNGLRLGGLSTAIRLLRSRPRLIRG*			GGTAATCGCG	TTGACTTATT	0	S	0	0	0	0	0
9972	4315	an	AN5667.1	58.m07309	AO070342000259	0	-172	-95					ATGGATTACGTCTTGGCGGACTCTCCACAGCGATCCGTCTGCTCCGTTCGCGCCCACGCCTCATTCGCGGCTGATTGA	ATGGATTACGTCTTGGCGGACTCTCCACAGCGATCCGTCTGCTCCGTTCGCGCCCACGCCTCATTCGCGGCTGATTGA			MDYVLADSPQRSVCSVRAHASFAAD*	MDYVLADSPQRSVCSVRAHASFAAD*			GCGATGCCTA	CTTATTTATC	0	S	0	0	0	0	0
9974	4315	ao	AN5667.1	58.m07309	AO070342000259	0					-200	-189	ATGGCAGAGTGA			ATGGCAGAGTGA	MAE*			MAE*	CCGACCCGCG	TTTTCGTCTT	0	S	0	0	0	0	0
9976	4316	af	AN4350.1	58.m07970	AO070240000028	0			-103	-77			ATGATACCATCTTATCGTTCTGTCTGA		ATGATACCATCTTATCGTTCTGTCTGA		MIPSYRSV*		MIPSYRSV*		ATTCTCATGA	GACTCCACTG	0	E	0	0	0	0	0
9975	4316	an	AN4350.1	58.m07970	AO070240000028	0	-142	-74					ATGCGACTCGCTTCGGTCCCCAAATTATCCGTCCTCTTAAATCGCTGCGTTACTGATTCCCGTATCTGA	ATGCGACTCGCTTCGGTCCCCAAATTATCCGTCCTCTTAAATCGCTGCGTTACTGATTCCCGTATCTGA			MRLASVPKLSVLLNRCVTDSRI*	MRLASVPKLSVLLNRCVTDSRI*			TTGATAAAGG	CATTGACGTC	0	E	0	0	0	0	0
9977	4316	ao	AN4350.1	58.m07970	AO070240000028	0					-171	-145	ATGTTTCTTCAAGCGTCTCATTCTTGA			ATGTTTCTTCAAGCGTCTCATTCTTGA	MFLQASHS*			MFLQASHS*	GTGGATGTGA	TCTCAGTGCT	0	E	0	0	0	0	0
9980	4317	af	AN4637.1	57.m05548	AO070248000017	0			-154	-107			ATGAGCCCCGGCTCTATCCCCCTTGATCGACCTTGTGATTGGTCATAA		ATGAGCCCCGGCTCTATCCCCCTTGATCGACCTTGTGATTGGTCATAA		MSPGSIPLDRPCDWS*		MSPGSIPLDRPCDWS*		ATTATCCTCG	AACAGCAGCC	0	O	0	0	0	0	0
9978	4317	an	AN4637.1	57.m05548	AO070248000017	0	-133	-116					ATGAGTCCGCTCCTATGA	ATGAGTCCGCTCCTATGA			MSPLL*	MSPLL*			CCTCCCCTCA	CGGACACACG	0	O	0	0	0	0	0

9979	4317	an	AN4637.1	57.m05548	AO070248000017	0	-119	-87					ATGACGGACACACGACCCTCGGACTGTTCTTGA	ATGACGGACACACGACCCTCGGACTGTTCTTGA			MTDTRPSDCS*	MTDTRPSDCS*			GTCCGCTCCT	CTGACAGTGT	0	O	0	0	0	0	0
9981	4317	ao	AN4637.1	57.m05548	AO070248000017	0					-175	-128	ATGAGTGCCCGCTTTATCCTCCTTCGACGACCGTCCGATTGGTCATAG			ATGAGTGCCCGCTTTATCCTCCTTCGACGACCGTCCGATTGGTCATAG	MSARFILLRRPSDWS*			MSARFILLRRPSDWS*	TCCCCTCTCG	CTCTCAGTCA	0	O	0	0	0	0	0
9982	4319	an	AN5768.1	69.m14831	AO070249000004	0	-171	-151					ATGGTGCACCAGCATACGTAA	ATGGTGCACCAGCATACGTAA			MVHQHT*	MVHQHT*			ATACCTACCC	TACCCCAGCG	0		FG07425.1	MG07482.1	0	0	0
9983	4319	an	AN5768.1	69.m14831	AO070249000004	0	-123	-25					ATGATTGTCCTCCTTACTGAAGTCCCTACGATCTCCGCGTTCGACCTCTCCACCACACAATATTCTTTTCCACCCACCGTGCGCAATCGTAGGTGGTAG	ATGATTGTCCTCCTTACTGAAGTCCCTACGATCTCCGCGTTCGACCTCTCCACCACACAATATTCTTTTCCACCCACCGTGCGCAATCGTAGGTGGTAG			MIVLLTEVPTISAFDLSTTQYSFPPTVRNRRW*	MIVLLTEVPTISAFDLSTTQYSFPPTVRNRRW*			TTTTTATACT	GCGCAGTTTC	0		FG07425.1	MG07482.1	0	0	0
9984	4319	ao	AN5768.1	69.m14831	AO070249000004	0					-235	-188	ATGAATTGTTTTGCCTCCCTGCTGAATTGCTACTTTTTATTTTTTTAA			ATGAATTGTTTTGCCTCCCTGCTGAATTGCTACTTTTTATTTTTTTAA	MNCFASLLNCYFLFF*			MNCFASLLNCYFLFF*	TGCCACTTAC	AATTTATTTA	0		FG07425.1	MG07482.1	0	0	0
9986	4320	af	AN4378.1	58.m08998	AO070261000021	0			-157	-95			ATGGGGTCGTTTTGCAGTCGAGAATTGAATATATATCCTCCATCTGGGAGCTTAGTTCTATAG		ATGGGGTCGTTTTGCAGTCGAGAATTGAATATATATCCTCCATCTGGGAGCTTAGTTCTATAG		MGSFCSRELNIYPPSGSLVL*		MGSFCSRELNIYPPSGSLVL*		TTCGGTGACA	ATCACTTTTG	0	G	0	0	0	0	0
9987	4320	ao	AN4378.1	58.m08998	AO070261000021	0					-194	-156	ATGTCGTCGTCCTTCCTTCGATCCTTCCGCATTCGGTGA			ATGTCGTCGTCCTTCCTTCGATCCTTCCGCATTCGGTGA	MSSSFLRSFRIR*			MSSSFLRSFRIR*	GTCATCGGGG	CCATGGAGCC	0	G	0	0	0	0	0
9988	4320	ao	AN4378.1	58.m08998	AO070261000021	0					-153	-76	ATGGAGCCGTTTCACTCTCGAGAATCAACGCTTACATCTCTATCGGATTCTCTCGCGATAAGTTTTGAATGGTCGTGA			ATGGAGCCGTTTCACTCTCGAGAATCAACGCTTACATCTCTATCGGATTCTCTCGCGATAAGTTTTGAATGGTCGTGA	MEPFHSRESTLTSLSDSLAISFEWS*			MEPFHSRESTLTSLSDSLAISFEWS*	TTCGGTGACC	GCGCTCCTGG	0	G	0	0	0	0	0
9989	4320	ao	AN4378.1	58.m08998	AO070261000021	0					-85	-23	ATGGTCGTGAGCGCTCCTGGGTTGTTACTCTGCGATCTCCGAAGTTCACACGAGACTACGTGA			ATGGTCGTGAGCGCTCCTGGGTTGTTACTCTGCGATCTCCGAAGTTCACACGAGACTACGTGA	MVVSAPGLLLCDLRSSHETT*			MVVSAPGLLLCDLRSSHETT*	TAAGTTTTGA	GCTGTGGTCG	0	G	0	0	0	0	0
9990	4321	ao	AN1089.1	70.m15143	AO070285000061	0					-232	-164	ATGTCCTTTTTTCACCTTCAATCCGGTGTTTCTCTTTCTTTTAGCCCTGCTTCGCTTCCTTTCTTTTGA			ATGTCCTTTTTTCACCTTCAATCCGGTGTTTCTCTTTCTTTTAGCCCTGCTTCGCTTCCTTTCTTTTGA	MSFFHLQSGVSLSFSPASLPFF*			MSFFHLQSGVSLSFSPASLPFF*	CGTTCCTTTT	AACTGCTTCT	0	R	0	0	0	0	0
9991	4321	ao	AN1089.1	70.m15143	AO070285000061	0					-75	-49	ATGATCCGAAATTGTTTCTTCGTTTGA			ATGATCCGAAATTGTTTCTTCGTTTGA	MIRNCFFV*			MIRNCFFV*	TGAGACGTCG	AAAATAAAAA	0	R	0	0	0	0	0
9993	4322	af	AN4959.1	59.m08864	AO070288000021	0			-181	-170			ATGTTGCCATGA		ATGTTGCCATGA		MLP*		MLP*		CGAGAGATAG	CCAGCAGTGA	0	D	0	0	0	0	0
9994	4322	af	AN4959.1	59.m08864	AO070288000021	0			-173	-105			ATGACCAGCAGTGAGTGTATATCTTGTTTGTTTACGAGGAATTATTCCCTACTTGCAACAGCCAACTAA		ATGACCAGCAGTGAGTGTATATCTTGTTTGTTTACGAGGAATTATTCCCTACTTGCAACAGCCAACTAA		MTSSECISCLFTRNYSLLATAN*		MTSSECISCLFTRNYSLLATAN*		AGATGTTGCC	CCCAAACTCA	0	D	0	0	0	0	0
9995	4322	af	AN4959.1	59.m08864	AO070288000021	0			-67	-47			ATGGCCGCCGAAATCTCCTAG		ATGGCCGCCGAAATCTCCTAG		MAAEIS*		MAAEIS*		TTGAGACCTC	GGAGGTACTT	0	D	0	0	0	0	0
9992	4322	an	AN4959.1	59.m08864	AO070288000021	0	-145	-134					ATGGACCAGTGA	ATGGACCAGTGA			MDQ*	MDQ*			TGAACGTTGG	GTCGCGGCCT	0	D	0	0	0	0	0
9996	4322	ao	AN4959.1	59.m08864	AO070288000021	0					-152	-102	ATGACCAGCAGTGAGTACGAAAAACTTCCTCATCCCTTCCGCGGACATTGA			ATGACCAGCAGTGAGTACGAAAAACTTCCTCATCCCTTCCGCGGACATTGA	MTSSEYEKLPHPFRGH*			MTSSEYEKLPHPFRGH*	ACATAGACCG	CTGACGAAAC	0	D	0	0	0	0	0
9997	4322	ao	AN4959.1	59.m08864	AO070288000021	0					-67	-23	ATGGCCCCCCAAGTCCCCCAGGGAAGCGCTGCTGAGCTCTCCTAG			ATGGCCCCCCAAGTCCCCCAGGGAAGCGCTGCTGAGCTCTCCTAG	MAPQVPQGSAAELS*			MAPQVPQGSAAELS*	TCGACATCTC	CGGTCGAAAA	0	D	0	0	0	0	0
9999	4323	af	AN2057.1	58.m07659	AO070292000042	0			-204	-85			ATGAATGAATCTGGCACGTCGGAAGTGATAGTGACCTTGATGACGGGGGCGGCATGGTCACGTGATCAATTGGATTTTCCGGGCCGAAGCTCGACTTTCTTTTTCATGAGTACCGGTTGA		ATGAATGAATCTGGCACGTCGGAAGTGATAGTGACCTTGATGACGGGGGCGGCATGGTCACGTGATCAATTGGATTTTCCGGGCCGAAGCTCGACTTTCTTTTTCATGAGTACCGGTTGA		MNESGTSEVIVTLMTGAAWSRDQLDFPGRSSTFFFMSTG*		MNESGTSEVIVTLMTGAAWSRDQLDFPGRSSTFFFMSTG*		TATTTTGTCA	TCGCGTTGTT	0	J	0	MG06378.1	0	YGL068W	0
10000	4323	af	AN2057.1	58.m07659	AO070292000042	0			-200	-177			ATGAATCTGGCACGTCGGAAGTGA		ATGAATCTGGCACGTCGGAAGTGA		MNLARRK*		MNLARRK*		TTGTCAATGA	TAGTGACCTT	0	J	0	MG06378.1	0	YGL068W	0
10001	4323	af	AN2057.1	58.m07659	AO070292000042	0			-165	-85			ATGACGGGGGCGGCATGGTCACGTGATCAATTGGATTTTCCGGGCCGAAGCTCGACTTTCTTTTTCATGAGTACCGGTTGA		ATGACGGGGGCGGCATGGTCACGTGATCAATTGGATTTTCCGGGCCGAAGCTCGACTTTCTTTTTCATGAGTACCGGTTGA		MTGAAWSRDQLDFPGRSSTFFFMSTG*		MTGAAWSRDQLDFPGRSSTFFFMSTG*		AGTGACCTTG	TCGCGTTGTT	0	J	0	MG06378.1	0	YGL068W	0
10002	4323	af	AN2057.1	58.m07659	AO070292000042	0			-151	-140			ATGGTCACGTGA		ATGGTCACGTGA		MVT*		MVT*		CGGGGGCGGC	TCAATTGGAT	0	J	0	MG06378.1	0	YGL068W	0
10003	4323	af	AN2057.1	58.m07659	AO070292000042	0			-99	-85			ATGAGTACCGGTTGA		ATGAGTACCGGTTGA		MSTG*		MSTG*		TTTCTTTTTC	TCGCGTTGTT	0	J	0	MG06378.1	0	YGL068W	0
9998	4323	an	AN2057.1	58.m07659	AO070292000042	0	-213	-148					ATGATTGTACCATATATCCTAAAGTCTGATCGAGCCGTAGATAGAACCTGGTGTTGTGTCACGTGA	ATGATTGTACCATATATCCTAAAGTCTGATCGAGCCGTAGATAGAACCTGGTGTTGTGTCACGTGA			MIVPYILKSDRAVDRTWCCVT*	MIVPYILKSDRAVDRTWCCVT*			AATCGTCAGC	CGGTACCAGA	0	J	0	MG06378.1	0	YGL068W	0
10004	4323	ao	AN2057.1	58.m07659	AO070292000042	0					-270	-229	ATGGTGTTTTATTTTTTATATATTTGTCTACCTTTATATTGA			ATGGTGTTTTATTTTTTATATATTTGTCTACCTTTATATTGA	MVFYFLYICLPLY*			MVFYFLYICLPLY*	AGTATGAACT	CCAGAAACTG	0	J	0	MG06378.1	0	YGL068W	0
10008	4327	an	AN6228.1	72.m19426	AO070304000079	0	-183	-112					ATGTGGATTCCTTGTCCTTTCCTTTCCTCGTCCGCCACAAGTGGTGGTAACACTCGCACATTTGGTCCGTGA	ATGTGGATTCCTTGTCCTTTCCTTTCCTCGTCCGCCACAAGTGGTGGTAACACTCGCACATTTGGTCCGTGA			MWIPCPFLSSSATSGGNTRTFGP*	MWIPCPFLSSSATSGGNTRTFGP*			AACCAGCTAC	CAGTCTCTAA	0	R	0	0	0	0	0
10009	4327	ao	AN6228.1	72.m19426	AO070304000079	0					-217	-179	ATGCTCTTTTTCCCTCTCGCTCTAAAAACCCATAGCTGA			ATGCTCTTTTTCCCTCTCGCTCTAAAAACCCATAGCTGA	MLFFPLALKTHS*			MLFFPLALKTHS*	TCATTCACGG	TCTTTCCCCC	0	R	0	0	0	0	0
10012	4329	af	AN3377.1	66.m04648	AO070317000062	0			-231	-166			ATGATCATTTGGAGTAGCGATGGAATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGA		ATGATCATTTGGAGTAGCGATGGAATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGA		MIIWSSDGMLAGTVQVSLARI*		MIIWSSDGMLAGTVQVSLARI*		CGTCCGGGAC	TGATAATCAT	0		0	0	0	0	0
10013	4329	af	AN3377.1	66.m04648	AO070317000062	0			-212	-93			ATGGAATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGATGATAATCATGAGGTTACTTTCAACCTGCTGGACAGGCCCAACCGCATGCGACTCTTCTCTCCAAGGTATTAA		ATGGAATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGATGATAATCATGAGGTTACTTTCAACCTGCTGGACAGGCCCAACCGCATGCGACTCTTCTCTCCAAGGTATTAA		MECLRALFRSAWQGSDDNHEVTFNLLDRPNRMRLFSPRY*		MECLRALFRSAWQGSDDNHEVTFNLLDRPNRMRLFSPRY*		TGGAGTAGCG	AGGTATTAAA	0		0	0	0	0	0
10014	4329	af	AN3377.1	66.m04648	AO070317000062	0			-207	-166			ATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGA		ATGCTTGCGGGCACTGTTCAGGTCAGCTTGGCAAGGATCTGA		MLAGTVQVSLARI*		MLAGTVQVSLARI*		TAGCGATGGA	TGATAATCAT	0		0	0	0	0	0
10015	4329	af	AN3377.1	66.m04648	AO070317000062	0			-119	-93			ATGCGACTCTTCTCTCCAAGGTATTAA		ATGCGACTCTTCTCTCCAAGGTATTAA		MRLFSPRY*		MRLFSPRY*		GCCCAACCGC	AGGTATTAAA	0		0	0	0	0	0
10010	4329	an	AN3377.1	66.m04648	AO070317000062	0	-196	-152					ATGGAGAGGACGAGGGGACTGCTAATGGCTTGTCAAATATTTTAA	ATGGAGAGGACGAGGGGACTGCTAATGGCTTGTCAAATATTTTAA			MERTRGLLMACQIF*	MERTRGLLMACQIF*			GGGATTGAAA	ACTGGCGTAG	0		0	0	0	0	0
10011	4329	an	AN3377.1	66.m04648	AO070317000062	0	-172	-152					ATGGCTTGTCAAATATTTTAA	ATGGCTTGTCAAATATTTTAA			MACQIF*	MACQIF*			GGGACTGCTA	ACTGGCGTAG	0		0	0	0	0	0
10017	4329	ao	AN3377.1	66.m04648	AO070317000062	0					-248	-156	ATGCGAAACTCCATGTGCCATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG			ATGCGAAACTCCATGTGCCATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG	MRNSMCHDSPQPDPMAMPRATLRSGRDQEI*			MRNSMCHDSPQPDPMAMPRATLRSGRDQEI*	GAAGCGACAG	CTGCCCAGAT	0		0	0	0	0	0
10018	4329	ao	AN3377.1	66.m04648	AO070317000062	0					-236	-156	ATGTGCCATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG			ATGTGCCATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG	MCHDSPQPDPMAMPRATLRSGRDQEI*			MCHDSPQPDPMAMPRATLRSGRDQEI*	GCGAAACTCC	CTGCCCAGAT	0		0	0	0	0	0
10019	4329	ao	AN3377.1	66.m04648	AO070317000062	0					-229	-182	ATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAA			ATGATTCTCCACAACCCGACCCGATGGCCATGCCTCGTGCAACTCTAA	MILHNPTRWPCLVQL*			MILHNPTRWPCLVQL*	TCCATGTGCC	GATCAGGACG	0		0	0	0	0	0
10020	4329	ao	AN3377.1	66.m04648	AO070317000062	0					-206	-156	ATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG			ATGGCCATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG	MAMPRATLRSGRDQEI*			MAMPRATLRSGRDQEI*	ACCCGACCCG	CTGCCCAGAT	0		0	0	0	0	0
10021	4329	ao	AN3377.1	66.m04648	AO070317000062	0					-200	-156	ATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG			ATGCCTCGTGCAACTCTAAGATCAGGACGAGATCAGGAGATATAG	MPRATLRSGRDQEI*			MPRATLRSGRDQEI*	CCCGATGGCC	CTGCCCAGAT	0		0	0	0	0	0
10022	4332	ao	AN4519.1	57.m05609	AO070321000125	0					-251	-228	ATGAAAGAAGGAAGACTGAAATAG			ATGAAAGAAGGAAGACTGAAATAG	MKEGRLK*			MKEGRLK*	ATACAGGGCA	GCAATATCGC	0	RP	0	0	0	0	0
10023	4332	ao	AN4519.1	57.m05609	AO070321000125	0					-169	-59	ATGCTTTTTTTGGGTGAGCGTCTGCCAAGAATCAGGGTGGAGCAGCGGAACAGGAAAGGTTCCGCCTTATCAGCTCTGCCGCCTAGTAAGACTACTGGTTGTATATCTTAG			ATGCTTTTTTTGGGTGAGCGTCTGCCAAGAATCAGGGTGGAGCAGCGGAACAGGAAAGGTTCCGCCTTATCAGCTCTGCCGCCTAGTAAGACTACTGGTTGTATATCTTAG	MLFLGERLPRIRVEQRNRKGSALSALPPSKTTGCIS*			MLFLGERLPRIRVEQRNRKGSALSALPPSKTTGCIS*	CTCTGGTCTG	GACCACAGCT	0	RP	0	0	0	0	0
10024	4333	af	AN6591.1	62.m03207	AO070326000039	0			-241	-224			ATGCTGACCGCCTTGTAG		ATGCTGACCGCCTTGTAG		MLTAL*		MLTAL*		CCCGCCATCA	ATTCCCAAAG	0	YU	0	0	0	0	0
10028	4334	af	AN6615.1	62.m03212	AO070326000064	0			-245	-186			ATGCCTTCTACATACCATGGATATCCAGTCATGAGTCCACAACTAGGTTCTGTCTTGTAA		ATGCCTTCTACATACCATGGATATCCAGTCATGAGTCCACAACTAGGTTCTGTCTTGTAA		MPSTYHGYPVMSPQLGSVL*		MPSTYHGYPVMSPQLGSVL*		TCAAAGCTTC	TATTCTCTTC	0	K	0	0	0	0	0
10029	4334	af	AN6615.1	62.m03212	AO070326000064	0			-229	-212			ATGGATATCCAGTCATGA		ATGGATATCCAGTCATGA		MDIQS*		MDIQS*		TCTACATACC	GTCCACAACT	0	K	0	0	0	0	0
10030	4334	af	AN6615.1	62.m03212	AO070326000064	0			-215	-186			ATGAGTCCACAACTAGGTTCTGTCTTGTAA		ATGAGTCCACAACTAGGTTCTGTCTTGTAA		MSPQLGSVL*		MSPQLGSVL*		ATATCCAGTC	TATTCTCTTC	0	K	0	0	0	0	0
10025	4334	an	AN6615.1	62.m03212	AO070326000064	0	-229	-143					ATGCCTACACCCGCTCCTTTCTCATTTCCTCCTTACCTTATTTCATTTCATGCGCCGAAACACACGCATTCCCGTACGCCTATCTAA	ATGCCTACACCCGCTCCTTTCTCATTTCCTCCTTACCTTATTTCATTTCATGCGCCGAAACACACGCATTCCCGTACGCCTATCTAA			MPTPAPFSFPPYLISFHAPKHTHSRTPI*	MPTPAPFSFPPYLISFHAPKHTHSRTPI*			TGGATCGTGT	GCTACAGGTG	0	K	0	0	0	0	0
10026	4334	an	AN6615.1	62.m03212	AO070326000064	0	-180	-115					ATGCGCCGAAACACACGCATTCCCGTACGCCTATCTAAGCTACAGGTGAGCGTGCAAGCCACTTAG	ATGCGCCGAAACACACGCATTCCCGTACGCCTATCTAAGCTACAGGTGAGCGTGCAAGCCACTTAG			MRRNTRIPVRLSKLQVSVQAT*	MRRNTRIPVRLSKLQVSVQAT*			ATTTCATTTC	GTCCCTAACC	0	K	0	0	0	0	0
10027	4334	an	AN6615.1	62.m03212	AO070326000064	0	-65	-12					ATGATTGTGTTCAGTCCGCGTCTGGCTGACAAACGGTGTGGTTTGAAGGCCTAG	ATGATTGTGTTCAGTCCGCGTCTGGCTGACAAACGGTGTGGTTTGAAGGCCTAG			MIVFSPRLADKRCGLKA*	MIVFSPRLADKRCGLKA*			ACACCGTGTC	TTATCTCCGA	0	K	0	0	0	0	0
10031	4334	ao	AN6615.1	62.m03212	AO070326000064	0					-224	-213	ATGCAGCCATGA			ATGCAGCCATGA	MQP*			MQP*	CTTCCTGGAT	GTCTTTGTTT	0	K	0	0	0	0	0
10032	4334	ao	AN6615.1	62.m03212	AO070326000064	0					-216	-196	ATGAGTCTTTGTTTTTTCTAA			ATGAGTCTTTGTTTTTTCTAA	MSLCFF*			MSLCFF*	ATATGCAGCC	TTTCTTGTGA	0	K	0	0	0	0	0
10033	4334	ao	AN6615.1	62.m03212	AO070326000064	0					-141	-130	ATGTGTTACTAA			ATGTGTTACTAA	MCY*			MCY*	TTCTTATTTC	TTAAATAATT	0	K	0	0	0	0	0
10036	4336	af	AN1116.1	70.m15119	AO070331000108	0			-71	-33			ATGCTCCGTTCCTACACTGATGCCCCACTTCGATCCTGA		ATGCTCCGTTCCTACACTGATGCCCCACTTCGATCCTGA		MLRSYTDAPLRS*		MLRSYTDAPLRS*		TTGCCGAGGT	CGAGCTGACA	0	K	0	0	0	0	0
10037	4336	ao	AN1116.1	70.m15119	AO070331000108	0					-76	-50	ATGCTTAGCCCCCGCAAGAGTCAATAA			ATGCTTAGCCCCCGCAAGAGTCAATAA	MLSPRKSQ*			MLSPRKSQ*	CTTTAAGCGT	TTTATCGTGG	0	K	0	0	0	0	0
10038	4337	an	AN2983.1	59.m09031	AO070337000139	0	-187	-125					ATGTCTAATCTGATCTGTGCACCCGTTTACCACGCCGACATTACCGCGCAGCTCCCTCTGTGA	ATGTCTAATCTGATCTGTGCACCCGTTTACCACGCCGACATTACCGCGCAGCTCCCTCTGTGA			MSNLICAPVYHADITAQLPL*	MSNLICAPVYHADITAQLPL*			TCTTCTTTGT	TCCCGGCTTG	0	Y	0	0	0	0	0
10048	4342	an	AN7572.1	72.m19591	AO070343000419	0	-164	-144					ATGCAGCGAATGAATCCGTAG	ATGCAGCGAATGAATCCGTAG			MQRMNP*	MQRMNP*			TGGCCGGTTA	CCAACCAACG	0	R	0	0	0	0	0
10046	4342	conserved	AN7572.1	72.m19591	AO070343000419	0	-175	-164	-191	-180	-181	-170	ATGGCCsGTTrr	ATGGCCGGTTAA	ATGGCCCGTTAG	ATGGCCCGTTGA	MAg*	MAG*	MAR*	MAR*	CrryyymGCC	TsywGCGrAT	0	R	0	0	0	0	0
10047	4342	conserved	AN7572.1	72.m19591	AO070343000419	0	-155	-144	-171	-160	-161	-150	ATGmATyCrTAr	ATGAATCCGTAG	ATGCATTCATAA	ATGAATCCATAA	Mnp*	MNP*	MHS*	MNP*	rrTsywGCGr	Cmhmvywhsd	0	R	0	0	0	0	0
10049	4343	af	AN9509.1	72.m19475	AO070241000002	0			-133	-119			ATGCTAATTGCCTAA		ATGCTAATTGCCTAA		MLIA*		MLIA*		TAAGCACAGT	TTTGAACAAT	0	D	0	0	0	0	0
10050	4343	ao	AN9509.1	72.m19475	AO070241000002	0					-157	-146	ATGGTCGCATGA			ATGGTCGCATGA	MVA*			MVA*	AACTTGTCGC	CTGCTGACGG	0	D	0	0	0	0	0
10051	4343	ao	AN9509.1	72.m19475	AO070241000002	0					-149	-132	ATGACTGCTGACGGATAA			ATGACTGCTGACGGATAA	MTADG*			MTADG*	GCATGGTCGC	TTTATTTTTT	0	D	0	0	0	0	0
10053	4347	af	AN1095.1	70.m15135	AO070285000047	0			-108	-55			ATGCCCGGTCCGACATTTCTCCACATCCGCATCCCGAAGATCTTTGTCCCGTAA		ATGCCCGGTCCGACATTTCTCCACATCCGCATCCCGAAGATCTTTGTCCCGTAA		MPGPTFLHIRIPKIFVP*		MPGPTFLHIRIPKIFVP*		GAGGAAAACG	TATCAATTCG	0	J	0	0	0	0	0
10052	4347	an	AN1095.1	70.m15135	AO070285000047	0	-235	-215					ATGAGGCATACAATCAACTAA	ATGAGGCATACAATCAACTAA			MRHTIN*	MRHTIN*			AATTCATTGA	AAGATTGATC	0	J	0	0	0	0	0
10054	4347	ao	AN1095.1	70.m15135	AO070285000047	0					-184	-173	ATGATATTTTAA			ATGATATTTTAA	MIF*			MIF*	CACAGAAGTT	AAATTAGGAC	0	J	0	0	0	0	0
10058	4348	af	AN8783.1	71.m15597	AO070289000008	0			-174	-157			ATGCCTCCGTGGGAGTAG		ATGCCTCCGTGGGAGTAG		MPPWE*		MPPWE*		CGACGGCGCT	TGTGTTTTGG	0	D	FG05504.1	0	0	0	0
10059	4348	af	AN8783.1	71.m15597	AO070289000008	0			-85	-56			ATGAGCTCCGCAGCCTCAATGCGTCTATGA		ATGAGCTCCGCAGCCTCAATGCGTCTATGA		MSSAASMRL*		MSSAASMRL*		CGGAGTTGAC	CCGTAACTCA	0	D	FG05504.1	0	0	0	0
10060	4348	af	AN8783.1	71.m15597	AO070289000008	0			-67	-56			ATGCGTCTATGA		ATGCGTCTATGA		MRL*		MRL*		CGCAGCCTCA	CCGTAACTCA	0	D	FG05504.1	0	0	0	0

10055	4348	an	AN8783.1	71.m15597	AO070289000008	0	-230	-192					ATGCGCCGCTGGGATAATTTGCGGAGGCCTGAATATTAA	ATGCGCCGCTGGGATAATTTGCGGAGGCCTGAATATTAA			MRRWDNLRRPEY*	MRRWDNLRRPEY*			TGAAGTTCCG	GGCATAAACA	0	D	FG05504.1	0	0	0	0
10056	4348	an	AN8783.1	71.m15597	AO070289000008	0	-180	-166					ATGTCGGGGAACTGA	ATGTCGGGGAACTGA			MSGN*	MSGN*			GCATAAACAC	ACAAAGCAAA	0	D	FG05504.1	0	0	0	0
10057	4348	an	AN8783.1	71.m15597	AO070289000008	0	-62	-51					ATGCAGGATTGA	ATGCAGGATTGA			MQD*	MQD*			CACATCTTCG	GGACGGCATA	0	D	FG05504.1	0	0	0	0
10062	4348	ao	AN8783.1	71.m15597	AO070289000008	0					-158	-36	ATGTTGCTACGACAACGAGGCTTTGGCTTGGCTTACGGCAAGCGATCACCATCACAGATGTCACGGAGACAAGCCACACAAGCGACCACGTTATTGAACATTCCGGATGGCCTGAACTACTAA			ATGTTGCTACGACAACGAGGCTTTGGCTTGGCTTACGGCAAGCGATCACCATCACAGATGTCACGGAGACAAGCCACACAAGCGACCACGTTATTGAACATTCCGGATGGCCTGAACTACTAA	MLLRQRGFGLAYGKRSPSQMSRRQATQATTLLNIPDGLNY*			MLLRQRGFGLAYGKRSPSQMSRRQATQATTLLNIPDGLNY*	GTGGCTCTGT	CCTTTCATAC	0	D	FG05504.1	0	0	0	0
10063	4348	ao	AN8783.1	71.m15597	AO070289000008	0					-101	-36	ATGTCACGGAGACAAGCCACACAAGCGACCACGTTATTGAACATTCCGGATGGCCTGAACTACTAA			ATGTCACGGAGACAAGCCACACAAGCGACCACGTTATTGAACATTCCGGATGGCCTGAACTACTAA	MSRRQATQATTLLNIPDGLNY*			MSRRQATQATTLLNIPDGLNY*	ACCATCACAG	CCTTTCATAC	0	D	FG05504.1	0	0	0	0
10065	4350	af	AN1711.1	72.m19761	AO070297000053	0			-158	-42			ATGATGTTTGATAAGCAGACAAACACATCAAAAAAAATGTTTCCTCTGCGGGGCAAAAGCAGTTATTCATCATCCTTCCAAGAGTCTACGACTCTGATTCTATATCCTATTCTTGA		ATGATGTTTGATAAGCAGACAAACACATCAAAAAAAAATGTTTCCTCTGCGGGGCAAAAGCAGTTATTCATCATCCTTCCAAGAGTCTACGACTCTGATTCTATATCCTATTCTTGA		MMFDKQTNTSKKNVSSAGQKQLFIILPRVYDSDSISYS*		MMFDKQTNTSKKNVSSAGQKQLFIILPRVYDSDSISYS*		CTGACCAAGC	GCTCTCTGTA	0	J	FG09760.1	0	NCU08663.1	0	0
10066	4350	af	AN1711.1	72.m19761	AO070297000053	0			-155	-42			ATGTTTGATAAGCAGACAAACACATCAAAAAAAAATGTTTCCTCTGCGGGGCAAAAGCAGTTATTCATCATCCTTCCAAGAGTCTACGACTCTGATTCTATATCCTATTCTTGA		ATGTTTGATAAGCAGACAAACACATCAAAAAAAAATGTTTCCTCTGCGGGGCAAAAGCAGTTATTCATCATCCTTCCAAGAGTCTACGACTCTGATTCTATATCCTATTCTTGA		MFDKQTNTSKKNVSSAGQKQLFIILPRVYDSDSISYS*		MFDKQTNTSKKNVSSAGQKQLFIILPRVYDSDSISYS*		ACCAAGCATG	GCTCTCTGTA	0	J	FG09760.1	0	NCU08663.1	0	0
10064	4350	an	AN1711.1	72.m19761	AO070297000053	0	-196	-164					ATGATCTATCAGGTCTTAGCAGAGATAAGATAG	ATGATCTATCAGGTCTTAGCAGAGATAAGATAG			MIYQVLAEIR*	MIYQVLAEIR*			ATCTCTTATA	GAAATCACAA	0	J	FG09760.1	0	NCU08663.1	0	0
10067	4350	ao	AN1711.1	72.m19761	AO070297000053	0					-161	-66	ATGACAAACACATCCATTATTAAGCAATCAAACAAAGCAAACGGAAATCTTTCCCCGCGGCAAAAAAAAAAAAGTTACAAATCCAGTAACCCTTAG			ATGACAAACACATCCATTATTAAGCAATCAAACAAAGCAAACGGAAATCTTTCCCCGCGGCAAAAAAAAAAAAGTTACAAATCCAGTAACCCTTAG	MTNTSIIKQSNKANGNLSPRQKKKSYKSSNP*			MTNTSIIKQSNKANGNLSPRQKKKSYKSSNP*	CAGAGCAAAC	AGTTCACTTC	0	J	FG09760.1	0	NCU08663.1	0	0
10070	4353	ao	AN5871.1	72.m19263	AO070308000137	0					-124	-62	ATGGCATTTGTTCCCAGTGTATCTTACAGTGGGATCATTGCAGAATTATTACCAATCGATTGA			ATGGCATTTGTTCCCAGTGTATCTTACAGTGGGATCATTGCAGAATTATTACCAATCGATTGA	MAFVPSVSYSGIIAELLPID*			MAFVPSVSYSGIIAELLPID*	GTTACTTCAC	AGTCATTCGA	0	A	FG06161.1	MG07132.1	0	0	0
10072	4355	af	AN3391.1	70.m15714	AO070309000063	0			-136	-71			ATGTGGGGGAAAAGTCAAAGTCCGGGTGAAGTGAGTACTCCCGAAGCGTATGCCCCCTTGACATAG		ATGTGGGGGAAAAGTCAAAGTCCGGGTGAAGTGAGTACTCCCGAAGCGTATGCCCCCTTGACATAG		MWGKSQSPGEVSTPEAYAPLT*		MWGKSQSPGEVSTPEAYAPLT*		GCACTGTTCG	GGTAATAATG	0	R	0	0	0	0	0
10073	4355	af	AN3391.1	70.m15714	AO070309000063	0			-87	-76			ATGCCCCCTTGA		ATGCCCCCTTGA		MPP*		MPP*		CCCGAAGCGT	CATAGGGTAA	0	R	0	0	0	0	0
10074	4355	af	AN3391.1	70.m15714	AO070309000063	0			-63	-10			ATGTGCTTTCGCATTGTTCCACCCATGGCCCCCCCGCGTTCGGAGCTGCGTTAG		ATGTGCTTTCGCATTGTTCCACCCATGGCCCCCCCGCGTTCGGAGCTGCGTTAG		MCFRIVPPMAPPRSELR*		MCFRIVPPMAPPRSELR*		TAGGGTAATA	CTAGGCACCA	0	R	0	0	0	0	0
10071	4355	an	AN3391.1	70.m15714	AO070309000063	0	-190	-158					ATGCGGGGAGCTAGGCGAATTCTCGACCGATAG	ATGCGGGGAGCTAGGCGAATTCTCGACCGATAG			MRGARRILDR*	MRGARRILDR*			AGGGGTTCAC	GGTTAGGTCA	0	R	0	0	0	0	0
10078	4358	af	AN0235.1	54.m06363	AO070318000080	0			-79	-47			ATGAAACCCCCATCTTCATCCTACAGCGATTGA		ATGAAACCCCCATCTTCATCCTACAGCGATTGA		MKPPSSSYSD*		MKPPSSSYSD*		GAAGAGCCTG	TTACCTGCAA	0	T	0	0	0	0	0
10077	4358	an	AN0235.1	54.m06363	AO070318000080	0	-61	-23					ATGAGACGATATCCCCCCCAACGCCGTCGCTCGACCTGA	ATGAGACGATATCCCCCCCAACGCCGTCGCTCGACCTGA			MRRYPPQRRRST*	MRRYPPQRRRST*			CATCCTACCG	TCCCACATTG	0	T	0	0	0	0	0
10081	4359	af	AN1210.1	70.m15011	AO070331000216	0			-83	-66			ATGACACCGGCTAGGTGA		ATGACACCGGCTAGGTGA		MTPAR*		MTPAR*		GCTGCCTCCC	TTTGCTACTA	0	K	0	0	0	0	0
10079	4359	an	AN1210.1	70.m15011	AO070331000216	0	-217	-125					ATGGATTTTTACTCCGAACCAGTCTCTCGTTCTACCGTGCTCCTGTCTGCGATTGACGCAAGCAATCCGAGGCACGGCTTCCCGAACCCATAG	ATGGATTTTTACTCCGAACCAGTCTCTCGTTCTACCGTGCTCCTGTCTGCGATTGACGCAAGCAATCCGAGGCACGGCTTCCCGAACCCATAG			MDFYSEPVSRSTVLLSAIDASNPRHGFPNP*	MDFYSEPVSRSTVLLSAIDASNPRHGFPNP*			TCTTCTTTTC	TAACGCAAGC	0	K	0	0	0	0	0
10080	4359	an	AN1210.1	70.m15011	AO070331000216	0	-66	-52					ATGCTGAGGAGCTGA	ATGCTGAGGAGCTGA			MLRS*	MLRS*			CGACAGACAT	AACCCTTGAA	0	K	0	0	0	0	0
10082	4359	ao	AN1210.1	70.m15011	AO070331000216	0					-290	-270	ATGTCTCTTTATATCTTCTAG			ATGTCTCTTTATATCTTCTAG	MSLYIF*			MSLYIF*	TGTCTGTTTC	TCTAGTCTCT	0	K	0	0	0	0	0
10083	4359	ao	AN1210.1	70.m15011	AO070331000216	0					-82	-29	ATGCCAGGAAGCCAGTCGGACTTGCTGCTAGGAGTAGCTGATTCATGCCTCTGA			ATGCCAGGAAGCCAGTCGGACTTGCTGCTAGGAGTAGCTGATTCATGCCTCTGA	MPGSQSDLLLGVADSCL*			MPGSQSDLLLGVADSCL*	GCCGCCTTTC	TTAAGACACC	0	K	0	0	0	0	0
10084	4362	af	AN5751.1	69.m14849	AO070341000008	0			-131	-99			ATGCCGGGTTTCGATCAGTTCTCCAGCCCATAA		ATGCCGGGTTTCGATCAGTTCTCCAGCCCATAA		MPGFDQFSSP*		MPGFDQFSSP*		TGACCATCTG	CCCCGCGGGA	0	L	0	0	0	0	0
10085	4362	ao	AN5751.1	69.m14849	AO070341000008	0					-122	-90	ATGATGGCTCATTTATATCCCCTTCAACCATAA			ATGATGGCTCATTTATATCCCCTTCAACCATAA	MMAHLYPLQP*			MMAHLYPLQP*	CGTGTTTTGG	CGTCATAACC	0	L	0	0	0	0	0
10086	4362	ao	AN5751.1	69.m14849	AO070341000008	0					-119	-90	ATGGCTCATTTATATCCCCTTCAACCATAA			ATGGCTCATTTATATCCCCTTCAACCATAA	MAHLYPLQP*			MAHLYPLQP*	GTTTTGGATG	CGTCATAACC	0	L	0	0	0	0	0
10087	4363	af	AN4183.1	69.m14960	AO070341000083	0			-235	-206			ATGGGTGTAACGCTTCAAAGGACTCACTGA		ATGGGTGTAACGCTTCAAAGGACTCACTGA		MGVTLQRTH*		MGVTLQRTH*		TGGACACGAG	TTTTGTTTTT	0	OT	0	0	0	0	0
10088	4363	ao	AN4183.1	69.m14960	AO070341000083	0					-98	-87	ATGTATCGGTGA			ATGTATCGGTGA	MYR*			MYR*	AGCCCCTTAG	CCTTCGATGC	0	OT	0	0	0	0	0
10089	4363	ao	AN4183.1	69.m14960	AO070341000083	0					-80	-39	ATGCTGCGACCAAATCTCAAAACCCATCACTACCCCGCTTGA			ATGCTGCGACCAAATCTCAAAACCCATCACTACCCCGCTTGA	MLRPNLKTHHYPA*			MLRPNLKTHHYPA*	GTGACCTTCG	CGCCATTAGC	0	OT	0	0	0	0	0
10090	4364	an	AN7576.1	72.m19595	AO070343000423	0	-222	-202					ATGTGCCATTTTTACGCTTAG	ATGTGCCATTTTTACGCTTAG			MCHFYA*	MCHFYA*			GACTGTTTGG	TAACTTGCAT	0	TZ	0	MG04377.1	0	0	0
10091	4366	an	AN4210.1	54.m07041	AO070231000014	0	-64	-14					ATGCTGATTCCTCCAAAAGGCTTGCGCGGACTTATCCTCGATCCCCGCTAA	ATGCTGATTCCTCCAAAAGGCTTGCGCGGACTTATCCTCGATCCCCGCTAA			MLIPPKGLRGLILDPR*	MLIPPKGLRGLILDPR*			TCGTCGGCGG	GGGGGTTGTT	0	KTDL	0	0	0	0	0
10092	4366	ao	AN4210.1	54.m07041	AO070231000014	0					-102	-52	ATGCTGACGTCAAAAGAAAGCTTGCGCGGACTGCTCCTCGATCCCCATTAA			ATGCTGACGTCAAAAGAAAGCTTGCGCGGACTGCTCCTCGATCCCCATTAA	MLTSKESLRGLLLDPH*			MLTSKESLRGLLLDPH*	CCACCAGCGA	GGGGGGGTTG	0	KTDL	0	0	0	0	0
10094	4367	an	AN4369.1	58.m07958	AO070261000009	0	-209	-165					ATGCTAAGCGCATCGCCCACTATCCCCAACCATCCTTTCAACTAG	ATGCTAAGCGCATCGCCCACTATCCCCAACCATCCTTTCAACTAG			MLSASPTIPNHPFN*	MLSASPTIPNHPFN*			CCAGTGTTGG	TTCTCAATCG	0	T	0	0	0	0	0
10093	4367	conserved	AN4369.1	58.m07958	AO070261000009	0	-90	-64	-109	-83	-107	-81	ATGyTCATTGAdTyywsysTbwshTAA	ATGCTCATTGATTCTACCGTGTGTTAA	ATGCTCATTGAGTTCTGTCTCACCTAA	ATGTTCATTGAATCTTCTCTTTCATAA	MIldstvc*	MLIDSTVC*	MLIEFCLT*	MFIESSLS*	khmbsTGAGG	Tydsyksksd	0	T	0	0	0	0	0
10098	4368	af	AN4612.1	57.m05529	AO070267000028	0			-151	-77			ATGTCCGGCCGCTTTTACGGAATGGGCAATAATCCAGTGCTGCTTTTATTGGCCTGTAGACCCTCCAGGGAATAA		ATGTCCGGCCGCTTTTACGGAATGGGCAATAATCCAGTGCTGCTTTTATTGGCCTGTAGACCCTCCAGGGAATAA		MSGRFYGMGNNPVLLLLACRPSRE*		MSGRFYGMGNNPVLLLLACRPSRE*		CGGAAGGCCG	ACAATGAGGA	0		0	0	0	0	0
10099	4368	af	AN4612.1	57.m05529	AO070267000028	0			-130	-77			ATGGGCAATAATCCAGTGCTGCTTTTATTGGCCTGTAGACCCTCCAGGGAATAA		ATGGGCAATAATCCAGTGCTGCTTTTATTGGCCTGTAGACCCTCCAGGGAATAA		MGNNPVLLLLACRPSRE*		MGNNPVLLLLACRPSRE*		CTTTTACGGA	ACAATGAGGA	0		0	0	0	0	0
10100	4368	af	AN4612.1	57.m05529	AO070267000028	0			-73	-17			ATGAGGAACAGCAGGCAAGAAGACAGCAACACATCTACACCCAGACAATTATACTAG		ATGAGGAACAGCAGGCAAGAAGACAGCAACACATCTACACCCAGACAATTATACTAG		MRNSRQEDSNTSTPRQLY*		MRNSRQEDSNTSTPRQLY*		GGAATAAACA	TAACGGATAC	0		0	0	0	0	0
10095	4368	an	AN4612.1	57.m05529	AO070267000028	0	-259	-248					ATGCTGTTGTGA	ATGCTGTTGTGA			MLL*	MLL*			GCGAGTTGTG	AGAGCTGATG	0		0	0	0	0	0
10096	4368	an	AN4612.1	57.m05529	AO070267000028	0	-240	-163					ATGCGGTTGATGAACCGGGAAAGGGTGCGACAAGCAAGAACGGAAGCAACGAGGTTTGTCCGGAGACCCGAGGACTAG	ATGCGGTTGATGAACCGGGAAAGGGTGCGACAAGCAAGAACGGAAGCAACGAGGTTTGTCCGGAGACCCGAGGACTAG			MRLMNRERVRQARTEATRFVRRPED*	MRLMNRERVRQARTEATRFVRRPED*			TGAAGAGCTG	CCCCTTTTGG	0		0	0	0	0	0
10097	4368	an	AN4612.1	57.m05529	AO070267000028	0	-231	-163					ATGAACCGGGAAAGGGTGCGACAAGCAAGAACGGAAGCAACGAGGTTTGTCCGGAGACCCGAGGACTAG	ATGAACCGGGAAAGGGTGCGACAAGCAAGAACGGAAGCAACGAGGTTTGTCCGGAGACCCGAGGACTAG			MNRERVRQARTEATRFVRRPED*	MNRERVRQARTEATRFVRRPED*			GATGCGGTTG	CCCCTTTTGG	0		0	0	0	0	0
10101	4368	ao	AN4612.1	57.m05529	AO070267000028	0					-89	-72	ATGCAGCAGTTGTCATGA			ATGCAGCAGTTGTCATGA	MQQLS*			MQQLS*	CTGTAAACAA	AACTCCAACT	0		0	0	0	0	0
10102	4368	ao	AN4612.1	57.m05529	AO070267000028	0					-75	-49	ATGAAACTCCAACTTCATACTTTCTAA			ATGAAACTCCAACTTCATACTTTCTAA	MKLQLHTF*			MKLQLHTF*	AGCAGTTGTC	GTATATTCAT	0		0	0	0	0	0
10105	4370	af	AN8784.1	71.m15598	AO070289000009	0			-200	-108			ATGTCAACTCCGTCAGTGTCTCTCAGAATCGGGCCAAGCCTCAAGAGGTGGTTGTCGCAGCAACCAAAACACACTACTCCCACGGAGGCATAG		ATGTCAACTCCGTCAGTGTCTCTCAGAATCGGGCCAAGCCTCAAGAGGTGGTTGTCGCAGCAACCAAAACACACTACTCCCACGGAGGCATAG		MSTPSVSLRIGPSLKRWLSQQPKHTTPTEA*		MSTPSVSLRIGPSLKRWLSQQPKHTTPTEA*		TGCGGAGCTC	CGCCGTCGGT	0		0	0	0	0	0
10103	4370	an	AN8784.1	71.m15598	AO070289000009	0	-207	-166					ATGGGGTGCGTTGTCGCAGCAACGGGCCTCAAAACGGCTTAG	ATGGGGTGCGTTGTCGCAGCAACGGGCCTCAAAACGGCTTAG			MGCVVAATGLKTA*	MGCVVAATGLKTA*			CGAGACCACA	TGTCTTTTGC	0		0	0	0	0	0
10104	4370	an	AN8784.1	71.m15598	AO070289000009	0	-137	-45					ATGTGTTTATGCCTTAATATTCAGGCCTCCGCAAATTATCCCAGCGGCGCATCGGAACTTCAACCTCAACTTGAACTGGTTCCAACGTCTTAA	ATGTGTTTATGCCTTAATATTCAGGCCTCCGCAAATTATCCCAGCGGCGCATCGGAACTTCAACCTCAACTTGAACTGGTTCCAACGTCTTAA			MCLCLNIQASANYPSGASELQPQLELVPTS*	MCLCLNIQASANYPSGASELQPQLELVPTS*			GTTCCCCGAC	CAGAGGAAAG	0		0	0	0	0	0
10106	4370	ao	AN8784.1	71.m15598	AO070289000009	0					-244	-176	ATGTTCAATAACGTGGTCGCTTGTGTGGCTTGTCTCCGTGACATCTGTGATGGTGATCGCTTGCCGTAA			ATGTTCAATAACGTGGTCGCTTGTGTGGCTTGTCTCCGTGACATCTGTGATGGTGATCGCTTGCCGTAA	MFNNVVACVACLRDICDGDRLP*			MFNNVVACVACLRDICDGDRLP*	GCCATCCGGA	GCCAAGCCAA	0		0	0	0	0	0
10107	4370	ao	AN8784.1	71.m15598	AO070289000009	0					-195	-115	ATGGTGATCGCTTGCCGTAAGCCAAGCCAAAGCCTCGTTGTCGTAGCAACATACAGAGCCACTACACCCAGAGGGGTATAG			ATGGTGATCGCTTGCCGTAAGCCAAGCCAAAGCCTCGTTGTCGTAGCAACATACAGAGCCACTACACCCAGAGGGGTATAG	MVIACRKPSQSLVVVATYRATTPRGV*			MVIACRKPSQSLVVVATYRATTPRGV*	GACATCTGTG	CGGCGCCAAG	0		0	0	0	0	0
10112	4371	af	AN5123.1	54.m06901	AO070291000056	0			-220	-35			ATGAGGCAGCGGATAATGGATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAGAGCCCAAGATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		ATGAGGCAGCGGATAATGGATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAGAGCCCAAGATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		MRQRIMDAIGTAPLVQEGPSIIDNQSCSSLEPKMSCVVLVLINTILLPSLCLALAPSFSAV*		MRQRIMDAIGTAPLVQEGPSIIDNQSCSSLEPKMSCVVLVLINTILLPSLCLALAPSFSAV*		ATAGTCCCAG	TTCCACTGCC	0	GQ	0	MG08569.1	NCU01704.1	0	0
10113	4371	af	AN5123.1	54.m06901	AO070291000056	0			-205	-35			ATGGATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAGAGCCCAAGATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		ATGGATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAGAGCCCAAGATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		MDAIGTAPLVQEGPSIIDNQSCSSLEPKMSCVVLVLINTILLPSLCLALAPSFSAV*		MDAIGTAPLVQEGPSIIDNQSCSSLEPKMSCVVLVLINTILLPSLCLALAPSFSAV*		GCAGCGGATA	TTCCACTGCC	0	GQ	0	MG08569.1	NCU01704.1	0	0
10114	4371	af	AN5123.1	54.m06901	AO070291000056	0			-201	-130			ATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAG		ATGCCATTGGGACTGCCCCGCTTGTCCAGGAAGGCCCTTCTATTATTGATAATCAGAGTTGCAGTAGTCTAG		MPLGLPRLSRKALLLLIIRVAVV*		MPLGLPRLSRKALLLLIIRVAVV*		CGGATAATGG	AGCCCAAGAT	0	GQ	0	MG08569.1	NCU01704.1	0	0
10115	4371	af	AN5123.1	54.m06901	AO070291000056	0			-121	-35			ATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		ATGAGCTGCGTGGTCTTAGTTCTTATAAATACAATCCTGCTCCCAAGTCTCTGTCTCGCTTTGGCACCATCCTTCTCTGCTGTATAG		MSCVVLVLINTILLPSLCLALAPSFSAV*		MSCVVLVLINTILLPSLCLALAPSFSAV*		AGAGCCCAAG	TTCCACTGCC	0	GQ	0	MG08569.1	NCU01704.1	0	0
10108	4371	an	AN5123.1	54.m06901	AO070291000056	0	-203	-189					ATGGTCTCTTATTAA	ATGGTCTCTTATTAA			MVSY*	MVSY*			TCTACCCCGC	ATGACGTCGA	0	GQ	0	MG08569.1	NCU01704.1	0	0
10109	4371	an	AN5123.1	54.m06901	AO070291000056	0	-188	-123					ATGACGTCGAAAAATGGACCGCGACCCGCACGGCGTAACTCCGTGGTAGGAATGGATAAAGTCTAA	ATGACGTCGAAAAATGGACCGCGACCCGCACGGCGTAACTCCGTGGTAGGAATGGATAAAGTCTAA			MTSKNGPRPARRNSVVGMDKV*	MTSKNGPRPARRNSVVGMDKV*			CTCTTATTAA	CCTGTCTCAA	0	GQ	0	MG08569.1	NCU01704.1	0	0
10110	4371	an	AN5123.1	54.m06901	AO070291000056	0	-175	-140					ATGGACCGCGACCCGCACGGCGTAACTCCGTGGTAG	ATGGACCGCGACCCGCACGGCGTAACTCCGTGGTAG			MDRDPHGVTPW*	MDRDPHGVTPW*			ACGTCGAAAA	GAATGGATAA	0	GQ	0	MG08569.1	NCU01704.1	0	0

10111	4371	an	AN5123.1	54.m06901	AO070291000056	0	-137	-123					ATGGATAAAGTCTAA	ATGGATAAAGTCTAA			MDKV*	MDKV*			CGTGGTAGGA	CCTGTCTCAA	0	GQ	0	MG08569.1	NCU01704.1	0	0
10116	4371	ao	AN5123.1	54.m06901	AO070291000056	0					-239	-90	ATGAGGGGCTGCGGGCAAATGACGTCGGAACATTGTGGAGCCCCTGACACTCATTTCTTTACGCCTATAGACCCTCGATACTACAGTTGCATTGCGTCCCATTATAAATTCACTACACCTTTTTCCTCCAGTATTCTGATCGACTGCTGA			ATGAGGGGCTGCGGGCAAATGACGTCGGAACATTGTGGAGCCCCTGACACTCATTTCTTTACGCCTATAGACCCTCGATACTACAGTTGCATTGCGTCCCATTATAAATTCACTACACCTTTTTCCTCCAGTATTCTGATCGACTGCTGA	MRGCGQMTSEHCGAPDTHFFTPIDPRYYSCIASHYKFTTPFSSSILIDC*			MRGCGQMTSEHCGAPDTHFFTPIDPRYYSCIASHYKFTTPFSSSILIDC*	TGTAGGTTCC	AGACTGTACC	0	GQ	0	MG08569.1	NCU01704.1	0	0
10117	4371	ao	AN5123.1	54.m06901	AO070291000056	0					-221	-90	ATGACGTCGGAACATTGTGGAGCCCCTGACACTCATTTCTTTACGCCTATAGACCCTCGATACTACAGTTGCATTGCGTCCCATTATAAATTCACTACACCTTTTTCCTCCAGTATTCTGATCGACTGCTGA			ATGACGTCGGAACATTGTGGAGCCCCTGACACTCATTTCTTTACGCCTATAGACCCTCGATACTACAGTTGCATTGCGTCCCATTATAAATTCACTACACCTTTTTCCTCCAGTATTCTGATCGACTGCTGA	MTSEHCGAPDTHFFTPIDPRYYSCIASHYKFTTPFSSSILIDC*			MTSEHCGAPDTHFFTPIDPRYYSCIASHYKFTTPFSSSILIDC*	CTGCGGGCAA	AGACTGTACC	0	GQ	0	MG08569.1	NCU01704.1	0	0
10129	4381	af	AN0317.1	54.m06441	AO070334000015	0			-129	-103			ATGCTCGTGGCATCATCTTCACTCTAG		ATGCTCGTGGCATCATCTTCACTCTAG		MLVASSSL*		MLVASSSL*		TTGACGATCT	TCCACAGCAT	0	TU	0	0	0	0	0
10128	4381	an	AN0317.1	54.m06441	AO070334000015	0	-95	-81					ATGCTCGTCAACTGA	ATGCTCGTCAACTGA			MLVN*	MLVN*			CCGACCATCT	CATCTGTCCC	0	TU	0	0	0	0	0
10130	4381	ao	AN0317.1	54.m06441	AO070334000015	0					-116	-93	ATGCCCGTGGCATCTTCTGGATAA			ATGCCCGTGGCATCTTCTGGATAA	MPVASSG*			MPVASSG*	TTGGCCATCC	GCTGACAGCC	0	TU	0	0	0	0	0
10133	4382	af	AN0302.1	54.m06459	AO070334000037	0			-176	-18			ATGCGCGCCTCATCTAACCTTCGATTTCGACAGAGAACCCTCACCAATGCGAAAAGTTGCATTCACGAAGTATTACAGCGACTCCGGATAGATGAACTGAATGGAACATATTCCTCTATACAGAAGAATATCTCCTTATCTCGGATTCCAACGCCTTGA		ATGCGCGCCTCATCTAACCTTCGATTTCGACAGAGAACCCTCACCAATGCGAAAAGTTGCATTCACGAAGTATTACAGCGACTCCGGATAGATGAACTGAATGGAACATATTCCTCTATACAGAAGAATATCTCCTTATCTCGGATTCCAACGCCTTGA		MRASSNLRFRQRTLTNAKSCIHEVLQRLRIDELNGTYSSIQKNISLSRIPTP*		MRASSNLRFRQRTLTNAKSCIHEVLQRLRIDELNGTYSSIQKNISLSRIPTP*		TCACAGTTTT	AGCCCTTGTC	0	Y	0	0	0	0	0
10134	4382	af	AN0302.1	54.m06459	AO070334000037	0			-130	-86			ATGCGAAAAGTTGCATTCACGAAGTATTACAGCGACTCCGGATAG		ATGCGAAAAGTTGCATTCACGAAGTATTACAGCGACTCCGGATAG		MRKVAFTKYYSDSG*		MRKVAFTKYYSDSG*		ACCCTCACCA	ATGAACTGAA	0	Y	0	0	0	0	0
10131	4382	an	AN0302.1	54.m06459	AO070334000037	0	-141	-127					ATGCGCTCTCGTTGA	ATGCGCTCTCGTTGA			MRSR*	MRSR*			CTTGTTCTTG	CTTGCCGACC	0	Y	0	0	0	0	0
10132	4382	an	AN0302.1	54.m06459	AO070334000037	0	-98	-69					ATGAGTTTATTGTTCTCTACGCCTGGATAA	ATGAGTTTATTGTTCTCTACGCCTGGATAA			MSLLFSTPG*	MSLLFSTPG*			TCCCGGTTGA	ATACTCCGCC	0	Y	0	0	0	0	0
10135	4384	af	AN2898.1	59.m08748	AO070338000110	0			-242	-144			ATGCGCATCGGAGATCGAGCAAGCCTCAAAACACCGATATTCTTTCAGGAACTCAGGGTCTCAGTTCCGTTCGTCGCAACCTTCAAACCTACCCTCTGA		ATGCGCATCGGAGATCGAGCAAGCCTCAAAACACCGATATTCTTTCAGGAACTCAGGGTCTCAGTTCCGTTCGTCGCAACCTTCAAACCTACCCTCTGA		MRIGDRASLKTPIFFQELRVSVPFVATFKPTL*		MRIGDRASLKTPIFFQELRVSVPFVATFKPTL*		CGATTGGCGC	TCTTCGCGTC	0	B	0	0	0	0	0
10136	4386	ao	AN3731.1	69.m15388	AO070342000286	0					-87	-76	ATGTCATACTAA			ATGTCATACTAA	MSY*			MSY*	GGTACTTGAC	ACTCCGACCA	0	S	0	0	0	0	0
10137	4387	an	AN2136.1	72.m19704	AO070343000181	0	-150	-49					ATGGATTCTGCCCATACCCTATTCCTGCCGTCTCCCTCTACCTTGAACCTCCCCACCCTCGACTTGTCCTCTCGACCAACGAACAGCCGGTTGATCCTATAA	ATGGATTCTGCCCATACCCTATTCCTGCCGTCTCCCTCTACCTTGAACCTCCCCACCCTCGACTTGTCCTCTCGACCAACGAACAGCCGGTTGATCCTATAA			MDSAHTLFLPSPSTLNLPTLDLSSRPTNSRLIL*	MDSAHTLFLPSPSTLNLPTLDLSSRPTNSRLIL*			GTAGGTTTGG	TCCATGTAGT	0		FG07133.1	MG07063.1	NCU01243.1	0	0
10138	4387	ao	AN2136.1	72.m19704	AO070343000181	0					-166	-56	ATGGATATTGCCCATACCCTCCCTCCCTCCTGGCCGCTCTCTCTGCCTCTTGCCTCTTCCCCACCCTCGCCGCCGGGTCCACTCTCGCACCCTATTCGAACATTCGATTAA			ATGGATATTGCCCATACCCTCCCTCCCTCCTGGCCGCTCTCTCTGCCTCTTGCCTCTTCCCCACCCTCGCCGCCGGGTCCACTCTCGCACCCTATTCGAACATTCGATTAA	MDIAHTLPPSWPLSLPLASSPPSPPGPLSHPIRTFD*			MDIAHTLPPSWPLSLPLASSPPSPPGPLSHPIRTFD*	GTAGGTTTGG	TCGAATCATT	0		FG07133.1	MG07063.1	NCU01243.1	0	0
10141	4392	af	AN6369.1	72.m19491	AO070279000072	0			-178	-65			ATGAAATTTTGTCGACTGTGGCTGCGAACCATTGATCTCATCACACATCGATCCTTGTTTTATTTAAGTTTGAGAATCCTTCAAAAATGTCTCAATCCCCTCCGTTGTCTTTAG		ATGAAATTTTGTCGACTGTGGCTGCGAACCATTGATCTCATCACACATCGATCCTTGTTTTATTTAAGTTTGAGAATCCTTCAAAAATGTCTCAATCCCCTCCGTTGTCTTTAG		MKFCRLWLRTIDLITHRSLFYLSLRILQKCLNPLRCL*		MKFCRLWLRTIDLITHRSLFYLSLRILQKCLNPLRCL*		AATAAGCTCC	TCCTTCTGTC	0	Q	0	MG08918.1	NCU00290.1	0	0
10139	4392	an	AN6369.1	72.m19491	AO070279000072	0	-188	-39					ATGGATCTCCCCTGGTCCCTGCGAACTAGTACACGACTGGAATTTCAAGGTTTCTTTACTCTGTACTCGAATTCGAGTCAAATGCGTGGACATCGACGCTTGCAAGGCCTGTTTTCATCAAGGACAAACATCTGCCCTGAATTTCTATAA	ATGGATCTCCCCTGGTCCCTGCGAACTAGTACACGACTGGAATTTCAAGGTTTCTTTACTCTGTACTCGAATTCGAGTCAAATGCGTGGACATCGACGCTTGCAAGGCCTGTTTTCATCAAGGACAAACATCTGCCCTGAATTTCTATAA			MDLPWSLRTSTRLEFQGFFTLYSNSSQMRGHRRLQGLFSSRTNICPEFL*	MDLPWSLRTSTRLEFQGFFTLYSNSSQMRGHRRLQGLFSSRTNICPEFL*			GGCAGATAAA	TCCTCCCACT	0	Q	0	MG08918.1	NCU00290.1	0	0
10140	4392	an	AN6369.1	72.m19491	AO070279000072	0	-107	-39					ATGCGTGGACATCGACGCTTGCAAGGCCTGTTTTCATCAAGGACAAACATCTGCCCTGAATTTCTATAA	ATGCGTGGACATCGACGCTTGCAAGGCCTGTTTTCATCAAGGACAAACATCTGCCCTGAATTTCTATAA			MRGHRRLQGLFSSRTNICPEFL*	MRGHRRLQGLFSSRTNICPEFL*			TTCGAGTCAA	TCCTCCCACT	0	Q	0	MG08918.1	NCU00290.1	0	0
10142	4392	ao	AN6369.1	72.m19491	AO070279000072	0					-171	-103	ATGACTGCACCTGACTCGCTTCTCGTTGGACACCGACAGGGATCCCGTCGCGGGTTGCCAACGCTCTAA			ATGACTGCACCTGACTCGCTTCTCGTTGGACACCGACAGGGATCCCGTCGCGGGTTGCCAACGCTCTAA	MTAPDSLLVGHRQGSRRGLPTL*			MTAPDSLLVGHRQGSRRGLPTL*	GATTAGATAC	AAATCCAACT	0	Q	0	MG08918.1	NCU00290.1	0	0
10145	4393	af	AN5155.1	54.m06863	AO070291000012	0			-214	-176			ATGCGAATCCATGGAAAGCCGCAACGGAACTGGCCATGA		ATGCGAATCCATGGAAAGCCGCAACGGAACTGGCCATGA		MRIHGKPQRNWP*		MRIHGKPQRNWP*		GTCTGGACAA	TCCAAACCAT	0	A	0	0	0	0	0
10146	4393	af	AN5155.1	54.m06863	AO070291000012	0			-204	-127			ATGGAAAGCCGCAACGGAACTGGCCATGATCCAAACCATGAAGTCATAATGGATCGGTGGTTTCTATACGAGAGGTAG		ATGGAAAGCCGCAACGGAACTGGCCATGATCCAAACCATGAAGTCATAATGGATCGGTGGTTTCTATACGAGAGGTAG		MESRNGTGHDPNHEVIMDRWFLYER*		MESRNGTGHDPNHEVIMDRWFLYER*		ATGCGAATCC	ATACTTTAGA	0	A	0	0	0	0	0
10147	4393	af	AN5155.1	54.m06863	AO070291000012	0			-179	-156			ATGATCCAAACCATGAAGTCATAA		ATGATCCAAACCATGAAGTCATAA		MIQTMKS*		MIQTMKS*		GGAACTGGCC	TGGATCGGTG	0	A	0	0	0	0	0
10148	4393	af	AN5155.1	54.m06863	AO070291000012	0			-167	-156			ATGAAGTCATAA		ATGAAGTCATAA		MKS*		MKS*		GATCCAAACC	TGGATCGGTG	0	A	0	0	0	0	0
10149	4393	af	AN5155.1	54.m06863	AO070291000012	0			-156	-127			ATGGATCGGTGGTTTCTATACGAGAGGTAG		ATGGATCGGTGGTTTCTATACGAGAGGTAG		MDRWFLYER*		MDRWFLYER*		TGAAGTCATA	ATACTTTAGA	0	A	0	0	0	0	0
10143	4393	an	AN5155.1	54.m06863	AO070291000012	0	-179	-105					ATGATCTTCATTCTCTCACAGCTATTCAGAAGAGTCGGCACTATTCAATGCGCAACTCCAAATGTCTTGATATAA	ATGATCTTCATTCTCTCACAGCTATTCAGAAGAGTCGGCACTATTCAATGCGCAACTCCAAATGTCTTGATATAA			MIFILSQLFRRVGTIQCATPNVLI*	MIFILSQLFRRVGTIQCATPNVLI*			CTGTCGCGGG	GTTAGCAGTC	0	A	0	0	0	0	0
10144	4393	an	AN5155.1	54.m06863	AO070291000012	0	-132	-100					ATGCGCAACTCCAAATGTCTTGATATAAGTTAG	ATGCGCAACTCCAAATGTCTTGATATAAGTTAG			MRNSKCLDIS*	MRNSKCLDIS*			GCACTATTCA	CAGTCGCAAC	0	A	0	0	0	0	0
10150	4393	ao	AN5155.1	54.m06863	AO070291000012	0					-210	-196	ATGGAAACATGTTGA			ATGGAAACATGTTGA	METC*			METC*	GCTGCGATCC	TCTCGACTTC	0	A	0	0	0	0	0
10151	4393	ao	AN5155.1	54.m06863	AO070291000012	0					-202	-89	ATGTTGATCTCGACTTCTCTATCAATCCTTCCCTCGATGGGACCCCGGCGATCAGAAACAATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG			ATGTTGATCTCGACTTCTCTATCAATCCTTCCCTCGATGGGACCCCGGCGATCAGAAACAATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG	MLISTSLSILPSMGPRRSETMQFLPLHGQKNVVNEIC*			MLISTSLSILPSMGPRRSETMQFLPLHGQKNVVNEIC*	CCATGGAAAC	CTCCCACACA	0	A	0	0	0	0	0
10152	4393	ao	AN5155.1	54.m06863	AO070291000012	0					-166	-89	ATGGGACCCCGGCGATCAGAAACAATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG			ATGGGACCCCGGCGATCAGAAACAATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG	MGPRRSETMQFLPLHGQKNVVNEIC*			MGPRRSETMQFLPLHGQKNVVNEIC*	CCTTCCCTCG	CTCCCACACA	0	A	0	0	0	0	0
10153	4393	ao	AN5155.1	54.m06863	AO070291000012	0					-142	-89	ATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG			ATGCAATTTCTGCCGCTGCACGGTCAGAAAAATGTTGTGAACGAAATCTGTTAG	MQFLPLHGQKNVVNEIC*			MQFLPLHGQKNVVNEIC*	ATCAGAAACA	CTCCCACACA	0	A	0	0	0	0	0
10156	4394	af	AN2049.1	58.m07637	AO070292000016	0			-217	-200			ATGCCATACCTTCGATGA		ATGCCATACCTTCGATGA		MPYLR*		MPYLR*		CATTACTTTC	TCTGTTCTCG	0	A	0	0	0	0	0
10157	4394	af	AN2049.1	58.m07637	AO070292000016	0			-203	-153			ATGATCTGTTCTCGCTTGAAAGCGTTTATGCTGTTTTTGTTTCTCAACTAA		ATGATCTGTTCTCGCTTGAAAGCGTTTATGCTGTTTTTGTTTCTCAACTAA		MICSRLKAFMLFLFLN*		MICSRLKAFMLFLFLN*		CATACCTTCG	CCCGACGCCA	0	A	0	0	0	0	0
10154	4394	an	AN2049.1	58.m07637	AO070292000016	0	-267	-226					ATGTTGACCTCGACCAACTATTCAAACTCTCAAAGTCAATGA	ATGTTGACCTCGACCAACTATTCAAACTCTCAAAGTCAATGA			MLTSTNYSNSQSQ*	MLTSTNYSNSQSQ*			GATAGCTTTG	GTCGAGGCCC	0	A	0	0	0	0	0
10162	4395	af	AN5614.1	58.m07537	AO070301000013	0			-202	-176			ATGCGTCATGAGATCTCAATAGACTGA		ATGCGTCATGAGATCTCAATAGACTGA		MRHEISID*		MRHEISID*		AGACTCGAGT	TTTATCTTCA	0		0	0	0	YNL279W	YNL279W
10161	4395	an	AN5614.1	58.m07537	AO070301000013	0	-195	-73					ATGCGGTATGAATTCTCAATAGATTGCATCTCAAATATATCCTACGACATAGGTGCTGCTGGCCAGCGTTTTTTACAATCCCGAGATACTTATTTTCCTCCCTCCGCGGTCATCAGTCTTTAA	ATGCGGTATGAATTCTCAATAGATTGCATCTCAAATATATCCTACGACATAGGTGCTGCTGGCCAGCGTTTTTTACAATCCCGAGATACTTATTTTCCTCCCTCCGCGGTCATCAGTCTTTAA			MRYEFSIDCISNISYDIGAAGQRFLQSRDTYFPPSAVISL*	MRYEFSIDCISNISYDIGAAGQRFLQSRDTYFPPSAVISL*			GATAGATTTC	CGCTCGACAT	0		0	0	0	YNL279W	YNL279W
10160	4395	conserved	AN5614.1	58.m07537	AO070301000013	0	-188	-174	-195	-181	-219	-205	ATGrvwyyyCwwTAr	ATGAATTCTCAATAG	ATGAGATCTCAATAG	ATGGCTCTCCTTTAA	Mnsq*	MNSQ*	MRSQ*	MALL*	wbywTGyGky	wyTGhhyyhy	0		0	0	0	YNL279W	YNL279W
10163	4397	an	AN0077.1	71.m16046	AO070311000138	0	-146	-90					ATGGTGGGGCTAGAGATAACGTTGCTGCTACAATATATCTCCAACCTTGTCTTATAA	ATGGTGGGGCTAGAGATAACGTTGCTGCTACAATATATCTCCAACCTTGTCTTATAA			MVGLEITLLLQYISNLVL*	MVGLEITLLLQYISNLVL*			AAGAATGTAA	CCCAGAGCTC	0	QR	0	MG08311.1	0	0	0
10166	4398	af	AN4239.1	54.m06802	AO070324000175	0			-175	-158			ATGATTATATATGCCTGA		ATGATTATATATGCCTGA		MIIYA*		MIIYA*		GCACGTGGCA	GGCATACAAC	0		FG01193.1	0	0	0	0
10167	4398	af	AN4239.1	54.m06802	AO070324000175	0			-165	-7			ATGCCTGAGGCATACAACGCGTGGCGCGCTGTCCGGAAAAAAGAAACCCCGTGCAGCTCACAAGTCGCAATGGATCCAAGTGAGGCTGTCCCTGGGGATAGATCCCGTTACCAGCATCGGGCCATCTTAAGGTTCACTGTATTGGACGTCATCACTTGA		ATGCCTGAGGCATACAACGCGTGGCGCGCTGTCCGGAAAAAAGAAACCCCGTGCAGCTCACAAGTCGCAATGGATCCAAGTGAGGCTGTCCCTGGGGATAGATCCCGTTACCAGCATCGGGCCATCTTAAGGTTCACTGTATTGGACGTCATCACTTGA		MPEAYNAWRAVRKKETPCSSQVAMDPSEAVPGDRSRYQHRAILRFTVLDVIT*		MPEAYNAWRAVRKKETPCSSQVAMDPSEAVPGDRSRYQHRAILRFTVLDVIT*		ATGATTATAT	GCTACAATGG	0		FG01193.1	0	0	0	0
10168	4398	af	AN4239.1	54.m06802	AO070324000175	0			-96	-7			ATGGATCCAAGTGAGGCTGTCCCTGGGGATAGATCCCGTTACCAGCATCGGGCCATCTTAAGGTTCACTGTATTGGACGTCATCACTTGA		ATGGATCCAAGTGAGGCTGTCCCTGGGGATAGATCCCGTTACCAGCATCGGGCCATCTTAAGGTTCACTGTATTGGACGTCATCACTTGA		MDPSEAVPGDRSRYQHRAILRFTVLDVIT*		MDPSEAVPGDRSRYQHRAILRFTVLDVIT*		ACAAGTCGCA	GCTACAATGG	0		FG01193.1	0	0	0	0
10165	4398	an	AN4239.1	54.m06802	AO070324000175	0	-143	-120					ATGACTTGCATTTTGGAAAAATGA	ATGACTTGCATTTTGGAAAAATGA			MTCILEK*	MTCILEK*			GAATTATCAC	ATTTCCGTGA	0		FG01193.1	0	0	0	0
10170	4399	af	AN0463.1	54.m06605	AO070328000174	0			-188	-6			ATGCCTAGAGGTGACTACTCGCATGTAGCGACCCCTCCTCATTCCTTCGATCGGGAAGATTACGTATCACACTCTCAGATACCGATCCGTTGCTCGCCTCCATCGATTGGCGCACTGCCCCTCGTTTCTCGAACGGCCGTTGAAAACCACTGCGGGGCTTGCCCTGTGTCGCTCCCTTCATAG		ATGCCTAGAGGTGACTACTCGCATGTAGCGACCCCTCCTCATTCCTTCGATCGGGAAGATTACGTATCACACTCTCAGATACCGATCCGTTGCTCGCCTCCATCGATTGGCGCACTGCCCCTCGTTTCTCGAACGGCCGTTGAAAACCACTGCGGGGCTTGCCCTGTGTCGCTCCCTTCATAG		MPRGDYSHVATPPHSFDREDYVSHSQIPIRCSPPSIGALPLVSRTAVENHCGACPVSLPS*		MPRGDYSHVATPPHSFDREDYVSHSQIPIRCSPPSIGALPLVSRTAVENHCGACPVSLPS*		GTCGAGACAT	CAGATATGCC	0	T	0	0	0	0	0
10169	4399	an	AN0463.1	54.m06605	AO070328000174	0	-147	-88					ATGTCGCGGCTTGTCCCCTTGATCAAACCAGAATTCCTGCTTTCTTTCTGCCTCCGCTGA	ATGTCGCGGCTTGTCCCCTTGATCAAACCAGAATTCCTGCTTTCTTTCTGCCTCCGCTGA			MSRLVPLIKPEFLLSFCLR*	MSRLVPLIKPEFLLSFCLR*			GGATTACTGC	ACCGCTGCCC	0	T	0	0	0	0	0
10171	4400	ao	AN0279.1	54.m06503	AO070334000092	0					-189	-73	ATGTCAACCTTCCCCGCCCCGTGTCTTGATTTTAATTACTGGAACTCCCGCATCTTTATTACTTGGTCGTCACTACTTCCAATTACTTGTCCCCTTCTCTTACTTATACCCATCTAA			ATGTCAACCTTCCCCGCCCCGTGTCTTGATTTTAATTACTGGAACTCCCGCATCTTTATTACTTGGTCGTCACTACTTCCAATTACTTGTCCCCTTCTCTTACTTATACCCATCTAA	MSTFPAPCLDFNYWNSRIFITWSSLLPITCPLLLLIPI*			MSTFPAPCLDFNYWNSRIFITWSSLLPITCPLLLLIPI*	ATTATATTAA	CCGACTGTCA	0	K	0	0	0	0	0
10172	4401	af	AN1562.1	55.m03078	AO070339000292	0			-119	-39			ATGGGGTTGTTCCGCACAGTCGACAATCTCGACATACGCGGACTCCGTATGGAGTGCAGCGTGTCGCGTCACCCGTTCTAA		ATGGGGTTGTTCCGCACAGTCGACAATCTCGACATACGCGGACTCCGTATGGAGTGCAGCGTGTCGCGTCACCCGTTCTAA		MGLFRTVDNLDIRGLRMECSVSRHPF*		MGLFRTVDNLDIRGLRMECSVSRHPF*		CTTAAATACG	AGCAGAGTCA	0		0	0	0	0	0
10173	4401	af	AN1562.1	55.m03078	AO070339000292	0			-71	-39			ATGGAGTGCAGCGTGTCGCGTCACCCGTTCTAA		ATGGAGTGCAGCGTGTCGCGTCACCCGTTCTAA		MECSVSRHPF*		MECSVSRHPF*		CGGACTCCGT	AGCAGAGTCA	0		0	0	0	0	0
10174	4401	ao	AN1562.1	55.m03078	AO070339000292	0					-129	-61	ATGATTATTGCGACCCATACCCCGGGATTCTATTGGGAAAGTGGGAGCGTCCGTCCCCTGCATATATAG			ATGATTATTGCGACCCATACCCCGGGATTCTATTGGGAAAGTGGGAGCGTCCGTCCCCTGCATATATAG	MIIATHTPGFYWESGSVRPLHI*			MIIATHTPGFYWESGSVRPLHI*	CAGGGAAACA	GGCCTCCCCC	0		0	0	0	0	0
10175	4405	ao	AN0837.1	70.m15437	AO070255000006	0					-182	-165	ATGCCCAATAATTATTGA			ATGCCCAATAATTATTGA	MPNNY*			MPNNY*	GGTTAATTAT	CCTTCTCCTT	0	A	0	0	0	0	0
10180	4406	af	AN5829.1	72.m18956	AO070260000017	0			-132	-112			ATGCCGTATGAACTGCTTTGA		ATGCCGTATGAACTGCTTTGA		MPYELL*		MPYELL*		AGATCGACGG	TCAGATCTTG	0	Z	0	0	0	0	0

10181	4406	af	AN5829.1	72.m18956	AO070260000017	0			-125	-6			ATGAACTGCTTTGATCAGATCTTGTGGGAACGGGCCGGACTGCTCTGCGCTGGTCAACTTCCGATCCCCTTTGTGTTGATGGTTGAAAGCTACGACTCGTCTGTTCCGTCTGAAAGATAG		ATGAACTGCTTTGATCAGATCTTGTGGGAACGGGCCGGACTGCTCTGCGCTGGTCAACTTCCGATCCCCTTTGTGTTGATGGTTGAAAGCTACGACTCGTCTGTTCCGTCTGAAAGATAG		MNCFDQILWERAGLLCAGQLPIPFVLMVESYDSSVPSER*		MNCFDQILWERAGLLCAGQLPIPFVLMVESYDSSVPSER*		CGGATGCCGT	GATTCATGGC	0	Z	0	0	0	0	0
10176	4406	an	AN5829.1	72.m18956	AO070260000017	0	-236	-222					ATGCTTCCAGAATAG	ATGCTTCCAGAATAG			MLPE*	MLPE*			TAACTAGCTC	AAACAGCGGC	0	Z	0	0	0	0	0
10177	4406	an	AN5829.1	72.m18956	AO070260000017	0	-202	-170					ATGATAATCACTGCTGCTGGCCAGCCCCGTTGA	ATGATAATCACTGCTGCTGGCCAGCCCCGTTGA			MIITAAGQPR*	MIITAAGQPR*			CAAGGCCTTG	AATCTCGACT	0	Z	0	0	0	0	0
10178	4406	an	AN5829.1	72.m18956	AO070260000017	0	-107	-93					ATGGAAGCTTTCTAA	ATGGAAGCTTTCTAA			MEAF*	MEAF*			GGTATAGTCA	CACGACGGTC	0	Z	0	0	0	0	0
10179	4406	an	AN5829.1	72.m18956	AO070260000017	0	-67	-20					ATGAGAGCCGACGATTGCAGCTCTGACAGAGACCTTGTTGCACTGTGA	ATGAGAGCCGACGATTGCAGCTCTGACAGAGACCTTGTTGCACTGTGA			MRADDCSSDRDLVAL*	MRADDCSSDRDLVAL*			GCGCGTGTGC	TGGTCTAACT	0	Z	0	0	0	0	0
10183	4406	ao	AN5829.1	72.m18956	AO070260000017	0					-104	-90	ATGGACCCCGCATAG			ATGGACCCCGCATAG	MDPA*			MDPA*	GAAAGGTCAA	CGCAGCGCTT	0	Z	0	0	0	0	0
10186	4408	af	AN2442.1	69.m15216	AO070264000033	0			-271	-179			ATGTCAACTGGAACAAGGCCCTGTCCAACGAACAACCTTACATCAGCCACGCTGCTGGTACAATGTATCTCAACATCATCTCCTCTTGACTGA		ATGTCAACTGGAACAAGGCCCTGTCCAACGAACAACCTTACATCAGCCACGCTGCTGGTACAATGTATCTCAACATCATCTCCTCTTGACTGA		MSTGTRPCPTNNLTSATLLVQCISTSSPLD*		MSTGTRPCPTNNLTSATLLVQCISTSSPLD*		TGATATCTCC	CTCTTAGATG	0		0	0	0	0	0
10187	4408	af	AN2442.1	69.m15216	AO070264000033	0			-209	-183			ATGTATCTCAACATCATCTCCTCTTGA		ATGTATCTCAACATCATCTCCTCTTGA		MYLNIISS*		MYLNIISS*		TGCTGGTACA	CTGACTCTTA	0		0	0	0	0	0
10188	4408	af	AN2442.1	69.m15216	AO070264000033	0			-171	-103			ATGAGCAGAGCCCTTTGTCATGTTTTGTTGAAGATAAACCTTTTGTCTCTTTGTATTGCGAACCGATGA		ATGAGCAGAGCCCTTTGTCATGTTTTGTTGAAGATAAACCTTTTGTCTCTTTGTATTGCGAACCGATGA		MSRALCHVLLKINLLSLCIANR*		MSRALCHVLLKINLLSLCIANR*		TGACTCTTAG	TCTCATCCTC	0		0	0	0	0	0
10189	4408	af	AN2442.1	69.m15216	AO070264000033	0			-152	-141			ATGTTTTGTTGA		ATGTTTTGTTGA		MFC*		MFC*		GCCCTTTGTC	AGATAAACCT	0		0	0	0	0	0
10190	4408	af	AN2442.1	69.m15216	AO070264000033	0			-106	-20			ATGATCTCATCCTCTCCAAGTGGCCAGTGTTGGGAGGCTTCTTCTAGTTTACGACGCCTCCTCATTTGGTCAGGATCTGCCTTTTGA		ATGATCTCATCCTCTCCAAGTGGCCAGTGTTGGGAGGCTTCTTCTAGTTTACGACGCCTCCTCATTTGGTCAGGATCTGCCTTTTGA		MISSSPSGQCWEASSSLRRLLIWSGSAF*		MISSSPSGQCWEASSSLRRLLIWSGSAF*		TTGCGAACCG	CAGAAGTCAA	0		0	0	0	0	0
10184	4408	an	AN2442.1	69.m15216	AO070264000033	0	-133	-122					ATGGTCTTCTGA	ATGGTCTTCTGA			MVF*	MVF*			TCAGAGGCAT	ATAGTCATAT	0		0	0	0	0	0
10185	4408	an	AN2442.1	69.m15216	AO070264000033	0	-108	-94					ATGCATACTCGCTGA	ATGCATACTCGCTGA			MHTR*	MHTR*			GTCATATATC	CTGTGCTATC	0		0	0	0	0	0
10191	4408	ao	AN2442.1	69.m15216	AO070264000033	0					-169	-140	ATGATGCACTCAGAATTTCCGTCATTCTGA			ATGATGCACTCAGAATTTCCGTCATTCTGA	MMHSEFPSF*			MMHSEFPSF*	GTTCTAGGAC	TACCATTATA	0		0	0	0	0	0
10192	4408	ao	AN2442.1	69.m15216	AO070264000033	0					-166	-140	ATGCACTCAGAATTTCCGTCATTCTGA			ATGCACTCAGAATTTCCGTCATTCTGA	MHSEFPSF*			MHSEFPSF*	CTAGGACATG	TACCATTATA	0		0	0	0	0	0
10193	4408	ao	AN2442.1	69.m15216	AO070264000033	0					-76	-62	ATGTCTTGTACTTGA			ATGTCTTGTACTTGA	MSCT*			MSCT*	CTCGCCGCGA	CGCCTGAACT	0		0	0	0	0	0
10195	4412	af	AN4473.1	58.m07846	AO070305000112	0			-163	-92			ATGCTCGACTATCAAATGGCTTATCATCGCCATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAA		ATGCTCGACTATCAAATGGCTTATCATCGCCATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAA		MLDYQMAYHRHAGGIPTDQPRYI*		MLDYQMAYHRHAGGIPTDQPRYI*		ACTAGCTCAA	TGGTAGCCAG	0	R	0	MG10414.1	0	0	0
10196	4412	af	AN4473.1	58.m07846	AO070305000112	0			-148	-92			ATGGCTTATCATCGCCATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAA		ATGGCTTATCATCGCCATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAA		MAYHRHAGGIPTDQPRYI*		MAYHRHAGGIPTDQPRYI*		CGACTATCAA	TGGTAGCCAG	0	R	0	MG10414.1	0	0	0
10197	4412	af	AN4473.1	58.m07846	AO070305000112	0			-132	-31			ATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAATGGTAGCCAGGTGCCCCATGAATATGATCCATGGAGGCAAGAAAACGAACCTGGGGTATAA		ATGCTGGGGGAATCCCCACTGATCAGCCACGTTATATATAATGGTAGCCAGGTGCCCCATGAATATGATCCATGGAGGCAAGAAAACGAACCTGGGGTATAA		MLGESPLISHVIYNGSQVPHEYDPWRQENEPGV*		MLGESPLISHVIYNGSQVPHEYDPWRQENEPGV*		TATCATCGCC	CAAAAACTGG	0	R	0	MG10414.1	0	0	0
10194	4412	an	AN4473.1	58.m07846	AO070305000112	0	-145	-119					ATGATATACCGGCGTCATCCAAGCTGA	ATGATATACCGGCGTCATCCAAGCTGA			MIYRRHPS*	MIYRRHPS*			GCATTGACAG	GCCGATACCC	0	R	0	MG10414.1	0	0	0
10198	4412	ao	AN4473.1	58.m07846	AO070305000112	0					-247	-182	ATGATTGGGGTCATTGCGCTGAGAGACTTTCGCCAGTTGCGCGGCCTTGGTAGCTATATAACATAG			ATGATTGGGGTCATTGCGCTGAGAGACTTTCGCCAGTTGCGCGGCCTTGGTAGCTATATAACATAG	MIGVIALRDFRQLRGLGSYIT*			MIGVIALRDFRQLRGLGSYIT*	TATCGGCGCC	CAATACCATC	0	R	0	MG10414.1	0	0	0
10200	4413	an	AN4486.1	57.m05645	AO070311000037	0	-209	-171					ATGCTTTTCACTTATCGGTCTCGAGCAATCCCGCATTAA	ATGCTTTTCACTTATCGGTCTCGAGCAATCCCGCATTAA			MLFTYRSRAIPH*	MLFTYRSRAIPH*			GCGCAATCGC	TCATTACACC	0		0	0	0	0	0
10203	4417	af	AN2852.1	59.m08695	AO070338000173	0			-142	-98			ATGACTCTTGTGGTAATCCTCCGATCTGCCCCTCGTGTGCGATAG		ATGACTCTTGTGGTAATCCTCCGATCTGCCCCTCGTGTGCGATAG		MTLVVILRSAPRVR*		MTLVVILRSAPRVR*		TGTGCCTTCC	GTCTTGCATC	0		0	0	0	0	0
10201	4417	an	AN2852.1	59.m08695	AO070338000173	0	-183	-172					ATGACTCGGTAA	ATGACTCGGTAA			MTR*	MTR*			TGTGCCTTCC	AGCTGTTTCC	0		0	0	0	0	0
10204	4417	ao	AN2852.1	59.m08695	AO070338000173	0					-230	-219	ATGAACCTGTGA			ATGAACCTGTGA	MNL*			MNL*	CTATTGCTCG	GAAACGTCAA	0		0	0	0	0	0
10205	4417	ao	AN2852.1	59.m08695	AO070338000173	0					-61	-38	ATGCTTCTACGCCGACCGCCTTAA			ATGCTTCTACGCCGACCGCCTTAA	MLLRRPP*			MLLRRPP*	GCTCCCTTGC	TCGATCCCGA	0		0	0	0	0	0
10211	4420	af	AN2083.1	57.m05782	AO070341000236	0			-182	-90			ATGTTGCCTAGAACTGGATATATGTGTGCACAGACCACTATCGATGTCATAGGGATCAGACGCGTCGACGACGCGAACCGCATCGCATTATGA		ATGTTGCCTAGAACTGGATATATGTGTGCACAGACCACTATCGATGTCATAGGGATCAGACGCGTCGACGACGCGAACCGCATCGCATTATGA		MLPRTGYMCAQTTIDVIGIRRVDDANRIAL*		MLPRTGYMCAQTTIDVIGIRRVDDANRIAL*		ACCTAGGCGA	CCCATCCGCA	0	S	0	0	0	0	0
10212	4420	af	AN2083.1	57.m05782	AO070341000236	0			-161	-90			ATGTGTGCACAGACCACTATCGATGTCATAGGGATCAGACGCGTCGACGACGCGAACCGCATCGCATTATGA		ATGTGTGCACAGACCACTATCGATGTCATAGGGATCAGACGCGTCGACGACGCGAACCGCATCGCATTATGA		MCAQTTIDVIGIRRVDDANRIAL*		MCAQTTIDVIGIRRVDDANRIAL*		AACTGGATAT	CCCATCCGCA	0	S	0	0	0	0	0
10213	4420	af	AN2083.1	57.m05782	AO070341000236	0			-93	-16			ATGACCCATCCGCAGCCGCAACTCTACTTAGACTCATGGTTTTGTTTCGTTCTTTTTAGTTCCAAAATACTAATATAG		ATGACCCATCCGCAGCCGCAACTCTACTTAGACTCATGGTTTTGTTTCGTTCTTTTTAGTTCCAAAATACTAATATAG		MTHPQPQLYLDSWFCFVLFSSKILI*		MTHPQPQLYLDSWFCFVLFSSKILI*		GCATCGCATT	CTACTTCGAT	0	S	0	0	0	0	0
10210	4420	an	AN2083.1	57.m05782	AO070341000236	0	-123	-40					ATGAACAGTTACCTAAATTATAGTGGTACGAGCTCTTGCCTTGATCCGACCAACCACTTTATTCAGGCCCATGCCTCGCCGTGA	ATGAACAGTTACCTAAATTATAGTGGTACGAGCTCTTGCCTTGATCCGACCAACCACTTTATTCAGGCCCATGCCTCGCCGTGA			MNSYLNYSGTSSCLDPTNHFIQAHASP*	MNSYLNYSGTSSCLDPTNHFIQAHASP*			TCGAGTCATA	AACCCACTCA	0	S	0	0	0	0	0
10215	4420	ao	AN2083.1	57.m05782	AO070341000236	0					-245	-219	ATGCAACATGGACGCTGTTTGCCTTAA			ATGCAACATGGACGCTGTTTGCCTTAA	MQHGRCLP*			MQHGRCLP*	CATCATACGA	GGTTCAGGCC	0	S	0	0	0	0	0
10216	4420	ao	AN2083.1	57.m05782	AO070341000236	0					-238	-98	ATGGACGCTGTTTGCCTTAAGGTTCAGGCCGTCAACAGTCCTATCCGAGTTAAATGGCCTTCTGTGCACAGACCACCCGTTTATGGTTTAGCGACGCGTCGTCGCGTTACCCCAGTCGACACAATCAATAAGCAGAGTTAG			ATGGACGCTGTTTGCCTTAAGGTTCAGGCCGTCAACAGTCCTATCCGAGTTAAATGGCCTTCTGTGCACAGACCACCCGTTTATGGTTTAGCGACGCGTCGTCGCGTTACCCCAGTCGACACAATCAATAAGCAGAGTTAG	MDAVCLKVQAVNSPIRVKWPSVHRPPVYGLATRRRVTPVDTINKQS*			MDAVCLKVQAVNSPIRVKWPSVHRPPVYGLATRRRVTPVDTINKQS*	CGAATGCAAC	CTAAGACAAC	0	S	0	0	0	0	0
10217	4420	ao	AN2083.1	57.m05782	AO070341000236	0					-185	-108	ATGGCCTTCTGTGCACAGACCACCCGTTTATGGTTTAGCGACGCGTCGTCGCGTTACCCCAGTCGACACAATCAATAA			ATGGCCTTCTGTGCACAGACCACCCGTTTATGGTTTAGCGACGCGTCGTCGCGTTACCCCAGTCGACACAATCAATAA	MAFCAQTTRLWFSDASSRYPSRHNQ*			MAFCAQTTRLWFSDASSRYPSRHNQ*	TCCGAGTTAA	GCAGAGTTAG	0	S	0	0	0	0	0
10219	4421	af	AN4112.1	54.m07047	AO070342000107	0			-279	-235			ATGATGATACCACGTGTGGTGGTGCTCTCACTCCGTCCTCTGTAG		ATGATGATACCACGTGTGGTGGTGCTCTCACTCCGTCCTCTGTAG		MMIPRVVVLSLRPL*		MMIPRVVVLSLRPL*		TGCTGATGAT	CAACTGACGT	0	Y	0	0	0	0	0
10220	4421	af	AN4112.1	54.m07047	AO070342000107	0			-276	-235			ATGATACCACGTGTGGTGGTGCTCTCACTCCGTCCTCTGTAG		ATGATACCACGTGTGGTGGTGCTCTCACTCCGTCCTCTGTAG		MIPRVVVLSLRPL*		MIPRVVVLSLRPL*		TGATGATATG	CAACTGACGT	0	Y	0	0	0	0	0
10218	4421	an	AN4112.1	54.m07047	AO070342000107	0	-183	-133					ATGACGTCAGCTCACCGCCTACCGATTCCGACATTTTATTTACACCGTTAG	ATGACGTCAGCTCACCGCCTACCGATTCCGACATTTTATTTACACCGTTAG			MTSAHRLPIPTFYLHR*	MTSAHRLPIPTFYLHR*			AGCGTGGACC	TTCGTCTCAA	0	Y	0	0	0	0	0
10221	4421	ao	AN4112.1	54.m07047	AO070342000107	0					-212	-195	ATGCTCCAGTCACGTTAG			ATGCTCCAGTCACGTTAG	MLQSR*			MLQSR*	CTGACATCAG	ATGAAATCAC	0	Y	0	0	0	0	0
10222	4421	ao	AN4112.1	54.m07047	AO070342000107	0					-194	-177	ATGAAATCACTCCACTGA			ATGAAATCACTCCACTGA	MKSLH*			MKSLH*	GTCACGTTAG	CGTCAGCTCA	0	Y	0	0	0	0	0
10223	4425	af	AN0846.1	70.m15445	AO070216000005	0			-172	-131			ATGCCTTGTTCTTCCCTGAACCTCTTTGAAATCTCTCACTGA		ATGCCTTGTTCTTCCCTGAACCTCTTTGAAATCTCTCACTGA		MPCSSLNLFEISH*		MPCSSLNLFEISH*		CGTGCCAGTC	TTTCTGTGAC	0		0	0	0	0	0
10224	4426	an	AN1356.1	70.m14874	AO070237000004	0	-224	-24					ATGGAGCGTGGGTGGAGCTATCATCTTGTCTTGAGAGCGAGACTGGGTGGTAAGGTATGTGGGGAGGTATATAAGAGGGACGACGAAGCTGAGTCCATTCAGATGTCTAATTATTTGATTGCCCTTTTATCCATCATTTTTTCTTTGTTAATCATTACCTCTTCTGATCTTTATACATTCATTGTCTGTATAGATCGATAG	ATGGAGCGTGGGTGGAGCTATCATCTTGTCTTGAGAGCGAGACTGGGTGGTAAGGTATGTGGGGAGGTATATAAGAGGGACGACGAAGCTGAGTCCATTCAGATGTCTAATTATTTGATTGCCCTTTTATCCATCATTTTTTCTTTGTTAATCATTACCTCTTCTGATCTTTATACATTCATTGTCTGTATAGATCGATAG			MERGWSYHLVLRARLGGKVCGEVYKRDDEAESIQMSNYLIALLSIIFSLLIITSSDLYTFIVCIDR*	MERGWSYHLVLRARLGGKVCGEVYKRDDEAESIQMSNYLIALLSIIFSLLIITSSDLYTFIVCIDR*			GATGAAGAAA	ACTCACTACT	0		0	0	0	0	0
10225	4426	an	AN1356.1	70.m14874	AO070237000004	0	-168	-151					ATGTGGGGAGGTATATAA	ATGTGGGGAGGTATATAA			MWGGI*	MWGGI*			GTGGTAAGGT	GAGGGACGAC	0		0	0	0	0	0
10226	4426	an	AN1356.1	70.m14874	AO070237000004	0	-122	-24					ATGTCTAATTATTTGATTGCCCTTTTATCCATCATTTTTTCTTTGTTAATCATTACCTCTTCTGATCTTTATACATTCATTGTCTGTATAGATCGATAG	ATGTCTAATTATTTGATTGCCCTTTTATCCATCATTTTTTCTTTGTTAATCATTACCTCTTCTGATCTTTATACATTCATTGTCTGTATAGATCGATAG			MSNYLIALLSIIFSLLIITSSDLYTFIVCIDR*	MSNYLIALLSIIFSLLIITSSDLYTFIVCIDR*			GTCCATTCAG	ACTCACTACT	0		0	0	0	0	0
10227	4426	ao	AN1356.1	70.m14874	AO070237000004	0					-144	-130	ATGTATATCCTGTAG			ATGTATATCCTGTAG	MYIL*			MYIL*	CGATATTGAC	TATATACATA	0		0	0	0	0	0
10228	4427	an	AN2509.1	59.m08475	AO070263000057	0	-205	-188					ATGAGCCGTTTATGGTAA	ATGAGCCGTTTATGGTAA			MSRLW*	MSRLW*			ACTCCTTCCG	TTTTGGTAGC	0		0	0	0	YJR078W	0
10229	4427	an	AN2509.1	59.m08475	AO070263000057	0	-194	-165					ATGGTAATTTTGGTAGCTTTGACCTGCTGA	ATGGTAATTTTGGTAGCTTTGACCTGCTGA			MVILVALTC*	MVILVALTC*			TGAGCCGTTT	GACTATTGTC	0		0	0	0	YJR078W	0
10230	4427	an	AN2509.1	59.m08475	AO070263000057	0	-140	-105					ATGAGTTCCTGGCCCAATTTGTCTACTGCAAGTTGA	ATGAGTTCCTGGCCCAATTTGTCTACTGCAAGTTGA			MSSWPNLSTAS*	MSSWPNLSTAS*			ACTTGTGTTC	GGTCTCACCT	0		0	0	0	YJR078W	0
10231	4427	ao	AN2509.1	59.m08475	AO070263000057	0					-216	-184	ATGTATGTTCTTCCCTACTCTCTGGCCACCTAG			ATGTATGTTCTTCCCTACTCTCTGGCCACCTAG	MYVLPYSLAT*			MYVLPYSLAT*	GGCTTTAAGG	ACTGGTTTCC	0		0	0	0	YJR078W	0
10232	4427	ao	AN2509.1	59.m08475	AO070263000057	0					-212	-171	ATGTTCTTCCCTACTCTCTGGCCACCTAGACTGGTTTCCTGA			ATGTTCTTCCCTACTCTCTGGCCACCTAGACTGGTTTCCTGA	MFFPTLWPPRLVS*			MFFPTLWPPRLVS*	TTAAGGATGT	GACTAACCCG	0		0	0	0	YJR078W	0
10234	4429	ao	AN7628.1	71.m15822	AO070294000038	0					-233	-219	ATGACTTTTGATTGA			ATGACTTTTGATTGA	MTFD*			MTFD*	AGGGGGCAAG	TTAAGCGGGA	0	A	0	0	0	0	0
10241	4430	af	AN4458.1	58.m07866	AO070305000135	0			-233	-147			ATGGAAATGACTCAAAAAGTAGATACTCTCCTGAGCTCAGAAGTCCACCTGAGGACTCTTGAGCAGAACGTGATAACTGGTGAATAA		ATGGAAATGACTCAAAAAGTAGATACTCTCCTGAGCTCAGAAGTCCACCTGAGGACTCTTGAGCAGAACGTGATAACTGGTGAATAA		MEMTQKVDTLLSSEVHLRTLEQNVITGE*		MEMTQKVDTLLSSEVHLRTLEQNVITGE*		ATAGGGACCA	TGGGAAGCGC	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10242	4430	af	AN4458.1	58.m07866	AO070305000135	0			-227	-147			ATGACTCAAAAAGTAGATACTCTCCTGAGCTCAGAAGTCCACCTGAGGACTCTTGAGCAGAACGTGATAACTGGTGAATAA		ATGACTCAAAAAGTAGATACTCTCCTGAGCTCAGAAGTCCACCTGAGGACTCTTGAGCAGAACGTGATAACTGGTGAATAA		MTQKVDTLLSSEVHLRTLEQNVITGE*		MTQKVDTLLSSEVHLRTLEQNVITGE*		ACCAATGGAA	TGGGAAGCGC	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10243	4430	af	AN4458.1	58.m07866	AO070305000135	0			-147	-115			ATGGGAAGCGCATTGGTGACGCTGCATGTTTGA		ATGGGAAGCGCATTGGTGACGCTGCATGTTTGA		MGSALVTLHV*		MGSALVTLHV*		CTGGTGAATA	CATGTTTGCA	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10235	4430	an	AN4458.1	58.m07866	AO070305000135	0	-248	-234					ATGGCTGCTAGGTAG	ATGGCTGCTAGGTAG			MAAR*	MAAR*			TCGGCCGAGG	ACAATAAATG	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10236	4430	an	AN4458.1	58.m07866	AO070305000135	0	-216	-178					ATGACACGTATTCAGAGCCAAAAATGTCTATATAATTAA	ATGACACGTATTCAGAGCCAAAAATGTCTATATAATTAA			MTRIQSQKCLYN*	MTRIQSQKCLYN*			ATGAAATGAC	TCCAAAAAAC	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10237	4430	an	AN4458.1	58.m07866	AO070305000135	0	-193	-182					ATGTCTATATAA	ATGTCTATATAA			MSI*	MSI*			AGAGCCAAAA	TTAATCCAAA	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10238	4430	an	AN4458.1	58.m07866	AO070305000135	0	-162	-118					ATGGTTTTGCTAAAGCTTCAAGTGAGCTCCGCTGTCGAGCAATGA	ATGGTTTTGCTAAAGCTTCAAGTGAGCTCCGCTGTCGAGCAATGA			MVLLKLQVSSAVEQ*	MVLLKLQVSSAVEQ*			AAAACGCGGG	TGCAAGACGA	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10239	4430	an	AN4458.1	58.m07866	AO070305000135	0	-121	-62					ATGATGCAAGACGAACTGTGTTTGTCCTGTTTGCATGCGTCCCTGGGTCTTCCGCCGTGA	ATGATGCAAGACGAACTGTGTTTGTCCTGTTTGCATGCGTCCCTGGGTCTTCCGCCGTGA			MMQDELCLSCLHASLGLPP*	MMQDELCLSCLHASLGLPP*			CTGTCGAGCA	GGTTTTCCAT	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10240	4430	an	AN4458.1	58.m07866	AO070305000135	0	-118	-62					ATGCAAGACGAACTGTGTTTGTCCTGTTTGCATGCGTCCCTGGGTCTTCCGCCGTGA	ATGCAAGACGAACTGTGTTTGTCCTGTTTGCATGCGTCCCTGGGTCTTCCGCCGTGA			MQDELCLSCLHASLGLPP*	MQDELCLSCLHASLGLPP*			TCGAGCAATG	GGTTTTCCAT	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10244	4430	ao	AN4458.1	58.m07866	AO070305000135	0					-203	-192	ATGACCCTTTGA			ATGACCCTTTGA	MTL*			MTL*	ACTAAGAGAA	ACGTTTGCTT	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C

10245	4430	ao	AN4458.1	58.m07866	AO070305000135	0					-127	-23	ATGTATGACGCTGTATGTACCGGGTGTTTGTTATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAG			ATGTATGACGCTGTATGTACCGGGTGTTTGTTATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAG	MYDAVCTGCLLCLHSAAPSRLRSFQSRGARIFVS*			MYDAVCTGCLLCLHSAAPSRLRSFQSRGARIFVS*	TACGACTAAC	TTCACCTTTA	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10246	4430	ao	AN4458.1	58.m07866	AO070305000135	0					-113		ATGTACCGGGTGTTTGTTATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAGTTCACCTTTACACAGAGTCATGA			ATGTACCGGGTGTTTGTTATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAGTTCACCTTTACACAGAGTCATGA	MYRVFVMFALRGPIASSQLSIPRSQNLRFLVHLYTES*			MYRVFVMFALRGPIASSQLSIPRSQNLRFLVHLYTES*	ATGACGCTGT	TGTCCAAGAG	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10247	4430	ao	AN4458.1	58.m07866	AO070305000135	0					-95		ATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAGTTCACCTTTACACAGAGTCATGA			ATGTTTGCACTCCGCGGCCCCATCGCGTCTTCGCAGCTTTCAATCCCGCGGAGCCAGAATCTTCGTTTCTTAGTTCACCTTTACACAGAGTCATGA	MFALRGPIASSQLSIPRSQNLRFLVHLYTES*			MFALRGPIASSQLSIPRSQNLRFLVHLYTES*	GGTGTTTGTT	TGTCCAAGAG	0	Z	FG06789.1	MG08169.1	0	YFR005C	YFR005C
10248	4431	af	AN4253.1	65.m07425	AO070309000123	0			-249	-208			ATGTGCGGCTCTTGGCTCTCCTTCTGTCCATCCCTCCGCTGA		ATGTGCGGCTCTTGGCTCTCCTTCTGTCCATCCCTCCGCTGA		MCGSWLSFCPSLR*		MCGSWLSFCPSLR*		CTAGTGGGCG	ATTTTTCCCG	0		0	0	0	0	0
10249	4431	ao	AN4253.1	65.m07425	AO070309000123	0					-180	-106	ATGAAAATTTCCCGGAAGATCCTCACGCAACAATTACACCTAATCGAATTGAATGCTCTAACTCCTCTCAACTAA			ATGAAAATTTCCCGGAAGATCCTCACGCAACAATTACACCTAATCGAATTGAATGCTCTAACTCCTCTCAACTAA	MKISRKILTQQLHLIELNALTPLN*			MKISRKILTQQLHLIELNALTPLN*	CCAACTACGG	CTCGGTGTGT	0		0	0	0	0	0
10250	4436	af	AN6072.1	72.m19948	AO070340000116	0			-122	-108			ATGTACGTCTTCTGA		ATGTACGTCTTCTGA		MYVF*		MYVF*		AACACACAAC	TCCAGGATTC	0	E	0	MG09290.1	NCU08111.1	YDR465C	0
10251	4437	af	AN6081.1	72.m19926	AO070340000131	0			-159	-139			ATGCTGATTCCTTTAAATTGA		ATGCTGATTCCTTTAAATTGA		MLIPLN*		MLIPLN*		GCTACTATAT	TCGCTAATTT	0	ZR	0	0	0	0	0
10252	4438	an	AN5934.1	72.m19195	AO070340000336	0	-205	-59					ATGGGTAATTTATTCTGCCGTTTTTTTATGCGCTACGCTACTCTCGCGCGTGGCAAAGCCTAGGCGGTCTACAACCATTTCAACAGTCAACACCACATTCTTACTTTGGTGATATTAGTATGAACAGACATTTCAGGCCTGTTTAG	ATGGGTAATTTATTCTGCCGTTTTTTTATGCGCTACGCTACTCTCGCGCGTGGCAAAGCCTAGGCGGTCTACAACCATTTCAACAGTCAACACCACATTCTTACTTTGGTGATATTAGTATGAACAGACATTTCAGGCCTGTTTAG			MGNLFCRFFYALRYSRAWQSLGGLQPFQQSTPHSYFGDISMNRHFRPV*	MGNLFCRFFYALRYSRAWQSLGGLQPFQQSTPHSYFGDISMNRHFRPV*			CTAGACCTAT	AATATTCTCC	0	S	0	0	0	0	0
10253	4438	an	AN5934.1	72.m19195	AO070340000336	0	-177	-142					ATGCGCTACGCTACTCTCGCGCGTGGCAAAGCCTAG	ATGCGCTACGCTACTCTCGCGCGTGGCAAAGCCTAG			MRYATLARGKA*	MRYATLARGKA*			CGTTTTTTTT	GCGGTCTACA	0	S	0	0	0	0	0
10254	4438	an	AN5934.1	72.m19195	AO070340000336	0	-85	-59					ATGAACAGACATTTCAGGCCTGTTTAG	ATGAACAGACATTTCAGGCCTGTTTAG			MNRHFRPV*	MNRHFRPV*			TGATATTAGT	AATATTCTCC	0	S	0	0	0	0	0
10255	4438	ao	AN5934.1	72.m19195	AO070340000336	0					-187	-116	ATGCCAAAAGATACAGAAAACAACTACTCAGACAAGAAACCAACCCCACTATACCATCATAGAATGTACTGA			ATGCCAAAAGATACAGAAAACAACTACTCAGACAAGAAACCAACCCCACTATACCATCATAGAATGTACTGA	MPKDTENNYSDKKPTPLYHHRMY*			MPKDTENNYSDKKPTPLYHHRMY*	AGTAGGCGGT	CATTGCGTGC	0	S	0	0	0	0	0
10256	4438	ao	AN5934.1	72.m19195	AO070340000336	0					-82	-56	ATGAAACTACACCGTCTAGACACATAG			ATGAAACTACACCGTCTAGACACATAG	MKLHRLDT*			MKLHRLDT*	ATCAAAATTA	ATTCTATCCA	0	S	0	0	0	0	0
10262	4440	af	AN5206.1	69.m14903	AO070199000006	0			-170	-87			ATGCTCTGCTTGCACAGCTGTCATAGTATCCATTTCCCCGGCTATAGACCGCGGGTCAACATTCTTCCCGTGGTCGCATACTAG		ATGCTCTGCTTGCACAGCTGTCATAGTATCCATTTCCCCGGCTATAGACCGCGGGTCAACATTCTTCCCGTGGTCGCATACTAG		MLCLHSCHSIHFPGYRPRVNILPVVAY*		MLCLHSCHSIHFPGYRPRVNILPVVAY*		GAAGAAAACG	TCATACTAAT	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10257	4440	an	AN5206.1	69.m14903	AO070199000006	0	-225	-166					ATGCTATCCATTCCTATATCTCGCTGCAAGTTTATCGATACCGGATCGGAAGATCTATGA	ATGCTATCCATTCCTATATCTCGCTGCAAGTTTATCGATACCGGATCGGAAGATCTATGA			MLSIPISRCKFIDTGSEDL*	MLSIPISRCKFIDTGSEDL*			CAGGCTAGAT	GATATAGCCT	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10258	4440	an	AN5206.1	69.m14903	AO070199000006	0	-169	-152					ATGAGATATAGCCTGTAA	ATGAGATATAGCCTGTAA			MRYSL*	MRYSL*			CGGAAGATCT	ATGACAGTCG	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10259	4440	an	AN5206.1	69.m14903	AO070199000006	0	-151	-134					ATGACAGTCGGAAGATGA	ATGACAGTCGGAAGATGA			MTVGR*	MTVGR*			TAGCCTGTAA	ACGGGTTGCT	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10260	4440	an	AN5206.1	69.m14903	AO070199000006	0	-137	-27					ATGAACGGGTTGCTCAACCTGAAATCCCGATTCCTCGGCGATATGCCCGGATCATTATTCTTCCCGTCGCCATACAAAATCAATTCCCTCCGATTGCGGACGTTTTCCTAG	ATGAACGGGTTGCTCAACCTGAAATCCCGATTCCTCGGCGATATGCCCGGATCATTATTCTTCCCGTCGCCATACAAAATCAATTCCCTCCGATTGCGGACGTTTTCCTAG			MNGLLNLKSRFLGDMPGSLFFPSPYKINSLRLRTFS*	MNGLLNLKSRFLGDMPGSLFFPSPYKINSLRLRTFS*			CAGTCGGAAG	CCAGCAGGAA	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10261	4440	an	AN5206.1	69.m14903	AO070199000006	0	-95	-27					ATGCCCGGATCATTATTCTTCCCGTCGCCATACAAAATCAATTCCCTCCGATTGCGGACGTTTTCCTAG	ATGCCCGGATCATTATTCTTCCCGTCGCCATACAAAATCAATTCCCTCCGATTGCGGACGTTTTCCTAG			MPGSLFFPSPYKINSLRLRTFS*	MPGSLFFPSPYKINSLRLRTFS*			CCTCGGCGAT	CCAGCAGGAA	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10263	4440	ao	AN5206.1	69.m14903	AO070199000006	0					-178	-149	ATGCCGAACTCCTCCAATATGTTTCTGTAG			ATGCCGAACTCCTCCAATATGTTTCTGTAG	MPNSSNMFL*			MPNSSNMFL*	TTCCCCTTCA	TTCCGTTTGA	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10264	4440	ao	AN5206.1	69.m14903	AO070199000006	0					-160	-149	ATGTTTCTGTAG			ATGTTTCTGTAG	MFL*			MFL*	CTCCTCCAAT	TTCCGTTTGA	0	E	FG01392.1	MG01566.1	0	YIL094C	0
10265	4443	an	AN4410.1	58.m07898	AO070273000030	0	-189	-34					ATGTTCTCTCGCTTCCTTATATTACTCAGAGTATTGGAAATGGGGCAAATCGCACCCGGTGACTTTCACATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA	ATGTTCTCTCGCTTCCTTATATTACTCAGAGTATTGGAAATGGGGCAAATCGCACCCGGTGACTTTCACATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA			MFSRFLILLRVLEMGQIAPGDFHMSRMRSRPSQGRSRPNTPQPSTLLIPYS*	MFSRFLILLRVLEMGQIAPGDFHMSRMRSRPSQGRSRPNTPQPSTLLIPYS*			ACTAATTGAC	CCTCTATCCA	0	R	0	0	0	0	0
10266	4443	an	AN4410.1	58.m07898	AO070273000030	0	-150	-34					ATGGGGCAAATCGCACCCGGTGACTTTCACATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA	ATGGGGCAAATCGCACCCGGTGACTTTCACATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA			MGQIAPGDFHMSRMRSRPSQGRSRPNTPQPSTLLIPYS*	MGQIAPGDFHMSRMRSRPSQGRSRPNTPQPSTLLIPYS*			AGTATTGGAA	CCTCTATCCA	0	R	0	0	0	0	0
10267	4443	an	AN4410.1	58.m07898	AO070273000030	0	-120	-34					ATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA	ATGTCACGAATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA			MSRMRSRPSQGRSRPNTPQPSTLLIPYS*	MSRMRSRPSQGRSRPNTPQPSTLLIPYS*			TGACTTTCAC	CCTCTATCCA	0	R	0	0	0	0	0
10268	4443	an	AN4410.1	58.m07898	AO070273000030	0	-111	-34					ATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA	ATGCGGAGTCGTCCTAGCCAAGGTAGATCCAGGCCTAACACACCCCAACCCTCGACTCTCCTCATTCCATACTCTTGA			MRSRPSQGRSRPNTPQPSTLLIPYS*	MRSRPSQGRSRPNTPQPSTLLIPYS*			CATGTCACGA	CCTCTATCCA	0	R	0	0	0	0	0
10269	4443	ao	AN4410.1	58.m07898	AO070273000030	0					-149	-93	ATGTCACGGGCGGAGTTGCCGACAAAACAAGGCCAACAACCCTCCAAAATCTCATGA			ATGTCACGGGCGGAGTTGCCGACAAAACAAGGCCAACAACCCTCCAAAATCTCATGA	MSRAELPTKQGQQPSKIS*			MSRAELPTKQGQQPSKIS*	CCGCATTCAC	GCTGCTGCAT	0	R	0	0	0	0	0
10270	4443	ao	AN4410.1	58.m07898	AO070273000030	0					-96	-1	ATGAGCTGCTGCATCCATCATACCATTAATGAGCTTGCCACTCTCTTAGTGCCCTCTTCCTATATTTATTGCCCTCCGTGGCCCCAGGCAACCTAG			ATGAGCTGCTGCATCCATCATACCATTAATGAGCTTGCCACTCTCTTAGTGCCCTCTTCCTATATTTATTGCCCTCCGTGGCCCCAGGCAACCTAG	MSCCIHHTINELATLLVPSSYIYCPPWPQAT*			MSCCIHHTINELATLLVPSSYIYCPPWPQAT*	CCAAAATCTC	ATGGAGGTAT	0	R	0	0	0	0	0
10271	4443	ao	AN4410.1	58.m07898	AO070273000030	0					-68	-48	ATGAGCTTGCCACTCTCTTAG			ATGAGCTTGCCACTCTCTTAG	MSLPLS*			MSLPLS*	CATACCATTA	TGCCCTCTTC	0	R	0	0	0	0	0
10275	4444	af	AN1084.1	70.m15158	AO070285000084	0			-234	-130			ATGCTGTTTATCGTGGCGCGATCTAGGTATCCAGGTAGGTACATATCAAGTCCCAATGAGCGACCTCCGCAATCCCGCAGCTGTGATTGGGCGACTCATGACTAA		ATGCTGTTTATCGTGGCGCGATCTAGGTATCCAGGTAGGTACATATCAAGTCCCAATGAGCGACCTCCGCAATCCCGCAGCTGTGATTGGGCGACTCATGACTAA		MLFIVARSRYPGRYISSPNERPPQSRSCDWATHD*		MLFIVARSRYPGRYISSPNERPPQSRSCDWATHD*		GCCTACTGTG	GCAAACTCCC	0	J	FG07182.1	0	0	0	0
10272	4444	an	AN1084.1	70.m15158	AO070285000084	0	-214	-200					ATGGAGCGACTCTAG	ATGGAGCGACTCTAG			MERL*	MERL*			GGAACAAAGT	CATAGGACGG	0	J	FG07182.1	0	0	0	0
10273	4444	an	AN1084.1	70.m15158	AO070285000084	0	-156	-142					ATGCTCCGTTGCTGA	ATGCTCCGTTGCTGA			MLRC*	MLRC*			AACATCCGCA	TTGGTTAATA	0	J	FG07182.1	0	0	0	0
10274	4444	an	AN1084.1	70.m15158	AO070285000084	0	-130	-110					ATGACTAAGCACATCTCCTAA	ATGACTAAGCACATCTCCTAA			MTKHIS*	MTKHIS*			TGGTTAATAG	AATTTTCGGG	0	J	FG07182.1	0	0	0	0
10276	4444	ao	AN1084.1	70.m15158	AO070285000084	0					-203	-183	ATGTTCCATAATACTCCGTAG			ATGTTCCATAATACTCCGTAG	MFHNTP*			MFHNTP*	ACCCAAGTTG	TTGGATGGGG	0	J	FG07182.1	0	0	0	0
10277	4444	ao	AN1084.1	70.m15158	AO070285000084	0					-178	-146	ATGGGGAAAGCCTCCGCAATTCGGCACCTGTGA			ATGGGGAAAGCCTCCGCAATTCGGCACCTGTGA	MGKASAIRHL*			MGKASAIRHL*	CCGTAGTTGG	TTGGACAACA	0	J	FG07182.1	0	0	0	0
10278	4445	af	AN5108.1	54.m06914	AO070291000071	0			-229	-119			ATGACGCAATTCCTAATTCGAAACAGGAGATTAACGTTCTATGTTTGTCTTTCTTTAGGCCGCGAGTTTTCCTACATGCGATTCCGGAAGACAAAGGCTCGGAGTGTTTAG		ATGACGCAATTCCTAATTCGAAACAGGAGATTAACGTTCTATGTTTGTCTTTCTTTAGGCCGCGAGTTTTCCTACATGCGATTCCGGAAGACAAAGGCTCGGAGTGTTTAG		MTQFLIRNRRLTFYVCLSLGREFSYMRFRKTKARSV*		MTQFLIRNRRLTFYVCLSLGREFSYMRFRKTKARSV*		TTTTAGCTTC	CGCCCTCTAG	0	A	0	0	0	0	0
10279	4445	af	AN5108.1	54.m06914	AO070291000071	0			-189	-172			ATGTTTGTCTTTCTTTAG		ATGTTTGTCTTTCTTTAG		MFVFL*		MFVFL*		TTAACGTTCT	GCCGCGAGTT	0	A	0	0	0	0	0
10280	4445	af	AN5108.1	54.m06914	AO070291000071	0			-154	-119			ATGCGATTCCGGAAGACAAAGGCTCGGAGTGTTTAG		ATGCGATTCCGGAAGACAAAGGCTCGGAGTGTTTAG		MRFRKTKARSV*		MRFRKTKARSV*		GTTTTCCTAC	CGCCCTCTAG	0	A	0	0	0	0	0
10281	4445	ao	AN5108.1	54.m06914	AO070291000071	0					-257	-201	ATGTCTGTACGTATACAAGTTTTGATAACTGACCTTGTAGAAAGAGCATGGGTTTAG			ATGTCTGTACGTATACAAGTTTTGATAACTGACCTTGTAGAAAGAGCATGGGTTTAG	MSVRIQVLITDLVERAWV*			MSVRIQVLITDLVERAWV*	TTTTGATCTC	CTAATTGACC	0	A	0	0	0	0	0
10282	4445	ao	AN5108.1	54.m06914	AO070291000071	0					-210	-193	ATGGGTTTAGCTAATTGA			ATGGGTTTAGCTAATTGA	MGLAN*			MGLAN*	TAGAAAGAGC	CCAGGCGATC	0	A	0	0	0	0	0
10283	4445	ao	AN5108.1	54.m06914	AO070291000071	0					-176	-114	ATGCTCTTGCCCACTTTTTCCACGTCGGATTATCGTACAACGAACCCGCATGGGTCCCAGTGA			ATGCTCTTGCCCACTTTTTCCACGTCGGATTATCGTACAACGAACCCGCATGGGTCCCAGTGA	MLLPTFSTSDYRTTNPHGSQ*			MLLPTFSTSDYRTTNPHGSQ*	GATCGTTGTG	CTTGGACTTG	0	A	0	0	0	0	0
10284	4445	ao	AN5108.1	54.m06914	AO070291000071	0					-127	-80	ATGGGTCCCAGTGACTTGGACTTGAAGAAGACGGGAGTAACGAGATAG			ATGGGTCCCAGTGACTTGGACTTGAAGAAGACGGGAGTAACGAGATAG	MGPSDLDLKKTGVTR*			MGPSDLDLKKTGVTR*	ACGAACCCGC	CATATTCAAA	0	A	0	0	0	0	0
10286	4447	af	AN1639.1	58.m07718	AO070299000037	0			-170				ATGTCATGCATTCCTGGACTACAAGCACTGTTGATGCTGTCGGCGATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		ATGTCATGCATTCCTGGACTACAAGCACTGTTGATGCTGTCGGCGATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		MSCIPGLQALLMLSAMWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		MSCIPGLQALLMLSAMWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		CTCCAAACTA	TGTCGGGACT	0	O	0	0	0	0	0
10287	4447	af	AN1639.1	58.m07718	AO070299000037	0			-165	-106			ATGCATTCCTGGACTACAAGCACTGTTGATGCTGTCGGCGATGTGGAGGGGCTCAGCTGA		ATGCATTCCTGGACTACAAGCACTGTTGATGCTGTCGGCGATGTGGAGGGGCTCAGCTGA		MHSWTTSTVDAVGDVEGLS*		MHSWTTSTVDAVGDVEGLS*		AACTAATGTC	TGACATATTT	0	O	0	0	0	0	0
10288	4447	af	AN1639.1	58.m07718	AO070299000037	0			-137				ATGCTGTCGGCGATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		ATGCTGTCGGCGATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		MLSAMWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		MLSAMWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		AGCACTGTTG	TGTCGGGACT	0	O	0	0	0	0	0
10289	4447	af	AN1639.1	58.m07718	AO070299000037	0			-125				ATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		ATGTGGAGGGGCTCAGCTGATGACATATTTGGTCCAAAACAGAAAACCACCATATCCCTCTTTCCCACCGTCAACATCCTCCTTCCTCCATTCATCTCCCTGGCTGGTCAAATTCCGCCGCCATAA		MWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		MWRGSADDIFGPKQKTTISLFPTVNILLPPFISLAGQIPPP*		GCTGTCGGCG	TGTCGGGACT	0	O	0	0	0	0	0
10285	4447	an	AN1639.1	58.m07718	AO070299000037	0	-88	-11					ATGACATATCGAGATCCGAAGCTCTCGAGCTGTCAACATCATTCTTCTCCCAACTTTTTTCTCCGACATAAACTCTAA	ATGACATATCGAGATCCGAAGCTCTCGAGCTGTCAACATCATTCTTCTCCCAACTTTTTTCTCCGACATAAACTCTAA			MTYRDPKLSSCQHHSSPNFFLRHKL*	MTYRDPKLSSCQHHSSPNFFLRHKL*			GGAGGGGCTG	CTCCGTCACA	0	O	0	0	0	0	0
10293	4448	af	AN1614.1	58.m07709	AO070299000065	0			-113	-81			ATGCTTGCCCGTCTGCGTAGGATGACTCCATAA		ATGCTTGCCCGTCTGCGTAGGATGACTCCATAA		MLARLRRMTP*		MLARLRRMTP*		TCAACCCGGG	TAATAGATAT	0	IR	0	0	0	0	0
10294	4448	af	AN1614.1	58.m07709	AO070299000065	0			-92	-81			ATGACTCCATAA		ATGACTCCATAA		MTP*		MTP*		TCTGCGTAGG	TAATAGATAT	0	IR	0	0	0	0	0
10290	4448	an	AN1614.1	58.m07709	AO070299000065	0	-193	-176					ATGGTATCTCCGCTGTGA	ATGGTATCTCCGCTGTGA			MVSPL*	MVSPL*			TCGTCCCCGG	TGCTTAATGA	0	IR	0	0	0	0	0
10291	4448	an	AN1614.1	58.m07709	AO070299000065	0	-176	-156					ATGCTTAATGATAGACTCTAG	ATGCTTAATGATAGACTCTAG			MLNDRL*	MLNDRL*			CTCCGCTGTG	TCACATTCAT	0	IR	0	0	0	0	0

10292	4448	an	AN1614.1	58.m07709	AO070299000065	0	-169	-137					ATGATAGACTCTAGTCACATTCATAGACTCTAG	ATGATAGACTCTAGTCACATTCATAGACTCTAG			MIDSSHIHRL*	MIDSSHIHRL*			GTGATGCTTA	TCTCACTCAT	0	IR	0	0	0	0	0
10295	4448	ao	AN1614.1	58.m07709	AO070299000065	0					-179	-165	ATGCTTATAAATTGA			ATGCTTATAAATTGA	MLIN*			MLIN*	ATTCTTCGAG	CCGAGCCCCG	0	IR	0	0	0	0	0
10296	4448	ao	AN1614.1	58.m07709	AO070299000065	0					-115	-92	ATGGCTTATCTGACAGCAATATAG			ATGGCTTATCTGACAGCAATATAG	MAYLTAI*			MAYLTAI*	CCCATCTGGC	CTATTCTTAG	0	IR	0	0	0	0	0
10301	4449	af	AN6275.1	72.m19365	AO070304000006	0			-161	-117			ATGCGCAGCACTCTCCCCACCACAGTTGCACTCTTCTCCAGATAA		ATGCGCAGCACTCTCCCCACCACAGTTGCACTCTTCTCCAGATAA		MRSTLPTTVALFSR*		MRSTLPTTVALFSR*		TCCACATTAG	ATCACGCGCG	0		0	0	0	0	0
10297	4449	an	AN6275.1	72.m19365	AO070304000006	0	-237	-223					ATGATCGCTCTTTGA	ATGATCGCTCTTTGA			MIAL*	MIAL*			TACGATATCT	ATGTATTTAC	0		0	0	0	0	0
10298	4449	an	AN6275.1	72.m19365	AO070304000006	0	-222	-205					ATGTATTTACTCAAATGA	ATGTATTTACTCAAATGA			MYLLK*	MYLLK*			CGCTCTTTGA	ATCATTCAGA	0		0	0	0	0	0
10299	4449	an	AN6275.1	72.m19365	AO070304000006	0	-208	-122					ATGAATCATTCAGACTTCTGCCGCCATCGTTACGGATCATCTCAACCACTCCTTTTATTGTTTCACGGCCATACCTTGCACAACTGA	ATGAATCATTCAGACTTCTGCCGCCATCGTTACGGATCATCTCAACCACTCCTTTTATTGTTTCACGGCCATACCTTGCACAACTGA			MNHSDFCRHRYGSSQPLLLLFHGHTLHN*	MNHSDFCRHRYGSSQPLLLLFHGHTLHN*			ATTTACTCAA	CGTCGTATGT	0		0	0	0	0	0
10300	4449	an	AN6275.1	72.m19365	AO070304000006	0	-115	-68					ATGTTGCGCGAAGTCAGCATTGATATATCTCCCTCCCAATCCTGCTGA	ATGTTGCGCGAAGTCAGCATTGATATATCTCCCTCCCAATCCTGCTGA			MLREVSIDISPSQSC*	MLREVSIDISPSQSC*			CTGACGTCGT	GTATTATAAG	0		0	0	0	0	0
10302	4449	ao	AN6275.1	72.m19365	AO070304000006	0					-93	-40	ATGACAAGAGGACTATCGCCCATCTCGATTCGCACGAGACCCAACCAGTTTTAG			ATGACAAGAGGACTATCGCCCATCTCGATTCGCACGAGACCCAACCAGTTTTAG	MTRGLSPISIRTRPNQF*			MTRGLSPISIRTRPNQF*	ATTGGAGCGC	GGCCCACGAA	0		0	0	0	0	0
10305	4450	af	AN3746.1	65.m07388	AO070309000076	0			-144	-31			ATGCTGATGCAGACAGGTCGATTAGATTCCCCTCATAGAGCTTGCACATCCAGTGGGCGCTTGATATATCACTTTTCCCTCCCTGGCGTGTTTTTGCGATACCCCTTCAAGTGA		ATGCTGATGCAGACAGGTCGATTAGATTCCCCTCATAGAGCTTGCACATCCAGTGGGCGCTTGATATATCACTTTTCCCTCCCTGGCGTGTTTTTGCGATACCCCTTCAAGTGA		MLMQTGRLDSPHRACTSSGRLIYHFSLPGVFLRYPFK*		MLMQTGRLDSPHRACTSSGRLIYHFSLPGVFLRYPFK*		CGTGCTGACC	ATTGCTCCGC	0	T	0	0	0	0	0
10306	4450	af	AN3746.1	65.m07388	AO070309000076	0			-138	-31			ATGCAGACAGGTCGATTAGATTCCCCTCATAGAGCTTGCACATCCAGTGGGCGCTTGATATATCACTTTTCCCTCCCTGGCGTGTTTTTGCGATACCCCTTCAAGTGA		ATGCAGACAGGTCGATTAGATTCCCCTCATAGAGCTTGCACATCCAGTGGGCGCTTGATATATCACTTTTCCCTCCCTGGCGTGTTTTTGCGATACCCCTTCAAGTGA		MQTGRLDSPHRACTSSGRLIYHFSLPGVFLRYPFK*		MQTGRLDSPHRACTSSGRLIYHFSLPGVFLRYPFK*		GACCATGCTG	ATTGCTCCGC	0	T	0	0	0	0	0
10303	4450	an	AN3746.1	65.m07388	AO070309000076	0	-181	-131					ATGTTGATGGTCGGTTTCCTGCTCTCATACCGGCAACTCATCTCCTGCTGA	ATGTTGATGGTCGGTTTCCTGCTCTCATACCGGCAACTCATCTCCTGCTGA			MLMVGFLLSYRQLISC*	MLMVGFLLSYRQLISC*			AACTAGCGGA	CTGTTTTTTT	0	T	0	0	0	0	0
10304	4450	an	AN3746.1	65.m07388	AO070309000076	0	-175	-131					ATGGTCGGTTTCCTGCTCTCATACCGGCAACTCATCTCCTGCTGA	ATGGTCGGTTTCCTGCTCTCATACCGGCAACTCATCTCCTGCTGA			MVGFLLSYRQLISC*	MVGFLLSYRQLISC*			CGGAATGTTG	CTGTTTTTTT	0	T	0	0	0	0	0
10307	4450	ao	AN3746.1	65.m07388	AO070309000076	0					-131	-120	ATGATTTTGTGA			ATGATTTTGTGA	MIL*			MIL*	GTGCTAACAT	GTAATAGGTC	0	T	0	0	0	0	0
10311	4452	af	AN8675.1	62.m03480	AO070315000094	0			-98	-78			ATGGCACCTTTATTTGGATAA		ATGGCACCTTTATTTGGATAA		MAPLFG*		MAPLFG*		TTCAATTATC	CTACTGAAAG	0	S	0	0	NCU07447.1	0	0
10308	4452	an	AN8675.1	62.m03480	AO070315000094	0	-104	-63					ATGGAATATTATTTTCGATATTCCTTCTCTCATCCTATCTAA	ATGGAATATTATTTTCGATATTCCTTCTCTCATCCTATCTAA			MEYYFRYSFSHPI*	MEYYFRYSFSHPI*			AACCGTGAAT	TGTCCTGCGG	0	S	0	0	NCU07447.1	0	0
10309	4452	an	AN8675.1	62.m03480	AO070315000094	0	-63	-40					ATGTCCTGCGGTGCCCGAGACTAA	ATGTCCTGCGGTGCCCGAGACTAA			MSCGARD*	MSCGARD*			ATCCTATCTA	TCTCCCCACT	0	S	0	0	NCU07447.1	0	0
10312	4452	ao	AN8675.1	62.m03480	AO070315000094	0					-100	-62	ATGGCGACTGTACTTCGAATCTTGCCGAAACCCTTTTAA			ATGGCGACTGTACTTCGAATCTTGCCGAAACCCTTTTAA	MATVLRILPKPF*			MATVLRILPKPF*	TTTCTAGAAT	TGTGTTGCGG	0	S	0	0	NCU07447.1	0	0
10313	4452	ao	AN8675.1	62.m03480	AO070315000094	0					-62	-12	ATGTGTTGCGGAGTCTGGTCTACCGTCCCCCACTTAACGACCAATGCATGA			ATGTGTTGCGGAGTCTGGTCTACCGTCCCCCACTTAACGACCAATGCATGA	MCCGVWSTVPHLTTNA*			MCCGVWSTVPHLTTNA*	AACCCTTTTA	AGATACTCGT	0	S	0	0	NCU07447.1	0	0
10315	4453	af	AN7717.1	71.m15742	AO070325000130	0			-251	-186			ATGCTGTTTTCCATTTTGAGAGGACGCCAGGTCAATAATCCTCACGTATCATTGAGAACCCGCTGA		ATGCTGTTTTCCATTTTGAGAGGACGCCAGGTCAATAATCCTCACGTATCATTGAGAACCCGCTGA		MLFSILRGRQVNNPHVSLRTR*		MLFSILRGRQVNNPHVSLRTR*		TGCCCTGGCG	TTATTAGCAT	0		0	0	0	0	0
10314	4453	an	AN7717.1	71.m15742	AO070325000130	0	-91	-77					ATGAGGGGCAAATAA	ATGAGGGGCAAATAA			MRGK*	MRGK*			TCATCCCTTG	CACCCGACCC	0		0	0	0	0	0
10316	4453	ao	AN7717.1	71.m15742	AO070325000130	0					-202	-158	ATGACTGTCAATTCATTTGTGAAGTATGTAGCTAATGGTCATTAA			ATGACTGTCAATTCATTTGTGAAGTATGTAGCTAATGGTCATTAA	MTVNSFVKYVANGH*			MTVNSFVKYVANGH*	TTACTGTTTC	GTACCCAATT	0		0	0	0	0	0
10317	4453	ao	AN7717.1	71.m15742	AO070325000130	0					-168	-100	ATGGTCATTAAGTACCCAATTTTTTTTTGGTTCAGCACCGCTTTTCTTTCCCCTAAACCCCCTCCTTAA			ATGGTCATTAAGTACCCAATTTTTTTTTGGTTCAGCACCGCTTTTCTTTCCCCTAAACCCCCTCCTTAA	MVIKYPIFFWFSTAFLSPKPPP*			MVIKYPIFFWFSTAFLSPKPPP*	TATGTAGCTA	TCATCCCTTT	0		0	0	0	0	0
10319	4454	af	AN5573.1	58.m07499	AO070328000033	0			-170	-135			ATGCAATTGATACACTTCTGTGCGCTACTTGCATGA		ATGCAATTGATACACTTCTGTGCGCTACTTGCATGA		MQLIHFCALLA*		MQLIHFCALLA*		TTGTGAAGTA	GGGCTGCCTT	0		0	0	0	0	0
10320	4454	af	AN5573.1	58.m07499	AO070328000033	0			-138	-70			ATGAGGGCTGCCTTACCTCTTTCAAACACTCTCAAGCAATTATCCATAAATCCCCCTCACTTCCACTAA		ATGAGGGCTGCCTTACCTCTTTCAAACACTCTCAAGCAATTATCCATAAATCCCCCTCACTTCCACTAA		MRAALPLSNTLKQLSINPPHFH*		MRAALPLSNTLKQLSINPPHFH*		CGCTACTTGC	ACCGTACCGG	0		0	0	0	0	0
10318	4454	an	AN5573.1	58.m07499	AO070328000033	0	-180	-169					ATGATCCCTTGA	ATGATCCCTTGA			MIP*	MIP*			ATAATCCCTT	ACTTCCGTTG	0		0	0	0	0	0
10321	4457	af	AN2889.1	59.m08736	AO070338000125	0			-213	-172			ATGACGCTGTTGGTCGTTCTCCGCAGCGCTAAACCGCTTTGA		ATGACGCTGTTGGTCGTTCTCCGCAGCGCTAAACCGCTTTGA		MTLLVVLRSAKPL*		MTLLVVLRSAKPL*		ATTCCGCCGG	GTCTATAGAA	0	RP	0	0	0	0	0
10322	4457	ao	AN2889.1	59.m08736	AO070338000125	0					-179	-6	ATGCTTCGCATGAATTCCTCCGCGCCGCTAACCCGATTTGGGAGGGCATCGGATACCCGCGCGTTGCTCTTGCATTCACTGCCTGGACAAACACTCACTGGCACATTCCTCTACCTTGGCTATGAACTAGTGAATGGGCGGATTAATGATATACCCCGAGGGACCTCCCACTGA			ATGCTTCGCATGAATTCCTCCGCGCCGCTAACCCGATTTGGGAGGGCATCGGATACCCGCGCGTTGCTCTTGCATTCACTGCCTGGACAAACACTCACTGGCACATTCCTCTACCTTGGCTATGAACTAGTGAATGGGCGGATTAATGATATACCCCGAGGGACCTCCCACTGA	MLRMNSSAPLTRFGRASDTRALLLHSLPGQTLTGTFLYLGYELVNGRINDIPRGTSH*			MLRMNSSAPLTRFGRASDTRALLLHSLPGQTLTGTFLYLGYELVNGRINDIPRGTSH*	TGACATTCTC	TCACCATGGC	0	RP	0	0	0	0	0
10323	4457	ao	AN2889.1	59.m08736	AO070338000125	0					-170	-6	ATGAATTCCTCCGCGCCGCTAACCCGATTTGGGAGGGCATCGGATACCCGCGCGTTGCTCTTGCATTCACTGCCTGGACAAACACTCACTGGCACATTCCTCTACCTTGGCTATGAACTAGTGAATGGGCGGATTAATGATATACCCCGAGGGACCTCCCACTGA			ATGAATTCCTCCGCGCCGCTAACCCGATTTGGGAGGGCATCGGATACCCGCGCGTTGCTCTTGCATTCACTGCCTGGACAAACACTCACTGGCACATTCCTCTACCTTGGCTATGAACTAGTGAATGGGCGGATTAATGATATACCCCGAGGGACCTCCCACTGA	MNSSAPLTRFGRASDTRALLLHSLPGQTLTGTFLYLGYELVNGRINDIPRGTSH*			MNSSAPLTRFGRASDTRALLLHSLPGQTLTGTFLYLGYELVNGRINDIPRGTSH*	CATGCTTCGC	TCACCATGGC	0	RP	0	0	0	0	0
10325	4458	af	AN2735.1	54.m07004	AO070338000216	0			-211	-173			ATGCCCAATGCAGTGTTAGGGCCGGAGTCGGTGTATTAA		ATGCCCAATGCAGTGTTAGGGCCGGAGTCGGTGTATTAA		MPNAVLGPESVY*		MPNAVLGPESVY*		CATTGCAAAA	GCCTGTACAG	0	S	0	0	0	0	0
10326	4458	af	AN2735.1	54.m07004	AO070338000216	0			-204	-193			ATGCAGTGTTAG		ATGCAGTGTTAG		MQC*		MQC*		AAAATGCCCA	GGCCGGAGTC	0	S	0	0	0	0	0
10327	4458	af	AN2735.1	54.m07004	AO070338000216	0			-140	-111			ATGACTTATACAAGTCTCGTTGGGGCTTGA		ATGACTTATACAAGTCTCGTTGGGGCTTGA		MTYTSLVGA*		MTYTSLVGA*		TGACAAATCG	TCGCTCGCGC	0	S	0	0	0	0	0
10324	4458	an	AN2735.1	54.m07004	AO070338000216	0	-182	-123					ATGATTATACGGAGTACGACCAGAGCAAGACCATTGCATACTGAATATACACAATATTAG	ATGATTATACGGAGTACGACCAGAGCAAGACCATTGCATACTGAATATACACAATATTAG			MIIRSTTRARPLHTEYTQY*	MIIRSTTRARPLHTEYTQY*			CAGAGAGAAT	ACTGAGTTTT	0	S	0	0	0	0	0
10328	4458	ao	AN2735.1	54.m07004	AO070338000216	0					-220	-131	ATGTCCGCAGAGAGATCAGATAGGGCATGCAAGCATGCATTTAGTGGTATACTTCTGGAAGTTTATGATACTATTCCTTTGATCCTCTAA			ATGTCCGCAGAGAGATCAGATAGGGCATGCAAGCATGCATTTAGTGGTATACTTCTGGAAGTTTATGATACTATTCCTTTGATCCTCTAA	MSAERSDRACKHAFSGILLEVYDTIPLIL*			MSAERSDRACKHAFSGILLEVYDTIPLIL*	GCAGAAAAAA	TTGATTACTG	0	S	0	0	0	0	0
10329	4458	ao	AN2735.1	54.m07004	AO070338000216	0					-194	-177	ATGCAAGCATGCATTTAG			ATGCAAGCATGCATTTAG	MQACI*			MQACI*	CAGATAGGGC	TGGTATACTT	0	S	0	0	0	0	0
10330	4458	ao	AN2735.1	54.m07004	AO070338000216	0					-186	-139	ATGCATTTAGTGGTATACTTCTGGAAGTTTATGATACTATTCCTTTGA			ATGCATTTAGTGGTATACTTCTGGAAGTTTATGATACTATTCCTTTGA	MHLVVYFWKFMILFL*			MHLVVYFWKFMILFL*	GCATGCAAGC	TCCTCTAATT	0	S	0	0	0	0	0
10331	4458	ao	AN2735.1	54.m07004	AO070338000216	0					-156	-139	ATGATACTATTCCTTTGA			ATGATACTATTCCTTTGA	MILFL*			MILFL*	CTGGAAGTTT	TCCTCTAATT	0	S	0	0	0	0	0
10332	4458	ao	AN2735.1	54.m07004	AO070338000216	0					-102	-55	ATGTACTTTACTGGTCACAGCACTACAATCCGTTATTGTATTTTCTGA			ATGTACTTTACTGGTCACAGCACTACAATCCGTTATTGTATTTTCTGA	MYFTGHSTTIRYCIF*			MYFTGHSTTIRYCIF*	AAGGTAGCTT	CACCACATTA	0	S	0	0	0	0	0
10333	4460	af	AN6006.1	72.m19136	AO070340000272	0			-286	-167			ATGTTTTCTTCTTGTGGCCCAGTCCTGGTAGTCTGTGCTTTTGCTGTGCTGCCCTCTTGCTTTGATTATCACTACTGGACAAACTACCGGGAAAATAATCTGCACCCTATCCTTCTCTGA		ATGTTTTCTTCTTGTGGCCCAGTCCTGGTAGTCTGTGCTTTTGCTGTGCTGCCCTCTTGCTTTGATTATCACTACTGGACAAACTACCGGGAAAATAATCTGCACCCTATCCTTCTCTGA		MFSSCGPVLVVCAFAVLPSCFDYHYWTNYRENNLHPILL*		MFSSCGPVLVVCAFAVLPSCFDYHYWTNYRENNLHPILL*		TAACCACTGA	CCACTGTCTA	0	YU	0	0	0	0	0
10334	4460	ao	AN6006.1	72.m19136	AO070340000272	0					-157	-110	ATGTGCACTTTTGCACTTTCTTTACTACAACATCTCCCCGCGACATAA			ATGTGCACTTTTGCACTTTCTTTACTACAACATCTCCCCGCGACATAA	MCTFALSLLQHLPAT*			MCTFALSLLQHLPAT*	AACAAACCCA	CTTTCTCGGC	0	YU	0	0	0	0	0
10337	4461	af	AN3623.1	58.m07410	AO070342000128	0			-226	-212			ATGACAACTGGATAG		ATGACAACTGGATAG		MTTG*		MTTG*		AACAATTCGA	GTATCGGATA	0	OT	0	0	0	0	0
10338	4461	af	AN3623.1	58.m07410	AO070342000128	0			-79	-32			ATGTCGGTTTACGCTCGACTGTCTCGCCCAATGTCCTACAGCAGCTGA		ATGTCGGTTTACGCTCGACTGTCTCGCCCAATGTCCTACAGCAGCTGA		MSVYARLSRPMSYSS*		MSVYARLSRPMSYSS*		TTCCCCTTGC	CCTCCATTAA	0	OT	0	0	0	0	0
10335	4461	an	AN3623.1	58.m07410	AO070342000128	0	-233						ATGTTTGCATTAACTGCAAACCCCTGGACCTCATTTCTCGCTCCATCTGCGGAGTACTGTACACTAATCACCAGTTATCCAACAACACCAGCCACGAGCCTAATCACCAATGCTCGCCCCGTTTCAGACGTACCTCGAACTATACATTCAGCTGAACTTATACGCTATCATCGGCAGCACCTAACTTGCACATTCAACCTGCAACTCAGCTCAAGCTCCAGCACTCAGCACTGA	ATGTTTGCATTAACTGCAAACCCCTGGACCTCATTTCTCGCTCCATCTGCGGAGTACTGTACACTAATCACCAGTTATCCAACAACACCAGCCACGAGCCTAATCACCAATGCTCGCCCCGTTTCAGACGTACCTCGAACTATACATTCAGCTGAACTTATACGCTATCATCGGCAGCACCTAACTTGCACATTCAACCTGCAACTCAGCTCAAGCTCCAGCACTCAGCACTGA			MFALTANPWTSFLAPSAEYCTLITSYPTTPATSLITNARPVSDVPRTIHSAELIRYHRQHLTCTFNLQLSSSSSTQH*	MFALTANPWTSFLAPSAEYCTLITSYPTTPATSLITNARPVSDVPRTIHSAELIRYHRQHLTCTFNLQLSSSSSTQH*			AGTGGAGGAT	TGGACCAAGT	0	OT	0	0	0	0	0
10336	4461	an	AN3623.1	58.m07410	AO070342000128	0	-124	-50					ATGCTCGCCCCGTTTCAGACGTACCTCGAACTATACATTCAGCTGAACTTATACGCTATCATCGGCAGCACCTAA	ATGCTCGCCCCGTTTCAGACGTACCTCGAACTATACATTCAGCTGAACTTATACGCTATCATCGGCAGCACCTAA			MLAPFQTYLELYIQLNLYAIIGST*	MLAPFQTYLELYIQLNLYAIIGST*			CTAATCACCA	CTTGCACATT	0	OT	0	0	0	0	0
10340	4461	ao	AN3623.1	58.m07410	AO070342000128	0					-249	-238	ATGTGGGGATAA			ATGTGGGGATAA	MWG*			MWG*	TAGTTATCAC	ATGTCATTGT	0	OT	0	0	0	0	0
10341	4461	ao	AN3623.1	58.m07410	AO070342000128	0					-237	-124	ATGTCATTGTTTGCATTCCAAACAAACACCCCATTCGGGACATCACTTGGATATCATCACCATTGCTTTCAGCAAACATCTCCCATTCACACCGACAGACTGCATAGTTTCTAA			ATGTCATTGTTTGCATTCCAAACAAACACCCCATTCGGGACATCACTTGGATATCATCACCATTGCTTTCAGCAAACATCTCCCATTCACACCGACAGACTGCATAGTTTCTAA	MSLFAFQTNTPFGTSLGYHHHCFQQTSPIHTDRLHSF*			MSLFAFQTNTPFGTSLGYHHHCFQQTSPIHTDRLHSF*	GTGGGGATAA	GCGGCAATAG	0	OT	0	0	0	0	0
10343	4463	af	AN5891.1	72.m19239	AO070245000016	0			-102	-73			ATGCCTGTTGGGTCTGAACGGGTTATTTGA		ATGCCTGTTGGGTCTGAACGGGTTATTTGA		MPVGSERVI*		MPVGSERVI*		GGTAGGTGGC	AGCCCTCAAC	0	R	0	0	0	0	0
10342	4463	an	AN5891.1	72.m19239	AO070245000016	0	-99	-82					ATGTGGTTAGGGATATAA	ATGTGGTTAGGGATATAA			MWLGI*	MWLGI*			CTTTCGTGAT	TCGATCCCAT	0	R	0	0	0	0	0
10344	4463	ao	AN5891.1	72.m19239	AO070245000016	0					-100	-83	ATGCGTGCTGGGCTTTGA			ATGCGTGCTGGGCTTTGA	MRAGL*			MRAGL*	AATAAGTGAC	CGGTTTATCC	0	R	0	0	0	0	0
10347	4466	af	AN8821.1	71.m15632	AO070276000021	0			-259	-200			ATGACATATCCGGTAGACGTAGAGCGGTTCGTAAATACGGATCGGCAATTTTCTTCATGA		ATGACATATCCGGTAGACGTAGAGCGGTTCGTAAATACGGATCGGCAATTTTCTTCATGA		MTYPVDVERFVNTDRQFSS*		MTYPVDVERFVNTDRQFSS*		GTTCCCTGGG	GAGGCCACGA	0		FG05966.1	0	0	0	0
10348	4466	af	AN8821.1	71.m15632	AO070276000021	0			-203	-159			ATGAGAGGCCACGAAAATACCCCTGGCTATCTGTCTAAAAACTAA		ATGAGAGGCCACGAAAATACCCCTGGCTATCTGTCTAAAAACTAA		MRGHENTPGYLSKN*		MRGHENTPGYLSKN*		AATTTTCTTC	AAAGACTGTG	0		FG05966.1	0	0	0	0
10349	4466	af	AN8821.1	71.m15632	AO070276000021	0			-133	-86			ATGTTCTGCTCTGGAGGCAACTCCCATTCCGCCAAGACAACTCGATAA		ATGTTCTGCTCTGGAGGCAACTCCCATTCCGCCAAGACAACTCGATAA		MFCSGGNSHSAKTTR*		MFCSGGNSHSAKTTR*		GTGGGAACCC	TTCCCGTTTT	0		FG05966.1	0	0	0	0
10345	4466	an	AN8821.1	71.m15632	AO070276000021	0	-144	-118					ATGCATCCGCTAAGTATGCTTCTGTAG	ATGCATCCGCTAAGTATGCTTCTGTAG			MHPLSMLL*	MHPLSMLL*			ACCTCGTAAA	GGCTACCGCG	0		FG05966.1	0	0	0	0
10346	4466	an	AN8821.1	71.m15632	AO070276000021	0	-129	-118					ATGCTTCTGTAG	ATGCTTCTGTAG			MLL*	MLL*			TCCGCTAAGT	GGCTACCGCG	0		FG05966.1	0	0	0	0
10350	4466	ao	AN8821.1	71.m15632	AO070276000021	0					-170	-132	ATGCAGCATTGGAGTGTATCAAGAATTGTTTCGTCGTAA			ATGCAGCATTGGAGTGTATCAAGAATTGTTTCGTCGTAA	MQHWSVSRIVSS*			MQHWSVSRIVSS*	AAACATCCGT	TACTGGGAAT	0		FG05966.1	0	0	0	0

10351	4467	af	AN0579.1	69.m15690	AO070280000001	0			-169	-26			ATGGGCGGGTTTTCCCTTTACGAACACGAACAACCAAGGGGGCTACAAAACCGTACAGTCGTCTGGTTCTCTTTCACACTTTCTGAGGCCTGTCGCTTTTCAGGCAAACTATCAAGTAGTCTTTTTTGTGTTTTTAAATATTGA		ATGGGCGGGTTTTCCCTTTACGAACACGAACAACCAAGGGGGCTACAAAACCGTACAGTCGTCTGGTTCTCTTTCACACTTTCTGAGGCCTGTCGCTTTTCAGGCAAACTATCAAGTAGTCTTTTTTGTGTTTTTAAATATTGA		MGGFSLYEHEQPRGLQNRTVVWFSFTLSEACRFSGKLSSSLFCVFKY*		MGGFSLYEHEQPRGLQNRTVVWFSFTLSEACRFSGKLSSSLFCVFKY*		CTTTGGAATT	TAGACACTGT	0	Q	0	0	0	0	0
10352	4468	af	AN7465.1	57.m05876	AO070287000061	0			-256	-179			ATGCGATTATTGATTTGCTACTTGACTGGATCTGTTGCGGTTCTGTGTTTGTTTTTCTTGTCTCTTCGGAGGCTTTAG		ATGCGATTATTGATTTGCTACTTGACTGGATCTGTTGCGGTTCTGTGTTTGTTTTTCTTGTCTCTTCGGAGGCTTTAG		MRLLICYLTGSVAVLCFFLSLRRL*		MRLLICYLTGSVAVLCFFLSLRRL*		ATCGCAGTAC	GTGCAGGAAA	0	D	FG00509.1	0	0	0	0
10354	4469	af	AN6675.1	65.m07305	AO070289000014	0			-232	-170			ATGGCCGTGGAGCCTTCTATTTGGTGCCGTTGCTATTCATTTTATGCATACTCCAAGTCATGA		ATGGCCGTGGAGCCTTCTATTTGGTGCCGTTGCTATTCATTTTATGCATACTCCAAGTCATGA		MAVEPSIWCRCYSFYAYSKS*		MAVEPSIWCRCYSFYAYSKS*		GTAGCCCGTC	GTTGCGCTTC	0	R	0	0	0	0	0
10355	4469	af	AN6675.1	65.m07305	AO070289000014	0			-189	-148			ATGCATACTCCAAGTCATGAGTTGCGCTTCTATGTTGCTTGA		ATGCATACTCCAAGTCATGAGTTGCGCTTCTATGTTGCTTGA		MHTPSHELRFYVA*		MHTPSHELRFYVA*		TATTCATTTT	TTTGGTTTCT	0	R	0	0	0	0	0
10356	4469	af	AN6675.1	65.m07305	AO070289000014	0			-173	-93			ATGAGTTGCGCTTCTATGTTGCTTGATTTGGTTTCTCTGCAAAACACCGCACGGCCTGGAAACTTTACGCTTGGTATTTGA		ATGAGTTGCGCTTCTATGTTGCTTGATTTGGTTTCTCTGCAAAACACCGCACGGCCTGGAAACTTTACGCTTGGTATTTGA		MSCASMLLDLVSLQNTARPGNFTLGI*		MSCASMLLDLVSLQNTARPGNFTLGI*		ACTCCAAGTC	GGCTCAGCGG	0	R	0	0	0	0	0
10357	4469	af	AN6675.1	65.m07305	AO070289000014	0			-158	-93			ATGTTGCTTGATTTGGTTTCTCTGCAAAACACCGCACGGCCTGGAAACTTTACGCTTGGTATTTGA		ATGTTGCTTGATTTGGTTTCTCTGCAAAACACCGCACGGCCTGGAAACTTTACGCTTGGTATTTGA		MLLDLVSLQNTARPGNFTLGI*		MLLDLVSLQNTARPGNFTLGI*		TTGCGCTTCT	GGCTCAGCGG	0	R	0	0	0	0	0
10353	4469	an	AN6675.1	65.m07305	AO070289000014	0	-163	-107					ATGTTTGGCTTTTCCCAGGGACTGCGTCGTGTCTTGCGTTGTTATTCACCACATTGA	ATGTTTGGCTTTTCCCAGGGACTGCGTCGTGTCTTGCGTTGTTATTCACCACATTGA			MFGFSQGLRRVLRCYSPH*	MFGFSQGLRRVLRCYSPH*			CTCGTCAGTC	GGCGGGTCTC	0	R	0	0	0	0	0
10358	4469	ao	AN6675.1	65.m07305	AO070289000014	0					-242	-180	ATGGCTGTGACACCGCTGCCCTTCATTTCTTTGCGATTTTATGCATTTTCCGGTTGCTATTGA			ATGGCTGTGACACCGCTGCCCTTCATTTCTTTGCGATTTTATGCATTTTCCGGTTGCTATTGA	MAVTPLPFISLRFYAFSGCY*			MAVTPLPFISLRFYAFSGCY*	TTCGCCGCCG	GTCATGATTG	0	R	0	0	0	0	0
10359	4469	ao	AN6675.1	65.m07305	AO070289000014	0					-202	-173	ATGCATTTTCCGGTTGCTATTGAGTCATGA			ATGCATTTTCCGGTTGCTATTGAGTCATGA	MHFPVAIES*			MHFPVAIES*	TTGCGATTTT	TTGGCATTTC	0	R	0	0	0	0	0
10360	4469	ao	AN6675.1	65.m07305	AO070289000014	0					-176	-108	ATGATTGGCATTTCTCCTTTACTTGACCCGGTTTCCTTATGCTACGCGGCGCCGCGAGACTCTGTTTGA			ATGATTGGCATTTCTCCTTTACTTGACCCGGTTTCCTTATGCTACGCGGCGCCGCGAGACTCTGTTTGA	MIGISPLLDPVSLCYAAPRDSV*			MIGISPLLDPVSLCYAAPRDSV*	CTATTGAGTC	TTGCAACGTG	0	R	0	0	0	0	0
10361	4469	ao	AN6675.1	65.m07305	AO070289000014	0					-138	-97	ATGCTACGCGGCGCCGCGAGACTCTGTTTGATTGCAACGTGA			ATGCTACGCGGCGCCGCGAGACTCTGTTTGATTGCAACGTGA	MLRGAARLCLIAT*			MLRGAARLCLIAT*	CGGTTTCCTT	GGCTGAGCGA	0	R	0	0	0	0	0
10362	4470	af	AN2263.1	71.m15904	AO070295000026	0			-228	-19			ATGCTGGATGACTCAGCATCTTATCTTATCCGCGCGGGGCCTTTCTTTTCTCTCTGGAAATCTTCAACATCATTAATAATACCACTATCCTTCTTTTTCCTTTGCCTCCGAGCATTAACCTCCTCTCTTTCCCTCTGGATACGACCTCTCTCTAATTCTACAAGGGAAAGAATTTTTCTTATTCAAAAGTGGTGGAAGTCAGCGGATTGA		ATGCTGGATGACTCAGCATCTTATCTTATCCGCGCGGGGCCTTTCTTTTCTCTCTGGAAATCTTCAACATCATTAATAATACCACTATCCTTCTTTTTCCTTTGCCTCCGAGCATTAACCTCCTCTCTTTCCCTCTGGATACGACCTCTCTCTAATTCTACAAGGGAAAGAATTTTTCTTATTCAAAAGTGGTGGAAGTCAGCGGATTGA		MLDDSASYLIRAGPFFSLWKSSTSLIIPLSFFFLCLRALTSSLSLWIRPLSNSTRERIFLIQKWWKSAD*		MLDDSASYLIRAGPFFSLWKSSTSLIIPLSFFFLCLRALTSSLSLWIRPLSNSTRERIFLIQKWWKSAD*		ACGGTCCTTG	ACTGCACACA	0	R	0	MG07525.1	0	YGL099W	YGL099W
10363	4470	af	AN2263.1	71.m15904	AO070295000026	0			-221	-153			ATGACTCAGCATCTTATCTTATCCGCGCGGGGCCTTTCTTTTCTCTCTGGAAATCTTCAACATCATTAA		ATGACTCAGCATCTTATCTTATCCGCGCGGGGCCTTTCTTTTCTCTCTGGAAATCTTCAACATCATTAA		MTQHLILSARGLSFLSGNLQHH*		MTQHLILSARGLSFLSGNLQHH*		TTGATGCTGG	TAATACCACT	0	R	0	MG07525.1	0	YGL099W	YGL099W
10364	4470	ao	AN2263.1	71.m15904	AO070295000026	0					-157	-143	ATGGAACAAAATTAA			ATGGAACAAAATTAA	MEQN*			MEQN*	TCATCGCCAA	TAATTCTCCG	0	R	0	MG07525.1	0	YGL099W	YGL099W
10365	4471	an	AN7256.1	72.m19794	AO070297000012	0	-245	-99					ATGTATTCTCGGAATTGCTGCACAGGTGTAGTTGGACGGTGTCGGTATCTGACGGGATCGTTCCGAGCCTCGGCACCAGGCCGTATCGGGCTGATCAGTTGGATCGTGACAGTCCGGGGATATGGAGACTTTCACTTAAGACTTTAG	ATGTATTCTCGGAATTGCTGCACAGGTGTAGTTGGACGGTGTCGGTATCTGACGGGATCGTTCCGAGCCTCGGCACCAGGCCGTATCGGGCTGATCAGTTGGATCGTGACAGTCCGGGGATATGGAGACTTTCACTTAAGACTTTAG			MYSRNCCTGVVGRCRYLTGSFRASAPGRIGLISWIVTVRGYGDFHLRL*	MYSRNCCTGVVGRCRYLTGSFRASAPGRIGLISWIVTVRGYGDFHLRL*			AGGGGCGGAA	ACTCCCGACC	0		0	0	0	0	0
10366	4471	an	AN7256.1	72.m19794	AO070297000012	0	-124	-107					ATGGAGACTTTCACTTAA	ATGGAGACTTTCACTTAA			METFT*	METFT*			GTCCGGGGAT	GACTTTAGAC	0		0	0	0	0	0
10367	4471	ao	AN7256.1	72.m19794	AO070297000012	0					-227	-147	ATGGGTAGGACAAAAGTTGTGAAGGACGGGTTGTCAAGTGCACGCAAATTGATTCGGTCGAGCACAGCGATTTGTCTGTAA			ATGGGTAGGACAAAAGTTGTGAAGGACGGGTTGTCAAGTGCACGCAAATTGATTCGGTCGAGCACAGCGATTTGTCTGTAA	MGRTKVVKDGLSSARKLIRSSTAICL*			MGRTKVVKDGLSSARKLIRSSTAICL*	AGGGTAGTTC	CCTCCGAACC	0		0	0	0	0	0
10368	4471	ao	AN7256.1	72.m19794	AO070297000012	0					-99	-73	ATGCTCTGCGTTGACATTTCCCTATAA			ATGCTCTGCGTTGACATTTCCCTATAA	MLCVDISL*			MLCVDISL*	TGCTAGTCAG	ATCCACAACG	0		0	0	0	0	0
10370	4474	ao	AN8211.1	53.m03763	AO070310000102	0					-76	-50	ATGACTGCCCCCTTCCATCCGCGATAA			ATGACTGCCCCCTTCCATCCGCGATAA	MTAPFHPR*			MTAPFHPR*	TTCGCCTCGG	GACACGCGCA	0	R	0	0	0	0	0
10369	4474	conserved	AN8211.1	53.m03763	AO070310000102	0	-98	-54	-96	-52	-94	-50	ATGbGyyTTTCGCmTmGGrykmybkCyyCCTTCCrTCCGCGATAA	ATGGGTTTTTCGCATAGGACGCTGGCTTCCTTCCGTCCGCGATAA	ATGCGCTTTTCGCATCGGGCTCCCTCTCCCTTCCATCCGCGATAA	ATGTGCCTTTCGCCTCGGATGACTGCCCCCTTCCATCCGCGATAA	MgfShRtlasFrPR*	MGFSHRTLASFRPR*	MRFSHRAPSPFHPR*	MCLSPRMTAPFHPR*	vwbbyyyyym	rmsmCssssm	0	R	0	0	0	0	0
10371	4475	an	AN0093.1	71.m15368	AO070311000122	0	-131	-108					ATGGCCTTGCTAATACTCCTCTGA	ATGGCCTTGCTAATACTCCTCTGA			MALLILL*	MALLILL*			TGAGATAACA	TCTTAGTTAC	0	Y	FG02562.1	MG05259.1	NCU06271.1	0	0
10372	4475	an	AN0093.1	71.m15368	AO070311000122	0	-82	-53					ATGATTCCCATAAGCATTTTAGCGCCTTGA	ATGATTCCCATAAGCATTTTAGCGCCTTGA			MIPISILAP*	MIPISILAP*			TCTCTCATCG	AATTGTTCCA	0	Y	FG02562.1	MG05259.1	NCU06271.1	0	0
10373	4475	ao	AN0093.1	71.m15368	AO070311000122	0					-105	-82	ATGGCTTATCTTCAACTCCTGTAG			ATGGCTTATCTTCAACTCCTGTAG	MAYLQLL*			MAYLQLL*	CCACCACCCC	TTCTGGAGGC	0	Y	FG02562.1	MG05259.1	NCU06271.1	0	0
10374	4480	ao	AN0265.1	54.m06967	AO070334000094	0					-188	-150	ATGTACCTGACTCCACTATTGACCGCTCGTGATCTTTAA			ATGTACCTGACTCCACTATTGACCGCTCGTGATCTTTAA	MYLTPLLTARDL*			MYLTPLLTARDL*	GCAAGATTGA	CAGCAACCTG	0	GOT	0	0	0	0	0
10375	4481	af	AN1500.1	55.m03010	AO070334000217	0			-264	-229			ATGCTCGCATTTCCCATCAGCATCGATTTCCTTTAG		ATGCTCGCATTTCCCATCAGCATCGATTTCCTTTAG		MLAFPISIDFL*		MLAFPISIDFL*		TTCTTCAGGT	CGATCTACCA	0	R	0	0	0	0	0
10376	4481	af	AN1500.1	55.m03010	AO070334000217	0			-199	-179			ATGAAGGAATATGATGATTGA		ATGAAGGAATATGATGATTGA		MKEYDD*		MKEYDD*		CAACATCACA	TAACCAACCT	0	R	0	0	0	0	0
10377	4481	af	AN1500.1	55.m03010	AO070334000217	0			-189	-76			ATGATGATTGATAACCAACCTCTTTCAGATTCTCCGCCTCGATCTCCTTATTGGAACGCAGACCTTGTCTTTTACCGAATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		ATGATGATTGATAACCAACCTCTTTCAGATTCTCCGCCTCGATCTCCTTATTGGAACGCAGACCTTGTCTTTTACCGAATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		MMIDNQPLSDSPPRSPYWNADLVFYRMVGTSTVDYRA*		MMIDNQPLSDSPPRSPYWNADLVFYRMVGTSTVDYRA*		ATGAAGGAAT	GACGTCTGCA	0	R	0	0	0	0	0
10378	4481	af	AN1500.1	55.m03010	AO070334000217	0			-186	-76			ATGATTGATAACCAACCTCTTTCAGATTCTCCGCCTCGATCTCCTTATTGGAACGCAGACCTTGTCTTTTACCGAATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		ATGATTGATAACCAACCTCTTTCAGATTCTCCGCCTCGATCTCCTTATTGGAACGCAGACCTTGTCTTTTACCGAATGGTGGGGACTAGCACAGTCGACTATCGAGCTTAG		MIDNQPLSDSPPRSPYWNADLVFYRMVGTSTVDYRA*		MIDNQPLSDSPPRSPYWNADLVFYRMVGTSTVDYRA*		AAGGAATATG	GACGTCTGCA	0	R	0	0	0	0	0
10380	4481	ao	AN1500.1	55.m03010	AO070334000217	0					-320	-282	ATGTTTTCCCGTGCGGCCCGTTCCTCCTATGAAACTTAA			ATGTTTTCCCGTGCGGCCCGTTCCTCCTATGAAACTTAA	MFSRAARSSYET*			MFSRAARSSYET*	GAAAGATTGT	TCCATCGCTT	0	R	0	0	0	0	0
10381	4481	ao	AN1500.1	55.m03010	AO070334000217	0					-292	-245	ATGAAACTTAATCCATCGCTTGCTATGCGCGCAAGCCGACAAGAATGA			ATGAAACTTAATCCATCGCTTGCTATGCGCGCAAGCCGACAAGAATGA	MKLNPSLAMRASRQE*			MKLNPSLAMRASRQE*	CGTTCCTCCT	TTCAAGTCTC	0	R	0	0	0	0	0
10382	4481	ao	AN1500.1	55.m03010	AO070334000217	0					-268	-245	ATGCGCGCAAGCCGACAAGAATGA			ATGCGCGCAAGCCGACAAGAATGA	MRASRQE*			MRASRQE*	ATCGCTTGCT	TTCAAGTCTC	0	R	0	0	0	0	0
10383	4481	ao	AN1500.1	55.m03010	AO070334000217	0					-248	-225	ATGATTCAAGTCTCCCTTCAGTGA			ATGATTCAAGTCTCCCTTCAGTGA	MIQVSLQ*			MIQVSLQ*	GCCGACAAGA	AGATAGTAAT	0	R	0	0	0	0	0
10384	4481	ao	AN1500.1	55.m03010	AO070334000217	0					-216	-199	ATGGTGGCTGACGATTGA			ATGGTGGCTGACGATTGA	MVADD*			MVADD*	GAAGATAGTA	CACTAATAGT	0	R	0	0	0	0	0
10389	4485	af	AN1148.1	70.m15090	AO070331000139	0			-247	-203			ATGAAGACCTTTCCTGATTGGGTGATTAGCTGTTGGTGCCACTGA		ATGAAGACCTTTCCTGATTGGGTGATTAGCTGTTGGTGCCACTGA		MKTFPDWVISCWCH*		MKTFPDWVISCWCH*		AAACTGTCGA	GACTGATCAG	0	I	0	0	0	0	0
10390	4485	af	AN1148.1	70.m15090	AO070331000139	0			-159	-142			ATGTTTGGGCTACATTAA		ATGTTTGGGCTACATTAA		MFGLH*		MFGLH*		GGCGACGGGT	CTTCCTACTC	0	I	0	0	0	0	0
10391	4485	af	AN1148.1	70.m15090	AO070331000139	0			-105	-79			ATGATCAATGTTTCGAGTTCTTTCTAG		ATGATCAATGTTTCGAGTTCTTTCTAG		MINVSSSF*		MINVSSSF*		GAGCCTATAC	CAGGTGATCA	0	I	0	0	0	0	0
10392	4485	af	AN1148.1	70.m15090	AO070331000139	0			-98	-72			ATGTTTCGAGTTCTTTCTAGCAGGTGA		ATGTTTCGAGTTCTTTCTAGCAGGTGA		MFRVLSSR*		MFRVLSSR*		TACATGATCA	TCAAAGATCG	0	I	0	0	0	0	0
10387	4485	an	AN1148.1	70.m15090	AO070331000139	0	-89	-60					ATGTCTGGCCTTTCACCTTTAAATGCTTGA	ATGTCTGGCCTTTCACCTTTAAATGCTTGA			MSGLSPLNA*	MSGLSPLNA*			CTGACTACCT	TTCTTCTTAA	0	I	0	0	0	0	0
10388	4485	an	AN1148.1	70.m15090	AO070331000139	0	-67	-50					ATGCTTGATTCTTCTTAA	ATGCTTGATTCTTCTTAA			MLDSS*	MLDSS*			TCACCTTTAA	TATTCGACAC	0	I	0	0	0	0	0
10393	4485	ao	AN1148.1	70.m15090	AO070331000139	0					-80	-54	ATGTTTGGGATTGTTGGTAGAGGCTAA			ATGTTTGGGATTGTTGGTAGAGGCTAA	MFGIVGRG*			MFGIVGRG*	TCCTGTTTTC	ACCATTCTTT	0	I	0	0	0	0	0
10396	4486	af	AN3660.1	58.m07438	AO070342000025	0			-243	-223			ATGTATCGTTTTCATGCATGA		ATGTATCGTTTTCATGCATGA		MYRFHA*		MYRFHA*		CTACAAAAGG	ATCACGTGAG	0	R	FG08400.1	0	NCU03924.1	0	0
10397	4486	af	AN3660.1	58.m07438	AO070342000025	0			-230	-96			ATGCATGAATCACGTGAGAAGGCGTCGCGATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAGGACCATCTAGGTGTTGCACTTCTTACACTTTAGCTACTTCATCGCCGTGA		ATGCATGAATCACGTGAGAAGGCGTCGCGATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAGGACCATCTAGGTGTTGCACTTCTTACACTTTAGCTACTTCATCGCCGTGA		MHESREKASRCLASARRILQASFAAQSLGPSRCCTSYTLATSSP*		MHESREKASRCLASARRILQASFAAQSLGPSRCCTSYTLATSSP*		TATCGTTTTC	TACTTGTACT	0	R	FG08400.1	0	NCU03924.1	0	0
10398	4486	af	AN3660.1	58.m07438	AO070342000025	0			-226	-146			ATGAATCACGTGAGAAGGCGTCGCGATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAG		ATGAATCACGTGAGAAGGCGTCGCGATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAG		MNHVRRRRDASRRRVASFKHHSQLSR*		MNHVRRRRDASRRRVASFKHHSQLSR*		GTTTTCATGC	GACCATCTAG	0	R	FG08400.1	0	NCU03924.1	0	0
10399	4486	af	AN3660.1	58.m07438	AO070342000025	0			-201	-136			ATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAGGACCATCTAG		ATGCCTCGCGTCGGCGCGTCGCATCCTTCAAGCATCATTCGCAGCTCAGTCGCTAGGACCATCTAG		MPRVGASHPSSIIRSSVARTI*		MPRVGASHPSSIIRSSVARTI*		AGGCGTCGCG	GTGTTGCACT	0	R	FG08400.1	0	NCU03924.1	0	0
10394	4486	an	AN3660.1	58.m07438	AO070342000025	0	-240	-181					ATGGTTGGCCCTCTAATGAAAGAAACTGCACGTGACTTGGTGTCGCCAGGCGCGACTTGA	ATGGTTGGCCCTCTAATGAAAGAAACTGCACGTGACTTGGTGTCGCCAGGCGCGACTTGA			MVGPLMKETARDLVSPGAT*	MVGPLMKETARDLVSPGAT*			AGGCACGTTG	GCGCGTCGCA	0	R	FG08400.1	0	NCU03924.1	0	0
10395	4486	an	AN3660.1	58.m07438	AO070342000025	0	-225	-181					ATGAAAGAAACTGCACGTGACTTGGTGTCGCCAGGCGCGACTTGA	ATGAAAGAAACTGCACGTGACTTGGTGTCGCCAGGCGCGACTTGA			MKETARDLVSPGAT*	MKETARDLVSPGAT*			TGGCCCTCTA	GCGCGTCGCA	0	R	FG08400.1	0	NCU03924.1	0	0
10400	4486	ao	AN3660.1	58.m07438	AO070342000025	0					-197	-174	ATGGTAAACTGTACGCGCACGTGA			ATGGTAAACTGTACGCGCACGTGA	MVNCTRT*			MVNCTRT*	CGTACCAAAG	CCAGGTGTCG	0	R	FG08400.1	0	NCU03924.1	0	0
10404	4488	af	AN7597.1	72.m19615	AO070343000314	0			-144	-130			ATGGGACCAACCTGA		ATGGGACCAACCTGA		MGPT*		MGPT*		TCGATCGTGT	GGTGGATCCT	0	T	0	0	0	YJL212C	YJL212C
10401	4488	an	AN7597.1	72.m19615	AO070343000314	0	-276	-211					ATGCTACGCCAGCCGATTAGAGGAGGTACCATTAATTCCCTATATCTCGTTGATAACAATGGTTAG	ATGCTACGCCAGCCGATTAGAGGAGGTACCATTAATTCCCTATATCTCGTTGATAACAATGGTTAG			MLRQPIRGGTINSLYLVDNNG*	MLRQPIRGGTINSLYLVDNNG*			ACGGCGCGCC	TCAATCATTG	0	T	0	0	0	YJL212C	YJL212C
10402	4488	an	AN7597.1	72.m19615	AO070343000314	0	-218	-192					ATGGTTAGTCAATCATTGTTCAGGTGA	ATGGTTAGTCAATCATTGTTCAGGTGA			MVSQSLFR*	MVSQSLFR*			GTTGATAACA	TTATTGCTGG	0	T	0	0	0	YJL212C	YJL212C
10403	4488	an	AN7597.1	72.m19615	AO070343000314	0	-180	-43					ATGGATGTGAATTACCTGGCCAGACAGATAACGTGCGGACAGTCAAAAGGGTGCCGTCCTCCCTGGTCTGCTGTAACACTTGCCCTTTTCTTCTCACCCACCGCCTATCCTCCTCTCCTACCATCTCCGTCCCATTGA	ATGGATGTGAATTACCTGGCCAGACAGATAACGTGCGGACAGTCAAAAGGGTGCCGTCCTCCCTGGTCTGCTGTAACACTTGCCCTTTTCTTCTCACCCACCGCCTATCCTCCTCTCCTACCATCTCCGTCCCATTGA			MDVNYLARQITCGQSKGCRPPWSAVTLALFFSPTAYPPLLPSPSH*	MDVNYLARQITCGQSKGCRPPWSAVTLALFFSPTAYPPLLPSPSH*			TATTGCTGGA	GTGCTCAACT	0	T	0	0	0	YJL212C	YJL212C
10406	4489	af	AN7560.1	72.m19581	AO070343000400	0			-168	-130			ATGCTTAGCACAACCCGAATACATTCTTCAGAATTGTAG		ATGCTTAGCACAACCCGAATACATTCTTCAGAATTGTAG		MLSTTRIHSSEL*		MLSTTRIHSSEL*		CAGGGAGACA	ACTGCATCTG	0		FG05608.1	0	NCU03316.1	0	0
10407	4489	af	AN7560.1	72.m19581	AO070343000400	0			-104	-15			ATGAAGACGACTCTTGGCCTCGCGGTGACATCAACAGCGGATCCTTTCGCTTCCTCATCCCCACCATCTTCAACCTCCGCATTGCAGTAA		ATGAAGACGACTCTTGGCCTCGCGGTGACATCAACAGCGGATCCTTTCGCTTCCTCATCCCCACCATCTTCAACCTCCGCATTGCAGTAA		MKTTLGLAVTSTADPFASSSPPSSTSALQ*		MKTTLGLAVTSTADPFASSSPPSSTSALQ*		AGGCTGTGCT	AGAAGTCCAG	0		FG05608.1	0	NCU03316.1	0	0
10405	4489	an	AN7560.1	72.m19581	AO070343000400	0	-149	-90					ATGAGATTTTGTATTCAGCTCGTTTGGAAAGCGTACTTCTTGGCTGCGGCCTGGCGGTGA	ATGAGATTTTGTATTCAGCTCGTTTGGAAAGCGTACTTCTTGGCTGCGGCCTGGCGGTGA			MRFCIQLVWKAYFLAAAWR*	MRFCIQLVWKAYFLAAAWR*			AAATCCATAA	CTTCAAGAAC	0		FG05608.1	0	NCU03316.1	0	0

10408	4489	ao	AN7560.1	72.m19581	AO070343000400	0					-265	-236	ATGAAGGATATACCACTCAATTCGCCATGA			ATGAAGGATATACCACTCAATTCGCCATGA	MKDIPLNSP*			MKDIPLNSP*	AGCGGGCCAT	ATCTATAGCT	0		FG05608.1	0	NCU03316.1	0	0
10409	4489	ao	AN7560.1	72.m19581	AO070343000400	0					-239	-228	ATGAATCTATAG			ATGAATCTATAG	MNL*			MNL*	TCAATTCGCC	CTATAGTATC	0		FG05608.1	0	NCU03316.1	0	0
10410	4489	ao	AN7560.1	72.m19581	AO070343000400	0					-216	-136	ATGAGTGAGTACAAGCGAGAGACGAGCTACTCAAAACCAATAATAATACAAGAATCACCAATTATTCAAGCTCCATTGTAG			ATGAGTGAGTACAAGCGAGAGACGAGCTACTCAAAACCAATAATAATACAAGAATCACCAATTATTCAAGCTCCATTGTAG	MSEYKRETSYSKPIIIQESPIIQAPL*			MSEYKRETSYSKPIIIQESPIIQAPL*	TATAGTATCA	CAAACCTTGC	0		FG05608.1	0	NCU03316.1	0	0
10411	4491	af	AN6654.1	62.m03256	AO070269000012	0			-237	-187			ATGATCGCTTATCTATTATCGGCTCCTATCCTTGTCTGTAATATGCAATAG		ATGATCGCTTATCTATTATCGGCTCCTATCCTTGTCTGTAATATGCAATAG		MIAYLLSAPILVCNMQ*		MIAYLLSAPILVCNMQ*		AATTCCTATC	CACCGGTGTG	0	E	0	MG02538.1	0	0	0
10412	4491	ao	AN6654.1	62.m03256	AO070269000012	0					-207	-136	ATGGACAATGGCAAGGAAGCAGTTTATCTCCTATGCGGTCATTTGATCCGCATGACGATAAGGCGCCGATAA			ATGGACAATGGCAAGGAAGCAGTTTATCTCCTATGCGGTCATTTGATCCGCATGACGATAAGGCGCCGATAA	MDNGKEAVYLLCGHLIRMTIRRR*			MDNGKEAVYLLCGHLIRMTIRRR*	TATGATGTGA	CAGATGACCC	0	E	0	MG02538.1	0	0	0
10413	4491	ao	AN6654.1	62.m03256	AO070269000012	0					-200	-162	ATGGCAAGGAAGCAGTTTATCTCCTATGCGGTCATTTGA			ATGGCAAGGAAGCAGTTTATCTCCTATGCGGTCATTTGA	MARKQFISYAVI*			MARKQFISYAVI*	TGAATGGACA	TCCGCATGAC	0	E	0	MG02538.1	0	0	0
10414	4491	ao	AN6654.1	62.m03256	AO070269000012	0					-156	-136	ATGACGATAAGGCGCCGATAA			ATGACGATAAGGCGCCGATAA	MTIRRR*			MTIRRR*	TTTGATCCGC	CAGATGACCC	0	E	0	MG02538.1	0	0	0
10415	4491	ao	AN6654.1	62.m03256	AO070269000012	0					-132	-91	ATGACCCGCTGTGGCTCCTTCGTTCCGCCCACACCTTCTTAG			ATGACCCGCTGTGGCTCCTTCGTTCCGCCCACACCTTCTTAG	MTRCGSFVPPTPS*			MTRCGSFVPPTPS*	CCGATAACAG	ACCGCGATTC	0	E	0	MG02538.1	0	0	0
10416	4491	ao	AN6654.1	62.m03256	AO070269000012	0					-62	-30	ATGTCTTTCGACCACTTTTATTCCTATATTTGA			ATGTCTTTCGACCACTTTTATTCCTATATTTGA	MSFDHFYSYI*			MSFDHFYSYI*	TTGCAGGCTC	ACTGACGTTG	0	E	0	MG02538.1	0	0	0
10417	4492	af	AN4442.1	58.m09016	AO070273000012	0			-254	-129			ATGACCGAATGTCATCGGTACAGTAGAGTGACCACTAGCATTCATCCATCGGCCTGGCCGGTCGTTACCCTTCCTGATACTAAATCATCGATGTGCCCAGATTCCTCCAAGCGCATATTTCTTTGA		ATGACCGAATGTCATCGGTACAGTAGAGTGACCACTAGCATTCATCCATCGGCCTGGCCGGTCGTTACCCTTCCTGATACTAAATCATCGATGTGCCCAGATTCCTCCAAGCGCATATTTCTTTGA		MTECHRYSRVTTSIHPSAWPVVTLPDTKSSMCPDSSKRIFL*		MTECHRYSRVTTSIHPSAWPVVTLPDTKSSMCPDSSKRIFL*		CTCAGCGACC	CTGTTGGCTT	0	O	0	0	0	0	0
10418	4492	af	AN4442.1	58.m09016	AO070273000012	0			-246	-229			ATGTCATCGGTACAGTAG		ATGTCATCGGTACAGTAG		MSSVQ*		MSSVQ*		CCATGACCGA	AGTGACCACT	0	O	0	0	0	0	0
10419	4492	af	AN4442.1	58.m09016	AO070273000012	0			-164	-129			ATGTGCCCAGATTCCTCCAAGCGCATATTTCTTTGA		ATGTGCCCAGATTCCTCCAAGCGCATATTTCTTTGA		MCPDSSKRIFL*		MCPDSSKRIFL*		TAAATCATCG	CTGTTGGCTT	0	O	0	0	0	0	0
10420	4494	ao	AN6279.1	72.m19361	AO070308000038	0					-174	-46	ATGTTTACGGCTTCTGCTCGAAGCCGTCTCTCCACACTTTCGCGGCCCCGTCTCTCTCCTACCAACTCTCTTCTTGCTAGATCTGCTGTGGTATGGCTCGCGCAATTGACCTCATTTCTACGCCCCTGA			ATGTTTACGGCTTCTGCTCGAAGCCGTCTCTCCACACTTTCGCGGCCCCGTCTCTCTCCTACCAACTCTCTTCTTGCTAGATCTGCTGTGGTATGGCTCGCGCAATTGACCTCATTTCTACGCCCCTGA	MFTASARSRLSTLSRPRLSPTNSLLARSAVVWLAQLTSFLRP*			MFTASARSRLSTLSRPRLSPTNSLLARSAVVWLAQLTSFLRP*	GTCCAGAGGG	ATTGGATTCG	0	I	0	MG01721.1	0	0	0
10421	4494	ao	AN6279.1	72.m19361	AO070308000038	0					-82	-23	ATGGCTCGCGCAATTGACCTCATTTCTACGCCCCTGAATTGGATTCGAATGGCATGTTAA			ATGGCTCGCGCAATTGACCTCATTTCTACGCCCCTGAATTGGATTCGAATGGCATGTTAA	MARAIDLISTPLNWIRMAC*			MARAIDLISTPLNWIRMAC*	CTGCTGTGGT	CTGGCATATG	0	I	0	MG01721.1	0	0	0
10424	4495	af	AN5673.1	65.m07399	AO070309000086	0			-81	-61			ATGATCATGCCTGCTTGCTGA		ATGATCATGCCTGCTTGCTGA		MIMPAC*		MIMPAC*		TTTGCTGCCG	TGATAGTGCT	0		0	0	0	0	0
10425	4495	af	AN5673.1	65.m07399	AO070309000086	0			-75	-61			ATGCCTGCTTGCTGA		ATGCCTGCTTGCTGA		MPAC*		MPAC*		GCCGATGATC	TGATAGTGCT	0		0	0	0	0	0
10426	4495	af	AN5673.1	65.m07399	AO070309000086	0			-61	-23			ATGATAGTGCTGCTCTTGCTTATGGAAGCTTTCCCATAA		ATGATAGTGCTGCTCTTGCTTATGGAAGCTTTCCCATAA		MIVLLLLMEAFP*		MIVLLLLMEAFP*		CTGCTTGCTG	CCCCGAAACT	0		0	0	0	0	0
10423	4495	an	AN5673.1	65.m07399	AO070309000086	0	-64	-47					ATGCATTCCCGCTATTGA	ATGCATTCCCGCTATTGA			MHSRY*	MHSRY*			CCCGCTCATT	TGGTGGACGG	0		0	0	0	0	0
10428	4495	ao	AN5673.1	65.m07399	AO070309000086	0					-210	-40	ATGTTGTTGATTCTTTCTGGGTTCCTCTCCCTCTGTTCCCTACGCCCTAGACTCAGCTTCTTCGACAATATCAAACTGTTAGATCTAATTCTTCACAGAATTTTTCGGCTTTCGGACCGAACCAAGTTCATCACCGATACGGGTCCCCGTCATGATGCAGTAGGGGCTTGA			ATGTTGTTGATTCTTTCTGGGTTCCTCTCCCTCTGTTCCCTACGCCCTAGACTCAGCTTCTTCGACAATATCAAACTGTTAGATCTAATTCTTCACAGAATTTTTCGGCTTTCGGACCGAACCAAGTTCATCACCGATACGGGTCCCCGTCATGATGCAGTAGGGGCTTGA	MLLILSGFLSLCSLRPRLSFFDNIKLLDLILHRIFRLSDRTKFITDTGPRHDAVGA*			MLLILSGFLSLCSLRPRLSFFDNIKLLDLILHRIFRLSDRTKFITDTGPRHDAVGA*	TCCTTCGCGC	CCGAGGATCT	0		0	0	0	0	0
10433	4497	af	AN6572.1	62.m03169	AO070326000015	0			-241	-206			ATGCCCGCTTCTTATCTCCCAGTCCAAATCCACTGA		ATGCCCGCTTCTTATCTCCCAGTCCAAATCCACTGA		MPASYLPVQIH*		MPASYLPVQIH*		AGCATAAATA	TAAGCTCGTC	0	R	0	0	0	0	0
10434	4497	af	AN6572.1	62.m03169	AO070326000015	0			-163	-113			ATGTGGGCAGAAAAAGGCGGATGCGAGAGGAACGATGCAAGTAAGCAATAA		ATGTGGGCAGAAAAAGGCGGATGCGAGAGGAACGATGCAAGTAAGCAATAA		MWAEKGGCERNDASKQ*		MWAEKGGCERNDASKQ*		CCGGCGGTGG	TGGTCCGATG	0	R	0	0	0	0	0
10435	4497	af	AN6572.1	62.m03169	AO070326000015	0			-143	-120			ATGCGAGAGGAACGATGCAAGTAA		ATGCGAGAGGAACGATGCAAGTAA		MREERCK*		MREERCK*		AAAAAGGCGG	GCAATAATGG	0	R	0	0	0	0	0
10436	4497	af	AN6572.1	62.m03169	AO070326000015	0			-129	-100			ATGCAAGTAAGCAATAATGGTCCGATGTGA		ATGCAAGTAAGCAATAATGGTCCGATGTGA		MQVSNNGPM*		MQVSNNGPM*		GAGAGGAACG	GCTTCTGATC	0	R	0	0	0	0	0
10437	4497	af	AN6572.1	62.m03169	AO070326000015	0			-113	-36			ATGGTCCGATGTGAGCTTCTGATCGATTTTCCGCAAGTTGATACTACCCTCTCGCATTACATCATGCGATTAAGCTAG		ATGGTCCGATGTGAGCTTCTGATCGATTTTCCGCAAGTTGATACTACCCTCTCGCATTACATCATGCGATTAAGCTAG		MVRCELLIDFPQVDTTLSHYIMRLS*		MVRCELLIDFPQVDTTLSHYIMRLS*		GTAAGCAATA	ACCAAGAGCT	0	R	0	0	0	0	0
10430	4497	an	AN6572.1	62.m03169	AO070326000015	0	-151	-62					ATGGCAGAATTGACTCGAAAAGAATCTCTAGAAGATGACGGAAACAAACTACAGCAAAACCAACGGGATTTAACCATGCGAGTGCGTTGA	ATGGCAGAATTGACTCGAAAAGAATCTCTAGAAGATGACGGAAACAAACTACAGCAAAACCAACGGGATTTAACCATGCGAGTGCGTTGA			MAELTRKESLEDDGNKLQQNQRDLTMRVR*	MAELTRKESLEDDGNKLQQNQRDLTMRVR*			GCGGTAAGCT	TTACGGGCAC	0	R	0	0	0	0	0
10431	4497	an	AN6572.1	62.m03169	AO070326000015	0	-117	-79					ATGACGGAAACAAACTACAGCAAAACCAACGGGATTTAA	ATGACGGAAACAAACTACAGCAAAACCAACGGGATTTAA			MTETNYSKTNGI*	MTETNYSKTNGI*			TCTCTAGAAG	CCATGCGAGT	0	R	0	0	0	0	0
10432	4497	an	AN6572.1	62.m03169	AO070326000015	0	-76	-62					ATGCGAGTGCGTTGA	ATGCGAGTGCGTTGA			MRVR*	MRVR*			GGATTTAACC	TTACGGGCAC	0	R	0	0	0	0	0
10439	4497	ao	AN6572.1	62.m03169	AO070326000015	0					-73	-11	ATGACAAATTGCGCCCGTTCGTCATGCGAGCTCATTAGACCGGACACAAAACTGATATTCTAG			ATGACAAATTGCGCCCGTTCGTCATGCGAGCTCATTAGACCGGACACAAAACTGATATTCTAG	MTNCARSSCELIRPDTKLIF*			MTNCARSSCELIRPDTKLIF*	TGGTCAACCT	GATTTATACT	0	R	0	0	0	0	0
10447	4502	af	AN5491.1	69.m15461	AO070341000394	0			-65	-48			ATGTCCCTGCTCCGATGA		ATGTCCCTGCTCCGATGA		MSLLR*		MSLLR*		TCATCTTATT	CATTCGAAAC	0	U	0	0	0	0	0
10449	4502	ao	AN5491.1	69.m15461	AO070341000394	0					-66	-49	ATGATACCCACCCGATGA			ATGATACCCACCCGATGA	MIPTR*			MIPTR*	TTTTCATATT	CACCTGCGGT	0	U	0	0	0	0	0
10451	4508	af	AN1695.1	58.m07771	AO070305000019	0			-167	-135			ATGTCTCTCTCTCTCTCCCTCTCTTCACGGTAA		ATGTCTCTCTCTCTCTCCCTCTCTTCACGGTAA		MSLSLSLSSR*		MSLSLSLSSR*		CTACCTGTAC	AGTCATCTAC	0	S	0	0	0	0	0
10452	4508	af	AN1695.1	58.m07771	AO070305000019	0			-119	-15			ATGCCCTCAGAACTAGTCACCGGTGAGAACCTAGCGGGAGCTTTGGTTGCAGCGCAAGAACGTTACGTACCGAGAAAGACGTTTCACGGATTCCTCAACGAGTGA		ATGCCCTCAGAACTAGTCACCGGTGAGAACCTAGCGGGAGCTTTGGTTGCAGCGCAAGAACGTTACGTACCGAGAAAGACGTTTCACGGATTCCTCAACGAGTGA		MPSELVTGENLAGALVAAQERYVPRKTFHGFLNE*		MPSELVTGENLAGALVAAQERYVPRKTFHGFLNE*		TCTACTTACC	GCAGCAGCAG	0	S	0	0	0	0	0
10453	4508	ao	AN1695.1	58.m07771	AO070305000019	0					-213	-199	ATGCCCTTGGTGTAG			ATGCCCTTGGTGTAG	MPLV*			MPLV*	AAGACCACGT	CCAGAGCTCC	0	S	0	0	0	0	0
10454	4515	af	AN1175.1	70.m15042	AO070331000170	0			-172	-143			ATGCAAATCAAACAAAGCAAACACAGATAA		ATGCAAATCAAACAAAGCAAACACAGATAA		MQIKQSKHR*		MQIKQSKHR*		AATCCCCACC	AAAAAAGACA	0	A	0	0	0	0	0
10455	4515	af	AN1175.1	70.m15042	AO070331000170	0			-118	-11			ATGGTCGAGGACGCATGGACATTGAAGAAAGGAAAAATATACGCCATTGCCATTAAACAAGTCGGACCCCTTCCTGCTTCTTCCTGCATGAATAAAACAAAACCTTAG		ATGGTCGAGGACGCATGGACATTGAAGAAAGGAAAAATATACGCCATTGCCATTAAACAAGTCGGACCCCTTCCTGCTTCTTCCTGCATGAATAAAACAAAACCTTAG		MVEDAWTLKKGKIYAIAIKQVGPLPASSCMNKTKP*		MVEDAWTLKKGKIYAIAIKQVGPLPASSCMNKTKP*		TAAAAGAAAA	ATCACCAGTC	0	A	0	0	0	0	0
10456	4515	af	AN1175.1	70.m15042	AO070331000170	0			-104	-63			ATGGACATTGAAGAAAGGAAAAATATACGCCATTGCCATTAA		ATGGACATTGAAGAAAGGAAAAATATACGCCATTGCCATTAA		MDIEERKNIRHCH*		MDIEERKNIRHCH*		TCGAGGACGC	ACAAGTCGGA	0	A	0	0	0	0	0
10458	4515	ao	AN1175.1	70.m15042	AO070331000170	0					-62	-51	ATGTCTGTATGA			ATGTCTGTATGA	MSV*			MSV*	AAAAAAGATT	TTGTCTTCGG	0	A	0	0	0	0	0
10459	4520	an	AN1344.1	70.m14889	AO070247000020	0	-86	-54					ATGTCGCCCGCCCTGACTCAAGAGTCCCGCTGA	ATGTCGCCCGCCCTGACTCAAGAGTCCCGCTGA			MSPALTQESR*	MSPALTQESR*			AATTTCCCGC	CTGATGTGCA	0	J	0	0	0	0	0
10460	4520	ao	AN1344.1	70.m14889	AO070247000020	0					-104	-75	ATGACTCAATCTACTAACCATTGCACATAG			ATGACTCAATCTACTAACCATTGCACATAG	MTQSTNHCT*			MTQSTNHCT*	CGTGTGCGGC	ACACCAAGGA	0	J	0	0	0	0	0
10461	4522	af	AN6644.1	62.m03242	AO070295000021	0			-89				ATGCGGCTATCGTCGATATTGTATCACTCTCATCTCTACCTTGATAGTGAGGTATCGTTGTACAGGCCACAGCATAGGCTGATTATCTGA		ATGCGGCTATCGTCGATATTGTATCACTCTCATCTCTACCTTGATAGTGAGGTATCGTTGTACAGGCCACAGCATAGGCTGATTATCTGA		MRLSSILYHSHLYLDSEVSLYRPQHRLII*		MRLSSILYHSHLYLDSEVSLYRPQHRLII*		ATAGTCGGCT	TGCCTCCGGT	0	E	0	0	0	0	0
10464	4523	af	AN1459.1	55.m02963	AO070306000075	0			-179	-165			ATGTGCTTTCCGTGA		ATGTGCTTTCCGTGA		MCFP*		MCFP*		CCGTACTACC	TCATCGTTGT	0	O	0	0	0	0	0
10465	4523	af	AN1459.1	55.m02963	AO070306000075	0			-141	-127			ATGGCGATCCTCTGA		ATGGCGATCCTCTGA		MAIL*		MAIL*		TTATTGCTCA	TCCTGGAGCT	0	O	0	0	0	0	0
10463	4523	an	AN1459.1	55.m02963	AO070306000075	0	-146	-120					ATGCAGCTTTCTTGTCCAATTCCATAG	ATGCAGCTTTCTTGTCCAATTCCATAG			MQLSCPIP*	MQLSCPIP*			CGATCCGACT	CTAATTTGAA	0	O	0	0	0	0	0
10466	4523	ao	AN1459.1	55.m02963	AO070306000075	0					-168	-151	ATGATGTCCTTTTCCTGA			ATGATGTCCTTTTCCTGA	MMSFS*			MMSFS*	CTTTCTCTAT	TTGCTTTCTG	0	O	0	0	0	0	0
10467	4523	ao	AN1459.1	55.m02963	AO070306000075	0					-165	-151	ATGTCCTTTTCCTGA			ATGTCCTTTTCCTGA	MSFS*			MSFS*	TCTCTATATG	TTGCTTTCTG	0	O	0	0	0	0	0
10468	4523	ao	AN1459.1	55.m02963	AO070306000075	0					-139	-113	ATGTCATCGCATGGAGAATATTCCTGA			ATGTCATCGCATGGAGAATATTCCTGA	MSSHGEYS*			MSSHGEYS*	TGCTTTCTGT	GTTTCTATTC	0	O	0	0	0	0	0
10469	4523	ao	AN1459.1	55.m02963	AO070306000075	0					-129	-91	ATGGAGAATATTCCTGAGTTTCTATTCTCCTTGCTCTAG			ATGGAGAATATTCCTGAGTTTCTATTCTCCTTGCTCTAG	MENIPEFLFSLL*			MENIPEFLFSLL*	ATGTCATCGC	CTAACCAATT	0	O	0	0	0	0	0
10470	4525	af	AN0919.1	70.m15526	AO070320000099	0			-174	-82			ATGTCTAGCTCACCAAAGAAATGGGAGCTCCATTCATTACTATTATTGATTGACCCTTTTCCAGTCCTCGAACCCCCAAGAGGCGATAGTTAA		ATGTCTAGCTCACCAAAGAAATGGGAGCTCCATTCATTACTATTATTGATTGACCCTTTTCCAGTCCTCGAACCCCCAAGAGGCGATAGTTAA		MSSSPKKWELHSLLLLIDPFPVLEPPRGDS*		MSSSPKKWELHSLLLLIDPFPVLEPPRGDS*		TAGTTAGTAC	AAGAAACAAG	0	F	0	0	0	0	0
10471	4525	af	AN0919.1	70.m15526	AO070320000099	0			-154	-122			ATGGGAGCTCCATTCATTACTATTATTGATTGA		ATGGGAGCTCCATTCATTACTATTATTGATTGA		MGAPFITIID*		MGAPFITIID*		CACCAAAGAA	CCCTTTTCCA	0	F	0	0	0	0	0
10473	4526	af	AN4843.1	59.m09135	AO070327000126	0			-105	-94			ATGCTTTATTAG		ATGCTTTATTAG		MLY*		MLY*		TGCCCCGCCA	ACCGAGCAAT	0	G	0	0	0	YJL221C	0
10472	4526	an	AN4843.1	59.m09135	AO070327000126	0	-157	-125					ATGGCTGGACAGCCGCCAGCTTACGAGGGGTAA	ATGGCTGGACAGCCGCCAGCTTACGAGGGGTAA			MAGQPPAYEG*	MAGQPPAYEG*			TGTAACAACA	GGTCTCCGCC	0	G	0	0	0	YJL221C	0
10474	4526	ao	AN4843.1	59.m09135	AO070327000126	0					-176	-30	ATGCACCCACCGATAATTTCTCCGCTCGAGAAAGGAGCTGCCCCGCGGTGGGTGTTATCGGATAGCAAGCTGCCCCTCCCAGCAACAACAAAACATATAGATAAACTGAAGCCTCCCTCTTTCTTTTGTATATTCAAGTTACTCTAG			ATGCACCCACCGATAATTTCTCCGCTCGAGAAAGGAGCTGCCCCGCGGTGGGTGTTATCGGATAGCAAGCTGCCCCTCCCAGCAACAACAAAACATATAGATAAACTGAAGCCTCCCTCTTTCTTTTGTATATTCAAGTTACTCTAG	MHPPIISPLEKGAAPRWVLSDSKLPLPATTKHIDKLKPPSFFCIFKLL*			MHPPIISPLEKGAAPRWVLSDSKLPLPATTKHIDKLKPPSFFCIFKLL*	TAGGTCGGCA	GAAATCATAT	0	G	0	0	0	YJL221C	0
10475	4528	an	AN4775.1	59.m09208	AO070329000077	0	-254	-168					ATGGAGGAGACGTTTCCCCTTATTAGTATATGGACTCCGGACTGGAATGAAATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGA	ATGGAGGAGACGTTTCCCCTTATTAGTATATGGACTCCGGACTGGAATGAAATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGA			MEETFPLISIWTPDWNEMSRDRKLGQLD*	MEETFPLISIWTPDWNEMSRDRKLGQLD*			GACGAGATTG	CGCCGCAAGC	0	O	FG09432.1	MG02608.1	0	0	0
10476	4528	an	AN4775.1	59.m09208	AO070329000077	0	-225	-205					ATGGACTCCGGACTGGAATGA	ATGGACTCCGGACTGGAATGA			MDSGLE*	MDSGLE*			TTATTAGTAT	AATGTCACGT	0	O	FG09432.1	MG02608.1	0	0	0
10477	4528	an	AN4775.1	59.m09208	AO070329000077	0	-208	-125					ATGAAATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGACGCCGCAAGCTCCAGATGCAATCATACTCCATCATCACTCTGA	ATGAAATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGACGCCGCAAGCTCCAGATGCAATCATACTCCATCATCACTCTGA			MKCHVIGSSASLTDAASSRCNHTPSSL*	MKCHVIGSSASLTDAASSRCNHTPSSL*			CCGGACTGGA	CCTTATCCCC	0	O	FG09432.1	MG02608.1	0	0	0
10478	4528	an	AN4775.1	59.m09208	AO070329000077	0	-203	-168					ATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGA	ATGTCACGTGATAGGAAGCTCGGCCAGCTTGACTGA			MSRDRKLGQLD*	MSRDRKLGQLD*			CTGGAATGAA	CGCCGCAAGC	0	O	FG09432.1	MG02608.1	0	0	0
10483	4530	af	AN5749.1	69.m14847	AO070341000006	0			-186	-172			ATGAACAACCTTTGA		ATGAACAACCTTTGA		MNNL*		MNNL*		GTCGAGGCGG	CCGTTGTTGT	0	E	0	0	0	0	0
10484	4530	af	AN5749.1	69.m14847	AO070341000006	0			-120	-91			ATGGAATATACCGTGGTTTACCCTTGCTAG		ATGGAATATACCGTGGTTTACCCTTGCTAG		MEYTVVYPC*		MEYTVVYPC*		CCTCTCTATC	TTCATCAACT	0	E	0	0	0	0	0
10479	4530	an	AN5749.1	69.m14847	AO070341000006	0	-235	-215					ATGCAGGTTCATTATGATTGA	ATGCAGGTTCATTATGATTGA			MQVHYD*	MQVHYD*			TCAGGGTGGA	GAGAGGATGG	0	E	0	0	0	0	0
10480	4530	an	AN5749.1	69.m14847	AO070341000006	0	-222	-190					ATGATTGAGAGAGGATGGTCGCTTGTGTACTGA	ATGATTGAGAGAGGATGGTCGCTTGTGTACTGA			MIERGWSLVY*	MIERGWSLVY*			CAGGTTCATT	GATCTCTGTA	0	E	0	0	0	0	0

10481	4530	an	AN5749.1	69.m14847	AO070341000006	0	-208	-179					ATGGTCGCTTGTGTACTGAGATCTCTGTAG	ATGGTCGCTTGTGTACTGAGATCTCTGTAG			MVACVLRSL*	MVACVLRSL*			TTGAGAGAGG	TTTATTCTAT	0	E	0	0	0	0	0
10485	4530	ao	AN5749.1	69.m14847	AO070341000006	0					-165	-94	ATGCACGTGACATGCGCTGGACCCTCGGAACAGAAAACCCCAATTCACTTGCGCCATTTACGTAGAACTTGA			ATGCACGTGACATGCGCTGGACCCTCGGAACAGAAAACCCCAATTCACTTGCGCCATTTACGTAGAACTTGA	MHVTCAGPSEQKTPIHLRHLRRT*			MHVTCAGPSEQKTPIHLRHLRRT*	CTTCTCCGGG	GATAACATCG	0	E	0	0	0	0	0
10486	4530	ao	AN5749.1	69.m14847	AO070341000006	0					-154	-101	ATGCGCTGGACCCTCGGAACAGAAAACCCCAATTCACTTGCGCCATTTACGTAG			ATGCGCTGGACCCTCGGAACAGAAAACCCCAATTCACTTGCGCCATTTACGTAG	MRWTLGTENPNSLAPFT*			MRWTLGTENPNSLAPFT*	TGCACGTGAC	AACTTGAGAT	0	E	0	0	0	0	0
10488	4532	af	AN4341.1	58.m07983	AO070240000016	0			-171	-115			ATGACGTTGTCAAGGTGGCCTCGATCTGTGCGTTCCGCCCATTGGCGGTACCACTAA		ATGACGTTGTCAAGGTGGCCTCGATCTGTGCGTTCCGCCCATTGGCGGTACCACTAA		MTLSRWPRSVRSAHWRYH*		MTLSRWPRSVRSAHWRYH*		TGTGATCGAA	ACAAACGATA	0		0	0	0	0	0
10489	4532	af	AN4341.1	58.m07983	AO070240000016	0			-78	-43			ATGCTATACAACACGATGGAGAGACGGAATTTCTGA		ATGCTATACAACACGATGGAGAGACGGAATTTCTGA		MLYNTMERRNF*		MLYNTMERRNF*		CACTATTGCC	GATTTACACT	0		0	0	0	0	0
10490	4532	af	AN4341.1	58.m07983	AO070240000016	0			-63	-43			ATGGAGAGACGGAATTTCTGA		ATGGAGAGACGGAATTTCTGA		MERRNF*		MERRNF*		ATACAACACG	GATTTACACT	0		0	0	0	0	0
10487	4532	an	AN4341.1	58.m07983	AO070240000016	0	-112	-86					ATGACGTTGTCACGTTGCCAGAACTGA	ATGACGTTGTCACGTTGCCAGAACTGA			MTLSRCQN*	MTLSRCQN*			AGTAGCGCAA	TCGGATCTTC	0		0	0	0	0	0
10492	4532	ao	AN4341.1	58.m07983	AO070240000016	0					-202	-35	ATGAACTCTCGTAACTTGGATGACGTTGTCATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAATCCGTCGGCGGCGTTTCTGCCCGCCTTTCAACACAGCATCTAATTGTACCCACCTGAAACTACCACACAAGGCCATTGTCAACGCCATGGTAAATGACGGTTGA			ATGAACTCTCGTAACTTGGATGACGTTGTCATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAATCCGTCGGCGGCGTTTCTGCCCGCCTTTCAACACAGCATCTAATTGTACCCACCTGAAACTACCACACAAGGCCATTGTCAACGCCATGGTAAATGACGGTTGA	MNSRNLDDVVMLASLSFLPHLIRRRRFCPPFNTASNCTHLKLPHKAIVNAMVNDG*			MNSRNLDDVVMLASLSFLPHLIRRRRFCPPFNTASNCTHLKLPHKAIVNAMVNDG*	TCGTGGAACA	CTAGTTCAAT	0		0	0	0	0	0
10493	4532	ao	AN4341.1	58.m07983	AO070240000016	0					-183	-139	ATGACGTTGTCATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAA			ATGACGTTGTCATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAA	MTLSCWPLSRFCPI*			MTLSCWPLSRFCPI*	CGTAACTTGG	TCCGTCGGCG	0		0	0	0	0	0
10494	4532	ao	AN4341.1	58.m07983	AO070240000016	0					-172	-35	ATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAATCCGTCGGCGGCGTTTCTGCCCGCCTTTCAACACAGCATCTAATTGTACCCACCTGAAACTACCACACAAGGCCATTGTCAACGCCATGGTAAATGACGGTTGA			ATGTTGGCCTCTCTCTCGTTTCTGCCCCATTTAATCCGTCGGCGGCGTTTCTGCCCGCCTTTCAACACAGCATCTAATTGTACCCACCTGAAACTACCACACAAGGCCATTGTCAACGCCATGGTAAATGACGGTTGA	MLASLSFLPHLIRRRRFCPPFNTASNCTHLKLPHKAIVNAMVNDG*			MLASLSFLPHLIRRRRFCPPFNTASNCTHLKLPHKAIVNAMVNDG*	TGACGTTGTC	CTAGTTCAAT	0		0	0	0	0	0
10501	4534	af	AN9010.1	52.m03996	AO070289000056	0			-194	-66			ATGACAGCAAGGCAGCGGAACAGGCCCGTCAGAACCATTGGGAAATCCAGCCCACGGGAACACCCCACAGTCTGGGGTAAAAGTTGGGGTAAGCGATCAACATGGGGAAGCGGGAATCCATCGATATAA		ATGACAGCAAGGCAGCGGAACAGGCCCGTCAGAACCATTGGGAAATCCAGCCCACGGGAACACCCCACAGTCTGGGGTAAAAGTTGGGGTAAGCGATCAACATGGGGAAGCGGGAATCCATCGATATAA		MTARQRNRPVRTIGKSSPREHPTVWGKSWGKRSTWGSGNPSI*		MTARQRNRPVRTIGKSSPREHPTVWGKSWGKRSTWGSGNPSI*		GGGCAGTGGA	GTAGATCGAC	0	G	0	0	0	0	0
10502	4534	af	AN9010.1	52.m03996	AO070289000056	0			-93	-7			ATGGGGAAGCGGGAATCCATCGATATAAGTAGATCGACACCCTGCATCTTCCTTCTTTCATCACTACGGTTGCATCCCCCTCTATAA		ATGGGGAAGCGGGAATCCATCGATATAAGTAGATCGACACCCTGCATCTTCCTTCTTTCATCACTACGGTTGCATCCCCCTCTATAA		MGKRESIDISRSTPCIFLLSSLRLHPPL*		MGKRESIDISRSTPCIFLLSSLRLHPPL*		AGCGATCAAC	GCCATTATGT	0	G	0	0	0	0	0
10498	4534	an	AN9010.1	52.m03996	AO070289000056	0	-186	-40					ATGGAGCACGCAAGCTTCCCCTCGCCGGCATTTTGGTGGCATTGCGGGGTATCATTCCGCTATCTGGGGAAGGGTCTGAAGTCTTCTAGGGCAAAAAATGCGGGGTTGAAGGTCTTCTCTTTAAGAATGCCAACGCTGGCCTCCTGA	ATGGAGCACGCAAGCTTCCCCTCGCCGGCATTTTGGTGGCATTGCGGGGTATCATTCCGCTATCTGGGGAAGGGTCTGAAGTCTTCTAGGGCAAAAAATGCGGGGTTGAAGGTCTTCTCTTTAAGAATGCCAACGCTGGCCTCCTGA			MEHASFPSPAFWWHCGVSFRYLGKGLKSSRAKNAGLKVFSLRMPTLAS*	MEHASFPSPAFWWHCGVSFRYLGKGLKSSRAKNAGLKVFSLRMPTLAS*			ACCATACCCT	GTGTAATTCC	0	G	0	0	0	0	0
10499	4534	an	AN9010.1	52.m03996	AO070289000056	0	-89	-78					ATGCGGGGTTGA	ATGCGGGGTTGA			MRG*	MRG*			AGGGCAAAAA	AGGTCTTCTC	0	G	0	0	0	0	0
10503	4534	ao	AN9010.1	52.m03996	AO070289000056	0					-108	-88	ATGGACTTTCTGTGTTTATAA			ATGGACTTTCTGTGTTTATAA	MDFLCL*			MDFLCL*	AGCTCAAAGC	GCAGGTCGAT	0	G	0	0	0	0	0
10504	4535	an	AN2281.1	71.m15926	AO070295000058	0	-146	-60					ATGACTTGTCACGTCCGCCTCTCTCTTGCTCTATCTTTCTTACCGTCTCACACTTTGCTCAATTTATCACCTGACCGAGTTATATGA	ATGACTTGTCACGTCCGCCTCTCTCTTGCTCTATCTTTCTTACCGTCTCACACTTTGCTCAATTTATCACCTGACCGAGTTATATGA			MTCHVRLSLALSFLPSHTLLNLSPDRVI*	MTCHVRLSLALSFLPSHTLLNLSPDRVI*			ATCGCCATCA	TGAACTGCAT	0	MU	0	0	0	0	0
10509	4535	ao	AN2281.1	71.m15926	AO070295000058	0					-250	-194	ATGATTTCACGTTGCTATCGAACTTTAGCCGAGGCCGCGCCAGACGGTTGGCCATGA			ATGATTTCACGTTGCTATCGAACTTTAGCCGAGGCCGCGCCAGACGGTTGGCCATGA	MISRCYRTLAEAAPDGWP*			MISRCYRTLAEAAPDGWP*	GCACCACCCC	TTTTATCATT	0	MU	0	0	0	0	0
10510	4535	ao	AN2281.1	71.m15926	AO070295000058	0					-197	-102	ATGATTTTATCATTCCCCGACCGTCTCGCTCGGCTGTTGTCATTGATGATCGGTCCTTCTTCACCTCCTCTCCCCTTTTATATTCCCTGGCATTAG			ATGATTTTATCATTCCCCGACCGTCTCGCTCGGCTGTTGTCATTGATGATCGGTCCTTCTTCACCTCCTCTCCCCTTTTATATTCCCTGGCATTAG	MILSFPDRLARLLSLMIGPSSPPLPFYIPWH*			MILSFPDRLARLLSLMIGPSSPPLPFYIPWH*	ACGGTTGGCC	CTTGCCTCTG	0	MU	0	0	0	0	0
10511	4535	ao	AN2281.1	71.m15926	AO070295000058	0					-152	-102	ATGATCGGTCCTTCTTCACCTCCTCTCCCCTTTTATATTCCCTGGCATTAG			ATGATCGGTCCTTCTTCACCTCCTCTCCCCTTTTATATTCCCTGGCATTAG	MIGPSSPPLPFYIPWH*			MIGPSSPPLPFYIPWH*	GTTGTCATTG	CTTGCCTCTG	0	MU	0	0	0	0	0
10515	4537	af	AN3124.1	59.m08612	AO070303000023	0			-232	-179			ATGTCAATGTGGCAGCCTGAAGAAGATGGCATCAACGAGCGACTTCCATTTTAG		ATGTCAATGTGGCAGCCTGAAGAAGATGGCATCAACGAGCGACTTCCATTTTAG		MSMWQPEEDGINERLPF*		MSMWQPEEDGINERLPF*		ACAGAAGTAC	GACGTGTTGT	0	Z	0	0	0	0	0
10516	4537	af	AN3124.1	59.m08612	AO070303000023	0			-226	-179			ATGTGGCAGCCTGAAGAAGATGGCATCAACGAGCGACTTCCATTTTAG		ATGTGGCAGCCTGAAGAAGATGGCATCAACGAGCGACTTCCATTTTAG		MWQPEEDGINERLPF*		MWQPEEDGINERLPF*		GTACATGTCA	GACGTGTTGT	0	Z	0	0	0	0	0
10517	4537	af	AN3124.1	59.m08612	AO070303000023	0			-207	-142			ATGGCATCAACGAGCGACTTCCATTTTAGGACGTGTTGTCTGGACAACCAAAGCCTAACCCGATGA		ATGGCATCAACGAGCGACTTCCATTTTAGGACGTGTTGTCTGGACAACCAAAGCCTAACCCGATGA		MASTSDFHFRTCCLDNQSLTR*		MASTSDFHFRTCCLDNQSLTR*		CCTGAAGAAG	GGAAAGAGAA	0	Z	0	0	0	0	0
10518	4537	af	AN3124.1	59.m08612	AO070303000023	0			-145	-86			ATGAGGAAAGAGAATATCGTCCCTGTCAACTGTGGAAACCATCCAGAGCTGCTGCCATGA		ATGAGGAAAGAGAATATCGTCCCTGTCAACTGTGGAAACCATCCAGAGCTGCTGCCATGA		MRKENIVPVNCGNHPELLP*		MRKENIVPVNCGNHPELLP*		GCCTAACCCG	AATTGTCACT	0	Z	0	0	0	0	0
10513	4537	an	AN3124.1	59.m08612	AO070303000023	0	-169	-77					ATGAAGACAAACCAAAGCTCCGCCCGTCCCAGAGTTGATGGCCAGCTGCATTTATTGACCATTATTCAATCGACATCCACCATCCTTGCATAG	ATGAAGACAAACCAAAGCTCCGCCCGTCCCAGAGTTGATGGCCAGCTGCATTTATTGACCATTATTCAATCGACATCCACCATCCTTGCATAG			MKTNQSSARPRVDGQLHLLTIIQSTSTILA*	MKTNQSSARPRVDGQLHLLTIIQSTSTILA*			GCTAACCCAA	CCAGTTCATC	0	Z	0	0	0	0	0
10514	4537	an	AN3124.1	59.m08612	AO070303000023	0	-132	-112					ATGGCCAGCTGCATTTATTGA	ATGGCCAGCTGCATTTATTGA			MASCIY*	MASCIY*			CCCAGAGTTG	CCATTATTCA	0	Z	0	0	0	0	0
10519	4537	ao	AN3124.1	59.m08612	AO070303000023	0					-237	-28	ATGAAGGGGGCATCAACCCCATTTCGGCTCGTGAAGATGAAGTTGCCTGGACAACAGGACACTAACCTAAAGGGGAATGACAGACTCAGCATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA			ATGAAGGGGGCATCAACCCCATTTCGGCTCGTGAAGATGAAGTTGCCTGGACAACAGGACACTAACCTAAAGGGGAATGACAGACTCAGCATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA	MKGASTPFRLVKMKLPGQQDTNLKGNDRLSMTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*			MKGASTPFRLVKMKLPGQQDTNLKGNDRLSMTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*	TTTCGGCCTG	ACAATCGGCA	0	Z	0	0	0	0	0
10520	4537	ao	AN3124.1	59.m08612	AO070303000023	0					-201	-28	ATGAAGTTGCCTGGACAACAGGACACTAACCTAAAGGGGAATGACAGACTCAGCATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA			ATGAAGTTGCCTGGACAACAGGACACTAACCTAAAGGGGAATGACAGACTCAGCATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA	MKLPGQQDTNLKGNDRLSMTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*			MKLPGQQDTNLKGNDRLSMTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*	GCTCGTGAAG	ACAATCGGCA	0	Z	0	0	0	0	0
10521	4537	ao	AN3124.1	59.m08612	AO070303000023	0					-161	-144	ATGACAGACTCAGCATGA			ATGACAGACTCAGCATGA	MTDSA*			MTDSA*	CTAAAGGGGA	CATCTCAAAG	0	Z	0	0	0	0	0
10522	4537	ao	AN3124.1	59.m08612	AO070303000023	0					-147	-28	ATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA			ATGACATCTCAAAGTGGAAACCCATCAACTGCTTCACGTTATAACGATCCGACTAAGCCAGGCCAACGTGGAGACGGCGATACTAACCCACTTCTTGCTGTCGTGTCTCCTCTTACGTGA	MTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*			MTSQSGNPSTASRYNDPTKPGQRGDGDTNPLLAVVSPLT*	CAGACTCAGC	ACAATCGGCA	0	Z	0	0	0	0	0
10525	4538	af	AN1796.1	72.m19548	AO070309000135	0			-127	-107			ATGATACCCTTATCTGTTTGA		ATGATACCCTTATCTGTTTGA		MIPLSV*		MIPLSV*		TTTTTGCAGC	GCCGCCAAAA	0	L	0	0	0	YDR182W	0
10523	4538	an	AN1796.1	72.m19548	AO070309000135	0	-158	-138					ATGTCGTCGCTTACCCAGTAA	ATGTCGTCGCTTACCCAGTAA			MSSLTQ*	MSSLTQ*			CTTGAACACG	CGTACTTGCA	0	L	0	0	0	YDR182W	0
10527	4538	ao	AN1796.1	72.m19548	AO070309000135	0					-160	-128	ATGATGCTTTGTGTTCCCAATTTGAAGCGTTGA			ATGATGCTTTGTGTTCCCAATTTGAAGCGTTGA	MMLCVPNLKR*			MMLCVPNLKR*	TCGGTTGACC	GTGTCATTGT	0	L	0	0	0	YDR182W	0
10528	4538	ao	AN1796.1	72.m19548	AO070309000135	0					-157	-128	ATGCTTTGTGTTCCCAATTTGAAGCGTTGA			ATGCTTTGTGTTCCCAATTTGAAGCGTTGA	MLCVPNLKR*			MLCVPNLKR*	GTTGACCATG	GTGTCATTGT	0	L	0	0	0	YDR182W	0
10529	4538	ao	AN1796.1	72.m19548	AO070309000135	0					-110	-60	ATGAGAACCAAGTACGCCGCTTGCCGACATCCCATCAGAACTTCCGTGTAA			ATGAGAACCAAGTACGCCGCTTGCCGACATCCCATCAGAACTTCCGTGTAA	MRTKYAACRHPIRTSV*			MRTKYAACRHPIRTSV*	TGTTCTCCCA	AGGCGGAGCA	0	L	0	0	0	YDR182W	0
10533	4539	af	AN8679.1	62.m03392	AO070315000099	0			-162	-85			ATGAAAAGTCCCACCGTATACATGGGCAGGAGATTCCTGCTTGCTAGGAAGTGCTCCATTGCCTGCCACCCGACGTGA		ATGAAAAGTCCCACCGTATACATGGGCAGGAGATTCCTGCTTGCTAGGAAGTGCTCCATTGCCTGCCACCCGACGTGA		MKSPTVYMGRRFLLARKCSIACHPT*		MKSPTVYMGRRFLLARKCSIACHPT*		TCAAGGACGG	TGATAGCTGG	0	O	0	0	0	0	0
10534	4539	af	AN8679.1	62.m03392	AO070315000099	0			-85	-47			ATGATAGCTGGGTTTGCTCATCATATAGCATCACACTAA		ATGATAGCTGGGTTTGCTCATCATATAGCATCACACTAA		MIAGFAHHIASH*		MIAGFAHHIASH*		ACCCGACGTG	ATCTTTTTCT	0	O	0	0	0	0	0
10532	4539	an	AN8679.1	62.m03392	AO070315000099	0	-82	-41					ATGATAGCGGGGCCATCTATACTGCGCAGCAAGCTACACTAA	ATGATAGCGGGGCCATCTATACTGCGCAGCAAGCTACACTAA			MIAGPSILRSKLH*	MIAGPSILRSKLH*			TGCCTACGTG	AATCGGCCCT	0	O	0	0	0	0	0
10535	4539	ao	AN8679.1	62.m03392	AO070315000099	0					-152	-75	ATGGTCGTCGACGCACCACCACCAATGGGCTGGAAGGTCCTTGCGAAGAGGGGTTCTACAGCTTGTCACCCGACGTGA			ATGGTCGTCGACGCACCACCACCAATGGGCTGGAAGGTCCTTGCGAAGAGGGGTTCTACAGCTTGTCACCCGACGTGA	MVVDAPPPMGWKVLAKRGSTACHPT*			MVVDAPPPMGWKVLAKRGSTACHPT*	TCTTACACGG	TGGTAGTCGG	0	O	0	0	0	0	0
10536	4539	ao	AN8679.1	62.m03392	AO070315000099	0					-75	-37	ATGGTAGTCGGAGTTGTCCATTGTAACTGCAGTACTTAA			ATGGTAGTCGGAGTTGTCCATTGTAACTGCAGTACTTAA	MVVGVVHCNCST*			MVVGVVHCNCST*	ACCCGACGTG	CCTTTCTTTC	0	O	0	0	0	0	0
10531	4539	conserved	AN8679.1	62.m03392	AO070315000099	0	-132	-82	-141	-85	-128	-75	ATGGGywGsArrdyyCTdshdrvkmGsvrdTshhymrbybbbyvymmshsrwsrTGA	ATGGGTTGCAGGACTCTACAAAGGCGCCAATCACTAAGCCTGCCTACGTGA	ATGGGCAGGAGATTCCTGCTTGCTAGGAAGTGCTCCATTGCCTGCCACCCGACGTGA	ATGGGCTGGAAGGTCCTTGCGAAGAGGGGTTCTACAGCTTGTCACCCGACGTGA	MGcrtLqrRqslslpt*	MGCRTLQRRQSLSLPT*	MGRRFLLARKCSIACHPT*	MGWKVLAKRGSTACHPT*	vmCmsyAymm	TGrTAGybGG	0	O	0	0	0	0	0
10539	4540	af	AN4534.1	57.m05587	AO070321000148	0			-205	-173			ATGGACAGGGTAATTCCTCCCGTGCTCTCTTGA		ATGGACAGGGTAATTCCTCCCGTGCTCTCTTGA		MDRVIPPVLS*		MDRVIPPVLS*		GCATTGATTA	ATCGCTAAGC	0	S	0	0	0	0	0
10537	4540	an	AN4534.1	57.m05587	AO070321000148	0	-239	-177					ATGAAGTCCCCAGTAGTTGTCGACCGCACGACTTCAAGCAAGTCGACCTCAATGACAGCCTGA	ATGAAGTCCCCAGTAGTTGTCGACCGCACGACTTCAAGCAAGTCGACCTCAATGACAGCCTGA			MKSPVVVDRTTSSKSTSMTA*	MKSPVVVDRTTSSKSTSMTA*			GCGACTCGCA	TAGCGATACT	0	S	0	0	0	0	0
10538	4540	an	AN4534.1	57.m05587	AO070321000148	0	-188	-177					ATGACAGCCTGA	ATGACAGCCTGA			MTA*	MTA*			GTCGACCTCA	TAGCGATACT	0	S	0	0	0	0	0
10540	4540	ao	AN4534.1	57.m05587	AO070321000148	0					-237	-181	ATGAGTATGAAACCTTCAATTGGATCCGCAGTCCTTGGGTTAATGCGTAAAAGGTAA			ATGAGTATGAAACCTTCAATTGGATCCGCAGTCCTTGGGTTAATGCGTAAAAGGTAA	MSMKPSIGSAVLGLMRKR*			MSMKPSIGSAVLGLMRKR*	ACAGCCTCTG	AAGGTACAAG	0	S	0	0	0	0	0
10541	4540	ao	AN4534.1	57.m05587	AO070321000148	0					-231	-181	ATGAAACCTTCAATTGGATCCGCAGTCCTTGGGTTAATGCGTAAAAGGTAA			ATGAAACCTTCAATTGGATCCGCAGTCCTTGGGTTAATGCGTAAAAGGTAA	MKPSIGSAVLGLMRKR*			MKPSIGSAVLGLMRKR*	TCTGATGAGT	AAGGTACAAG	0	S	0	0	0	0	0
10542	4540	ao	AN4534.1	57.m05587	AO070321000148	0					-195	-181	ATGCGTAAAAGGTAA			ATGCGTAAAAGGTAA	MRKR*			MRKR*	CCTTGGGTTA	AAGGTACAAG	0	S	0	0	0	0	0
10544	4541	af	AN8120.1	53.m03831	AO070322000028	0			-145	-47			ATGCCGCGTAACCCGGGCTCGATCCAATGTCCTAGGAGCCACCAGAAGGGGTTGCCGATGAAACAACGATGGGGAACACTCGGGGAGAATCCCTCCTAA		ATGCCGCGTAACCCGGGCTCGATCCAATGTCCTAGGAGCCACCAGAAGGGGTTGCCGATGAAACAACGATGGGGAACACTCGGGGAGAATCCCTCCTAA		MPRNPGSIQCPRSHQKGLPMKQRWGTLGENPS*		MPRNPGSIQCPRSHQKGLPMKQRWGTLGENPS*		ACAGGCCTGG	CTTCCAACTT	0	S	0	0	0	0	0
10545	4541	af	AN8120.1	53.m03831	AO070322000028	0			-88	-47			ATGAAACAACGATGGGGAACACTCGGGGAGAATCCCTCCTAA		ATGAAACAACGATGGGGAACACTCGGGGAGAATCCCTCCTAA		MKQRWGTLGENPS*		MKQRWGTLGENPS*		GGGGTTGCCG	CTTCCAACTT	0	S	0	0	0	0	0
10546	4541	ao	AN8120.1	53.m03831	AO070322000028	0					-205	-179	ATGCCGCCTTTCCCTCAAAGGGTCTAG			ATGCCGCCTTTCCCTCAAAGGGTCTAG	MPPFPQRV*			MPPFPQRV*	GGAGGTCTCG	CGTGGCGACT	0	S	0	0	0	0	0

10548	4543	af	AN1221.1	70.m15002	AO070331000223	0			-267	-151			ATGCACGCGAGCAGACTCGATATTCTAGCTGTTGTTGCTGCAACGAGACGCGTGACAGACGCCAAGCTTGTCTTCGCGAATCGCGACATCTGTGAAAGGACTTTCCCCACCAGCTGA		ATGCACGCGAGCAGACTCGATATTCTAGCTGTTGTTGCTGCAACGAGACGCGTGACAGACGCCAAGCTTGTCTTCGCGAATCGCGACATCTGTGAAAGGACTTTCCCCACCAGCTGA		MHASRLDILAVVAATRRVTDAKLVFANRDICERTFPTS*		MHASRLDILAVVAATRRVTDAKLVFANRDICERTFPTS*		TGTCCTCGAC	CCGTTTCTGT	0	T	0	0	0	0	0
10550	4543	ao	AN1221.1	70.m15002	AO070331000223	0					-252	-220	ATGTGCGTCAGTCGAAGGTTGTTCGAACCGTGA			ATGTGCGTCAGTCGAAGGTTGTTCGAACCGTGA	MCVSRRLFEP*			MCVSRRLFEP*	GTCATTTTCC	CGCGTGATGC	0	T	0	0	0	0	0
10551	4543	ao	AN1221.1	70.m15002	AO070331000223	0					-213	-34	ATGCCAAGAGGGCCCCAATTTAATCGCGTCGTCGCGGGCCAGCATTTTCGGGACATAGATTTAGTGACCCTATCAATCCATATCATATCATTATCTCTCGATTACTCAATTATACCGAGTCCCTCTTGGCATTACGCTTTGTCAAGTCGAGCCTTGATTATCCTTCTTCTTCCTTTATGA			ATGCCAAGAGGGCCCCAATTTAATCGCGTCGTCGCGGGCCAGCATTTTCGGGACATAGATTTAGTGACCCTATCAATCCATATCATATCATTATCTCTCGATTACTCAATTATACCGAGTCCCTCTTGGCATTACGCTTTGTCAAGTCGAGCCTTGATTATCCTTCTTCTTCCTTTATGA	MPRGPQFNRVVAGQHFRDIDLVTLSIHIISLSLDYSIIPSPSWHYALSSRALIILLLPL*			MPRGPQFNRVVAGQHFRDIDLVTLSIHIISLSLDYSIIPSPSWHYALSSRALIILLLPL*	GTGACGCGTG	AAGCACACAA	0	T	0	0	0	0	0
10553	4545	af	AN2184.1	72.m19039	AO070340000082	0			-157	-131			ATGCGTTTCGGGTTCCAATCCAGCTAG		ATGCGTTTCGGGTTCCAATCCAGCTAG		MRFGFQSS*		MRFGFQSS*		CAACTTCTAA	ATGCTGTTTC	0	S	0	MG04663.1	NCU07577.1	0	0
10554	4545	af	AN2184.1	72.m19039	AO070340000082	0			-130	-104			ATGCTGTTTCTTCTTGTCTGTGTATAG		ATGCTGTTTCTTCTTGTCTGTGTATAG		MLFLLVCV*		MLFLLVCV*		ATCCAGCTAG	ATAAACTACT	0	S	0	MG04663.1	NCU07577.1	0	0
10556	4545	ao	AN2184.1	72.m19039	AO070340000082	0					-240	-190	ATGCTTTTGGCCTCACATCTTCTTCACTTGGTTCTTCGATATTTCTGTTGA			ATGCTTTTGGCCTCACATCTTCTTCACTTGGTTCTTCGATATTTCTGTTGA	MLLASHLLHLVLRYFC*			MLLASHLLHLVLRYFC*	TTTCATTTGC	TATGTCATTT	0	S	0	MG04663.1	NCU07577.1	0	0
10557	4545	ao	AN2184.1	72.m19039	AO070340000082	0					-188	-165	ATGTCATTTTCTGGCTCAGGTTAG			ATGTCATTTTCTGGCTCAGGTTAG	MSFSGSG*			MSFSGSG*	TTCTGTTGAT	CTCAGGATTA	0	S	0	MG04663.1	NCU07577.1	0	0
10563	4546	af	AN1927.1	69.m14944	AO070341000108	0			-265	-167			ATGCGATCGCAAGCTCGAATTGTTCCTGACTCTATCAAATTTGTCGCGCGATCATGCTTGCTGCGTCAAGTTCACAGCGCCGAGGACACACGGCGCTAG		ATGCGATCGCAAGCTCGAATTGTTCCTGACTCTATCAAATTTGTCGCGCGATCATGCTTGCTGCGTCAAGTTCACAGCGCCGAGGACACACGGCGCTAG		MRSQARIVPDSIKFVARSCLLRQVHSAEDTRR*		MRSQARIVPDSIKFVARSCLLRQVHSAEDTRR*		TCAATCCCAC	CCCCTTCAAC	0		0	0	0	0	0
10564	4546	af	AN1927.1	69.m14944	AO070341000108	0			-212	-27			ATGCTTGCTGCGTCAAGTTCACAGCGCCGAGGACACACGGCGCTAGCCCCTTCAACATGCCTCTCCGCCCAGGCAATTTTAGCCTGTAAAACCTTGCGTGCTGTCACTCGCGTCCTTCCGTCCTCCAACTACCTCCTTCCGTCATCACTCCGGAGCCTCGCTCCACCATCAACACCCACCTTCTAG		ATGCTTGCTGCGTCAAGTTCACAGCGCCGAGGACACACGGCGCTAGCCCCTTCAACATGCCTCTCCGCCCAGGCAATTTTAGCCTGTAAAACCTTGCGTGCTGTCACTCGCGTCCTTCCGTCCTCCAACTACCTCCTTCCGTCATCACTCCGGAGCCTCGCTCCACCATCAACACCCACCTTCTAG		MLAASSSQRRGHTALAPSTCLSAQAILACKTLRAVTRVLPSSNYLLPSSLRSLAPPSTPTF*		MLAASSSQRRGHTALAPSTCLSAQAILACKTLRAVTRVLPSSNYLLPSSLRSLAPPSTPTF*		TCGCGCGATC	GCGTGATTAT	0		0	0	0	0	0
10565	4546	af	AN1927.1	69.m14944	AO070341000108	0			-156	-124			ATGCCTCTCCGCCCAGGCAATTTTAGCCTGTAA		ATGCCTCTCCGCCCAGGCAATTTTAGCCTGTAA		MPLRPGNFSL*		MPLRPGNFSL*		CCCCTTCAAC	AACCTTGCGT	0		0	0	0	0	0
10559	4546	an	AN1927.1	69.m14944	AO070341000108	0	-241	-161					ATGCGCTCTGAATTTCTGCTTCATGTCGCGCGATTATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAG	ATGCGCTCTGAATTTCTGCTTCATGTCGCGCGATTATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAG			MRSEFLLHVARLCLLCSTQIAESSRR*	MRSEFLLHVARLCLLCSTQIAESSRR*			CGTCAGATTC	CCCCTTCAAA	0		0	0	0	0	0
10560	4546	an	AN1927.1	69.m14944	AO070341000108	0	-219	-118					ATGTCGCGCGATTATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAGCCCCTTCAAAATGCCCCCCGCCCAAGTAGTTTTTAGCCTGTAA	ATGTCGCGCGATTATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAGCCCCTTCAAAATGCCCCCCGCCCAAGTAGTTTTTAGCCTGTAA			MSRDYVCCALLKSPRAVGASPFKMPPAQVVFSL*	MSRDYVCCALLKSPRAVGASPFKMPPAQVVFSL*			TTTCTGCTTC	AACCTTGCCT	0		0	0	0	0	0
10561	4546	an	AN1927.1	69.m14944	AO070341000108	0	-206	-132					ATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAGCCCCTTCAAAATGCCCCCCGCCCAAGTAG	ATGTTTGCTGTGCTCTACTCAAATCGCCGAGAGCAGTCGGCGCTAGCCCCTTCAAAATGCCCCCCGCCCAAGTAG			MFAVLYSNRREQSALAPSKCPPPK*	MFAVLYSNRREQSALAPSKCPPPK*			TCGCGCGATT	TTTTTAGCCT	0		0	0	0	0	0
10562	4546	an	AN1927.1	69.m14944	AO070341000108	0	-150	-118					ATGCCCCCCGCCCAAGTAGTTTTTAGCCTGTAA	ATGCCCCCCGCCCAAGTAGTTTTTAGCCTGTAA			MPPAQVVFSL*	MPPAQVVFSL*			CCCCTTCAAA	AACCTTGCCT	0		0	0	0	0	0
10566	4546	ao	AN1927.1	69.m14944	AO070341000108	0					-284	-225	ATGAAACTATATTCTCGTCCCCGAGCCTTCATCAGATTCAGCGATCTTCATTTTCTGTAA			ATGAAACTATATTCTCGTCCCCGAGCCTTCATCAGATTCAGCGATCTTCATTTTCTGTAA	MKLYSRPRAFIRFSDLHFL*			MKLYSRPRAFIRFSDLHFL*	TCATCCAAGT	ATCAATCGCG	0		0	0	0	0	0
10567	4548	an	AN5616.1	58.m08957	AO070301000016	0	-271	-251					ATGTCTCCAGCCTTGGATTAG	ATGTCTCCAGCCTTGGATTAG			MSPALD*	MSPALD*			AGTGCAGTGA	GGCTCCGATA	0	E	FG01560.1	MG03264.1	NCU03347.1	YJL060W	YJL060W
10568	4548	an	AN5616.1	58.m08957	AO070301000016	0	-217	-200					ATGTCGCAAGCGGGATGA	ATGTCGCAAGCGGGATGA			MSQAG*	MSQAG*			TAGACCGCGG	TTCATTCTCC	0	E	FG01560.1	MG03264.1	NCU03347.1	YJL060W	YJL060W
10569	4548	an	AN5616.1	58.m08957	AO070301000016	0	-203	-6					ATGATTCATTCTCCAACCTCCGTCCCTCAGTTACATTTTGCCCCTCTTTCACCCTTTGCCCCTCTTAACTATTCTCTATGCTCTCGAGTTCTCGTTCTTCTGCCACGCTCCTTAAATCCTTCAATTCATCGAGTCTTCTTTCCTGCTCCCCAAGGTCAAGACTCAGCCTCCGCATCCCAAGGTTCCAATTCGGAGTAA	ATGATTCATTCTCCAACCTCCGTCCCTCAGTTACATTTTGCCCCTCTTTCACCCTTTGCCCCTCTTAACTATTCTCTATGCTCTCGAGTTCTCGTTCTTCTGCCACGCTCCTTAAATCCTTCAATTCATCGAGTCTTCTTTCCTGCTCCCCAAGGTCAAGACTCAGCCTCCGCATCCCAAGGTTCCAATTCGGAGTAA			MIHSPTSVPQLHFAPLSPFAPLNYSLCSRVLVLLPRSLNPSIHRVFFPAPQGQDSASASQGSNSE*	MIHSPTSVPQLHFAPLSPFAPLNYSLCSRVLVLLPRSLNPSIHRVFFPAPQGQDSASASQGSNSE*			CGCAAGCGGG	GAGCGATGTC	0	E	FG01560.1	MG03264.1	NCU03347.1	YJL060W	YJL060W
10577	4554	ao	AN4814.1	59.m09162	AO070329000018	0					-69	-52	ATGGGCTGCAGCCCGTGA			ATGGGCTGCAGCCCGTGA	MGCSP*			MGCSP*	TTGCCCATTC	ACTTCTTTTC	0	S	0	0	0	0	0
10578	4555	af	AN8061.1	53.m03913	AO070330000013	0			-190	-95			ATGCTTTACAAGTCCACACATGACTTGCAGGTTCTGACTCCATATACTTCAATTGGGCCCGAAGATTTATATTATCTGAGGCTGTTGCAGCTGTAG		ATGCTTTACAAGTCCACACATGACTTGCAGGTTCTGACTCCATATACTTCAATTGGGCCCGAAGATTTATATTATCTGAGGCTGTTGCAGCTGTAG		MLYKSTHDLQVLTPYTSIGPEDLYYLRLLQL*		MLYKSTHDLQVLTPYTSIGPEDLYYLRLLQL*		TACTCGGATT	AGCTCAAGCC	0	O	0	0	0	0	0
10579	4555	af	AN8061.1	53.m03913	AO070330000013	0			-171	-154			ATGACTTGCAGGTTCTGA		ATGACTTGCAGGTTCTGA		MTCRF*		MTCRF*		AAGTCCACAC	CTCCATATAC	0	O	0	0	0	0	0
10580	4555	ao	AN8061.1	53.m03913	AO070330000013	0					-150	-118	ATGAAAATCACACACAATAACCTCACCATCTAA			ATGAAAATCACACACAATAACCTCACCATCTAA	MKITHNNLTI*			MKITHNNLTI*	TCTCCCAATT	CTCATCATAC	0	O	0	0	0	0	0
10585	4557	af	AN9099.1	66.m04767	AO070332000175	0			-118	-53			ATGAGCGTGGTACTGCCTCGAGAGAAAGCTCGCGTGAGGGCCGTCGGATGCCCCCTTCGTCACTAA		ATGAGCGTGGTACTGCCTCGAGAGAAAGCTCGCGTGAGGGCCGTCGGATGCCCCCTTCGTCACTAA		MSVVLPREKARVRAVGCPLRH*		MSVVLPREKARVRAVGCPLRH*		TAACCGTGGA	AAGTACCCGC	0	R	0	0	0	0	0
10586	4557	ao	AN9099.1	66.m04767	AO070332000175	0					-147	-121	ATGCTACGCATTTCACTATCGTCATAG			ATGCTACGCATTTCACTATCGTCATAG	MLRISLSS*			MLRISLSS*	ACATTGACAA	TCATTCGAGC	0	R	0	0	0	0	0
10588	4558	af	AN7392.1	55.m03254	AO070334000209	0			-176	-123			ATGTCCGATGCTAAGGCGACGCTGTCTCCGATAAGCACCATATGGTCTCGATGA		ATGTCCGATGCTAAGGCGACGCTGTCTCCGATAAGCACCATATGGTCTCGATGA		MSDAKATLSPISTIWSR*		MSDAKATLSPISTIWSR*		ATCCAGGAAG	TTGACGGTCA	0	E	0	0	0	0	0
10589	4558	af	AN7392.1	55.m03254	AO070334000209	0			-169	-143			ATGCTAAGGCGACGCTGTCTCCGATAA		ATGCTAAGGCGACGCTGTCTCCGATAA		MLRRRCLR*		MLRRRCLR*		AAGATGTCCG	GCACCATATG	0	E	0	0	0	0	0
10590	4558	af	AN7392.1	55.m03254	AO070334000209	0			-135	-97			ATGGTCTCGATGATTGACGGTCACACGAGGCGACAATAG		ATGGTCTCGATGATTGACGGTCACACGAGGCGACAATAG		MVSMIDGHTRRQ*		MVSMIDGHTRRQ*		TAAGCACCAT	CCAGACCAGA	0	E	0	0	0	0	0
10591	4558	af	AN7392.1	55.m03254	AO070334000209	0			-126	-97			ATGATTGACGGTCACACGAGGCGACAATAG		ATGATTGACGGTCACACGAGGCGACAATAG		MIDGHTRRQ*		MIDGHTRRQ*		TATGGTCTCG	CCAGACCAGA	0	E	0	0	0	0	0
10587	4558	an	AN7392.1	55.m03254	AO070334000209	0	-114	-76					ATGATTGTAACACCAAATGATAAGCCGATACGACGCTGA	ATGATTGTAACACCAAATGATAAGCCGATACGACGCTGA			MIVTPNDKPIRR*	MIVTPNDKPIRR*			CTCTTATCTC	GGATACTAGG	0	E	0	0	0	0	0
10592	4558	ao	AN7392.1	55.m03254	AO070334000209	0					-162	-148	ATGGGGTGTCACTAA			ATGGGGTGTCACTAA	MGCH*			MGCH*	ACACCTTCGC	CTGTGCCCCT	0	E	0	0	0	0	0
10593	4562	an	AN1948.1	58.m07348	AO070342000213	0	-123	-61					ATGAAAAGAGAGAGTAAGAGAGCTTCAGGTGTCTGGGAGAGGGAAAAAGTCGGCAGACCATGA	ATGAAAAGAGAGAGTAAGAGAGCTTCAGGTGTCTGGGAGAGGGAAAAAGTCGGCAGACCATGA			MKRESKRASGVWEREKVGRP*	MKRESKRASGVWEREKVGRP*			CTCACTCTGG	ACTTTCTGGC	0	A	0	0	0	0	0
10594	4562	an	AN1948.1	58.m07348	AO070342000213	0	-64	-44					ATGAACTTTCTGGCTGCCTGA	ATGAACTTTCTGGCTGCCTGA			MNFLAA*	MNFLAA*			TCGGCAGACC	AGGAGTTATA	0	A	0	0	0	0	0
10598	4563	af	AN8799.1	71.m15606	AO070276000061	0			-252	-199			ATGCAGCCAATCGGAGCCCAGCAGAATCCAGCAGTTGGTCGCCCTGACATCTAG		ATGCAGCCAATCGGAGCCCAGCAGAATCCAGCAGTTGGTCGCCCTGACATCTAG		MQPIGAQQNPAVGRPDI*		MQPIGAQQNPAVGRPDI*		GGTCCAAGGC	CCCTGAGCCC	0	J	0	MG04871.1	0	0	0
10599	4563	af	AN8799.1	71.m15606	AO070276000061	0			-103	-62			ATGAGTGACGGATTGCTCCAGGATAGAGATATATCGGTCTAG		ATGAGTGACGGATTGCTCCAGGATAGAGATATATCGGTCTAG		MSDGLLQDRDISV*		MSDGLLQDRDISV*		GACTTTCAAG	CTCCTTTCTC	0	J	0	MG04871.1	0	0	0
10597	4563	an	AN8799.1	71.m15606	AO070276000061	0	-135	-106					ATGCGGCCTAGTGGGGAAGATTCCGTCTAG	ATGCGGCCTAGTGGGGAAGATTCCGTCTAG			MRPSGEDSV*	MRPSGEDSV*			TTGAAGCCAA	ATCTTTTGAG	0	J	0	MG04871.1	0	0	0
10600	4563	ao	AN8799.1	71.m15606	AO070276000061	0					-218	-180	ATGGATGCGCCAGAGGGTCATCATCCAATGATAAACTAG			ATGGATGCGCCAGAGGGTCATCATCCAATGATAAACTAG	MDAPEGHHPMIN*			MDAPEGHHPMIN*	CAAGCATTCA	ATTTCCAATG	0	J	0	MG04871.1	0	0	0
10601	4563	ao	AN8799.1	71.m15606	AO070276000061	0					-214	-188	ATGCGCCAGAGGGTCATCATCCAATGA			ATGCGCCAGAGGGTCATCATCCAATGA	MRQRVIIQ*			MRQRVIIQ*	CATTCAATGG	TAAACTAGAT	0	J	0	MG04871.1	0	0	0
10602	4563	ao	AN8799.1	71.m15606	AO070276000061	0					-191	-180	ATGATAAACTAG			ATGATAAACTAG	MIN*			MIN*	TCATCATCCA	ATTTCCAATG	0	J	0	MG04871.1	0	0	0
10603	4563	ao	AN8799.1	71.m15606	AO070276000061	0					-172	-107	ATGCGGTGGGAGCATCACCCTAATCTTCTAGCCCTGAGCCCTAATTACTGTCCCAGTCGGGTCTAG			ATGCGGTGGGAGCATCACCCTAATCTTCTAGCCCTGAGCCCTAATTACTGTCCCAGTCGGGTCTAG	MRWEHHPNLLALSPNYCPSRV*			MRWEHHPNLLALSPNYCPSRV*	TAGATTTCCA	ATCGGATCTT	0	J	0	MG04871.1	0	0	0
10604	4563	ao	AN8799.1	71.m15606	AO070276000061	0					-94	-77	ATGGCTGCCCCAGAATGA			ATGGCTGCCCCAGAATGA	MAAPE*			MAAPE*	CGGATCTTTA	TAGAAGCTTT	0	J	0	MG04871.1	0	0	0
10609	4564	af	AN8613.1	59.m09389	AO070299000102	0			-99	-40			ATGCCAAGCCAAGGATTTCCAGACCTCATCGGATACCCGAATACCCGCACTTCTCACTGA		ATGCCAAGCCAAGGATTTCCAGACCTCATCGGATACCCGAATACCCGCACTTCTCACTGA		MPSQGFPDLIGYPNTRTSH*		MPSQGFPDLIGYPNTRTSH*		GAAATAAGAG	TCGGAGACCC	0		0	0	0	0	0
10605	4564	an	AN8613.1	59.m09389	AO070299000102	0	-219	-121					ATGACTCCGCGAGGGCAACATATATACGCAAACCCGCCGGTCCTTTCCTTCATGGATTATCGCTGCTCCAGGCACATTACACAGTTTATGACAAGATGA	ATGACTCCGCGAGGGCAACATATATACGCAAACCCGCCGGTCCTTTCCTTCATGGATTATCGCTGCTCCAGGCACATTACACAGTTTATGACAAGATGA			MTPRGQHIYANPPVLSFMDYRCSRHITQFMTR*	MTPRGQHIYANPPVLSFMDYRCSRHITQFMTR*			AATTCAAACT	GCGAAGGAGT	0		0	0	0	0	0
10606	4564	an	AN8613.1	59.m09389	AO070299000102	0	-168	-121					ATGGATTATCGCTGCTCCAGGCACATTACACAGTTTATGACAAGATGA	ATGGATTATCGCTGCTCCAGGCACATTACACAGTTTATGACAAGATGA			MDYRCSRHITQFMTR*	MDYRCSRHITQFMTR*			CCTTTCCTTC	GCGAAGGAGT	0		0	0	0	0	0
10607	4564	an	AN8613.1	59.m09389	AO070299000102	0	-132	-121					ATGACAAGATGA	ATGACAAGATGA			MTR*	MTR*			TACACAGTTT	GCGAAGGAGT	0		0	0	0	0	0
10608	4564	an	AN8613.1	59.m09389	AO070299000102	0	-124	-71					ATGAGCGAAGGAGTGCTGGCCGCCCAATCTGCAGGGAGACGCAGGCGAGGATGA	ATGAGCGAAGGAGTGCTGGCCGCCCAATCTGCAGGGAGACGCAGGCGAGGATGA			MSEGVLAAQSAGRRRRG*	MSEGVLAAQSAGRRRRG*			TTATGACAAG	CACAGAAAGA	0		0	0	0	0	0
10610	4564	ao	AN8613.1	59.m09389	AO070299000102	0					-267	-223	ATGCGACAGTATCACTTCGTCGTGGGAAGAGCAATCTCATTCTAA			ATGCGACAGTATCACTTCGTCGTGGGAAGAGCAATCTCATTCTAA	MRQYHFVVGRAISF*			MRQYHFVVGRAISF*	CCGCCAATAC	ACATAAAACG	0		0	0	0	0	0
10611	4565	ao	AN4511.1	57.m05617	AO070311000067	0					-118	-89	ATGTTGTCGCAGAGAAACCAGCTTCATTGA			ATGTTGTCGCAGAGAAACCAGCTTCATTGA	MLSQRNQLH*			MLSQRNQLH*	TAACTCGGCA	AATTTGGATA	0		0	0	NCU02937.1	0	0
10618	4567	af	AN0889.1	70.m15493	AO070320000058	0			-199	-47			ATGTTTATCACCACGTGCCACTATCGCAAAGCCAAGATGCAAAAGAAGCTTCACCGACGACATTTTGTTTCATATTATCTCTCTCTTTTTTCCGAGTGGAAAGTCAGGAATGCCGTTATCTTGCGCGAATTAGATGTCTATGCCCTAGATTAG		ATGTTTATCACCACGTGCCACTATCGCAAAGCCAAGATGCAAAAGAAGCTTCACCGACGACATTTTGTTTCATATTATCTCTCTCTTTTTTCCGAGTGGAAAGTCAGGAATGCCGTTATCTTGCGCGAATTAGATGTCTATGCCCTAGATTAG		MFITTCHYRKAKMQKKLHRRHFVSYYLSLFSEWKVRNAVILRELDVYALD*		MFITTCHYRKAKMQKKLHRRHFVSYYLSLFSEWKVRNAVILRELDVYALD*		CGTGATTAAG	AGTTCGTTCT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10619	4567	af	AN0889.1	70.m15493	AO070320000058	0			-163	-47			ATGCAAAAGAAGCTTCACCGACGACATTTTGTTTCATATTATCTCTCTCTTTTTTCCGAGTGGAAAGTCAGGAATGCCGTTATCTTGCGCGAATTAGATGTCTATGCCCTAGATTAG		ATGCAAAAGAAGCTTCACCGACGACATTTTGTTTCATATTATCTCTCTCTTTTTTCCGAGTGGAAAGTCAGGAATGCCGTTATCTTGCGCGAATTAGATGTCTATGCCCTAGATTAG		MQKKLHRRHFVSYYLSLFSEWKVRNAVILRELDVYALD*		MQKKLHRRHFVSYYLSLFSEWKVRNAVILRELDVYALD*		CAAAGCCAAG	AGTTCGTTCT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10620	4567	af	AN0889.1	70.m15493	AO070320000058	0			-90	-67			ATGCCGTTATCTTGCGCGAATTAG		ATGCCGTTATCTTGCGCGAATTAG		MPLSCAN*		MPLSCAN*		AAAGTCAGGA	ATGTCTATGC	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10621	4567	af	AN0889.1	70.m15493	AO070320000058	0			-66	-52			ATGTCTATGCCCTAG		ATGTCTATGCCCTAG		MSMP*		MSMP*		CGCGAATTAG	ATTAGAGTTC	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10612	4567	an	AN0889.1	70.m15493	AO070320000058	0	-230	-216					ATGAAGACCAGATAA	ATGAAGACCAGATAA			MKTR*	MKTR*			GGGTTTGACG	TAACTGAGCA	0	R	FG09745.1	MG06080.1	0	YHR168W	0

10613	4567	an	AN0889.1	70.m15493	AO070320000058	0	-156	-55					ATGACGTCAAAAATGCCTGGCAAAGCTTTTGAGCGTCATGGCCGTGACATAGCTGAAGAGCATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGA	ATGACGTCAAAAATGCCTGGCAAAGCTTTTGAGCGTCATGGCCGTGACATAGCTGAAGAGCATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGA			MTSKMPGKAFERHGRDIAEEHEKLGFQLTHSLH*	MTSKMPGKAFERHGRDIAEEHEKLGFQLTHSLH*			ATAAGATCAC	CCGAGCACGT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10614	4567	an	AN0889.1	70.m15493	AO070320000058	0	-144	-55					ATGCCTGGCAAAGCTTTTGAGCGTCATGGCCGTGACATAGCTGAAGAGCATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGA	ATGCCTGGCAAAGCTTTTGAGCGTCATGGCCGTGACATAGCTGAAGAGCATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGA			MPGKAFERHGRDIAEEHEKLGFQLTHSLH*	MPGKAFERHGRDIAEEHEKLGFQLTHSLH*			GACGTCAAAA	CCGAGCACGT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10615	4567	an	AN0889.1	70.m15493	AO070320000058	0	-119	-105					ATGGCCGTGACATAG	ATGGCCGTGACATAG			MAVT*	MAVT*			TTTGAGCGTC	CTGAAGAGCA	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10616	4567	an	AN0889.1	70.m15493	AO070320000058	0	-95	-12					ATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGACCGAGCACGTCCCGACAATTGTTGCAGGATGAGCGACACCTAG	ATGAAAAGCTCGGTTTCCAGCTTACCCACTCGCTCCATTGACCGAGCACGTCCCGACAATTGTTGCAGGATGAGCGACACCTAG			MKSSVSSLPTRSIDRARPDNCCRMSDT*	MKSSVSSLPTRSIDRARPDNCCRMSDT*			GCTGAAGAGC	CACAATATAC	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10623	4567	ao	AN0889.1	70.m15493	AO070320000058	0					-231	-76	ATGTATCGTTTATCATCAGGTGCTGATAAGGTCACGTGTGATGCAGGTTTGCTCCAGAGCTATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAGATTGA			ATGTATCGTTTATCATCAGGTGCTGATAAGGTCACGTGTGATGCAGGTTTGCTCCAGAGCTATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAGATTGA	MYRLSSGADKVTCDAGLLQSYDNIDYQIHYSQLLGRKVLCKSDGRRKMLLD*			MYRLSSGADKVTCDAGLLQSYDNIDYQIHYSQLLGRKVLCKSDGRRKMLLD*	AGGCATCGAT	CTTTAGGCTT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10624	4567	ao	AN0889.1	70.m15493	AO070320000058	0					-191	-81	ATGCAGGTTTGCTCCAGAGCTATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAG			ATGCAGGTTTGCTCCAGAGCTATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAG	MQVCSRAMTTSTIRYTIHNYSEEKCFASQTEEGKCF*			MQVCSRAMTTSTIRYTIHNYSEEKCFASQTEEGKCF*	GTCACGTGTG	ATTGACTTTA	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10625	4567	ao	AN0889.1	70.m15493	AO070320000058	0					-170	-81	ATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAG			ATGACAACATCGACTATCAGATACACTATTCACAATTACTCGGAAGAAAAGTGCTTTGCAAGTCAGACGGAAGAAGGAAAATGCTTTTAG	MTTSTIRYTIHNYSEEKCFASQTEEGKCF*			MTTSTIRYTIHNYSEEKCFASQTEEGKCF*	CTCCAGAGCT	ATTGACTTTA	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10626	4567	ao	AN0889.1	70.m15493	AO070320000058	0					-90	-76	ATGCTTTTAGATTGA			ATGCTTTTAGATTGA	MLLD*			MLLD*	AAGAAGGAAA	CTTTAGGCTT	0	R	FG09745.1	MG06080.1	0	YHR168W	0
10627	4568	ao	AN0903.1	70.m15512	AO070320000077	0					-216	-202	ATGATTGTTTTATAA			ATGATTGTTTTATAA	MIVL*			MIVL*	TTATTATTCA	ATTAATATAC	0		FG05167.1	0	NCU03501.1	0	0
10628	4568	ao	AN0903.1	70.m15512	AO070320000077	0					-176	-159	ATGTGGTTCCATGAATGA			ATGTGGTTCCATGAATGA	MWFHE*			MWFHE*	TCCATCTGAG	TCACTACAGC	0		FG05167.1	0	NCU03501.1	0	0
10629	4568	ao	AN0903.1	70.m15512	AO070320000077	0					-166	-71	ATGAATGATCACTACAGCAACAACAACCATTACTACTACTTACCTCATCTACAAACGTCATCCTTTGCATATACACGAATCATACGAGTGTATTGA			ATGAATGATCACTACAGCAACAACAACCATTACTACTACTTACCTCATCTACAAACGTCATCCTTTGCATATACACGAATCATACGAGTGTATTGA	MNDHYSNNNHYYYLPHLQTSSFAYTRIIRVY*			MNDHYSNNNHYYYLPHLQTSSFAYTRIIRVY*	ATGTGGTTCC	CAACAACTAC	0		FG05167.1	0	NCU03501.1	0	0
10630	4568	ao	AN0903.1	70.m15512	AO070320000077	0					-162	-31	ATGATCACTACAGCAACAACAACCATTACTACTACTTACCTCATCTACAAACGTCATCCTTTGCATATACACGAATCATACGAGTGTATTGACAACAACTACCATCTCCCAATCCTCAGCCGTATTTGTTAA			ATGATCACTACAGCAACAACAACCATTACTACTACTTACCTCATCTACAAACGTCATCCTTTGCATATACACGAATCATACGAGTGTATTGACAACAACTACCATCTCCCAATCCTCAGCCGTATTTGTTAA	MITTATTTITTTYLIYKRHPLHIHESYECIDNNYHLPILSRIC*			MITTATTTITTTYLIYKRHPLHIHESYECIDNNYHLPILSRIC*	GGTTCCATGA	CATCTGCCCG	0		FG05167.1	0	NCU03501.1	0	0
10633	4569	af	AN3421.1	67.m02958	AO070323000200	0			-298	-119			ATGATAAAATCTGGCAGACTATGCGATAATAGTGAACATGGATTGCATCACTATGTCTACTACACAATAACTGATCGTCTAGCACTTCGATTTGAGGGTTTATTATGTTCACAAGTCAGCAACCTAGCCCCTCCTGTATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAA		ATGATAAAATCTGGCAGACTATGCGATAATAGTGAACATGGATTGCATCACTATGTCTACTACACAATAACTGATCGTCTAGCACTTCGATTTGAGGGTTTATTATGTTCACAAGTCAGCAACCTAGCCCCTCCTGTATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAA		MIKSGRLCDNSEHGLHHYVYYTITDRLALRFEGLLCSQVSNLAPPVCRTDIGPYQLSPQ*		MIKSGRLCDNSEHGLHHYVYYTITDRLALRFEGLLCSQVSNLAPPVCRTDIGPYQLSPQ*		ACAGAGCTGA	CTCCGCAGTC	0		FG08465.1	MG09333.1	0	0	0
10634	4569	af	AN3421.1	67.m02958	AO070323000200	0			-261	-229			ATGGATTGCATCACTATGTCTACTACACAATAA		ATGGATTGCATCACTATGTCTACTACACAATAA		MDCITMSTTQ*		MDCITMSTTQ*		AATAGTGAAC	CTGATCGTCT	0		FG08465.1	MG09333.1	0	0	0
10635	4569	af	AN3421.1	67.m02958	AO070323000200	0			-246	-229			ATGTCTACTACACAATAA		ATGTCTACTACACAATAA		MSTTQ*		MSTTQ*		TTGCATCACT	CTGATCGTCT	0		FG08465.1	MG09333.1	0	0	0
10636	4569	af	AN3421.1	67.m02958	AO070323000200	0			-194	-102			ATGTTCACAAGTCAGCAACCTAGCCCCTCCTGTATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAACTCCGCAGTCAGCGTAA		ATGTTCACAAGTCAGCAACCTAGCCCCTCCTGTATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAACTCCGCAGTCAGCGTAA		MFTSQQPSPSCMSHGHRSISTISAVTPQSA*		MFTSQQPSPSCMSHGHRSISTISAVTPQSA*		AGGGTTTATT	GCACCCCGTC	0		FG08465.1	MG09333.1	0	0	0
10637	4569	af	AN3421.1	67.m02958	AO070323000200	0			-161	-102			ATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAACTCCGCAGTCAGCGTAA		ATGTCGCACGGACATAGGTCCATATCAACTATCTCCGCAGTAACTCCGCAGTCAGCGTAA		MSHGHRSISTISAVTPQSA*		MSHGHRSISTISAVTPQSA*		CCCCTCCTGT	GCACCCCGTC	0		FG08465.1	MG09333.1	0	0	0
10638	4569	af	AN3421.1	67.m02958	AO070323000200	0			-84	-37			ATGTATTTAATCCTTGACCCGCAGGCTACTTGTTTGATCTTCCCTTGA		ATGTATTTAATCCTTGACCCGCAGGCTACTTGTTTGATCTTCCCTTGA		MYLILDPQATCLIFP*		MYLILDPQATCLIFP*		GTCTTCAGCC	ATGATCTCAA	0		FG08465.1	MG09333.1	0	0	0
10631	4569	an	AN3421.1	67.m02958	AO070323000200	0	-191	-126					ATGGCTGACGCCAAGGCCGACTCCCGGACTTATCGACATCGACAGTATCTCCGGCTGAGTAGGTAG	ATGGCTGACGCCAAGGCCGACTCCCGGACTTATCGACATCGACAGTATCTCCGGCTGAGTAGGTAG			MADAKADSRTYRHRQYLRLSR*	MADAKADSRTYRHRQYLRLSR*			TCGTTGACAG	TCCCCTGGTC	0		FG08465.1	MG09333.1	0	0	0
10632	4569	an	AN3421.1	67.m02958	AO070323000200	0	-112	-47					ATGAATAGCACAGGGATCATCTATAAAGGTCGATTGCCTCTGATTATCGACTTCACTCCTACCTGA	ATGAATAGCACAGGGATCATCTATAAAGGTCGATTGCCTCTGATTATCGACTTCACTCCTACCTGA			MNSTGIIYKGRLPLIIDFTPT*	MNSTGIIYKGRLPLIIDFTPT*			CCTGGTCAGC	TGCGAGAAAT	0		FG08465.1	MG09333.1	0	0	0
10640	4569	ao	AN3421.1	67.m02958	AO070323000200	0					-208	-188	ATGCAGCTTGGCAGGCGTTAA			ATGCAGCTTGGCAGGCGTTAA	MQLGRR*			MQLGRR*	AGCCTTGAAG	CTCCGTGTCA	0		FG08465.1	MG09333.1	0	0	0
10641	4569	ao	AN3421.1	67.m02958	AO070323000200	0					-119	-81	ATGTATAAAGAGCCCCAGCCCACTTTTTGCATTCAATAA			ATGTATAAAGAGCCCCAGCCCACTTTTTGCATTCAATAA	MYKEPQPTFCIQ*			MYKEPQPTFCIQ*	TAAGTCCTAC	ATTTTTGATC	0		FG08465.1	MG09333.1	0	0	0
10643	4571	an	AN3095.1	59.m08648	AO070334000137	0	-114	-91					ATGGCTCCGCGTTATATCCCTTAG	ATGGCTCCGCGTTATATCCCTTAG			MAPRYIP*	MAPRYIP*			TGAAGACCTT	ATGTCCTGAT	0	S	0	0	0	0	0
10645	4574	af	AN1261.1	70.m14958	AO070214000004	0			-165	-133			ATGTCTTATAAATCGTCGTTTCCTACAATGTAG		ATGTCTTATAAATCGTCGTTTCCTACAATGTAG		MSYKSSFPTM*		MSYKSSFPTM*		CGGGTCGGGC	TCAGTTTCTT	0		FG05613.1	0	0	0	0
10644	4574	an	AN1261.1	70.m14958	AO070214000004	0	-209	-183					ATGCGCTTGGGTATAAATCGGCTTTGA	ATGCGCTTGGGTATAAATCGGCTTTGA			MRLGINRL*	MRLGINRL*			ACTCTTCGGA	TCTTTCTTTC	0		FG05613.1	0	0	0	0
10646	4574	ao	AN1261.1	70.m14958	AO070214000004	0					-215	-117	ATGTTTCGTCCTCATGTAGAACTTTTTCCATTTGTTTCTCCTTTTCCTTCGTTTTCAAGCAAAAGTCTGTCCTTCCGCAGCATCTTCTGGCTTCTTTGA			ATGTTTCGTCCTCATGTAGAACTTTTTCCATTTGTTTCTCCTTTTCCTTCGTTTTCAAGCAAAAGTCTGTCCTTCCGCAGCATCTTCTGGCTTCTTTGA	MFRPHVELFPFVSPFPSFSSKSLSFRSIFWLL*			MFRPHVELFPFVSPFPSFSSKSLSFRSIFWLL*	TATATAGGCC	TACCCCATTT	0		FG05613.1	0	0	0	0
10653	4576	af	AN5799.1	72.m18927	AO070260000050	0			-264	-139			ATGTATATATTTATAATACGCTGTCGAATGAAAGGTGCCTTGATTTATATATATCACCTGGTCGATATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		ATGTATATATTTATAATACGCTGTCGAATGAAAGGTGCCTTGATTTATATATATCACCTGGTCGATATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		MYIFIIRCRMKGALIYIYHLVDMYQAHKNFSNWTCLVSYHL*		MYIFIIRCRMKGALIYIYHLVDMYQAHKNFSNWTCLVSYHL*		CAGGTTAATT	ACCGCGGGCA	0	E	0	0	0	0	0
10654	4576	af	AN5799.1	72.m18927	AO070260000050	0			-237	-139			ATGAAAGGTGCCTTGATTTATATATATCACCTGGTCGATATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		ATGAAAGGTGCCTTGATTTATATATATCACCTGGTCGATATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		MKGALIYIYHLVDMYQAHKNFSNWTCLVSYHL*		MKGALIYIYHLVDMYQAHKNFSNWTCLVSYHL*		ACGCTGTCGA	ACCGCGGGCA	0	E	0	0	0	0	0
10655	4576	af	AN5799.1	72.m18927	AO070260000050	0			-198	-139			ATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		ATGTACCAAGCACACAAAAATTTCAGCAATTGGACATGCCTTGTTAGTTATCACCTGTAG		MYQAHKNFSNWTCLVSYHL*		MYQAHKNFSNWTCLVSYHL*		CCTGGTCGAT	ACCGCGGGCA	0	E	0	0	0	0	0
10656	4576	af	AN5799.1	72.m18927	AO070260000050	0			-163	-152			ATGCCTTGTTAG		ATGCCTTGTTAG		MPC*		MPC*		GCAATTGGAC	TTATCACCTG	0	E	0	0	0	0	0
10647	4576	an	AN5799.1	72.m18927	AO070260000050	0	-201	-157					ATGCATTACATGTGTACTTTTAAATCATGCGTATGTGGCACTTGA	ATGCATTACATGTGTACTTTTAAATCATGCGTATGTGGCACTTGA			MHYMCTFKSCVCGT*	MHYMCTFKSCVCGT*			ACTTATCATT	TTCTCCACTC	0	E	0	0	0	0	0
10648	4576	an	AN5799.1	72.m18927	AO070260000050	0	-192	-157					ATGTGTACTTTTAAATCATGCGTATGTGGCACTTGA	ATGTGTACTTTTAAATCATGCGTATGTGGCACTTGA			MCTFKSCVCGT*	MCTFKSCVCGT*			TATGCATTAC	TTCTCCACTC	0	E	0	0	0	0	0
10649	4576	an	AN5799.1	72.m18927	AO070260000050	0	-175	-116					ATGCGTATGTGGCACTTGATTCTCCACTCGCCTATGACACACTCTGGTTACATAAGGTGA	ATGCGTATGTGGCACTTGATTCTCCACTCGCCTATGACACACTCTGGTTACATAAGGTGA			MRMWHLILHSPMTHSGYIR*	MRMWHLILHSPMTHSGYIR*			CTTTTAAATC	GTGCTTACTA	0	E	0	0	0	0	0
10650	4576	an	AN5799.1	72.m18927	AO070260000050	0	-169	-116					ATGTGGCACTTGATTCTCCACTCGCCTATGACACACTCTGGTTACATAAGGTGA	ATGTGGCACTTGATTCTCCACTCGCCTATGACACACTCTGGTTACATAAGGTGA			MWHLILHSPMTHSGYIR*	MWHLILHSPMTHSGYIR*			AATCATGCGT	GTGCTTACTA	0	E	0	0	0	0	0
10651	4576	an	AN5799.1	72.m18927	AO070260000050	0	-142	-116					ATGACACACTCTGGTTACATAAGGTGA	ATGACACACTCTGGTTACATAAGGTGA			MTHSGYIR*	MTHSGYIR*			CCACTCGCCT	GTGCTTACTA	0	E	0	0	0	0	0
10652	4576	an	AN5799.1	72.m18927	AO070260000050	0	-99	-43					ATGCTCGTCCTCCGCCAGCTGTTACCGCACATTCTCGTTTCACAAGTGTGCTTATAA	ATGCTCGTCCTCCGCCAGCTGTTACCGCACATTCTCGTTTCACAAGTGTGCTTATAA			MLVLRQLLPHILVSQVCL*	MLVLRQLLPHILVSQVCL*			ACTACTCAGC	CGTCTTCCTC	0	E	0	0	0	0	0
10658	4577	af	AN4365.1	58.m09005	AO070261000008	0			-147	-52			ATGCTACATCATAGTCTAACGATGTTTCATATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		ATGCTACATCATAGTCTAACGATGTTTCATATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		MLHHSLTMFHMPLWWQLRSKTGQGPYNAIIM*		MLHHSLTMFHMPLWWQLRSKTGQGPYNAIIM*		TCTAGATCCG	GACAGTCCGT	0	L	0	0	0	0	0
10659	4577	af	AN4365.1	58.m09005	AO070261000008	0			-126	-52			ATGTTTCATATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		ATGTTTCATATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		MFHMPLWWQLRSKTGQGPYNAIIM*		MFHMPLWWQLRSKTGQGPYNAIIM*		TAGTCTAACG	GACAGTCCGT	0	L	0	0	0	0	0
10660	4577	af	AN4365.1	58.m09005	AO070261000008	0			-117	-52			ATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		ATGCCACTCTGGTGGCAACTTCGTTCAAAGACTGGCCAAGGGCCATACAATGCTATAATCATGTGA		MPLWWQLRSKTGQGPYNAIIM*		MPLWWQLRSKTGQGPYNAIIM*		GATGTTTCAT	GACAGTCCGT	0	L	0	0	0	0	0
10657	4577	an	AN4365.1	58.m09005	AO070261000008	0	-149	-93					ATGGAAGTGACCTTGGCGTCTTCTGGACCTTCTGGACCTTCTGTGCGGCGATCTTAG	ATGGAAGTGACCTTGGCGTCTTCTGGACCTTCTGGACCTTCTGTGCGGCGATCTTAG			MEVTLASSGPSGPSVRRS*	MEVTLASSGPSGPSVRRS*			GCTGAACAAG	CTTAGCTCAG	0	L	0	0	0	0	0
10661	4577	ao	AN4365.1	58.m09005	AO070261000008	0					-141	-103	ATGGTAGCAACTCCGCCTCTCATTCTTTCCTTTTCCTAA			ATGGTAGCAACTCCGCCTCTCATTCTTTCCTTTTCCTAA	MVATPPLILSFS*			MVATPPLILSFS*	TCATTCTAAT	CATACTTTCT	0	L	0	0	0	0	0
10662	4577	ao	AN4365.1	58.m09005	AO070261000008	0					-86	-72	ATGGAGGTAACTTGA			ATGGAGGTAACTTGA	MEVT*			MEVT*	TTCTTGTGCC	ACCCCGGAAT	0	L	0	0	0	0	0
10663	4577	ao	AN4365.1	58.m09005	AO070261000008	0					-63	-31	ATGGCAATATGTGGCGGCAATCACCTTCTGTAA			ATGGCAATATGTGGCGGCAATCACCTTCTGTAA	MAICGGNHLL*			MAICGGNHLL*	GAACCCCGGA	ACCATGTACC	0	L	0	0	0	0	0
10665	4578	ao	AN5566.1	52.m03724	AO070279000055	0					-256	-182	ATGCGGGGAATCCTGAGCGGTGAGATGGGCGGCGAGAGATACTGCCCCAGTGCCCCTCCATGTAACACCACGTGA			ATGCGGGGAATCCTGAGCGGTGAGATGGGCGGCGAGAGATACTGCCCCAGTGCCCCTCCATGTAACACCACGTGA	MRGILSGEMGGERYCPSAPPCNTT*			MRGILSGEMGGERYCPSAPPCNTT*	GATTCGCTCA	TGGGCCAAGC	0	F	FG10358.1	MG00919.1	NCU02325.1	0	0
10666	4578	ao	AN5566.1	52.m03724	AO070279000055	0					-232	-182	ATGGGCGGCGAGAGATACTGCCCCAGTGCCCCTCCATGTAACACCACGTGA			ATGGGCGGCGAGAGATACTGCCCCAGTGCCCCTCCATGTAACACCACGTGA	MGGERYCPSAPPCNTT*			MGGERYCPSAPPCNTT*	GAGCGGTGAG	TGGGCCAAGC	0	F	FG10358.1	MG00919.1	NCU02325.1	0	0
10667	4578	ao	AN5566.1	52.m03724	AO070279000055	0					-182	-126	ATGGGCCAAGCGGGGCATTTCTGGACAGGAACGCCATGTGATTGGCTGATCGCGTGA			ATGGGCCAAGCGGGGCATTTCTGGACAGGAACGCCATGTGATTGGCTGATCGCGTGA	MGQAGHFWTGTPCDWLIA*			MGQAGHFWTGTPCDWLIA*	ACACCACGTG	CTCAGGGCAA	0	F	FG10358.1	MG00919.1	NCU02325.1	0	0
10670	4582	ao	AN6261.1	72.m19396	AO070304000028	0					-238	-167	ATGAATAATTTCCGTCGCGTCTCCCCACATTTTCAACGCGTCTTCCCGACATCCACTTTCGAGCGATTCTGA			ATGAATAATTTCCGTCGCGTCTCCCCACATTTTCAACGCGTCTTCCCGACATCCACTTTCGAGCGATTCTGA	MNNFRRVSPHFQRVFPTSTFERF*			MNNFRRVSPHFQRVFPTSTFERF*	AAGTTCCGCC	ATTGGCCACC	0		0	0	0	0	0

10673	4583	af	AN6254.1	72.m19981	AO070304000034	0			-274	-128			ATGAATGACACCCTCTCAAACCGAGACTCTGATTGGCTGAGAGGGCCCGGGATCGGTTGGCATTGCCGAAGCACGCATGGGCTCGGAGGCTTGATCTATCGCCGACTCAGAATTTATCTAAGGCCCCCTCTGGCTGACAGATGGTAG		ATGAATGACACCCTCTCAAACCGAGACTCTGATTGGCTGAGAGGGCCCGGGATCGGTTGGCATTGCCGAAGCACGCATGGGCTCGGAGGCTTGATCTATCGCCGACTCAGAATTTATCTAAGGCCCCCTCTGGCTGACAGATGGTAG		MNDTLSNRDSDWLRGPGIGWHCRSTHGLGGLIYRRLRIYLRPPLADRW*		MNDTLSNRDSDWLRGPGIGWHCRSTHGLGGLIYRRLRIYLRPPLADRW*		TACATCGAAC	TCTTACGAAT	0	C	0	0	0	YLR348C	0
10674	4583	af	AN6254.1	72.m19981	AO070304000034	0			-270	-235			ATGACACCCTCTCAAACCGAGACTCTGATTGGCTGA		ATGACACCCTCTCAAACCGAGACTCTGATTGGCTGA		MTPSQTETLIG*		MTPSQTETLIG*		TCGAACATGA	GAGGGCCCGG	0	C	0	0	0	YLR348C	0
10675	4583	af	AN6254.1	72.m19981	AO070304000034	0			-198	-181			ATGGGCTCGGAGGCTTGA		ATGGGCTCGGAGGCTTGA		MGSEA*		MGSEA*		CGAAGCACGC	TCTATCGCCG	0	C	0	0	0	YLR348C	0
10676	4583	af	AN6254.1	72.m19981	AO070304000034	0			-134	-96			ATGGTAGTCTTACGAATTACGACTTATCGCGGCCATTAA		ATGGTAGTCTTACGAATTACGACTTATCGCGGCCATTAA		MVVLRITTYRGH*		MVVLRITTYRGH*		TGGCTGACAG	TTAACATTGC	0	C	0	0	0	YLR348C	0
10672	4583	an	AN6254.1	72.m19981	AO070304000034	0	-165	-142					ATGCTGATTGGTCCACCCCGCTGA	ATGCTGATTGGTCCACCCCGCTGA			MLIGPPR*	MLIGPPR*			GAAAACCGAG	CGTTTCCGAG	0	C	0	0	0	YLR348C	0
10679	4583	ao	AN6254.1	72.m19981	AO070304000034	0					-220	-134	ATGATTGGCTGGTTGCCTCCAGCACCGGTTATGCTGCCGAAGACCGCTGCGGGCTCGGAGATAGATCAAGTCTCCGACGCATTTTAA			ATGATTGGCTGGTTGCCTCCAGCACCGGTTATGCTGCCGAAGACCGCTGCGGGCTCGGAGATAGATCAAGTCTCCGACGCATTTTAA	MIGWLPPAPVMLPKTAAGSEIDQVSDAF*			MIGWLPPAPVMLPKTAAGSEIDQVSDAF*	AACCGAGTCT	GAAATTCCCG	0	C	0	0	0	YLR348C	0
10680	4583	ao	AN6254.1	72.m19981	AO070304000034	0					-190	-134	ATGCTGCCGAAGACCGCTGCGGGCTCGGAGATAGATCAAGTCTCCGACGCATTTTAA			ATGCTGCCGAAGACCGCTGCGGGCTCGGAGATAGATCAAGTCTCCGACGCATTTTAA	MLPKTAAGSEIDQVSDAF*			MLPKTAAGSEIDQVSDAF*	AGCACCGGTT	GAAATTCCCG	0	C	0	0	0	YLR348C	0
10686	4584	af	AN6309.1	72.m19325	AO070308000064	0			-218	-78			ATGAGTGTTATCAAGGACTTCTTGCCCTTGAGTTGCGCCTGTCAAGTGAAAGGCGGCATGTTGGAGTCGATATCGACACCATGTAATTCAGGCATCAAAAGAGTTTCCTCAATTGGGCACGTGCGGAACTCTGTATCATGA		ATGAGTGTTATCAAGGACTTCTTGCCCTTGAGTTGCGCCTGTCAAGTGAAAGGCGGCATGTTGGAGTCGATATCGACACCATGTAATTCAGGCATCAAAAGAGTTTCCTCAATTGGGCACGTGCGGAACTCTGTATCATGA		MSVIKDFLPLSCACQVKGGMLESISTPCNSGIKRVSSIGHVRNSVS*		MSVIKDFLPLSCACQVKGGMLESISTPCNSGIKRVSSIGHVRNSVS*		AGCCGCAGAG	TCGCGGCCCT	0	Y	FG05460.1	MG05004.1	0	0	0
10687	4584	af	AN6309.1	72.m19325	AO070308000064	0			-161	-78			ATGTTGGAGTCGATATCGACACCATGTAATTCAGGCATCAAAAGAGTTTCCTCAATTGGGCACGTGCGGAACTCTGTATCATGA		ATGTTGGAGTCGATATCGACACCATGTAATTCAGGCATCAAAAGAGTTTCCTCAATTGGGCACGTGCGGAACTCTGTATCATGA		MLESISTPCNSGIKRVSSIGHVRNSVS*		MLESISTPCNSGIKRVSSIGHVRNSVS*		GAAAGGCGGC	TCGCGGCCCT	0	Y	FG05460.1	MG05004.1	0	0	0
10688	4584	af	AN6309.1	72.m19325	AO070308000064	0			-81	-40			ATGATCGCGGCCCTATCGTCATCTTCCGCAACGCAGTTCTAA		ATGATCGCGGCCCTATCGTCATCTTCCGCAACGCAGTTCTAA		MIAALSSSSATQF*		MIAALSSSSATQF*		ACTCTGTATC	ATTCCTATCA	0	Y	FG05460.1	MG05004.1	0	0	0
10681	4584	an	AN6309.1	72.m19325	AO070308000064	0	-159	-130					ATGAGACATGACATCATGCGATTATTCTGA	ATGAGACATGACATCATGCGATTATTCTGA			MRHDIMRLF*	MRHDIMRLF*			AAGACGAAAG	TGATCAGATA	0	Y	FG05460.1	MG05004.1	0	0	0
10682	4584	an	AN6309.1	72.m19325	AO070308000064	0	-152	-114					ATGACATCATGCGATTATTCTGATGATCAGATAAGATAA	ATGACATCATGCGATTATTCTGATGATCAGATAAGATAA			MTSCDYSDDQIR*	MTSCDYSDDQIR*			AAGATGAGAC	GAATAAATTA	0	Y	FG05460.1	MG05004.1	0	0	0
10683	4584	an	AN6309.1	72.m19325	AO070308000064	0	-144	-130					ATGCGATTATTCTGA	ATGCGATTATTCTGA			MRLF*	MRLF*			ACATGACATC	TGATCAGATA	0	Y	FG05460.1	MG05004.1	0	0	0
10684	4584	an	AN6309.1	72.m19325	AO070308000064	0	-130	-119					ATGATCAGATAA	ATGATCAGATAA			MIR*	MIR*			GATTATTCTG	GATAAGAATA	0	Y	FG05460.1	MG05004.1	0	0	0
10685	4584	an	AN6309.1	72.m19325	AO070308000064	0	-100	-38					ATGCGATTTTACCGTAATCTCCAGCCTCCGGCCAACCTTGCAAGTGCCATCTTCCGTCCATAA	ATGCGATTTTACCGTAATCTCCAGCCTCCGGCCAACCTTGCAAGTGCCATCTTCCGTCCATAA			MRFYRNLQPPANLASAIFRP*	MRFYRNLQPPANLASAIFRP*			TAAATTACGC	TCCAACATCC	0	Y	FG05460.1	MG05004.1	0	0	0
10689	4584	ao	AN6309.1	72.m19325	AO070308000064	0					-243	-160	ATGAACCTCATTCTTAAATACAAACCCCATCCCAATGTCAACAGTATACTCCGTAAATCAGGGTTCCGGACCTCATCTCCATGA			ATGAACCTCATTCTTAAATACAAACCCCATCCCAATGTCAACAGTATACTCCGTAAATCAGGGTTCCGGACCTCATCTCCATGA	MNLILKYKPHPNVNSILRKSGFRTSSP*			MNLILKYKPHPNVNSILRKSGFRTSSP*	TACCTAAATT	TTAAATACAA	0	Y	FG05460.1	MG05004.1	0	0	0
10690	4584	ao	AN6309.1	72.m19325	AO070308000064	0					-209	-156	ATGTCAACAGTATACTCCGTAAATCAGGGTTCCGGACCTCATCTCCATGATTAA			ATGTCAACAGTATACTCCGTAAATCAGGGTTCCGGACCTCATCTCCATGATTAA	MSTVYSVNQGSGPHLHD*			MSTVYSVNQGSGPHLHD*	CCCCATCCCA	ATACAATGGC	0	Y	FG05460.1	MG05004.1	0	0	0
10691	4584	ao	AN6309.1	72.m19325	AO070308000064	0					-150	-121	ATGGCCCGTGCAGTACATTCAATACCGTAA			ATGGCCCGTGCAGTACATTCAATACCGTAA	MARAVHSIP*			MARAVHSIP*	ATTAAATACA	CAGAACCCAG	0	Y	FG05460.1	MG05004.1	0	0	0
10693	4586	af	AN0891.1	70.m15490	AO070320000062	0			-127	-77			ATGCTGATTCGTCTCGAAATTTTCGGCAAACTATCCCCTCGTTCCACTTGA		ATGCTGATTCGTCTCGAAATTTTCGGCAAACTATCCCCTCGTTCCACTTGA		MLIRLEIFGKLSPRST*		MLIRLEIFGKLSPRST*		CTTAACATGA	CCTGCGACAA	0		0	0	0	0	0
10692	4586	an	AN0891.1	70.m15490	AO070320000062	0	-122	-48					ATGCGTGCTGACCAACTTCGGTATACCACAGCAGCGTTCTTTTCTGCGTACATTCATTACGGGTCTTTCAGTTGA	ATGCGTGCTGACCAACTTCGGTATACCACAGCAGCGTTCTTTTCTGCGTACATTCATTACGGGTCTTTCAGTTGA			MRADQLRYTTAAFFSAYIHYGSFS*	MRADQLRYTTAAFFSAYIHYGSFS*			AATCGCCTAC	GACATGGTGG	0		0	0	0	0	0
10694	4589	an	AN7745.1	71.m15773	AO070325000172	0	-240	-214					ATGCTCGGCCAATTCTCCGGCTCTTGA	ATGCTCGGCCAATTCTCCGGCTCTTGA			MLGQFSGS*	MLGQFSGS*			ACCGCGCGTG	TCAGTCTCAG	0	U	0	0	0	0	0
10695	4589	an	AN7745.1	71.m15773	AO070325000172	0	-194	-174					ATGTTGGCTCGTGATGACTGA	ATGTTGGCTCGTGATGACTGA			MLARDD*	MLARDD*			GTTGCGCTCT	CGGTCACGTT	0	U	0	0	0	0	0
10696	4589	an	AN7745.1	71.m15773	AO070325000172	0	-181	-86					ATGACTGACGGTCACGTTACTCTTTTGTCCTCCTCATTTCTTTACCTCTCGTGTCTTAGCATCCTTCCTCCTTATACGATCTTCACCGTCGCTTAA	ATGACTGACGGTCACGTTACTCTTTTGTCCTCCTCATTTCTTTACCTCTCGTGTCTTAGCATCCTTCCTCCTTATACGATCTTCACCGTCGCTTAA			MTDGHVTLLSSSFLYLSCLSILPPYTIFTVA*	MTDGHVTLLSSSFLYLSCLSILPPYTIFTVA*			TTGGCTCGTG	AGCGCGGAGC	0	U	0	0	0	0	0
10697	4589	ao	AN7745.1	71.m15773	AO070325000172	0					-196	-185	ATGACCCTCTGA			ATGACCCTCTGA	MTL*			MTL*	TACTGTCGTA	TCGCCACGCC	0	U	0	0	0	0	0
10698	4589	ao	AN7745.1	71.m15773	AO070325000172	0					-63	-52	ATGTTCTGCTGA			ATGTTCTGCTGA	MFC*			MFC*	CCTCTATAGA	AGGCGATGAG	0	U	0	0	0	0	0
10699	4590	ao	AN5340.1	69.m15568	AO070333000183	0					-119	-84	ATGGGTCCCTCTGAGGTGACTATCGGCACGTGTTGA			ATGGGTCCCTCTGAGGTGACTATCGGCACGTGTTGA	MGPSEVTIGTC*			MGPSEVTIGTC*	GGCACACGTG	TAAGGCATCC	0	A	0	0	0	0	0
10700	4591	af	AN2883.1	59.m08730	AO070338000131	0			-239	-192			ATGAACAGGAACCAAGATATAGCAGAGGATGATGAATCACGAAAGTAG		ATGAACAGGAACCAAGATATAGCAGAGGATGATGAATCACGAAAGTAG		MNRNQDIAEDDESRK*		MNRNQDIAEDDESRK*		CCAGTAGAGA	CAGAAGCAGC	0	J	0	0	0	0	0
10701	4591	af	AN2883.1	59.m08730	AO070338000131	0			-211	-134			ATGATGAATCACGAAAGTAGCAGAAGCAGCTCTTTAATCGTGGGGTCGCGGGGCAGCGATTATCTGAGTGGTGCCTGA		ATGATGAATCACGAAAGTAGCAGAAGCAGCTCTTTAATCGTGGGGTCGCGGGGCAGCGATTATCTGAGTGGTGCCTGA		MMNHESSRSSSLIVGSRGSDYLSGA*		MMNHESSRSSSLIVGSRGSDYLSGA*		ATAGCAGAGG	GGCATACACG	0	J	0	0	0	0	0
10702	4591	af	AN2883.1	59.m08730	AO070338000131	0			-208	-134			ATGAATCACGAAAGTAGCAGAAGCAGCTCTTTAATCGTGGGGTCGCGGGGCAGCGATTATCTGAGTGGTGCCTGA		ATGAATCACGAAAGTAGCAGAAGCAGCTCTTTAATCGTGGGGTCGCGGGGCAGCGATTATCTGAGTGGTGCCTGA		MNHESSRSSSLIVGSRGSDYLSGA*		MNHESSRSSSLIVGSRGSDYLSGA*		GCAGAGGATG	GGCATACACG	0	J	0	0	0	0	0
10703	4591	ao	AN2883.1	59.m08730	AO070338000131	0					-131	-87	ATGGACCTTAGTCATACCTGCCTATTCCCACTTAGTCCATTTTAG			ATGGACCTTAGTCATACCTGCCTATTCCCACTTAGTCCATTTTAG	MDLSHTCLFPLSPF*			MDLSHTCLFPLSPF*	GGGGCCATCT	GTCAATCACG	0	J	0	0	0	0	0
10704	4592	an	AN0440.1	54.m06630	AO070338000297	0	-93	-76					ATGAACATGGGCTATTGA	ATGAACATGGGCTATTGA			MNMGY*	MNMGY*			CGGTAAAGGC	GGCCCAATCC	0	B	0	0	0	YDR176W	0
10705	4592	an	AN0440.1	54.m06630	AO070338000297	0	-87	-76					ATGGGCTATTGA	ATGGGCTATTGA			MGY*	MGY*			AGGCATGAAC	GGCCCAATCC	0	B	0	0	0	YDR176W	0
10707	4592	ao	AN0440.1	54.m06630	AO070338000297	0					-230	-132	ATGATGGAGTACAGAAGAGAACACGGCCAGAGCCTCTTGCAGGGCTTATATTTTCGAACTGCGACCAGCTGCCGAAGCGCGCTTCATGAAGCCTCATAA			ATGATGGAGTACAGAAGAGAACACGGCCAGAGCCTCTTGCAGGGCTTATATTTTCGAACTGCGACCAGCTGCCGAAGCGCGCTTCATGAAGCCTCATAA	MMEYRREHGQSLLQGLYFRTATSCRSALHEAS*			MMEYRREHGQSLLQGLYFRTATSCRSALHEAS*	TATCCTGATA	GCCATACAAT	0	B	0	0	0	YDR176W	0
10708	4592	ao	AN0440.1	54.m06630	AO070338000297	0					-227	-132	ATGGAGTACAGAAGAGAACACGGCCAGAGCCTCTTGCAGGGCTTATATTTTCGAACTGCGACCAGCTGCCGAAGCGCGCTTCATGAAGCCTCATAA			ATGGAGTACAGAAGAGAACACGGCCAGAGCCTCTTGCAGGGCTTATATTTTCGAACTGCGACCAGCTGCCGAAGCGCGCTTCATGAAGCCTCATAA	MEYRREHGQSLLQGLYFRTATSCRSALHEAS*			MEYRREHGQSLLQGLYFRTATSCRSALHEAS*	CCTGATAATG	GCCATACAAT	0	B	0	0	0	YDR176W	0
10709	4592	ao	AN0440.1	54.m06630	AO070338000297	0					-145	-119	ATGAAGCCTCATAAGCCATACAATTGA			ATGAAGCCTCATAAGCCATACAATTGA	MKPHKPYN*			MKPHKPYN*	AGCGCGCTTC	AACGCCAAAC	0	B	0	0	0	YDR176W	0
10710	4592	ao	AN0440.1	54.m06630	AO070338000297	0					-87	-76	ATGGAATATTAA			ATGGAATATTAA	MEY*			MEY*	ACCGAAAATA	AGCCATCCAA	0	B	0	0	0	YDR176W	0
10732	4594	an	AN5489.1	69.m15463	AO070341000396	0	-188	-69					ATGACTCTCGCTCGCCAGCAGTCCAGAATCCAATATAACCGCTTTGGGACATCATTTTGCCGAGGAGAACTCACCACCATCATCACAGTCCCAGCAGGATTCCTTAACTGCCGGTTTTAG	ATGACTCTCGCTCGCCAGCAGTCCAGAATCCAATATAACCGCTTTGGGACATCATTTTGCCGAGGAGAACTCACCACCATCATCACAGTCCCAGCAGGATTCCTTAACTGCCGGTTTTAG			MTLARQQSRIQYNRFGTSFCRGELTTIITVPAGFLNCRF*	MTLARQQSRIQYNRFGTSFCRGELTTIITVPAGFLNCRF*			CTTCAATTCT	AAATTCACAT	0	Z	0	0	0	0	0
10736	4599	af	AN7250.1	72.m19799	AO070297000005	0			-147	-28			ATGCGGAGAGACGGGATTGCGCAATTCTGGTGCGGAGTCCATATCTGTAATCGCACGTTCAATCAGTCGGAGAACGTGGAGATAATTGCTACCCCCATTGGGACCAAAAAAATCAACTAA		ATGCGGAGAGACGGGATTGCGCAATTCTGGTGCGGAGTCCATATCTGTAATCGCACGTTCAATCAGTCGGAGAACGTGGAGATAATTGCTACCCCCATTGGGACCAAAAAAATCAACTAA		MRRDGIAQFWCGVHICNRTFNQSENVEIIATPIGTKKIN*		MRRDGIAQFWCGVHICNRTFNQSENVEIIATPIGTKKIN*		TCAGAAAGGT	ATCTACAGGA	0	P	0	0	0	0	0
10735	4599	an	AN7250.1	72.m19799	AO070297000005	0	-99	-34					ATGGGCTCTGGGTTACGACTAGAGCAAGGAAAACTTCACGATAAGCTGAAATCGCGGATAATCTGA	ATGGGCTCTGGGTTACGACTAGAGCAAGGAAAACTTCACGATAAGCTGAAATCGCGGATAATCTGA			MGSGLRLEQGKLHDKLKSRII*	MGSGLRLEQGKLHDKLKSRII*			AGCGCTTCAC	TTACTTTTGG	0	P	0	0	0	0	0
10737	4599	ao	AN7250.1	72.m19799	AO070297000005	0					-215	-168	ATGCCGAGAACGTCGGATTCCCCATCTCACGAGGCGCATTTCTATTGA			ATGCCGAGAACGTCGGATTCCCCATCTCACGAGGCGCATTTCTATTGA	MPRTSDSPSHEAHFY*			MPRTSDSPSHEAHFY*	TCCCCGAGTT	GCGAGTCCCT	0	P	0	0	0	0	0
10739	4600	af	AN8253.1	53.m03708	AO070310000052	0			-194	-168			ATGGAGAGCCTCGACTTTGCCAGTTGA		ATGGAGAGCCTCGACTTTGCCAGTTGA		MESLDFAS*		MESLDFAS*		GAGTCACTGC	CGAACTGATA	0	O	0	0	0	0	0
10738	4600	an	AN8253.1	53.m03708	AO070310000052	0	-266	-252					ATGGTCAACGTCTGA	ATGGTCAACGTCTGA			MVNV*	MVNV*			GTTTGAGAAA	ATAGACAATA	0	O	0	0	0	0	0
10740	4600	ao	AN8253.1	53.m03708	AO070310000052	0					-188	-156	ATGATTTGTCGGCCACTGATAAGCCCGCGCTAA			ATGATTTGTCGGCCACTGATAAGCCCGCGCTAA	MICRPLISPR*			MICRPLISPR*	GGCGGATCCA	GATAAGGATA	0	O	0	0	0	0	0
10741	4601	an	AN2470.1	53.m03715	AO070310000056	0	-230	-219					ATGTCATGGTGA	ATGTCATGGTGA			MSW*	MSW*			TGATCATGTG	TGCATCCCTT	0	ER	0	0	0	0	0
10742	4601	an	AN2470.1	53.m03715	AO070310000056	0	-225	-121					ATGGTGATGCATCCCTTCTTCATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA	ATGGTGATGCATCCCTTCTTCATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA			MVMHPFFMAVMSSSIQQLSSQNREELFLFSYSFS*	MVMHPFFMAVMSSSIQQLSSQNREELFLFSYSFS*			ATGTGATGTC	TATTGAAAGC	0	ER	0	0	0	0	0
10743	4601	an	AN2470.1	53.m03715	AO070310000056	0	-219	-121					ATGCATCCCTTCTTCATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA	ATGCATCCCTTCTTCATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA			MHPFFMAVMSSSIQQLSSQNREELFLFSYSFS*	MHPFFMAVMSSSIQQLSSQNREELFLFSYSFS*			TGTCATGGTG	TATTGAAAGC	0	ER	0	0	0	0	0
10744	4601	an	AN2470.1	53.m03715	AO070310000056	0	-204	-121					ATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA	ATGGCTGTCATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA			MAVMSSSIQQLSSQNREELFLFSYSFS*	MAVMSSSIQQLSSQNREELFLFSYSFS*			TCCCTTCTTC	TATTGAAAGC	0	ER	0	0	0	0	0
10745	4601	an	AN2470.1	53.m03715	AO070310000056	0	-195	-121					ATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA	ATGTCATCTAGTATACAGCAGCTCTCGAGCCAGAACAGAGAAGAACTCTTTCTATTCTCATATTCCTTCAGTTAA			MSSSIQQLSSQNREELFLFSYSFS*	MSSSIQQLSSQNREELFLFSYSFS*			CATGGCTGTC	TATTGAAAGC	0	ER	0	0	0	0	0
10749	4601	ao	AN2470.1	53.m03715	AO070310000056	0					-234	-52	ATGACTGGAATGTATCATTATTACCCCAGTCCTCTCCAGACTGGAGAAGCCCAGGGAATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGACTGGAATGTATCATTATTACCCCAGTCCTCTCCAGACTGGAGAAGCCCAGGGAATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MTGMYHYYPSPLQTGEAQGMTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*			MTGMYHYYPSPLQTGEAQGMTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*	AAAAAGGTCC	TTGAAGCCGT	0	ER	0	0	0	0	0

10750	4601	ao	AN2470.1	53.m03715	AO070310000056	0					-225	-52	ATGTATCATTATTACCCCAGTCCTCTCCAGACTGGAGAAGCCCAGGGAATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGTATCATTATTACCCCAGTCCTCTCCAGACTGGAGAAGCCCAGGGAATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MYHYYPSPLQTGEAQGMTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*			MYHYYPSPLQTGEAQGMTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*	CATGACTGGA	TTGAAGCCGT	0	ER	0	0	0	0	0
10751	4601	ao	AN2470.1	53.m03715	AO070310000056	0					-177	-52	ATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGACTATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*			MTMVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*	AGCCCAGGGA	TTGAAGCCGT	0	ER	0	0	0	0	0
10752	4601	ao	AN2470.1	53.m03715	AO070310000056	0					-171	-52	ATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA			ATGGTTGGGCGTTCCAAGATTTTTGCCCCAGGCCGATTCATAGTGATGTCAGTCCTGATGATGTACTCAACAACCACTATTGAAATATCACCTTTTAATCCACGCATGCACCATCCATAA	MVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*			MVGRSKIFAPGRFIVMSVLMMYSTTTIEISPFNPRMHHP*	GGGAATGACT	TTGAAGCCGT	0	ER	0	0	0	0	0
10759	4602	af	AN2505.1	59.m08485	AO070312000059	0			-181	-89			ATGGATAACTGTGTCTCCACAGTTGGAGATCGTCATTATCCTTTACTGCTCGCACCACCATCACTGTCATCACATCATCACAGCGTATTTTAA		ATGGATAACTGTGTCTCCACAGTTGGAGATCGTCATTATCCTTTACTGCTCGCACCACCATCACTGTCATCACATCATCACAGCGTATTTTAA		MDNCVSTVGDRHYPLLLAPPSLSSHHHSVF*		MDNCVSTVGDRHYPLLLAPPSLSSHHHSVF*		GACATCCAAG	CTACAGCATT	0		0	0	0	0	0
10757	4602	an	AN2505.1	59.m08485	AO070312000059	0	-137	-39					ATGCACACGGCGCATACTCATTCTCCACAACACCGGCCTGGGACAGTGTTACTCCAATGTCTGACGCGCCCTGACGGCTCCGGTACGTCTCTCCCTTAG	ATGCACACGGCGCATACTCATTCTCCACAACACCGGCCTGGGACAGTGTTACTCCAATGTCTGACGCGCCCTGACGGCTCCGGTACGTCTCTCCCTTAG			MHTAHTHSPQHRPGTVLLQCLTRPDGSGTSLP*	MHTAHTHSPQHRPGTVLLQCLTRPDGSGTSLP*			TTAAAGGCTC	CTCGTAGGCC	0		0	0	0	0	0
10758	4602	an	AN2505.1	59.m08485	AO070312000059	0	-81	-64					ATGTCTGACGCGCCCTGA	ATGTCTGACGCGCCCTGA			MSDAP*	MSDAP*			TGTTACTCCA	CGGCTCCGGT	0		0	0	0	0	0
10760	4602	ao	AN2505.1	59.m08485	AO070312000059	0					-242	-210	ATGCTTGTTAGAGCCGCATTCCTGAACTACTAA			ATGCTTGTTAGAGCCGCATTCCTGAACTACTAA	MLVRAAFLNY*			MLVRAAFLNY*	AATGATCCTC	AACATGCTCT	0		0	0	0	0	0
10761	4602	ao	AN2505.1	59.m08485	AO070312000059	0					-206	-165	ATGCTCTCAGCTGGTTCATTCCGTCTCCAAGGGTGTGGGTAA			ATGCTCTCAGCTGGTTCATTCCGTCTCCAAGGGTGTGGGTAA	MLSAGSFRLQGCG*			MLSAGSFRLQGCG*	CTACTAAAAC	TCTTCACACT	0		0	0	0	0	0
10764	4603	af	AN4177.1	56.m02500	AO070319000001	0			-197	-165			ATGAGGATGCCGCTCTTCATGGCGTGTGGGTGA		ATGAGGATGCCGCTCTTCATGGCGTGTGGGTGA		MRMPLFMACG*		MRMPLFMACG*		AGAAGACCCA	TATCATACTT	0		0	0	0	0	0
10765	4603	af	AN4177.1	56.m02500	AO070319000001	0			-191	-165			ATGCCGCTCTTCATGGCGTGTGGGTGA		ATGCCGCTCTTCATGGCGTGTGGGTGA		MPLFMACG*		MPLFMACG*		CCCAATGAGG	TATCATACTT	0		0	0	0	0	0
10766	4603	af	AN4177.1	56.m02500	AO070319000001	0			-179	-165			ATGGCGTGTGGGTGA		ATGGCGTGTGGGTGA		MACG*		MACG*		GCCGCTCTTC	TATCATACTT	0		0	0	0	0	0
10762	4603	an	AN4177.1	56.m02500	AO070319000001	0	-175	-116					ATGATTTCGCGGGCCGTTCCACTTCCCGAAGGTCCCGGTAGTGAGCCTGAGACGCCATGA	ATGATTTCGCGGGCCGTTCCACTTCCCGAAGGTCCCGGTAGTGAGCCTGAGACGCCATGA			MISRAVPLPEGPGSEPETP*	MISRAVPLPEGPGSEPETP*			CGTTTTATCC	CGCCATACAG	0		0	0	0	0	0
10763	4603	an	AN4177.1	56.m02500	AO070319000001	0	-119	-78					ATGACGCCATACAGACGTCTTCCTTCGTGGAGACTACGATAG	ATGACGCCATACAGACGTCTTCCTTCGTGGAGACTACGATAG			MTPYRRLPSWRLR*	MTPYRRLPSWRLR*			CTGAGACGCC	ATCTACAATA	0		0	0	0	0	0
10767	4603	ao	AN4177.1	56.m02500	AO070319000001	0					-153	-142	ATGAGGTCATGA			ATGAGGTCATGA	MRS*			MRS*	TCAAGGGGTT	CATCCGAGGT	0		0	0	0	0	0
10768	4603	ao	AN4177.1	56.m02500	AO070319000001	0					-145	-59	ATGACATCCGAGGTACAGCTTCTTCAACTCTTGCTTATAACAGATGGTATATATAAGACTTCGAGCACACCAGTGTCTTTACTTTAG			ATGACATCCGAGGTACAGCTTCTTCAACTCTTGCTTATAACAGATGGTATATATAAGACTTCGAGCACACCAGTGTCTTTACTTTAG	MTSEVQLLQLLLITDGIYKTSSTPVSLL*			MTSEVQLLQLLLITDGIYKTSSTPVSLL*	TTATGAGGTC	TATGTTCAAC	0		0	0	0	0	0
10769	4603	ao	AN4177.1	56.m02500	AO070319000001	0					-102	-13	ATGGTATATATAAGACTTCGAGCACACCAGTGTCTTTACTTTAGTATGTTCAACTCATTACTGAACTACATACTATACTTCGTTGCCTGA			ATGGTATATATAAGACTTCGAGCACACCAGTGTCTTTACTTTAGTATGTTCAACTCATTACTGAACTACATACTATACTTCGTTGCCTGA	MVYIRLRAHQCLYFSMFNSLLNYILYFVA*			MVYIRLRAHQCLYFSMFNSLLNYILYFVA*	CTTATAACAG	ACGTACTAGA	0		0	0	0	0	0
10771	4604	an	AN0977.1	70.m15615	AO070320000180	0	-62	-6					ATGCGACCAACCGCGACTGACGTGGATCTATGCGCAGCCTGTAATTGTTATCGTTGA	ATGCGACCAACCGCGACTGACGTGGATCTATGCGCAGCCTGTAATTGTTATCGTTGA			MRPTATDVDLCAACNCYR*	MRPTATDVDLCAACNCYR*			TGAAATGTGA	CCGCGATGCC	0		0	0	0	0	0
10775	4605	af	AN3924.1	69.m15005	AO070324000120	0			-155	-135			ATGAACGAGGAAGCAATCTGA		ATGAACGAGGAAGCAATCTGA		MNEEAI*		MNEEAI*		TACAGAGGAA	AGAACCAAAG	0	K	FG01036.1	MG00484.1	0	0	0
10774	4605	an	AN3924.1	69.m15005	AO070324000120	0	-103	-92					ATGTACACGTGA	ATGTACACGTGA			MYT*	MYT*			CATCCTCGCA	ACTAGCTCCA	0	K	FG01036.1	MG00484.1	0	0	0
10776	4605	ao	AN3924.1	69.m15005	AO070324000120	0					-160	-146	ATGACCAGAGACTAA			ATGACCAGAGACTAA	MTRD*			MTRD*	CACCCAAAGA	ATGAGAATAT	0	K	FG01036.1	MG00484.1	0	0	0
10777	4605	ao	AN3924.1	69.m15005	AO070324000120	0					-145	-131	ATGAGAATATCCTAA			ATGAGAATATCCTAA	MRIS*			MRIS*	CAGAGACTAA	TTCCAATACC	0	K	FG01036.1	MG00484.1	0	0	0
10778	4606	an	AN3217.1	67.m02926	AO070330000062	0	-180	-31					ATGACAGATATAATAGCCTCAGGCAGAAAAGAACCACGTGATTCGGAGATAGAGGTGGCCCGTATATCCGTCTGCCGGCCTTCCGCGACTTCAAGACACAGTCCAACCCTTTCATTCCAGACAACTCGTTACTGGCGAGGAGTGGCCTAG	ATGACAGATATAATAGCCTCAGGCAGAAAAGAACCACGTGATTCGGAGATAGAGGTGGCCCGTATATCCGTCTGCCGGCCTTCCGCGACTTCAAGACACAGTCCAACCCTTTCATTCCAGACAACTCGTTACTGGCGAGGAGTGGCCTAG			MTDIIASGRKEPRDSEIEVARISVCRPSATSRHSPTLSFQTTRYWRGVA*	MTDIIASGRKEPRDSEIEVARISVCRPSATSRHSPTLSFQTTRYWRGVA*			AAACGATAGA	TCCAGACTTA	0		0	0	0	0	0
10781	4607	af	AN4070.1	54.m06713	AO070342000059	0			-112	-71			ATGTTGATCAGAGCTTCTGTTATTGCTACGACTTGTCACTGA		ATGTTGATCAGAGCTTCTGTTATTGCTACGACTTGTCACTGA		MLIRASVIATTCH*		MLIRASVIATTCH*		GCTCCTTTGC	AGAGCGATCA	0	S	0	0	0	0	0
10779	4607	an	AN4070.1	54.m06713	AO070342000059	0	-154	-77					ATGCGATCTGATGCATCACCCTGCACCCGCTGGACGCGCCCCGATAGGCTGGTTCCCGTTGGCAGTCTTCTAGTTTGA	ATGCGATCTGATGCATCACCCTGCACCCGCTGGACGCGCCCCGATAGGCTGGTTCCCGTTGGCAGTCTTCTAGTTTGA			MRSDASPCTRWTRPDRLVPVGSLLV*	MRSDASPCTRWTRPDRLVPVGSLLV*			ATATGCTCTG	GATCTGGAGT	0	S	0	0	0	0	0
10780	4607	an	AN4070.1	54.m06713	AO070342000059	0	-144	-82					ATGCATCACCCTGCACCCGCTGGACGCGCCCCGATAGGCTGGTTCCCGTTGGCAGTCTTCTAG	ATGCATCACCCTGCACCCGCTGGACGCGCCCCGATAGGCTGGTTCCCGTTGGCAGTCTTCTAG			MHHPAPAGRAPIGWFPLAVF*	MHHPAPAGRAPIGWFPLAVF*			ATGCGATCTG	TTTGAGATCT	0	S	0	0	0	0	0
10782	4607	ao	AN4070.1	54.m06713	AO070342000059	0					-73	-56	ATGTTTATCATTATCTGA			ATGTTTATCATTATCTGA	MFIII*			MFIII*	GGTTTTGGAA	TGACCGGGTG	0	S	0	0	0	0	0
10786	4613	af	AN1454.1	55.m02959	AO070302000024	0			-256	-74			ATGGCAGGCAAACGGACGGAGATACCTATACAAGAGGCTTGTCAAGGCGAAGACCTTGTTCGCGAGTTTTTCCGGACCGTCGGCCCTTTCTACGCTTATGTCATCCGCCAACCCGGCCTTCCTTCTGCGTGGGGGACGGTGTACGGGATACGGAGTATCTGCGGAACGCGAAGCCGCATGTAA		ATGGCAGGCAAACGGACGGAGATACCTATACAAGAGGCTTGTCAAGGCGAAGACCTTGTTCGCGAGTTTTTCCGGACCGTCGGCCCTTTCTACGCTTATGTCATCCGCCAACCCGGCCTTCCTTCTGCGTGGGGGACGGTGTACGGGATACGGAGTATCTGCGGAACGCGAAGCCGCATGTAA		MAGKRTEIPIQEACQGEDLVREFFRTVGPFYAYVIRQPGLPSAWGTVYGIRSICGTRSRM*		MAGKRTEIPIQEACQGEDLVREFFRTVGPFYAYVIRQPGLPSAWGTVYGIRSICGTRSRM*		TCGACTGTCA	ATAATGATAA	0	Z	FG00428.1	MG04771.1	0	0	0
10787	4613	af	AN1454.1	55.m02959	AO070302000024	0			-159	-70			ATGTCATCCGCCAACCCGGCCTTCCTTCTGCGTGGGGGACGGTGTACGGGATACGGAGTATCTGCGGAACGCGAAGCCGCATGTAAATAA		ATGTCATCCGCCAACCCGGCCTTCCTTCTGCGTGGGGGACGGTGTACGGGATACGGAGTATCTGCGGAACGCGAAGCCGCATGTAAATAA		MSSANPAFLLRGGRCTGYGVSAEREAACK*		MSSANPAFLLRGGRCTGYGVSAEREAACK*		TTCTACGCTT	TGATAATCAA	0	Z	FG00428.1	MG04771.1	0	0	0
10788	4613	af	AN1454.1	55.m02959	AO070302000024	0			-70	-53			ATGATAATCAATTCGTAG		ATGATAATCAATTCGTAG		MIINS*		MIINS*		CATGTAAATA	AGGGCCTGGA	0	Z	FG00428.1	MG04771.1	0	0	0
10783	4613	an	AN1454.1	55.m02959	AO070302000024	0	-190	-155					ATGGCAAGCCGGCAGAGGAGGTTCGGATGCTGGTGA	ATGGCAAGCCGGCAGAGGAGGTTCGGATGCTGGTGA			MASRQRRFGCW*	MASRQRRFGCW*			GTGATCGATA	CCGAACAAGA	0	Z	FG00428.1	MG04771.1	0	0	0
10784	4613	an	AN1454.1	55.m02959	AO070302000024	0	-164	-39					ATGCTGGTGACCGAACAAGACGAAGTTCCTGTCGCGAGTTTTTCCGGACCCGTCGGACCTGCGCTTATGTCATCCTCATCCAGTCCACGCTTCCATTCACGCAGTGTATACTCCCCAAGTAAATAA	ATGCTGGTGACCGAACAAGACGAAGTTCCTGTCGCGAGTTTTTCCGGACCCGTCGGACCTGCGCTTATGTCATCCTCATCCAGTCCACGCTTCCATTCACGCAGTGTATACTCCCCAAGTAAATAA			MLVTEQDEVPVASFSGPVGPALMSSSSSPRFHSRSVYSPSK*	MLVTEQDEVPVASFSGPVGPALMSSSSSPRFHSRSVYSPSK*			GGAGGTTCGG	TATTCCCAGG	0	Z	FG00428.1	MG04771.1	0	0	0
10785	4613	an	AN1454.1	55.m02959	AO070302000024	0	-98	-39					ATGTCATCCTCATCCAGTCCACGCTTCCATTCACGCAGTGTATACTCCCCAAGTAAATAA	ATGTCATCCTCATCCAGTCCACGCTTCCATTCACGCAGTGTATACTCCCCAAGTAAATAA			MSSSSSPRFHSRSVYSPSK*	MSSSSSPRFHSRSVYSPSK*			ACCTGCGCTT	TATTCCCAGG	0	Z	FG00428.1	MG04771.1	0	0	0
10789	4613	ao	AN1454.1	55.m02959	AO070302000024	0					-244	-227	ATGGCTGGCAATCGATAG			ATGGCTGGCAATCGATAG	MAGNR*			MAGNR*	TCAATTGGCA	GATACTCAGA	0	Z	FG00428.1	MG04771.1	0	0	0
10790	4613	ao	AN1454.1	55.m02959	AO070302000024	0					-156	-106	ATGTCATCCGCCGACCCGGACTCTGGGCGCGGGACGGGGAAGTCCAACTAA			ATGTCATCCGCCGACCCGGACTCTGGGCGCGGGACGGGGAAGTCCAACTAA	MSSADPDSGRGTGKSN*			MSSADPDSGRGTGKSN*	GCCTGTGCTT	CGCGCATAAC	0	Z	FG00428.1	MG04771.1	0	0	0
10791	4618	af	AN6171.1	72.m19002	AO070340000034	0			-232	-137			ATGTTAGACAAGCAACACTATACCCGAATAAGTATGATAAACCCGACCACTGGTTCAGATCACATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		ATGTTAGACAAGCAACACTATACCCGAATAAGTATGATAAACCCGACCACTGGTTCAGATCACATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		MLDKQHYTRISMINPTTGSDHMAVCTVCTAY*		MLDKQHYTRISMINPTTGSDHMAVCTVCTAY*		AACAGCAACA	ACCACCAGCA	0	A	FG10219.1	0	NCU01008.1	0	0
10792	4618	af	AN6171.1	72.m19002	AO070340000034	0			-199	-137			ATGATAAACCCGACCACTGGTTCAGATCACATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		ATGATAAACCCGACCACTGGTTCAGATCACATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		MINPTTGSDHMAVCTVCTAY*		MINPTTGSDHMAVCTVCTAY*		CCGAATAAGT	ACCACCAGCA	0	A	FG10219.1	0	NCU01008.1	0	0
10793	4618	af	AN6171.1	72.m19002	AO070340000034	0			-169	-137			ATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		ATGGCAGTTTGCACAGTTTGCACCGCGTACTAA		MAVCTVCTAY*		MAVCTVCTAY*		TTCAGATCAC	ACCACCAGCA	0	A	FG10219.1	0	NCU01008.1	0	0
10795	4621	an	AN4234.1	54.m06782	AO070234000012	0	-202	-158					ATGTTTTGCTGGCACCGCCGCAGCACAGCAAGGAACCAGGCCTAG	ATGTTTTGCTGGCACCGCCGCAGCACAGCAAGGAACCAGGCCTAG			MFCWHRRSTARNQA*	MFCWHRRSTARNQA*			AAGACCGGCC	TAAAGTTGTC	0	G	0	0	0	0	0
10796	4624	af	AN0332.1	54.m06425	AO070318000008	0			-204	-109			ATGGCACTAGCATGGTTTGATATTAGTCATCCTAATGATTCCTCATCCTTCTTCTCCCCTAGTGCCCTCCCTTCTCCTTGTGTCCCAACTGTTTAA		ATGGCACTAGCATGGTTTGATATTAGTCATCCTAATGATTCCTCATCCTTCTTCTCCCCTAGTGCCCTCCCTTCTCCTTGTGTCCCAACTGTTTAA		MALAWFDISHPNDSSSFFSPSALPSPCVPTV*		MALAWFDISHPNDSSSFFSPSALPSPCVPTV*		GTCACTCTAT	CAAGACAAAG	0	R	0	0	0	0	0
10797	4624	af	AN0332.1	54.m06425	AO070318000008	0			-170	-72			ATGATTCCTCATCCTTCTTCTCCCCTAGTGCCCTCCCTTCTCCTTGTGTCCCAACTGTTTAACAAGACAAAGTCACCGGCAAGGCTATTAAACAACTAA		ATGATTCCTCATCCTTCTTCTCCCCTAGTGCCCTCCCTTCTCCTTGTGTCCCAACTGTTTAACAAGACAAAGTCACCGGCAAGGCTATTAAACAACTAA		MIPHPSSPLVPSLLLVSQLFNKTKSPARLLNN*		MIPHPSSPLVPSLLLVSQLFNKTKSPARLLNN*		AGTCATCCTA	AACAAATCTA	0	R	0	0	0	0	0
10798	4625	an	AN7680.1	57.m05457	AO070325000070	0	-234	-169					ATGTCTATCTACTTTGCCAGTATTTCAAACGCTAAAAGGGCTCCGATCAACAATTTTTTGCAATAA	ATGTCTATCTACTTTGCCAGTATTTCAAACGCTAAAAGGGCTCCGATCAACAATTTTTTGCAATAA			MSIYFASISNAKRAPINNFLQ*	MSIYFASISNAKRAPINNFLQ*			ACCTTTGCAA	AGTCTACGTA	0	Z	0	0	0	0	0
10799	4625	an	AN7680.1	57.m05457	AO070325000070	0	-118	-17					ATGTATAACCAGGTGGACCGTGCGAGACACGGGGAAAGCTGTCCTCCCGCCCTACTTACCTGTACAGCACAAACTCACTCTTTCCCCTCACGAACTCCCTAA	ATGTATAACCAGGTGGACCGTGCGAGACACGGGGAAAGCTGTCCTCCCGCCCTACTTACCTGTACAGCACAAACTCACTCTTTCCCCTCACGAACTCCCTAA			MYNQVDRARHGESCPPALLTCTAQTHSFPSRTP*	MYNQVDRARHGESCPPALLTCTAQTHSFPSRTP*			TGATCGTCTC	TTTCATTGCT	0	Z	0	0	0	0	0
10802	4629	af	AN4530.1	57.m05596	AO070321000140	0			-174	-121			ATGATTTGTGAAGGCAACAGTGTCTCTTCCTCCATTGGCTTGATTGAGTGTTAA		ATGATTTGTGAAGGCAACAGTGTCTCTTCCTCCATTGGCTTGATTGAGTGTTAA		MICEGNSVSSSIGLIEC*		MICEGNSVSSSIGLIEC*		GGTTTTCTTC	GCACCTCCTT	0	J	0	0	0	0	0
10803	4638	af	AN1467.1	55.m02969	AO070306000090	0			-243	-229			ATGGACAAAGCGTAG		ATGGACAAAGCGTAG		MDKA*		MDKA*		CTCCAATTGC	AGGACTTCAT	0	T	0	MG00166.1	NCU00958.1	0	0
10807	4639	af	AN1025.1	70.m15210	AO070312000120	0			-157	-131			ATGCTCCAGCCGCGCTTGACCACTTGA		ATGCTCCAGCCGCGCTTGACCACTTGA		MLQPRLTT*		MLQPRLTT*		TTCGTTCCGG	TTGTTTACGT	0	T	0	0	0	0	0
10806	4639	an	AN1025.1	70.m15210	AO070312000120	0	-138	-97					ATGAATAATAGCCTTGGCTTGACCGACCATTTCGCGCTCTGA	ATGAATAATAGCCTTGGCTTGACCGACCATTTCGCGCTCTGA			MNNSLGLTDHFAL*	MNNSLGLTDHFAL*			TAAACCATCG	ACCTGTACTG	0	T	0	0	0	0	0
10808	4639	ao	AN1025.1	70.m15210	AO070312000120	0					-173	-63	ATGCAAAACCTGGTCTTACTACCTCACCCCTGTGTCGCCAAAGCATTTGATAGCAACACCGCGGGCGCACCCCGAGCGTCGTCGTCATTGACAATTTTGGTACCTTGGTGA			ATGCAAAACCTGGTCTTACTACCTCACCCCTGTGTCGCCAAAGCATTTGATAGCAACACCGCGGGCGCACCCCGAGCGTCGTCGTCATTGACAATTTTGGTACCTTGGTGA	MQNLVLLPHPCVAKAFDSNTAGAPRASSSLTILVPW*			MQNLVLLPHPCVAKAFDSNTAGAPRASSSLTILVPW*	TTGCTGTCGG	ACCTTTCGCG	0	T	0	0	0	0	0

10810	4647	af	AN8884.1	56.m02296	AO070293000016	0			-270	-76			ATGATCGATTGTCCTCTCCAATCTATAAGTTCCTCCTTCGCATACGCTTCAAATCTGAGTTTCTCCCTCGGATCGTCCTCAATTGATTTTTTTTTGTTTTTCATTTCTCATCTTTCATTGCTTTTCTACAAATTTTTTCTTCTTTTACCCTACCAGGCTTTCTCTCTTGTTCGGTTGTATCGAAGCTTATTATAG		ATGATCGATTGTCCTCTCCAATCTATAAGTTCCTCCTTCGCATACGCTTCAAATCTGAGTTTCTCCCTCGGATCGTCCTCAATTGATTTTTTTTTGTTTTTCATTTCTCATCTTTCATTGCTTTTCTACAAATTTTTTCTTCTTTTACCCTACCAGGCTTTCTCTCTTGTTCGGTTGTATCGAAGCTTATTATAG		MIDCPLQSISSSFAYASNLSFSLGSSSIDFFLFFISHLSLLFYKFFLLLPYQAFSLVRLYRSLL*		MIDCPLQSISSSFAYASNLSFSLGSSSIDFFLFFISHLSLLFYKFFLLLPYQAFSLVRLYRSLL*		TCATGATCTC	TCATCATCCC	0		0	0	0	0	0
10815	4651	af	AN2591.1	58.m08876	AO070245000015	0			-191	-168			ATGGTAGAAGCAAGAAGTTGCTGA		ATGGTAGAAGCAAGAAGTTGCTGA		MVEARSC*		MVEARSC*		TTTTGGAGAC	ACATATTACA	0	G	0	0	0	0	0
10813	4651	an	AN2591.1	58.m08876	AO070245000015	0	-178	-113					ATGCAACCCTGGACAGTTGGAGTCCGAGGGATGACTGATAGCAACCCCGCACTCCAGACTGATTGA	ATGCAACCCTGGACAGTTGGAGTCCGAGGGATGACTGATAGCAACCCCGCACTCCAGACTGATTGA			MQPWTVGVRGMTDSNPALQTD*	MQPWTVGVRGMTDSNPALQTD*			GAATACTCGG	ATAATTCGCT	0	G	0	0	0	0	0
10814	4651	an	AN2591.1	58.m08876	AO070245000015	0	-148	-113					ATGACTGATAGCAACCCCGCACTCCAGACTGATTGA	ATGACTGATAGCAACCCCGCACTCCAGACTGATTGA			MTDSNPALQTD*	MTDSNPALQTD*			AGTCCGAGGG	ATAATTCGCT	0	G	0	0	0	0	0
10816	4651	ao	AN2591.1	58.m08876	AO070245000015	0					-166	-134	ATGTCTGTAGAATGGAAGCCACGCTGGCAATGA			ATGTCTGTAGAATGGAAGCCACGCTGGCAATGA	MSVEWKPRWQ*			MSVEWKPRWQ*	TGTCCCATGA	GTGTACTTGG	0	G	0	0	0	0	0
10817	4651	ao	AN2591.1	58.m08876	AO070245000015	0					-105	-91	ATGTGCGCGGGGTAA			ATGTGCGCGGGGTAA	MCAG*			MCAG*	AGGGCCGATC	GTTACATCTC	0	G	0	0	0	0	0
10822	4652	af	AN7524.1	69.m15112	AO070258000032	0			-141	-127			ATGGGATACAGTTGA		ATGGGATACAGTTGA		MGYS*		MGYS*		ACTACATAAC	TCTCATCAGA	0	V	0	0	0	0	0
10818	4652	an	AN7524.1	69.m15112	AO070258000032	0	-238	-35					ATGACATTCCCTTCTAGTTACTCCGTTCGCAGCTCCATAAAACGACCATGTCGTCGTTCTCATTCATCGCCCATTCCTTTCGATGACGAACGGTCCTGGCTACCGGCTAACTCCACTGTTCCAGCTTCGCCCATGATCGTCCTGTGTCTATACCATTCCCCTGAACGACTCTTCGCACTCCCATCTCCCCCCTTCCAACCCTGA	ATGACATTCCCTTCTAGTTACTCCGTTCGCAGCTCCATAAAACGACCATGTCGTCGTTCTCATTCATCGCCCATTCCTTTCGATGACGAACGGTCCTGGCTACCGGCTAACTCCACTGTTCCAGCTTCGCCCATGATCGTCCTGTGTCTATACCATTCCCCTGAACGACTCTTCGCACTCCCATCTCCCCCCTTCCAACCCTGA			MTFPSSYSVRSSIKRPCRRSHSSPIPFDDERSWLPANSTVPASPMIVLCLYHSPERLFALPSPPFQP*	MTFPSSYSVRSSIKRPCRRSHSSPIPFDDERSWLPANSTVPASPMIVLCLYHSPERLFALPSPPFQP*			TCAGTTCCCT	ACTAGTGCCC	0	V	0	0	0	0	0
10819	4652	an	AN7524.1	69.m15112	AO070258000032	0	-191	-153					ATGTCGTCGTTCTCATTCATCGCCCATTCCTTTCGATGA	ATGTCGTCGTTCTCATTCATCGCCCATTCCTTTCGATGA			MSSFSFIAHSFR*	MSSFSFIAHSFR*			TAAAACGACC	CGAACGGTCC	0	V	0	0	0	0	0
10820	4652	an	AN7524.1	69.m15112	AO070258000032	0	-156	-103					ATGACGAACGGTCCTGGCTACCGGCTAACTCCACTGTTCCAGCTTCGCCCATGA	ATGACGAACGGTCCTGGCTACCGGCTAACTCCACTGTTCCAGCTTCGCCCATGA			MTNGPGYRLTPLFQLRP*	MTNGPGYRLTPLFQLRP*			ATTCCTTTCG	TCGTCCTGTG	0	V	0	0	0	0	0
10821	4652	an	AN7524.1	69.m15112	AO070258000032	0	-106	-35					ATGATCGTCCTGTGTCTATACCATTCCCCTGAACGACTCTTCGCACTCCCATCTCCCCCCTTCCAACCCTGA	ATGATCGTCCTGTGTCTATACCATTCCCCTGAACGACTCTTCGCACTCCCATCTCCCCCCTTCCAACCCTGA			MIVLCLYHSPERLFALPSPPFQP*	MIVLCLYHSPERLFALPSPPFQP*			AGCTTCGCCC	ACTAGTGCCC	0	V	0	0	0	0	0
10824	4660	af	AN3029.1	59.m08990	AO070337000071	0			-178	-161			ATGCCGGTCTCGTTTTAA		ATGCCGGTCTCGTTTTAA		MPVSF*		MPVSF*		GGGAAACGTG	GTGTTGCACC	0	U	0	0	0	0	0
10823	4660	an	AN3029.1	59.m08990	AO070337000071	0	-208	-197					ATGACAGAATAA	ATGACAGAATAA			MTE*	MTE*			CGGGGATATA	TTAGCTAGGC	0	U	0	0	0	0	0
10825	4660	ao	AN3029.1	59.m08990	AO070337000071	0					-178	-167	ATGACGCTTTAA			ATGACGCTTTAA	MTL*			MTL*	GCCTTTGGGG	TTCTACCCTA	0	U	0	0	0	0	0
10830	4661	af	AN6707.1	65.m07278	AO070339000137	0			-258	-193			ATGATGGGCGCATCCCATCGGTATAAGGTGCCTGAAGAAGCTATAATTGCATATTTAAATAATTAA		ATGATGGGCGCATCCCATCGGTATAAGGTGCCTGAAGAAGCTATAATTGCATATTTAAATAATTAA		MMGASHRYKVPEEAIIAYLNN*		MMGASHRYKVPEEAIIAYLNN*		GTTCGGGCAG	ATATTATATG	0	KL	0	0	0	0	0
10831	4661	af	AN6707.1	65.m07278	AO070339000137	0			-255	-193			ATGGGCGCATCCCATCGGTATAAGGTGCCTGAAGAAGCTATAATTGCATATTTAAATAATTAA		ATGGGCGCATCCCATCGGTATAAGGTGCCTGAAGAAGCTATAATTGCATATTTAAATAATTAA		MGASHRYKVPEEAIIAYLNN*		MGASHRYKVPEEAIIAYLNN*		CGGGCAGATG	ATATTATATG	0	KL	0	0	0	0	0
10832	4661	af	AN6707.1	65.m07278	AO070339000137	0			-153	-82			ATGTTACGTAGTGGTACTTATCAGCTTGGAAGATTTCTGATAAGAGAAATGTTTGAACTGTTTGCCTCGTAG		ATGTTACGTAGTGGTACTTATCAGCTTGGAAGATTTCTGATAAGAGAAATGTTTGAACTGTTTGCCTCGTAG		MLRSGTYQLGRFLIREMFELFAS*		MLRSGTYQLGRFLIREMFELFAS*		CCCGAAAAAA	ATAGCATAAT	0	KL	0	0	0	0	0
10833	4661	af	AN6707.1	65.m07278	AO070339000137	0			-105	-82			ATGTTTGAACTGTTTGCCTCGTAG		ATGTTTGAACTGTTTGCCTCGTAG		MFELFAS*		MFELFAS*		GATAAGAGAA	ATAGCATAAT	0	KL	0	0	0	0	0
10826	4661	an	AN6707.1	65.m07278	AO070339000137	0	-214	-161					ATGGGTTTTGGCAGGCAGGATTCTTCATGGCCTACCAGTTGGGATGAAATCTAA	ATGGGTTTTGGCAGGCAGGATTCTTCATGGCCTACCAGTTGGGATGAAATCTAA			MGFGRQDSSWPTSWDEI*	MGFGRQDSSWPTSWDEI*			CGGCGTAGAC	ATCGATAAGA	0	KL	0	0	0	0	0
10827	4661	an	AN6707.1	65.m07278	AO070339000137	0	-188	-168					ATGGCCTACCAGTTGGGATGA	ATGGCCTACCAGTTGGGATGA			MAYQLG*	MAYQLG*			AGGATTCTTC	AATCTAAATC	0	KL	0	0	0	0	0
10828	4661	an	AN6707.1	65.m07278	AO070339000137	0	-171	-109					ATGAAATCTAAATCGATAAGACGCCTTGAGAGCGTGCCACAAGGGAGGAAGTGTAGACCGTAG	ATGAAATCTAAATCGATAAGACGCCTTGAGAGCGTGCCACAAGGGAGGAAGTGTAGACCGTAG			MKSKSIRRLESVPQGRKCRP*	MKSKSIRRLESVPQGRKCRP*			ACCAGTTGGG	ATGAAAAAGT	0	KL	0	0	0	0	0
10829	4661	an	AN6707.1	65.m07278	AO070339000137	0	-108	-28					ATGAAAAAGTTGGTTATCGGGCCTGATAAGGCCGTCCGTGTTTGCACTGTTTGGGCTCCTTATCGCCGTGACATTCTCTGA	ATGAAAAAGTTGGTTATCGGGCCTGATAAGGCCGTCCGTGTTTGCACTGTTTGGGCTCCTTATCGCCGTGACATTCTCTGA			MKKLVIGPDKAVRVCTVWAPYRRDIL*	MKKLVIGPDKAVRVCTVWAPYRRDIL*			TAGACCGTAG	AGAACTTCCT	0	KL	0	0	0	0	0
10835	4661	ao	AN6707.1	65.m07278	AO070339000137	0					-245	-198	ATGGACTCTGGAAAAATGGCGGAAACATGCCCGGCATCGACCGACTAA			ATGGACTCTGGAAAAATGGCGGAAACATGCCCGGCATCGACCGACTAA	MDSGKMAETCPASTD*			MDSGKMAETCPASTD*	CACCATTGAC	TTAAACATCG	0	KL	0	0	0	0	0
10836	4661	ao	AN6707.1	65.m07278	AO070339000137	0					-230	-198	ATGGCGGAAACATGCCCGGCATCGACCGACTAA			ATGGCGGAAACATGCCCGGCATCGACCGACTAA	MAETCPASTD*			MAETCPASTD*	CTCTGGAAAA	TTAAACATCG	0	KL	0	0	0	0	0
10837	4661	ao	AN6707.1	65.m07278	AO070339000137	0					-219	-118	ATGCCCGGCATCGACCGACTAATTAAACATCGTATAAGGCAGGAGTCGAGAACCTCTGGAAAAAGCAGGGAGAAGAATGCGACACTTCGAGGGGATCCGTAG			ATGCCCGGCATCGACCGACTAATTAAACATCGTATAAGGCAGGAGTCGAGAACCTCTGGAAAAAGCAGGGAGAAGAATGCGACACTTCGAGGGGATCCGTAG	MPGIDRLIKHRIRQESRTSGKSREKNATLRGDP*			MPGIDRLIKHRIRQESRTSGKSREKNATLRGDP*	TGGCGGAAAC	AAATATTTCT	0	KL	0	0	0	0	0
10838	4661	ao	AN6707.1	65.m07278	AO070339000137	0					-143	-99	ATGCGACACTTCGAGGGGATCCGTAGAAATATTTCTATCAGATAA			ATGCGACACTTCGAGGGGATCCGTAGAAATATTTCTATCAGATAA	MRHFEGIRRNISIR*			MRHFEGIRRNISIR*	AGGGAGAAGA	GAAGGGTGTT	0	KL	0	0	0	0	0
10839	4662	ao	AN5199.1	69.m14898	AO070237000029	0					-241	-221	ATGACCCTAGATAGTAGATAA			ATGACCCTAGATAGTAGATAA	MTLDSR*			MTLDSR*	GGTGCGCTTA	ACTAAGCCGG	0	O	0	0	0	0	0
10840	4664	an	AN6323.1	72.m19441	AO070304000044	0	-196	-32					ATGGTCGTGATCTATAGCCTGAGGTATACGTCAGGCACCAGATTTGAGGCCTTATTTCTGAGGCAGCAACAAACCCGGGAGAGTTCCCCTGGCGCGGTCAATAACAACATTCCAAACACAACGGCCGTCCCCGCCTCTCCTTACAGCCTGGAGTTCTCCTTCTGA	ATGGTCGTGATCTATAGCCTGAGGTATACGTCAGGCACCAGATTTGAGGCCTTATTTCTGAGGCAGCAACAAACCCGGGAGAGTTCCCCTGGCGCGGTCAATAACAACATTCCAAACACAACGGCCGTCCCCGCCTCTCCTTACAGCCTGGAGTTCTCCTTCTGA			MVVIYSLRYTSGTRFEALFLRQQQTRESSPGAVNNNIPNTTAVPASPYSLEFSF*	MVVIYSLRYTSGTRFEALFLRQQQTRESSPGAVNNNIPNTTAVPASPYSLEFSF*			GAGGTAAGTC	GTCATTGCAG	0	DZ	0	0	0	0	0
10841	4664	ao	AN6323.1	72.m19441	AO070304000044	0					-166	-122	ATGCCTCAGGCTACCAAGAATCCTTCCGCGCGGATCGCGTCCTGA			ATGCCTCAGGCTACCAAGAATCCTTCCGCGCGGATCGCGTCCTGA	MPQATKNPSARIAS*			MPQATKNPSARIAS*	AGATTATCTG	GGCTCCGAAC	0	DZ	0	0	0	0	0
10842	4665	ao	AN5870.1	72.m19264	AO070308000136	0					-236	-138	ATGCGGCCCCTCAGGCCAATCAGATTTGTCTCAGGCCTTCTTCCTCCTGGGACTAGTCTAGTGCTTTGCTCTCTGTTCCATGAGTTACTTCAACGCTGA			ATGCGGCCCCTCAGGCCAATCAGATTTGTCTCAGGCCTTCTTCCTCCTGGGACTAGTCTAGTGCTTTGCTCTCTGTTCCATGAGTTACTTCAACGCTGA	MRPLRPIRFVSGLLPPGTSLVLCSLFHELLQR*			MRPLRPIRFVSGLLPPGTSLVLCSLFHELLQR*	GGGAAACTTT	CTTCTTCGTC	0		0	0	0	0	0
10843	4665	ao	AN5870.1	72.m19264	AO070308000136	0					-157	-59	ATGAGTTACTTCAACGCTGACTTCTTCGTCGCTCCACTGCCCCGGCCGAAAGCTATCTCGGTTTTCACTATATCATTCCTGTGGGCCCTGATTTTCTGA			ATGAGTTACTTCAACGCTGACTTCTTCGTCGCTCCACTGCCCCGGCCGAAAGCTATCTCGGTTTTCACTATATCATTCCTGTGGGCCCTGATTTTCTGA	MSYFNADFFVAPLPRPKAISVFTISFLWALIF*			MSYFNADFFVAPLPRPKAISVFTISFLWALIF*	TCTCTGTTCC	AGATTCAACA	0		0	0	0	0	0
10844	4669	an	AN4873.1	59.m08769	AO070338000087	0	-110	-57					ATGCGACCTGCATATACTGATCTGTATGGTCTCTCCCAGTCCTGCAATAAGTGA	ATGCGACCTGCATATACTGATCTGTATGGTCTCTCCCAGTCCTGCAATAAGTGA			MRPAYTDLYGLSQSCNK*	MRPAYTDLYGLSQSCNK*			TACCTTGTCT	TCTGTCCAAC	0	R	0	0	0	0	0
10845	4669	ao	AN4873.1	59.m08769	AO070338000087	0					-110	-63	ATGGTTTTATGCAACATGCGCAAAGCTTTCCGGAGTACTTACATATAG			ATGGTTTTATGCAACATGCGCAAAGCTTTCCGGAGTACTTACATATAG	MVLCNMRKAFRSTYI*			MVLCNMRKAFRSTYI*	TGCGTGAGGT	AATTAGATCT	0	R	0	0	0	0	0
10846	4669	ao	AN4873.1	59.m08769	AO070338000087	0					-95	-63	ATGCGCAAAGCTTTCCGGAGTACTTACATATAG			ATGCGCAAAGCTTTCCGGAGTACTTACATATAG	MRKAFRSTYI*			MRKAFRSTYI*	TTTATGCAAC	AATTAGATCT	0	R	0	0	0	0	0
10847	4670	af	AN5952.1	72.m19168	AO070340000305	0			-226	-188			ATGGATTACGTTAACACCATTGGTCAGCCGTGTCAGTAA		ATGGATTACGTTAACACCATTGGTCAGCCGTGTCAGTAA		MDYVNTIGQPCQ*		MDYVNTIGQPCQ*		CCGCTCAGCC	GCAACGGCAG	0	E	0	0	0	0	0
10848	4670	af	AN5952.1	72.m19168	AO070340000305	0			-148	-137			ATGGAGGGGTGA		ATGGAGGGGTGA		MEG*		MEG*		GATTGTCGTC	CAACCCTGGG	0	E	0	0	0	0	0
10849	4670	af	AN5952.1	72.m19168	AO070340000305	0			-114	-103			ATGCTGCCATGA		ATGCTGCCATGA		MLP*		MLP*		GCAACGGACA	AGTGCCTAGC	0	E	0	0	0	0	0
10850	4670	af	AN5952.1	72.m19168	AO070340000305	0			-106	-77			ATGAAGTGCCTAGCCCTTTCACGAGACTGA		ATGAAGTGCCTAGCCCTTTCACGAGACTGA		MKCLALSRD*		MKCLALSRD*		CAATGCTGCC	CGGTGCCTTG	0	E	0	0	0	0	0
10851	4672	an	AN4332.1	58.m07986	AO070240000011	0	-104	-84					ATGTCCCGGTCGTTGGGTTGA	ATGTCCCGGTCGTTGGGTTGA			MSRSLG*	MSRSLG*			CGTACGCTGA	TCCGCACCGG	0	U	0	0	0	0	0
10854	4674	af	AN0560.1	69.m15287	AO070272000037	0			-258	-238			ATGGCAAGGTATTCCCTTTGA		ATGGCAAGGTATTCCCTTTGA		MARYSL*		MARYSL*		CAACAAGGGG	CGACTGGAAG	0	U	FG09816.1	0	0	0	0
10855	4674	af	AN0560.1	69.m15287	AO070272000037	0			-89	-39			ATGTTGCAATGCTTGCGCTTTCTTCAGCTTTTTGATAGCCTAATCATCTAA		ATGTTGCAATGCTTGCGCTTTCTTCAGCTTTTTGATAGCCTAATCATCTAA		MLQCLRFLQLFDSLII*		MLQCLRFLQLFDSLII*		TTAGCTCGTC	TCGATCTGAC	0	U	FG09816.1	0	0	0	0
10856	4674	af	AN0560.1	69.m15287	AO070272000037	0			-81	-55			ATGCTTGCGCTTTCTTCAGCTTTTTGA		ATGCTTGCGCTTTCTTCAGCTTTTTGA		MLALSSAF*		MLALSSAF*		TCATGTTGCA	TAGCCTAATC	0	U	FG09816.1	0	0	0	0
10852	4674	an	AN0560.1	69.m15287	AO070272000037	0	-201	-145					ATGCGGACTTCGAAGCTCGTCGGCACCTTGACGGAAGCTGCGATGGGACAATTTTGA	ATGCGGACTTCGAAGCTCGTCGGCACCTTGACGGAAGCTGCGATGGGACAATTTTGA			MRTSKLVGTLTEAAMGQF*	MRTSKLVGTLTEAAMGQF*			GCTGCGTTGG	ACTGACTGAG	0	U	FG09816.1	0	0	0	0
10853	4674	an	AN0560.1	69.m15287	AO070272000037	0	-159	-145					ATGGGACAATTTTGA	ATGGGACAATTTTGA			MGQF*	MGQF*			GGAAGCTGCG	ACTGACTGAG	0	U	FG09816.1	0	0	0	0
10857	4674	ao	AN0560.1	69.m15287	AO070272000037	0					-200	-162	ATGTTTATTTGGTCTATGGGGACGAGACTGGGGAAGTGA			ATGTTTATTTGGTCTATGGGGACGAGACTGGGGAAGTGA	MFIWSMGTRLGK*			MFIWSMGTRLGK*	GGGGAAAGGG	CGCTTTTCTC	0	U	FG09816.1	0	0	0	0
10858	4674	ao	AN0560.1	69.m15287	AO070272000037	0					-185	-162	ATGGGGACGAGACTGGGGAAGTGA			ATGGGGACGAGACTGGGGAAGTGA	MGTRLGK*			MGTRLGK*	TATTTGGTCT	CGCTTTTCTC	0	U	FG09816.1	0	0	0	0
10860	4676	an	AN1094.1	70.m15137	AO070285000053	0	-164	-102					ATGCTGGCAGGGAAAACCTTGATTTTTGATTTTTTTTTAATTATTTTCATCCTTGAATTGTGA	ATGCTGGCAGGGAAAACCTTGATTTTTGATTTTTTTTTAATTATTTTCATCCTTGAATTGTGA			MLAGKTLIFDFFLIIFILEL*	MLAGKTLIFDFFLIIFILEL*			GCCTCTATCA	ATCATCAAAC	0	C	0	0	0	0	0
10861	4677	af	AN3135.1	59.m08590	AO070303000009	0			-229	-203			ATGGTCGCCTCATCTCATTCGCTTTGA		ATGGTCGCCTCATCTCATTCGCTTTGA		MVASSHSL*		MVASSHSL*		CTCAACTTTA	CGTACAAAGA	0	S	0	0	0	0	0
10866	4678	af	AN8700.1	62.m03368	AO070315000128	0			-198	-31			ATGATTGAACTTTGTTATTCTGCTGGACTACTGACGCGTATAAGAAGCGCAGACTTGCTGGCTGATCGACATGACTATTTCCCTGTTTCCCTCTCAATAGTGCCAGGTCATTGCTTTCTGCGGCATTGGGCCAATCTATGGTTTCTTTTTCTCGTTTCTGTCCTATAA		ATGATTGAACTTTGTTATTCTGCTGGACTACTGACGCGTATAAGAAGCGCAGACTTGCTGGCTGATCGACATGACTATTTCCCTGTTTCCCTCTCAATAGTGCCAGGTCATTGCTTTCTGCGGCATTGGGCCAATCTATGGTTTCTTTTTCTCGTTTCTGTCCTATAA		MIELCYSAGLLTRIRSADLLADRHDYFPVSLSIVPGHCFLRHWANLWFLFLVSVL*		MIELCYSAGLLTRIRSADLLADRHDYFPVSLSIVPGHCFLRHWANLWFLFLVSVL*		AGCTTGGTTT	TCGAGCCACT	0	GEPR	0	0	0	0	0
10867	4678	af	AN8700.1	62.m03368	AO070315000128	0			-128	-99			ATGACTATTTCCCTGTTTCCCTCTCAATAG		ATGACTATTTCCCTGTTTCCCTCTCAATAG		MTISLFPSQ*		MTISLFPSQ*		GCTGATCGAC	TGCCAGGTCA	0	GEPR	0	0	0	0	0
10862	4678	an	AN8700.1	62.m03368	AO070315000128	0	-163	-44					ATGGCTGGTTTGTGCTTTATAAAGTCTTGCAAGACCCGCAATGTTAAGATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA	ATGGCTGGTTTGTGCTTTATAAAGTCTTGCAAGACCCGCAATGTTAAGATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA			MAGLCFIKSCKTRNVKMPMLIRSLGISYLLHQSPHILLH*	MAGLCFIKSCKTRNVKMPMLIRSLGISYLLHQSPHILLH*			GAGGGGCTAG	CCTTAATCCG	0	GEPR	0	0	0	0	0
10863	4678	an	AN8700.1	62.m03368	AO070315000128	0	-123	-16					ATGTTAAGATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGACCTTAATCCGTTCACCTTTTCTACTTGA	ATGTTAAGATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGACCTTAATCCGTTCACCTTTTCTACTTGA			MLRCPCLFEAWVFLTYCTSLHIFYYIDLNPFTFST*	MLRCPCLFEAWVFLTYCTSLHIFYYIDLNPFTFST*			AAGACCCGCA	TTGATAACCG	0	GEPR	0	0	0	0	0
10864	4678	an	AN8700.1	62.m03368	AO070315000128	0	-115	-44					ATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA	ATGCCCATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA			MPMLIRSLGISYLLHQSPHILLH*	MPMLIRSLGISYLLHQSPHILLH*			CAATGTTAAG	CCTTAATCCG	0	GEPR	0	0	0	0	0
10865	4678	an	AN8700.1	62.m03368	AO070315000128	0	-109	-44					ATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA	ATGCTTATTCGAAGCTTGGGTATTTCTTACCTACTGCACCAGTCTCCACATATTTTATTACATTGA			MLIRSLGISYLLHQSPHILH*	MLIRSLGISYLLHQSPHILH*			TAAGATGCCC	CCTTAATCCG	0	GEPR	0	0	0	0	0

10868	4678	ao	AN8700.1	62.m03368	AO070315000128	0					-252	-97	ATGCTTATTGCGGAAGGCAACACTTTTACTTATAATCCGGGGATTATAAGATGCAGGCTTGAGCTTAGAGAAAGCTTGTTATACGTACTTAATCTACCCTACATTTGCTTGACTTCTTACTATTGCCTTGACCCCAAACGTGAGGCATACAACTGA			ATGCTTATTGCGGAAGGCAACACTTTTACTTATAATCCGGGGATTATAAGATGCAGGCTTGAGCTTAGAGAAAGCTTGTTATACGTACTTAATCTACCCTACATTTGCTTGACTTCTTACTATTGCCTTGACCCCAAACGTGAGGCATACAACTGA	MLIAEGNTFTYNPGIIRCRLELRESLLYVLNLPYICLTSYYCLDPKREAYN*			MLIAEGNTFTYNPGIIRCRLELRESLLYVLNLPYICLTSYYCLDPKREAYN*	TCGTCGATCC	TGACCTTATG	0	GEPR	0	0	0	0	0
10869	4678	ao	AN8700.1	62.m03368	AO070315000128	0					-202	-191	ATGCAGGCTTGA			ATGCAGGCTTGA	MQA*			MQA*	GGATTATAAG	GCTTAGAGAA	0	GEPR	0	0	0	0	0
10870	4678	ao	AN8700.1	62.m03368	AO070315000128	0					-97	-35	ATGACCTTATGTGTCTGCTGCAGAATTGCGCGGATTGAACTTCTAACTCGAATATATCCCTAA			ATGACCTTATGTGTCTGCTGCAGAATTGCGCGGATTGAACTTCTAACTCGAATATATCCCTAA	MTLCVCCRIARIELLTRIYP*			MTLCVCCRIARIELLTRIYP*	CATACAACTG	TTCCTACTTT	0	GEPR	0	0	0	0	0
10871	4678	ao	AN8700.1	62.m03368	AO070315000128	0					-89	-60	ATGTGTCTGCTGCAGAATTGCGCGGATTGA			ATGTGTCTGCTGCAGAATTGCGCGGATTGA	MCLLQNCAD*			MCLLQNCAD*	TGATGACCTT	ACTTCTAACT	0	GEPR	0	0	0	0	0
10877	4679	af	AN1563.1	55.m03084	AO070339000290	0			-292	-221			ATGAGGATAACCTCGGTTAGCGGCGTCCAATTAGTAATTCAAGAGTGGGGATTTCTGGATAAGGCCCGATAA		ATGAGGATAACCTCGGTTAGCGGCGTCCAATTAGTAATTCAAGAGTGGGGATTTCTGGATAAGGCCCGATAA		MRITSVSGVQLVIQEWGFLDKAR*		MRITSVSGVQLVIQEWGFLDKAR*		TCACTGTCAT	GGAAATTCCC	0	HE	FG02203.1	MG05506.1	0	0	0
10878	4679	af	AN1563.1	55.m03084	AO070339000290	0			-206	-12			ATGGTCCATGGCGATTCTATCATCTCCTTCGCGATATTTGCAATTATTGGCGACAATTGCTCATCTGGACATTCTGAGCCAGGCAATCTGGGTCGGTATTACTGCGTCCAAAATCCCCTCTCATACCTGGTCGTTTCTGGGTGGTCGACTGTCCTCTTTCTAATCTCTTTCAGCGTTTGGGGTGTCGAGTGTTGA		ATGGTCCATGGCGATTCTATCATCTCCTTCGCGATATTTGCAATTATTGGCGACAATTGCTCATCTGGACATTCTGAGCCAGGCAATCTGGGTCGGTATTACTGCGTCCAAAATCCCCTCTCATACCTGGTCGTTTCTGGGTGGTCGACTGTCCTCTTTCTAATCTCTTTCAGCGTTTGGGGTGTCGAGTGTTGA		MVHGDSIISFAIFAIIGDNCSSGHSEPGNLGRYYCVQNPLSYLVVSGWSTVLFLISFSVWGVEC*		MVHGDSIISFAIFAIIGDNCSSGHSEPGNLGRYYCVQNPLSYLVVSGWSTVLFLISFSVWGVEC*		ATTCCCCATA	CAACGGGAAA	0	HE	FG02203.1	MG05506.1	0	0	0
10879	4679	af	AN1563.1	55.m03084	AO070339000290	0			-199	-44			ATGGCGATTCTATCATCTCCTTCGCGATATTTGCAATTATTGGCGACAATTGCTCATCTGGACATTCTGAGCCAGGCAATCTGGGTCGGTATTACTGCGTCCAAAATCCCCTCTCATACCTGGTCGTTTCTGGGTGGTCGACTGTCCTCTTTCTAA		ATGGCGATTCTATCATCTCCTTCGCGATATTTGCAATTATTGGCGACAATTGCTCATCTGGACATTCTGAGCCAGGCAATCTGGGTCGGTATTACTGCGTCCAAAATCCCCTCTCATACCTGGTCGTTTCTGGGTGGTCGACTGTCCTCTTTCTAA		MAILSSPSRYLQLLATIAHLDILSQAIWVGITASKIPSHTWSFLGGRLSSF*		MAILSSPSRYLQLLATIAHLDILSQAIWVGITASKIPSHTWSFLGGRLSSF*		ATAATGGTCC	TCTCTTTCAG	0	HE	FG02203.1	MG05506.1	0	0	0
10872	4679	an	AN1563.1	55.m03084	AO070339000290	0	-236	-177					ATGGCACGAAATGGCTCTGGCATAATGAATTCTTGCGTGACCATGGGTCAATTTTGCTAA	ATGGCACGAAATGGCTCTGGCATAATGAATTCTTGCGTGACCATGGGTCAATTTTGCTAA			MARNGSGIMNSCVTMGQFC*	MARNGSGIMNSCVTMGQFC*			ACAACCAACA	AACACCGTTC	0	HE	FG02203.1	MG05506.1	0	0	0
10873	4679	an	AN1563.1	55.m03084	AO070339000290	0	-226	-212					ATGGCTCTGGCATAA	ATGGCTCTGGCATAA			MALA*	MALA*			ATGGCACGAA	TGAATTCTTG	0	HE	FG02203.1	MG05506.1	0	0	0
10874	4679	an	AN1563.1	55.m03084	AO070339000290	0	-212	-177					ATGAATTCTTGCGTGACCATGGGTCAATTTTGCTAA	ATGAATTCTTGCGTGACCATGGGTCAATTTTGCTAA			MNSCVTMGQFC*	MNSCVTMGQFC*			CTCTGGCATA	AACACCGTTC	0	HE	FG02203.1	MG05506.1	0	0	0
10875	4679	an	AN1563.1	55.m03084	AO070339000290	0	-194	-177					ATGGGTCAATTTTGCTAA	ATGGGTCAATTTTGCTAA			MGQFC*	MGQFC*			TTGCGTGACC	AACACCGTTC	0	HE	FG02203.1	MG05506.1	0	0	0
10876	4679	an	AN1563.1	55.m03084	AO070339000290	0	-83	-60					ATGACAACCCCGCTTACTATATAA	ATGACAACCCCGCTTACTATATAA			MTTPLTI*	MTTPLTI*			TGAACTAAGG	ACCCCCCTCC	0	HE	FG02203.1	MG05506.1	0	0	0
10892	4682	af	AN1151.1	69.m15307	AO070226000022	0			-117	-28			ATGCCGTTCCCCCGCATTATGAAGATGAAAGTATGGAGAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		ATGCCGTTCCCCCGCATTATGAAGATGAAAGTATGGAGAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		MPFPRIMKMKVWRKKKSSQCSSNSSIMLL*		MPFPRIMKMKVWRKKKSSQCSSNSSIMLL*		CCGTCATGGA	GATCCAATCG	0	G	FG09485.1	MG01335.1	NCU04071.1	0	0
10893	4682	af	AN1151.1	69.m15307	AO070226000022	0			-99	-28			ATGAAGATGAAAGTATGGAGAAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		ATGAAGATGAAAGTATGGAGAAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		MKMKVWRKKKSSQCSSNSSIMLL*		MKMKVWRKKKSSQCSSNSSIMLL*		CCCCCGCATT	GATCCAATCG	0	G	FG09485.1	MG01335.1	NCU04071.1	0	0
10894	4682	af	AN1151.1	69.m15307	AO070226000022	0			-93	-28			ATGAAAGTATGGAGAAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		ATGAAAGTATGGAGAAAAAAAAAAATCATCTCAATGTAGTTCAAATTCATCAATTATGTTACTTTGA		MKVWRKKKSSQCSSNSSIMLL*		MKVWRKKKSSQCSSNSSIMLL*		CATTATGAAG	GATCCAATCG	0	G	FG09485.1	MG01335.1	NCU04071.1	0	0
10895	4682	af	AN1151.1	69.m15307	AO070226000022	0			-85	-56			ATGGAGAAAAAAAAAAATCATCTCAATGTAG		ATGGAGAAAAAAAAAAATCATCTCAATGTAG		MEKKKIISM*		MEKKKIISM*		AGATGAAAGT	TTCAAATTCA	0	G	FG09485.1	MG01335.1	NCU04071.1	0	0
10899	4684	af	AN7307.1	72.m19758	AO070297000055	0			-241	-230			ATGAAGATATGA		ATGAAGATATGA		MKI*		MKI*		CCGGGCGACT	GGACATTGGG	0	S	FG04255.1	0	0	0	0
10900	4684	af	AN7307.1	72.m19758	AO070297000055	0			-233	-123			ATGAGGACATTGGGAGAGCATTGGGTTTCGAACCAGTTCGAAGCGCATGTCCGCGTTCGACTATTCGCGTCCATCACTTCCCCGTCTGGCATGCACAAACGCGACTGTTGA		ATGAGGACATTGGGAGAGCATTGGGTTTCGAACCAGTTCGAAGCGCATGTCCGCGTTCGACTATTCGCGTCCATCACTTCCCCGTCTGGCATGCACAAACGCGACTGTTGA		MRTLGEHWVSNQFEAHVRVRLFASITSPSGMHKRDC*		MRTLGEHWVSNQFEAHVRVRLFASITSPSGMHKRDC*		CTATGAAGAT	GAGACAATCG	0	S	FG04255.1	0	0	0	0
10901	4684	af	AN7307.1	72.m19758	AO070297000055	0			-187	-95			ATGTCCGCGTTCGACTATTCGCGTCCATCACTTCCCCGTCTGGCATGCACAAACGCGACTGTTGAGAGACAATCGCCAAAGCGACACTATTGA		ATGTCCGCGTTCGACTATTCGCGTCCATCACTTCCCCGTCTGGCATGCACAAACGCGACTGTTGAGAGACAATCGCCAAAGCGACACTATTGA		MSAFDYSRPSLPRLACTNATVERQSPKRHY*		MSAFDYSRPSLPRLACTNATVERQSPKRHY*		TTCGAAGCGC	ATCCTTGAAT	0	S	FG04255.1	0	0	0	0
10902	4684	af	AN7307.1	72.m19758	AO070297000055	0			-143	-123			ATGCACAAACGCGACTGTTGA		ATGCACAAACGCGACTGTTGA		MHKRDC*		MHKRDC*		CCCGTCTGGC	GAGACAATCG	0	S	FG04255.1	0	0	0	0
10897	4684	an	AN7307.1	72.m19758	AO070297000055	0	-150	-22					ATGTGCAACTCTCGACAAAAACCACGCCCTCCAAGTCGTCGGGGTCCAGTCCCCTTTCAATTCTCCCTTTCCTCCGATGGACATAGTAAAGGGTCTTGCTGGCCAGTATCTTTAGCTTCAGTCAAATAA	ATGTGCAACTCTCGACAAAAACCACGCCCTCCAAGTCGTCGGGGTCCAGTCCCCTTTCAATTCTCCCTTTCCTCCGATGGACATAGTAAAGGGTCTTGCTGGCCAGTATCTTTAGCTTCAGTCAAATAA			MCNSRQKPRPPSRRGPVPFQFSLSSDGHSKGSCWPVSLASVK*	MCNSRQKPRPPSRRGPVPFQFSLSSDGHSKGSCWPVSLASVK*			GCCAGCCGCA	ATCCGTCCTC	0	S	FG04255.1	0	0	0	0
10898	4684	an	AN7307.1	72.m19758	AO070297000055	0	-74	-36					ATGGACATAGTAAAGGGTCTTGCTGGCCAGTATCTTTAG	ATGGACATAGTAAAGGGTCTTGCTGGCCAGTATCTTTAG			MDIVKGLAGQYL*	MDIVKGLAGQYL*			CTTTCCTCCG	CTTCAGTCAA	0	S	FG04255.1	0	0	0	0
10903	4684	ao	AN7307.1	72.m19758	AO070297000055	0					-286	-248	ATGTCTCCCAGGCTATTCGGAAATTCTCCGAGAGGGTGA			ATGTCTCCCAGGCTATTCGGAAATTCTCCGAGAGGGTGA	MSPRLFGNSPRG*			MSPRLFGNSPRG*	GTGACCTTTC	CCCCTCCGAT	0	S	FG04255.1	0	0	0	0
10908	4686	af	AN4484.1	57.m05647	AO070311000033	0			-156	-115			ATGTGGCCTCCGTTTATCACTTTACCTGCCACCTACATCTGA		ATGTGGCCTCCGTTTATCACTTTACCTGCCACCTACATCTGA		MWPPFITLPATYI*		MWPPFITLPATYI*		TCTTTTCGCT	ATCATCCAGT	0	R	0	0	0	0	0
10909	4686	af	AN4484.1	57.m05647	AO070311000033	0			-101	-54			ATGTCCTTTGTAATCACCGCTCACCGTGAAGCTGTCGGCCCACGGTGA		ATGTCCTTTGTAATCACCGCTCACCGTGAAGCTGTCGGCCCACGGTGA		MSFVITAHREAVGPR*		MSFVITAHREAVGPR*		ATCCAGTGAC	CAATAACGCT	0	R	0	0	0	0	0
10904	4686	an	AN4484.1	57.m05647	AO070311000033	0	-187	-134					ATGCCCTGTTCCGCTATGCGCCCTCGCCGACTGGTCCCCTCCGAATGTTCTTGA	ATGCCCTGTTCCGCTATGCGCCCTCGCCGACTGGTCCCCTCCGAATGTTCTTGA			MPCSAMRPRRLVPSECS*	MPCSAMRPRRLVPSECS*			GTCTTGACTG	AACGACTTAA	0	R	0	0	0	0	0
10905	4686	an	AN4484.1	57.m05647	AO070311000033	0	-172	-134					ATGCGCCCTCGCCGACTGGTCCCCTCCGAATGTTCTTGA	ATGCGCCCTCGCCGACTGGTCCCCTCCGAATGTTCTTGA			MRPRRLVPSECS*	MRPRRLVPSECS*			CTGTTCCGCT	AACGACTTAA	0	R	0	0	0	0	0
10906	4686	an	AN4484.1	57.m05647	AO070311000033	0	-143	-99					ATGTTCTTGAAACGACTTAAGTGTCATGATCCTCACTCCAATTGA	ATGTTCTTGAAACGACTTAAGTGTCATGATCCTCACTCCAATTGA			MFLKRLKCHDPHSN*	MFLKRLKCHDPHSN*			TCCCCTCCGA	CAATCGCCAG	0	R	0	0	0	0	0
10907	4686	an	AN4484.1	57.m05647	AO070311000033	0	-118	-80					ATGATCCTCACTCCAATTGACAATCGCCAGTATTTGTGA	ATGATCCTCACTCCAATTGACAATCGCCAGTATTTGTGA			MILTPIDNRQYL*	MILTPIDNRQYL*			CTTAAGTGTC	CCGCGGTTCC	0	R	0	0	0	0	0
10910	4686	ao	AN4484.1	57.m05647	AO070311000033	0					-175	-158	ATGCGACGCCAGCATTAA			ATGCGACGCCAGCATTAA	MRRQH*			MRRQH*	TGCTTTCGAT	CCCTCCTGGA	0	R	0	0	0	0	0
10911	4686	ao	AN4484.1	57.m05647	AO070311000033	0					-118	-83	ATGATATTACTCTGCAGCGGCCCCATAGTTTGGTAA			ATGATATTACTCTGCAGCGGCCCCATAGTTTGGTAA	MILLCSGPIVW*			MILLCSGPIVW*	TCTTGGTATC	TAATATTCAG	0	R	0	0	0	0	0
10914	4687	af	AN4761.1	59.m09222	AO070327000055	0			-215	-177			ATGGCGAGTCGCATTTCGATTCATTACTCTCGTTTATAA		ATGGCGAGTCGCATTTCGATTCATTACTCTCGTTTATAA		MASRISIHYSRL*		MASRISIHYSRL*		TAATTTTGTC	CCCAAATTCA	0	O	0	0	0	0	0
10912	4687	an	AN4761.1	59.m09222	AO070327000055	0	-262	-245					ATGGCGCTGTGTGACTAG	ATGGCGCTGTGTGACTAG			MALCD*	MALCD*			CCTTTCGGTC	TTACGACTGC	0	O	0	0	0	0	0
10913	4687	an	AN4761.1	59.m09222	AO070327000055	0	-108	-97					ATGATTTTTTAA	ATGATTTTTTAA			MIF*	MIF*			CGACCTTTAA	TTCCCGATCT	0	O	0	0	0	0	0
10915	4687	ao	AN4761.1	59.m09222	AO070327000055	0					-242	-207	ATGGCGTATAGTCTGCTAACCTACTACTCTCGTTGA			ATGGCGTATAGTCTGCTAACCTACTACTCTCGTTGA	MAYSLLTYYSR*			MAYSLLTYYSR*	GTGTTCTGTC	TTGATTGTCC	0	O	0	0	0	0	0
10916	4687	ao	AN4761.1	59.m09222	AO070327000055	0					-85	-29	ATGATCTTCGTTCCTTTTTCATCTCTCTGGATACTGTTCCTTTCTTCCGATCTCTAG			ATGATCTTCGTTCCTTTTTCATCTCTCTGGATACTGTTCCTTTCTTCCGATCTCTAG	MIFVPFSSLWILFLSSDL*			MIFVPFSSLWILFLSSDL*	ATATCTTCGG	TCTTTTTTTA	0	O	0	0	0	0	0
10917	4688	ao	AN0258.1	54.m06523	AO070334000100	0					-228	-163	ATGTTTCCAAAACATAATTTCTTTGCGGTTGTACAAAGTAATGAACATATATATTTACTCGCCTGA			ATGTTTCCAAAACATAATTTCTTTGCGGTTGTACAAAGTAATGAACATATATATTTACTCGCCTGA	MFPKHNFFAVVQSNEHIYLLA*			MFPKHNFFAVVQSNEHIYLLA*	TTCATTTTAC	TTCCACCCGA	0	L	0	0	0	0	0
10918	4688	ao	AN0258.1	54.m06523	AO070334000100	0					-188	-141	ATGAACATATATATTTACTCGCCTGATTCCACCCGACCGCCCGGCTAG			ATGAACATATATATTTACTCGCCTGATTCCACCCGACCGCCCGGCTAG	MNIYIYSPDSTRPPG*			MNIYIYSPDSTRPPG*	GTACAAAGTA	CCTTAAATGG	0	L	0	0	0	0	0
10919	4688	ao	AN0258.1	54.m06523	AO070334000100	0					-134	-30	ATGGCTGCATTCCCTCGGCATCTGCCAACAACCAACAACATAATTTATCTCCGGAGTAGCGGTCACAATTACATTCCCACCATTCCACCACCAGCTCCTCCGTAA			ATGGCTGCATTCCCTCGGCATCTGCCAACAACCAACAACATAATTTATCTCCGGAGTAGCGGTCACAATTACATTCCCACCATTCCACCACCAGCTCCTCCGTAA	MAAFPRHLPTTNNIIYLRSSGHNYIPTIPPPAPP*			MAAFPRHLPTTNNIIYLRSSGHNYIPTIPPPAPP*	CTAGCCTTAA	AACACCAAGT	0	L	0	0	0	0	0
10920	4689	af	AN6132.1	72.m19030	AO070340000067	0			-248	-36			ATGCCTGGCCGTCGCTCTGTGCAAATTCACGCTCATCTAACGCCAAATTTGCTGCAGAAAGTGGTCTTTTCAGATCATCTTGTATCACTTCATTATCCTTCAAAATTCTCATGTGTTCTCAATGCTGAATTATCAAGCCCCGCTGCGAGGCCAGATCGTGACTCAGACCCGCTTCGCCTCTTGAGTACTAACTATCGCACGCATTCCCCCTAA		ATGCCTGGCCGTCGCTCTGTGCAAATTCACGCTCATCTAACGCCAAATTTGCTGCAGAAAGTGGTCTTTTCAGATCATCTTGTATCACTTCATTATCCTTCAAAATTCTCATGTGTTCTCAATGCTGAATTATCAAGCCCCGCTGCGAGGCCAGATCGTGACTCAGACCCGCTTCGCCTCTTGAGTACTAACTATCGCACGCATTCCCCCTAA		MPGRRSVQIHAHLTPNLLQKVVFSDHLVSLHYPSKFSCVLNAELSSPAARPDRDSDPLRLLSTNYRTHSP*		MPGRRSVQIHAHLTPNLLQKVVFSDHLVSLHYPSKFSCVLNAELSSPAARPDRDSDPLRLLSTNYRTHSP*		ATCTATTCTT	TCACTGCACC	0		0	0	0	0	0
10921	4689	af	AN6132.1	72.m19030	AO070340000067	0			-138	-121			ATGTGTTCTCAATGCTGA		ATGTGTTCTCAATGCTGA		MCSQC*		MCSQC*		CAAAATTCTC	ATTATCAAGC	0		0	0	0	0	0
10922	4689	af	AN6132.1	72.m19030	AO070340000067	0			-127	-65			ATGCTGAATTATCAAGCCCCGCTGCGAGGCCAGATCGTGACTCAGACCCGCTTCGCCTCTTGA		ATGCTGAATTATCAAGCCCCGCTGCGAGGCCAGATCGTGACTCAGACCCGCTTCGCCTCTTGA		MLNYQAPLRGQIVTQTRFAS*		MLNYQAPLRGQIVTQTRFAS*		TGTGTTCTCA	GTACTAACTA	0		0	0	0	0	0
10928	4694	af	AN2056.1	58.m07644	AO070292000026	0			-230	-120			ATGCCAAGTCTTTGCATGCCTAGAGAAAGCTCGTGCCCTGTCTTATCCCGGGGTTATGTCAACGGAGCTGCCCAGACTTCGGCTCCCGCTCCACAGACTAAACCACCTTAG		ATGCCAAGTCTTTGCATGCCTAGAGAAAGCTCGTGCCCTGTCTTATCCCGGGGTTATGTCAACGGAGCTGCCCAGACTTCGGCTCCCGCTCCACAGACTAAACCACCTTAG		MPSLCMPRESSCPVLSRGYVNGAAQTSAPAPQTKPP*		MPSLCMPRESSCPVLSRGYVNGAAQTSAPAPQTKPP*		TTCAACCTTG	CGCAGCTCCG	0	S	FG06749.1	0	0	0	0
10929	4694	af	AN2056.1	58.m07644	AO070292000026	0			-215	-120			ATGCCTAGAGAAAGCTCGTGCCCTGTCTTATCCCGGGGTTATGTCAACGGAGCTGCCCAGACTTCGGCTCCCGCTCCACAGACTAAACCACCTTAG		ATGCCTAGAGAAAGCTCGTGCCCTGTCTTATCCCGGGGTTATGTCAACGGAGCTGCCCAGACTTCGGCTCCCGCTCCACAGACTAAACCACCTTAG		MPRESSCPVLSRGYVNGAAQTSAPAPQTKPP*		MPRESSCPVLSRGYVNGAAQTSAPAPQTKPP*		AAGTCTTTGC	CGCAGCTCCG	0	S	FG06749.1	0	0	0	0
10926	4694	an	AN2056.1	58.m07644	AO070292000026	0	-215	-180					ATGGTGGACTTGGAGGTCTGGGCTCCACCAAACTAG	ATGGTGGACTTGGAGGTCTGGGCTCCACCAAACTAG			MVDLEVWAPPN*	MVDLEVWAPPN*			GTCGCGTCTA	GCTTTTGCGG	0	S	FG06749.1	0	0	0	0
10927	4694	an	AN2056.1	58.m07644	AO070292000026	0	-153	-142					ATGCCACCCTAA	ATGCCACCCTAA			MPP*	MPP*			TCAATTGATT	CCCAACAACT	0	S	FG06749.1	0	0	0	0
10930	4694	ao	AN2056.1	58.m07644	AO070292000026	0					-184	-149	ATGTCAAAATGCCCAGAGTTCGGCTCCACAGACTAA			ATGTCAAAATGCCCAGAGTTCGGCTCCACAGACTAA	MSKCPEFGSTD*			MSKCPEFGSTD*	GGAAATTACT	GTGAACTTTC	0	S	FG06749.1	0	0	0	0
10931	4694	ao	AN2056.1	58.m07644	AO070292000026	0					-176	-45	ATGCCCAGAGTTCGGCTCCACAGACTAAGTGAACTTTCGCCCCAATCGCTTTTGCGACGAACGTCAATTCGAGCCGACAACCTTCCCGTTCCCTCTCTTCCTCCTTCTCCGCCACGTCGCCATCTTTCTTGA			ATGCCCAGAGTTCGGCTCCACAGACTAAGTGAACTTTCGCCCCAATCGCTTTTGCGACGAACGTCAATTCGAGCCGACAACCTTCCCGTTCCCTCTCTTCCTCCTTCTCCGCCACGTCGCCATCTTTCTTGA	MPRVRLHRLSELSPQSLLRRTSIRADNLPVPSLPPSPPRRHLS*			MPRVRLHRLSELSPQSLLRRTSIRADNLPVPSLPPSPPRRHLS*	CTATGTCAAA	CAGCTCCGAA	0	S	FG06749.1	0	0	0	0
10933	4696	af	AN0117.1	71.m15396	AO070311000104	0			-229	-215			ATGGTCCCACCTTAG		ATGGTCCCACCTTAG		MVPP*		MVPP*		TGATCGTAGG	CATGTTGCCG	0	B	FG05072.1	0	0	0	0
10934	4696	af	AN0117.1	71.m15396	AO070311000104	0			-213	-199			ATGTTGCCGTCATAG		ATGTTGCCGTCATAG		MLPS*		MLPS*		CCACCTTAGC	TCGAATAGTA	0	B	FG05072.1	0	0	0	0

10932	4696	an	AN0117.1	71.m15396	AO070311000104	0	-213	-76					ATGAGAATCCACTTGCCTCGTAGTTCTCAGATCTTCCCTTTCACTCATTACATTACCTCGAGTCCCCTGTCAAAAGCTCGTACTGTTTGTCGATTGGAAGACTCTTTTGGGCCCCGCGCGCTATCGATTTCTCCCTGA	ATGAGAATCCACTTGCCTCGTAGTTCTCAGATCTTCCCTTTCACTCATTACATTACCTCGAGTCCCCTGTCAAAAGCTCGTACTGTTTGTCGATTGGAAGACTCTTTTGGGCCCCGCGCGCTATCGATTTCTCCCTGA			MRIHLPRSSQIFPFTHYITSSPLSKARTVCRLEDSFGPRALSISP*	MRIHLPRSSQIFPFTHYITSSPLSKARTVCRLEDSFGPRALSISP*			AGGTAGCTTC	TCTTCGATCT	0	B	FG05072.1	0	0	0	0
10935	4700	an	AN1293.1	70.m14915	AO070303000055	0	-237	-184					ATGAATCTTCAGAAGCAGATGTCCTCTGTATATAAAAGCCTGTTCATGATATAA	ATGAATCTTCAGAAGCAGATGTCCTCTGTATATAAAAGCCTGTTCATGATATAA			MNLQKQMSSVYKSLFMI*	MNLQKQMSSVYKSLFMI*			TCGATAGCAT	ATACAAGAAA	0		FG01324.1	MG06354.1	0	0	0
10936	4700	an	AN1293.1	70.m14915	AO070303000055	0	-219	-184					ATGTCCTCTGTATATAAAAGCCTGTTCATGATATAA	ATGTCCTCTGTATATAAAAGCCTGTTCATGATATAA			MSSVYKSLFMI*	MSSVYKSLFMI*			TCAGAAGCAG	ATACAAGAAA	0		FG01324.1	MG06354.1	0	0	0
10937	4700	ao	AN1293.1	70.m14915	AO070303000055	0					-182	-159	ATGTCCGTAGCATGCACACCATAG			ATGTCCGTAGCATGCACACCATAG	MSVACTP*			MSVACTP*	AACGACAATC	ACTACGTTAG	0		FG01324.1	MG06354.1	0	0	0
10938	4700	ao	AN1293.1	70.m14915	AO070303000055	0					-171	-76	ATGCACACCATAGACTACGTTAGCCTAGACCCTCAGGCAATAATATCGACTGATATGACGTACCCACGTGACCGCCCACATAGTTTCCCCGCATGA			ATGCACACCATAGACTACGTTAGCCTAGACCCTCAGGCAATAATATCGACTGATATGACGTACCCACGTGACCGCCCACATAGTTTCCCCGCATGA	MHTIDYVSLDPQAIISTDMTYPRDRPHSFPA*			MHTIDYVSLDPQAIISTDMTYPRDRPHSFPA*	TGTCCGTAGC	AGCCAACGAC	0		FG01324.1	MG06354.1	0	0	0
10939	4700	ao	AN1293.1	70.m14915	AO070303000055	0					-117	-76	ATGACGTACCCACGTGACCGCCCACATAGTTTCCCCGCATGA			ATGACGTACCCACGTGACCGCCCACATAGTTTCCCCGCATGA	MTYPRDRPHSFPA*			MTYPRDRPHSFPA*	ATCGACTGAT	AGCCAACGAC	0		FG01324.1	MG06354.1	0	0	0
10940	4701	af	AN5710.1	54.m06825	AO070324000150	0			-254	-216			ATGAGGGCGCCACACGTGGAGCTCGGCGGGCGGGACTAA		ATGAGGGCGCCACACGTGGAGCTCGGCGGGCGGGACTAA		MRAPHVELGGRD*		MRAPHVELGGRD*		CAAGACGCCG	CAATCATAAT	0	U	0	0	0	0	0
10944	4702	af	AN6608.1	62.m03189	AO070326000057	0			-263	-210			ATGTTCCTTTCTACAATCAAGACATGCCTCGAATCCATATATTTGATGTATTAG		ATGTTCCTTTCTACAATCAAGACATGCCTCGAATCCATATATTTGATGTATTAG		MFLSTIKTCLESIYLMY*		MFLSTIKTCLESIYLMY*		GCTTTGGACG	TGCGATATAA	0		0	0	0	0	0
10945	4702	af	AN6608.1	62.m03189	AO070326000057	0			-240	-184			ATGCCTCGAATCCATATATTTGATGTATTAGTGCGATATAACCGGGCGGTTCGGTGA		ATGCCTCGAATCCATATATTTGATGTATTAGTGCGATATAACCGGGCGGTTCGGTGA		MPRIHIFDVLVRYNRAVR*		MPRIHIFDVLVRYNRAVR*		CAATCAAGAC	TGTTGTTTCC	0		0	0	0	0	0
10946	4702	af	AN6608.1	62.m03189	AO070326000057	0			-184	-146			ATGTTGTTTCCAGTTTGGTACATATACCCCTCATATTAA		ATGTTGTTTCCAGTTTGGTACATATACCCCTCATATTAA		MLFPVWYIYPSY*		MLFPVWYIYPSY*		CGGTTCGGTG	TAGTTTGATA	0		0	0	0	0	0
10941	4702	an	AN6608.1	62.m03189	AO070326000057	0	-238	-194					ATGTGGGAATCTAAAGATGCTCGACACGGGTGTATTGAAGAGTGA	ATGTGGGAATCTAAAGATGCTCGACACGGGTGTATTGAAGAGTGA			MWESKDARHGCIEE*	MWESKDARHGCIEE*			CTGTCTTTCG	AAGACCTCTC	0		0	0	0	0	0
10942	4702	an	AN6608.1	62.m03189	AO070326000057	0	-222	-118					ATGCTCGACACGGGTGTATTGAAGAGTGAAAGACCTCTCACTTTGTGTGATGCAGTGCACAGTCCGATTCTGATACATATATCCGCGCCTGCTTTTTCATCATAA	ATGCTCGACACGGGTGTATTGAAGAGTGAAAGACCTCTCACTTTGTGTGATGCAGTGCACAGTCCGATTCTGATACATATATCCGCGCCTGCTTTTTCATCATAA			MLDTGVLKSERPLTLCDAVHSPILIHISAPAFSS*	MLDTGVLKSERPLTLCDAVHSPILIHISAPAFSS*			GAATCTAAAG	TTTTCGCTTC	0		0	0	0	0	0
10943	4702	an	AN6608.1	62.m03189	AO070326000057	0	-173	-150					ATGCAGTGCACAGTCCGATTCTGA	ATGCAGTGCACAGTCCGATTCTGA			MQCTVRF*	MQCTVRF*			ACTTTGTGTG	TACATATATC	0		0	0	0	0	0
10947	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-243	-181	ATGGGAATTTGGCATAATAATGCTAATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGA			ATGGGAATTTGGCATAATAATGCTAATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGA	MGIWHNNANGLQSDRPQNSM*			MGIWHNNANGLQSDRPQNSM*	CTTTGTCTCT	TGTCACACTT	0		0	0	0	0	0
10948	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-224	-132	ATGCTAATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGATGTCACACTTGATTCTGATACATTAAATATACCCCTCGTGCTTTTCTAA			ATGCTAATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGATGTCACACTTGATTCTGATACATTAAATATACCCCTCGTGCTTTTCTAA	MLMVCKVIGLKTPCDVTLDSDTLNIPLVLF*			MLMVCKVIGLKTPCDVTLDSDTLNIPLVLF*	TGGCATAATA	TGAGCATATC	0		0	0	0	0	0
10949	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-218	-132	ATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGATGTCACACTTGATTCTGATACATTAAATATACCCCTCGTGCTTTTCTAA			ATGGTCTGCAAAGTGATAGGCCTCAAAACTCCATGTGATGTCACACTTGATTCTGATACATTAAATATACCCCTCGTGCTTTTCTAA	MVCKVIGLKTPCDVTLDSDTLNIPLVLF*			MVCKVIGLKTPCDVTLDSDTLNIPLVLF*	AATAATGCTA	TGAGCATATC	0		0	0	0	0	0
10950	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-181	-155	ATGTCACACTTGATTCTGATACATTAA			ATGTCACACTTGATTCTGATACATTAA	MSHLILIH*			MSHLILIH*	ACTCCATGTG	ATATACCCCT	0		0	0	0	0	0
10951	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-132	-55	ATGAGCATATCTTTCCGCCTTCACCACCCTCGCTTTATGTTTTCACCTGTGAACCATAGCCTGATATATTACCCATAG			ATGAGCATATCTTTCCGCCTTCACCACCCTCGCTTTATGTTTTCACCTGTGAACCATAGCCTGATATATTACCCATAG	MSISFRLHHPRFMFSPVNHSLIYYP*			MSISFRLHHPRFMFSPVNHSLIYYP*	TGCTTTTCTA	TTGACTTGGA	0		0	0	0	0	0
10952	4702	ao	AN6608.1	62.m03189	AO070326000057	0					-96	-55	ATGTTTTCACCTGTGAACCATAGCCTGATATATTACCCATAG			ATGTTTTCACCTGTGAACCATAGCCTGATATATTACCCATAG	MFSPVNHSLIYYP*			MFSPVNHSLIYYP*	CCCTCGCTTT	TTGACTTGGA	0		0	0	0	0	0
10957	4704	af	AN1818.1	58.m07683	AO070333000196	0			-159	-136			ATGGTGAAATTGAAAATAGCCTAA		ATGGTGAAATTGAAAATAGCCTAA		MVKLKIA*		MVKLKIA*		ATTGGACTAG	ACGACAGAGC	0	G	0	0	0	0	0
10953	4704	an	AN1818.1	58.m07683	AO070333000196	0	-249	-40					ATGGAAATGCCAATTAGCCTAAAACCGCCGCTGTTCGGTCTCGCGTCCGAGCCCAGGGGTCTCTCGCGGGACTCGTACAGTGCATGCCAATGCCAATTGATCTATAAAACCCAGCGGCCGGCTCTTGATCTGGCTCTTCTCATCATCAAAAGCTCTGGCAGCTTGCATTCCTTAGTATTCGCATTCCATTCATTCGTACTTTTCCTTTGA	ATGGAAATGCCAATTAGCCTAAAACCGCCGCTGTTCGGTCTCGCGTCCGAGCCCAGGGGTCTCTCGCGGGACTCGTACAGTGCATGCCAATGCCAATTGATCTATAAAACCCAGCGGCCGGCTCTTGATCTGGCTCTTCTCATCATCAAAAGCTCTGGCAGCTTGCATTCCTTAGTATTCGCATTCCATTCATTCGTACTTTTCCTTTGA			MEMPISLKPPLFGLASEPRGLSRDSYSACQCQLIYKTQRPALDLALLIIKSSGSLHSLVFAFHSFVLFL*	MEMPISLKPPLFGLASEPRGLSRDSYSACQCQLIYKTQRPALDLALLIIKSSGSLHSLVFAFHSFVLFL*			CGCTCTCAAG	TATCGCTACT	0	G	0	0	0	0	0
10954	4704	an	AN1818.1	58.m07683	AO070333000196	0	-243	-40					ATGCCAATTAGCCTAAAACCGCCGCTGTTCGGTCTCGCGTCCGAGCCCAGGGGTCTCTCGCGGGACTCGTACAGTGCATGCCAATGCCAATTGATCTATAAAACCCAGCGGCCGGCTCTTGATCTGGCTCTTCTCATCATCAAAAGCTCTGGCAGCTTGCATTCCTTAGTATTCGCATTCCATTCATTCGTACTTTTCCTTTGA	ATGCCAATTAGCCTAAAACCGCCGCTGTTCGGTCTCGCGTCCGAGCCCAGGGGTCTCTCGCGGGACTCGTACAGTGCATGCCAATGCCAATTGATCTATAAAACCCAGCGGCCGGCTCTTGATCTGGCTCTTCTCATCATCAAAAGCTCTGGCAGCTTGCATTCCTTAGTATTCGCATTCCATTCATTCGTACTTTTCCTTTGA			MPISLKPPLFGLASEPRGLSRDSYSACQCQLIYKTQRPALDLALLIIKSSGSLHSLVFAFHSFVLFL*	MPISLKPPLFGLASEPRGLSRDSYSACQCQLIYKTQRPALDLALLIIKSSGSLHSLVFAFHSFVLFL*			CAAGATGGAA	TATCGCTACT	0	G	0	0	0	0	0
10955	4704	an	AN1818.1	58.m07683	AO070333000196	0	-166	-143					ATGCCAATGCCAATTGATCTATAA	ATGCCAATGCCAATTGATCTATAA			MPMPIDL*	MPMPIDL*			CGTACAGTGC	AACCCAGCGG	0	G	0	0	0	0	0
10956	4704	an	AN1818.1	58.m07683	AO070333000196	0	-160	-143					ATGCCAATTGATCTATAA	ATGCCAATTGATCTATAA			MPIDL*	MPIDL*			GTGCATGCCA	AACCCAGCGG	0	G	0	0	0	0	0
10958	4704	ao	AN1818.1	58.m07683	AO070333000196	0					-146	-96	ATGGTGAAACAGGCTGAAGAACAGTTCCTGGCAGGTCAAATGAGAATGTAA			ATGGTGAAACAGGCTGAAGAACAGTTCCTGGCAGGTCAAATGAGAATGTAA	MVKQAEEQFLAGQMRM*			MVKQAEEQFLAGQMRM*	CGTGGCTATC	ATAGGGCCAT	0	G	0	0	0	0	0
10959	4704	ao	AN1818.1	58.m07683	AO070333000196	0					-107	-96	ATGAGAATGTAA			ATGAGAATGTAA	MRM*			MRM*	GGCAGGTCAA	ATAGGGCCAT	0	G	0	0	0	0	0
10960	4705	af	AN2970.1	59.m09047	AO070337000156	0			-244	-182			ATGCCCCACAACCACGTGTGGGCCCCGCTCGCGCGCATGTCCGAAGAGTCAGCGTACAGGTAA		ATGCCCCACAACCACGTGTGGGCCCCGCTCGCGCGCATGTCCGAAGAGTCAGCGTACAGGTAA		MPHNHVWAPLARMSEESAYR*		MPHNHVWAPLARMSEESAYR*		TCCTCTGGCG	GCTGACCGAC	0	P	FG06718.1	0	NCU00088.1	0	0
10961	4705	af	AN2970.1	59.m09047	AO070337000156	0			-208	-182			ATGTCCGAAGAGTCAGCGTACAGGTAA		ATGTCCGAAGAGTCAGCGTACAGGTAA		MSEESAYR*		MSEESAYR*		GCTCGCGCGC	GCTGACCGAC	0	P	FG06718.1	0	NCU00088.1	0	0
10962	4705	ao	AN2970.1	59.m09047	AO070337000156	0					-253	-236	ATGTCCATGATTACGTAG			ATGTCCATGATTACGTAG	MSMIT*			MSMIT*	TTGTTCTGGA	GAGGCGAAGG	0	P	FG06718.1	0	NCU00088.1	0	0
10963	4705	ao	AN2970.1	59.m09047	AO070337000156	0					-247	-236	ATGATTACGTAG			ATGATTACGTAG	MIT*			MIT*	TGGAATGTCC	GAGGCGAAGG	0	P	FG06718.1	0	NCU00088.1	0	0
10964	4705	ao	AN2970.1	59.m09047	AO070337000156	0					-134	-105	ATGACTCTTTTTGTGTCAAACTTTTTGTAA			ATGACTCTTTTTGTGTCAAACTTTTTGTAA	MTLFVSNFL*			MTLFVSNFL*	CGGTTTTGGA	ACTCTGTTCG	0	P	FG06718.1	0	NCU00088.1	0	0
10967	4707	af	AN8741.1	62.m03339	AO070250000041	0			-102	-88			ATGGTTCCACCGTAG		ATGGTTCCACCGTAG		MVPP*		MVPP*		GCCTTCATAT	CCATCTTCCC	0	R	0	0	0	0	0
10965	4707	an	AN8741.1	62.m03339	AO070250000041	0	-218	-204					ATGGCTTTGGGATAG	ATGGCTTTGGGATAG			MALG*	MALG*			ATACATCTGG	CGTCGTCTCC	0	R	0	0	0	0	0
10966	4707	an	AN8741.1	62.m03339	AO070250000041	0	-186	-151					ATGCTTACCTGCTCGCCACGTTTTTTGACTACTTGA	ATGCTTACCTGCTCGCCACGTTTTTTGACTACTTGA			MLTCSPRFLTT*	MLTCSPRFLTT*			TCCATCATAT	ACTCCTCGAT	0	R	0	0	0	0	0
10968	4707	ao	AN8741.1	62.m03339	AO070250000041	0					-114	-100	ATGGTTCGGGTGTAG			ATGGTTCGGGTGTAG	MVRV*			MVRV*	GTCTTCATAT	CCACGTTTTG	0	R	0	0	0	0	0
10969	4710	an	AN0232.1	72.m19983	AO070304000024	0	-219	-196					ATGAAAGAATCCTCTGACCCTTAA	ATGAAAGAATCCTCTGACCCTTAA			MKESSDP*	MKESSDP*			ATTGTATAGG	TGATGATGGG	0	OK	0	MG01086.1	NCU01511.1	0	0
10970	4710	an	AN0232.1	72.m19983	AO070304000024	0	-196	-179					ATGATGATGGGAAGCTGA	ATGATGATGGGAAGCTGA			MMMGS*	MMMGS*			CTGACCCTTA	AAGGATCTGG	0	OK	0	MG01086.1	NCU01511.1	0	0
10971	4710	an	AN0232.1	72.m19983	AO070304000024	0	-193	-179					ATGATGGGAAGCTGA	ATGATGGGAAGCTGA			MMGS*	MMGS*			ACCCTTAATG	AAGGATCTGG	0	OK	0	MG01086.1	NCU01511.1	0	0
10972	4710	an	AN0232.1	72.m19983	AO070304000024	0	-190	-179					ATGGGAAGCTGA	ATGGGAAGCTGA			MGS*	MGS*			CTTAATGATG	AAGGATCTGG	0	OK	0	MG01086.1	NCU01511.1	0	0
10973	4710	an	AN0232.1	72.m19983	AO070304000024	0	-167	-87					ATGGAAGTTGGCGCAACGGAAGGCTCCGATGGAGACAGTTCCTGTCAGTGTCAATGGAAGCTGGAGCGGGGCAGAAGCTAA	ATGGAAGTTGGCGCAACGGAAGGCTCCGATGGAGACAGTTCCTGTCAGTGTCAATGGAAGCTGGAGCGGGGCAGAAGCTAA			MEVGATEGSDGDSSCQCQWKLERGRS*	MEVGATEGSDGDSSCQCQWKLERGRS*			AGGATCTGGG	GGGACAGACA	0	OK	0	MG01086.1	NCU01511.1	0	0
10974	4710	an	AN0232.1	72.m19983	AO070304000024	0	-114	-55					ATGGAAGCTGGAGCGGGGCAGAAGCTAAGGGACAGACAACAAACCCCTCACTGCCAGTGA	ATGGAAGCTGGAGCGGGGCAGAAGCTAAGGGACAGACAACAAACCCCTCACTGCCAGTGA			MEAGAGQKLRDRQQTPHCQ*	MEAGAGQKLRDRQQTPHCQ*			GTCAGTGTCA	CCACACCACA	0	OK	0	MG01086.1	NCU01511.1	0	0
10975	4710	ao	AN0232.1	72.m19983	AO070304000024	0					-224	-117	ATGAAGAGAACTGTCATGGAGCCTGGAGGTGGTATCGGCAGTCTCCGCTGGTTCGGCGAACGAATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA			ATGAAGAGAACTGTCATGGAGCCTGGAGGTGGTATCGGCAGTCTCCGCTGGTTCGGCGAACGAATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA	MKRTVMEPGGGIGSLRWFGERMPSMADSNSKSMIK*			MKRTVMEPGGGIGSLRWFGERMPSMADSNSKSMIK*	GAAAACCATC	CTGGACGCCC	0	OK	0	MG01086.1	NCU01511.1	0	0
10976	4710	ao	AN0232.1	72.m19983	AO070304000024	0					-209	-117	ATGGAGCCTGGAGGTGGTATCGGCAGTCTCCGCTGGTTCGGCGAACGAATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA			ATGGAGCCTGGAGGTGGTATCGGCAGTCTCCGCTGGTTCGGCGAACGAATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA	MEPGGGIGSLRWFGERMPSMADSNSKSMIK*			MEPGGGIGSLRWFGERMPSMADSNSKSMIK*	GAGAACTGTC	CTGGACGCCC	0	OK	0	MG01086.1	NCU01511.1	0	0
10977	4710	ao	AN0232.1	72.m19983	AO070304000024	0					-161	-117	ATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA			ATGCCGTCCATGGCCGACAGCAACTCTAAATCAATGATTAAATAA	MPSMADSNSKSMIK*			MPSMADSNSKSMIK*	CGGCGAACGA	CTGGACGCCC	0	OK	0	MG01086.1	NCU01511.1	0	0
10978	4710	ao	AN0232.1	72.m19983	AO070304000024	0					-152	-117	ATGGCCGACAGCAACTCTAAATCAATGATTAAATAA			ATGGCCGACAGCAACTCTAAATCAATGATTAAATAA	MADSNSKSMIK*			MADSNSKSMIK*	AATGCCGTCC	CTGGACGCCC	0	OK	0	MG01086.1	NCU01511.1	0	0
10979	4710	ao	AN0232.1	72.m19983	AO070304000024	0					-128	-117	ATGATTAAATAA			ATGATTAAATAA	MIK*			MIK*	CTCTAAATCA	CTGGACGCCC	0	OK	0	MG01086.1	NCU01511.1	0	0
10980	4711	an	AN3866.1	58.m07838	AO070305000102	0	-217	-167					ATGGGTTTGCTTGTTATTATTCGTGGTCTGTATCTCTCGCTTATGGTTTAG	ATGGGTTTGCTTGTTATTATTCGTGGTCTGTATCTCTCGCTTATGGTTTAG			MGLLVIIRGLYLSLMV*	MGLLVIIRGLYLSLMV*			GGCTACGCGT	ATATATACTA	0	E	0	0	0	0	0
10981	4712	ao	AN0086.1	71.m15362	AO070311000130	0					-168	-55	ATGCGAACCGTTCCCCTTTCAGCAGCCCCGATTTTCGCTCAGATACCGCAGTCATCGACTCAGCCTCCCCCGGATCTCCACAAAACACTTTTCATGCTCAGTGGATCCTGTTAA			ATGCGAACCGTTCCCCTTTCAGCAGCCCCGATTTTCGCTCAGATACCGCAGTCATCGACTCAGCCTCCCCCGGATCTCCACAAAACACTTTTCATGCTCAGTGGATCCTGTTAA	MRTVPLSAAPIFAQIPQSSTQPPPDLHKTLFMLSGSC*			MRTVPLSAAPIFAQIPQSSTQPPPDLHKTLFMLSGSC*	TGTTGTTTGC	CACTACTTCG	0	G	0	0	0	0	0
10982	4712	ao	AN0086.1	71.m15362	AO070311000130	0					-75	-55	ATGCTCAGTGGATCCTGTTAA			ATGCTCAGTGGATCCTGTTAA	MLSGSC*			MLSGSC*	AACACTTTTC	CACTACTTCG	0	G	0	0	0	0	0
10986	4716	af	AN4540.1	57.m05981	AO070321000158	0			-279	-196			ATGCAAACGGTGGATACTATGCGCAATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAG		ATGCAAACGGTGGATACTATGCGCAATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAG		MQTVDTMRNDEDQLPEASLPNLVSNYF*		MQTVDTMRNDEDQLPEASLPNLVSNYF*		ACATCATGAA	TCATAAATGA	0	ER	0	0	0	0	0
10987	4716	af	AN4540.1	57.m05981	AO070321000158	0			-261	-196			ATGCGCAATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAG		ATGCGCAATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAG		MRNDEDQLPEASLPNLVSNYF*		MRNDEDQLPEASLPNLVSNYF*		GGTGGATACT	TCATAAATGA	0	ER	0	0	0	0	0

10988	4716	af	AN4540.1	57.m05981	AO070321000158	0			-254	-186			ATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAGTCATAAATGA		ATGACGAAGACCAATTACCCGAAGCAAGCCTCCCAAATCTGGTATCCAATTATTTTTAGTCATAAATGA		MTKTNYPKQASQIWYPIIFSHK*		MTKTNYPKQASQIWYPIIFSHK*		ACTATGCGCA	AATACCTGCA	0	ER	0	0	0	0	0
10989	4716	af	AN4540.1	57.m05981	AO070321000158	0			-189	-139			ATGAAATACCTGCAAGCTGGATGCTGCCCCGCATCAAAGAACAATATGTGA		ATGAAATACCTGCAAGCTGGATGCTGCCCCGCATCAAAGAACAATATGTGA		MKYLQAGCCPASKNNM*		MKYLQAGCCPASKNNM*		TTAGTCATAA	GGGACTGCCG	0	ER	0	0	0	0	0
10990	4716	af	AN4540.1	57.m05981	AO070321000158	0			-169	-98			ATGCTGCCCCGCATCAAAGAACAATATGTGAGGGACTGCCGTTATCGGTGTGGAGCAGCCCAATCTTTCTAA		ATGCTGCCCCGCATCAAAGAACAATATGTGAGGGACTGCCGTTATCGGTGTGGAGCAGCCCAATCTTTCTAA		MLPRIKEQYVRDCRYRCGAAQSF*		MLPRIKEQYVRDCRYRCGAAQSF*		TGCAAGCTGG	ATTCACTCCG	0	ER	0	0	0	0	0
10983	4716	an	AN4540.1	57.m05981	AO070321000158	0	-219	-205					ATGCTCAGACCTTAA	ATGCTCAGACCTTAA			MLRP*	MLRP*			ACACCTGGAA	GTTAACCTCG	0	ER	0	0	0	0	0
10984	4716	an	AN4540.1	57.m05981	AO070321000158	0	-101	-54					ATGATGCCGAGATTTATCCAGCTTCTCCTGCACCCCGCGTCGAAATAA	ATGATGCCGAGATTTATCCAGCTTCTCCTGCACCCCGCGTCGAAATAA			MMPRFIQLLLHPASK*	MMPRFIQLLLHPASK*			TGTATCGTAT	AAAGAAAGGG	0	ER	0	0	0	0	0
10985	4716	an	AN4540.1	57.m05981	AO070321000158	0	-98	-54					ATGCCGAGATTTATCCAGCTTCTCCTGCACCCCGCGTCGAAATAA	ATGCCGAGATTTATCCAGCTTCTCCTGCACCCCGCGTCGAAATAA			MPRFIQLLLHPASK*	MPRFIQLLLHPASK*			ATCGTATATG	AAAGAAAGGG	0	ER	0	0	0	0	0
10992	4716	ao	AN4540.1	57.m05981	AO070321000158	0					-197	-159	ATGAGAGTGTTGGGGGTAACAGCCCCACAGTTATCATAA			ATGAGAGTGTTGGGGGTAACAGCCCCACAGTTATCATAA	MRVLGVTAPQLS*			MRVLGVTAPQLS*	ATTTTAGCTG	ATCGAGGGGC	0	ER	0	0	0	0	0
10993	4716	ao	AN4540.1	57.m05981	AO070321000158	0					-121	-14	ATGTGGGGGTCTTGGTTTCTCCAAAACGGCACATTTTACGTGCTTCGATTCAATGACCCAACTCTGCGAAGAAGACATTCCTTGTATACACCTTCCTCCACAACATAG			ATGTGGGGGTCTTGGTTTCTCCAAAACGGCACATTTTACGTGCTTCGATTCAATGACCCAACTCTGCGAAGAAGACATTCCTTGTATACACCTTCCTCCACAACATAG	MWGSWFLQNGTFYVLRFNDPTLRRRHSLYTPSSTT*			MWGSWFLQNGTFYVLRFNDPTLRRRHSLYTPSSTT*	CGTTCATCGG	ATCAGTCTAC	0	ER	0	0	0	0	0
10997	4717	af	AN6587.1	62.m03176	AO070326000035	0			-68	-39			ATGGCAGGATTAAGTCGGACAGACCATTGA		ATGGCAGGATTAAGTCGGACAGACCATTGA		MAGLSRTDH*		MAGLSRTDH*		GTAGGTCTCA	TTGCTGCGAT	0	J	0	0	0	0	0
10994	4717	an	AN6587.1	62.m03176	AO070326000035	0	-109	-62					ATGACCGTTATAACAGGACATCAAAGAAAGGTAAGTCAATGCCGATGA	ATGACCGTTATAACAGGACATCAAAGAAAGGTAAGTCAATGCCGATGA			MTVITGHQRKVSQCR*	MTVITGHQRKVSQCR*			GTGTGTTGAA	TAGTGACTCG	0	J	0	0	0	0	0
10995	4717	an	AN6587.1	62.m03176	AO070326000035	0	-71	-36					ATGCCGATGATAGTGACTCGACTTTCGAGTGACTGA	ATGCCGATGATAGTGACTCGACTTTCGAGTGACTGA			MPMIVTRLSSD*	MPMIVTRLSSD*			AGGTAAGTCA	CTGGCTTCAA	0	J	0	0	0	0	0
10996	4717	an	AN6587.1	62.m03176	AO070326000035	0	-65	-36					ATGATAGTGACTCGACTTTCGAGTGACTGA	ATGATAGTGACTCGACTTTCGAGTGACTGA			MIVTRLSSD*	MIVTRLSSD*			GTCAATGCCG	CTGGCTTCAA	0	J	0	0	0	0	0
10998	4717	ao	AN6587.1	62.m03176	AO070326000035	0					-142	-92	ATGGTGAAATGGCCGCGATGGCAGCAAACGCAAGCGCGGTACATCATGTGA			ATGGTGAAATGGCCGCGATGGCAGCAAACGCAAGCGCGGTACATCATGTGA	MVKWPRWQQTQARYIM*			MVKWPRWQQTQARYIM*	AGTTAGATAC	GTGGCAGGTA	0	J	0	0	0	0	0
10999	4717	ao	AN6587.1	62.m03176	AO070326000035	0					-134	-81	ATGGCCGCGATGGCAGCAAACGCAAGCGCGGTACATCATGTGAGTGGCAGGTAG			ATGGCCGCGATGGCAGCAAACGCAAGCGCGGTACATCATGTGAGTGGCAGGTAG	MAAMAANASAVHHVSGR*			MAAMAANASAVHHVSGR*	ACATGGTGAA	TTGGGATGAG	0	J	0	0	0	0	0
11000	4717	ao	AN6587.1	62.m03176	AO070326000035	0					-125	-81	ATGGCAGCAAACGCAAGCGCGGTACATCATGTGAGTGGCAGGTAG			ATGGCAGCAAACGCAAGCGCGGTACATCATGTGAGTGGCAGGTAG	MAANASAVHHVSGR*			MAANASAVHHVSGR*	AATGGCCGCG	TTGGGATGAG	0	J	0	0	0	0	0
11002	4720	af	AN1362.1	70.m14867	AO070243000002	0			-249	-175			ATGTATCACGTGTCACAAACGTCACTGCGGGTCCGAACCCAATCACAAGCGTCCGTTGTCTGGAGCTTTGGATAG		ATGTATCACGTGTCACAAACGTCACTGCGGGTCCGAACCCAATCACAAGCGTCCGTTGTCTGGAGCTTTGGATAG		MYHVSQTSLRVRTQSQASVVWSFG*		MYHVSQTSLRVRTQSQASVVWSFG*		GGCGGGACCT	GAGGTGGTCT	0		0	0	0	0	0
11003	4720	af	AN1362.1	70.m14867	AO070243000002	0			-148	-107			ATGACCCTGAATTACTTTCTGCCTACAGATACCTTCACCTGA		ATGACCCTGAATTACTTTCTGCCTACAGATACCTTCACCTGA		MTLNYFLPTDTFT*		MTLNYFLPTDTFT*		AATAACGGCA	TACTTTCAAT	0		0	0	0	0	0
11001	4720	an	AN1362.1	70.m14867	AO070243000002	0	-176	-120					ATGAGAGAGCTCCAACTCAAGCCTCCAATAATCAGTCGCAACAGAACATCGCATTAG	ATGAGAGAGCTCCAACTCAAGCCTCCAATAATCAGTCGCAACAGAACATCGCATTAG			MRELQLKPPIISRNRTSH*	MRELQLKPPIISRNRTSH*			AGAGTGGCTG	CTTTCTGCCT	0		0	0	0	0	0
11004	4720	ao	AN1362.1	70.m14867	AO070243000002	0					-236	-204	ATGGGTGCCCATCACGTGGCGCAACGTCACTGA			ATGGGTGCCCATCACGTGGCGCAACGTCACTGA	MGAHHVAQRH*			MGAHHVAQRH*	TAGATAAGCG	GCATCGAAGC	0		0	0	0	0	0
11006	4722	af	AN3826.1	58.m07802	AO070305000062	0			-149	-75			ATGCGCGGAGTCTTGGCGCGGCAGGCCGAAGGACAGCTGGAGCATACAAACCAACAGCCAACAGTGAGACACTGA		ATGCGCGGAGTCTTGGCGCGGCAGGCCGAAGGACAGCTGGAGCATACAAACCAACAGCCAACAGTGAGACACTGA		MRGVLARQAEGQLEHTNQQPTVRH*		MRGVLARQAEGQLEHTNQQPTVRH*		GAAAAGGGAA	CTGAAAGTTA	0	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11009	4722	ao	AN3826.1	58.m07802	AO070305000062	0					-172	-47	ATGGTCCGTGCACTGCGGACGGAAAAGGCGGAGAGTCTTGGCAGGGCGATTGATATGGAAAAGGGACAGCTGGACCAACCGACAAACACGAACAGTTTCCCAGGCCAATTTCACCGGGCCTGTTGA			ATGGTCCGTGCACTGCGGACGGAAAAGGCGGAGAGTCTTGGCAGGGCGATTGATATGGAAAAGGGACAGCTGGACCAACCGACAAACACGAACAGTTTCCCAGGCCAATTTCACCGGGCCTGTTGA	MVRALRTEKAESLGRAIDMEKGQLDQPTNTNSFPGQFHRAC*			MVRALRTEKAESLGRAIDMEKGQLDQPTNTNSFPGQFHRAC*	GGCATATCCG	CCCCGTTCGG	0	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11010	4722	ao	AN3826.1	58.m07802	AO070305000062	0					-118	-47	ATGGAAAAGGGACAGCTGGACCAACCGACAAACACGAACAGTTTCCCAGGCCAATTTCACCGGGCCTGTTGA			ATGGAAAAGGGACAGCTGGACCAACCGACAAACACGAACAGTTTCCCAGGCCAATTTCACCGGGCCTGTTGA	MEKGQLDQPTNTNSFPGQFHRAC*			MEKGQLDQPTNTNSFPGQFHRAC*	GGCGATTGAT	CCCCGTTCGG	0	R	FG00694.1	MG01168.1	NCU00924.1	0	0
11012	4725	an	AN2664.1	71.m15162	AO070343000349	0	-119	-9					ATGAGATCCAGGACCCTGGTTGCTTCCCCACAGTATAAGTGCGGGCGAAACGGCCTGCCGGAGGCTCACGCCAGGGCAATTGAATCACTGGGCCTCAATCGTCTTGACTGA	ATGAGATCCAGGACCCTGGTTGCTTCCCCACAGTATAAGTGCGGGCGAAACGGCCTGCCGGAGGCTCACGCCAGGGCAATTGAATCACTGGGCCTCAATCGTCTTGACTGA			MRSRTLVASPQYKCGRNGLPEAHARAIESLGLNRLD*	MRSRTLVASPQYKCGRNGLPEAHARAIESLGLNRLD*			CACCCCGACC	TTGTCGAAAT	0		0	0	NCU06861.1	0	0
11013	4725	ao	AN2664.1	71.m15162	AO070343000349	0					-68	-6	ATGATATATTACCAAACAACAACAAACTTTCCCCGGACATTACCCCAGATCCCCAGCAATTGA			ATGATATATTACCAAACAACAACAAACTTTCCCCGGACATTACCCCAGATCCCCAGCAATTGA	MIYYQTTTNFPRTLPQIPSN*			MIYYQTTTNFPRTLPQIPSN*	GTCTTGGCTA	TCAAAATGTT	0		0	0	NCU06861.1	0	0
11016	4728	ao	AN1795.1	72.m19547	AO070309000136	0					-219	-202	ATGATGCTACTGATATAG			ATGATGCTACTGATATAG	MMLLI*			MMLLI*	ACTACTAGCG	TCCTTTTTTT	0	P	0	0	0	0	0
11017	4728	ao	AN1795.1	72.m19547	AO070309000136	0					-216	-202	ATGCTACTGATATAG			ATGCTACTGATATAG	MLLI*			MLLI*	ACTAGCGATG	TCCTTTTTTT	0	P	0	0	0	0	0
11020	4729	af	AN6809.1	53.m04197	AO070317000043	0			-151	-116			ATGATCGGATCGACGTTACACAAAGAGCGATCCTAG		ATGATCGGATCGACGTTACACAAAGAGCGATCCTAG		MIGSTLHKERS*		MIGSTLHKERS*		CCGATGCGGT	ACGCGTCCGG	0	I	0	0	0	0	0
11018	4729	an	AN6809.1	53.m04197	AO070317000043	0	-245	-195					ATGCATAATGCATCACAGCCACCTTGCAAAAACGCTAATCAATCTGACTAG	ATGCATAATGCATCACAGCCACCTTGCAAAAACGCTAATCAATCTGACTAG			MHNASQPPCKNANQSD*	MHNASQPPCKNANQSD*			TGCAGGAAAA	CGGTCTAAAA	0	I	0	0	0	0	0
11019	4729	an	AN6809.1	53.m04197	AO070317000043	0	-238	-92					ATGCATCACAGCCACCTTGCAAAAACGCTAATCAATCTGACTAGCGGTCTAAAAAAACGAAAAAGCAAAAAGGTCACACAACATCGATTCATCACCTTCTCACCTTGTCAACAAACTGTCCTGATCCTGTCTCTGATTGCTGTTTGA	ATGCATCACAGCCACCTTGCAAAAACGCTAATCAATCTGACTAGCGGTCTAAAAAAACGAAAAAGCAAAAAGGTCACACAACATCGATTCATCACCTTCTCACCTTGTCAACAAACTGTCCTGATCCTGTCTCTGATTGCTGTTTGA			MHHSHLAKTLINLTSGLKKRKSKKVTQHRFITFSPCQQTVLILSLIAV*	MHHSHLAKTLINLTSGLKKRKSKKVTQHRFITFSPCQQTVLILSLIAV*			AAAATGCATA	CCTCCCTCTC	0	I	0	0	0	0	0
11021	4729	ao	AN6809.1	53.m04197	AO070317000043	0					-215	-171	ATGCAGGTTAACCGAACCCCGGCAGCAAGGGTTGGCTGCACATAA			ATGCAGGTTAACCGAACCCCGGCAGCAAGGGTTGGCTGCACATAA	MQVNRTPAARVGCT*			MQVNRTPAARVGCT*	ATCCCTGTGT	ATACAATGCA	0	I	0	0	0	0	0
11022	4729	ao	AN6809.1	53.m04197	AO070317000043	0					-165	-61	ATGCAAAGCACACCGCTCCTGACACGTTGTCTGACAACGCACTCCTCCTCCTCCTCCTTATTTTCCCGGCTCGTAGTGACTCGCTTACTAGTCAGGTTGAGCTGA			ATGCAAAGCACACCGCTCCTGACACGTTGTCTGACAACGCACTCCTCCTCCTCCTCCTTATTTTCCCGGCTCGTAGTGACTCGCTTACTAGTCAGGTTGAGCTGA	MQSTPLLTRCLTTHSSSSSLFSRLVVTRLLVRLS*			MQSTPLLTRCLTTHSSSSSLFSRLVVTRLLVRLS*	CATAAATACA	ACCGAATTCT	0	I	0	0	0	0	0
11023	4732	af	AN8116.1	53.m03826	AO070322000022	0			-133	-116			ATGACCTTCAGGATCTGA		ATGACCTTCAGGATCTGA		MTFRI*		MTFRI*		TCCACCCTTG	GACCTTTGGA	0	R	0	0	0	0	0
11024	4732	ao	AN8116.1	53.m03826	AO070322000022	0					-238	-179	ATGTTGATTTTTTACTGCTTTTGTTCGCACACTCATTTGTTATCGTTGATGATACCGTGA			ATGTTGATTTTTTACTGCTTTTGTTCGCACACTCATTTGTTATCGTTGATGATACCGTGA	MLIFYCFCSHTHLLSLMIP*			MLIFYCFCSHTHLLSLMIP*	TGGTCCTTCT	GTGTATCATC	0	R	0	0	0	0	0
11025	4732	ao	AN8116.1	53.m03826	AO070322000022	0					-190	-179	ATGATACCGTGA			ATGATACCGTGA	MIP*			MIP*	GTTATCGTTG	GTGTATCATC	0	R	0	0	0	0	0
11026	4734	af	AN9104.1	66.m04565	AO070332000169	0			-238	-203			ATGTTTGTCGCCTTTACTTTCCACTTTCTTCTGTGA		ATGTTTGTCGCCTTTACTTTCCACTTTCTTCTGTGA		MFVAFTFHFLL*		MFVAFTFHFLL*		AGATACCAGC	CTGCAACCGG	0	Y	0	0	0	0	0
11027	4734	af	AN9104.1	66.m04565	AO070332000169	0			-119	-102			ATGGCATCATCTTCCTGA		ATGGCATCATCTTCCTGA		MASSS*		MASSS*		TGGCGATTGC	GTAAAGGATA	0	Y	0	0	0	0	0
11028	4734	af	AN9104.1	66.m04565	AO070332000169	0			-68	-54			ATGATATATCTCTAG		ATGATATATCTCTAG		MIYL*		MIYL*		GCGCTCCCAA	ACAGGTCAAC	0	Y	0	0	0	0	0
11029	4734	ao	AN9104.1	66.m04565	AO070332000169	0					-94	-59	ATGTTACATTGCCTCACTAGCGCTCTACCTCAATGA			ATGTTACATTGCCTCACTAGCGCTCTACCTCAATGA	MLHCLTSALPQ*			MLHCLTSALPQ*	TTACAATTGC	TTTAATTTCA	0	Y	0	0	0	0	0
11030	4736	af	AN6190.1	72.m19288	AO070308000111	0			-194	-174			ATGGGCTTCTGGCTACGGTAG		ATGGGCTTCTGGCTACGGTAG		MGFWLR*		MGFWLR*		TTCCCTGGTC	CCTTAGAGCC	0	D	0	0	0	0	0
11031	4736	af	AN6190.1	72.m19288	AO070308000111	0			-140	-48			ATGGTCTCGGCCATCGATCTCCGCAGCAGTAGCTCTCCTGCTCCATCAATTACCACCAGCGTCAGGTCGAGTGGCCCGCCGTCCTCACAGTGA		ATGGTCTCGGCCATCGATCTCCGCAGCAGTAGCTCTCCTGCTCCATCAATTACCACCAGCGTCAGGTCGAGTGGCCCGCCGTCCTCACAGTGA		MVSAIDLRSSSSPAPSITTSVRSSGPPSSQ*		MVSAIDLRSSSSPAPSITTSVRSSGPPSSQ*		GATCTGGGCA	CAGGCCGTGT	0	D	0	0	0	0	0
11032	4736	ao	AN6190.1	72.m19288	AO070308000111	0					-185	-96	ATGAGCTCCGCCGGTGGTATCTCCGTCTCCGTCCCGTCATTCCTTCCAGAAGCTCCGCTTGGCCTAAGCGCCTCCTCCGTCTCTCCTTAA			ATGAGCTCCGCCGGTGGTATCTCCGTCTCCGTCCCGTCATTCCTTCCAGAAGCTCCGCTTGGCCTAAGCGCCTCCTCCGTCTCTCCTTAA	MSSAGGISVSVPSFLPEAPLGLSASSVSP*			MSSAGGISVSVPSFLPEAPLGLSASSVSP*	CTGACTAGTC	CAGCTTGTTT	0	D	0	0	0	0	0
11034	4737	af	AN8687.1	62.m03487	AO070315000106	0			-76	-29			ATGATCCCAGATGAGTCACTCATTTTGTTTCAAATAAACCTCCTCTGA		ATGATCCCAGATGAGTCACTCATTTTGTTTCAAATAAACCTCCTCTGA		MIPDESLILFQINLL*		MIPDESLILFQINLL*		ATTTATTGGC	GCTTCTCCTT	0	K	0	0	0	0	0
11035	4737	af	AN8687.1	62.m03487	AO070315000106	0			-66	-40			ATGAGTCACTCATTTTGTTTCAAATAA		ATGAGTCACTCATTTTGTTTCAAATAA		MSHSFCFK*		MSHSFCFK*		ATGATCCCAG	ACCTCCTCTG	0	K	0	0	0	0	0
11033	4737	an	AN8687.1	62.m03487	AO070315000106	0	-178	-131					ATGCGAGTTGCTGCCTTGAAATCCAGGCAAAGACGATATCTTGACTAA	ATGCGAGTTGCTGCCTTGAAATCCAGGCAAAGACGATATCTTGACTAA			MRVAALKSRQRRYLD*	MRVAALKSRQRRYLD*			CAGTTAGGCA	CTTATCCGCC	0	K	0	0	0	0	0
11036	4737	ao	AN8687.1	62.m03487	AO070315000106	0					-128	-117	ATGACTCCATAG			ATGACTCCATAG	MTP*			MTP*	TCTATCAACT	CTCCTCCACT	0	K	0	0	0	0	0
11039	4738	af	AN0888.1	70.m15494	AO070320000057	0			-175	-44			ATGACGTTGCTTTCATTAACTAATGTGTGGAGTGAAAAGGAGAGAAAACGCAGTTTAAAAAGCACAATTGTAGTAAGAAGTCATCTCAGCCTTCTTCTATTATCTACTCATCTCTATCTCTCTCGGAACTGA		ATGACGTTGCTTTCATTAACTAATGTGTGGAGTGAAAAGGAGAGAAAACGCAGTTTAAAAAGCACAATTGTAGTAAGAAGTCATCTCAGCCTTCTTCTATTATCTACTCATCTCTATCTCTCTCGGAACTGA		MTLLSLTNVWSEKERKRSLKSTIVVRSHLSLLLLSTHLYLSRN*		MTLLSLTNVWSEKERKRSLKSTIVVRSHLSLLLLSTHLYLSRN*		TCGCTCTGCA	TAGGCTCTGA	0	BT	0	0	0	0	0
11040	4738	af	AN0888.1	70.m15494	AO070320000057	0			-153	-118			ATGTGTGGAGTGAAAAGGAGAGAAAACGCAGTTTAA		ATGTGTGGAGTGAAAAGGAGAGAAAACGCAGTTTAA		MCGVKRRENAV*		MCGVKRRENAV*		TCATTAACTA	AAAGCACAAT	0	BT	0	0	0	0	0
11037	4738	an	AN0888.1	70.m15494	AO070320000057	0	-175	-155					ATGGCACAACTTGATAATTAA	ATGGCACAACTTGATAATTAA			MAQLDN*	MAQLDN*			GCCTTGGCGT	TCTTCTCTGA	0	BT	0	0	0	0	0
11038	4738	an	AN0888.1	70.m15494	AO070320000057	0	-96	-49					ATGGCAAAACACGTCTTTATAACTTTCTTGACCTTCTCCCCTCCTTGA	ATGGCAAAACACGTCTTTATAACTTTCTTGACCTTCTCCCCTCCTTGA			MAKHVFITFLTFSPP*	MAKHVFITFLTFSPP*			AGCAGCGAAA	GATTTCACCT	0	BT	0	0	0	0	0
11042	4738	ao	AN0888.1	70.m15494	AO070320000057	0					-245	-186	ATGAATTGCTGTAGTCTTCACTGTAAGCTACTAAATAGTGCGACCGGACTTAAAATATAA			ATGAATTGCTGTAGTCTTCACTGTAAGCTACTAAATAGTGCGACCGGACTTAAAATATAA	MNCCSLHCKLLNSATGLKI*			MNCCSLHCKLLNSATGLKI*	CCTCAAAATT	TCCCCGCATG	0	BT	0	0	0	0	0
11043	4738	ao	AN0888.1	70.m15494	AO070320000057	0					-178	-164	ATGACGTTGCGGTAA			ATGACGTTGCGGTAA	MTLR*			MTLR*	TAATCCCCGC	AATAAGAGTG	0	BT	0	0	0	0	0
11044	4738	ao	AN0888.1	70.m15494	AO070320000057	0					-118	-47	ATGCAACACTCATCACTTACAAACCACCATTATCTTACCATACCCTCACTTACAAATTGGTGCCGGCGATAG			ATGCAACACTCATCACTTACAAACCACCATTATCTTACCATACCCTCACTTACAAATTGGTGCCGGCGATAG	MQHSSLTNHHYLTIPSLTNWCRR*			MQHSSLTNHHYLTIPSLTNWCRR*	GCCACAACAA	CAATTCTATC	0	BT	0	0	0	0	0
11046	4739	af	AN1750.1	69.m15051	AO070324000043	0			-205	-59			ATGTATAAATTGCCGTCCAGTTGGATCTCTGGTAGAAATTCAATGTGGGGAGATGAAGCGATAAGATTAAAATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAAAAAAGATCATCACCGCTTCCATTGA		ATGTATAAATTGCCGTCCAGTTGGATCTCTGGTAGAAATTCAATGTGGGGAGATGAAGCGATAAGATTAAAATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAAAAAAGATCATCACCGCTTCCATTGA		MYKLPSSWISGRNSMWGDEAIRLKCVKRRASFLPLFFISSKKDHHRFH*		MYKLPSSWISGRNSMWGDEAIRLKCVKRRASFLPLFFISSKKDHHRFH*		GGCAGTGTAG	TTTGCGTCGC	0	A	0	0	0	0	0

11047	4739	af	AN1750.1	69.m15051	AO070324000043	0			-163	-59			ATGTGGGGAGATGAAGCGATAAGATTAAAATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAAAAAAGATCATCACCGCTTCCATTGA		ATGTGGGGAGATGAAGCGATAAGATTAAAATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAAAAAAGATCATCACCGCTTCCATTGA		MWGDEAIRLKCVKRRASFLPLFFISSKKDHHRFH*		MWGDEAIRLKCVKRRASFLPLFFISSKKDHHRFH*		TAGAAATTCA	TTTGCGTCGC	0	A	0	0	0	0	0
11048	4739	af	AN1750.1	69.m15051	AO070324000043	0			-153	-142			ATGAAGCGATAA		ATGAAGCGATAA		MKR*		MKR*		ATGTGGGGAG	GATTAAAATG	0	A	0	0	0	0	0
11049	4739	af	AN1750.1	69.m15051	AO070324000043	0			-134	-84			ATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAA		ATGCGTAAAAAGGCGGGCCTCTTTTCTGCCGCTTTTTTTCATCTCAAGTAA		MRKKAGLFSAAFFHLK*		MRKKAGLFSAAFFHLK*		TAAGATTAAA	AAAAGATCAT	0	A	0	0	0	0	0
11045	4739	an	AN1750.1	69.m15051	AO070324000043	0	-206	-186					ATGGGCGACAAAAAGGAATAG	ATGGGCGACAAAAAGGAATAG			MGDKKE*	MGDKKE*			TCGATTCCCA	AGGAGGGGTC	0	A	0	0	0	0	0
11050	4739	ao	AN1750.1	69.m15051	AO070324000043	0					-195	-184	ATGGGTAGGTAA			ATGGGTAGGTAA	MGR*			MGR*	AACTATACCA	AGAAGAGTGA	0	A	0	0	0	0	0
11051	4739	ao	AN1750.1	69.m15051	AO070324000043	0					-167	-129	ATGAATTTCTCCGTGGGGCAGAGGCGGGCGTGCCGATAA			ATGAATTTCTCCGTGGGGCAGAGGCGGGCGTGCCGATAA	MNFSVGQRRACR*			MNFSVGQRRACR*	GTGATTTTCA	GATTGACTCT	0	A	0	0	0	0	0
11052	4741	an	AN5149.1	69.m14886	AO070237000016	0	-195	-154					ATGCGCACTTTGGGCAATTCTAGCAATTTCTTTCCTTTGTGA	ATGCGCACTTTGGGCAATTCTAGCAATTTCTTTCCTTTGTGA			MRTLGNSSNFFPL*	MRTLGNSSNFFPL*			GTAGCCCCTT	TGCTTGATGC	0	GO	0	0	0	0	0
11053	4741	an	AN5149.1	69.m14886	AO070237000016	0	-154	-128					ATGCTTGATGCTCCTTCACTTCTCTAA	ATGCTTGATGCTCCTTCACTTCTCTAA			MLDAPSLL*	MLDAPSLL*			TTCCTTTGTG	TACAATCTTG	0	GO	0	0	0	0	0
11054	4741	an	AN5149.1	69.m14886	AO070237000016	0	-147	-97					ATGCTCCTTCACTTCTCTAATACAATCTTGCTCACTATTGCAGTTCTTTGA	ATGCTCCTTCACTTCTCTAATACAATCTTGCTCACTATTGCAGTTCTTTGA			MLLHFSNTILLTIAVL*	MLLHFSNTILLTIAVL*			GTGATGCTTG	CAATCCATTC	0	GO	0	0	0	0	0
11055	4741	ao	AN5149.1	69.m14886	AO070237000016	0					-220	-173	ATGTGGATTTCAAGGCAGAGCATCCTTTGTCTGTATCTCGTTGTTTAA			ATGTGGATTTCAAGGCAGAGCATCCTTTGTCTGTATCTCGTTGTTTAA	MWISRQSILCLYLVV*			MWISRQSILCLYLVV*	CTAAATCAGT	CCTTCCCTAA	0	GO	0	0	0	0	0
11056	4741	ao	AN5149.1	69.m14886	AO070237000016	0					-155	-99	ATGGAACCACCTCTCATCAATGATCCTGTCCTTTGTCAATTCATCCTCTTGCTATAG			ATGGAACCACCTCTCATCAATGATCCTGTCCTTTGTCAATTCATCCTCTTGCTATAG	MEPPLINDPVLCQFILLL*			MEPPLINDPVLCQFILLL*	TAAGCCATCA	CTGCCTTGAT	0	GO	0	0	0	0	0
11057	4741	ao	AN5149.1	69.m14886	AO070237000016	0					-136	-11	ATGATCCTGTCCTTTGTCAATTCATCCTCTTGCTATAGCTGCCTTGATCTGACATCGGCCGGCCATCTTTTCTTCTCCTTCCCAAGGACCATCACCTTGCAACCTACGTCCGCGAGGAGCTGTTAA			ATGATCCTGTCCTTTGTCAATTCATCCTCTTGCTATAGCTGCCTTGATCTGACATCGGCCGGCCATCTTTTCTTCTCCTTCCCAAGGACCATCACCTTGCAACCTACGTCCGCGAGGAGCTGTTAA	MILSFVNSSSCYSCLDLTSAGHLFFSFPRTITLQPTSARSC*			MILSFVNSSSCYSCLDLTSAGHLFFSFPRTITLQPTSARSC*	CCTCTCATCA	CTTAGCCAGT	0	GO	0	0	0	0	0
11060	4745	af	AN0470.1	54.m06599	AO070328000168	0			-172	-122			ATGATGAATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		ATGATGAATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		MMNDFMLELGSLGVDD*		MMNDFMLELGSLGVDD*		ATCTGAAATA	GCAGCAGTGG	0	J	0	0	0	0	0
11061	4745	af	AN0470.1	54.m06599	AO070328000168	0			-169	-122			ATGAATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		ATGAATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		MNDFMLELGSLGVDD*		MNDFMLELGSLGVDD*		TGAAATAATG	GCAGCAGTGG	0	J	0	0	0	0	0
11062	4745	af	AN0470.1	54.m06599	AO070328000168	0			-165	-55			ATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAAGCAGCAGTGGAGAGGAAAATCATTCTTTGCGGCTCCGACGAAGCCAAGGACGGAGGAGGGCAATTGA		ATGACTTCATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAAGCAGCAGTGGAGAGGAAAATCATTCTTTGCGGCTCCGACGAAGCCAAGGACGGAGGAGGGCAATTGA		MTSCWNWGVLASMTKQQWRGKSFFAAPTKPRTEEGN*		MTSCWNWGVLASMTKQQWRGKSFFAAPTKPRTEEGN*		ATAATGATGA	ACACTCACTC	0	J	0	0	0	0	0
11063	4745	af	AN0470.1	54.m06599	AO070328000168	0			-157	-122			ATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		ATGCTGGAATTGGGGAGTCTTGGCGTCGATGACTAA		MLELGSLGVDD*		MLELGSLGVDD*		GAATGACTTC	GCAGCAGTGG	0	J	0	0	0	0	0
11064	4745	af	AN0470.1	54.m06599	AO070328000168	0			-129	-55			ATGACTAAGCAGCAGTGGAGAGGAAAATCATTCTTTGCGGCTCCGACGAAGCCAAGGACGGAGGAGGGCAATTGA		ATGACTAAGCAGCAGTGGAGAGGAAAATCATTCTTTGCGGCTCCGACGAAGCCAAGGACGGAGGAGGGCAATTGA		MTKQQWRGKSFFAAPTKPRTEEGN*		MTKQQWRGKSFFAAPTKPRTEEGN*		CTTGGCGTCG	ACACTCACTC	0	J	0	0	0	0	0
11058	4745	an	AN0470.1	54.m06599	AO070328000168	0	-177	-163					ATGATTTCACCTTGA	ATGATTTCACCTTGA			MISP*	MISP*			TGCAGATTAG	CGAGACGATG	0	J	0	0	0	0	0
11059	4745	an	AN0470.1	54.m06599	AO070328000168	0	-155	-129					ATGTCTTGGCGGACTTTGCTACTGTAA	ATGTCTTGGCGGACTTTGCTACTGTAA			MSWRTLLL*	MSWRTLLL*			TGACGAGACG	AAACTAGCTG	0	J	0	0	0	0	0
11065	4745	ao	AN0470.1	54.m06599	AO070328000168	0					-220	-176	ATGCTCTTTCCTTGTCTATTCTATACTAGTACTGGAGCGGTATGA			ATGCTCTTTCCTTGTCTATTCTATACTAGTACTGGAGCGGTATGA	MLFPCLFYTSTGAV*			MLFPCLFYTSTGAV*	GTTCTGTTTG	CTTCATCATC	0	J	0	0	0	0	0
11066	4745	ao	AN0470.1	54.m06599	AO070328000168	0					-179	-135	ATGACTTCATCATCTTTCATGAGCCTGTCGATTCTTGGCGGATGA			ATGACTTCATCATCTTTCATGAGCCTGTCGATTCTTGGCGGATGA	MTSSSFMSLSILGG*			MTSSSFMSLSILGG*	CTGGAGCGGT	TGACTAAGCG	0	J	0	0	0	0	0
11067	4745	ao	AN0470.1	54.m06599	AO070328000168	0					-161	-135	ATGAGCCTGTCGATTCTTGGCGGATGA			ATGAGCCTGTCGATTCTTGGCGGATGA	MSLSILGG*			MSLSILGG*	ATCATCTTTC	TGACTAAGCG	0	J	0	0	0	0	0
11068	4745	ao	AN0470.1	54.m06599	AO070328000168	0					-138	-34	ATGATGACTAAGCGCTCGTGCAGAGGAAAATCGTTCGCCGGAATTCCCAAAGCAGAGGGCGAACGAGACCATCGTCGGTTCAGCTGTAGCCCACCCTTTTTTTAA			ATGATGACTAAGCGCTCGTGCAGAGGAAAATCGTTCGCCGGAATTCCCAAAGCAGAGGGCGAACGAGACCATCGTCGGTTCAGCTGTAGCCCACCCTTTTTTTAA	MMTKRSCRGKSFAGIPKAEGERDHRRFSCSPPFF*			MMTKRSCRGKSFAGIPKAEGERDHRRFSCSPPFF*	TTCTTGGCGG	CTCCAGCTCA	0	J	0	0	0	0	0
11069	4745	ao	AN0470.1	54.m06599	AO070328000168	0					-135	-34	ATGACTAAGCGCTCGTGCAGAGGAAAATCGTTCGCCGGAATTCCCAAAGCAGAGGGCGAACGAGACCATCGTCGGTTCAGCTGTAGCCCACCCTTTTTTTAA			ATGACTAAGCGCTCGTGCAGAGGAAAATCGTTCGCCGGAATTCCCAAAGCAGAGGGCGAACGAGACCATCGTCGGTTCAGCTGTAGCCCACCCTTTTTTTAA	MTKRSCRGKSFAGIPKAEGERDHRRFSCSPPFF*			MTKRSCRGKSFAGIPKAEGERDHRRFSCSPPFF*	TTGGCGGATG	CTCCAGCTCA	0	J	0	0	0	0	0
11074	4749	af	AN6114.1	72.m19045	AO070340000090	0			-227	-204			ATGGATACCAACATGAGAGATTGA		ATGGATACCAACATGAGAGATTGA		MDTNMRD*		MDTNMRD*		CGCACTTCAT	TGGATTCTGG	0	L	FG01896.1	0	NCU01321.1	0	0
11075	4749	af	AN6114.1	72.m19045	AO070340000090	0			-215	-204			ATGAGAGATTGA		ATGAGAGATTGA		MRD*		MRD*		GGATACCAAC	TGGATTCTGG	0	L	FG01896.1	0	NCU01321.1	0	0
11076	4749	af	AN6114.1	72.m19045	AO070340000090	0			-204	-49			ATGGATTCTGGCTCTCAAACGAACTTGCGACACCACGCACATATGAGACCCACTAACGCTGCCATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		ATGGATTCTGGCTCTCAAACGAACTTGCGACACCACGCACATATGAGACCCACTAACGCTGCCATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		MDSGSQTNLRHHAHMRPTNAAMLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		MDSGSQTNLRHHAHMRPTNAAMLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		TGAGAGATTG	TCGCCTAATT	0	L	FG01896.1	0	NCU01321.1	0	0
11077	4749	af	AN6114.1	72.m19045	AO070340000090	0			-162	-49			ATGAGACCCACTAACGCTGCCATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		ATGAGACCCACTAACGCTGCCATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		MRPTNAAMLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		MRPTNAAMLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		CCACGCACAT	TCGCCTAATT	0	L	FG01896.1	0	NCU01321.1	0	0
11078	4749	af	AN6114.1	72.m19045	AO070340000090	0			-141	-49			ATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		ATGCTCACGACATACCTTTATATAATATTGTATATAAAAACCATACATTGGCTTCTTGGTTACTATTATTATCACCCTCAATGCAGCGAGTGA		MLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		MLTTYLYIILYIKTIHWLLGYYYYHPQCSE*		TAACGCTGCC	TCGCCTAATT	0	L	FG01896.1	0	NCU01321.1	0	0
11070	4749	an	AN6114.1	72.m19045	AO070340000090	0	-138	-64					ATGCTGCCGAGTCTTCAATCATGGATGCATAATTGCGCTGCACGAGCTACAAAACCTTGTATGTACGGTTTATGA	ATGCTGCCGAGTCTTCAATCATGGATGCATAATTGCGCTGCACGAGCTACAAAACCTTGTATGTACGGTTTATGA			MLPSLQSWMHNCAARATKPCMYGL*	MLPSLQSWMHNCAARATKPCMYGL*			AGAGAATACG	AGCAGAGTTA	0	L	FG01896.1	0	NCU01321.1	0	0
11071	4749	an	AN6114.1	72.m19045	AO070340000090	0	-118	-107					ATGGATGCATAA	ATGGATGCATAA			MDA*	MDA*			GTCTTCAATC	TTGCGCTGCA	0	L	FG01896.1	0	NCU01321.1	0	0
11072	4749	an	AN6114.1	72.m19045	AO070340000090	0	-114	-64					ATGCATAATTGCGCTGCACGAGCTACAAAACCTTGTATGTACGGTTTATGA	ATGCATAATTGCGCTGCACGAGCTACAAAACCTTGTATGTACGGTTTATGA			MHNCAARATKPCMYGL*	MHNCAARATKPCMYGL*			TCAATCATGG	AGCAGAGTTA	0	L	FG01896.1	0	NCU01321.1	0	0
11073	4749	an	AN6114.1	72.m19045	AO070340000090	0	-78	-64					ATGTACGGTTTATGA	ATGTACGGTTTATGA			MYGL*	MYGL*			AAAACCTTGT	AGCAGAGTTA	0	L	FG01896.1	0	NCU01321.1	0	0
11080	4749	ao	AN6114.1	72.m19045	AO070340000090	0					-177	-160	ATGATGTCTGACCCTTAA			ATGATGTCTGACCCTTAA	MMSDP*			MMSDP*	TCAAAAAACA	TGACAATTCA	0	L	FG01896.1	0	NCU01321.1	0	0
11081	4749	ao	AN6114.1	72.m19045	AO070340000090	0					-174	-160	ATGTCTGACCCTTAA			ATGTCTGACCCTTAA	MSDP*			MSDP*	AAAAACAATG	TGACAATTCA	0	L	FG01896.1	0	NCU01321.1	0	0
11082	4749	ao	AN6114.1	72.m19045	AO070340000090	0					-160	-35	ATGACAATTCATCTCCAACTTAACGTGCATAATGGGGGATTAATGCTTGACTTGTTCTACGTCACATCTATATTGAATTTCTATATATATACACCTCTGTTCATTACCTTATATACAATGCACTAA			ATGACAATTCATCTCCAACTTAACGTGCATAATGGGGGATTAATGCTTGACTTGTTCTACGTCACATCTATATTGAATTTCTATATATATACACCTCTGTTCATTACCTTATATACAATGCACTAA	MTIHLQLNVHNGGLMLDLFYVTSILNFYIYTPLFITLYTMH*			MTIHLQLNVHNGGLMLDLFYVTSILNFYIYTPLFITLYTMH*	CTGACCCTTA	CATATACACG	0	L	FG01896.1	0	NCU01321.1	0	0
11083	4749	ao	AN6114.1	72.m19045	AO070340000090	0					-129	-118	ATGGGGGATTAA			ATGGGGGATTAA	MGD*			MGD*	AACGTGCATA	TGCTTGACTT	0	L	FG01896.1	0	NCU01321.1	0	0
11084	4749	ao	AN6114.1	72.m19045	AO070340000090	0					-118	-35	ATGCTTGACTTGTTCTACGTCACATCTATATTGAATTTCTATATATATACACCTCTGTTCATTACCTTATATACAATGCACTAA			ATGCTTGACTTGTTCTACGTCACATCTATATTGAATTTCTATATATATACACCTCTGTTCATTACCTTATATACAATGCACTAA	MLDLFYVTSILNFYIYTPLFITLYTMH*			MLDLFYVTSILNFYIYTPLFITLYTMH*	TGGGGGATTA	CATATACACG	0	L	FG01896.1	0	NCU01321.1	0	0
11088	4751	af	AN3073.1	59.m08925	AO070224000013	0			-181	-146			ATGTCTTGCTTCTCGAACAAGCCCAAACAAACGTAG		ATGTCTTGCTTCTCGAACAAGCCCAAACAAACGTAG		MSCFSNKPKQT*		MSCFSNKPKQT*		AGTTTTAATT	GACGTGTACT	0	J	0	MG06566.1	NCU06866.1	0	0
11089	4751	af	AN3073.1	59.m08925	AO070224000013	0			-134	-72			ATGACCTCCGCGACCGTGATTCTGCCGTGCGGAAACAGCAGCACTCGGTCCGAGCCGAACTGA		ATGACCTCCGCGACCGTGATTCTGCCGTGCGGAAACAGCAGCACTCGGTCCGAGCCGAACTGA		MTSATVILPCGNSSTRSEPN*		MTSATVILPCGNSSTRSEPN*		ACGTGTACTG	GCGGAGAAGA	0	J	0	MG06566.1	NCU06866.1	0	0
11085	4751	an	AN3073.1	59.m08925	AO070224000013	0	-225	-145					ATGACCATATACATAATCATTAAAACCCAGGCATTGACCTCTCTTCCAATTTTATATCGCATCTCTTCGATGTCGAAATAG	ATGACCATATACATAATCATTAAAACCCAGGCATTGACCTCTCTTCCAATTTTATATCGCATCTCTTCGATGTCGAAATAG			MTIYIIIKTQALTSLPILYRISSMSK*	MTIYIIIKTQALTSLPILYRISSMSK*			CTCCTGGTCT	TGCAGTATTA	0	J	0	MG06566.1	NCU06866.1	0	0
11086	4751	an	AN3073.1	59.m08925	AO070224000013	0	-156	-145					ATGTCGAAATAG	ATGTCGAAATAG			MSK*	MSK*			CATCTCTTCG	TGCAGTATTA	0	J	0	MG06566.1	NCU06866.1	0	0
11087	4751	an	AN3073.1	59.m08925	AO070224000013	0	-125	-108					ATGATCGGTTATCGATAA	ATGATCGGTTATCGATAA			MIGYR*	MIGYR*			ATCGATAAGA	GCTTGGTTGG	0	J	0	MG06566.1	NCU06866.1	0	0
11091	4752	af	AN6817.1	65.m07380	AO070309000070	0			-186	-121			ATGCAGAATATCGGCCGTGCCGAGGCAGTTTCGCTGCAAGTTCAAGGATACTTGCGAAAAAAGTAG		ATGCAGAATATCGGCCGTGCCGAGGCAGTTTCGCTGCAAGTTCAAGGATACTTGCGAAAAAAGTAG		MQNIGRAEAVSLQVQGYLRKK*		MQNIGRAEAVSLQVQGYLRKK*		TGATAACTGA	ACAGATAACC	0	R	0	MG10413.1	0	0	0
11090	4752	an	AN6817.1	65.m07380	AO070309000070	0	-174	-160					ATGCCTGCTTACTGA	ATGCCTGCTTACTGA			MPAY*	MPAY*			TGATGTAATA	GCAGTAAGCT	0	R	0	MG10413.1	0	0	0
11092	4752	ao	AN6817.1	65.m07380	AO070309000070	0					-171	-121	ATGGAGTTAGCAGCCGAGGTTCATTCGTCGCCTTGTCTTAGCGACCGCTGA			ATGGAGTTAGCAGCCGAGGTTCATTCGTCGCCTTGTCTTAGCGACCGCTGA	MELAAEVHSSPCLSDR*			MELAAEVHSSPCLSDR*	CAATTCGGTT	GTCTTTGTCA	0	R	0	MG10413.1	0	0	0
11096	4755	af	AN1871.1	57.m05746	AO070341000188	0			-75	-31			ATGGCCGAGTTGCCTCAACCATTGCAGACTGGCGGTTCTCATTGA		ATGGCCGAGTTGCCTCAACCATTGCAGACTGGCGGTTCTCATTGA		MAELPQPLQTGGSH*		MAELPQPLQTGGSH*		CCATTAATCA	ATGTTCACGC	0		0	0	0	0	0
11093	4755	an	AN1871.1	57.m05746	AO070341000188	0	-210	-175					ATGCAGGGAGCCAATCAGCCTTCCCGCTGTGTCTGA	ATGCAGGGAGCCAATCAGCCTTCCCGCTGTGTCTGA			MQGANQPSRCV*	MQGANQPSRCV*			CGGGTTCTTG	TCATGCTTCG	0		0	0	0	0	0
11094	4755	an	AN1871.1	57.m05746	AO070341000188	0	-172	-110					ATGCTTCGTCATCTACTTTCCCAGTCGCTGGAGCTTAGACGGCAGTGTTTCATTTCCTTATAA	ATGCTTCGTCATCTACTTTCCCAGTCGCTGGAGCTTAGACGGCAGTGTTTCATTTCCTTATAA			MLRHLLSQSLELRRQCFISL*	MLRHLLSQSLELRRQCFISL*			GTGTCTGATC	AGCACTTTTT	0		0	0	0	0	0
11095	4755	an	AN1871.1	57.m05746	AO070341000188	0	-64	-20					ATGCAAACCACCAGCTTTCCTGCATTCAAAACATCTACTGGATAA	ATGCAAACCACCAGCTTTCCTGCATTCAAAACATCTACTGGATAA			MQTTSFPAFKTSTG*	MQTTSFPAFKTSTG*			GCTTACATCT	CTTCCCGCGT	0		0	0	0	0	0
11098	4755	ao	AN1871.1	57.m05746	AO070341000188	0					-94	-71	ATGGCATCGATCCAAGGTGCTTGA			ATGGCATCGATCCAAGGTGCTTGA	MASIQGA*			MASIQGA*	ACCAAGCTTC	CAGGGCATCC	0		0	0	0	0	0
11100	4756	af	AN1413.1	55.m03241	AO070242000017	0			-87	-52			ATGTATTGCCTTCTTGATTGTTTTGGACTGTATTAG		ATGTATTGCCTTCTTGATTGTTTTGGACTGTATTAG		MYCLLDCFGLY*		MYCLLDCFGLY*		TGACATTGCA	GTTGATAAAG	0	A	FG04907.1	0	0	0	0
11099	4756	an	AN1413.1	55.m03241	AO070242000017	0	-100	-74					ATGTCTCTGGCCGCACAGCACAGCTGA	ATGTCTCTGGCCGCACAGCACAGCTGA			MSLAAQHS*	MSLAAQHS*			TTCTCTGGCA	AGTGCAACGA	0	A	FG04907.1	0	0	0	0

11101	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-230	-147	ATGTCTCTAATGTCAATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA			ATGTCTCTAATGTCAATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA	MSLMSMDSTKQLPLLLRDSWNKFICST*			MSLMSMDSTKQLPLLLRDSWNKFICST*	TTGGCGTGTG	CTTAGATGCT	0	A	FG04907.1	0	0	0	0
11102	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-221	-147	ATGTCAATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA			ATGTCAATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA	MSMDSTKQLPLLLRDSWNKFICST*			MSMDSTKQLPLLLRDSWNKFICST*	GATGTCTCTA	CTTAGATGCT	0	A	FG04907.1	0	0	0	0
11103	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-215	-147	ATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA			ATGGATAGCACTAAGCAGCTTCCCTTGTTGTTGAGAGACTCTTGGAATAAATTTATTTGCAGCACATGA	MDSTKQLPLLLRDSWNKFICST*			MDSTKQLPLLLRDSWNKFICST*	TCTAATGTCA	CTTAGATGCT	0	A	FG04907.1	0	0	0	0
11104	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-141	-82	ATGCTCCCAGATTTGTTATTCTGCTTCTCCATTATTTATGCAATGGTTTTTCTTGCATAA			ATGCTCCCAGATTTGTTATTCTGCTTCTCCATTATTTATGCAATGGTTTTTCTTGCATAA	MLPDLLFCFSIIYAMVFLA*			MLPDLLFCFSIIYAMVFLA*	CATGACTTAG	AGGCAGTTGA	0	A	FG04907.1	0	0	0	0
11105	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-104	-72	ATGCAATGGTTTTTCTTGCATAAAGGCAGTTGA			ATGCAATGGTTTTTCTTGCATAAAGGCAGTTGA	MQWFFLHKGS*			MQWFFLHKGS*	TCCATTATTT	AAAGACAGAT	0	A	FG04907.1	0	0	0	0
11106	4756	ao	AN1413.1	55.m03241	AO070242000017	0					-99	-82	ATGGTTTTTCTTGCATAA			ATGGTTTTTCTTGCATAA	MVFLA*			MVFLA*	TATTTATGCA	AGGCAGTTGA	0	A	FG04907.1	0	0	0	0
11109	4758	af	AN0581.1	69.m15267	AO070280000003	0			-130	-119			ATGGAGGGCTGA		ATGGAGGGCTGA		MEG*		MEG*		CTGTATTTCA	GAACGCTTCA	0	R	0	0	0	YDR338C	0
11110	4758	af	AN0581.1	69.m15267	AO070280000003	0			-84	-49			ATGACAGCTGCTGCGTATATCAGCATCCTTCGATAG		ATGACAGCTGCTGCGTATATCAGCATCCTTCGATAG		MTAAAYISILR*		MTAAAYISILR*		GACCGGGTGG	ATTCGGCAAA	0	R	0	0	0	YDR338C	0
11107	4758	an	AN0581.1	69.m15267	AO070280000003	0	-190	-122					ATGCAAATACTGGACTATCATTTGAGCTTAAGCGACATCTTTCCTTCTCCAACTCCCCTCTGTCTTTGA	ATGCAAATACTGGACTATCATTTGAGCTTAAGCGACATCTTTCCTTCTCCAACTCCCCTCTGTCTTTGA			MQILDYHLSLSDIFPSPTPLCL*	MQILDYHLSLSDIFPSPTPLCL*			GTCGAGCGCG	CTCTTTAACT	0	R	0	0	0	YDR338C	0
11108	4758	an	AN0581.1	69.m15267	AO070280000003	0	-61	-38					ATGAGGATATCGCGACAACAGTGA	ATGAGGATATCGCGACAACAGTGA			MRISRQQ*	MRISRQQ*			CACCACCGCG	CTAACGACCT	0	R	0	0	0	YDR338C	0
11111	4758	ao	AN0581.1	69.m15267	AO070280000003	0					-275	-231	ATGGCTGAAAGCTCTTTAGAGGCAAAATCTGCTGATGGAGCGTAA			ATGGCTGAAAGCTCTTTAGAGGCAAAATCTGCTGATGGAGCGTAA	MAESSLEAKSADGA*			MAESSLEAKSADGA*	CTTTATTTCA	TATGATTACT	0	R	0	0	0	YDR338C	0
11112	4758	ao	AN0581.1	69.m15267	AO070280000003	0					-241	-215	ATGGAGCGTAATATGATTACTACCTAG			ATGGAGCGTAATATGATTACTACCTAG	MERNMITT*			MERNMITT*	AAATCTGCTG	TACCTACACC	0	R	0	0	0	YDR338C	0
11113	4758	ao	AN0581.1	69.m15267	AO070280000003	0					-229	-215	ATGATTACTACCTAG			ATGATTACTACCTAG	MITT*			MITT*	GGAGCGTAAT	TACCTACACC	0	R	0	0	0	YDR338C	0
11114	4758	ao	AN0581.1	69.m15267	AO070280000003	0					-116	-69	ATGTCTTTGGCACCATTAGATCATGGTGAGAAAGTTTCCTTAAATTAG			ATGTCTTTGGCACCATTAGATCATGGTGAGAAAGTTTCCTTAAATTAG	MSLAPLDHGEKVSLN*			MSLAPLDHGEKVSLN*	TCGAGATTGT	AATTTTCCAT	0	R	0	0	0	YDR338C	0
11115	4758	ao	AN0581.1	69.m15267	AO070280000003	0					-94	-74	ATGGTGAGAAAGTTTCCTTAA			ATGGTGAGAAAGTTTCCTTAA	MVRKFP*			MVRKFP*	CCATTAGATC	ATTAGAATTT	0	R	0	0	0	YDR338C	0
11116	4759	an	AN1050.1	70.m15207	AO070312000117	0	-147	-109					ATGCCTCGGCTTCCCCTCGGCCCCAGACTGCGAGCATAG	ATGCCTCGGCTTCCCCTCGGCCCCAGACTGCGAGCATAG			MPRLPLGPRLRA*	MPRLPLGPRLRA*			CTTTCAGAAA	TCAAGAGGCA	0	I	0	0	0	0	0
11117	4759	an	AN1050.1	70.m15207	AO070312000117	0	-91	-8					ATGTCTTCTCGTCCATCATCCTTTCTCCTCTTCATTCTCATTCACTTTCATCCCATCACTAAAAGTCAGCCTACAATTCAATAA	ATGTCTTCTCGTCCATCATCCTTTCTCCTCTTCATTCTCATTCACTTTCATCCCATCACTAAAAGTCAGCCTACAATTCAATAA			MSSRPSSFLLFILIHFHPITKSQPTIQ*	MSSRPSSFLLFILIHFHPITKSQPTIQ*			GCAACTCCTC	CTACAACATG	0	I	0	0	0	0	0
11118	4759	ao	AN1050.1	70.m15207	AO070312000117	0					-183	-142	ATGATGTGTTATTCCAATACCCTCTCACAAGTAGCGGTTTAG			ATGATGTGTTATTCCAATACCCTCTCACAAGTAGCGGTTTAG	MMCYSNTLSQVAV*			MMCYSNTLSQVAV*	TTGGTAAGTG	ACCACTGCCC	0	I	0	0	0	0	0
11119	4759	ao	AN1050.1	70.m15207	AO070312000117	0					-180	-142	ATGTGTTATTCCAATACCCTCTCACAAGTAGCGGTTTAG			ATGTGTTATTCCAATACCCTCTCACAAGTAGCGGTTTAG	MCYSNTLSQVAV*			MCYSNTLSQVAV*	GTAAGTGATG	ACCACTGCCC	0	I	0	0	0	0	0
11120	4760	af	AN1931.1	69.m14947	AO070341000104	0			-165	-73			ATGTCTGGCACGTGCGGCCGTCATCGGGCATCCACAATTGGCTGCCTCAGGCCGCACCGCATCCGCCACTTGGTGATTGTCATCCACTATTGA		ATGTCTGGCACGTGCGGCCGTCATCGGGCATCCACAATTGGCTGCCTCAGGCCGCACCGCATCCGCCACTTGGTGATTGTCATCCACTATTGA		MSGTCGRHRASTIGCLRPHRIRHLVIVIHY*		MSGTCGRHRASTIGCLRPHRIRHLVIVIHY*		TCCGTCTTGC	ATTCCCCAAA	0	T	0	0	0	0	0
11121	4760	ao	AN1931.1	69.m14947	AO070341000104	0					-195	-124	ATGCATTCAATGAACTGCACACCCGGCACGTGTCCCCCACCCAATCGGGCATCCACATTGATTGGAGCCTGA			ATGCATTCAATGAACTGCACACCCGGCACGTGTCCCCCACCCAATCGGGCATCCACATTGATTGGAGCCTGA	MHSMNCTPGTCPPPNRASTLIGA*			MHSMNCTPGTCPPPNRASTLIGA*	TGTTAATTGA	GGCTGTCCAG	0	T	0	0	0	0	0
11122	4760	ao	AN1931.1	69.m14947	AO070341000104	0					-186	-124	ATGAACTGCACACCCGGCACGTGTCCCCCACCCAATCGGGCATCCACATTGATTGGAGCCTGA			ATGAACTGCACACCCGGCACGTGTCCCCCACCCAATCGGGCATCCACATTGATTGGAGCCTGA	MNCTPGTCPPPNRASTLIGA*			MNCTPGTCPPPNRASTLIGA*	AATGCATTCA	GGCTGTCCAG	0	T	0	0	0	0	0
11123	4762	af	AN0591.1	69.m15257	AO070280000017	0			-225	-142			ATGAGGTACCTTAGTACATGGAAACTTCGTTATTCTCTGCAATTTCTCCTTGACGAACTATATGATCCTATCTCTCATCTGTGA		ATGAGGTACCTTAGTACATGGAAACTTCGTTATTCTCTGCAATTTCTCCTTGACGAACTATATGATCCTATCTCTCATCTGTGA		MRYLSTWKLRYSLQFLLDELYDPISHL*		MRYLSTWKLRYSLQFLLDELYDPISHL*		AGAGTCTCTC	CAGCGCTGAC	0	EH	0	0	0	0	0
11124	4762	af	AN0591.1	69.m15257	AO070280000017	0			-208	-173			ATGGAAACTTCGTTATTCTCTGCAATTTCTCCTTGA		ATGGAAACTTCGTTATTCTCTGCAATTTCTCCTTGA		METSLFSAISP*		METSLFSAISP*		ACCTTAGTAC	CGAACTATAT	0	EH	0	0	0	0	0
11125	4762	af	AN0591.1	69.m15257	AO070280000017	0			-164	-57			ATGATCCTATCTCTCATCTGTGACAGCGCTGACTTTGCTGATAAGTCAGTGATACAGCGACATCACATTCCGTCCCCGCTACAACGTCCACCAAAGCTGCATACCTGA		ATGATCCTATCTCTCATCTGTGACAGCGCTGACTTTGCTGATAAGTCAGTGATACAGCGACATCACATTCCGTCCCCGCTACAACGTCCACCAAAGCTGCATACCTGA		MILSLICDSADFADKSVIQRHHIPSPLQRPPKLHT*		MILSLICDSADFADKSVIQRHHIPSPLQRPPKLHT*		GACGAACTAT	TAAGTACGCG	0	EH	0	0	0	0	0
11126	4765	af	AN3802.1	57.m05972	AO070337000226	0			-127	-107			ATGATACATACAGCATCGTGA		ATGATACATACAGCATCGTGA		MIHTAS*		MIHTAS*		CCTTTATCGT	TAGAATCGGC	0		0	0	0	0	0
11128	4765	ao	AN3802.1	57.m05972	AO070337000226	0					-88	-68	ATGATTTTACCCTTTGATTGA			ATGATTTTACCCTTTGATTGA	MILPFD*			MILPFD*	GACCATCATC	AGCTTTACTC	0		0	0	0	0	0
11132	4767	af	AN1993.1	58.m07603	AO070301000084	0			-238	-155			ATGGTTATTCACATGAGTCAAAAAAATACACAACTCACCCGCTGCATCTCCGACTCGGATCTGCTACTTCTCGACTCTTATTAG		ATGGTTATTCACATGAGTCAAAAAAATACACAACTCACCCGCTGCATCTCCGACTCGGATCTGCTACTTCTCGACTCTTATTAG		MVIHMSQKNTQLTRCISDSDLLLLDSY*		MVIHMSQKNTQLTRCISDSDLLLLDSY*		GAATTTCCCT	GATTGATCTC	0	E	0	0	0	0	0
11133	4767	af	AN1993.1	58.m07603	AO070301000084	0			-226	-155			ATGAGTCAAAAAAATACACAACTCACCCGCTGCATCTCCGACTCGGATCTGCTACTTCTCGACTCTTATTAG		ATGAGTCAAAAAAATACACAACTCACCCGCTGCATCTCCGACTCGGATCTGCTACTTCTCGACTCTTATTAG		MSQKNTQLTRCISDSDLLLLDSY*		MSQKNTQLTRCISDSDLLLLDSY*		GGTTATTCAC	GATTGATCTC	0	E	0	0	0	0	0
11130	4767	an	AN1993.1	58.m07603	AO070301000084	0	-250	-227					ATGAGTGTTGGCTTTTACCCGTGA	ATGAGTGTTGGCTTTTACCCGTGA			MSVGFYP*	MSVGFYP*			CAGCGATCGG	TCGGCCCATC	0	E	0	0	0	0	0
11131	4767	an	AN1993.1	58.m07603	AO070301000084	0	-208	-149					ATGAGTCAAAGAAAACATTCACACAAACATCACGCAGCATCTCCGACTCGGCCACCCTAG	ATGAGTCAAAGAAAACATTCACACAAACATCACGCAGCATCTCCGACTCGGCCACCCTAG			MSQRKHSHKHHAASPTRPP*	MSQRKHSHKHHAASPTRPP*			TCGCTCTCAC	CTGGCTGCTG	0	E	0	0	0	0	0
11138	4768	af	AN1045.1	70.m15201	AO070336000078	0			-269	-219			ATGTTGTACATTGCTTATGCTTCGCGCGACTGGCGCAGTGTCATACTCTGA		ATGTTGTACATTGCTTATGCTTCGCGCGACTGGCGCAGTGTCATACTCTGA		MLYIAYASRDWRSVIL*		MLYIAYASRDWRSVIL*		TAAGGCTCCT	ATCTGGACTT	0	R	0	0	0	0	0
11139	4768	af	AN1045.1	70.m15201	AO070336000078	0			-253	-158			ATGCTTCGCGCGACTGGCGCAGTGTCATACTCTGAATCTGGACTTGCGGAGTTGACTCACATTCAATCGTTATCACTTACTGTTTCAATGAATTAA		ATGCTTCGCGCGACTGGCGCAGTGTCATACTCTGAATCTGGACTTGCGGAGTTGACTCACATTCAATCGTTATCACTTACTGTTTCAATGAATTAA		MLRATGAVSYSESGLAELTHIQSLSLTVSMN*		MLRATGAVSYSESGLAELTHIQSLSLTVSMN*		TACATTGCTT	ATTTCATTTT	0	R	0	0	0	0	0
11134	4768	an	AN1045.1	70.m15201	AO070336000078	0	-272	-156					ATGGTACCCGTCCTGCTGCAGCATTTTGCGCTTGAATGCAGCCTCGCTCATCGGCGCGTCGGCCGTTCGCGATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGA	ATGGTACCCGTCCTGCTGCAGCATTTTGCGCTTGAATGCAGCCTCGCTCATCGGCGCGTCGGCCGTTCGCGATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGA			MVPVLLQHFALECSLAHRRVGRSRCPSEIPCRYLSYRS*	MVPVLLQHFALECSLAHRRVGRSRCPSEIPCRYLSYRS*			AAGGATCTTG	ATCAAAACTC	0	R	0	0	0	0	0
11135	4768	an	AN1045.1	70.m15201	AO070336000078	0	-237	-127					ATGCAGCCTCGCTCATCGGCGCGTCGGCCGTTCGCGATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGAATCAAAACTCAGCCTTGCTGAAACCTTAG	ATGCAGCCTCGCTCATCGGCGCGTCGGCCGTTCGCGATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGAATCAAAACTCAGCCTTGCTGAAACCTTAG			MQPRSSARRPFAMSLRDSLSLFVLSVMNQNSALLKP*	MQPRSSARRPFAMSLRDSLSLFVLSVMNQNSALLKP*			TTGCGCTTGA	CGCGCATACT	0	R	0	0	0	0	0
11136	4768	an	AN1045.1	70.m15201	AO070336000078	0	-201	-127					ATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGAATCAAAACTCAGCCTTGCTGAAACCTTAG	ATGTCCCTCCGAGATTCCTTGTCGCTATTTGTCTTATCGGTCATGAATCAAAACTCAGCCTTGCTGAAACCTTAG			MSLRDSLSLFVLSVMNQNSALLKP*	MSLRDSLSLFVLSVMNQNSALLKP*			GCCGTTCGCG	CGCGCATACT	0	R	0	0	0	0	0
11137	4768	an	AN1045.1	70.m15201	AO070336000078	0	-159	-127					ATGAATCAAAACTCAGCCTTGCTGAAACCTTAG	ATGAATCAAAACTCAGCCTTGCTGAAACCTTAG			MNQNSALLKP*	MNQNSALLKP*			CTTATCGGTC	CGCGCATACT	0	R	0	0	0	0	0
11142	4768	ao	AN1045.1	70.m15201	AO070336000078	0					-258	-145	ATGGCTCTAGCGCGGACCTCAAGTCATTGTCCTTGTCCAAAGGAACGGATTGACTCACGTGTAGAGATGACTCCGCTTTATGCTTGTTTTATACCCTTGTCTACTCTCTCATAG			ATGGCTCTAGCGCGGACCTCAAGTCATTGTCCTTGTCCAAAGGAACGGATTGACTCACGTGTAGAGATGACTCCGCTTTATGCTTGTTTTATACCCTTGTCTACTCTCTCATAG	MALARTSSHCPCPKERIDSRVEMTPLYACFIPLSTLS*			MALARTSSHCPCPKERIDSRVEMTPLYACFIPLSTLS*	CATCCTCCGC	ACCGTATTAA	0	R	0	0	0	0	0
11143	4768	ao	AN1045.1	70.m15201	AO070336000078	0					-192	-145	ATGACTCCGCTTTATGCTTGTTTTATACCCTTGTCTACTCTCTCATAG			ATGACTCCGCTTTATGCTTGTTTTATACCCTTGTCTACTCTCTCATAG	MTPLYACFIPLSTLS*			MTPLYACFIPLSTLS*	ACGTGTAGAG	ACCGTATTAA	0	R	0	0	0	0	0
11144	4768	ao	AN1045.1	70.m15201	AO070336000078	0					-179	-135	ATGCTTGTTTTATACCCTTGTCTACTCTCTCATAGACCGTATTAA			ATGCTTGTTTTATACCCTTGTCTACTCTCTCATAGACCGTATTAA	MLVLYPCLLSHRPY*			MLVLYPCLLSHRPY*	ACTCCGCTTT	TGCTCTGCGA	0	R	0	0	0	0	0
11145	4768	ao	AN1045.1	70.m15201	AO070336000078	0					-135	-94	ATGCTCTGCGAAACGCGTGTCGACGTTTACACTAACCATTAA			ATGCTCTGCGAAACGCGTGTCGACGTTTACACTAACCATTAA	MLCETRVDVYTNH*			MLCETRVDVYTNH*	GACCGTATTA	TTGACAATTA	0	R	0	0	0	0	0
11148	4774	af	AN5591.1	58.m07515	AO070328000012	0			-145	-86			ATGATACACAAGCATCTTGACTTTGGCTTAATCATCACCTTTGTGTCCTCTACGGAATAA		ATGATACACAAGCATCTTGACTTTGGCTTAATCATCACCTTTGTGTCCTCTACGGAATAA		MIHKHLDFGLIITFVSSTE*		MIHKHLDFGLIITFVSSTE*		CTTGCTATCC	TTCGAGCGGC	0	E	0	0	0	0	0
11146	4774	an	AN5591.1	58.m07515	AO070328000012	0	-224	-204					ATGCGGTCGATGCGCGACTAG	ATGCGGTCGATGCGCGACTAG			MRSMRD*	MRSMRD*			CTACTGGGCA	AATTGAATAG	0	E	0	0	0	0	0
11147	4774	an	AN5591.1	58.m07515	AO070328000012	0	-215	-204					ATGCGCGACTAG	ATGCGCGACTAG			MRD*	MRD*			AATGCGGTCG	AATTGAATAG	0	E	0	0	0	0	0
11150	4779	af	AN1309.1	59.m09385	AO070266000049	0			-136	-35			ATGACTTTAAGGCCAAGCTGCGCTCGGACACGACTGCCGTCCAGGGTGTCTATAAAGAGCCGGGTCCCTTTTCATATTCTTTCCCAATCTTGTTCTCTGTAG		ATGACTTTAAGGCCAAGCTGCGCTCGGACACGACTGCCGTCCAGGGTGTCTATAAAGAGCCGGGTCCCTTTTCATATTCTTTCCCAATCTTGTTCTCTGTAG		MTLRPSCARTRLPSRVSIKSRVPFHILSQSCSL*		MTLRPSCARTRLPSRVSIKSRVPFHILSQSCSL*		GACGTCCTGG	GACCTCTCAA	0	UR	0	0	0	0	0
11149	4779	an	AN1309.1	59.m09385	AO070266000049	0	-250	-218					ATGGTTTGTTATTCTTTGAACGGTGATATATAG	ATGGTTTGTTATTCTTTGAACGGTGATATATAG			MVCYSLNGDI*	MVCYSLNGDI*			AGGCTGGTTG	GGTTTTCGGT	0	UR	0	0	0	0	0
11151	4779	ao	AN1309.1	59.m09385	AO070266000049	0					-192	-160	ATGACCCCATTGGCCTGGATACGGTCGACTTGA			ATGACCCCATTGGCCTGGATACGGTCGACTTGA	MTPLAWIRST*			MTPLAWIRST*	CTTGAGTCCC	TTCAGTCTTT	0	UR	0	0	0	0	0
11152	4780	ao	AN8903.1	56.m02313	AO070293000036	0					-262	-212	ATGATTATTATTATCATAATAATAATAATAAATATTATATATATTTTTTAA			ATGATTATTATTATCATAATAATAATAATAAATATTATATATATTTTTTAA	MIIIIIIIINIIYIF*			MIIIIIIIINIIYIF*	TTTTCTTTTC	TTTGAGTGAC	0	E	0	0	0	0	0
11153	4780	ao	AN8903.1	56.m02313	AO070293000036	0					-146	-126	ATGAACCACCACATGTATTAA			ATGAACCACCACATGTATTAA	MNHHMY*			MNHHMY*	CTCGTCCCAC	AAGCCCCAAG	0	E	0	0	0	0	0
11154	4781	af	AN4743.1	59.m09236	AO070327000077	0			-242	-207			ATGTCCTCTTTATCGTATACAATTGCATCGTCCTAA		ATGTCCTCTTTATCGTATACAATTGCATCGTCCTAA		MSSLSYTIASS*		MSSLSYTIASS*		ATCTTTTTTT	CTCATTTGAC	0	R	0	0	0	0	0
11155	4782	af	AN8400.1	59.m09197	AO070329000063	0			-256	-74			ATGCCTATGAGTCTGGCCGAATCTGGCCGTGACTATAAAATCCTTTATTGGCCGGAGCACTCAACTCCGTTTCGTCAAGGATGCTTTATATATCATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGAAGAATCAACGCGCGCTGAAACCGATGAAGACGAGGGGTATATAA		ATGCCTATGAGTCTGGCCGAATCTGGCCGTGACTATAAAATCCTTTATTGGCCGGAGCACTCAACTCCGTTTCGTCAAGGATGCTTTATATATCATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGAAGAATCAACGCGCGCTGAAACCGATGAAGACGAGGGGTATATAA		MPMSLAESGRDYKILYWPEHSTPFRQGCFIYHATELQRRSTVVRSLKNQRALKPMKTRGI*		MPMSLAESGRDYKILYWPEHSTPFRQGCFIYHATELQRRSTVVRSLKNQRALKPMKTRGI*		TGGTCCGGTC	GGATCACTTG	0	GEPR	0	0	0	0	0
11156	4782	af	AN8400.1	59.m09197	AO070329000063	0			-250	-74			ATGAGTCTGGCCGAATCTGGCCGTGACTATAAAATCCTTTATTGGCCGGAGCACTCAACTCCGTTTCGTCAAGGATGCTTTATATATCATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGAAGAATCAACGCGCGCTGAAACCGATGAAGACGAGGGGTATATAA		ATGAGTCTGGCCGAATCTGGCCGTGACTATAAAATCCTTTATTGGCCGGAGCACTCAACTCCGTTTCGTCAAGGATGCTTTATATATCATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGAAGAATCAACGCGCGCTGAAACCGATGAAGACGAGGGGTATATAA		MSLAESGRDYKILYWPEHSTPFRQGCFIYHATELQRRSTVVRSLKNQRALKPMKTRGI*		MSLAESGRDYKILYWPEHSTPFRQGCFIYHATELQRRSTVVRSLKNQRALKPMKTRGI*		GGTCATGCCT	GGATCACTTG	0	GEPR	0	0	0	0	0

11157	4782	af	AN8400.1	59.m09197	AO070329000063	0			-176	-153			ATGCTTTATATATCATGCTACTGA		ATGCTTTATATATCATGCTACTGA		MLYISCY*		MLYISCY*		TTCGTCAAGG	GCTTCAAAGA	0	GEPR	0	0	0	0	0
11158	4782	af	AN8400.1	59.m09197	AO070329000063	0			-162	-118			ATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGA		ATGCTACTGAGCTTCAAAGACGGAGTACAGTCGTGCGGAGTCTGA		MLLSFKDGVQSCGV*		MLLSFKDGVQSCGV*		TTTATATATC	AGAATCAACG	0	GEPR	0	0	0	0	0
11159	4782	af	AN8400.1	59.m09197	AO070329000063	0			-94	-74			ATGAAGACGAGGGGTATATAA		ATGAAGACGAGGGGTATATAA		MKTRGI*		MKTRGI*		GCTGAAACCG	GGATCACTTG	0	GEPR	0	0	0	0	0
11162	4782	ao	AN8400.1	59.m09197	AO070329000063	0					-225	-79	ATGATGTCGTCCGCCCGTTGCTCAACTCCCTTATTGGTCGGAACACTGCCCTCCGCTACCCTTATAGATGATATTCAGGCTGGAACGGAGCACTGTCGTGCGATCAGCCTCACTCACCCCTCGGAGGTCGACCGAAAACAATCGTGA			ATGATGTCGTCCGCCCGTTGCTCAACTCCCTTATTGGTCGGAACACTGCCCTCCGCTACCCTTATAGATGATATTCAGGCTGGAACGGAGCACTGTCGTGCGATCAGCCTCACTCACCCCTCGGAGGTCGACCGAAAACAATCGTGA	MMSSARCSTPLLVGTLPSATLIDDIQAGTEHCRAISLTHPSEVDRKQS*			MMSSARCSTPLLVGTLPSATLIDDIQAGTEHCRAISLTHPSEVDRKQS*	TTCGCATCTC	GAACAGATTG	0	GEPR	0	0	0	0	0
11163	4782	ao	AN8400.1	59.m09197	AO070329000063	0					-222	-79	ATGTCGTCCGCCCGTTGCTCAACTCCCTTATTGGTCGGAACACTGCCCTCCGCTACCCTTATAGATGATATTCAGGCTGGAACGGAGCACTGTCGTGCGATCAGCCTCACTCACCCCTCGGAGGTCGACCGAAAACAATCGTGA			ATGTCGTCCGCCCGTTGCTCAACTCCCTTATTGGTCGGAACACTGCCCTCCGCTACCCTTATAGATGATATTCAGGCTGGAACGGAGCACTGTCGTGCGATCAGCCTCACTCACCCCTCGGAGGTCGACCGAAAACAATCGTGA	MSSARCSTPLLVGTLPSATLIDDIQAGTEHCRAISLTHPSEVDRKQS*			MSSARCSTPLLVGTLPSATLIDDIQAGTEHCRAISLTHPSEVDRKQS*	GCATCTCATG	GAACAGATTG	0	GEPR	0	0	0	0	0
11165	4787	an	AN1697.1	58.m07773	AO070305000021	0	-187	-137					ATGTCTTGTTCCTCATTGTCATTCTCCTCCGTCGCCTCTCTCCGTCATTAA	ATGTCTTGTTCCTCATTGTCATTCTCCTCCGTCGCCTCTCTCCGTCATTAA			MSCSSLSFSSVASLRH*	MSCSSLSFSSVASLRH*			CATCCCCTGT	TTCTAGACTG	0	AR	0	0	0	0	0
11166	4790	af	AN6499.1	62.m03087	AO070222000013	0			-205	-38			ATGCCCCTCCCTCCTGCTCCACCCCCGCTCTACCTCAAGTGCTTTCTTTCACCTTCGACCGGTTGTGCTTCTTCCATCAACATTTCCCCAATCTTGCGTTGGTCCAATTCTGTCAGTTGTCCGCCTTACTCACACGCGATACAGAGAACGTTACTTTCTTGTTCTTAA		ATGCCCCTCCCTCCTGCTCCACCCCCGCTCTACCTCAAGTGCTTTCTTTCACCTTCGACCGGTTGTGCTTCTTCCATCAACATTTCCCCAATCTTGCGTTGGTCCAATTCTGTCAGTTGTCCGCCTTACTCACACGCGATACAGAGAACGTTACTTTCTTGTTCTTAA		MPLPPAPPPLYLKCFLSPSTGCASSINISPILRWSNSVSCPPYSHAIQRTLLSCS*		MPLPPAPPPLYLKCFLSPSTGCASSINISPILRWSNSVSCPPYSHAIQRTLLSCS*		TACAGCCAGC	TTGACAGCTA	0	C	0	0	0	0	0
11168	4791	af	AN5881.1	72.m19250	AO070245000027	0			-166	-86			ATGTGTTTGTTGTTTAGCAGGCGGAACGGAAAACTTGGCGTATGTTTTGTCTTGTATTGCTCCTCCAAAAGTTTGTCTTGA		ATGTGTTTGTTGTTTAGCAGGCGGAACGGAAAACTTGGCGTATGTTTTGTCTTGTATTGCTCCTCCAAAAGTTTGTCTTGA		MCLLFSRRNGKLGVCFVLYCSSKSLS*		MCLLFSRRNGKLGVCFVLYCSSKSLS*		CGGGGCCGTG	TAATCAAGTT	0		0	0	0	0	0
11169	4791	af	AN5881.1	72.m19250	AO070245000027	0			-125	-48			ATGTTTTGTCTTGTATTGCTCCTCCAAAAGTTTGTCTTGATAATCAAGTTATCTGGCCGGAGCACATGTGAAGGGTAA		ATGTTTTGTCTTGTATTGCTCCTCCAAAAGTTTGTCTTGATAATCAAGTTATCTGGCCGGAGCACATGTGAAGGGTAA		MFCLVLLLQKFVLIIKLSGRSTCEG*		MFCLVLLLQKFVLIIKLSGRSTCEG*		AACTTGGCGT	TGCAACGTCC	0		0	0	0	0	0
11167	4791	an	AN5881.1	72.m19250	AO070245000027	0	-277	-59					ATGCCACGGTCCGCCATTGCCATCCAGAACGGTTTTAGTTCCACCTGGTTCAGCTCATTCACCACTGCTAGCGCGGCTTATATAAGCCGAGCTCCCCCATCTTTTTTCGCCGTGCTGTTGTTTTGTTTAGTCTACTCCCCCAAGCTGGTTCAAGCTCAGAAGGTCGTTCTTGGCCAGTTCTCACTTAATCTGAGCTTTATACTGGCTCACGCTGTCTAA	ATGCCACGGTCCGCCATTGCCATCCAGAACGGTTTTAGTTCCACCTGGTTCAGCTCATTCACCACTGCTAGCGCGGCTTATATAAGCCGAGCTCCCCCATCTTTTTTCGCCGTGCTGTTGTTTTGTTTAGTCTACTCCCCCAAGCTGGTTCAAGCTCAGAAGGTCGTTCTTGGCCAGTTCTCACTTAATCTGAGCTTTATACTGGCTCACGCTGTCTAA			MPRSAIAIQNGFSSTWFSSFTTASAAYISRAPPSFFAVLLFCLVYSPKLVQAQKVVLGQFSLNLSFILAHAV*	MPRSAIAIQNGFSSTWFSSFTTASAAYISRAPPSFFAVLLFCLVYSPKLVQAQKVVLGQFSLNLSFILAHAV*			CGTCGAATCT	TATACTGGAA	0		0	0	0	0	0
11171	4791	ao	AN5881.1	72.m19250	AO070245000027	0					-195	-109	ATGCGCTTTTTCTCATTGTGTTGTTGGATGTTTACACAAGTGGGACGCAAAGCTTGCCCTCAGCTTGTTGTCTTTGTCTTGCCATAG			ATGCGCTTTTTCTCATTGTGTTGTTGGATGTTTACACAAGTGGGACGCAAAGCTTGCCCTCAGCTTGTTGTCTTTGTCTTGCCATAG	MRFFSLCCWMFTQVGRKACPQLVVFVLP*			MRFFSLCCWMFTQVGRKACPQLVVFVLP*	TCACAATTGT	GTAAGTCCAG	0		0	0	0	0	0
11172	4791	ao	AN5881.1	72.m19250	AO070245000027	0					-168	-109	ATGTTTACACAAGTGGGACGCAAAGCTTGCCCTCAGCTTGTTGTCTTTGTCTTGCCATAG			ATGTTTACACAAGTGGGACGCAAAGCTTGCCCTCAGCTTGTTGTCTTTGTCTTGCCATAG	MFTQVGRKACPQLVVFVLP*			MFTQVGRKACPQLVVFVLP*	GTGTTGTTGG	GTAAGTCCAG	0		0	0	0	0	0
11178	4792	af	AN0980.1	70.m15621	AO070250000038	0			-165	-91			ATGTCTGTGGCTTGGAGATTTGTGGATGGTGAAGTGGCTTGGGGGTGTGAGAACCGGCGATCTAAAAGTCTTTAA		ATGTCTGTGGCTTGGAGATTTGTGGATGGTGAAGTGGCTTGGGGGTGTGAGAACCGGCGATCTAAAAGTCTTTAA		MSVAWRFVDGEVAWGCENRRSKSL*		MSVAWRFVDGEVAWGCENRRSKSL*		CTAATCAATA	TAGCCTGTGC	0	G	0	0	0	0	0
11179	4792	af	AN0980.1	70.m15621	AO070250000038	0			-140	-63			ATGGTGAAGTGGCTTGGGGGTGTGAGAACCGGCGATCTAAAAGTCTTTAATAGCCTGTGCGTGCCATCCCGTTTGTAG		ATGGTGAAGTGGCTTGGGGGTGTGAGAACCGGCGATCTAAAAGTCTTTAATAGCCTGTGCGTGCCATCCCGTTTGTAG		MVKWLGGVRTGDLKVFNSLCVPSRL*		MVKWLGGVRTGDLKVFNSLCVPSRL*		AGATTTGTGG	GTGTTGGAAC	0	G	0	0	0	0	0
11173	4792	an	AN0980.1	70.m15621	AO070250000038	0	-247	-170					ATGCTTCATCCCAGCATGGATTTGACCACAGAAGGTAACATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA	ATGCTTCATCCCAGCATGGATTTGACCACAGAAGGTAACATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA			MLHPSMDLTTEGNMARLSTPLGLWN*	MLHPSMDLTTEGNMARLSTPLGLWN*			CCCCACATCT	CGATCGTCTT	0	G	0	0	0	0	0
11174	4792	an	AN0980.1	70.m15621	AO070250000038	0	-232	-170					ATGGATTTGACCACAGAAGGTAACATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA	ATGGATTTGACCACAGAAGGTAACATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA			MDLTTEGNMARLSTPLGLWN*	MDLTTEGNMARLSTPLGLWN*			TCATCCCAGC	CGATCGTCTT	0	G	0	0	0	0	0
11175	4792	an	AN0980.1	70.m15621	AO070250000038	0	-208	-170					ATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA	ATGGCTCGATTGTCGACTCCACTTGGCCTCTGGAACTGA			MARLSTPLGLWN*	MARLSTPLGLWN*			AGAAGGTAAC	CGATCGTCTT	0	G	0	0	0	0	0
11176	4792	an	AN0980.1	70.m15621	AO070250000038	0	-135	-109					ATGCGGAGGCTTGGTCGTAAGGTCTAA	ATGCGGAGGCTTGGTCGTAAGGTCTAA			MRRLGRKV*	MRRLGRKV*			CTACTCTAGG	GCGATGCTCA	0	G	0	0	0	0	0
11177	4792	an	AN0980.1	70.m15621	AO070250000038	0	-105	-34					ATGCTCAACCCGCTTCACCAAGTCCCAGAACATAAATTGGGCCGAGCTTCAGCCAGGTACCATGCACGGTAG	ATGCTCAACCCGCTTCACCAAGTCCCAGAACATAAATTGGGCCGAGCTTCAGCCAGGTACCATGCACGGTAG			MLNPLHQVPEHKLGRASARYHAR*	MLNPLHQVPEHKLGRASARYHAR*			GGTCTAAGCG	ACAGCCCACA	0	G	0	0	0	0	0
11180	4792	ao	AN0980.1	70.m15621	AO070250000038	0					-176	-126	ATGATGCAATGTTCTTTACTCCATCCAGGAATTGCTCCTAGTGTGGGGTAA			ATGATGCAATGTTCTTTACTCCATCCAGGAATTGCTCCTAGTGTGGGGTAA	MMQCSLLHPGIAPSVG*			MMQCSLLHPGIAPSVG*	CAGACTCACA	AAAGCACGAT	0	G	0	0	0	0	0
11181	4792	ao	AN0980.1	70.m15621	AO070250000038	0					-173	-126	ATGCAATGTTCTTTACTCCATCCAGGAATTGCTCCTAGTGTGGGGTAA			ATGCAATGTTCTTTACTCCATCCAGGAATTGCTCCTAGTGTGGGGTAA	MQCSLLHPGIAPSVG*			MQCSLLHPGIAPSVG*	ACTCACAATG	AAAGCACGAT	0	G	0	0	0	0	0
11182	4792	ao	AN0980.1	70.m15621	AO070250000038	0					-168	-136	ATGTTCTTTACTCCATCCAGGAATTGCTCCTAG			ATGTTCTTTACTCCATCCAGGAATTGCTCCTAG	MFFTPSRNCS*			MFFTPSRNCS*	CAATGATGCA	TGTGGGGTAA	0	G	0	0	0	0	0
11183	4792	ao	AN0980.1	70.m15621	AO070250000038	0					-117	-43	ATGGATTTTGGCCGGCTACTTGGCGGTCCTTCATACTACTATTTATTAGGGCATGGGTCCCCGTCCACGGCTTGA			ATGGATTTTGGCCGGCTACTTGGCGGTCCTTCATACTACTATTTATTAGGGCATGGGTCCCCGTCCACGGCTTGA	MDFGRLLGGPSYYYLLGHGSPSTA*			MDFGRLLGGPSYYYLLGHGSPSTA*	AAAAAGCACG	GATCAAGTTT	0	G	0	0	0	0	0
11190	4797	af	AN6627.1	62.m03223	AO070326000078	0			-196	-164			ATGTTGGAAATCGGACAGTTTGAGTATGAGTGA		ATGTTGGAAATCGGACAGTTTGAGTATGAGTGA		MLEIGQFEYE*		MLEIGQFEYE*		AAGAGGGGGG	TGTTGAAGTG	0	U	0	0	0	0	0
11191	4797	af	AN6627.1	62.m03223	AO070326000078	0			-171	-28			ATGAGTGATGTTGAAGTGTGTTTATACGTGGCTGGACTCGGTCTGATCGCCGGAGAGCTCTCACCTTTTCCGCCCACGGTTCCCCACCATAGTGGCCACTACACACACTTGTCCGTTCTCCAAAACCCACGCTGCTCGCACTGA		ATGAGTGATGTTGAAGTGTGTTTATACGTGGCTGGACTCGGTCTGATCGCCGGAGAGCTCTCACCTTTTCCGCCCACGGTTCCCCACCATAGTGGCCACTACACACACTTGTCCGTTCTCCAAAACCCACGCTGCTCGCACTGA		MSDVEVCLYVAGLGLIAGELSPFPPTVPHHSGHYTHLSVLQNPRCSH*		MSDVEVCLYVAGLGLIAGELSPFPPTVPHHSGHYTHLSVLQNPRCSH*		CAGTTTGAGT	ATAATATACA	0	U	0	0	0	0	0
11192	4797	af	AN6627.1	62.m03223	AO070326000078	0			-164	-126			ATGTTGAAGTGTGTTTATACGTGGCTGGACTCGGTCTGA		ATGTTGAAGTGTGTTTATACGTGGCTGGACTCGGTCTGA		MLKCVYTWLDSV*		MLKCVYTWLDSV*		AGTATGAGTG	TCGCCGGAGA	0	U	0	0	0	0	0
11193	4797	ao	AN6627.1	62.m03223	AO070326000078	0					-207	-16	ATGTCTAAGTTGCAGAATTGTGCAGAGTCGGAGGAGAGTGAAATAGTGGTCGGAGTGGGTGTTTATACGTGGCTGAACTCTTGGGAGGTGAAGGTCGAGGCTTTCCGCCCGCAGGATAATTTCCCCACAGTGCGGATCTTCTTGCCTTCTCCTACAGCCCATACCTTACACACCTCGACGCAATTTATTTAG			ATGTCTAAGTTGCAGAATTGTGCAGAGTCGGAGGAGAGTGAAATAGTGGTCGGAGTGGGTGTTTATACGTGGCTGAACTCTTGGGAGGTGAAGGTCGAGGCTTTCCGCCCGCAGGATAATTTCCCCACAGTGCGGATCTTCTTGCCTTCTCCTACAGCCCATACCTTACACACCTCGACGCAATTTATTTAG	MSKLQNCAESEESEIVVGVGVYTWLNSWEVKVEAFRPQDNFPTVRIFLPSPTAHTLHTSTQFI*			MSKLQNCAESEESEIVVGVGVYTWLNSWEVKVEAFRPQDNFPTVRIFLPSPTAHTLHTSTQFI*	TAATTAAGGA	CAAAGCTTAG	0	U	0	0	0	0	0
11194	4800	an	AN2344.1	63.m00601	AO070343000375	0	-101	-69					ATGGAGTCGTCAGGCACTTGCGGGATTGTATAA	ATGGAGTCGTCAGGCACTTGCGGGATTGTATAA			MESSGTCGIV*	MESSGTCGIV*			GGGTAGTCCT	AAGCCCTAAC	0	G	0	0	0	0	0
11195	4800	ao	AN2344.1	63.m00601	AO070343000375	0					-199	-83	ATGCAAATGTCATTGGTCGTCCCCCACAAGACAGGAACCACATCCCGTATTCACAGCTGCTTCGGCCAGCGTTTCGGCAGTTCTGGGTCTTCTGCAAGGGCACATCCTTTGCGTTGA			ATGCAAATGTCATTGGTCGTCCCCCACAAGACAGGAACCACATCCCGTATTCACAGCTGCTTCGGCCAGCGTTTCGGCAGTTCTGGGTCTTCTGCAAGGGCACATCCTTTGCGTTGA	MQMSLVVPHKTGTTSRIHSCFGQRFGSSGSSARAHPLR*			MQMSLVVPHKTGTTSRIHSCFGQRFGSSGSSARAHPLR*	GGAATCAATT	GACCACGGTA	0	G	0	0	0	0	0
11196	4800	ao	AN2344.1	63.m00601	AO070343000375	0					-193	-83	ATGTCATTGGTCGTCCCCCACAAGACAGGAACCACATCCCGTATTCACAGCTGCTTCGGCCAGCGTTTCGGCAGTTCTGGGTCTTCTGCAAGGGCACATCCTTTGCGTTGA			ATGTCATTGGTCGTCCCCCACAAGACAGGAACCACATCCCGTATTCACAGCTGCTTCGGCCAGCGTTTCGGCAGTTCTGGGTCTTCTGCAAGGGCACATCCTTTGCGTTGA	MSLVVPHKTGTTSRIHSCFGQRFGSSGSSARAHPLR*			MSLVVPHKTGTTSRIHSCFGQRFGSSGSSARAHPLR*	AATTATGCAA	GACCACGGTA	0	G	0	0	0	0	0
11197	4804	an	AN3717.1	69.m15422	AO070341000346	0	-249	-235					ATGCACACAGTGTGA	ATGCACACAGTGTGA			MHTV*	MHTV*			TGAAAAAGAC	AAAGTGGAAT	0	H	FG08923.1	0	NCU01922.1	0	0
11198	4804	ao	AN3717.1	69.m15422	AO070341000346	0					-190	-80	ATGAACCTTGTCAGAGCTTCCTTCTGGAGTGCCATTGCTCAACATAAATACGGCGTGTTTCCCTCTGTTCATTTTATTCTGTTCTTCAATCACCATCTCTCAACTCATTGA			ATGAACCTTGTCAGAGCTTCCTTCTGGAGTGCCATTGCTCAACATAAATACGGCGTGTTTCCCTCTGTTCATTTTATTCTGTTCTTCAATCACCATCTCTCAACTCATTGA	MNLVRASFWSAIAQHKYGVFPSVHFILFFNHHLSTH*			MNLVRASFWSAIAQHKYGVFPSVHFILFFNHHLSTH*	ACAAGAGGCC	ATTATATTGA	0	H	FG08923.1	0	NCU01922.1	0	0
11199	4806	ao	AN5778.1	69.m14819	AO070249000023	0					-112	-44	ATGGTTACGACGCCCCTCGGACACGATAACCAAACTGCGTCAACAACTTCAGAAGCAATCGGAATTTAA			ATGGTTACGACGCCCCTCGGACACGATAACCAAACTGCGTCAACAACTTCAGAAGCAATCGGAATTTAA	MVTTPLGHDNQTASTTSEAIGI*			MVTTPLGHDNQTASTTSEAIGI*	CGCGTCATCG	TATTGACCGA	0	Z	FG00610.1	0	0	0	0
11201	4807	af	AN4385.1	58.m08969	AO070261000030	0			-238	-206			ATGCCATTTGTTGGCGAGCGGATTTCTTTCTGA		ATGCCATTTGTTGGCGAGCGGATTTCTTTCTGA		MPFVGERISF*		MPFVGERISF*		ACTTCTCATC	CACATTCTTT	0	T	0	MG04100.1	NCU01335.1	0	0
11202	4807	af	AN4385.1	58.m08969	AO070261000030	0			-136	-77			ATGACTGATCCGGCCAACCCCTGGCTCCTGCCCTTTTTCTACCGATCATTTTCCATCTGA		ATGACTGATCCGGCCAACCCCTGGCTCCTGCCCTTTTTCTACCGATCATTTTCCATCTGA		MTDPANPWLLPFFYRSFSI*		MTDPANPWLLPFFYRSFSI*		GCGTGCTGAC	AACCACCTGG	0	T	0	MG04100.1	NCU01335.1	0	0
11200	4807	an	AN4385.1	58.m08969	AO070261000030	0	-133	-26					ATGAGTGATCCGACCGATTCCCGGCACCTGCCTTTTCCTCTTCCCACCGTGCTCAAGATTGTACATTCCAAGCCGACGTTTCAAGTCCGAATCGAGCCTTGCTCATAA	ATGAGTGATCCGACCGATTCCCGGCACCTGCCTTTTCCTCTTCCCACCGTGCTCAAGATTGTACATTCCAAGCCGACGTTTCAAGTCCGAATCGAGCCTTGCTCATAA			MSDPTDSRHLPFPLPTVLKIVHSKPTFQVRIEPCS*	MSDPTDSRHLPFPLPTVLKIVHSKPTFQVRIEPCS*			GCGTGCTGAT	GTACCATCTC	0	T	0	MG04100.1	NCU01335.1	0	0
11203	4807	ao	AN4385.1	58.m08969	AO070261000030	0					-215	-48	ATGTGCTTTATTGCTCTATTTCCAACTCTCACTAATAGTGTGTGGTCTCGAAAGACAGGTTTTGCTGCTGATATGAACAGTACTCTCCGATCGCCTGGCTCCTGCCTTCAGCCGTGCCGTTCCTCTCCTGAAACCACAAGGTCCGAGACTACCTGTCAACCTCAGTGA			ATGTGCTTTATTGCTCTATTTCCAACTCTCACTAATAGTGTGTGGTCTCGAAAGACAGGTTTTGCTGCTGATATGAACAGTACTCTCCGATCGCCTGGCTCCTGCCTTCAGCCGTGCCGTTCCTCTCCTGAAACCACAAGGTCCGAGACTACCTGTCAACCTCAGTGA	MCFIALFPTLTNSVWSRKTGFAADMNSTLRSPGSCLQPCRSSPETTRSETTCQPQ*			MCFIALFPTLTNSVWSRKTGFAADMNSTLRSPGSCLQPCRSSPETTRSETTCQPQ*	CTCCCTATTT	ATCCAGACTT	0	T	0	MG04100.1	NCU01335.1	0	0
11204	4807	ao	AN4385.1	58.m08969	AO070261000030	0					-143	-48	ATGAACAGTACTCTCCGATCGCCTGGCTCCTGCCTTCAGCCGTGCCGTTCCTCTCCTGAAACCACAAGGTCCGAGACTACCTGTCAACCTCAGTGA			ATGAACAGTACTCTCCGATCGCCTGGCTCCTGCCTTCAGCCGTGCCGTTCCTCTCCTGAAACCACAAGGTCCGAGACTACCTGTCAACCTCAGTGA	MNSTLRSPGSCLQPCRSSPETTRSETTCQPQ*			MNSTLRSPGSCLQPCRSSPETTRSETTCQPQ*	TGCTGCTGAT	ATCCAGACTT	0	T	0	MG04100.1	NCU01335.1	0	0

11205	4809	an	AN9377.1	52.m03906	AO070315000006	0	-183	-109					ATGCCCAGTGCTCCCTCTACCTATAAAGAGTGGACATTCGTTCGTTCAATTGCAAACCCTTTGATCTTCTCATAG	ATGCCCAGTGCTCCCTCTACCTATAAAGAGTGGACATTCGTTCGTTCAATTGCAAACCCTTTGATCTTCTCATAG			MPSAPSTYKEWTFVRSIANPLIFS*	MPSAPSTYKEWTFVRSIANPLIFS*			GCCGTGGGGG	TTAGCAATCC	0		0	0	0	0	0
11206	4809	ao	AN9377.1	52.m03906	AO070315000006	0					-174	-160	ATGTCCAGGACTTGA			ATGTCCAGGACTTGA	MSRT*			MSRT*	CCAAAATCCC	ACTTGATCGT	0		0	0	0	0	0
11208	4812	af	AN3733.1	69.m15382	AO070342000279	0			-234	-178			ATGAGTGACCTTTACTCCAGCCTCTCGTTCAGTTTGTTGAAGTGTTTATTCTTGTAA		ATGAGTGACCTTTACTCCAGCCTCTCGTTCAGTTTGTTGAAGTGTTTATTCTTGTAA		MSDLYSSLSFSLLKCLFL*		MSDLYSSLSFSLLKCLFL*		GAGTAGTAGA	AGTTTCTCTC	0	G	0	0	0	YLR057W	0
11209	4812	af	AN3733.1	69.m15382	AO070342000279	0			-135	-91			ATGATCACATCCTTATTCCCGTCACTCTTTTATTCCTCTTGTTGA		ATGATCACATCCTTATTCCCGTCACTCTTTTATTCCTCTTGTTGA		MITSLFPSLFYSSC*		MITSLFPSLFYSSC*		TTGGTATCTC	GGTTTTGATT	0	G	0	0	0	YLR057W	0
11207	4812	an	AN3733.1	69.m15382	AO070342000279	0	-197	-180					ATGAAAATCAGAAATTGA	ATGAAAATCAGAAATTGA			MKIRN*	MKIRN*			TCGAGATGCC	ACCCCCTTTC	0	G	0	0	0	YLR057W	0
11210	4812	ao	AN3733.1	69.m15382	AO070342000279	0					-99	-67	ATGTCGCTCTTCATCCTTCTTTTCTACCCTTAA			ATGTCGCTCTTCATCCTTCTTTTCTACCCTTAA	MSLFILLFYP*			MSLFILLFYP*	TGGATTTTTC	TTCCCCTTTT	0	G	0	0	0	YLR057W	0
11211	4816	an	AN0694.1	70.m15297	AO070343000519	0	-192	-133					ATGAGCAGCCCTAGTCCGCCTGTCAGCATGACATCACAACAAGCAAGCAAGCCTATATAG	ATGAGCAGCCCTAGTCCGCCTGTCAGCATGACATCACAACAAGCAAGCAAGCCTATATAG			MSSPSPPVSMTSQQASKPI*	MSSPSPPVSMTSQQASKPI*			TTGCTGATCC	AACCGTCCGT	0		0	0	0	0	0
11212	4816	an	AN0694.1	70.m15297	AO070343000519	0	-165	-133					ATGACATCACAACAAGCAAGCAAGCCTATATAG	ATGACATCACAACAAGCAAGCAAGCCTATATAG			MTSQQASKPI*	MTSQQASKPI*			GCCTGTCAGC	AACCGTCCGT	0		0	0	0	0	0
11213	4816	ao	AN0694.1	70.m15297	AO070343000519	0					-246	-178	ATGTACTGGACATGGTGGACTTTTACCGTCAGAATGACATCATCCAGGTCGATGATCTGGATATCATAG			ATGTACTGGACATGGTGGACTTTTACCGTCAGAATGACATCATCCAGGTCGATGATCTGGATATCATAG	MYWTWWTFTVRMTSSRSMIWIS*			MYWTWWTFTVRMTSSRSMIWIS*	GGGGGCTCGA	TTGATGCCAT	0		0	0	0	0	0
11214	4816	ao	AN0694.1	70.m15297	AO070343000519	0					-213	-178	ATGACATCATCCAGGTCGATGATCTGGATATCATAG			ATGACATCATCCAGGTCGATGATCTGGATATCATAG	MTSSRSMIWIS*			MTSSRSMIWIS*	TACCGTCAGA	TTGATGCCAT	0		0	0	0	0	0
11215	4816	ao	AN0694.1	70.m15297	AO070343000519	0					-195	-178	ATGATCTGGATATCATAG			ATGATCTGGATATCATAG	MIWIS*			MIWIS*	ATCCAGGTCG	TTGATGCCAT	0		0	0	0	0	0
11216	4816	ao	AN0694.1	70.m15297	AO070343000519	0					-164	-39	ATGCCAATGGTATATAGCATTGCTATCGCACTGCTCGGGTTGTCTACATCAGATCATTCGAAACAAATCTACGATACCACGATATTCAACGCTACAAACTACTTCAATTTCCATCAACATCTCTAG			ATGCCAATGGTATATAGCATTGCTATCGCACTGCTCGGGTTGTCTACATCAGATCATTCGAAACAAATCTACGATACCACGATATTCAACGCTACAAACTACTTCAATTTCCATCAACATCTCTAG	MPMVYSIAIALLGLSTSDHSKQIYDTTIFNATNYFNFHQHL*			MPMVYSIAIALLGLSTSDHSKQIYDTTIFNATNYFNFHQHL*	ATGCCATGAG	AACACTTGGA	0		0	0	0	0	0
11217	4816	ao	AN0694.1	70.m15297	AO070343000519	0					-158	-39	ATGGTATATAGCATTGCTATCGCACTGCTCGGGTTGTCTACATCAGATCATTCGAAACAAATCTACGATACCACGATATTCAACGCTACAAACTACTTCAATTTCCATCAACATCTCTAG			ATGGTATATAGCATTGCTATCGCACTGCTCGGGTTGTCTACATCAGATCATTCGAAACAAATCTACGATACCACGATATTCAACGCTACAAACTACTTCAATTTCCATCAACATCTCTAG	MVYSIAIALLGLSTSDHSKQIYDTTIFNATNYFNFHQHL*			MVYSIAIALLGLSTSDHSKQIYDTTIFNATNYFNFHQHL*	TGAGATGCCA	AACACTTGGA	0		0	0	0	0	0
11218	4820	af	AN4209.1	54.m07042	AO070231000015	0			-251	-234			ATGGTACTCAATAAGTGA		ATGGTACTCAATAAGTGA		MVLNK*		MVLNK*		TTGGCCCAGA	TTGTGATTGT	0	R	FG05384.1	0	0	0	0
11221	4826	af	AN1846.1	58.m07665	AO070292000059	0			-243	-64			ATGTCCTTTGCACTCTCGCACTCTACTTCCTGTCTCTGGATGTACCTTTCAATTTCTCAGCCTAGCTGTCCACCGGTGTCTATCATCTCTTCCTACTCGCCAGCCATCCATCCTCTGAAGGCAAGGGGATCGAAAACAACAATAAGCAAAGACGATTTGCCCTTTTCCAGGACTCCCTAA		ATGTCCTTTGCACTCTCGCACTCTACTTCCTGTCTCTGGATGTACCTTTCAATTTCTCAGCCTAGCTGTCCACCGGTGTCTATCATCTCTTCCTACTCGCCAGCCATCCATCCTCTGAAGGCAAGGGGATCGAAAACAACAATAAGCAAAGACGATTTGCCCTTTTCCAGGACTCCCTAA		MSFALSHSTSCLWMYLSISQPSCPPVSIISSYSPAIHPLKARGSKTTISKDDLPFSRTP*		MSFALSHSTSCLWMYLSISQPSCPPVSIISSYSPAIHPLKARGSKTTISKDDLPFSRTP*		ATCTGTCTAA	CCCCCACCCC	0		0	0	0	0	0
11222	4826	af	AN1846.1	58.m07665	AO070292000059	0			-204	-64			ATGTACCTTTCAATTTCTCAGCCTAGCTGTCCACCGGTGTCTATCATCTCTTCCTACTCGCCAGCCATCCATCCTCTGAAGGCAAGGGGATCGAAAACAACAATAAGCAAAGACGATTTGCCCTTTTCCAGGACTCCCTAA		ATGTACCTTTCAATTTCTCAGCCTAGCTGTCCACCGGTGTCTATCATCTCTTCCTACTCGCCAGCCATCCATCCTCTGAAGGCAAGGGGATCGAAAACAACAATAAGCAAAGACGATTTGCCCTTTTCCAGGACTCCCTAA		MYLSISQPSCPPVSIISSYSPAIHPLKARGSKTTISKDDLPFSRTP*		MYLSISQPSCPPVSIISSYSPAIHPLKARGSKTTISKDDLPFSRTP*		CTGTCTCTGG	CCCCCACCCC	0		0	0	0	0	0
11220	4826	an	AN1846.1	58.m07665	AO070292000059	0	-121	-95					ATGCAGCCTTTAACTCAGGCGGCTTGA	ATGCAGCCTTTAACTCAGGCGGCTTGA			MQPLTQAA*	MQPLTQAA*			AACACTTCAG	CTTGAGTGCA	0		0	0	0	0	0
11223	4826	ao	AN1846.1	58.m07665	AO070292000059	0					-145	-113	ATGTATCGTCCATCTTCGCAGCCCGGCTGTTAG			ATGTATCGTCCATCTTCGCAGCCCGGCTGTTAG	MYRPSSQPGC*			MYRPSSQPGC*	ACCTCTTCAG	CCAGTCTGAG	0		0	0	0	0	0
11228	4827	af	AN9481.1	71.m15629	AO070276000025	0			-243	-208			ATGATAAAGACCCTGACACTCCTCGGGCTCATTTAA		ATGATAAAGACCCTGACACTCCTCGGGCTCATTTAA		MIKTLTLLGLI*		MIKTLTLLGLI*		TATTTCCTAG	GTGTCAAAAT	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11229	4827	af	AN9481.1	71.m15629	AO070276000025	0			-132	-100			ATGGCCCTAGCTCCCGCCCGCCCCTCCAGATAG		ATGGCCCTAGCTCCCGCCCGCCCCTCCAGATAG		MALAPARPSR*		MALAPARPSR*		GCTCTCCGCT	CAATCCCCGA	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11224	4827	an	AN9481.1	71.m15629	AO070276000025	0	-236	-195					ATGATGATACGGCCAAACATTACCCGTTCAAAATTTTCGTGA	ATGATGATACGGCCAAACATTACCCGTTCAAAATTTTCGTGA			MMIRPNITRSKFS*	MMIRPNITRSKFS*			TTATGCTAAT	GCAAGTCTCA	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11225	4827	an	AN9481.1	71.m15629	AO070276000025	0	-233	-195					ATGATACGGCCAAACATTACCCGTTCAAAATTTTCGTGA	ATGATACGGCCAAACATTACCCGTTCAAAATTTTCGTGA			MIRPNITRSKFS*	MIRPNITRSKFS*			TGCTAATATG	GCAAGTCTCA	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11226	4827	an	AN9481.1	71.m15629	AO070276000025	0	-140	-120					ATGTCTTATGTCCCTAGGTAG	ATGTCTTATGTCCCTAGGTAG			MSYVPR*	MSYVPR*			CATTTGCACT	GGAGTACTTA	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11227	4827	an	AN9481.1	71.m15629	AO070276000025	0	-133	-35					ATGTCCCTAGGTAGGGAGTACTTAGTCTGCGTGGTTCCGCTCCCCGCCAGTCTCCGCCGTCAAGCTTCGCTGCACCTCAACTTTGAATCCCAGCTTTGA	ATGTCCCTAGGTAGGGAGTACTTAGTCTGCGTGGTTCCGCTCCCCGCCAGTCTCCGCCGTCAAGCTTCGCTGCACCTCAACTTTGAATCCCAGCTTTGA			MSLGREYLVCVVPLPASLRRQASLHLNFESQL*	MSLGREYLVCVVPLPASLRRQASLHLNFESQL*			ACTATGTCTT	CAATTGTCTT	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11230	4827	ao	AN9481.1	71.m15629	AO070276000025	0					-246	-220	ATGACCCTCACTCTCCCTATGCTATAA			ATGACCCTCACTCTCCCTATGCTATAA	MTLTLPML*			MTLTLPML*	TTAATACGTT	ACTAACCCAT	0	P	FG05981.1	MG07326.1	NCU03588.1	0	0
11231	4829	an	AN1917.1	69.m14935	AO070341000123	0	-93	-55					ATGGTTAAGCTCATTCCTCACTGCCAATGCCGCTGCTGA	ATGGTTAAGCTCATTCCTCACTGCCAATGCCGCTGCTGA			MVKLIPHCQCRC*	MVKLIPHCQCRC*			CGGTCAGTTC	ACGAAACCGA	0	C	0	0	0	0	0
11232	4829	an	AN1917.1	69.m14935	AO070341000123	0	-67	-41					ATGCCGCTGCTGAACGAAACCGACTAA	ATGCCGCTGCTGAACGAAACCGACTAA			MPLLNETD*	MPLLNETD*			CTCACTGCCA	TTACCCATAG	0	C	0	0	0	0	0
11233	4829	ao	AN1917.1	69.m14935	AO070341000123	0					-116	-6	ATGGTCACACATGCTCTGCTCTCATTGCTATTACCGTCATCTGCTCAAATTTGCGCCCGGCACTGCGACGGTGTGCTGACTTTCCAGGCTTATTGTAATTCCTGTTTGTGA			ATGGTCACACATGCTCTGCTCTCATTGCTATTACCGTCATCTGCTCAAATTTGCGCCCGGCACTGCGACGGTGTGCTGACTTTCCAGGCTTATTGTAATTCCTGTTTGTGA	MVTHALLSLLLPSSAQICARHCDGVLTFQAYCNSCL*			MVTHALLSLLLPSSAQICARHCDGVLTFQAYCNSCL*	CGGTTAGTGG	TCAAAATGGC	0	C	0	0	0	0	0
11234	4829	ao	AN1917.1	69.m14935	AO070341000123	0					-106	-38	ATGCTCTGCTCTCATTGCTATTACCGTCATCTGCTCAAATTTGCGCCCGGCACTGCGACGGTGTGCTGA			ATGCTCTGCTCTCATTGCTATTACCGTCATCTGCTCAAATTTGCGCCCGGCACTGCGACGGTGTGCTGA	MLCSHCYYRHLLKFAPGTATVC*			MLCSHCYYRHLLKFAPGTATVC*	ATGGTCACAC	CTTTCCAGGC	0	C	0	0	0	0	0
11243	4838	ao	AN1426.1	55.m03264	AO070242000026	0					-267	-166	ATGTTTGTACATTGCATTCAAGGCCGCCTAATGGCTGCATACAGGCCGCCCCCCCTCCCACTATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGA			ATGTTTGTACATTGCATTCAAGGCCGCCTAATGGCTGCATACAGGCCGCCCCCCCTCCCACTATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGA	MFVHCIQGRLMAAYRPPPLPLCGPLVNARSLLP*			MFVHCIQGRLMAAYRPPPLPLCGPLVNARSLLP*	CGCAATCCAA	CGTATAAAAG	0	OE	FG08454.1	MG02309.1	0	0	0
11244	4838	ao	AN1426.1	55.m03264	AO070242000026	0					-237	-166	ATGGCTGCATACAGGCCGCCCCCCCTCCCACTATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGA			ATGGCTGCATACAGGCCGCCCCCCCTCCCACTATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGA	MAAYRPPPLPLCGPLVNARSLLP*			MAAYRPPPLPLCGPLVNARSLLP*	AGGCCGCCTA	CGTATAAAAG	0	OE	FG08454.1	MG02309.1	0	0	0
11245	4838	ao	AN1426.1	55.m03264	AO070242000026	0					-205	-137	ATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGACGTATAAAAGTCAGAGGATATTCCTCTGA			ATGTGGGCCACTTGTCAATGCTCGAAGTCTGCTACCTTGACGTATAAAAGTCAGAGGATATTCCTCTGA	MWATCQCSKSATLTYKSQRIFL*			MWATCQCSKSATLTYKSQRIFL*	CCCTCCCACT	TCGCTGACCT	0	OE	FG08454.1	MG02309.1	0	0	0
11246	4838	ao	AN1426.1	55.m03264	AO070242000026	0					-188	-159	ATGCTCGAAGTCTGCTACCTTGACGTATAA			ATGCTCGAAGTCTGCTACCTTGACGTATAA	MLEVCYLDV*			MLEVCYLDV*	CCACTTGTCA	AAGTCAGAGG	0	OE	FG08454.1	MG02309.1	0	0	0
11252	4841	an	AN0685.1	70.m15287	AO070343000533	0	-218	-180					ATGGTCTTGTGCATATCCCTCACATTTTACGATACCTGA	ATGGTCTTGTGCATATCCCTCACATTTTACGATACCTGA			MVLCISLTFYDT*	MVLCISLTFYDT*			TTAGCAGTCA	TCAGCCCAAT	0		0	0	0	0	0
11253	4841	ao	AN0685.1	70.m15287	AO070343000533	0					-195	-73	ATGAAAATAAAATATTTCAAAATCTCTTCCATTGTCCCAAAGAGTCTGTCGCAACTCTCCTCTCTCCATTTATATAAATCCTTATCGGTGCCCCACACTCGAACCCAAAAAAATAAAATATAA			ATGAAAATAAAATATTTCAAAATCTCTTCCATTGTCCCAAAGAGTCTGTCGCAACTCTCCTCTCTCCATTTATATAAATCCTTATCGGTGCCCCACACTCGAACCCAAAAAAATAAAATATAA	MKIKYFKISSIVPKSLSQLSSLHLYKSLSVPHTRTQKNKI*			MKIKYFKISSIVPKSLSQLSSLHLYKSLSVPHTRTQKNKI*	ATTTTCAGAA	TTCTTCAACA	0		0	0	0	0	0
11256	4844	af	AN1859.1	58.m07653	AO070292000036	0			-244	-200			ATGTGCCTCATGAGTTCCTTAATAAAATTGCTGCAGCTAAGCTAA		ATGTGCCTCATGAGTTCCTTAATAAAATTGCTGCAGCTAAGCTAA		MCLMSSLIKLLQLS*		MCLMSSLIKLLQLS*		CGTCCTTTAT	ATCTACGGAA	0	K	0	0	0	0	0
11257	4844	af	AN1859.1	58.m07653	AO070292000036	0			-235	-200			ATGAGTTCCTTAATAAAATTGCTGCAGCTAAGCTAA		ATGAGTTCCTTAATAAAATTGCTGCAGCTAAGCTAA		MSSLIKLLQLS*		MSSLIKLLQLS*		TATGTGCCTC	ATCTACGGAA	0	K	0	0	0	0	0
11254	4844	an	AN1859.1	58.m07653	AO070292000036	0	-261	-247					ATGAAGTCGGTATGA	ATGAAGTCGGTATGA			MKSV*	MKSV*			GCGCATTCTC	GGCGGAACCC	0	K	0	0	0	0	0
11255	4844	an	AN1859.1	58.m07653	AO070292000036	0	-250	-74					ATGAGGCGGAACCCACTGCGGAAGAAGCTCTGCCGGAGCTCAATCGCACCACCACTTCCAGGCTGCCTTATCAGGTCCTTATCACTACTGTCACGTGCTTTACTCTTGCCCGTTGAAAAAGAACGCGCTCGGCCAGCTTTGTCGCCTTCAACTTTGCGTCATCCAAATTTGCTTTAA	ATGAGGCGGAACCCACTGCGGAAGAAGCTCTGCCGGAGCTCAATCGCACCACCACTTCCAGGCTGCCTTATCAGGTCCTTATCACTACTGTCACGTGCTTTACTCTTGCCCGTTGAAAAAGAACGCGCTCGGCCAGCTTTGTCGCCTTCAACTTTGCGTCATCCAAATTTGCTTTAA			MRRNPLRKKLCRSSIAPPLPGCLIRSLSLLSRALLLPVEKERARPALSPSTLRHPNLL*	MRRNPLRKKLCRSSIAPPLPGCLIRSLSLLSRALLLPVEKERARPALSPSTLRHPNLL*			TGAAGTCGGT	AATCCACGTA	0	K	0	0	0	0	0
11258	4844	ao	AN1859.1	58.m07653	AO070292000036	0					-178	-104	ATGCTTCCCGCCGCGTTGTCACGTGCCACTGGCAATTCCCGCGGTGATTTCGCGACAAGACTAGATAAGATCTAG			ATGCTTCCCGCCGCGTTGTCACGTGCCACTGGCAATTCCCGCGGTGATTTCGCGACAAGACTAGATAAGATCTAG	MLPAALSRATGNSRGDFATRLDKI*			MLPAALSRATGNSRGDFATRLDKI*	CCCCATCGTC	GCACTCAAGC	0	K	0	0	0	0	0
11259	4845	an	AN1830.1	52.m03901	AO070292000077	0	-173	-3					ATGACCCGCAATCCCCGGTGGCCAGCGCCACGCCGTCAACCCACCTCCCCGCAGGCTACCCCAAGTTGGACGGTTAGGAAGCCGAGCTTTTGCCGGGTCCGTATATATAGCCTGTCCGTCGGTGCCGGAAGCACCCATTCTTTGTGCAGTCTGTACTTGTATGCTTGTTGA	ATGACCCGCAATCCCCGGTGGCCAGCGCCACGCCGTCAACCCACCTCCCCGCAGGCTACCCCAAGTTGGACGGTTAGGAAGCCGAGCTTTTGCCGGGTCCGTATATATAGCCTGTCCGTCGGTGCCGGAAGCACCCATTCTTTGTGCAGTCTGTACTTGTATGCTTGTTGA			MTRNPRWPAPRRQPTSPQATPSWTVRKPSFCRVRIYSLSVGAGSTHSLCSLYLYAC*	MTRNPRWPAPRRQPTSPQATPSWTVRKPSFCRVRIYSLSVGAGSTHSLCSLYLYAC*			AAGCCCCCAG	AAATGCCTTT	0	R	0	0	0	0	0
11260	4845	ao	AN1830.1	52.m03901	AO070292000077	0					-66	-40	ATGAACTTGGATGTTTCTCCGCGGTAA			ATGAACTTGGATGTTTCTCCGCGGTAA	MNLDVSPR*			MNLDVSPR*	AAGTAGTCCC	ACACGTAAGT	0	R	0	0	0	0	0
11262	4847	an	AN4691.1	71.m15674	AO070284000047	0	-201	-181					ATGCTAGTTCGTGTATCGTGA	ATGCTAGTTCGTGTATCGTGA			MLVRVS*	MLVRVS*			ACTGCTTTGC	CCTGGCTCCT	0	IQR	0	MG02544.1	0	0	0
11273	4850	af	AN7469.1	57.m05953	AO070287000057	0			-219	-112			ATGTTCCCCCACGTTGTTCGCCGGGTCCTTGGAGCAATACGAGCATCTTCCGCCATGTTTTTCGACCAGTTTCCATCAGTCATACACAAGAGTTCTAACCCGTCGTGA		ATGTTCCCCCACGTTGTTCGCCGGGTCCTTGGAGCAATACGAGCATCTTCCGCCATGTTTTTCGACCAGTTTCCATCAGTCATACACAAGAGTTCTAACCCGTCGTGA		MFPHVVRRVLGAIRASSAMFFDQFPSVIHKSSNPS*		MFPHVVRRVLGAIRASSAMFFDQFPSVIHKSSNPS*		ACCGTCACAA	CTCCGCTTCT	0	H	0	0	0	0	0
11274	4850	af	AN7469.1	57.m05953	AO070287000057	0			-165	-112			ATGTTTTTCGACCAGTTTCCATCAGTCATACACAAGAGTTCTAACCCGTCGTGA		ATGTTTTTCGACCAGTTTCCATCAGTCATACACAAGAGTTCTAACCCGTCGTGA		MFFDQFPSVIHKSSNPS*		MFFDQFPSVIHKSSNPS*		ATCTTCCGCC	CTCCGCTTCT	0	H	0	0	0	0	0

11275	4850	ao	AN7469.1	57.m05953	AO070287000057	0					-156	-22	ATGCATTCATTCCGTCATGGCCGATACCCCCGCATCGCCCGCCTTATCGATACCGCGGCCTTCTTCCACATTCCACCATTTTGCTCACTTTCAATTGCTGCTCATCGCCAGACAAACGCTGGATTTAGTCCATAG			ATGCATTCATTCCGTCATGGCCGATACCCCCGCATCGCCCGCCTTATCGATACCGCGGCCTTCTTCCACATTCCACCATTTTGCTCACTTTCAATTGCTGCTCATCGCCAGACAAACGCTGGATTTAGTCCATAG	MHSFRHGRYPRIARLIDTAAFFHIPPFCSLSIAAHRQTNAGFSP*			MHSFRHGRYPRIARLIDTAAFFHIPPFCSLSIAAHRQTNAGFSP*	ACCAATCAAC	ATTTGTTATA	0	H	0	0	0	0	0
11280	4851	af	AN6898.1	71.m16034	AO070314000023	0			-276	-205			ATGGTTCCACTGGGAAATTTCATGACAGCAGGCGTTGGACTAGACCCAAAAGGGGCTGGCAGCAGCATGTGA		ATGGTTCCACTGGGAAATTTCATGACAGCAGGCGTTGGACTAGACCCAAAAGGGGCTGGCAGCAGCATGTGA		MVPLGNFMTAGVGLDPKGAGSSM*		MVPLGNFMTAGVGLDPKGAGSSM*		GGTTATGGCG	CTCCCGCAGT	0	U	0	MG05208.1	0	YKL002W	YKL002W
11281	4851	af	AN6898.1	71.m16034	AO070314000023	0			-133	-59			ATGTCACCGCATCACATTCACCGCAGGCTTCTATCTGATAAACATACTGCTGCGCATAAAAATTGCCGTCTGTGA		ATGTCACCGCATCACATTCACCGCAGGCTTCTATCTGATAAACATACTGCTGCGCATAAAAATTGCCGTCTGTGA		MSPHHIHRRLLSDKHTAAHKNCRL*		MSPHHIHRRLLSDKHTAAHKNCRL*		AGGTGGGTTG	GAAGCACGTT	0	U	0	MG05208.1	0	YKL002W	YKL002W
11277	4851	an	AN6898.1	71.m16034	AO070314000023	0	-161	-129					ATGGTATGGTGGCTGCCATGTGACCCCCCGTAA	ATGGTATGGTGGCTGCCATGTGACCCCCCGTAA			MVWWLPCDPP*	MVWWLPCDPP*			ATGTCTCAAA	AGCCGGCCGT	0	U	0	MG05208.1	0	YKL002W	YKL002W
11278	4851	an	AN6898.1	71.m16034	AO070314000023	0	-156	-139					ATGGTGGCTGCCATGTGA	ATGGTGGCTGCCATGTGA			MVAAM*	MVAAM*			TCAAAATGGT	CCCCCCGTAA	0	U	0	MG05208.1	0	YKL002W	YKL002W
11279	4851	an	AN6898.1	71.m16034	AO070314000023	0	-103	-89					ATGTCTGGAGCCTGA	ATGTCTGGAGCCTGA			MSGA*	MSGA*			CGTTACATAC	TGTCACCGCA	0	U	0	MG05208.1	0	YKL002W	YKL002W
11282	4851	ao	AN6898.1	71.m16034	AO070314000023	0					-135	-10	ATGTCACCGCGCGGCTTCGGATCGAATCAGATATTCCCCTCTCCAATCTTGCCCCCTTCATTTGTACCTTTCACGCAGCCTCTTTGGTTTTGTTTCTCATTGTTTGTTACTGGGCATCTTTCTTGA			ATGTCACCGCGCGGCTTCGGATCGAATCAGATATTCCCCTCTCCAATCTTGCCCCCTTCATTTGTACCTTTCACGCAGCCTCTTTGGTTTTGTTTCTCATTGTTTGTTACTGGGCATCTTTCTTGA	MSPRGFGSNQIFPSPILPPSFVPFTQPLWFCFSLFVTGHLS*			MSPRGFGSNQIFPSPILPPSFVPFTQPLWFCFSLFVTGHLS*	CTTAGGTTTG	CTGGCCAAGA	0	U	0	MG05208.1	0	YKL002W	YKL002W
11276	4851	conserved	AN6898.1	71.m16034	AO070314000023	0	-171	-139	-255	-205	-237	-205	ATGwChsmArrbGkkdkrsTvGmysCmAwrkGrGCTGGCAGCAGCATGTGA	ATGTCTCAAAATGGTATGGTGGCTGCCATGTGA	ATGACAGCAGGCGTTGGACTAGACCCAAAAGGGGCTGGCAGCAGCATGTGA	ATGTCCCAAAAGGGGTTGGTCGCCGCCATGTGA	Msqngmvaam*	MSQNGMVAAM*	MTAGVGLDPKGAGSSM*	MSQKGLVAAM*	kGGAAAwwyy	CysyCsshvh	0	U	0	MG05208.1	0	YKL002W	YKL002W
11285	4852	af	AN2860.1	59.m08704	AO070338000162	0			-173	-57			ATGGTGCGTTCAGGACGCTGCGTGCCAGACTTAAAAAGATGGGCGGTGGTCCCTGGCTTGGAGGGGCTGCTTTTCTCTCCTTTCCTCTCTATCCTCGTATCTGTCCTTGACTCTTGA		ATGGTGCGTTCAGGACGCTGCGTGCCAGACTTAAAAAGATGGGCGGTGGTCCCTGGCTTGGAGGGGCTGCTTTTCTCTCCTTTCCTCTCTATCCTCGTATCTGTCCTTGACTCTTGA		MVRSGRCVPDLKRWAVVPGLEGLLFSPFLSILVSVLDS*		MVRSGRCVPDLKRWAVVPGLEGLLFSPFLSILVSVLDS*		ACCAAGTGGG	CTGTCACACA	0	Q	0	0	0	0	0
11286	4852	af	AN2860.1	59.m08704	AO070338000162	0			-135	-64			ATGGGCGGTGGTCCCTGGCTTGGAGGGGCTGCTTTTCTCTCCTTTCCTCTCTATCCTCGTATCTGTCCTTGA		ATGGGCGGTGGTCCCTGGCTTGGAGGGGCTGCTTTTCTCTCCTTTCCTCTCTATCCTCGTATCTGTCCTTGA		MGGGPWLGGAAFLSFPLYPRICP*		MGGGPWLGGAAFLSFPLYPRICP*		ACTTAAAAAG	CTCTTGACTG	0	Q	0	0	0	0	0
11283	4852	an	AN2860.1	59.m08704	AO070338000162	0	-183	-169					ATGTCACGATGGTAA	ATGTCACGATGGTAA			MSRW*	MSRW*			GTCCTGGATA	CGAGGTGTCA	0	Q	0	0	0	0	0
11284	4852	an	AN2860.1	59.m08704	AO070338000162	0	-175	-131					ATGGTAACGAGGTGTCATTCATTGCACCCCCACTCGCAGGCCTGA	ATGGTAACGAGGTGTCATTCATTGCACCCCCACTCGCAGGCCTGA			MVTRCHSLHPHSQA*	MVTRCHSLHPHSQA*			TAATGTCACG	AAGTGTGTTT	0	Q	0	0	0	0	0
11287	4852	ao	AN2860.1	59.m08704	AO070338000162	0					-176	-156	ATGGCTCCGCAGCCCTGTTAG			ATGGCTCCGCAGCCCTGTTAG	MAPQPC*			MAPQPC*	CCGTAATTGC	TTTGTTGGCG	0	Q	0	0	0	0	0
11291	4858	af	AN5445.1	69.m15489	AO070333000112	0			-243	-193			ATGGAGTTTGCCTCTCCTGCCCTAGTCCAGCCTCATATAATCAAACGATGA		ATGGAGTTTGCCTCTCCTGCCCTAGTCCAGCCTCATATAATCAAACGATGA		MEFASPALVQPHIIKR*		MEFASPALVQPHIIKR*		CTTCTCCTTC	ACCAAGGCTC	0		0	0	0	0	0
11292	4858	af	AN5445.1	69.m15489	AO070333000112	0			-196	-104			ATGAACCAAGGCTCTCTTACTACAGTCGATCGTAGTTTGTGCTTGCACACCCTCCCCCGCATCCGTGCCCTCACCGGGTCTGGTCTGCATTGA		ATGAACCAAGGCTCTCTTACTACAGTCGATCGTAGTTTGTGCTTGCACACCCTCCCCCGCATCCGTGCCCTCACCGGGTCTGGTCTGCATTGA		MNQGSLTTVDRSLCLHTLPRIRALTGSGLH*		MNQGSLTTVDRSLCLHTLPRIRALTGSGLH*		TAATCAAACG	GGCGCTATAG	0		0	0	0	0	0
11289	4858	an	AN5445.1	69.m15489	AO070333000112	0	-203	-60					ATGTCCTCTGCGAACGATGGTACTAAGGTCATCTCGGATCCTCGATTGTCGTCTGTGCTCGCACATCGTCCGTCCCAATCCCCTTGCTGGGAGGGTCTCCGCCGCTGTGACGTACAGCTCAACGAGGACGCTCCTCCACTCTGA	ATGTCCTCTGCGAACGATGGTACTAAGGTCATCTCGGATCCTCGATTGTCGTCTGTGCTCGCACATCGTCCGTCCCAATCCCCTTGCTGGGAGGGTCTCCGCCGCTGTGACGTACAGCTCAACGAGGACGCTCCTCCACTCTGA			MSSANDGTKVISDPRLSSVLAHRPSQSPCWEGLRRCDVQLNEDAPPL*	MSSANDGTKVISDPRLSSVLAHRPSQSPCWEGLRRCDVQLNEDAPPL*			CACTGGGTCC	ACCGAATTGC	0		0	0	0	0	0
11290	4858	an	AN5445.1	69.m15489	AO070333000112	0	-187	-47					ATGGTACTAAGGTCATCTCGGATCCTCGATTGTCGTCTGTGCTCGCACATCGTCCGTCCCAATCCCCTTGCTGGGAGGGTCTCCGCCGCTGTGACGTACAGCTCAACGAGGACGCTCCTCCACTCTGAACCGAATTGCTGA	ATGGTACTAAGGTCATCTCGGATCCTCGATTGTCGTCTGTGCTCGCACATCGTCCGTCCCAATCCCCTTGCTGGGAGGGTCTCCGCCGCTGTGACGTACAGCTCAACGAGGACGCTCCTCCACTCTGAACCGAATTGCTGA			MVLRSSRILDCRLCSHIVRPNPLAGRVSAAVTYSSTRTLLHSEPNC*	MVLRSSRILDCRLCSHIVRPNPLAGRVSAAVTYSSTRTLLHSEPNC*			TCTGCGAACG	ACCATCCCTG	0		0	0	0	0	0
11293	4858	ao	AN5445.1	69.m15489	AO070333000112	0					-213	-112	ATGCAAACGATGATATCACAGTCTCTCCGTAATTACGACTGTCGCTTGTGCCTGCACGCTCTCCCTCGCGTCCATTCCCTTCTCGGGAACGGTCTGCTGTGA			ATGCAAACGATGATATCACAGTCTCTCCGTAATTACGACTGTCGCTTGTGCCTGCACGCTCTCCCTCGCGTCCATTCCCTTCTCGGGAACGGTCTGCTGTGA	MQTMISQSLRNYDCRLCLHALPRVHSLLGNGLL*			MQTMISQSLRNYDCRLCLHALPRVHSLLGNGLL*	ATACCCGTCC	GTTGCTGACT	0		0	0	0	0	0
11294	4858	ao	AN5445.1	69.m15489	AO070333000112	0					-204	-112	ATGATATCACAGTCTCTCCGTAATTACGACTGTCGCTTGTGCCTGCACGCTCTCCCTCGCGTCCATTCCCTTCTCGGGAACGGTCTGCTGTGA			ATGATATCACAGTCTCTCCGTAATTACGACTGTCGCTTGTGCCTGCACGCTCTCCCTCGCGTCCATTCCCTTCTCGGGAACGGTCTGCTGTGA	MISQSLRNYDCRLCLHALPRVHSLLGNGLL*			MISQSLRNYDCRLCLHALPRVHSLLGNGLL*	CATGCAAACG	GTTGCTGACT	0		0	0	0	0	0
11296	4861	an	AN3914.1	69.m15015	AO070324000101	0	-255	-67					ATGACTGCCCTTTCACATTTGGATGTCTCTGGTCGTTCGACCTGCACCTTCCTTGATAGACCGGACGCCGAAGCTGCTGCATTGAGGACCACGACATCCCAGCAACAACAACAACCGTCAAATCTCGACAAACCTCCATATCCTTGTGTTTTCTTACCGTCGCAACTCTCGCTTTTTATTCTTGACTGA	ATGACTGCCCTTTCACATTTGGATGTCTCTGGTCGTTCGACCTGCACCTTCCTTGATAGACCGGACGCCGAAGCTGCTGCATTGAGGACCACGACATCCCAGCAACAACAACAACCGTCAAATCTCGACAAACCTCCATATCCTTGTGTTTTCTTACCGTCGCAACTCTCGCTTTTTATTCTTGACTGA			MTALSHLDVSGRSTCTFLDRPDAEAAALRTTTSQQQQQPSNLDKPPYPCVFLPSQLSLFILD*	MTALSHLDVSGRSTCTFLDRPDAEAAALRTTTSQQQQQPSNLDKPPYPCVFLPSQLSLFILD*			ACTAGAAATG	CAAATTGTAC	0	G	0	0	0	0	0
11297	4861	an	AN3914.1	69.m15015	AO070324000101	0	-233	-171					ATGTCTCTGGTCGTTCGACCTGCACCTTCCTTGATAGACCGGACGCCGAAGCTGCTGCATTGA	ATGTCTCTGGTCGTTCGACCTGCACCTTCCTTGATAGACCGGACGCCGAAGCTGCTGCATTGA			MSLVVRPAPSLIDRTPKLLH*	MSLVVRPAPSLIDRTPKLLH*			TCACATTTGG	GGACCACGAC	0	G	0	0	0	0	0
11299	4862	af	AN9361.1	71.m15139	AO070333000266	0			-203	-159			ATGCCTAGAACAAAGCAATTAAGCTCCTGTTATGAAACCTTTTGA		ATGCCTAGAACAAAGCAATTAAGCTCCTGTTATGAAACCTTTTGA		MPRTKQLSSCYETF*		MPRTKQLSSCYETF*		CTCTTCAGTA	GTCCAGACTT	0	M	0	0	0	0	0
11300	4862	af	AN9361.1	71.m15139	AO070333000266	0			-105	-91			ATGGGGGGGGGTTGA		ATGGGGGGGGGTTGA		MGGG*		MGGG*		CTGAATCAAT	GCTTGCTCCA	0	M	0	0	0	0	0
11298	4862	an	AN9361.1	71.m15139	AO070333000266	0	-161	-120					ATGCTGGTATCTTTACCTTTTCGCCCTACGGGGATGGTATAA	ATGCTGGTATCTTTACCTTTTCGCCCTACGGGGATGGTATAA			MLVSLPFRPTGMV*	MLVSLPFRPTGMV*			ACCGTGCAAT	TAGCGTCATC	0	M	0	0	0	0	0
11301	4862	ao	AN9361.1	71.m15139	AO070333000266	0					-162	-148	ATGTTTCAGAATTAG			ATGTTTCAGAATTAG	MFQN*			MFQN*	AAGGTATTGC	AAACTCGGGA	0	M	0	0	0	0	0
11303	4864	af	AN8100.1	69.m14871	AO070281000022	0			-202	-185			ATGAGGCTGGTTGAATAA		ATGAGGCTGGTTGAATAA		MRLVE*		MRLVE*		CGGAGTGGTT	TCAATTATCT	0	P	0	0	0	0	0
11304	4864	af	AN8100.1	69.m14871	AO070281000022	0			-171	-154			ATGACTTCAATTGATTAA		ATGACTTCAATTGATTAA		MTSID*		MTSID*		ATTATCTACA	TACAAGGTGA	0	P	0	0	0	0	0
11305	4864	af	AN8100.1	69.m14871	AO070281000022	0			-134	-123			ATGCGCTTATAA		ATGCGCTTATAA		MRL*		MRL*		AGATTATTAT	GCTGGGGTCT	0	P	0	0	0	0	0
11302	4864	an	AN8100.1	69.m14871	AO070281000022	0	-111	-49					ATGGAGTCTGTTGTTGTCTCGCCTATACGCAAACACCGAACACTGCTATTACCGCATAAATAG	ATGGAGTCTGTTGTTGTCTCGCCTATACGCAAACACCGAACACTGCTATTACCGCATAAATAG			MESVVVSPIRKHRTLLLPHK*	MESVVVSPIRKHRTLLLPHK*			CTCATCTCTG	CCCCTCACCA	0	P	0	0	0	0	0
11306	4864	ao	AN8100.1	69.m14871	AO070281000022	0					-151	-83	ATGGAGTCCGTTACCGTCAAAAATTTACTAGTACAAAACCACCAGAAAATATTAGTATTACCCATATAG			ATGGAGTCCGTTACCGTCAAAAATTTACTAGTACAAAACCACCAGAAAATATTAGTATTACCCATATAG	MESVTVKNLLVQNHQKILVLPI*			MESVTVKNLLVQNHQKILVLPI*	ATATCTTCTG	CCAGACCCAC	0	P	0	0	0	0	0
11308	4865	an	AN2109.1	57.m05963	AO070341000274	0	-120	-91					ATGAGATTTGTTGCGTCATACCCCAGCTAA	ATGAGATTTGTTGCGTCATACCCCAGCTAA			MRFVASYPS*	MRFVASYPS*			CTATTTCACT	CTCGGTCAGC	0	DO	0	0	0	0	0
11310	4867	ao	AN5980.1	72.m19163	AO070340000300	0					-218	-180	ATGATCTGGTACCATTTTTTGTATCAGTCTACCATTTAA			ATGATCTGGTACCATTTTTTGTATCAGTCTACCATTTAA	MIWYHFLYQSTI*			MIWYHFLYQSTI*	GTCAGTATAC	AACGGTCCCC	0		0	0	0	0	0
11311	4867	ao	AN5980.1	72.m19163	AO070340000300	0					-124	-110	ATGGGTTTGATTTGA			ATGGGTTTGATTTGA	MGLI*			MGLI*	ATCCGTCGTC	ATCTGGGGTT	0		0	0	0	0	0
11316	4868	af	AN2048.1	58.m07636	AO070292000015	0			-220	-188			ATGGAGCTGCGGATGTCGGCGATATCTTTGTGA		ATGGAGCTGCGGATGTCGGCGATATCTTTGTGA		MELRMSAISL*		MELRMSAISL*		ATTGTTGGTG	TTGCGACAAG	0	U	FG01890.1	0	0	0	0
11317	4868	af	AN2048.1	58.m07636	AO070292000015	0			-208	-188			ATGTCGGCGATATCTTTGTGA		ATGTCGGCGATATCTTTGTGA		MSAISL*		MSAISL*		GGAGCTGCGG	TTGCGACAAG	0	U	FG01890.1	0	0	0	0
11314	4868	an	AN2048.1	58.m07636	AO070292000015	0	-227	-186					ATGTCTGTCGCTGGATCGCCGTTCCAAGTTACGTCGTGGTAA	ATGTCTGTCGCTGGATCGCCGTTCCAAGTTACGTCGTGGTAA			MSVAGSPFQVTSW*	MSVAGSPFQVTSW*			CTTCAGGTTG	TTCAACGCCG	0	U	FG01890.1	0	0	0	0
11315	4868	an	AN2048.1	58.m07636	AO070292000015	0	-73	-53					ATGATGCTCAGTATAGCTTAA	ATGATGCTCAGTATAGCTTAA			MMLSIA*	MMLSIA*			TTTCCGACCA	AGGACACTCA	0	U	FG01890.1	0	0	0	0
11318	4868	ao	AN2048.1	58.m07636	AO070292000015	0					-213	-163	ATGGTCGTGTGTATTCGGTATCTATATGATGAACAGTTCTGCTTTCTATGA			ATGGTCGTGTGTATTCGGTATCTATATGATGAACAGTTCTGCTTTCTATGA	MVVCIRYLYDEQFCFL*			MVVCIRYLYDEQFCFL*	GGAAGTATTG	CTTTACGCCT	0	U	FG01890.1	0	0	0	0
11319	4868	ao	AN2048.1	58.m07636	AO070292000015	0					-188	-114	ATGATGAACAGTTCTGCTTTCTATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAG			ATGATGAACAGTTCTGCTTTCTATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAG	MMNSSAFYDFTPVANQSALSLYSG*			MMNSSAFYDFTPVANQSALSLYSG*	CGGTATCTAT	GCCTGCGACT	0	U	FG01890.1	0	0	0	0
11320	4868	ao	AN2048.1	58.m07636	AO070292000015	0					-185	-114	ATGAACAGTTCTGCTTTCTATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAG			ATGAACAGTTCTGCTTTCTATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAG	MNSSAFYDFTPVANQSALSLYSG*			MNSSAFYDFTPVANQSALSLYSG*	TATCTATATG	GCCTGCGACT	0	U	FG01890.1	0	0	0	0
11321	4868	ao	AN2048.1	58.m07636	AO070292000015	0					-166	-95	ATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAGGCCTGCGACTAACCACTAA			ATGACTTTACGCCTGTCGCGAATCAAAGTGCCCTTTCTTTATACTCGGGCTAGGCCTGCGACTAACCACTAA	MTLRLSRIKVPFLYTRARPATNH*			MTLRLSRIKVPFLYTRARPATNH*	TCTGCTTTCT	CCTAAGCCAT	0	U	FG01890.1	0	0	0	0
11322	4868	ao	AN2048.1	58.m07636	AO070292000015	0					-78	-58	ATGATGTTCAAGACAACCTAA			ATGATGTTCAAGACAACCTAA	MMFKTT*			MMFKTT*	CCATTGGCCG	AGGACACTCC	0	U	FG01890.1	0	0	0	0
11313	4868	conserved	AN2048.1	58.m07636	AO070292000015	0	-70	-53	-76	-59	-75	-58	ATGhTCmrkryArsyTAr	ATGCTCAGTATAGCTTAA	ATGATCCGGGCAAGCTAG	ATGTTCAAGACAACCTAA	Mlsia*	MLSIA*	MIRAS*	MFKTT*	yhGrCCrAyG	rssrCwCTCm	0	U	FG01890.1	0	0	0	0
11325	4872	af	AN5346.1	69.m15558	AO070333000176	0			-221	-144			ATGGAGTTATGGTACGGAGTAACTCCGTACTCCGTAGTCCGCAAGACAAACGCGTATACGATAGCTTCACCGTTTTGA		ATGGAGTTATGGTACGGAGTAACTCCGTACTCCGTAGTCCGCAAGACAAACGCGTATACGATAGCTTCACCGTTTTGA		MELWYGVTPYSVVRKTNAYTIASPF*		MELWYGVTPYSVVRKTNAYTIASPF*		GATTGCTATT	GCCTGTCTCA	0	O	0	MG10494.1	0	0	0
11326	4872	af	AN5346.1	69.m15558	AO070333000176	0			-213	-82			ATGGTACGGAGTAACTCCGTACTCCGTAGTCCGCAAGACAAACGCGTATACGATAGCTTCACCGTTTTGAGCCTGTCTCAATTGCCTTTGTATCCACGACGAGAATTCTTCCCTGTCGGCAATATGTTATAA		ATGGTACGGAGTAACTCCGTACTCCGTAGTCCGCAAGACAAACGCGTATACGATAGCTTCACCGTTTTGAGCCTGTCTCAATTGCCTTTGTATCCACGACGAGAATTCTTCCCTGTCGGCAATATGTTATAA		MVRSNSVLRSPQDKRVYDSFTVLSLSQLPLYPRREFFPVGNML*		MVRSNSVLRSPQDKRVYDSFTVLSLSQLPLYPRREFFPVGNML*		TTATGGAGTT	GTGGTTATCA	0	O	0	MG10494.1	0	0	0
11323	4872	an	AN5346.1	69.m15558	AO070333000176	0	-221	-183					ATGCCTGAGGAACTAGGCTCTACACCAATTCCTATCTGA	ATGCCTGAGGAACTAGGCTCTACACCAATTCCTATCTGA			MPEELGSTPIPI*	MPEELGSTPIPI*			TCGCACTCTT	GACCACGTTG	0	O	0	MG10494.1	0	0	0
11324	4872	an	AN5346.1	69.m15558	AO070333000176	0	-98	-48					ATGCTGTACACGTCAGTATCACCGTCGGTCCACGCACACTCTCAGAGTTGA	ATGCTGTACACGTCAGTATCACCGTCGGTCCACGCACACTCTCAGAGTTGA			MLYTSVSPSVHAHSQS*	MLYTSVSPSVHAHSQS*			GGGGCTGTGA	ATCCCGCAAG	0	O	0	MG10494.1	0	0	0
11328	4872	ao	AN5346.1	69.m15558	AO070333000176	0					-226	-140	ATGATAGAGTGTGGGGGGAAGAGGACCGGGCCATGTTTACTCCGTCTAACAACCGATCGTCATCCTGCACCACCTTTACAGGATTAG			ATGATAGAGTGTGGGGGGAAGAGGACCGGGCCATGTTTACTCCGTCTAACAACCGATCGTCATCCTGCACCACCTTTACAGGATTAG	MIECGGKRTGPCLLRLTTDRHPAPPLQD*			MIECGGKRTGPCLLRLTTDRHPAPPLQD*	CGCGGTTGAT	AGCTCTTGCG	0	O	0	MG10494.1	0	0	0

§S3 Upstream open reading frames (uORFs)

11329	4872	ao	AN5346.1	69.m15558	AO070333000176	0					-194	-36	ATGTTTACTCCGTCTAACAACCGATCGTCATCCTGCACCACCTTTACAGGATTAGAGCTCTTGCGGATCTTTCAAACACCTCGCTGGCATACAGTGAAAACCCTCCATGGTCTCAAGATAGTCAATTGTCCTCCTTTGCGCATTATGATTGATATCTAA			ATGTTTACTCCGTCTAACAACCGATCGTCATCCTGCACCACCTTTACAGGATTAGAGCTCTTGCGGATCTTTCAAACACCTCGCTGGCATACAGTGAAAACCCTCCATGGTCTCAAGATAGTCAATTGTCCTCCTTTGCGCATTATGATTGATATCTAA	MFTPSNNRSSSCTTFTGLELLRIFQTPRWHTVKTLHGLKIVNCPPLRIMIDI*			MFTPSNNRSSSCTTFTGLELLRIFQTPRWHTVKTLHGLKIVNCPPLRIMIDI*	GGACCGGGCC	ACTATCTAAT	0	O	0	MG10494.1	0	0	0
11330	4872	ao	AN5346.1	69.m15558	AO070333000176	0					-88	-74	ATGGTCTCAAGATAG			ATGGTCTCAAGATAG	MVSR*			MVSR*	AAAACCCTCC	TCAATTGTCC	0	O	0	MG10494.1	0	0	0
11333	4873	af	AN2745.1	54.m06686	AO070338000226	0			-206	-141			ATGATGATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		ATGATGATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		MMMMQKMATYCQQRDKQPLFP*		MMMMQKMATYCQQRDKQPLFP*		ATAATAAAGA	CCGCCAAAGC	0	R	FG01906.1	MG07515.1	0	0	0
11334	4873	af	AN2745.1	54.m06686	AO070338000226	0			-203	-141			ATGATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		ATGATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		MMMQKMATYCQQRDKQPLFP*		MMMQKMATYCQQRDKQPLFP*		ATAAAGAATG	CCGCCAAAGC	0	R	FG01906.1	MG07515.1	0	0	0
11335	4873	af	AN2745.1	54.m06686	AO070338000226	0			-200	-141			ATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		ATGATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		MMQKMATYCQQRDKQPLFP*		MMQKMATYCQQRDKQPLFP*		AAGAATGATG	CCGCCAAAGC	0	R	FG01906.1	MG07515.1	0	0	0
11336	4873	af	AN2745.1	54.m06686	AO070338000226	0			-197	-141			ATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		ATGCAAAAGATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		MQKMATYCQQRDKQPLFP*		MQKMATYCQQRDKQPLFP*		AATGATGATG	CCGCCAAAGC	0	R	FG01906.1	MG07515.1	0	0	0
11337	4873	af	AN2745.1	54.m06686	AO070338000226	0			-188	-141			ATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		ATGGCAACCTACTGTCAACAGAGGGATAAACAGCCGCTCTTCCCGTGA		MATYCQQRDKQPLFP*		MATYCQQRDKQPLFP*		GATGCAAAAG	CCGCCAAAGC	0	R	FG01906.1	MG07515.1	0	0	0
11332	4873	an	AN2745.1	54.m06686	AO070338000226	0	-161	-144					ATGAGTTGTAACTTGTGA	ATGAGTTGTAACTTGTGA			MSCNL*	MSCNL*			ATAGCATTTT	CGGTCAAGGA	0	R	FG01906.1	MG07515.1	0	0	0
11338	4873	ao	AN2745.1	54.m06686	AO070338000226	0					-253	-242	ATGGAGAGATAG			ATGGAGAGATAG	MER*			MER*	GAGGGAAAGA	CGTGAAGCGA	0	R	FG01906.1	MG07515.1	0	0	0
11339	4873	ao	AN2745.1	54.m06686	AO070338000226	0					-151	-59	ATGGTTTCTTCCCCACGGCGGAGCTTCAATTCAATTACGTTCACGACAATAATTTCCCACCTTATTTCCTTTGTTTCTATAAACAATCACTAA			ATGGTTTCTTCCCCACGGCGGAGCTTCAATTCAATTACGTTCACGACAATAATTTCCCACCTTATTTCCTTTGTTTCTATAAACAATCACTAA	MVSSPRRSFNSITFTTIISHLISFVSINNH*			MVSSPRRSFNSITFTTIISHLISFVSINNH*	AATTGGGCTG	TTAACTATTC	0	R	FG01906.1	MG07515.1	0	0	0
11340	4874	af	AN7513.1	69.m15155	AO070258000018	0			-281	-270			ATGCCTTGTTGA		ATGCCTTGTTGA		MPC*		MPC*		AACGGGATTG	AGCGGGGTGG	0	K	0	0	0	0	0
11342	4876	af	AN5400.1	69.m15773	AO070333000134	0			-212	-180			ATGCAACTAGCCAAACGGCTCTCCTTCTCCTGA		ATGCAACTAGCCAAACGGCTCTCCTTCTCCTGA		MQLAKRLSFS*		MQLAKRLSFS*		CCTACTAATC	CAAGCTACTT	0	P	0	0	0	0	0
11343	4876	af	AN5400.1	69.m15773	AO070333000134	0			-94	-68			ATGATGCCGAAAGACCGTCGTCGATGA		ATGATGCCGAAAGACCGTCGTCGATGA		MMPKDRRR*		MMPKDRRR*		CCTGACGTGA	TCGCAAATAT	0	P	0	0	0	0	0
11344	4876	af	AN5400.1	69.m15773	AO070333000134	0			-91	-68			ATGCCGAAAGACCGTCGTCGATGA		ATGCCGAAAGACCGTCGTCGATGA		MPKDRRR*		MPKDRRR*		GACGTGAATG	TCGCAAATAT	0	P	0	0	0	0	0
11345	4876	af	AN5400.1	69.m15773	AO070333000134	0			-71	-15			ATGATCGCAAATATCCCCTTATCTACCCCGTTCCCGATCATGGTCAGTGAAAAGTGA		ATGATCGCAAATATCCCCTTATCTACCCCGTTCCCGATCATGGTCAGTGAAAAGTGA		MIANIPLSTPFPIMVSEK*		MIANIPLSTPFPIMVSEK*		ACCGTCGTCG	CAACTACCAG	0	P	0	0	0	0	0
11341	4876	an	AN5400.1	69.m15773	AO070333000134	0	-125	-108					ATGGAGGGGTCTAGCTGA	ATGGAGGGGTCTAGCTGA			MEGSS*	MEGSS*			AATAGCGAGA	GGGGGTGTCG	0	P	0	0	0	0	0
11347	4876	ao	AN5400.1	69.m15773	AO070333000134	0					-144	-106	ATGTCACGGACTCGTGATTTCACGGCCATAGCCCTATAA			ATGTCACGGACTCGTGATTTCACGGCCATAGCCCTATAA	MSRTRDFTAIAL*			MSRTRDFTAIAL*	ATCGCGAGTC	AATGAAACCG	0	P	0	0	0	0	0
11349	4878	af	AN0564.1	69.m15283	AO070272000041	0			-166	-104			ATGGCTCGAATTTGTTCGTATTCGACACTTTTTTCCTCCGGAGGATGTCGTGGGATATCTTAA		ATGGCTCGAATTTGTTCGTATTCGACACTTTTTTCCTCCGGAGGATGTCGTGGGATATCTTAA		MARICSYSTLFSSGGCRGIS*		MARICSYSTLFSSGGCRGIS*		TTGACTCGCG	ATGCCATGAG	0	R	0	0	0	0	0
11348	4878	an	AN0564.1	69.m15283	AO070272000041	0	-129	-106					ATGCACGATTTCCCAGCCGGCTAG	ATGCACGATTTCCCAGCCGGCTAG			MHDFPAG*	MHDFPAG*			TATCGTCGCG	ACGTGCGGAG	0	R	0	0	0	0	0
11350	4878	ao	AN0564.1	69.m15283	AO070272000041	0					-160	-149	ATGGCCTTTTGA			ATGGCCTTTTGA	MAF*			MAF*	TGGCGTGGTC	TTTGTTCTGC	0	R	0	0	0	0	0
11355	4880	an	AN5811.1	72.m18941	AO070260000036	0	-222	-157					ATGTATTGGAGATCAAGCTCAAATGAGGTCATTGGCTTAGTCACATATGTTATTAAAGCGCCCTAA	ATGTATTGGAGATCAAGCTCAAATGAGGTCATTGGCTTAGTCACATATGTTATTAAAGCGCCCTAA			MYWRSSSNEVIGLVTYVIKAP*	MYWRSSSNEVIGLVTYVIKAP*			AACTCGAAGA	CAGCTCAATC	0		FG06524.1	MG09114.1	0	0	0
11356	4880	an	AN5811.1	72.m18941	AO070260000036	0	-200	-183					ATGAGGTCATTGGCTTAG	ATGAGGTCATTGGCTTAG			MRSLA*	MRSLA*			TCAAGCTCAA	TCACATATGT	0		FG06524.1	MG09114.1	0	0	0
11357	4880	an	AN5811.1	72.m18941	AO070260000036	0	-176	-105					ATGTTATTAAAGCGCCCTAACAGCTCAATCTTAAAAGCTTGGGTATCTCAATTCTCAATTTATCAAGCCTAA	ATGTTATTAAAGCGCCCTAACAGCTCAATCTTAAAAGCTTGGGTATCTCAATTCTCAATTTATCAAGCCTAA			MLLKRPNSSILKAWVSQFSIYQA*	MLLKRPNSSILKAWVSQFSIYQA*			TTAGTCACAT	GCCGACACCA	0		FG06524.1	MG09114.1	0	0	0
11361	4881	af	AN0442.1	54.m06632	AO070338000299	0			-221	-180			ATGCCAATTGACTTGTTCCACTTAACGTGTTGTAATAGGTAA		ATGCCAATTGACTTGTTCCACTTAACGTGTTGTAATAGGTAA		MPIDLFHLTCCNR*		MPIDLFHLTCCNR*		TTAGATTTCG	TTCATAATTT	0	Z	FG09305.1	MG03612.1	0	0	0
11362	4881	af	AN0442.1	54.m06632	AO070338000299	0			-131	-120			ATGTTGTGGTAA		ATGTTGTGGTAA		MLW*		MLW*		AAAAGCCTTA	AAGACTGCAT	0	Z	FG09305.1	MG03612.1	0	0	0
11358	4881	an	AN0442.1	54.m06632	AO070338000299	0	-184	-134					ATGGGGTCCATCCGCCATACTTCCTGGGGGCACTGCGGGCCCCATGCATGA	ATGGGGTCCATCCGCCATACTTCCTGGGGGCACTGCGGGCCCCATGCATGA			MGSIRHTSWGHCGPHA*	MGSIRHTSWGHCGPHA*			TAGTCCTTAC	CTACCTAAAT	0	Z	FG09305.1	MG03612.1	0	0	0
11359	4881	an	AN0442.1	54.m06632	AO070338000299	0	-141	-67					ATGCATGACTACCTAAATAGGACTAGCCCCTGTCCAGTGTCCACAGCTGATCTTATCGATAAGTTCGTCACTTGA	ATGCATGACTACCTAAATAGGACTAGCCCCTGTCCAGTGTCCACAGCTGATCTTATCGATAAGTTCGTCACTTGA			MHDYLNRTSPCPVSTADLIDKFVT*	MHDYLNRTSPCPVSTADLIDKFVT*			TGCGGGCCCC	GCTTCATTTC	0	Z	FG09305.1	MG03612.1	0	0	0
11360	4881	an	AN0442.1	54.m06632	AO070338000299	0	-137	-126					ATGACTACCTAA	ATGACTACCTAA			MTT*	MTT*			GGCCCCATGC	ATAGGACTAG	0	Z	FG09305.1	MG03612.1	0	0	0
11363	4881	ao	AN0442.1	54.m06632	AO070338000299	0					-221	-189	ATGCATTGGGGTATATACACCTCAGAAATATAG			ATGCATTGGGGTATATACACCTCAGAAATATAG	MHWGIYTSEI*			MHWGIYTSEI*	TATTCAAAAC	AACCGACTCC	0	Z	FG09305.1	MG03612.1	0	0	0
11364	4883	an	AN2273.1	71.m15918	AO070295000049	0	-209	-183					ATGGAGGGGCAGCAGATGAACACCTGA	ATGGAGGGGCAGCAGATGAACACCTGA			MEGQQMNT*	MEGQQMNT*			AAGAATTACT	AACTCCAGGC	0		0	MG06267.1	0	0	0
11365	4883	an	AN2273.1	71.m15918	AO070295000049	0	-194	-183					ATGAACACCTGA	ATGAACACCTGA			MNT*	MNT*			GGGGCAGCAG	AACTCCAGGC	0		0	MG06267.1	0	0	0
11366	4883	ao	AN2273.1	71.m15918	AO070295000049	0					-166	-23	ATGATGGTCCGGAGGGGCAGCAACAGAAAGAAGATCCGGATCATATGCCGTACCGTACTGTACGGAGCGTATTGCATCGCATCAGGGGAGTCGCCGTCTACAACTCTCCATACTACAACCACCTCTTTTTCTGCTATCGCATAA			ATGATGGTCCGGAGGGGCAGCAACAGAAAGAAGATCCGGATCATATGCCGTACCGTACTGTACGGAGCGTATTGCATCGCATCAGGGGAGTCGCCGTCTACAACTCTCCATACTACAACCACCTCTTTTTCTGCTATCGCATAA	MMVRRGSNRKKIRIICRTVLYGAYCIASGESPSTTLHTTTTSFSAIA*			MMVRRGSNRKKIRIICRTVLYGAYCIASGESPSTTLHTTTTSFSAIA*	TGGGGGAGGG	CTTACAGTAT	0		0	MG06267.1	0	0	0
11367	4883	ao	AN2273.1	71.m15918	AO070295000049	0					-163	-23	ATGGTCCGGAGGGGCAGCAACAGAAAGAAGATCCGGATCATATGCCGTACCGTACTGTACGGAGCGTATTGCATCGCATCAGGGGAGTCGCCGTCTACAACTCTCCATACTACAACCACCTCTTTTTCTGCTATCGCATAA			ATGGTCCGGAGGGGCAGCAACAGAAAGAAGATCCGGATCATATGCCGTACCGTACTGTACGGAGCGTATTGCATCGCATCAGGGGAGTCGCCGTCTACAACTCTCCATACTACAACCACCTCTTTTTCTGCTATCGCATAA	MVRRGSNRKKIRIICRTVLYGAYCIASGESPSTTLHTTTTSFSAIA*			MVRRGSNRKKIRIICRTVLYGAYCIASGESPSTTLHTTTTSFSAIA*	GGGAGGGATG	CTTACAGTAT	0		0	MG06267.1	0	0	0
11368	4884	an	AN1981.1	58.m08945	AO070301000066	0	-235	-197					ATGATGGAACAGAAAAGGGACGACGTGAAGCTATGTTGA	ATGATGGAACAGAAAAGGGACGACGTGAAGCTATGTTGA			MMEQKRDDVKLC*	MMEQKRDDVKLC*			AAGAGTTGGA	GTGGCAGCTG	0	O	0	0	0	YJL031C	0
11369	4884	an	AN1981.1	58.m08945	AO070301000066	0	-232	-197					ATGGAACAGAAAAGGGACGACGTGAAGCTATGTTGA	ATGGAACAGAAAAGGGACGACGTGAAGCTATGTTGA			MEQKRDDVKLC*	MEQKRDDVKLC*			AGTTGGAATG	GTGGCAGCTG	0	O	0	0	0	YJL031C	0
11370	4884	an	AN1981.1	58.m08945	AO070301000066	0	-203	-177					ATGTTGAGTGGCAGCTGCTTGTATTGA	ATGTTGAGTGGCAGCTGCTTGTATTGA			MLSGSCLY*	MLSGSCLY*			ACGTGAAGCT	CAGACAACAC	0	O	0	0	0	YJL031C	0
11372	4884	ao	AN1981.1	58.m08945	AO070301000066	0					-178	-14	ATGAGGCAGTATAGTATGGCACGTGACGTCCCGATAGGGAAAGCACTCCAAACGGAGTTGAGCAGCCGTGACTTCTACTTCATCGTTCTCCTTACTGGTAGGCCTGTGAAAACCATCCGTTCCTGGTGGTGGCACGTTTCAACTAGTCAGGTGTTTCATAGATAG			ATGAGGCAGTATAGTATGGCACGTGACGTCCCGATAGGGAAAGCACTCCAAACGGAGTTGAGCAGCCGTGACTTCTACTTCATCGTTCTCCTTACTGGTAGGCCTGTGAAAACCATCCGTTCCTGGTGGTGGCACGTTTCAACTAGTCAGGTGTTTCATAGATAG	MRQYSMARDVPIGKALQTELSSRDFYFIVLLTGRPVKTIRSWWWHVSTSQVFHR*			MRQYSMARDVPIGKALQTELSSRDFYFIVLLTGRPVKTIRSWWWHVSTSQVFHR*	TCCCGTATAG	ACAACAGGTC	0	O	0	0	0	YJL031C	0
11373	4884	ao	AN1981.1	58.m08945	AO070301000066	0					-163	-14	ATGGCACGTGACGTCCCGATAGGGAAAGCACTCCAAACGGAGTTGAGCAGCCGTGACTTCTACTTCATCGTTCTCCTTACTGGTAGGCCTGTGAAAACCATCCGTTCCTGGTGGTGGCACGTTTCAACTAGTCAGGTGTTTCATAGATAG			ATGGCACGTGACGTCCCGATAGGGAAAGCACTCCAAACGGAGTTGAGCAGCCGTGACTTCTACTTCATCGTTCTCCTTACTGGTAGGCCTGTGAAAACCATCCGTTCCTGGTGGTGGCACGTTTCAACTAGTCAGGTGTTTCATAGATAG	MARDVPIGKALQTELSSRDFYFIVLLTGRPVKTIRSWWWHVSTSQVFHR*			MARDVPIGKALQTELSSRDFYFIVLLTGRPVKTIRSWWWHVSTSQVFHR*	GCAGTATAGT	ACAACAGGTC	0	O	0	0	0	YJL031C	0
11377	4887	af	AN6331.1	72.m19450	AO070304000109	0			-205	-167			ATGGCCGAAATTGACCTCTTGATATTGCTGGCGGTCTGA		ATGGCCGAAATTGACCTCTTGATATTGCTGGCGGTCTGA		MAEIDLLILLAV*		MAEIDLLILLAV*		AACCCGCACG	TATCCCGACC	0	R	0	0	0	0	0
11376	4887	an	AN6331.1	72.m19450	AO070304000109	0	-191	-168					ATGTTTTGCGTCTCTACGGGTTGA	ATGTTTTGCGTCTCTACGGGTTGA			MFCVSTG*	MFCVSTG*			ACCCCTTTTC	GATGCTCTGA	0	R	0	0	0	0	0
11378	4887	ao	AN6331.1	72.m19450	AO070304000109	0					-246	-211	ATGTCCCCTCACTCTGACCTCTACATCATGGCCTGA			ATGTCCCCTCACTCTGACCTCTACATCATGGCCTGA	MSPHSDLYIMA*			MSPHSDLYIMA*	AGCTCTTATT	GTATACTTTG	0	R	0	0	0	0	0
11382	4889	af	AN6196.1	72.m19294	AO070308000103	0			-161	-141			ATGATGGTTTGTTTTTGTTGA		ATGATGGTTTGTTTTTGTTGA		MMVCFC*		MMVCFC*		CAGAGATGAC	TGATCTTAGC	0		0	0	0	0	0
11383	4889	af	AN6196.1	72.m19294	AO070308000103	0			-158	-141			ATGGTTTGTTTTTGTTGA		ATGGTTTGTTTTTGTTGA		MVCFC*		MVCFC*		AGATGACATG	TGATCTTAGC	0		0	0	0	0	0
11384	4889	af	AN6196.1	72.m19294	AO070308000103	0			-141	-127			ATGATCTTAGCATGA		ATGATCTTAGCATGA		MILA*		MILA*		GTTTTTGTTG	TCCTGTATCG	0		0	0	0	0	0
11385	4889	af	AN6196.1	72.m19294	AO070308000103	0			-130	-107			ATGATCCTGTATCGAGTTCTGTGA		ATGATCCTGTATCGAGTTCTGTGA		MILYRVL*		MILYRVL*		TGATCTTAGC	TTGTCCTGAA	0		0	0	0	0	0
11379	4889	an	AN6196.1	72.m19294	AO070308000103	0	-189	-85					ATGCCCCGGGCCGAGCCAAAAAAGTTCCTCCTTCGTGCTTTCAATGCCTATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAATAGCTGCTCTTGATTGA	ATGCCCCGGGCCGAGCCAAAAAAGTTCCTCCTTCGTGCTTTCAATGCCTATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAATAGCTGCTCTTGATTGA			MPRAEPKKFLLRAFNAYGTHTHLPFASIVIAALD*	MPRAEPKKFLLRAFNAYGTHTHLPFASIVIAALD*			CCGCCTACAA	AGATTGATTT	0		0	0	0	0	0
11380	4889	an	AN6196.1	72.m19294	AO070308000103	0	-146	-102					ATGCCTATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAA	ATGCCTATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAA			MPMGLTLTCLLLQL*	MPMGLTLTCLLLQL*			CGTGCTTTCA	TAGCTGCTCT	0		0	0	0	0	0
11381	4889	an	AN6196.1	72.m19294	AO070308000103	0	-140	-102					ATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAA	ATGGGACTCACACTCACTTGCCTTTTGCTTCAATTGTAA			MGLTLTCLLLQL*	MGLTLTCLLLQL*			TTCAATGCCT	TAGCTGCTCT	0		0	0	0	0	0
11386	4889	ao	AN6196.1	72.m19294	AO070308000103	0					-172	-161	ATGCTTCAATAG			ATGCTTCAATAG	MLQ*			MLQ*	CTTCTTTTTC	TAGCCTACAA	0		0	0	0	0	0
11387	4889	ao	AN6196.1	72.m19294	AO070308000103	0					-151	-104	ATGAACGTTTCTTGGATACTGCTCAGCTTTATCGACAATTGTGGCTAG			ATGAACGTTTCTTGGATACTGCTCAGCTTTATCGACAATTGTGGCTAG	MNVSWILLSFIDNCG*			MNVSWILLSFIDNCG*	GTAGCCTACA	GGTCCTCTAA	0		0	0	0	0	0
11392	4892	af	AN4781.1	59.m09202	AO070329000069	0			-83	-51			ATGATGTTTTCATCCAGACTCAATTGCATCTAA		ATGATGTTTTCATCCAGACTCAATTGCATCTAA		MMFSSRLNCI*		MMFSSRLNCI*		ACCATTACAC	GCTCCACCTC	0	CH	0	0	0	0	0
11393	4892	af	AN4781.1	59.m09202	AO070329000069	0			-80	-51			ATGTTTTCATCCAGACTCAATTGCATCTAA		ATGTTTTCATCCAGACTCAATTGCATCTAA		MFSSRLNCI*		MFSSRLNCI*		ATTACACATG	GCTCCACCTC	0	CH	0	0	0	0	0
11389	4892	an	AN4781.1	59.m09202	AO070329000069	0	-182	-144					ATGATTTCAGTAATGACGTCGGGCGTGGATGTATCATAG	ATGATTTCAGTAATGACGTCGGGCGTGGATGTATCATAG			MISVMTSGVDVS*	MISVMTSGVDVS*			CCTCAATCAC	CTCCAAAGAT	0	CH	0	0	0	0	0
11390	4892	an	AN4781.1	59.m09202	AO070329000069	0	-170	-144					ATGACGTCGGGCGTGGATGTATCATAG	ATGACGTCGGGCGTGGATGTATCATAG			MTSGVDVS*	MTSGVDVS*			GATTTCAGTA	CTCCAAAGAT	0	CH	0	0	0	0	0
11391	4892	an	AN4781.1	59.m09202	AO070329000069	0	-154	-77					ATGTATCATAGCTCCAAAGATTTCAATTGCTTCAATTACAGCTCTCAACCTTCGACTATCTTCAGTACAAGCGAATGA	ATGTATCATAGCTCCAAAGATTTCAATTGCTTCAATTACAGCTCTCAACCTTCGACTATCTTCAGTACAAGCGAATGA			MYHSSKDFNCFNYSSQPSTIFSTSE*	MYHSSKDFNCFNYSSQPSTIFSTSE*			TCGGGCGTGG	TTCAGTCAAT	0	CH	0	0	0	0	0
11394	4892	ao	AN4781.1	59.m09202	AO070329000069	0					-185	-126	ATGATCACACCCCAATACTACATACTCCACACTCATCAATACAATCAAACCAACCAGTAA			ATGATCACACCCCAATACTACATACTCCACACTCATCAATACAATCAAACCAACCAGTAA	MITPQYYILHTHQYNQTNQ*			MITPQYYILHTHQYNQTNQ*	CATCAATCAC	TACCCATCAA	0	CH	0	0	0	0	0
11397	4894	af	AN7353.1	72.m20007	AO070278000047	0			-225	-145			ATGCTTCACCGGGTCGTTTCCACTTTCTTCCCTCCACCCCGCCCAGCACACGCAGGGTCTGACAGATGGGGGCGCCAATGA		ATGCTTCACCGGGTCGTTTCCACTTTCTTCCCTCCACCCCGCCCAGCACACGCAGGGTCTGACAGATGGGGGCGCCAATGA		MLHRVVSTFFPPPRPAHAGSDRWGRQ*		MLHRVVSTFFPPPRPAHAGSDRWGRQ*		TAAACACTGT	AATGCCGGCA	0	R	0	0	0	0	0

11398	4894	af	AN7353.1	72.m20007	AO070278000047	0			-160	-74			ATGGGGGCGCCAATGAAATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAA		ATGGGGGCGCCAATGAAATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAA		MGAPMKCRQKHGSWVLHIRISNRIPRYI*		MGAPMKCRQKHGSWVLHIRISNRIPRYI*		GGTCTGACAG	TATGAACTTC	0	R	0	0	0	0	0
11399	4894	af	AN7353.1	72.m20007	AO070278000047	0			-148	-74			ATGAAATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAA		ATGAAATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAA		MKCRQKHGSWVLHIRISNRIPRYI*		MKCRQKHGSWVLHIRISNRIPRYI*		GGGGGCGCCA	TATGAACTTC	0	R	0	0	0	0	0
11400	4894	af	AN7353.1	72.m20007	AO070278000047	0			-143	-96			ATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAA		ATGCCGGCAGAAGCATGGCAGCTGGGTGCTACATATCCGGATTTCTAA		MPAEAWQLGATYPDF*		MPAEAWQLGATYPDF*		CGCCAATGAA	TCGTATTCCA	0	R	0	0	0	0	0
11401	4894	af	AN7353.1	72.m20007	AO070278000047	0			-129	-10			ATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAATATGAACTTCGTGCCTCTGTACAGTCTCGATTGTCAATACTGCCTGTGTATCTGTACCATTTAA		ATGGCAGCTGGGTGCTACATATCCGGATTTCTAATCGTATTCCAAGGTATATATAATATGAACTTCGTGCCTCTGTACAGTCTCGATTGTCAATACTGCCTGTGTATCTGTACCATTTAA		MAAGCYISGFLIVFQGIYNMNFVPLYSLDCQYCLCICTI*		MAAGCYISGFLIVFQGIYNMNFVPLYSLDCQYCLCICTI*		CGGCAGAAGC	ACCGTCGGTA	0	R	0	0	0	0	0
11402	4894	af	AN7353.1	72.m20007	AO070278000047	0			-72	-10			ATGAACTTCGTGCCTCTGTACAGTCTCGATTGTCAATACTGCCTGTGTATCTGTACCATTTAA		ATGAACTTCGTGCCTCTGTACAGTCTCGATTGTCAATACTGCCTGTGTATCTGTACCATTTAA		MNFVPLYSLDCQYCLCICTI*		MNFVPLYSLDCQYCLCICTI*		TATATATAAT	ACCGTCGGTA	0	R	0	0	0	0	0
11403	4894	ao	AN7353.1	72.m20007	AO070278000047	0					-167	-156	ATGTACCTTTAA			ATGTACCTTTAA	MYL*			MYL*	ATATCAATAA	GGGTTCGACC	0	R	0	0	0	0	0
11405	4895	af	AN4089.1	54.m06734	AO070342000092	0			-239	-201			ATGTCCCGATGCCTTCGATGTCCTGATTCTTGTACTTGA		ATGTCCCGATGCCTTCGATGTCCTGATTCTTGTACTTGA		MSRCLRCPDSCT*		MSRCLRCPDSCT*		AGGGCTTTTG	CTATGACTCT	0	J	0	0	0	0	0
11406	4895	af	AN4089.1	54.m06734	AO070342000092	0			-231	-214			ATGCCTTCGATGTCCTGA		ATGCCTTCGATGTCCTGA		MPSMS*		MPSMS*		TGATGTCCCG	TTCTTGTACT	0	J	0	0	0	0	0
11407	4895	af	AN4089.1	54.m06734	AO070342000092	0			-198	-142			ATGACTCTTCGCATGTGCATCCTATCAACACCCAGATGGAGTCGCCAGCAGTGCTGA		ATGACTCTTCGCATGTGCATCCTATCAACACCCAGATGGAGTCGCCAGCAGTGCTGA		MTLRMCILSTPRWSRQQC*		MTLRMCILSTPRWSRQQC*		GTACTTGACT	ATTGCAGACT	0	J	0	0	0	0	0
11408	4895	af	AN4089.1	54.m06734	AO070342000092	0			-186	-142			ATGTGCATCCTATCAACACCCAGATGGAGTCGCCAGCAGTGCTGA		ATGTGCATCCTATCAACACCCAGATGGAGTCGCCAGCAGTGCTGA		MCILSTPRWSRQQC*		MCILSTPRWSRQQC*		GACTCTTCGC	ATTGCAGACT	0	J	0	0	0	0	0
11409	4895	af	AN4089.1	54.m06734	AO070342000092	0			-163	-125			ATGGAGTCGCCAGCAGTGCTGAATTGCAGACTGAAATAA		ATGGAGTCGCCAGCAGTGCTGAATTGCAGACTGAAATAA		MESPAVLNCRLK*		MESPAVLNCRLK*		CAACACCCAG	GCAGACAACG	0	J	0	0	0	0	0
11404	4895	an	AN4089.1	54.m06734	AO070342000092	0	-134	-102					ATGGGCTTTCTATTTTCTATCTCATTCATCTAG	ATGGGCTTTCTATTTTCTATCTCATTCATCTAG			MGFLFSISFI*	MGFLFSISFI*			AGCTTTATCA	CATCAGCAGC	0	J	0	0	0	0	0
11410	4896	af	AN1326.1	70.m14905	AO070303000090	0			-239	-126			ATGATCGATCTGTGTCTCCCTCATTCTCACGAAGTTACAAGACTCCGAGGACGGGGTGTTTTTTTTTTCTTCAAACAGATTACCACCTTTGAGTCGGACCAACAGGGGCTGTGA		ATGATCGATCTGTGTCTCCCTCATTCTCACGAAGTTACAAGACTCCGAGGACGGGGTGTTTTTTTTTTCTTCAAACAGATTACCACCTTTGAGTCGGACCAACAGGGGCTGTGA		MIDLCLPHSHEVTRLRGRGVFFFFKQITTFESDQQGL*		MIDLCLPHSHEVTRLRGRGVFFFFKQITTFESDQQGL*		TTCTGGCCAA	GGTACGGAGT	0	R	0	0	0	0	0
11411	4896	ao	AN1326.1	70.m14905	AO070303000090	0					-202	-179	ATGCCACTGACAATCACCTTGTGA			ATGCCACTGACAATCACCTTGTGA	MPLTITL*			MPLTITL*	CCGTGATTCA	GCAGCGCAGG	0	R	0	0	0	0	0
11415	4899	af	AN2771.1	59.m09272	AO070327000013	0			-238	-140			ATGCTCGGAGTATACATTCAGACTAGCCTTCTTAGGAAAGGCGCCTCAATGCACGGCTATCCCTTATCGAGACTAGCTCCCTCGACGTTCCCAATTTAG		ATGCTCGGAGTATACATTCAGACTAGCCTTCTTAGGAAAGGCGCCTCAATGCACGGCTATCCCTTATCGAGACTAGCTCCCTCGACGTTCCCAATTTAG		MLGVYIQTSLLRKGASMHGYPLSRLAPSTFPI*		MLGVYIQTSLLRKGASMHGYPLSRLAPSTFPI*		AAGTACCTTG	GCTTTTGAGC	0	S	0	0	0	0	0
11416	4899	af	AN2771.1	59.m09272	AO070327000013	0			-190	-140			ATGCACGGCTATCCCTTATCGAGACTAGCTCCCTCGACGTTCCCAATTTAG		ATGCACGGCTATCCCTTATCGAGACTAGCTCCCTCGACGTTCCCAATTTAG		MHGYPLSRLAPSTFPI*		MHGYPLSRLAPSTFPI*		AGGCGCCTCA	GCTTTTGAGC	0	S	0	0	0	0	0
11417	4899	af	AN2771.1	59.m09272	AO070327000013	0			-121	-98			ATGATTTCATTATTTTATTTTTGA		ATGATTTCATTATTTTATTTTTGA		MISLFYF*		MISLFYF*		GCCGCATCAG	TTAACTATTA	0	S	0	0	0	0	0
11412	4899	an	AN2771.1	59.m09272	AO070327000013	0	-191	-180					ATGGTCACATGA	ATGGTCACATGA			MVT*	MVT*			TTTGGGAGAT	TCTACTAGTA	0	S	0	0	0	0	0
11413	4899	an	AN2771.1	59.m09272	AO070327000013	0	-183	-172					ATGATCTACTAG	ATGATCTACTAG			MIY*	MIY*			ATATGGTCAC	TACCATCATG	0	S	0	0	0	0	0
11414	4899	an	AN2771.1	59.m09272	AO070327000013	0	-129	-43					ATGGCTGACTCAACAATATTTCCTCTTAGCGTCTCCCGCTCTCGACCGCCGCGGCCTGGCCGATTTGAATTCTCGAAAGTTGCATAA	ATGGCTGACTCAACAATATTTCCTCTTAGCGTCTCCCGCTCTCGACCGCCGCGGCCTGGCCGATTTGAATTCTCGAAAGTTGCATAA			MADSTIFPLSVSRSRPPRPGRFEFSKVA*	MADSTIFPLSVSRSRPPRPGRFEFSKVA*			TTTGAGCCGC	TTTCATCTTC	0	S	0	0	0	0	0
11418	4899	ao	AN2771.1	59.m09272	AO070327000013	0					-109	-41	ATGATGACTCATCCTTCATGCAGTTCCCGATTTAATTTTAGTTCGATGCTTTTTCTTTATCTCCGATAA			ATGATGACTCATCCTTCATGCAGTTCCCGATTTAATTTTAGTTCGATGCTTTTTCTTTATCTCCGATAA	MMTHPSCSSRFNFSSMLFLYLR*			MMTHPSCSSRFNFSSMLFLYLR*	TTTGAGCCGC	TCAATCTATC	0	S	0	0	0	0	0
11419	4899	ao	AN2771.1	59.m09272	AO070327000013	0					-106	-41	ATGACTCATCCTTCATGCAGTTCCCGATTTAATTTTAGTTCGATGCTTTTTCTTTATCTCCGATAA			ATGACTCATCCTTCATGCAGTTCCCGATTTAATTTTAGTTCGATGCTTTTTCTTTATCTCCGATAA	MTHPSCSSRFNFSSMLFLYLR*			MTHPSCSSRFNFSSMLFLYLR*	GAGCCGCATG	TCAATCTATC	0	S	0	0	0	0	0
11420	4899	ao	AN2771.1	59.m09272	AO070327000013	0					-92	-75	ATGCAGTTCCCGATTTAA			ATGCAGTTCCCGATTTAA	MQFPI*			MQFPI*	CTCATCCTTC	TTTTAGTTCG	0	S	0	0	0	0	0
11421	4899	ao	AN2771.1	59.m09272	AO070327000013	0					-64	-41	ATGCTTTTTCTTTATCTCCGATAA			ATGCTTTTTCTTTATCTCCGATAA	MLFLYLR*			MLFLYLR*	TTTTAGTTCG	TCAATCTATC	0	S	0	0	0	0	0
11422	4902	ao	AN0559.1	69.m15288	AO070272000036	0					-190	-32	ATGATCCTCCGCCTTCAAAATTGTCAGAACATGAGAAAAGCGTCACTTCCCCAGTCTCGTCCCCATAGACCAAATAAACATCCCTTTCCCCGGTTCGGTCGGACTCGCCTGAGGCACTGGACTTATTCTACCTCTGTGCTTTCTTTTATCCTTCTTTAA			ATGATCCTCCGCCTTCAAAATTGTCAGAACATGAGAAAAGCGTCACTTCCCCAGTCTCGTCCCCATAGACCAAATAAACATCCCTTTCCCCGGTTCGGTCGGACTCGCCTGAGGCACTGGACTTATTCTACCTCTGTGCTTTCTTTTATCCTTCTTTAA	MILRLQNCQNMRKASLPQSRPHRPNKHPFPRFGRTRLRHWTYSTSVLSFILL*			MILRLQNCQNMRKASLPQSRPHRPNKHPFPRFGRTRLRHWTYSTSVLSFILL*	CGGAAGAACA	TAAATAATTA	0	U	FG09817.1	MG06097.1	NCU06632.1	0	0
11423	4902	ao	AN0559.1	69.m15288	AO070272000036	0					-160	-32	ATGAGAAAAGCGTCACTTCCCCAGTCTCGTCCCCATAGACCAAATAAACATCCCTTTCCCCGGTTCGGTCGGACTCGCCTGAGGCACTGGACTTATTCTACCTCTGTGCTTTCTTTTATCCTTCTTTAA			ATGAGAAAAGCGTCACTTCCCCAGTCTCGTCCCCATAGACCAAATAAACATCCCTTTCCCCGGTTCGGTCGGACTCGCCTGAGGCACTGGACTTATTCTACCTCTGTGCTTTCTTTTATCCTTCTTTAA	MRKASLPQSRPHRPNKHPFPRFGRTRLRHWTYSTSVLSFILL*			MRKASLPQSRPHRPNKHPFPRFGRTRLRHWTYSTSVLSFILL*	TTGTCAGAAC	TAAATAATTA	0	U	FG09817.1	MG06097.1	NCU06632.1	0	0
11424	4906	an	AN4214.1	54.m06959	AO070231000010	0	-238	-143					ATGATACATCGCCCCAATTTACCATATCAACGAAGCTTGGCTGGCAACATCCGCTGTGATCCTTACCGCTATTGCTCGTTTACTAGGATGGCCTGA	ATGATACATCGCCCCAATTTACCATATCAACGAAGCTTGGCTGGCAACATCCGCTGTGATCCTTACCGCTATTGCTCGTTTACTAGGATGGCCTGA			MIHRPNLPYQRSLAGNIRCDPYRYCSFTRMA*	MIHRPNLPYQRSLAGNIRCDPYRYCSFTRMA*			CCGCCCTCGC	TTACCGTGAA	0	A	0	0	0	0	0
11425	4906	ao	AN4214.1	54.m06959	AO070231000010	0					-124	-17	ATGATCGGGGAGAAATCTAGCGAATTCATTCTCTTTAATCTCACCAAACAAGCAAACCTGTACCCTCAACTTGGTTCCAGCTGGACTGGCCTTGTTTCCTTGAGTTAA			ATGATCGGGGAGAAATCTAGCGAATTCATTCTCTTTAATCTCACCAAACAAGCAAACCTGTACCCTCAACTTGGTTCCAGCTGGACTGGCCTTGTTTCCTTGAGTTAA	MIGEKSSEFILFNLTKQANLYPQLGSSWTGLVSLS*			MIGEKSSEFILFNLTKQANLYPQLGSSWTGLVSLS*	TTGGGATGGC	ATTCATTGCT	0	A	0	0	0	0	0
11430	4908	af	AN0693.1	70.m15296	AO070343000520	0			-247	-209			ATGCAACCTAATGCTTGTACGGAGGGTATGTCGTCATAA		ATGCAACCTAATGCTTGTACGGAGGGTATGTCGTCATAA		MQPNACTEGMSS*		MQPNACTEGMSS*		TGCGGTGAAT	TGGCAAAACT	0		0	0	0	0	0
11431	4908	af	AN0693.1	70.m15296	AO070343000520	0			-237	-58			ATGCTTGTACGGAGGGTATGTCGTCATAATGGCAAAACTCACCAGCCTTGCCAGGATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAACAGCGTTGAAATCTGCTCTTCGCATACGTTTAGGAATCCCATCACCTCAAAGACTTACTCAAGAGACCTTTTCGCATCACTTATAA		ATGCTTGTACGGAGGGTATGTCGTCATAATGGCAAAACTCACCAGCCTTGCCAGGATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAACAGCGTTGAAATCTGCTCTTCGCATACGTTTAGGAATCCCATCACCTCAAAGACTTACTCAAGAGACCTTTTCGCATCACTTATAA		MLVRRVCRHNGKTHQPCQDDDGLQSQQLQHITALKSALRIRLGIPSPQRLTQETFSHHL*		MLVRRVCRHNGKTHQPCQDDDGLQSQQLQHITALKSALRIRLGIPSPQRLTQETFSHHL*		ATGCAACCTA	ATCAGTCTAC	0		0	0	0	0	0
11432	4908	af	AN0693.1	70.m15296	AO070343000520	0			-220	-209			ATGTCGTCATAA		ATGTCGTCATAA		MSS*		MSS*		TACGGAGGGT	TGGCAAAACT	0		0	0	0	0	0
11433	4908	af	AN0693.1	70.m15296	AO070343000520	0			-209	-144			ATGGCAAAACTCACCAGCCTTGCCAGGATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		ATGGCAAAACTCACCAGCCTTGCCAGGATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		MAKLTSLARMMTVSSHNSSNI*		MAKLTSLARMMTVSSHNSSNI*		TGTCGTCATA	CAGCGTTGAA	0		0	0	0	0	0
11434	4908	af	AN0693.1	70.m15296	AO070343000520	0			-182	-144			ATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		ATGATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		MMTVSSHNSSNI*		MMTVSSHNSSNI*		CCTTGCCAGG	CAGCGTTGAA	0		0	0	0	0	0
11435	4908	af	AN0693.1	70.m15296	AO070343000520	0			-179	-144			ATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		ATGACGGTCTCCAGTCACAACAGCTCCAACATATAA		MTVSSHNSSNI*		MTVSSHNSSNI*		TGCCAGGATG	CAGCGTTGAA	0		0	0	0	0	0
11426	4908	an	AN0693.1	70.m15296	AO070343000520	0	-166	-125					ATGATTCATGCCAATGGATGCAGGCATACTCCCTTCTTATAA	ATGATTCATGCCAATGGATGCAGGCATACTCCCTTCTTATAA			MIHANGCRHTPFL*	MIHANGCRHTPFL*			TAACGTCATC	GATCAAGTAG	0		0	0	0	0	0
11427	4908	an	AN0693.1	70.m15296	AO070343000520	0	-159	-115					ATGCCAATGGATGCAGGCATACTCCCTTCTTATAAGATCAAGTAG	ATGCCAATGGATGCAGGCATACTCCCTTCTTATAAGATCAAGTAG			MPMDAGILPSYKIK*	MPMDAGILPSYKIK*			ATCATGATTC	ACCACTACAT	0		0	0	0	0	0
11428	4908	an	AN0693.1	70.m15296	AO070343000520	0	-153	-115					ATGGATGCAGGCATACTCCCTTCTTATAAGATCAAGTAG	ATGGATGCAGGCATACTCCCTTCTTATAAGATCAAGTAG			MDAGILPSYKIK*	MDAGILPSYKIK*			ATTCATGCCA	ACCACTACAT	0		0	0	0	0	0
11429	4908	an	AN0693.1	70.m15296	AO070343000520	0	-149	-90					ATGCAGGCATACTCCCTTCTTATAAGATCAAGTAGACCACTACATCTTTGTTTCTTGTAG	ATGCAGGCATACTCCCTTCTTATAAGATCAAGTAGACCACTACATCTTTGTTTCTTGTAG			MQAYSLLIRSSRPLHLCFL*	MQAYSLLIRSSRPLHLCFL*			ATGCCAATGG	AATCATCGAA	0		0	0	0	0	0
11436	4908	ao	AN0693.1	70.m15296	AO070343000520	0					-199	-188	ATGTCGTCATAG			ATGTCGTCATAG	MSS*			MSS*	GACATCGGCT	GTGTAACAAC	0		0	0	0	0	0
11437	4908	ao	AN0693.1	70.m15296	AO070343000520	0					-154	-131	ATGCACCCAACAACAAACATATAA			ATGCACCCAACAACAAACATATAA	MHPTTNI*			MHPTTNI*	CCATTAAATC	GTAACCAGGA	0		0	0	0	0	0
11438	4909	an	AN0504.1	69.m15297	AO070226000008	0	-104	-75					ATGTGTGCATCGGCTATGCTGCCAATTTGA	ATGTGTGCATCGGCTATGCTGCCAATTTGA			MCASAMLPI*	MCASAMLPI*			GAGCACGTTT	GCTTGATTTT	0	DT	FG01464.1	0	0	0	0
11439	4909	an	AN0504.1	69.m15297	AO070226000008	0	-89	-75					ATGCTGCCAATTTGA	ATGCTGCCAATTTGA			MLPI*	MLPI*			TGCATCGGCT	GCTTGATTTT	0	DT	FG01464.1	0	0	0	0
11440	4909	ao	AN0504.1	69.m15297	AO070226000008	0					-272	-144	ATGATAAGGCGGTTACGGGACACCAGAGGGCCCAATCACGCGATCTCGAGATACCCAACAACCACGTGTGGGGAAAAGCGTCACTTGATCTTAATTAATGATTCAATCCAACCTTTTGCGACGTTCTAG			ATGATAAGGCGGTTACGGGACACCAGAGGGCCCAATCACGCGATCTCGAGATACCCAACAACCACGTGTGGGGAAAAGCGTCACTTGATCTTAATTAATGATTCAATCCAACCTTTTGCGACGTTCTAG	MIRRLRDTRGPNHAISRYPTTTCGEKRHLILINDSIQPFATF*			MIRRLRDTRGPNHAISRYPTTTCGEKRHLILINDSIQPFATF*	AGCAAAAAGA	ATATTCGTCC	0	DT	FG01464.1	0	0	0	0
11441	4909	ao	AN0504.1	69.m15297	AO070226000008	0					-175	-83	ATGATTCAATCCAACCTTTTGCGACGTTCTAGATATTCGTCCCCGGTGCAAATAGACGGCCTTCGCTCAATAATTTCTTTCCCCTTCTTTTGA			ATGATTCAATCCAACCTTTTGCGACGTTCTAGATATTCGTCCCCGGTGCAAATAGACGGCCTTCGCTCAATAATTTCTTTCCCCTTCTTTTGA	MIQSNLLRRSRYSSPVQIDGLRSIISFPFF*			MIQSNLLRRSRYSSPVQIDGLRSIISFPFF*	ATCTTAATTA	CCGTTCTGAC	0	DT	FG01464.1	0	0	0	0
11445	4911	af	AN5103.1	54.m06964	AO070291000076	0			-238	-203			ATGATCATGCCTATCCGAGTACGATACCTTTCCTGA		ATGATCATGCCTATCCGAGTACGATACCTTTCCTGA		MIMPIRVRYLS*		MIMPIRVRYLS*		TCTTTTATTT	AAAGGTAATT	0	C	0	0	0	0	0
11446	4911	af	AN5103.1	54.m06964	AO070291000076	0			-232	-203			ATGCCTATCCGAGTACGATACCTTTCCTGA		ATGCCTATCCGAGTACGATACCTTTCCTGA		MPIRVRYLS*		MPIRVRYLS*		ATTTATGATC	AAAGGTAATT	0	C	0	0	0	0	0
11442	4911	an	AN5103.1	54.m06964	AO070291000076	0	-201	-157					ATGATGAACTTTGCAGTTATTTCCGATCCGGACTCAATCCTTTAG	ATGATGAACTTTGCAGTTATTTCCGATCCGGACTCAATCCTTTAG			MMNFAVISDPDSIL*	MMNFAVISDPDSIL*			AATCAAGAGT	CCATCTCTGC	0	C	0	0	0	0	0
11443	4911	an	AN5103.1	54.m06964	AO070291000076	0	-198	-157					ATGAACTTTGCAGTTATTTCCGATCCGGACTCAATCCTTTAG	ATGAACTTTGCAGTTATTTCCGATCCGGACTCAATCCTTTAG			MNFAVISDPDSIL*	MNFAVISDPDSIL*			CAAGAGTATG	CCATCTCTGC	0	C	0	0	0	0	0
11451	4911	ao	AN5103.1	54.m06964	AO070291000076	0					-148	-101	ATGCTTTCTATCCATCACATTCTCTCATACTATCCTCACAAATCTTAA			ATGCTTTCTATCCATCACATTCTCTCATACTATCCTCACAAATCTTAA	MLSIHHILSYYPHKS*			MLSIHHILSYYPHKS*	AAATTTCTGG	TTCATTGTCT	0	C	0	0	0	0	0
11453	4912	af	AN3673.1	58.m07433	AO070342000015	0			-243	-157			ATGGGATCATGGGGACAGGCAACTCTGCATATTTCCATTGGCATCGGTCACAACTCCAACTACACCGCATGGAGGATCCGCGGATAA		ATGGGATCATGGGGACAGGCAACTCTGCATATTTCCATTGGCATCGGTCACAACTCCAACTACACCGCATGGAGGATCCGCGGATAA		MGSWGQATLHISIGIGHNSNYTAWRIRG*		MGSWGQATLHISIGIGHNSNYTAWRIRG*		CAGGCTAAGT	TTCGAACAAA	0	O	FG01377.1	MG05621.1	0	0	0
11454	4912	af	AN3673.1	58.m07433	AO070342000015	0			-235	-119			ATGGGGACAGGCAACTCTGCATATTTCCATTGGCATCGGTCACAACTCCAACTACACCGCATGGAGGATCCGCGGATAATTCGAACAAACACACATATGCTTGAAAGCCCTTCATAG		ATGGGGACAGGCAACTCTGCATATTTCCATTGGCATCGGTCACAACTCCAACTACACCGCATGGAGGATCCGCGGATAATTCGAACAAACACACATATGCTTGAAAGCCCTTCATAG		MGTGNSAYFHWHRSQLQLHRMEDPRIIRTNTHMLESPS*		MGTGNSAYFHWHRSQLQLHRMEDPRIIRTNTHMLESPS*		GTATGGGATC	TTCCAAATTC	0	O	FG01377.1	MG05621.1	0	0	0
11455	4912	af	AN3673.1	58.m07433	AO070342000015	0			-175	-119			ATGGAGGATCCGCGGATAATTCGAACAAACACACATATGCTTGAAAGCCCTTCATAG		ATGGAGGATCCGCGGATAATTCGAACAAACACACATATGCTTGAAAGCCCTTCATAG		MEDPRIIRTNTHMLESPS*		MEDPRIIRTNTHMLESPS*		ACTACACCGC	TTCCAAATTC	0	O	FG01377.1	MG05621.1	0	0	0

11456	4912	af	AN3673.1	58.m07433	AO070342000015	0			-139	-119			ATGCTTGAAAGCCCTTCATAG		ATGCTTGAAAGCCCTTCATAG		MLESPS*		MLESPS*		AAACACACAT	TTCCAAATTC	0	O	FG01377.1	MG05621.1	0	0	0
11452	4912	an	AN3673.1	58.m07433	AO070342000015	0	-225	-109					ATGGAGTTTGTCCAGCACCAGCTCCGTCGACGCAACAGAACTACAAACCCCAATCTCAAATTCACACGAGCACGAGGCGAATCAATCGGCACCATCTGGAGCTGCATAAAAACATAA	ATGGAGTTTGTCCAGCACCAGCTCCGTCGACGCAACAGAACTACAAACCCCAATCTCAAATTCACACGAGCACGAGGCGAATCAATCGGCACCATCTGGAGCTGCATAAAAACATAA			MEFVQHQLRRRNRTTNPNLKFTRARGESIGTIWSCIKT*	MEFVQHQLRRRNRTTNPNLKFTRARGESIGTIWSCIKT*			CGCGGCGGAC	GACCTTCCGA	0	O	FG01377.1	MG05621.1	0	0	0
11458	4913	af	AN0445.1	54.m06637	AO070338000307	0			-238	-89			ATGCGGTTTGCCTCGCGCTCGCCTAATTTGCTAGCGTCCCACACACAACACCTCGCAAAAGAGATCATCTTTCCCTTCAATCTTTCCAGAGCGACATCGACGACAACCGACGACCTGCCACGCCGACAAGGTGCGTTTTCGCGTCCCTAA		ATGCGGTTTGCCTCGCGCTCGCCTAATTTGCTAGCGTCCCACACACAACACCTCGCAAAAGAGATCATCTTTCCCTTCAATCTTTCCAGAGCGACATCGACGACAACCGACGACCTGCCACGCCGACAAGGTGCGTTTTCGCGTCCCTAA		MRFASRSPNLLASHTQHLAKEIIFPFNLSRATSTTTDDLPRRQGAFSRP*		MRFASRSPNLLASHTQHLAKEIIFPFNLSRATSTTTDDLPRRQGAFSRP*		TGGTTGGTGG	AATTGCGATA	0	J	0	0	0	0	0
11457	4913	an	AN0445.1	54.m06637	AO070338000307	0	-116	-105					ATGTCAAGTTGA	ATGTCAAGTTGA			MSS*	MSS*			CCGACAAGGT	ACATTCTGTT	0	J	0	0	0	0	0
11459	4913	ao	AN0445.1	54.m06637	AO070338000307	0					-233	-183	ATGCGGAAGATCTCGCCTAATTTCCTAGCGTCCCACACACAACCTCGTTGA			ATGCGGAAGATCTCGCCTAATTTCCTAGCGTCCCACACACAACCTCGTTGA	MRKISPNFLASHTQPR*			MRKISPNFLASHTQPR*	TGGTTGGTGG	AGAGATCTCG	0	J	0	0	0	0	0
11460	4913	ao	AN0445.1	54.m06637	AO070338000307	0					-110	-84	ATGTTTATAATACCCAGCTCTTCCTGA			ATGTTTATAATACCCAGCTCTTCCTGA	MFIIPSSS*			MFIIPSSS*	CCGACAAGGT	GTTCTCAAGA	0	J	0	0	0	0	0
11462	4914	af	AN7569.1	72.m19588	AO070343000415	0			-103	-89			ATGAAAGGTTCCTGA		ATGAAAGGTTCCTGA		MKGS*		MKGS*		ATCCCATCTG	GCACCAAGTT	0	C	0	0	0	YGR096W	0
11461	4914	an	AN7569.1	72.m19588	AO070343000415	0	-85	-56					ATGACCGAGGCAACTGCGTGCATCCCTTAA	ATGACCGAGGCAACTGCGTGCATCCCTTAA			MTEATACIP*	MTEATACIP*			TAACTTCCCG	TCACTCCATT	0	C	0	0	0	YGR096W	0
11463	4914	ao	AN7569.1	72.m19588	AO070343000415	0					-158	-138	ATGAACTATTCAACCCATTGA			ATGAACTATTCAACCCATTGA	MNYSTH*			MNYSTH*	AAAATTTCCC	AATCTTATAA	0	C	0	0	0	YGR096W	0
11464	4915	af	AN6325.1	72.m19443	AO070304000043	0			-178	-167			ATGAAGATGTGA		ATGAAGATGTGA		MKM*		MKM*		GCCTGCGTTC	ATCATAGTGA	0	R	0	MG01783.1	0	0	0
11465	4915	af	AN6325.1	72.m19443	AO070304000043	0			-94	-74			ATGCCAGAGAATCCAACCTAG		ATGCCAGAGAATCCAACCTAG		MPENPT*		MPENPT*		CTTATCGCAT	ATTTACACTT	0	R	0	MG01783.1	0	0	0
11466	4915	ao	AN6325.1	72.m19443	AO070304000043	0					-103	-86	ATGCTACTTGTCACCTAG			ATGCTACTTGTCACCTAG	MLLVT*			MLLVT*	CTTCTCGTGC	ACCTCAGAAC	0	R	0	MG01783.1	0	0	0
11471	4920	af	AN3034.1	59.m08984	AO070337000075	0			-159	-142			ATGGCAGAAGCTCCCTAG		ATGGCAGAAGCTCCCTAG		MAEAP*		MAEAP*		ATCATCGGAA	TCTTGGCGGC	0	C	FG07041.1	0	0	0	0
11467	4920	an	AN3034.1	59.m08984	AO070337000075	0	-191	-162					ATGTCGTGGTCTCAACTGCAATATAGTTAA	ATGTCGTGGTCTCAACTGCAATATAGTTAA			MSWSQLQYS*	MSWSQLQYS*			TACCGGCTTC	TGATGTACTC	0	C	FG07041.1	0	0	0	0
11468	4920	an	AN3034.1	59.m08984	AO070337000075	0	-162	-13					ATGATGTACTCCGCAGAAGCTGGAGCTCTAAGTCTTGGCAGCGCTTATCCTCATTGGGAAATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA	ATGATGTACTCCGCAGAAGCTGGAGCTCTAAGTCTTGGCAGCGCTTATCCTCATTGGGAAATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA			MMYSAEAGALSLGSAYPHWEMLTSSDPNLLPSILVFKPSTISSHPNVHF*	MMYSAEAGALSLGSAYPHWEMLTSSDPNLLPSILVFKPSTISSHPNVHF*			AATATAGTTA	GCTACATTCA	0	C	FG07041.1	0	0	0	0
11469	4920	an	AN3034.1	59.m08984	AO070337000075	0	-159	-13					ATGTACTCCGCAGAAGCTGGAGCTCTAAGTCTTGGCAGCGCTTATCCTCATTGGGAAATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA	ATGTACTCCGCAGAAGCTGGAGCTCTAAGTCTTGGCAGCGCTTATCCTCATTGGGAAATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA			MYSAEAGALSLGSAYPHWEMLTSSDPNLLPSILVFKPSTISSHPNVHF*	MYSAEAGALSLGSAYPHWEMLTSSDPNLLPSILVFKPSTISSHPNVHF*			ATAGTTAATG	GCTACATTCA	0	C	FG07041.1	0	0	0	0
11470	4920	an	AN3034.1	59.m08984	AO070337000075	0	-102	-13					ATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA	ATGTTAACATCATCCGACCCGAATCTTTTGCCTTCGATTCTCGTCTTCAAACCATCAACAATTTCCTCCCATCCCAACGTCCATTTCTAA			MLTSSDPNLLPSILVFKPSTISSHPNVHF*	MLTSSDPNLLPSILVFKPSTISSHPNVHF*			TCATTGGGAA	GCTACATTCA	0	C	FG07041.1	0	0	0	0
11472	4920	ao	AN3034.1	59.m08984	AO070337000075	0					-169	-149	ATGTTGGGACGGAAAGGATGA			ATGTTGGGACGGAAAGGATGA	MLGRKG*			MLGRKG*	CCCTCTTCAG	ATGCCTCAGG	0	C	FG07041.1	0	0	0	0
11473	4920	ao	AN3034.1	59.m08984	AO070337000075	0					-152	-54	ATGAATGCCTCAGGCCGACCGGTCGAGAGCTCCCGAGCTTGTTCTTGGCAAGCGGTAACATCATCAGTTTCCTGTTCGTCACCTCCAAACTTTCATTAA			ATGAATGCCTCAGGCCGACCGGTCGAGAGCTCCCGAGCTTGTTCTTGGCAAGCGGTAACATCATCAGTTTCCTGTTCGTCACCTCCAAACTTTCATTAA	MNASGRPVESSRACSWQAVTSSVSCSSPPNFH*			MNASGRPVESSRACSWQAVTSSVSCSSPPNFH*	GACGGAAAGG	AATTCTCCTC	0	C	FG07041.1	0	0	0	0
11474	4920	ao	AN3034.1	59.m08984	AO070337000075	0					-148	-95	ATGCCTCAGGCCGACCGGTCGAGAGCTCCCGAGCTTGTTCTTGGCAAGCGGTAA			ATGCCTCAGGCCGACCGGTCGAGAGCTCCCGAGCTTGTTCTTGGCAAGCGGTAA	MPQADRSRAPELVLGKR*			MPQADRSRAPELVLGKR*	GAAAGGATGA	CATCATCAGT	0	C	FG07041.1	0	0	0	0
11475	4922	ao	AN5022.1	59.m09494	AO070338000182	0					-184	-170	ATGCGGAGACAATAA			ATGCGGAGACAATAA	MRRQ*			MRRQ*	CTTAGCCCCA	ACAAAAAGTG	0	Z	FG10315.1	MG08423.1	NCU07196.1	0	0
11480	4924	af	AN3814.1	57.m05668	AO070311000012	0			-327	-283			ATGTGTCCCAATTGCTTCTACTTGATGGGTTCGCCGTGCTCTTGA		ATGTGTCCCAATTGCTTCTACTTGATGGGTTCGCCGTGCTCTTGA		MCPNCFYLMGSPCS*		MCPNCFYLMGSPCS*		TGGAGTGTCC	TGGCCTTGCA	0	O	0	0	0	0	0
11481	4924	af	AN3814.1	57.m05668	AO070311000012	0			-303	-283			ATGGGTTCGCCGTGCTCTTGA		ATGGGTTCGCCGTGCTCTTGA		MGSPCS*		MGSPCS*		CTTCTACTTG	TGGCCTTGCA	0	O	0	0	0	0	0
11482	4924	af	AN3814.1	57.m05668	AO070311000012	0			-283	-254			ATGGCCTTGCAAAGGACGGCGCATCCCTAG		ATGGCCTTGCAAAGGACGGCGCATCCCTAG		MALQRTAHP*		MALQRTAHP*		CGTGCTCTTG	CACTGGGCCT	0	O	0	0	0	0	0
11483	4924	af	AN3814.1	57.m05668	AO070311000012	0			-222	-22			ATGCAGTCAACTACCGGCTTCCCACGTGGGAGCCTGAGGCCAGCAACCTTCCCGACGGCTTACCTAAACTGGCACACATGGAACTTTTCGGCTGACGCAATATGTTCCCATTGCACTTTTAGTCACGTGATTCCCCCCCTTTTCCTCCCCCCTCCCAAAAATTCGGTCGCCGTATTGACCCGCTTCTGCCCCTCCTTTTAG		ATGCAGTCAACTACCGGCTTCCCACGTGGGAGCCTGAGGCCAGCAACCTTCCCGACGGCTTACCTAAACTGGCACACATGGAACTTTTCGGCTGACGCAATATGTTCCCATTGCACTTTTAGTCACGTGATTCCCCCCCTTTTCCTCCCCCCTCCCAAAAATTCGGTCGCCGTATTGACCCGCTTCTGCCCCTCCTTTTAG		MQSTTGFPRGSLRPATFPTAYLNWHTWNFSADAICSHCTFSHVIPPLFLPPPKNSVAVLTRFCPSF*		MQSTTGFPRGSLRPATFPTAYLNWHTWNFSADAICSHCTFSHVIPPLFLPPPKNSVAVLTRFCPSF*		AGCTTGGTAT	TTCCAGCACC	0	O	0	0	0	0	0
11484	4924	af	AN3814.1	57.m05668	AO070311000012	0			-145	-128			ATGGAACTTTTCGGCTGA		ATGGAACTTTTCGGCTGA		MELFG*		MELFG*		ACTGGCACAC	CGCAATATGT	0	O	0	0	0	0	0
11485	4924	af	AN3814.1	57.m05668	AO070311000012	0			-121	-101			ATGTTCCCATTGCACTTTTAG		ATGTTCCCATTGCACTTTTAG		MFPLHF*		MFPLHF*		CTGACGCAAT	TCACGTGATT	0	O	0	0	0	0	0
11476	4924	an	AN3814.1	57.m05668	AO070311000012	0	-336	-298					ATGCCAGTTCATCAGATTAGCCTTCATTACAGCTGTTAA	ATGCCAGTTCATCAGATTAGCCTTCATTACAGCTGTTAA			MPVHQISLHYSC*	MPVHQISLHYSC*			TGAGTCCTCC	ACAATGTATT	0	O	0	0	0	0	0
11477	4924	an	AN3814.1	57.m05668	AO070311000012	0	-294	-247					ATGTATTCTACTTCAATTCTTTGGGCAGCCGAGCCGCCCGAAGAGTGA	ATGTATTCTACTTCAATTCTTTGGGCAGCCGAGCCGCCCGAAGAGTGA			MYSTSILWAAEPPEE*	MYSTSILWAAEPPEE*			CTGTTAAACA	TTGTATTTCT	0	O	0	0	0	0	0
11486	4924	ao	AN3814.1	57.m05668	AO070311000012	0					-360	-241	ATGAATTGGCCACGGCGTTGGGTCTGGTTGCTTCCATCCAATGCTGTTCCTTTCCAATCCCTTAGCCCAAAGTCCACCCCCAGGCTAAGGGAGAGGCCAACCAACCATATGGCGGCCTGA			ATGAATTGGCCACGGCGTTGGGTCTGGTTGCTTCCATCCAATGCTGTTCCTTTCCAATCCCTTAGCCCAAAGTCCACCCCCAGGCTAAGGGAGAGGCCAACCAACCATATGGCGGCCTGA	MNWPRRWVWLLPSNAVPFQSLSPKSTPRLRERPTNHMAA*			MNWPRRWVWLLPSNAVPFQSLSPKSTPRLRERPTNHMAA*	TCCCGGTGAG	GGCCACCACA	0	O	0	0	0	0	0
11487	4924	ao	AN3814.1	57.m05668	AO070311000012	0					-320	-273	ATGCTGTTCCTTTCCAATCCCTTAGCCCAAAGTCCACCCCCAGGCTAA			ATGCTGTTCCTTTCCAATCCCTTAGCCCAAAGTCCACCCCCAGGCTAA	MLFLSNPLAQSPPPG*			MLFLSNPLAQSPPPG*	CTTCCATCCA	GGGAGAGGCC	0	O	0	0	0	0	0
11488	4924	ao	AN3814.1	57.m05668	AO070311000012	0					-252	-241	ATGGCGGCCTGA			ATGGCGGCCTGA	MAA*			MAA*	AACCAACCAT	GGCCACCACA	0	O	0	0	0	0	0
11489	4925	af	AN0454.1	54.m06615	AO070328000182	0			-219	-43			ATGCTTTGCTCGATTATTTTGTGTTGTAATCAAAGCAGATTATCTTTAAAGTCTATTTATTTATTGAAGCAAGTCGGAAACGTGGATGACTGTTGCTCTGCTTTAAGTCAGGCTGACTCTCGCCTCGTATCAGTAATCCTCTCTTCACACTCTGTGATCTTCTTCGGGTGCTACTAG		ATGCTTTGCTCGATTATTTTGTGTTGTAATCAAAGCAGATTATCTTTAAAGTCTATTTATTTATTGAAGCAAGTCGGAAACGTGGATGACTGTTGCTCTGCTTTAAGTCAGGCTGACTCTCGCCTCGTATCAGTAATCCTCTCTTCACACTCTGTGATCTTCTTCGGGTGCTACTAG		MLCSIILCCNQSRLSLKSIYLLKQVGNVDDCCSALSQADSRLVSVILSSHSVIFFGCY*		MLCSIILCCNQSRLSLKSIYLLKQVGNVDDCCSALSQADSRLVSVILSSHSVIFFGCY*		TGTCTTGCGT	AATTTTATCC	0	E	0	0	0	0	0
11490	4925	af	AN0454.1	54.m06615	AO070328000182	0			-134	-114			ATGACTGTTGCTCTGCTTTAA		ATGACTGTTGCTCTGCTTTAA		MTVALL*		MTVALL*		GGAAACGTGG	GTCAGGCTGA	0	E	0	0	0	0	0
11491	4925	ao	AN0454.1	54.m06615	AO070328000182	0					-264	-235	ATGGTCGCGGATCTTTATATAGTATGTTAA			ATGGTCGCGGATCTTTATATAGTATGTTAA	MVADLYIVC*			MVADLYIVC*	TTCTTTGCTA	TATATCTCCG	0	E	0	0	0	0	0
11492	4925	ao	AN0454.1	54.m06615	AO070328000182	0					-241	-191	ATGTTAATATATCTCCGCCACCCGCCTAGTTCCGTTTTGGATGGCAGGTGA			ATGTTAATATATCTCCGCCACCCGCCTAGTTCCGTTTTGGATGGCAGGTGA	MLIYLRHPPSSVLDGR*			MLIYLRHPPSSVLDGR*	TTTATATAGT	ATTGTTGAAT	0	E	0	0	0	0	0
11493	4925	ao	AN0454.1	54.m06615	AO070328000182	0					-201	-79	ATGGCAGGTGAATTGTTGAATGTCCGTTCGCAGCCGTCAGACCTTATCAGTCCGCCCCGCCCACCATAACTTGGTCCCTCCTCCCTCCAACCGTGGTTCAATTAACTTTTCCCTACAACAATAG			ATGGCAGGTGAATTGTTGAATGTCCGTTCGCAGCCGTCAGACCTTATCAGTCCGCCCCGCCCACCATAACTTGGTCCCTCCTCCCTCCAACCGTGGTTCAATTAACTTTTCCCTACAACAATAG	MAGELLNVRSQPSDLISPPAHHNLVPPPSNRGSINFSLQQ*			MAGELLNVRSQPSDLISPPAHHNLVPPPSNRGSINFSLQQ*	TCCGTTTTGG	CTTTTTCTTC	0	E	0	0	0	0	0
11494	4925	ao	AN0454.1	54.m06615	AO070328000182	0					-182	-33	ATGTCCGTTCGCAGCCGTCAGACCTTATCAGTCCGCCCCGCCCACCATAACTTGGTCCCTCCTCCCTCCAACCGTGGTTCAATTAACTTTTCCCTACAACAATAGCTTTTTCTTCTTTCGATGTTCACAATCATTTTGTAATCTGTGGTGA			ATGTCCGTTCGCAGCCGTCAGACCTTATCAGTCCGCCCCGCCCACCATAACTTGGTCCCTCCTCCCTCCAACCGTGGTTCAATTAACTTTTCCCTACAACAATAGCTTTTTCTTCTTTCGATGTTCACAATCATTTTGTAATCTGTGGTGA	MSVRSRQTLSVRPPTITWSLLPPTVVQLTFPYNNSFFFFRCSQSFCNLW*			MSVRSRQTLSVRPPTITWSLLPPTVVQLTFPYNNSFFFFRCSQSFCNLW*	GAATTGTTGA	CAAGAATATC	0	E	0	0	0	0	0
11496	4929	an	AN7367.1	69.m15484	AO070239000027	0	-231	-163					ATGAATGAATGGCGGGATTTGATGCTCAACGCTGCAGGTAGGCTATACGCACCTAGCGATCTGCGATAA	ATGAATGAATGGCGGGATTTGATGCTCAACGCTGCAGGTAGGCTATACGCACCTAGCGATCTGCGATAA			MNEWRDLMLNAAGRLYAPSDLR*	MNEWRDLMLNAAGRLYAPSDLR*			TTAATCACAA	ACAAACCCCG	0	E	0	0	0	0	0
11497	4929	an	AN7367.1	69.m15484	AO070239000027	0	-227	-210					ATGAATGGCGGGATTTGA	ATGAATGGCGGGATTTGA			MNGGI*	MNGGI*			TCACAAATGA	TGCTCAACGC	0	E	0	0	0	0	0
11498	4929	an	AN7367.1	69.m15484	AO070239000027	0	-223	-191					ATGGCGGGATTTGATGCTCAACGCTGCAGGTAG	ATGGCGGGATTTGATGCTCAACGCTGCAGGTAG			MAGFDAQRCR*	MAGFDAQRCR*			AAATGAATGA	GCTATACGCA	0	E	0	0	0	0	0
11499	4929	an	AN7367.1	69.m15484	AO070239000027	0	-210	-163					ATGCTCAACGCTGCAGGTAGGCTATACGCACCTAGCGATCTGCGATAA	ATGCTCAACGCTGCAGGTAGGCTATACGCACCTAGCGATCTGCGATAA			MLNAAGRLYAPSDLR*	MLNAAGRLYAPSDLR*			GCGGGATTTG	ACAAACCCCG	0	E	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_consensus	context_down_consensus	within 60bp	COG category	fg_uorf_utr	mg_uorf_utr	nc_uorf_utr	sc_uorf_100bp	sc_cooccur_orf_100bp
6578	3178	conserved	AN1179.1	70.m15038	AO070331000175	1	-27	-10	-27	-10	-27	-10	ATGTCATyCCbTybyTrA	ATGTCATCCCCTCGTTAA	ATGTCATCCCGTCCTTGA	ATGTCATTCCTTTTCTGA	MSspr*	MSSPR*	MSSRP*	MSFLF*	dyhvGATCCG	yTmGyCTCAA	0	U	0	0	0	0	0
5687	2862	conserved	AN1341.1	70.m15733	AO070247000023	1	-31	-20	-46	-35	-34	-23	ATGGGCyGTTGA	ATGGGCCGTTGA	ATGGGCCGTTGA	ATGGGCTGTTGA	MGr*	MGR*	MGR*	MGC*	TkdyyTTGGA	vyyvyymrhw	1	U	FG01552.1	0	0	0	0
6597	3186	conserved	AN9125.1	66.m04585	AO070332000149	1	-52	-26	-62	-36	-65	-39	ATGChmdyTywymAdsvybTbCGGTGA	ATGCAATTTTACCAACGCCTGCGGTGA	ATGCTCACTTTCAATGCCGTCCGGTGA	ATGCCAGTTCATAAGCATTTTCGGTGA	MqfyqrlR*	MQFYQRLR*	MLTFNAVR*	MPVHKHFR*	mkmwyykAmh	ywbbwCkCyy	0	K	FG00778.1	0	NCU00727.1	YNR003C	0
698	516	conserved	AN5151.1	69.m14882	AO070237000013	1	-48	-37	-365	-354	-101	-90	ATGydsvTTTGA	ATGTACCTTTGA	ATGCGGGTTTGA	ATGCTGATTTGA	Myl*	MYL*	MRV*	MLI*	mhhsmAGrhy	TmTbsmmdwd	0	RT	0	0	0	0	0
2846	1792	conserved	AN8723.1	62.m03343	AO070315000151	1	-93	-40	-93	-40	-93	-40	ATGAAmTysGGTCCrTysyvTCymymCrswTysAGAwCGryyGGyGCwTCyTAG	ATGAACTTCGGTCCGTCCTGTCCATCCACATTGAGATCGGCTGGTGCATCCTAG	ATGAAATCGGGTCCATTGTCTCTATACGGTTCCAGATCGATCGGCGCTTCTTAG	ATGAAATTCGGTCCGTCCCATCTCCACACATCGAGAACGACCGGCGCTTCCTAG	MnfGPscpstlRsaGAS*	MNFGPSCPSTLRSAGAS*	MKSGPLSLYGSRSIGAS*	MKFGPSHLHTSRTTGAS*	vvyhAsCATC	ACTybwGTCr	0		0	0	0	0	0
6221	3048	conserved	AN1014.1	70.m15232	AO070312000004	1	-67	-41	-120	-94	-73	-47	ATGTTvbCyywmGyyGAyyCyGGmTrr	ATGTTGCCTTACGTTGATTCCGGATAA	ATGTTCGCCTTCGCCGACCCTGGATAG	ATGTTATCCCAAGTTGACTCTGGCTGA	MlpyvDsG*	MLPYVDSG*	MFAFADPG*	MLSQVDSG*	bhbbmTrGhy	wvyywwwwby	0	I	0	0	NCU01751.1	YKL188C	YKL188C
1983	1287	conserved	AN6642.1	62.m03239	AO070295000022	1	-101	-54	-86	-39	-139	-92	ATGGACTCkCAyTssyTkGwdGAyACrATmTAyATGrAGCCTCCyTAr	ATGGACTCGCATTCCTTGGTTGACACGATCTATATGGAGCCTCCCTAA	ATGGACTCTCACTCGCTTGAAGATACGATATACATGAAGCCTCCTTAG	ATGGACTCGCATTGCCTGGAGGATACAATCTATATGGAGCCTCCCTAA	MDSHsLvDTIYMePP*	MDSHSLVDTIYMEPP*	MDSHSLEDTIYMKPP*	MDSHCLEDTIYMEPP*	sTbbwkGTGy	rrdmmmbsmh	0	P	0	0	0	0	0
1984	1287	conserved	AN6642.1	62.m03239	AO070295000022	1	-68	-54	-53	-39	-106	-92	ATGrAGCCTCCyTAr	ATGGAGCCTCCCTAA	ATGAAGCCTCCTTAG	ATGGAGCCTCCCTAA	MePP*	MEPP*	MKPP*	MEPP*	yACrATmTAy	rrdmmmbsmh	0	P	0	0	0	0	0
5131	2655	conserved	AN5528.1	69.m15427	AO070341000360	1	-69	-58	-59	-48	-67	-56	ATGsTyyCyTGA	ATGCTCCCCTGA	ATGGTCTCTTGA	ATGGTTCCTTGA	Mlp*	MLP*	MVS*	MVP*	CrCkmywAhr	skAhAvrbhG	0	U	0	0	NCU05029.1	0	0
3384	2032	conserved	AN8846.1	71.m15980	AO070271000030	1	-87	-64	-260	-237	-89	-66	ATGAyCmrybkbyGsTwydCdTrA	ATGATCCGTTGGCGCTTTGCATAA	ATGACCCACCTTCGGTACACTTGA	ATGATCAGTGTCTGGTACTCGTAA	Mirwrfa*	MIRWRFA*	MTHLRYT*	MISVWYS*	CmkywATymA	rwwyyysrAr	0	G	0	0	0	0	0
2203	1408	conserved	AN5966.1	72.m19965	AO070340000323	1	-100	-83	-175	-158	-77	-60	ATGAwCGGGATACCGTGA	ATGATCGGGATACCGTGA	ATGAACGGGATACCGTGA	ATGATCGGGATACCGTGA	MiGIP*	MIGIP*	MNGIP*	MIGIP*	TyTGyrATCr	AmyyydysyC	0	R	0	0	0	0	0
2179	1396	conserved	AN5452.1	69.m15743	AO070239000031	1	-105	-85	-103	-83	-106	-86	ATGGGAdTrvTwyyAywhTrA	ATGGGAGTACTTTTATTATAA	ATGGGATTGATTCTATTCTGA	ATGGGAATGGTATCACATTAA	MGvlll*	MGVLLL*	MGLILF*	MGMVSH*	mTCTGCAGCA	AGwCAmmywd	0	A	0	MG06457.1	0	0	0
6416	3115	conserved	AN8009.1	53.m03858	AO070322000058	1	-191	-126	-317	-141	-325	-125	ATGACAGGTGTTCGdyykGGryywvhsyykGwhGhyykGhsmTyhyhsTdybdyAwsyTsdhCydsysTGTskkTmTyyyTTTrrsskkkrkrsmCsyCkmrsrrrmsGwkrGACrmwsssmrwmGkCwGwswGrArssskryCGkkykkAsrwkryAswGTCmkrwCkTkmTswrrTTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGGCCGGGGTCAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGATCTGGGTTTCTGTCTGAAGACTGGTGCTTTTTGTTCGGTATGCTCGACTGCTCTGTGGTTATTTTTTTGACCTGGAGAGACGCCTCGCAGACGGATGGACGCTCCCAGTCGTCAGTCAGAAACCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	ATGACAGGTGTTCGTCTTGGACCTGCCCTGGTTGCCTGGCCATCCCCCTACTTCATGCTGTCCCTGCGTGTCTGTCTCCCTTTAGGGGTTGTGCCCCTCGAAGGAGACGTGAGACAAAGGGCAAAGGCTGAGTGGAGGGGTACCGGGTGTACGAGGCAGAGTCCGGTCGTTCTGAGATTATACTGTCATAACTTGATCTAG	MTGVRpGsnpvvlrlychnLi*	MTGVRPGSNPVVLRLYCHNLI*	MTGVRSGFLSEDWCFLFGMLDCSVVIFLTWRDASQTDGRSQSSVRNPVVLRLYCHNLI*	MTGVRLGPALVAWPSPYFMLSLRVCLPLGVVPLEGDVRQRAKAEWRGTGCTRQSPVVLRLYCHNLI*	ywGCwysCGC	ATAATACTAG	0	P	FG01672.1	0	0	0	0
10042	4339	conserved	AN2902.1	59.m08753	AO070338000104	1	-143	-132	-159	-148	-143	-132	ATGGmkCCmTAG	ATGGCTCCATAG	ATGGATCCCTAG	ATGGCGCCATAG	MaP*	MAP*	MDP*	MAP*	mkCkwCGGGC	Ckrybrrrmv	0	K	0	MG03485.1	NCU09300.1	0	0
1303	917	conserved	AN4670.1	71.m15658	AO070284000036	1	-171	-160	-308	-297	-158	-147	ATGArbCyhTrA	ATGAGGCTCTGA	ATGAGTCCATAA	ATGAACCCTTGA	Mrl*	MRL*	MSP*	MNP*	bhmksArGCC	wyTsssvrsd	0	R	0	0	0	0	0
3357	2016	conserved	AN1779.1	69.m15647	AO070324000017	1	-177	-163	-188	-174	-129	-115	ATGrCbTyTyTsTrA	ATGGCCTTTCTCTGA	ATGACTTCTCTCTAA	ATGGCGTCTTTGTGA	MafL*	MAFL*	MTSL*	MASL*	mryryswACA	kykAmvvTyy	0	LD	0	0	0	0	0
1652	1125	conserved	AN1546.1	55.m03274	AO070339000308	1	-185	-174	-657	-646	-177	-166	ATGkykyTGTGA	ATGTTTCTGTGA	ATGGCTTTGTGA	ATGTCGCTGTGA	MfL*	MFL*	MAL*	MSL*	yArymCAGTG	rATGAsydGG	0	B	0	0	0	0	0
116	85	conserved	AN1521.1	55.m03040	AO070334000239	1	-207	-196	-283	-272	-282	-271	ATGArybryTrA	ATGAATCATTAA	ATGAGCGACTGA	ATGAGCTGCTGA	Mnh*	MNH*	MSD*	MSC*	kmbwsykryC	khTyhbddyh	0	K	0	0	0	0	0
7940	3651	conserved	AN1349.1	70.m14884	AO070237000012	1	-254	-201	-250	-197	-260	-207	ATGGCGAAyTwCsyTkTyhmrAGATATGyCGTCwTTCyTTTTkGGCTTGTGTGA	ATGGCGAATTACGTTGTCTCAAGATATGTCGTCTTTCCTTTTTGGCTTGTGTGA	ATGGCGAACTTCCCTTTTCAGAGATATGTCGTCATTCTTTTTGGGCTTGTGTGA	ATGGCGAATTACGTTTTCAAGAGATATGCCGTCTTTCTTTTTGGGCTTGTGTGA	MANyvvsRYvVfpFwLV*	MANYVVSRYVVFPFWLV*	MANFPFQRYVVILFGLV*	MANYVFKRYAVFLFGLV*	AGCTTTCChT	AGTGGGATyT	0	A	0	0	0	0	0
10206	4418	conserved	AN0412.1	54.m06662	AO070338000255	1	-228	-211	-292	-275	-300	-283	ATGysTykTATATyATrr	ATGTCTCTTATATTATAG	ATGCGTTGTATATCATGA	ATGCCTTGTATATCATGA	Mslll*	MSLIL*	MRCIS*	MPCIS*	CmyhmmCAyC	ymvTChTysk	0	RP	0	0	0	0	0
1355	936	conserved	AN1082.1	70.m15156	AO070285000082	1	-243	-217	-285	-259	-116	-90	ATGrTyyyhvykyvyTTyrryysyTAA	ATGATTCTAGCGTCCTTCAATTCCTAA	ATGGTCCTCACTCGTTTTAGTCGCTAA	ATGGTTTCTCTTCATTTCGACCGTTAA	MilasFns*	MILASFNS*	MVLTRFSR*	MVSLHFDR*	ysvwGvmyCk	hhwvTCTyTC	0	F	FG05143.1	MG08146.1	0	0	0
9060	4027	conserved	AN4984.1	59.m08886	AO070288000052	1	-236	-222	-265	-251	-629	-615	ATGyywwTywwCTAA	ATGCTTTTCAACTAA	ATGTCAATCATCTAA	ATGTTATTTTACTAA	Mlfn*	MLFN*	MSII*	MLFY*	kwdTCyCyyC	GmGAhwyymA	0	R	0	0	0	0	0
9102	4038	conserved	AN6843.1	71.m15300	AO070314000096	1	-278	-237	-157	-116	-166	-125	ATGGCTbTCbCGmAGCwCwrGkGGbyTkyTbwCdGGvdCTGA	ATGGCTGTCTCGCAGCTCAAGGGGTCTTCTTTCTGGAACTGA	ATGGCTTTCGCGAAGCTCAAGTGGCCTGTTGACAGGCGCTGA	ATGGCTCTCCCGAAGCACTGGTGGGTTGCTCTCGGGGTCTGA	MAvsqlkgssfwn*	MAVSQLKGSSFWN*	MAFAKLKWPVDRR*	MALPKHWWVALGV*	GhrCyyTmAG	rrCCAChACr	0	J	FG09003.1	MG04008.1	0	YML025C	YML025C
7939	3651	conserved	AN1349.1	70.m14884	AO070237000012	1	-418	-401	-398	-381	-430	-413	ATGAwmmArTCkyTyTGA	ATGATCAAATCTCTTTGA	ATGAAACAGTCGTTTTGA	ATGAACAAGTCGCTCTGA	MikSl*	MIKSL*	MKQSF*	MNKSL*	srsAAAAryC	CmAymGTGTA	0	A	0	0	0	0	0
958	700	conserved	AN8076.1	53.m03929	AO070330000034	0	-11	1	-11	1	-11	1	ATGryCyGGTGA	ATGGTCCGGTGA	ATGACCTGGTGA	ATGACCTGGTGA	Mvr*	MVR*	MTW*	MTW*	myyTTywrky	TGTCTkCrCG	1	A	0	0	0	0	0
3046	1907	conserved	AN4597.1	57.m05519	AO070267000013	0	-38	1	-38	1	-38	1	ATGmGryhyyyybwwdCvdryydyAbyhyhmydhymTAA	ATGCGATACCTTCTATCATACTTTAGTCTACCTCTCTAA	ATGAGGCTTTCTGATACCAGTTGCATTTTTACGACATAA	ATGAGGCCCTCCTTTGCGGACCATACCACCATATCATAA	MRyllsyfslpl*	MRYLLSYFSLPL*	MRLSDTSCIFTT*	MRPSFADHTTIS*	mhyyGsCTTs	TGwCrTCwwy	1	BD	0	0	0	0	0
8333	3765	conserved	AN0244.1	54.m06697	AO070338000236	0	-23	1	-23	1	-23	1	ATGrwyATkCGrACrThyyGCTGA	ATGAACATTCGGACATACCGCTGA	ATGGTTATGCGAACGTCCTGCTGA	ATGGTCATTCGAACATTTTGCTGA	MniRTyr*	MNIRTYR*	MVMRTSC*	MVIRTFC*	wbwbrrAGmr	TGAGCTCCAh	1	U	0	0	0	0	0
10199	4413	conserved	AN4486.1	57.m05645	AO070311000037	0	-26	1	-26	1	-26	1	ATGCTyCTGyyGyyrCCrGyCCCGTrA	ATGCTTCTGTCGTCACCAGCCCCGTGA	ATGCTTCTGCTGCTGCCGGCCCCGTAA	ATGCTCCTGCTGCCACCAGTCCCGTAA	MLLssPaP*	MLLSSPAP*	MLLLLPAP*	MLLLPPVP*	vmdvskAATA	TGGGAGGTry	1		0	0	0	0	0
1051	757	conserved	AN1854.1	58.m08938	AO070292000029	0	-57	-4	-51	-4	-51	-4	ATGsTkywThyvmsvArrrhdrkhhymmkwmmhhvhCwvvmmACkwvrACGTGA	ATGGTGTTTTCCAGAAAGGTTGGATCAAGAACAACTCAACACACGACGACGTGA	ATGGTTCATATACGGAGAGCGAGTACCATACATCGACTGGCCACTTGA	ATGCTTCTTCCGCCCAAAAAAATCCTACTTCACTACCTCACAACTTAA	MvfsrkvgsrttqhTtt*	MVFSRKVGSRTTQHTTT*	MVHIRRASTIHRLAT*	MLLPPKKILLHYLTT*	yvvbGwGrCm	CsrATGACvm	1		0	0	0	0	0
8001	3673	conserved	AN0118.1	71.m15397	AO070311000095	0	-36	-10	-39	-13	-39	-13	ATGmTmmmsdysrGyydmTwCyyrTAr	ATGATACAGTCGGGTTACTTCTCATAG	ATGCTAACCGTGGGTCGCTACCTGTAA	ATGATCACCACCAGCTTATTCTCATAA	Miqsgyfs*	MIQSGYFS*	MLTVGRYL*	MITTSLFS*	yvrmmymTys	rkwrTyryvr	1	Z	0	0	0	0	0
5165	2671	conserved	AN3144.1	59.m08521	AO070256000047	0	-23	-12	-25	-14	-23	-12	ATGCTCymmTAA	ATGCTCCCATAA	ATGCTCCCATAA	ATGCTCTACTAA	MLp*	MLP*	MLP*	MLY*	TyyhyyTCCC	yCbrmdyCwm	1	R	FG04221.1	MG09837.1	0	YDR323C	0
7348	3451	conserved	AN2905.1	59.m08756	AO070338000100	0	-23	-12	-23	-12	-23	-12	ATGGGTTGGTAA	ATGGGTTGGTAA	ATGGGTTGGTAA	ATGGGTTGGTAA	MGW*	MGW*	MGW*	MGW*	sdCyTTGCAG	rACCrCACGA	1	K	0	0	0	0	0

uORF_id	ortholog_cluster_id	species	an_gene	af_gene	ao_gene	in_utr	an_rel_start	an_rel_stop	af_rel_start	af_rel_stop	ao_rel_start	ao_rel_stop	consensus_dna	an_dna	af_dna	ao_dna	consensus_aa	an_aa	af_aa	ao_aa	context_up_consensus	context_down_consensus	within 60bp	COG category	fg_uorf_utr	mg_uorf_utr	nc_uorf_utr	sc_uorf_100bp	sc_cooccur_orf_100bp
1528	1046	conserved	AN1494.1	55.m03004	AO070334000211	0	-60	-13	-60	-13	-60	-13	ATGACGGTrGAkGryCAGskwrGCGCTCGyGGCGCAGTrCACGAyTGA	ATGACGGTGGATGGTCAGCTTGGCGCTCGTGGCGCAGTACACGACTGA	ATGACGGTGGATGGTCAGCGTGGCGCTCGCGGCGCAGTGCACGATTGA	ATGACGGTAGAGGACCAGGGAAGCGCTCGCGGCGCAGTGCACGACTGA	MTVdgQlgARGAVHD*	MTVDGQLGARGAVHD*	MTVDGQRGARGAVHD*	MTVEDQGSARGAVHD*	krrsyTGGAC	GTAyyyTGCG	1	K	0	0	NCU02052.1	0	0
5	4	conserved	AN0877.1	70.m15480	AO070320000036	0	-34	-14	-34	-14	-34	-14	ATGTGTkGTGAyCACGGmTGA	ATGTGTTGTGATCACGGATGA	ATGTGTTGTGACCACGGCTGA	ATGTGTGGTGACCACGGATGA	MCcDHG*	MCCDHG*	MCCDHG*	MCGDHG*	yrrrTGysmv	hhAyTyGCTC	1		0	0	0	0	0
2923	1844	conserved	AN4864.1	59.m09108	AO070329000150	0	-30	-16	-27	-13	-35	-21	ATGGrwsACmvbTrA	ATGGAAGACCACTGA	ATGGGAGACAGGTGA	ATGGGTCACCCTTAA	Medh*	MEDH*	MGDR*	MGHP*	TwyksrGyCA	whvydhyhhv	1	GE	0	MG09310.1	0	YOR002W	0
9193	4076	conserved	AN1168.1	70.m15052	AO070331000162	0	-37	-20	-37	-20	-37	-20	ATGTCTrCmTTCGGyTAG	ATGTCTGCATTCGGCTAG	ATGTCTACATTCGGCTAG	ATGTCTGCCTTCGGTTAG	MSaFG*	MSAFG*	MSTFG*	MSAFG*	GCrGyyTGCr	ysvAyyrwwy	1	PT	FG01364.1	0	0	YGR217W	YGR217W
173	138	conserved	AN5627.1	58.m08920	AO070301000027	0	-33	-22	-37	-26	-34	-23	ATGAAbCywTAA	ATGAAGCTATAA	ATGAATCCTTAA	ATGAACCTATAA	Mkl*	MKL*	MNP*	MNL*	bwhhsAACvd	kmhyCrmwkw	1	YU	0	0	0	0	0
8916	3977	conserved	AN5885.1	72.m19245	AO070245000022	0	-36	-22	-60	-46	-56	-42	ATGyyGsyykywTrA	ATGTCGGTTGTTTGA	ATGCTGCTCTCATAA	ATGCCGGCTGTTTGA	Msvv*	MSVV*	MLLS*	MPAV*	CbTkrrvCAC	drmvrTvsbd	1	G	0	0	0	0	0
5549	2804	conserved	AN4460.1	58.m07864	AO070305000133	0	-52	-41	-49	-38	-51	-40	ATGGCGCGmTAr	ATGGCGCGCTAA	ATGGCGCGCTAG	ATGGCGCGATAG	MAR*	MAR*	MAR*	MAR*	krkwyrkrks	wwhbywyrsm	1	A	FG06788.1	0	NCU03628.1	0	0

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
AN0001.1					
AN0002.1					
AN0003.1					
AN0004.1					
AN0005.1					
AN0006.1					
AN0007.1					
AN0008.1					
AN0009.1	FG10203.1	MG00771.1			
AN0010.1					
AN0011.1					
AN0012.1		MG01764.1			
AN0013.1					
AN0014.1					
AN0015.1					
AN0016.1					
AN0017.1					
AN0018.1					
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AN0024.1					
AN0025.1					
AN0026.1					
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AN0028.1					
AN0029.1					
AN0030.1					
AN0031.1		MG06493.1			
AN0032.1					
AN0033.1					
AN0034.1		MG04014.1		YFL053W	
AN0035.1					
AN0036.1		MG08569.1	NCU01704.1		
AN0037.1					
AN0038.1					
AN0039.1				YNL011C	
AN0040.1	FG05516.1		NCU00276.1		
AN0041.1					
AN0042.1					
AN0043.1	FG02725.1	MG05031.1	NCU09517.1		
AN0044.1	FG02724.1	MG05032.1			
AN0045.1					
AN0046.1				YPR033C	YPR033C
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AN0050.1	FG07302.1		NCU06417.1		
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AN0063.1			NCU00182.1		
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AN0065.1		MG06406.1	NCU07885.1		
AN0066.1				YKL120W	YKL120W
AN0067.1					
AN0068.1					

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AN0077.1		MG08311.1			
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AN0093.1	FG02562.1	MG05259.1	NCU06271.1		
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AN0117.1	FG05072.1				
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AN0120.1				YMR028W	
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AN0124.1	FG09784.1	MG07119.1	NCU07722.1		
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AN0127.1		MG03139.1			
AN0128.1				YOL141W	YOL141W
AN0129.1					
AN0130.1				YML005W	
AN0131.1				YLR250W	
AN0132.1					
AN0133.1	FG10757.1			YGL120C	
AN0134.1			NCU01613.1		
AN0135.1	FG10861.1	MG03876.1			
AN0136.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0138.1	FG10862.1				
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AN0141.1	FG10860.1	MG03881.1		YKR056W	
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AN0167.1	FG05648.1	MG06077.1			
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AN0193.1	FG04272.1		NCU08029.1		
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0233.1	FG05720.1		NCU05853.1		
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AN0239.1	FG00191.1		NCU00671.1		
AN0240.1					
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AN0243.1	FG04985.1				
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AN0247.1	FG00732.1				
AN0248.1		MG06786.1	NCU00813.1		
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AN0251.1					
AN0252.1	FG06875.1	MG09916.1	NCU09119.1		
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AN0255.1					
AN0256.1	FG05380.1				
AN0257.1				YPR128C	
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AN0259.1		MG03683.1	NCU03216.1		
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AN0272.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0301.1	FG01026.1	MG00333.1	NCU07363.1		
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AN0321.1	FG00843.1	MG06984.1		YOR207C	
AN0322.1			NCU00606.1		
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0349.1	FG04314.1		NCU05427.1		
AN0350.1					
AN0351.1	FG05023.1				
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AN0354.1	FG00478.1	MG05734.1			
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AN0356.1	FG05024.1	MG00068.1			
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AN0385.1	FG05696.1	MG02125.1			
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0433.1	FG01516.1	MG03653.1	NCU08389.1	YOR312C	
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AN0436.1	FG00715.1	MG04518.1		YDR255C	
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AN0440.1				YDR176W	
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AN0451.1	FG07315.1	MG08624.1			
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AN0472.1	FG08757.1		NCU07076.1		
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AN0476.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0543.1					
AN0544.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0554.1		MG03900.1			
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AN0556.1				YMR224C	YMR224C
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AN0558.1					
AN0559.1	FG09817.1	MG06097.1	NCU06632.1		
AN0560.1	FG09816.1				
AN0561.1	FG09732.1	MG04146.1			
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AN0574.1					
AN0575.1					
AN0576.1	FG05306.1	MG06100.1			
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AN0582.1	FG09724.1	MG07124.1	NCU07717.1		
AN0583.1		MG04179.1			
AN0584.1					
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AN0589.1		MG08049.1	NCU04439.1		
AN0590.1	FG09767.1	MG04180.1	NCU07713.1		
AN0591.1					
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AN0593.1	FG05284.1	MG01687.1			
AN0594.1					
AN0595.1	FG09786.1				
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AN0599.1		MG01176.1			
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AN0606.1			NCU06895.1		
AN0607.1					
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AN0610.1					
AN0611.1					
AN0612.1		MG09900.1			

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0621.1					
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AN0623.1			NCU08977.1		
AN0624.1			NCU09466.1		
AN0625.1	FG06776.1	MG05721.1	NCU00308.1		
AN0626.1					
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AN0628.1		MG08725.1	NCU00780.1		
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AN0633.1					
AN0634.1					
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AN0636.1	FG00960.1	MG03933.1	NCU09757.1	YPL175W	YPL175W
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AN0639.1					
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AN0651.1			NCU06493.1		
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AN0673.1			NCU07171.1		
AN0674.1					
AN0675.1					
AN0676.1	FG09993.1	MG00961.1			
AN0677.1					
AN0678.1					
AN0679.1					
AN0680.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0707.1				YOR048C	
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AN0720.1	FG09628.1		NCU07266.1		
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AN0726.1	FG01351.1				
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AN0730.1		MG00297.1	NCU04450.1		
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AN0742.1					
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AN0746.1					
AN0747.1	FG00863.1	MG03600.1			
AN0748.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN0756.1					
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AN0758.1	FG10426.1		NCU08167.1		
AN0759.1					
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AN0762.1			NCU04124.1	YKL179C	
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AN0764.1		MG02619.1			
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AN0767.1					
AN0768.1					
AN0769.1				YKL025C	
AN0770.1			NCU01928.1		
AN0771.1					
AN0772.1					
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AN0868.1		MG02999.1	NCU00580.1		
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AN0871.1		MG10490.1			
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AN0874.1		MG06313.1			
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AN0877.1					
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AN0946.1	FG00292.1			YOR206W	
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AN1013.1			NCU04331.1		
AN1014.1			NCU01751.1	YKL188C	YKL188C
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AN1019.1	FG09616.1				
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AN1087.1					
AN1088.1					

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AN1100.1	FG10203.1	MG00771.1			
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AN1103.1	FG04103.1	MG05196.1			
AN1104.1	FG02563.1	MG05258.1			
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AN1119.1		MG04539.1			
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AN1122.1				YPL220W	YPL220W
AN1123.1	FG00341.1				
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AN1126.1			NCU08340.1		
AN1127.1		MG04441.1			
AN1128.1			NCU08338.1		
AN1129.1					
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AN1132.1					
AN1133.1	FG09422.1	MG03089.1	NCU02463.1		
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AN1136.1	FG05701.1		NCU06022.1	YDR287W	
AN1137.1	FG05704.1				
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AN1150.1	FG01573.1	MG02375.1	NCU05410.1	YOL140W	
AN1151.1	FG09485.1	MG01335.1	NCU04071.1		
AN1152.1		MG09883.1			
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AN1155.1					
AN1156.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1166.1	FG01016.1	MG04444.1	NCU02707.1	YLR448W	
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AN1173.1			NCU04403.1		
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AN1181.1		MG05526.1			
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AN1198.1		MG04826.1	NCU02727.1		
AN1199.1	FG10375.1				
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AN1201.1	FG01333.1	MG06345.1			
AN1202.1		MG09400.1			
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AN1207.1					
AN1208.1	FG01337.1	MG05616.1	NCU02966.1		
AN1209.1				YGR232W	
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AN1211.1	FG01152.1	MG04827.1			
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AN1222.1		MG00383.1			
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AN1246.1		MG05063.1			
AN1247.1				YOR292C	
AN1248.1					
AN1249.1				YKL012W	
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AN1257.1	FG10282.1	MG04092.1	NCU00244.1		
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AN1261.1	FG05613.1				
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AN1270.1	FG05614.1	MG05156.1			
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AN1286.1		MG00590.1			
AN1287.1		MG07912.1	NCU05633.1		
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1354.1		MG10652.1	NCU01022.1		
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AN1357.1		MG01003.1			
AN1358.1					
AN1359.1					
AN1360.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1367.1	FG11603.1	MG09313.1	NCU03321.1		
AN1368.1					
AN1369.1					
AN1370.1					
AN1371.1					
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AN1376.1		MG01295.1	NCU04699.1		
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AN1378.1	FG08359.1				
AN1379.1	FG10280.1				
AN1380.1	FG08614.1		NCU07451.1	YGR264C	
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AN1425.1					
AN1426.1	FG08454.1	MG02309.1			
AN1427.1					
AN1428.1		MG00620.1			

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1454.1	FG00428.1	MG04771.1			
AN1455.1	FG00430.1		NCU02708.1		
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AN1460.1		MG02400.1	NCU03369.1		
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AN1467.1		MG00166.1	NCU00958.1		
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AN1477.1	FG08946.1		NCU01900.1		
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AN1484.1		MG04396.1	NCU01965.1		
AN1485.1			NCU03124.1		
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AN1488.1					
AN1489.1	FG06669.1	MG05309.1	NCU00226.1		
AN1490.1					
AN1491.1	FG02532.1	MG05682.1	NCU00157.1		
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AN1493.1					
AN1494.1			NCU02052.1		
AN1495.1				YFL017W-A	
AN1496.1					

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AN1513.1				YGR012W	YGR012W
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AN1522.1				YGL010W	
AN1523.1	FG00637.1				
AN1524.1	FG00417.1				
AN1525.1				YML055W	
AN1526.1	FG05601.1		NCU00966.1	YKL207W	
AN1527.1					
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AN1536.1		MG04758.1			
AN1537.1					
AN1538.1				YGR005C	
AN1539.1	FG00623.1	MG00336.1			
AN1540.1					
AN1541.1		MG00652.1	NCU02056.1		
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AN1543.1				YJR051W	
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AN1563.1	FG02203.1	MG05506.1			
AN1564.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1597.1	FG00828.1		NCU01598.1		
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AN1624.1		MG00892.1	NCU02250.1		
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AN1632.1					

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AN1699.1	FG10790.1	MG03418.1			
AN1700.1					

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AN1710.1				YPL104W	
AN1711.1	FG09760.1		NCU08663.1		
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AN1715.1		MG10677.1			
AN1716.1					
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AN1718.1					
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AN1721.1			NCU08363.1		
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AN1723.1					
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AN1726.1	FG09240.1	MG03840.1			
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AN1733.1	FG01141.1	MG00189.1	NCU03076.1	YHR037W	YHR037W
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AN1742.1					
AN1743.1		MG03839.1			
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AN1746.1					
AN1747.1					
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AN1751.1		MG00559.1	NCU04040.1		
AN1752.1	FG08463.1	MG00929.1			YFR030W
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AN1754.1			NCU07061.1		
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AN1757.1	FG05365.1		NCU05942.1		
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AN1766.1	FG05127.1	MG07444.1			
AN1767.1		MG00645.1			
AN1768.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1775.1	FG02191.1		NCU05644.1		
AN1776.1	FG02192.1	MG03758.1	NCU05645.1		
AN1777.1					
AN1778.1	FG09312.1	MG00599.1			
AN1779.1					
AN1780.1	FG09309.1	MG00596.1	NCU05971.1		
AN1781.1					
AN1782.1					
AN1783.1					
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AN1828.1					
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AN1836.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1849.1					
AN1850.1				YKR087C	
AN1851.1	FG06761.1		NCU07567.1		
AN1852.1					
AN1853.1	FG01866.1				
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AN1856.1					
AN1857.1					
AN1858.1		MG00755.1			
AN1859.1					
AN1860.1	FG06738.1		NCU00360.1	YLR290C	
AN1861.1				YGR129W	YGR129W
AN1862.1					
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AN1865.1		MG04225.1			
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AN1876.1					
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AN1883.1	FG06098.1		NCU02639.1		
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AN1886.1	FG09882.1	MG08318.1	NCU09035.1		
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AN1892.1	FG06415.1			YJL143W	
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AN1896.1	FG06449.1	MG00317.1	NCU05537.1		
AN1897.1					
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AN1900.1	FG09462.1		NCU04713.1		
AN1901.1					
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AN1903.1					
AN1904.1				YJR064W	YJR064W

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1915.1	FG08760.1				
AN1916.1					
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AN1918.1	FG08601.1		NCU09873.1		
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AN1965.1		MG07148.1			
AN1966.1					
AN1967.1					
AN1968.1		MG03250.1			
AN1969.1	FG04412.1				
AN1970.1					
AN1971.1				YDR190C	YDR190C
AN1972.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN1981.1				YJL031C	
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AN1988.1	FG05181.1			YIL068C	
AN1989.1		MG07162.1	NCU06761.1		
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AN1994.1					
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AN1999.1		MG01048.1	NCU05982.1	YOL096C	
AN2000.1					
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AN2002.1			NCU05999.1		
AN2003.1					
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AN2027.1					
AN2028.1					
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AN2030.1	FG01866.1				
AN2031.1					
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AN2033.1					
AN2034.1					
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AN2036.1					
AN2037.1					
AN2038.1					
AN2039.1					
AN2040.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN2053.1			NCU00356.1		
AN2054.1					
AN2055.1		MG05176.1			
AN2056.1	FG06749.1				
AN2057.1		MG06378.1		YGL068W	
AN2058.1					
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AN2061.1		MG03880.1			
AN2062.1				YJL034W	
AN2063.1					
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AN2076.1			NCU04840.1		
AN2077.1	FG08439.1				
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AN2088.1	FG01054.1				
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AN2094.1				YDR141C	
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AN2104.1		MG04742.1			
AN2105.1	FG00358.1	MG04741.1	NCU00505.1	YGR074W	
AN2106.1					
AN2107.1	FG01359.1	MG00521.1			
AN2108.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN2114.1			NCU08315.1		
AN2115.1					
AN2116.1				YLL056C	
AN2117.1					
AN2118.1					
AN2119.1			NCU04090.1		
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AN2134.1					
AN2135.1					
AN2136.1	FG07133.1	MG07063.1	NCU01243.1		
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AN2138.1					
AN2139.1	FG07145.1	MG07058.1		YOR258W	
AN2140.1		MG07209.1			
AN2141.1					
AN2142.1					
AN2143.1	FG07139.1	MG07070.1			
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AN2148.1					
AN2149.1					
AN2150.1		MG10357.1			
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AN2153.1		MG07084.1	NCU08026.1		
AN2154.1					
AN2155.1		MG06151.1		YGL091C	
AN2156.1					
AN2157.1					
AN2158.1		MG01176.1			
AN2159.1					
AN2160.1					
AN2161.1		MG10359.1			
AN2162.1					
AN2163.1					
AN2164.1					
AN2165.1					
AN2166.1					
AN2167.1					
AN2168.1					
AN2169.1		MG06521.1			
AN2170.1					
AN2171.1					
AN2172.1				YNL025C	YNL025C
AN2173.1				YNL083W	YNL083W
AN2174.1					
AN2175.1					
AN2176.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN2178.1					
AN2179.1					
AN2180.1					
AN2181.1	FG05301.1				
AN2182.1					
AN2183.1					
AN2184.1		MG04663.1	NCU07577.1		
AN2185.1	FG06686.1				
AN2186.1					
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AN2188.1					
AN2189.1					
AN2190.1	FG07428.1				
AN2191.1					
AN2192.1					
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AN2194.1					
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AN2233.1		MG01432.1	NCU07019.1		
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AN2237.1	FG08454.1	MG02309.1			
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AN2239.1					
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AN2241.1					
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AN2243.1		MG01743.1			
AN2244.1		MG08640.1	NCU01183.1		

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN2249.1					
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AN2251.1					
AN2252.1					
AN2253.1					
AN2254.1					
AN2255.1					
AN2256.1					
AN2257.1					
AN2258.1	FG06661.1				
AN2259.1					
AN2260.1					
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3034.1	FG07041.1				
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AN3055.1		MG03855.1	NCU09707.1		
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AN3059.1	FG06055.1	MG00901.1			
AN3060.1					

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AN3148.1				YDR104C	YDR104C
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AN3264.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3363.1	FG00697.1				
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AN3367.1	FG09386.1		NCU06059.1		
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AN3370.1			NCU06057.1		
AN3371.1			NCU06056.1		
AN3372.1					
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AN3378.1	FG09214.1		NCU00799.1		
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3413.1		MG09222.1	NCU06047.1		
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AN3421.1	FG08465.1	MG09333.1			
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AN3425.1			NCU04256.1		
AN3426.1					
AN3427.1	FG10156.1		NCU04273.1	YNL175C	YNL175C
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AN3456.1			NCU02430.1		
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AN3458.1				YKR085C	
AN3459.1	FG09893.1	MG00256.1			
AN3460.1			NCU02402.1		
AN3461.1			NCU05075.1		
AN3462.1				YGL143C	
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AN3466.1	FG07970.1	MG03149.1	NCU02438.1		
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AN3468.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3536.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3581.1		MG01284.1		YHR106W	
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AN3583.1	FG09156.1		NCU03219.1	YNL238W	
AN3584.1		MG03638.1		YJL036W	
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AN3588.1	FG01233.1		NCU07472.1		
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AN3590.1		MG09900.1			
AN3591.1	FG00490.1				
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AN3593.1					
AN3594.1	FG02011.1	MG06743.1			
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AN3604.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3619.1				YNL250W	
AN3620.1	FG00281.1	MG03676.1			
AN3621.1		MG03677.1			
AN3622.1		MG03726.1			
AN3623.1					
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AN3626.1		MG01256.1	NCU03194.1		
AN3627.1		MG05250.1			
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AN3635.1		MG05167.1	NCU04412.1		
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AN3658.1				YKL221W	
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AN3669.1					
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AN3671.1		MG05635.1			
AN3672.1	FG07303.1		NCU06416.1		

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3674.1					
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AN3677.1	FG00604.1		NCU07300.1		
AN3678.1		MG05379.1	NCU07301.1		
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AN3680.1					
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AN3686.1				YGL220W	
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AN3689.1	FG07044.1	MG00859.1	NCU06882.1		
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AN3692.1	FG00333.1				
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AN3700.1	FG04922.1	MG01176.1			
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AN3714.1	FG07960.1		NCU02378.1		
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AN3717.1	FG08923.1		NCU01922.1		
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AN3740.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN3745.1	FG07107.1	MG09302.1		YOR294W	
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AN3749.1	FG07112.1	MG09306.1			
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AN3751.1		MG05695.1	NCU00161.1		
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AN3756.1					
AN3757.1		MG00142.1			
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AN3760.1					
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AN3772.1					
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AN3776.1			NCU09654.1		
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AN3778.1	FG05299.1	MG06109.1	NCU09746.1		
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AN3928.1	FG02469.1	MG03098.1	NCU06110.1		
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AN3937.1	FG00566.1	MG07744.1		YGR093W	
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AN4048.1	FG05311.1		NCU05309.1		
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AN4050.1		MG00652.1	NCU02056.1		
AN4051.1	FG07925.1	MG03446.1			
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AN4053.1	FG00748.1	MG00744.1			
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AN4159.1	FG10264.1			YPR035W	YPR035W
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AN4161.1				YMR114C	
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AN4163.1	FG09870.1	MG04719.1			
AN4164.1					
AN4165.1				YML012W	
AN4166.1					
AN4167.1		MG01044.1			
AN4168.1	FG09497.1	MG02506.1			
AN4169.1					
AN4170.1		MG01045.1	NCU03887.1		
AN4171.1				YNL047C	YNL047C
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AN4201.1	FG07277.1	MG10188.1			
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AN4207.1				YPR029C	
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AN4209.1	FG05384.1				
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AN4215.1	FG02097.1				
AN4216.1	FG02096.1	MG05446.1	NCU01218.1		

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AN4222.1			NCU01827.1	YHR010W	
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AN4224.1					
AN4225.1					
AN4226.1	FG01446.1				
AN4227.1					
AN4228.1					
AN4229.1					
AN4230.1		MG09516.1			
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AN4232.1		MG00087.1	NCU04503.1	YHR066W	
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AN4239.1	FG01193.1				
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AN4282.1	FG01604.1				
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AN4284.1					

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AN4303.1	FG04571.1			YGR007W	
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AN4349.1		MG01106.1			
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AN4351.1				YOR275C	
AN4352.1	FG07963.1				

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN4412.1		MG03931.1			
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AN4417.1	FG10865.1	MG03886.1			
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AN4419.1				YIR026C	
AN4420.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN4428.1	FG04398.1				
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AN4430.1	FG06282.1	MG01104.1			
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AN4433.1					
AN4434.1		MG03928.1			
AN4435.1			NCU03360.1		
AN4436.1					
AN4437.1					
AN4438.1					
AN4439.1	FG01611.1	MG06214.1	NCU08736.1		
AN4440.1	FG01670.1	MG03908.1	NCU03334.1		
AN4441.1					
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AN4443.1		MG06712.1			
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AN4445.1				YGR002C	
AN4446.1	FG10067.1	MG08096.1			
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AN4458.1	FG06789.1	MG08169.1		YFR005C	YFR005C
AN4459.1					
AN4460.1	FG06788.1		NCU03628.1		
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AN4467.1					
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AN4470.1	FG06843.1	MG01592.1			
AN4471.1	FG05585.1	MG06429.1	NCU07864.1	YKL021C	
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AN4487.1					
AN4488.1					

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AN4496.1			NCU06648.1		
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AN4869.1		MG01153.1	NCU10061.1	YGL011C	
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AN4875.1	FG10780.1	MG00920.1	NCU02271.1	YDR282C	YDR282C
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AN4916.1	FG06587.1				
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AN4923.1		MG01026.1	NCU03922.1		
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AN4986.1		MG02749.1			
AN4987.1	FG09908.1	MG07335.1			
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AN5013.1		MG06005.1			
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AN5019.1	FG07880.1	MG05888.1	NCU08434.1		
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AN5109.1	FG06240.1	MG03160.1	NCU01759.1		
AN5110.1	FG05197.1		NCU01758.1		
AN5111.1					
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AN5114.1	FG00834.1	MG06959.1		YNL072W	
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AN5116.1		MG08570.1			
AN5117.1					
AN5118.1					
AN5119.1				YML014W	
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AN5121.1	FG10738.1	MG01059.1			
AN5122.1	FG10737.1			YDR226W	
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AN5167.1					
AN5168.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN5185.1			NCU03872.1		
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AN5236.1	FG00257.1				

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AN5486.1		MG06196.1		YLR351C	YLR351C
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AN5519.1	FG06007.1			YJL024C	
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AN5523.1	FG06051.1	MG03860.1			
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AN5525.1	FG07953.1		NCU02366.1		
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AN5528.1			NCU05029.1		
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AN5530.1	FG01187.1	MG05375.1			
AN5531.1		MG00378.1			
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AN5536.1			NCU04507.1		
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AN5566.1	FG10358.1	MG00919.1	NCU02325.1		
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AN5576.1					

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AN5586.1		MG01288.1			
AN5587.1		MG01302.1			
AN5588.1	FG01475.1				
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AN5592.1	FG10511.1				
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AN5595.1			NCU03458.1		
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AN5599.1	FG08766.1				
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AN5601.1		MG08564.1		YNR050C	
AN5602.1			NCU04087.1		
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AN5604.1	FG09280.1	MG08895.1			
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AN5606.1	FG00818.1	MG03947.1	NCU03463.1		
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AN5614.1				YNL279W	YNL279W
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AN5616.1	FG01560.1	MG03264.1	NCU03347.1	YJL060W	YJL060W
AN5617.1					
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AN5641.1					
AN5642.1	FG10270.1		NCU03874.1		
AN5643.1	FG10269.1				
AN5644.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN5656.1	FG10120.1				
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AN5658.1	FG04564.1	MG09541.1	NCU04130.1		
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AN5660.1					
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AN5662.1				YIL078W	YIL078W
AN5663.1					
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AN5668.1			NCU05077.1		
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AN5675.1	FG05735.1			YDR330W	
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AN5681.1	FG07078.1	MG00145.1			
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AN5692.1				YLR324W	YLR324W
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AN5719.1	FG10368.1				
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AN5725.1			NCU06779.1	YNL048W	YNL048W
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AN5727.1		MG09726.1	NCU00972.1		
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AN5732.1	FG01642.1		NCU05421.1		
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AN5746.1		MG10607.1			
AN5747.1	FG01198.1				
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AN5758.1			NCU08161.1		
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AN5774.1	FG05736.1		NCU00770.1		
AN5775.1					
AN5776.1					
AN5777.1		MG04555.1			
AN5778.1	FG00610.1				
AN5779.1					
AN5780.1					

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AN5788.1			NCU00778.1		
AN5789.1			NCU00777.1		
AN5790.1	FG05733.1	MG01995.1			
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AN5815.1	FG06959.1	MG00479.1		YPL209C	
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AN5871.1	FG06161.1	MG07132.1			
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AN5875.1	FG06203.1				
AN5876.1			NCU07504.1		
AN5877.1	FG07539.1				
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AN5880.1	FG09587.1				
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AN5903.1		MG06176.1			
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AN5906.1					
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AN5908.1	FG06702.1		NCU07550.1		
AN5909.1	FG09678.1				
AN5910.1		MG06274.1			
AN5911.1					
AN5912.1		MG04976.1			
AN5913.1		MG03880.1	NCU01754.1		
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AN5915.1		MG06273.1			
AN5916.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN5960.1			NCU07830.1		
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AN5977.1				YGL157W	
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AN5980.1					
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AN5984.1					

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AN5986.1	FG08941.1	MG02921.1	NCU01906.1	YOR120W	
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AN6253.1		MG03217.1	NCU01512.1		
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AN6267.1		MG01121.1			
AN6268.1					
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AN6272.1	FG01927.1		NCU08005.1		
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AN6732.1	FG05235.1	MG09470.1	NCU06617.1		

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AN6796.1	FG08979.1	MG01679.1	NCU06603.1	YDR533C	
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AN6798.1	FG03666.1				
AN6799.1					
AN6800.1					

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AN6843.1	FG09003.1	MG04008.1		YML025C	YML025C
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AN6866.1	FG09602.1		NCU07725.1		
AN6867.1					
AN6868.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN6894.1	FG05403.1		NCU00181.1		
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AN6896.1					
AN6897.1			NCU00436.1		
AN6898.1		MG05208.1		YKL002W	YKL002W
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AN6900.1	FG06702.1	MG08905.1	NCU07550.1		
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AN6904.1	FG06703.1	MG08906.1			
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AN6936.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7004.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7140.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7194.1	FG10124.1	MG00738.1	NCU01419.1		
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AN7208.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7219.1					
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AN7273.1		MG00114.1			
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AN7276.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7293.1	FG06758.1	MG00127.1	NCU07563.1		
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AN7299.1		MG06316.1	NCU00422.1		
AN7300.1					
AN7301.1	FG02528.1	MG05686.1	NCU00163.1		
AN7302.1					
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AN7307.1	FG04255.1				
AN7308.1					
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AN7313.1	FG11366.1	MG03844.1	NCU06861.1		
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AN7325.1		MG08071.1			
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AN7344.1			NCU06522.1		

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7412.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7422.1	FG02640.1		NCU05777.1		
AN7423.1	FG10122.1	MG00685.1	NCU03606.1		
AN7424.1					
AN7425.1					
AN7426.1					
AN7427.1					
AN7428.1	FG10226.1		NCU06672.1	YHR171W	YHR171W
AN7429.1				YHR144C	
AN7430.1	FG09984.1		NCU07156.1		
AN7431.1				YKL059C	
AN7432.1					
AN7433.1					
AN7434.1					
AN7435.1				YML021C	YML021C
AN7436.1					
AN7437.1			NCU07504.1		
AN7438.1					
AN7439.1				YPR175W	
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AN7478.1					
AN7479.1	FG08865.1	MG08897.1			
AN7480.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN7487.1					
AN7488.1		MG10533.1			
AN7489.1					
AN7490.1					
AN7491.1					
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AN7498.1					
AN7499.1					
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AN7501.1		MG04137.1			
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AN7503.1				YDR365C	
AN7504.1		MG04163.1			
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AN9098.1					
AN9099.1					
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AN9101.1	FG10185.1	MG07295.1	NCU01284.1		
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AN9103.1	FG02433.1		NCU05850.1		
AN9104.1					
AN9105.1					
AN9106.1				YDR058C	
AN9107.1					
AN9108.1		MG00755.1	NCU01402.1		
AN9109.1					
AN9110.1					
AN9111.1					
AN9112.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN9115.1					
AN9116.1					
AN9117.1					
AN9118.1					
AN9119.1		MG04717.1			
AN9120.1	FG00843.1				
AN9121.1					
AN9122.1					
AN9123.1					
AN9124.1					
AN9125.1	FG00778.1		NCU00727.1	YNR003C	
AN9126.1					
AN9127.1					
AN9128.1		MG07309.1			
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AN9137.1					
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AN9141.1		MG09463.1	NCU08857.1		
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AN9143.1					
AN9144.1					
AN9145.1					
AN9146.1					
AN9147.1					
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AN9151.1					
AN9152.1					
AN9153.1					
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AN9155.1					
AN9156.1					
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AN9162.1			NCU02126.1		
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AN9170.1				YMR058W	
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AN9174.1					
AN9175.1					
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AN9178.1					
AN9179.1				YPR127W	
AN9180.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN9248.1					

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AN9270.1					
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AN9272.1					
AN9273.1					
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AN9275.1		MG06133.1			
AN9276.1					
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AN9278.1	FG01141.1	MG00189.1	NCU03076.1		
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AN9281.1					
AN9282.1					
AN9283.1					
AN9284.1					
AN9285.1					
AN9286.1					
AN9287.1	FG02360.1	MG09314.1	NCU03322.1		
AN9288.1		MG01176.1			
AN9289.1					
AN9290.1		MG03499.1			
AN9291.1					
AN9292.1					
AN9293.1			NCU06324.1		
AN9294.1					
AN9295.1					
AN9296.1					
AN9297.1					
AN9298.1			NCU06198.1		
AN9299.1	FG02000.1	MG06747.1	NCU04109.1		
AN9300.1					
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AN9303.1	FG00828.1	MG03212.1	NCU01598.1		
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AN9306.1					
AN9307.1					
AN9308.1					
AN9309.1					
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AN9316.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN9334.1					
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AN9337.1					
AN9338.1					
AN9339.1	FG06733.1	MG06442.1			
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AN9344.1					
AN9345.1				YPL171C	
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AN9356.1			NCU02019.1		
AN9357.1				YIR035C	
AN9358.1					
AN9359.1				YMR033W	
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AN9383.1					
AN9384.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN9389.1					
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AN9392.1					
AN9393.1					
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AN9395.1					
AN9396.1					YKR035W-A
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AN9399.1				YLR015W	
AN9400.1				YMR293C	
AN9401.1		MG02566.1			
AN9402.1	FG00259.1	MG02819.1			
AN9403.1		MG10569.1			
AN9404.1					
AN9405.1					
AN9406.1					
AN9407.1					
AN9408.1		MG04118.1			
AN9409.1					
AN9410.1				YDR444W	
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AN9412.1					
AN9413.1					
AN9414.1					
AN9415.1					
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AN9438.1				YDR435C	
AN9439.1					
AN9440.1					
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AN9449.1					
AN9450.1					
AN9451.1					
AN9452.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
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AN9456.1					
AN9457.1					
AN9458.1					
AN9459.1					
AN9460.1		MG07324.1	NCU06677.1		
AN9461.1	FG07381.1		NCU03796.1	YGL059W	YGL059W
AN9462.1					
AN9463.1				YPL242C	
AN9464.1					
AN9465.1	FG01154.1				
AN9466.1					
AN9467.1					
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AN9469.1				YOR150W	
AN9470.1		MG05283.1			
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AN9476.1					
AN9477.1					
AN9478.1					
AN9479.1					
AN9480.1					
AN9481.1	FG05981.1	MG07326.1	NCU03588.1		
AN9482.1					
AN9483.1					
AN9484.1					
AN9485.1					
AN9486.1				YOR196C	
AN9487.1					
AN9488.1					
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AN9491.1					
AN9492.1					
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AN9498.1					
AN9499.1					
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AN9504.1		MG03026.1			
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AN9516.1					
AN9517.1					
AN9518.1					
AN9519.1					
AN9520.1					

an_gene	fg_uorf_utr_or_60bp	mg_uorf_utr_or_60bp	nc_uorf_utr_or_60bp	sc_uorf_100bp	sc_cooccur_orf_100bp
AN9521.1					
AN9522.1	FG07173.1	MG09516.1			
AN9523.1					
AN9524.1					
AN9525.1					
AN9526.1					
AN9527.1					
AN9528.1	FG02596.1		NCU06193.1		
AN9529.1					
AN9530.1					
AN9531.1					
AN9532.1					
AN9533.1					
AN9534.1					
AN9535.1					
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AN9537.1					
AN9538.1					
AN9539.1					
AN9540.1					
AN9541.1					

§S4 Conserved Non-Coding conpats

Method:

To search for conserved non-coding conpats with enriched statistical signals, we started with the set of 4936 ortholog triplets and 1000bp upstream and downstream regions multiply aligned using MLAGAN. The High-scoring Conserved Sequence (HCS) blocks were identified as described in the paper, and aligned all-vs-all to identify the best local alignment between pairs. Local alignments were clustered to identify commonly occurring subconpats (occur >= 4 different HCS) termed conpats. We identified all conpat co-occurrences (where the conpat appears upstream of 3 orthologous genes, or downstream of 3 orthologs) by using MAST with an expect

Co-occurrence Enrichment - conpat occurs more often than random conpats of same length and degeneracy. Pvalue assigned by comparing observed co-occurrences to distribution of 1000 simulated conpats of same length

Upstream vs Downstream - conpat occurs preferentially upstream or downstream of genes. Pvalue assigned by binomial distribution (# upstream occurrence, total occurrences, background probability=0.56). Background

Category Enrichment - conpat occurs preferentially near genes having related functional categories. Pvalue for each category C assigned by hypergeometric distribution (# co-occurrences upstream of genes in category C, total # co-occurrences, # all genes in category C, # all genes) with the Bonferroni correction for multiple testing.

Cell Location Enrichment - conpat occurs preferentially near genes having related cellular location, based on the GO cell location category for the A. nidulans gene's best bi-directional hit (BBH) to S. cerevisiae. Pvalue for each category C assigned by hypergeometric distribution (# co-occurrences upstream of genes in category C, total # co-occurrences, # all genes in category C, # all genes) with the Bonferroni correction for multiple testing. The total number of genes is all A. nidulans genes having a three-way ortholog in Aspergillus, and the number of

Definitions:

Three-way orthologs: Pairwise orthologs are defined as best bidirectional hits (within all-vs-all comparison of genome protein sets) using blastp (e<1e-5) and requiring > 60% coverage of each gene. Three-way orthologs

Tabs:

conpats: 69 conpats showed co-occurrence enrichment (p < 0.01) and either upstream or downstream

conpat_sites: sites of co-occurring conpats, 2 lines per ortholog (for upstream co-occurring conpats, and

conpat_matrices.ace: conpat matrix in ACE file format (multiple alignment HCS subsequences). X=any

factors: sequences of known factors used in similarity searches

an_cats: for all three-way orthologs, the A. nidulans locus, description, COG category, yeast best bi-directional hit (BBH), yeast GO cellular location category

top35: the top 35 conpats sorted by the number of HCS

Data fields:

conpats tab:

ID: unique conpat identifier.

Conpat Consensus: sequence logo (generated by WebLogo program [Crooks GE et all, Genome Research, 2004]) based on HCS multiple alignment.

Similar Sequence: name of known factor with a similar binding sequence, based on CompareACE score > 0.85. Set of known factors in tab "factors".

HCS: number of HCS blocks clustered together to generate conpat

5' Sites: number of ortholog triplets (An, Af, Ao) that the conpat co-occurred upstream of. All ortholog triplets were aligned including 1000 bp upstream. If a neighboring gene is located within 1000bp upstream, the upstream non-coding alignment is split in half, otherwise the entire 1000bp upstream alignment is split in half.

3' Sites: number of ortholog triplets (An, Af, Ao) that the conpat co-occurred downstream of. All ortholog triplets were aligned including 1000 bp downstream. If a neighboring gene is located within 1000bp downstream, the downstream non-coding alignment is split in half, otherwise the entire 1000bp downstream alignment is split in half.

5' /3' Bias? "up" indicates that the conpat preferentially occurrs upstream of genes (pvalue < 0.01 based on binomial distribution). "down" indicates a downstream preference.

% Aligned: percent of upstream co-occurrences that overlap an HCS (if 5'/3' bias="up", use downstream co-occurrences otherwise).

Strand Bias? "yes" indicates that the conpat co-occurred more often on the + strand (same strand as gene) than on the - strand (binomial distribution, pvalue < 0.01). "no" indicates that no such preference was observed. Note: there will be no preference for reverse-complement palindrome conpats.

Sites/Gene: average number of times a conpat is found upstream of the gene (if 5'/3' bias = "up") or downstream of the gene (if 5'/3' bias = "down").

Enriched in COG categories: categories showing enrichment (pvalue < 0.01 as described above), after multiple category testing. The number of genes in this category are

Enriched in cell location: categories showing enrichment (pvalue < 0.01 as described above), after multiple category testing. The number of genes in this category are

Bits / Base: average number of information content bits contained in the weight matrix.

Conpat Consensus: ASCII representation of the conpat weight matrix. BE VERY CAREFUL if you use this as it's much better to use the underlying weight matrix representation (see conpat_matrices.ace). The ASCII representation has capital letters representing bases with > 1 bit of information from the weight matrix, and lowercase

conpat_sites tab:

conpat ID: unique conpat identifier.

Conpat Consensus: see above

Similar Sequence: see above

conpat 5' / 3' Bias: upsteam/downstream bias of the conpat, see above

Site 5' / 3' of Locus: "up" if the site is upstream of the given gene, "down" if the site is downstream of the given gene

AF Locus: locus of the A. fumigatus ortholog

AN Locus: locus of the A. nidulans ortholog

AO Locus: locus of the A. oryzae ortholog

Locus Description: name of the A. nidulans locus

COG Category: COG category for AN locus (multiple letters indicate locus is in multiple categories)

COG Cat Enriched: 1 if the conpat in enriched in this category (p<0.01)

(Bonferonni correction).

 # AF sites: number of conpat sites upstream/downstream of this gene in A. fumigatus

 # AN sites: number of conpat sites upstream/downstream of this gene in A. nidulans

 # AO sites: number of conpat sites upstream/downstream of this gene in A. oryzae

Overlap HCS: 1 if any of the sites overlaps an HCS

conpat start.

conpat start.

conpat start.

AN 5' UTR Len: if "Site 5'/3' of Locus"="up", then report the length of the EST alignment that overlaps a gene to the 5' end (indicating a lowerbound for the 5' UTR length) or "No EST" if no EST aligns to this gene. NOTE: just the maximum aligned length is given and introns may be present within the 5' UTR.

In AN 5' UTR: 1 if "AN 5' UTR Len">0 and the "AN dist from gene" < "AN 5' UTR Len"

downstream of this gene

In AN 3' UTR: 1 if "AN 3' UTR Len">0 and the "AN dist from gene" < "AN 3' UTR Len"

ID	Conpat Consensus	Similar Sequence	# HCS	# 5' Sites	# 3' Sites	5' /3' Bias?	% Aligned	Strand Bias?	Sites/ Gene	Enriched in COG categories (# genes in category)	Enriched in cell location (# genes in category)	Bits / Base	Conpat Consensus
1821		bHLH	36	115	8	up^{3}	35%	yes^{3}	1.1	J:Translation, ribosomal structure, biogenesis (16)^{1}	nucleus (22)	1.9	TCACGTG
1622		areA/gln3	19	25	3	up^{1}	60%		1.1		nucleus (8)	1.6	ATCTTATC
234			17	46	11	up^{2}	35%		1.2	A:RNA processing, modification (8)		1.3	GTTTGTCnTGTTTG
1934		bHLH	16	36	3	up^{3}	47%	yes^{1}	1.1	I:Lipid transport, metabolism (10)^{2}		1.8	TCACATGA
1710		puf3	16	5	20	down^{1}	30%	yes^{3}	1.0			1.6	TGTATATA
896			15	14	2	up	43%	yes	1.0			1.6	TGGTCCGTGC
1602			14	34	0	up^{3}	50%		1.1		nucleolus (4)	1.8	AGGCGGT
1879			13	24	1	up^{2}	63%	yes	1.1			1.8	CTTATCGAT
1132			12	14	2	up	36%	yes^{3}	1.1			1.6	CCCCTCT
2683			10	27	1	up^{3}	48%	yes^{1}	1.1			1.7	TCTCCGC
2223			9	5	16	down	63%	yes^{3}	1.0			1.8	GGCGTTG
1291		yAP1	9	21	1	up^{2}	62%	yes	1.1			1.8	TGAGTCAG
992			9	1	21	down^{3}	86%	yes^{3}	1.1			1.8	GCATAGCG
2611			9	0	17	down^{3}	59%		1.1			1.8	TGTACAT
1739			9	9	0	up	44%	yes^{1}	1.2	J:Translation, ribosomal structure, biogenesis (4)		1.5	GGGCTTAGGG
418			9	33	1	up^{3}	45%		1.2			1.4	CAAACAGTGCAAA
2077		puf3	9	1	9	down	56%	yes	1.0		mitochondrion (4)^{1}	1.3	TGTACAAATA
973			8	74	6	up^{3}	36%	yes^{1}	1.1	A:RNA processing, modification (12)^{1}	nucleolus (8)^{2}	1.8	CACCGCCT
2488			8	37	4	up^{3}	38%	yes^{2}	1.1	T:Signal transduction mechanisms (11)^{2}	cytoplasm (13)^{1}	1.7	TACCCCGC
1144		puf3	8	2	11	down	36%	yes^{3}	1.3		mitochondrion (6)^{3}	1.7	TGTACTAT
1635			8	13	1	up	69%	yes^{3}	1.2	J:Translation, ribosomal structure, biogenesis (8)^{3}	cytoplasm (8)^{2}	1.6	CGACAACCC
1940			8	2	19	down^{2}	47%	yes^{3}	1.2	D:Cell cycle/division, chrom. partitioning (5)^{1}		1.4	GTbGGCGTT
2199		bHLH	7	40	3	up^{3}	30%		1.0			1.8	CCACGTGC
1426			7	14	1	up	50%		1.0	C:Energy production, conversion (5)^{1}		1.7	CCCGAGGT
2525		stuA/mbp1	6	18	1	up^{1}	39%	yes	1.3	L:Replication, recombination, repair (10)^{3}	nucleus (8)^{1}	1.9	GACGCGT
813		yATF-B	6	11	1	up	45%		1.1			1.8	ACGTCAC
1650			6	11	0	up	73%		1.1	J:Translation, ribosomal structure, biogenesis (4)	nucleolus (4)^{2}	1.7	GAAATTT
2093			6	44	5	up^{3}	30%	yes^{3}	1.1	I:Lipid transport, metabolism (8)		1.7	CCCCGCAC
1998			6	25	1	up^{3}	40%	yes	1.0	I:Lipid transport, metabolism (7)^{1}	peroxisome (2)^{1}	1.7	CCTCGGCA
2497			6	0	8	down	100%	yes^{2}	1.0			1.6	TGCATAG
751			6	25	2	up^{2}	40%		1.1			1.6	ACCGCCTTCC
2483		cpcA/gcn4	5	19	4	up	26%		1.2	J:Translation, ribosomal structure, biogenesis (7)^{2}	cytoplasm (12)^{3}	2.0	TGAGTCA
2249			5	36	0	up^{3}	25%		1.2	J:Translation, ribosomal structure, biogenesis (13)^{3}	nucleolus (8)^{3}nucleus (12)^{1}	1.9	TTTTTTT
1059			5	12	1	up	92%		1.1			1.9	TCGGCCCG
2451			5	0	10	down^{1}	80%		1.0		cell periphery (2)	1.9	GATATCC
2677			5	34	6	up^{2}	62%	yes^{3}	1.1			1.8	TCACCGC
1723			5	18	2	up	50%		1.0			1.7	TCTCGTGA
2919			5	53	2	up^{3}	30%	yes^{3}	1.1		cytoplasm (16)	1.7	TCCCCGC
1581			5	1	8	down	38%	yes^{3}	1.0			1.7	TGCATATA
2215			5	1	10	down	40%	yes^{3}	1.1			1.7	ATTCCCC
252			5	12	0	up^{1}	25%		1.1			1.6	ACGCGTAAAGTGGTT
2032			5	18	1	up^{1}	39%		1.1	(7)^{1}		1.6	GAAGCTCTC
1971			5	11	1	up	82%		1.1			1.5	CGCCGGCCG
1872			5	0	13	down^{2}	69%	yes	1.0			1.5	TATGATAC
1093			5	83	6	up^{3}	16%	yes^{3}	1.4		cytoplasm (26)^{2}nucleus (17)	1.5	CCCCTCCCCC
1453			5	4	12	down	33%		1.1			1.5	TTTGGTCTT
855			5	12	1	up	58%	yes	1.2			1.4	TTCCGCCCGC

ID	Conpat Consensus	Similar Sequence	# HCS	# 5' Sites	# 3' Sites	5' /3' Bias?	% Aligned	Strand Bias?	Sites/ Gene	Enriched in COG categories (# genes in category)	Enriched in cell location (# genes in category)	Bits / Base	Conpat Consensus
2194			5	2	14	down^{1}	21%	yes^{3}	1.0			1.4	GGvGTTTGGAG
616			5	19	1	up^{1}	37%		1.0	L:Replication, recombination, repair (7)^{3}		1.4	CGCGAAdTCACGTG
652			5	263	32	up^{3}	8%	yes^{3}	1.9	C:Energy production, conversion (24)	cytoplasm (50)	1.3	CTCTCCTTCTCCCC
45			5	400	243	up^{1}	3%	yes^{3}	1.9		cytoplasm (75)^{1}	1.3	TTTCTTTTTCTTTTTTTT
2662			4	2	25	down^{3}	56%	yes^{3}	1.0			1.9	GAGATACC
2253			4	1	8	down	50%		1.1			1.9	TTTGGTTT
2529			4	30	2	up^{3}	30%	yes	1.0			1.8	ACGTGAC
1230			4	14	1	up	29%	yes^{3}	1.1			1.7	TTACCCCTC
2236			4	18	2	up	67%		1.0		late Golgi (2)nucleolus (5)^{2}	1.7	GCAGAATC
1407			4	40	3	up^{3}	30%	yes	1.1	J:Translation, ribosomal structure, biogenesis (9)^{1}		1.6	CCCGTGACT
1475			4	24	53	down^{3}	26%	yes^{3}	1.6			1.6	TTTCCTTT
328			4	3	12	down	83%	yes^{3}	1.1			1.6	GCATAGCATGGCGT
2287			4	33	0	up^{3}	6%	yes^{3}	1.3			1.6	TTCTTCCTT
843			4	13	1	up	38%		1.0			1.5	TGAGCCTCGG
2378		puf3	4	2	11	down	73%	yes^{1}	1.0		mitochondrion (4)	1.5	TGTACAGAA
347			4	15	1	up	47%		1.0	J:Translation, ribosomal structure, biogenesis (5)	nucleolus (4)^{1}	1.5	wmAAAAGTTC
1183			4	22	4	up	59%		1.1			1.5	AAACAAGGCA
344			4	14	2	up	50%		1.1			1.5	GGCAAAATdAAC
336			4	4	31	down^{3}	23%	yes^{3}	1.1	K:Transcription (7)		1.4	GGCGTTTGGG
698			4	121	16	up^{3}	10%	yes^{3}	1.7		mitochondrion (13)cytoplasm (27)	1.3	CCCTCCATCTCCA
233			4	108	36	up^{3}	6%	yes^{3}	1.6	C:Energy production, conversion (14)	mitochondrion (12)	1.3	TCTCCTTTCCTCyC
1270			4	26	5	up^{1}	12%	yes^{3}	1.3			1.3	CTTTTCCGTCC
Similar sequence determined comparing pattern with known factors in yeast and Aspergillus via CompareACE (score cutoff 0.85)													
Pvalues indicated by superscript: ^{1}pvalue < 1e-3, ^{2}pvalue < 1e-4, ^{3}pvalue < 1e-5													

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTT		up	down	71.m16041	AN0047.1	AO070314000125	GTP-binding protein GP-1				1	3	3	0	44	53	110			272	1
45	TTTCTTTTTCTTTTTTT		up	down	71.m15325	AN0056.1	AO070314000131	hypothetical protein [Neurospora crassa]				1	2	3	0	98	205	8			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	71.m15359	AN0081.1	AO070311000136	G-protein beta subunit				3	2	3	0	61	282	14			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15366	AN0091.1	AO070311000124	Putative protein methyltransferase involved in meiosis and transcriptional silencing (Dot1)	DK		0.939027978679397 4.15828392190872	1	1	2	0	207	66	182			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	71.m15386	AN0111.1	AO070311000109	mRNA splicing factor	A		1.249	1	1	1	0	276	74	146			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06496	AN0266.1	AO070334000087	Splicing factor, arginine/serine-rich	A		1.249	1	2	1	0	28	53	64	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15437	AN0837.1	AO070255000006	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	2	2	0	24	214	89	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15477	AN0874.1	AO070320000033	Poly(A) polymerase and related nucleotidyltransferases	A		1.249	3	2	3	0	91	98	162	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m14844	AN1379.1	AO070243000010	mRNA export protein (contains WD40 repeats)	A		1.249	1	1	1	0	12	210	245	135	0		
45	TTTCTTTTTCTTTTTTT		up	down	71.m16065	AN0182.1	AO070321000058	Ras-related GTPase				1	1	1	0	248	280	255			341	1
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07773	AN1697.1	AO070305000021	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	A		1.249	3	1	2	0	96	441	115	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15051	AN1750.1	AO070324000043	RNA helicase	A		1.249	1	1	1	0	94	30	29	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07347	AN1949.1	AO070342000215	ATP-dependent RNA helicase pitchoune	A		1.249	1	2	1	0	78	111	309	51	0		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07602	AN1992.1	AO070301000083	U4/U6.U5 snRNP associated protein	A		1.249	1	1	2	1	226	144	124	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19690	AN2151.1	AO070343000200	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	1	1	0	118	80	340	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08713	AN2868.1	AO070338000154	Oligoribonuclease (3'->5' exoribonuclease)	A		1.249	1	1	1	0	115	377	187	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m14962	AN3958.1	AO070341000080	DNA alkylation damage repair protein	A		1.249	1	1	2	0	237	91	13	64	0		
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06491	AN0293.1	AO070334000049	Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold				1	1	1	0	12	14	137			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	54.m06459	AN0302.1	AO070334000037	Nucleolar GTPase/ATPase p130	Y		0.123	6	5	2	1	71	109	151			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06765	AN4206.1	AO070231000018	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	1	1	1	0	79	40	122	34	0		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m08025	AN4298.1	AO070189000008	U3 small nucleolar ribonucleoprotein (snoRNP) subunit - Mpp10p	A		1.249	2	1	1	0	65	164	65	143	0		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06392	AN0359.1	AO070318000037	Translation initiation factor 3, subunit b (eIF-3b)	J		0.203	1	2	1	0	44	4	31			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15682	AN4696.1	AO070329000189	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	2	1	0	243	209	102	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19952	AN5931.1	AO070340000344	ATP-dependent RNA helicase	A		1.249	4	4	4	0	121	67	57	111	1		
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06638	AN0446.1	AO070338000308	Uncharacterized protein PSP1 (suppressor of DNA polymerase alpha mutations in yeast)				1	3	3	0	190	130	230			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	65.m07245	AN6725.1	AO070339000169	Protein involved in mRNA turnover and stability	A		1.249	1	1	1	1	144	40	47	45	1		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06605	AN0463.1	AO070328000174	Signaling protein DOCK180	T		0.089	1	2	3	0	113	47	27			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	53.m03883	AN8034.1	AO070322000125	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	2	3	0	107	177	297	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03908	AN8038.1	AO070330000008	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A		1.249	2	1	3	0	280	22	25	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03926	AN8073.1	AO070330000031	tRNA and rRNA cytosine-C5-methylase (nucleolar protein NOL1/NOP2)	A		1.249	1	1	2	0	78	20	13	8	0		
45	TTTCTTTTTCTTTTTTTT		up	down	69.m15281	AN0565.1	AO070272000043	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				3	3	3	1	68	84	84			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09109	AN4862.1	AO070329000148	Ran GTPase-activating protein	AYT		1.24930147251137 0.123290877849902 0.0887649648758591	2	1	2	0	20	152	68	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	69.m15270	AN0575.1	AO070272000054	Calmodulin-binding protein CRAG, contains DENN domain	T		0.089	2	1	2	0	150	202	112			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19479	AN2426.1	AO070241000005	Histone H4	B		6.721	1	1	1	0	116	383	410	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		6.721	4	3	4	0	42	110	208	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15648	AN0634.1	AO070318000124	GTP-binding ADP-ribosylation factor-like protein yARL3	U		3.418	1	1	1	0	185	66	117			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	53.m04190	AN8042.1	AO070330000004	Histone deacetylase complex, catalytic component HDA1	B		6.721	2	2	1	0	92	242	306	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m14994	AN1226.1	AO070331000235	Sirtuin 5 and related class III sirtuins (SIR2 family)	BK		6.72131997613286 4.15828392190872	1	1	2	0	47	152	94	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15259	AN0655.1	AO070343000571	hypothetical protein [Neurospora crassa]				1	5	4	0	156	102	19			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m15267	AN0664.1	AO070343000556	Phosphoinositide-specific phospholipase C	T		0.089	2	3	3	0	57	89	175			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15494	AN0888.1	AO070320000057	Uncharacterized conserved protein, contains JmjC domain	BT		6.72131997613286 0.08876496487585591	1	1	1	0	122	157	87	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15252	AN0595.1	AO070280000021	NADP/FAD dependent oxidoreductase	C		0.327	2	3	2	0	51	218	420	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15785	AN0775.1	AO070316000063	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.327	1	1	2	0	104	196	232	87	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15316	AN0709.1	AO070343000497	FOG: Zn-finger				1	1	2	0	412	309	385			731	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m15456	AN0870.1	AO070320000023	Mitochondrial phosphate carrier protein	C		0.327	2	1	2	0	57	438	27	15	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15319	AN0734.1	AO070343000495	Histone H4	B		6.721	2	1	1	0	6	6	8			342	1
45	TTTCTTTTTCTTTTTTT		up	down	70.m15349	AN0751.1	AO070343000448	predicted protein [Neurospora crassa]				1	1	2	0	33	360	77			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15137	AN1094.1	AO070285000053	NADH-dehydrogenase (ubiquinone)	C		0.327	3	2	3	0	32	122	69	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	55.m03061	AN1543.1	AO070339000311	Fumarate reductase, flavoprotein subunit	C		0.327	2	1	2	0	31	314	227	43	0		
45	TTTCTTTTTCTTTTTTT		up	up	55.m03067	AN1547.1	AO070339000307	Acetyl-CoA hydrolase	C		0.327	3	2	4	0	52	352	42	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07694	AN1624.1	AO070299000090	Mitochondrial F1F0-ATP synthase, subunit c/ATP9/proteolipid	C		0.327	2	3	2	0	45	356	325	79	0		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15053	AN1752.1	AO070324000041	NADP/FAD dependent oxidoreductase	C		0.327	1	2	1	0	51	51	77	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15424	AN0823.1	AO070255000022	Uncharacterized conserved protein				1	1	1	0	32	25	49			233	1
45	TTTCTTTTTCTTTTTTT		up	up	57.m05769	AN2069.1	AO070341000218	Cytochrome b5	C		0.327	1	2	3	0	360	125	134	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15944	AN2295.1	AO070295000075	Succinyl-CoA synthetase, alpha subunit	C		0.327	1	1	1	0	17	164	159	137	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15445	AN0846.1	AO070216000005	predicted protein [Neurospora crassa]				1	1	1	0	69	150	148			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15449	AN0849.1	AO070216000008	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z		5.801	1	2	2	0	268	171	118			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m15453	AN0854.1	AO070320000001	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	1	1	0	65	53	41			308	1
45	TTTCTTTTTCTTTTTTT		up	up	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		0.327	1	2	2	1	60	307	340	104	0		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C		0.327	3	2	3	0	24	154	247	187	1		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06583	AN4007.1	AO070328000146	Succinyl-CoA:alpha-ketoacid-CoA transferase	C		0.327	1	1	2	0	73	309	234	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07847	AN4462.1	AO070305000113	Pyruvate carboxylase	C		0.327	3	3	2	0	271	34	305	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07480	AN5534.1	AO070328000057	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.327	2	1	1	0	46	182	143	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07331	AN5634.1	AO070342000238	Isocitrate lyase	C		0.327	2	1	2	0	146	348	360	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.327	1	2	1	0	227	135	43	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15490	AN0891.1	AO070320000062	Positive regulator of purine utilization				1	1	1	0	16	3	181			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m15508	AN0899.1	AO070320000073	Nucleolar GTPase/ATPase p130	Y		0.123	1	3	4	1	165	3	34			7	1
45	TTTCTTTTTCTTTTTTT		up	up	62.m03250	AN6650.1	AO070269000001	Citrate synthase	C		0.327	2	1	2	0	33	382	162	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15522	AN0913.1	AO070320000094	Phosphatidylinositol synthase	I		3.913	1	1	2	0	375	313	169			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	65.m07257	AN6717.1	AO070339000157	NAD-dependent malate dehydrogenase	C		0.327	2	1	3	0	37	160	141	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03685	AN8275.1	AO070310000026	Citrate synthase	C		0.327	1	1	2	0	76	77	89	73	0		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03362	AN8707.1	AO070315000134	Fumarase	C		0.327	4	1	1	0	62	113	54	89	0		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		0.123290877849902 3.41751618934886	2	1	2	0	93	113	98			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	62.m03322	AN8755.1	AO070250000017	Isocitrate lyase	C		0.327	2	1	2	0	32	237	295	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15535	AN0928.1	AO070320000113	hypothetical protein ((AL451014) putative protein [Neurospora crassa])				1	1	1	0	42	7	22			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	65.m07308	AN8785.1	AO070289000010	Mitochondrial aspartate/glutamate carrier protein Aralar/Citrin (contains EF-hand Ca2+-binding domains)	C		0.327	2	4	6	0	64	15	2	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15600	AN0953.1	AO070320000154	Predicted small GTPase involved in nuclear protein import	U		3.418	1	2	1	0	312	232	367			35	0
45	TTTCTTTTTCTTTTTTT		up	up	52.m04030	AN9403.1	AO070274000014	Pyruvate dehydrogenase E1, beta subunit	C		0.327	1	1	1	0	25	317	207	101	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15609	AN0973.1	AO070320000174	FOG: Zn-finger				2	1	2	0	11	152	172			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m15619	AN0979.1	AO070320000183	Nucleolar GTPase/ATPase p130	Y		0.123	1	3	2	0	269	27	23			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	54.m07025	AN3894.1	AO070324000132	Aconitase/homoaconitase (aconitase superfamily)	CE		0.327086752378182 0.255777139620395	1	1	1	0	73	172	209	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15433	AN5525.1	AO070341000364	Aconitase/homoaconitase (aconitase superfamily)	CE		0.3270867 52378182 0.2557771 39620395	1	1	2	0	144	344	387	111	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15214	AN0997.1	AO070312000043	Ribonuclease III domain proteins	J		0.203	1	1	2	0	165	139	173			120	0
45	TTTCTTTTTCTTTTTTT		up	up	70.m15237	AN1019.1	AO070343000596	Cullins	D		0.939	2	2	2	0	133	157	94	69	0		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15234	AN1016.1	AO070312000002	G-protein alpha subunit (small G protein superfamily)	DT		0.9390279 78679397 0.0887649 64875859 1	1	2	3	0	283	117	110			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19677	AN2163.1	AO070343000222	Mitotic spindle checkpoint protein	D		0.939	1	1	4	0	301	104	63	242	1		
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15961	AN8830.1	AO070271000049	Checkpoint kinase and related serine/threonine protein kinases	D		0.939	1	2	1	0	155	74	38	121	1		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15197	AN1039.1	AO070336000074	HLH transcription factor EBF/Olf-1 and related DNA binding proteins	K		4.158	2	2	3	0	11	131	8			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15290	AN0687.1	AO070343000527	Spermidine synthase	E		0.256	4	2	2	0	27	377	272	123	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15221	AN1003.1	AO070312000031	Isocitrate dehydrogenase, alpha subunit	E		0.256	2	2	1	0	47	174	197	48	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15165	AN1073.1	AO070218000012	H+/oligopeptide symporter	E		0.256	3	2	2	0	34	252	233	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15191	AN1052.1	AO070336000059	von Willebrand factor and related coagulation proteins	V		9.308	2	1	1	0	137	205	165			368	1
45	TTTCTTTTTCTTTTTTT		up	up	55.m02926	AN1429.1	AO070242000022	Choline dehydrogenase and related flavoproteins	E		0.256	1	1	3	0	215	410	315	48	0		
45	TTTCTTTTTCTTTTTTTT		up	up	55.m02949	AN1446.1	AO070302000003	Cystathionine beta-lyases/cystathionine gamma-synthases	E		0.256	1	1	3	0	55	181	143	214	1		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07723	AN1631.1	AO070299000043	Amino acid transporters	E		0.256	3	1	3	0	300	153	34	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15036	AN1733.1	AO070324000063	Delta-1-pyrroline-5-carboxylate dehydrogenase	E		0.256	1	2	2	0	48	213	108	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15138	AN1093.1	AO070285000054	Vacuolar sorting protein VPS1, dynamin, and related proteins	U		3.418	2	1	1	0	30	1	258			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07598	AN1990.1	AO070301000078	Alpha-isopropylmalate synthase/homocitrate synthase	E		0.256	1	1	1	0	408	265	185	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15137	AN1094.1	AO070285000053	NADH-dehydrogenase (ubiquinone)	C		0.327	4	1	4	0	119	125	83			569	1
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07603	AN1993.1	AO070301000084	Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT1/GOT2	E		0.256	2	1	3	0	77	430	101	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15836	AN2229.1	AO070326000151	Homoserine acetyltransferase	E		0.256	1	1	1	0	96	61	54	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m15119	AN1116.1	AO070331000108	Transcription regulator XNP/ATRX, DEAD-box superfamily	K		4.158	2	1	3	0	24	232	51			50	0
45	TTTCTTTTTCTTTTTTT		up	down	70.m15114	AN1126.1	AO070331000119	GTP-binding ADP-ribosylation factor Arf1	U		3.418	1	2	2	0	171	173	165			286	1
45	TTTCTTTTTCTTTTTTT		up	up	59.m08957	AN3058.1	AO070337000016	Glycine/serine hydroxymethyltransferase	E		0.256	2	1	2	0	77	392	111	66	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15054	AN1166.1	AO070331000160	60s ribosomal protein L6	J		0.203	1	1	1	0	282	265	259			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	67.m02904	AN3304.1	AO070274000035	Amino acid transporters	E		0.256	1	1	1	0	52	329	65	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04660	AN3359.1	AO070317000081	Amino acid transporters	E		0.256	1	1	2	0	207	248	134	23	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15040	AN1177.1	AO070331000173	Vesicle coat complex COPI, beta subunit	U		3.418	1	1	1	0	84	14	137			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m08894	AN4159.1	AO070342000188	Glutamine synthetase	E		0.256	2	1	2	0	185	197	280	167	0		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07953	AN4376.1	AO070261000018	Glutamate/leucine/phenylalanine/valine dehydrogenases	E		0.256	3	1	2	0	73	384	331	100	0		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		0.256	5	2	4	0	24	235	220	66	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m09156	AN4819.1	AO070327000168	Glutamine synthetase	E		0.256	2	1	1	0	72	119	186	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06889	AN5134.1	AO070291000041	Glutamate synthase	E		0.256	2	1	1	0	262	309	209	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m14988	AN1231.1	AO070331000243	DNA polymerase IV (family X)	L		0.635	1	1	1	0	304	18	317			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	69.m14806	AN5790.1	AO070249000036	Isocitrate dehydrogenase, gamma subunit	E		0.256	1	1	5	0	428	420	47	205	0		
45	TTTCTTTTTCTTTTTTT		up	down	70.m14963	AN1251.1	AO070214000014	FOG: Zn-finger				3	4	3	0	58	208	132			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m14969	AN1255.1	AO070223000014	Chromodomain-helicase DNA-binding protein	K		4.158	2	2	2	0	69	186	16			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	70.m14961	AN1258.1	AO070214000012	predicted protein [Neurospora crassa]				1	1	1	0	260	286	158			12	0
45	TTTCTTTTTCTTTTTTT		up	up	72.m18963	AN5835.1	AO070260000010	Glycine/serine hydroxymethyltransferase	E		0.256	2	1	3	0	65	439	221	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19248	AN5883.1	AO070245000025	5,10-methylenetetrahydrofolate reductase	E		0.256	1	1	2	0	381	136	103	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	56.m02313	AN8903.1	AO070293000036	H+/oligopeptide symporter	E		0.256	3	1	2	0	6	138	64	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m04148	AN9506.1	AO070266000019	Amino acid transporters	E		0.256	2	1	2	0	69	255	121	51	0		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07391	AN3591.1	AO070342000143	Methylmalonate semialdehyde dehydrogenase	EG		0.2557771 39620395 1.0681502 5630857	1	1	1	0	88	124	666	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03251	AN6651.1	AO070269000002	ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	EJ		0.255777139620395 0.203093081833132	2	2	3	0	233	283	288	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		0.089	1	2	1	0	291	212	101			831	1
45	TTTCTTTTTCTTTTTTT		up	up	65.m07309	AN0490.1	AO070321000178	CTP synthase (UTP-ammonia lyase)	F		2.256	2	1	1	0	73	68	65	39	0		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05527	AN4603.1	AO070267000024	Dihydroorotase and related enzymes	F		2.256	1	2	3	0	21	307	129	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19247	AN5884.1	AO070245000024	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F		2.256	1	3	2	0	138	106	147	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	70.m14828	AN1394.1	AO070233000008	Septin CDC10 and related P-loop GTPases	DTZ		0.939027978679397 0.0887649648758591 5.80101679073153	1	1	1	0	206	103	122			356	1
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03232	AN6637.1	AO070326000089	Glutamine phosphoribosylpyrophosphate amidotransferase	F		2.256	2	2	4	0	144	25	2	415	1		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03757	AN8216.1	AO070310000096	Nucleoside diphosphate kinase	F		2.256	1	2	1	0	62	167	136	111	0		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04541	AN9083.1	AO070332000196	Adenine phosphoribosyl transferases	F		2.256	5	3	4	0	3	253	404	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	55.m03263	AN1437.1	AO070232000002	hypothetical protein [Neurospora crassa]				2	1	3	0	68	99	37			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	65.m07264	AN6711.1	AO070339000151	Ribose-phosphate pyrophosphokinase	FE		2.25564684014177 0.255777139620395	2	1	1	0	104	34	31	113	1		
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15460	AN5493.1	AO070341000392	Concentrative Na+-nucleoside cotransporter CNT1/CNT2	FP		2.25564684014177 1.35806928644389	1	1	1	0	156	264	29	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15291	AN0688.1	AO070343000525	Transketolase	G		1.068	5	1	4	0	47	330	172	66	0		
45	TTTCTTTTTCTTTTTTT		up	up	55.m02960	AN1457.1	AO070306000072	Permease of the major facilitator superfamily	G		1.068	1	1	1	0	154	95	400	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	55.m02969	AN1467.1	AO070306000090	Serine/threonine protein phosphatase	T		0.089	1	1	2	0	291	6	178			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07672	AN1827.1	AO070292000070	Chitinase	G		1.068	1	1	2	0	61	341	532	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	55.m02977	AN1475.1	AO070306000098	Cytoskeleton-associated protein and related proteins	Z		5.801	0	1	1	0	356	152	366			392	1
45	TTTCTTTTTCTTTTTTT		up	down	55.m03039	AN1520.1	AO070334000238	Nucleolar GTPase/ATPase p130	Y		0.123	1	3	1	0	263	13	190			328	1
45	TTTCTTTTTCTTTTTTT		up	up	71.m15917	AN2272.1	AO070295000048	Possible pfkB family carbohydrate kinase	G		1.068	1	1	1	0	67	118	83	91	0		
45	TTTCTTTTTCTTTTTTT		up	up	71.m16112	AN2282.1	AO070295000059	Permease of the major facilitator superfamily	G		1.068	1	2	1	0	61	441	247	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08711	AN2867.1	AO070338000157	Phosphoglucomutase	G		1.068	1	1	1	0	126	46	31	29	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08724	AN2875.1	AO070338000136	Fructose 1,6-bisphosphate aldolase	G		1.068	1	2	4	0	362	134	91	43	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m09058	AN2936.1	AO070337000172	Alpha-mannosidase	G		1.068	1	1	1	0	122	264	289	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08959	AN3059.1	AO070337000014	Phosphoglycerate mutase	G		1.068	1	1	1	0	146	74	76	25	0		
45	TTTCTTTTTCTTTTTTT		up	up	52.m03703	AN3307.1	AO070330000183	Glycogen synthase	G		1.068	4	2	2	0	121	142	28	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	52.m03702	AN3308.1	AO070330000181	Alpha-amylase	G		1.068	2	2	3	0	391	88	125	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m09022	AN1635.1	AO070299000058	mRNA processing protein	A		1.249	1	1	1	0	93	122	181			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07718	AN1639.1	AO070299000037	Thioredoxin-like protein	O		0.952	1	2	1	1	359	248	348			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07719	AN1652.1	AO070299000039	FOG: Zn-finger				2	3	3	0	352	175	369			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06782	AN4234.1	AO070234000012	Phosphoglucomutase/phosphomannomutase	G		1.068	1	2	1	0	90	135	128	77	0		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05514	AN4591.1	AO070267000007	Phosphoglucomutase/phosphomannomutase	G		1.068	1	1	1	0	10	25	45	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	54.m06876	AN5144.1	AO070291000029	Fructose-6-phosphate 2-kinase/fructose-2,6-biphosphatase	G		1.068	1	2	4	0	28	366	13	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15037	AN1731.1	AO070324000062	Proline oxidase	E		0.256	1	1	2	0	195	4	7			137	1
45	TTTCTTTTTCTTTTTTT		up	up	69.m14907	AN5210.1	AO070337000270	Pyruvate kinase	G		1.068	3	1	3	0	28	416	48	60	0		
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15435	AN5523.1	AO070341000366	Trehalose-6-phosphate synthase component TPS1 and related subunits	G		1.068	1	1	3	0	320	163	136	201	1		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19991	AN6286.1	AO070308000006	Glucosidase I	G		1.068	1	1	4	0	67	266	293	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03095	AN6508.1	AO070270000001	Glycogen synthase kinase-3	G		1.068	1	3	3	0	411	36	69	36	0		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15236	AN6900.1	AO070314000015	Triosephosphate isomerase	G		1.068	2	1	2	0	82	221	126	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07673	AN1828.1	AO070292000071	predicted protein [Neurospora crassa]				4	1	1	0	54	142	312			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05882	AN7459.1	AO070287000066	Hexokinase	G		1.068	3	1	1	0	61	23	0	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03857	AN8010.1	AO070322000057	Glycogen synthase	G		1.068	4	3	3	0	127	74	96	293	1		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		1.068	2	1	3	0	130	314	270	146	0		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		1.068	5	3	1	0	262	19	66	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTT		up	down	57.m05716	AN1902.1	AO070341000151	Nucleolar GTPase/ATPase p130	Y		0.123	1	2	3	0	33	24	62			505	1
45	TTTCTTTTTCTTTTTTT		up	down	69.m14936	AN1918.1	AO070341000122	Phosphoenolpyruvate carboxykinase (ATP)	C		0.327	3	1	4	0	14	19	10			195	1
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09373	AN3113.1	AO070303000036	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE		1.06815025630857 0.255777139620395	4	2	6	0	109	243	73	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m14947	AN1931.1	AO070341000104	Predicted GTPase-activating protein	T		0.089	1	1	2	0	86	94	108			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07359	AN1940.1	AO070342000196	Nucleolar GTPase/ATPase p130	Y		0.123	2	3	2	0	21	21	43			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15335	AN0726.1	AO070343000481	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		1.06815025630857 0.951548363056541	1	2	3	0	205	163	38	170	1		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07346	AN1950.1	AO070342000218	conserved hypothetical protein [Neurospora crassa]				3	3	3	0	103	17	110			496	1
45	TTTCTTTTTCTTTTTTTT		up	up	55.m03185	AN1602.1	AO070339000250	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		1.06815025630857 0.951548363056541	1	1	1	0	38	391	403	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		0.987	4	3	3	0	22	163	133	193	1		
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05936	AN7660.1	AO070268000029	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H		0.987	2	2	2	0	69	183	280	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07570	AN1965.1	AO070301000046	Ribose-phosphate pyrophosphokinase	FE		2.25564684014177 0.255777139620395	3	3	1	0	105	3	326			133	1
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15639	AN0243.1	AO070284000073	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.913	1	1	1	0	42	181	273	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15636	AN0640.1	AO070318000141	Sphingolipid hydroxylase	I		3.913	1	1	2	0	395	101	206	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15426	AN0824.1	AO070255000021	Short-chain acyl-CoA dehydrogenase	I		3.913	2	2	1	0	75	87	106	25	0		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m14873	AN1357.1	AO070237000003	Phosphorylcholine transferase/cholinephosphate cytidylyltransferase	I		3.913	3	1	3	0	124	182	137	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07709	AN1614.1	AO070299000065	SAM-dependent methyltransferases	I		3.913	2	1	2	0	187	241	309	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07604	AN1995.1	AO070301000090	Spindle pole body protein	Z		5.801	2	1	1	0	207	213	128			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m08943	AN2001.1	AO070301000099	predicted protein [Neurospora crassa]				1	1	1	0	218	156	186			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07617	AN2008.1	AO070179000004	Predicted hydrolase (HAD superfamily)				3	3	2	1	63	141	177			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07618	AN2009.1	AO070179000005	Transcription factor PRD and related proteins, contain PAX and HOX domains	K		4.158	1	1	3	0	304	17	41			673	1
45	TTTCTTTTTCTTTTTTT		up	up	58.m07772	AN1696.1	AO070305000020	Predicted acyltransferases	I		3.913	2	1	2	0	382	165	49	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m08942	AN2011.1	AO070202000001	P-type ATPase				1	1	1	0	10	1	415			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05768	AN2068.1	AO070341000217	Vigilin	I		3.913	2	2	2	0	364	115	26	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		3.913	6	3	4	0	12	38	71	298	1		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09454	AN4997.1	AO070288000080	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.913	1	1	4	0	29	131	142	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07643	AN2055.1	AO070292000025	hypothetical protein [Neurospora crassa]				2	2	2	0	27	42	138			447	1
45	TTTCTTTTTCTTTTTTT		up	up	58.m07549	AN5626.1	AO070301000025	Acyl-CoA synthetase	I		3.913	1	1	3	0	407	175	142	66	0		
45	TTTCTTTTTCTTTTTTT		up	up	65.m07239	AN6731.1	AO070339000175	Fatty acid desaturase	I		3.913	3	1	3	0	107	331	326	7	0		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03303	AN7204.1	AO070293000065	Fatty acid desaturase	I		3.913	2	2	2	0	25	188	195	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03827	AN8117.1	AO070322000025	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme	I		3.913	3	2	5	0	183	218	231	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03736	AN8233.1	AO070310000075	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.913	1	1	3	0	85	251	169	117	0		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05770	AN2072.1	AO070341000219	Ubiquitin C-terminal hydrolase	O		0.952	2	1	1	0	160	325	12			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05806	AN2105.1	AO070341000263	Small nuclear ribonucleoprotein SMD1 and related snRNPs	A		1.249	1	1	3	0	48	83	27			57	0
45	TTTCTTTTTCTTTTTTT		up	up	53.m03681	AN8280.1	AO070310000020	Long-chain acyl-CoA synthetases (AMP-forming)	I		3.913	3	3	1	0	80	43	137	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19711	AN2130.1	AO070278000033	Ras1 guanine nucleotide exchange factor	T		0.089	3	2	1	0	31	40	3			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	52.m04034	AN9407.1	AO070274000010	3-oxoacyl-[acyl-carrier protein] reductase	I		3.913	1	2	4	0	217	3	23	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	52.m04035	AN9408.1	AO070274000009	Enoyl reductase domain of yeast-type FAS1	I		3.913	2	2	4	0	359	17	20	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		3.418	2	1	2	0	39	456	226			144	0

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45	TTTCTTTTTCTTTTTTTT		up	up	54.m06529	AN0254.1	AO070334000106	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE		3.91278222556957 0.255777139620395	2	1	5	0	42	147	126	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06444	AN0314.1	AO070334000018	Aspartyl-tRNA synthetase	J		0.203	2	1	2	0	137	205	121	69	0		
45	TTTCTTTTTCTTTTTTTT		up	up	54.m06616	AN0455.1	AO070328000183	Acetyltransferases, including N-acetylases of ribosomal proteins	J		0.203	1	1	1	0	29	113	70	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19688	AN2153.1	AO070343000202	Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	J		0.203	1	2	2	0	225	142	282	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19677	AN2163.1	AO070343000222	Mitotic spindle checkpoint protein	D		0.939	3	1	7	0	100	295	57			274	0
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09062	AN2932.1	AO070337000175	Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases	J		0.203	1	1	3	0	283	86	6	275	1		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15855	AN2210.1	AO070294000012	Predicted transporter (ABC superfamily)				2	3	1	0	81	9	11			344	1
45	TTTCTTTTTCTTTTTTT		up	up	54.m06579	AN4015.1	AO070328000151	Translation initiation factor 5A (eIF-5A)	J		0.203	2	3	2	0	86	113	157	70	0		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		0.203	3	3	2	1	126	283	77	96	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08665	AN5014.1	AO070334000120	60S ribosomal protein L22	J		0.203	1	1	1	0	327	81	82	70	0		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15881	AN2247.1	AO070326000126	Myosin class II heavy chain	Z		5.801	2	1	2	0	21	2	8			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		0.203	1	1	1	0	50	187	131	101	0		
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15895	AN2255.1	AO070326000108	Transcription regulator XNP/ATRX, DEAD-box superfamily	K		4.158	3	1	1	0	34	135	178			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15896	AN2256.1	AO070326000107	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL		4.15828392190872 0.6349440929397	2	1	1	0	9	24	191			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15450	AN0176.1	AO070321000065	GATA-4/5/6 transcription factors	K		4.158	1	2	2	0	208	218	79	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06667	AN0407.1	AO070338000247	RNA polymerase III transcription factor TFIIIC	K		4.158	1	2	2	0	315	176	299	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15524	AN0917.1	AO070320000097	Transcriptional coactivator CAPER (RRM superfamily)	K		4.158	1	1	1	0	46	227	354	168	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15059	AN1162.1	AO070331000152	Elongation factor 1 beta/delta chain	K		4.158	1	1	1	0	41	117	113	17	0		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07590	AN1984.1	AO070301000069	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K		4.158	1	1	1	0	261	258	114	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		0.327	2	1	4	1	111	306	21			307	1
45	TTTCTTTTTCTTTTTTT		up	up	59.m08698	AN2854.1	AO070338000167	Transcription factor of the Forkhead/HNF3 family	K		4.158	1	1	1	0	185	76	245	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	72.m19478	AN2425.1	AO070241000006	Protein phosphatase, regulatory subunit PPP1R3C/D	OT		0.951548363056541 0.0887649648758591	1	2	2	0	257	232	219			489	1
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		4.158	4	4	2	0	88	112	48	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	54.m06748	AN4187.1	AO070342000108	SNF2 family DNA-dependent ATPase domain-containing protein	K		4.158	3	2	4	0	105	440	201	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C		0.327	1	1	3	0	54	88	7			207	1
45	TTTCTTTTTCTTTTTTTT		up	down	69.m15197	AN2459.1	AO070264000014	Protein phosphatase 1, regulatory subunit, and related proteins	T		0.089	1	1	5	0	1	106	2			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	69.m15203	AN2464.1	AO070264000006	Protein transporter of the TRAM (translocating chain-associating membrane) superfamily	U		3.418	1	1	1	0	88	147	234			341	1
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07962	AN4361.1	AO070261000004	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		4.158	1	1	3	0	242	199	270	263	1		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08494	AN2496.1	AO070312000124	Putative transmembrane protein cmp44E				1	2	2	0	48	9	146			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	59.m09383	AN2499.1	AO070312000049	RNA polymerase II elongator associated protein				1	1	2	0	184	147	59			675	1
45	TTTCTTTTTCTTTTTTT		up	down	54.m06688	AN2743.1	AO070338000228	Translation initiation factor 3, subunit a (eIF-3a)	J		0.203	3	3	2	0	75	44	63			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	54.m06687	AN2744.1	AO070338000227	predicted protein [Neurospora crassa]				1	8	1	0	105	7	23			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	54.m06683	AN2748.1	AO070338000223	FOG: Zn-finger				1	1	3	0	515	380	55			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06680	AN2749.1	AO070338000221	WASP-interacting protein VRP1/WIP, contains WH2 domain	Z		5.801	2	2	2	0	48	122	131			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	54.m06682	AN2750.1	AO070338000222					3	1	1	0	105	139	448			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09500	AN2756.1	AO070327000037	Actin-binding protein SLA2/Huntingtin-interacting protein Hip1	Z		5.801	2	1	3	0	202	99	162			207	1
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09254	AN2757.1	AO070327000036	Uncharacterized conserved protein TEX2, contains PH domain				1	1	1	0	158	174	128			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	59.m09264	AN2760.1	AO070327000022	Lactoylglutathione lyase and related lyases	E		0.256	2	1	1	0	281	39	6			295	1
45	TTTCTTTTTCTTTTTTT		up	up	59.m08799	AN4900.1	AO070338000044	RNA polymerase II, large subunit	K		4.158	2	2	2	0	18	162	185	662	1		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09488	AN2766.1	AO070327000031	Phosphatidylinositol-4-phosphate 5-kinase	T		0.089	1	1	1	0	381	400	360			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19202	AN5929.1	AO070340000354	Calcium-responsive transcription coactivator	K		4.158	2	2	3	0	200	163	69	No EST	No EST		

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45	TTTCTTTTTCTTTTTTTT		up	up	72.m19132	AN6012.1	AO070340000266	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K		4.158	2	3	3	0	278	73	20	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19649	AN7608.1	AO070343000269	RNA Polymerase C (III) 37 kDa subunit	K		4.158	1	1	1	0	261	235	167	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m04172	AN8272.1	AO070310000029	RNA polymerase III (C) subunit	K		4.158	1	1	1	0	169	43	55	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		4.158	1	3	2	0	187	299	357	157	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15474	AN0872.1	AO070320000030	CDC45 (cell division cycle 45)-like protein	L		0.635	2	1	1	0	35	236	66	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		6.721	4	2	3	0	94	106	155			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15174	AN1060.1	AO070218000003	DNA damage-responsive repressor GIS1/RPH1, jumonji superfamily	L		0.635	1	3	1	0	198	170	488	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08744	AN2895.1	AO070338000115	Uncharacterized conserved protein				1	1	1	0	14	28	59			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	59.m08751	AN2901.1	AO070338000106	Arginase	E		0.256	2	1	1	0	5	156	63			67	0
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L		0.635	1	1	1	0	230	12	3	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19611	AN7589.1	AO070343000303	Predicted hydrolase involved in interstrand cross-link repair	L		0.635	1	1	3	0	180	179	73	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03793	AN8185.1	AO070310000139	5'-3' exonuclease XRN1/KEM1/SEP1 involved in DNA strand exchange and mRNA turnover	LD		0.6349440929397 0.939027978679397	1	1	1	0	216	46	46	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09062	AN2932.1	AO070337000175	Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases	J		0.203	1	1	2	0	249	302	277			624	1
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15386	AN3729.1	AO070342000283	1,3-beta-glucan synthase/callose synthase catalytic subunit	M		6.643	2	2	1	1	371	95	23	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	56.m03102	AN4372.1	AO070275000045	Endopolygalacturonase	M		6.643	2	1	2	0	95	464	358	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09028	AN2985.1	AO070337000137	Predicted transporter (major facilitator superfamily)				1	1	2	0	13	307	3			130	0
45	TTTCTTTTTCTTTTTTT		up	down	59.m09022	AN2992.1	AO070337000126	Translation initiation factor 2, beta subunit (eIF-2beta)	J		0.203	1	3	1	0	43	79	104			355	1
45	TTTCTTTTTCTTTTTTT		up	down	59.m09013	AN3001.1	AO070337000111	Mitogen-activated protein kinase kinase (MAP2K)	T		0.089	3	2	2	0	43	144	107			320	1
45	TTTCTTTTTCTTTTTTT		up	down	59.m08981	AN3036.1	AO070337000078	predicted protein [Neurospora crassa]				1	1	2	0	238	24	15			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19590	AN7571.1	AO070343000417	Predicted mechanosensitive ion channel	M		6.643	3	1	1	0	134	238	63	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09479	AN3445.1	AO070265000021	Extracellular protein SEL-1 and related proteins	MOT		6.642878635625 0.951548363056541 0.0887649648758591	1	1	4	0	20	446	262	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08932	AN3067.1	AO070337000006	DNA polymerase epsilon, catalytic subunit A	L		0.635	1	1	2	0	14	32	15			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15462	AN0866.1	AO070320000017	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O		0.952	3	3	3	0	50	172	148	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08919	AN3079.1	AO070224000007					1	1	3	0	97	32	30			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15455	AN0871.1	AO070320000029	Gpi-anchor transamidase	O		0.952	1	1	1	0	54	256	64	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08918	AN3080.1	AO070224000006	Vesicle coat complex COPII, subunit SFB3	U		3.418	1	1	1	0	122	36	439			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15203	AN1047.1	AO070313000109	Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	O		0.952	2	2	4	0	127	366	195	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15130	AN1102.1	AO070285000036	Serine palmitoyltransferase	O		0.952	1	1	4	0	58	245	27	150	0		
45	TTTCTTTTTCTTTTTTT		up	up	55.m02957	AN1455.1	AO070302000021	Oligosaccharyltransferase, STT3 subunit	O		0.952	2	1	2	0	7	160	132	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07660	AN1851.1	AO070292000043	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O		0.952	1	1	1	0	39	109	115	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09373	AN3113.1	AO070303000036	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE		1.06815025630857 0.255777139620395	1	1	1	0	387	367	116			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		0.952	2	4	1	0	188	105	179	173	1		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				3	3	3	0	219	179	248			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19685	AN2157.1	AO070343000208	Aspartyl protease	O		0.952	2	1	1	0	196	401	216	278	0		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08584	AN3142.1	AO070303000002	Nucleolar GTPase/ATPase p130	Y		0.123	1	2	5	0	387	157	119			297	1
45	TTTCTTTTTCTTTTTTT		up	down	59.m08506	AN3145.1	AO070312000163	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	2	2	0	58	66	70			386	1
45	TTTCTTTTTCTTTTTTT		up	down	59.m08562	AN3172.1	AO070256000018	40S ribosomal protein SA (P40)/Laminin receptor 1	J		0.203	1	1	1	0	216	116	200			399	1
45	TTTCTTTTTCTTTTTTTT		up	down	59.m08573	AN3181.1	AO070256000007	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	T		0.089	1	1	1	0	175	37	66			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	down	59.m08571	AN3183.1	AO070256000009	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B		6.721	2	1	1	0	114	301	357			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m09263	AN2761.1	AO070327000023	Ubiquitin-protein ligase	O		0.952	4	4	5	0	159	271	140	144	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08754	AN2903.1	AO070338000102	Aspartyl protease	O		0.952	1	1	1	0	90	384	448	70	0		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07379	AN3581.1	AO070342000168	Thioredoxin reductase	O		0.952	3	2	2	0	132	39	72	163	1		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07392	AN3592.1	AO070342000144	Calnexin	O		0.952	1	3	3	0	188	295	34	126	0		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06754	AN4192.1	AO070342000112	Molecular chaperone (DnaJ superfamily)	O		0.952	2	1	2	0	2	415	89	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15667	AN4683.1	AO070284000018	Oligosaccharyltransferase, beta subunit	O		0.952	1	1	1	0	62	146	132	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09275	AN3422.1	AO070327000010	Mitogen-activated protein kinase kinase (MAP2K)	T		0.089	1	1	2	0	146	175	37			376	1
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09280	AN3426.1	AO070327000005	Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	A		1.249	2	1	1	0	322	231	28			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09222	AN4761.1	AO070327000055	Dolichyl-phosphate-mannose:protein O-mannosyl transferase	O		0.952	1	1	1	0	231	183	344	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	54.m06917	AN5105.1	AO070291000074	Dolichyl-phosphate-mannose:protein O-mannosyl transferase	O		0.952	2	2	3	1	259	312	175	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15458	AN5495.1	AO070341000391	Ubiquitin-protein ligase	O		0.952	1	1	3	0	49	140	48	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19133	AN6010.1	AO070340000269	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	O		0.952	2	3	3	0	96	320	331	149	0		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		0.952	2	2	2	0	22	182	177	140	0		
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07441	AN3659.1	AO070342000029	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		0.0887649648758591 5.80101679073153	1	1	1	0	151	45	52			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19291	AN6193.1	AO070308000106	Mitochondrial ATP-dependent protease PIM1/LON	O		0.952	1	1	1	0	77	155	80	128	0		
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07430	AN3669.1	AO070342000010	Protein involved in cell differentiation/sexual development				4	2	5	0	134	145	135			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	69.m15403	AN3696.1	AO070341000317	Equilibrative nucleoside transporter protein	F		2.256	2	1	1	0	79	102	117			326	1
45	TTTCTTTTTCTTTTTTT		up	up	62.m03116	AN6528.1	AO070270000028	Prenyl protein protease	O		0.952	1	1	1	0	252	380	266	58	0		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15380	AN3735.1	AO070342000272	GTPase-activating protein				1	2	1	0	349	291	284			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19795	AN7254.1	AO070297000010	AAA+-type ATPase	O		0.952	1	1	2	0	4	261	235	106	0		
45	TTTCTTTTTCTTTTTTT		up	down	65.m07351	AN3765.1	AO070309000034					1	1	1	0	281	167	295			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	65.m07196	AN3781.1	AO070289000057	Na+/Pi symporter	P		1.358	1	1	1	0	13	15	11			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19566	AN7549.1	AO070277000046	AAA+-type ATPase	O		0.952	1	1	1	0	36	189	176	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05667	AN3815.1	AO070311000013	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z		5.801	3	3	5	0	61	46	63			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07830	AN3853.1	AO070305000093	Metalloendoprotease HMP1 (insulinase superfamily)	O		0.952	1	1	1	0	187	135	141			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07841	AN3869.1	AO070305000105	Mevalonate kinase MVK/ERG12	I		3.913	2	1	1	0	27	172	84			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19586	AN7567.1	AO070343000413	Glutaredoxin-related protein	O		0.952	1	3	2	0	161	140	76	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19597	AN7579.1	AO070343000426	26S proteasome regulatory complex, subunit RPN10/PSMD4	O		0.952	1	1	1	0	98	114	141	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m14999	AN3929.1	AO070341000037	Permease of the major facilitator superfamily	G		1.068	1	1	1	0	495	136	234			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	69.m14975	AN3946.1	AO070341000066	Mitotic checkpoint serine/threonine protein kinase	D		0.939	1	3	1	0	91	49	319			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	53.m03928	AN8075.1	AO070330000033	Deoxyhypusine synthase	O		0.952	2	1	1	0	66	5	483	35	1		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06592	AN3999.1	AO070328000163	E3 ubiquitin protein ligase	O		0.952	1	2	3	0	417	185	317			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m09455	AN8605.1	AO070314000022	Cyclophilin type peptidyl-prolyl cis-trans isomerase	O		0.952	1	1	1	0	55	464	129	32	0		
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03392	AN8679.1	AO070315000099	RAB proteins geranylgeranyltransferase component A (RAB escort protein)	O		0.952	1	2	1	0	176	214	399	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19478	AN2425.1	AO070241000006	Protein phosphatase, regulatory subunit PPP1R3C/D	OT		0.951548363056541 0.0887649648758591	2	2	2	0	238	154	273	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06562	AN4034.1	AO070328000126	CCAAT-binding factor, subunit A (HAP3)	K		4.158	1	2	2	0	335	328	276			2	0
45	TTTCTTTTTCTTTTTTT		up	down	54.m06733	AN4088.1	AO070342000091	predicted protein [Neurospora crassa]				2	3	2	0	309	272	296			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15641	AN0241.1	AO070284000071	Cu2+/Zn2+ superoxide dismutase SOD1	P		1.358	1	1	4	0	243	243	13	123	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15760	AN1181.1	AO070331000179	Ammonia permease	P		1.358	1	2	1	0	209	302	290	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	55.m02974	AN1472.1	AO070306000093	Tellurite resistance protein and related permeases	P		1.358	1	1	4	0	283	431	322	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07716	AN1630.1	AO070299000035	Catalase (peroxidase I)	P		1.358	1	2	2	0	149	370	311	69	0		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19547	AN1795.1	AO070309000136	Zn2+ transporter ZNT1 and related Cd2+/Zn2+ transporters (cation diffusion facilitator superfamily)	P		1.358	2	1	2	0	220	303	284	137	0		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05611	AN4517.1	AO070321000123	Heavy metal exporter HMT1, ABC superfamily	P		1.358	3	2	3	0	101	0	45	556	1		
45	TTTCTTTTTCTTTTTTT		up	up	59.m09466	AN4859.1	AO070329000143	Plasma membrane H+-transporting ATPase	P		1.358	5	3	2	1	96	133	185	103	0		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15495	AN5440.1	AO070333000102	Catalase (peroxidase I)	P		1.358	1	1	1	0	133	126	65	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06765	AN4206.1	AO070231000018	Splicing coactivator SRm160/300, subunit SRm300	A		1.249	2	1	1	0	237	271	73			456	1

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06959	AN4214.1	AO070231000010	Alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)	A		1.249	2	1	2	0	57	47	402			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	69.m15483	AN5449.1	AO070239000028	Arylsulfatase A and related enzymes	P		1.358	5	3	2	0	124	203	131	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m14939	AN5549.1	AO070341000115	Inorganic phosphate transporter	P		1.358	1	2	1	0	182	438	175	308	0		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06778	AN4237.1	AO070234000004	predicted protein [Neurospora crassa]				2	1	1	0	77	222	185			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	54.m07034	AN4238.1	AO070234000002	Ribosomal protein S6 kinase and related proteins	T		0.089	3	2	3	0	34	141	87			151	1
45	TTTCTTTTTCTTTTTTT		up	up	72.m18948	AN5821.1	AO070260000024	Ca2+/H+ antiporter VCX1 and related proteins	P		1.358	1	1	4	0	162	262	54	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m08010	AN4314.1	AO070230000002	predicted protein [Neurospora crassa]				4	1	3	0	43	141	166			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m08007	AN4317.1	AO070230000006	Vesicle coat complex COPII, subunit SEC13	U		3.418	1	1	2	0	14	31	13			118	1
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19051	AN6107.1	AO070340000100	Cl- channel CLC-3 and related proteins (CLC superfamily)	P		1.358	2	1	2	0	94	311	46	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03875	AN8029.1	AO070322000075	Na+/K+ transporter	P		1.358	1	1	1	0	437	90	74	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m08810	AN4906.1	AO070338000039	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ		1.35806928644389 0.66935342495277	1	1	1	0	36	115	501	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15198	AN1041.1	AO070336000075	Ca2+-modulated nonselective cation channel polycystin	PT		1.35806928644389 0.0887649648758591	1	1	1	0	62	332	399	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				3	1	4	0	357	243	206			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	58.m07907	AN4418.1	AO070273000039	predicted protein [Neurospora crassa]				1	1	1	0	274	271	423			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15374	AN0771.1	AO070316000073	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q		0.669	1	2	1	0	134	279	198	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15122	AN1111.1	AO070285000025	Flavin-containing monooxygenase	Q		0.669	2	2	1	0	69	415	253	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07850	AN4465.1	AO070305000119	Putative growth response protein	T		0.089	1	1	4	1	22	12	24			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07862	AN4472.1	AO070305000131	Putative transcription factor HALR/MLL3, involved in embryonic development				1	1	1	0	35	86	181			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15558	AN5318.1	AO070334000168	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q		0.669	1	2	1	0	156	228	303	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05654	AN4479.1	AO070311000025	FOG: HAMP domain	T		0.089	2	1	2	0	19	277	25			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m18952	AN5823.1	AO070260000021	Lysine/ornithine N-monooxygenase	Q		0.669	2	1	4	0	16	374	74	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03878	AN8928.1	AO070281000035	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q		0.669	1	1	1	0	202	86	262	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15438	AN0163.1	AO070321000084	Rho GDP-dissociation inhibitor	T		0.089	1	2	1	0	164	300	367	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05641	AN4490.1	AO070311000042	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K		4.158	1	3	1	0	44	33	103			279	1
45	TTTCTTTTTCTTTTTTT		up	down	57.m05629	AN4501.1	AO070311000054	Multifunctional chaperone (14-3-3 family)	O		0.952	1	1	2	0	12	186	86			508	1
45	TTTCTTTTTCTTTTTTT		up	down	57.m05616	AN4513.1	AO070311000069	Kinesin-like protein	Z		5.801	1	1	1	0	93	14	228			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15270	AN0575.1	AO070272000054	Calmodulin-binding protein CRAG, contains DENN domain	T		0.089	4	2	2	0	187	147	73	117	0		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05597	AN4529.1	AO070321000139					2	2	2	0	12	52	24			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	57.m05584	AN4537.1	AO070321000154	Ypt/Rab-specific GTPase-activating protein GYP6	U		3.418	1	1	1	0	14	98	235			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15539	AN0931.1	AO070320000122	Mitogen-activated protein kinase kinase (MAP2K)	T		0.089	1	1	4	0	383	84	26	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05579	AN4546.1	AO070321000159	PolyC-binding proteins alphaCP-1 and related KH domain proteins	A		1.249	1	3	1	0	353	104	136			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	57.m05557	AN4547.1	AO070321000185	Vesicle coat complex COPI, gamma subunit	U		3.418	1	3	2	0	88	83	87			148	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m15629	AN0988.1	AO070318000150	LAMMER dual specificity kinases	T		0.089	1	2	3	0	44	64	49	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05501	AN4579.1	AO070316000166	predicted protein [Neurospora crassa]				2	1	1	0	26	100	56			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15050	AN1171.1	AO070331000166	Serine/threonine protein kinase	T		0.089	1	1	3	0	93	129	118	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05520	AN4598.1	AO070267000015	LST7 amino acid permease Golgi transport protein	UE		3.41751618934886 0.255777139620395	1	1	1	0	307	239	125			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		0.089	2	1	3	0	165	396	29	400	1		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05543	AN4632.1	AO070340000375	FOG: FHA domain	T		0.089	3	2	1	0	101	238	373			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m08643	AN3101.1	AO070334000142	Sensory transduction histidine kinase	T		0.089	2	3	7	0	270	87	49	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08628	AN3110.1	AO070303000041	3-phosphoinositide-dependent protein kinase (PDK1)	T		0.089	1	2	2	0	313	106	186	391	1		
45	TTTCTTTTTCTTTTTTTT		up	up	65.m07375	AN3752.1	AO070309000065	Uncharacterized conserved protein, contains TBC domain	T		0.089	4	2	3	0	86	10	0	471	1		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15694	AN4706.1	AO070329000170	Myosin class II heavy chain	Z		5.801	1	1	1	0	113	134	185			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06745	AN4189.1	AO070342000110	Mitogen-activated protein kinase kinase (MAP2K)	T		0.089	1	2	4	0	319	27	112	No EST	No EST		

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45	TTTCTTTTTCTTTTTTT		up	down	71.m15707	AN4719.1	AO070311000002	RhoGEF GTPase	T		0.089	1	2	3	0	336	95	133			595	1
45	TTTCTTTTTCTTTTTTT		up	up	57.m05654	AN4479.1	AO070311000025	FOG: HAMP domain	T		0.089	2	3	7	0	314	61	82	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09224	AN4759.1	AO070327000057	Guanine nucleotide exchange factor	U		3.418	2	1	2	0	226	227	200			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05648	AN4483.1	AO070311000032	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		0.089	5	3	7	0	37	190	48	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09211	AN4771.1	AO070329000081	WD40 repeat protein				1	1	1	0	22	7	43			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m08914	AN5011.1	AO070224000003	FGF receptor activating protein 1	T		0.089	3	3	1	0	67	69	133	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07516	AN5592.1	AO070328000011	Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	T		0.089	1	1	4	0	408	350	75	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09157	AN4818.1	AO070327000169	Signal transduction histidine kinase	T		0.089	1	1	1	0	103	68	226			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19897	AN5849.1	AO070281000056	Serine/threonine protein kinase	T		0.089	2	3	1	0	182	1	305	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m09148	AN4824.1	AO070327000153	Galactosyltransferases	G		1.068	1	1	1	0	5	5	5			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19237	AN5893.1	AO070245000013	G protein signaling regulators	T		0.089	4	4	8	0	93	26	23	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19290	AN6192.1	AO070308000109	Serine/threonine protein kinase	T		0.089	3	3	1	0	179	49	332	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08765	AN4870.1	AO070338000090	predicted protein [Neurospora crassa]				1	1	2	0	17	37	62			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		0.089	3	1	2	0	155	42	47	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19330	AN6304.1	AO070308000059	Stress-activated MAP kinase-interacting protein, Sin1p	T		0.089	1	1	1	0	217	103	80	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19797	AN7252.1	AO070297000007	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T		0.089	1	1	2	0	483	139	223	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15723	AN7697.1	AO070325000104	Sensory transduction histidine kinase	T		0.089	3	2	2	0	79	7	9	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03738	AN8231.1	AO070310000077	S-adenosylmethionine decarboxylase	T		0.089	3	1	1	1	252	104	210	9	0		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08826	AN4923.1	AO070338000020	Hydroxymethylglutaryl-CoA synthase	I		3.913	1	1	1	0	30	119	39			208	1
45	TTTCTTTTTCTTTTTTT		up	down	59.m08828	AN4926.1	AO070338000017	hypothetical protein [Neurospora crassa]				1	1	1	0	202	340	224			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				1	1	1	0	162	226	306			431	1
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07325	AN5638.1	AO070342000239	OTU (ovarian tumor)-like cysteine protease	TO		0.08876496487585591 0.951548363056541	1	1	1	0	31	211	220	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m07434	AN3664.1	AO070342000020	C-type lectin	TV		0.08876496487585591 9.30761496067453	1	1	5	0	175	100	11	248	1		
45	TTTCTTTTTCTTTTTTT		up	down	59.m08886	AN4984.1	AO070288000052	Cyclin				4	2	3	0	54	215	196			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	59.m08887	AN4985.1	AO070288000053	Serine/threonine protein kinase	T		0.089	2	1	3	0	272	240	94			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	54.m07007	AN0409.1	AO070338000252	Nischarin, modulator of integrin alpha5 subunit action	TZ		0.08876496487585591 5.80101679073153	2	3	2	0	256	6	28	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15264	AN0585.1	AO070280000007	Actin regulatory protein (Wiskott-Aldrich syndrome protein)	TZ		0.08876496487585591 5.80101679073153	2	2	3	0	415	81	51	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	71.m16009	AN8869.1	AO070271000002	Armadillo/beta-Catenin/plakoglobin	TZ		0.08876496487585591 5.80101679073153	1	1	1	0	348	314	373	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	59.m09454	AN4997.1	AO070288000080	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.913	1	3	1	0	267	107	15			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06965	AN0261.1	AO070334000097	Vesicle coat complex COPII, subunit SEC23	U		3.418	1	2	1	0	317	32	23	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15529	AN0922.1	AO070320000101	Medium subunit of clathrin adaptor complex	U		3.418	1	1	2	0	6	42	37	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15040	AN1177.1	AO070331000173	Vesicle coat complex COPI, beta subunit	U		3.418	1	1	2	0	42	172	27	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09385	AN1309.1	AO070266000049	Vacuolar sorting protein VPS1, dynamin, and related proteins	U		3.418	1	1	1	0	54	502	405	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05726	AN1892.1	AO070341000163	Mitochondrial import inner membrane translocase, subunit TIM17	U		3.418	3	1	1	0	3	152	304	242	1		
45	TTTCTTTTTCTTTTTTT		up	up	69.m14938	AN1921.1	AO070341000116	Peroxisomal biogenesis protein (peroxin)	U		3.418	1	2	2	0	184	115	4	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07577	AN1973.1	AO070301000057	V-SNARE	U		3.418	1	2	1	0	271	152	335	214	1		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06880	AN5141.1	AO070291000035	Superfamily II DNA and RNA helicases	LKJ		0.6349440929397 4.15828392190872 0.203093081833132	2	1	2	0	133	296	328			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		3.418	1	4	2	0	87	46	55	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m09076	AN2945.1	AO070337000194	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U		3.418	1	2	2	0	338	123	70	18	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08918	AN3080.1	AO070224000006	Vesicle coat complex COPII, subunit SFB3	U		3.418	1	1	1	0	31	215	355	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15505	AN5404.1	AO070333000090	Reticulon	U		3.418	1	3	6	0	187	256	38	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19327	AN6307.1	AO070308000062	Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	U		3.418	1	1	2	0	266	64	7	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	56.m02547	AN6412.1	AO070339000013	Vesicular amine transporter	U		3.418	1	1	1	0	207	201	29	45	0		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15563	AN5343.1	AO070333000181	Kinesin (SMY1 subfamily)	Z		5.801	1	3	1	1	52	16	13			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	53.m04098	AN8053.1	AO070322000147	Inositol polyphosphate 5-phosphatase and related proteins	U		3.418	2	1	3	0	226	81	22	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15748	AN7721.1	AO070325000136	Transport protein Sec61, alpha subunit	UO		3.41751618934886 0.951548363056541	2	1	2	0	44	130	129	106	0		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05577	AN4544.1	AO070321000162	Dual specificity phosphatase	V		9.308	2	1	4	0	210	325	24	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19094	AN6059.1	AO070340000190	HVA22/DP1 gene product-related proteins	V		9.308	2	2	2	0	279	123	196	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15493	AN5441.1	AO070333000104	Ribosomal protein S18	J		0.203	2	1	1	0	13	18	192			211	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m14985	AN1233.1	AO070331000247	Nucleolar GTPase/ATPase p130	Y		0.123	2	1	2	0	324	154	30	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m18986	AN5857.1	AO070340000013	Nucleolar GTPase/ATPase p130	Y		0.123	1	2	4	0	94	363	295	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15461	AN5491.1	AO070341000394	Cytoplasm to vacuole targeting protein	U		3.418	1	1	1	0	93	104	5			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19015	AN6150.1	AO070340000052	Nucleolar GTPase/ATPase p130	Y		0.123	1	1	2	0	55	370	124	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15515	AN0906.1	AO070320000082	Karyopherin (importin) beta 1	YU		0.123290877849902 3.41751618934886	6	2	3	0	70	404	58	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15450	AN5513.1	AO070341000383	predicted protein [Neurospora crassa]				3	1	2	0	27	213	56			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		0.123290877849902 3.41751618934886	2	2	1	0	18	314	156	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15031	AN1190.1	AO070331000190	Nuclear pore complex, rNup107 component (sc Nup84)	YU		0.123290877849902 3.41751618934886	1	1	1	0	290	192	201	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07479	AN5533.1	AO070328000058	Cell division protein	D		0.939	1	1	1	0	82	206	144			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15160	AN2120.1	AO070332000051	Karyopherin (importin) beta 3	YU		0.123290877849902 3.41751618934886	2	2	6	1	188	167	90	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	58.m08920	AN5627.1	AO070301000027	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	YU		0.123290877849902 3.41751618934886	2	2	3	0	375	16	71	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06442	AN0316.1	AO070334000016	Alpha tubulin	Z		5.801	1	2	3	0	182	196	102	27	0		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15763	AN1182.1	AO070331000182	Beta tubulin	Z		5.801	2	2	1	0	43	170	149	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07499	AN5573.1	AO070328000033	predicted protein [Neurospora crassa]				1	1	2	0	38	6	3			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07509	AN5588.1	AO070328000021	AAA+-type ATPase containing the peptidase M41 domain	O		0.952	1	2	1	0	29	3	113			132	1
45	TTTCTTTTTCTTTTTTT		up	down	58.m07508	AN5589.1	AO070328000022	Ribulose kinase and related carbohydrate kinases	G		1.068	1	1	1	0	61	169	63			413	1
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05667	AN3815.1	AO070311000013	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z		5.801	3	1	1	0	245	267	90	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07534	AN5610.1	AO070301000010	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q		0.669	1	0	2	0	105	0	18			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15259	AN6875.1	AO070314000048	Kinesin-like protein	Z		5.801	1	1	2	0	425	158	90	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05838	AN7501.1	AO070287000012	LisH motif-containing protein	Z		5.801	1	1	2	1	137	184	109	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15420	AN0137.1	AO070321000115	Predicted starch-binding protein				2	1	2	0	113	161	92	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15446	AN0173.1	AO070321000071					1	1	1	0	7	327	303	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07562	AN5640.1	AO070301000036	Histone acetyltransferase (MYST family)	B		6.721	2	1	3	0	137	69	269			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15479	AN0213.1	AO070323000085					2	1	2	0	45	124	149	354	1		
45	TTTCTTTTTCTTTTTTT		up	down	58.m07334	AN5642.1	AO070342000232	predicted protein [Neurospora crassa]				1	2	1	0	186	119	121			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06482	AN0287.1	AO070334000066	WD40 repeat protein				3	1	2	0	221	108	168	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15290	AN0557.1	AO070272000032	Cdc4 and related F-box and WD-40 proteins				1	1	2	0	78	65	78	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		0.203	2	2	1	1	34	38	45			438	1
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06842	AN5722.1	AO070324000128	Protein phosphatase 2C/pyruvate dehydrogenase (lipoamide) phosphatase	T		0.089	1	1	1	0	368	190	101			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	54.m06848	AN5728.1	AO070324000123	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	T		0.089	1	1	2	0	288	155	60			528	1
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15281	AN0565.1	AO070272000043	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				2	1	1	0	43	326	205	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	69.m15631	AN5745.1	AO070341000002	Translation initiation factor eIF3, p35 subunit	J		0.203	1	1	1	0	48	42	47			221	1
45	TTTCTTTTTCTTTTTTT		up	down	69.m14851	AN5753.1	AO070329000011					1	1	1	0	311	201	194			372	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m15259	AN0655.1	AO070343000571	hypothetical protein [Neurospora crassa]				1	1	2	0	240	312	235	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15292	AN0689.1	AO070343000524	acetate regulatory DNA binding protein FacB [Emericella nidulans]				1	1	1	0	224	212	217	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15369	AN0766.1	AO070316000078	hypothetical protein [Novosphingobium aromaticivorans]				3	1	5	0	53	350	67	377	1		
45	TTTCTTTTTCTTTTTTT		up	down	72.m18953	AN5822.1	AO070260000020	Cyclin-dependent kinase WEE1	D		0.939	2	1	2	0	322	401	142			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15407	AN0806.1	AO070239000011	WD40 repeat protein				2	2	3	0	366	130	8	379	1		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15424	AN0823.1	AO070255000022	Uncharacterized conserved protein				3	1	1	0	14	281	382	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				1	1	4	0	184	238	210			28	0
45	TTTCTTTTTCTTTTTTT		up	up	70.m15460	AN0867.1	AO070320000018	hypothetical protein [Neurospora crassa]				1	1	2	0	87	422	127	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19916	AN5836.1	AO070340000001	RNA polymerase II, large subunit	K		4.158	1	1	1	0	165	17	62			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	70.m15535	AN0928.1	AO070320000113	hypothetical protein ((AL451014) putative protein [Neurospora crassa])				2	1	2	0	130	5	61	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15609	AN0973.1	AO070320000174	FOG: Zn-finger				4	1	5	0	87	256	13	103	0		
45	TTTCTTTTTCTTTTTTT		up	down	72.m18986	AN5857.1	AO070340000013	Nucleolar GTPase/ATPase p130	Y		0.123	1	1	1	0	450	0	85			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m15626	AN0986.1	AO070318000155	PHD Zn-finger proteins				3	2	2	0	208	2	245	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15236	AN1018.1	AO070343000597	Uncharacterized conserved protein				1	1	1	0	100	164	272	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19239	AN5891.1	AO070245000016	PHD Zn-finger proteins				1	1	1	0	55	247	151			344	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m15201	AN1045.1	AO070336000078	FOG: RRM domain				2	1	1	0	43	427	94	192	0		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19237	AN5893.1	AO070245000013	G protein signaling regulators	T		0.089	1	1	1	0	263	279	424			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	72.m19953	AN5915.1	AO070340000372	Golgi proteins involved in ER retention (RER)	U		3.418	1	2	2	0	197	26	161			425	1
45	TTTCTTTTTCTTTTTTT		up	up	70.m15143	AN1089.1	AO070285000061	Thioredoxin binding protein TBP-2/VDUP1				3	2	5	0	107	317	60	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m15141	AN1091.1	AO070285000058	FOG: RRM domain				2	2	4	0	241	225	32	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19202	AN5929.1	AO070340000354	Calcium-responsive transcription coactivator	K		4.158	1	2	1	0	202	174	237			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	70.m14958	AN1261.1	AO070214000004	hypothetical protein [Neurospora crassa]				1	2	3	0	13	188	260	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m14896	AN1337.1	AO070303000102	predicted protein [Neurospora crassa]				2	1	1	0	108	141	135	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19186	AN5970.1	AO070340000328	Thioredoxin/protein disulfide isomerase	O		0.952	2	1	1	0	34	62	40			48	0
45	TTTCTTTTTCTTTTTTTT		up	up	70.m14875	AN1355.1	AO070237000005	Permease of the drug/metabolite transporter (DMT) superfamily				1	1	3	0	176	256	0	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				1	2	2	1	270	158	226	189	1		
45	TTTCTTTTTCTTTTTTT		up	up	70.m14839	AN1382.1	AO070243000014	hypothetical protein [Neurospora crassa]				1	1	1	0	194	103	123	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19109	AN6050.1	AO070340000215					1	1	1	0	163	194	39			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	55.m02933	AN1423.1	AO070232000019	Permease of the major facilitator superfamily				2	0	3	0	158	0	155	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	55.m02928	AN1427.1	AO070242000025	Uncharacterized conserved protein				1	2	5	0	349	236	108	419	1		
45	TTTCTTTTTCTTTTTTT		up	up	55.m02945	AN1438.1	AO070232000003	hypothetical protein [Neurospora crassa]				2	2	2	0	253	180	50	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	55.m03059	AN1540.1	AO070334000264	predicted protein [Neurospora crassa]				1	2	1	0	258	207	395	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19931	AN6118.1	AO070340000086	Amino acid transporters	E		0.256	1	1	1	0	27	306	167			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	72.m19029	AN6136.1	AO070340000066	Protein involved in mRNA turnover and stability	A		1.249	1	1	2	0	34	55	84			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07732	AN1666.1	AO070299000048	Nucleolar GTPase				1	2	1	0	94	69	72	122	1		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19900	AN6168.1	AO070340000030	NADP+-dependent malic enzyme	C		0.327	1	1	1	0	0	134	0			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07663	AN1847.1	AO070292000057					2	2	2	0	14	214	209	248	1		
45	TTTCTTTTTCTTTTTTTT		up	up	57.m05742	AN1876.1	AO070341000183	Predicted membrane protein, contains two CBS domains				1	1	1	0	15	375	356	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07338	AN1955.1	AO070342000226					2	1	2	0	170	188	146	49	0		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19294	AN6196.1	AO070308000103					1	2	2	0	0	109	26			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTT		up	up	58.m07337	AN1956.1	AO070342000227	Predicted helicase				1	1	1	0	71	15	112	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07568	AN1963.1	AO070301000044					1	3	1	0	487	44	79	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19306	AN6208.1	AO070308000085					1	1	1	0	158	76	223			164	1
45	TTTCTTTTTCTTTTTTT		up	up	58.m08942	AN2011.1	AO070202000001	P-type ATPase				1	2	3	0	18	101	183	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19434	AN6221.1	AO070304000053	GATA-4/5/6 transcription factors	K		4.158	2	1	2	0	187	219	193			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	72.m19980	AN6247.1	AO070304000102	predicted protein [Neurospora crassa]				1	1	1	0	250	8	249			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07624	AN2016.1	AO070202000009	amyR [Emericella nidulans]				1	1	3	0	262	342	305	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19981	AN6254.1	AO070304000034	Mitochondrial oxoglutarate/malate carrier proteins	C		0.327	1	1	1	0	256	361	0			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	72.m19395	AN6262.1	AO070304000027	predicted protein [Neurospora crassa]				1	1	2	0	138	66	19			220	1
45	TTTCTTTTTCTTTTTTT		up	up	58.m07632	AN2044.1	AO070292000011	hypothetical protein [Neurospora crassa]				1	2	1	0	346	88	20	7	0		
45	TTTCTTTTTCTTTTTTTT		up	down	72.m19363	AN6277.1	AO070304000003	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)				1	1	1	0	219	158	171			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	58.m07643	AN2055.1	AO070292000025	hypothetical protein [Neurospora crassa]				4	2	4	0	106	263	21	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07644	AN2056.1	AO070292000026	Uncharacterized conserved protein				1	2	1	0	44	260	263	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05773	AN2070.1	AO070341000226	PHD finger protein AF10				1	1	1	0	310	131	0	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19709	AN2132.1	AO070278000027	predicted protein [Neurospora crassa]				1	1	1	0	175	200	14	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19508	AN6347.1	AO070275000012	Serine/threonine protein kinase				1	2	3	0	42	5	122			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	down	72.m19507	AN6348.1	AO070275000017	Mitochondrial import inner membrane translocase, subunit TIM23	U		3.418	2	1	1	0	148	450	159			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	69.m14881	AN2190.1	AO070247000014	Predicted methyltransferase				1	2	3	0	279	9	22	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	62.m03439	AN6500.1	AO070222000014	60S ribosomal protein L28	J		0.203	1	1	1	0	146	150	153			212	1
45	TTTCTTTTTCTTTTTTT		up	up	71.m15846	AN2219.1	AO070326000185	related to ahmp1 protein [MIPS] [Neurospora crassa]				1	1	2	0	12	286	13	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	62.m03095	AN6508.1	AO070270000001	Glycogen synthase kinase-3	G		1.068	2	1	4	0	225	223	232			45	0
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15877	AN2243.1	AO070326000130	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				1	1	2	0	377	381	62	307	0		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15889	AN2251.1	AO070326000115	Predicted membrane protein				2	1	2	0	125	276	12	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15938	AN2290.1	AO070295000069	FOG: Zn-finger				3	2	3	0	173	7	15	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08497	AN2492.1	AO070312000128	Uncharacterized conserved protein				1	3	3	0	15	81	47	128	1		
45	TTTCTTTTTCTTTTTTT		up	down	62.m03155	AN6568.1	AO070326000011	Uncharacterized conserved protein				2	1	2	0	56	169	74			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	62.m03168	AN6574.1	AO070326000017	E3 ubiquitin ligase involved in syntaxin degradation	O		0.952	1	1	1	0	101	44	96			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	62.m03177	AN6588.1	AO070326000036					1	1	2	0	331	320	313			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m08697	AN2855.1	AO070338000169	FOG: Zn-finger				4	2	2	0	88	200	104	180	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08714	AN2869.1	AO070338000153	Predicted transporter (major facilitator superfamily)				3	2	1	0	105	282	332	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08919	AN3079.1	AO070224000007					2	1	3	0	148	237	129	139	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				1	2	1	0	213	210	307	106	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				2	2	3	0	142	132	257	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	65.m07300	AN6680.1	AO070289000022	predicted protein [Neurospora crassa]				1	1	2	0	115	88	10			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	65.m07490	AN6696.1	AO070339000127	hypothetical protein [Neurospora crassa]				1	2	2	0	98	63	94			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m08614	AN3122.1	AO070303000025	hypothetical protein [Neurospora crassa]				1	1	1	0	173	159	143	254	1		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04639	AN3371.1	AO070281000010	predicted protein [Neurospora crassa]				3	2	3	0	329	310	81	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07398	AN3600.1	AO070342000153	hypothetical protein [Neurospora crassa]				1	2	3	0	454	305	212	276	0		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06552	AN4019.1	AO070328000118	Permease of the major facilitator superfamily				1	3	1	0	489	10	112	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07369	AN4148.1	AO070342000182	Predicted transporter (major facilitator superfamily)				1	2	3	0	140	301	257	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15289	AN6828.1	AO070314000111	Nucleolar GTPase/ATPase p130	Y		0.123	2	2	3	0	4	28	15			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	69.m15618	AN4170.1	AO070341000092	Thioredoxin binding protein TBP-2/VDUP1				1	1	4	0	142	308	94	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m14953	AN4171.1	AO070341000090	hypothetical protein [Neurospora crassa]				3	1	1	0	33	206	95	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15255	AN6880.1	AO070314000044	Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	KIT		4.15828392190872 3.91278222556957 0.0887649648758591	1	1	3	0	229	60	43			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				3	2	3	0	127	86	88	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15234	AN6902.1	AO070314000013	Protein involved in mRNA turnover	A		1.249	1	1	1	0	17	21	39			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05647	AN4484.1	AO070311000033	PHD finger protein				3	1	3	0	159	455	81	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05645	AN4486.1	AO070311000037	hypothetical protein [Neurospora crassa]				1	2	1	0	243	129	296	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05570	AN4558.1	AO070321000170	hypothetical protein [Neurospora crassa]				1	1	2	0	256	263	128	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19795	AN7254.1	AO070297000010	AAA+-type ATPase	O		0.952	1	1	1	0	141	1	16			136	1
45	TTTCTTTTTCTTTTTTTT		up	down	72.m19770	AN7296.1	AO070297000039	Sister chromatid cohesion complex Cohesin, subunit PDS5	D		0.939	2	2	2	0	103	6	220			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15672	AN4689.1	AO070284000044					1	1	1	0	234	55	174	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19727	AN7350.1	AO070278000050	FOG: RRM domain				2	1	2	0	465	317	335			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	72.m20006	AN7352.1	AO070278000048	E3 ubiquitin ligase involved in syntaxin degradation	O		0.952	1	1	1	0	21	205	45			280	1

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTT		up	down	57.m05902	AN7441.1	AO070229000013	Actin-related protein - Arp4p/Act3p	Z		5.801	1	3	1	0	192	21	105			453	1
45	TTTCTTTTTCTTTTTTT		up	down	57.m05889	AN7454.1	AO070287000072	hypothetical protein [Neurospora crassa]				2	2	1	0	121	183	23			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15704	AN4716.1	AO070311000005	hypothetical protein [Neurospora crassa]				2	1	2	0	379	133	113	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m09236	AN4743.1	AO070327000077	Ras-related small GTPase, Rho type				3	4	4	0	233	200	89	100	0		
45	TTTCTTTTTCTTTTTTT		up	up	59.m09204	AN4779.1	AO070329000071	NIPSNAP1 protein				2	2	2	0	137	56	35	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	57.m05861	AN7480.1	AO070287000037	FOG: RRM domain				1	2	3	0	272	256	164			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	59.m09162	AN4814.1	AO070329000018	Predicted membrane protein				2	2	2	0	191	277	141	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	72.m19562	AN7545.1	AO070277000042	CCAAT-binding factor, subunit B (HAP2)	K		4.158	1	2	3	0	362	13	59			304	1
45	TTTCTTTTTCTTTTTTT		up	up	59.m09409	AN4880.1	AO070338000081	Jacalin-like lectin domain-containing protein				2	1	2	0	168	444	178	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m08812	AN4908.1	AO070338000038	Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondrial morphology/distribution, also found associated with eIF-3				2	2	1	0	130	68	151	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08815	AN4912.1	AO070338000036	hypothetical protein [Neurospora crassa]				2	1	1	0	3	485	189	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08878	AN4975.1	AO070288000042	FAD-dependent oxidoreductase				1	1	1	0	60	156	23	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08886	AN4984.1	AO070288000052	Cyclin				2	2	2	0	12	156	59	74	0		
45	TTTCTTTTTCTTTTTTTT		up	up	59.m08894	AN4991.1	AO070288000071	aureobasidin-resistance protein; AurA [Aspergillus nidulans]				1	2	1	0	435	106	46	420	1		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08896	AN4993.1	AO070288000076	N-acetyltransferase				2	1	2	0	30	10	35	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	59.m08680	AN5026.1	AO070338000185	PHD finger protein AF10				3	2	1	0	315	126	68	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15822	AN7628.1	AO070294000038	mRNA deadenylase subunit	A		1.249	1	2	3	0	322	75	79			414	1
45	TTTCTTTTTCTTTTTTT		up	up	59.m08678	AN5048.1	AO070338000188	Transcription factor, contains HOX domain				1	2	2	0	71	356	208	138	0		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06882	AN5140.1	AO070291000036	Permease of the major facilitator superfamily				1	1	2	0	91	463	151	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	57.m05947	AN7681.1	AO070325000071	Mod5 protein sorting/negative effector of RNA Pol III synthesis	K		4.158	2	1	2	0	30	25	37			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	54.m06862	AN5156.1	AO070291000011	Cyclin				2	1	3	0	145	451	297	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	71.m15720	AN7698.1	AO070325000103	Myosin class I heavy chain	Z		5.801	3	3	1	0	17	12	27			311	1
45	TTTCTTTTTCTTTTTTT		up	down	71.m15729	AN7700.1	AO070325000106	FOG: RRM domain				2	2	2	0	197	74	243			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05706	AN5226.1	AO070337000252	Predicted membrane protein				5	2	4	0	200	319	58	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15778	AN5236.1	AO070325000177	Predicted membrane protein				1	2	1	0	254	22	26	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	53.m03863	AN8016.1	AO070322000065	Predicted ATP-dependent RNA helicase FAL1, involved in rRNA maturation, DEAD-box superfamily	J		0.203	1	2	2	0	337	203	110			251	1
45	TTTCTTTTTCTTTTTTT		up	up	69.m15506	AN5405.1	AO070333000118	predicted protein [Neurospora crassa]				2	2	1	0	156	137	109	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	69.m15524	AN5407.1	AO070333000121	Predicted GTPase activator NB4S/EVI5 (contains TBC domain)/Calmodulin-binding protein Pollux (contains PTB and TBC domains)				3	1	1	0	143	274	155	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	69.m15489	AN5445.1	AO070333000112					1	2	1	0	280	256	217	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	53.m03908	AN8038.1	AO070330000008	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A		1.249	2	3	2	0	164	11	14			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	53.m03907	AN8039.1	AO070330000007	Histone 2A	B		6.721	2	2	2	0	252	326	125			383	1
45	TTTCTTTTTCTTTTTTT		up	up	58.m07489	AN5563.1	AO070328000044	Aldo/keto reductase family proteins				1	1	1	0	533	352	434	278	0		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07499	AN5573.1	AO070328000033	predicted protein [Neurospora crassa]				2	1	6	1	248	272	108	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	58.m07334	AN5642.1	AO070342000232	predicted protein [Neurospora crassa]				2	3	3	0	193	38	33	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	54.m06835	AN5716.1	AO070324000136	FOG: CBS domain				1	1	1	0	130	224	100	30	0		
45	TTTCTTTTTCTTTTTTT		up	down	53.m03888	AN8055.1	AO070322000145	RNA-binding Ran Zn-finger protein and related proteins				1	2	3	0	223	44	224			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	69.m14857	AN5740.1	AO070341000019	Ras-related small GTPase, Rho type				3	2	2	0	266	408	271	83	0		
45	TTTCTTTTTCTTTTTTTT		up	up	69.m14853	AN5755.1	AO070341000014	hypothetical protein (related to a-agglutinin core protein AGA1 [imported] - Neurospora crassa)				1	3	2	0	553	12	1	575	1		
45	TTTCTTTTTCTTTTTTTT		up	down	56.m02396	AN8105.1	AO070323000021	Non-ribosomal peptide synthetase modules and related proteins	Q		0.669	1	2	1	0	26	89	364			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				3	2	5	0	85	16	14	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	53.m03799	AN8181.1	AO070310000145	predicted protein [Neurospora crassa]				2	1	1	0	85	93	130			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19214	AN5917.1	AO070340000369	Predicted transporter (major facilitator superfamily)				2	1	2	0	316	52	484	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19965	AN5966.1	AO070340000323	FOG: Zn-finger				1	2	2	0	210	193	248	438	1		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19109	AN6050.1	AO070340000215					3	1	3	0	61	354	0	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19074	AN6084.1	AO070340000134	predicted protein [Neurospora crassa]				1	1	3	0	195	119	83	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				4	4	4	0	405	32	1	386	1		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19303	AN6204.1	AO070308000089	cell wall beta-glucan assembly; Kre6p [Saccharomyces cerevisiae]				1	1	2	0	471	82	81	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				2	1	3	0	41	36	40			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	53.m03696	AN8261.1	AO070310000040	Protein kinase PCTAIRE and related kinases				1	1	3	0	30	47	31			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19306	AN6208.1	AO070308000085					4	3	2	0	362	164	162	270	1		
45	TTTCTTTTTCTTTTTTTT		up	down	53.m03693	AN8268.1	AO070310000034	RasGAP SH3 binding protein rasputin, contains NTF2 and RRM domains	T		0.089	2	2	6	0	15	378	6			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19316	AN6217.1	AO070308000074	Cdc4 and related F-box and WD-40 proteins				1	2	3	0	316	95	109	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	72.m19363	AN6277.1	AO070304000003	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)				2	3	5	0	191	51	131	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
45	TTTCTTTTTCTTTTTTT		up	up	72.m19339	AN6295.1	AO070308000053	predicted protein [Neurospora crassa]				1	1	2	0	397	86	100	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03118	AN6530.1	AO070270000030	Predicted membrane protein				2	1	2	0	39	122	69	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03135	AN6538.1	AO070270000046	LRR-containing protein				3	4	1	0	48	42	231	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03196	AN6601.1	AO070326000052	Transmembrane protein				1	1	1	0	52	124	106	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	62.m03234	AN6639.1	AO070326000091	Uncharacterized protein involved in propionate catabolism				3	3	1	0	9	233	240	21	0		
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15293	AN6823.1	AO070314000102	hypothetical protein ((AL513443) hypothetical protein [Neurospora crassa])				2	1	2	0	391	92	72	288	1		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15271	AN6858.1	AO070314000075	predicted protein [Neurospora crassa]				3	2	1	0	189	187	283	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	62.m03362	AN8707.1	AO070315000134	Fumarase	C		0.327	1	3	1	0	131	103	380			116	1
45	TTTCTTTTTCTTTTTTT		up	down	62.m03358	AN8710.1	AO070315000137	FOG: Low-complexity				1	1	1	0	118	131	31			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	62.m03343	AN8723.1	AO070315000151	predicted protein [Neurospora crassa]				1	1	2	0	364	49	188			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	72.m19729	AN7348.1	AO070278000051	Uncharacterized conserved protein				1	2	2	0	104	172	139	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	62.m03339	AN8741.1	AO070250000041	FOG: Zn-finger				1	1	1	0	110	31	32			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05873	AN7471.1	AO070287000055	Predicted carbohydrate kinase, contains PfkB domain				1	1	1	0	81	38	85	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	57.m05861	AN7480.1	AO070287000037	FOG: RRM domain				1	2	3	0	216	348	71	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19651	AN7610.1	AO070343000266	putative transcription factor [Emericella nidulans]				2	1	4	0	327	149	79	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	65.m07308	AN8785.1	AO070289000010	Mitochondrial aspartate/glutamate carrier protein Aralar/Citrin (contains EF-hand Ca2+-binding domains)	C		0.327	2	1	2	0	26	118	71			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	71.m15859	AN7623.1	AO070294000020	hypothetical protein [Neurospora crassa]				1	1	1	0	125	39	281	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15957	AN8825.1	AO070271000056	Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	U		3.418	1	3	1	0	91	38	212			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	57.m05419	AN7657.1	AO070268000020	GEL1 protein [Aspergillus fumigatus]				2	3	2	0	90	305	346	158	0		
45	TTTCTTTTTCTTTTTTTT		up	down	71.m15961	AN8830.1	AO070271000049	Checkpoint kinase and related serine/threonine protein kinases	D		0.939	1	2	3	0	471	151	344			327	1
45	TTTCTTTTTCTTTTTTT		up	down	71.m15980	AN8846.1	AO070271000030	Protein involved in beta-1,3-glucan synthesis	G		1.068	1	1	2	0	16	148	328			165	1
45	TTTCTTTTTCTTTTTTT		up	up	53.m03888	AN8055.1	AO070322000145	RNA-binding Ran Zn-finger protein and related proteins				5	4	3	1	48	181	95	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	71.m16001	AN8863.1	AO070271000008	Nucleosome assembly protein NAP-1	BD		6.72131997613286 0.939027978679397	2	3	2	0	224	67	267			No EST	No EST
45	TTTCTTTTTCTTTTTTTT		up	up	53.m03775	AN8200.1	AO070310000119	hypothetical protein ((AL513466) putative protein [Neurospora crassa])				1	1	1	0	228	33	186	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				3	1	2	0	311	192	177	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	53.m04209	AN8262.1	AO070310000038	related to G protein coupled receptor like protein [Neurospora crassa]				1	1	1	0	107	73	117	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	72.m19891	AN8312.1	AO070307000026	Neutral protease II precursor (Deuterolysin) (NPII)				1	1	1	0	92	419	501	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	62.m03339	AN8741.1	AO070250000041	FOG: Zn-finger				2	2	1	0	64	36	109	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	down	66.m04555	AN9096.1	AO070332000179					3	2	5	0	38	35	60			370	1
45	TTTCTTTTTCTTTTTTT		up	up	62.m03324	AN8751.1	AO070250000011	NDR and related serine/threonine kinases				4	2	4	0	35	11	10	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	71.m15604	AN8797.1	AO070276000063	hypothetical protein ((AL513442) conserved hypothetical protein [Neurospora crassa])				1	1	3	0	310	302	171	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15985	AN8850.1	AO070271000026	Uncharacterized conserved protein				1	1	2	0	128	3	80	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04555	AN9096.1	AO070332000179					1	2	1	0	255	158	40	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	down	58.m07216	AN9204.1	AO070338000019	Acetyltransferases, including N-acetylases of ribosomal proteins	J		0.203	1	1	2	0	139	218	353			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	down	52.m04075	AN9357.1	AO070315000043	Predicted dehydrogenase	Q		0.669	1	1	1	0	192	122	25			No EST	No EST
45	TTTCTTTTTCTTTTTTT		up	up	66.m04767	AN9099.1	AO070332000175	SPRY domain-containing proteins				1	1	1	0	211	98	77	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04760	AN9108.1	AO070332000164	predicted protein [Neurospora crassa]				1	1	3	0	107	35	469	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	66.m04608	AN9146.1	AO070332000116	hypothetical protein [Neurospora crassa]				1	1	3	0	462	41	51	No EST	No EST		
45	TTTCTTTTTCTTTTTTTT		up	up	66.m04586	AN9149.1	AO070332000147	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain				1	2	1	0	138	7	42	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	52.m03906	AN9377.1	AO070315000006	Allergen Asp f 4				1	1	1	0	132	422	421	No EST	No EST		
45	TTTCTTTTTCTTTTTTT		up	up	71.m15215	AN9451.1	AO070219000021	predicted protein [Neurospora crassa]				2	1	2	0	114	88	131	127	1		
233	TCTCCTTTCCTCyC		up	down	71.m16041	AN0047.1	AO070314000125	GTP-binding protein GP-1				1	1	1	0	63	133	138			272	1
233	TCTCCTTTCCTCyC		up	up	71.m15331	AN0051.1	AO070314000138	Isopenicillin N synthase and related dioxygenases				1	1	1	0	207	136	91	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	71.m15444	AN0170.1	AO070321000076	Thioredoxin	O		0.837	1	1	1	0	182	214	72	207	0		
233	TCTCCTTTCCTCyC		up	up	54.m06529	AN0254.1	AO070334000106	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE		4.28577529470617 0.745375778970292	1	1	2	0	303	147	247	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	69.m15270	AN0575.1	AO070272000054	Calmodulin-binding protein CRAG, contains DENN domain	T		5.000	2	5	2	0	429	49	72	117	1		
233	TCTCCTTTCCTCyC		up	down	70.m15259	AN0655.1	AO070343000571	hypothetical protein [Neurospora crassa]				2	1	2	0	150	234	20			No EST	No EST

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233	TCTCCTTTCCTCyC		up	down	70.m15286	AN0684.1	AO070343000534	Nucleolar GTPase/ATPase p130	Y		12.715	1	1	1	0	163	155	149			61	0
233	TCTCCTTTCCTCyC		up	up	70.m15290	AN0687.1	AO070343000527	Spermidine synthase	E		0.745	2	2	2	0	86	228	273	123	0		
233	TCTCCTTTCCTCyC		up	up	70.m15335	AN0726.1	AO070343000481	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		5.05419317961222 0.837307665519789	1	1	2	0	185	155	73	170	1		
233	TCTCCTTTCCTCyC		up	up	70.m15361	AN0747.1	AO070343000435	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O		0.837	1	1	1	0	31	180	217	29	0		
233	TCTCCTTTCCTCyC		up	down	70.m15793	AN0809.1	AO070239000006	RNA polymerase II, large subunit	K		1.015	1	1	1	0	17	169	266			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	70.m15460	AN0867.1	AO070320000018	hypothetical protein [Neurospora crassa]				1	1	1	0	90	164	436	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m15456	AN0870.1	AO070320000023	Mitochondrial phosphate carrier protein	C	1	0.004	2	3	1	0	55	349	314	15	0		
233	TCTCCTTTCCTCyC		up	up	70.m15524	AN0917.1	AO070320000097	Transcriptional coactivator CAPER (RRM superfamily)	K		1.015	1	1	2	0	51	352	117	168	0		
233	TCTCCTTTCCTCyC		up	down	70.m15807	AN0924.1	AO070320000103	Uncharacterized conserved protein				2	1	3	0	47	168	77			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	70.m15813	AN0937.1	AO070320000128	NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIT-4 [Neurospora crassa]				1	2	1	0	144	55	62	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	70.m15600	AN0953.1	AO070320000154	Predicted small GTPase involved in nuclear protein import	U		5.620	1	2	2	0	317	17	328			35	1
233	TCTCCTTTCCTCyC		up	up	70.m15626	AN0986.1	AO070318000155	PHD Zn-finger proteins				3	3	1	0	302	12	28	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m15221	AN1003.1	AO070312000031	Isocitrate dehydrogenase, alpha subunit	E		0.745	1	1	1	0	65	186	207	48	0		
233	TCTCCTTTCCTCyC		up	up	70.m15130	AN1102.1	AO070285000036	Serine palmitoyltransferase	O		0.837	2	1	1	0	57	245	275	150	0		
233	TCTCCTTTCCTCyC		up	down	70.m15114	AN1126.1	AO070331000119	GTP-binding ADP-ribosylation factor Arf1	U		5.620	2	1	2	1	145	178	141			286	1
233	TCTCCTTTCCTCyC		up	up	70.m15059	AN1162.1	AO070331000152	Elongation factor 1 beta/delta chain	K		1.015	1	1	1	0	49	124	144	17	0		
233	TCTCCTTTCCTCyC		up	up	70.m15772	AN1165.1	AO070331000157	Predicted 3-ketosphinganine reductase	Q		6.045	1	1	1	0	126	0	117	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m15040	AN1177.1	AO070331000173	Vesicle coat complex COPI, beta subunit	U		5.620	1	1	1	0	38	103	48	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		8.467	2	1	1	0	40	165	210	193	1		
233	TCTCCTTTCCTCyC		up	up	70.m14923	AN1284.1	AO070332000035	Predicted GTP-binding protein (ODN superfamily)				5	1	3	0	5	292	196	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m14890	AN1343.1	AO070247000021	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K		1.015	1	1	2	0	335	126	46	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				3	2	1	1	147	163	241	189	1		
233	TCTCCTTTCCTCyC		up	up	55.m02926	AN1429.1	AO070242000022	Choline dehydrogenase and related flavoproteins	E		0.745	1	1	3	0	217	412	325	48	0		
233	TCTCCTTTCCTCyC		up	up	55.m02925	AN1430.1	AO070242000021	NAD-dependent aldehyde dehydrogenases	C	1	0.004	1	1	2	0	215	451	69	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	55.m03039	AN1520.1	AO070334000238	Nucleolar GTPase/ATPase p130	Y		12.715	2	2	1	0	202	123	209			328	1
233	TCTCCTTTCCTCyC		up	up	55.m03042	AN1523.1	AO070334000241	F0F1-type ATP synthase, alpha subunit	C	1	0.004	1	2	1	0	90	311	332	68	0		
233	TCTCCTTTCCTCyC		up	up	55.m03067	AN1547.1	AO070339000307	Acetyl-CoA hydrolase	C	1	0.004	3	1	4	0	64	433	34	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	58.m07718	AN1639.1	AO070299000037	Thioredoxin-like protein	O		0.837	1	2	1	1	358	385	350			No EST	No EST
233	TCTCCTTTCCTCyC		up	down	58.m07719	AN1652.1	AO070299000039	FOG: Zn-finger				1	1	2	0	387	318	196			No EST	No EST
233	TCTCCTTTCCTCyC		up	down	58.m07734	AN1669.1	AO070299000051	FOG: Immunoglobin and related proteins	P		4.659	1	1	1	0	43	247	275			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	58.m08869	AN1933.1	AO070342000200	Predicted membrane protein				2	2	2	0	42	307	431	391	1		
233	TCTCCTTTCCTCyC		up	down	58.m07643	AN2055.1	AO070292000025	hypothetical protein [Neurospora crassa]				1	1	1	0	37	49	58			447	1
233	TCTCCTTTCCTCyC		up	up	58.m07644	AN2056.1	AO070292000026	Uncharacterized conserved protein				1	1	1	0	387	330	271	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		0.837	3	2	3	0	190	101	47	173	1		
233	TCTCCTTTCCTCyC		up	up	57.m05769	AN2069.1	AO070341000218	Cytochrome b5	C	1	0.004	3	1	2	0	87	158	139	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	57.m05777	AN2078.1	AO070341000231	Thyroid hormone receptor-associated protein complex, subunit TRAP240	K		1.015	1	1	1	0	237	7	135			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	72.m19708	AN2133.1	AO070278000026	Armadillo/beta-Catenin/plakoglobin	TZ		4.99979971356992 8.41157787507119	1	1	1	0	65	84	180	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		5.620	3	1	1	0	88	170	185	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	72.m19677	AN2163.1	AO070343000222	Mitotic spindle checkpoint protein	D		8.010	1	3	4	0	56	288	7			274	0
233	TCTCCTTTCCTCyC		up	up	69.m14881	AN2190.1	AO070247000014	Predicted methyltransferase				1	1	4	0	285	0	21	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	71.m15855	AN2210.1	AO070294000012	Predicted transporter (ABC superfamily)				1	2	1	0	76	9	165			344	1
233	TCTCCTTTCCTCyC		up	up	71.m15889	AN2251.1	AO070326000115	Predicted membrane protein				1	1	2	0	207	274	179	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	71.m15896	AN2256.1	AO070326000107	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL		1.01548329749935 4.34546556837552	1	1	1	0	144	34	182			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C	1	0.004	2	1	2	1	59	312	309	104	0		
233	TCTCCTTTCCTCyC		up	up	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C	1	0.004	2	1	1	0	176	267	352	187	0		
233	TCTCCTTTCCTCyC		up	down	54.m06688	AN2743.1	AO070338000228	Translation initiation factor 3, subunit a (eIF-3a)	J		4.370	1	1	1	0	169	58	68			No EST	No EST
233	TCTCCTTTCCTCyC		up	down	54.m06687	AN2744.1	AO070338000227	predicted protein [Neurospora crassa]				1	2	1	0	4	174	455			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	59.m09263	AN2761.1	AO070327000023	Ubiquitin-protein ligase	O		0.837	4	2	6	0	162	267	106	144	0		
233	TCTCCTTTCCTCyC		up	up	59.m08698	AN2854.1	AO070338000167	Transcription factor of the Forkhead/HNF3 family	K		1.015	1	2	1	0	278	20	41	No EST	No EST		

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233	TCTCCTTTCCTCyC		up	up	59.m08697	AN2855.1	AO070338000169	FOG: Zn-finger				3	2	2	0	90	202	106	180	0		
233	TCTCCTTTCCTCyC		up	up	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		10.093	4	3	3	0	230	109	136	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	59.m09023	AN2989.1	AO070337000133	FOG: RRM domain				2	1	3	0	89	391	10	183	0		
233	TCTCCTTTCCTCyC		up	down	59.m08989	AN3031.1	AO070331000089	Pyridoxalphosphate-dependent enzyme/predicted threonine synthase	E		0.745	1	1	1	0	20	87	57			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	59.m08957	AN3058.1	AO070337000016	Glycine/serine hydroxymethyltransferase	E		0.745	2	1	3	0	59	438	134	66	0		
233	TCTCCTTTCCTCyC		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				3	2	1	1	415	320	299	106	0		
233	TCTCCTTTCCTCyC		up	up	59.m09373	AN3113.1	AO070303000036	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE		5.05419317961222 0.745375778970292	1	1	2	0	103	276	174	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				2	3	4	0	241	36	257	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				2	1	1	0	227	237	246			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	66.m04660	AN3359.1	AO070317000081	Amino acid transporters	E		0.745	1	1	2	0	221	215	135	23	0		
233	TCTCCTTTCCTCyC		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		4.286	3	5	1	0	11	40	76	298	1		
233	TCTCCTTTCCTCyC		up	up	66.m04618	AN3416.1	AO070203000005	SNARE protein Syntaxin 1 and related proteins	U		5.620	1	1	1	0	280	162	158	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	69.m15402	AN3691.1	AO070341000316	AAA+-type ATPase	O		0.837	1	1	2	0	125	357	382	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	69.m15386	AN3729.1	AO070342000283	1,3-beta-glucan synthase/callose synthase catalytic subunit	M		10.683	2	1	1	0	365	41	135	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	69.m15382	AN3733.1	AO070342000279	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	G		5.054	1	1	2	0	440	117	130	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	65.m07367	AN3757.1	AO070309000049	Predicted alpha/beta hydrolase BEM46				1	1	1	0	212	5	283			No EST	No EST
233	TCTCCTTTCCTCyC		up	down	69.m14970	AN3955.1	AO070341000068	Uncharacterized conserved protein				2	1	1	0	165	160	199			209	1
233	TCTCCTTTCCTCyC		up	up	54.m06579	AN4015.1	AO070328000151	Translation initiation factor 5A (eIF-5A)	J		4.370	1	1	2	0	87	117	187	70	0		
233	TCTCCTTTCCTCyC		up	up	54.m06544	AN4026.1	AO070328000109					1	1	1	0	169	222	84	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	54.m06728	AN4087.1	AO070342000080	40S ribosomal protein S3	J		4.370	1	1	1	0	6	10	32			60	1
233	TCTCCTTTCCTCyC		up	up	54.m06745	AN4189.1	AO070342000110	Mitogen-activated protein kinase kinase (MAP2K)	T		5.000	1	1	2	0	207	193	125	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m06754	AN4192.1	AO070342000112	Molecular chaperone (DnaJ superfamily)	O		0.837	1	1	1	0	7	397	403	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m07041	AN4210.1	AO070231000014	Signaling protein SWIFT and related BRCT domain proteins	KTDL		1.01548329749935 4.99979971356992 8.01033033227436 4.34546556837552	1	1	1	0	172	216	293	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		4.370	2	1	2	1	118	287	3	96	0		
233	TCTCCTTTCCTCyC		up	down	54.m06803	AN4240.1	AO070324000174	Protein involved in glucose derepression and pre-vacuolar endosome protein sorting	U		5.620	1	1	1	0	36	34	38			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	58.m08000	AN4323.1	AO070230000015	Branched chain aminotransferase BCAT1, pyridoxal phosphate enzymes type IV superfamily	E		0.745	1	1	1	0	87	27	121	270	1		
233	TCTCCTTTCCTCyC		up	up	58.m07962	AN4361.1	AO070261000004	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		1.015	1	2	3	0	241	210	155	263	1		
233	TCTCCTTTCCTCyC		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				1	2	1	0	232	98	266	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	57.m05648	AN4483.1	AO070311000032	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		5.000	2	2	5	0	94	338	209	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	57.m05978	AN4514.1	AO070311000070	Peptide methionine sulfoxide reductase	O		0.837	1	1	2	0	28	307	39	174	0		
233	TCTCCTTTCCTCyC		up	up	57.m05527	AN4603.1	AO070267000024	Dihydroorotase and related enzymes	F		7.266	2	1	2	0	23	367	494	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	71.m15670	AN4687.1	AO070284000042	3-Methylcrotonyl-CoA carboxylase, non-biotin containing subunit/Acetyl-CoA carboxylase carboxyl transferase, subunit beta	EI		0.745375778970292 4.28577529470617	1	1	1	0	164	2	110	135	1		
233	TCTCCTTTCCTCyC		up	up	59.m08812	AN4908.1	AO070338000038	Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondrial morphology/distribution, also found associated with eIF-3				2	1	1	0	132	140	118	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	59.m09454	AN4997.1	AO070288000080	Phosphatidylinositol transfer protein SEC14 and related proteins	I		4.286	1	1	4	0	227	288	17	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	59.m09454	AN4997.1	AO070288000080	Phosphatidylinositol transfer protein SEC14 and related proteins	I		4.286	1	2	1	0	2	112	17			No EST	No EST
233	TCTCCTTTCCTCyC		up	down	59.m08914	AN5011.1	AO070224000003	FGF receptor activating protein 1	T		5.000	1	1	1	0	148	303	29			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	59.m08680	AN5026.1	AO070338000185	PHD finger protein AF10				1	3	2	0	386	231	39	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m06902	AN5122.1	AO070291000057	Adenylate kinase	F		7.266	3	1	1	0	80	200	222	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m06889	AN5134.1	AO070291000041	Glutamate synthase	E		0.745	2	1	2	0	253	311	58	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
233	TCTCCTTTCCTCyC		up	down	69.m14917	AN5218.1	AO070337000261	Activating transcription factor 4	K		1.015	1	1	1	0	19	51	51			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	69.m15489	AN5445.1	AO070333000112					2	1	1	0	286	264	228	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	69.m15483	AN5449.1	AO070239000028	Arylsulfatase A and related enzymes	P		4.659	2	3	4	0	191	205	110	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	58.m07334	AN5642.1	AO070342000232	predicted protein [Neurospora crassa]				1	2	1	0	192	90	182	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		4.370	2	1	1	0	44	195	129	101	0		
233	TCTCCTTTCCTCyC		up	down	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		4.370	2	3	2	1	25	64	27			438	1
233	TCTCCTTTCCTCyC		up	up	69.m14857	AN5740.1	AO070341000019	Ras-related small GTPase, Rho type				1	2	2	0	503	35	276	83	1		
233	TCTCCTTTCCTCyC		up	down	69.m15631	AN5745.1	AO070341000002	Translation initiation factor eIF3, p35 subunit	J		4.370	1	1	1	1	84	83	81			221	1
233	TCTCCTTTCCTCyC		up	up	69.m14848	AN5750.1	AO070341000007	predicted protein [Neurospora crassa]				2	1	1	0	252	169	299	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	72.m18953	AN5822.1	AO070260000020	Cyclin-dependent kinase WEE1	D		8.010	1	1	2	0	414	406	146			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	72.m19237	AN5893.1	AO070245000013	G protein signaling regulators	T		5.000	2	2	1	0	16	34	33	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	72.m19202	AN5929.1	AO070340000354	Calcium-responsive transcription coactivator	K		1.015	2	2	1	0	136	335	197	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	72.m19952	AN5931.1	AO070340000344	ATP-dependent RNA helicase	A		2.363	2	2	1	0	126	61	65	111	1		
233	TCTCCTTTCCTCyC		up	up	72.m19141	AN5999.1	AO070340000277	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				2	1	2	0	212	300	255	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		0.837	1	2	2	0	103	212	161	140	0		
233	TCTCCTTTCCTCyC		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				2	2	2	0	448	43	4	386	1		
233	TCTCCTTTCCTCyC		up	down	72.m19980	AN6247.1	AO070304000102	predicted protein [Neurospora crassa]				2	4	1	0	77	18	65			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	72.m18968	AN6299.1	AO070260000007	Uncharacterized conserved protein				1	1	1	0	531	231	160	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	72.m19507	AN6348.1	AO070275000017	Mitochondrial import inner membrane translocase, subunit TIM23	U		5.620	1	1	1	0	33	119	106	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	62.m03095	AN6508.1	AO070270000001	Glycogen synthase kinase-3	G		5.054	1	2	1	0	410	35	147	36	1		
233	TCTCCTTTCCTCyC		up	up	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	1	0.004	2	1	1	0	230	62	397	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	62.m03135	AN6538.1	AO070270000046	LRR-containing protein				1	1	2	0	329	179	129	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	62.m03196	AN6601.1	AO070326000052	Transmembrane protein				1	1	1	0	60	129	118	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	62.m03250	AN6650.1	AO070269000001	Citrate synthase	C	1	0.004	1	2	2	0	42	150	335	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	62.m03302	AN6669.1	AO070321000010	Predicted transporter (major facilitator superfamily)				2	1	1	0	98	469	453	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	65.m07257	AN6717.1	AO070339000157	NAD-dependent malate dehydrogenase	C	1	0.004	2	1	3	0	64	168	159	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	65.m07239	AN6731.1	AO070339000175	Fatty acid desaturase	I		4.286	2	2	2	0	161	97	396	7	0		
233	TCTCCTTTCCTCyC		up	up	71.m15271	AN6858.1	AO070314000075	predicted protein [Neurospora crassa]				1	2	1	0	222	195	293	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	71.m15255	AN6880.1	AO070314000044	Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	KIT		1.01548329749935 4.28577529470617 4.99979971356992	1	1	2	0	234	122	92			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	72.m19589	AN7570.1	AO070343000416	Alpha tubulin	Z		8.412	1	1	3	0	124	393	190	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	72.m19601	AN7580.1	AO070343000328	predicted protein [Neurospora crassa]				1	1	1	0	22	12	167			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	57.m05936	AN7660.1	AO070268000029	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H		8.467	2	1	2	0	31	195	275	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	71.m15720	AN7698.1	AO070325000103	Myosin class I heavy chain	Z		8.412	1	1	1	0	226	240	26			311	1
233	TCTCCTTTCCTCyC		up	up	71.m15734	AN7710.1	AO070325000117	Predicted phosphatase/phosphohexomutase				1	1	1	0	97	300	364	184	0		
233	TCTCCTTTCCTCyC		up	up	71.m15748	AN7721.1	AO070325000136	Transport protein Sec61, alpha subunit	UO		5.62034359867491 0.83730765519789	2	1	2	0	41	177	119	106	0		
233	TCTCCTTTCCTCyC		up	down	71.m15776	AN7750.1	AO070325000175	Protein predicted to be involved in carbohydrate metabolism	G		5.054	1	2	1	0	12	215	160			No EST	No EST
233	TCTCCTTTCCTCyC		up	up	53.m03857	AN8010.1	AO070322000057	Glycogen synthase	G		5.054	2	2	2	0	204	82	106	293	1		
233	TCTCCTTTCCTCyC		up	up	53.m03827	AN8117.1	AO070322000025	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme	I		4.286	1	2	4	0	213	219	303	No EST	No EST		
233	TCTCCTTTCCTCyC		up	down	53.m03827	AN8117.1	AO070322000025	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme	I		4.286	1	1	1	0	435	367	472			499	1
233	TCTCCTTTCCTCyC		up	up	53.m04128	AN8235.1	AO070310000073	predicted protein [Neurospora crassa]				1	2	1	0	206	217	139	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	53.m03692	AN8269.1	AO070310000033	Molecular chaperone (HSP90 family)	O		0.837	3	1	2	0	225	159	179	336	1		
233	TCTCCTTTCCTCyC		up	up	53.m03686	AN8274.1	AO070310000027	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	1	0.004	2	1	1	1	234	307	264	158	0		
233	TCTCCTTTCCTCyC		up	up	53.m03685	AN8275.1	AO070310000026	Citrate synthase	C	1	0.004	1	1	1	0	72	79	133	73	0		
233	TCTCCTTTCCTCyC		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		1.015	1	1	2	1	180	138	432	157	1		
233	TCTCCTTTCCTCyC		up	up	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		5.054	2	2	2	0	505	33	11	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	71.m15961	AN8830.1	AO070271000049	Checkpoint kinase and related serine/threonine protein kinases	D		8.010	1	1	2	0	157	65	12	121	1		

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233	TCTCCTTTCCTCyC		up	up	56.m02292	AN8881.1	AO070293000011	Mitochondrial carnitine-acylcarnitine carrier protein	C	1	0.004	1	1	1	0	61	261	238	334	1		
233	TCTCCTTTCCTCyC		up	up	56.m03091	AN8945.1	AO070319000047	methyltransferase [Gibberella zeae]				1	1	1	0	43	350	387	125	0		
233	TCTCCTTTCCTCyC		up	up	66.m04571	AN9112.1	AO070332000162	Alcohol dehydrogenase, class V	Q		6.045	1	1	1	1	117	41	40	No EST	No EST		
233	TCTCCTTTCCTCyC		up	up	53.m04180	AN9411.1	AO070310000008	NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit	C	1	0.004	1	1	4	0	29	107	102	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	71.m15415	AN0131.1	AO070321000122	hypothetical protein [Neurospora crassa]				2	1	1	1	113	2	2	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	71.m16051	AN0161.1	AO070321000086	mRNA cleavage and polyadenylation factor IA/II complex, subunit CLP1	A	1	0.004	1	1	1	0	141	59	204	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	71.m15442	AN0167.1	AO070321000079	Translation initiation factor 2B, alpha subunit (eIF-2Balpha/GCN3)	J		2.330	1	0	0	0	135	0	0	68	1		
234	GTTTGTCnTGTTTG		up	down	54.m06638	AN0446.1	AO070338000308	Uncharacterized protein PSP1 (suppressor of DNA polymerase alpha mutations in yeast)				1	1	1	0	370	20	558			No EST	No EST
234	GTTTGTCnTGTTTG		up	up	69.m15266	AN0582.1	AO070280000004	Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	L		5.416	2	1	1	1	5	101	142	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	70.m15453	AN0854.1	AO070320000001	Splicing coactivator SRm160/300, subunit SRm300	A	1	0.004	1	1	2	0	303	422	40	355	0		
234	GTTTGTCnTGTTTG		up	down	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		6.00093143789754 5.94832756554461	2	1	1	0	172	126	23			No EST	No EST
234	GTTTGTCnTGTTTG		up	up	70.m15042	AN1175.1	AO070331000170	Nucleolar protein NOP52/RRP1	A	1	0.004	1	1	2	0	150	80	76	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	70.m14972	AN1249.1	AO070223000012	Spliceosomal protein FBP11/Splicing factor PRP40	A	1	0.004	1	1	1	1	126	26	27	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	70.m14858	AN1371.1	AO070215000010	predicted protein [Neurospora crassa]				1	2	1	0	166	7	268	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	69.m15042	AN1728.1	AO070324000059	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit	C		6.389	1	1	1	0	166	88	80	40	0		
234	GTTTGTCnTGTTTG		up	up	58.m07660	AN1851.1	AO070292000043	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O		0.468	1	1	1	0	135	17	21	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	58.m07634	AN2046.1	AO070292000013					1	2	1	0	264	137	130	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	57.m05779	AN2080.1	AO070341000233	Polypeptide release factor 3	J		2.330	1	1	2	0	176	242	20	55	0		
234	GTTTGTCnTGTTTG		up	up	72.m19703	AN2137.1	AO070343000182	Cyclin B and related kinase-activating proteins	D		4.635	2	2	1	0	272	200	6	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	72.m19688	AN2153.1	AO070343000202	Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	J		2.330	2	1	1	1	166	338	364	No EST	No EST		
234	GTTTGTCnTGTTTG		up	down	71.m15855	AN2210.1	AO070294000012	Predicted transporter (ABC superfamily)				1	1	1	0	86	172	204			344	1
234	GTTTGTCnTGTTTG		up	up	71.m15831	AN2234.1	AO070326000145	predicted protein [Neurospora crassa]				0	1	0	1	116	27	0	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	71.m15902	AN2261.1	AO070326000103	Phosphatidylglycerolphosphate synthase	I		6.392	1	1	1	1	9	47	56	47	0		
234	GTTTGTCnTGTTTG		up	up	59.m08499	AN2490.1	AO070312000130	Uncharacterized conserved protein, contains N-recognin-type Zn-finger				2	1	1	1	132	99	213	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	59.m09034	AN2980.1	AO070337000142	60S ribosomal protein L35A/L37	J		2.330	1	2	2	1	33	371	425	81	0		
234	GTTTGTCnTGTTTG		up	up	59.m08916	AN3082.1	AO070224000004	mRNA cleavage and polyadenylation factor II complex, subunit CFT2 (CPSF subunit)	A	1	0.004	2	1	1	0	243	124	207	No EST	No EST		
234	GTTTGTCnTGTTTG		up	down	59.m08584	AN3142.1	AO070303000002	Nucleolar GTPase/ATPase p130	Y		6.001	1	1	3	0	308	207	228			297	1
234	GTTTGTCnTGTTTG		up	up	59.m08516	AN3147.1	AO070256000043	Glycolipid transfer protein	G		5.131	1	2	1	0	192	16	26	70	1		
234	GTTTGTCnTGTTTG		up	up	58.m07385	AN3586.1	AO070342000163	Monooxygenase involved in coenzyme Q (ubiquinone) biosynthesis	HC		3.15808680457693 6.38936712971506	1	1	1	0	89	408	340	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	58.m07441	AN3659.1	AO070342000029	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		6.25460287399896 4.12027664947604	1	1	1	0	411	34	36	No EST	No EST		
234	GTTTGTCnTGTTTG		up	down	58.m07982	AN4342.1	AO070240000017	Tryptophan-rich basic nuclear protein				3	1	2	0	73	262	422			No EST	No EST
234	GTTTGTCnTGTTTG		up	down	58.m07958	AN4369.1	AO070261000009	Ras1 guanine nucleotide exchange factor	T		6.255	1	1	1	0	426	320	269			No EST	No EST
234	GTTTGTCnTGTTTG		up	down	58.m07878	AN4447.1	AO070273000006	Signal transduction histidine kinase	T		6.255	1	1	1	0	58	110	222			101	0
234	GTTTGTCnTGTTTG		up	up	58.m07866	AN4458.1	AO070305000135	Spindle pole body protein - Sad1p	Z		4.120	1	1	1	1	106	69	67	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	58.m07864	AN4460.1	AO070305000133	WD40-repeat-containing subunit of the 18S rRNA processing complex	A	1	0.004	1	1	1	1	155	249	219	No EST	No EST		
234	GTTTGTCnTGTTTG		up	down	59.m09218	AN4767.1	AO070327000046	Scaffold/matrix specific factor hnRNP-U/SAF-A, contains SPRY domain	A	1	0.004	1	1	1	0	8	34	64			274	1
234	GTTTGTCnTGTTTG		up	up	59.m09211	AN4771.1	AO070329000081	WD40 repeat protein				2	1	1	1	76	311	330	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	59.m08812	AN4908.1	AO070338000038	Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondrial morphology/distribution, also found associated with eIF-3				1	1	1	0	208	17	13	No EST	No EST		
234	GTTTGTCnTGTTTG		up	down	59.m08873	AN4969.1	AO070288000035	Centromere-associated protein HEC1	D		4.635	1	1	2	0	182	430	28			No EST	No EST
234	GTTTGTCnTGTTTG		up	down	54.m06911	AN5111.1	AO070291000068	E3 ubiquitin ligase interacting with arginine methyltransferase	O		0.468	1	1	1	0	347	95	20			465	1
234	GTTTGTCnTGTTTG		up	up	69.m15498	AN5438.1	AO070333000100	Hsp90 co-chaperone CNS1 (contains TPR repeats)	O		0.468	1	1	1	1	79	146	154	54	0		
234	GTTTGTCnTGTTTG		up	up	69.m15743	AN5452.1	AO070239000031	Splicing factor 3b, subunit 3	A	1	0.004	2	1	1	0	42	87	56	179	1		

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234	GTTTGTCnTGTTTG		up	up	69.m15436	AN5522.1	AO070341000367	predicted protein [Neurospora crassa]				1	1	1	0	257	4	58	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	69.m15615	AN5744.1	AO070341000001	Multifunctional chaperone (14-3-3 family)	O		0.468	1	1	2	0	260	252	255	141	0		
234	GTTTGTCnTGTTTG		up	up	69.m14811	AN5786.1	AO070249000032	hypothetical protein [Neurospora crassa]				1	1	1	0	52	53	33	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	72.m19228	AN5902.1	AO070248000040	Alpha-1,2 glucosyltransferase/transcriptional activator	OKIT		0.4677043 88108704 3.6904929 5931665 6.3917198 0243256 6.2546028 7399896	1	1	1	0	121	18	24	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	72.m19002	AN6171.1	AO070340000034	U3 small nucleolar ribonucleoprotein (snoRNP) component	A	1	0.004	1	2	2	0	149	59	223	41	0		
234	GTTTGTCnTGTTTG		up	up	72.m18993	AN6176.1	AO070340000023	predicted protein [Neurospora crassa]				2	2	1	0	279	141	70	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	62.m03131	AN6543.1	AO070270000041	Armadillo/beta-catenin-like repeat-containing protein	O		0.468	1	1	3	0	321	235	186	139	0		
234	GTTTGTCnTGTTTG		up	up	62.m03124	AN6549.1	AO070270000036	RNA polymerase II transcriptional regulation mediator	K		3.690	1	1	1	1	156	71	87	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	65.m07278	AN6707.1	AO070339000137	DNA or RNA helicases of superfamily II	KL		3.6904929 5931665 5.4158710 8820351	1	1	1	0	78	67	69	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	71.m16029	AN6921.1	AO070313000060	HSP90 co-chaperone p23	O		0.468	1	1	1	0	225	64	80	71	1		
234	GTTTGTCnTGTTTG		up	up	57.m05449	AN7673.1	AO070325000053	Putative zinc transporter	P		8.333	2	1	1	1	29	40	41	26	0		
234	GTTTGTCnTGTTTG		up	up	57.m05454	AN7677.1	AO070325000067	hypothetical protein [Neurospora crassa]				1	1	2	0	288	70	79	82	1		
234	GTTTGTCnTGTTTG		up	up	53.m03887	AN8056.1	AO070322000144	Chromosome condensation complex Condensin, subunit G	BD		8.0483430 1133854 4.6345362 347303	1	1	1	1	206	73	88	161	1		
234	GTTTGTCnTGTTTG		up	up	53.m03779	AN8194.1	AO070310000126	emp24/gp25L/p24 family of membrane trafficking proteins	U		5.948	1	1	2	0	142	162	150	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	53.m03758	AN8215.1	AO070310000097	5,10-methylenetetrahydrofolate reductase	E		5.264	1	1	1	0	346	25	134	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	62.m03475	AN8670.1	AO070315000087	Nucleolar GTPase/ATPase p130	Y		6.001	1	1	1	0	291	177	173	No EST	No EST		
234	GTTTGTCnTGTTTG		up	up	62.m03370	AN8699.1	AO070315000126	Ubiquitin-specific protease	O		0.468	1	1	1	1	137	33	46	46	1		
234	GTTTGTCnTGTTTG		up	down	62.m03358	AN8710.1	AO070315000137	FOG: Low-complexity				1	1	1	0	83	163	30			No EST	No EST
234	GTTTGTCnTGTTTG		up	up	66.m04582	AN9116.1	AO070332000151	Nicotinic acid phosphoribosyltransferase	H		3.158	1	1	1	0	187	154	150	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	71.m15403	AN0122.1	AO070311000090	ATP-dependent Lon protease, bacterial type	O		2.247	1	1	1	0	93	293	296	78	0		
252	ACGCGTAAAGTGGTT		up	up	71.m15484	AN0228.1	AO070323000081	DNA replication licensing factor, MCM6 component	L		0.023	1	1	1	1	248	198	206	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	58.m08995	AN1660.1	AO070299000020	FOG: Immunoglobin and related proteins	P		1.455	1	1	1	0	263	85	107	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	69.m15675	AN2460.1	AO070264000013	Splicing coactivator SRm160/300, subunit SRm300	A		0.353	2	1	1	0	196	297	356	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	59.m08977	AN3040.1	AO070337000054	Projectin/twitchin and related proteins	Z		0.139	1	1	1	0	125	107	227	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	58.m07862	AN4472.1	AO070305000131	Putative transcription factor HALR/MLL3, involved in embryonic development				1	1	1	0	23	319	253	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	57.m05851	AN7493.1	AO070287000024	predicted protein [Neurospora crassa]				1	1	1	0	170	41	33	145	1		
252	ACGCGTAAAGTGGTT		up	up	53.m03853	AN7994.1	AO070322000052	DNA replication licensing factor, MCM5 component	L		0.023	1	1	1	1	133	117	125	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	53.m03916	AN8065.1	AO070330000021	Actin-related protein Arp2/3 complex, subunit ARPC3	Z		0.139	1	1	1	1	80	26	26	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	53.m04127	AN8236.1	AO070310000072	Putative growth response protein	T		2.049	1	1	1	0	134	187	37	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	62.m03399	AN8671.1	AO070315000088	tRNA-splicing endonuclease positive effector (SEN1)	A		0.353	1	1	2	0	471	11	8	No EST	No EST		
252	ACGCGTAAAGTGGTT		up	up	62.m03468	AN8713.1	AO070315000139	Structure-specific endonuclease ERCC1-XPF, catalytic component XPF/ERCC4	L		0.023	1	1	1	0	4	181	140	4	0		
328	GCATAGCATGGCGT		down	down	70.m15351	AN0716.1	AO070343000451	Uncharacterized conserved protein				1	1	1	0	74	43	72			No EST	No EST
328	GCATAGCATGGCGT		down	up	70.m14935	AN1272.1	AO070332000020	Casein kinase II, beta subunit	TDK		5.4051789 2753173 2.1737045 8663162 6.2429177 5748114	1	1	1	0	290	23	23	No EST	No EST		

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328	GCATAGCATGGCGT		down	down	70.m14899	AN1335.1	AO070303000097	G-protein beta subunit-like protein (contains WD40 repeats)				1	1	1	1	106	63	59			No EST	No EST
328	GCATAGCATGGCGT		down	down	69.m14936	AN1918.1	AO070341000122	Phosphoenolpyruvate carboxykinase (ATP)	C		3.169	1	1	1	1	38	78	59			195	1
328	GCATAGCATGGCGT		down	down	59.m08521	AN3144.1	AO070256000047	FYVE finger-containing protein				1	2	1	1	112	67	126			257	1
328	GCATAGCATGGCGT		down	up	59.m08819	AN4916.1	AO070338000027	40S ribosomal protein S7	J		3.295	1	1	1	0	158	49	205	82	1		
328	GCATAGCATGGCGT		down	down	69.m15562	AN5344.1	AO070333000180	Ubiquitin-protein ligase	O		3.745	1	1	1	1	193	73	197			173	1
328	GCATAGCATGGCGT		down	down	65.m07417	AN5693.1	AO070309000108	Uncharacterized conserved protein				1	1	1	1	211	75	186			319	1
328	GCATAGCATGGCGT		down	down	72.m19257	AN5875.1	AO070308000144	rRNA processing protein	JD		3.29482238215225 2.17370458663162	1	1	1	1	101	103	105			173	1
328	GCATAGCATGGCGT		down	down	65.m07490	AN6696.1	AO070339000127	hypothetical protein [Neurospora crassa]				1	1	1	1	128	111	121			No EST	No EST
328	GCATAGCATGGCGT		down	down	71.m15293	AN6823.1	AO070314000102	hypothetical protein ((AL513443) hypothetical protein [Neurospora crassa])				1	3	2	1	58	12	47			No EST	No EST
328	GCATAGCATGGCGT		down	up	72.m20022	AN7304.1	AO070297000051	Mitochondrial solute carrier protein	C		3.169	1	1	1	0	374	196	88	No EST	No EST		
328	GCATAGCATGGCGT		down	down	57.m05871	AN7473.1	AO070287000053	mRNA capping enzyme, guanylyltransferase (alpha) subunit	A		2.885	1	1	1	0	104	32	64			No EST	No EST
328	GCATAGCATGGCGT		down	down	53.m03757	AN8216.1	AO070310000096	Nucleoside diphosphate kinase	F		1.265	1	2	1	1	281	230	286			113	0
328	GCATAGCATGGCGT		down	down	52.m04075	AN9357.1	AO070315000043	Predicted dehydrogenase	Q		2.649	1	1	1	1	154	90	110			No EST	No EST
336	GGCGTTTGGG		down	down	54.m06624	AN0433.1	AO070338000284	60S ribosomal protein L18A	J		4.519	1	1	1	1	338	86	13			No EST	No EST
336	GGCGTTTGGG		down	down	54.m06621	AN0436.1	AO070338000281	Predicted E3 ubiquitin ligase	O		1.236	1	1	1	0	128	79	130			No EST	No EST
336	GGCGTTTGGG		down	down	70.m15630	AN0989.1	AO070318000148	SWI-SNF chromatin-remodeling complex protein	B		3.829	1	1	1	1	107	108	126			No EST	No EST
336	GGCGTTTGGG		down	down	70.m15197	AN1039.1	AO070336000074	HLH transcription factor EBF/Olf-1 and related DNA binding proteins	K	1	0.002	1	1	1	0	5	48	194			No EST	No EST
336	GGCGTTTGGG		down	down	70.m15119	AN1116.1	AO070331000108	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	1	0.002	1	1	1	1	132	122	115			50	0
336	GGCGTTTGGG		down	down	70.m14969	AN1255.1	AO070223000014	Chromodomain-helicase DNA-binding protein	K	1	0.002	1	2	1	0	141	100	122			No EST	No EST
336	GGCGTTTGGG		down	down	58.m07780	AN1713.1	AO070305000029	Predicted esterase of the alpha-beta hydrolase superfamily				1	1	1	0	144	145	174			No EST	No EST
336	GGCGTTTGGG		down	down	58.m07647	AN1855.1	AO070292000031	hypothetical protein [Neurospora crassa]				1	1	1	0	82	126	160			No EST	No EST
336	GGCGTTTGGG		down	down	58.m08944	AN2000.1	AO070301000095	Ubiquitin and ubiquitin-like proteins	O		1.236	1	1	1	0	19	60	54			184	1
336	GGCGTTTGGG		down	down	72.m19657	AN2181.1	AO070343000260	Transcription initiation factor IIA, gamma subunit	K	1	0.002	3	1	1	0	24	104	140			No EST	No EST
336	GGCGTTTGGG		down	down	71.m15825	AN2238.1	AO070326000135	Molecular chaperone (DnaJ superfamily)	O		1.236	1	1	1	0	31	87	45			231	1
336	GGCGTTTGGG		down	down	54.m06686	AN2745.1	AO070338000226	Acetyltransferase, (GNAT) family				1	1	1	1	64	42	70			No EST	No EST
336	GGCGTTTGGG		down	down	59.m08753	AN2902.1	AO070338000104	TFIIF-interacting CTD phosphatases, including NLI-interacting factor	K	1	0.002	1	1	1	0	118	11	205			295	1
336	GGCGTTTGGG		down	down	59.m08521	AN3144.1	AO070256000047	FYVE finger-containing protein				2	2	2	1	98	76	103			257	1
336	GGCGTTTGGG		down	down	59.m08579	AN3178.1	AO070256000001	Component of histone deacetylase complex (breast carcinoma metastasis suppressor 1 protein in human)	DK	1	1.6755847560646 0.00154964124728046	2	2	1	0	94	91	90			No EST	No EST
336	GGCGTTTGGG		down	down	58.m07808	AN3830.1	AO070305000068	Threonine/serine dehydratases	E		4.334	1	1	1	0	117	59	82			218	1
336	GGCGTTTGGG		down	up	54.m07041	AN4210.1	AO070231000014	Signaling protein SWIFT and related BRCT domain proteins	KTDL	1	0.00154964124728046 2.64516856168208 1.6755847560646 5.32683350592104	1	2	1	1	394	167	147	No EST	No EST		
336	GGCGTTTGGG		down	down	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				1	1	1	0	132	189	217			431	1
336	GGCGTTTGGG		down	down	69.m15442	AN5517.1	AO070341000376	Cdc4 and related F-box and WD-40 proteins				1	1	1	0	247	250	210			No EST	No EST
336	GGCGTTTGGG		down	down	54.m06817	AN5702.1	AO070324000158	Uncharacterized conserved protein				1	1	1	0	101	146	139			No EST	No EST
336	GGCGTTTGGG		down	down	72.m19269	AN5865.1	AO070308000129	GTP-binding protein CRFG/NOG1 (ODN superfamily)				1	1	1	0	109	160	99			163	1
336	GGCGTTTGGG		down	down	72.m19252	AN5879.1	AO070245000029	Uncharacterized conserved protein, contains ML domain				2	1	1	0	3	190	173			388	1
336	GGCGTTTGGG		down	up	72.m19170	AN5954.1	AO070340000308	RNA polymerase I-associated factor - PAF67	JK	1	4.51914823078007 0.00154964124728046	2	1	1	1	96	391	449	No EST	No EST		
336	GGCGTTTGGG		down	up	72.m19188	AN5972.1	AO070340000330	Vesicle coat complex COPI, beta' subunit	U		1.484	1	1	1	1	28	64	287	370	1		
336	GGCGTTTGGG		down	down	72.m19518	AN6340.1	AO070298000007	Kinesin (KAR3 subfamily)	Z		4.486	1	1	1	0	71	87	47			348	1
336	GGCGTTTGGG		down	down	72.m19646	AN7601.1	AO070343000271	hypothetical protein [Neurospora crassa]				2	1	2	1	364	261	476			No EST	No EST

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336	GGCGTTTGGG		down	down	71.m15822	AN7628.1	AO070294000038	mRNA deadenylase subunit	A		2.705	1	1	1	0	428	93	417			414	1
336	GGCGTTTGGG		down	down	57.m05947	AN7681.1	AO070325000071	Mod5 protein sorting/negative effector of RNA Pol III synthesis	K	1	0.002	1	1	1	0	140	168	159			No EST	No EST
336	GGCGTTTGGG		down	down	57.m05465	AN7688.1	AO070325000082	Protein similar to predicted member of the intramitochondrial sorting protein family	U		1.484	1	1	1	0	65	59	61			No EST	No EST
336	GGCGTTTGGG		down	down	53.m03844	AN8002.1	AO070322000044	Anaphase-promoting complex (APC), Cdc16 subunit	DO		1.6755847560646 1.23567660162831	1	1	1	0	40	44	41			No EST	No EST
336	GGCGTTTGGG		down	down	53.m03884	AN8059.1	AO070322000124	Mitochondrial import inner membrane translocase, subunit TIM22	U		1.484	1	2	1	0	94	47	84			170	1
336	GGCGTTTGGG		down	down	62.m03398	AN8672.1	AO070315000089	P-type ATPase				1	1	1	0	148	157	163			No EST	No EST
336	GGCGTTTGGG		down	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J		4.519	1	1	1	1	48	199	208	73	0		
336	GGCGTTTGGG		down	down	66.m04759	AN9086.1	AO070332000191	Transport protein particle (TRAPP) complex subunit	U		1.484	1	1	2	1	42	32	43			No EST	No EST
336	GGCGTTTGGG		down	down	52.m03849	AN9362.1	AO070315000035	U2 snRNP splicing factor, small subunit, and related proteins	A		2.705	1	1	1	0	33	21	31			No EST	No EST
344	GGCAAAATdAAC		up	up	54.m06376	AN0373.1	AO070318000051					1	1	2	1	114	345	90	No EST	No EST		
344	GGCAAAATdAAC		up	up	70.m15259	AN0655.1	AO070343000571	hypothetical protein [Neurospora crassa]				1	1	1	0	187	362	355	No EST	No EST		
344	GGCAAAATdAAC		up	up	70.m15803	AN0810.1	AO070239000005	Extracellular protein SEL-1 and related proteins	MOT		2.04012406070323 4.95255424673632 1.59531876539979	1	1	1	1	184	191	217	No EST	No EST		
344	GGCAAAATdAAC		up	up	70.m15019	AN1200.1	AO070331000206	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein	JK		4.54832475240168 4.21171440392101	1	1	1	1	62	116	110	No EST	No EST		
344	GGCAAAATdAAC		up	down	55.m02974	AN1472.1	AO070306000093	Tellurite resistance protein and related permeases	P		3.479	1	1	1	0	162	117	373			No EST	No EST
344	GGCAAAATdAAC		up	up	69.m15077	AN1778.1	AO070324000018	Ketopantoate hydroxymethyltransferase	H		2.440	1	1	1	0	373	92	140	No EST	No EST		
344	GGCAAAATdAAC		up	up	71.m15938	AN2290.1	AO070295000069	FOG: Zn-finger				1	1	1	1	474	83	121	No EST	No EST		
344	GGCAAAATdAAC		up	up	71.m15179	AN2692.1	AO070313000096					1	1	1	1	354	319	259	204	0		
344	GGCAAAATdAAC		up	up	59.m09061	AN2933.1	AO070337000174	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	BT		2.22297029653099 1.59531876539979	2	1	1	0	239	30	143	No EST	No EST		
344	GGCAAAATdAAC		up	down	54.m06799	AN4219.1	AO070315000080	RNA polymerase III subunit C11	K		4.212	1	1	1	0	230	172	235			No EST	No EST
344	GGCAAAATdAAC		up	up	58.m07928	AN4395.1	AO070261000040	hypothetical protein [Neurospora crassa]				1	1	1	0	443	96	55	762	1		
344	GGCAAAATdAAC		up	up	58.m07911	AN4421.1	AO070273000044	Glycolate oxidase	C		4.407	1	1	1	1	10	283	283	No EST	No EST		
344	GGCAAAATdAAC		up	up	58.m07861	AN4471.1	AO070305000130	WD40 repeat-containing protein				1	1	1	1	94	173	285	36	0		
344	GGCAAAATdAAC		up	up	54.m06876	AN5144.1	AO070291000029	Fructose-6-phosphate 2-kinase/fructose-2,6-biphosphatase	G		4.704	1	1	1	0	253	341	111	No EST	No EST		
344	GGCAAAATdAAC		up	up	62.m03256	AN6654.1	AO070269000012	Glutamine synthetase	E		4.677	1	1	1	0	42	93	198	No EST	No EST		
344	GGCAAAATdAAC		up	up	53.m03875	AN8029.1	AO070322000075	Na+/K+ transporter	P		3.479	1	1	1	0	349	96	393	No EST	No EST		
347	wmAAAAGTTC		up	up	70.m15249	AN0647.1	AO070343000582	U3 small nucleolar ribonucleoprotein (snoRNP) component	A		1.940	1	1	1	1	65	264	265	No EST	No EST		
347	wmAAAAGTTC		up	up	70.m15127	AN1105.1	AO070285000033	Translocase of outer mitochondrial membrane complex, subunit TOM22	U		0.145	1	1	1	0	135	94	64	62	0		
347	wmAAAAGTTC		up	up	58.m07589	AN1983.1	AO070301000068	WD40 repeat-containing protein				1	1	1	1	134	305	155	No EST	No EST		
347	wmAAAAGTTC		up	up	69.m15160	AN2120.1	AO070332000051	Karyopherin (importin) beta 3	YU		0.654716680693002 0.144705130355008	1	1	1	0	245	422	380	No EST	No EST		
347	wmAAAAGTTC		up	up	65.m07390	AN3745.1	AO070309000078	Regulator of ribosome synthesis	J	1	0.002	1	1	1	1	120	57	69	No EST	No EST		
347	wmAAAAGTTC		up	up	58.m07811	AN3832.1	AO070305000070	Mitochondrial elongation factor	J	1	0.002	1	1	1	1	81	74	59	No EST	No EST		
347	wmAAAAGTTC		up	up	54.m07028	AN4251.1	AO070324000161	Mitochondrial/chloroplast ribosomal protein S2	J	1	0.002	2	1	1	1	17	317	248	23	0		
347	wmAAAAGTTC		up	up	58.m07861	AN4471.1	AO070305000130	WD40 repeat-containing protein				1	1	1	0	231	180	291	36	0		
347	wmAAAAGTTC		up	up	57.m05499	AN4581.1	AO070316000164	Protein involved in high osmolarity signaling pathway	T		0.807	1	1	1	0	78	110	122	No EST	No EST		
347	wmAAAAGTTC		up	up	59.m09234	AN4751.1	AO070327000068	Predicted DEAD-box-containing helicase				1	1	1	0	113	56	62	No EST	No EST		
347	wmAAAAGTTC		up	up	59.m08868	AN4965.1	AO070288000030	Negative regulator of transcription	K		2.003	1	1	1	0	39	130	145	No EST	No EST		
347	wmAAAAGTTC		up	up	59.m08913	AN5010.1	AO070224000002	HAT (Half-A-TPR) repeat-containing protein				1	1	1	1	62	130	101	No EST	No EST		
347	wmAAAAGTTC		up	down	54.m07022	AN5720.1	AO070324000130	Predicted membrane protein				1	1	2	0	77	91	62			147	1
347	wmAAAAGTTC		up	up	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		0.807	1	1	2	0	337	183	188	No EST	No EST		

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347	wmAAAAGTTC		up	up	72.m19789	AN7260.1	AO070297000018	Protein involved in the nuclear export of pre-ribosomes	JU	1	0.00225896730723546 0.144705130355008	1	1	1	0	57	35	44	No EST	No EST		
347	wmAAAAGTTC		up	up	71.m15986	AN8851.1	AO070271000025	Pseudouridine synthase	J	1	0.002	1	1	1	1	133	49	110	92	1		
418	CAAACAGTGCAAA		up	up	71.m15415	AN0131.1	AO070321000122	hypothetical protein [Neurospora crassa]				1	1	1	1	165	2	2	No EST	No EST		
418	CAAACAGTGCAAA		up	up	71.m15442	AN0167.1	AO070321000079	Translation initiation factor 2B, alpha subunit (eIF-2Balpha/GCN3)	J		3.648	1	0	0	0	136	0	0	68	1		
418	CAAACAGTGCAAA		up	up	71.m15474	AN0211.1	AO070321000033	U2-associated snRNP A' protein	A		0.069	1	2	1	0	243	176	72	No EST	No EST		
418	CAAACAGTGCAAA		up	up	70.m15056	AN1164.1	AO070331000156	Disrupter of silencing SAS10	B		4.261	1	1	1	0	118	25	114	No EST	No EST		
418	CAAACAGTGCAAA		up	up	70.m15042	AN1175.1	AO070331000170	Nucleolar protein NOP52/RRP1	A		0.069	1	1	1	0	151	80	91	No EST	No EST		
418	CAAACAGTGCAAA		up	up	70.m14858	AN1371.1	AO070215000010	predicted protein [Neurospora crassa]				1	1	1	0	167	8	269	No EST	No EST		
418	CAAACAGTGCAAA		up	up	69.m15042	AN1728.1	AO070324000059	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit	C		4.899	1	1	1	0	166	89	81	40	0		
418	CAAACAGTGCAAA		up	up	58.m07634	AN2046.1	AO070292000013					1	2	1	0	264	138	131	No EST	No EST		
418	CAAACAGTGCAAA		up	up	72.m19688	AN2153.1	AO070343000202	Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	J		3.648	1	1	2	1	167	338	104	No EST	No EST		
418	CAAACAGTGCAAA		up	up	71.m15831	AN2234.1	AO070326000145	predicted protein [Neurospora crassa]				1	1	1	1	116	28	1	No EST	No EST		
418	CAAACAGTGCAAA		up	up	71.m15902	AN2261.1	AO070326000103	Phosphatidylglycerolphosphate synthase	I		3.516	1	1	1	1	9	48	57	47	0		
418	CAAACAGTGCAAA		up	up	59.m08499	AN2490.1	AO070312000130	Uncharacterized conserved protein, contains N-recognin-type Zn-finger				1	1	1	1	133	99	213	No EST	No EST		
418	CAAACAGTGCAAA		up	up	59.m08916	AN3082.1	AO070224000004	mRNA cleavage and polyadenylation factor II complex, subunit CFT2 (CPSF subunit)	A		0.069	1	1	2	1	244	124	207	No EST	No EST		
418	CAAACAGTGCAAA		up	up	59.m08516	AN3147.1	AO070256000043	Glycolipid transfer protein	G		4.427	2	1	2	0	22	17	18	70	1		
418	CAAACAGTGCAAA		up	up	58.m07441	AN3659.1	AO070342000029	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		3.77910280071952 1.67867605822275	1	1	1	0	411	35	37	No EST	No EST		
418	CAAACAGTGCAAA		up	up	58.m07838	AN3866.1	AO070305000102	Threonine/serine dehydratases	E		3.779	2	1	1	0	73	250	94	No EST	No EST		
418	CAAACAGTGCAAA		up	up	58.m07866	AN4458.1	AO070305000135	Spindle pole body protein - Sad1p	Z		1.679	1	1	1	1	106	70	68	No EST	No EST		
418	CAAACAGTGCAAA		up	up	58.m07864	AN4460.1	AO070305000133	WD40-repeat-containing subunit of the 18S rRNA processing complex	A		0.069	1	1	1	1	156	249	219	No EST	No EST		
418	CAAACAGTGCAAA		up	up	59.m09211	AN4771.1	AO070329000081	WD40 repeat protein				1	1	1	1	126	311	330	No EST	No EST		
418	CAAACAGTGCAAA		up	up	69.m15498	AN5438.1	AO070333000100	Hsp90 co-chaperone CNS1 (contains TPR repeats)	O		1.510	1	1	1	1	79	147	155	54	0		
418	CAAACAGTGCAAA		up	up	69.m15743	AN5452.1	AO070239000031	Splicing factor 3b, subunit 3	A		0.069	2	2	1	0	43	87	56	179	1		
418	CAAACAGTGCAAA		up	up	69.m15436	AN5522.1	AO070341000367	predicted protein [Neurospora crassa]				1	1	2	0	258	4	58	No EST	No EST		
418	CAAACAGTGCAAA		up	up	69.m14811	AN5786.1	AO070249000032	hypothetical protein [Neurospora crassa]				1	1	1	1	53	53	33	No EST	No EST		
418	CAAACAGTGCAAA		up	up	72.m19228	AN5902.1	AO070248000040	Alpha-1,2 glucosyltransferase/transcriptional activator	OKIT		1.51021223864604 1.33930810390672 3.51562528375586 3.77910280071952	2	1	1	0	106	19	25	No EST	No EST		
418	CAAACAGTGCAAA		up	up	72.m18993	AN6176.1	AO070340000023	predicted protein [Neurospora crassa]				2	2	1	0	239	132	70	No EST	No EST		
418	CAAACAGTGCAAA		up	up	62.m03124	AN6549.1	AO070270000036	RNA polymerase II transcriptional regulation mediator	K		1.339	1	1	1	1	157	71	78	No EST	No EST		
418	CAAACAGTGCAAA		up	up	65.m07278	AN6707.1	AO070339000137	DNA or RNA helicases of superfamily II	KL		1.33930810390672 5.23435349295246	1	1	1	0	78	68	70	No EST	No EST		
418	CAAACAGTGCAAA		up	up	71.m16029	AN6921.1	AO070313000060	HSP90 co-chaperone p23	O		1.510	1	1	1	0	226	64	80	71	1		
418	CAAACAGTGCAAA		up	down	72.m19648	AN7600.1	AO070343000270	Sulfite reductase (ferredoxin)	P		5.588	1	1	1	0	129	70	94			No EST	No EST
418	CAAACAGTGCAAA		up	up	71.m15820	AN7630.1	AO070294000040	Angio-associated migratory cell protein (contains WD40 repeats)				1	0	1	0	260	0	65	31	1		
418	CAAACAGTGCAAA		up	up	53.m03779	AN8194.1	AO070310000126	emp24/gp25L/p24 family of membrane trafficking proteins	U		4.755	1	1	1	1	143	162	176	No EST	No EST		
418	CAAACAGTGCAAA		up	up	53.m03758	AN8215.1	AO070310000097	5,10-methylenetetrahydrofolate reductase	E		3.779	1	1	1	0	346	26	135	No EST	No EST		
418	CAAACAGTGCAAA		up	up	62.m03370	AN8699.1	AO070315000126	Ubiquitin-specific protease	O		1.510	1	2	1	1	137	34	47	46	1		
418	CAAACAGTGCAAA		up	up	66.m04582	AN9116.1	AO070332000151	Nicotinic acid phosphoribosyltransferase	H		4.514	1	2	1	1	188	99	150	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	70.m15454	AN0855.1	AO070320000002	DNA repair protein, SNF2 family	L	1	0.000	1	1	1	1	96	104	117	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	70.m15223	AN1005.1	AO070312000029	Gamma-tubulin complex, DGRIP91/SPC98 component	Z		2.722	1	1	1	0	62	27	56	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	70.m14981	AN1237.1	AO070331000251	DNA repair protein RAD51/RHP55	L	1	0.000	1	1	1	1	284	21	37	No EST	No EST		

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616	CGCGAAdTCACGTG		up	up	70.m14968	AN1254.1	AO070223000015	FOG: Zn-finger				1	2	1	0	146	100	214	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	70.m14915	AN1293.1	AO070303000055	predicted protein [Neurospora crassa]				1	1	1	0	138	174	163	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	59.m09039	AN2973.1	AO070337000148	SNF2 family DNA-dependent ATPase	B		2.156	1	1	1	1	163	15	16	No EST	No EST		
616	CGCGAAdTCACGTG		up	down	59.m09280	AN3426.1	AO070327000005	Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	A		4.989	1	1	1	1	266	104	217			No EST	No EST
616	CGCGAAdTCACGTG		up	up	69.m15402	AN3691.1	AO070341000316	AAA+-type ATPase	O		2.343	1	1	1	0	236	178	261	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	57.m05686	AN3797.1	AO070337000231	3'-5' DNA helicase	L	1	0.000	1	1	1	0	66	94	119	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L	1	0.000	1	1	1	0	113	271	119	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	59.m08784	AN4888.1	AO070338000070	Thiamine pyrophosphate-requiring enzyme	EH		3.7802019 8310986 2.3442755 3434079	1	1	1	0	160	179	206	72	0		
616	CGCGAAdTCACGTG		up	up	59.m08882	AN4980.1	AO070288000047	Ribosomal protein S6 kinase and related proteins	T		3.780	1	1	1	1	233	62	59	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	59.m08904	AN5006.1	AO070255000034	Mismatch repair ATPase MSH2 (MutS family)	L	1	0.000	1	1	1	0	123	59	71	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	58.m07509	AN5588.1	AO070328000021	AAA+-type ATPase containing the peptidase M41 domain	O		2.343	1	1	1	0	272	330	111	164	0		
616	CGCGAAdTCACGTG		up	up	72.m19745	AN7325.1	AO070297000077	DNA polymerase delta, catalytic subunit	L	1	0.000	1	1	1	0	189	105	113	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	72.m19562	AN7545.1	AO070277000042	CCAAT-binding factor, subunit B (HAP2)	K		3.615	1	1	1	0	537	2	2	No EST	No EST		
616	CGCGAAdTCACGTG		up	up	57.m05407	AN7649.1	AO070268000005	Mitochondrial import inner membrane translocase, subunit TIM9	U		3.744	1	1	1	0	155	253	324	30	0		
616	CGCGAAdTCACGTG		up	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J		3.752	1	1	1	1	146	100	108	73	0		
616	CGCGAAdTCACGTG		up	up	62.m03468	AN8713.1	AO070315000139	Structure-specific endonuclease ERCC1-XPF, catalytic component XPF/ERCC4	L	1	0.000	1	1	1	1	58	128	85	4	0		
616	CGCGAAdTCACGTG		up	up	66.m04576	AN9109.1	AO070332000159	hypothetical protein [Neurospora crassa]				1	1	2	1	326	109	41	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15322	AN0048.1	AO070314000127	predicted protein [Neurospora crassa]				1	1	1	0	82	131	74	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15354	AN0076.1	AO070311000140	5'-3' exonuclease	L		1.361	2	1	2	0	85	157	3	49	0		
652	CTCTCCTTCTCCCC		up	up	71.m15359	AN0081.1	AO070311000136	G-protein beta subunit				2	2	3	0	125	285	317	153	0		
652	CTCTCCTTCTCCCC		up	up	71.m15360	AN0082.1	AO070311000135	Conserved phosducin-like protein	T		0.026	1	1	1	0	13	518	150	350	0		
652	CTCTCCTTCTCCCC		up	up	71.m15366	AN0091.1	AO070311000124	Putative protein methyltransferase involved in meiosis and transcriptional silencing (Dot1)	DK		2.8895232 7378684 2.8431548 1300744	1	1	1	0	195	87	80	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15380	AN0106.1	AO070311000113	Serine/threonine protein kinase	T		0.026	1	1	3	0	175	400	57	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15396	AN0117.1	AO070311000104	Histone H4	B		5.793	1	1	2	0	50	230	174	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15423	AN0140.1	AO070321000112	Actin-related protein Arp2/3 complex, subunit Arp3	Z		6.542	1	1	2	0	178	311	302	148	0		
652	CTCTCCTTCTCCCC		up	down	71.m16050	AN0162.1	AO070321000085	Nuclear localization sequence binding protein	K		2.843	2	1	2	0	335	261	13			153	0
652	CTCTCCTTCTCCCC		up	up	71.m15438	AN0163.1	AO070321000084	Rho GDP-dissociation inhibitor	T		0.026	1	1	2	0	315	421	175	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15479	AN0213.1	AO070323000085					3	1	2	0	423	113	113	354	1		
652	CTCTCCTTCTCCCC		up	up	71.m15641	AN0241.1	AO070284000071	Cu2+/Zn2+ superoxide dismutase SOD1	P		5.479	2	3	3	0	83	55	13	123	1		
652	CTCTCCTTCTCCCC		up	up	54.m06529	AN0254.1	AO070334000106	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE		3.7717892 2161064 4.2732569 4043449	2	3	2	0	163	102	315	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06482	AN0287.1	AO070334000066	WD40 repeat protein				2	1	2	0	102	32	231	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	54.m06459	AN0302.1	AO070334000037	Nucleolar GTPase/ATPase p130	Y		1.553	2	2	2	0	74	152	142			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	54.m06397	AN0357.1	AO070318000033	Cytochrome c1	C	1	0.006	1	1	1	1	71	208	214	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15273	AN0573.1	AO070272000052	Ypt/Rab GTPase activating protein	U		0.495	1	1	2	0	26	42	106	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15270	AN0575.1	AO070272000054	Calmodulin-binding protein CRAG, contains DENN domain	T		0.026	3	6	4	0	234	48	71	117	1		
652	CTCTCCTTCTCCCC		up	up	69.m15252	AN0595.1	AO070280000021	NADP/FAD dependent oxidoreductase	C	1	0.006	2	2	3	0	59	220	241	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15290	AN0687.1	AO070343000527	Spermidine synthase	E		4.273	1	1	2	0	53	433	284	123	0		
652	CTCTCCTTCTCCCC		up	up	70.m15335	AN0726.1	AO070343000481	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		4.0708802 464128 1.3114938 2861186	1	1	2	0	208	154	69	170	1		
652	CTCTCCTTCTCCCC		up	up	70.m15320	AN0733.1	AO070343000494	Histones H3 and H4	B		5.793	1	1	1	1	112	267	286	86	0		
652	CTCTCCTTCTCCCC		up	up	70.m15361	AN0747.1	AO070343000435	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O		1.311	1	1	1	0	24	185	226	29	0		
652	CTCTCCTTCTCCCC		up	up	70.m15785	AN0775.1	AO070316000063	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	1	0.006	1	1	2	0	107	159	252	87	0		
652	CTCTCCTTCTCCCC		up	down	70.m15415	AN0816.1	AO070288000088	RNA polymerase II transcription initiation factor TFIIA, large chain	K		2.843	1	1	1	0	45	53	49			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	70.m15426	AN0824.1	AO070255000021	Short-chain acyl-CoA dehydrogenase	I		3.772	3	2	2	0	64	89	85	25	0		
652	CTCTCCTTCTCCCC		up	up	70.m15437	AN0837.1	AO070255000006	Splicing coactivator SRm160/300, subunit SRm300	A		3.918	2	1	2	0	35	133	174	No EST	No EST		

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652	CTCTCCTTCTCCCC		up	up	70.m15462	AN0866.1	AO070320000017	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O		1.311	3	2	2	0	62	370	458	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15456	AN0870.1	AO070320000023	Mitochondrial phosphate carrier protein	C	1	0.006	2	2	2	0	56	401	79	15	0		
652	CTCTCCTTCTCCCC		up	up	70.m15488	AN0893.1	AO070320000065	Adenylosuccinate synthase	F		2.123	3	1	1	0	251	79	108	235	1		
652	CTCTCCTTCTCCCC		up	up	70.m15515	AN0906.1	AO070320000082	Karyopherin (importin) beta 1	YU		1.55270850176354 0.494755743050251	3	2	5	0	186	460	29	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	70.m15515	AN0906.1	AO070320000082	Karyopherin (importin) beta 1	YU		1.55270850176354 0.494755743050251	1	1	2	0	427	420	302			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		1.55270850176354 0.494755743050251	1	2	1	0	111	297	309	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15540	AN0932.1	AO070320000123	Pyridine nucleotide-disulphide oxidoreductase	Q		1.766	2	1	1	0	229	141	235	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15813	AN0937.1	AO070320000128	NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIT-4 [Neurospora crassa]				2	1	1	0	137	219	55	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15626	AN0986.1	AO070318000155	PHD Zn-finger proteins				2	3	2	0	404	75	27	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15221	AN1003.1	AO070312000031	Isocitrate dehydrogenase, alpha subunit	E		4.273	1	2	1	0	66	142	206	48	0		
652	CTCTCCTTCTCCCC		up	up	70.m15195	AN1037.1	AO070336000072	Fatty acid desaturase	I		3.772	1	3	4	0	390	101	82	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15203	AN1047.1	AO070313000109	Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	O		1.311	1	1	3	0	39	376	105	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15171	AN1062.1	AO070218000006	possible endozepine [Aspergillus fumigatus]				1	1	1	0	142	101	46	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15141	AN1091.1	AO070285000058	FOG: RRM domain				2	4	1	0	250	7	281	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15137	AN1094.1	AO070285000053	NADH-dehydrogenase (ubiquinone)	C	1	0.006	3	1	2	0	26	377	470	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15118	AN1117.1	AO070331000109	Putative cargo transport protein ERV29	U		0.495	2	2	2	0	135	237	276	192	0		
652	CTCTCCTTCTCCCC		up	up	70.m15114	AN1126.1	AO070331000119	GTP-binding ADP-ribosylation factor Arf1	U		0.495	1	2	1	0	254	119	69	108	0		
652	CTCTCCTTCTCCCC		up	up	70.m15059	AN1162.1	AO070331000152	Elongation factor 1 beta/delta chain	K		2.843	1	1	2	0	43	104	118	17	0		
652	CTCTCCTTCTCCCC		up	up	70.m15772	AN1165.1	AO070331000157	Predicted 3-ketosphinganine reductase	Q		1.766	1	1	2	0	127	106	82	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15040	AN1177.1	AO070331000173	Vesicle coat complex COPI, beta subunit	U		0.495	2	2	1	1	52	102	166	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15763	AN1182.1	AO070331000182	Beta tubulin	Z		6.542	2	1	2	0	94	195	150	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		4.326	5	2	2	0	21	157	162	193	1		
652	CTCTCCTTCTCCCC		up	up	70.m14994	AN1226.1	AO070331000235	Sirtuin 5 and related class III sirtuins (SIR2 family)	BK		5.79316725520768 2.84315481300744	1	1	3	0	50	54	2	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	70.m14980	AN1238.1	AO070331000252	hypothetical protein [Neurospora crassa]				1	1	1	0	193	124	121			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	70.m14923	AN1284.1	AO070332000035	Predicted GTP-binding protein (ODN superfamily)				3	1	2	0	64	308	178	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m14906	AN1325.1	AO070303000088	Protein interacting with poly(A)-binding protein	A		3.918	2	3	5	0	256	27	4	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m14896	AN1337.1	AO070303000102	predicted protein [Neurospora crassa]				2	1	3	0	93	134	47	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		0.026	3	3	4	0	93	298	1	400	1		
652	CTCTCCTTCTCCCC		up	down	70.m14847	AN1376.1	AO070243000006	Phospholipid methyltransferase	I		3.772	1	1	1	0	183	182	187			202	1
652	CTCTCCTTCTCCCC		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				5	3	4	1	144	119	176	189	1		
652	CTCTCCTTCTCCCC		up	down	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				1	1	3	0	45	103	39			363	1
652	CTCTCCTTCTCCCC		up	up	70.m14826	AN1396.1	AO070233000012	Glycerol-3-phosphate dehydrogenase	C	1	0.006	1	3	3	0	358	220	166	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	55.m02936	AN1420.1	AO070232000016	Putative Zn-finger protein				1	4	1	0	9	14	426	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	55.m02933	AN1423.1	AO070232000019	Permease of the major facilitator superfamily				1	1	2	0	292	2	149	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	55.m02926	AN1429.1	AO070242000022	Choline dehydrogenase and related flavoproteins	E		4.273	1	2	2	0	222	348	436	48	0		
652	CTCTCCTTCTCCCC		up	up	55.m03263	AN1437.1	AO070232000002	hypothetical protein [Neurospora crassa]				1	2	1	0	404	14	52	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	55.m03042	AN1523.1	AO070334000241	F0F1-type ATP synthase, alpha subunit	C	1	0.006	2	3	3	0	56	310	331	68	0		
652	CTCTCCTTCTCCCC		up	up	55.m03061	AN1543.1	AO070339000311	Fumarate reductase, flavoprotein subunit	C	1	0.006	1	1	3	0	34	314	162	43	0		
652	CTCTCCTTCTCCCC		up	up	55.m03067	AN1547.1	AO070339000307	Acetyl-CoA hydrolase	C	1	0.006	3	2	3	0	58	353	27	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07694	AN1624.1	AO070299000090	Mitochondrial F1F0-ATP synthase, subunit c/ATP9/proteolipid	C	1	0.006	4	3	1	0	54	413	439	79	0		
652	CTCTCCTTCTCCCC		up	up	58.m07716	AN1630.1	AO070299000035	Catalase (peroxidase I)	P		5.479	3	1	2	0	72	391	312	69	0		
652	CTCTCCTTCTCCCC		up	up	58.m07732	AN1666.1	AO070299000048	Nucleolar GTPase				1	1	1	0	97	113	82	122	1		
652	CTCTCCTTCTCCCC		up	up	58.m07772	AN1696.1	AO070305000020	Predicted acyltransferases	I		3.772	2	1	2	0	458	135	99	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	58.m07773	AN1697.1	AO070305000021	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	A		3.918	2	1	1	0	43	11	319			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	69.m15047	AN1744.1	AO070324000052	Predicted sugar phosphate isomerase involved in capsule formation	M		8.182	1	2	1	0	162	133	58	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
652	CTCTCCTTCTCCCC		up	up	58.m07713	AN1810.1	AO070299000061	Ornithine aminotransferase	E		4.273	2	1	1	0	0	103	244	33	0		
652	CTCTCCTTCTCCCC		up	down	58.m07668	AN1843.1	AO070292000064	Protein involved in meiotic recombination/predicted coiled-coil protein	D		2.890	2	3	2	0	267	240	276			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	58.m07660	AN1851.1	AO070292000043	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O		1.311	1	1	1	0	39	116	116	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m14935	AN1917.1	AO070341000123	Mitochondrial oxoglutarate/malate carrier proteins	C	1	0.006	1	4	3	0	487	60	145	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m14938	AN1921.1	AO070341000116	Peroxisomal biogenesis protein (peroxin)	U		0.495	1	1	2	0	187	316	10	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07338	AN1955.1	AO070342000226					1	2	1	0	177	387	378	49	0		
652	CTCTCCTTCTCCCC		up	up	58.m08946	AN1980.1	AO070301000065	Rab6 GTPase activator GAPCenA and related TBC domain proteins				2	2	1	0	136	86	247	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07644	AN2056.1	AO070292000026	Uncharacterized conserved protein				1	1	2	0	53	337	274	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		1.311	1	2	2	0	259	100	46	173	1		
652	CTCTCCTTCTCCCC		up	up	57.m05768	AN2068.1	AO070341000217	Vigilin	I		3.772	4	4	3	0	49	23	35	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05769	AN2069.1	AO070341000218	Cytochrome b5	C	1	0.006	4	2	2	0	85	137	135	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05787	AN2086.1	AO070341000244	Nuclear pore complex, Nup214/CAN component	YU		1.55270850176354 0.494755743050251	2	1	3	0	71	211	108	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15160	AN2120.1	AO070332000051	Karyopherin (importin) beta 3	YU		1.55270850176354 0.494755743050251	2	1	2	0	175	233	148	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19708	AN2133.1	AO070278000026	Armadillo/beta-Catenin/plakoglobin	TZ		0.0264658986385493 6.54158420983836	1	1	1	0	185	84	157	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19704	AN2136.1	AO070343000181	hypothetical protein [Neurospora crassa]				1	2	2	0	116	43	11	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19703	AN2137.1	AO070343000182	Cyclin B and related kinase-activating proteins	D		2.890	2	3	2	0	92	101	172	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		0.495	2	2	1	0	41	48	53	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19690	AN2151.1	AO070343000200	Splicing coactivator SRm160/300, subunit SRm300	A		3.918	1	2	2	0	326	72	72	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19677	AN2163.1	AO070343000222	Mitotic spindle checkpoint protein	D		2.890	2	2	5	0	367	5	35	242	1		
652	CTCTCCTTCTCCCC		up	up	72.m19038	AN2185.1	AO070340000081	Mitochondrial endonuclease	F		2.123	1	1	1	0	67	465	459	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15847	AN2215.1	AO070326000186	Uncharacterized conserved protein, contains GRAM domain				1	1	2	0	180	206	43	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15846	AN2219.1	AO070326000185	related to ahmp1 protein [MIPS] [Neurospora crassa]				2	2	1	0	14	284	12	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15889	AN2251.1	AO070326000115	Predicted membrane protein				1	1	1	0	214	276	188	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15917	AN2272.1	AO070295000048	Possible pfkB family carbohydrate kinase	G		4.071	1	2	2	0	70	57	49	91	1		
652	CTCTCCTTCTCCCC		up	up	71.m15923	AN2278.1	AO070295000054	Chromatin remodeling complex SWI/SNF, component SWI2 and related ATPases (DNA/RNA helicase superfamily)	BK		5.79316725520768 2.84315481300744	2	2	2	1	312	136	102	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15925	AN2280.1	AO070295000057	Uncharacterized conserved protein				2	2	1	0	185	343	306	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15938	AN2290.1	AO070295000069	FOG: Zn-finger				2	3	3	0	358	26	14	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15946	AN2297.1	AO070295000078	hypothetical protein [Neurospora crassa]				1	2	2	1	206	66	38	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C	1	0.006	3	2	3	1	48	309	495	104	0		
652	CTCTCCTTCTCCCC		up	down	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C	1	0.006	1	2	1	1	145	89	142			307	1
652	CTCTCCTTCTCCCC		up	up	72.m19478	AN2425.1	AO070241000006	Protein phosphatase, regulatory subunit PPP1R3C/D	OT		1.31149382861186 0.0264658986385493	1	1	2	0	209	156	143	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C	1	0.006	4	5	3	0	114	163	158	187	1		
652	CTCTCCTTCTCCCC		up	up	59.m08455	AN2525.1	AO070286000098	Serine racemase	TE		0.0264658986385493 4.27325694043449	1	1	1	0	42	36	3	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06673	AN2731.1	AO070338000213	Molecular chaperone (DnaJ superfamily)	O		1.311	2	1	2	0	98	308	353	113	0		
652	CTCTCCTTCTCCCC		up	down	54.m06688	AN2743.1	AO070338000228	Translation initiation factor 3, subunit a (eIF-3a)	J		1.424	2	2	1	0	76	57	230			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	54.m06682	AN2750.1	AO070338000222					3	1	2	0	117	256	166	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	54.m06682	AN2750.1	AO070338000222					2	1	3	0	102	144	18			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
652	CTCTCCTTCTCCCC		up	up	59.m09254	AN2757.1	AO070327000036	Uncharacterized conserved protein TEX2, contains PH domain				1	2	3	0	184	337	190	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m09263	AN2761.1	AO070327000023	Ubiquitin-protein ligase	O		1.311	4	1	4	0	146	280	131	144	0		
652	CTCTCCTTCTCCCC		up	up	59.m08697	AN2855.1	AO070338000169	FOG: Zn-finger				6	3	1	0	99	168	278	180	1		
652	CTCTCCTTCTCCCC		up	down	59.m08704	AN2860.1	AO070338000162	Alcohol dehydrogenase, class V	Q		1.766	1	1	2	0	252	390	55			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	59.m08713	AN2868.1	AO070338000154	Oligoribonuclease (3'->5' exoribonuclease)	A		3.918	2	1	1	0	3	379	137	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		5.793	4	4	5	0	237	79	44	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08724	AN2875.1	AO070338000136	Fructose 1,6-bisphosphate aldolase	G		4.071	2	2	5	0	52	180	101	43	0		
652	CTCTCCTTCTCCCC		up	up	59.m08731	AN2884.1	AO070338000130					2	2	2	0	406	32	94	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	59.m08751	AN2901.1	AO070338000106	Arginase	E		4.273	1	1	1	0	31	178	260			67	0
652	CTCTCCTTCTCCCC		up	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		2.843	4	2	1	0	90	43	48	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m09062	AN2932.1	AO070337000175	Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases	J		1.424	1	2	1	0	286	68	84	275	1		
652	CTCTCCTTCTCCCC		up	down	59.m09055	AN2939.1	AO070337000169	Ca2+-binding transmembrane protein LETM1/MRS7				1	1	1	0	28	83	46			239	1
652	CTCTCCTTCTCCCC		up	up	59.m09023	AN2989.1	AO070337000133	FOG: RRM domain				1	3	6	0	90	382	13	183	0		
652	CTCTCCTTCTCCCC		up	up	59.m08981	AN3036.1	AO070337000078	predicted protein [Neurospora crassa]				1	1	1	0	502	26	32	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	59.m08979	AN3038.1	AO070337000055	hypothetical protein [Neurospora crassa]				2	1	1	0	261	202	482			41	0
652	CTCTCCTTCTCCCC		up	up	59.m08957	AN3058.1	AO070337000016	Glycine/serine hydroxymethyltransferase	E		4.273	2	1	2	0	70	394	385	66	0		
652	CTCTCCTTCTCCCC		up	up	59.m08959	AN3059.1	AO070337000014	Phosphoglycerate mutase	G		4.071	2	2	4	0	139	14	19	25	1		
652	CTCTCCTTCTCCCC		up	up	59.m08921	AN3075.1	AO070224000009	hypothetical protein [Neurospora crassa]				2	1	2	0	206	370	263	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				4	2	1	1	216	206	294	106	0		
652	CTCTCCTTCTCCCC		up	up	59.m08628	AN3110.1	AO070303000041	3-phosphoinositide-dependent protein kinase (PDK1)	T		0.026	1	4	2	0	165	119	197	391	1		
652	CTCTCCTTCTCCCC		up	up	59.m08626	AN3112.1	AO070303000038	Protoporphyrinogen oxidase	H		4.326	4	4	2	0	70	36	365	57	1		
652	CTCTCCTTCTCCCC		up	down	59.m09373	AN3113.1	AO070303000036	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE		4.0708802 464128 4.2732569 4043449	2	1	1	0	234	304	110			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				2	1	5	0	253	124	272	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	67.m02904	AN3304.1	AO070274000035	Amino acid transporters	E		4.273	1	1	2	0	56	291	79	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		3.772	2	2	3	0	15	82	75	298	1		
652	CTCTCCTTCTCCCC		up	up	66.m04618	AN3416.1	AO070203000005	SNARE protein Syntaxin 1 and related proteins	U		0.495	1	3	1	0	230	145	288	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07376	AN3578.1	AO070342000171	Predicted MutS-related protein involved in mismatch repair	L		1.361	1	3	2	0	429	58	99	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07379	AN3581.1	AO070342000168	Thioredoxin reductase	O		1.311	3	1	1	1	148	33	210	163	1		
652	CTCTCCTTCTCCCC		up	up	58.m07392	AN3592.1	AO070342000144	Calnexin	O		1.311	2	2	1	0	131	288	239	126	0		
652	CTCTCCTTCTCCCC		up	up	58.m07398	AN3600.1	AO070342000153	hypothetical protein [Neurospora crassa]				1	1	1	0	281	357	251	276	0		
652	CTCTCCTTCTCCCC		up	up	58.m07399	AN3602.1	AO070342000154	Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	K		2.843	3	2	1	1	92	340	357	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07414	AN3627.1	AO070342000123	hypothetical protein [Neurospora crassa]				1	1	1	0	421	412	325	212	0		
652	CTCTCCTTCTCCCC		up	up	58.m07442	AN3658.1	AO070342000030	Monocarboxylate transporter	G		4.071	1	2	1	0	236	222	390	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07434	AN3664.1	AO070342000020	C-type lectin	TV		0.0264658 98638549 3 10.260727 4006116	2	2	1	0	154	92	393	248	1		
652	CTCTCCTTCTCCCC		up	up	58.m07428	AN3667.1	AO070342000004	HMG-box transcription factor	K		2.843	2	2	1	0	224	49	73	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15386	AN3729.1	AO070342000283	1,3-beta-glucan synthase/callose synthase catalytic subunit	M		8.182	4	2	2	1	386	11	15	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	69.m15380	AN3735.1	AO070342000272	GTPase-activating protein				1	1	1	0	360	320	285			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	65.m07375	AN3752.1	AO070309000065	Uncharacterized conserved protein, contains TBC domain	T		0.026	2	1	2	0	296	139	5	471	1		
652	CTCTCCTTCTCCCC		up	up	69.m15012	AN3915.1	AO070324000102	Aquaporin (major intrinsic protein family)	G		4.071	1	0	1	0	345	0	185	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	69.m14999	AN3929.1	AO070341000037	Permease of the major facilitator superfamily	G		4.071	1	0	1	0	496	141	345			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	54.m06579	AN4015.1	AO070328000151	Translation initiation factor 5A (eIF-5A)	J		1.424	2	2	2	0	96	141	198	70	0		
652	CTCTCCTTCTCCCC		up	up	54.m06570	AN4042.1	AO070328000135	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI		1.7655108 524824 3.7717892 2161064	1	1	3	0	20	411	347	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06564	AN4046.1	AO070328000129	Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)				1	1	2	1	86	14	82	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07369	AN4148.1	AO070342000182	Predicted transporter (major facilitator superfamily)				1	3	1	0	543	89	437	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m14951	AN4169.1	AO070341000094	hypothetical protein [Neurospora crassa]				2	2	3	0	274	181	53	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06745	AN4189.1	AO070342000110	Mitogen-activated protein kinase kinase (MAP2K)	T		0.026	1	2	2	0	369	9	95	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06772	AN4215.1	AO070231000009	Glutaredoxin and related proteins	O		1.311	1	3	1	0	85	224	422	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		1.424	5	3	2	1	125	260	316	96	0		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
652	CTCTCCTTCTCCCC		up	up	54.m06779	AN4236.1	AO070234000007	26S proteasome regulatory complex, ATPase RPT5	O		1.311	2	1	2	0	80	92	66	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m07034	AN4238.1	AO070234000002	Ribosomal protein S6 kinase and related proteins	T		0.026	1	1	1	0	217	278	52	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	65.m07433	AN4259.1	AO070277000032	Uncharacterized conserved protein, contains PCI domain				2	1	1	0	20	166	137	10	0		
652	CTCTCCTTCTCCCC		up	down	65.m07454	AN4276.1	AO070277000008	FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations				2	1	1	0	21	277	361			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	58.m08010	AN4314.1	AO070230000002	predicted protein [Neurospora crassa]				4	3	1	0	99	35	129	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07962	AN4361.1	AO070261000004	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		2.843	1	2	3	0	242	209	155	263	1		
652	CTCTCCTTCTCCCC		up	up	58.m07927	AN4394.1	AO070261000039					1	1	2	0	31	246	45	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				4	3	2	0	75	76	80	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07889	AN4437.1	AO070273000018	SOK1 kinase belonging to the STE20/SPS1/GC kinase family	T		0.026	1	1	2	0	248	200	249	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		4.273	3	4	4	0	59	190	50	66	0		
652	CTCTCCTTCTCCCC		up	up	58.m07847	AN4462.1	AO070305000113	Pyruvate carboxylase	C	1	0.006	2	2	5	0	130	228	12	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	58.m07860	AN4470.1	AO070305000129	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	J		1.424	1	1	1	0	401	78	49			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	57.m05654	AN4479.1	AO070311000025	FOG: HAMP domain	T		0.026	2	3	3	0	201	51	166	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05648	AN4483.1	AO070311000032	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		0.026	3	1	3	0	57	388	49	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05635	AN4496.1	AO070311000048	Predicted E3 ubiquitin ligase	O		1.311	1	3	2	0	30	64	90	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05604	AN4524.1	AO070321000132	predicted protein [Neurospora crassa]				1	1	2	0	200	111	106	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05554	AN4563.1	AO070321000191	Casein kinase (serine/threonine/tyrosine protein kinase)	T		0.026	3	2	1	0	62	70	80	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15682	AN4696.1	AO070329000189	Splicing coactivator SRm160/300, subunit SRm300	A		3.918	1	2	2	0	315	286	116	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15501	AN4732.1	AO070323000052	predicted protein [Neurospora crassa]				2	2	3	0	298	145	91	444	1		
652	CTCTCCTTCTCCCC		up	up	59.m09236	AN4743.1	AO070327000077	Ras-related small GTPase, Rho type				2	2	4	0	375	199	82	100	0		
652	CTCTCCTTCTCCCC		up	up	59.m09227	AN4756.1	AO070327000060	DNA-binding protein C1D involved in regulation of double-strand break repair	L		1.361	1	1	1	0	175	15	12	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m09204	AN4779.1	AO070329000071	NIPSNAP1 protein				3	3	1	0	140	51	313	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m09459	AN4820.1	AO070327000167	Aldehyde dehydrogenase	C	1	0.006	1	1	2	0	26	470	175	23	0		
652	CTCTCCTTCTCCCC		up	up	59.m09466	AN4859.1	AO070329000143	Plasma membrane H+-transporting ATPase	P		5.479	3	1	3	1	109	316	305	103	0		
652	CTCTCCTTCTCCCC		up	up	59.m09409	AN4880.1	AO070338000081	Jacalin-like lectin domain-containing protein				3	1	1	0	167	511	211	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08826	AN4923.1	AO070338000020	Hydroxymethylglutaryl-CoA synthase	I		3.772	3	2	4	0	40	403	314	172	0		
652	CTCTCCTTCTCCCC		up	up	59.m08856	AN4951.1	AO070288000003	Membrane coat complex Retromer, subunit VPS35	U		0.495	1	1	2	0	83	272	206	186	0		
652	CTCTCCTTCTCCCC		up	up	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				3	1	2	0	211	218	82	345	1		
652	CTCTCCTTCTCCCC		up	up	59.m08876	AN4973.1	AO070288000039	predicted protein [Neurospora crassa]				2	2	1	0	248	42	257	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08890	AN4987.1	AO070288000055	cAMP-dependent protein kinase types I and II, regulatory subunit	T		0.026	1	1	3	0	51	268	257	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08894	AN4991.1	AO070288000071	aureobasidin-resistance protein; AurA [Aspergillus nidulans]				2	1	1	0	51	111	48	420	1		
652	CTCTCCTTCTCCCC		up	up	59.m09454	AN4997.1	AO070288000080	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.772	1	2	3	0	114	127	7	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	59.m08669	AN5057.1	AO070338000201	Protein tyrosine phosphatase CDC14	V		10.261	2	1	1	0	381	164	169	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06903	AN5121.1	AO070291000058	26S proteasome regulatory complex, subunit RPN8/PSMD7	O		1.311	1	1	1	0	155	205	185	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06894	AN5129.1	AO070291000048	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O		1.311	3	1	2	0	5	478	331	141	0		
652	CTCTCCTTCTCCCC		up	up	54.m06889	AN5134.1	AO070291000041	Glutamate synthase	E		4.273	2	2	2	0	266	251	194	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m14882	AN5151.1	AO070237000013	Predicted membrane proteins, contain hemolysin III domain	T		0.026	2	0	3	0	282	0	33	228	1		
652	CTCTCCTTCTCCCC		up	up	54.m06857	AN5166.1	AO070291000006	CDP-diacylglycerol synthase	I		3.772	1	1	3	0	147	120	100	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m14907	AN5210.1	AO070337000270	Pyruvate kinase	G		4.071	3	1	2	0	71	425	46	60	0		
652	CTCTCCTTCTCCCC		up	up	57.m05706	AN5226.1	AO070337000252	Predicted membrane protein				2	1	3	0	97	220	228	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15562	AN5344.1	AO070333000180	Ubiquitin-protein ligase	O		1.311	1	2	1	0	178	32	138	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15551	AN5356.1	AO070333000156	Mitochondrial carnitine-acylcarnitine carrier protein	C	1	0.006	2	3	2	0	50	240	222	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15505	AN5404.1	AO070333000090	Reticulon	U		0.495	1	2	4	0	190	252	286	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15492	AN5442.1	AO070333000105	Serine carboxypeptidases (lysosomal cathepsin A)	OE		1.31149382861186 4.27325694043449	3	1	1	0	51	23	20	82	1		
652	CTCTCCTTCTCCCC		up	up	69.m15489	AN5445.1	AO070333000112					1	2	4	0	273	257	206	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	69.m15483	AN5449.1	AO070239000028	Arylsulfatase A and related enzymes	P		5.479	3	3	2	0	153	236	231	No EST	No EST		

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652	CTCTCCTTCTCCCC		up	up	69.m15746	AN5482.1	AO070341000403	GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein superfamily	U		0.495	1	2	1	0	138	138	302	124	0		
652	CTCTCCTTCTCCCC		up	up	69.m15460	AN5493.1	AO070341000392	Concentrative Na+-nucleoside cotransporter CNT1/CNT2	FP		2.12346893341593 5.47872319697198	1	1	1	0	159	75	32	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07475	AN5529.1	AO070328000064	NDR and related serine/threonine kinases				2	2	3	0	104	290	107	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	58.m07508	AN5589.1	AO070328000022	Ribulose kinase and related carbohydrate kinases	G		4.071	2	2	1	0	246	356	180	439	1		
652	CTCTCCTTCTCCCC		up	up	58.m07528	AN5604.1	AO070301000002	Fructose-1,6-bisphosphatase	G		4.071	1	1	0	0	165	44	0	181	1		
652	CTCTCCTTCTCCCC		up	up	58.m07549	AN5626.1	AO070301000025	Acyl-CoA synthetase	I		3.772	3	4	4	0	270	133	87	66	0		
652	CTCTCCTTCTCCCC		up	up	65.m07399	AN5673.1	AO070309000086	hypothetical protein [Neurospora crassa]				1	1	1	0	200	125	148	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	65.m07414	AN5688.1	AO070309000104	Cyclopropane fatty acid synthase and related methyltransferases	M		8.182	1	1	2	0	27	269	336	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06825	AN5710.1	AO070324000150	Cytosolic sorting protein GGA2/TOM1	U		0.495	1	1	1	0	36	46	51	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		1.424	2	2	2	0	45	181	9	101	0		
652	CTCTCCTTCTCCCC		up	up	69.m14857	AN5740.1	AO070341000019	Ras-related small GTPase, Rho type				3	1	4	0	257	189	225	83	0		
652	CTCTCCTTCTCCCC		up	up	69.m14855	AN5758.1	AO070341000017	Guanine nucleotide exchange factor	U		0.495	3	1	1	0	76	157	114	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				1	3	3	0	119	26	73	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m18963	AN5835.1	AO070260000010	Glycine/serine hydroxymethyltransferase	E		4.273	1	1	1	0	316	422	452	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19247	AN5884.1	AO070245000024	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F		2.123	2	1	1	0	157	112	144	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19202	AN5929.1	AO070340000354	Calcium-responsive transcription coactivator	K		2.843	2	2	1	0	137	335	203	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19952	AN5931.1	AO070340000344	ATP-dependent RNA helicase	A		3.918	2	3	3	0	163	68	64	111	1		
652	CTCTCCTTCTCCCC		up	up	72.m19141	AN5999.1	AO070340000277	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				1	1	1	0	229	171	254	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19133	AN6010.1	AO070340000269	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	O		1.311	3	3	2	0	125	371	325	149	0		
652	CTCTCCTTCTCCCC		up	up	72.m19936	AN6017.1	AO070340000258	Translation initiation factor 3, subunit g (eIF-3g)	J		1.424	3	1	3	0	146	126	343	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		1.311	1	3	2	0	112	162	170	140	0		
652	CTCTCCTTCTCCCC		up	up	72.m19041	AN6119.1	AO070340000085	Zinc carboxypeptidase				1	1	1	0	6	410	476	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				2	4	4	0	449	42	8	386	1		
652	CTCTCCTTCTCCCC		up	up	72.m19434	AN6221.1	AO070304000053	GATA-4/5/6 transcription factors	K		2.843	2	1	1	0	37	372	447	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	72.m19420	AN6233.1	AO070304000087	Molecular chaperone (DnaJ superfamily)	O		1.311	1	2	1	0	102	441	24			No EST	No EST
652	CTCTCCTTCTCCCC		up	down	72.m19414	AN6243.1	AO070304000097	MAPK related serine/threonine protein kinase	T		0.026	1	1	2	0	27	157	80			No EST	No EST
652	CTCTCCTTCTCCCC		up	down	72.m19980	AN6247.1	AO070304000102	predicted protein [Neurospora crassa]				2	2	1	0	76	17	252			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		0.026	2	1	2	0	482	17	15	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19981	AN6254.1	AO070304000034	Mitochondrial oxoglutarate/malate carrier proteins	C	1	0.006	1	1	1	0	47	103	190	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19363	AN6277.1	AO070304000003	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)				2	4	2	0	187	126	212	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	62.m03075	AN6487.1	AO070222000002	Aspartyl protease	O		1.311	1	1	1	0	106	153	117			58	0
652	CTCTCCTTCTCCCC		up	up	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	1	0.006	2	1	1	0	230	53	46	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03135	AN6538.1	AO070270000046	LRR-containing protein				3	4	4	0	297	156	128	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03155	AN6568.1	AO070326000011	Uncharacterized conserved protein				1	2	1	0	92	48	230	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03158	AN6578.1	AO070326000025	Gluconate transport-inducing protein	TG		0.0264658986385493 4.0708802464128	2	1	1	0	172	178	294	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03177	AN6588.1	AO070326000036					4	2	2	0	426	20	32	414	1		
652	CTCTCCTTCTCCCC		up	up	62.m03234	AN6639.1	AO070326000091	Uncharacterized protein involved in propionate catabolism				3	1	2	0	14	242	217	21	0		
652	CTCTCCTTCTCCCC		up	up	62.m03250	AN6650.1	AO070269000001	Citrate synthase	C	1	0.006	1	2	1	0	43	358	334	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03251	AN6651.1	AO070269000002	ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	EJ		4.27325694043449 1.42402407718168	1	1	1	0	17	231	317	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03302	AN6669.1	AO070321000010	Predicted transporter (major facilitator superfamily)				3	2	2	0	82	388	409	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15289	AN6828.1	AO070314000111	Nucleolar GTPase/ATPase p130	Y		1.553	1	2	1	0	115	29	44	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19777	AN7287.1	AO070297000028	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	1	0.006	2	2	3	1	146	61	77	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	72.m19727	AN7350.1	AO070278000050	FOG: RRM domain				6	2	2	0	59	167	222			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	57.m05909	AN7438.1	AO070229000006	Thyroid hormone receptor-associated coactivator complex component (TRAP170)	K		2.843	1	1	2	1	36	466	248	No EST	No EST		

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652	CTCTCCTTCTCCCC		up	up	57.m05873	AN7471.1	AO070287000055	Predicted carbohydrate kinase, contains PfkB domain				1	1	2	0	86	37	53	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05872	AN7472.1	AO070287000054	Oligosaccharyltransferase, alpha subunit (ribophorin I)	O		1.311	1	1	2	0	59	51	52	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	57.m05855	AN7474.1	AO070287000028	RNA-binding protein (contains RRM and Pumilio-like repeats)				1	1	1	0	165	146	171			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	57.m05861	AN7480.1	AO070287000037	FOG: RRM domain				2	2	3	0	46	139	294	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	57.m05838	AN7501.1	AO070287000012	LisH motif-containing protein	Z		6.542	2	2	3	1	119	152	98	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19589	AN7570.1	AO070343000416	Alpha tubulin	Z		6.542	1	1	1	0	104	362	383	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	72.m19615	AN7597.1	AO070343000314	Sexual differentiation process protein ISP4	T		0.026	1	2	1	0	193	216	314	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	72.m19650	AN7609.1	AO070343000267	Mitochondrial/chloroplast DNA-directed RNA polymerase RPO41, provides primers for DNA replication-initiation	KL		2.84315481300744 1.36078872407156	2	1	1	0	221	32	221			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	72.m19651	AN7610.1	AO070343000266	putative transcription factor [Emericella nidulans]				3	1	3	0	224	160	153	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15723	AN7697.1	AO070325000104	Sensory transduction histidine kinase	T		0.026	3	1	1	0	135	10	10	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15748	AN7721.1	AO070325000136	Transport protein Sec61, alpha subunit	UO		0.494755743050251 1.31149382861186	2	2	3	0	121	84	81	106	1		
652	CTCTCCTTCTCCCC		up	up	71.m15792	AN7760.1	AO070286000007	Amphiphysin	U		0.495	1	1	3	0	229	205	312	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	52.m03642	AN7950.1	AO070342000340	Cellobiohydrolase A (1,4-beta-cellobiosidase A)	G		4.071	1	1	1	0	128	323	433	79	0		
652	CTCTCCTTCTCCCC		up	up	53.m03851	AN7996.1	AO070322000049	hypothetical protein ((AL513410) hypothetical protein [Neurospora crassa])				2	2	1	0	382	364	2	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03908	AN8038.1	AO070330000008	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A		3.918	2	1	1	0	282	253	99	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		4.071	2	1	3	0	133	319	55	146	0		
652	CTCTCCTTCTCCCC		up	up	53.m04098	AN8053.1	AO070322000147	Inositol polyphosphate 5-phosphatase and related proteins	U		0.495	1	1	3	0	424	91	186	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03888	AN8055.1	AO070322000145	RNA-binding Ran Zn-finger protein and related proteins				2	5	3	1	48	88	266	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03827	AN8117.1	AO070322000025	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme	I		3.772	2	1	4	0	214	241	246	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03757	AN8216.1	AO070310000096	Nucleoside diphosphate kinase	F		2.123	1	1	1	0	65	168	132	111	0		
652	CTCTCCTTCTCCCC		up	up	53.m03738	AN8231.1	AO070310000077	S-adenosylmethionine decarboxylase	T		0.026	1	1	3	1	253	107	77	9	0		
652	CTCTCCTTCTCCCC		up	up	53.m04128	AN8235.1	AO070310000073	predicted protein [Neurospora crassa]				1	3	2	0	309	251	75	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				1	2	2	0	82	193	166	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	53.m03692	AN8269.1	AO070310000033	Molecular chaperone (HSP90 family)	O		1.311	1	5	2	0	109	27	178	336	1		
652	CTCTCCTTCTCCCC		up	up	53.m03687	AN8273.1	AO070310000028	Ubiquinol cytochrome c reductase, subunit QCR2	C	1	0.006	2	1	2	0	26	122	10	120	0		
652	CTCTCCTTCTCCCC		up	up	53.m03686	AN8274.1	AO070310000027	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	1	0.006	3	2	1	1	241	276	263	158	0		
652	CTCTCCTTCTCCCC		up	up	53.m03681	AN8280.1	AO070310000020	Long-chain acyl-CoA synthetases (AMP-forming)	I		3.772	2	1	1	0	275	227	92	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	65.m07461	AN8285.1	AO070277000003	Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7	DKL		2.88952327378684 2.84315481300744 1.36078872407156	1	1	1	0	128	109	485			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	55.m03152	AN8655.1	AO070296000035	hypothetical protein [Neurospora crassa]				1	1	3	0	145	169	178	260	1		
652	CTCTCCTTCTCCCC		up	up	62.m03407	AN8667.1	AO070269000068	GATA-4/5/6 transcription factors	K		2.843	1	1	2	0	191	489	329	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		2.843	1	3	3	1	121	234	358	157	0		
652	CTCTCCTTCTCCCC		up	up	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		4.071	1	2	3	0	496	47	51	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03388	AN8683.1	AO070315000103	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ		5.47872319697198 1.7655108524824	1	1	2	0	274	184	125	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03339	AN8741.1	AO070250000041	FOG: Zn-finger				2	2	2	0	66	249	293	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	62.m03324	AN8751.1	AO070250000011	NDR and related serine/threonine kinases				2	1	2	0	50	15	29	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15631	AN8820.1	AO070276000022	Serine-threonine phosphatase 2B, catalytic subunit				1	1	1	0	247	111	253	338	1		
652	CTCTCCTTCTCCCC		up	up	71.m15956	AN8824.1	AO070271000057	Translation initiation factor 6 (eIF-6)	J		1.424	1	1	2	0	180	113	178	129	1		
652	CTCTCCTTCTCCCC		up	up	71.m15967	AN8836.1	AO070271000042	p21-activated serine/threonine protein kinase	T		0.026	2	1	3	0	310	337	32	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	71.m15980	AN8846.1	AO070271000030	Protein involved in beta-1,3-glucan synthesis	G		4.071	3	2	5	0	191	129	166	355	1		
652	CTCTCCTTCTCCCC		up	up	71.m15984	AN8849.1	AO070271000027	Uncharacterized conserved protein				1	1	2	0	156	159	89	No EST	No EST		
652	CTCTCCTTCTCCCC		up	up	56.m02292	AN8881.1	AO070293000011	Mitochondrial carnitine-acylcarnitine carrier protein	C	1	0.006	1	2	3	0	62	230	152	334	1		
652	CTCTCCTTCTCCCC		up	up	56.m02296	AN8884.1	AO070293000016	hypothetical protein [Neurospora crassa]				1	1	1	0	363	115	140	197	1		
652	CTCTCCTTCTCCCC		up	up	66.m04541	AN9083.1	AO070332000196	Adenine phosphoribosyl transferases	F		2.123	4	2	4	0	4	438	438	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	66.m04545	AN9087.1	AO070332000190	Calcium-responsive transcription coactivator	K		2.843	1	1	2	0	111	337	96			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
652	CTCTCCTTCTCCCC		up	down	66.m04605	AN9147.1	AO070332000117	von Willebrand factor and related coagulation proteins	V		10.261	1	1	1	0	165	172	166			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	66.m04586	AN9149.1	AO070332000147	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain				3	2	2	0	81	2	312	No EST	No EST		
652	CTCTCCTTCTCCCC		up	down	59.m09152	AN9446.1	AO070327000156	Pantothenate kinase PanK and related proteins	H		4.326	1	2	1	0	305	320	286			No EST	No EST
652	CTCTCCTTCTCCCC		up	up	54.m06486	AN9448.1	AO070334000061	predicted protein [Neurospora crassa]				2	1	1	0	255	21	15	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15347	AN0071.1	AO070314000160	Splicing coactivator SRm160/300, subunit SRm300	A		4.832	1	1	1	0	123	359	387	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15354	AN0076.1	AO070311000140	5'-3' exonuclease	L		3.011	1	1	1	0	83	147	3	49	0		
698	CCCTCCATCTCCA		up	up	71.m15396	AN0117.1	AO070311000104	Histone H4	B		4.540	1	2	1	0	51	185	238	No EST	No EST		
698	CCCTCCATCTCCA		up	up	54.m06397	AN0357.1	AO070318000033	Cytochrome c1	C		0.033	1	1	1	1	69	208	201	No EST	No EST		
698	CCCTCCATCTCCA		up	up	54.m06664	AN0410.1	AO070294000082	Serine/threonine specific protein phosphatase PP1, catalytic subunit	T		0.596	3	2	1	0	28	67	368	No EST	No EST		
698	CCCTCCATCTCCA		up	down	54.m06624	AN0433.1	AO070338000284	60S ribosomal protein L18A	J		2.999	1	1	1	0	19	19	19			No EST	No EST
698	CCCTCCATCTCCA		up	up	69.m15270	AN0575.1	AO070272000054	Calmodulin-binding protein CRAG, contains DENN domain	T		0.596	2	3	2	0	417	51	115	117	1		
698	CCCTCCATCTCCA		up	up	69.m15264	AN0585.1	AO070280000007	Actin regulatory protein (Wiskott-Aldrich syndrome protein)	TZ		0.596443066422955 6.16407457777101	1	2	1	0	555	72	127	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15292	AN0689.1	AO070343000524	acetate regulatory DNA binding protein FacB [Emericella nidulans]				1	1	1	0	307	254	211	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15361	AN0747.1	AO070343000435	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O		2.492	1	1	2	0	25	177	216	29	0		
698	CCCTCCATCTCCA		up	up	70.m15785	AN0775.1	AO070316000063	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.033	1	1	1	0	105	159	275	87	0		
698	CCCTCCATCTCCA		up	up	70.m15426	AN0824.1	AO070255000021	Short-chain acyl-CoA dehydrogenase	I		3.241	1	2	2	0	84	84	85	25	0		
698	CCCTCCATCTCCA		up	up	70.m15437	AN0837.1	AO070255000006	Splicing coactivator SRm160/300, subunit SRm300	A		4.832	2	1	1	0	26	127	458	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15456	AN0870.1	AO070320000023	Mitochondrial phosphate carrier protein	C		0.033	2	1	1	0	63	446	373	15	0		
698	CCCTCCATCTCCA		up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		1.63418710566978 1.63987537586578	1	2	2	0	89	135	177	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15540	AN0932.1	AO070320000123	Pyridine nucleotide-disulphide oxidoreductase	Q		4.522	1	1	2	0	321	141	243	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15609	AN0973.1	AO070320000174	FOG: Zn-finger				3	2	2	0	161	151	148	103	0		
698	CCCTCCATCTCCA		up	up	70.m15137	AN1094.1	AO070285000053	NADH-dehydrogenase (ubiquinone)	C		0.033	3	1	2	0	33	377	24	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15136	AN1096.1	AO070285000048	von Willebrand factor and related coagulation proteins	V		4.375	1	2	1	0	78	449	95	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15118	AN1117.1	AO070331000109	Putative cargo transport protein ERV29	U		1.640	1	1	1	0	136	256	280	192	0		
698	CCCTCCATCTCCA		up	up	70.m15059	AN1162.1	AO070331000152	Elongation factor 1 beta/delta chain	K		5.011	1	3	2	0	50	98	112	17	0		
698	CCCTCCATCTCCA		up	down	70.m15038	AN1179.1	AO070331000176	Vacuolar import and degradation protein	U		1.640	1	2	2	0	105	78	55			158	1
698	CCCTCCATCTCCA		up	up	70.m14906	AN1325.1	AO070303000088	Protein interacting with poly(A)-binding protein	A		4.832	2	1	2	0	107	162	91	No EST	No EST		
698	CCCTCCATCTCCA		up	down	70.m14875	AN1355.1	AO070237000005	Permease of the drug/metabolite transporter (DMT) superfamily				1	1	2	0	24	116	50			No EST	No EST
698	CCCTCCATCTCCA		up	up	70.m14873	AN1357.1	AO070237000003	Phosphorylcholine transferase/cholinephosphate cytidylyltransferase	I		3.241	1	1	3	0	135	387	148	No EST	No EST		
698	CCCTCCATCTCCA		up	up	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		0.596	3	2	3	0	156	290	0	400	1		
698	CCCTCCATCTCCA		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				2	2	3	0	294	122	176	189	1		
698	CCCTCCATCTCCA		up	up	55.m02990	AN1484.1	AO070334000191	Valyl-tRNA synthetase	J		2.999	1	1	2	0	33	243	75	102	0		
698	CCCTCCATCTCCA		up	down	58.m07773	AN1697.1	AO070305000021	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	A		4.832	1	1	1	0	90	15	317			No EST	No EST
698	CCCTCCATCTCCA		up	up	57.m05369	AN1800.1	AO070335000095	Signal transduction histidine kinase	T		0.596	1	1	1	0	41	391	295	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m07667	AN1844.1	AO070292000063	palFp [Emericella nidulans]				1	1	1	0	40	233	485	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m07665	AN1846.1	AO070292000059					1	1	1	0	212	102	229	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05742	AN1876.1	AO070341000183	Predicted membrane protein, contains two CBS domains				1	1	2	0	18	369	341	No EST	No EST		
698	CCCTCCATCTCCA		up	down	58.m07346	AN1950.1	AO070342000218	conserved hypothetical protein [Neurospora crassa]				3	1	1	0	55	214	212			496	1
698	CCCTCCATCTCCA		up	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		2.492	1	2	1	0	259	101	140	173	1		
698	CCCTCCATCTCCA		up	up	57.m05768	AN2068.1	AO070341000217	Vigilin	I		3.241	4	3	2	0	47	26	39	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19691	AN2150.1	AO070343000199	Prolyl-tRNA synthetase	J		2.999	1	1	1	0	25	45	12	66	1		
698	CCCTCCATCTCCA		up	up	72.m20002	AN2154.1	AO070343000203	hypothetical protein [Neurospora crassa]				2	1	2	0	333	413	49	No EST	No EST		
698	CCCTCCATCTCCA		up	up	69.m14881	AN2190.1	AO070247000014	Predicted methyltransferase				1	1	1	0	282	4	271	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15846	AN2219.1	AO070326000185	related to ahmp1 protein [MIPS] [Neurospora crassa]				1	1	1	0	12	288	6	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15923	AN2278.1	AO070295000054	Chromatin remodeling complex SWI/SNF, component SWI2 and related ATPases (DNA/RNA helicase superfamily)	BK		4.53955386654454 5.01135951213957	2	2	1	1	347	85	102	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
698	CCCTCCATCTCCA		up	up	71.m15946	AN2297.1	AO070295000078	hypothetical protein [Neurospora crassa]				1	2	1	0	52	119	449	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		0.033	2	3	2	1	57	300	507	104	0		
698	CCCTCCATCTCCA		up	up	63.m00601	AN2344.1	AO070343000375	Permease of the major facilitator superfamily	G		0.139	1	1	1	0	271	37	81	No EST	No EST		
698	CCCTCCATCTCCA		up	up	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C		0.033	3	2	2	0	5	256	161	187	0		
698	CCCTCCATCTCCA		up	down	54.m06687	AN2744.1	AO070338000227	predicted protein [Neurospora crassa]				1	1	1	0	110	189	158			No EST	No EST
698	CCCTCCATCTCCA		up	up	59.m08697	AN2855.1	AO070338000169	FOG: Zn-finger				3	2	2	0	88	164	166	180	1		
698	CCCTCCATCTCCA		up	up	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		4.540	2	2	2	0	326	380	139	No EST	No EST		
698	CCCTCCATCTCCA		up	up	59.m08724	AN2875.1	AO070338000136	Fructose 1,6-bisphosphate aldolase	G		0.139	1	3	4	0	366	180	99	43	0		
698	CCCTCCATCTCCA		up	up	59.m09058	AN2936.1	AO070337000172	Alpha-mannosidase	G		0.139	2	1	1	0	133	306	279	No EST	No EST		
698	CCCTCCATCTCCA		up	up	59.m09023	AN2989.1	AO070337000133	FOG: RRM domain				1	2	3	0	93	394	13	183	0		
698	CCCTCCATCTCCA		up	up	59.m08957	AN3058.1	AO070337000016	Glycine/serine hydroxymethyltransferase	E		4.573	1	2	2	0	77	394	136	66	0		
698	CCCTCCATCTCCA		up	up	59.m08959	AN3059.1	AO070337000014	Phosphoglycerate mutase	G		0.139	1	1	2	1	223	14	19	25	1		
698	CCCTCCATCTCCA		up	up	59.m08662	AN3085.1	AO070334000123	Predicted phosphatase				3	1	1	0	160	488	103	166	0		
698	CCCTCCATCTCCA		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				3	3	1	1	210	6	302	106	1		
698	CCCTCCATCTCCA		up	up	59.m08628	AN3110.1	AO070303000041	3-phosphoinositide-dependent protein kinase (PDK1)	T		0.596	2	1	2	0	45	107	157	391	1		
698	CCCTCCATCTCCA		up	up	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				3	1	2	0	239	124	355	No EST	No EST		
698	CCCTCCATCTCCA		up	up	59.m08584	AN3142.1	AO070303000002	Nucleolar GTPase/ATPase p130	Y		1.634	1	1	1	0	320	230	211	No EST	No EST		
698	CCCTCCATCTCCA		up	up	52.m03702	AN3308.1	AO070330000181	Alpha-amylase	G		0.139	2	1	1	0	215	284	140	No EST	No EST		
698	CCCTCCATCTCCA		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		3.241	2	1	3	0	15	70	100	298	1		
698	CCCTCCATCTCCA		up	up	58.m07379	AN3581.1	AO070342000168	Thioredoxin reductase	O		2.492	3	1	1	1	62	111	142	163	1		
698	CCCTCCATCTCCA		up	up	58.m07398	AN3600.1	AO070342000153	hypothetical protein [Neurospora crassa]				1	2	1	0	282	96	228	276	1		
698	CCCTCCATCTCCA		up	up	69.m15419	AN3712.1	AO070341000341	Predicted hydrolase related to dienelactone hydrolase				2	1	1	0	164	306	366	68	0		
698	CCCTCCATCTCCA		up	up	57.m05667	AN3815.1	AO070311000013	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z		6.164	3	2	2	0	282	11	13	No EST	No EST		
698	CCCTCCATCTCCA		up	down	54.m06570	AN4042.1	AO070328000135	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI		4.52227748369821 3.24079585970098	1	1	2	0	48	87	18			410	1
698	CCCTCCATCTCCA		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		2.999	6	5	4	1	116	170	226	96	0		
698	CCCTCCATCTCCA		up	up	54.m06782	AN4234.1	AO070234000012	Phosphoglucomutase/phosphomannomutase	G		0.139	1	1	1	0	221	184	121	77	0		
698	CCCTCCATCTCCA		up	up	65.m07433	AN4259.1	AO070277000032	Uncharacterized conserved protein, contains PCI domain				3	1	1	0	13	160	140	10	0		
698	CCCTCCATCTCCA		up	up	58.m08998	AN4378.1	AO070261000021	Fucose permease	G		0.139	2	1	1	0	297	368	161	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m07927	AN4394.1	AO070261000039					2	2	1	0	29	48	31	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				2	5	1	0	20	98	91	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		4.573	4	1	4	0	28	226	235	66	0		
698	CCCTCCATCTCCA		up	up	58.m07847	AN4462.1	AO070305000113	Pyruvate carboxylase	C		0.033	2	3	3	0	122	35	19	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05648	AN4483.1	AO070311000032	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		0.596	3	2	1	0	46	382	469	No EST	No EST		
698	CCCTCCATCTCCA		up	down	57.m05642	AN4489.1	AO070304000089	putative transcriptional activator protein [Schizosaccharomyces pombe]				1	1	0	0	38	67	113			No EST	No EST
698	CCCTCCATCTCCA		up	down	57.m05543	AN4632.1	AO070340000375	FOG: FHA domain	T		0.596	1	1	1	0	315	248	219			No EST	No EST
698	CCCTCCATCTCCA		up	up	71.m15674	AN4691.1	AO070284000047	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQ		3.24079585970098 4.52227748369821	1	1	2	0	281	155	19	No EST	No EST		
698	CCCTCCATCTCCA		up	up	59.m09466	AN4859.1	AO070329000143	Plasma membrane H+-transporting ATPase	P		6.317	2	2	2	1	110	260	344	103	0		
698	CCCTCCATCTCCA		up	up	59.m08876	AN4973.1	AO070288000039	predicted protein [Neurospora crassa]				2	1	2	0	40	220	208	No EST	No EST		
698	CCCTCCATCTCCA		up	up	59.m09404	AN4978.1	AO070288000045	Alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)	A		4.832	1	1	1	0	342	59	79	329	1		
698	CCCTCCATCTCCA		up	up	59.m08894	AN4991.1	AO070288000071	aureobasidin-resistance protein; AurA [Aspergillus nidulans]				2	1	3	0	52	111	48	420	1		
698	CCCTCCATCTCCA		up	up	59.m08680	AN5026.1	AO070338000185	PHD finger protein AF10				1	2	3	0	390	214	37	No EST	No EST		
698	CCCTCCATCTCCA		up	up	54.m06902	AN5122.1	AO070291000057	Adenylate kinase	F		7.057	2	2	2	0	78	191	91	No EST	No EST		
698	CCCTCCATCTCCA		up	up	69.m14907	AN5210.1	AO070337000270	Pyruvate kinase	G		0.139	2	1	2	0	69	428	404	60	0		
698	CCCTCCATCTCCA		up	up	69.m15489	AN5445.1	AO070333000112					2	2	1	0	280	275	163	No EST	No EST		
698	CCCTCCATCTCCA		up	up	69.m15483	AN5449.1	AO070239000028	Arylsulfatase A and related enzymes	P		6.317	5	2	1	0	26	228	236	No EST	No EST		
698	CCCTCCATCTCCA		up	up	58.m07480	AN5534.1	AO070328000057	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.033	1	2	2	0	261	179	127	No EST	No EST		
698	CCCTCCATCTCCA		up	up	65.m07414	AN5688.1	AO070309000104	Cyclopropane fatty acid synthase and related methyltransferases	M		9.070	1	1	1	0	36	267	336	No EST	No EST		
698	CCCTCCATCTCCA		up	down	65.m07417	AN5693.1	AO070309000108	Uncharacterized conserved protein				1	1	1	0	196	332	19			319	0
698	CCCTCCATCTCCA		up	up	54.m06846	AN5726.1	AO070324000125	FOG: Zn-finger				2	2	1	0	159	41	85	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				2	3	2	0	83	29	379	No EST	No EST		
698	CCCTCCATCTCCA		up	down	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				1	2	3	0	357	71	29			28	0

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
698	CCCTCCATCTCCA		up	up	72.m19247	AN5884.1	AO070245000024	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F		7.057	1	1	1	0	161	116	142	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19245	AN5885.1	AO070245000022	Glycogen synthase	G		0.139	1	1	2	0	111	59	3	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19244	AN5886.1	AO070245000021	3-isopropylmalate dehydratase (aconitase superfamily)	E		4.573	1	1	1	0	188	338	290	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19237	AN5893.1	AO070245000013	G protein signaling regulators	T		0.596	2	3	2	0	26	31	36	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19952	AN5931.1	AO070340000344	ATP-dependent RNA helicase	A		4.832	1	2	2	0	160	72	68	111	1		
698	CCCTCCATCTCCA		up	up	72.m19192	AN5975.1	AO070340000331	Mannitol-1-phosphate/altronate dehydrogenases	G		0.139	2	1	1	0	279	356	206	114	0		
698	CCCTCCATCTCCA		up	up	72.m19109	AN6050.1	AO070340000215					2	1	1	0	465	50	177	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19094	AN6059.1	AO070340000190	HVA22/DP1 gene product-related proteins	V		4.375	1	1	2	0	355	205	99	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		2.492	1	1	2	0	115	304	170	140	0		
698	CCCTCCATCTCCA		up	down	72.m19085	AN6091.1	AO070340000149	predicted protein [Neurospora crassa]				2	1	2	0	177	94	352			74	0
698	CCCTCCATCTCCA		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				2	1	2	0	446	84	45	386	1		
698	CCCTCCATCTCCA		up	up	72.m19978	AN6231.1	AO070304000084	Tryptophan synthase beta chain	E		4.573	3	1	2	0	100	420	122	81	0		
698	CCCTCCATCTCCA		up	up	72.m19422	AN6232.1	AO070304000085	Vacuolar H+-ATPase V1 sector, subunit B	C		0.033	1	1	1	0	54	175	233	No EST	No EST		
698	CCCTCCATCTCCA		up	down	72.m19414	AN6243.1	AO070304000097	MAPK related serine/threonine protein kinase	T		0.596	1	1	1	0	27	165	213			No EST	No EST
698	CCCTCCATCTCCA		up	up	72.m19981	AN6254.1	AO070304000034	Mitochondrial oxoglutarate/malate carrier proteins	C		0.033	1	1	1	0	40	106	188	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19368	AN6271.1	AO070304000013	predicted protein [Neurospora crassa]				1	2	1	0	156	212	117	No EST	No EST		
698	CCCTCCATCTCCA		up	up	72.m19363	AN6277.1	AO070304000003	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)				1	2	2	0	184	123	215	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03095	AN6508.1	AO070270000001	Glycogen synthase kinase-3	G		0.139	1	3	2	1	145	38	154	36	0		
698	CCCTCCATCTCCA		up	down	62.m03095	AN6508.1	AO070270000001	Glycogen synthase kinase-3	G		0.139	1	1	2	0	404	323	377			45	0
698	CCCTCCATCTCCA		up	up	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.033	2	3	1	0	143	54	43	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03135	AN6538.1	AO070270000046	LRR-containing protein				2	1	2	0	298	182	132	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03177	AN6588.1	AO070326000036					2	2	4	0	433	74	35	414	1		
698	CCCTCCATCTCCA		up	up	62.m03214	AN6618.1	AO070326000068	Ypt/Rab-specific GTPase-activating protein GYP7 and related proteins	T		0.596	1	1	1	0	329	128	112	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03234	AN6639.1	AO070326000091	Uncharacterized protein involved in propionate catabolism				3	1	2	0	11	275	253	21	0		
698	CCCTCCATCTCCA		up	up	65.m07276	AN6703.1	AO070339000139	Permeases of the major facilitator superfamily	GEP		0.138974198029415 4.57317855211283 6.31669793202208	1	1	1	0	308	350	317	No EST	No EST		
698	CCCTCCATCTCCA		up	up	65.m07257	AN6717.1	AO070339000157	NAD-dependent malate dehydrogenase	C		0.033	2	1	1	0	89	171	140	No EST	No EST		
698	CCCTCCATCTCCA		up	up	71.m15289	AN6828.1	AO070314000111	Nucleolar GTPase/ATPase p130	Y		1.634	1	1	1	0	359	256	41	No EST	No EST		
698	CCCTCCATCTCCA		up	up	52.m03964	AN6941.1	AO070335000169					1	1	3	0	182	303	230	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05873	AN7471.1	AO070287000055	Predicted carbohydrate kinase, contains PfkB domain				1	1	1	0	82	43	86	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05872	AN7472.1	AO070287000054	Oligosaccharyltransferase, alpha subunit (ribophorin I)	O		2.492	1	2	1	0	102	44	50	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05408	AN7650.1	AO070268000006	Rho GTPase-activating protein	TZ		0.596443066422955 6.16407457777101	2	1	1	0	362	163	51	No EST	No EST		
698	CCCTCCATCTCCA		up	up	57.m05936	AN7660.1	AO070268000029	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H		7.524	1	1	2	0	79	198	319	No EST	No EST		
698	CCCTCCATCTCCA		up	down	71.m15729	AN7700.1	AO070325000106	FOG: RRM domain				1	1	1	0	470	204	305			No EST	No EST
698	CCCTCCATCTCCA		up	up	53.m03738	AN8231.1	AO070310000077	S-adenosylmethionine decarboxylase	T		0.596	1	2	1	1	259	105	212	9	0		
698	CCCTCCATCTCCA		up	up	53.m03736	AN8233.1	AO070310000075	Phosphatidylinositol transfer protein SEC14 and related proteins	I		3.241	1	1	2	0	82	256	217	117	0		
698	CCCTCCATCTCCA		up	up	53.m03681	AN8280.1	AO070310000020	Long-chain acyl-CoA synthetases (AMP-forming)	I		3.241	1	1	1	0	84	245	135	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03407	AN8667.1	AO070269000068	GATA-4/5/6 transcription factors	K		5.011	1	2	1	0	194	128	341	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		5.011	1	2	1	1	119	300	432	157	0		
698	CCCTCCATCTCCA		up	up	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		0.139	3	2	1	0	428	18	45	No EST	No EST		
698	CCCTCCATCTCCA		up	up	62.m03343	AN8723.1	AO070315000151	predicted protein [Neurospora crassa]				2	2	2	0	128	158	142	123	0		
698	CCCTCCATCTCCA		up	up	62.m03324	AN8751.1	AO070250000011	NDR and related serine/threonine kinases				4	2	3	0	53	7	29	No EST	No EST		
698	CCCTCCATCTCCA		up	down	71.m15583	AN8787.1	AO070276000074	Nuclear mRNA export factor receptor LOS1/Exportin-t (importin beta superfamily)	YUJ		1.63418710566978 1.63987537586578 2.99910605205111	1	1	1	0	87	135	328			356	1
698	CCCTCCATCTCCA		up	up	71.m15996	AN8858.1	AO070271000015	Transcription factor of the Forkhead/HNF3 family	K		5.011	1	1	1	0	503	14	175	No EST	No EST		

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698	CCCTCCATCTCCA		up	up	56.m02292	AN8881.1	AO070293000011	Mitochondrial carnitine-acylcarnitine carrier protein	C		0.033	2	2	2	1	75	229	152	334	1		
698	CCCTCCATCTCCA		up	up	54.m06486	AN9448.1	AO070334000061	predicted protein [Neurospora crassa]				1	1	2	0	536	29	19	No EST	No EST		
751	ACCGCCTTCC		up	up	54.m06468	AN0275.1	AO070334000082	Cystine transporter Cystinosin	E		2.077	1	1	1	0	185	80	105	No EST	No EST		
751	ACCGCCTTCC		up	up	54.m06464	AN0298.1	AO070334000044	Polyadenylation factor I complex, subunit, Yth1 (CPSF subunit)	A		0.013	1	1	1	0	283	343	173	No EST	No EST		
751	ACCGCCTTCC		up	up	70.m15804	AN0834.1	AO070255000011	Molecular chaperone (DnaJ superfamily)	O		0.153	1	1	1	1	283	204	254	No EST	No EST		
751	ACCGCCTTCC		up	up	70.m15196	AN1038.1	AO070336000073	Putative transmembrane protein				1	1	1	0	153	126	163	No EST	No EST		
751	ACCGCCTTCC		up	up	70.m15175	AN1059.1	AO070218000002	Carnitine O-acyltransferase CPT2/YAT1	I		3.376	1	1	1	1	89	386	437	No EST	No EST		
751	ACCGCCTTCC		up	down	70.m14988	AN1231.1	AO070331000243	DNA polymerase IV (family X)	L		4.385	2	1	1	1	64	303	376			No EST	No EST
751	ACCGCCTTCC		up	up	70.m14844	AN1379.1	AO070243000010	mRNA export protein (contains WD40 repeats)	A		0.013	1	1	1	0	298	84	142	135	1		
751	ACCGCCTTCC		up	up	58.m07724	AN1638.1	AO070299000044	Puromycin-sensitive aminopeptidase and related aminopeptidases	EO		2.07748989269454 0.152930127007461	1	1	1	0	209	148	125	No EST	No EST		
751	ACCGCCTTCC		up	up	72.m19694	AN2147.1	AO070343000196	rRNA processing protein Rrp5	A		0.013	1	1	2	0	140	68	10	No EST	No EST		
751	ACCGCCTTCC		up	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		1.624	1	1	1	1	441	38	43	No EST	No EST		
751	ACCGCCTTCC		up	up	59.m09061	AN2933.1	AO070337000174	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	BT		2.3361163957962 0.239446389529943	1	1	1	0	279	88	101	No EST	No EST		
751	ACCGCCTTCC		up	up	69.m15728	AN3726.1	AO070342000289	RAN guanine nucleotide release factor	T		0.239	2	1	1	0	13	262	319	233	0		
751	ACCGCCTTCC		up	up	65.m07368	AN3756.1	AO070309000050	20S proteasome, regulatory subunit beta type PSMB6/PSMB9/PRE3	O		0.153	1	1	1	1	217	29	32	No EST	No EST		
751	ACCGCCTTCC		up	up	54.m06583	AN4007.1	AO070328000146	Succinyl-CoA:alpha-ketoacid-CoA transferase	C		1.801	1	1	1	1	337	180	192	No EST	No EST		
751	ACCGCCTTCC		up	up	54.m06790	AN4226.1	AO070234000023	Sof1-like rRNA processing protein (contains WD40 repeats)	A		0.013	1	1	1	0	69	61	21	55	0		
751	ACCGCCTTCC		up	up	58.m07981	AN4346.1	AO070240000018	Nucleolar RNA-binding protein NIFK				1	1	1	1	22	16	46	24	1		
751	ACCGCCTTCC		up	up	58.m07904	AN4415.1	AO070273000036	Holocytochrome c synthase/heme-lyase	CO		1.80141857718525 0.152930127007461	1	1	2	0	133	39	105	No EST	No EST		
751	ACCGCCTTCC		up	up	59.m09126	AN4850.1	AO070327000106	RNA-binding protein RBM5 and related proteins, contain G-patch and RRM domains				1	1	1	0	84	222	38	No EST	No EST		
751	ACCGCCTTCC		up	up	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				2	1	1	1	96	131	157	345	1		
751	ACCGCCTTCC		up	down	72.m19268	AN5866.1	AO070308000130	Arylalkylamine N-acetyltransferase				1	1	1	1	55	70	82			No EST	No EST
751	ACCGCCTTCC		up	up	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		0.239	1	1	1	0	322	204	224	No EST	No EST		
751	ACCGCCTTCC		up	up	72.m19497	AN6363.1	AO070279000049	Serine/threonine protein kinase involved in cell cycle control	TD		0.239446389529943 2.99677563026662	1	1	1	1	126	22	36	No EST	No EST		
751	ACCGCCTTCC		up	up	65.m07285	AN6698.1	AO070339000130	Uncharacterized conserved protein				1	1	1	0	79	378	282	32	0		
751	ACCGCCTTCC		up	up	57.m05423	AN7659.1	AO070268000028	ATP-dependent RNA helicase	A		0.013	1	1	1	1	376	23	22	172	1		
751	ACCGCCTTCC		up	up	53.m03900	AN8044.1	AO070292000105	N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	O		0.153	2	1	1	0	345	365	103	No EST	No EST		
751	ACCGCCTTCC		up	up	53.m03925	AN8072.1	AO070330000030	hypothetical protein B13N20.140 [imported] - Neurospora crassa				1	1	1	0	76	25	24	No EST	No EST		
751	ACCGCCTTCC		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		1.624	1	1	1	1	236	237	312	157	0		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	70.m15166	AN1066.1	AO070218000011	hypothetical protein [Aspergillus fumigatus]				1	1	1	0	214	66	120	121	1		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	70.m14867	AN1362.1	AO070243000002	hypothetical protein [Neurospora crassa]				1	1	1	1	224	22	19	93	1		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	58.m07780	AN1713.1	AO070305000029	Predicted esterase of the alpha-beta hydrolase superfamily				1	1	1	0	303	45	24	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	down	71.m15826	AN2237.1	AO070326000136	Carboxypeptidase C (cathepsin A)	E		2.845	1	1	1	1	263	359	382			58	0
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	67.m02931	AN3223.1	AO070330000073	Pyrophosphate-dependent phosphofructo-1-kinase	G		1.662	3	1	1	1	171	285	290	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	58.m09011	AN4299.1	AO070207000001	conserved hypothetical protein [Neurospora crassa]				1	1	1	0	154	224	302	52	0		

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813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	59.m09399	AN4914.1	AO070338000033	Acetate kinase	C		1.517	1	1	1	0	1	85	155	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	59.m08869	AN4966.1	AO070288000031	Uncharacterized conserved protein				1	1	1	0	87	237	244	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	72.m19071	AN6079.1	AO070340000129	Predicted RNA-binding protein				1	1	1	1	95	149	168	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	62.m03178	AN6589.1	AO070326000037	Glycosylphosphatidylinositol anchor synthesis protein	T		1.648	1	1	1	1	478	26	23	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	53.m03745	AN8228.1	AO070310000083	Predicted ATPase, nucleotide-binding	D		1.020	1	1	1	1	206	175	81	No EST	No EST		
813	ACGTCAC	yATF-B (KWCGTCA) [yeast_motifs_all];	up	up	62.m03470	AN8698.1	AO070315000125	Actin-related protein Arp2/3 complex, subunit ARPC4	Z		0.932	1	1	1	0	21	170	167	52	0		
843	TGAGCCTCGG		up	up	71.m15403	AN0122.1	AO070311000090	ATP-dependent Lon protease, bacterial type	O		2.652	1	1	1	1	219	89	58	78	0		
843	TGAGCCTCGG		up	up	54.m06472	AN0271.1	AO070334000077	dUTPase	F		0.948	1	1	1	0	116	21	19	42	1		
843	TGAGCCTCGG		up	up	54.m06470	AN0273.1	AO070334000079	FOG: Zn-finger				1	1	1	0	337	169	390	No EST	No EST		
843	TGAGCCTCGG		up	up	70.m15321	AN0732.1	AO070343000493	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)				1	1	1	0	476	81	59	No EST	No EST		
843	TGAGCCTCGG		up	up	70.m14974	AN1246.1	AO070223000009	3-phosphoglycerate kinase	G		2.478	1	1	1	1	326	62	169	12	0		
843	TGAGCCTCGG		up	up	55.m03268	AN1524.1	AO070334000242	Methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase	H		1.241	1	1	1	0	220	281	19	No EST	No EST		
843	TGAGCCTCGG		up	up	55.m03061	AN1543.1	AO070339000311	Fumarate reductase, flavoprotein subunit	C		0.612	1	1	1	1	188	203	117	43	0		
843	TGAGCCTCGG		up	up	71.m15945	AN2296.1	AO070295000077	RFX family transcription factor	K		2.190	1	1	1	0	16	93	51	No EST	No EST		
843	TGAGCCTCGG		up	up	59.m08450	AN2529.1	AO070300000122	Enoyl-CoA isomerase	I		0.624	1	1	1	1	284	174	157	No EST	No EST		
843	TGAGCCTCGG		up	up	72.m18955	AN5828.1	AO070260000018	Cytochrome b5	C		0.612	1	1	1	0	196	64	59	No EST	No EST		
843	TGAGCCTCGG		up	up	72.m19960	AN5916.1	AO070340000370	Enoyl-CoA hydratase/carnithine racemase	I		0.624	1	1	1	0	195	50	63	14	0		
843	TGAGCCTCGG		up	up	62.m03428	AN6555.1	AO070270000059	Alpha/beta hydrolase				1	1	1	0	48	84	335	No EST	No EST		
843	TGAGCCTCGG		up	down	62.m03225	AN6629.1	AO070326000081	60S ribosomal protein L14	J		3.790	1	1	1	1	9	8	13			122	1
843	TGAGCCTCGG		up	up	72.m19794	AN7256.1	AO070297000012	25D9-5p [Aspergillus fumigatus]				1	1	1	1	128	142	194	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	70.m15019	AN1200.1	AO070331000206	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein	JK		0.698254065528167 2.40236233920571	3	1	2	1	71	110	64	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	59.m09033	AN2981.1	AO070337000141	Glucose-6-phosphate 1-dehydrogenase	G		2.754	1	1	1	1	143	499	116	121	0		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	69.m14970	AN3955.1	AO070341000068	Uncharacterized conserved protein				1	1	1	0	5	77	5	442	1		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	58.m07362	AN4163.1	AO070342000193	G protein beta subunit-like protein	T		2.733	1	1	1	1	42	136	312	77	0		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	69.m14951	AN4169.1	AO070341000094	hypothetical protein [Neurospora crassa]				1	1	1	0	124	79	331	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	57.m05642	AN4489.1	AO070304000089	putative transcriptional activator protein [Schizosaccharomyces pombe]				1	1	1	0	352	245	84	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	69.m15461	AN5491.1	AO070341000394	Cytoplasm to vacuole targeting protein	U		2.616	2	1	1	0	1	67	117	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	down	72.m18960	AN5832.1	AO070260000013	Ras-related GTPase				1	3	1	0	322	47	472			28	0
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	57.m05846	AN7496.1	AO070287000019	FOG: Immunoglobin and related proteins	P		1.940	1	1	1	1	243	229	225	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	53.m03750	AN8224.1	AO070310000088	Glutamyl-tRNA synthetase	J		0.698	1	1	2	1	15	37	17	34	0		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				1	3	1	1	148	155	358	No EST	No EST		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	53.m03687	AN8273.1	AO070310000028	Ubiquinol cytochrome c reductase, subunit QCR2	C		2.535	2	1	1	1	44	9	29	120	1		
855	TTCCGCCCGC	TEA1 a (CGGNCGG) [yeast_motifs_all];	up	up	62.m03474	AN8691.1	AO070315000112	Ribonucleases P/MRP protein subunit	A		2.308	1	1	1	0	142	76	90	No EST	No EST		
896	TGGTCCGTGC		up	up	70.m15466	AN0862.1	AO070320000011	Molecular chaperone Prefoldin, subunit 4	O		1.053	1	1	2	1	116	249	115	No EST	No EST		
896	TGGTCCGTGC		up	up	70.m15576	AN0944.1	AO070320000139	ATP-dependent RNA helicase	A		0.453	1	1	1	0	142	199	154	No EST	No EST		
896	TGGTCCGTGC		up	up	70.m15243	AN1024.1	AO070343000587	Chromatin remodeling complex WSTF-ISWI, small subunit	K		1.944	1	1	1	1	291	16	18	No EST	No EST		
896	TGGTCCGTGC		up	up	58.m07732	AN1666.1	AO070299000048	Nucleolar GTPase				1	1	1	1	175	12	12	122	1		
896	TGGTCCGTGC		up	down	54.m06739	AN4096.1	AO070342000097	hypothetical protein [Neurospora crassa]				1	1	1	1	354	192	218			No EST	No EST
896	TGGTCCGTGC		up	down	57.m05487	AN4565.1	AO070250000008	Unnamed protein				1	1	1	1	107	125	110			No EST	No EST
896	TGGTCCGTGC		up	up	59.m08665	AN5014.1	AO070334000120	60S ribosomal protein L22	J		0.017	1	1	1	1	273	145	147	70	0		

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896	TGGTCCGTGC		up	up	69.m14840	AN5742.1	AO070193000003	Fucose permease	G		2.171	1	1	1	0	243	317	442	No EST	No EST		
896	TGGTCCGTGC		up	up	72.m20019	AN7291.1	AO070297000031	Translation initiation factor 5B (eIF-5B)	J		0.017	1	1	1	0	208	8	8	No EST	No EST		
896	TGGTCCGTGC		up	up	57.m05836	AN7503.1	AO070287000009	Uncharacterized conserved protein				1	1	1	0	190	5	15	99	1		
896	TGGTCCGTGC		up	up	57.m05457	AN7680.1	AO070325000070	Myosin class II heavy chain	Z		1.337	1	1	1	0	112	288	172	No EST	No EST		
896	TGGTCCGTGC		up	up	53.m03917	AN8066.1	AO070330000022	tRNA(1-methyladenosine) methyltransferase, subunit GCD10	J		0.017	1	1	1	1	145	303	292	No EST	No EST		
896	TGGTCCGTGC		up	up	53.m03929	AN8076.1	AO070330000034	Splicing coactivator SRm160/300, subunit SRm300	A		0.453	1	1	1	1	244	261	293	824	1		
896	TGGTCCGTGC		up	up	52.m03716	AN8104.1	AO070338000145	hypothetical protein [Neurospora crassa]				1	1	1	0	248	27	26	No EST	No EST		
896	TGGTCCGTGC		up	up	53.m03708	AN8253.1	AO070310000052	Predicted RNA-binding protein Nob1p involved in 26S proteasome assembly	O		1.053	1	1	1	0	123	309	305	83	0		
896	TGGTCCGTGC		up	up	52.m04033	AN9406.1	AO070274000011	tRNA methyltransferase	J		0.017	1	1	1	0	110	45	67	No EST	No EST		
973	CACCGCCT		up	up	71.m15368	AN0093.1	AO070311000122	Nucleolar GTPase/ATPase p130	Y		0.416	1	0	1	0	220	0	2	No EST	No EST		
973	CACCGCCT		up	up	71.m15417	AN0133.1	AO070321000120	mRNA splicing factor ATP-dependent RNA helicase	A	1	0.000	1	2	1	0	182	100	93	No EST	No EST		
973	CACCGCCT		up	up	54.m06468	AN0275.1	AO070334000082	Cystine transporter Cystinosin	E		4.394	1	1	1	0	188	79	104	No EST	No EST		
973	CACCGCCT		up	up	54.m06464	AN0298.1	AO070334000044	Polyadenylation factor I complex, subunit, Yth1 (CPSF subunit)	A	1	0.000	1	2	1	0	286	272	172	No EST	No EST		
973	CACCGCCT		up	up	54.m06619	AN0430.1	AO070338000280	hypothetical protein [Neurospora crassa]				1	1	1	0	350	218	183	No EST	No EST		
973	CACCGCCT		up	up	69.m15269	AN0576.1	AO070272000056	Protein kinase containing WD40 repeats	T		1.940	1	1	1	0	222	149	174	No EST	No EST		
973	CACCGCCT		up	up	69.m15690	AN0579.1	AO070280000001	Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	Q		5.000	1	1	1	1	176	268	288	51	0		
973	CACCGCCT		up	up	69.m15266	AN0582.1	AO070280000004	Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	L		5.664	1	1	1	1	64	55	106	No EST	No EST		
973	CACCGCCT		up	up	69.m15260	AN0589.1	AO070280000011	RNA Helicase	A	1	0.000	1	1	1	0	90	71	62	16	0		
973	CACCGCCT		up	up	70.m15804	AN0834.1	AO070255000011	Molecular chaperone (DnaJ superfamily)	O		0.126	1	1	1	0	282	207	257	No EST	No EST		
973	CACCGCCT		up	up	70.m15629	AN0988.1	AO070318000150	LAMMER dual specificity kinases	T		1.940	1	1	1	1	311	189	132	No EST	No EST		
973	CACCGCCT		up	up	70.m15237	AN1019.1	AO070343000596	Cullins	D		5.966	1	1	1	1	494	43	1	69	1		
973	CACCGCCT		up	up	70.m15196	AN1038.1	AO070336000073	Putative transmembrane protein				1	1	1	0	156	129	166	No EST	No EST		
973	CACCGCCT		up	up	70.m15203	AN1047.1	AO070313000109	Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	O		0.126	2	2	3	0	234	6	6	No EST	No EST		
973	CACCGCCT		up	up	70.m14862	AN1367.1	AO070215000014	WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis	J		0.728	1	1	1	0	55	33	19	No EST	No EST		
973	CACCGCCT		up	up	70.m14844	AN1379.1	AO070243000010	mRNA export protein (contains WD40 repeats)	A	1	0.000	1	2	1	0	297	87	145	135	1		
973	CACCGCCT		up	up	55.m02969	AN1467.1	AO070306000090	Serine/threonine protein phosphatase	T		1.940	2	1	2	1	383	84	131	177	1		
973	CACCGCCT		up	up	55.m03057	AN1538.1	AO070334000262	Transcription initiation factor IIF, small subunit (RAP30)	K		3.580	1	2	1	1	207	165	175	No EST	No EST		
973	CACCGCCT		up	up	58.m07724	AN1638.1	AO070299000044	Puromycin-sensitive aminopeptidase and related aminopeptidases	EO		4.39369814917025 0.126123344831786	2	1	1	0	212	147	124	No EST	No EST		
973	CACCGCCT		up	up	58.m07570	AN1965.1	AO070301000046	Ribose-phosphate pyrophosphokinase	FE		8.15609785366271 4.39369814917025	1	1	1	0	283	83	29	125	1		
973	CACCGCCT		up	up	58.m07575	AN1970.1	AO070301000054	Mitochondrial/chloroplast ribosomal protein L28	J		0.728	1	1	1	0	180	28	24	No EST	No EST		
973	CACCGCCT		up	up	72.m19694	AN2147.1	AO070343000196	rRNA processing protein Rrp5	A	1	0.000	2	2	2	1	139	13	13	No EST	No EST		
973	CACCGCCT		up	up	71.m15881	AN2247.1	AO070326000126	Myosin class II heavy chain	Z		5.717	1	1	1	0	163	87	66	No EST	No EST		
973	CACCGCCT		up	up	54.m06683	AN2748.1	AO070338000223	FOG: Zn-finger				1	1	1	0	139	30	29	No EST	No EST		
973	CACCGCCT		up	up	59.m08713	AN2868.1	AO070338000154	Oligoribonuclease (3'->5' exoribonuclease)	A	1	0.000	2	1	1	1	208	324	354	No EST	No EST		
973	CACCGCCT		up	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		3.580	1	1	1	1	444	37	42	No EST	No EST		
973	CACCGCCT		up	down	59.m08982	AN3035.1	AO070337000077	5'-3' exonuclease	L		5.664	1	2	1	0	412	318	446			No EST	No EST
973	CACCGCCT		up	up	59.m08566	AN3176.1	AO070256000014	ATP-dependent RNA helicase	A	1	0.000	1	1	1	1	126	156	144	No EST	No EST		
973	CACCGCCT		up	up	59.m09501	AN3423.1	AO070327000008	Transcription elongation factor SPT6	A	1	0.000	1	1	1	0	297	49	116	No EST	No EST		
973	CACCGCCT		up	down	59.m09483	AN3453.1	AO070265000029	Ubiquitin C-terminal hydrolase	O		0.126	1	2	1	0	177	230	207			75	0
973	CACCGCCT		up	up	57.m05696	AN3787.1	AO070337000242	Peptide:N-glycanase	O		0.126	1	1	1	0	215	85	96	No EST	No EST		
973	CACCGCCT		up	up	58.m07818	AN3842.1	AO070305000077	GTPase Rab5/YPT51 and related small G protein superfamily GTPases	U		2.771	1	1	1	1	288	7	9	151	1		
973	CACCGCCT		up	up	54.m07047	AN4112.1	AO070342000107	Nucleolar GTPase/ATPase p130	Y		0.416	1	1	1	0	203	36	79	No EST	No EST		
973	CACCGCCT		up	up	54.m06754	AN4192.1	AO070342000112	Molecular chaperone (DnaJ superfamily)	O		0.126	1	1	1	1	98	483	453	No EST	No EST		
973	CACCGCCT		up	up	54.m06790	AN4226.1	AO070234000023	Sof1-like rRNA processing protein (contains WD40 repeats)	A	1	0.000	1	1	1	1	140	50	30	55	1		
973	CACCGCCT		up	up	58.m08016	AN4308.1	AO070207000013	Mitochondrial/chloroplast ribosomal protein L3	J		0.728	1	1	1	0	46	173	216	11	0		
973	CACCGCCT		up	down	58.m09007	AN4333.1	AO070240000012	predicted protein [Neurospora crassa]				1	1	1	0	327	200	382			No EST	No EST
973	CACCGCCT		up	up	58.m07981	AN4346.1	AO070240000018	Nucleolar RNA-binding protein NIFK				1	1	1	1	25	15	45	24	1		
973	CACCGCCT		up	down	58.m07937	AN4387.1	AO070261000033	Mitochondrial FAD carrier protein	C		2.877	1	1	1	0	320	146	321			No EST	No EST

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973	CACCGCCT		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				1	1	1	1	244	78	82	No EST	No EST		
973	CACCGCCT		up	up	58.m07904	AN4415.1	AO070273000036	Holocytochrome c synthase/heme-lyase	CO		2.87699093111136 0.126123344831786	1	1	2	0	132	42	104	No EST	No EST		
973	CACCGCCT		up	up	58.m07860	AN4470.1	AO070305000129	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	J		0.728	1	1	2	0	186	38	68	97	1		
973	CACCGCCT		up	up	58.m07861	AN4471.1	AO070305000130	WD40 repeat-containing protein				1	1	1	0	122	146	258	36	0		
973	CACCGCCT		up	up	57.m05499	AN4581.1	AO070316000164	Protein involved in high osmolarity signaling pathway	T		1.940	1	1	1	0	112	52	62	No EST	No EST		
973	CACCGCCT		up	up	59.m09126	AN4850.1	AO070327000106	RNA-binding protein RBM5 and related proteins, contain G-patch and RRM domains				1	1	1	0	83	225	41	No EST	No EST		
973	CACCGCCT		up	up	59.m09108	AN4864.1	AO070329000150	Glucosyltransferase - Alg6p	GE		1.81077964157289 4.39369814917025	1	1	2	1	276	34	60	No EST	No EST		
973	CACCGCCT		up	up	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				2	1	1	1	99	130	156	345	1		
973	CACCGCCT		up	up	59.m09494	AN5022.1	AO070338000182	Dynactin, subunit p25	Z		5.717	1	1	3	0	118	57	10	No EST	No EST		
973	CACCGCCT		up	up	54.m06817	AN5702.1	AO070324000158	Uncharacterized conserved protein				2	1	1	0	96	68	128	No EST	No EST		
973	CACCGCCT		up	up	54.m06828	AN5713.1	AO070324000145	Chaperonin complex component, TCP-1 eta subunit (CCT7)	O		0.126	1	1	1	1	189	85	70	No EST	No EST		
973	CACCGCCT		up	down	72.m19268	AN5866.1	AO070308000130	Arylalkylamine N-acetyltransferase				1	1	1	1	54	69	81			No EST	No EST
973	CACCGCCT		up	up	72.m19263	AN5871.1	AO070308000137	Predicted RNA methylase involved in rRNA processing	A	1	0.000	1	1	1	0	231	131	15	No EST	No EST		
973	CACCGCCT		up	up	72.m19188	AN5972.1	AO070340000330	Vesicle coat complex COPI, beta' subunit	U		2.771	1	1	1	1	282	23	55	370	1		
973	CACCGCCT		up	up	72.m19097	AN6061.1	AO070340000187	hypothetical protein [Schizosaccharomyces pombe]				1	1	1	0	459	8	45	32	1		
973	CACCGCCT		up	up	72.m19947	AN6073.1	AO070340000117	Prohibitin-like protein	O		0.126	1	1	1	0	86	71	70	No EST	No EST		
973	CACCGCCT		up	up	72.m19048	AN6110.1	AO070340000096	Uncharacterized conserved protein				1	1	1	1	113	11	11	No EST	No EST		
973	CACCGCCT		up	up	72.m19002	AN6171.1	AO070340000034	U3 small nucleolar ribonucleoprotein (snoRNP) component	A	1	0.000	1	1	2	0	110	88	166	41	0		
973	CACCGCCT		up	up	72.m19323	AN6311.1	AO070308000066	Cl- channel CLC-3 and related proteins (CLC superfamily)	P		5.876	1	1	1	1	137	23	22	No EST	No EST		
973	CACCGCCT		up	up	72.m19493	AN6367.1	AO070279000053	Phosphatidylinositol-4-phosphate 5-kinase and related FYVE finger-containing proteins	T		1.940	1	1	1	0	190	52	41	No EST	No EST		
973	CACCGCCT		up	up	62.m03148	AN6561.1	AO070326000002	Uncharacterized conserved protein				1	1	1	1	143	95	138	55	0		
973	CACCGCCT		up	up	62.m03207	AN6591.1	AO070326000039	Nuclear export receptor CSE1/CAS (importin beta superfamily)	YU		0.416033420152047 2.77134743294217	1	1	1	1	228	157	154	No EST	No EST		
973	CACCGCCT		up	up	65.m07285	AN6698.1	AO070339000130	Uncharacterized conserved protein				1	1	1	0	82	377	281	32	0		
973	CACCGCCT		up	up	65.m07244	AN6726.1	AO070339000170	20S proteasome, regulatory subunit alpha type PSMA2/PRE8	O		0.126	1	1	1	0	187	22	40	No EST	No EST		
973	CACCGCCT		up	up	72.m19795	AN7254.1	AO070297000010	AAA+-type ATPase	O		0.126	1	1	1	0	249	57	74	106	1		
973	CACCGCCT		up	up	72.m19751	AN7312.1	AO070297000060	tRNA nucleotidyltransferase/poly(A) polymerase	J		0.728	1	1	1	0	143	121	134	No EST	No EST		
973	CACCGCCT		up	up	69.m15143	AN7525.1	AO070258000031	ATPases involved in chromosome partitioning	D		5.966	1	2	1	0	19	10	8	No EST	No EST		
973	CACCGCCT		up	up	72.m19649	AN7608.1	AO070343000269	RNA Polymerase C (III) 37 kDa subunit	K		3.580	1	1	1	1	143	187	113	No EST	No EST		
973	CACCGCCT		up	up	57.m05423	AN7659.1	AO070268000028	ATP-dependent RNA helicase	A	1	0.000	1	1	1	0	379	22	21	172	1		
973	CACCGCCT		up	down	71.m15755	AN7731.1	AO070325000145	Nuclear transport receptor LGL2 (importin beta superfamily)	YU		0.416033420152047 2.77134743294217	1	1	1	0	32	20	22			No EST	No EST
973	CACCGCCT		up	up	53.m03900	AN8044.1	AO070292000105	N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	O		0.126	2	1	2	0	348	33	71	No EST	No EST		
973	CACCGCCT		up	up	53.m03925	AN8072.1	AO070330000030	hypothetical protein B13N20.140 [imported] - Neurospora crassa				1	1	1	0	75	28	27	No EST	No EST		
973	CACCGCCT		up	up	53.m03694	AN8264.1	AO070310000036	hypothetical protein [Schizosaccharomyces pombe]				2	2	2	0	171	286	332	No EST	No EST		
973	CACCGCCT		up	up	58.m08926	AN8488.1	AO070299000105	SNARE protein YKT6, synaptobrevin/VAMP syperfamily	U		2.771	1	1	1	0	90	71	32	No EST	No EST		
973	CACCGCCT		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		3.580	1	1	1	1	239	236	311	157	0		
973	CACCGCCT		up	up	62.m03389	AN8682.1	AO070315000102	Exosomal 3'-5' exoribonuclease complex, subunit Rrp43	J		0.728	1	1	2	1	121	385	87	No EST	No EST		
973	CACCGCCT		up	up	62.m03357	AN8712.1	AO070315000138	Translation initiation factor 1A (eIF-1A)	J		0.728	1	0	1	0	247	0	1	96	1		
973	CACCGCCT		up	up	71.m15960	AN8828.1	AO070271000052	Transport protein particle (TRAPP) complex subunit	U		2.771	1	1	1	0	148	220	77	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
973	CACCGCCT		up	up	52.m04024	AN9398.1	AO070274000018	Cell adhesion complex protein bystin				1	1	1	0	251	155	20	No EST	No EST		
973	CACCGCCT		up	up	53.m03781	AN9461.1	AO070310000129	Dehydrogenase kinase	T		1.940	1	1	1	0	67	69	116	No EST	No EST		
973	CACCGCCT		up	up	62.m03341	AN9504.1	AO070315000153	Ras GTPase activating protein RasGAP/neurofibromin	V		6.906	2	1	2	1	294	49	35	No EST	No EST		
992	GCATAGCG		down	down	71.m16095	AN0226.1	AO070284000066	Ubiquitin-protein ligase	O		0.900	1	1	1	0	97	52	112			No EST	No EST
992	GCATAGCG		down	down	54.m06984	AN0321.1	AO070334000005	RNA polymerase III, second largest subunit	K		0.297	1	1	1	1	103	70	66			No EST	No EST
992	GCATAGCG		down	down	70.m14899	AN1335.1	AO070303000097	G-protein beta subunit-like protein (contains WD40 repeats)				1	1	1	1	111	68	64			No EST	No EST
992	GCATAGCG		down	down	58.m07735	AN1668.1	AO070299000050	Predicted E3 ubiquitin ligase containing RING finger, subunit of transcription/repair factor TFIIH and CDK-activating kinase assembly factor	O		0.900	1	1	1	1	103	46	93			No EST	No EST
992	GCATAGCG		down	down	69.m14936	AN1918.1	AO070341000122	Phosphoenolpyruvate carboxykinase (ATP)	C		3.002	1	1	1	1	43	78	59			195	1
992	GCATAGCG		down	down	59.m08753	AN2902.1	AO070338000104	TFIIF-interacting CTD phosphatases, including NLI-interacting factor	K		0.297	2	1	2	0	94	113	180			295	1
992	GCATAGCG		down	up	59.m09040	AN2967.1	AO070337000149	tRNA-dihydrouridine synthase	J		1.457	1	1	1	0	20	461	500	No EST	No EST		
992	GCATAGCG		down	down	59.m08521	AN3144.1	AO070256000047	FYVE finger-containing protein				2	2	1	1	94	72	126			257	1
992	GCATAGCG		down	down	69.m15409	AN3705.1	AO070341000329	Uncharacterized conserved protein				1	1	1	1	76	76	84			No EST	No EST
992	GCATAGCG		down	down	65.m07425	AN4253.1	AO070309000123	predicted protein [Neurospora crassa]				1	1	1	1	98	142	112			288	1
992	GCATAGCG		down	down	57.m05571	AN4559.1	AO070321000169	Molecular chaperone (DnaJ superfamily)	O		0.900	1	1	1	1	125	119	121			12	0
992	GCATAGCG		down	down	59.m09173	AN4803.1	AO070329000036	Ribosomal protein S4	J		1.457	1	1	1	1	81	71	71			164	1
992	GCATAGCG		down	down	59.m08812	AN4908.1	AO070338000038	Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondrial morphology/distribution, also found associated with eIF-3				2	1	1	0	242	253	244			No EST	No EST
992	GCATAGCG		down	down	54.m06906	AN5119.1	AO070291000062	Predicted methyltransferase				2	1	1	1	58	177	201			No EST	No EST
992	GCATAGCG		down	down	69.m15442	AN5517.1	AO070341000376	Cdc4 and related F-box and WD-40 proteins				1	1	1	1	196	202	165			No EST	No EST
992	GCATAGCG		down	down	65.m07417	AN5693.1	AO070309000108	Uncharacterized conserved protein				2	1	1	1	78	75	186			319	1
992	GCATAGCG		down	down	72.m19257	AN5875.1	AO070308000144	rRNA processing protein	JD		1.45682789386515 2.45984236489557	1	1	1	1	101	98	105			173	1
992	GCATAGCG		down	down	72.m19327	AN6307.1	AO070308000062	Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	U		3.017	1	1	1	1	6	25	6			No EST	No EST
992	GCATAGCG		down	down	65.m07490	AN6696.1	AO070339000127	hypothetical protein [Neurospora crassa]				1	2	1	1	128	111	121			No EST	No EST
992	GCATAGCG		down	down	71.m15293	AN6823.1	AO070314000102	hypothetical protein ((AL513443) hypothetical protein [Neurospora crassa])				1	2	1	1	58	12	47			No EST	No EST
992	GCATAGCG		down	down	53.m03693	AN8268.1	AO070310000034	RasGAP SH3 binding protein rasputin, contains NTF2 and RRM domains	T		3.017	1	1	1	1	312	319	433			No EST	No EST
992	GCATAGCG		down	down	66.m04585	AN9125.1	AO070332000149	RNA polymerase III, subunit C34	K		0.297	1	1	1	1	44	33	36			72	1
1059	TCGGCCCG		up	up	71.m15469	AN0204.1	AO070321000040	ATP-dependent RNA helicase	A		2.596	1	1	1	1	102	60	78	37	0		
1059	TCGGCCCG		up	up	54.m06472	AN0271.1	AO070334000077	dUTPase	F		1.139	1	1	1	1	122	17	15	42	1		
1059	TCGGCCCG		up	up	70.m15479	AN0876.1	AO070320000035	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family				1	1	1	1	37	378	177	No EST	No EST		
1059	TCGGCCCG		up	up	70.m15135	AN1095.1	AO070285000047	Mitochondrial/chloroplast ribosomal protein L15/L10	J		2.965	1	1	1	1	95	307	336	No EST	No EST		
1059	TCGGCCCG		up	up	69.m15077	AN1778.1	AO070324000018	Ketopantoate hydroxymethyltransferase	H		1.497	1	1	1	1	499	4	8	No EST	No EST		
1059	TCGGCCCG		up	up	59.m08568	AN3186.1	AO070256000012	5'-3' exonuclease	L		2.232	1	1	1	1	142	42	60	No EST	No EST		
1059	TCGGCCCG		up	up	57.m05587	AN4534.1	AO070321000148	Uncharacterized conserved protein				1	1	1	1	96	108	149	No EST	No EST		
1059	TCGGCCCG		up	up	69.m14874	AN5177.1	AO070247000008	WD40 repeat protein				1	1	1	1	85	207	154	No EST	No EST		
1059	TCGGCCCG		up	up	69.m14806	AN5790.1	AO070249000036	Isocitrate dehydrogenase, gamma subunit	E		3.074	1	1	1	0	226	329	304	205	0		
1059	TCGGCCCG		up	up	72.m19149	AN5991.1	AO070340000286	AAA+-type ATPase	O		1.313	2	1	1	1	156	60	31	No EST	No EST		
1059	TCGGCCCG		up	up	72.m19133	AN6010.1	AO070340000269	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	O		1.313	2	1	1	1	61	283	287	149	0		
1059	TCGGCCCG		up	down	62.m03439	AN6500.1	AO070222000014	60S ribosomal protein L28	J		2.965	1	1	1	1	343	309	339			212	0
1059	TCGGCCCG		up	up	72.m19644	AN7603.1	AO070343000273	Vacuolar H+-ATPase V0 sector, subunit c''	C		2.852	1	1	1	1	172	61	79	No EST	No EST		
1093	CCCCTCCCCC		up	up	54.m06397	AN0357.1	AO070318000033	Cytochrome c1	C		0.346	2	1	2	1	61	207	200	No EST	No EST		
1093	CCCCTCCCCC		up	up	54.m06659	AN0417.1	AO070338000265	Sec61 protein translocation complex, beta subunit	O		2.434	1	1	2	0	21	299	139	No EST	No EST		
1093	CCCCTCCCCC		up	down	69.m15252	AN0595.1	AO070280000021	NADP/FAD dependent oxidoreductase	C		0.346	1	1	1	0	57	4	201			No EST	No EST
1093	CCCCTCCCCC		up	up	70.m15291	AN0688.1	AO070343000525	Transketolase	G		0.045	1	2	3	0	58	275	296	66	0		
1093	CCCCTCCCCC		up	up	70.m15358	AN0756.1	AO070343000444	Beta-galactosidase	G		0.045	1	1	1	0	39	227	201	No EST	No EST		
1093	CCCCTCCCCC		up	down	70.m15391	AN0781.1	AO070316000055	Atu related protein [imported] - Neurospora crassa				2	1	4	0	38	231	70			374	1
1093	CCCCTCCCCC		up	up	70.m15397	AN0787.1	AO070239000021	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	G		0.045	1	1	1	0	106	421	316	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15515	AN0906.1	AO070320000082	Karyopherin (importin) beta 1	YU		0.550091990129638 0.464854686559532	2	1	1	0	60	462	55	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1093	CCCCTCCCCC		up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		0.5500919 90129638 0.4648546 86559532	1	2	1	0	116	272	181	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15540	AN0932.1	AO070320000123	Pyridine nucleotide-disulphide oxidoreductase	Q		4.204	1	1	1	0	321	140	242	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15233	AN1015.1	AO070312000003	Glycogen phosphorylase	G		0.045	3	1	3	0	246	60	249	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15137	AN1094.1	AO070285000053	NADH-dehydrogenase (ubiquinone)	C		0.346	2	2	1	0	28	363	496	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15118	AN1117.1	AO070331000109	Putative cargo transport protein ERV29	U		0.465	2	2	1	0	143	264	275	192	0		
1093	CCCCTCCCCC		up	up	70.m15040	AN1177.1	AO070331000173	Vesicle coat complex COPI, beta subunit	U		0.465	1	2	1	1	57	165	165	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		5.373	4	1	2	0	55	152	150	193	1		
1093	CCCCTCCCCC		up	up	70.m14906	AN1325.1	AO070303000088	Protein interacting with poly(A)-binding protein	A		5.059	1	1	1	0	299	196	94	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		1.436	1	2	1	0	160	297	349	400	1		
1093	CCCCTCCCCC		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				3	4	3	1	275	121	175	189	1		
1093	CCCCTCCCCC		up	up	70.m14839	AN1382.1	AO070243000014	hypothetical protein [Neurospora crassa]				1	1	1	0	202	175	144	No EST	No EST		
1093	CCCCTCCCCC		up	up	70.m14826	AN1396.1	AO070233000012	Glycerol-3-phosphate dehydrogenase	C		0.346	3	1	2	0	358	286	5	No EST	No EST		
1093	CCCCTCCCCC		up	down	55.m03263	AN1437.1	AO070232000002	hypothetical protein [Neurospora crassa]				1	1	1	0	436	183	331			No EST	No EST
1093	CCCCTCCCCC		up	up	58.m08961	AN1720.1	AO070305000035	predicted protein [Neurospora crassa]				1	1	1	0	354	236	256	No EST	No EST		
1093	CCCCTCCCCC		up	up	69.m15048	AN1745.1	AO070324000051	Nicotinic acid mononucleotide adenylyltransferase	H		5.373	1	1	1	0	184	205	349	No EST	No EST		
1093	CCCCTCCCCC		up	down	58.m07668	AN1843.1	AO070292000064	Protein involved in meiotic recombination/predicted coiled-coil protein	D		6.111	3	3	2	1	266	165	281			No EST	No EST
1093	CCCCTCCCCC		up	up	57.m05716	AN1902.1	AO070341000151	Nucleolar GTPase/ATPase p130	Y		0.550	1	1	1	1	80	137	122	469	1		
1093	CCCCTCCCCC		up	up	58.m08946	AN1980.1	AO070301000065	Rab6 GTPase activator GAPCenA and related TBC domain proteins				1	2	1	0	143	37	185	No EST	No EST		
1093	CCCCTCCCCC		up	up	72.m19708	AN2133.1	AO070278000026	Armadillo/beta-Catenin/plakoglobin	TZ		1.4357064 521095 5.9601885 8219753	1	3	1	0	184	23	156	No EST	No EST		
1093	CCCCTCCCCC		up	up	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		0.465	2	1	1	0	85	50	52	No EST	No EST		
1093	CCCCTCCCCC		up	up	71.m15917	AN2272.1	AO070295000048	Possible pfkB family carbohydrate kinase	G		0.045	1	1	1	0	123	46	45	91	1		
1093	CCCCTCCCCC		up	up	71.m15938	AN2290.1	AO070295000069	FOG: Zn-finger				2	1	1	0	358	25	16	No EST	No EST		
1093	CCCCTCCCCC		up	up	69.m15223	AN2435.1	AO070264000043	ATP-citrate lyase	C		0.346	2	3	2	0	115	165	160	187	1		
1093	CCCCTCCCCC		up	up	71.m15179	AN2692.1	AO070313000096					1	1	1	0	255	134	112	204	1		
1093	CCCCTCCCCC		up	down	54.m06688	AN2743.1	AO070338000228	Translation initiation factor 3, subunit a (eIF-3a)	J		1.736	1	2	1	0	75	56	232			No EST	No EST
1093	CCCCTCCCCC		up	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		4.024	2	2	1	1	85	40	45	No EST	No EST		
1093	CCCCTCCCCC		up	up	59.m08981	AN3036.1	AO070337000078	predicted protein [Neurospora crassa]				2	1	1	0	151	22	34	No EST	No EST		
1093	CCCCTCCCCC		up	up	59.m08959	AN3059.1	AO070337000014	Phosphoglycerate mutase	G		0.045	1	1	2	1	227	13	18	25	1		
1093	CCCCTCCCCC		up	up	59.m08649	AN3094.1	AO070334000135	Rab6 GTPase activator GAPCenA and related TBC domain proteins				1	1	2	0	82	373	15	No EST	No EST		
1093	CCCCTCCCCC		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				1	3	1	1	325	129	307	106	0		
1093	CCCCTCCCCC		up	up	59.m08623	AN3114.1	AO070303000035	predicted protein [Neurospora crassa]				3	1	2	0	153	127	326	No EST	No EST		
1093	CCCCTCCCCC		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		3.919	1	1	1	0	34	365	104	298	0		
1093	CCCCTCCCCC		up	up	54.m07029	AN3503.1	AO070306000124	Permease of the major facilitator superfamily	G		0.045	1	1	1	0	94	221	228	No EST	No EST		
1093	CCCCTCCCCC		up	up	58.m07376	AN3578.1	AO070342000171	Predicted MutS-related protein involved in mismatch repair	L		4.897	2	1	1	0	235	442	89	No EST	No EST		
1093	CCCCTCCCCC		up	up	58.m07414	AN3627.1	AO070342000123	hypothetical protein [Neurospora crassa]				2	2	1	0	256	188	463	212	1		
1093	CCCCTCCCCC		up	up	65.m07359	AN3763.1	AO070309000041	Predicted transporter (major facilitator superfamily)				1	1	1	0	158	332	391	No EST	No EST		
1093	CCCCTCCCCC		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		1.736	3	1	1	1	147	262	315	96	0		
1093	CCCCTCCCCC		up	up	58.m07953	AN4376.1	AO070261000018	Glutamate/leucine/phenylalanine/valine dehydrogenases	E		3.677	1	1	2	0	176	126	38	100	0		
1093	CCCCTCCCCC		up	down	58.m07953	AN4376.1	AO070261000018	Glutamate/leucine/phenylalanine/valine dehydrogenases	E		3.677	1	1	1	0	8	5	26			168	1
1093	CCCCTCCCCC		up	up	58.m07928	AN4395.1	AO070261000040	hypothetical protein [Neurospora crassa]				1	2	1	0	279	77	203	762	1		
1093	CCCCTCCCCC		up	up	58.m07925	AN4401.1	AO070261000045	Asparagine synthase (glutamine-hydrolyzing)	E		3.677	1	1	1	0	99	65	99	341	1		
1093	CCCCTCCCCC		up	up	58.m07892	AN4433.1	AO070273000024	FOG: PPR repeat				1	1	1	0	221	76	59	No EST	No EST		
1093	CCCCTCCCCC		up	up	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		3.677	2	2	2	0	249	231	148	66	0		
1093	CCCCTCCCCC		up	up	58.m07847	AN4462.1	AO070305000113	Pyruvate carboxylase	C		0.346	2	3	3	0	126	256	44	No EST	No EST		
1093	CCCCTCCCCC		up	up	57.m05654	AN4479.1	AO070311000025	FOG: HAMP domain	T		1.436	1	1	2	0	206	170	315	No EST	No EST		
1093	CCCCTCCCCC		up	up	59.m09466	AN4859.1	AO070329000143	Plasma membrane H+-transporting ATPase	P		5.124	1	1	1	0	114	315	352	103	0		
1093	CCCCTCCCCC		up	up	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				3	2	1	1	93	218	271	345	1		
1093	CCCCTCCCCC		up	up	59.m08876	AN4973.1	AO070288000039	predicted protein [Neurospora crassa]				2	2	1	0	40	219	278	No EST	No EST		
1093	CCCCTCCCCC		up	up	69.m15551	AN5356.1	AO070333000156	Mitochondrial carnitine-acylcarnitine carrier protein	C		0.346	1	2	1	0	50	242	350	No EST	No EST		
1093	CCCCTCCCCC		up	up	58.m07475	AN5529.1	AO070328000064	NDR and related serine/threonine kinases				1	1	3	1	106	315	128	No EST	No EST		
1093	CCCCTCCCCC		up	up	58.m07489	AN5563.1	AO070328000044	Aldo/keto reductase family proteins				1	1	2	0	127	285	433	278	0		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1093	CCCCTCCCCC		up	up	58.m07508	AN5589.1	AO070328000022	Ribulose kinase and related carbohydrate kinases	G		0.045	1	1	1	0	423	355	179	439	1		
1093	CCCCTCCCCC		up	up	58.m07549	AN5626.1	AO070301000025	Acyl-CoA synthetase	I		3.919	1	3	2	0	374	216	174	66	0		
1093	CCCCTCCCCC		up	up	72.m19247	AN5884.1	AO070245000024	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F		4.092	1	2	1	0	194	120	194	No EST	No EST		
1093	CCCCTCCCCC		up	up	72.m19952	AN5931.1	AO070340000344	ATP-dependent RNA helicase	A		5.059	1	1	2	0	165	64	125	111	1		
1093	CCCCTCCCCC		up	up	72.m19291	AN6193.1	AO070308000106	Mitochondrial ATP-dependent protease PIM1/LON	O		2.434	1	1	1	0	29	41	90	128	1		
1093	CCCCTCCCCC		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				2	1	2	0	451	19	12	386	1		
1093	CCCCTCCCCC		up	up	72.m19978	AN6231.1	AO070304000084	Tryptophan synthase beta chain	E		3.677	1	1	1	0	120	286	467	81	0		
1093	CCCCTCCCCC		up	up	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		1.436	1	2	1	0	318	19	8	No EST	No EST		
1093	CCCCTCCCCC		up	up	72.m19329	AN6305.1	AO070308000060	cAMP-dependent protein kinase catalytic subunit (PKA)	T		1.436	1	1	1	0	144	94	361	No EST	No EST		
1093	CCCCTCCCCC		up	up	62.m03087	AN6499.1	AO070222000013	NAD-dependent malate dehydrogenase	C		0.346	2	2	2	0	192	373	375	105	0		
1093	CCCCTCCCCC		up	up	62.m03157	AN6570.1	AO070326000013	Protein involved in Snf1 protein kinase complex assembly	G		0.045	1	1	1	0	48	292	438	No EST	No EST		
1093	CCCCTCCCCC		up	up	62.m03158	AN6578.1	AO070326000025	Gluconate transport-inducing protein	TG		1.4357064 521095 0.0454095 52872867 4	3	2	2	0	69	159	25	No EST	No EST		
1093	CCCCTCCCCC		up	up	62.m03234	AN6639.1	AO070326000091	Uncharacterized protein involved in propionate catabolism				1	2	1	0	46	205	274	21	0		
1093	CCCCTCCCCC		up	up	65.m07502	AN6688.1	AO070339000095	Septin family protein (P-loop GTPase)	DZU		6.1114106 4805511 5.9601885 8219753 0.4648546 86559532	1	1	1	0	253	175	170	835	1		
1093	CCCCTCCCCC		up	up	71.m15272	AN6859.1	AO070314000076	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains	AK		5.0590706 0003855 4.0235542 6282144	1	1	2	1	265	295	68	78	0		
1093	CCCCTCCCCC		up	up	57.m05909	AN7438.1	AO070229000006	Thyroid hormone receptor-associated coactivator complex component (TRAP170)	K		4.024	1	1	1	0	35	471	332	No EST	No EST		
1093	CCCCTCCCCC		up	up	57.m05843	AN7498.1	AO070287000016	HEAT repeat-containing protein				1	1	1	1	147	129	23	No EST	No EST		
1093	CCCCTCCCCC		up	up	72.m19619	AN7594.1	AO070343000316	Uncharacterized conserved protein				1	1	1	0	254	226	211	74	0		
1093	CCCCTCCCCC		up	up	71.m15748	AN7721.1	AO070325000136	Transport protein Sec61, alpha subunit	UO		0.4648546 86559532 2.4344603 6577448	1	1	1	0	146	88	90	106	1		
1093	CCCCTCCCCC		up	up	71.m16099	AN7741.1	AO070325000162	Adaptor complexes medium subunit family	U		0.465	1	1	1	0	59	151	278	No EST	No EST		
1093	CCCCTCCCCC		up	up	53.m03857	AN8010.1	AO070322000057	Glycogen synthase	G		0.045	1	1	3	0	351	237	175	293	1		
1093	CCCCTCCCCC		up	up	53.m03891	AN8051.1	AO070292000094	predicted protein [Neurospora crassa]				1	2	3	0	136	229	308	No EST	No EST		
1093	CCCCTCCCCC		up	up	53.m03888	AN8055.1	AO070322000145	RNA-binding Ran Zn-finger protein and related proteins				1	3	2	1	251	220	250	No EST	No EST		
1093	CCCCTCCCCC		up	up	53.m03687	AN8273.1	AO070310000028	Ubiquinol cytochrome c reductase, subunit QCR2	C		0.346	1	1	1	0	26	126	146	120	0		
1093	CCCCTCCCCC		up	up	53.m04091	AN8277.1	AO070310000023	Cystathionine beta-lyases/cystathionine gamma-synthases	E		3.677	1	1	1	0	168	472	184	57	0		
1093	CCCCTCCCCC		up	up	62.m03407	AN8667.1	AO070269000068	GATA-4/5/6 transcription factors	K		4.024	1	3	2	0	190	488	363	No EST	No EST		
1093	CCCCTCCCCC		up	up	62.m03324	AN8751.1	AO070250000011	NDR and related serine/threonine kinases				3	1	2	0	55	66	28	No EST	No EST		
1093	CCCCTCCCCC		up	up	66.m04541	AN9083.1	AO070332000196	Adenine phosphoribosyl transferases	F		4.092	2	1	1	0	267	470	437	No EST	No EST		
1093	CCCCTCCCCC		up	up	54.m06486	AN9448.1	AO070334000061	predicted protein [Neurospora crassa]				1	1	1	0	540	17	12	No EST	No EST		
1093	CCCCTCCCCC		up	up	53.m03730	AN9521.1	AO070310000069	Ca2+-binding protein, EF-Hand protein superfamily	T		1.436	1	1	1	0	166	278	357	No EST	No EST		
1132	CCCCTCT		up	up	71.m15444	AN0170.1	AO070321000076	Thioredoxin	O		1.228	1	1	1	1	266	6	8	207	1		
1132	CCCCTCT		up	up	54.m06442	AN0316.1	AO070334000016	Alpha tubulin	Z		0.215	1	1	1	0	181	200	265	27	0		
1132	CCCCTCT		up	up	70.m15248	AN0646.1	AO070343000583	RNA helicase nonsense mRNA reducing factor (pNORF1)	A		2.191	1	1	1	1	229	23	26	59	1		
1132	CCCCTCT		up	up	70.m14845	AN1378.1	AO070243000008	predicted protein [Neurospora crassa]				2	2	1	0	307	127	209	189	1		
1132	CCCCTCT		up	up	69.m14935	AN1917.1	AO070341000123	Mitochondrial oxoglutarate/malate carrier proteins	C		0.684	2	1	1	0	249	200	228	No EST	No EST		
1132	CCCCTCT		up	down	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		1.228	1	1	1	1	9	8	7			130	1
1132	CCCCTCT		up	up	58.m07379	AN3581.1	AO070342000168	Thioredoxin reductase	O		1.228	1	1	1	0	314	35	2	163	1		
1132	CCCCTCT		up	up	58.m07404	AN3606.1	AO070342000159	predicted protein [Neurospora crassa]				1	1	1	1	368	188	193	No EST	No EST		
1132	CCCCTCT		up	down	58.m07982	AN4342.1	AO070240000017	Tryptophan-rich basic nuclear protein				2	1	1	0	101	290	451			No EST	No EST
1132	CCCCTCT		up	up	59.m09224	AN4759.1	AO070327000057	Guanine nucleotide exchange factor	U		2.434	1	1	2	1	257	158	215	No EST	No EST		

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1132	CCCCTCT		up	up	59.m08831	AN4929.1	AO070338000014	Drebrins and related actin binding proteins	Z		0.215	1	1	1	0	275	241	435	No EST	No EST		
1132	CCCCTCT		up	up	69.m14907	AN5210.1	AO070337000270	Pyruvate kinase	G		2.533	1	1	1	0	76	373	400	60	0		
1132	CCCCTCT		up	up	62.m03227	AN6631.1	AO070326000083	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	C		0.684	1	1	1	0	32	197	209	35	0		
1132	CCCCTCT		up	up	72.m19727	AN7350.1	AO070278000050	FOG: RRM domain				1	1	1	0	196	342	255	131	0		
1132	CCCCTCT		up	up	71.m15815	AN7784.1	AO070286000028	GTPase-activating protein VRP				1	1	1	1	287	214	104	No EST	No EST		
1132	CCCCTCT		up	up	54.m06486	AN9448.1	AO070334000061	predicted protein [Neurospora crassa]				1	1	1	0	537	28	18	No EST	No EST		
1144	TGTACTAT		down	down	71.m15318	AN0043.1	AO070314000122	Phytoene/squalene synthetase	I		2.139	1	7	1	0	96	25	24			No EST	No EST
1144	TGTACTAT		down	up	54.m06657	AN0418.1	AO070338000266	Urea transporter	E		0.095	1	1	1	0	444	420	289	No EST	No EST		
1144	TGTACTAT		down	down	70.m15575	AN0943.1	AO070320000138	Mitochondrial F1F0-ATP synthase, subunit g/ATP20	C		0.470	1	1	1	1	63	62	61			121	1
1144	TGTACTAT		down	down	70.m15221	AN1003.1	AO070312000031	Isocitrate dehydrogenase, alpha subunit	E		0.095	1	1	1	0	17	18	18			109	1
1144	TGTACTAT		down	down	69.m15651	AN1780.1	AO070324000015	Putative Xaa-Pro aminopeptidase	E		0.095	2	1	1	0	43	46	39			No EST	No EST
1144	TGTACTAT		down	down	59.m08453	AN2526.1	AO070220000001	Ketol-acid reductoisomerase	EH		0.094805583893341 1.08531454807399	1	1	1	1	42	41	37			105	1
1144	TGTACTAT		down	down	54.m06576	AN4036.1	AO070328000140	Predicted GTPase activator protein	T		2.307	1	1	1	0	82	54	39			No EST	No EST
1144	TGTACTAT		down	down	58.m08016	AN4308.1	AO070207000013	Mitochondrial/chloroplast ribosomal protein L3	J		0.534	1	1	2	1	33	26	30			91	1
1144	TGTACTAT		down	down	59.m08910	AN5008.1	AO070255000045	Cytochrome c oxidase, subunit VIb/COX12	C		0.470	2	1	1	0	66	91	74			No EST	No EST
1144	TGTACTAT		down	up	72.m19104	AN6054.1	AO070340000200	Mitochondrial genome maintenance protein MGM101, mitochondrial precursor				1	1	2	0	181	66	56	8	0		
1144	TGTACTAT		down	down	71.m15299	AN6842.1	AO070314000097	Phosphatidylethanolamine binding protein				1	1	1	1	64	33	58			No EST	No EST
1144	TGTACTAT		down	down	72.m19714	AN7361.1	AO070278000038	Glutamyl-tRNA synthetase (mitochondrial)	J		0.534	1	1	1	0	241	49	26			70	1
1144	TGTACTAT		down	down	57.m05825	AN7508.1	AO070258000011	hypothetical protein [Neurospora crassa]				1	1	1	0	57	69	74			No EST	No EST
1183	AAACAAGGCA		up	up	71.m15415	AN0131.1	AO070321000122	hypothetical protein [Neurospora crassa]				2	1	1	1	114	3	3	No EST	No EST		
1183	AAACAAGGCA		up	down	70.m15311	AN0704.1	AO070343000506	Uncharacterized protein SFI1 involved in G(2)-M transition	D		6.515	1	1	1	0	57	165	37			No EST	No EST
1183	AAACAAGGCA		up	down	70.m15426	AN0824.1	AO070255000021	Short-chain acyl-CoA dehydrogenase	I		4.144	1	2	1	0	81	153	169			304	1
1183	AAACAAGGCA		up	up	70.m15042	AN1175.1	AO070331000170	Nucleolar protein NOP52/RRP1	A		0.068	1	1	1	1	153	81	92	No EST	No EST		
1183	AAACAAGGCA		up	down	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		7.599	1	1	1	1	62	69	59			360	1
1183	AAACAAGGCA		up	up	69.m15042	AN1728.1	AO070324000059	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit	C		4.141	1	1	1	1	167	91	83	40	0		
1183	AAACAAGGCA		up	up	58.m07660	AN1851.1	AO070292000043	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O		1.338	1	1	1	1	51	18	22	No EST	No EST		
1183	AAACAAGGCA		up	up	72.m19667	AN2173.1	AO070343000244	Predicted mitochondrial carrier protein	F		2.264	1	1	1	1	240	107	86	181	1		
1183	AAACAAGGCA		up	up	71.m15881	AN2247.1	AO070326000126	Myosin class II heavy chain	Z		0.726	1	1	1	1	122	132	105	No EST	No EST		
1183	AAACAAGGCA		up	up	71.m15945	AN2296.1	AO070295000077	RFX family transcription factor	K		0.455	1	1	1	0	45	29	90	No EST	No EST		
1183	AAACAAGGCA		up	up	59.m08499	AN2490.1	AO070312000130	Uncharacterized conserved protein, contains N-recognin-type Zn-finger				2	1	1	1	39	100	214	No EST	No EST		
1183	AAACAAGGCA		up	up	59.m08916	AN3082.1	AO070224000004	mRNA cleavage and polyadenylation factor II complex, subunit CFT2 (CPSF subunit)	A		0.068	1	1	1	1	246	125	208	No EST	No EST		
1183	AAACAAGGCA		up	up	54.m07043	AN4201.1	AO070231000023	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ		4.14390833818174 3.89274281632885	2	2	1	0	64	95	25	No EST	No EST		
1183	AAACAAGGCA		up	up	58.m07864	AN4460.1	AO070305000133	WD40-repeat-containing subunit of the 18S rRNA processing complex	A		0.068	1	1	1	1	158	250	220	No EST	No EST		
1183	AAACAAGGCA		up	up	69.m15743	AN5452.1	AO070239000031	Splicing factor 3b, subunit 3	A		0.068	1	1	1	0	45	88	280	179	1		
1183	AAACAAGGCA		up	up	69.m15436	AN5522.1	AO070341000367	predicted protein [Neurospora crassa]				1	1	1	0	260	5	59	No EST	No EST		
1183	AAACAAGGCA		up	up	69.m14811	AN5786.1	AO070249000032	hypothetical protein [Neurospora crassa]				1	1	1	1	55	54	34	No EST	No EST		
1183	AAACAAGGCA		up	up	65.m07278	AN6707.1	AO070339000137	DNA or RNA helicases of superfamily II	KL		0.45535230595195 3.75771934080085	1	1	1	1	79	70	72	No EST	No EST		
1183	AAACAAGGCA		up	up	71.m16029	AN6921.1	AO070313000060	HSP90 co-chaperone p23	O		1.338	1	1	1	0	228	65	81	71	1		
1183	AAACAAGGCA		up	up	57.m05902	AN7441.1	AO070229000013	Actin-related protein - Arp4p/Act3p	Z		0.726	1	1	1	0	52	45	161	144	1		
1183	AAACAAGGCA		up	down	57.m05902	AN7441.1	AO070229000013	Actin-related protein - Arp4p/Act3p	Z		0.726	1	1	1	0	273	70	102			453	1
1183	AAACAAGGCA		up	up	57.m05835	AN7504.1	AO070287000007	predicted protein [Neurospora crassa]				1	1	1	0	92	4	56	No EST	No EST		
1183	AAACAAGGCA		up	up	57.m05828	AN7511.1	AO070258000009	beta (1-3) glucanosyltransferase Gel3p [Aspergillus fumigatus]				1	1	1	0	311	348	462	178	0		
1183	AAACAAGGCA		up	up	71.m15820	AN7630.1	AO070294000040	Angio-associated migratory cell protein (contains WD40 repeats)				1	2	1	1	261	2	67	31	1		
1183	AAACAAGGCA		up	up	53.m04181	AN7997.1	AO070322000048	RNA polymerase III transcription factor (TF)IIIC subunit	K		0.455	1	1	1	0	230	265	177	No EST	No EST		
1183	AAACAAGGCA		up	up	62.m03370	AN8699.1	AO070315000126	Ubiquitin-specific protease	O		1.338	1	1	1	1	138	36	49	46	1		
1230	TTACCCCTC		up	up	71.m15641	AN0241.1	AO070284000071	Cu2+/Zn2+ superoxide dismutase SOD1	P		2.409	1	1	1	0	119	234	363	123	0		
1230	TTACCCCTC		up	up	54.m06621	AN0436.1	AO070338000281	Predicted E3 ubiquitin ligase	O		1.579	1	1	1	1	274	177	346	No EST	No EST		

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1230	TTACCCCTC		up	up	69.m15293	AN0554.1	AO070272000027	Aldehyde dehydrogenase	C		0.879	1	1	1	0	147	77	107	17	0		
1230	TTACCCCTC		up	up	70.m15312	AN0705.1	AO070343000504	Isoleucyl-tRNA synthetase	J		0.189	1	1	1	0	70	78	87	36	0		
1230	TTACCCCTC		up	up	57.m05745	AN1873.1	AO070341000189	Predicted phosphoglycerate mutase	G		1.132	1	1	1	1	61	189	291	No EST	No EST		
1230	TTACCCCTC		up	up	54.m06800	AN4218.1	AO070315000081	Translation elongation factor EF-1 alpha/Tu	J		0.189	1	1	1	1	308	166	222	96	0		
1230	TTACCCCTC		up	up	59.m09109	AN4862.1	AO070329000148	Ran GTPase-activating protein	AYT		2.81639696385209 0.923969068570605 3.23787140287071	1	1	1	0	1	205	227	No EST	No EST		
1230	TTACCCCTC		up	up	72.m19122	AN6035.1	AO070340000253	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	M		1.412	1	1	1	0	256	142	81	No EST	No EST		
1230	TTACCCCTC		up	up	62.m03087	AN6499.1	AO070222000013	NAD-dependent malate dehydrogenase	C		0.879	1	2	2	0	218	358	372	105	0		
1230	TTACCCCTC		up	up	71.m15250	AN6889.1	AO070314000032	hypothetical protein [Neurospora crassa]				1	1	1	0	193	77	52	No EST	No EST		
1230	TTACCCCTC		up	up	57.m05859	AN7479.1	AO070287000036	Asparaginyl-tRNA synthetase	J		0.189	1	1	1	1	333	190	264	97	0		
1230	TTACCCCTC		up	up	72.m19654	AN7620.1	AO070343000264	Uncharacterized conserved protein				1	1	1	0	140	364	253	No EST	No EST		
1230	TTACCCCTC		up	up	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		1.132	1	1	1	0	23	482	462	146	0		
1230	TTACCCCTC		up	down	53.m03797	AN8182.1	AO070310000143	Septin family protein (P-loop GTPase)	DZU		6.45029020252672 6.69416221306746 4.69906365271842	1	1	1	1	95	103	93			349	1
1230	TTACCCCTC		up	up	70.m15333	AN9437.1	AO070343000483	Predicted E3 ubiquitin ligase	O		1.579	1	1	1	0	6	155	166	No EST	No EST		
1270	CTTTTCCGTCC		up	up	58.m07773	AN1697.1	AO070305000021	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	A		4.877	2	2	1	0	180	273	152	No EST	No EST		
1270	CTTTTCCGTCC		up	up	55.m03061	AN1543.1	AO070339000311	Fumarate reductase, flavoprotein subunit	C		0.955	1	1	1	0	105	273	225	43	0		
1270	CTTTTCCGTCC		up	up	59.m09440	AN2999.1	AO070337000118	NADP-dependent isocitrate dehydrogenase	C		0.955	1	1	1	0	506	63	73	No EST	No EST		
1270	CTTTTCCGTCC		up	up	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.955	1	1	1	0	144	61	41	No EST	No EST		
1270	CTTTTCCGTCC		up	up	65.m07283	AN6694.1	AO070339000132	DNA replication checkpoint protein CHL12/CTF18	DL		4.39644867756451 4.68037978614166	1	1	1	1	267	201	473	No EST	No EST		
1270	CTTTTCCGTCC		up	up	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		3.089	3	3	2	0	29	197	230	66	0		
1270	CTTTTCCGTCC		up	up	59.m09156	AN4819.1	AO070327000168	Glutamine synthetase	E		3.089	2	1	1	0	18	235	159	No EST	No EST		
1270	CTTTTCCGTCC		up	up	54.m06742	AN4102.1	AO070342000101	Beta-glucosidase-related glycosidases	G		3.131	1	1	1	0	86	113	65	No EST	No EST		
1270	CTTTTCCGTCC		up	up	69.m14907	AN5210.1	AO070337000270	Pyruvate kinase	G		3.131	1	1	2	1	209	341	281	60	0		
1270	CTTTTCCGTCC		up	down	58.m07659	AN2057.1	AO070292000042	Mitochondrial/chloroplast ribosomal protein L12	J		3.806	1	1	1	1	140	122	160			334	1
1270	CTTTTCCGTCC		up	up	70.m15636	AN0640.1	AO070318000141	Sphingolipid hydroxylase	I		2.732	1	1	2	0	201	37	36	No EST	No EST		
1270	CTTTTCCGTCC		up	up	57.m05768	AN2068.1	AO070341000217	Vigilin	I		2.732	1	2	1	0	477	18	18	No EST	No EST		
1270	CTTTTCCGTCC		up	up	54.m06684	AN2747.1	AO070338000224	RNA polymerase subunit K	K		4.888	1	2	1	1	177	10	10	No EST	No EST		
1270	CTTTTCCGTCC		up	up	70.m15462	AN0866.1	AO070320000017	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O		3.587	2	1	3	0	60	365	258	No EST	No EST		
1270	CTTTTCCGTCC		up	up	59.m09263	AN2761.1	AO070327000023	Ubiquitin-protein ligase	O		3.587	2	1	1	0	258	284	240	144	0		
1270	CTTTTCCGTCC		up	up	72.m19699	AN2142.1	AO070343000188	Karyopherin (importin) alpha	U		0.293	4	1	1	0	66	46	48	No EST	No EST		
1270	CTTTTCCGTCC		up	down	59.m08643	AN3101.1	AO070334000142	Sensory transduction histidine kinase	T		3.422	1	1	1	0	188	251	179			No EST	No EST
1270	CTTTTCCGTCC		up	down	59.m08561	AN3171.1	AO070256000019	Ras-related small GTPase, Rho type				1	1	1	1	142	140	161			No EST	No EST
1270	CTTTTCCGTCC		up	up	62.m03223	AN6627.1	AO070326000078	Signal recognition particle receptor, alpha subunit	U		0.293	1	1	1	0	96	4	19	No EST	No EST		
1270	CTTTTCCGTCC		up	up	71.m15957	AN8825.1	AO070271000056	Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	U		0.293	2	1	1	0	237	232	243	No EST	No EST		
1270	CTTTTCCGTCC		up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		2.25138065907798 0.292507935544752	1	1	1	0	115	296	105	No EST	No EST		
1270	CTTTTCCGTCC		up	up	59.m09279	AN3425.1	AO070327000006	Interferon-related protein PC4 like	Z		1.110	1	1	1	0	315	14	295	No EST	No EST		
1270	CTTTTCCGTCC		up	up	71.m15259	AN6875.1	AO070314000048	Kinesin-like protein	Z		1.110	1	1	1	0	96	213	361	No EST	No EST		
1270	CTTTTCCGTCC		up	down	62.m03096	AN6510.1	AO070270000003	Translocase of outer mitochondrial membrane complex, subunit TOM40	U		0.293	1	1	1	0	120	100	88			463	1
1270	CTTTTCCGTCC		up	up	70.m14839	AN1382.1	AO070243000014	hypothetical protein [Neurospora crassa]				1	1	1	0	191	14	135	No EST	No EST		
1270	CTTTTCCGTCC		up	up	55.m03078	AN1562.1	AO070339000292	predicted protein [Neurospora crassa]				1	2	1	0	179	445	44	No EST	No EST		
1270	CTTTTCCGTCC		up	up	58.m07667	AN1844.1	AO070292000063	palFp [Emericella nidulans]				1	1	2	0	51	256	52	No EST	No EST		
1270	CTTTTCCGTCC		up	up	58.m07644	AN2056.1	AO070292000026	Uncharacterized conserved protein				1	1	1	0	47	336	279	No EST	No EST		
1270	CTTTTCCGTCC		up	up	71.m15938	AN2290.1	AO070295000069	FOG: Zn-finger				1	1	1	0	530	21	317	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1270	CTTTTCCGTCC		up	up	62.m03343	AN8723.1	AO070315000151	predicted protein [Neurospora crassa]				1	1	3	0	143	273	146	123	0		
1270	CTTTTCCGTCC		up	down	62.m03402	AN9500.1	AO070205000004	Cyclin				2	1	2	1	156	189	174			No EST	No EST
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	54.m06468	AN0275.1	AO070334000082	Cystine transporter Cystinosin	E		0.022	1	1	1	0	210	58	81	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15311	AN0495.1	AO070226000029	Formyltetrahydrofolate hydrolase	F		1.591	1	1	1	0	136	72	100	43	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15260	AN0589.1	AO070280000011	RNA Helicase	A		0.253	1	1	1	1	122	30	17	16	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m15350	AN0717.1	AO070343000449	Histidinol phosphate aminotransferase	E		0.022	1	1	1	0	113	30	123	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m15158	AN1084.1	AO070285000084	Mitochondrial translation elongation factor Tu	J		0.015	1	1	1	1	128	118	125	52	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m14959	AN1260.1	AO070214000005	mRNA splicing factor PRP31	A		0.253	1	1	1	0	122	67	83	40	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m07569	AN1964.1	AO070301000045	40S ribosomal protein S6	J		0.015	1	2	1	0	129	288	336	58	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05779	AN2080.1	AO070341000233	Polypeptide release factor 3	J		0.015	1	1	1	1	122	105	79	55	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	71.m15904	AN2263.1	AO070295000026	Predicted GTP-binding protein MMR1				1	1	1	1	212	48	64	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m08964	AN3851.1	AO070305000089	Putative N2,N2-dimethylguanosine tRNA methyltransferase	A		0.253	1	1	1	1	113	55	69	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m07895	AN4430.1	AO070273000027	Acetolactate synthase, small subunit	E		0.022	1	1	1	1	146	136	153	38	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05643	AN4488.1	AO070311000040	predicted protein [Neurospora crassa]				1	1	1	0	519	60	13	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05569	AN4557.1	AO070321000171	AAA+-type ATPase containing the peptidase M41 domain	O		2.830	1	1	1	1	219	222	149	148	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	down	59.m09189	AN4792.1	AO070329000054	Proteins containing the FAD binding domain	C		3.002	1	1	1	1	254	126	213			No EST	No EST
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15491	AN5443.1	AO070333000106	Predicted exosome subunit	J		0.015	1	2	2	0	186	81	88	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	72.m19170	AN5954.1	AO070340000308	RNA polymerase I-associated factor - PAF67	JK		0.0154573118753153 2.95574128653908	1	1	1	1	208	293	353	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	72.m19489	AN6371.1	AO070279000075	hypothetical protein [Neurospora crassa]				1	1	1	1	393	118	57	308	1		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15238	AN6390.1	AO070343000155	Homogentisate 1,2-dioxygenase	E		0.022	1	2	2	1	116	88	95	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05914	AN7430.1	AO070229000001	Glutamine amidotransferase/cyclase	E		0.022	1	1	1	1	212	96	45	45	0		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	72.m19584	AN7565.1	AO070343000408					1	1	1	1	90	196	70	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	71.m15766	AN7736.1	AO070325000157	Ankyrin repeat protein				2	2	1	0	180	312	221	No EST	No EST		
1291	TGAGTCAG	yAP1 (STGACTMA) [yeast_motifs_all];	up	up	52.m04030	AN9403.1	AO070274000014	Pyruvate dehydrogenase E1, beta subunit	C		3.002	1	1	1	1	198	185	89	101	0		
1407	CCCGTGACT		up	up	54.m06978	AN0304.1	AO070334000034	Fe2+/Zn2+ regulated transporter	P		4.838	1	1	1	0	377	94	49	116	1		
1407	CCCGTGACT		up	up	70.m15484	AN0881.1	AO070320000049	Alkylated DNA repair protein	L		1.004	1	2	1	0	18	107	41	No EST	No EST		
1407	CCCGTGACT		up	up	70.m15630	AN0989.1	AO070318000148	SWI-SNF chromatin-remodeling complex protein	B		4.324	1	2	1	1	311	16	17	No EST	No EST		
1407	CCCGTGACT		up	down	70.m15172	AN1061.1	AO070218000005	Amino acid transporters	E		3.523	1	1	1	0	160	119	258			No EST	No EST
1407	CCCGTGACT		up	up	70.m15021	AN1198.1	AO070331000203	Aminomethyl transferase	E		3.523	1	1	1	1	103	242	216	No EST	No EST		
1407	CCCGTGACT		up	up	70.m14989	AN1230.1	AO070331000242	Inner membrane protein required for assembly of the F0 sector of ATP synthase	O		0.405	1	1	1	1	137	30	21	No EST	No EST		
1407	CCCGTGACT		up	down	70.m14905	AN1326.1	AO070303000090	Protein kinase				1	1	1	0	222	267	207			130	0
1407	CCCGTGACT		up	up	55.m02913	AN1405.1	AO070242000008					1	1	1	0	130	423	408	No EST	No EST		
1407	CCCGTGACT		up	up	55.m02950	AN1448.1	AO070302000005	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	J	1	0.001	1	1	1	0	180	78	60	No EST	No EST		
1407	CCCGTGACT		up	up	58.m07665	AN1846.1	AO070292000059					1	1	1	0	274	249	328	No EST	No EST		
1407	CCCGTGACT		up	up	58.m08869	AN1933.1	AO070342000200	Predicted membrane protein				1	2	1	0	288	30	237	391	1		
1407	CCCGTGACT		up	up	58.m08945	AN1981.1	AO070301000066	Protein geranylgeranyltransferase type II, alpha subunit	O		0.405	1	1	1	0	134	48	85	No EST	No EST		
1407	CCCGTGACT		up	up	58.m07590	AN1984.1	AO070301000069	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K		0.630	1	2	1	0	347	152	188	No EST	No EST		

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1407	CCCGTGACT		up	up	71.m15940	AN2292.1	AO070295000071	Protein required for cell viability; Yil019wp [Saccharomyces cerevisiae]				1	1	1	0	51	28	30	No EST	No EST		
1407	CCCGTGACT		up	up	54.m06686	AN2745.1	AO070338000226	Acetyltransferase, (GNAT) family				1	1	1	1	138	128	137	No EST	No EST		
1407	CCCGTGACT		up	up	59.m08755	AN2904.1	AO070338000101	26S proteasome regulatory complex, ATPase RPT3	O		0.405	1	1	1	0	201	317	400	95	0		
1407	CCCGTGACT		up	up	59.m08756	AN2905.1	AO070338000100	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	K		0.630	1	1	1	0	468	26	34	No EST	No EST		
1407	CCCGTGACT		up	up	59.m09022	AN2992.1	AO070337000126	Translation initiation factor 2, beta subunit (eIF-2beta)	J	1	0.001	1	1	1	0	171	18	25	83	1		
1407	CCCGTGACT		up	up	67.m02926	AN3217.1	AO070330000062	putative transcriptional activator with fungal binuclear cluster domain [Schizosaccharomyces pombe]				1	1	1	0	97	82	109	70	0		
1407	CCCGTGACT		up	up	58.m07438	AN3660.1	AO070342000025	Methyltransferase-like protein				1	1	1	1	214	132	178	No EST	No EST		
1407	CCCGTGACT		up	up	54.m06715	AN4073.1	AO070342000062	40S ribosomal protein S12	J	1	0.001	1	2	1	0	178	29	57	No EST	No EST		
1407	CCCGTGACT		up	up	58.m07362	AN4163.1	AO070342000193	G protein beta subunit-like protein	T		3.623	1	2	1	1	190	12	173	77	1		
1407	CCCGTGACT		up	up	58.m07955	AN4377.1	AO070261000012	predicted protein [Neurospora crassa]				1	2	1	0	185	49	105	No EST	No EST		
1407	CCCGTGACT		up	up	57.m05585	AN4536.1	AO070321000153	Serine/threonine protein kinase	TKL		3.62315832294026 0.629803315005952 1.00359496612816	1	1	1	1	417	33	7	No EST	No EST		
1407	CCCGTGACT		up	up	59.m09460	AN4788.1	AO070329000059	RNA splicing factor - Slu7p	A		1.536	1	1	1	0	25	63	82	No EST	No EST		
1407	CCCGTGACT		up	up	59.m08819	AN4916.1	AO070338000027	40S ribosomal protein S7	J	1	0.001	1	1	1	0	228	43	140	82	1		
1407	CCCGTGACT		up	down	63.m00628	AN5049.1	AO070338000189	Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	P		4.838	1	1	1	0	258	81	128			No EST	No EST
1407	CCCGTGACT		up	up	58.m07493	AN5569.1	AO070328000037	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB1	KL		0.629803315005952 1.00359496612816	1	1	1	0	205	109	182	No EST	No EST		
1407	CCCGTGACT		up	up	65.m07407	AN5681.1	AO070309000096	Predicted E3 ubiquitin ligase, integral peroxisomal membrane protein	O		0.405	2	1	1	1	43	83	89	52	0		
1407	CCCGTGACT		up	up	54.m06834	AN5715.1	AO070324000138	40s ribosomal protein S26	J	1	0.001	1	1	1	1	173	189	60	No EST	No EST		
1407	CCCGTGACT		up	up	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J	1	0.001	1	1	1	1	204	29	2	101	1		
1407	CCCGTGACT		up	up	69.m14856	AN5741.1	AO070341000018	predicted protein [Neurospora crassa]				1	1	1	0	92	360	295	No EST	No EST		
1407	CCCGTGACT		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		0.405	1	1	1	0	241	77	77	140	1		
1407	CCCGTGACT		up	up	72.m19412	AN6245.1	AO070304000099	predicted protein [Neurospora crassa]				1	1	1	0	134	107	310	No EST	No EST		
1407	CCCGTGACT		up	up	62.m03227	AN6631.1	AO070326000083	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	C		4.065	1	1	1	0	106	103	127	35	0		
1407	CCCGTGACT		up	up	71.m15298	AN6841.1	AO070314000098	Mitochondrial inner membrane protease, subunit IMP1	O		0.405	1	1	1	0	96	17	26	No EST	No EST		
1407	CCCGTGACT		up	up	57.m05838	AN7501.1	AO070287000012	LisH motif-containing protein	Z		4.789	1	1	1	0	235	131	29	No EST	No EST		
1407	CCCGTGACT		up	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J	1	0.001	1	1	1	1	146	105	113	73	0		
1407	CCCGTGACT		up	up	62.m03454	AN8722.1	AO070315000150	ATP-dependent RNA helicase	A		1.536	1	1	1	1	281	173	197	186	1		
1407	CCCGTGACT		up	up	71.m15986	AN8851.1	AO070271000025	Pseudouridine synthase	J	1	0.001	1	1	1	0	209	73	36	92	1		
1407	CCCGTGACT		up	up	56.m02291	AN8880.1	AO070293000010	Sortilin and related receptors				1	1	1	0	287	49	83	No EST	No EST		
1407	CCCGTGACT		up	up	52.m03843	AN9360.1	AO070315000040	Protein containing a U1-type Zn-finger and implicated in RNA splicing or processing	A		1.536	1	1	1	0	199	31	218	No EST	No EST		
1407	CCCGTGACT		up	up	72.m19967	AN9468.1	AO070340000317	40S ribosomal protein S16	J	1	0.001	1	1	1	0	42	44	58	73	1		
1426	CCCGAGGT		up	up	71.m15403	AN0122.1	AO070311000090	ATP-dependent Lon protease, bacterial type	O		0.877	1	1	1	1	218	92	61	78	0		
1426	CCCGAGGT		up	up	54.m06650	AN0426.1	AO070338000276	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I		0.011	1	1	1	1	325	95	166	No EST	No EST		
1426	CCCGAGGT		up	down	70.m15270	AN0667.1	AO070343000553	Mannose-6-phosphate isomerase	G		2.406	1	1	1	0	175	130	132			17	0
1426	CCCGAGGT		up	up	70.m15622	AN0981.1	AO070318000167	Long chain fatty acid elongase	I		0.011	1	1	1	0	432	34	29	No EST	No EST		
1426	CCCGAGGT		up	up	71.m15534	AN2332.1	AO070323000014	Succinate dehydrogenase, Fe-S protein subunit	C	1	0.001	1	1	1	1	234	260	324	138	0		
1426	CCCGAGGT		up	up	59.m09097	AN2916.1	AO070329000155	Succinate dehydrogenase, flavoprotein subunit	C	1	0.001	1	1	1	1	139	158	175	No EST	No EST		
1426	CCCGAGGT		up	up	59.m09078	AN2925.1	AO070337000214	Peroxisome assembly factor 2 containing the AAA+-type ATPase domain	O		0.877	1	1	2	1	284	170	147	No EST	No EST		
1426	CCCGAGGT		up	up	59.m09056	AN2938.1	AO070337000168	Peroxisomal NUDIX hydrolase	L		1.366	1	1	1	1	117	133	205	No EST	No EST		
1426	CCCGAGGT		up	up	59.m08411	AN3191.1	AO070338000263	Esterase/lipase	I		0.011	1	1	1	0	178	174	44	No EST	No EST		
1426	CCCGAGGT		up	up	54.m06786	AN4230.1	AO070234000016	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I		0.011	1	1	1	1	182	35	70	No EST	No EST		
1426	CCCGAGGT		up	up	65.m07435	AN4261.1	AO070277000030					1	1	1	0	109	99	91	No EST	No EST		
1426	CCCGAGGT		up	up	54.m07051	AN5113.1	AO070291000066	Peroxisomal biogenesis protein (peroxin 16)	U		1.739	1	0	1	0	190	0	4	No EST	No EST		
1426	CCCGAGGT		up	up	72.m18955	AN5828.1	AO070260000018	Cytochrome b5	C	1	0.001	1	1	1	0	195	63	62	No EST	No EST		
1426	CCCGAGGT		up	up	72.m19901	AN6167.1	AO070343000365	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	1	0.001	1	1	1	0	136	242	165	No EST	No EST		
1426	CCCGAGGT		up	up	56.m02337	AN9014.1	AO070321000049	Glycolate oxidase	C	1	0.001	0	1	1	0	177	15	89	No EST	No EST		
1453	TTTGGTCTT		down	down	70.m14971	AN1256.1	AO070223000013	RNAse L inhibitor, ABC superfamily	A		0.530	1	1	1	0	283	228	123			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1453	TTTGGTCTT		down	down	58.m07718	AN1639.1	AO070299000037	Thioredoxin-like protein	O		3.370	1	1	1	1	232	261	222			No EST	No EST
1453	TTTGGTCTT		down	up	58.m08938	AN1854.1	AO070292000029	hypothetical protein [Schizosaccharomyces pombe]				1	1	1	0	77	86	140	No EST	No EST		
1453	TTTGGTCTT		down	down	54.m06676	AN2734.1	AO070338000217	60S acidic ribosomal protein P0	J		0.786	1	1	1	1	277	255	270			151	0
1453	TTTGGTCTT		down	down	59.m09039	AN2973.1	AO070337000148	SNF2 family DNA-dependent ATPase	B		0.111	1	1	1	0	57	25	39			No EST	No EST
1453	TTTGGTCTT		down	down	59.m09009	AN3005.1	AO070337000107	Protein involved in vacuole import and degradation	U		0.766	1	2	2	0	173	10	83			241	1
1453	TTTGGTCTT		down	down	59.m08502	AN3188.1	AO070312000135	Phosphatidylserine decarboxylase	I		2.871	1	1	2	1	403	392	229			182	0
1453	TTTGGTCTT		down	up	58.m07411	AN3624.1	AO070342000127	Cation transport ATPase	P		6.449	1	1	1	0	165	60	353	No EST	No EST		
1453	TTTGGTCTT		down	down	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		0.786	1	1	1	1	103	133	105			438	1
1453	TTTGGTCTT		down	down	72.m19026	AN6138.1	AO070340000064	DNA-binding cell division cycle control protein	D		1.956	1	1	1	0	109	45	104			No EST	No EST
1453	TTTGGTCTT		down	up	62.m03226	AN6630.1	AO070326000082	Transcription factor containing NAC and TS-N domains	K		2.703	1	1	1	1	236	101	174	276	1		
1453	TTTGGTCTT		down	down	71.m15272	AN6859.1	AO070314000076	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains	AK		0.5296256 43536033 2.7026576 3160642	1	1	1	0	175	123	168			No EST	No EST
1453	TTTGGTCTT		down	down	57.m05468	AN7687.1	AO070325000085	Translocase of outer mitochondrial membrane complex, subunit TOM70/TOM72	U		0.766	1	1	1	0	353	155	296			No EST	No EST
1453	TTTGGTCTT		down	down	53.m04190	AN8042.1	AO070330000004	Histone deacetylase complex, catalytic component HDA1	B		0.111	1	1	1	0	26	326	277			137	0
1453	TTTGGTCTT		down	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		2.703	1	1	1	1	131	355	423	157	0		
1453	TTTGGTCTT		down	down	52.m03971	AN9297.1	AO070279000023	Myosin-crossreactive antigen				1	1	1	0	18	66	128			194	1
1475	TTTCCTTT		down	down	71.m15325	AN0056.1	AO070314000131	hypothetical protein [Neurospora crassa]				1	1	2	0	278	137	198			No EST	No EST
1475	TTTCCTTT		down	down	71.m16046	AN0077.1	AO070311000138	Iron/ascorbate family oxidoreductases	Q		5.896	1	2	1	1	302	206	339			No EST	No EST
1475	TTTCCTTT		down	down	71.m15404	AN0123.1	AO070311000089	Predicted mitochondrial ribosomal protein L23	J		2.883	1	1	1	0	23	55	22			No EST	No EST
1475	TTTCCTTT		down	up	71.m15450	AN0176.1	AO070321000065	GATA-4/5/6 transcription factors	K		2.063	2	1	1	0	208	223	259	No EST	No EST		
1475	TTTCCTTT		down	up	71.m16095	AN0226.1	AO070284000066	Ubiquitin-protein ligase	O		2.175	1	1	3	0	141	405	37	119	0		
1475	TTTCCTTT		down	up	54.m06965	AN0261.1	AO070334000097	Vesicle coat complex COPII, subunit SEC23	U		2.806	1	2	1	0	319	32	25	No EST	No EST		
1475	TTTCCTTT		down	down	54.m06503	AN0279.1	AO070334000092	Transcription factor, Myb superfamily	K		2.063	2	1	2	0	36	112	146			No EST	No EST
1475	TTTCCTTT		down	down	54.m06398	AN0356.1	AO070318000032	predicted protein [Neurospora crassa]				1	1	1	0	196	189	242			75	0
1475	TTTCCTTT		down	down	54.m06391	AN0360.1	AO070318000038	RNA polymerase I transcription factor UAF	K		2.063	1	1	2	0	91	142	103			393	1
1475	TTTCCTTT		down	down	69.m15281	AN0565.1	AO070272000043	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				4	3	5	1	319	362	191			No EST	No EST
1475	TTTCCTTT		down	down	69.m15273	AN0573.1	AO070272000052	Ypt/Rab GTPase activating protein	U		2.806	2	1	2	0	107	18	27			No EST	No EST
1475	TTTCCTTT		down	down	70.m15259	AN0655.1	AO070343000571	hypothetical protein [Neurospora crassa]				2	2	2	0	165	113	77			No EST	No EST
1475	TTTCCTTT		down	down	70.m15280	AN0676.1	AO070343000539	Gamma tubulin	Z		0.087	1	2	1	1	46	18	404			98	1
1475	TTTCCTTT		down	down	70.m15319	AN0734.1	AO070343000495	Histone H4	B		7.994	4	2	1	1	11	85	158			342	1
1475	TTTCCTTT		down	up	70.m15369	AN0766.1	AO070316000078	hypothetical protein [Novosphingobium aromaticivorans]				1	1	4	0	54	355	41	377	1		
1475	TTTCCTTT		down	up	70.m15460	AN0867.1	AO070320000018	hypothetical protein [Neurospora crassa]				2	2	2	1	87	130	137	No EST	No EST		
1475	TTTCCTTT		down	up	70.m15477	AN0874.1	AO070320000033	Poly(A) polymerase and related nucleotidyltransferases	A		6.261	1	1	1	0	180	115	172	No EST	No EST		
1475	TTTCCTTT		down	down	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		6.2508640 0985864 2.8058037 5590618	1	2	2	0	49	99	103			No EST	No EST
1475	TTTCCTTT		down	up	70.m15143	AN1089.1	AO070285000061	Thioredoxin binding protein TBP-2/VDUP1				4	3	3	0	136	5	61	No EST	No EST		
1475	TTTCCTTT		down	down	70.m15054	AN1166.1	AO070331000160	60s ribosomal protein L6	J		2.883	2	1	1	0	263	274	261			No EST	No EST
1475	TTTCCTTT		down	up	70.m15031	AN1190.1	AO070331000190	Nuclear pore complex, rNup107 component (sc Nup84)	YU		6.2508640 0985864 2.8058037 5590618	1	1	2	0	300	197	196	No EST	No EST		
1475	TTTCCTTT		down	down	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		8.153	2	1	1	1	60	129	57			360	1
1475	TTTCCTTT		down	up	70.m14985	AN1233.1	AO070331000247	Nucleolar GTPase/ATPase p130	Y		6.251	2	1	2	0	312	164	99	No EST	No EST		
1475	TTTCCTTT		down	down	55.m03042	AN1523.1	AO070334000241	F0F1-type ATP synthase, alpha subunit	C		2.510	1	1	2	1	390	372	99			403	1
1475	TTTCCTTT		down	down	58.m07708	AN1613.1	AO070299000064					1	1	1	0	114	138	278			No EST	No EST
1475	TTTCCTTT		down	down	58.m07754	AN1677.1	AO070299000001	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQ		5.0794773 239054 5.8962951 2247155	1	1	1	0	43	125	23			240	1
1475	TTTCCTTT		down	down	69.m14936	AN1918.1	AO070341000122	Phosphoenolpyruvate carboxykinase (ATP)	C		2.510	4	1	4	1	14	19	20			195	1
1475	TTTCCTTT		down	down	58.m07346	AN1950.1	AO070342000218	conserved hypothetical protein [Neurospora crassa]				2	2	1	0	104	216	203			496	1
1475	TTTCCTTT		down	down	58.m07606	AN1997.1	AO070301000092	FOG: Zn-finger				2	2	2	1	110	148	111			No EST	No EST
1475	TTTCCTTT		down	down	58.m07617	AN2008.1	AO070179000004	Predicted hydrolase (HAD superfamily)				2	1	2	1	68	142	185			No EST	No EST

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1475	TTTCCTTT		down	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		2.175	1	1	1	0	165	197	188	173	0		
1475	TTTCCTTT		down	up	57.m05773	AN2070.1	AO070341000226	PHD finger protein AF10				2	1	1	0	156	129	168	No EST	No EST		
1475	TTTCCTTT		down	up	69.m15160	AN2120.1	AO070332000051	Karyopherin (importin) beta 3	YU		6.25086400985864 2.80580375590618	1	1	3	0	193	252	187	No EST	No EST		
1475	TTTCCTTT		down	down	72.m19712	AN2129.1	AO070278000034	COP9 signalosome, subunit CSN5	OT		2.17463453024612 0.696605565444995	1	2	1	0	266	288	285			No EST	No EST
1475	TTTCCTTT		down	down	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		2.510	3	2	3	1	26	10	24			307	1
1475	TTTCCTTT		down	up	59.m09396	AN2911.1	AO070338000094	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K		2.063	1	1	1	0	235	482	298	No EST	No EST		
1475	TTTCCTTT		down	down	59.m09068	AN2927.1	AO070337000182	Dual specificity; serine/threonine and tyrosine kinase	D		2.033	1	2	1	0	119	40	129			No EST	No EST
1475	TTTCCTTT		down	down	59.m08612	AN3124.1	AO070303000023	Kinesin-like protein	Z		0.087	1	1	2	0	38	4	69			146	1
1475	TTTCCTTT		down	down	59.m08573	AN3181.1	AO070256000007	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	T		0.697	1	2	1	0	180	20	102			No EST	No EST
1475	TTTCCTTT		down	up	59.m09479	AN3445.1	AO070265000021	Extracellular protein SEL-1 and related proteins	MOT		10.7749188504509 2.17463453024612 0.696605565444995	1	2	2	0	29	233	262	No EST	No EST		
1475	TTTCCTTT		down	up	69.m14984	AN3940.1	AO070341000052	Predicted alpha-helical protein, potentially involved in replication/repair	L		4.771	2	1	1	1	131	228	232	No EST	No EST		
1475	TTTCCTTT		down	down	69.m14975	AN3946.1	AO070341000066	Mitotic checkpoint serine/threonine protein kinase	D		2.033	1	1	2	0	91	172	313			No EST	No EST
1475	TTTCCTTT		down	down	54.m06707	AN4064.1	AO070342000052	Mitochondrial ADP/ATP carrier proteins	C		2.510	1	1	1	0	202	176	180			No EST	No EST
1475	TTTCCTTT		down	down	54.m06733	AN4088.1	AO070342000091	predicted protein [Neurospora crassa]				1	2	1	0	249	283	509			No EST	No EST
1475	TTTCCTTT		down	down	54.m06794	AN4223.1	AO070234000027	Cytoskeleton-associated protein and related proteins	Z		0.087	3	1	1	1	167	120	135			247	1
1475	TTTCCTTT		down	down	58.m07927	AN4394.1	AO070261000039					2	2	2	0	284	109	278			No EST	No EST
1475	TTTCCTTT		down	up	57.m05647	AN4484.1	AO070311000033	PHD finger protein				3	1	1	0	263	460	184	No EST	No EST		
1475	TTTCCTTT		down	down	71.m15687	AN4699.1	AO070329000175	predicted protein [Neurospora crassa]				1	1	1	0	381	320	273			No EST	No EST
1475	TTTCCTTT		down	up	59.m09466	AN4859.1	AO070329000143	Plasma membrane H+-transporting ATPase	P		5.019	4	1	1	1	253	164	166	103	0		
1475	TTTCCTTT		down	down	59.m08868	AN4965.1	AO070288000030	Negative regulator of transcription	K		2.063	2	1	2	0	177	273	324			No EST	No EST
1475	TTTCCTTT		down	down	59.m09404	AN4978.1	AO070288000045	Alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)	A		6.261	1	1	1	0	89	119	280			No EST	No EST
1475	TTTCCTTT		down	up	59.m08665	AN5014.1	AO070334000120	60S ribosomal protein L22	J		2.883	1	1	1	0	332	88	84	70	0		
1475	TTTCCTTT		down	down	69.m14876	AN5179.1	AO070247000010	Diphthamide biosynthesis protein	J		2.883	1	1	1	0	181	207	76			170	0
1475	TTTCCTTT		down	up	69.m15483	AN5449.1	AO070239000028	Arylsulfatase A and related enzymes	P		5.019	3	2	1	0	29	205	238	No EST	No EST		
1475	TTTCCTTT		down	down	58.m07499	AN5573.1	AO070328000033	predicted protein [Neurospora crassa]				1	1	1	0	155	287	371			No EST	No EST
1475	TTTCCTTT		down	up	58.m07334	AN5642.1	AO070342000232	predicted protein [Neurospora crassa]				2	1	3	0	198	163	38	No EST	No EST		
1475	TTTCCTTT		down	down	54.m06820	AN5705.1	AO070324000154	Golgi protein	U		2.806	1	1	1	0	163	224	107			No EST	No EST
1475	TTTCCTTT		down	down	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		2.883	1	2	1	1	25	37	27			438	1
1475	TTTCCTTT		down	down	54.m06848	AN5728.1	AO070324000123	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	T		0.697	2	1	1	0	274	292	58			528	1
1475	TTTCCTTT		down	down	72.m19916	AN5836.1	AO070340000001	RNA polymerase II, large subunit	K		2.063	1	1	2	0	164	20	46			No EST	No EST
1475	TTTCCTTT		down	down	72.m19954	AN5911.1	AO070248000037	Actin-related protein	Z		0.087	1	1	1	0	2	180	13			No EST	No EST
1475	TTTCCTTT		down	down	72.m19145	AN5995.1	AO070340000282	Carbonic anhydrase				2	1	1	0	39	6	18			No EST	No EST
1475	TTTCCTTT		down	down	72.m19290	AN6192.1	AO070308000109	Serine/threonine protein kinase	T		0.697	1	1	1	0	31	186	273			No EST	No EST
1475	TTTCCTTT		down	down	72.m19409	AN6251.1	AO070304000036	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T		0.697	2	1	1	0	106	86	109			No EST	No EST
1475	TTTCCTTT		down	down	72.m19508	AN6347.1	AO070275000012	Serine/threonine protein kinase				1	1	1	0	47	47	127			No EST	No EST
1475	TTTCCTTT		down	down	62.m03201	AN6597.1	AO070326000046	Protein kinase PITSLRE and related kinases				1	2	1	0	113	51	36			No EST	No EST
1475	TTTCCTTT		down	up	62.m03196	AN6601.1	AO070326000052	Transmembrane protein				1	1	1	0	67	129	107	No EST	No EST		
1475	TTTCCTTT		down	up	62.m03214	AN6618.1	AO070326000068	Ypt/Rab-specific GTPase-activating protein GYP7 and related proteins	T		0.697	1	2	1	0	115	112	127	No EST	No EST		
1475	TTTCCTTT		down	up	65.m07245	AN6725.1	AO070339000169	Protein involved in mRNA turnover and stability	A		6.261	1	2	1	1	139	35	46	45	1		
1475	TTTCCTTT		down	up	65.m07227	AN6740.1	AO070339000186					1	1	3	0	429	62	34	No EST	No EST		

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1475	TTTCCTTT		down	down	57.m05403	AN7626.1	AO070294000087	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		0.696605565444995 0.0870047362491821	1	2	1	0	20	10	89			No EST	No EST
1475	TTTCCTTT		down	down	62.m03408	AN8666.1	AO070269000070	von Willebrand factor and related coagulation proteins	V		5.723	2	1	2	0	60	424	116			No EST	No EST
1475	TTTCCTTT		down	down	62.m03339	AN8741.1	AO070250000041	FOG: Zn-finger				2	1	2	1	92	38	30			No EST	No EST
1475	TTTCCTTT		down	down	71.m15957	AN8825.1	AO070271000056	Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	U		2.806	1	2	1	0	100	37	200			No EST	No EST
1475	TTTCCTTT		down	down	71.m15961	AN8830.1	AO070271000049	Checkpoint kinase and related serine/threonine protein kinases	D		2.033	1	2	5	0	211	159	222			327	1
1475	TTTCCTTT		down	down	66.m04555	AN9096.1	AO070332000179					2	3	1	0	97	36	299			370	1
1475	TTTCCTTT		down	down	62.m03402	AN9500.1	AO070205000004	Cyclin				4	1	2	1	32	66	52			No EST	No EST
1581	TGCATATA		down	down	69.m15252	AN0595.1	AO070280000021	NADP/FAD dependent oxidoreductase	C		0.234	1	1	1	1	100	68	66			No EST	No EST
1581	TGCATATA		down	down	70.m15234	AN1016.1	AO070312000002	G-protein alpha subunit (small G protein superfamily)	DT		0.955622978532695 0.307523087264298	1	1	1	0	415	448	454			No EST	No EST
1581	TGCATATA		down	down	69.m15037	AN1731.1	AO070324000062	Proline oxidase	E		1.676	1	1	1	1	124	85	119			137	1
1581	TGCATATA		down	down	59.m08494	AN2496.1	AO070312000124	Putative transmembrane protein cmp44E				1	1	1	0	122	104	133			No EST	No EST
1581	TGCATATA		down	up	59.m08506	AN3145.1	AO070312000163	Splicing coactivator SRm160/300, subunit SRm300	A		4.479	1	1	1	0	26	468	545	No EST	No EST		
1581	TGCATATA		down	down	58.m07387	AN3587.1	AO070342000137	Ubiquitin-specific protease	O		0.488	1	1	1	0	37	35	39			No EST	No EST
1581	TGCATATA		down	down	54.m07034	AN4238.1	AO070234000002	Ribosomal protein S6 kinase and related proteins	T		0.308	1	1	1	0	63	38	38			151	1
1581	TGCATATA		down	down	58.m07904	AN4415.1	AO070273000036	Holocytochrome c synthase/heme-lyase	CO		0.233637461301134 0.487836716418576	1	1	1	0	50	131	25			No EST	No EST
1581	TGCATATA		down	down	72.m19781	AN7284.1	AO070297000024	Mitochondrial ribosomal protein L17	J		1.591	1	1	1	1	152	105	144			No EST	No EST
1602	AGGCGGT		up	up	71.m15417	AN0133.1	AO070321000120	mRNA splicing factor ATP-dependent RNA helicase	A		0.330	1	1	1	0	183	100	93	No EST	No EST		
1602	AGGCGGT		up	up	54.m06468	AN0275.1	AO070334000082	Cystine transporter Cystinosin	E		3.543	1	1	1	0	188	80	105	No EST	No EST		
1602	AGGCGGT		up	up	69.m15266	AN0582.1	AO070280000004	Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	L		4.866	1	1	1	1	65	55	106	No EST	No EST		
1602	AGGCGGT		up	up	70.m15629	AN0988.1	AO070318000150	LAMMER dual specificity kinases	T		0.803	1	1	1	1	311	190	133	No EST	No EST		
1602	AGGCGGT		up	up	70.m15237	AN1019.1	AO070343000596	Cullins	D		1.884	1	1	1	1	494	44	2	69	1		
1602	AGGCGGT		up	up	70.m15196	AN1038.1	AO070336000073	Putative transmembrane protein				1	1	1	0	156	129	166	No EST	No EST		
1602	AGGCGGT		up	up	70.m15203	AN1047.1	AO070313000109	Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	O		1.485	1	1	1	0	486	6	6	No EST	No EST		
1602	AGGCGGT		up	up	70.m14862	AN1367.1	AO070215000014	WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis	J		0.656	1	1	1	0	56	33	19	No EST	No EST		
1602	AGGCGGT		up	up	55.m02969	AN1467.1	AO070306000090	Serine/threonine protein phosphatase	T		0.803	2	1	2	1	384	84	131	177	1		
1602	AGGCGGT		up	up	55.m03057	AN1538.1	AO070334000262	Transcription initiation factor IIF, small subunit (RAP30)	K		3.086	1	1	2	1	207	166	156	No EST	No EST		
1602	AGGCGGT		up	up	58.m07570	AN1965.1	AO070301000046	Ribose-phosphate pyrophosphokinase	FE		3.58211435600003 3.54258558033525	1	1	1	0	284	83	29	125	1		
1602	AGGCGGT		up	up	58.m07575	AN1970.1	AO070301000054	Mitochondrial/chloroplast ribosomal protein L28	J		0.656	1	1	1	0	181	28	24	No EST	No EST		
1602	AGGCGGT		up	up	72.m19694	AN2147.1	AO070343000196	rRNA processing protein Rrp5	A		0.330	2	2	2	1	140	13	13	No EST	No EST		
1602	AGGCGGT		up	up	59.m09061	AN2933.1	AO070337000174	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	BT		4.01701212915162 0.803304288730723	1	1	1	0	282	88	101	No EST	No EST		
1602	AGGCGGT		up	up	54.m06754	AN4192.1	AO070342000112	Molecular chaperone (DnaJ superfamily)	O		1.485	1	1	1	1	98	484	454	No EST	No EST		
1602	AGGCGGT		up	up	58.m07861	AN4471.1	AO070305000130	WD40 repeat-containing protein				1	1	1	0	122	147	259	36	0		
1602	AGGCGGT		up	up	57.m05499	AN4581.1	AO070316000164	Protein involved in high osmolarity signaling pathway	T		0.803	1	1	1	1	112	53	63	No EST	No EST		
1602	AGGCGGT		up	up	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				1	1	1	1	306	131	157	345	1		
1602	AGGCGGT		up	up	54.m06828	AN5713.1	AO070324000145	Chaperonin complex component, TCP-1 eta subunit (CCT7)	O		1.485	1	1	1	1	189	86	71	No EST	No EST		
1602	AGGCGGT		up	up	72.m19263	AN5871.1	AO070308000137	Predicted RNA methylase involved in rRNA processing	A		0.330	1	1	1	0	231	132	16	No EST	No EST		
1602	AGGCGGT		up	up	72.m19188	AN5972.1	AO070340000330	Vesicle coat complex COPI, beta' subunit	U		1.721	1	1	1	1	283	23	55	370	1		

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1602	AGGCGGT		up	up	72.m19097	AN6061.1	AO070340000187	hypothetical protein [Schizosaccharomyces pombe]				1	1	1	0	459	9	46	32	1		
1602	AGGCGGT		up	up	72.m19947	AN6073.1	AO070340000117	Prohibitin-like protein	O		1.485	1	1	1	0	87	71	70	No EST	No EST		
1602	AGGCGGT		up	up	72.m19048	AN6110.1	AO070340000096	Uncharacterized conserved protein				1	1	1	1	114	11	11	No EST	No EST		
1602	AGGCGGT		up	up	72.m19323	AN6311.1	AO070308000066	Cl- channel CLC-3 and related proteins (CLC superfamily)	P		4.858	1	1	1	1	137	24	23	No EST	No EST		
1602	AGGCGGT		up	up	62.m03148	AN6561.1	AO070326000002	Uncharacterized conserved protein				1	1	1	1	143	96	139	55	0		
1602	AGGCGGT		up	up	62.m03207	AN6591.1	AO070326000039	Nuclear export receptor CSE1/CAS (importin beta superfamily)	YU		2.76099808291866 1.72095378687229	1	1	1	1	228	158	155	No EST	No EST		
1602	AGGCGGT		up	up	72.m19751	AN7312.1	AO070297000060	tRNA nucleotidyltransferase/poly(A) polymerase	J		0.656	1	1	1	0	144	121	134	No EST	No EST		
1602	AGGCGGT		up	up	69.m15143	AN7525.1	AO070258000031	ATPases involved in chromosome partitioning	D		1.884	1	1	1	0	20	10	8	No EST	No EST		
1602	AGGCGGT		up	up	57.m05423	AN7659.1	AO070268000028	ATP-dependent RNA helicase	A		0.330	1	1	1	1	379	23	22	172	1		
1602	AGGCGGT		up	up	53.m03925	AN8072.1	AO070330000030	hypothetical protein B13N20.140 [imported] - Neurospora crassa				1	1	1	0	76	28	27	No EST	No EST		
1602	AGGCGGT		up	up	58.m08926	AN8488.1	AO070299000105	SNARE protein YKT6, synaptobrevin/VAMP syperfamily	U		1.721	1	1	1	0	91	72	32	No EST	No EST		
1602	AGGCGGT		up	up	62.m03394	AN8676.1	AO070315000096	Regulator of arginine metabolism and related MADS box-containing transcription factors	K		3.086	1	1	1	1	239	237	312	157	0		
1602	AGGCGGT		up	up	62.m03357	AN8712.1	AO070315000138	Translation initiation factor 1A (eIF-1A)	J		0.656	1	0	1	0	248	0	1	96	1		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	71.m15475	AN0212.1	AO070321000032	predicted protein [Neurospora crassa]				1	1	1	1	348	125	16	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	69.m15311	AN0495.1	AO070226000029	Formyltetrahydrofolate hydrolase	F		2.031	1	1	1	0	156	58	79	43	0		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	down	69.m15281	AN0565.1	AO070272000043	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				1	1	1	1	186	180	180			No EST	No EST
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	down	70.m15670	AN0609.1	AO070280000031	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ		2.98535660617829 4.06214900466041	2	2	1	0	136	214	347			No EST	No EST
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	70.m15605	AN0956.1	AO070320000158	tRNA-dihydrouridine synthase	J		1.940	1	1	1	1	213	8	18	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	69.m15052	AN1751.1	AO070324000042	SAM-dependent methyltransferase/cell division protein FtsJ	D		0.862	1	1	1	1	114	1	1	No EST	No EST		

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1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	58.m07336	AN1957.1	AO070342000228	RNA Methylase, SpoU family	A		0.086	1	1	1	1	119	82	55	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	58.m07589	AN1983.1	AO070301000068	WD40 repeat-containing protein				1	1	1	1	212	230	80	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	72.m19695	AN2146.1	AO070343000195	Transcription regulator XNP/ATRX, DEAD-box superfamily	K		0.495	1	2	2	1	95	517	328	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	71.m15940	AN2292.1	AO070295000071	Protein required for cell viability; Yil019wp [Saccharomyces cerevisiae]				1	1	1	1	61	19	21	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	59.m08751	AN2901.1	AO070338000106	Arginase	E		0.052	2	1	1	0	107	242	152	246	1		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	down	59.m09424	AN2977.1	AO070337000144	Mitochondrial phosphate carrier protein	C		3.029	1	1	1	1	261	220	233			107	0
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	59.m08566	AN3176.1	AO070256000014	ATP-dependent RNA helicase	A		0.086	1	1	1	0	114	168	157	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	66.m04635	AN3367.1	AO070281000025	Translin-associated protein X				1	1	1	1	96	75	141	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	59.m09314	AN3451.1	AO070265000026	Chromosome condensation complex Condensin, subunit D2	BD		2.3361163957962 0.861758226124602	1	1	1	0	215	146	121	51	0		

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1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	69.m15412	AN3707.1	AO070341000332	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E		0.052	1	1	1	0	96	178	61	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	58.m08007	AN4317.1	AO070230000006	Vesicle coat complex COPII, subunit SEC13	U		3.357	1	1	1	1	288	26	18	76	1		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	58.m07989	AN4331.1	AO070240000009	Structure-specific endonuclease ERCC1-XPF, ERCC1 component	L		3.206	1	1	1	1	53	5	4	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	71.m15491	AN4721.1	AO070323000062	DEAH-box RNA helicase	A		0.086	1	1	1	0	224	52	85	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	59.m09207	AN4776.1	AO070329000076	Phospholipase/carboxyhydrolase	E		0.052	1	1	1	0	171	124	218	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	69.m14806	AN5790.1	AO070249000036	Isocitrate dehydrogenase, gamma subunit	E		0.052	1	1	1	0	233	322	297	205	0		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	72.m19170	AN5954.1	AO070340000308	RNA polymerase I-associated factor - PAF67	JK		1.94045711732845 0.495263856202323	1	1	1	1	183	317	379	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	72.m19434	AN6221.1	AO070304000053	GATA-4/5/6 transcription factors	K		0.495	1	2	1	0	113	18	378	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	72.m19978	AN6231.1	AO070304000084	Tryptophan synthase beta chain	E		0.052	1	1	1	1	322	185	229	81	0		

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1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	57.m05898	AN7447.1	AO070229000019	HAT repeat protein	A		0.086	1	1	1	1	130	85	121	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	57.m05843	AN7498.1	AO070287000016	HEAT repeat-containing protein				1	1	1	1	113	164	59	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				1	1	2	1	445	100	126	No EST	No EST		
1622	ATCTTATC	areA_new (WGATAAGR) [aspergillus_motifs_all]; DAL81 (GATAAG) [yeast_motifs_all];GLN3 (GATAAk) [yeast_motifs_all];	up	up	62.m03387	AN8684.1	AO070315000104	Predicted N-acetyltransferase				1	2	1	0	176	277	250	No EST	No EST		
1635	CGACAACCC		up	up	70.m15054	AN1166.1	AO070331000160	60s ribosomal protein L6	J	1	0.000	1	1	1	1	50	172	187	No EST	No EST		
1635	CGACAACCC		up	up	70.m14890	AN1343.1	AO070247000021	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K		2.503	1	1	1	1	155	181	170	No EST	No EST		
1635	CGACAACCC		up	up	70.m14888	AN1345.1	AO070247000019	40S ribosomal protein S23	J	1	0.000	1	1	1	0	263	20	13	No EST	No EST		
1635	CGACAACCC		up	up	59.m09034	AN2980.1	AO070337000142	60S ribosomal protein L35A/L37	J	1	0.000	1	2	1	1	78	368	422	81	0		
1635	CGACAACCC		up	up	66.m04623	AN3413.1	AO070281000039	40S ribosomal protein S2/30S ribosomal protein S5	J	1	0.000	1	1	2	1	71	235	158	74	0		
1635	CGACAACCC		up	up	69.m14960	AN4183.1	AO070341000083	Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	OT		3.03057110657774 2.8127765805243	1	1	1	0	455	144	52	No EST	No EST		
1635	CGACAACCC		up	up	54.m06795	AN4222.1	AO070234000028	60S ribosomal protein L27	J	1	0.000	1	1	1	1	24	386	358	87	0		
1635	CGACAACCC		up	up	57.m05712	AN5222.1	AO070337000256	40S ribosomal protein S11	J	1	0.000	1	1	1	0	64	131	167	116	0		
1635	CGACAACCC		up	up	54.m06834	AN5715.1	AO070324000138	40s ribosomal protein S26	J	1	0.000	1	1	2	1	80	285	146	No EST	No EST		
1635	CGACAACCC		up	up	72.m19924	AN6083.1	AO070340000133	60s ribosomal protein L10	J	1	0.000	1	1	1	1	44	185	199	No EST	No EST		
1635	CGACAACCC		up	up	57.m05844	AN7497.1	AO070287000017	NADH:ubiquinone oxidoreductase, NDUFS4/18 kDa subunit	C		2.630	1	1	1	0	1	81	76	No EST	No EST		
1635	CGACAACCC		up	down	72.m19589	AN7570.1	AO070343000416	Alpha tubulin	Z		6.078	1	1	1	1	107	97	90			No EST	No EST
1635	CGACAACCC		up	up	57.m05434	AN7664.1	AO070268000037	Ca2+ transporting ATPase	P		2.044	1	1	1	1	205	308	289	No EST	No EST		
1635	CGACAACCC		up	up	71.m16001	AN8863.1	AO070271000008	Nucleosome assembly protein NAP-1	BD		1.28914594752066 1.83988758623835	2	1	1	1	6	438	487	72	0		
1650	GAAATTT		up	up	71.m15469	AN0204.1	AO070321000040	ATP-dependent RNA helicase	A		0.203	2	1	1	1	3	71	88	37	0		
1650	GAAATTT		up	up	54.m06965	AN0261.1	AO070334000097	Vesicle coat complex COPII, subunit SEC23	U		1.256	1	1	2	0	102	19	67	No EST	No EST		
1650	GAAATTT		up	up	55.m02940	AN1434.1	AO070232000012	Nucleolar protein involved in 40S ribosome biogenesis	J	1	0.004	1	1	1	0	43	30	43	No EST	No EST		
1650	GAAATTT		up	up	59.m08591	AN3134.1	AO070303000010	Chaperonin complex component, TCP-1 gamma subunit (CCT3)	O		0.110	1	1	1	1	152	89	93	No EST	No EST		
1650	GAAATTT		up	up	65.m07433	AN4259.1	AO070277000032	Uncharacterized conserved protein, contains PCI domain				1	1	1	1	134	97	81	10	0		
1650	GAAATTT		up	up	58.m08981	AN4412.1	AO070273000032	Nuclear exosomal RNA helicase MTR4, DEAD-box superfamily	A		0.203	1	1	1	1	90	51	76	No EST	No EST		
1650	GAAATTT		up	up	69.m15625	AN5203.1	AO070199000002	Ribosomal protein S8	J	1	0.004	1	1	1	1	275	52	20	No EST	No EST		
1650	GAAATTT		up	up	54.m06828	AN5713.1	AO070324000145	Chaperonin complex component, TCP-1 eta subunit (CCT7)	O		0.110	1	1	1	1	145	128	108	No EST	No EST		
1650	GAAATTT		up	up	72.m19047	AN6111.1	AO070340000094	Exosomal 3'-5' exoribonuclease complex, subunit Rrp45	J	1	0.004	1	1	1	0	54	55	78	66	1		
1650	GAAATTT		up	up	71.m15986	AN8851.1	AO070271000025	Pseudouridine synthase	J	1	0.004	3	1	1	1	3	134	113	92	0		

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1650	GAAATTT		up	up	66.m04584	AN9124.1	AO070332000148	Molecular co-chaperone STI1	O		0.110	1	1	1	1	146	79	98	No EST	No EST		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	70.m15472	AN0857.1	AO070320000004	predicted protein [Neurospora crassa]				1	1	1	0	115	13	43			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	70.m15493	AN0889.1	AO070320000058	Predicted GTP-binding protein (ODN superfamily)				1	1	1	0	96	18	95			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	70.m15807	AN0924.1	AO070320000103	Uncharacterized conserved protein				1	1	1	1	337	328	402			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	70.m15733	AN1341.1	AO070247000023	Membrane coat complex Retromer, subunit VPS29/PEP11	U		4.891	1	1	1	1	36	129	23			189	1
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	58.m07598	AN1990.1	AO070301000078	Alpha-isopropylmalate synthase/homocitrate synthase	E		2.453	1	1	1	0	279	314	290			62	0
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	72.m19694	AN2147.1	AO070343000196	rRNA processing protein Rrp5	A		1.648	1	1	1	1	74	54	57			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	up	56.m02312	AN2583.1	AO070329000004	Glyceraldehyde 3-phosphate dehydrogenase	G		2.501	1	1	2	0	8	85	153	No EST	No EST		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	54.m06671	AN2730.1	AO070338000210	Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	P		4.211	1	1	1	0	139	155	167			197	1
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	71.m15507	AN2830.1	AO070330000102	Sterol desaturase	I		2.078	1	1	1	0	175	33	133			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	59.m08516	AN3147.1	AO070256000043	Glycolipid transfer protein	G		2.501	1	1	1	0	289	48	86			107	1
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	66.m04638	AN3370.1	AO070281000023	Mannosyltransferase	G		2.501	1	1	1	0	30	131	6			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	58.m07830	AN3853.1	AO070305000093	Metalloendoprotease HMP1 (insulinase superfamily)	O		3.161	1	1	1	0	137	34	95			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	65.m07435	AN4261.1	AO070277000030					1	1	1	0	15	15	49			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	59.m09109	AN4862.1	AO070329000148	Ran GTPase-activating protein	AYT		1.64785526868742 1.81716589396935 2.45302771106611	1	1	1	1	390	381	373			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	59.m08861	AN4956.1	AO070288000018	Thiamine pyrophosphate-requiring enzyme	EH		2.45302771106611 3.15497620525398	1	1	1	1	305	354	309			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	up	54.m06872	AN5188.1	AO070291000024	Ribonuclease H	L		7.315	1	2	1	0	194	29	92	No EST	No EST		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	up	69.m14895	AN5196.1	AO070237000026	mRNA splicing factor				1	1	1	0	347	71	16	No EST	No EST		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	72.m19243	AN5887.1	AO070245000020	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	C		2.046	1	1	1	0	21	229	50			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	72.m19228	AN5902.1	AO070248000040	Alpha-1,2 glucosyltransferase/transcriptional activator	OKIT		3.16127869756242 4.7571240768546 2.07785656819965 2.45302771106611	1	1	2	0	65	28	63			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	up	72.m19045	AN6114.1	AO070340000090	DNA polymerase IV (family X)	L		7.315	1	1	2	0	105	187	206	50	0		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	up	72.m19000	AN6169.1	AO070340000031	hypothetical protein [Neurospora crassa]				1	1	1	0	122	20	486	No EST	No EST		
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	69.m15185	AN7193.1	AO070252000009	Aldo/keto reductase family proteins				1	1	1	0	20	33	70			64	1
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	57.m05844	AN7497.1	AO070287000017	NADH:ubiquinone oxidoreductase, NDUFS4/18 kDa subunit	C		2.046	1	1	1	1	21	23	21			No EST	No EST
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	53.m03735	AN8234.1	AO070310000074	predicted protein [Neurospora crassa]				1	1	1	0	90	45	125			18	0
1710	TGTATATA	efficiency_element1 (TATATA) [polya];	down	down	62.m03402	AN9500.1	AO070205000004	Cyclin				1	1	1	0	279	248	238			No EST	No EST
1723	TCTCGTGA		up	up	69.m15282	AN0993.1	AO070272000042	Permease of the major facilitator superfamily	G		3.776	1	1	1	0	303	183	205	No EST	No EST		
1723	TCTCGTGA		up	up	70.m15145	AN1069.1	AO070285000067	hypothetical protein [Neurospora crassa]				1	1	1	1	353	148	212	No EST	No EST		
1723	TCTCGTGA		up	up	70.m14981	AN1237.1	AO070331000251	DNA repair protein RAD51/RHP55	L		3.134	1	1	1	1	283	67	44	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1723	TCTCGTGA		up	down	70.m14905	AN1326.1	AO070303000090	Protein kinase				1	1	2	0	221	266	206			130	0
1723	TCTCGTGA		up	up	55.m03042	AN1523.1	AO070334000241	F0F1-type ATP synthase, alpha subunit	C		1.382	1	1	1	0	197	212	234	68	0		
1723	TCTCGTGA		up	up	69.m15067	AN1769.1	AO070324000028	Salt-sensitive 3'-phosphoadenosine-5'-phosphatase HAL2/SAL1	FP		1.76647600425002 3.08099500429545	1	1	1	0	236	106	51	212	1		
1723	TCTCGTGA		up	up	58.m07665	AN1846.1	AO070292000059					1	1	1	1	276	248	327	No EST	No EST		
1723	TCTCGTGA		up	up	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		1.382	1	1	1	1	159	228	425	104	0		
1723	TCTCGTGA		up	up	59.m08733	AN2886.1	AO070338000128	predicted protein [Neurospora crassa]				1	1	1	1	33	184	206	No EST	No EST		
1723	TCTCGTGA		up	up	59.m08756	AN2905.1	AO070338000100	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	K		3.562	1	1	1	0	470	25	33	No EST	No EST		
1723	TCTCGTGA		up	up	59.m09034	AN2980.1	AO070337000142	60S ribosomal protein L35A/L37	J		0.391	1	1	1	1	222	235	283	81	0		
1723	TCTCGTGA		up	up	69.m15402	AN3691.1	AO070341000316	AAA+-type ATPase	O		3.724	1	1	1	0	235	185	268	No EST	No EST		
1723	TCTCGTGA		up	up	54.m06757	AN4194.1	AO070315000084	ARK protein kinase family	T		1.683	1	1	1	0	164	108	60	No EST	No EST		
1723	TCTCGTGA		up	up	58.m07559	AN5646.1	AO070301000034	3-oxoacyl CoA thiolase	I		3.676	1	1	1	1	259	66	64	27	0		
1723	TCTCGTGA		up	up	54.m06834	AN5715.1	AO070324000138	40s ribosomal protein S26	J		0.391	1	1	1	1	175	188	59	No EST	No EST		
1723	TCTCGTGA		up	up	54.m06840	AN5719.1	AO070324000131	60s acidic ribosomal protein P1	J		0.391	1	2	1	0	203	5	4	101	1		
1723	TCTCGTGA		up	up	69.m14850	AN5752.1	AO070341000009	subunit of RNA polymerase II holoenzyme/mediator complex; Srb5p [Saccharomyces cerevisiae]				1	1	2	0	81	166	218	No EST	No EST		
1723	TCTCGTGA		up	up	69.m15695	AN6391.1	AO070343000154	Serine/threonine protein phosphatase 2A, catalytic subunit	T		1.683	1	1	1	1	71	190	221	208	1		
1723	TCTCGTGA		up	up	72.m19779	AN7285.1	AO070297000027	predicted protein [Neurospora crassa]				1	1	1	0	269	47	90	No EST	No EST		
1723	TCTCGTGA		up	down	53.m03908	AN8038.1	AO070330000008	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A		5.176	1	1	1	1	98	72	74			No EST	No EST
1739	GGGCTTAGGG		up	up	70.m15648	AN0634.1	AO070318000124	GTP-binding ADP-ribosylation factor-like protein yARL3	U		0.845	2	1	2	0	253	212	146	No EST	No EST		
1739	GGGCTTAGGG		up	up	70.m15293	AN0690.1	AO070343000523	N-methyltransferase				1	1	1	0	143	12	7	No EST	No EST		
1739	GGGCTTAGGG		up	up	58.m07605	AN1996.1	AO070301000091	Uncharacterized conserved protein				1	1	1	0	366	208	218	No EST	No EST		
1739	GGGCTTAGGG		up	up	59.m09034	AN2980.1	AO070337000142	60S ribosomal protein L35A/L37	J	1	0.001	1	1	2	1	168	293	265	81	0		
1739	GGGCTTAGGG		up	up	66.m04623	AN3413.1	AO070281000039	40S ribosomal protein S2/30S ribosomal protein S5	J	1	0.001	1	1	1	1	182	91	62	74	0		
1739	GGGCTTAGGG		up	up	54.m06802	AN4239.1	AO070324000175	hypothetical protein [Neurospora crassa]				1	1	1	0	202	266	347	No EST	No EST		
1739	GGGCTTAGGG		up	up	54.m06863	AN5155.1	AO070291000012	Subunit of tRNA-specific adenosine-34 deaminase	A		0.724	2	1	2	1	232	136	163	No EST	No EST		
1739	GGGCTTAGGG		up	up	54.m06834	AN5715.1	AO070324000138	40s ribosomal protein S26	J	1	0.001	1	1	1	1	150	211	82	No EST	No EST		
1739	GGGCTTAGGG		up	up	71.m15606	AN8799.1	AO070276000061	tRNA(1-methyladenosine) methyltransferase, subunit GCD14	J	1	0.001	1	1	1	0	181	21	46	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15474	AN0211.1	AO070321000033	U2-associated snRNP A' protein	A		0.011	1	1	1	0	235	73	116	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06978	AN0304.1	AO070334000034	Fe2+/Zn2+ regulated transporter	P		4.342	1	1	1	0	379	96	51	116	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06443	AN0315.1	AO070334000017	hypothetical protein [Neurospora crassa]				1	1	1	0	439	43	69	220	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06392	AN0359.1	AO070318000037	Translation initiation factor 3, subunit b (eIF-3b)	J	1	0.001	1	1	1	0	190	333	111	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06650	AN0426.1	AO070338000276	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I		3.432	1	1	1	0	368	41	128	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06630	AN0440.1	AO070338000297	Histone acetyltransferases PCAF/SAGA/ADA, subunit TADA3L/NGG1	B		2.884	2	1	2	0	291	196	181	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15255	AN0593.1	AO070280000019	Predicted dehydrogenase				1	1	1	0	409	16	47	92	1		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15484	AN0881.1	AO070320000049	Alkylated DNA repair protein	L		0.020	1	1	1	0	18	133	43	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15630	AN0989.1	AO070318000148	SWI-SNF chromatin-remodeling complex protein	B		2.884	1	1	1	0	313	18	17	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15208	AN1027.1	AO070312000118					1	1	1	0	121	28	31	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15144	AN1068.1	AO070285000068	predicted protein [Neurospora crassa]				1	1	1	0	155	69	109	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15059	AN1162.1	AO070331000152	Elongation factor 1 beta/delta chain	K		0.373	1	1	1	0	177	33	18	17	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14981	AN1237.1	AO070331000251	DNA repair protein RAD51/RHP55	L		0.020	1	1	1	1	291	21	37	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14968	AN1254.1	AO070223000015	FOG: Zn-finger				1	1	1	0	146	107	221	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14945	AN1266.1	AO070332000014	RNA helicase	A		0.011	1	1	1	1	241	14	28	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14915	AN1293.1	AO070303000055	predicted protein [Neurospora crassa]				1	1	1	0	145	154	108	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14867	AN1362.1	AO070243000002	hypothetical protein [Neurospora crassa]				1	1	1	1	237	10	7	93	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	55.m02913	AN1405.1	AO070242000008					2	1	1	0	118	422	408	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	55.m02950	AN1448.1	AO070302000005	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	J	1	0.001	1	1	1	1	182	78	60	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	55.m03045	AN1528.1	AO070334000247	DNA repair/transcription protein Mms19	LK		0.0201565823997405 0.372854930474872	2	2	2	1	64	21	27	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m09021	AN1634.1	AO070299000045	U5 snRNP-like RNA helicase subunit	A		0.011	1	1	1	0	103	126	78	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	58.m07753	AN1675.1	AO070299000004	Lysophospholipase	I		3.432	1	1	1	0	288	213	365			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07777	AN1701.1	AO070305000027	Uncharacterized protein conserved in bacteria				1	1	1	0	277	36	34	No EST	No EST		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15042	AN1728.1	AO070324000059	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit	C		2.772	1	2	1	0	123	110	132	40	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07653	AN1859.1	AO070292000036	Transcription initiation factor IIF, auxiliary subunit	K		0.373	1	1	1	1	120	29	28	83	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07347	AN1949.1	AO070342000215	ATP-dependent RNA helicase pitchoune	A		0.011	1	1	1	1	128	389	248	51	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m08945	AN1981.1	AO070301000066	Protein geranylgeranyltransferase type II, alpha subunit	O		1.732	1	1	1	1	136	48	40	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07659	AN2057.1	AO070292000042	Mitochondrial/chloroplast ribosomal protein L12	J	1	0.001	1	1	1	1	140	36	86	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05776	AN2077.1	AO070341000230	WD40 repeat protein				1	1	1	0	145	71	80	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05790	AN2088.1	AO070341000246	Uncharacterized conserved protein				1	1	1	1	129	302	334	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	69.m15162	AN2123.1	AO070306000102	Transcriptional coactivator	K		0.373	1	1	1	1	367	309	365			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19657	AN2181.1	AO070343000260	Transcription initiation factor IIA, gamma subunit	K		0.373	1	1	1	0	99	5	22	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15853	AN2213.1	AO070294000009	26S proteasome regulatory complex, ATPase RPT2	O		1.732	1	1	1	0	31	278	266	107	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15903	AN2262.1	AO070295000025	Uncharacterized conserved protein				1	1	1	0	128	119	132	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15913	AN2268.1	AO070295000040	Mitochondrial/chloroplast ribosomal protein L5/L7	J	1	0.001	1	1	1	0	80	221	224	29	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15940	AN2292.1	AO070295000071	Protein required for cell viability; Yil019wp [Saccharomyces cerevisiae]				1	1	1	1	53	28	30	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15511	AN2308.1	AO070323000046	Cl- channel CLC-3 and related proteins (CLC superfamily)	P		4.342	1	1	1	1	24	235	262	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08450	AN2529.1	AO070300000122	Enoyl-CoA isomerase	I		3.432	1	1	1	1	281	180	163	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06676	AN2734.1	AO070338000217	60S acidic ribosomal protein P0	J	1	0.001	1	1	1	1	160	42	82	61	1		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	54.m06684	AN2747.1	AO070338000224	RNA polymerase subunit K	K		0.373	1	1	1	0	343	170	137			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09260	AN2764.1	AO070327000027	5'-3' exonuclease	L		0.020	1	1	1	0	219	88	95	237	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09356	AN2848.1	AO070334000119	Component of the U4/U6.U5 snRNP/mitosis protein DIM1	AD		0.0107343307758018 4.71234722941693	1	1	1	0	73	84	121	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	59.m08733	AN2886.1	AO070338000128	predicted protein [Neurospora crassa]				1	1	1	1	269	219	341			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08747	AN2897.1	AO070338000111	predicted protein [Neurospora crassa]				1	1	1	1	147	163	148	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09055	AN2939.1	AO070337000169	Ca2+-binding transmembrane protein LETM1/MRS7				1	1	1	0	20	93	147	112	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09039	AN2973.1	AO070337000148	SNF2 family DNA-dependent ATPase	B		2.884	1	1	1	1	163	22	24	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09022	AN2992.1	AO070337000126	Translation initiation factor 2, beta subunit (eIF-2beta)	J	1	0.001	1	1	1	0	171	18	27	83	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08547	AN3156.1	AO070256000036	Translation initiation factor 2, alpha subunit (eIF-2alpha)	J	1	0.001	1	1	1	0	275	48	105	165	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08563	AN3173.1	AO070256000017	Mitochondrial/choloroplast ribosomal protein S15	J	1	0.001	1	1	1	0	130	40	26	34	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08566	AN3176.1	AO070256000014	ATP-dependent RNA helicase	A		0.011	1	1	1	0	153	118	111	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	67.m02926	AN3217.1	AO070330000062	putative transcriptional activator with fungal binuclear cluster domain [Schizosaccharomyces pombe]				1	1	1	0	97	82	111	70	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	67.m02932	AN3224.1	AO070330000074	predicted protein [Neurospora crassa]				1	1	1	0	94	377	374	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	66.m04640	AN3372.1	AO070281000014	FOG: Low-complexity				1	1	1	0	9	1	1	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09501	AN3423.1	AO070327000008	Transcription elongation factor SPT6	A		0.011	1	1	1	0	342	10	75	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	59.m09280	AN3426.1	AO070327000005	Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	A		0.011	1	1	1	1	273	111	224			No EST	No EST

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07389	AN3589.1	AO070342000140	Putative dynamitin	Z		4.093	1	1	1	0	136	280	160	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m08910	AN3644.1	AO070328000090	Ubiquitin-conjugating enzyme E2	O		1.732	2	1	2	1	192	51	17	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07438	AN3660.1	AO070342000025	Methyltransferase-like protein				1	1	1	1	214	132	178	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	57.m05665	AN3818.1	AO070311000015	predicted protein [Neurospora crassa]				1	1	1	0	439	357	537			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	58.m07804	AN3828.1	AO070305000065					1	1	1	0	150	97	160			No EST	No EST
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07811	AN3832.1	AO070305000070	Mitochondrial elongation factor	J	1	0.001	1	1	1	1	110	49	33	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15009	AN3919.1	AO070324000114	Nuclear polyadenylated RNA binding protein	A		0.011	1	1	1	0	280	272	4	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14995	AN3932.1	AO070341000043	20S proteasome, regulatory subunit beta type PSMB5/PSMB8/PRE2	O		1.732	1	1	1	1	172	24	41	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14989	AN3937.1	AO070341000048	Uncharacterized conserved protein				1	1	1	0	53	44	42	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06550	AN4021.1	AO070328000119	Zn finger protein				2	2	1	0	161	168	10	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06715	AN4073.1	AO070342000062	40S ribosomal protein S12	J	1	0.001	1	2	1	0	178	31	33	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07362	AN4163.1	AO070342000193	G protein beta subunit-like protein	T		1.867	1	1	1	1	193	14	173	77	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06773	AN4216.1	AO070231000008	conserved hypothetical protein [Neurospora crassa]				1	1	1	1	86	20	56	18	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07963	AN4364.1	AO070261000007	Chitinase	M		6.344	1	1	1	0	358	87	101	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m09004	AN4428.1	AO070273000065	Amino acid transporter protein	E		1.867	1	1	1	0	79	295	217	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05535	AN4617.1	AO070267000034	Exosomal 3'-5' exoribonuclease complex subunit Rrp40	J	1	0.001	1	1	1	0	142	32	39	No EST	No EST		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15697	AN4709.1	AO070329000166	Phosphatidylinositol 3-kinase VPS34, involved in signal transduction	TU		1.86706454107343 3.23788186140762	1	1	1	0	211	43	23	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09460	AN4788.1	AO070329000059	RNA splicing factor - Slu7p	A		0.011	1	1	1	0	25	63	84	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08904	AN5006.1	AO070255000034	Mismatch repair ATPase MSH2 (MutS family)	L		0.020	1	1	1	0	131	66	71	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14897	AN5198.1	AO070237000028	Predicted transporter (major facilitator superfamily)				1	1	1	1	100	72	109	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14913	AN5215.1	AO070337000264	WD-repeat protein WDR6, WD repeat superfamily				1	1	1	0	198	13	13	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15743	AN5452.1	AO070239000031	Splicing factor 3b, subunit 3	A		0.011	2	1	1	1	273	74	41	179	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15746	AN5482.1	AO070341000403	GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein superfamily	U		3.238	1	1	1	0	210	57	101	124	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15723	AN5496.1	AO070341000389	predicted protein [Neurospora crassa]				1	1	1	1	61	42	7	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15455	AN5498.1	AO070341000387	Transcription initiation factor IIE, beta subunit	K		0.373	1	1	1	0	251	41	34	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15451	AN5512.1	AO070341000384	Magnesium-dependent phosphatase				1	1	1	0	137	177	97	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07493	AN5569.1	AO070328000037	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB1	KL		0.372854930474872 0.0201565823997405	1	1	1	0	207	111	184	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07509	AN5588.1	AO070328000021	AAA+-type ATPase containing the peptidase M41 domain	O		1.732	1	1	1	0	272	105	111	164	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07525	AN5601.1	AO070328000003	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	E		1.867	1	1	1	0	128	116	68	12	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	65.m07407	AN5681.1	AO070309000096	Predicted E3 ubiquitin ligase, integral peroxisomal membrane protein	O		1.732	2	2	2	1	182	70	91	52	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06844	AN5724.1	AO070324000127	Inner membrane protein translocase involved in respiratory chain assembly	OU		1.73223080721335 3.23788186140762	1	1	1	1	196	28	12	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14856	AN5741.1	AO070341000018	predicted protein [Neurospora crassa]				1	1	1	0	92	360	297	No EST	No EST		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15631	AN5745.1	AO070341000002	Translation initiation factor eIF3, p35 subunit	J	1	0.001	1	1	1	0	225	46	73	102	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19252	AN5879.1	AO070245000029	Uncharacterized conserved protein, contains ML domain				1	1	1	1	21	135	130	110	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19960	AN5916.1	AO070340000370	Enoyl-CoA hydratase/carnithine racemase	I		3.432	1	1	1	0	211	38	51	14	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19117	AN6041.1	AO070340000241	Uncharacterized conserved protein				1	1	1	0	215	108	48	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19104	AN6054.1	AO070340000200	Mitochondrial genome maintenance protein MGM101, mitochondrial precursor				1	1	1	0	77	179	134	8	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19058	AN6069.1	AO070340000110	ATP-dependent DNA ligase I	L		0.020	1	1	1	0	212	34	91	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		1.732	1	1	1	1	243	77	77	140	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19030	AN6132.1	AO070340000067	predicted protein [Neurospora crassa]				1	1	1	1	348	227	132	103	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19422	AN6232.1	AO070304000085	Vacuolar H+-ATPase V1 sector, subunit B	C		2.772	1	1	1	0	168	83	138	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19400	AN6256.1	AO070304000032	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	O		1.732	1	1	1	0	163	71	76	22	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19369	AN6272.1	AO070304000012	Ferredoxin/adrenodoxin reductase	F		6.661	1	1	1	0	101	287	49	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19450	AN6331.1	AO070304000109	Proteins containing the RNA recognition motif				1	1	1	1	290	58	55	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	62.m03111	AN6522.1	AO070270000021	Mitochondrial GTPase	J	1	0.001	1	1	1	0	82	197	391	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	62.m03227	AN6631.1	AO070326000083	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	C		2.772	1	1	1	1	109	105	129	35	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15298	AN6841.1	AO070314000098	Mitochondrial inner membrane protease, subunit IMP1	O		1.732	1	1	1	0	98	19	26	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15245	AN6895.1	AO070314000026	DNA helicase PIF1/RRM3	D		4.712	1	1	1	1	143	39	73	No EST	No EST		

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1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m20020	AN7292.1	AO070297000033	Soluble epoxide hydrolase	I		3.432	1	1	1	1	158	47	89	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19764	AN7301.1	AO070297000049	Glucosyltransferase - Alg8p	K		0.373	1	1	1	0	127	100	153	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19745	AN7325.1	AO070297000077	DNA polymerase delta, catalytic subunit	L		0.020	1	1	1	0	196	85	113	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19585	AN7566.1	AO070343000409	3'-5' exonuclease	L		0.020	2	1	1	0	208	151	116	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15815	AN7784.1	AO070286000028	GTPase-activating protein VRP				1	1	1	1	337	146	44	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m03906	AN8040.1	AO070330000006	Protein involved in inorganic phosphate transport	P		4.342	2	1	1	0	157	230	273	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	down	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		0.044	2	1	1	0	195	298	426			216	0
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m03886	AN8057.1	AO070322000143	Cysteine synthase	E		1.867	1	1	1	1	129	189	165	10	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m04172	AN8272.1	AO070310000029	RNA polymerase III (C) subunit	K		0.373	1	1	1	0	202	17	26	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J	1	0.001	1	1	1	1	146	107	115	73	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	62.m03454	AN8722.1	AO070315000150	ATP-dependent RNA helicase	A		0.011	1	1	1	1	284	175	199	186	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15603	AN8796.1	AO070276000064	GTP-binding protein	T		1.867	1	1	1	0	282	67	65	172	1		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15965	AN8835.1	AO070271000044	Glycyl-tRNA synthetase and related class II tRNA synthetase	J	1	0.001	1	1	1	0	4	165	169	42	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	56.m02287	AN8874.1	AO070293000003	Vacuolar sorting protein VPS1, dynamin, and related proteins	U		3.238	1	1	1	0	293	243	34	186	0		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	56.m02291	AN8880.1	AO070293000010	Sortilin and related receptors				1	1	1	0	289	49	83	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	66.m04517	AN9057.1	AO070176000001	predicted protein [Neurospora crassa]				1	1	1	0	226	8	63	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	66.m04576	AN9109.1	AO070332000159	hypothetical protein [Neurospora crassa]				1	3	1	1	353	71	49	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	52.m03843	AN9360.1	AO070315000040	Protein containing a U1-type Zn-finger and implicated in RNA splicing or processing	A		0.011	1	2	1	0	202	18	218	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15786	AN9436.1	AO070343000484	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 5'-3' helicase subunit RAD3	KL		0.372854930474872 0.0201565823997405	1	1	1	1	129	47	48	No EST	No EST		
1821	TCACGTG	Cbf1 (RTCACRTG) [yeast_motifs_all];PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19967	AN9468.1	AO070340000317	40S ribosomal protein S16	J	1	0.001	1	1	2	0	45	44	50	73	1		
1872	TATGATAC		down	down	54.m06658	AN0416.1	AO070338000264	hypothetical protein [Neurospora crassa]				1	1	1	1	206	116	189			No EST	No EST
1872	TATGATAC		down	down	70.m15319	AN0734.1	AO070343000495	Histone H4	B		1.128	1	1	1	1	239	248	233			342	1
1872	TATGATAC		down	down	58.m08946	AN1980.1	AO070301000065	Rab6 GTPase activator GAPCenA and related TBC domain proteins				1	1	1	0	53	119	158			No EST	No EST
1872	TATGATAC		down	down	58.m07387	AN3587.1	AO070342000137	Ubiquitin-specific protease	O		0.292	1	1	1	0	83	73	76			No EST	No EST
1872	TATGATAC		down	down	54.m06954	AN4072.1	AO070342000061	FOG: Ankyrin repeat				1	1	1	1	89	54	93			No EST	No EST
1872	TATGATAC		down	down	58.m07882	AN4443.1	AO070273000010	Methionine synthase II (cobalamin-independent)	E		2.461	1	1	1	1	105	101	99			353	1
1872	TATGATAC		down	down	71.m15664	AN4674.1	AO070284000032	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		2.4776088850601 0.291943312568149	1	1	1	1	98	87	93			350	1
1872	TATGATAC		down	down	54.m06853	AN5163.1	AO070291000002	von Willebrand factor and related coagulation proteins	V		0.589	1	1	1	0	54	56	34			No EST	No EST
1872	TATGATAC		down	down	72.m19445	AN6326.1	AO070304000041	Vigilin	I		2.315	1	1	1	1	394	466	368			No EST	No EST
1872	TATGATAC		down	down	62.m03114	AN6525.1	AO070270000024	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C		0.612	1	1	1	1	96	92	95			135	1
1872	TATGATAC		down	down	62.m03168	AN6574.1	AO070326000017	E3 ubiquitin ligase involved in syntaxin degradation	O		0.292	1	1	1	1	63	35	37			No EST	No EST
1872	TATGATAC		down	down	53.m03716	AN8251.1	AO070310000057	putative transcriptional activator [Aspergillus nidulans]				1	1	1	1	59	80	64			No EST	No EST
1872	TATGATAC		down	down	56.m02292	AN8881.1	AO070293000011	Mitochondrial carnitine-acylcarnitine carrier protein	C		0.612	1	1	1	0	83	61	42			356	1
1879	CTTATCGAT		up	up	71.m15643	AN0239.1	AO070284000068	Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	TU		3.12886473589624 0.993284467686079	1	1	1	0	455	26	15	No EST	No EST		
1879	CTTATCGAT		up	up	69.m15311	AN0495.1	AO070226000029	Formyltetrahydrofolate hydrolase	F		3.069	1	1	1	1	153	51	81	43	0		
1879	CTTATCGAT		up	up	70.m15293	AN0690.1	AO070343000523	N-methyltransferase				1	1	1	1	120	34	38	No EST	No EST		
1879	CTTATCGAT		up	up	55.m03022	AN1510.1	AO070334000228	Endoplasmic reticulum membrane-associated oxidoreductin involved in disulfide bond formation	OU		3.76201827084848 0.993284467686079	1	1	1	0	123	44	118	217	1		
1879	CTTATCGAT		up	up	55.m03268	AN1524.1	AO070334000242	Methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase	H		3.814	1	1	1	1	112	269	359	No EST	No EST		
1879	CTTATCGAT		up	up	55.m03045	AN1528.1	AO070334000247	DNA repair/transcription protein Mms19	LK		4.92697828093621 2.41624650000689	1	1	1	1	50	71	66	No EST	No EST		
1879	CTTATCGAT		up	up	55.m03058	AN1539.1	AO070334000263	COP9 signalosome, subunit CSN4	OT		3.76201827084848 3.12886473589624	1	1	1	0	145	176	208	No EST	No EST		
1879	CTTATCGAT		up	up	55.m03275	AN1559.1	AO070339000294	Predicted coiled-coil protein				1	1	1	1	213	102	106	97	0		
1879	CTTATCGAT		up	up	58.m08960	AN1719.1	AO070305000034	predicted protein [Neurospora crassa]				1	1	1	0	257	240	185	No EST	No EST		
1879	CTTATCGAT		up	up	58.m08870	AN1934.1	AO070342000199	predicted protein [Neurospora crassa]				1	1	1	0	62	83	306	No EST	No EST		
1879	CTTATCGAT		up	up	71.m15180	AN2693.1	AO070313000094	Uncharacterized conserved protein				1	1	1	0	136	66	42	No EST	No EST		
1879	CTTATCGAT		up	down	59.m09069	AN2926.1	AO070337000185	Uncharacterized conserved protein related to ribosomal protein S8E				1	2	1	0	153	257	234			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
1879	CTTATCGAT		up	up	59.m08513	AN3153.1	AO070256000033	Hismacro and SEC14 domain-containing proteins	BK		3.5405513681339 2.41624650000689	1	1	1	1	323	204	347	76	0		
1879	CTTATCGAT		up	up	69.m14975	AN3946.1	AO070341000066	Mitotic checkpoint serine/threonine protein kinase	D		4.582	1	1	2	1	211	133	18	No EST	No EST		
1879	CTTATCGAT		up	up	58.m07907	AN4418.1	AO070273000039	predicted protein [Neurospora crassa]				1	2	1	1	64	354	364	No EST	No EST		
1879	CTTATCGAT		up	up	58.m09004	AN4428.1	AO070273000065	Amino acid transporter protein	E		5.174	1	1	1	1	94	277	201	No EST	No EST		
1879	CTTATCGAT		up	up	57.m05596	AN4530.1	AO070321000140	Meiotic cell division protein Pelota/DOM34	J		5.242	1	1	1	1	275	38	21	No EST	No EST		
1879	CTTATCGAT		up	up	71.m15660	AN4672.1	AO070284000034	Predicted PRP38-like splicing factor				1	1	1	0	86	100	75	13	0		
1879	CTTATCGAT		up	up	59.m09234	AN4751.1	AO070327000068	Predicted DEAD-box-containing helicase				1	1	2	1	143	30	33	No EST	No EST		
1879	CTTATCGAT		up	up	54.m06845	AN5725.1	AO070324000126	Glycosyltransferase	M		3.299	1	1	1	0	154	23	54	No EST	No EST		
1879	CTTATCGAT		up	up	72.m19424	AN6229.1	AO070304000080	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C		5.271	2	1	1	1	101	161	75	15	0		
1879	CTTATCGAT		up	up	71.m15236	AN6900.1	AO070314000015	Triosephosphate isomerase	G		5.153	1	1	1	1	216	95	56	No EST	No EST		
1879	CTTATCGAT		up	up	71.m15220	AN6912.1	AO070219000017	predicted protein [Neurospora crassa]				1	1	1	0	74	43	41	No EST	No EST		
1879	CTTATCGAT		up	up	72.m19584	AN7565.1	AO070343000408					2	1	1	1	11	161	14	No EST	No EST		
1879	CTTATCGAT		up	up	53.m03783	AN9460.1	AO070310000131	Signal peptidase complex subunit	U		0.993	1	1	1	1	240	55	64	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	71.m15414	AN0130.1	AO070311000080	Putative methyltransferase				1	1	1	1	177	195	161	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	54.m06521	AN0260.1	AO070334000098	Eukaryotic-type DNA primase, large subunit	L		2.669	1	2	1	0	351	131	110	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	54.m06455	AN0303.1	AO070334000035	predicted protein [Neurospora crassa]				1	1	1	0	109	301	248	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	54.m06650	AN0426.1	AO070338000276	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I	1	0.000	1	1	1	1	315	106	176	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	69.m15269	AN0576.1	AO070272000056	Protein kinase containing WD40 repeats	T		3.868	1	1	1	0	209	162	185	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	70.m15258	AN0654.1	AO070343000572	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase	H		1.380	2	3	2	0	219	110	149	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	70.m15361	AN0747.1	AO070343000435	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O		1.772	1	1	1	1	131	89	122	29	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	70.m15403	AN0802.1	AO070239000016	Protein involved in plasmid maintenance/nuclear protein involved in lipid metabolism	I	1	0.000	2	1	1	1	176	242	221	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	70.m15443	AN0843.1	AO070216000003	Ribosomal protein S7	J		3.779	1	1	1	1	76	406	295	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	67.m02992	AN0949.1	AO070343000236	Sterol desaturase	I	1	0.000	2	1	1	0	115	311	395	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	70.m15232	AN1014.1	AO070312000004	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I	1	0.000	1	1	1	0	245	160	163	147	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	55.m02942	AN1442.1	AO070232000005	Preprotein translocase subunit Sec66	U		2.017	1	1	1	0	325	88	120	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	55.m03022	AN1510.1	AO070334000228	Endoplasmic reticulum membrane-associated oxidoreductin involved in disulfide bond formation	OU		1.77203658376353 2.01666925932491	1	1	1	1	90	267	409	217	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	58.m07754	AN1677.1	AO070299000001	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQ	1	2.16537437769743e-05 5.19950971613616	1	1	1	1	260	207	220	98	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	58.m07603	AN1993.1	AO070301000084	Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT1/GOT2	E		4.193	1	1	1	1	222	259	289	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	72.m20002	AN2154.1	AO070343000203	hypothetical protein [Neurospora crassa]				1	1	2	1	94	378	375	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	59.m08493	AN2497.1	AO070312000123	Palmitoyl protein thioesterase	IO	1	2.16537437769743e-05 1.77203658376353	1	1	1	0	183	205	258	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	71.m15507	AN2830.1	AO070330000102	Sterol desaturase	I	1	0.000	1	1	1	0	140	423	192	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	59.m08735	AN2888.1	AO070338000126	predicted protein [Neurospora crassa]				1	1	1	0	188	64	86	74	1		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	66.m04623	AN3413.1	AO070281000039	40S ribosomal protein S2/30S ribosomal protein S5	J		3.779	1	1	1	1	232	14	14	74	1		

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1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L		2.669	1	1	1	0	120	111	118	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	58.m07955	AN4377.1	AO070261000012	predicted protein [Neurospora crassa]				2	1	1	0	187	48	80	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	58.m07898	AN4410.1	AO070273000030	Uncharacterized conserved protein, contains WD40 repeat and BROMO domains				1	1	1	1	170	62	42	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	54.m06857	AN5166.1	AO070291000006	CDP-diacylglycerol synthase	I	1	0.000	1	1	1	1	243	58	61	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	down	69.m14876	AN5179.1	AO070247000010	Diphthamide biosynthesis protein	J		3.779	1	1	1	1	219	239	229			170	0
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	57.m05713	AN5221.1	AO070337000257	FOG: Immunoglobin and related proteins	P		2.579	1	1	1	1	183	21	31	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	69.m15570	AN5338.1	AO070333000229	Predicted flavoprotein involved in K+ transport	P		2.579	1	1	1	0	276	201	249	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	69.m15469	AN5484.1	AO070341000401	2-enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/Peroxisomal 3-ketoacyl-CoA-thiolase, sterol-binding domain and related enzymes	I	1	0.000	1	1	1	0	167	355	365	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	58.m07559	AN5646.1	AO070301000034	3-oxoacyl CoA thiolase	I	1	0.000	1	1	1	1	297	39	34	27	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	69.m14845	AN5747.1	AO070341000004	26S proteasome regulatory complex, ATPase RPT4	O		1.772	1	1	1	0	202	322	310	88	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	72.m19339	AN6295.1	AO070308000053	predicted protein [Neurospora crassa]				1	1	1	1	500	6	6	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	down	62.m03256	AN6654.1	AO070269000012	Glutamine synthetase	E		4.193	2	1	2	0	257	139	220			No EST	No EST
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	65.m07257	AN6717.1	AO070339000157	NAD-dependent malate dehydrogenase	C		3.654	1	1	1	0	226	87	8	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	72.m19588	AN7569.1	AO070343000415	Mitochondrial solute carrier protein	C		3.654	0	0	0	0	0	191	187	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	57.m05407	AN7649.1	AO070268000005	Mitochondrial import inner membrane translocase, subunit TIM9	U		2.017	1	2	3	0	154	231	279	30	0		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	57.m05936	AN7660.1	AO070268000029	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H		1.380	1	1	1	1	120	135	224	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	53.m03866	AN8020.1	AO070322000068	conserved hypothetical protein [Neurospora crassa]				2	1	1	0	162	172	46	No EST	No EST		
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	down	62.m03336	AN8744.1	AO070250000031	Glycolate oxidase	C		3.654	1	1	1	1	248	202	256			No EST	No EST
1934	TCACATGA	Cbf1 (RTCACRTG) [yeast_motifs_all];	up	up	53.m03781	AN9461.1	AO070310000129	Dehydrogenase kinase	T		3.868	1	1	1	1	88	46	92	No EST	No EST		
1940	GTbGGCGTT		down	down	71.m15463	AN0193.1	AO070321000051	Thiamine pyrophosphokinase	F		1.658	1	2	1	1	105	57	88			No EST	No EST
1940	GTbGGCGTT		down	down	70.m15311	AN0704.1	AO070343000506	Uncharacterized protein SFI1 involved in G(2)-M transition	D	1	0.001	1	2	1	0	22	20	67			No EST	No EST
1940	GTbGGCGTT		down	up	70.m15313	AN0706.1	AO070343000503	ER-Golgi vesicle-tethering protein p115	U		1.438	1	1	1	0	207	65	65	No EST	No EST		
1940	GTbGGCGTT		down	down	70.m15609	AN0973.1	AO070320000174	FOG: Zn-finger				1	1	1	0	199	60	111			No EST	No EST
1940	GTbGGCGTT		down	down	55.m03022	AN1510.1	AO070334000228	Endoplasmic reticulum membrane-associated oxidoreductin involved in disulfide bond formation	OU		2.10904431214641 1.43790304829778	1	1	2	0	96	35	79			121	1
1940	GTbGGCGTT		down	down	57.m05781	AN2082.1	AO070341000235	Uncharacterized conserved protein, contains BSD domain				1	1	1	0	35	143	149			267	1
1940	GTbGGCGTT		down	down	72.m19704	AN2136.1	AO070343000181	hypothetical protein [Neurospora crassa]				1	1	1	1	487	586	365			No EST	No EST
1940	GTbGGCGTT		down	down	71.m15945	AN2296.1	AO070295000077	RFX family transcription factor	K		0.263	1	1	1	1	122	127	148			No EST	No EST
1940	GTbGGCGTT		down	down	59.m09050	AN2965.1	AO070337000162	Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	DO	1	0.000502048888692969 2.10904431214641	2	1	1	0	95	38	97			No EST	No EST
1940	GTbGGCGTT		down	down	59.m08579	AN3178.1	AO070256000001	Component of histone deacetylase complex (breast carcinoma metastasis suppressor 1 protein in human)	DK	1	0.000502048888692969 0.263353780159277	2	1	1	0	91	24	26			No EST	No EST
1940	GTbGGCGTT		down	down	58.m07896	AN4408.1	AO070273000028	hypothetical protein [Magnaporthe grisea]				2	1	1	0	34	52	47			No EST	No EST
1940	GTbGGCGTT		down	down	59.m09174	AN4802.1	AO070329000037	60S ribosomal protein L21	J		3.377	1	1	1	1	26	26	30			483	1
1940	GTbGGCGTT		down	down	59.m08850	AN4945.1	AO070166000001	hypothetical protein [Neurospora crassa]				1	1	1	0	55	49	72			No EST	No EST

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1940	GTbGGCGTT		down	down	54.m06846	AN5726.1	AO070324000125	FOG: Zn-finger				1	1	1	0	155	108	173			No EST	No EST
1940	GTbGGCGTT		down	down	72.m19141	AN5999.1	AO070340000277	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				1	1	1	1	121	86	94			334	1
1940	GTbGGCGTT		down	down	72.m19026	AN6138.1	AO070340000064	DNA-binding cell division cycle control protein	D	1	0.001	1	1	1	1	97	292	149			No EST	No EST
1940	GTbGGCGTT		down	down	71.m15218	AN6914.1	AO070219000019	Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	ZD	1	2.4499096 6706483 0.0005020 48888692 969	1	4	2	1	77	21	20			134	1
1940	GTbGGCGTT		down	down	57.m05465	AN7688.1	AO070325000082	Protein similar to predicted member of the intramitochondrial sorting protein family	U		1.438	1	1	1	1	62	56	58			No EST	No EST
1940	GTbGGCGTT		down	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J		3.377	1	1	1	1	45	203	212	73	0		
1940	GTbGGCGTT		down	down	66.m04563	AN9102.1	AO070332000171	DNA-dependent RNA polymerase I	K		0.263	1	1	1	1	86	50	111			No EST	No EST
1940	GTbGGCGTT		down	down	54.m06486	AN9448.1	AO070334000061	predicted protein [Neurospora crassa]				1	1	1	0	96	73	74			No EST	No EST
1971	CGCCGGCCG		up	up	70.m15313	AN0706.1	AO070343000503	ER-Golgi vesicle-tethering protein p115	U		2.511	1	2	1	0	31	30	259	No EST	No EST		
1971	CGCCGGCCG		up	up	70.m15054	AN1166.1	AO070331000160	60s ribosomal protein L6	J		0.610	1	2	1	1	60	67	177	No EST	No EST		
1971	CGCCGGCCG		up	up	55.m02969	AN1467.1	AO070306000090	Serine/threonine protein phosphatase	T		0.108	1	1	1	1	379	87	148	177	1		
1971	CGCCGGCCG		up	up	54.m06583	AN4007.1	AO070328000146	Succinyl-CoA:alpha-ketoacid-CoA transferase	C		2.427	1	1	1	1	339	179	191	No EST	No EST		
1971	CGCCGGCCG		up	up	71.m15705	AN4717.1	AO070311000004	cAMP-dependent protein kinase catalytic subunit (PKA)	T		0.108	1	1	1	0	303	78	61	No EST	No EST		
1971	CGCCGGCCG		up	down	59.m08879	AN4976.1	AO070288000043	TATA-box binding protein (TBP), component of TFIID and TFIIIB	K		5.195	1	1	1	0	293	278	309			506	1
1971	CGCCGGCCG		up	up	58.m07314	AN5660.1	AO070342000252	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		2.6590987 0597145 2.9405141 6265446	1	1	2	1	94	401	316	597	1		
1971	CGCCGGCCG		up	up	72.m19056	AN6067.1	AO070340000108	Translation initiation factor 5 (eIF-5)	J		0.610	1	1	1	1	278	219	238	No EST	No EST		
1971	CGCCGGCCG		up	up	72.m19558	AN7542.1	AO070277000038	predicted protein [Neurospora crassa]				1	1	1	1	38	434	522	123	0		
1971	CGCCGGCCG		up	up	57.m05408	AN7650.1	AO070268000006	Rho GTPase-activating protein	TZ		0.1083492 38735247 1.4912272 738168	1	2	1	1	195	311	289	No EST	No EST		
1971	CGCCGGCCG		up	up	71.m15780	AN7748.1	AO070325000180	S-M checkpoint control protein CID1 and related nucleotidyltransferases	D		1.632	1	1	1	1	269	167	187	No EST	No EST		
1971	CGCCGGCCG		up	up	66.m04577	AN9121.1	AO070332000155	ESDC [Aspergillus nidulans]				1	1	1	1	322	192	223	460	1		
1998	CCTCGGCA		up	up	71.m15403	AN0122.1	AO070311000090	ATP-dependent Lon protease, bacterial type	O		1.185	1	1	1	1	217	93	62	78	0		
1998	CCTCGGCA		up	down	70.m15270	AN0667.1	AO070343000553	Mannose-6-phosphate isomerase	G		2.164	2	1	1	0	162	129	131			17	0
1998	CCTCGGCA		up	up	70.m15459	AN0868.1	AO070320000019	Acyl-CoA thioesterase	I	1	0.000	1	1	1	1	146	128	217	No EST	No EST		
1998	CCTCGGCA		up	up	57.m05985	AN1882.1	AO070341000166	NADH:flavin oxidoreductase/12-oxophytodienoate reductase	C		0.024	1	1	1	0	183	196	191	23	0		
1998	CCTCGGCA		up	up	71.m15926	AN2281.1	AO070295000058	Peroxisomal assembly protein PEX3	MU		1.9375673 4665627 1.6998660 2403297	1	1	1	1	176	251	297	121	0		
1998	CCTCGGCA		up	up	53.m04034	AN2577.1	AO070234000010	Peroxisomal multifunctional beta-oxidation protein and related enzymes	I	1	0.000	1	1	1	0	114	260	125	No EST	No EST		
1998	CCTCGGCA		up	up	59.m09262	AN2762.1	AO070327000024	Glutaryl-CoA dehydrogenase	E		2.926	1	1	2	0	167	221	111	No EST	No EST		
1998	CCTCGGCA		up	up	59.m09078	AN2925.1	AO070337000214	Peroxisome assembly factor 2 containing the AAA+-type ATPase domain	O		1.185	1	1	2	1	283	171	253	No EST	No EST		
1998	CCTCGGCA		up	up	59.m09056	AN2938.1	AO070337000168	Peroxisomal NUDIX hydrolase	L		2.850	1	1	1	1	116	134	206	No EST	No EST		
1998	CCTCGGCA		up	up	54.m06786	AN4230.1	AO070234000016	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I	1	0.000	1	1	1	1	181	36	71	No EST	No EST		
1998	CCTCGGCA		up	up	65.m07435	AN4261.1	AO070277000030					1	1	1	0	110	98	90	No EST	No EST		
1998	CCTCGGCA		up	up	53.m03677	AN4280.1	AO070310000016	Predicted mitochondrial carrier protein	C		0.024	1	1	1	0	365	200	201	No EST	No EST		
1998	CCTCGGCA		up	up	54.m07051	AN5113.1	AO070291000066	Peroxisomal biogenesis protein (peroxin 16)	U		1.700	1	1	1	0	189	1	5	No EST	No EST		
1998	CCTCGGCA		up	up	69.m15551	AN5356.1	AO070333000156	Mitochondrial carnitine-acylcarnitine carrier protein	C		0.024	1	1	1	0	369	153	177	No EST	No EST		
1998	CCTCGGCA		up	up	58.m07559	AN5646.1	AO070301000034	3-oxoacyl CoA thiolase	I	1	0.000	1	1	1	1	211	104	108	27	0		
1998	CCTCGGCA		up	up	65.m07407	AN5681.1	AO070309000096	Predicted E3 ubiquitin ligase, integral peroxisomal membrane protein	O		1.185	1	1	1	1	169	94	120	52	0		
1998	CCTCGGCA		up	up	72.m18955	AN5828.1	AO070260000018	Cytochrome b5	C		0.024	1	1	1	0	194	62	63	No EST	No EST		
1998	CCTCGGCA		up	up	72.m19150	AN5990.1	AO070340000287	Acyl-CoA synthetase	I	1	0.000	1	1	1	0	215	43	84	No EST	No EST		
1998	CCTCGGCA		up	up	72.m19295	AN6195.1	AO070308000098	FOG: Zn-finger				1	1	1	0	89	476	443	386	0		
1998	CCTCGGCA		up	up	72.m19305	AN6207.1	AO070308000086	Dehydrogenase kinase	T		2.926	1	1	1	0	156	186	236	No EST	No EST		
1998	CCTCGGCA		up	up	69.m15243	AN6394.1	AO070343000149	Acyl-CoA dehydrogenases	I	1	0.000	1	1	1	0	202	16	26	No EST	No EST		

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1998	CCTCGGCA		up	up	72.m19794	AN7256.1	AO070297000012	25D9-5p [Aspergillus fumigatus]				1	1	1	0	126	146	198	No EST	No EST		
1998	CCTCGGCA		up	up	72.m19792	AN7258.1	AO070297000014	Peroxisomal membrane protein MPV17 and related proteins				1	1	1	1	298	164	251	368	1		
1998	CCTCGGCA		up	up	72.m19779	AN7285.1	AO070297000027	predicted protein [Neurospora crassa]				1	1	1	1	228	101	130	No EST	No EST		
1998	CCTCGGCA		up	up	52.m04095	AN8415.1	AO070302000056	Acyl-CoA dehydrogenases	I	1	0.000	1	1	1	0	144	348	76	No EST	No EST		
1998	CCTCGGCA		up	up	66.m04774	AN9075.1	AO070332000206	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C		0.024	1	1	1	0	206	163	232	No EST	No EST		
2032	GAAGCTCTC		up	up	71.m15635	AN1133.1	AO070276000007	N-methyl-D-aspartate receptor glutamate-binding subunit	T		2.262	1	1	1	0	128	88	118	37	0		
2032	GAAGCTCTC		up	up	70.m14980	AN1238.1	AO070331000252	hypothetical protein [Neurospora crassa]				1	1	1	0	121	92	115	No EST	No EST		
2032	GAAGCTCTC		up	up	55.m03042	AN1523.1	AO070334000241	F0F1-type ATP synthase, alpha subunit	C		0.829	1	1	1	0	100	306	327	68	0		
2032	GAAGCTCTC		up	up	58.m07776	AN1700.1	AO070305000026	26S proteasome regulatory complex, subunit RPN2/PSMD1	O	1	0.000	1	1	1	0	95	177	42	No EST	No EST		
2032	GAAGCTCTC		up	up	58.m07660	AN1851.1	AO070292000043	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O	1	0.000	1	1	1	0	6	51	55	No EST	No EST		
2032	GAAGCTCTC		up	up	57.m05786	AN2085.1	AO070341000243	20S proteasome, regulatory subunit beta type PSMB7/PSMB10/PUP1	O	1	0.000	2	1	2	1	198	107	42	52	0		
2032	GAAGCTCTC		up	down	71.m15826	AN2237.1	AO070326000136	Carboxypeptidase C (cathepsin A)	E		2.262	1	1	1	1	224	320	132			58	0
2032	GAAGCTCTC		up	up	71.m15877	AN2243.1	AO070326000130	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)				1	1	1	1	70	481	443	307	0		
2032	GAAGCTCTC		up	up	69.m15673	AN2456.1	AO070264000017	Uncharacterized conserved protein				1	1	1	1	175	80	190	No EST	No EST		
2032	GAAGCTCTC		up	up	59.m08733	AN2886.1	AO070338000128	predicted protein [Neurospora crassa]				1	1	1	0	192	69	195	No EST	No EST		
2032	GAAGCTCTC		up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L		1.880	1	1	1	0	137	156	174	No EST	No EST		
2032	GAAGCTCTC		up	up	69.m14995	AN3932.1	AO070341000043	20S proteasome, regulatory subunit beta type PSMB5/PSMB8/PRE2	O	1	0.000	1	1	1	0	137	67	94	No EST	No EST		
2032	GAAGCTCTC		up	up	57.m05618	AN4510.1	AO070311000065	Leucine rich repeat proteins, some proteins contain F-box				1	1	1	0	136	43	68	No EST	No EST		
2032	GAAGCTCTC		up	up	57.m05507	AN4583.1	AO070316000171	HSP90 co-chaperone CPR7/Cyclophilin	O	1	0.000	1	1	1	1	174	74	26	22	0		
2032	GAAGCTCTC		up	up	71.m15778	AN5236.1	AO070325000177	Predicted membrane protein				1	1	1	0	123	165	157	No EST	No EST		
2032	GAAGCTCTC		up	up	69.m15433	AN5525.1	AO070341000364	Aconitase/homoaconitase (aconitase superfamily)	CE		0.829017516177287 2.26161746616916	2	1	2	1	4	442	381	111	0		
2032	GAAGCTCTC		up	up	72.m19133	AN6010.1	AO070340000269	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	O	1	0.000	1	1	1	1	219	289	293	149	0		
2032	GAAGCTCTC		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O	1	0.000	1	1	1	1	228	90	92	140	1		
2032	GAAGCTCTC		up	up	72.m19767	AN7299.1	AO070297000045	Metallopeptidase				2	2	1	0	212	56	76	67	1		
2077	TGTACAAATA		down	up	70.m15319	AN0734.1	AO070343000495	Histone H4	B		4.372	1	1	1	1	131	288	282	69	0		
2077	TGTACAAATA		down	down	70.m15127	AN1105.1	AO070285000033	Translocase of outer mitochondrial membrane complex, subunit TOM22	U		1.409	1	1	1	0	464	385	490			240	0
2077	TGTACAAATA		down	down	58.m07726	AN1636.1	AO070299000057	hypothetical protein [Neurospora crassa]				1	1	1	0	151	162	128			No EST	No EST
2077	TGTACAAATA		down	down	59.m08563	AN3173.1	AO070256000017	Mitochondrial/choloroplast ribosomal protein S15	J		0.274	1	1	1	0	164	122	162			No EST	No EST
2077	TGTACAAATA		down	down	57.m05641	AN4490.1	AO070311000042	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K		1.266	1	1	1	1	141	252	176			279	1
2077	TGTACAAATA		down	down	58.m07520	AN5596.1	AO070328000008	Permease of the major facilitator superfamily				1	1	1	1	73	55	72			275	1
2077	TGTACAAATA		down	down	72.m19947	AN6073.1	AO070340000117	Prohibitin-like protein	O		1.724	1	1	1	1	86	77	121			No EST	No EST
2077	TGTACAAATA		down	down	71.m15300	AN6843.1	AO070314000096	Mitochondrial/chloroplast ribosomal protein L4	J		0.274	1	1	1	1	60	52	52			91	1
2077	TGTACAAATA		down	down	71.m15724	AN7699.1	AO070325000105	predicted protein [Neurospora crassa]				1	1	1	0	98	64	98			84	1
2077	TGTACAAATA		down	down	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		1.509	1	1	1	1	499	336	475			No EST	No EST
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	54.m06529	AN0254.1	AO070334000106	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE	1	0.00765114272370187 2.06767721409258	2	1	2	0	114	365	392	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	54.m06476	AN0267.1	AO070334000073	Myosin regulatory light chain, EF-Hand protein superfamily	Z		3.244	1	1	1	0	160	142	78	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15297	AN0504.1	AO070226000008	Serine/threonine specific protein phosphatase involved in cell cycle control, PP2A-related	DT		1.22510205640882 2.06767721409258	2	1	1	0	1	61	43	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15255	AN0593.1	AO070280000019	Predicted dehydrogenase				1	1	1	1	370	69	100	92	1		

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2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15258	AN0654.1	AO070343000572	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase	H		6.796	1	1	1	0	228	190	239	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15221	AN1003.1	AO070312000031	Isocitrate dehydrogenase, alpha subunit	E		2.068	1	1	1	0	114	152	173	48	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m14919	AN1289.1	AO070303000050	Uncharacterized conserved protein				1	2	1	0	143	84	234	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m14915	AN1293.1	AO070303000055	predicted protein [Neurospora crassa]				1	1	1	0	120	169	130	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m20005	AN2138.1	AO070343000183	ATP-dependent RNA helicase A	A		6.245	1	1	2	0	118	4	4	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	62.m03412	AN2320.1	AO070269000057	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	C		1.481	1	1	1	0	122	54	40	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	63.m00601	AN2344.1	AO070343000375	Permease of the major facilitator superfamily	G		3.911	1	2	1	1	253	55	63	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19463	AN2412.1	AO070236000002	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		2.068	1	1	1	0	98	312	413	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m04034	AN2577.1	AO070234000010	Peroxisomal multifunctional beta-oxidation protein and related enzymes	I	1	0.008	1	2	1	0	105	244	134	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15522	AN3312.1	AO070333000132	Reductases with broad range of substrate specificities				1	1	2	0	70	172	255	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	59.m09280	AN3426.1	AO070327000005	Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	A		6.245	1	1	1	1	266	104	217			No EST	No EST
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15404	AN3695.1	AO070341000319	Isochorismate synthase	E		2.068	1	1	1	1	50	253	214	61	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15413	AN3708.1	AO070341000333	Zinc-binding protein of the histidine triad (HIT) family	T		2.068	1	1	1	0	124	124	105	5	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07818	AN3842.1	AO070305000077	GTPase Rab5/YPT51 and related small G protein superfamily GTPases	U		5.159	1	1	1	0	283	12	14	151	1		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	54.m07043	AN4201.1	AO070231000023	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ	1	0.00765114272370187 2.09063644481557	2	1	1	0	161	262	249	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07872	AN4453.1	AO070273000002	Mitochondrial inheritance and actin cytoskeleton organization protein	Z		3.244	1	1	1	1	115	406	37	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05570	AN4558.1	AO070321000170	hypothetical protein [Neurospora crassa]				1	1	1	0	97	345	412	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05486	AN4647.1	AO070316000121	Peroxisomal phytanoyl-CoA hydroxylase	I	1	0.008	1	1	1	0	71	57	113	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m08864	AN4959.1	AO070288000021	Protein required for S-phase initiation or completion	D		1.225	1	1	1	0	281	51	65	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m14875	AN5178.1	AO070247000009	Alcohol dehydrogenase, class IV	C		1.481	2	1	1	1	60	101	143	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	69.m15495	AN5440.1	AO070333000102	Catalase (peroxidase I)	P		6.961	1	1	1	0	236	188	249			No EST	No EST
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15371	AN5669.1	AO070342000262	Succinyl-CoA:alpha-ketoacid-CoA transferase	C		1.481	1	1	1	1	196	256	251	22	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m14821	AN5776.1	AO070249000021	SWI-SNF chromatin-remodeling complex protein	B		6.551	1	1	1	0	221	229	270	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m18983	AN5850.1	AO070317000138	Hydroxysteroid 17-beta dehydrogenase 11	Q		2.091	1	1	1	0	128	213	254	13	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	72.m19268	AN5866.1	AO070308000130	Arylalkylamine N-acetyltransferase				1	1	1	0	35	56	64			No EST	No EST
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19958	AN5913.1	AO070248000033	Alcohol dehydrogenase, class V	Q		2.091	1	1	1	0	177	155	380	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19960	AN5916.1	AO070340000370	Enoyl-CoA hydratase/carnithine racemase	I	1	0.008	1	1	1	0	166	82	91	14	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19150	AN5990.1	AO070340000287	Acyl-CoA synthetase	I	1	0.008	1	1	1	0	12	241	284	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	72.m19143	AN5997.1	AO070340000279	40S ribosomal protein S15	J		2.368	1	1	1	1	117	125	120			294	1
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19944	AN6037.1	AO070340000248	Glucose-6-phosphate isomerase	G		3.911	1	0	1	1	52	0	4	173	1		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19071	AN6079.1	AO070340000129	Predicted RNA-binding protein				1	1	1	1	102	141	160	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19424	AN6229.1	AO070304000080	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C		1.481	1	1	1	1	119	182	115	15	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19339	AN6295.1	AO070308000053	predicted protein [Neurospora crassa]				1	1	1	0	372	116	127	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07697	AN6438.1	AO070299000087	Dipeptidyl aminopeptidase	O		2.899	1	1	1	0	69	199	195	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15250	AN6889.1	AO070314000032	hypothetical protein [Neurospora crassa]				1	1	1	0	191	80	55	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05876	AN7465.1	AO070287000061	Sister chromatid cohesion complex Cohesin, subunit RAD21/SCC1	D		1.225	1	2	1	1	69	90	79	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15153	AN7514.1	AO070258000020	Nucleolar GTPase/ATPase p130	Y		4.819	1	1	1	0	312	131	3	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19591	AN7572.1	AO070343000419	NDR and related serine/threonine kinases				1	1	2	1	392	128	147	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m03866	AN8020.1	AO070322000068	conserved hypothetical protein [Neurospora crassa]				1	1	1	0	309	79	209	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m09197	AN8400.1	AO070329000063	Permeases of the major facilitator superfamily	GEP		3.910554805366 2.06767721409258 6.96075923361899	1	1	1	0	299	158	134	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	52.m04095	AN8415.1	AO070302000056	Acyl-CoA dehydrogenases	I	1	0.008	1	1	1	1	126	364	96	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15603	AN8796.1	AO070276000064	GTP-binding protein	T		2.068	1	1	2	0	113	280	268	172	0		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15193	AN8968.1	AO070342000435	hypothetical protein [Neurospora crassa]				1	1	1	0	129	15	11	No EST	No EST		
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	59.m08384	AN9291.1	AO070339000229	Permeases of the major facilitator superfamily	GEP		3.910554805366 2.06767721409258 6.96075923361899	1	1	1	0	5	11	302			No EST	No EST
2093	CCCCGCAC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m04094	AN9522.1	AO070310000070	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I	1	0.008	1	1	1	1	183	47	7	No EST	No EST		
2194	GGvGTTTGGAG		down	down	54.m06521	AN0260.1	AO070334000098	Eukaryotic-type DNA primase, large subunit	L		0.618	1	2	1	1	254	82	264			No EST	No EST
2194	GGvGTTTGGAG		down	down	70.m15416	AN0817.1	AO070288000087	Putative transcriptional repressor regulating G2/M transition	KD		1.00827858320546 0.451190227357433	1	1	1	1	107	102	122			No EST	No EST
2194	GGvGTTTGGAG		down	up	69.m14936	AN1918.1	AO070341000122	Phosphoenolpyruvate carboxykinase (ATP)	C		4.068	1	1	2	1	158	279	215	52	0		
2194	GGvGTTTGGAG		down	down	59.m08579	AN3178.1	AO070256000001	Component of histone deacetylase complex (breast carcinoma metastasis suppressor 1 protein in human)	DK		0.451190227357433 1.00827858320546	1	1	1	0	57	91	90			No EST	No EST
2194	GGvGTTTGGAG		down	down	65.m07390	AN3745.1	AO070309000078	Regulator of ribosome synthesis	J		4.198	1	1	1	1	97	77	94			No EST	No EST
2194	GGvGTTTGGAG		down	down	58.m07808	AN3830.1	AO070305000068	Threonine/serine dehydratases	E		1.473	1	1	1	0	117	59	82			218	1
2194	GGvGTTTGGAG		down	down	54.m07047	AN4112.1	AO070342000107	Nucleolar GTPase/ATPase p130	Y		1.232	1	1	1	0	172	174	281			No EST	No EST
2194	GGvGTTTGGAG		down	down	58.m07904	AN4415.1	AO070273000036	Holocytochrome c synthase/heme-lyase	CO		4.06814775625896 2.10567113864815	1	1	1	0	70	41	43			No EST	No EST
2194	GGvGTTTGGAG		down	down	59.m08858	AN4953.1	AO070288000006	Ras-related small GTPase, Rho type				1	1	1	0	132	189	217			431	1
2194	GGvGTTTGGAG		down	down	71.m15298	AN6841.1	AO070314000098	Mitochondrial inner membrane protease, subunit IMP1	O		2.106	1	1	1	0	59	30	26			No EST	No EST
2194	GGvGTTTGGAG		down	down	57.m05879	AN7463.1	AO070287000063	Ammonia permease	P		3.212	1	1	1	0	45	280	121			No EST	No EST
2194	GGvGTTTGGAG		down	up	57.m05846	AN7496.1	AO070287000019	FOG: Immunoglobin and related proteins	P		3.212	1	1	1	1	167	295	300	No EST	No EST		
2194	GGvGTTTGGAG		down	down	57.m05465	AN7688.1	AO070325000082	Protein similar to predicted member of the intramitochondrial sorting protein family	U		4.173	1	1	1	0	65	59	61			No EST	No EST
2194	GGvGTTTGGAG		down	down	57.m05337	AN7777.1	AO070286000057	Amino acid transporters	E		1.473	1	1	1	0	77	116	15			No EST	No EST
2194	GGvGTTTGGAG		down	down	53.m03915	AN8064.1	AO070330000020	Replication factor C, subunit RFC5	L		0.618	1	1	1	0	128	290	70			No EST	No EST
2194	GGvGTTTGGAG		down	down	62.m03398	AN8672.1	AO070315000089	P-type ATPase				1	1	1	0	148	157	163			No EST	No EST
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	71.m15474	AN0211.1	AO070321000033	U2-associated snRNP A' protein	A		4.024	1	1	1	0	234	73	116	No EST	No EST		

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2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06476	AN0267.1	AO070334000073	Myosin regulatory light chain, EF-Hand protein superfamily	Z		0.655	1	1	1	0	156	146	82	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06650	AN0426.1	AO070338000276	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I		2.485	1	1	1	0	368	40	127	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06630	AN0440.1	AO070338000297	Histone acetyltransferases PCAF/SAGA/ADA, subunit TADA3L/NGG1	B		5.322	1	1	1	0	290	196	201	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15349	AN0751.1	AO070343000448	predicted protein [Neurospora crassa]				1	1	1	0	179	329	219	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15474	AN0872.1	AO070320000030	CDC45 (cell division cycle 45)-like protein	L		1.235	1	1	1	1	247	68	173	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15484	AN0881.1	AO070320000049	Alkylated DNA repair protein	L		1.235	1	1	1	0	17	133	43	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15535	AN0928.1	AO070320000113	hypothetical protein ((AL451014) putative protein [Neurospora crassa])				1	1	1	0	364	96	75	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15208	AN1027.1	AO070312000118					1	1	1	0	120	27	31	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m14897	AN1334.1	AO070303000099	Component of vacuolar transporter chaperone (Vtc) involved in vacuole fusion	UO		2.65208787590796 4.06027204839289	1	1	1	0	411	56	58	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	down	70.m14849	AN1374.1	AO070215000001	Uncharacterized conserved protein				1	1	1	0	187	176	179			No EST	No EST
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	55.m02950	AN1448.1	AO070302000005	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	J		4.691	1	1	1	0	182	77	59	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	down	58.m07753	AN1675.1	AO070299000004	Lysophospholipase	I		2.485	0	1	1	0	288	212	365			No EST	No EST
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07653	AN1859.1	AO070292000036	Transcription initiation factor IIF, auxiliary subunit	K		0.775	1	1	1	0	119	29	28	83	1		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	58.m07590	AN1984.1	AO070301000069	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K		0.775	2	2	2	1	349	56	63	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05776	AN2077.1	AO070341000230	WD40 repeat protein				1	1	1	0	144	71	80	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08450	AN2529.1	AO070300000122	Enoyl-CoA isomerase	I		2.485	1	1	1	1	281	179	162	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09356	AN2848.1	AO070334000119	Component of the U4/U6.U5 snRNP/mitosis protein DIM1	AD		4.02439412175509 5.97244600957524	1	1	1	0	73	83	120	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08759	AN2909.1	AO070338000097	Putative arsenite-translocating ATPase	P		1.157	1	1	1	0	346	20	19	58	1		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m09097	AN2916.1	AO070329000155	Succinate dehydrogenase, flavoprotein subunit	C		4.347	1	1	1	1	182	115	132	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	67.m02932	AN3224.1	AO070330000074	predicted protein [Neurospora crassa]				1	1	1	0	93	377	374	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	66.m04640	AN3372.1	AO070281000014	FOG: Low-complexity				1	1	1	0	9	1	9	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14994	AN3933.1	AO070341000044	RNA polymerase I, second largest subunit	K		0.775	1	1	1	1	308	272	227	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m14989	AN3937.1	AO070341000048	Uncharacterized conserved protein				1	1	1	0	53	44	42	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05645	AN4486.1	AO070311000037	hypothetical protein [Neurospora crassa]				2	1	2	0	416	27	28	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05643	AN4488.1	AO070311000040	predicted protein [Neurospora crassa]				1	1	1	1	498	81	34	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05570	AN4558.1	AO070321000170	hypothetical protein [Neurospora crassa]				1	1	1	0	312	128	169	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	59.m08893	AN4990.1	AO070288000060	Uncharacterized membrane protein				1	1	1	1	505	57	35	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m07051	AN5113.1	AO070291000066	Peroxisomal biogenesis protein (peroxin 16)	U		2.652	1	1	1	0	156	30	35	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06878	AN5143.1	AO070291000032	Protein involved in vacuolar polyphosphate accumulation, contains SPX domain	P		1.157	0	0	0	0	297	0	0	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	69.m15563	AN5343.1	AO070333000181	Kinesin (SMY1 subfamily)	Z		0.655	1	1	1	1	157	278	210	200	0		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06826	AN5711.1	AO070324000151	Uncharacterized conserved protein				1	1	1	0	139	20	30	No EST	No EST		

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2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	54.m06844	AN5724.1	AO070324000127	Inner membrane protein translocase involved in respiratory chain assembly	OU		4.06027204839289 2.65208787590796	1	1	1	1	196	27	11	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19252	AN5879.1	AO070245000029	Uncharacterized conserved protein, contains ML domain				1	1	1	1	20	135	130	110	0		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19023	AN6141.1	AO070340000061	Imidazoleglycerol-phosphate synthase subunit H-like	H		5.563	1	1	1	1	113	114	119	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19422	AN6232.1	AO070304000085	Vacuolar H+-ATPase V1 sector, subunit B	C		4.347	1	1	1	0	167	83	138	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	72.m19499	AN6359.1	AO070279000047	Cdc4 and related F-box and WD-40 proteins				1	1	1	0	445	52	210	276	1		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	57.m05422	AN7658.1	AO070268000027	Cdc42-interacting protein CIP4	Z		0.655	1	1	1	0	131	243	227	227	0		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m03906	AN8040.1	AO070330000006	Protein involved in inorganic phosphate transport	P		1.157	1	1	1	0	173	229	273	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m04127	AN8236.1	AO070310000072	Putative growth response protein	T		4.336	1	1	1	0	181	150	1	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	70.m15786	AN9436.1	AO070343000484	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 5'-3' helicase subunit RAD3	KL		0.775142541545787 1.23519380446543	1	1	1	0	128	46	48	No EST	No EST		
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	down	53.m03848	AN9467.1	AO070322000047	Serine/threonine protein phosphatase 2A, regulatory subunit	T		4.336	1	1	1	0	302	321	317			No EST	No EST
2199	CCACGTGC	PHO4 (CACGTG) [yeast_motifs_all];	up	up	53.m04094	AN9522.1	AO070310000070	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I		2.485	1	1	1	1	179	51	11	No EST	No EST		
2215	ATTCCCC		down	down	71.m15326	AN0055.1	AO070314000132	TmpA [Emericella nidulans]				1	1	1	0	322	330	125			68	0
2215	ATTCCCC		down	down	71.m16065	AN0182.1	AO070321000058	Ras-related GTPase				1	1	1	1	236	234	240			341	1
2215	ATTCCCC		down	down	69.m15036	AN1733.1	AO070324000063	Delta-1-pyrroline-5-carboxylate dehydrogenase	E		1.261	1	1	1	1	29	31	25			No EST	No EST
2215	ATTCCCC		down	down	58.m07665	AN1846.1	AO070292000059					1	1	1	0	101	74	38			162	1
2215	ATTCCCC		down	down	71.m15842	AN2224.1	AO070326000179	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U		1.196	1	1	1	0	36	60	37			No EST	No EST
2215	ATTCCCC		down	down	59.m08758	AN2907.1	AO070338000098	Translation initiation factor 3, subunit e (eIF-3e)	J		0.261	1	1	1	0	161	82	69			No EST	No EST
2215	ATTCCCC		down	down	59.m08952	AN3062.1	AO070337000011	Myosin class II heavy chain	Z		0.066	1	1	1	0	75	99	83			No EST	No EST
2215	ATTCCCC		down	down	59.m09174	AN4802.1	AO070329000037	60S ribosomal protein L21	J		0.261	1	1	1	1	133	128	130			483	1
2215	ATTCCCC		down	down	71.m15259	AN6875.1	AO070314000048	Kinesin-like protein	Z		0.066	1	1	2	0	108	94	74			No EST	No EST
2215	ATTCCCC		down	up	71.m15815	AN7784.1	AO070286000028	GTPase-activating protein VRP				1	1	1	1	290	211	101	No EST	No EST		
2215	ATTCCCC		down	down	62.m03398	AN8672.1	AO070315000089	P-type ATPase				2	1	1	1	134	143	149			No EST	No EST
2223	GGCGTTG		down	down	70.m15630	AN0989.1	AO070318000148	SWI-SNF chromatin-remodeling complex protein	B		0.254	1	1	1	1	107	108	126			No EST	No EST
2223	GGCGTTG		down	up	70.m15237	AN1019.1	AO070343000596	Cullins	D		3.164	1	1	1	0	438	117	71	69	0		
2223	GGCGTTG		down	down	70.m15739	AN1247.1	AO070223000010	Peroxisomal membrane protein MPV17 and related proteins				1	1	1	1	86	278	111			374	1
2223	GGCGTTG		down	down	57.m05735	AN1880.1	AO070341000169	predicted protein [Neurospora crassa]				1	1	1	0	226	245	246			286	1
2223	GGCGTTG		down	up	72.m19711	AN2130.1	AO070278000033	Ras1 guanine nucleotide exchange factor	T		5.282	1	1	1	1	99	110	117	No EST	No EST		
2223	GGCGTTG		down	down	72.m19466	AN2415.1	AO070228000029	RNA polymerase I and III, subunit RPA40/RPC40	K		0.228	1	1	1	1	48	52	47			No EST	No EST
2223	GGCGTTG		down	down	59.m08476	AN2508.1	AO070263000056	Cysteine desulfurase NFS1	E		1.754	1	1	1	0	87	32	143			92	1
2223	GGCGTTG		down	down	71.m16097	AN2754.1	AO070276000006	Amino acid transporter protein	E		1.754	1	1	1	0	237	173	266			No EST	No EST
2223	GGCGTTG		down	down	59.m09408	AN4878.1	AO070338000082	Transcription factor	K		0.228	1	1	1	1	297	230	350			303	1
2223	GGCGTTG		down	down	58.m07558	AN5648.1	AO070301000033	Uncharacterized conserved protein				1	1	1	1	264	258	267			No EST	No EST
2223	GGCGTTG		down	down	54.m06846	AN5726.1	AO070324000125	FOG: Zn-finger				1	1	1	0	158	111	176			No EST	No EST
2223	GGCGTTG		down	down	69.m14857	AN5740.1	AO070341000019	Ras-related small GTPase, Rho type				1	1	2	1	245	255	248			126	0
2223	GGCGTTG		down	up	72.m19980	AN6247.1	AO070304000102	predicted protein [Neurospora crassa]				1	1	1	0	7	509	499	325	0		
2223	GGCGTTG		down	down	72.m19504	AN6351.1	AO070275000048	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U		1.545	2	1	1	1	55	45	89			49	1
2223	GGCGTTG		down	up	53.m03907	AN8039.1	AO070330000007	Histone 2A	B		0.254	2	1	1	0	171	74	323	319	1		
2223	GGCGTTG		down	down	53.m03887	AN8056.1	AO070322000144	Chromosome condensation complex Condensin, subunit G	BD		0.253871390377446 3.16419799073092	1	1	1	0	31	32	30			No EST	No EST
2223	GGCGTTG		down	down	62.m03393	AN8677.1	AO070315000097	Galactosyltransferases	G		4.471	1	1	1	1	276	215	286			No EST	No EST
2223	GGCGTTG		down	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J		4.367	1	1	1	1	48	202	211	73	0		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2223	GGCGTTG		down	down	71.m15583	AN8787.1	AO070276000074	Nuclear mRNA export factor receptor LOS1/Exportin-t (importin beta superfamily)	YUJ		1.38559238191041 1.54506181317591 4.36711979457036	1	1	1	1	267	273	232			356	1
2223	GGCGTTG		down	down	66.m04545	AN9087.1	AO070332000190	Calcium-responsive transcription coactivator	K		0.228	1	1	1	0	173	196	177			No EST	No EST
2223	GGCGTTG		down	down	52.m03849	AN9362.1	AO070315000035	U2 snRNP splicing factor, small subunit, and related proteins	A		3.990	1	1	1	1	33	21	31			No EST	No EST
2236	GCAGAATC		up	up	70.m15611	AN0966.1	AO070320000170	Uncharacterized conserved protein BCNT				1	1	1	0	78	4	10	No EST	No EST		
2236	GCAGAATC		up	up	70.m15019	AN1200.1	AO070331000206	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein	JK		0.273786162161689 0.846221949021435	1	1	1	1	65	117	111	No EST	No EST		
2236	GCAGAATC		up	up	70.m15003	AN1222.1	AO070331000222	S-adenosylmethionine synthetase	H		1.581	1	1	1	1	241	80	69	193	1		
2236	GCAGAATC		up	up	69.m15051	AN1750.1	AO070324000043	RNA helicase	A		0.768	1	1	1	1	105	43	28	No EST	No EST		
2236	GCAGAATC		up	up	69.m14944	AN1927.1	AO070341000108	hypothetical protein [Neurospora crassa]				1	1	1	1	330	231	251	No EST	No EST		
2236	GCAGAATC		up	up	58.m07638	AN2050.1	AO070292000017	Vesicle coat protein clathrin, light chain	U		1.048	1	1	1	1	148	75	78	91	1		
2236	GCAGAATC		up	up	69.m15220	AN2438.1	AO070264000041	Predicted GTPase				1	1	1	1	19	30	47	No EST	No EST		
2236	GCAGAATC		up	up	59.m08566	AN3176.1	AO070256000014	ATP-dependent RNA helicase	A		0.768	1	1	1	0	14	147	133	No EST	No EST		
2236	GCAGAATC		up	up	58.m07374	AN3576.1	AO070342000173	Uncharacterized membrane protein NPD008/CGI-148				1	1	1	1	154	49	92	No EST	No EST		
2236	GCAGAATC		up	up	54.m06709	AN4065.1	AO070342000055	KRR1-interacting protein involved in 40S ribosome biogenesis	J		0.274	1	2	1	1	113	30	19	No EST	No EST		
2236	GCAGAATC		up	up	54.m06728	AN4087.1	AO070342000080	40S ribosomal protein S3	J		0.274	1	1	1	1	6	311	165	No EST	No EST		
2236	GCAGAATC		up	up	58.m07861	AN4471.1	AO070305000130	WD40 repeat-containing protein				1	1	1	1	97	174	286	36	0		
2236	GCAGAATC		up	up	59.m09126	AN4850.1	AO070327000106	RNA-binding protein RBM5 and related proteins, contain G-patch and RRM domains				1	1	1	1	72	238	52	No EST	No EST		
2236	GCAGAATC		up	down	58.m07512	AN5585.1	AO070328000019	3-keto sterol reductase	I		3.164	1	1	1	0	44	163	145			No EST	No EST
2236	GCAGAATC		up	up	72.m19294	AN6196.1	AO070308000103					1	1	1	1	245	114	146	No EST	No EST		
2236	GCAGAATC		up	up	72.m19322	AN6312.1	AO070308000067	predicted protein [Neurospora crassa]				1	1	1	0	128	132	167	No EST	No EST		
2236	GCAGAATC		up	up	65.m07298	AN6682.1	AO070289000024	8-oxoguanine DNA glycosylase	L		2.194	1	2	1	0	86	10	104	No EST	No EST		
2236	GCAGAATC		up	up	69.m15144	AN7526.1	AO070258000030	Apoptosis antagonizing transcription factor/protein transport protein	KU		0.846221949021435 1.04788844714934	1	1	1	0	75	16	7	No EST	No EST		
2236	GCAGAATC		up	up	53.m03895	AN8049.1	AO070292000101	NADH:ubiquinone oxidoreductase, NDUFS6/13 kDa subunit	C		2.565	1	1	1	0	155	16	16	No EST	No EST		
2236	GCAGAATC		up	down	62.m03377	AN8693.1	AO070315000115	Serine/threonine protein kinase	D		4.561	1	1	1	0	79	201	85			No EST	No EST
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	54.m06594	AN0476.1	AO070328000164	Mitochondrial ribosomal protein L27	J	1	0.000	1	1	1	1	122	10	12	9	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	65.m07309	AN0490.1	AO070321000178	CTP synthase (UTP-ammonia lyase)	F		0.081	1	1	2	0	123	69	20	39	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	69.m15266	AN0582.1	AO070280000004	Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	L		1.907	1	1	1	1	95	23	76	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	69.m15260	AN0589.1	AO070280000011	RNA Helicase	A	1	0.002	1	1	1	1	106	57	44	16	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15249	AN0647.1	AO070343000582	U3 small nucleolar ribonucleoprotein (snoRNP) component	A	1	0.002	2	1	1	1	3	263	264	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15576	AN0944.1	AO070320000139	ATP-dependent RNA helicase	A	1	0.002	1	1	1	0	185	230	188	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15580	AN0946.1	AO070320000143	Predicted protein involved in nuclear export of pre-ribosomes	J	1	0.000	1	1	1	0	99	6	3	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15605	AN0956.1	AO070320000158	tRNA-dihydrouridine synthase	J	1	0.000	1	1	1	0	158	53	68	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15042	AN1175.1	AO070331000170	Nucleolar protein NOP52/RRP1	A	1	0.002	1	1	1	0	137	96	108	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m15019	AN1200.1	AO070331000206	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein	JK	1	2.54117069140594e-08 2.46556524184544	1	1	2	1	62	121	91	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m14875	AN1355.1	AO070237000005	Permease of the drug/metabolite transporter (DMT) superfamily				1	1	1	0	188	256	49	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	70.m14862	AN1367.1	AO070215000014	WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis	J	1	0.000	1	1	1	0	5	88	50	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	58.m07732	AN1666.1	AO070299000048	Nucleolar GTPase				1	1	1	0	140	100	72	122	1		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	72.m19761	AN1711.1	AO070297000053	NMD protein affecting ribosome stability and mRNA decay	J	1	0.000	1	1	1	0	122	79	34	23	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	69.m15051	AN1750.1	AO070324000043	RNA helicase	A	1	0.002	1	1	1	0	95	40	25	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	58.m07570	AN1965.1	AO070301000046	Ribose-phosphate pyrophosphokinase	FE		0.0808018695609068 1.64366554181311	1	1	1	0	222	129	88	125	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	57.m05792	AN2090.1	AO070341000248	Protein containing repeated kelch motifs				1	2	1	0	163	80	128	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	59.m09061	AN2933.1	AO070337000174	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	BT		3.17627995048343 2.99527759330682	1	1	4	0	242	151	1	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	59.m08928	AN3069.1	AO070337000005	Ribosome biogenesis protein - Nop56p/Sik1p	AJ	1	0.00206108813997884 2.54117069140594e-08	1	1	2	1	177	16	13	109	1		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	65.m07390	AN3745.1	AO070309000078	Regulator of ribosome synthesis	J	1	0.000	1	1	1	1	119	61	73	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	58.m07803	AN3827.1	AO070305000064	Protein required for normal rRNA processing	A	1	0.002	2	1	1	0	81	30	110	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	58.m07811	AN3832.1	AO070305000070	Mitochondrial elongation factor	J	1	0.000	1	1	1	1	80	78	63	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	58.m07837	AN3865.1	AO070305000101	Methionyl-tRNA synthetase	J	1	0.000	1	1	1	0	110	37	67	9	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L		1.907	1	1	1	0	231	22	0	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	54.m06579	AN4015.1	AO070328000151	Translation initiation factor 5A (eIF-5A)	J	1	0.000	1	1	1	0	190	190	128	70	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	54.m06784	AN4232.1	AO070234000014	RNA-binding protein required for 60S ribosomal subunit biogenesis	J	1	0.000	1	1	1	0	100	16	34	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	65.m07411	AN5685.1	AO070309000100	Uncharacterized conserved protein				1	1	1	0	99	9	14	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	69.m14807	AN5789.1	AO070249000035	Predicted protein carboxyl methylase				1	1	1	1	247	35	53	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	72.m19269	AN5865.1	AO070308000129	GTP-binding protein CRFG/NOG1 (ODN superfamily)				1	1	1	0	92	15	12	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	62.m03156	AN6569.1	AO070326000012	Predicted metalloprotease with chaperone activity (RNAse H/HSP70 fold)	O		2.165	2	1	1	0	140	90	81	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	65.m07264	AN6711.1	AO070339000151	Ribose-phosphate pyrophosphokinase	FE		0.0808018695609068 1.64366554181311	1	1	1	0	115	34	29	113	1		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	62.m03303	AN7204.1	AO070293000065	Fatty acid desaturase	I		3.326	2	1	1	0	30	188	195	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	57.m05914	AN7430.1	AO070229000001	Glutamine amidotransferase/cyclase	E		1.644	1	1	1	0	241	76	18	45	0		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	53.m04172	AN8272.1	AO070310000029	RNA polymerase III (C) subunit	K		2.466	1	1	1	0	73	47	60	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	52.m04024	AN9398.1	AO070274000018	Cell adhesion complex protein bystin				1	1	1	0	137	183	62	No EST	No EST		
2249	TTTTTTT	positioning_element2 (AAAAAA) [polya];	up	up	52.m04033	AN9406.1	AO070274000011	tRNA methyltransferase	J	1	0.000	1	1	1	0	83	68	99	No EST	No EST		
2253	TTTGGTTT		down	up	70.m15468	AN0861.1	AO070320000009	predicted protein [Neurospora crassa]				1	1	1	0	226	94	15	No EST	No EST		
2253	TTTGGTTT		down	down	72.m19355	AN1150.1	AO070308000028	Acetylornithine aminotransferase	E		2.794	1	1	1	0	69	62	186			No EST	No EST
2253	TTTGGTTT		down	down	58.m07718	AN1639.1	AO070299000037	Thioredoxin-like protein	O		0.813	1	1	1	1	198	226	189			No EST	No EST
2253	TTTGGTTT		down	down	57.m05818	AN2112.1	AO070341000294	3-carboxymuconate cyclase	G		2.826	2	1	1	0	147	211	202			No EST	No EST

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2253	TTTGGTTT		down	down	65.m07256	AN6718.1	AO070339000158	ATPases of the AAA+ class	O		0.813	1	1	1	0	13	65	272			No EST	No EST
2253	TTTGGTTT		down	down	71.m15272	AN6859.1	AO070314000076	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains	AK		2.22482137311558 2.34087518282749	1	1	1	1	158	118	146			No EST	No EST
2253	TTTGGTTT		down	down	71.m15720	AN7698.1	AO070325000103	Myosin class I heavy chain	Z		1.444	1	2	2	0	161	44	42			311	1
2253	TTTGGTTT		down	down	65.m07308	AN8785.1	AO070289000010	Mitochondrial aspartate/glutamate carrier protein Aralar/Citrin (contains EF-hand Ca2+-binding domains)	C		2.513	1	1	1	1	110	32	27			No EST	No EST
2253	TTTGGTTT		down	down	71.m15583	AN8787.1	AO070276000074	Nuclear mRNA export factor receptor LOS1/Exportin-t (importin beta superfamily)	YUJ		0.615487511470356 2.6227681264767 2.65115798769945	1	1	1	1	117	107	84			356	1
2287	TTCTTCCTT		up	up	70.m15397	AN0787.1	AO070239000021	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	G		1.502	1	1	1	0	122	7	335	No EST	No EST		
2287	TTCTTCCTT		up	up	70.m15426	AN0824.1	AO070255000021	Short-chain acyl-CoA dehydrogenase	I		1.165	1	1	1	0	86	66	90	25	0		
2287	TTCTTCCTT		up	up	70.m15462	AN0866.1	AO070320000017	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O		2.034	1	1	1	0	262	382	461	No EST	No EST		
2287	TTCTTCCTT		up	up	55.m03061	AN1543.1	AO070339000311	Fumarate reductase, flavoprotein subunit	C		0.377	2	1	2	0	22	292	54	43	0		
2287	TTCTTCCTT		up	up	55.m03274	AN1546.1	AO070339000308	Histone deacetylase complex, SIN3 component	B		0.726	1	1	1	0	127	372	436	320	0		
2287	TTCTTCCTT		up	up	58.m07716	AN1630.1	AO070299000035	Catalase (peroxidase I)	P		1.677	1	1	1	0	168	417	355	69	0		
2287	TTCTTCCTT		up	up	58.m07713	AN1810.1	AO070299000061	Ornithine aminotransferase	E		3.203	1	1	1	0	95	105	174	33	0		
2287	TTCTTCCTT		up	up	57.m05742	AN1876.1	AO070341000183	Predicted membrane protein, contains two CBS domains				1	2	1	0	26	196	363	No EST	No EST		
2287	TTCTTCCTT		up	up	58.m07644	AN2056.1	AO070292000026	Uncharacterized conserved protein				1	1	1	0	5	353	270	No EST	No EST		
2287	TTCTTCCTT		up	up	57.m05760	AN2062.1	AO070341000205	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O		2.034	3	2	2	0	149	103	87	173	1		
2287	TTCTTCCTT		up	up	57.m05768	AN2068.1	AO070341000217	Vigilin	I		1.165	2	1	2	0	383	143	38	No EST	No EST		
2287	TTCTTCCTT		up	up	59.m08719	AN2871.1	AO070338000143	SWI-SNF chromatin-remodeling complex protein	B		0.726	2	2	2	0	334	111	138	No EST	No EST		
2287	TTCTTCCTT		up	up	59.m08644	AN3100.1	AO070334000141	predicted protein [Neurospora crassa]				3	1	2	1	215	333	314	106	0		
2287	TTCTTCCTT		up	up	66.m04646	AN3376.1	AO070281000020	Squalene synthetase	I		1.165	1	1	2	0	14	125	78	298	1		
2287	TTCTTCCTT		up	up	54.m06745	AN4189.1	AO070342000110	Mitogen-activated protein kinase kinase (MAP2K)	T		0.574	1	1	1	0	309	25	123	No EST	No EST		
2287	TTCTTCCTT		up	up	58.m08010	AN4314.1	AO070230000002	predicted protein [Neurospora crassa]				2	1	1	0	179	43	17	No EST	No EST		
2287	TTCTTCCTT		up	up	58.m08982	AN4411.1	AO070273000031	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				1	1	2	0	165	202	1	No EST	No EST		
2287	TTCTTCCTT		up	up	58.m07847	AN4462.1	AO070305000113	Pyruvate carboxylase	C		0.377	1	1	3	0	273	35	133	No EST	No EST		
2287	TTCTTCCTT		up	up	59.m08876	AN4973.1	AO070288000039	predicted protein [Neurospora crassa]				2	2	2	0	45	176	221	No EST	No EST		
2287	TTCTTCCTT		up	up	59.m09453	AN4998.1	AO070255000029	Ras GTPase-activating protein family - IQGAP	T		0.574	1	1	1	0	453	470	505	No EST	No EST		
2287	TTCTTCCTT		up	up	57.m05712	AN5222.1	AO070337000256	40S ribosomal protein S11	J		3.367	1	1	1	0	101	95	131	116	1		
2287	TTCTTCCTT		up	up	69.m15615	AN5744.1	AO070341000001	Multifunctional chaperone (14-3-3 family)	O		2.034	1	1	1	0	88	83	168	141	1		
2287	TTCTTCCTT		up	up	72.m19897	AN5849.1	AO070281000056	Serine/threonine protein kinase	T		0.574	1	1	1	0	210	249	115	No EST	No EST		
2287	TTCTTCCTT		up	up	72.m19123	AN6033.1	AO070340000255	Predicted GTPase-activating protein	T		0.574	1	1	1	0	310	196	230	No EST	No EST		
2287	TTCTTCCTT		up	up	65.m07257	AN6717.1	AO070339000157	NAD-dependent malate dehydrogenase	C		0.377	2	1	1	0	103	161	139	No EST	No EST		
2287	TTCTTCCTT		up	up	71.m15236	AN6900.1	AO070314000015	Triosephosphate isomerase	G		1.502	1	1	1	0	82	218	163	No EST	No EST		
2287	TTCTTCCTT		up	up	72.m19777	AN7287.1	AO070297000028	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C		0.377	1	1	2	0	173	240	412	No EST	No EST		
2287	TTCTTCCTT		up	up	56.m02393	AN7388.1	AO070293000057	Catalase (peroxidase I)	P		1.677	1	1	1	0	179	307	14	No EST	No EST		
2287	TTCTTCCTT		up	up	62.m03324	AN8751.1	AO070250000011	NDR and related serine/threonine kinases				2	2	1	0	341	9	24	No EST	No EST		
2287	TTCTTCCTT		up	up	71.m15604	AN8797.1	AO070276000063	hypothetical protein ((AL513442) conserved hypothetical protein [Neurospora crassa])				1	1	1	0	100	103	435	No EST	No EST		
2287	TTCTTCCTT		up	up	71.m15980	AN8846.1	AO070271000030	Protein involved in beta-1,3-glucan synthesis	G		1.502	1	1	2	0	335	289	251	355	1		
2287	TTCTTCCTT		up	up	66.m04571	AN9112.1	AO070332000162	Alcohol dehydrogenase, class V	Q		3.745	1	1	1	1	116	47	46	No EST	No EST		
2287	TTCTTCCTT		up	up	66.m04608	AN9146.1	AO070332000116	hypothetical protein [Neurospora crassa]				1	1	1	0	179	41	58	No EST	No EST		
2378	TGTACAGAA		down	down	70.m15361	AN0747.1	AO070343000435	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O		2.573	1	1	1	1	124	115	105			141	1
2378	TGTACAGAA		down	down	70.m15382	AN0776.1	AO070316000062	60S ribosomal protein L22	J		0.077	1	1	1	1	64	70	63			283	1
2378	TGTACAGAA		down	down	70.m15214	AN0997.1	AO070312000043	Ribonuclease III domain proteins	J		0.077	1	1	1	1	119	105	120			120	1
2378	TGTACAGAA		down	down	70.m14921	AN1287.1	AO070303000048	Prohibitins and stomatins of the PID superfamily	C		0.470	1	1	1	0	317	258	300			No EST	No EST
2378	TGTACAGAA		down	down	57.m05716	AN1902.1	AO070341000151	Nucleolar GTPase/ATPase p130	Y		0.578	2	1	1	0	173	276	420			505	1
2378	TGTACAGAA		down	down	71.m15519	AN2315.1	AO070323000037	F0F1-type ATP synthase, beta subunit	C		0.470	1	1	1	1	90	68	83			307	1
2378	TGTACAGAA		down	down	71.m16072	AN2317.1	AO070323000039	Actin depolymerizing factor	Z		1.305	1	1	1	1	263	251	253			345	1
2378	TGTACAGAA		down	up	54.m06889	AN5134.1	AO070291000041	Glutamate synthase	E		3.983	1	1	1	0	116	54	84	No EST	No EST		
2378	TGTACAGAA		down	down	58.m07520	AN5596.1	AO070328000008	Permease of the major facilitator superfamily				1	1	1	1	74	56	73			275	1
2378	TGTACAGAA		down	up	65.m07286	AN6697.1	AO070339000128	hypothetical protein [Neurospora crassa]				1	1	1	0	347	207	190	193	0		

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2378	TGTACAGAA		down	down	53.m03929	AN8076.1	AO070330000034	Splicing coactivator SRm160/300, subunit SRm300	A		1.920	1	1	1	1	106	137	233			No EST	No EST
2378	TGTACAGAA		down	down	53.m03749	AN8225.1	AO070310000087	Ribosomal protein L1	J		0.077	1	1	1	1	40	17	29			No EST	No EST
2378	TGTACAGAA		down	down	66.m04578	AN9120.1	AO070332000154	RNA polymerase II, second largest subunit	K		2.004	1	1	1	0	42	2	31			102	1
2451	GATATCC		down	down	70.m15369	AN0766.1	AO070316000078	hypothetical protein [Novosphingobium aromaticivorans]				1	1	1	1	144	99	133			222	1
2451	GATATCC		down	down	70.m14828	AN1394.1	AO070233000008	Septin CDC10 and related P-loop GTPases	DTZ		1.51923914920482 0.59518574358162 1.38438496613063	1	1	1	1	172	169	175			356	1
2451	GATATCC		down	down	55.m02962	AN1458.1	AO070306000074	predicted protein [Neurospora crassa]				1	1	1	0	134	106	127			171	1
2451	GATATCC		down	down	59.m08861	AN4956.1	AO070288000018	Thiamine pyrophosphate-requiring enzyme	EH		2.52234850439796 1.1465025928533	1	1	1	1	56	128	42			No EST	No EST
2451	GATATCC		down	down	72.m19365	AN6275.1	AO070304000006	predicted protein [Neurospora crassa]				1	1	1	0	297	235	365			No EST	No EST
2451	GATATCC		down	down	62.m03225	AN6629.1	AO070326000081	60S ribosomal protein L14	J		2.413	1	1	1	1	136	128	142			122	0
2451	GATATCC		down	down	65.m07261	AN6709.1	AO070339000154	Guanine nucleotide exchange factor	U		2.391	1	1	1	1	48	48	48			No EST	No EST
2451	GATATCC		down	down	57.m05879	AN7463.1	AO070287000063	Ammonia permease	P		1.708	1	1	1	1	63	75	49			No EST	No EST
2451	GATATCC		down	down	72.m19601	AN7580.1	AO070343000328	predicted protein [Neurospora crassa]				1	1	1	1	142	153	127			No EST	No EST
2451	GATATCC		down	down	71.m15967	AN8836.1	AO070271000042	p21-activated serine/threonine protein kinase	T		0.595	1	1	1	1	191	127	183			No EST	No EST
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m15312	AN0705.1	AO070343000504	Isoleucyl-tRNA synthetase	J	1	0.000	1	1	1	0	110	47	57	36	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	down	70.m15314	AN0707.1	AO070343000502	5'-3' exonuclease HKE1/RAT1	LA		3.47484323080616 2.99358537946206	1	1	1	1	353	383	376			No EST	No EST
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m15350	AN0717.1	AO070343000449	Histidinol phosphate aminotransferase	E	1	0.000	1	1	1	0	114	31	123	No EST	No EST		

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2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m15488	AN0893.1	AO070320000065	Adenylosuccinate synthase	F		1.105	1	1	1	0	402	33	51	235	1		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	70.m14889	AN1344.1	AO070247000020	Translation initiation factor 2B, beta subunit (eIF-2Bbeta/GCD7)	J	1	0.000	1	1	1	0	107	336	353	71	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05730	AN1883.1	AO070306000016	Argininosuccinate synthase	E	1	0.000	1	1	2	0	58	330	265	47	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05779	AN2080.1	AO070341000233	Polypeptide release factor 3	J	1	0.000	1	1	1	1	122	105	79	55	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	71.m15904	AN2263.1	AO070295000026	Predicted GTP-binding protein MMR1				1	1	1	1	213	48	64	No EST	No EST		

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2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	62.m03436	AN2409.1	AO070298000018	Phosphoserine aminotransferase	HE	1	1.4065653 2060447 0.0001191 15766590 459	2	1	1	0	103	141	307	12	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	59.m09022	AN2992.1	AO070337000126	Translation initiation factor 2, beta subunit (eIF-2beta)	J	1	0.000	1	1	1	0	181	6	16	83	1		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15368	AN3429.1	AO070265000003	Amidases related to nicotinamidase	Q		0.584	1	1	1	0	95	108	51	4	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	down	65.m07362	AN3760.1	AO070309000043	Cell growth-regulating nucleolar protein	D		3.817	1	1	1	0	205	229	409			93	0
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m07895	AN4430.1	AO070273000027	Acetolactate synthase, small subunit	E	1	0.000	1	1	1	1	147	136	153	38	0		

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2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05569	AN4557.1	AO070321000171	AAA+-type ATPase containing the peptidase M41 domain	O		2.202	1	1	1	1	220	222	149	148	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	down	59.m09189	AN4792.1	AO070329000054	Proteins containing the FAD binding domain	C		2.624	1	1	1	1	255	127	214			No EST	No EST
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	69.m15491	AN5443.1	AO070333000106	Predicted exosome subunit	J	1	0.000	1	2	2	0	186	81	88	No EST	No EST		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m07525	AN5601.1	AO070328000003	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	E	1	0.000	1	1	1	0	114	164	76	12	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	58.m07534	AN5610.1	AO070301000010	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q		0.584	1	2	1	0	93	188	284	No EST	No EST		

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2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	71.m15275	AN6864.1	AO070314000084	Translation initiation factor 2B, delta subunit (eIF-2Bdelta/GCD2)	J	1	0.000	1	1	1	0	126	148	158	No EST	No EST		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	57.m05914	AN7430.1	AO070229000001	Glutamine amidotransferase/cyclase	E	1	0.000	1	1	2	1	213	96	45	45	0		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	down	72.m19567	AN7550.1	AO070277000047	Type I phosphodiesterase/nucleotide pyrophosphatase				1	1	1	0	283	219	278			No EST	No EST
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	71.m15749	AN7722.1	AO070325000137	Putative glutamate/ornithine acetyltransferase	E	1	0.000	2	1	2	0	134	119	132	No EST	No EST		
2483	TGAGTCA	cpcA (ATGACTCA) [aspergillus_motifs_all]; Bas1 (TGACTC) [yeast_motifs_all];GCN4 (ATGACTCAT) [yeast_motifs_all];GCN4 b:General control of nitrogen and purine metabolism (RRTGACTCA) [yeast_motifs_all];yAP1 (STGACTMA) [yeast_motifs_all];	up	up	53.m03750	AN8224.1	AO070310000088	Glutamyl-tRNA synthetase	J	1	0.000	1	1	1	0	1	58	53	34	0		

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2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15380	AN0106.1	AO070311000113	Serine/threonine protein kinase	T	1	0.000	1	1	1	0	153	267	362	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15461	AN0191.1	AO070321000052	RNA polymerase II elongator complex, subunit ELP4	BK		4.82475367478436 0.58986654995859	1	1	1	1	58	80	75	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15648	AN0634.1	AO070318000124	GTP-binding ADP-ribosylation factor-like protein yARL3	U		2.245	1	1	1	1	310	181	120	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15312	AN0705.1	AO070343000504	Isoleucyl-tRNA synthetase	J		4.084	1	1	2	1	70	79	50	36	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15808	AN0926.1	AO070320000110	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		3.38429275323496 2.24544317942041	1	1	1	0	155	228	219	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15539	AN0931.1	AO070320000122	Mitogen-activated protein kinase kinase (MAP2K)	T	1	0.000	1	1	1	1	237	237	282	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m14974	AN1246.1	AO070223000009	3-phosphoglycerate kinase	G		1.182	1	1	1	0	169	239	315	12	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	55.m02991	AN1485.1	AO070334000192	Casein kinase II, alpha subunit	TDK	1	1.40538440589522e-05 0.668283214252526 0.58986654995859	1	1	1	0	64	173	160	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07743	AN1662.1	AO070299000024	Uncharacterized conserved protein				2	1	1	0	54	138	81	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05745	AN1873.1	AO070341000189	Predicted phosphoglycerate mutase	G		1.182	1	1	1	1	61	182	284	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15204	AN2455.1	AO070264000021	C4-type Zn-finger protein				1	1	2	1	165	78	132	36	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	59.m09067	AN2928.1	AO070337000181	von Willebrand factor and related coagulation proteins	V		11.545	1	1	1	0	382	2	104			No EST	No EST
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m09082	AN2960.1	AO070337000210	Probable taurine catabolism dioxygenase	Q		1.206	1	1	2	1	183	295	312	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m08647	AN3096.1	AO070334000138	Protein arginine N-methyltransferase PRMT1 and related enzymes	OKT	1	3.99278482883074 0.58986654995859 1.40538440589522e-05	1	1	2	1	192	70	47	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15412	AN3707.1	AO070341000332	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E		4.162	1	1	1	0	135	69	47	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15413	AN3708.1	AO070341000333	Zinc-binding protein of the histidine triad (HIT) family	T	1	0.000	1	1	1	0	126	122	103	5	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15727	AN3719.1	AO070341000350	Mitogen-activated protein kinase	T	1	0.000	1	1	1	1	366	126	153	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	65.m07383	AN3748.1	AO070309000072	ATP phosphoribosyltransferase	E		4.162	1	1	1	0	20	349	403	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05656	AN3824.1	AO070311000023	Phenylalanyl-tRNA synthetase, beta subunit	J		4.084	1	2	1	0	176	324	322	10	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m14968	AN3954.1	AO070341000069	6-phosphogluconate dehydrogenase	G		1.182	2	2	2	1	38	193	152	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	54.m06799	AN4219.1	AO070315000080	RNA polymerase III subunit C11	K		0.590	1	1	1	0	349	342	465			No EST	No EST
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07997	AN4326.1	AO070240000003	Casein kinase II, beta subunit	TDK	1	1.40538440589522e-05 0.668283214252526 0.58986654995859	1	1	1	1	105	53	53	No EST	No EST		

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2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m09016	AN4442.1	AO070273000012	Ubiquitin fusion degradation protein-2	O		3.993	1	1	1	0	48	123	266	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05648	AN4483.1	AO070311000032	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	1	0.000	1	1	1	0	234	84	206	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15705	AN4717.1	AO070311000004	cAMP-dependent protein kinase catalytic subunit (PKA)	T	1	0.000	1	1	1	1	309	73	56	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	71.m15491	AN4721.1	AO070323000062	DEAH-box RNA helicase	A		3.864	1	1	1	0	55	176	76			153	0
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15746	AN5482.1	AO070341000403	GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein superfamily	U		2.245	1	1	1	0	237	32	74	124	1		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m08888	AN5737.1	AO070255000002	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQ		2.08922618330662 1.20646061954303	1	1	1	0	84	116	3	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19071	AN6079.1	AO070340000129	Predicted RNA-binding protein				1	1	1	1	104	139	158	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19006	AN6159.1	AO070340000043	Sterol O-acyltransferase/Diacylglycerol O-acyltransferase	I		2.089	1	1	1	0	107	132	70	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19497	AN6363.1	AO070279000049	Serine/threonine protein kinase involved in cell cycle control	TD	1	1.40538440589522e-05 0.668283214252526	1	1	1	0	139	12	26	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	62.m03192	AN6604.1	AO070326000055	hypothetical protein [Neurospora crassa]				1	1	1	0	55	408	159	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	62.m03451	AN6655.1	AO070269000011	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQ		2.08922618330662 1.20646061954303	1	1	1	0	231	92	95	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	67.m02939	AN6795.1	AO070335000198	antigenic cell wall protein MP1 [Aspergillus flavus]				1	1	1	0	201	83	133	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15250	AN6889.1	AO070314000032	hypothetical protein [Neurospora crassa]				2	1	1	0	24	78	53	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05460	AN7418.1	AO070323000154	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC		5.07176216053754 4.94470653849616	1	1	1	0	269	223	343	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	down	71.m15821	AN7629.1	AO070294000039	predicted protein [Neurospora crassa]				1	1	1	1	54	58	88			117	1
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15732	AN7708.1	AO070325000115	Aldo/keto reductases, related to diketogulonate reductase				1	1	1	0	174	319	336	No EST	No EST		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		1.182	1	2	1	0	23	239	463	146	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15603	AN8796.1	AO070276000064	GTP-binding protein	T	1	0.000	1	1	1	1	47	282	279	172	0		
2488	TACCCCGC	MIG1b (GCGGGG) [yeast_motifs_all];	up	up	66.m04519	AN9067.1	AO070332000219	FOG: RRM domain				1	1	1	0	213	317	312	38	0		
2497	TGCATAG		down	down	54.m06984	AN0321.1	AO070334000005	RNA polymerase III, second largest subunit	K		0.098	1	1	1	1	102	69	65			No EST	No EST
2497	TGCATAG		down	down	59.m09221	AN4762.1	AO070327000054	predicted protein [Neurospora crassa]				1	1	1	1	128	108	103			124	1
2497	TGCATAG		down	down	59.m09174	AN4802.1	AO070329000037	60S ribosomal protein L21	J		0.134	1	1	1	1	126	121	123			483	1
2497	TGCATAG		down	down	54.m06906	AN5119.1	AO070291000062	Predicted methyltransferase				2	1	1	1	57	179	203			No EST	No EST
2497	TGCATAG		down	down	69.m15442	AN5517.1	AO070341000376	Cdc4 and related F-box and WD-40 proteins				1	1	1	1	195	201	164			No EST	No EST
2497	TGCATAG		down	down	72.m19327	AN6307.1	AO070308000062	Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	U		0.787	1	1	1	1	5	24	5			No EST	No EST
2497	TGCATAG		down	down	62.m03225	AN6629.1	AO070326000081	60S ribosomal protein L14	J		0.134	1	1	1	1	19	18	23			122	1
2497	TGCATAG		down	down	66.m04585	AN9125.1	AO070332000149	RNA polymerase III, subunit C34	K		0.098	1	1	1	1	43	32	35			72	1
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	71.m15484	AN0228.1	AO070323000081	DNA replication licensing factor, MCM6 component	L	1	0.000	2	2	1	1	200	207	244	No EST	No EST		

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2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	down	54.m06654	AN0421.1	AO070338000267	RNA-binding protein (RRM superfamily)				1	1	1	1	139	109	149			283	1
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	70.m15474	AN0872.1	AO070320000030	CDC45 (cell division cycle 45)-like protein	L	1	0.000	1	2	1	0	229	88	192	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	70.m15807	AN0924.1	AO070320000103	Uncharacterized conserved protein				1	1	1	0	423	105	53	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	70.m15002	AN1221.1	AO070331000223	Serine/threonine protein kinase	T		1.885	2	1	2	0	2	390	240	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	70.m14981	AN1237.1	AO070331000251	DNA repair protein RAD51/RHP55	L	1	0.000	2	2	2	1	85	43	59	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	58.m07794	AN1708.1	AO070305000041	Mismatch repair ATPase MSH6 (MutS family)	L	1	0.000	1	1	1	0	172	4	4	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	72.m19700	AN2141.1	AO070343000187	Predicted telomere binding protein				1	1	2	1	244	105	78	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	59.m08498	AN2491.1	AO070312000129	DNA replication licensing factor, MCM2 component	L	1	0.000	2	1	2	1	162	139	181	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	59.m08756	AN2905.1	AO070338000100	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	K		0.604	1	1	1	0	188	321	299	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	58.m08972	AN4407.1	AO070273000067	DNA repair and recombination protein RAD52/RAD22	L	1	0.000	0	1	1	0	245	9	180	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	59.m09119	AN4854.1	AO070327000089	hypothetical protein ((AL451015) conserved hypothetical protein [Neurospora crassa])				1	1	1	0	117	291	218	40	0		

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2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	54.m06909	AN5114.1	AO070291000065	Ribonuclease HI	L	1	0.000	1	1	1	0	131	7	85	251	1		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	69.m15442	AN5517.1	AO070341000376	Cdc4 and related F-box and WD-40 proteins				1	1	1	1	65	454	465	370	0		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	58.m07541	AN5617.1	AO070301000017	ATPase related to the helicase subunit of the Holliday junction resolvase	L	1	0.000	2	2	2	0	131	194	86	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	72.m19202	AN5929.1	AO070340000354	Calcium-responsive transcription coactivator	K		0.604	1	2	2	1	73	151	162	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	72.m19148	AN5992.1	AO070340000285	DNA replication licensing factor, MCM7 component	L	1	0.000	1	1	1	1	203	55	9	56	1		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	72.m19334	AN6300.1	AO070308000056	Replication factor C, subunit RFC3	DL	1	1.41470193026362 4.32898199375738e-11	2	1	1	0	96	234	221	No EST	No EST		
2525	GACGCGT	(wCGCGw stuA) [aspergillus_motifs_all]; MBP1 (ACGCGTnA) [yeast_motifs_all];SWI6 (ACGCGT) [yeast_motifs_all];	up	up	53.m03916	AN8065.1	AO070330000021	Actin-related protein Arp2/3 complex, subunit ARPC3	Z		1.317	1	1	1	0	107	7	7	No EST	No EST		
2529	ACGTGAC		up	up	54.m06978	AN0304.1	AO070334000034	Fe2+/Zn2+ regulated transporter	P		3.684	1	1	1	0	378	95	50	116	1		
2529	ACGTGAC		up	up	54.m06392	AN0359.1	AO070318000037	Translation initiation factor 3, subunit b (eIF-3b)	J		0.018	1	1	1	0	189	335	110	No EST	No EST		
2529	ACGTGAC		up	up	70.m15630	AN0989.1	AO070318000148	SWI-SNF chromatin-remodeling complex protein	B		0.625	1	1	2	0	312	17	18	No EST	No EST		
2529	ACGTGAC		up	up	70.m14945	AN1266.1	AO070332000014	RNA helicase	A		0.697	1	1	1	1	242	13	27	No EST	No EST		
2529	ACGTGAC		up	up	55.m02950	AN1448.1	AO070302000005	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	J		0.018	1	1	1	0	181	79	61	No EST	No EST		
2529	ACGTGAC		up	up	58.m07653	AN1859.1	AO070292000036	Transcription initiation factor IIF, auxiliary subunit	K		0.800	1	1	1	1	121	28	27	83	1		
2529	ACGTGAC		up	up	58.m08945	AN1981.1	AO070301000066	Protein geranylgeranyltransferase type II, alpha subunit	O		0.886	1	1	1	0	135	49	41	No EST	No EST		
2529	ACGTGAC		up	up	58.m07659	AN2057.1	AO070292000042	Mitochondrial/chloroplast ribosomal protein L12	J		0.018	1	1	1	0	141	35	88	No EST	No EST		
2529	ACGTGAC		up	up	71.m15903	AN2262.1	AO070295000025	Uncharacterized conserved protein				1	1	1	0	127	120	134	No EST	No EST		
2529	ACGTGAC		up	up	71.m15940	AN2292.1	AO070295000071	Protein required for cell viability; Yil019wp [Saccharomyces cerevisiae]				1	1	1	0	52	29	31	No EST	No EST		
2529	ACGTGAC		up	down	59.m08733	AN2886.1	AO070338000128	predicted protein [Neurospora crassa]				1	1	1	1	270	220	342			No EST	No EST
2529	ACGTGAC		up	up	59.m08747	AN2897.1	AO070338000111	predicted protein [Neurospora crassa]				1	1	1	0	160	165	150	No EST	No EST		
2529	ACGTGAC		up	up	59.m09039	AN2973.1	AO070337000148	SNF2 family DNA-dependent ATPase	B		0.625	1	1	1	0	161	24	25	No EST	No EST		
2529	ACGTGAC		up	up	59.m09022	AN2992.1	AO070337000126	Translation initiation factor 2, beta subunit (eIF-2beta)	J		0.018	1	1	1	0	172	19	26	83	1		
2529	ACGTGAC		up	up	69.m15009	AN3919.1	AO070324000114	Nuclear polyadenylated RNA binding protein	A		0.697	1	1	1	0	279	271	5	No EST	No EST		
2529	ACGTGAC		up	up	69.m14995	AN3932.1	AO070341000043	20S proteasome, regulatory subunit beta type PSMB5/PSMB8/PRE2	O		0.886	1	1	1	1	173	25	43	No EST	No EST		
2529	ACGTGAC		up	up	54.m06715	AN4073.1	AO070342000062	40S ribosomal protein S12	J		0.018	1	1	1	0	179	48	32	No EST	No EST		
2529	ACGTGAC		up	up	58.m07362	AN4163.1	AO070342000193	G protein beta subunit-like protein	T		2.593	1	1	1	1	194	13	174	77	1		
2529	ACGTGAC		up	up	71.m15658	AN4670.1	AO070284000036	FOG: WD40 repeat				1	1	1	0	345	453	131	299	0		
2529	ACGTGAC		up	up	69.m15723	AN5496.1	AO070341000389	predicted protein [Neurospora crassa]				1	1	1	1	60	44	8	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2529	ACGTGAC		up	up	58.m07493	AN5569.1	AO070328000037	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB1	KL		0.7999239 40864314 1.5619338 7465504	1	1	1	0	206	110	183	No EST	No EST		
2529	ACGTGAC		up	up	69.m14856	AN5741.1	AO070341000018	predicted protein [Neurospora crassa]				1	1	1	0	93	361	296	No EST	No EST		
2529	ACGTGAC		up	up	72.m19080	AN6089.1	AO070340000143	Mitochondrial chaperonin, Cpn60/Hsp60p	O		0.886	1	1	1	1	242	78	78	140	1		
2529	ACGTGAC		up	up	62.m03227	AN6631.1	AO070326000083	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	C		3.625	1	1	1	0	107	104	128	35	0		
2529	ACGTGAC		up	up	72.m20020	AN7292.1	AO070297000033	Soluble epoxide hydrolase	I		3.611	1	1	1	0	157	49	91	No EST	No EST		
2529	ACGTGAC		up	up	72.m19764	AN7301.1	AO070297000049	Glucosyltransferase - Alg8p	K		0.800	1	1	1	0	128	99	152	No EST	No EST		
2529	ACGTGAC		up	up	72.m19745	AN7325.1	AO070297000077	DNA polymerase delta, catalytic subunit	L		1.562	1	2	2	1	168	87	114	No EST	No EST		
2529	ACGTGAC		up	down	53.m03905	AN8041.1	AO070330000005	Glyceraldehyde 3-phosphate dehydrogenase	G		2.080	2	1	1	0	196	297	425			216	0
2529	ACGTGAC		up	up	53.m03913	AN8061.1	AO070330000013	Peptidyl-prolyl cis-trans isomerase	O		0.886	1	1	1	1	296	42	53	No EST	No EST		
2529	ACGTGAC		up	up	62.m03491	AN8704.1	AO070315000132	60s ribosomal protein L24	J		0.018	1	1	1	1	147	106	114	73	0		
2529	ACGTGAC		up	up	71.m15603	AN8796.1	AO070276000064	GTP-binding protein	T		2.593	1	1	1	0	281	68	66	172	1		
2529	ACGTGAC		up	up	52.m03843	AN9360.1	AO070315000040	Protein containing a U1-type Zn-finger and implicated in RNA splicing or processing	A		0.697	1	1	1	0	200	32	219	No EST	No EST		
2611	TGTACAT		down	down	70.m15442	AN0842.1	AO070216000002	Predicted AMP-binding protein				1	1	1	1	265	161	306			No EST	No EST
2611	TGTACAT		down	down	70.m15523	AN0914.1	AO070320000095	Serine/threonine protein phosphatase	T		0.944	2	1	1	1	24	67	96			No EST	No EST
2611	TGTACAT		down	down	70.m14989	AN1230.1	AO070331000242	Inner membrane protein required for assembly of the F0 sector of ATP synthase	O		2.260	1	1	1	0	15	7	148			No EST	No EST
2611	TGTACAT		down	down	58.m07666	AN1845.1	AO070292000060	hypothetical protein [Neurospora crassa]				1	1	1	0	171	103	186			79	0
2611	TGTACAT		down	down	58.m08946	AN1980.1	AO070301000065	Rab6 GTPase activator GAPCenA and related TBC domain proteins				1	1	2	0	120	85	25			No EST	No EST
2611	TGTACAT		down	down	72.m19466	AN2415.1	AO070228000029	RNA polymerase I and III, subunit RPA40/RPC40	K		2.099	1	1	1	1	78	76	77			No EST	No EST
2611	TGTACAT		down	down	58.m07445	AN3655.1	AO070342000033	predicted protein [Neurospora crassa]				1	1	1	1	31	31	24			49	1
2611	TGTACAT		down	down	65.m07425	AN4253.1	AO070309000123	predicted protein [Neurospora crassa]				1	1	1	1	232	260	220			288	1
2611	TGTACAT		down	down	58.m07520	AN5596.1	AO070328000008	Permease of the major facilitator superfamily				1	1	1	1	77	59	76			275	1
2611	TGTACAT		down	down	69.m14848	AN5750.1	AO070341000007	predicted protein [Neurospora crassa]				1	1	1	1	58	115	70			No EST	No EST
2611	TGTACAT		down	down	72.m19214	AN5917.1	AO070340000369	Predicted transporter (major facilitator superfamily)				1	1	1	0	35	49	41			No EST	No EST
2611	TGTACAT		down	down	62.m03121	AN6533.1	AO070270000033	Targeting complex (TRAPP) subunit	U		2.205	1	1	1	0	19	280	298			No EST	No EST
2611	TGTACAT		down	down	62.m03432	AN6534.1	AO070270000051	Mannosyltransferase OCH1 and related enzymes	M		1.099	1	1	1	1	224	196	249			No EST	No EST
2611	TGTACAT		down	down	62.m03155	AN6568.1	AO070326000011	Uncharacterized conserved protein				1	1	2	1	161	192	21			No EST	No EST
2611	TGTACAT		down	down	71.m15820	AN7630.1	AO070294000040	Angio-associated migratory cell protein (contains WD40 repeats)				1	1	1	0	237	183	198			No EST	No EST
2611	TGTACAT		down	down	71.m15816	AN7783.1	AO070286000029	RhoGEF GTPase	T		0.944	1	1	1	0	221	266	316			No EST	No EST
2611	TGTACAT		down	down	53.m04180	AN9411.1	AO070310000008	NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit	C		2.168	1	1	1	1	199	165	207			207	1
2662	GAGATACC		down	down	71.m15450	AN0176.1	AO070321000065	GATA-4/5/6 transcription factors	K		1.985	1	1	1	1	95	119	91			No EST	No EST
2662	GAGATACC		down	down	54.m06490	AN0292.1	AO070334000050	Transcription initiation factor TFIID, subunit TAF5 (also component of histone acetyltransferase SAGA)	K		1.985	1	1	1	1	40	49	26			250	1
2662	GAGATACC		down	down	70.m15648	AN0634.1	AO070318000124	GTP-binding ADP-ribosylation factor-like protein yARL3	U		2.337	1	1	1	0	94	93	86			No EST	No EST
2662	GAGATACC		down	down	70.m14905	AN1326.1	AO070303000090	Protein kinase				1	1	1	1	88	95	85			130	1
2662	GAGATACC		down	down	70.m15731	AN1358.1	AO070237000002	Serine/threonine protein phosphatase	T		2.539	1	1	1	1	382	425	225			831	1
2662	GAGATACC		down	down	69.m15651	AN1780.1	AO070324000015	Putative Xaa-Pro aminopeptidase	E		4.023	1	1	1	1	23	27	18			No EST	No EST
2662	GAGATACC		down	down	58.m07667	AN1844.1	AO070292000063	palFp [Emericella nidulans]				1	1	1	1	118	61	75			No EST	No EST
2662	GAGATACC		down	down	59.m08724	AN2875.1	AO070338000136	Fructose 1,6-bisphosphate aldolase	G		4.003	1	1	1	0	67	61	43			No EST	No EST
2662	GAGATACC		down	down	59.m08977	AN3040.1	AO070337000054	Projectin/twitchin and related proteins	Z		3.473	1	1	1	0	59	55	60			No EST	No EST
2662	GAGATACC		down	down	59.m08590	AN3135.1	AO070303000009	Uncharacterized conserved protein				1	1	1	1	42	27	39			No EST	No EST
2662	GAGATACC		down	down	66.m04642	AN3374.1	AO070281000016	Chitinase	M		2.664	1	1	1	1	262	252	247			No EST	No EST
2662	GAGATACC		down	down	58.m07430	AN3669.1	AO070342000010	Protein involved in cell differentiation/sexual development				1	1	1	1	508	496	435			No EST	No EST
2662	GAGATACC		down	up	69.m15000	AN3928.1	AO070341000038	Protein involved in thiamine biosynthesis and DNA damage tolerance				1	1	1	1	245	62	62	429	1		
2662	GAGATACC		down	down	59.m08772	AN4876.1	AO070338000084	Vacuolar assembly/sorting protein VPS41	U		2.337	1	1	1	0	311	166	163			No EST	No EST
2662	GAGATACC		down	down	69.m15451	AN5512.1	AO070341000384	Magnesium-dependent phosphatase				1	1	1	0	93	82	93			No EST	No EST
2662	GAGATACC		down	down	69.m15439	AN5520.1	AO070341000371	60S ribosomal protein L7A	J		4.093	1	1	1	1	249	105	268			134	1
2662	GAGATACC		down	down	58.m07308	AN5668.1	AO070342000260	Golgi-associated protein/Nedd4 WW domain-binding protein				1	1	1	0	213	133	192			No EST	No EST
2662	GAGATACC		down	down	72.m19298	AN6200.1	AO070308000096	Uncharacterized conserved protein				1	1	1	0	258	184	320			113	0
2662	GAGATACC		down	down	72.m19981	AN6254.1	AO070304000034	Mitochondrial oxoglutarate/malate carrier proteins	C		4.130	1	1	1	1	210	242	246			No EST	No EST
2662	GAGATACC		down	down	72.m19322	AN6312.1	AO070308000067	predicted protein [Neurospora crassa]				1	1	1	0	138	93	142			No EST	No EST
2662	GAGATACC		down	down	71.m16031	AN6886.1	AO070314000039	PalH [Emericella nidulans]				1	1	1	0	266	192	302			No EST	No EST
2662	GAGATACC		down	down	72.m19797	AN7252.1	AO070297000007	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T		2.539	1	1	1	1	78	41	83			241	1

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2662	GAGATACC		down	down	72.m19730	AN7341.1	AO070278000053	predicted protein [Neurospora crassa]				1	2	1	0	183	72	254			483	1
2662	GAGATACC		down	down	72.m19567	AN7550.1	AO070277000047	Type I phosphodiesterase/nucleotide pyrophosphatase				1	1	1	0	71	95	55			No EST	No EST
2662	GAGATACC		down	down	57.m05423	AN7659.1	AO070268000028	ATP-dependent RNA helicase	A		4.116	1	1	1	1	121	216	66			No EST	No EST
2662	GAGATACC		down	up	53.m03738	AN8231.1	AO070310000077	S-adenosylmethionine decarboxylase	T		2.539	1	1	1	1	325	44	151	9	0		
2662	GAGATACC		down	down	71.m15611	AN8804.1	AO070276000054	hypothetical proline-rich protein; possible coiled-coil region [Schizosaccharomyces pombe]				2	1	1	1	47	58	33			No EST	No EST
2677	TCACCGC		up	up	71.m15417	AN0133.1	AO070321000120	mRNA splicing factor ATP-dependent RNA helicase	A		0.381	1	1	1	0	181	102	95	No EST	No EST		
2677	TCACCGC		up	up	71.m15474	AN0211.1	AO070321000033	U2-associated snRNP A' protein	A		0.381	1	1	1	1	200	101	144	No EST	No EST		
2677	TCACCGC		up	up	54.m06619	AN0430.1	AO070338000280	hypothetical protein [Neurospora crassa]				1	1	1	0	352	217	182	No EST	No EST		
2677	TCACCGC		up	up	69.m15690	AN0579.1	AO070280000001	Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	Q		5.606	1	1	1	1	178	267	287	51	0		
2677	TCACCGC		up	up	70.m15763	AN1182.1	AO070331000182	Beta tubulin	Z		1.872	1	1	1	1	155	139	124	No EST	No EST		
2677	TCACCGC		up	down	70.m14988	AN1231.1	AO070331000243	DNA polymerase IV (family X)	L		5.615	2	2	2	1	349	301	374			No EST	No EST
2677	TCACCGC		up	up	55.m02940	AN1434.1	AO070232000012	Nucleolar protein involved in 40S ribosome biogenesis	J		3.962	1	1	1	0	94	1	1	No EST	No EST		
2677	TCACCGC		up	up	58.m07733	AN1665.1	AO070299000047	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T		0.927	1	1	1	1	194	127	129	No EST	No EST		
2677	TCACCGC		up	up	72.m19692	AN2149.1	AO070343000198	Chaperonin complex component, TCP-1 alpha subunit (CCT1)	O		0.725	1	1	1	1	119	13	16	No EST	No EST		
2677	TCACCGC		up	down	59.m08476	AN2508.1	AO070263000056	Cysteine desulfurase NFS1	E		2.615	1	1	1	1	353	291	708			92	0
2677	TCACCGC		up	up	54.m06683	AN2748.1	AO070338000223	FOG: Zn-finger				1	1	1	0	141	29	28	No EST	No EST		
2677	TCACCGC		up	up	59.m08720	AN2872.1	AO070338000142	predicted protein [Neurospora crassa]				1	1	1	1	160	338	329	No EST	No EST		
2677	TCACCGC		up	up	59.m08929	AN3070.1	AO070337000004	Chaperonin complex component, TCP-1 zeta subunit (CCT6)	O		0.725	1	1	1	0	135	43	43	No EST	No EST		
2677	TCACCGC		up	up	59.m08566	AN3176.1	AO070256000014	ATP-dependent RNA helicase	A		0.381	1	1	1	1	128	155	143	No EST	No EST		
2677	TCACCGC		up	up	66.m04642	AN3374.1	AO070281000016	Chitinase	M		4.384	1	1	1	1	21	161	395	No EST	No EST		
2677	TCACCGC		up	up	59.m09329	AN3469.1	AO070265000045	Histone H2B	B		4.635	1	1	1	1	138	200	199	112	0		
2677	TCACCGC		up	up	69.m15021	AN3909.1	AO070324000094	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L		5.615	1	1	2	0	183	29	62	No EST	No EST		
2677	TCACCGC		up	up	54.m07047	AN4112.1	AO070342000107	Nucleolar GTPase/ATPase p130	Y		3.186	1	1	1	1	205	35	78	No EST	No EST		
2677	TCACCGC		up	up	54.m06790	AN4226.1	AO070234000023	Sof1-like rRNA processing protein (contains WD40 repeats)	A		0.381	1	1	1	1	142	49	29	55	1		
2677	TCACCGC		up	down	58.m09007	AN4333.1	AO070240000012	predicted protein [Neurospora crassa]				1	1	1	0	329	202	384			No EST	No EST
2677	TCACCGC		up	up	58.m07981	AN4346.1	AO070240000018	Nucleolar RNA-binding protein NIFK				1	1	1	1	27	14	44	24	1		
2677	TCACCGC		up	up	59.m09494	AN5022.1	AO070338000182	Dynactin, subunit p25	Z		1.872	1	1	1	0	120	56	108	No EST	No EST		
2677	TCACCGC		up	up	69.m14894	AN5195.1	AO070237000025	ER vesicle integral membrane protein involved in establishing cell polarity, signaling and protein degradation	OUT		0.724661043362525 0.725542603803205 0.926889563920066	1	1	1	0	228	92	266	No EST	No EST		
2677	TCACCGC		up	up	54.m06817	AN5702.1	AO070324000158	Uncharacterized conserved protein				1	1	1	1	210	70	130	No EST	No EST		
2677	TCACCGC		up	up	54.m06828	AN5713.1	AO070324000145	Chaperonin complex component, TCP-1 eta subunit (CCT7)	O		0.725	1	1	1	1	191	84	69	No EST	No EST		
2677	TCACCGC		up	down	72.m19268	AN5866.1	AO070308000130	Arylalkylamine N-acetyltransferase				1	1	1	1	53	68	80			No EST	No EST
2677	TCACCGC		up	up	72.m19188	AN5972.1	AO070340000330	Vesicle coat complex COPI, beta' subunit	U		0.726	1	1	1	1	274	25	57	370	1		
2677	TCACCGC		up	up	72.m19097	AN6061.1	AO070340000187	hypothetical protein [Schizosaccharomyces pombe]				1	1	1	0	461	7	44	32	1		
2677	TCACCGC		up	up	72.m19323	AN6311.1	AO070308000066	Cl- channel CLC-3 and related proteins (CLC superfamily)	P		2.600	1	1	1	1	139	22	21	No EST	No EST		
2677	TCACCGC		up	up	72.m19493	AN6367.1	AO070279000053	Phosphatidylinositol-4-phosphate 5-kinase and related FYVE finger-containing proteins	T		0.927	1	1	1	0	189	54	43	No EST	No EST		
2677	TCACCGC		up	up	62.m03148	AN6561.1	AO070326000002	Uncharacterized conserved protein				2	1	2	1	95	144	137	55	0		
2677	TCACCGC		up	down	62.m03168	AN6574.1	AO070326000017	E3 ubiquitin ligase involved in syntaxin degradation	O		0.725	1	1	1	0	171	136	172			No EST	No EST
2677	TCACCGC		up	up	71.m16034	AN6898.1	AO070314000023	Vacuolar assembly/sorting protein DID4	U		0.726	2	1	1	0	109	41	55	No EST	No EST		
2677	TCACCGC		up	up	72.m19648	AN7600.1	AO070343000270	Sulfite reductase (ferredoxin)	P		2.600	1	1	1	1	75	439	436	No EST	No EST		
2677	TCACCGC		up	up	53.m03900	AN8044.1	AO070292000105	N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	O		0.725	2	1	2	0	350	32	70	No EST	No EST		
2677	TCACCGC		up	up	62.m03389	AN8682.1	AO070315000102	Exosomal 3'-5' exoribonuclease complex, subunit Rrp43	J		3.962	1	1	1	1	123	384	314	No EST	No EST		
2677	TCACCGC		up	up	71.m15960	AN8828.1	AO070271000052	Transport protein particle (TRAPP) complex subunit	U		0.726	1	1	1	0	150	219	76	No EST	No EST		
2677	TCACCGC		up	down	71.m15215	AN9451.1	AO070219000021	predicted protein [Neurospora crassa]				1	1	1	0	189	114	134			No EST	No EST
2677	TCACCGC		up	up	53.m03781	AN9461.1	AO070310000129	Dehydrogenase kinase	T		0.927	1	1	1	1	69	68	115	No EST	No EST		
2677	TCACCGC		up	up	62.m03341	AN9504.1	AO070315000153	Ras GTPase activating protein RasGAP/neurofibromin	V		2.855	1	1	2	1	311	48	34	No EST	No EST		
2683	TCTCCGC		up	up	71.m16063	AN0085.1	AO070311000131					1	1	1	0	267	423	420	No EST	No EST		

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2683	TCTCCGC		up	up	54.m06982	AN0312.1	AO070334000021	RNA polymerase I transcription factor	K		0.907	1	1	1	0	323	111	97	No EST	No EST		
2683	TCTCCGC		up	up	70.m15267	AN0664.1	AO070343000556	Phosphoinositide-specific phospholipase C	T		0.467	1	1	1	1	276	191	67	No EST	No EST		
2683	TCTCCGC		up	up	70.m15442	AN0842.1	AO070216000002	Predicted AMP-binding protein				1	1	1	0	242	250	314	No EST	No EST		
2683	TCTCCGC		up	up	70.m15502	AN0896.1	AO070320000070	Succinate dehydrogenase membrane anchor subunit and related proteins	CU		3.0067064 9458921 3.1733082 9826823	1	1	1	1	189	28	28	44	1		
2683	TCTCCGC		up	up	70.m15196	AN1038.1	AO070336000073	Putative transmembrane protein				1	1	1	0	169	123	159	No EST	No EST		
2683	TCTCCGC		up	up	70.m15112	AN1122.1	AO070331000114	60S ribosomal protein L10A	J		5.120	1	1	1	1	114	128	48	61	0		
2683	TCTCCGC		up	up	70.m15103	AN1134.1	AO070331000125	QUINIC ACID UTILIZATION ACTIVATOR				1	1	1	0	257	163	248	No EST	No EST		
2683	TCTCCGC		up	up	70.m15050	AN1171.1	AO070331000166	Serine/threonine protein kinase	T		0.467	1	1	1	1	392	45	44	No EST	No EST		
2683	TCTCCGC		up	down	58.m07668	AN1843.1	AO070292000064	Protein involved in meiotic recombination/predicted coiled-coil protein	D		4.802	1	2	1	0	220	247	152			No EST	No EST
2683	TCTCCGC		up	up	69.m15162	AN2123.1	AO070306000102	Transcriptional coactivator	K		0.907	1	1	1	0	129	24	26	75	1		
2683	TCTCCGC		up	up	59.m09058	AN2936.1	AO070337000172	Alpha-mannosidase	G		3.456	1	1	1	0	198	190	177	No EST	No EST		
2683	TCTCCGC		up	up	59.m08551	AN3163.1	AO070256000032	Membrane protease subunits, stomatin/prohibitin homologs	O		2.300	1	1	1	0	415	223	196	No EST	No EST		
2683	TCTCCGC		up	up	58.m07387	AN3587.1	AO070342000137	Ubiquitin-specific protease	O		2.300	1	1	1	0	183	324	392	No EST	No EST		
2683	TCTCCGC		up	up	69.m14984	AN3940.1	AO070341000052	Predicted alpha-helical protein, potentially involved in replication/repair	L		5.086	2	1	1	0	72	361	375	No EST	No EST		
2683	TCTCCGC		up	up	58.m07997	AN4326.1	AO070240000003	Casein kinase II, beta subunit	TDK		0.4669370 05715596 4.8016308 7248282 0.9065511 92029075	1	1	1	1	61	72	92	No EST	No EST		
2683	TCTCCGC		up	up	58.m07978	AN4353.1	AO070240000022	Peroxisomal 3-ketoacyl-CoA-thiolase P-44/SCP2	I		5.193	1	1	1	0	131	328	312	No EST	No EST		
2683	TCTCCGC		up	up	59.m09135	AN4843.1	AO070327000126	Alpha-amylase	G		3.456	1	1	1	0	115	235	192	No EST	No EST		
2683	TCTCCGC		up	up	59.m08844	AN4940.1	AO070338000003	hypothetical protein [Schizosaccharomyces pombe]				1	1	1	1	356	42	44	90	1		
2683	TCTCCGC		up	up	69.m14839	AN5759.1	AO070193000004	Serine/threonine protein kinase	T		0.467	2	1	1	1	14	74	94	No EST	No EST		
2683	TCTCCGC		up	up	72.m18945	AN5817.1	AO070260000030	Gamma-glutamyl kinase	E		4.991	1	1	1	1	64	14	17	No EST	No EST		
2683	TCTCCGC		up	up	72.m19187	AN5971.1	AO070340000329	NADH:ubiquinone oxidoreductase, NDUFA5/B13 subunit	C		3.007	1	1	2	1	139	93	31	No EST	No EST		
2683	TCTCCGC		up	up	72.m19145	AN5995.1	AO070340000282	Carbonic anhydrase				1	1	1	0	158	1	1	213	1		
2683	TCTCCGC		up	up	72.m19648	AN7600.1	AO070343000270	Sulfite reductase (ferredoxin)	P		5.044	1	1	1	1	249	262	260	No EST	No EST		
2683	TCTCCGC		up	up	57.m05936	AN7660.1	AO070268000029	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H		4.082	1	1	1	1	148	122	166	No EST	No EST		
2683	TCTCCGC		up	up	53.m03884	AN8059.1	AO070322000124	Mitochondrial import inner membrane translocase, subunit TIM22	U		3.173	1	1	1	1	155	129	135	No EST	No EST		
2683	TCTCCGC		up	up	53.m03692	AN8269.1	AO070310000033	Molecular chaperone (HSP90 family)	O		2.300	1	1	2	0	425	33	43	336	1		
2683	TCTCCGC		up	up	62.m03387	AN8684.1	AO070315000104	Predicted N-acetyltransferase				2	2	1	1	161	316	266	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15331	AN0051.1	AO070314000138	Isopenicillin N synthase and related dioxygenases				1	1	1	0	306	96	6	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15440	AN0165.1	AO070321000081	Vesicle coat complex AP-3, beta subunit	U		4.003	1	1	1	0	178	331	302	78	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m16064	AN0179.1	AO070321000059	Predicted dehydrogenase	Q		4.020	1	1	1	0	134	343	337	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	54.m06475	AN0268.1	AO070334000074	MesA [Emericella nidulans]				1	1	1	1	296	42	42	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15251	AN0596.1	AO070280000022	Damage-specific DNA binding complex, subunit DDB1	L		5.070	1	1	1	0	75	289	367	No EST	No EST		

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2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15350	AN0717.1	AO070343000449	Histidinol phosphate aminotransferase	E		0.475	1	1	2	0	68	80	216	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15460	AN0867.1	AO070320000018	hypothetical protein [Neurospora crassa]				1	1	1	1	398	163	172	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15141	AN1091.1	AO070285000058	FOG: RRM domain				1	1	1	1	165	376	346	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m14915	AN1293.1	AO070303000055	predicted protein [Neurospora crassa]				1	1	1	0	122	168	129	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	70.m15733	AN1341.1	AO070247000023	Membrane coat complex Retromer, subunit VPS29/PEP11	U		4.003	1	1	1	1	215	301	294	96	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	55.m02938	AN1432.1	AO070232000014	Predicted RNA binding protein, contains G-patch and Zn-finger domains	A		4.149	1	1	1	1	164	171	169	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07764	AN1689.1	AO070305000009	Aldehyde dehydrogenase	C		3.093	1	1	1	0	105	175	107	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15036	AN1733.1	AO070324000063	Delta-1-pyrroline-5-carboxylate dehydrogenase	E		0.475	1	1	1	0	110	169	180	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15654	AN1761.1	AO070324000020	Ubiquitin-protein ligase	O		3.332	2	1	1	0	134	379	281	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15067	AN1769.1	AO070324000028	Salt-sensitive 3'-phosphoadenosine-5'-phosphatase HAL2/SAL1	FP		0.326346338872678 0.626586705080152	1	1	1	0	196	85	92	212	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m20005	AN2138.1	AO070343000183	ATP-dependent RNA helicase A	A		4.149	1	1	1	0	149	3	3	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m20010	AN2139.1	AO070343000184	Predicted hydrolase (HIT family)				1	1	1	0	158	4	5	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m16111	AN2270.1	AO070295000043	FOG: Zn-finger				1	1	1	1	48	370	232	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m08759	AN2909.1	AO070338000097	Putative arsenite-translocating ATPase	P		0.627	1	1	1	0	144	225	238	58	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m08953	AN3061.1	AO070337000012	AAA+-type ATPase	O		3.332	1	1	1	0	74	111	161	252	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	down	59.m08663	AN3084.1	AO070334000122	Predicted alpha/beta hydrolase				1	1	1	0	15	290	119			No EST	No EST

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2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07430	AN3669.1	AO070342000010	Protein involved in cell differentiation/sexual development				1	1	1	0	239	197	254	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15404	AN3695.1	AO070341000319	Isochorismate synthase	E		0.475	1	1	1	0	52	252	213	61	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15418	AN3714.1	AO070341000340	hypothetical protein [Neurospora crassa]				1	1	1	1	443	84	92	261	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	65.m07367	AN3757.1	AO070309000049	Predicted alpha/beta hydrolase BEM46				1	1	1	1	254	17	9	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05693	AN3789.1	AO070337000239	Predicted dioxygenase				1	2	1	0	5	40	281	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	54.m07043	AN4201.1	AO070231000023	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ		0.7669452 02613153 4.0202012 1986697	1	1	1	1	163	261	248	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07872	AN4453.1	AO070273000002	Mitochondrial inheritance and actin cytoskeleton organization protein	Z		3.090	2	2	1	1	117	339	36	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	57.m05618	AN4510.1	AO070311000065	Leucine rich repeat proteins, some proteins contain F-box				1	1	1	0	165	14	33	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15670	AN4687.1	AO070284000042	3-Methylcrotonyl-CoA carboxylase, non-biotin containing subunit/Acetyl-CoA carboxylase carboxyl transferase, subunit beta	EI		0.4749583 40076133 0.7669452 02613153	1	1	1	0	1	123	131	135	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	59.m08864	AN4959.1	AO070288000021	Protein required for S-phase initiation or completion	D		5.446	1	1	1	1	283	50	64	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	down	69.m15495	AN5440.1	AO070333000102	Catalase (peroxidase I)	P		0.627	1	1	1	0	238	190	251			No EST	No EST
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15460	AN5493.1	AO070341000392	Concentrative Na+-nucleoside cotransporter CNT1/CNT2	FP		0.3263463 38872678 0.6265867 05080152	1	1	1	0	276	192	159	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15723	AN5496.1	AO070341000389	predicted protein [Neurospora crassa]				1	1	1	0	32	72	38	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15435	AN5523.1	AO070341000366	Trehalose-6-phosphate synthase component TPS1 and related subunits	G		3.417	1	1	1	0	352	104	187	201	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07525	AN5601.1	AO070328000003	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	E		0.475	1	1	1	0	92	135	97	12	0		

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2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	58.m07314	AN5660.1	AO070342000252	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		3.41739963337731 3.3322854768967	1	1	1	0	388	261	123	597	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19960	AN5916.1	AO070340000370	Enoyl-CoA hydratase/carnithine racemase	I		0.767	1	1	1	0	165	84	93	14	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19114	AN6045.1	AO070340000237	Copper chaperone for superoxide dismutase	P		0.627	0	1	0	0	148	1	0	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19948	AN6072.1	AO070340000116	Guanidinoacetate methyltransferase and related proteins	E		0.475	1	1	1	0	259	30	19	93	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19074	AN6084.1	AO070340000134	predicted protein [Neurospora crassa]				2	1	1	0	57	95	208	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19017	AN6148.1	AO070340000054	Acetylcholinesterase/Butyrylcholinesterase	T		3.396	1	1	1	0	283	146	33	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19424	AN6229.1	AO070304000080	NADPH:quinone reductase and related Zn-dependent oxidoreductases	C		3.093	1	1	1	1	121	181	114	15	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	69.m15237	AN6389.1	AO070275000070	Carboxylesterase and related proteins				1	1	1	0	71	135	57	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	65.m07240	AN6730.1	AO070339000174	Xanthine/uracil permeases	F		0.326	1	2	1	0	141	131	268	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19797	AN7252.1	AO070297000007	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T		3.396	2	1	1	0	310	82	129	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m03773	AN7517.1	AO070310000116	hypothetical protein ((AL513466) hypothetical protein [Neurospora crassa])				1	1	1	0	142	160	188	53	0		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	72.m19595	AN7576.1	AO070343000423	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		3.39581483087136 3.09007587971242	1	1	1	1	333	151	162	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	71.m15820	AN7630.1	AO070294000040	Angio-associated migratory cell protein (contains WD40 repeats)				1	1	1	0	244	21	86	31	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m03857	AN8010.1	AO070322000057	Glycogen synthase	G		3.417	2	1	2	0	248	236	352	293	1		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m03866	AN8020.1	AO070322000068	conserved hypothetical protein [Neurospora crassa]				1	1	1	0	311	78	211	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	52.m04095	AN8415.1	AO070302000056	Acyl-CoA dehydrogenases	I		0.767	1	1	1	0	125	366	98	No EST	No EST		

Pattern ID	Conpat Consensus	Similar Sequence	Pattern 5' / 3' Bias	Site 5' / 3' of Locus	AF Locus	AN Locus	AO Locus	Locus Description	COG Category	COG Cat Enriched	COG Cat Pval	# AF sites	# AN sites	# AO sites	Overlap HCS	AF Dist to Gene	AN Dist to Gene	AO Dist to Gene	AN 5' UTR Len	In AN 5' UTR	AN 3' UTR Len	In AN 3' UTR
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	62.m03322	AN8755.1	AO070250000017	Isocitrate lyase	C		3.093	1	1	1	1	189	137	186	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	66.m04586	AN9149.1	AO070332000147	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain				1	1	1	1	302	215	206	No EST	No EST		
2919	TCCCCGC	creA (SYGGGG) [aspergillus_motifs_all]; MIG1b (GCGGGG) [yeast_motifs_all];	up	up	53.m04094	AN9522.1	AO070310000070	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I		0.767	1	1	1	1	185	46	6	No EST	No EST		

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# Motif 45 TTTCTTTTTCTTTTTTTT
Motif 45
TTTCTTTTTCTTTTTTTT
TTCCTTTTTTTTTTTTTT
TTTTTTTTTCTTTTCTTT
TTCCTTTTTCTTTTTTTC
TTTCTTTTTTTTTTTTTT
CTTTTCTTTCTTTCTTTT
CTTTTCTTTTTTTCTTTT
TTTTCTTTTCTTTCCTTT
CTTCTTTCTCTTTCTTCT
TTTCTTCGTCTTTCGTTT
TTTCTTCCTATTTCTCTT
TCTCTTCTTATTTCTTAT
TTTCCTCCTCTTCTTTCT
TTTTTCCGTTTATTTTTT
TTCCGTCTGCTCTTTTTC
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# Motif 233 TCTCCTTTCCTCyC
Motif 233
TCTCCTTTCCTCCC
TCTTCTTTCTTCCC
TCTCCGTCCCTCTC
TCTCCTTCCCTCCG
TCTCCTTCCATCTC
TCTTCTTTCCTATC
TCTCCATTCTTCTC
TTTTCTTTTTTCCC
TCTCCTTCCCACCG
TTTCCTTCCCCCCG
TCTACTTTCCTATC
GCTCCGTTTCTCTC
**************

# Motif 234 GTTTGTCnTGTTTG
Motif 234
GTTTGTCTTGTTTG
GTTTGTCTTGTTTG
GTTTGTCTTGTTTG
GTTTGTCCTGTTTG
GTTTGTCCTGTTTG
GTTTGTCCTGTTTG
GTTTGTTTTGTTTG
GTTTGTCTTGTTTG
GTTTGTCCTGTTTG
GTTTGTTCTGTTTG
GTTTGTCTTGTTTG
GTTTGTCTTGTTTG
XTTTGTTTTGTTTG
GTTTGTCTTGTTTG
GTTTGTTATGTTTG
GTTTGTTCTGTTTG
GTTTGTTCTGTTTG
GTTTGACCTGTTTG
GTTTGCTTTGTTTG
GTTTGCTTTGTTTG
GTTTGTCGTGTTTG
GTTTGTCTTGTTTX
GTTTGTCTTGTTTX
GTTTGTCTTGTTTX
GTTTGTTATGTTTG
GTTTGCGTTGTTTG
XTTTGCTTTGTTTG
GTTTGTCCTGTTTG
GTTTGCTCTGTTTG
GTTTGTTGTGTTTG
XTTTGCCATGTTTG
XTTTGTGCTGTTTG
XTTTGTGCTGTTTG
GTTTGCGCTGTTTG
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# Motif 45 TTTCTTTTTCTTTTTTTT
XTTTGTTGTGTTTG
XTTTGTCTGGTTTG
GTTTGACATGTTTG
XTTTGGCTTGTTTG
TTTTGTCTTGTTTG
GTTTGCACTGTTTG
GTTTGCACTGTTTG
XTTTGCCCTATTTG
GTTTGCACCGTTTG
GTTTGCACGGTTTG
GTTTGAGTAGTTTG
CCTTGTTCTGTTCA
GTTTTTCTCGTTCT
CCTCGTCCTCTTTA
GATTGTCTTGGTCT
AGTTTTCACGTTTT
CCTCATCCTCTTTA
**************

# Motif 252 ACGCGTAAAGTGGTT
Motif 252
ACGCGTAAAGTGGTT
ACGCGTAAAGTGGTT
ACGCGTAAAGTGGTT
ACGCGTAAAGTGGTT
ACGCGTTAAGTGGTT
ACGCGTAAAGTGGTT
ACGCGTAAAGTGGTT
ACGCGTTAAGTGGTT
ACGCGTTAAGTGGTT
ACGCGTTAAGTGGTT
ACGTGTAAAGTGGTT
ACGCGTTAATTGATT
XXGCGTAAAGTGGXX
XXGCGTAAAGTGGXX
XXGCGTTAAGTGGXX
***************

# Motif 328 GCATAGCATGGCGT
Motif 328
GCATAGCATGGCGT
GCATAGCATGGCGT
GCATAGCGTGGCGT
GCATAGCGTGGAGT
GGTTAGCATGGCGT
GCATAGCAAGGCGT
GCATAGCGTGGCGT
GCATAGCGTGGCGT
GCATAGCGTGGCGT
GGTTAGCATGGCGC
GGTTAGCATGGCGC
GCATGGCACGGAGT
**************

# Motif 336 GGCGTTTGGG
Motif 336
GGCGTTTGGG
GGCGTTTGGX
GGCGTTTTGG
GGCGTTTGGX
GGCGTTTGGX
GGTGTTTGGG
GGCGTTCGGG
GGCGTTGGGG
GGCGATTTCG
GGTGTTTCGG
GGCGTCGGGG
GGCGAGTTGA
**********
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# Motif 45 TTTCTTTTTCTTTTTTTT
# Motif 344 GGCAAAATdAAC
Motif 344
GTCAAAATGAAC
GGCAAAATGAAC
GGCAAAATGAAG
GGCGAAATGAAC
GTCAAAATAAAC
GTCAAAATAAAC
GTCAAAATAAAC
GGCAAAACGAAC
GGCGAAATAAAG
GGCAGAATAGAC
GGCAAAAATGAC
GTCAGAATGAGA
************

# Motif 347 wmAAAAGTTC
Motif 347
AAAAAAGTTC
AAAAAAGTTC
AAAAAAGTTC
AAAAAAGTTC
TCAAAAGTTC
TCAAAAGTTC
TCAAAAGTTC
TCAAAAGTTC
AAAAAAGTTG
AAAAAAGTTG
TCACAGTTTC
TCACACGTCC
**********

# Motif 418 CAAACAGTGCAAA
Motif 418
CAAACAGTGCAAA
CAAACAGTGCAAA
CAAACAGTGCAAA
XAAACAGTGCAAA
XAAACAGTGCAAA
CAAACATTGCAAA
CAAACAGTGCAAA
CAAACAGTGCAAA
CAAACTGTGCAAA
CAAACGGTGCAAA
CAAACGGTGCAAA
CAAACATTGCAAA
CAAACATTGCAAA
CAAACAGTACAAA
CAAATTGTGCAAA
CAAACAATGCAAA
XAAACAGTTCAAA
CAAATAGTACAAA
CAAACATTCCAAA
CAAACAATGCAAX
CAAACACTGCAAX
CAAACAAGTCAAA
TAAACTGTGCAAT
AAAACACTGCAAC
TAAGCAGAGCAAX
CATTGGGTGCAAA
CAAGATGTGTAAT
*************

# Motif 616 CGCGAAdTCACGTG
Motif 616
CGCGAAGTCACGTG
CGCCAAATCACGTG
CGCGAGGTCACGTG
CACGAAGTCACGTG
CACGAGGTCACGTG
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
CACGAGGTCACGTG
CACGAGATCACGTG
CGCGAAGTCACCTG
CGCCAAACCACGTG
CGCGCATTCACGTG
CACGAGATCACATG
ACCCAAATCACGTC
CGTCACTTCACGTG
AGCCAATTCACCTT
AGCCAAACCACCTC
**************

# Motif 652 CTCTCCTTCTCCCC
Motif 652
CTCTCCTTCTCCTT
CCCACCTTCTCCCC
CTCTCCTTCTCTTC
CTCTCCTTCTCTTC
CTCTCCTTCTCTTC
TCCTCCTTCTTCCC
CTCTCCTTCTTCCT
CCCCCCTTCTCCCC
TTCTCCTTCCCCTC
GCCACCTTCTCCCC
CTCTCCTCCCTCCT
CTCTCCTCCCTCCT
CCCTCCCTCTTCCT
TCCACCXTCCCCCC
CTCACCTCTTTCCC
**************

# Motif 698 CCCTCCATCTCCA
Motif 698
CCCTCCATCTCCA
CCCTCCATCTCCA
CCCTCCATCGCCA
CCCTTCATCTCCA
CCCTCCCCCTCCA
CCCTCCCCCTCCA
CACTCCATCTCCC
TCCTCTATCTCCT
CACTCCTTCCCCA
TCCTCCAGCTCTT
CACTCCTTTCCCA
TCTTCTATCTCTT
*************

# Motif 751 ACCGCCTTCC
Motif 751
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTTCC
ACCGCCTGCC
ACCGCCTGCC
GCCGCCTTCC
GCCGCCTTCC
ACCGCCTTTC
ACCGCCTCCC
ACCGCCTGCT
GCCGCCATCC
AGCGCCTTAC
AGCGCCCTCC
ACCGCTTTGC
**********

# Motif 813 ACGTCAC
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# Motif 45 TTTCTTTTTCTTTTTTTT
Motif 813
ACGTCAC
ACGTCAC
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ACGTCAC
ACGTCAC
ACGTCAC
XCGTCAC
XCGTCAC
ACGTCAC
XCGTCAC
ACGTCAG
ACGTCAT
*******

# Motif 843 TGAGCCTCGG
Motif 843
TGAGCCTCGG
TGAGCCTCGG
TGAGCCTCGG
TTAGCCTCGG
TGTGCCTCGG
TGAGCCTCAG
CGAGCCTCGG
CGAGCCTCGG
TTTGCCTCGG
TGAGGCTCGG
CGAACCTCGG
AGAGCCTTGT
**********

# Motif 855 TTCCGCCCGC
Motif 855
TTCCGGCCGC
TTCCGCCCGC
TCCCGCCCGA
TTCCGCCCGC
TTCCGCCCGC
TCCCGCCCGC
TTCCGCCCGC
CTCCGGCCGA
TGCCGCCCGC
TCCCGGCCGA
TTCCGGCTGA
TCCCGGCCGA
TTCCAGCCGA
TTTCGCCTGC
TTCCGGCGTA
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# Motif 896 TGGTCCGTGC
Motif 896
TGGTCCGTGC
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XGGTCCGTGC
XGGTCCGTGC
TGGTCCGTGC
TGGTCCGTGX
TGGTCCGTGX
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TGGTCCGTGX
TGGTCCGTGC
TGGTCCGTGC
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# Motif 45 TTTCTTTTTCTTTTTTTT
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XGGTCTGTGC
XGGTCTGTGC
XGGCCCGTGC
XGGTCTGTGC
TGGTCTGTGX
TGGTCTGTGX
TGGTTCGTGC
TGGACCGTGX
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# Motif 973 CACCGCCT
Motif 973
CACCGCCT
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CACCGCCT
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CACCGCCT
CACCGCCT
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CACCGCCT
CACCGCCT
CACCGCCT
CACCGCCT
CACCGCCT
CACCGCTT
CACCGCCT
GACCGCCT
GACCGCCT
CACCGCTT
CACCGCCT
CACCGCCC
CACCGCCT
CACCGCCT
CACCGCTT
TACCGCTT
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# Motif 992 GCATAGCG
Motif 992
GCATAGCG
GCATAGCG
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GCATAGCG
GCATAGCG
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# Motif 45 TTTCTTTTTCTTTTTTTT
GCATAGCG
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GCATAGCG
GCATAGCG
GCATAGCG
GCATAGCA
GCATAGCA
GCATAGCG
GCATAGCG
GCATAGCX
GCATAGCX
GCATAGCX
GCATAGCA
GCATGGCG
GCATCGCG
GCATCGCG
********

# Motif 1059 TCGGCCCG
Motif 1059
TCGGCCCG
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TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGCCCG
TCGGGCCG
TCGGGCCG
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TCGGGCCG
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# Motif 1093 CCCCTCCCCC
Motif 1093
CCCCTCCCCT
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CCCCTCCCCC
CCCCTCCCCT
GCCCTCCTCC
CCCCTCCCTT
GCCCGCCCCC
XCCCTCCTTC
XCCCTCCTTC
CGCCTCCCTC
CCCCTTCACC
CCTCTCCTTC
**********

# Motif 1132 CCCCTCT
Motif 1132
CCCCTCT
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CCCCTCT
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
CCCCTCT
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CCCCTCT
CCCCTCT
CCCCTCT
GCCCTCT
CCCCGCT
CCCCGCT
CCCCTCT
CCCCTCT
CCCCTCT
TCCCTCT
TCCCCCT
GCCCGCT
CCGCTCT
GCACTCT
CCTCCCT
CCCGTCT
TTCTTCT
*******

# Motif 1144 TGTACTAT
Motif 1144
TGTACTAT
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TGTACTAC
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TGTACAAT
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TGTACAAT
TGTACTAC
TGTACTAC
TGTACCAT
TGTACTAT
TGTGCTAT
TGTACAAT
TTTAATTT
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# Motif 1183 AAACAAGGCA
Motif 1183
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AAACAAAGCA
AAACAAGGCA
AAACAGGGCA
AAACACGGCA
AAACAAGACA
AAACAGAGCA
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
AAACGAAGCA
AAACGCGTCA
AAAGAATGCA
AAGCCAGGCA
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# Motif 1230 TTACCCCTC
Motif 1230
TTACCCCTC
TTACCCCTC
TTACCCCTC
TTACCCCTC
TTACCCCTC
TTACCCCTC
TTACCCCTC
TTACCCCGC
TTACCCCAC
CTACCCCAC
CTACCCCTT
CTACCCCTT
*********

# Motif 1270 CTTTTCCGTCC
Motif 1270
XTTTTCCGTCC
XTTTTCCGTCC
CTTTTCCGTCC
CTTTTCCGTCC
CTTCTCCGTCA
CTTTTCCCACC
CTTTTCCCACC
CCTGTCCGTCC
CCTTTCTGTCA
TTTCTCCGTCG
XTTTCCCGCCC
CCGTTTCGTCC
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# Motif 1291 TGAGTCAG
Motif 1291
TGAGTCAG
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TGACTCAG
TGACTCAG
TGAGTCAG
TGAGTCAG
TGAGTAAG
TGACTCAG
TGACTCAG
TTAGTCAG
TGAGTAAG
TTAGTCAG
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# Motif 1407 CCCGTGACT
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
Motif 1407
CCCGTGACT
CCCGTGACT
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CCCGTGACT
CCCGTGACT
XCCGTGACC
XCCGTGACC
XCCGTGACT
CCCGTGACC
CCCGTGACC
CCCGTGATT
CATGTGACT
*********

# Motif 1426 CCCGAGGT
Motif 1426
CCCGAGGT
CCCGAGGT
CCCGAGGT
XCCGAGGT
CCCGAGGT
CCCGAGGT
GCCGAGGT
GCCGAGGT
CCCGAGGT
CCCGAGGT
CCCGAGGT
CCCGAGGT
CCCGAGGT
CCCGAGGT
GCCGAGAT
GCCGAGAT
CCCGACGT
CCCGAGAT
GCCGACGT
GCCGAAGT
CCCGAGAC
********

# Motif 1453 TTTGGTCTT
Motif 1453
ATTGGTCTT
ATTGGTCTT
ATTGGTCTT
TTTGGTCTT
TTTGGTCTT
TTTGATCTT
TTTGGTCAT
TTTTGTCTT
TTTTGTCTT
TTTGGTCTG
TTTGCTCTT
TTAGGTCTT
TTTGGTCGT
TTGGCTCTT
TTTTTTCGG
*********

# Motif 1475 TTTCCTTT
Motif 1475
TTTCCTTT
TTTCCTTT
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TTTCCTTT
TTTCCTTT
TTTCCTTT
TTTGCTTT
TTTTCTTT
TTTTCTTT
```

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# Motif 45 TTTCTTTTTCTTTTTTTT
CTTCCTTT
CTTGCTTG
TTTGCTTC
********

# Motif 1581 TGCATATA
Motif 1581
TGCATATA
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TGCATATA
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TGCATATX
TGCATATX
TGCATATX
TGCATATA
TGCATATA
TGCATATA
TGCXTATA
TGCACATA
TGCATTTA
TGCGCATA
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# Motif 1602 AGGCGGT
Motif 1602
AGGCGGT
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AGGCGGT
XGGCGGT
XGGCGGT
AAGCGGT
XGGCGGC
*******
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
# Motif 1622 ATCTTATC
Motif 1622
ATCTTATC
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ATCTAATC
ATTTTATC
ATTTTATC
ACCTTATC
ATCGTATC
TTCTTATX
AGCTTATC
XTCTTAGC
XTCTTAGC
ACCTTATX
GTCTTATX
AGCTTGTC
********

# Motif 1635 CGACAACCC
Motif 1635
CGACAACCC
CGACAACCC
CGACAACCC
CGACAACCT
CGACAACCT
CGACAACCC
CGACAACCC
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
CGACAACCT
CGACAACCX
CGACAACCX
CGACAACCX
CGACAACCC
CGACAACCC
CGACAACCC
TGACAACCC
CGACACCCC
CGACAAACC
CAACAACCC
TGACAACCC
CGACCACCC
TGGCAACCC
TGGCAACCC
CGACGACCC
TGACAGCCC
*********

# Motif 1650 GAAATTT
Motif 1650
GAAATTT
GAAATTT
GAAATTT
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GAAAATT
GAAATTT
GAAATTT
GAAATTX
GAAATTX
GAAATTX
GAAATTT
GAAATTT
GAAAATT
GAAAATT
GAAAATT
GAATTTT
GAAATTT
CAAATTT
*******

# Motif 1710 TGTATATA
Motif 1710
TGTATATA
TGTATATA
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XGTATATA
XGTATATA
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
XGTATATA
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GGTATATA
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AGTATATA
TTTATATA
XXTATATA
AGTATATA
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TGTACATA
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TGTAAATA
TGTAAATA
TGTATAAT
TTTGTATA
GCTATATA
TGTATACT
AGTATATG
GTTGTATA
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# Motif 1723 TCTCGTGA
Motif 1723
TCTCGTGA
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TCCCGTGA
CCTCGTGA
CCTCGTGA
TCGCGTGA
TCTTGTGA
TCTCGTAA
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# Motif 1739 GGGCTTAGGG
Motif 1739
GGGCTTAGGG
GGGCTTAGGG
GGGCATAGGG
GGGCTTAGGG
GGGCTTAGGG
GGGCTTAGGG
GGGCATAGGG
GGGCATAGGG
GGGCTTAGGX
GGGCATAGGG
GGGCTTAGGX
GGGCTAAGGG
XGGCTTAGGG
XGGCTTAGGG
XGGCTTAGGG
GGGCATAGGX
XGGCTTAGGG
XGGCTTAGGG
XGGCATAGGG
GGGCTAAGGX
GGGCTCAGGX
GGGTATAGGG
XGGCTCAGGG
XGGCTCAGGG
GGGGATAGGG
XGGTTTAGGG
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```
# Motif 45 TTTCTTTTTCTTTTTTTT
GGGCTAGGGX
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# Motif 1821 TCACGTG
Motif 1821
TCACGTG
TCACGTG
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# Motif 45 TTTCTTTTTCTTTTTTTT
TCACGTG
TCACGTG
TCACGTG
TCACGTX
TCACGTX
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TCACGTG
TCACGTG
TCACGTG
TCACGTG
TCACCTG
TCACATG
TCGCGTG
GCACGTG
*******

# Motif 1872 TATGATAC
Motif 1872
TATGATAC
TCTGATAC
TCTGATAC
TATGATAC
TATGGTAC
TATGGTAC
GATGATAC
TATGATAC
GATGATCC
GATGATCC
TATGATAX
TATGATAX
TATGATAX
TACGATAC
TATGTTCC
********

# Motif 1879 CTTATCGAT
Motif 1879
CTTATCGAT
CTTATCGAT
CTTATCGAT
CTTATCGAT
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# Motif 45 TTTCTTTTTCTTTTTTTT
CTTATCGAT
CTTATCGAT
CTTATCGAT
CTTATCGAT
CTTATCGAT
XTTATCGAT
XTTATCGAT
XTTATCGAT
CTTATCGAT
CTTATCGAT
CTTATCGAT
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CTTATCGAT
TTTATCGAT
TTTATCGAT
TTTATCGAT
CTTATCAAT
CTCATCGAT
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# Motif 1934 TCACATGA
Motif 1934
TCACATGA
TCACATGA
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TCACATGA
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TCACATGA
TCACATGA
TCACATGX
TCACATGX
TCACATGX
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# Motif 45 TTTCTTTTTCTTTTTTTT
TCACATGA
TCACATGA
XCACATGA
XCACATGA
XCACATGA
XCACATGA
XCACATGA
XCACATGA
TCACATGC
TCACATGC
TCACATGC
TCACATGC
TCACATGT
TCACATGT
TCACATGG
TCACATAA
TTACATGA
********

# Motif 1940 GTbGGCGTT
Motif 1940
GTTGGCGTT
GTCGGCGTT
GTCGGCGTT
GTTGGCGTX
GTCGGCGTX
GTCGGCGTX
GTTGGCGTT
GTTGGCGTT
TTTGGCGTT
TTCGGCGTT
TTCGGCGTT
TTCGGCGTT
TTCGGCGTT
TTTGGCGTT
TTTGGCGTT
GTTGGCATT
GTTGGCATT
TTGGGCGTT
TTGGGCGTT
ATTGGCGTT
GACGGCGTT
GTCGGTGCA
GTTTGCGCA
GTCAGTGCA
*********

# Motif 1971 CGCCGGCCG
Motif 1971
CGCCGGCCG
CGCCGGCCG
CGCCGGTCG
CGCCTGCCG
CGCCTGCCG
CACCGGCCG
CGCCTGCCG
CGCCGTCCG
CGCCGTCCG
CGCCGGTCG
CGCCGATCG
CGCTGGTCG
CGCAGGCCG
CGCCCGCCG
CACCAGCCG
*********

# Motif 1998 CCTCGGCA
Motif 1998
CCTCGGCA
CCTCGGCA
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# Motif 45 TTTCTTTTTCTTTTTTTT
CCTCGGCA
CCTCGGCA
CCTCGGCA
CCTCGGCA
CCTCGGCA
CCTCGGTA
CCTCGGTA
CCTCGGTA
CCTCGGTA
CCTCGGTA
CCTCGGTA
XXTCGGCA
XXTCGGCA
XXTCGGCA
CCTCGGTA
CCTCGGCT
********

# Motif 2032 GAAGCTCTC
Motif 2032
GAAGCTCTC
GAAGCTCTC
GAAGCTCCC
AAAGCTCTC
AAAGCTCTC
AAAGCTCTC
GAAGCTTTC
GAAGCTCTC
GAAGCTCTC
GAAGCTCTC
AAAGCTCTC
GAAGCTCTX
GAAGCTCCX
GAAGCTCCX
GAGGTTTTC
*********

# Motif 2077 TGTACAAATA
Motif 2077
TGTACAAATA
TGTACAAATA
TGTACAAATA
TGTACAAATA
TGTACAAATA
TGTACAAATA
TGTACAAATX
TGTACAAATX
TATACAAATA
TATACAAATA
TATACAAATA
TGTATAAATA
TGTATAAATA
XATACAAATA
XATACAAATA
TGTACAAACA
TGTACCAATA
XXXACAAATA
TGTATAAAXX
TGTATAAAXX
TGTAAAAATX
XATACAAGTA
XXXACAGATA
XXXACAAGTA
TGTACAGAGC
TGTACAGAGC
TGTATAATXX
**********

# Motif 2093 CCCCGCAC
Motif 2093
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Motif 45 TTTCTTTTTCTTTTTTTT
CCCCGCAC
CCCCGCAC
CCCCGCAC
CCCCGCAC
CCCCGCAC
XCCCGCAC
XCCCGCAC
XCCCGCAC
CCCCGCAC
CCCCGCAC
XCCCGCAC
XCCCGCAC
CCCCGCAC
CCCCGCAT
CCCCGCAT
CCCCGCAT
CCCCGCAG
XCCCACAC
****

Motif 2194 GGvGTTTGGAG
Motif 2194
GGAGTTTGGAG
GGAGTTTGGAG
GGAGTTTGGAG
GTCGTTTGGAG
GTGGTTTGGAG
GTGGTTTGGAG
GTCGTTTGGAG
GTCGTTCGGAG
GGCGTTTGGAT
GGAGTTTGGGX
GTGGCTTGGAG
GGCGTCTGGAG
GGAGTTCGGAT
GGAGTTTGGTX
GGAGTTTCGGX
****

Motif 2199 CCACGTGC
Motif 2199
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGX
CCACGTGX
CCACGTGX
XCACGTGC
XCACGTGC
XCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
CCACGTGC
XCACGTGC
XCACGTGC
XCACGTGC
****

Motif 2215 ATTCCCC
Motif 2215
ATTCCCC
XTTCCCC
XTTCCCC
ATTCCCC

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# Motif 45 TTTCTTTTTCTTTTTTTT
ATTCCCC
ATTCCCC
ATTCCCC
ATTCCCC
GTTCCCC
ATTTCCC
ATTCCCC
ATTCCCC
XTTCCCT
ATTCCCC
ATTCCCA
*******

# Motif 2223 GGCGTTG
Motif 2223
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTA
GGCGTTC
GGCGTTC
GGCGTTC
GGCGTTC
GGCGTTG
GGCGTTG
GGCGTTG
GGCGTTA
GGCGTTA
GGCGTTA
*******

# Motif 2236 GCAGAATC
Motif 2236
GCAGAATC
GCAGAATC
GCAGAATC
GCAGAATC
GCAGAATC
GCAGAAAC
GCAGAAAC
GCAGAATA
GCAGAATA
GCAGAATA
GCAGAAAT
ACAGAAAC
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# Motif 2249 TTTTTTT
Motif 2249
TTTTTTT
TTTTTTT
TTTTTTT
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TTTTTTT
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# Motif 45 TTTCTTTTTCTTTTTTTT
TTTTTTT
TTTTTTT
TTTTTTT
TTTTTTT
TTTTTTT
TTTTTTT
ATTTTTT
*******

# Motif 2253 TTTGGTTT
Motif 2253
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGTTT
TTTGGATT
TCTGGATT
********

# Motif 2287 TTCTTCCTT
Motif 2287
TTCTTCCTT
XTCTTCCTT
TTCTTCCTT
TTCTTCCTC
TTCTTCCTC
TTCTTCCTC
CTCTTCCTT
TACTTCCTT
TACTTCCTT
TTCTTCCCT
XTATTCCTT
XTATTCCTT
*********

# Motif 2378 TGTACAGAA
Motif 2378
TGTACAGAA
TGTACAGAA
TGTACAGAA
TGTACAGAA
GGTACAGAA
TGTATAGAA
TGTATAGAA
TGTACAGXX
TGTACAGXX
TGTACAGXX
GGTACGGAA
GGTACGGTA
*********

# Motif 2451 GATATCC
Motif 2451
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
GATATCC
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# Motif 45 TTTCTTTTTCTTTTTTTT
GATATCC
GATATCT
GATATCT
GATACCC
*******

# Motif 2483 TGAGTCA
Motif 2483
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
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TGAGTCA
TGAGTCA
TGAGTCA
TGAGTCA
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# Motif 2488 TACCCCGC
Motif 2488
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGC
TACCCCGX
TACCCCGX
TACCCCGX
AACCCCGC
AACCCCGC
AACCCCGC
AACCCCGC
AACCCCGC
AACCCCGX
AACCCCGX
AACCCCGX
TGCCCCGC
TGCCCCGC
********

# Motif 2497 TGCATAG
Motif 2497
TGCATAG
TGCATAG
TGCATAG
TGCATAG
TGCATAG
TGCATAG
TGCATAG
TGCATAG
TGCACAG
TGCACAG
TGCACAG
TGCACAG
TGCACAG
XGCATAG
XGCATAG
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# Motif 45 TTTCTTTTTCTTTTTTTT
TGCCCAG
TTCXTAG
XGCACGG
*******

# Motif 2525 GACGCGT
Motif 2525
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
GACGCGT
XACGCGT
GACGCGT
XACGCGT
XACGCGT
*******

# Motif 2529 ACGTGAC
Motif 2529
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGTGAC
ACGCGAC
ACCTGAC
TCGCGAC
*******

# Motif 2611 TGTACAT
Motif 2611
TGTACAT
TGTACAT
TGTACAT
TGTACAT
TGTACAT
TGTACAT
XGTACAT
XGTACAT
XGTACAT
TGTACAT
TGTACAT
TGTACAT
TGTACAT
TGTACAT
TGTACAT
XGTACAT
XGTACAT
XGTACAT
TGTACAT
TGTACAT
TGTACAT
CGTACAT
CGTACAT
CGTACAT
TGTACAT
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# Motif 45 TTTCTTTTTCTTTTTTTT
TGTACAT
TTTACAT
*******

# Motif 2662 GAGATACC
Motif 2662
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
GAGATACC
AAGATACC
AAGATACC
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# Motif 2677 TCACCGC
Motif 2677
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
TCACCGC
ACACCGC
ACACCGC
XCACCGC
XCACCGC
XCACCGC
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# Motif 2683 TCTCCGC
Motif 2683
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGC
TCTCCGX
TCTCCGX
TCTCCGX
TCTCCGX
TCTCCGX
TCTCCGX
TCTCCGX
TCTCCGX
XCTCCGC
XCTCCGC
XCTCCGC
TCTCCGC
TCTCCGC
ACTCCGC
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# Motif 45 TTTCTTTTTCTTTTTTTT
TATCCGX
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# Motif 2919 TCCCCGC
Motif 2919
TCCCCGX
TCCCCGX
TCCCCGX
TCCCCGC
TCCCCGC
TCCCCGC
TCCCCGC
TCCCCGC
TCCCCGC
TCCCCGC
TCCCCGC
XCCCCGC
XCCCCGC
XCCCCGC
CCCCCGC
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Known Aspergillus Factors	
abaA	CATTCC
amdR	TCGGCGAA...AGCCAAT
AnCF	AGCCAAT
areA	HGATAR
areA_n	WGATAAGR
brlA	TCCCTyy
cpcA	ATGACTCA
creA	SYGGGG
facB_1	TCC........BGA
facB_2	TCS..........GSA
facB_3	GCA.........SGC
facB_4	TCS.........GGA
facB_5	GCC...........TGC
facB_6	GCA..........TGC
facB_7	GCA........GGC
nirA	CTCCGHCC
nit2_1	TATCTA
nit2_2	TAGTAGAGATA
nit2_3	TATCGC........TATCGT
nit2_4	GAGATA
pacC	GCCARG
penR1	CCAAT
prnA_1	CCGGnCCGG
prnA_2	CCGGnnCCGG
prnA_3	CCGGnnnCCGG
prnA_4	CCGGnnnnCCGG
prnA_5	CCGGnnnnnCCGG
prnA_6	CCGGnnnnnnCCGG
stuA	wCGCGw
UAY	CGS......SCG

Known S. cerevisiae Factors	
ABF1	RTCRYnnnnnACG
ACE2	GCTGGT
ADR1	GGAGA
Bas1	TGACTC
Cbf1	RTCACRTG
Cin5	TTACTAA
DAL81	GATAAG
Dig1	RTGAAACA
FKH1	TTGTTTACST
FKH2	TTGTTTACST
Gal4	CGGnnnnnnnnnnnCCG
GCN4	ATGACTCAT
GCR1	GGAAG
GLN3	GATAAk
HAP2	GCCAATCA
HAP4	TnRTTGGT
HSF1b	TTCTAGAA
INO2	CATGTGAAat
INO4	CATGTGAAat
Leu3	CCGGNNCCGG
MAC1	TTTGCTCA
MBP1	ACGCGTnA
MCM1a	TTWCCcnwwwrGGAAA
MET31	AAACTGTGGC
MET4	TGGCAAATG
MIG1	CCCCRSWWWW
MIG1b	GCGGGG
MSN2	CCCCT
MSN4	CCCCT
PDR1	CCGCGG
PHO4	CACGTG
PUF3	CHTGTAWATA
PUF4	WHTGTAHAWTA
PUF5	TGTAAYAWTA
PUT3	CGGnnnnnnnnnnCCG
RAP1	ACACCCATACATTT
REB1	CCGGGTAA
RLM1	CTAWWWWTAG
RME1	GAACCTCAA
SMP1	ACTACTAWWWWTAG
STE12	RTGAAACA
SWI4	CRCGAAAA
SWI5	KGCTGR
SWI6	ACGCGT
YAP1	TTACTAA

Known 3' Elements	
efficiency_element1	TATATA
efficiency_element2	TATGTA
efficiency_element3	TTTTTATA
efficiency_element4	TTTTTATA
polyA_site	AATAAAA
positioning_element1	AAGAA
positioning_element2	AAAAAA
positioning_element3	AATAAA
positioning_element4	TTAAGAAC
transcription_termination	TATATATATATATA

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN0012.1	predicted protein [Neurospora crassa]				
AN0013.1	Predicted transporter (major facilitator superfamily)	R			
AN0034.1	Dihydroxyacetone kinase/glycerone kinase	G	Carbohydrate transport, metabolism	YFL053W	
AN0038.1	Protein kinase ATM/Tel1, involved in telomere length regulation and DNA repair	TBLD			
AN0039.1	Uncharacterized conserved protein	S		YNL011C	
AN0040.1	Mitochondrial DNA polymerase gamma, catalytic subunit	L	Replication, recombination, repair	YOR330C	mitochondrion
AN0042.1	Mg2+ and Co2+ transporters	P	Inorganic ion transport, metabolism		
AN0043.1	Phytoene/squalene synthetase	I	Lipid transport, metabolism		
AN0044.1	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL		YLR032W	cytoplasm nucleus
AN0046.1	Histidyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YPR033C	cytoplasm
AN0047.1	GTP-binding protein GP-1	R			
AN0048.1	predicted protein [Neurospora crassa]				
AN0049.1	N-acetylglucosaminyl phosphatidylinositol de-N-acetylase	M		YMR281W	cytoplasm
AN0050.1	Predicted metal-dependent hydrolase of the TIM-barrel fold	R			
AN0051.1	Isopenicillin N synthase and related dioxygenases	R			
AN0052.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN0054.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN0055.1	TmpA [Emericella nidulans]				
AN0056.1	hypothetical protein [Neurospora crassa]				
AN0057.1	Tyrosyl-tRNA synthetase, cytoplasmic	J	Translation, ribosomal structure, biogenesis	YGR185C	cytoplasm
AN0058.1	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production, conversion		
AN0059.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN0060.1	Decapping enzyme complex, predicted pyrophosphatase DCP2	A	RNA processing, modification		
AN0061.1	predicted protein [Neurospora crassa]			YLR326W	
AN0062.1	Uncharacterized conserved protein	S			
AN0064.1	predicted protein [Neurospora crassa]				
AN0065.1	Histone H3 (Lys4) methyltransferase complex and RNA cleavage factor II complex, subunit SWD2	ABO		YKL018W	
AN0066.1	Mitochondrial oxaloacetate carrier protein	C	Energy production, conversion	YKL120W	mitochondrion
AN0067.1	Ribonucleotide reductase, beta subunit	F	Nucleotide transport, metabolism	YJL026W	cytoplasm nucleus
AN0069.1	WD40 repeat-containing protein	S			
AN0071.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN0072.1	Pseudouridine synthase	J	Translation, ribosomal structure, biogenesis	YNL292W	cytoplasm nucleus
AN0073.1	hypothetical protein ((AL513463) hypothetical protein [Neurospora crassa])				
AN0074.1	Nucleolar protein-like/EBNA1-binding protein	A	RNA processing, modification	YKL172W	
AN0075.1	Thioredoxin/protein disulfide isomerase	O	Posttranslational modification/turnover/chaperones		
AN0076.1	5'-3' exonuclease	L	Replication, recombination, repair		
AN0077.1	Iron/ascorbate family oxidoreductases	QR			
AN0078.1	SamB protein [Emericella nidulans]				
AN0081.1	G-protein beta subunit	R		YOR212W	cytoplasm
AN0082.1	Conserved phosducin-like protein	T	Signal transduction mechanisms		
AN0083.1	Transcription initiation factor IIF, auxiliary subunit	K	Transcription	YPL129W	nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0084.1	Ran-binding protein RANBP1 and related RanBD domain proteins	U	Intracellular trafficking/secretion/transport	YDR002W	
AN0085.1					
AN0086.1	Glycolipid 2-alpha-mannosyltransferase (alpha-1,2-mannosyltransferase)	G	Carbohydrate transport, metabolism	YIL085C	
AN0087.1	Predicted Rho GTPase-activating protein	R			
AN0088.1	Predicted membrane protein	S		YML018C	vacuolar membrane
AN0089.1	Ras-related GTPase	R		YML001W	cytoplasm nucleus
AN0090.1	WD40 repeat protein TipD	R			
AN0091.1	Putative protein methyltransferase involved in meiosis and transcriptional silencing (Dot1)	DK		YDR440W	cytoplasm nucleus
AN0092.1	Putative SAM-dependent rRNA methyltransferase SPB1	AR			
AN0093.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN0094.1					
AN0097.1	ATP-dependent DNA ligase IV	L	Replication, recombination, repair	YOR005C	
AN0106.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN0109.1	Spliceosomal protein snRNP-U1A/U2B	A	RNA processing, modification		
AN0111.1	mRNA splicing factor	A	RNA processing, modification	YDR416W	nucleus
AN0112.1	Pattern-formation protein/guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport		
AN0114.1	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	D	Cell cycle/division, chrom. partitioning		
AN0115.1	Conserved WD40 repeat-containing protein	S			
AN0116.1	Mitochondrial/chloroplast ribosomal protein L11	J	Translation, ribosomal structure, biogenesis	YNL185C	mitochondrion
AN0117.1	Histone H4	B	Chromatin structure, dynamics	YLR225C	cytoplasm
AN0118.1	Dyneins, heavy chain	Z	Cytoskeleton	YKR054C	cytoplasm
AN0120.1	Protein phosphatase 2A-associated protein	T	Signal transduction mechanisms	YMR028W	
AN0121.1	Porphobilinogen deaminase	H	Coenzyme transport, metabolism	YDL205C	cytoplasm nucleus
AN0122.1	ATP-dependent Lon protease, bacterial type	O	Posttranslational modification/turnover/chaperones		
AN0123.1	Predicted mitochondrial ribosomal protein L23	J	Translation, ribosomal structure, biogenesis		
AN0124.1	Serine/threonine protein kinase	TR		YNL207W	cytoplasm
AN0125.1	26S proteasome regulatory complex, subunit RPN1/PSMD2	O	Posttranslational modification/turnover/chaperones		
AN0126.1	DNA mismatch repair protein - MLH1 family	L	Replication, recombination, repair	YMR167W	cytoplasm nucleus
AN0127.1	Uncharacterized conserved protein, contains WD40 repeats	S		YFR021W	
AN0128.1	Carboxymethyl transferase	O	Posttranslational modification/turnover/chaperones	YOL141W	cytoplasm
AN0129.1	Dual specificity phosphatase	V	Defense mechanisms		
AN0130.1	Putative methyltransferase	R		YML005W	cytoplasm
AN0131.1	hypothetical protein [Neurospora crassa]			YLR250W	Golgi early Golgi
AN0132.1					
AN0133.1	mRNA splicing factor ATP-dependent RNA helicase	A	RNA processing, modification	YGL120C	nucleolus
AN0134.1	Protein kinase inhibitor	D	Cell cycle/division, chrom. partitioning	YBR133C	bud neck cytoplasm
AN0135.1	Myosin assembly protein/sexual cycle protein and related proteins	ODR			
AN0137.1	Predicted starch-binding protein	R		YPL110C	cytoplasm
AN0138.1	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB4	KL		YPR056W	nucleus
AN0139.1	Asparaginase	E	Amino acid transport, metabolism		
AN0140.1	Actin-related protein Arp2/3 complex, subunit Arp3	Z	Cytoskeleton	YJR065C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0141.1	tRNA uracil-5-methyltransferase and related tRNA-modifying enzymes	J	Translation, ribosomal structure, biogenesis	YKR056W	
AN0142.1	Ribosomal protein S5	J	Translation, ribosomal structure, biogenesis	YBR251W	mitochondrion
AN0144.1	Putative serine/threonine protein kinase	R			
AN0145.1	AFLJ [Aspergillus parasiticus]				
AN0154.1	Transcription initiation factor TFIID, subunit TAF10 (also component of histone acetyltransferase SAGA)	K	Transcription		
AN0156.1	Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	KIT			
AN0158.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR		YBR046C	cytoplasm nucleus
AN0159.1	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	AR			
AN0160.1	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport, metabolism		
AN0161.1	mRNA cleavage and polyadenylation factor IA/II complex, subunit CLP1	A	RNA processing, modification	YOR250C	
AN0162.1	Nuclear localization sequence binding protein	K	Transcription		
AN0163.1	Rho GDP-dissociation inhibitor	T	Signal transduction mechanisms	YDL135C	cytoplasm nucleus
AN0164.1	Serine/threonine specific protein phosphatase involved in glycogen accumulation, PP2A-related	GT		YNR032W	cytoplasm nucleus
AN0165.1	Vesicle coat complex AP-3, beta subunit	U	Intracellular trafficking/secretion/transport	YGR261C	Golgi early Golgi
AN0166.1	Centromere-associated protein NUF2	D	Cell cycle/division, chrom. partitioning	YOL069W	spindle pole
AN0167.1	Translation initiation factor 2B, alpha subunit (eIF-2Balpha/GCN3)	J	Translation, ribosomal structure, biogenesis	YKR026C	cytoplasm
AN0170.1	Thioredoxin	O	Posttranslational modification/turnover/chaperones	YGR209C	cytoplasm nucleus
AN0172.1	MHYT domain (predicted integral membrane sensor domain)	T	Signal transduction mechanisms		
AN0173.1					
AN0174.1	D-aspartate oxidase	E	Amino acid transport, metabolism		
AN0176.1	GATA-4/5/6 transcription factors	K	Transcription		
AN0179.1	Predicted dehydrogenase	Q		YMR226C	cytoplasm nucleus
AN0182.1	Ras-related GTPase	R		YGR152C	cytoplasm nucleus
AN0183.1	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes	EH		YMR178W	cytoplasm nucleus
AN0189.1	RNase MRP and P, subunit POP4/p29	A	RNA processing, modification		
AN0190.1	tRNA splicing endonuclease	J	Translation, ribosomal structure, biogenesis	YAR008W	
AN0191.1	RNA polymerase II elongator complex, subunit ELP4	BK		YPL101W	
AN0193.1	Thiamine pyrophosphokinase	F	Nucleotide transport, metabolism	YJR142W	
AN0201.1	Predicted transporter (major facilitator superfamily)	R			
AN0202.1	ARCA protein [Emericella nidulans]				
AN0204.1	ATP-dependent RNA helicase	A	RNA processing, modification	YKR024C	nucleolus nucleus
AN0205.1	Panthothenate synthetase	H	Coenzyme transport, metabolism	YIL145C	cytoplasm nucleus
AN0206.1	Glycerol-3-phosphate O-acyltransferase	I	Lipid transport, metabolism		
AN0209.1	Ammonia permease	P	Inorganic ion transport, metabolism		
AN0210.1	Nucleoside phosphatase	F	Nucleotide transport, metabolism	YER005W	Golgi early Golgi
AN0211.1	U2-associated snRNP A' protein	A	RNA processing, modification	YPL213W	nucleus
AN0212.1	predicted protein [Neurospora crassa]				
AN0213.1					
AN0219.1	Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	U	Intracellular trafficking/secretion/transport		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0224.1	Renal dipeptidase	O	Posttranslational modification/turnover/chaperones		
AN0226.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YDR054C	cytoplasm nucleus
AN0227.1					
AN0228.1	DNA replication licensing factor, MCM6 component	L	Replication, recombination, repair	YGL201C	cytoplasm nucleus
AN0229.1	Uncharacterized conserved protein	R		YMR266W	cell periphery
AN0232.1	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase	OK			
AN0233.1	Predicted transporter (major facilitator superfamily)	R			
AN0235.1	Serine/threonine protein kinase and endoribonuclease ERN1/IRE1, sensor of the unfolded protein response pathway	T	Signal transduction mechanisms		
AN0236.1	Polyadenylation factor I complex, subunit PFS2	A	RNA processing, modification		
AN0237.1	Uncharacterized conserved protein	S			
AN0238.1	Subtilisin-related protease/Vacuolar protease B	O	Posttranslational modification/turnover/chaperones		
AN0239.1	Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	TU			
AN0240.1	Transaldolase	G	Carbohydrate transport, metabolism	YLR354C	nucleus
AN0241.1	Cu2+/Zn2+ superoxide dismutase SOD1	P	Inorganic ion transport, metabolism	YJR104C	cytoplasm nucleus
AN0242.1	Transcriptional coactivator p100	K	Transcription		
AN0243.1	Phosphatidylinositol transfer protein SEC14 and related proteins	I	Lipid transport, metabolism		
AN0244.1	Vacuolar assembly/sorting protein VPS8	U	Intracellular trafficking/secretion/transport	YAL002W	endosome
AN0245.1	putative glucanase precursor [Schizosaccharomyces pombe]				
AN0246.1	Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	R			
AN0247.1	Predicted P-loop ATPase fused to an acetyltransferase	R		YNL132W	nucleolus
AN0248.1	Thioredoxin/protein disulfide isomerase	O	Posttranslational modification/turnover/chaperones		
AN0249.1	predicted protein [Neurospora crassa]				
AN0252.1	F0F1-type ATP synthase, gamma subunit	C	Energy production, conversion	YBR039W	mitochondrion
AN0253.1	DNA topoisomerase I	L	Replication, recombination, repair	YOL006C	nucleolus nucleus
AN0254.1	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE			
AN0255.1	Uncharacterized conserved protein	S			
AN0256.1	Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	OT			
AN0258.1	Micrococcal nuclease (thermonuclease) homologs	L	Replication, recombination, repair	YGL085W	mitochondrion
AN0259.1	Adenylate kinase	F	Nucleotide transport, metabolism	YER170W	mitochondrion
AN0260.1	Eukaryotic-type DNA primase, large subunit	L	Replication, recombination, repair	YKL045W	
AN0261.1	Vesicle coat complex COPII, subunit SEC23	U	Intracellular trafficking/secretion/transport	YPR181C	
AN0262.1	40S ribosomal protein S2	J	Translation, ribosomal structure, biogenesis	YEL054C	cytoplasm
AN0265.1	O-linked N-acetylglucosamine transferase OGT	GOT			
AN0266.1	Splicing factor, arginine/serine-rich	A	RNA processing, modification		
AN0267.1	Myosin regulatory light chain, EF-Hand protein superfamily	Z	Cytoskeleton		
AN0268.1	MesA [Emericella nidulans]				
AN0270.1	Pyridoxal/pyridoxine/pyridoxamine kinase	H	Coenzyme transport, metabolism	YEL029C	cytoplasm nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0271.1	dUTPase	F	Nucleotide transport, metabolism	YBR252W	cytoplasm nucleus
AN0272.1	Predicted aminoglycoside phosphotransferase	R			
AN0273.1	FOG: Zn-finger	R			
AN0275.1	Cystine transporter Cystinosin	E	Amino acid transport, metabolism	YCR075C	
AN0276.1	Unnamed protein	X			
AN0279.1	Transcription factor, Myb superfamily	K	Transcription		
AN0280.1	Alpha-glucosidases, family 31 of glycosyl hydrolases	G	Carbohydrate transport, metabolism		
AN0281.1	Ypt/Rab GTPase activating protein	U	Intracellular trafficking/secretion/transport	YMR055C	spindle pole
AN0287.1	WD40 repeat protein	R			
AN0290.1	F-actin capping protein, beta subunit	Z	Cytoskeleton	YIL034C	actin
AN0292.1	Transcription initiation factor TFIID, subunit TAF5 (also component of histone acetyltransferase SAGA)	K	Transcription	YBR198C	nucleus
AN0293.1	Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold	R		YHR075C	
AN0294.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN0295.1	Nuclear pore complex, rNpl4 component (sc Npl4)	YU		YBR170C	cytoplasm nucleus
AN0297.1	1,4-benzoquinone reductase-like; Trp repressor binding protein-like/protoplast-secreted protein	R		YDR032C	
AN0298.1	Polyadenylation factor I complex, subunit, Yth1 (CPSF subunit)	A	RNA processing, modification	YPR107C	nucleus
AN0299.1	Chitinase	G	Carbohydrate transport, metabolism		
AN0300.1	Asparaginase	E	Amino acid transport, metabolism	YLR160C	
AN0301.1	predicted protein [Neurospora crassa]				
AN0302.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN0303.1	predicted protein [Neurospora crassa]				
AN0304.1	Fe2+/Zn2+ regulated transporter	P	Inorganic ion transport, metabolism	YHR134W	
AN0305.1	WD40-repeat-containing subunit of the 18S rRNA processing complex	A	RNA processing, modification	YLR129W	cytoplasm nucleus
AN0306.1	Actin-related protein Arp2/3 complex, subunit ARPC2	Z	Cytoskeleton	YNR035C	actin
AN0308.1	Uncharacterized proteins of PilT N-term./Vapc superfamily	R			
AN0310.1	WD40 repeat-containing protein	S		YLR196W	nucleolus cytoplasm nucleus
AN0311.1	predicted protein [Neurospora crassa]				
AN0312.1	RNA polymerase I transcription factor	K	Transcription	YKL125W	nucleolus nucleus
AN0313.1	Esterase/lipase	I	Lipid transport, metabolism		
AN0314.1	Aspartyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis		
AN0315.1	hypothetical protein [Neurospora crassa]				
AN0316.1	Alpha tubulin	Z	Cytoskeleton	YML085C	spindle pole microtubule cytoplasm
AN0317.1	Synaptic vesicle protein EHS-1 and related EH domain proteins	TU			
AN0318.1	Plasma membrane H+-transporting ATPase	P	Inorganic ion transport, metabolism	YPL036W	
AN0320.1	Translational repressor MPT5/PUF4 and related RNA-binding proteins (Puf superfamily)	J	Translation, ribosomal structure, biogenesis		
AN0321.1	RNA polymerase III, second largest subunit	K	Transcription	YOR207C	nucleus
AN0323.1	Uncharacterized conserved protein	S			
AN0326.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN0328.1	Uncharacterized protein involved in protein-protein interaction, contains polyproline-binding GYF domain	R			
AN0329.1	Ubiquitin fusion-degradation protein	O	Posttranslational modification/turnover/chaperones	YGR048W	cytoplasm nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0330.1	NADH:flavin oxidoreductase/12-oxophytodienoate reductase	CR			
AN0331.1	predicted protein [Neurospora crassa]				
AN0332.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN0333.1					
AN0335.1	unknown [Emericella nidulans]				
AN0337.1					
AN0339.1	predicted protein [Neurospora crassa]				
AN0345.1	RNA-binding protein required for biogenesis of the ribosomal 60S subunit	J	Translation, ribosomal structure, biogenesis		
AN0347.1	GTPase Rab11/YPT3, small G protein superfamily	U	Intracellular trafficking/secretion/transport	YER031C	cytoplasm nucleus
AN0349.1	Putative ATP-dependent Clp-type protease (AAA+ ATPase superfamily)	O	Posttranslational modification/turnover/chaperones	YBR227C	mitochondrion
AN0351.1	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate reductase	C	Energy production, conversion	YDL022W	peroxisome
AN0352.1	Alpha amylase	G	Carbohydrate transport, metabolism	YPR184W	cytoplasm
AN0354.1	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	E	Amino acid transport, metabolism	YDR035W	cytoplasm nucleus
AN0356.1	predicted protein [Neurospora crassa]				
AN0357.1	Cytochrome c1	C	Energy production, conversion	YOR065W	mitochondrion
AN0358.1	Exocyst subunit - Sec10p	U	Intracellular trafficking/secretion/transport		
AN0359.1	Translation initiation factor 3, subunit b (eIF-3b)	J	Translation, ribosomal structure, biogenesis	YOR361C	cytoplasm
AN0360.1	RNA polymerase I transcription factor UAF	K	Transcription		
AN0361.1	Notchless-like WD40 repeat-containing protein	S			
AN0362.1	IgE-binding protein [Aspergillus fumigatus]				
AN0363.1	predicted protein [Neurospora crassa]				
AN0364.1	involved in sterol uptake; Upc2p [Saccharomyces cerevisiae]				
AN0365.1	predicted protein [Neurospora crassa]				
AN0369.1	Metallopeptidase	R			
AN0370.1	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport, metabolism		
AN0373.1					
AN0375.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN0379.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN0380.1	Cyclophilin-related peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN0381.1	Chaperonin complex component, TCP-1 beta subunit (CCT2)	O	Posttranslational modification/turnover/chaperones	YIL142W	
AN0385.1	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	EH			
AN0387.1	Deoxyribodipyrimidine photolyase	L	Replication, recombination, repair	YOR386W	cytoplasm nucleus
AN0388.1	hypothetical protein [Neurospora crassa]				
AN0391.1	hypothetical protein [Neurospora crassa]				
AN0392.1	hypothetical protein [Neurospora crassa]				
AN0394.1	Monodehydroascorbate/ferredoxin reductase	R		YNR074C	
AN0400.1					
AN0403.1	Monodehydroascorbate/ferredoxin reductase	R			
AN0404.1	Multidrug/pheromone exporter, ABC superfamily	Q			
AN0406.1	Predicted RNA-binding protein involved in translational regulation	JT			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0407.1	RNA polymerase III transcription factor TFIIIC	K	Transcription	YGR047C	cytoplasm nucleus
AN0408.1	Predicted esterase of the alpha-beta hydrolase superfamily	R			
AN0409.1	Nischarin, modulator of integrin alpha5 subunit action	TZ			
AN0410.1	Serine/threonine specific protein phosphatase PP1, catalytic subunit	TR		YER133W	cytoplasm nucleus
AN0411.1	Vesicle coat complex COPII, GTPase subunit SAR1	U	Intracellular trafficking/secretion/transport	YPL218W	
AN0412.1	FOG: Immunoglobin and related proteins	RP			
AN0414.1	Microtubule-associated protein Asp	Z	Cytoskeleton		
AN0416.1	hypothetical protein [Neurospora crassa]				
AN0417.1	Sec61 protein translocation complex, beta subunit	O	Posttranslational modification/turnover/chaperones		
AN0418.1	Urea transporter	E	Amino acid transport, metabolism	YHL016C	
AN0421.1	RNA-binding protein (RRM superfamily)	R		YPR112C	
AN0422.1	TEF-1 and related transcription factor, TEAD family	K	Transcription		
AN0425.1	Protein phosphatase 1, regulatory subunit, and related proteins	T	Signal transduction mechanisms		
AN0426.1	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I	Lipid transport, metabolism		
AN0428.1	Lysyl-tRNA synthetase (class II)	J	Translation, ribosomal structure, biogenesis		
AN0430.1	hypothetical protein [Neurospora crassa]				
AN0431.1	Urea amidohydrolase (urease) alpha subunit	E	Amino acid transport, metabolism		
AN0432.1	NADH-cytochrome b-5 reductase	HC		YKL150W	mitochondrion
AN0433.1	60S ribosomal protein L18A	J	Translation, ribosomal structure, biogenesis	YOR312C	cytoplasm
AN0436.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones	YDR255C	
AN0439.1	Nitrogen permease regulator NLRG/NPR2	P	Inorganic ion transport, metabolism		
AN0440.1	Histone acetyltransferases PCAF/SAGA/ADA, subunit TADA3L/NGG1	B	Chromatin structure, dynamics	YDR176W	nucleus
AN0442.1	Predicted actin-bundling protein	Z	Cytoskeleton		
AN0443.1	Threonine dehydrogenase and related Zn-dependent dehydrogenases	ER			
AN0444.1	E3 ubiquitin protein ligase	O	Posttranslational modification/turnover/chaperones		
AN0445.1	60s ribosomal protein L15	J	Translation, ribosomal structure, biogenesis	YMR121C	nucleolus nucleus
AN0446.1	Uncharacterized protein PSP1 (suppressor of DNA polymerase alpha mutations in yeast)	R			
AN0448.1	predicted protein [Neurospora crassa]				
AN0449.1	cAMP-regulated guanine nucleotide exchange factor	T	Signal transduction mechanisms		
AN0450.1	Uncharacterized conserved protein with similarity to predicted ATPase of the PP-loop superfamily	R			
AN0451.1	Sigma receptor and C-8 sterol isomerase	T	Signal transduction mechanisms	YMR202W	
AN0452.1	endoglucanase [Emericella desertorum]				
AN0454.1	Mu-crystallin	E	Amino acid transport, metabolism		
AN0455.1	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure, biogenesis		
AN0458.1					
AN0460.1	predicted protein [Neurospora crassa]				
AN0462.1	Exocyst protein Sec3	U	Intracellular trafficking/secretion/transport		
AN0463.1	Signaling protein DOCK180	T	Signal transduction mechanisms		
AN0464.1	Phosphoesterases	R			
AN0465.1	40S ribosomal protein S8	J	Translation, ribosomal structure, biogenesis	YER102W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0469.1	Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	P	Inorganic ion transport, metabolism	YNR013C	ER
AN0470.1	Ribosomal protein S7	J	Translation, ribosomal structure, biogenesis		
AN0471.1	Ca2+/H+ antiporter VCX1 and related proteins	P	Inorganic ion transport, metabolism	YDL128W	ER
AN0472.1	Predicted endo-1,3-beta-glucanase	G	Carbohydrate transport, metabolism	YNR067C	vacuole
AN0475.1	Uncharacterized conserved protein	S		YML093W	nucleolus nucleus
AN0476.1	Mitochondrial ribosomal protein L27	J	Translation, ribosomal structure, biogenesis		
AN0482.1	Predicted ubiquitin-conjugating enzyme	O	Posttranslational modification/turnover/chaperones		
AN0484.1	predicted protein [Neurospora crassa]				
AN0485.1	Phosphatidylinositol transfer protein PDR16 and related proteins	I	Lipid transport, metabolism		
AN0486.1	FOG: Zn-finger	R			
AN0489.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN0490.1	CTP synthase (UTP-ammonia lyase)	F	Nucleotide transport, metabolism	YBL039C	cytoplasm
AN0494.1	1,4-beta-D-glucan-cellobiohydrolyase [Aspergillus nidulans]				
AN0495.1	Formyltetrahydrofolate hydrolase	F	Nucleotide transport, metabolism		
AN0502.1	Fe-S oxidoreductase	C	Energy production, conversion	YPL207W	ER
AN0503.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN0504.1	Serine/threonine specific protein phosphatase involved in cell cycle control, PP2A-related	DT			
AN0505.1	Nonsense-mediated decay protein Upf3	A	RNA processing, modification		
AN0507.1	hypothetical protein [Neurospora crassa]				
AN0554.1	Aldehyde dehydrogenase	C	Energy production, conversion	YOR374W	mitochondrion
AN0555.1	hypothetical protein [Neurospora crassa]				
AN0556.1	DNA repair exonuclease MRE11	L	Replication, recombination, repair	YMR224C	cytoplasm nucleus
AN0557.1	Cdc4 and related F-box and WD-40 proteins	R			
AN0558.1	beta (1-3) glucanosyltransferase Gel2p [Aspergillus fumigatus]			YOL132W	
AN0559.1	Translocase of outer mitochondrial membrane complex, subunit TOM20	U	Intracellular trafficking/secretion/transport	YGR082W	mitochondrion
AN0560.1	Exocyst complex subunit	U	Intracellular trafficking/secretion/transport	YBR102C	cell periphery bud neck bud
AN0561.1	Predicted transporter (ABC superfamily)	R		YDR061W	mitochondrion
AN0562.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN0564.1	Multiple inositol polyphosphate phosphatase	R		YHR215W	vacuole
AN0565.1	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	R		YJL130C	cytoplasm
AN0568.1	predicted protein [Neurospora crassa]				
AN0569.1	Histone acetyltransferase SAGA/ADA, catalytic subunit PCAF/GCN5 and related proteins	BK			
AN0573.1	Ypt/Rab GTPase activating protein	U	Intracellular trafficking/secretion/transport		
AN0574.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN0575.1	Calmodulin-binding protein CRAG, contains DENN domain	T	Signal transduction mechanisms		
AN0576.1	Protein kinase containing WD40 repeats	T	Signal transduction mechanisms		
AN0577.1	hypothetical protein [Aspergillus fumigatus]				
AN0578.1	FOG: Zn-finger	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0579.1	Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	Q		YPL117C	cytoplasm nucleus
AN0581.1	Uncharacterized membrane protein, predicted efflux pump	R		YDR338C	
AN0582.1	Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	L	Replication, recombination, repair		
AN0583.1	ATP-dependent RNA helicase	A	RNA processing, modification	YDL031W	
AN0585.1	Actin regulatory protein (Wiskott-Aldrich syndrome protein)	TZ			
AN0589.1	RNA Helicase	A	RNA processing, modification	YJL033W	nucleolus
AN0590.1	Predicted molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN0591.1	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes	EH		YDL045C	cytoplasm
AN0593.1	Predicted dehydrogenase	R			
AN0594.1	Fry-like conserved proteins	R		YIL129C	
AN0595.1	NADP/FAD dependent oxidoreductase	C	Energy production, conversion	YHR042W	ER
AN0596.1	Damage-specific DNA binding complex, subunit DDB1	L	Replication, recombination, repair		
AN0597.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN0600.1	hypothetical protein ((AL513467) conserved hypothetical protein [Neurospora crassa])				
AN0604.1	UV damage repair endonuclease	L	Replication, recombination, repair		
AN0605.1	Uncharacterized conserved protein	S			
AN0606.1	Cytochrome P450 CYP2 subfamily	Q			
AN0607.1	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q			
AN0609.1	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ			
AN0623.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN0624.1	Hypothetical ORF; Ydr132cp [Saccharomyces cerevisiae]				
AN0625.1	Proliferation-associated nucleolar protein (NOL1)	D	Cell cycle/division, chrom. partitioning	YNL022C	nucleolus cytoplasm nucleus
AN0627.1	FYVE finger containing protein	R			
AN0628.1	Lactate dehydrogenase and related dehydrogenases	CHR			
AN0629.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones	YIR038C	
AN0631.1	Transcriptional co-repressor component	K	Transcription		
AN0632.1	U5 snRNP-associated RNA splicing factor	A	RNA processing, modification		
AN0633.1	cDNA sequence BC010311 [Mus musculus]				
AN0634.1	GTP-binding ADP-ribosylation factor-like protein yARL3	U	Intracellular trafficking/secretion/transport		
AN0635.1	predicted protein [Neurospora crassa]				
AN0636.1	N-acetylglucosaminyltransferase complex, subunit PIG-A/SPT14, required for phosphatidylinositol biosynthesis/Sulfolipid synthase	MOI		YPL175W	
AN0638.1	predicted protein [Neurospora crassa]				
AN0640.1	Sphingolipid hydroxylase	I	Lipid transport, metabolism		
AN0641.1	Microtubule-binding protein (translationally controlled tumor protein)	DZ		YKL056C	cytoplasm
AN0642.1	Signal recognition particle, subunit Srp19	U	Intracellular trafficking/secretion/transport		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0644.1	putative zinc finger transcription factor [Aspergillus fumigatus]				
AN0646.1	RNA helicase nonsense mRNA reducing factor (pNORF1)	A	RNA processing, modification	YMR080C	cytoplasm
AN0647.1	U3 small nucleolar ribonucleoprotein (snoRNP) component	A	RNA processing, modification	YNL075W	
AN0649.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN0651.1	G-protein alpha subunit (small G protein superfamily)	DT			
AN0653.1	Predicted MutS-related protein involved in mismatch repair	L	Replication, recombination, repair	YPL199C	cytoplasm
AN0654.1	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase	H	Coenzyme transport, metabolism	YPL069C	mitochondrion
AN0655.1	hypothetical protein [Neurospora crassa]				
AN0657.1	Translocase of outer mitochondrial membrane complex, subunit TOM37/Metaxin 1	U	Intracellular trafficking/secretion/transport		
AN0659.1	predicted protein [Neurospora crassa]				
AN0660.1	Uridine permease/thiamine transporter/allantoin transport	FH			
AN0661.1	unknown [Leptosphaeria maculans]				
AN0662.1	Adenine deaminase/adenosine deaminase	F	Nucleotide transport, metabolism		
AN0664.1	Phosphoinositide-specific phospholipase C	T	Signal transduction mechanisms		
AN0665.1	Vesicle coat complex COPI, epsilon subunit	U	Intracellular trafficking/secretion/transport		
AN0667.1	Mannose-6-phosphate isomerase	G	Carbohydrate transport, metabolism	YER003C	cytoplasm nucleus
AN0668.1	Histone acetyltransferase SAGA associated factor SGF29	R			
AN0670.1	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H	Coenzyme transport, metabolism	YBL033C	cytoplasm nucleus
AN0671.1	predicted protein [Neurospora crassa]				
AN0672.1	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport, metabolism		
AN0673.1	Actin-related protein Arp2/3 complex, subunit Arp2	Z	Cytoskeleton	YDL029W	
AN0675.1	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	C	Energy production, conversion		
AN0676.1	Gamma tubulin	Z	Cytoskeleton	YLR212C	spindle pole
AN0679.1	Phosphotyrosyl phosphatase activator	DT			
AN0681.1	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport, metabolism	YHR112C	cytoplasm
AN0682.1					
AN0684.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN0685.1	Hypothetical ORF; Ylr063wp [Saccharomyces cerevisiae]			YLR063W	cytoplasm
AN0686.1	Prohibitin	O	Posttranslational modification/turnover/chaperones	YGR132C	mitochondrion
AN0687.1	Spermidine synthase	E	Amino acid transport, metabolism	YPR069C	cytoplasm nucleus
AN0688.1	Transketolase	G	Carbohydrate transport, metabolism	YPR074C	cytoplasm nucleus
AN0689.1	acetate regulatory DNA binding protein FacB [Emericella nidulans]				
AN0690.1	N-methyltransferase	R			
AN0691.1					
AN0693.1	hypothetical protein ((AL513462) putative protein [Neurospora crassa])				
AN0694.1					
AN0696.1	Mitotic checkpoint protein MAD1	D	Cell cycle/division, chrom. partitioning		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0697.1	RhoA GTPase effector DIA/Diaphanous	TZ			
AN0699.1	Protein kinase PCTAIRE and related kinases	R			
AN0700.1	Predicted membrane protein	S		YGL114W	
AN0703.1	RAVE (regulator of V-ATPase assembly) complex subunit RAV1/DMX protein, WD repeat superfamily	R		YJR033C	
AN0704.1	Uncharacterized protein SFI1 involved in G(2)-M transition	D	Cell cycle/division, chrom. partitioning	YLL003W	spindle pole
AN0705.1	Isoleucyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YBL076C	cytoplasm
AN0706.1	ER-Golgi vesicle-tethering protein p115	U	Intracellular trafficking/secretion/transport		
AN0707.1	5'-3' exonuclease HKE1/RAT1	LA		YOR048C	nucleus
AN0709.1	FOG: Zn-finger	R			
AN0714.1	U1-like Zn-finger protein	R			
AN0716.1	Uncharacterized conserved protein	S			
AN0717.1	Histidinol phosphate aminotransferase	E	Amino acid transport, metabolism	YIL116W	cytoplasm
AN0719.1	Histone acetyltransferase PCAF/SAGA, subunit SUPT3H/SPT3	K	Transcription	YDR392W	nucleus
AN0720.1	Diphthine synthase	J	Translation, ribosomal structure, biogenesis	YLR172C	cytoplasm
AN0723.1	hypothetical protein [Neurospora crassa]				
AN0724.1	Permease of the major facilitator superfamily	R			
AN0725.1	Spindle pole body protein	Z	Cytoskeleton		
AN0726.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		YMR244W	
AN0727.1	Putative u4/u6 small nuclear ribonucleoprotein	A	RNA processing, modification		
AN0728.1	Uncharacterized conserved protein	S			
AN0729.1	Mannosyltransferase	MU			
AN0730.1	Uncharacterized conserved protein	S			
AN0731.1	Peroxisomal membrane protein MPV17 and related proteins	R			
AN0732.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN0733.1	Histones H3 and H4	B	Chromatin structure, dynamics	YNL031C	
AN0734.1	Histone H4	B	Chromatin structure, dynamics		
AN0746.1	Nucleoside-diphosphate-sugar epimerases	MG			
AN0747.1	Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	O	Posttranslational modification/turnover/chaperones	YLR163C	mitochondrion
AN0751.1	predicted protein [Neurospora crassa]				
AN0756.1	Beta-galactosidase	G	Carbohydrate transport, metabolism		
AN0757.1	tRNA cytosine-5-methylases and related enzymes of the NOL1/NOP2/sun superfamily	J	Translation, ribosomal structure, biogenesis		
AN0762.1	Transcription factor/CCAAT displacement protein CDP1	K	Transcription	YKL179C	lipid particle
AN0764.1	Protocatechuate 3,4-dioxygenase beta subunit	Q			
AN0765.1	Flavonol reductase/cinnamoyl-CoA reductase	V	Defense mechanisms		
AN0766.1	hypothetical protein [Novosphingobium aromaticivorans]				
AN0768.1	Secreted and surface protein containing fasciclin-like repeats	M			
AN0770.1	Predicted regulator of the ubiquitin pathway (contains UAS and UBX domains)	T	Signal transduction mechanisms		
AN0771.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q		YOR153W	cell periphery
AN0772.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0773.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ		YLR214W	
AN0774.1	Sorbitol dehydrogenase	Q			
AN0775.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	Energy production, conversion		
AN0776.1	60S ribosomal protein L22	J	Translation, ribosomal structure, biogenesis	YKL180W	cytoplasm
AN0778.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN0780.1	Aromatic amino acid aminotransferase and related proteins	E	Amino acid transport, metabolism	YER152C	cytoplasm nucleus
AN0781.1	Atu related protein [imported] - Neurospora crassa				
AN0782.1	Ankyrin	M			
AN0787.1	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	G	Carbohydrate transport, metabolism		
AN0794.1	Transcription initiation factor TFIID, subunit TAF9 (also component of histone acetyltransferase SAGA)	K	Transcription		
AN0796.1	Uncharacterized conserved protein	S			
AN0797.1	Histidinol dehydrogenase	E	Amino acid transport, metabolism	YCL030C	cytoplasm
AN0802.1	Protein involved in plasmid maintenance/nuclear protein involved in lipid metabolism	NI			
AN0803.1	Unnamed protein	X			
AN0804.1	Uncharacterized conserved protein	S		YGR024C	cytoplasm nucleus
AN0806.1	WD40 repeat protein	R		YNL035C	nucleus
AN0807.1	predicted protein [Neurospora crassa]				
AN0808.1	WD40 repeat protein	R		YAR003W	nucleus
AN0809.1	RNA polymerase II, large subunit	K	Transcription	YDL140C	nucleus
AN0810.1	Extracellular protein SEL-1 and related proteins	MOT			
AN0811.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism	YJR152W	
AN0812.1	Beta-glucosidase, lactase phlorizinhydrolase, and related proteins	G	Carbohydrate transport, metabolism		
AN0813.1	Kelch repeat-containing proteins	R			
AN0814.1	Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	DO		YGL116W	cytoplasm nucleus
AN0815.1	Failed axon connections (fax) protein/glutathione S-transferase-like protein	T	Signal transduction mechanisms		
AN0816.1	RNA polymerase II transcription initiation factor TFIIA, large chain	K	Transcription		
AN0817.1	Putative transcriptional repressor regulating G2/M transition	KD			
AN0818.1	Uncharacterized conserved protein	R		YLR401C	cytoplasm nucleus
AN0819.1	B-cell receptor-associated protein and related proteins	V	Defense mechanisms	YDL072C	ER
AN0821.1	hypothetical protein [Neurospora crassa]				
AN0822.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN0823.1	Uncharacterized conserved protein	S			
AN0824.1	Short-chain acyl-CoA dehydrogenase	I	Lipid transport, metabolism		
AN0827.1	Uncharacterized membrane protein	S		YJL091C	ER
AN0828.1	Amidases	J	Translation, ribosomal structure, biogenesis		
AN0829.1	Low-affinity cAMP phosphodiesterase	T	Signal transduction mechanisms		
AN0831.1	SPRY domain-containing proteins	R			
AN0832.1	Putative metallopeptidase	R			
AN0834.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones	YOR254C	ER

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0836.1	D-arabinono-1, 4-lactone oxidase	V	Defense mechanisms	YML086C	mitochondrion
AN0837.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN0838.1	ATP-dependent RNA helicase	A	RNA processing, modification		
AN0840.1	Alpha-isopropylmalate synthase/homocitrate synthase	E	Amino acid transport, metabolism	YNL104C	mitochondrion cytoplasm
AN0842.1	Predicted AMP-binding protein	R		YOR093C	
AN0843.1	Ribosomal protein S7	J	Translation, ribosomal structure, biogenesis	YJR123W	
AN0846.1	predicted protein [Neurospora crassa]				
AN0847.1	Molecular chaperones GRP170/SIL1, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones		
AN0848.1	hypothetical protein [Neurospora crassa]				
AN0849.1	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z	Cytoskeleton		
AN0854.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN0855.1	DNA repair protein, SNF2 family	L	Replication, recombination, repair	YBR073W	nucleus
AN0856.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN0857.1	predicted protein [Neurospora crassa]				
AN0858.1	Chaperone HSP104 and related ATP-dependent Clp proteases	O	Posttranslational modification/turnover/chaperones	YLL026W	cytoplasm
AN0860.1	predicted protein [Neurospora crassa]				
AN0861.1	predicted protein [Neurospora crassa]				
AN0862.1	Molecular chaperone Prefoldin, subunit 4	O	Posttranslational modification/turnover/chaperones	YNL153C	cytoplasm
AN0864.1	hypothetical protein ((AL451014) hypothetical protein [Neurospora crassa])				
AN0865.1	Putative trehalase	G	Carbohydrate transport, metabolism	YNL092W	
AN0866.1	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones		
AN0867.1	hypothetical protein [Neurospora crassa]				
AN0868.1	Acyl-CoA thioesterase	I	Lipid transport, metabolism		
AN0869.1					
AN0870.1	Mitochondrial phosphate carrier protein	C	Energy production, conversion	YJR077C	mitochondrion
AN0871.1	Gpi-anchor transamidase	O	Posttranslational modification/turnover/chaperones	YDR331W	ER
AN0872.1	CDC45 (cell division cycle 45)-like protein	L	Replication, recombination, repair		
AN0873.1	Predicted dehydrogenase	R			
AN0874.1	Poly(A) polymerase and related nucleotidyltransferases	A	RNA processing, modification	YKR002W	nucleus
AN0876.1	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	R			
AN0877.1	hypothetical protein (related to pathway-specific nitrogen regulator [imported] - Neurospora crassa)				
AN0879.1	Uncharacterized conserved protein	S			
AN0880.1	Peroxisomal targeting signal type 2 receptor	U	Intracellular trafficking/secretion/transport	YDR142C	
AN0881.1	Alkylated DNA repair protein	L	Replication, recombination, repair		
AN0885.1	Transcription factor MEIS1 and related HOX domain proteins	K	Transcription		
AN0886.1	Uncharacterized proteins, homologs of lactam utilization protein B	R			
AN0888.1	Uncharacterized conserved protein, contains JmjC domain	BT			
AN0889.1	Predicted GTP-binding protein (ODN superfamily)	R		YHR168W	
AN0891.1	Positive regulator of purine utilization				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0892.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN0893.1	Adenylosuccinate synthase	F	Nucleotide transport, metabolism	YNL220W	cytoplasm
AN0894.1	ATP-dependent RNA helicase pitchoune	A	RNA processing, modification		
AN0895.1	Predicted NAD-dependent oxidoreductase	R			
AN0896.1	Succinate dehydrogenase membrane anchor subunit and related proteins	CU		YLR164W	
AN0897.1	Predicted nucleic acid-binding protein ASMTL	D	Cell cycle/division, chrom. partitioning		
AN0899.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN0901.1	Multicopper oxidases	Q			
AN0902.1	predicted protein [Neurospora crassa]				
AN0903.1	hypothetical protein [Neurospora crassa]				
AN0904.1	predicted protein [Neurospora crassa]				
AN0905.1	Anaphase-promoting complex (APC), subunit 4	DO			
AN0906.1	Karyopherin (importin) beta 1	YU		YLR347C	nuclear periphery cytoplasm
AN0907.1	40S ribosomal protein S15/S22	J	Translation, ribosomal structure, biogenesis	YJL190C	nucleolus nucleus
AN0909.1	hypothetical protein ((AL451014) putative protein [Neurospora crassa])				
AN0910.1	Phosphatidylserine decarboxylase	I	Lipid transport, metabolism	YNL169C	mitochondrion
AN0912.1	3-isopropylmalate dehydrogenase	E	Amino acid transport, metabolism	YCL018W	
AN0913.1	Phosphatidylinositol synthase	I	Lipid transport, metabolism	YPR113W	ER
AN0914.1	Serine/threonine protein phosphatase	T	Signal transduction mechanisms		
AN0917.1	Transcriptional coactivator CAPER (RRM superfamily)	K	Transcription		
AN0918.1	Sphingolipid fatty acid hydroxylase	I	Lipid transport, metabolism	YMR272C	ER
AN0919.1	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F	Nucleotide transport, metabolism		
AN0920.1	predicted protein [Neurospora crassa]				
AN0922.1	Medium subunit of clathrin adaptor complex	U	Intracellular trafficking/secretion/transport		
AN0923.1	AAA ATPase containing von Willebrand factor type A (vWA) domain	R			
AN0924.1	Uncharacterized conserved protein	S			
AN0925.1	Phosphoinositide phosphatase SAC1	I	Lipid transport, metabolism		
AN0926.1	Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	YU		YBR017C	cytoplasm nucleus
AN0927.1	Ubiquitin C-terminal hydrolase	O	Posttranslational modification/turnover/chaperones		
AN0928.1	hypothetical protein ((AL451014) putative protein [Neurospora crassa])				
AN0929.1	Choline kinase	M		YLR133W	cytoplasm
AN0930.1	Predicted membrane protein	S			
AN0931.1	Mitogen-activated protein kinase kinase (MAP2K)	T	Signal transduction mechanisms		
AN0932.1	Pyridine nucleotide-disulphide oxidoreductase	Q		YPL091W	mitochondrion cytoplasm nucleus
AN0934.1					
AN0936.1	Threonyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YKL194C	mitochondrion
AN0937.1	NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIT-4 [Neurospora crassa]				
AN0938.1	Predicted transporter (major facilitator superfamily)	R			
AN0939.1	Predicted metal-dependent hydrolase of the TIM-barrel fold	R			
AN0941.1	Maltase glucoamylase and related hydrolases, glycosyl hydrolase family 31	G	Carbohydrate transport, metabolism		
AN0942.1	Sorbitol dehydrogenase	Q			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN0943.1	Mitochondrial F1F0-ATP synthase, subunit g/ATP20	C	Energy production, conversion	YPR020W	mitochondrion
AN0944.1	ATP-dependent RNA helicase	A	RNA processing, modification	YGL171W	
AN0945.1	Vacuolar sorting protein VPS28	U	Intracellular trafficking/secretion/transport		
AN0946.1	Predicted protein involved in nuclear export of pre-ribosomes	J	Translation, ribosomal structure, biogenesis	YOR206W	nucleolus nucleus
AN0947.1	Molybdenum cofactor biosynthesis pathway protein	H	Coenzyme transport, metabolism		
AN0949.1	Sterol desaturase	I	Lipid transport, metabolism		
AN0951.1	Predicted metal-dependent hydrolase (beta-lactamase superfamily)	R			
AN0953.1	Predicted small GTPase involved in nuclear protein import	U	Intracellular trafficking/secretion/transport	YGR163W	vacuolar membrane
AN0954.1	Predicted heme/steroid binding protein	R			
AN0955.1	40S ribosomal protein S25	J	Translation, ribosomal structure, biogenesis		
AN0956.1	tRNA-dihydrouridine synthase	J	Translation, ribosomal structure, biogenesis		
AN0957.1	predicted protein [Neurospora crassa]				
AN0960.1	G4P04 [Emericella nidulans]				
AN0966.1	Uncharacterized conserved protein BCNT	S			
AN0973.1	FOG: Zn-finger	R			
AN0977.1	predicted protein [Neurospora crassa]				
AN0978.1	Translation initiation factor 2B, gamma subunit (eIF-2Bgamma/GCD1)	J	Translation, ribosomal structure, biogenesis		
AN0979.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN0980.1	Beta-galactosidase	G	Carbohydrate transport, metabolism		
AN0981.1	Long chain fatty acid elongase	I	Lipid transport, metabolism		
AN0982.1	WASP-interacting protein VRP1/WIP, contains WH2 domain	Z	Cytoskeleton		
AN0984.1	Uncharacterized conserved protein	S		YOR243C	nucleus
AN0986.1	PHD Zn-finger proteins	R			
AN0987.1	hypothetical protein [Neurospora crassa]				
AN0988.1	LAMMER dual specificity kinases	T	Signal transduction mechanisms		
AN0989.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN0990.1	mRNA cleavage and polyadenylation factor II complex, BRR5 (CPSF subunit)	A	RNA processing, modification	YLR277C	nucleus
AN0991.1	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	H	Coenzyme transport, metabolism		
AN0993.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN0994.1	Dual specificity phosphatase	V	Defense mechanisms		
AN0997.1	Ribonuclease III domain proteins	J	Translation, ribosomal structure, biogenesis	YMR024W	mitochondrion
AN0998.1	hypothetical protein [Neurospora crassa]			YCR019W	
AN1001.1	Uncharacterized conserved protein	S			
AN1002.1	Sec5 subunit of exocyst complex	U	Intracellular trafficking/secretion/transport	YDR166C	cell periphery bud neck bud
AN1003.1	Isocitrate dehydrogenase, alpha subunit	E	Amino acid transport, metabolism	YOR136W	mitochondrion
AN1005.1	Gamma-tubulin complex, DGRIP91/SPC98 component	Z	Cytoskeleton		
AN1006.1	Sulfite oxidase, molybdopterin-binding component	C	Energy production, conversion		
AN1007.1	NAD(P)H-nitrite reductase	C	Energy production, conversion		
AN1008.1	Nitrate/nitrite transporter	P	Inorganic ion transport, metabolism		
AN1009.1	Uncharacterized conserved protein	S			
AN1010.1	hypothetical protein [Aspergillus fumigatus]				
AN1012.1	Predicted hydrolase (HAD superfamily)	R			
AN1013.1	60S ribosomal protein L5	J	Translation, ribosomal structure, biogenesis	YPL131W	cytoplasm
AN1014.1	Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	I	Lipid transport, metabolism	YKL188C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1015.1	Glycogen phosphorylase	G	Carbohydrate transport, metabolism	YPR160W	cytoplasm
AN1016.1	G-protein alpha subunit (small G protein superfamily)	DT		YER020W	cell periphery
AN1017.1	Mitogen-activated protein kinase	T	Signal transduction mechanisms	YLR113W	cytoplasm
AN1018.1	Uncharacterized conserved protein	S			
AN1019.1	Cullins	D	Cell cycle/division, chrom. partitioning	YDL132W	cytoplasm nucleus
AN1020.1	Uncharacterized protein containing double-stranded beta helix domain	S			
AN1021.1	hypothetical protein [Aspergillus fumigatus]				
AN1022.1	Uncharacterized conserved protein	S			
AN1023.1	Synaptic vesicle protein EHS-1 and related EH domain proteins	TU		YNL084C	
AN1024.1	Chromatin remodeling complex WSTF-ISWI, small subunit	K	Transcription	YFR038W	
AN1025.1	Chimaerin and related Rho GTPase activating proteins	T	Signal transduction mechanisms		
AN1026.1	hypothetical protein [Neurospora crassa]				
AN1027.1					
AN1028.1	predicted protein [Neurospora crassa]				
AN1037.1	Fatty acid desaturase	I	Lipid transport, metabolism		
AN1038.1	Putative transmembrane protein	R			
AN1039.1	HLH transcription factor EBF/Olf-1 and related DNA binding proteins	K	Transcription		
AN1041.1	Ca2+-modulated nonselective cation channel polycystin	PT			
AN1045.1	FOG: RRM domain	R			
AN1047.1	Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones	YBR169C	cytoplasm
AN1048.1	hypothetical protein [Neurospora crassa]				
AN1049.1	Protein involved in sister chromatid separation and/or segregation	D	Cell cycle/division, chrom. partitioning		
AN1050.1	3-oxoacyl CoA thiolase	I	Lipid transport, metabolism		
AN1051.1	DNA repair protein RHP57	L	Replication, recombination, repair		
AN1052.1	von Willebrand factor and related coagulation proteins	WV			
AN1053.1	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	AR			
AN1054.1	hypothetical protein [Aspergillus fumigatus]				
AN1056.1	Predicted NTPase (NACHT family)	T	Signal transduction mechanisms		
AN1057.1	Highly conserved protein containing a thioredoxin domain	R			
AN1058.1	Defense-related protein containing SCP domain	S			
AN1059.1	Carnitine O-acyltransferase CPT2/YAT1	I	Lipid transport, metabolism	YAR035W	
AN1060.1	DNA damage-responsive repressor GIS1/RPH1, jumonji superfamily	L	Replication, recombination, repair		
AN1061.1	Amino acid transporters	E	Amino acid transport, metabolism	YKL174C	
AN1062.1	possible endozepine [Aspergillus fumigatus]				
AN1063.1	NADH:ubiquinone oxidoreductase, NDUFA8/PGIV/19 kDa subunit	C	Energy production, conversion		
AN1065.1	Uncharacterized conserved protein	S		YPR133C	
AN1066.1	hypothetical protein [Aspergillus fumigatus]			YNR018W	mitochondrion
AN1068.1	predicted protein [Neurospora crassa]				
AN1069.1	hypothetical protein [Neurospora crassa]			YHR142W	vacuole bud neck cytoplasm bud
AN1073.1	H+/oligopeptide symporter	E	Amino acid transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1074.1	Glycine cleavage system H protein (lipoate-binding)	E	Amino acid transport, metabolism	YAL044C	mitochondrion
AN1075.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones	YKL034W	
AN1076.1	Putative Zn2+ transporter MSC2 (cation diffusion facilitator superfamily)	P	Inorganic ion transport, metabolism		
AN1080.1	Predicted mRNA cap-binding protein related to eIF-4E	J	Translation, ribosomal structure, biogenesis		
AN1082.1	Nucleoside phosphatase	F	Nucleotide transport, metabolism	YEL042W	Golgi
AN1083.1	Translation initiation factor 3 (IF-3)	J	Translation, ribosomal structure, biogenesis		
AN1084.1	Mitochondrial translation elongation factor Tu	J	Translation, ribosomal structure, biogenesis	YOR187W	mitochondrion
AN1085.1	GTP-binding protein	R		YOR165W	
AN1086.1	Predicted thioesterase	R			
AN1087.1	Cytochrome P450	Q			
AN1089.1	Thioredoxin binding protein TBP-2/VDUP1	R			
AN1090.1	Transcription factor BarH and related HOX domain proteins	R			
AN1091.1	FOG: RRM domain	R			
AN1092.1	Glucosamine 6-phosphate synthetases, contain amidotransferase and phosphosugar isomerase domains	M		YNL191W	cytoplasm
AN1093.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR		YOR211C	
AN1094.1	NADH-dehydrogenase (ubiquinone)	C	Energy production, conversion	YMR145C	mitochondrion
AN1095.1	Mitochondrial/chloroplast ribosomal protein L15/L10	J	Translation, ribosomal structure, biogenesis		
AN1096.1	von Willebrand factor and related coagulation proteins	WV			
AN1097.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN1099.1	FOG: Immunoglobin and related proteins	RP			
AN1102.1	Serine palmitoyltransferase	O	Posttranslational modification/turnover/chaperones	YDR062W	ER
AN1103.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN1104.1	Mitochondrial processing peptidase, alpha subunit	O	Posttranslational modification/turnover/chaperones		
AN1105.1	Translocase of outer mitochondrial membrane complex, subunit TOM22	U	Intracellular trafficking/secretion/transport	YNL131W	
AN1106.1	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B	Chromatin structure, dynamics		
AN1109.1	Predicted transporter (major facilitator superfamily)	R			
AN1110.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN1111.1	Flavin-containing monooxygenase	Q			
AN1114.1	Predicted DNA-binding protein	K	Transcription		
AN1115.1	Predicted inosine-uridine preferring nucleoside hydrolase	F	Nucleotide transport, metabolism		
AN1116.1	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	Transcription		
AN1117.1	Putative cargo transport protein ERV29	U	Intracellular trafficking/secretion/transport	YGR284C	ER
AN1118.1	predicted protein [Neurospora crassa]				
AN1121.1	predicted protein [Neurospora crassa]				
AN1122.1	60S ribosomal protein L10A	J	Translation, ribosomal structure, biogenesis	YPL220W	cytoplasm
AN1126.1	GTP-binding ADP-ribosylation factor Arf1	U	Intracellular trafficking/secretion/transport	YDL137W	late Golgi early Golgi
AN1128.1	predicted protein [Neurospora crassa]				
AN1129.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1131.1	hypothetical protein (related to cytosolic Cu/Zn superoxide dismutase [imported] - Neurospora crassa)				
AN1132.1	Pentafunctional AROM protein	E	Amino acid transport, metabolism		
AN1133.1	N-methyl-D-aspartate receptor glutamate-binding subunit	T	Signal transduction mechanisms	YNL305C	vacuole
AN1134.1	QUINIC ACID UTILIZATION ACTIVATOR				
AN1135.1	3-dehydroquinate dehydratase II	E	Amino acid transport, metabolism		
AN1136.1	Inositol monophosphatase	G	Carbohydrate transport, metabolism	YDR287W	
AN1137.1	Shikimate 5-dehydrogenase	E	Amino acid transport, metabolism		
AN1138.1	Predicted transporter (major facilitator superfamily)	R			
AN1139.1	Predicted dehydrogenases and related proteins	R			
AN1140.1	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport, metabolism		
AN1146.1	Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	P	Inorganic ion transport, metabolism		
AN1148.1	Acid sphingomyelinase and PHM5 phosphate metabolism protein	I	Lipid transport, metabolism	YDR452W	vacuole
AN1150.1	Acetylornithine aminotransferase	E	Amino acid transport, metabolism	YOL140W	mitochondrion
AN1151.1	3-carboxymuconate cyclase	G	Carbohydrate transport, metabolism		
AN1153.1	Spherulin 1A precursor				
AN1155.1	Exo-beta-1,3-glucanase	G	Carbohydrate transport, metabolism	YGR282C	vacuole
AN1156.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN1157.1	Nuclear-export-signal (NES)-containing protein/polyadenylated-RNA export factor	A	RNA processing, modification		
AN1158.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp44/Dis3	J	Translation, ribosomal structure, biogenesis	YDR293C	cytoplasm
AN1162.1	Elongation factor 1 beta/delta chain	K	Transcription	YAL003W	
AN1163.1	Chaperone HSP104 and related ATP-dependent Clp proteases	O	Posttranslational modification/turnover/chaperones	YDR258C	mitochondrion
AN1164.1	Disrupter of silencing SAS10	B	Chromatin structure, dynamics		
AN1165.1	Predicted 3-ketosphinganine reductase	Q		YBR265W	ER
AN1166.1	60s ribosomal protein L6	J	Translation, ribosomal structure, biogenesis	YLR448W	cytoplasm
AN1167.1	Cell membrane glycoprotein	R			
AN1168.1	Voltage-gated Ca2+ channels, alpha1 subunits	PT		YGR217W	cytoplasm
AN1170.1	Proteins containing SET domain	R			
AN1171.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN1175.1	Nucleolar protein NOP52/RRP1	A	RNA processing, modification		
AN1176.1	Sphingosine kinase, involved in sphingolipid metabolism	IT		YOR171C	
AN1177.1	Vesicle coat complex COPI, beta subunit	U	Intracellular trafficking/secretion/transport	YDR238C	Golgi early Golgi
AN1179.1	Vacuolar import and degradation protein	U	Intracellular trafficking/secretion/transport	YBR105C	cytoplasm nucleus
AN1180.1	MAPKKK (MAP kinase kinase kinase) SSK2 and related serine/threonine protein kinases	T	Signal transduction mechanisms		
AN1181.1	Ammonia permease	P	Inorganic ion transport, metabolism	YNL142W	cell periphery
AN1182.1	Beta tubulin	Z	Cytoskeleton	YFL037W	
AN1186.1	Purine-cytosine permease and related proteins	F	Nucleotide transport, metabolism		
AN1187.1	hypothetical protein ((AL451019) conserved hypothetical protein [Neurospora crassa])				
AN1188.1	Transcription elongation factor TAT-SF1	K	Transcription		
AN1189.1	Calcium transporting ATPase	P	Inorganic ion transport, metabolism	YGL006W	vacuolar membrane
AN1190.1	Nuclear pore complex, rNup107 component (sc Nup84)	YU			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1191.1	Ubiquitin-like proteins	O	Posttranslational modification/turnover/chaperones	YDR510W	cytoplasm nucleus
AN1193.1	Succinyl-CoA synthetase, beta subunit	C	Energy production, conversion		
AN1194.1	Adenosine 5'-phosphosulfate kinase	P	Inorganic ion transport, metabolism	YKL001C	cytoplasm
AN1195.1	Vacuolar H+-ATPase V1 sector, subunit C	C	Energy production, conversion	YKL080W	vacuolar membrane
AN1196.1	Uncharacterized conserved protein	S		YBL095W	mitochondrion
AN1198.1	Aminomethyl transferase	E	Amino acid transport, metabolism	YDR019C	mitochondrion
AN1199.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN1200.1	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein	JK		YDR060W	nucleolus
AN1201.1	Prolyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YER087W	
AN1202.1	ADP-ribose pyrophosphatase	F	Nucleotide transport, metabolism		
AN1205.1	Molecular chaperone Prefoldin, subunit 5	O	Posttranslational modification/turnover/chaperones	YML094W	cytoplasm
AN1207.1	Origin recognition complex, subunit 1, and related proteins	L	Replication, recombination, repair		
AN1208.1	Pleiotropic regulator 1	A	RNA processing, modification	YPL151C	cytoplasm nucleus
AN1209.1	26S proteasome regulatory complex, subunit PSMD10	O	Posttranslational modification/turnover/chaperones	YGR232W	cytoplasm nucleus
AN1210.1	Transcription factor TMF, TATA element modulatory factor	K	Transcription	YJR134C	Golgi early Golgi
AN1211.1	Vacuolar H+-ATPase V1 sector, subunit H	C	Energy production, conversion		
AN1212.1					
AN1213.1	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z	Cytoskeleton		
AN1215.1	GTPase	R		YER006W	nucleolus nucleus
AN1216.1	Predicted haloacid-halidohydrolase and related hydrolases	R		YIL053W	cytoplasm nucleus
AN1218.1	Predicted phosphoglycerate mutase	G	Carbohydrate transport, metabolism		
AN1219.1	Vesicle coat complex COPII, subunit SFB3	U	Intracellular trafficking/secretion/transport		
AN1221.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN1222.1	S-adenosylmethionine synthetase	H	Coenzyme transport, metabolism	YDR502C	
AN1226.1	Sirtuin 5 and related class III sirtuins (SIR2 family)	BK			
AN1229.1	SNARE protein GS28	U	Intracellular trafficking/secretion/transport	YHL031C	
AN1230.1	Inner membrane protein required for assembly of the F0 sector of ATP synthase	O	Posttranslational modification/turnover/chaperones	YLR393W	mitochondrion
AN1231.1	DNA polymerase IV (family X)	L	Replication, recombination, repair		
AN1232.1	predicted protein [Neurospora crassa]				
AN1233.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN1235.1	Puf family RNA-binding protein	J	Translation, ribosomal structure, biogenesis		
AN1237.1	DNA repair protein RAD51/RHP55	L	Replication, recombination, repair	YER095W	cytoplasm nucleus
AN1238.1	hypothetical protein [Neurospora crassa]				
AN1239.1	Uncharacterized conserved protein	S			
AN1240.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q			
AN1243.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN1244.1	Uncharacterized conserved protein	S		YKR018C	cytoplasm nucleus
AN1246.1	3-phosphoglycerate kinase	G	Carbohydrate transport, metabolism	YCR012W	cytoplasm nucleus
AN1247.1	Peroxisomal membrane protein MPV17 and related proteins	R		YOR292C	vacuole
AN1248.1	predicted protein [Neurospora crassa]				
AN1249.1	Spliceosomal protein FBP11/Splicing factor PRP40	A	RNA processing, modification	YKL012W	nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1251.1	FOG: Zn-finger	R			
AN1254.1	FOG: Zn-finger	R			
AN1255.1	Chromodomain-helicase DNA-binding protein	K	Transcription	YER164W	nucleus
AN1256.1	RNAse L inhibitor, ABC superfamily	A	RNA processing, modification	YDR091C	cytoplasm
AN1257.1	Glycosyl transferase, family 8 - glycogenin	G	Carbohydrate transport, metabolism		
AN1258.1	predicted protein [Neurospora crassa]				
AN1259.1	Cell cycle control protein (crooked neck)	D	Cell cycle/division, chrom. partitioning	YLR117C	nucleus
AN1260.1	mRNA splicing factor PRP31	A	RNA processing, modification		
AN1261.1	hypothetical protein [Neurospora crassa]				
AN1262.1					
AN1263.1	S-adenosylhomocysteine hydrolase	H	Coenzyme transport, metabolism	YER043C	cytoplasm
AN1264.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1265.1	FOG: Zn-finger	R			
AN1266.1	RNA helicase	A	RNA processing, modification	YBR237W	nucleus
AN1270.1	Translation initiation factor 3, subunit h (eIF-3h)	J	Translation, ribosomal structure, biogenesis		
AN1272.1	Casein kinase II, beta subunit	TDK		YOR039W	cytoplasm nucleus
AN1275.1	Uncharacterized conserved protein	S			
AN1276.1	Predicted transporter (major facilitator superfamily)	R			
AN1280.1	Ribosomal protein S11	J	Translation, ribosomal structure, biogenesis		
AN1281.1	Mitochondrial import inner membrane translocase, subunit TIM44	U	Intracellular trafficking/secretion/transport	YIL022W	mitochondrion
AN1282.1	TPR repeat-containing protein	R		YOR007C	cytoplasm
AN1283.1	WD40 repeat protein	R			
AN1284.1	Predicted GTP-binding protein (ODN superfamily)	R		YBR025C	cytoplasm
AN1286.1	Histone transcription regulator HIRA, WD repeat superfamily	DK		YBL008W	cytoplasm nucleus
AN1287.1	Prohibitins and stomatins of the PID superfamily	C	Energy production, conversion		
AN1288.1	RNA-binding protein LARP/SRO9 and related La domain proteins	OJ			
AN1289.1	Uncharacterized conserved protein	S			
AN1290.1	Predicted K+/H+-antiporter	P	Inorganic ion transport, metabolism	YJL094C	
AN1292.1	Lipid phosphate phosphatase and related enzymes of the PAP2 family	I	Lipid transport, metabolism		
AN1293.1	predicted protein [Neurospora crassa]				
AN1296.1	hypothetical protein [Neurospora crassa]			YJL087C	cytoplasm
AN1297.1	Membrane protein involved in ER to Golgi transport	U	Intracellular trafficking/secretion/transport	YBL102W	early Golgi
AN1299.1	Mitochondrial oxodicarboxylate carrier protein	C	Energy production, conversion		
AN1306.1	Actin regulatory proteins (gelsolin/villin family)	Z	Cytoskeleton		
AN1309.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR			
AN1319.1	60S ribosomal protein 15.5kD/SNU13, NHP2/L7A family (includes ribonuclease P subunit p38), involved in splicing	AJ		YEL026W	
AN1322.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR			
AN1324.1	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	AR			
AN1325.1	Protein interacting with poly(A)-binding protein	A	RNA processing, modification		
AN1326.1	Protein kinase	R			
AN1328.1	Subunit of the major N alpha-acetyltransferase	R		YHR013C	cytoplasm
AN1330.1	Defense-related protein containing SCP domain	S			
AN1331.1	conserved hypothetical protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1333.1	Dynein light chain	N			
AN1334.1	Component of vacuolar transporter chaperone (Vtc) involved in vacuole fusion	UO		YER072W	ER
AN1335.1	G-protein beta subunit-like protein (contains WD40 repeats)	R		YNL006W	
AN1336.1					
AN1337.1	predicted protein [Neurospora crassa]				
AN1339.1	Ubiquitin protein ligase RSP5/NEDD4	O	Posttranslational modification/turnover/chaperones	YER125W	
AN1340.1	Splicing factor RNPS1, SR protein superfamily	A	RNA processing, modification		
AN1341.1	Membrane coat complex Retromer, subunit VPS29/PEP11	U	Intracellular trafficking/secretion/transport		
AN1342.1	Alanine-glyoxylate aminotransferase AGT1	R		YFL030W	
AN1343.1	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K	Transcription		
AN1344.1	Translation initiation factor 2B, beta subunit (eIF-2Bbeta/GCD7)	J	Translation, ribosomal structure, biogenesis	YLR291C	cytoplasm
AN1345.1	40S ribosomal protein S23	J	Translation, ribosomal structure, biogenesis	YPR132W	cytoplasm
AN1346.1	hypothetical protein [Neurospora crassa]				
AN1348.1	Mitochondrial/chloroplast ribosomal protein L17	J	Translation, ribosomal structure, biogenesis	YJL063C	mitochondrion
AN1349.1	mRNA-binding protein Encore	A	RNA processing, modification		
AN1350.1	Uncharacterized conserved protein	S			
AN1352.1	Uncharacterized conserved protein	S		YNL024C-A	
AN1354.1	Uncharacterized conserved protein	S		YIL091C	nucleolus nucleus
AN1355.1	Permease of the drug/metabolite transporter (DMT) superfamily	R		YMR253C	early Golgi
AN1356.1					
AN1357.1	Phosphorylcholine transferase/cholinephosphate cytidylyltransferase	I	Lipid transport, metabolism		
AN1358.1	Serine/threonine protein phosphatase	T	Signal transduction mechanisms	YBL056W	cytoplasm nucleus
AN1359.1	RTX toxins and related Ca2+-binding proteins	Q			
AN1362.1	hypothetical protein [Neurospora crassa]				
AN1363.1	DEAH-box RNA helicase	A	RNA processing, modification		
AN1364.1	Thioredoxin-like protein	O	Posttranslational modification/turnover/chaperones		
AN1366.1	Nuclear AAA ATPase (VCP subfamily)	O	Posttranslational modification/turnover/chaperones	YLL034C	nucleolus nucleus
AN1367.1	WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis	J	Translation, ribosomal structure, biogenesis	YMR049C	nucleolus nucleus
AN1369.1	Uncharacterized conserved protein	S			
AN1370.1	Cell cycle-associated protein Mob1-1	D	Cell cycle/division, chrom. partitioning		
AN1371.1	predicted protein [Neurospora crassa]				
AN1372.1	Integral membrane protease of the rhomboid family involved in different forms of regulated intramembrane proteolysis	T	Signal transduction mechanisms		
AN1374.1	Uncharacterized conserved protein	S			
AN1375.1	predicted protein [Neurospora crassa]				
AN1376.1	Phospholipid methyltransferase	I	Lipid transport, metabolism	YJR073C	vacuole ER
AN1378.1	predicted protein [Neurospora crassa]				
AN1379.1	mRNA export protein (contains WD40 repeats)	A	RNA processing, modification	YER107C	nuclear periphery cytoplasm
AN1380.1	Methionyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YGR264C	cytoplasm
AN1381.1	Uncharacterized conserved protein	S			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1382.1	hypothetical protein [Neurospora crassa]				
AN1383.1	Regulator of ATP-sensitive K+ channels Alpha-endosulfine/ARPP-19 and related cAMP-regulated phosphoproteins	TU			
AN1384.1	Serine carboxypeptidases (lysosomal cathepsin A)	OE			
AN1385.1	WD40 repeat protein	R		YDR267C	cytoplasm
AN1386.1	SOK1 kinase belonging to the STE20/SPS1/GC kinase family	T	Signal transduction mechanisms		
AN1387.1	FOG: WD40 repeat	R		YGL213C	cytoplasm
AN1390.1	Copper chaperone	P	Inorganic ion transport, metabolism	YNL259C	cytoplasm
AN1391.1	predicted protein [Neurospora crassa]				
AN1394.1	Septin CDC10 and related P-loop GTPases	DTZ		YCR002C	cell periphery bud neck
AN1396.1	Glycerol-3-phosphate dehydrogenase	C	Energy production, conversion	YIL155C	mitochondrion
AN1397.1	Cytochrome P450 CYP2 subfamily	Q			
AN1402.1	Acetyltransferase (isoleucine patch superfamily)	R			
AN1403.1	Delta-aminolevulinic acid dehydratase	H	Coenzyme transport, metabolism	YGL040C	cytoplasm nucleus
AN1405.1					
AN1407.1	Uncharacterized conserved protein	S		YHR122W	cytoplasm
AN1408.1	U5 snRNP-specific protein	J	Translation, ribosomal structure, biogenesis		
AN1409.1	Acetyl-CoA acetyltransferase	I	Lipid transport, metabolism	YPL028W	nucleus
AN1413.1	mRNA cleavage and polyadenylation factor II complex, subunit CFT1 (CPSF subunit)	A	RNA processing, modification	YDR301W	nucleus
AN1416.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN1418.1	Glucosamine-6-phosphate isomerase	G	Carbohydrate transport, metabolism		
AN1420.1	Putative Zn-finger protein	R			
AN1421.1	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	Transcription		
AN1423.1	Permease of the major facilitator superfamily	R			
AN1424.1	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z	Cytoskeleton		
AN1426.1	Serine carboxypeptidases (lysosomal cathepsin A)	OE			
AN1427.1	Uncharacterized conserved protein	S			
AN1428.1	N-acetyl-glucosamine-6-phosphate deacetylase	G	Carbohydrate transport, metabolism		
AN1429.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN1430.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion		
AN1432.1	Predicted RNA binding protein, contains G-patch and Zn-finger domains	A	RNA processing, modification		
AN1433.1	Carboxylesterase and related proteins	R			
AN1434.1	Nucleolar protein involved in 40S ribosome biogenesis	J	Translation, ribosomal structure, biogenesis		
AN1436.1	predicted protein [Neurospora crassa]				
AN1437.1	hypothetical protein [Neurospora crassa]				
AN1438.1	hypothetical protein [Neurospora crassa]				
AN1440.1	AAA+-type ATPase containing the bromodomain	O	Posttranslational modification/turnover/chaperones		
AN1442.1	Preprotein translocase subunit Sec66	U	Intracellular trafficking/secretion/transport		
AN1443.1	Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains	T	Signal transduction mechanisms		
AN1444.1	hypothetical protein [Neurospora crassa]				
AN1445.1	Predicted methyltransferase	R		YIL110W	cytoplasm nucleus
AN1446.1	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport, metabolism	YAL012W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1448.1	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	J	Translation, ribosomal structure, biogenesis		
AN1450.1	hypothetical protein [Dictyostelium discoideum]				
AN1451.1					
AN1452.1	FOG: RRM domain	R		YOL041C	nucleolus
AN1454.1	Cytoplasmic dynein intermediate chain	Z	Cytoskeleton		
AN1455.1	Oligosaccharyltransferase, STT3 subunit	O	Posttranslational modification/turnover/chaperones	YGL022W	ER
AN1457.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN1458.1	predicted protein [Neurospora crassa]				
AN1459.1	Dolichyl-phosphate-mannose:protein O-mannosyl transferase	O	Posttranslational modification/turnover/chaperones	YJR143C	ER
AN1460.1	Pirin-related protein	R			
AN1461.1	Protein OS-9	R			
AN1464.1	Uncharacterized conserved protein	S			
AN1467.1	Serine/threonine protein phosphatase	T	Signal transduction mechanisms		
AN1468.1	U4/U6 small nuclear ribonucleoprotein Prp4 (contains WD40 repeats)	A	RNA processing, modification	YPR178W	cytoplasm nucleus
AN1469.1	Mitochondrial J-type chaperone	O	Posttranslational modification/turnover/chaperones	YGL018C	mitochondrion
AN1472.1	Tellurite resistance protein and related permeases	P	Inorganic ion transport, metabolism		
AN1474.1	RNA 3'-terminal phosphate cyclase	A	RNA processing, modification	YOL010W	nucleolus nucleus
AN1475.1	Cytoskeleton-associated protein and related proteins	ZR			
AN1476.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN1477.1	xylosidase [Penicillium herquei]				
AN1478.1	RNA helicase BRR2, DEAD-box superfamily	A	RNA processing, modification	YER172C	cytoplasm nucleus
AN1480.1	hypothetical protein [Neurospora crassa]			YIR032C	
AN1481.1	Predicted transporter (major facilitator superfamily)	R			
AN1482.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN1483.1	hypothetical protein [Neurospora crassa]				
AN1484.1	Valyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YGR094W	cytoplasm
AN1485.1	Casein kinase II, alpha subunit	TDK		YOR061W	cytoplasm nucleus
AN1486.1	Protein subunit of nuclear ribonuclease P (RNase P)	J	Translation, ribosomal structure, biogenesis		
AN1487.1	predicted protein [Neurospora crassa]				
AN1488.1	E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN1489.1	predicted protein [Neurospora crassa]				
AN1491.1	COP9 signalosome, subunit CSN1	OT			
AN1493.1	predicted protein [Neurospora crassa]				
AN1494.1	TATA binding protein associated factor	K	Transcription		
AN1498.1	ATP adenylyltransferase (5',5'''-P-1,P-4-tetraphosphate phosphorylase II)	F	Nucleotide transport, metabolism	YDR530C	cytoplasm nucleus
AN1500.1	FOG: Zn-finger	R			
AN1502.1	Beta-N-acetylhexosaminidase	G	Carbohydrate transport, metabolism		
AN1503.1	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	EM			
AN1504.1	WASP-interacting protein VRP1/WIP, contains WH2 domain	Z	Cytoskeleton		
AN1506.1	Fucose permease	G	Carbohydrate transport, metabolism		
AN1507.1	predicted protein [Neurospora crassa]				
AN1509.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1510.1	Endoplasmic reticulum membrane-associated oxidoreductin involved in disulfide bond formation	OU		YML130C	
AN1511.1	Peroxisomal biogenesis protein peroxin	U	Intracellular trafficking/secretion/transport		
AN1512.1	Amidases	JIT			
AN1513.1	Cysteine synthase	E	Amino acid transport, metabolism	YGR012W	mitochondrion
AN1516.1	Thiamine pyrophosphate-requiring enzyme	EH			
AN1519.1	Translation initiation factor 2C (eIF-2C) and related proteins	J	Translation, ribosomal structure, biogenesis		
AN1520.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN1521.1	DNA-directed RNA polymerase subunit E'	K	Transcription	YDR404C	nucleus
AN1522.1	Predicted membrane protein	S		YGL010W	ER
AN1523.1	F0F1-type ATP synthase, alpha subunit	C	Energy production, conversion	YBL099W	mitochondrion
AN1524.1	Methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase	H	Coenzyme transport, metabolism	YKR080W	cytoplasm nucleus
AN1525.1	predicted protein [Neurospora crassa]			YML055W	ER
AN1526.1	Uncharacterized conserved protein	S		YKL207W	
AN1527.1	predicted protein [Neurospora crassa]				
AN1528.1	DNA repair/transcription protein Mms19	LK			
AN1532.1					
AN1533.1	Predicted nucleolar protein involved in ribosome biogenesis	J	Translation, ribosomal structure, biogenesis	YPR144C	nucleus
AN1534.1	Mitochondrial F1F0-ATP synthase, subunit b/ATP4	C	Energy production, conversion	YPL078C	mitochondrion
AN1535.1	FOG: TPR repeat, SEL1 subfamily	R			
AN1536.1	Chromosome segregation ATPases	D	Cell cycle/division, chrom. partitioning		
AN1537.1	C3H1-type Zn-finger protein	R			
AN1538.1	Transcription initiation factor IIF, small subunit (RAP30)	K	Transcription	YGR005C	
AN1539.1	COP9 signalosome, subunit CSN4	OT			
AN1540.1	predicted protein [Neurospora crassa]				
AN1541.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion		
AN1543.1	Fumarate reductase, flavoprotein subunit	C	Energy production, conversion	YJR051W	mitochondrion
AN1544.1					
AN1545.1	Serine/threonine protein phosphatase 2A, regulatory subunit	T	Signal transduction mechanisms	YGL190C	cytoplasm
AN1546.1	Histone deacetylase complex, SIN3 component	B	Chromatin structure, dynamics		
AN1547.1	Acetyl-CoA hydrolase	C	Energy production, conversion	YBL015W	mitochondrion
AN1548.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1549.1					
AN1551.1	von Willebrand factor and related coagulation proteins	WV			
AN1554.1	Extracellular protein SEL-1 and related proteins	MOT			
AN1555.1	Chitin synthase/hyaluronan synthase (glycosyltransferases)	M		YBR023C	late Golgi
AN1556.1	FOG: WD40 repeat	R			
AN1558.1	Myosin class I heavy chain	Z	Cytoskeleton	YMR109W	actin
AN1559.1	Predicted coiled-coil protein	R			
AN1560.1	Polo-like serine/threonine protein kinase	D	Cell cycle/division, chrom. partitioning		
AN1562.1	predicted protein [Neurospora crassa]				
AN1563.1	Phosphoglycerate dehydrogenase and related dehydrogenases	HE			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1564.1	DNA mismatch repair protein - MLH2/PMS1/Pms2 family	L	Replication, recombination, repair		
AN1565.1	DHHC-type Zn-finger protein	R		YOL003C	
AN1570.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	C	Energy production, conversion		
AN1571.1	alpha-L-arabinofuranosidase [Emericella nidulans]				
AN1572.1	Tri7 [Fusarium sporotrichioides]				
AN1586.1	Copper amine oxidase	Q			
AN1602.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN1604.1	hypothetical protein (related to mutanase (mutA) gene [imported] - Neurospora crassa)				
AN1607.1	UDP-glucuronosyl and UDP-glucosyl transferase	GC			
AN1610.1					
AN1613.1					
AN1614.1	SAM-dependent methyltransferases	IR			
AN1624.1	Mitochondrial F1F0-ATP synthase, subunit c/ATP9/proteolipid	C	Energy production, conversion		
AN1628.1	Ca2+ transporting ATPase	P	Inorganic ion transport, metabolism		
AN1629.1	GTPase-activating protein that regulates ARFs (ADP-ribosylation factors), involved in ARF-mediated vesicular transport	U	Intracellular trafficking/secretion/transport		
AN1630.1	Catalase (peroxidase I)	P	Inorganic ion transport, metabolism		
AN1631.1	Amino acid transporters	E	Amino acid transport, metabolism	YGR055W	vacuole
AN1632.1	Serine/threonine-protein kinase involved in autophagy	OUT			
AN1633.1	predicted protein [Neurospora crassa]				
AN1634.1	U5 snRNP-like RNA helicase subunit	A	RNA processing, modification	YDR243C	cytoplasm nucleus
AN1635.1	mRNA processing protein	A	RNA processing, modification	YML046W	nucleus
AN1636.1	hypothetical protein [Neurospora crassa]				
AN1637.1	Molybdenum cofactor sulfurase	H	Coenzyme transport, metabolism		
AN1638.1	Puromycin-sensitive aminopeptidase and related aminopeptidases	EO		YKL157W	mitochondrion cytoplasm
AN1639.1	Thioredoxin-like protein	O	Posttranslational modification/turnover/chaperones		
AN1652.1	FOG: Zn-finger	R			
AN1660.1	FOG: Immunoglobin and related proteins	RP			
AN1661.1	Signaling protein RIC-8/synembryn (regulates neurotransmitter secretion)	T	Signal transduction mechanisms		
AN1662.1	Uncharacterized conserved protein	S		YPL225W	cytoplasm
AN1665.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	Signal transduction mechanisms	YJL057C	
AN1666.1	Nucleolar GTPase	R		YNR053C	nucleus
AN1667.1	predicted protein [Neurospora crassa]				
AN1668.1	Predicted E3 ubiquitin ligase containing RING finger, subunit of transcription/repair factor TFIIH and CDK-activating kinase assembly factor	O	Posttranslational modification/turnover/chaperones	YDR460W	nucleus
AN1669.1	FOG: Immunoglobin and related proteins	RP			
AN1673.1	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	E	Amino acid transport, metabolism		
AN1675.1	Lysophospholipase	I	Lipid transport, metabolism	YMR008C	
AN1677.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1681.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1683.1	Oligosaccharyltransferase, delta subunit (ribophorin II)	O	Posttranslational modification/turnover/chaperones	YMR149W	ER
AN1684.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN1685.1	Multiple inositol polyphosphate phosphatase	R			
AN1686.1	RNA polymerase II, large subunit	K	Transcription		
AN1688.1	Gluconolactonase	G	Carbohydrate transport, metabolism	YBR053C	
AN1689.1	Aldehyde dehydrogenase	C	Energy production, conversion		
AN1690.1	Uncharacterized conserved protein	S			
AN1692.1	Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes	O	Posttranslational modification/turnover/chaperones		
AN1693.1					
AN1694.1	Predicted nucleotidyltransferase	R			
AN1695.1	Conserved WD40 repeat-containing protein AN11	S		YPL247C	cytoplasm nucleus
AN1696.1	Predicted acyltransferases	I	Lipid transport, metabolism		
AN1697.1	Splicing coactivator SRm160/300, subunit SRm160 (contains PWI domain)	AR			
AN1698.1	RNA polymerase II transcription elongation factor DSIF/SUPT5H/SPT5	K	Transcription	YML010W	nucleus
AN1699.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN1700.1	26S proteasome regulatory complex, subunit RPN2/PSMD1	O	Posttranslational modification/turnover/chaperones	YIL075C	cytoplasm nucleus
AN1701.1	Uncharacterized protein conserved in bacteria	S			
AN1704.1	Beta, beta-carotene 15,15'-dioxygenase and related enzymes	Q			
AN1706.1	Glutaminyl cyclase	O	Posttranslational modification/turnover/chaperones	YFR018C	
AN1708.1	Mismatch repair ATPase MSH6 (MutS family)	L	Replication, recombination, repair	YDR097C	nucleus
AN1709.1	Tyrosyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis		
AN1710.1	Aspartyl-tRNA synthetase, mitochondrial	J	Translation, ribosomal structure, biogenesis	YPL104W	mitochondrion
AN1711.1	NMD protein affecting ribosome stability and mRNA decay	J	Translation, ribosomal structure, biogenesis	YHR170W	cytoplasm
AN1712.1	predicted protein [Neurospora crassa]				
AN1713.1	Predicted esterase of the alpha-beta hydrolase superfamily	R		YOR081C	lipid particle
AN1715.1	Mannose-6-phosphate isomerase	G	Carbohydrate transport, metabolism		
AN1719.1	predicted protein [Neurospora crassa]				
AN1720.1	predicted protein [Neurospora crassa]				
AN1721.1	Predicted endoplasmic reticulum membrane protein Lec35/MPDU1 involved in monosaccharide-P-dolichol utilization	R			
AN1722.1	Heme A farnesyltransferase	H	Coenzyme transport, metabolism	YPL172C	mitochondrion
AN1726.1	Branched chain alpha-keto acid dehydrogenase complex, alpha subunit	C	Energy production, conversion		
AN1728.1	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit	C	Energy production, conversion		
AN1729.1	PrnA protein [Emericella nidulans]				
AN1731.1	Proline oxidase	E	Amino acid transport, metabolism		
AN1733.1	Delta-1-pyrroline-5-carboxylate dehydrogenase	E	Amino acid transport, metabolism	YHR037W	mitochondrion
AN1734.1	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport, metabolism		
AN1735.1	Methylthioadenosine phosphorylase MTAP	F	Nucleotide transport, metabolism		
AN1742.1	Predicted beta-mannosidase	G	Carbohydrate transport, metabolism		
AN1743.1	Ubiquinone biosynthesis methyltransferase COQ5	H	Coenzyme transport, metabolism	YML110C	mitochondrion

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1744.1	Predicted sugar phosphate isomerase involved in capsule formation	M			
AN1745.1	Nicotinic acid mononucleotide adenylyltransferase	H	Coenzyme transport, metabolism	YGR010W	cytoplasm nucleus
AN1747.1	Uncharacterized conserved protein	S			
AN1748.1	Cytochrome P450	Q			
AN1750.1	RNA helicase	A	RNA processing, modification	YBR142W	nucleolus nucleus
AN1751.1	SAM-dependent methyltransferase/cell division protein FtsJ	DR		YBR061C	cytoplasm
AN1752.1	NADP/FAD dependent oxidoreductase	C	Energy production, conversion	YFR030W	cytoplasm
AN1753.1	Serine/threonine kinase TIP30/CC3	T	Signal transduction mechanisms	YER004W	ER
AN1757.1	20S proteasome, regulatory subunit alpha type PSMA4/PRE9	O	Posttranslational modification/turnover/chaperones	YGR135W	cytoplasm nucleus
AN1758.1	Transcription factor CA150	K	Transcription		
AN1761.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YEL012W	cytoplasm nucleus
AN1763.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1766.1	Predicted transporter (major facilitator superfamily)	R			
AN1767.1	Halotolerance protein HAL3 (contains flavoprotein domain)	PD			
AN1768.1	Cytosolic sorting protein GGA2/TOM1	U	Intracellular trafficking/secretion/transport		
AN1769.1	Salt-sensitive 3'-phosphoadenosine-5'-phosphatase HAL2/SAL1	FP		YOL064C	cytoplasm nucleus
AN1770.1	Mitochondrial/chloroplast ribosomal protein L6	J	Translation, ribosomal structure, biogenesis	YHR147C	cell periphery
AN1772.1	Feruloyl esterase B precursor (Ferulic acid esterase B) (FAEB) (FAE-I) (Cinnamoyl esterase) (CinnAE)				
AN1773.1	Predicted RNA-binding protein	R			
AN1775.1	GPI transamidase complex, GPI16/PIG-T component, involved in glycosylphosphatidylinositol anchor biosynthesis	MO		YHR188C	
AN1776.1	Spliceosome subunit	A	RNA processing, modification	YDL087C	nucleus
AN1777.1	Predicted transcription factor DATF1, contains PHD and TFS2M domains	K	Transcription		
AN1778.1	Ketopantoate hydroxymethyltransferase	H	Coenzyme transport, metabolism	YBR176W	mitochondrion
AN1779.1	Protein kinase essential for the initiation of DNA replication	LD			
AN1780.1	Putative Xaa-Pro aminopeptidase	E	Amino acid transport, metabolism	YER078C	mitochondrion
AN1781.1	Predicted flavin-nucleotide-binding protein	R			
AN1782.1	Sirtuin 5 and related class III sirtuins (SIR2 family)	BK			
AN1783.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1784.1	Polyketide synthase modules and related proteins	Q			
AN1795.1	Zn2+ transporter ZNT1 and related Cd2+/Zn2+ transporters (cation diffusion facilitator superfamily)	P	Inorganic ion transport, metabolism		
AN1796.1	Cell division control protein/predicted DNA repair exonuclease	L	Replication, recombination, repair	YDR182W	
AN1797.1	Predicted transporter (major facilitator superfamily)	R		YDL138W	
AN1798.1	Triglyceride lipase-cholesterol esterase	I	Lipid transport, metabolism	YLR020C	
AN1799.1	secretory lipase 5; Lip5; LIP [Candida albicans]				
AN1800.1	Signal transduction histidine kinase	T	Signal transduction mechanisms	YIL147C	cell periphery
AN1801.1	hypothetical serine-rich secreted protein [Schizosaccharomyces pombe]				
AN1808.1	Monoamine oxidase	E	Amino acid transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1810.1	Ornithine aminotransferase	E	Amino acid transport, metabolism	YLR438W	cytoplasm nucleus
AN1811.1	GPI-alpha-mannosyltransferase III (GPI10/PIG-B) involved in glycosylphosphatidylinositol anchor biosynthesis	MO		YGL142C	
AN1812.1	JUN-like bZIP transcription factor [Emericella nidulans]				
AN1817.1					
AN1818.1	Beta-1,4-xylanase	G	Carbohydrate transport, metabolism		
AN1820.1	hypothetical protein [Neurospora crassa]				
AN1822.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1824.1	predicted protein [Neurospora crassa]				
AN1826.1	Zn-dependent hydrolases, including glyoxylases	R			
AN1827.1	Chitinase	G	Carbohydrate transport, metabolism		
AN1828.1	predicted protein [Neurospora crassa]				
AN1830.1	Predicted transporter (major facilitator superfamily)	R			
AN1831.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1832.1	ANTIGEN 1 PRECURSOR (ASPND1)			YOL154W	vacuole
AN1833.1	Fe2+/Zn2+ regulated transporter	P	Inorganic ion transport, metabolism		
AN1835.1	hypothetical protein ((AL451019) conserved hypothetical protein [Neurospora crassa])				
AN1836.1	predicted protein [Neurospora crassa]				
AN1843.1	Protein involved in meiotic recombination/predicted coiled-coil protein	DR		YGL183C	
AN1844.1	palFp [Emericella nidulans]			YGL045W	
AN1845.1	hypothetical protein [Neurospora crassa]				
AN1846.1					
AN1847.1					
AN1848.1	TRANSCRIPTIONAL REGULATORY PROTEIN PRO1 [Neurospora crassa]				
AN1850.1	Peptidase family M48	O	Posttranslational modification/turnover/chaperones	YKR087C	mitochondrion
AN1851.1	Chaperonin complex component, TCP-1 theta subunit (CCT8)	O	Posttranslational modification/turnover/chaperones	YJL008C	
AN1854.1	hypothetical protein [Schizosaccharomyces pombe]				
AN1855.1	hypothetical protein [Neurospora crassa]				
AN1857.1	L-kynurenine hydrolase	E	Amino acid transport, metabolism	YLR231C	cytoplasm nucleus
AN1858.1	hypothetical protein [Neurospora crassa]				
AN1859.1	Transcription initiation factor IIF, auxiliary subunit	K	Transcription	YNL107W	cytoplasm nucleus
AN1860.1	Predicted oxidoreductase	R		YLR290C	mitochondrion
AN1865.1	Predicted transporter (major facilitator superfamily)	R			
AN1868.1	Alcohol dehydrogenase, class IV	C	Energy production, conversion		
AN1870.1	arabinan endo-1,5-alpha-L-arabinosidase A precursor [Bacteroides thetaiotaomicron VPI-5482]				
AN1871.1	predicted protein [Neurospora crassa]				
AN1873.1	Predicted phosphoglycerate mutase	G	Carbohydrate transport, metabolism		
AN1874.1	E3 ubiquitin protein ligase	O	Posttranslational modification/turnover/chaperones		
AN1875.1	C2H2-type Zn-finger protein	R		YBR267W	cytoplasm
AN1876.1	Predicted membrane protein, contains two CBS domains	S		YOL060C	vacuolar membrane
AN1878.1	Predicted membrane protein	S			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1880.1	predicted protein [Neurospora crassa]				
AN1881.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN1882.1	NADH:flavin oxidoreductase/12-oxophytodienoate reductase	CR			
AN1883.1	Argininosuccinate synthase	E	Amino acid transport, metabolism	YOL058W	cytoplasm
AN1884.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN1892.1	Mitochondrial import inner membrane translocase, subunit TIM17	U	Intracellular trafficking/secretion/transport	YJL143W	cytoplasm nucleus
AN1893.1	hypothetical protein [Neurospora crassa]				
AN1895.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones		
AN1896.1	Fumarylacetoacetase	G	Carbohydrate transport, metabolism		
AN1897.1	Homogentisate 1,2-dioxygenase	E	Amino acid transport, metabolism		
AN1900.1	Zn-finger protein	R			
AN1901.1	Cytochrome P450	Q		YHR007C	ER
AN1902.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN1904.1	Chaperonin complex component, TCP-1 epsilon subunit (CCT5)	O	Posttranslational modification/turnover/chaperones	YJR064W	
AN1905.1	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B	Chromatin structure, dynamics		
AN1907.1	DHHC-type Zn-finger proteins	R			
AN1908.1	Uncharacterized conserved protein	S			
AN1909.1	FOG: Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN1910.1					
AN1911.1	GDP-mannose pyrophosphorylase	GMO			
AN1912.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR			
AN1913.1	Lysyl-tRNA synthetase (class II)	J	Translation, ribosomal structure, biogenesis	YDR037W	
AN1915.1	Cytochrome oxidase assembly factor COX15	O	Posttranslational modification/turnover/chaperones	YER141W	mitochondrion
AN1916.1	mRNA cap methyltransferase	A	RNA processing, modification		
AN1917.1	Mitochondrial oxoglutarate/malate carrier proteins	C	Energy production, conversion		
AN1918.1	Phosphoenolpyruvate carboxykinase (ATP)	C	Energy production, conversion	YKR097W	
AN1920.1	Na+/H+ antiporter	P	Inorganic ion transport, metabolism		
AN1921.1	Peroxisomal biogenesis protein (peroxin)	U	Intracellular trafficking/secretion/transport	YOL147C	peroxisome
AN1922.1	26S proteasome regulatory complex, subunit RPN7/PSMD6	O	Posttranslational modification/turnover/chaperones	YPR108W	nucleus
AN1923.1	Alanine aminotransferase	E	Amino acid transport, metabolism	YLR089C	
AN1924.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN1927.1	hypothetical protein [Neurospora crassa]				
AN1929.1	hypothetical protein [Neurospora crassa]				
AN1931.1	Predicted GTPase-activating protein	T	Signal transduction mechanisms		
AN1933.1	Predicted membrane protein	S		YGR038W	ER
AN1934.1	predicted protein [Neurospora crassa]				
AN1937.1	REGULATORY PROTEIN WETA				
AN1938.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN1940.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN1945.1	Predicted phosphatases	R		YOR131C	cytoplasm nucleus
AN1947.1	hypothetical protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1948.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN1949.1	ATP-dependent RNA helicase pitchoune	A	RNA processing, modification	YMR290C	
AN1950.1	conserved hypothetical protein [Neurospora crassa]			YAL053W	cell periphery bud neck late Golgi bud
AN1952.1	hypothetical protein ((AL513411) putative protein [Neurospora crassa])				
AN1953.1	Actin and related proteins	Z	Cytoskeleton		
AN1954.1	Mitochondrial ribosomal protein S28	J	Translation, ribosomal structure, biogenesis		
AN1955.1					
AN1956.1	Predicted helicase	R			
AN1957.1	RNA Methylase, SpoU family	A	RNA processing, modification		
AN1959.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN1961.1	Uncharacterized protein of the uridine kinase family	F	Nucleotide transport, metabolism		
AN1962.1	HMG-box transcription factor	K	Transcription		
AN1963.1					
AN1964.1	40S ribosomal protein S6	J	Translation, ribosomal structure, biogenesis	YPL090C	cytoplasm
AN1965.1	Ribose-phosphate pyrophosphokinase	FE		YER099C	cytoplasm
AN1967.1	Peroxidase/oxygenase	R			
AN1968.1	Steroid reductase required for elongation of the very long chain fatty acids	I	Lipid transport, metabolism	YDL015C	ER
AN1969.1	Subunit of Golgi mannosyltransferase complex	GM			
AN1970.1	Mitochondrial/chloroplast ribosomal protein L28	J	Translation, ribosomal structure, biogenesis		
AN1971.1	DNA helicase, TBP-interacting protein	L	Replication, recombination, repair	YDR190C	nucleus
AN1973.1	V-SNARE	U	Intracellular trafficking/secretion/transport	YMR197C	
AN1974.1	Fe-S cluster biosynthesis protein ISA1 (contains a HesB-like domain)	P	Inorganic ion transport, metabolism		
AN1975.1	Uncharacterized conserved protein	S			
AN1976.1	Dosage compensation regulatory complex/histone acetyltransferase complex, subunit MSL-3/MRG15/EAF3, and related CHROMO domain-containing proteins	BK		YPR023C	nucleus
AN1980.1	Rab6 GTPase activator GAPCenA and related TBC domain proteins	R			
AN1981.1	Protein geranylgeranyltransferase type II, alpha subunit	O	Posttranslational modification/turnover/chaperones	YJL031C	
AN1982.1	Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	DO			
AN1983.1	WD40 repeat-containing protein	R			
AN1984.1	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K	Transcription	YLR399C	nucleus
AN1986.1	Mitochondrial matrix protein frataxin, involved in Fe/S protein biosynthesis	P	Inorganic ion transport, metabolism		
AN1987.1	hypothetical protein [Neurospora crassa]				
AN1988.1	Exocyst complex subunit SEC6	U	Intracellular trafficking/secretion/transport	YIL068C	cell periphery bud neck bud
AN1989.1	Glutamate decarboxylase/sphingosine phosphate lyase	E	Amino acid transport, metabolism	YDR294C	ER
AN1990.1	Alpha-isopropylmalate synthase/homocitrate synthase	E	Amino acid transport, metabolism	YDL131W	nucleus
AN1991.1	Uncharacterized conserved protein	S			
AN1992.1	U4/U6.U5 snRNP associated protein	A	RNA processing, modification		
AN1993.1	Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT1/GOT2	E	Amino acid transport, metabolism		
AN1995.1	Spindle pole body protein	Z	Cytoskeleton		
AN1996.1	Uncharacterized conserved protein	S		YDL001W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN1997.1	FOG: Zn-finger	R			
AN1999.1	Methyltransferases	H	Coenzyme transport, metabolism	YOL096C	mitochondrion
AN2000.1	Ubiquitin and ubiquitin-like proteins	OR		YLL039C	cytoplasm nucleus
AN2001.1	predicted protein [Neurospora crassa]				
AN2002.1	Beta subunit of farnesyltransferase	O	Posttranslational modification/turnover/chaperones	YDL090C	cytoplasm
AN2003.1	Uncharacterized conserved protein	R			
AN2004.1					
AN2005.1	Two-component phosphorelay intermediate involved in MAP kinase cascade regulation	T	Signal transduction mechanisms		
AN2006.1	predicted protein [Neurospora crassa]				
AN2007.1	Small nuclear ribonucleoprotein Sm D3	A	RNA processing, modification	YLR147C	
AN2008.1	Predicted hydrolase (HAD superfamily)	R		YHR100C	
AN2009.1	Transcription factor PRD and related proteins, contain PAX and HOX domains	K	Transcription		
AN2011.1	P-type ATPase	R		YMR162C	cytoplasm
AN2013.1	Predicted dehydrogenases and related proteins	R			
AN2014.1	Signal recognition particle, subunit Srp72	U	Intracellular trafficking/secretion/transport	YPL210C	ER
AN2015.1	Galactosyltransferases	G	Carbohydrate transport, metabolism		
AN2016.1	amyR [Emericella nidulans]				
AN2017.1	Maltase glucoamylase and related hydrolases, glycosyl hydrolase family 31	G	Carbohydrate transport, metabolism		
AN2026.1	predicted protein [Neurospora crassa]				
AN2037.1	CipA protein [Emericella nidulans]				
AN2042.1	NADP/FAD dependent oxidoreductase	C	Energy production, conversion		
AN2043.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN2044.1	hypothetical protein [Neurospora crassa]				
AN2045.1	1, 2-alpha-mannosidase	G	Carbohydrate transport, metabolism		
AN2046.1					
AN2047.1	Calmodulin and related proteins (EF-Hand superfamily)	T	Signal transduction mechanisms	YBR109C	cell periphery bud neck bud
AN2048.1	SNARE protein TLG2/Syntaxin 16	U	Intracellular trafficking/secretion/transport	YOL018C	
AN2049.1	Regulator of nuclear mRNA	A	RNA processing, modification		
AN2050.1	Vesicle coat protein clathrin, light chain	U	Intracellular trafficking/secretion/transport	YGR167W	late Golgi
AN2051.1	Cell division cycle 37 protein, CDC37	D	Cell cycle/division, chrom. partitioning	YDR168W	cytoplasm
AN2053.1	Nucleoside transporter	F	Nucleotide transport, metabolism	YAL022C	
AN2054.1	Serine/threonine kinase (haspin family)	D	Cell cycle/division, chrom. partitioning		
AN2055.1	hypothetical protein [Neurospora crassa]				
AN2056.1	Uncharacterized conserved protein	S		YNR021W	ER
AN2057.1	Mitochondrial/chloroplast ribosomal protein L12	J	Translation, ribosomal structure, biogenesis	YGL068W	mitochondrion
AN2058.1					
AN2059.1	hypothetical protein [Neurospora crassa]				
AN2060.1	exo-arabinanase [Penicillium chrysogenum]				
AN2061.1	Alcohol dehydrogenase, class V	Q			
AN2062.1	Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones	YJL034W	
AN2064.1	Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes	Q			
AN2065.1	PAB-dependent poly(A) ribonuclease, subunit PAN2	L	Replication, recombination, repair	YGL094C	cytoplasm
AN2068.1	Vigilin	I	Lipid transport, metabolism	YJL080C	ER
AN2069.1	Cytochrome b5	C	Energy production, conversion		
AN2070.1	PHD finger protein AF10	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2072.1	Ubiquitin C-terminal hydrolase	O	Posttranslational modification/turnover/chaperones	YER144C	
AN2073.1	Uncharacterized conserved protein, contains ankyrin and BTB/POZ domains	S			
AN2076.1	Phosphoprotein involved in cytoplasm to vacuole targeting and autophagy	U	Intracellular trafficking/secretion/transport		
AN2077.1	WD40 repeat protein	R		YGR145W	
AN2078.1	Thyroid hormone receptor-associated protein complex, subunit TRAP240	K	Transcription		
AN2080.1	Polypeptide release factor 3	J	Translation, ribosomal structure, biogenesis	YDR172W	cytoplasm
AN2081.1	hypothetical protein B23I11.70 [imported] - Neurospora crassa				
AN2082.1	Uncharacterized conserved protein, contains BSD domain	S			
AN2083.1	FOG: Low-complexity	S			
AN2085.1	20S proteasome, regulatory subunit beta type PSMB7/PSMB10/PUP1	O	Posttranslational modification/turnover/chaperones	YOR157C	cytoplasm nucleus
AN2086.1	Nuclear pore complex, Nup214/CAN component	YU			
AN2087.1	ATP-dependent DNA helicase	L	Replication, recombination, repair		
AN2088.1	Uncharacterized conserved protein	S			
AN2089.1	PolyC-binding proteins alphaCP-1 and related KH domain proteins	AR			
AN2090.1	Protein containing repeated kelch motifs	R		YPL263C	cytoplasm
AN2092.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN2094.1	Dopey and related predicted leucine zipper transcription factors	K	Transcription	YDR141C	early Golgi
AN2096.1	Acyltransferase required for palmitoylation of Hedgehog (Hh) family of secreted signaling proteins	T	Signal transduction mechanisms	YGL084C	ER
AN2099.1	mitochondrial alternative oxidase [Emericella nidulans]				
AN2101.1	RNA polymerase II, large subunit	K	Transcription		
AN2103.1	Uncharacterized conserved protein	S			
AN2104.1	Predicted N6-DNA-methyltransferase	J	Translation, ribosomal structure, biogenesis	YDR140W	cytoplasm nucleus
AN2105.1	Small nuclear ribonucleoprotein SMD1 and related snRNPs	A	RNA processing, modification	YGR074W	nucleus
AN2107.1	Predicted translation elongation factor	J	Translation, ribosomal structure, biogenesis		
AN2109.1	Anaphase-promoting complex (APC), subunit 2	DO			
AN2110.1	predicted protein [Neurospora crassa]				
AN2111.1	Predicted glutamine synthetase	F	Nucleotide transport, metabolism		
AN2112.1	3-carboxymuconate cyclase	G	Carbohydrate transport, metabolism		
AN2114.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN2115.1					
AN2119.1	Cholesterol transport protein (Niemann-Pick C disease protein)	I	Lipid transport, metabolism	YPL006W	vacuolar membrane
AN2120.1	Karyopherin (importin) beta 3	YU		YER110C	cytoplasm nucleus
AN2122.1	predicted protein [Neurospora crassa]				
AN2123.1	Transcriptional coactivator	K	Transcription	YOL135C	nucleus
AN2124.1	Lipid phosphate phosphatase and related enzymes of the PAP2 family	I	Lipid transport, metabolism	YDR284C	vacuolar membrane
AN2126.1	F-actin capping protein, alpha subunit	Z	Cytoskeleton	YKL007W	actin
AN2129.1	COP9 signalosome, subunit CSN5	OT			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2130.1	Ras1 guanine nucleotide exchange factor	T	Signal transduction mechanisms		
AN2132.1	predicted protein [Neurospora crassa]				
AN2133.1	Armadillo/beta-Catenin/plakoglobin	TZ			
AN2135.1	DNA-directed RNA polymerase III subunit	K	Transcription		
AN2136.1	hypothetical protein [Neurospora crassa]				
AN2137.1	Cyclin B and related kinase-activating proteins	D	Cell cycle/division, chrom. partitioning		
AN2138.1	ATP-dependent RNA helicase A	A	RNA processing, modification	YLR419W	cytoplasm
AN2139.1	Predicted hydrolase (HIT family)	R		YOR258W	cytoplasm nucleus
AN2140.1	Translocon-associated complex TRAP, alpha subunit	U	Intracellular trafficking/secretion/transport		
AN2141.1	Predicted telomere binding protein	R			
AN2142.1	Karyopherin (importin) alpha	U	Intracellular trafficking/secretion/transport	YNL189W	nuclear periphery cytoplasm
AN2143.1	Cohesin	D	Cell cycle/division, chrom. partitioning		
AN2144.1	Urease accessory protein UreH	O	Posttranslational modification/turnover/chaperones		
AN2145.1	Hypothetical ORF; Ydl237wp [Saccharomyces cerevisiae]				
AN2146.1	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	Transcription		
AN2147.1	rRNA processing protein Rrp5	A	RNA processing, modification	YMR229C	nucleolus
AN2148.1	WD40 repeat-containing protein L2DTL	S			
AN2149.1	Chaperonin complex component, TCP-1 alpha subunit (CCT1)	O	Posttranslational modification/turnover/chaperones	YDR212W	
AN2150.1	Prolyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YHR020W	
AN2151.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN2153.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	J	Translation, ribosomal structure, biogenesis		
AN2154.1	hypothetical protein [Neurospora crassa]			YGR157W	ER
AN2155.1	Predicted ATPase, nucleotide-binding	D	Cell cycle/division, chrom. partitioning	YGL091C	cytoplasm nucleus
AN2157.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones		
AN2158.1	Threonine dehydrogenase and related Zn-dependent dehydrogenases	ER			
AN2161.1	predicted protein [Neurospora crassa]			YGR111W	cytoplasm nucleus
AN2162.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN2163.1	Mitotic spindle checkpoint protein	D	Cell cycle/division, chrom. partitioning		
AN2164.1	Predicted importin 9	UY			
AN2165.1	Trans-aconitate methyltransferase	R			
AN2166.1	predicted protein [Neurospora crassa]				
AN2167.1	Annexin	U	Intracellular trafficking/secretion/transport		
AN2168.1	TNF receptor-associated factor	T	Signal transduction mechanisms		
AN2169.1	SNARE protein TLG1/Syntaxin 6	U	Intracellular trafficking/secretion/transport		
AN2172.1	CDK8 kinase-activating protein cyclin C	K	Transcription	YNL025C	nucleus
AN2173.1	Predicted mitochondrial carrier protein	F	Nucleotide transport, metabolism	YNL083W	mitochondrion
AN2174.1	Ubiquitin activating enzyme UBA1	O	Posttranslational modification/turnover/chaperones	YKL210W	cytoplasm nucleus
AN2176.1	predicted protein [Neurospora crassa]				
AN2177.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN2178.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN2179.1	FOG: Ankyrin repeat	R			
AN2180.1	Hexokinase	G	Carbohydrate transport, metabolism		
AN2181.1	Transcription initiation factor IIA, gamma subunit	K	Transcription	YKL058W	nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2182.1	predicted protein [Neurospora crassa]				
AN2183.1					
AN2184.1	Uncharacterized conserved protein	S			
AN2185.1	Mitochondrial endonuclease	F	Nucleotide transport, metabolism	YJL208C	mitochondrion
AN2188.1					
AN2190.1	Predicted methyltransferase	R			
AN2193.1					
AN2201.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN2208.1	Predicted dehydrogenases and related proteins	R			
AN2210.1	Predicted transporter (ABC superfamily)	R		YER036C	cytoplasm
AN2211.1	Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, cyclin H subunit	DKL		YPR025C	nucleus
AN2213.1	26S proteasome regulatory complex, ATPase RPT2	O	Posttranslational modification/turnover/chaperones	YDL007W	
AN2214.1	Uncharacterized conserved protein, contains WD40 repeat	S			
AN2215.1	Uncharacterized conserved protein, contains GRAM domain	S			
AN2216.1	Uncharacterized conserved protein	S			
AN2217.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN2218.1	Uncharacterized conserved protein	S			
AN2219.1	related to ahmp1 protein [MIPS] [Neurospora crassa]				
AN2222.1	ADP-ribosylation factor GTPase activator	TUZ		YDL226C	cytoplasm
AN2223.1	Mitochondrial elongation factor	J	Translation, ribosomal structure, biogenesis	YJL102W	mitochondrion
AN2224.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport	YOR132W	endosome
AN2226.1	KEKE-like motif-containing transcription regulator (Rlr1)/suppressor of sin4	K	Transcription		
AN2227.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN2228.1	ENSANGP00000004655 [Anopheles gambiae]				
AN2229.1	Homoserine acetyltransferase	E	Amino acid transport, metabolism	YNL277W	cytoplasm nucleus
AN2230.1	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport, metabolism		
AN2233.1	COP9 signalosome, subunit CSN6	OT			
AN2234.1	predicted protein [Neurospora crassa]				
AN2236.1	Uncharacterized conserved protein	S			
AN2237.1	Carboxypeptidase C (cathepsin A)	E	Amino acid transport, metabolism		
AN2238.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN2239.1	NADP-dependent flavoprotein reductase	C	Energy production, conversion	YPR048W	
AN2240.1	hypothetical protein [Neurospora crassa]				
AN2241.1	Repressor of drug resistance; Rdr1p [Saccharomyces cerevisiae]				
AN2242.1					
AN2243.1	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	R		YOR303W	cytoplasm
AN2244.1	GTP-binding protein DRG2 (ODN superfamily)	T	Signal transduction mechanisms	YGR173W	cytoplasm
AN2245.1	FOG: RRM domain	R			
AN2246.1	eIF-2alpha kinase GCN2	J	Translation, ribosomal structure, biogenesis	YDR283C	cytoplasm
AN2247.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN2248.1	4-aminobutyrate aminotransferase	E	Amino acid transport, metabolism	YGR019W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2251.1	Predicted membrane protein	S			
AN2255.1	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	Transcription		
AN2256.1	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL		YBR114W	cytoplasm nucleus
AN2258.1	hypothetical protein [Neurospora crassa]				
AN2259.1	hypothetical protein [Neurospora crassa]				
AN2261.1	Phosphatidylglycerolphosphate synthase	I	Lipid transport, metabolism	YCL004W	
AN2262.1	Uncharacterized conserved protein	S		YKL143W	cytoplasm
AN2263.1	Predicted GTP-binding protein MMR1	R		YGL099W	cytoplasm
AN2265.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN2266.1	Vacuolar sorting protein PEP3/VPS18	U	Intracellular trafficking/secretion/transport	YLR148W	endosome
AN2267.1					
AN2268.1	Mitochondrial/chloroplast ribosomal protein L5/L7	J	Translation, ribosomal structure, biogenesis	YDR237W	
AN2269.1	MEKK and related serine/threonine protein kinases	T	Signal transduction mechanisms	YLR362W	cytoplasm
AN2270.1	FOG: Zn-finger	R			
AN2271.1	Nonsense-mediated mRNA decay protein	A	RNA processing, modification		
AN2272.1	Possible pfkB family carbohydrate kinase	G	Carbohydrate transport, metabolism	YJR105W	cytoplasm nucleus
AN2273.1	predicted protein [Neurospora crassa]				
AN2274.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN2276.1	Adenosine deaminase	F	Nucleotide transport, metabolism		
AN2278.1	Chromatin remodeling complex SWI/SNF, component SWI2 and related ATPases (DNA/RNA helicase superfamily)	BK		YIL126W	nucleus
AN2279.1	Protein involved in membrane traffic (YOP1/TB2/DP1/HVA22 family)	U	Intracellular trafficking/secretion/transport	YPR028W	ER
AN2280.1	Uncharacterized conserved protein	S			
AN2281.1	Peroxisomal assembly protein PEX3	MU		YDR329C	peroxisome
AN2282.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN2283.1	RNA polymerase I 49 kDa subunit	K	Transcription		
AN2284.1	5-aminolevulinate synthase	H	Coenzyme transport, metabolism	YDR232W	mitochondrion
AN2285.1	SNF2 family DNA-dependent ATPase	L	Replication, recombination, repair		
AN2287.1	Amino acid transporters	E	Amino acid transport, metabolism	YDL210W	
AN2288.1	Sodium/hydrogen exchanger protein	P	Inorganic ion transport, metabolism	YDR456W	endosome
AN2289.1	Sucrose transporter and related proteins	G	Carbohydrate transport, metabolism		
AN2290.1	FOG: Zn-finger	R			
AN2292.1	Protein required for cell viability; Yil019wp [Saccharomyces cerevisiae]			YIL019W	cytoplasm nucleus
AN2293.1	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	E	Amino acid transport, metabolism	YIL020C	cytoplasm nucleus
AN2294.1	RNA polymerase II elongator complex, subunit ELP3/histone acetyltransferase	BK		YPL086C	cytoplasm
AN2295.1	Succinyl-CoA synthetase, alpha subunit	C	Energy production, conversion	YOR142W	mitochondrion
AN2296.1	RFX family transcription factor	K	Transcription		
AN2297.1	hypothetical protein [Neurospora crassa]				
AN2298.1	SMT3/SUMO-activating complex, AOS1/RAD31 component	O	Posttranslational modification/turnover/chaperones	YPR180W	nucleus
AN2299.1	hypothetical protein [Neurospora crassa]				
AN2300.1	Multidrug/pheromone exporter, ABC superfamily	Q			
AN2302.1	SCF ubiquitin ligase, Skp1 component	O	Posttranslational modification/turnover/chaperones	YDR328C	cytoplasm nucleus
AN2304.1	Nucleotide excision repair factor NEF2, RAD23 component	L	Replication, recombination, repair		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2306.1	Ubiquinol cytochrome c reductase, subunit RIP1	C	Energy production, conversion	YEL024W	mitochondrion
AN2307.1	hypothetical protein [Neurospora crassa]				
AN2308.1	Cl- channel CLC-3 and related proteins (CLC superfamily)	P	Inorganic ion transport, metabolism	YJR040W	
AN2311.1	Phosphomevalonate kinase	I	Lipid transport, metabolism	YMR220W	cytoplasm nucleus
AN2312.1	Stress responsive protein	R			
AN2313.1	hypothetical protein [Neurospora crassa]				
AN2314.1	1,4-alpha-glucan branching enzyme/starch branching enzyme II	G	Carbohydrate transport, metabolism	YEL011W	cytoplasm nucleus
AN2315.1	F0F1-type ATP synthase, beta subunit	C	Energy production, conversion	YJR121W	mitochondrion
AN2316.1	Cytochrome c oxidase, subunit IV/COX5b	C	Energy production, conversion	YNL052W	mitochondrion
AN2317.1	Actin depolymerizing factor	Z	Cytoskeleton	YLL050C	
AN2318.1	predicted protein [Neurospora crassa]				
AN2320.1	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	C	Energy production, conversion		
AN2321.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism	YAL067C	
AN2325.1	Putative alpha-1,2-mannosidase	G	Carbohydrate transport, metabolism		
AN2326.1	FOG: TPR repeat	R			
AN2327.1	Molybdopterin synthase sulfurylase	H	Coenzyme transport, metabolism	YHR111W	cytoplasm
AN2329.1	Permeases of the major facilitator superfamily	GEPR			
AN2330.1	late sexual development protein [Aspergillus nidulans]				
AN2332.1	Succinate dehydrogenase, Fe-S protein subunit	C	Energy production, conversion	YLL041C	mitochondrion
AN2334.1	Fructose/tagatose bisphosphate aldolase	G	Carbohydrate transport, metabolism		
AN2335.1	Predicted dehydrogenase	R			
AN2336.1	Phospholipase C	M			
AN2338.1	glycoprotein gp2 [Equine herpesvirus 4]				
AN2340.1	Myosin-crossreactive antigen	S			
AN2341.1	Uncharacterized conserved protein	S			
AN2342.1	hypothetical protein [Neurospora crassa]				
AN2343.1	Predicted oxidoreductase related to nitroreductase	R		YCL026C-B	cytoplasm nucleus
AN2344.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN2345.1	tryptophan dimethylallyltransferase (EC 2.5.1.34) - ergot fungus				
AN2348.1	Ankyrin	M			
AN2351.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			
AN2357.1	Aromatic-L-amino-acid/L-histidine decarboxylase	E	Amino acid transport, metabolism		
AN2359.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN2360.1	Purple acid phosphatase	G	Carbohydrate transport, metabolism		
AN2369.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN2378.1	Predicted dehydrogenases and related proteins	R			
AN2393.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN2395.1	Beta-galactosidase/beta-glucuronidase	G	Carbohydrate transport, metabolism		
AN2404.1	Predicted membrane protein	S			
AN2405.1	SAM-dependent methyltransferases	QR			
AN2406.1					
AN2409.1	Phosphoserine aminotransferase	HE			
AN2410.1	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	J	Translation, ribosomal structure, biogenesis		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2412.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	Signal transduction mechanisms	YOL016C	cytoplasm
AN2413.1	Ubiquitin conjugating enzyme	O	Posttranslational modification/turnover/chaperones		
AN2414.1	NADH:ubiquinone oxidoreductase, NDUFS2/49 kDa subunit	C	Energy production, conversion		
AN2415.1	RNA polymerase I and III, subunit RPA40/RPC40	K	Transcription	YPR110C	nucleolus nucleus
AN2416.1	NEDD8-activating complex, catalytic component UBA3	O	Posttranslational modification/turnover/chaperones	YPR066W	cytoplasm
AN2417.1	Uncharacterized conserved protein	S			
AN2418.1	Vacuolar sorting protein VPS33/slp1 (Sec1 family)	U	Intracellular trafficking/secretion/transport	YLR396C	vacuolar membrane
AN2419.1	SNAP-25 (synaptosome-associated protein) component of SNARE complex	U	Intracellular trafficking/secretion/transport		
AN2420.1	Splicing factor 3b, subunit 1	A	RNA processing, modification	YMR288W	cytoplasm nucleus
AN2421.1	FOG: Zn-finger	R			
AN2424.1	N-acetyl-beta-hexosaminidase	G	Carbohydrate transport, metabolism		
AN2425.1	Protein phosphatase, regulatory subunit PPP1R3C/D	OT			
AN2426.1	Histone H4	B	Chromatin structure, dynamics	YNL030W	nucleus
AN2427.1	Annexin	U	Intracellular trafficking/secretion/transport		
AN2428.1	Predicted mitochondrial carrier protein	C	Energy production, conversion		
AN2430.1	Guanine nucleotide-binding protein	R			
AN2431.1	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	YU			
AN2434.1	Uncharacterized conserved protein XAP-5	S			
AN2435.1	ATP-citrate lyase	C	Energy production, conversion		
AN2436.1	ATP-citrate lyase	C	Energy production, conversion		
AN2438.1	Predicted GTPase	R		YOR262W	cytoplasm
AN2439.1	Mitotic spindle checkpoint protein BUB3, WD repeat superfamily	D	Cell cycle/division, chrom. partitioning		
AN2440.1	Ribose 5-phosphate isomerase	G	Carbohydrate transport, metabolism	YOR095C	cytoplasm nucleus
AN2441.1	NEDD8-activating complex, APP-BP1/UBA5 component	O	Posttranslational modification/turnover/chaperones	YPL003W	
AN2442.1	hypothetical protein [Neurospora crassa]				
AN2446.1	hypothetical protein [Neurospora crassa]				
AN2447.1	hypothetical protein [Neurospora crassa]				
AN2449.1	Predicted tRNA-splicing endonuclease subunit	J	Translation, ribosomal structure, biogenesis		
AN2450.1	SMT3/SUMO-activating complex, catalytic component UBA2	O	Posttranslational modification/turnover/chaperones	YDR390C	nucleus
AN2453.1	Similar to cyclophilin-type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN2455.1	C4-type Zn-finger protein	R		YGR211W	cytoplasm nucleus
AN2456.1	Uncharacterized conserved protein	S			
AN2458.1	TATA-binding protein-interacting protein	R			
AN2459.1	Protein phosphatase 1, regulatory subunit, and related proteins	T	Signal transduction mechanisms		
AN2460.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN2461.1	Vacuolar assembly/sorting protein PEP5/VPS11	U	Intracellular trafficking/secretion/transport	YMR231W	endosome
AN2462.1	Predicted xylanase/chitin deacetylase	G	Carbohydrate transport, metabolism		
AN2464.1	Protein transporter of the TRAM (translocating chain-associating membrane) superfamily	U	Intracellular trafficking/secretion/transport	YHL003C	ER
AN2467.1	Uncharacterized protein involved in cytokinesis, contains TGc (transglutaminase/protease-like) domain	D	Cell cycle/division, chrom. partitioning		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2470.1	Threonine dehydrogenase and related Zn-dependent dehydrogenases	ER			
AN2478.1	Sugar phosphate isomerases/epimerases	G	Carbohydrate transport, metabolism		
AN2489.1	Cyclin C-dependent kinase CDK8	K	Transcription	YPL042C	
AN2490.1	Uncharacterized conserved protein, contains N-recognin-type Zn-finger	R			
AN2491.1	DNA replication licensing factor, MCM2 component	L	Replication, recombination, repair	YBL023C	cytoplasm nucleus
AN2492.1	Uncharacterized conserved protein	S			
AN2493.1	Alkaline phosphatase	P	Inorganic ion transport, metabolism		
AN2496.1	Putative transmembrane protein cmp44E	R			
AN2497.1	Palmitoyl protein thioesterase	IO			
AN2498.1	predicted protein [Neurospora crassa]				
AN2499.1	RNA polymerase II elongator associated protein	R			
AN2500.1	Predicted methyltransferase	R		YLR285W	cytoplasm
AN2502.1	similar to PH (pleckstrin homology) domain [Caenorhabditis elegans] [Dictyostelium discoideum]				
AN2505.1	hypothetical protein [Neurospora crassa]				
AN2506.1	Flavonol reductase/cinnamoyl-CoA reductase	V	Defense mechanisms		
AN2508.1	Cysteine desulfurase NFS1	E	Amino acid transport, metabolism	YCL017C	mitochondrion
AN2509.1	hypothetical protein [Neurospora crassa]			YJR078W	
AN2510.1	Uncharacterized conserved protein	S		YOR238W	cytoplasm
AN2512.1	RNA polymerase III, large subunit	K	Transcription	YOR116C	nucleus
AN2513.1	Serine/threonine protein kinase	R		YGR262C	cytoplasm nucleus
AN2514.1	Glutamate-cysteine ligase regulatory subunit	E	Amino acid transport, metabolism		
AN2515.1	Aldo/keto reductase family proteins	R		YJR096W	cytoplasm nucleus
AN2516.1	Amphiphysin	U	Intracellular trafficking/secretion/transport		
AN2518.1	Vesicle trafficking protein Sly1 (Sec1 family)	U	Intracellular trafficking/secretion/transport	YDR189W	Golgi early Golgi
AN2520.1	alpha-factor pheromone receptor; seven-transmembrane domain protein; Ste2p [Saccharomyces cerevisiae]				
AN2522.1	Serine/threonine protein kinase	R			
AN2523.1	Chitin synthase/hyaluronan synthase (glycosyltransferases)	M			
AN2525.1	Serine racemase	TE		YKL218C	
AN2526.1	Ketol-acid reductoisomerase	EH		YLR355C	
AN2528.1	Lysophospholipase L1 and related esterases	E	Amino acid transport, metabolism		
AN2529.1	Enoyl-CoA isomerase	I	Lipid transport, metabolism		
AN2531.1	Predicted transporter (major facilitator superfamily)	R			
AN2532.1	Copper amine oxidase	Q			
AN2533.1	Predicted beta-xylosidase	R			
AN2534.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN2536.1	Isopenicillin N synthase and related dioxygenases	R			
AN2537.1	putative pectate lyase [Streptomyces avermitilis MA-4680]				
AN2555.1	Serine carboxypeptidases (lysosomal cathepsin A)	OE		YGL203C	
AN2558.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN2559.1	Zinc-binding oxidoreductase	CR			
AN2560.1	Amino acid transporters	E	Amino acid transport, metabolism	YHL036W	vacuole
AN2561.1	bll6449 [Bradyrhizobium japonicum]				
AN2562.1	Uncharacterized conserved protein	S			
AN2569.1	Pectate lyase	G	Carbohydrate transport, metabolism		
AN2572.1	Dipeptidyl aminopeptidase	O	Posttranslational modification/turnover/chaperones		

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN2577.1	Peroxisomal multifunctional beta-oxidation protein and related enzymes	I	Lipid transport, metabolism		
AN2583.1	Glyceraldehyde 3-phosphate dehydrogenase	G	Carbohydrate transport, metabolism		
AN2584.1	Predicted transporter (major facilitator superfamily)	R			
AN2585.1	Predicted transporter (major facilitator superfamily)	R			
AN2591.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN2598.1	Urea transporter	E	Amino acid transport, metabolism		
AN2601.1	Predicted transporter (major facilitator superfamily)	R			
AN2602.1	Esterase/lipase	I	Lipid transport, metabolism		
AN2606.1	Pyoverdine/dityrosine biosynthesis protein	Q			
AN2607.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN2626.1	hypothetical protein [Neurospora crassa]				
AN2648.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN2649.1	hypothetical protein [Neurospora crassa]				
AN2664.1	hypothetical protein [Neurospora crassa]				
AN2667.1	hypothetical protein [Neurospora crassa]				
AN2674.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN2681.1	predicted protein [Neurospora crassa]				
AN2682.1	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production, conversion		
AN2684.1	Sterol reductase/lamin B receptor	IT		YGL012W	ER
AN2686.1	predicted protein [Neurospora crassa]				
AN2687.1	Ras-related small GTPase, Rho type	R			
AN2688.1	Sphingoid base-phosphate phosphatase	I	Lipid transport, metabolism		
AN2692.1					
AN2693.1	Uncharacterized conserved protein	R			
AN2694.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN2701.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN2703.1					
AN2721.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN2723.1	Histidinol dehydrogenase	E	Amino acid transport, metabolism		
AN2728.1	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	EM			
AN2729.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN2730.1	Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	P	Inorganic ion transport, metabolism	YBR294W	
AN2731.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones	YNL064C	cytoplasm nucleus
AN2733.1	Uroporphyrinogen decarboxylase	H	Coenzyme transport, metabolism	YDR047W	cytoplasm nucleus
AN2734.1	60S acidic ribosomal protein P0	J	Translation, ribosomal structure, biogenesis	YLR340W	
AN2735.1	WD repeat protein WDR4	S			
AN2736.1	Late Golgi protein sorting complex, subunit Vps53	U	Intracellular trafficking/secretion/transport	YJL029C	early Golgi
AN2737.1	mRNA export factor TAP/MEX67	A	RNA processing, modification	YPL169C	nuclear periphery
AN2738.1	COPII vesicle protein	U	Intracellular trafficking/secretion/transport	YAL042W	
AN2739.1	DNA polymerase theta/eta, DEAD-box superfamily	R			
AN2740.1	Cyclic nucleotide phosphodiesterase	T	Signal transduction mechanisms		
AN2741.1	Uncharacterized protein conserved in bacteria	O	Posttranslational modification/turnover/chaperones		
AN2743.1	Translation initiation factor 3, subunit a (eIF-3a)	J	Translation, ribosomal structure, biogenesis		
AN2744.1	predicted protein [Neurospora crassa]				
AN2745.1	Acetyltransferase, (GNAT) family	R		YPR131C	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2746.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN2747.1	RNA polymerase subunit K	K	Transcription	YPR187W	cytoplasm nucleus
AN2748.1	FOG: Zn-finger	R		YPR186C	cytoplasm nucleus
AN2749.1	WASP-interacting protein VRP1/WIP, contains WH2 domain	Z	Cytoskeleton		
AN2750.1					
AN2751.1	Uncharacterized conserved protein	S		YCR077C	cytoplasm
AN2752.1	Glycolipid 2-alpha-mannosyltransferase (alpha-1,2-mannosyltransferase)	G	Carbohydrate transport, metabolism	YOR099W	vacuole
AN2754.1	Amino acid transporter protein	E	Amino acid transport, metabolism		
AN2756.1	Actin-binding protein SLA2/Huntingtin-interacting protein Hip1	Z	Cytoskeleton		
AN2757.1	Uncharacterized conserved protein TEX2, contains PH domain	R			
AN2758.1	Protein involved in establishing cohesion between sister chromatids during DNA replication	L	Replication, recombination, repair		
AN2759.1	Protein required for 18S rRNA maturation and 40S ribosome biogenesis	J	Translation, ribosomal structure, biogenesis	YLR186W	cytoplasm nucleus
AN2760.1	Lactoylglutathione lyase and related lyases	E	Amino acid transport, metabolism		
AN2761.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YBR082C	cytoplasm nucleus
AN2762.1	Glutaryl-CoA dehydrogenase	E	Amino acid transport, metabolism		
AN2764.1	5'-3' exonuclease	L	Replication, recombination, repair	YKL113C	nucleus
AN2766.1	Phosphatidylinositol-4-phosphate 5-kinase	T	Signal transduction mechanisms		
AN2767.1	26S proteasome regulatory complex, subunit RPN3/PSMD3	O	Posttranslational modification/turnover/chaperones		
AN2771.1	Uncharacterized conserved protein	S			
AN2772.1	Anaphase-promoting complex (APC), subunit 1 (meiotic check point regulator/Tsg24)	DO			
AN2773.1	predicted protein [Neurospora crassa]				
AN2775.1	Predicted translation initiation factor related to eIF-3a	J	Translation, ribosomal structure, biogenesis		
AN2776.1	predicted protein [Neurospora crassa]				
AN2781.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN2782.1	hypothetical protein [Neurospora crassa]				
AN2793.1	3-isopropylmalate dehydrogenase	E	Amino acid transport, metabolism		
AN2794.1	Predicted transporter (major facilitator superfamily)	R			
AN2805.1					
AN2812.1	Na+/Pi symporter	P	Inorganic ion transport, metabolism		
AN2813.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q		YOR246C	lipid particle
AN2815.1	Mannitol-1-phosphate/altronate dehydrogenases	G	Carbohydrate transport, metabolism	YNR073C	
AN2822.1	Aquaporin (major intrinsic protein family)	G	Carbohydrate transport, metabolism		
AN2824.1	Metal-dependent amidase/aminoacylase/carboxypeptidase	R			
AN2825.1	Alcohol dehydrogenase, class V	Q			
AN2829.1	Amidases	JIT			
AN2830.1	Sterol desaturase	I	Lipid transport, metabolism		
AN2839.1	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport, metabolism		
AN2846.1	Glutathione peroxidase	O	Posttranslational modification/turnover/chaperones	YBR244W	cytoplasm nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2848.1	Component of the U4/U6.U5 snRNP/mitosis protein DIM1	AD		YPR082C	
AN2851.1	Prolyl 4-hydroxylase alpha subunit	E	Amino acid transport, metabolism		
AN2852.1	Hypothetical ORF; Yil130wp [Saccharomyces cerevisiae]			YIL130W	nucleus
AN2854.1	Transcription factor of the Forkhead/HNF3 family	K	Transcription		
AN2855.1	FOG: Zn-finger	R			
AN2857.1	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B	Chromatin structure, dynamics		
AN2858.1	Predicted dehydrogenases and related proteins	R			
AN2859.1	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	EM			
AN2860.1	Alcohol dehydrogenase, class V	Q		YMR318C	cytoplasm nucleus
AN2861.1	Beta-TrCP (transducin repeats containing)/Slimb proteins	S			
AN2862.1	Microtubule-binding protein involved in cell cycle control	DZ		YER016W	microtubule
AN2866.1	Predicted dehydrogenases and related proteins	R			
AN2867.1	Phosphoglucomutase	G	Carbohydrate transport, metabolism	YMR105C	cytoplasm nucleus
AN2868.1	Oligoribonuclease (3'->5' exoribonuclease)	A	RNA processing, modification		
AN2869.1	Predicted transporter (major facilitator superfamily)	R			
AN2871.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN2872.1	predicted protein [Neurospora crassa]				
AN2873.1	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	E	Amino acid transport, metabolism		
AN2875.1	Fructose 1,6-bisphosphate aldolase	G	Carbohydrate transport, metabolism	YKL060C	cytoplasm
AN2877.1	Oxysterol-binding protein	T	Signal transduction mechanisms	YPL145C	cytoplasm
AN2879.1	Amidases	JIT			
AN2880.1	Uncharacterized conserved protein	R			
AN2881.1	hypothetical protein [Neurospora crassa]				
AN2882.1	Homoserine dehydrogenase	E	Amino acid transport, metabolism	YJR139C	cytoplasm nucleus
AN2883.1	Translation initiation factor 5B (eIF-5B)	J	Translation, ribosomal structure, biogenesis		
AN2884.1					
AN2886.1	predicted protein [Neurospora crassa]				
AN2887.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN2888.1	predicted protein [Neurospora crassa]				
AN2889.1	FOG: Immunoglobin and related proteins	RP			
AN2890.1	Esterase/lipase	I	Lipid transport, metabolism		
AN2895.1	Uncharacterized conserved protein	S			
AN2896.1	Enoyl-CoA hydratase	I	Lipid transport, metabolism		
AN2897.1	predicted protein [Neurospora crassa]				
AN2898.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN2899.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN2900.1	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)	J	Translation, ribosomal structure, biogenesis	YBL080C	mitochondrion
AN2901.1	Arginase	E	Amino acid transport, metabolism	YPL111W	cytoplasm nucleus
AN2902.1	TFIIF-interacting CTD phosphatases, including NLI-interacting factor	K	Transcription	YMR277W	nucleus
AN2903.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones	YPL154C	vacuole
AN2904.1	26S proteasome regulatory complex, ATPase RPT3	O	Posttranslational modification/turnover/chaperones	YDR394W	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2905.1	DNA-binding proteins Bright/BRCAA1/RBP1 and related proteins containing BRIGHT domain	K	Transcription		
AN2906.1	Uncharacterized conserved protein NOF (Neighbor of FAU)	S			
AN2907.1	Translation initiation factor 3, subunit e (eIF-3e)	J	Translation, ribosomal structure, biogenesis		
AN2909.1	Putative arsenite-translocating ATPase	P	Inorganic ion transport, metabolism	YDL100C	ER
AN2911.1	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K	Transcription		
AN2913.1	predicted protein [Neurospora crassa]				
AN2914.1	Argininosuccinate lyase	E	Amino acid transport, metabolism	YHR018C	cytoplasm
AN2916.1	Succinate dehydrogenase, flavoprotein subunit	C	Energy production, conversion	YKL148C	
AN2917.1	26S proteasome regulatory complex, ATPase RPT1	O	Posttranslational modification/turnover/chaperones	YKL145W	nucleus
AN2918.1	Chaperonin complex component, TCP-1 delta subunit (CCT4)	O	Posttranslational modification/turnover/chaperones	YDL143W	
AN2919.1	FOG: Zn-finger	R			
AN2925.1	Peroxisome assembly factor 2 containing the AAA+-type ATPase domain	O	Posttranslational modification/turnover/chaperones		
AN2926.1	Uncharacterized conserved protein related to ribosomal protein S8E	R		YER126C	cytoplasm
AN2927.1	Dual specificity; serine/threonine and tyrosine kinase	D	Cell cycle/division, chrom. partitioning		
AN2928.1	von Willebrand factor and related coagulation proteins	WV			
AN2930.1	Predicted fumarylacetoacetate hydralase	R		YNL168C	mitochondrion
AN2932.1	Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases	J	Translation, ribosomal structure, biogenesis	YKR059W	cytoplasm
AN2933.1	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	BT			
AN2936.1	Alpha-mannosidase	G	Carbohydrate transport, metabolism	YGL156W	
AN2937.1					
AN2938.1	Peroxisomal NUDIX hydrolase	L	Replication, recombination, repair	YLR151C	
AN2939.1	Ca2+-binding transmembrane protein LETM1/MRS7	S		YPR125W	mitochondrion
AN2940.1	Uncharacterized conserved protein	S			
AN2941.1	predicted protein [Neurospora crassa]				
AN2944.1	TamA [Aspergillus nidulans]				
AN2945.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport		
AN2946.1	Dipeptidyl aminopeptidase	O	Posttranslational modification/turnover/chaperones	YHR028C	
AN2947.1	Phosphoinositide-specific phospholipase C	T	Signal transduction mechanisms		
AN2948.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones		
AN2951.1	UDP-glucose 4-epimerase	M			
AN2953.1	Uncharacterized conserved protein	S			
AN2954.1	von Willebrand factor and related coagulation proteins	WV			
AN2955.1	Glycosyltransferase	M			
AN2957.1	predicted protein [Neurospora crassa]				
AN2958.1	Predicted transporter (major facilitator superfamily)	R			
AN2959.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN2960.1	Probable taurine catabolism dioxygenase	Q			
AN2961.1	Uncharacterized conserved protein	S			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN2963.1	Structural maintenance of chromosome protein 1 (sister chromatid cohesion complex Cohesin, subunit SMC1)	D	Cell cycle/division, chrom. partitioning	YFL008W	cytoplasm nucleus
AN2964.1	Dihydrolipoamide acetyltransferase	C	Energy production, conversion	YGR193C	mitochondrion
AN2965.1	Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	DO		YGL003C	
AN2966.1	Aminopeptidase I zinc metalloprotease (M18)	E	Amino acid transport, metabolism		
AN2967.1	tRNA-dihydrouridine synthase	J	Translation, ribosomal structure, biogenesis	YNR015W	cytoplasm nucleus
AN2968.1	Inorganic pyrophosphatase/Nucleosome remodeling factor, subunit NURF38	C	Energy production, conversion	YBR011C	cytoplasm nucleus
AN2969.1	Replication factor C, subunit RFC4	L	Replication, recombination, repair		
AN2970.1	p-Nitrophenyl phosphatase	P	Inorganic ion transport, metabolism	YDL236W	cytoplasm nucleus
AN2971.1					
AN2973.1	SNF2 family DNA-dependent ATPase	B	Chromatin structure, dynamics		
AN2975.1	predicted protein [Neurospora crassa]				
AN2976.1	predicted protein [Neurospora crassa]				
AN2977.1	Mitochondrial phosphate carrier protein	C	Energy production, conversion	YER053C	mitochondrion
AN2980.1	60S ribosomal protein L35A/L37	J	Translation, ribosomal structure, biogenesis	YOR234C	cytoplasm
AN2981.1	Glucose-6-phosphate 1-dehydrogenase	G	Carbohydrate transport, metabolism	YNL241C	cytoplasm
AN2983.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN2985.1	Predicted transporter (major facilitator superfamily)	R			
AN2987.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN2988.1	Predicted cation transporter	P	Inorganic ion transport, metabolism	YER163C	cytoplasm nucleus
AN2989.1	FOG: RRM domain	R			
AN2992.1	Translation initiation factor 2, beta subunit (eIF-2beta)	J	Translation, ribosomal structure, biogenesis		
AN2995.1	Adaptor protein GRB2, contains SH2 and SH3 domains	T	Signal transduction mechanisms		
AN2996.1	Transcription factor MBF1	K	Transcription		
AN2997.1	Translation initiation factor 3, subunit i (eIF-3i)/TGF-beta receptor-interacting protein (TRIP-1)	JT		YMR146C	
AN2998.1	C1-tetrahydrofolate synthase	H	Coenzyme transport, metabolism	YGR204W	cytoplasm nucleus
AN2999.1	NADP-dependent isocitrate dehydrogenase	C	Energy production, conversion	YDL066W	mitochondrion
AN3000.1					
AN3001.1	Mitogen-activated protein kinase kinase (MAP2K)	T	Signal transduction mechanisms		
AN3002.1	hypothetical protein [Neurospora crassa]				
AN3004.1	Oxidation resistance protein	L	Replication, recombination, repair		
AN3005.1	Protein involved in vacuole import and degradation	U	Intracellular trafficking/secretion/transport	YNL212W	cytoplasm
AN3009.1					
AN3010.1	Uncharacterized conserved protein	S		YOL093W	cytoplasm nucleus
AN3013.1	hypothetical protein [Neurospora crassa]			YIR007W	cytoplasm
AN3014.1	TPR repeat-containing protein	A	RNA processing, modification	YPR189W	cytoplasm
AN3015.1	Uncharacterized conserved protein	S			
AN3016.1	unnamed protein product [Podospora anserina]				
AN3017.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN3018.1	Uncharacterized conserved protein	E	Amino acid transport, metabolism		
AN3019.1	26S proteasome regulatory complex, subunit RPN12/PSMD8	O	Posttranslational modification/turnover/chaperones	YFR052W	nucleus
AN3020.1	Predicted protease	O	Posttranslational modification/turnover/chaperones		
AN3022.1	Beta-tubulin folding cofactor C	O	Posttranslational modification/turnover/chaperones		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3023.1	Uncharacterized protein conserved in bacteria	S			
AN3024.1	Nucleosome assembly protein NAP-1	BD			
AN3026.1	Vesicle coat complex COPI, alpha subunit	U	Intracellular trafficking/secretion/transport	YDL145C	Golgi early Golgi
AN3028.1	SNF2 family DNA-dependent ATPase	L	Replication, recombination, repair		
AN3029.1	Vesicle coat complex AP-1/AP-2/AP-4, beta subunit	U	Intracellular trafficking/secretion/transport	YKL135C	late Golgi
AN3031.1	Pyridoxalphosphate-dependent enzyme/predicted threonine synthase	E	Amino acid transport, metabolism	YCR053W	cytoplasm nucleus
AN3033.1	Eukaryotic-type DNA primase, catalytic (small) subunit	L	Replication, recombination, repair	YIR008C	
AN3034.1	MAM33, mitochondrial matrix glycoprotein	C	Energy production, conversion	YIL070C	mitochondrion
AN3035.1	5'-3' exonuclease	L	Replication, recombination, repair		
AN3036.1	predicted protein [Neurospora crassa]				
AN3038.1	hypothetical protein [Neurospora crassa]				
AN3040.1	Projectin/twitchin and related proteins	Z	Cytoskeleton		
AN3044.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN3046.1	putative endoglucanase precursor [Cochliobolus heterostrophus]				
AN3051.1	hypothetical protein [Neurospora crassa]				
AN3053.1	Beta-glucanase/Beta-glucan synthetase	G	Carbohydrate transport, metabolism		
AN3055.1	Uncharacterized conserved protein	S			
AN3056.1	Uncharacterized MYND Zn-finger protein	R		YOL022C	cytoplasm
AN3058.1	Glycine/serine hydroxymethyltransferase	E	Amino acid transport, metabolism	YLR058C	cytoplasm nucleus
AN3059.1	Phosphoglycerate mutase	G	Carbohydrate transport, metabolism		
AN3061.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones	YPR173C	endosome
AN3062.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN3063.1	MADS box transcription factor	K	Transcription		
AN3064.1	Uncharacterized conserved protein, AMMECR1	S			
AN3065.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	Signal transduction mechanisms		
AN3067.1	DNA polymerase epsilon, catalytic subunit A	L	Replication, recombination, repair	YNL262W	cytoplasm nucleus
AN3069.1	Ribosome biogenesis protein - Nop56p/Sik1p	AJ			
AN3070.1	Chaperonin complex component, TCP-1 zeta subunit (CCT6)	O	Posttranslational modification/turnover/chaperones	YDR188W	
AN3071.1	Histone acetyltransferase (MYST family)	B	Chromatin structure, dynamics	YMR127C	cytoplasm nucleus
AN3073.1	Asparaginyl-tRNA synthetase (mitochondrial)	J	Translation, ribosomal structure, biogenesis	YCR024C	mitochondrion
AN3075.1	hypothetical protein [Neurospora crassa]				
AN3079.1					
AN3080.1	Vesicle coat complex COPII, subunit SFB3	U	Intracellular trafficking/secretion/transport	YHR098C	ER to Golgi
AN3081.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN3082.1	mRNA cleavage and polyadenylation factor II complex, subunit CFT2 (CPSF subunit)	A	RNA processing, modification		
AN3083.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN3084.1	Predicted alpha/beta hydrolase	R		YOR059C	
AN3085.1	Predicted phosphatase	R		YKR070W	mitochondrion
AN3088.1	Vacuolar H+-ATPase V0 sector, subunits c/c'	C	Energy production, conversion	YEL027W	ER
AN3089.1	predicted protein [Neurospora crassa]				
AN3090.1	G-protein alpha subunit (small G protein superfamily)	DT			
AN3091.1	M13 family peptidase	E	Amino acid transport, metabolism		
AN3092.1	Ras1 guanine nucleotide exchange factor	T	Signal transduction mechanisms		
AN3093.1	Myosin class V heavy chain	Z	Cytoskeleton		
AN3094.1	Rab6 GTPase activator GAPCenA and related TBC domain proteins	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3095.1	Conserved protein Mo25	S		YKL189W	cytoplasm nucleus
AN3096.1	Protein arginine N-methyltransferase PRMT1 and related enzymes	OKT		YBR034C	cytoplasm nucleus
AN3098.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones	YBR080C	Golgi early Golgi
AN3100.1	predicted protein [Neurospora crassa]				
AN3101.1	Sensory transduction histidine kinase	T	Signal transduction mechanisms		
AN3102.1	Sensory transduction histidine kinase	T	Signal transduction mechanisms		
AN3103.1					
AN3107.1	predicted protein [Neurospora crassa]				
AN3108.1	ACRIFLAVINE SENSITIVITY CONTROL PROTEIN ACR-2 [Neurospora crassa]				
AN3110.1	3-phosphoinositide-dependent protein kinase (PDK1)	T	Signal transduction mechanisms		
AN3112.1	Protoporphyrinogen oxidase	H	Coenzyme transport, metabolism		
AN3113.1	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE			
AN3114.1	predicted protein [Neurospora crassa]				
AN3115.1	Predicted transporter (major facilitator superfamily)	R			
AN3116.1	Transcription initiation factor TFIIIB, Brf1 subunit	K	Transcription		
AN3117.1	Cation transport ATPase	P	Inorganic ion transport, metabolism		
AN3118.1	Endonuclease MUS81	L	Replication, recombination, repair	YDR386W	
AN3119.1	Nucleoside-diphosphate-sugar epimerases	MG			
AN3120.1	hypothetical protein [Neurospora crassa]				
AN3122.1	hypothetical protein [Neurospora crassa]				
AN3123.1	K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	PT			
AN3124.1	Kinesin-like protein	Z	Cytoskeleton		
AN3125.1	predicted protein [Neurospora crassa]				
AN3126.1	Signal peptidase I	U	Intracellular trafficking/secretion/transport		
AN3128.1	Choline transporter-like protein	I	Lipid transport, metabolism		
AN3129.1	NAD+ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	KLO			
AN3130.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN3131.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones	YDR375C	mitochondrion
AN3132.1	Predicted Zn-dependent hydrolase (beta-lactamase superfamily)	R			
AN3134.1	Chaperonin complex component, TCP-1 gamma subunit (CCT3)	O	Posttranslational modification/turnover/chaperones	YJL014W	
AN3135.1	Uncharacterized conserved protein	S			
AN3136.1	Ubiquitin-conjugating enzyme	O	Posttranslational modification/turnover/chaperones		
AN3138.1	predicted protein [Neurospora crassa]				
AN3140.1					
AN3142.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN3143.1	Uncharacterized conserved protein	S			
AN3144.1	FYVE finger-containing protein	R		YDR323C	endosome
AN3145.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN3146.1	P-type ATPase	P	Inorganic ion transport, metabolism	YEL031W	ER
AN3147.1	Glycolipid transfer protein	G	Carbohydrate transport, metabolism		
AN3148.1	hypothetical protein. [Schizosaccharomyces pombe]			YDR104C	
AN3149.1	Mitochondrial inner membrane protease, subunit IMP2	OU			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3150.1	Gamma-glutamylcysteine synthetase	H	Coenzyme transport, metabolism	YJL101C	cytoplasm
AN3151.1					
AN3152.1	GATA-4/5/6 transcription factors	K	Transcription		
AN3153.1	Hismacro and SEC14 domain-containing proteins	BK			
AN3154.1	hypothetical protein [Neurospora crassa]			YDL056W	nucleus
AN3155.1	Receptor-activated Ca2+-permeable cation channels (STRPC family)	PT		YOR087W	ER cytoplasm
AN3156.1	Translation initiation factor 2, alpha subunit (eIF-2alpha)	J	Translation, ribosomal structure, biogenesis	YJR007W	cytoplasm
AN3157.1	Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	P	Inorganic ion transport, metabolism	YPR003C	ER
AN3163.1	Membrane protease subunits, stomatin/prohibitin homologs	O	Posttranslational modification/turnover/chaperones		
AN3164.1	predicted protein [Neurospora crassa]				
AN3165.1					
AN3167.1	Ribosome biogenesis protein - Nop58p/Nop5p	AJ		YOR310C	nucleolus
AN3168.1	Vacuolar H+-ATPase V0 sector, subunit d	C	Energy production, conversion	YLR447C	vacuolar membrane
AN3169.1	Ribose-phosphate pyrophosphokinase	FE		YOL061W	cytoplasm
AN3171.1	Ras-related small GTPase, Rho type	R			
AN3172.1	40S ribosomal protein SA (P40)/Laminin receptor 1	J	Translation, ribosomal structure, biogenesis	YGR214W	cytoplasm
AN3173.1	Mitochondrial/choloroplast ribosomal protein S15	J	Translation, ribosomal structure, biogenesis	YDR337W	mitochondrion
AN3175.1	acyltransferase family [Arabidopsis thaliana]				
AN3176.1	ATP-dependent RNA helicase	A	RNA processing, modification	YFL002C	nucleolus nucleus
AN3177.1	Predicted ER membrane protein	S		YOR311C	ER
AN3178.1	Component of histone deacetylase complex (breast carcinoma metastasis suppressor 1 protein in human)	DK			
AN3179.1	RNA polymerase II, large subunit	K	Transcription		
AN3180.1	Putative translation initiation inhibitor, yjgF family	J	Translation, ribosomal structure, biogenesis		
AN3181.1	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	T	Signal transduction mechanisms		
AN3183.1	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B	Chromatin structure, dynamics		
AN3184.1	Predicted mutarotase	G	Carbohydrate transport, metabolism		
AN3185.1	Actin and related proteins	Z	Cytoskeleton		
AN3186.1	5'-3' exonuclease	L	Replication, recombination, repair		
AN3188.1	Phosphatidylserine decarboxylase	I	Lipid transport, metabolism		
AN3191.1	Esterase/lipase	I	Lipid transport, metabolism		
AN3205.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion		
AN3208.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ			
AN3211.1	necrosis and ethylene inducing protein [Bacillus halodurans]				
AN3217.1	putative transcriptional activator with fungal binuclear cluster domain [Schizosaccharomyces pombe]				
AN3220.1	Permeases of the major facilitator superfamily	GEPR			
AN3221.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN3222.1	hypothetical protein [Neurospora crassa]			YOR155C	
AN3223.1	Pyrophosphate-dependent phosphofructo-1-kinase	G	Carbohydrate transport, metabolism	YGR240C	cytoplasm
AN3224.1	predicted protein [Neurospora crassa]				
AN3231.1	Mg2+ and Co2+ transporters	P	Inorganic ion transport, metabolism		
AN3233.1	Predicted transporter (major facilitator superfamily)	R			
AN3239.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3258.1	predicted protein [Neurospora crassa]				
AN3264.1	Predicted transporter (major facilitator superfamily)	R			
AN3268.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN3295.1	predicted protein [Neurospora crassa]				
AN3299.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones		
AN3300.1	ACRIFLAVINE SENSITIVITY CONTROL PROTEIN ACR-2 [Neurospora crassa]				
AN3301.1	Predicted transporter (major facilitator superfamily)	R			
AN3304.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN3305.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN3307.1	Glycogen synthase	G	Carbohydrate transport, metabolism		
AN3308.1	Alpha-amylase	G	Carbohydrate transport, metabolism		
AN3312.1	Reductases with broad range of substrate specificities	R			
AN3313.1	Ribosomal RNA adenine dimethylase	A	RNA processing, modification	YPL266W	
AN3337.1	hypothetical protein [Neurospora crassa]				
AN3341.1	Chromate transport protein ChrA	P	Inorganic ion transport, metabolism		
AN3344.1					
AN3347.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN3357.1	Predicted transporter (major facilitator superfamily)	R			
AN3358.1	Endo-beta-mannanase	G	Carbohydrate transport, metabolism		
AN3359.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN3361.1	Bacteriorhodopsin	R			
AN3362.1	Isoleucyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YPL040C	mitochondrion
AN3363.1	Kinesin-like protein	Z	Cytoskeleton	YBL063W	microtubule
AN3365.1	Mercaptopyruvate sulfurtransferase/thiosulfate sulfurtransferase	V	Defense mechanisms		
AN3366.1	unnamed protein product [Podospora anserina]				
AN3367.1	Translin-associated protein X	R			
AN3368.1	Beta-galactosidase/beta-glucuronidase	G	Carbohydrate transport, metabolism		
AN3370.1	Mannosyltransferase	G	Carbohydrate transport, metabolism	YJR013W	ER
AN3371.1	predicted protein [Neurospora crassa]				
AN3372.1	FOG: Low-complexity	S			
AN3373.1	Predicted DNA damage inducible protein	L	Replication, recombination, repair		
AN3374.1	Chitinase	M			
AN3375.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones	YIR004W	ER
AN3376.1	Squalene synthetase	I	Lipid transport, metabolism	YHR190W	ER
AN3377.1	pepstatin-insensitive acid protease [Talaromyces emersonii]				
AN3378.1	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E	Amino acid transport, metabolism	YLL062C	cytoplasm
AN3379.1					
AN3387.1					
AN3389.1	Endopolygalacturonase	M			
AN3390.1	Pectin methylesterase	G	Carbohydrate transport, metabolism		
AN3391.1	FOG: Zn-finger	R			
AN3392.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN3399.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3400.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN3405.1	Protein conjugation factor involved in autophagy	O	Posttranslational modification/turnover/chaperones		
AN3408.1	H+/oligopeptide symporter	E	Amino acid transport, metabolism	YKR093W	vacuole cell periphery
AN3410.1					
AN3411.1	Translation initiation factor 4F, cap-binding subunit (eIF-4E) and related cap-binding proteins	J	Translation, ribosomal structure, biogenesis	YOL139C	cytoplasm
AN3413.1	40S ribosomal protein S2/30S ribosomal protein S5	J	Translation, ribosomal structure, biogenesis	YGL123W	
AN3415.1	ADP-ribosylglycohydrolase	O	Posttranslational modification/turnover/chaperones		
AN3416.1	SNARE protein Syntaxin 1 and related proteins	U	Intracellular trafficking/secretion/transport	YMR183C	endosome
AN3417.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN3418.1	endo-1,4-beta-glucanase [Aspergillus nidulans]				
AN3419.1	Serine O-acetyltransferase	E	Amino acid transport, metabolism	YJL218W	
AN3421.1	predicted protein [Neurospora crassa]				
AN3422.1	Mitogen-activated protein kinase kinase (MAP2K)	T	Signal transduction mechanisms		
AN3423.1	Transcription elongation factor SPT6	A	RNA processing, modification	YGR116W	nucleus
AN3424.1	Oxysterol-binding protein	I	Lipid transport, metabolism		
AN3425.1	Interferon-related protein PC4 like	Z	Cytoskeleton		
AN3426.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	A	RNA processing, modification		
AN3427.1	Nuclear localization sequence binding protein	K	Transcription	YNL175C	nucleolus nucleus
AN3428.1	Uncharacterized conserved protein, contains ZZ-type Zn-finger	R			
AN3429.1	Amidases related to nicotinamidase	Q			
AN3430.1	hypothetical protein [Neurospora crassa]				
AN3431.1	Quinolinate phosphoribosyl transferase	F	Nucleotide transport, metabolism	YFR047C	cytoplasm nucleus
AN3432.1	Galactose mutarotase and related enzymes	G	Carbohydrate transport, metabolism	YNR071C	
AN3433.1	zinc cluster transcription factor Fcr1p [Candida albicans]				
AN3434.1	Ras-related GTPase	R			
AN3437.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN3438.1	Guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport		
AN3439.1	Uncharacterized conserved protein	S		YKR030W	
AN3440.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN3443.1	Phospholipase D1	I	Lipid transport, metabolism		
AN3444.1	Helicase of the DEAD superfamily	L	Replication, recombination, repair	YPL008W	cytoplasm nucleus
AN3445.1	Extracellular protein SEL-1 and related proteins	MOT			
AN3447.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN3449.1	OTU-like cysteine protease	TO		YFL044C	cytoplasm nucleus
AN3450.1	Serine/threonine protein kinase of the CDC7 subfamily involved in DNA synthesis, repair and recombination	L	Replication, recombination, repair	YDL017W	cytoplasm nucleus
AN3451.1	Chromosome condensation complex Condensin, subunit D2	BD		YLR272C	nucleolus cytoplasm nucleus
AN3452.1	Oxysterol-binding protein	T	Signal transduction mechanisms		
AN3453.1	Ubiquitin C-terminal hydrolase	O	Posttranslational modification/turnover/chaperones		
AN3454.1	unnamed protein product [Podospora anserina]			YMR129W	nuclear periphery
AN3455.1	Nucleolar RNA-associated protein (NRAP)	S		YGR090W	nucleolus nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3456.1	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport, metabolism	YJR130C	cytoplasm nucleus
AN3458.1	mitochondrial ribosomal protein YmL20 [Saccharomyces cerevisiae]			YKR085C	mitochondrion
AN3459.1	Metalloexopeptidases	E	Amino acid transport, metabolism	YFR044C	mitochondrion cytoplasm
AN3460.1	ATP-dependent RNA helicase	A	RNA processing, modification	YLR383W	cytoplasm nucleus
AN3461.1	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	Energy production, conversion	YBR291C	mitochondrion
AN3462.1	Mitochondrial polypeptide chain release factor	J	Translation, ribosomal structure, biogenesis	YGL143C	mitochondrion
AN3463.1	dsRNA-activated protein kinase inhibitor P58, contains TPR and DnaJ domains	V	Defense mechanisms		
AN3464.1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	O	Posttranslational modification/turnover/chaperones		
AN3466.1	Dihydrolipoamide succinyltransferase (2-oxoglutarate dehydrogenase, E2 subunit)	C	Energy production, conversion	YDR148C	mitochondrion
AN3469.1	Histone H2B	B	Chromatin structure, dynamics	YDR224C	nucleus
AN3489.1	Predicted membrane protein	R			
AN3498.1	Predicted transporter (major facilitator superfamily)	R			
AN3499.1	Predicted molecular chaperone distantly related to HSP70-fold metalloproteases	O	Posttranslational modification/turnover/chaperones		
AN3502.1					
AN3503.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism	YLR004C	
AN3504.1	Alpha-glucosidases, family 31 of glycosyl hydrolases	G	Carbohydrate transport, metabolism		
AN3508.1	hypothetical protein [Neurospora crassa]				
AN3511.1	Predicted Zn-dependent hydrolases of the beta-lactamase fold	R			
AN3515.1	Predicted transporter (major facilitator superfamily)	R		YBR298C	
AN3516.1	Alpha-amylase	G	Carbohydrate transport, metabolism		
AN3522.1	Globins and related hemoproteins	C	Energy production, conversion	YGR234W	cytoplasm
AN3527.1					
AN3533.1	predicted protein [Neurospora crassa]				
AN3535.1	predicted protein [Neurospora crassa]				
AN3536.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN3537.1	O-methyltransferase	Q			
AN3539.1					
AN3546.1					
AN3565.1	Zn-dependent hydrolases, including glyoxylases	R			
AN3569.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN3576.1	Uncharacterized membrane protein NPD008/CGI-148	R		YDR084C	late Golgi early Golgi
AN3577.1	Citrate lyase beta subunit	G	Carbohydrate transport, metabolism		
AN3578.1	Predicted MutS-related protein involved in mismatch repair	L	Replication, recombination, repair		
AN3579.1	Predicted membrane protein	S			
AN3580.1	Amine oxidase	Q			
AN3581.1	Thioredoxin reductase	O	Posttranslational modification/turnover/chaperones	YHR106W	mitochondrion
AN3582.1	hypothetical protein [Neurospora crassa]				
AN3583.1	Subtilisin-like proprotein convertase	O	Posttranslational modification/turnover/chaperones	YNL238W	early Golgi

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3584.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport	YJL036W	endosome
AN3586.1	Monooxygenase involved in coenzyme Q (ubiquinone) biosynthesis	HC		YGR255C	mitochondrion
AN3587.1	Ubiquitin-specific protease	O	Posttranslational modification/turnover/chaperones		
AN3588.1	Protein involved in dolichol pathway for N-glycosylation (mannosyltransferase family)	MU		YNR030W	ER
AN3589.1	Putative dynamitin	Z	Cytoskeleton		
AN3590.1	predicted protein [Neurospora crassa]				
AN3591.1	Methylmalonate semialdehyde dehydrogenase	EG			
AN3592.1	Calnexin	O	Posttranslational modification/turnover/chaperones	YAL058W	ER
AN3593.1	Class II aldolase/adducin N-terminal domain protein	G	Carbohydrate transport, metabolism	YJR024C	cytoplasm
AN3594.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport		
AN3595.1	hypothetical protein [Neurospora crassa]				
AN3596.1	hypothetical protein ((AL513463) conserved hypothetical protein [Neurospora crassa])				
AN3597.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN3600.1	hypothetical protein [Neurospora crassa]				
AN3602.1	Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	K	Transcription	YAL021C	cytoplasm
AN3603.1					
AN3604.1	Predicted DNA repair exonuclease SIA1	R			
AN3605.1	NADH-cytochrome b-5 reductase	HC			
AN3606.1	predicted protein [Neurospora crassa]				
AN3607.1	GATA-4/5/6 transcription factors	K	Transcription		
AN3612.1	Polyketide synthase modules and related proteins	Q			
AN3613.1	Endo-1,4-beta-xylanase 1 precursor (Xylanase 1) (1,4-beta-D-xylan xylanohydrolase 1)				
AN3619.1	DNA repair protein RAD50, ABC-type ATPase/SMC superfamily	L	Replication, recombination, repair	YNL250W	cytoplasm nucleus
AN3620.1	Checkpoint 9-1-1 complex, RAD1 component	DL			
AN3621.1	Histone acetyltransferase SAGA/ADA, catalytic subunit PCAF/GCN5 and related proteins	BK		YGR252W	nucleus
AN3622.1	hypothetical protein [Neurospora crassa]			YOR301W	
AN3623.1	COP9 signalosome, subunit CSN7	OT			
AN3624.1	Cation transport ATPase	P	Inorganic ion transport, metabolism	YDR270W	
AN3625.1	predicted protein [Neurospora crassa]				
AN3626.1	Phosphoribosylamidoimidazole-succinocarboxamide synthase	F	Nucleotide transport, metabolism	YOR128C	cytoplasm
AN3627.1	hypothetical protein [Neurospora crassa]				
AN3628.1	N-terminal acetyltransferase	B	Chromatin structure, dynamics	YDL040C	cytoplasm
AN3629.1	Formamidopyrimidine-DNA glycosylase	L	Replication, recombination, repair		
AN3632.1	Nuclear architecture related protein	Y	Nuclear structure	YNL240C	
AN3634.1	Anthranilate phosphoribosyltransferase	E	Amino acid transport, metabolism	YDR354W	cytoplasm nucleus
AN3635.1	predicted protein [Neurospora crassa]				
AN3636.1	hypothetical protein [Neurospora crassa]				
AN3642.1	Membrane coat complex Retromer, subunit VPS26	U	Intracellular trafficking/secretion/transport	YJL053W	endosome
AN3643.1	Uncharacterized conserved protein	S		YNL297C	early Golgi

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3644.1	Ubiquitin-conjugating enzyme E2	O	Posttranslational modification/turnover/chaperones	YGL087C	cytoplasm nucleus
AN3646.1	Uncharacterized conserved protein, contains RWD domain	S		YDR152W	cytoplasm
AN3648.1	Cyclin B and related kinase-activating proteins	D	Cell cycle/division, chrom. partitioning	YPR119W	nucleus
AN3649.1	Mitochondrial/chloroplast ribosomal protein L2	J	Translation, ribosomal structure, biogenesis	YEL050C	cytoplasm nucleus
AN3650.1	hypothetical protein [Neurospora crassa]				
AN3651.1	WD40 repeat protein	S			
AN3653.1	DNA replication helicase	L	Replication, recombination, repair	YHR164C	nucleus
AN3655.1	predicted protein [Neurospora crassa]				
AN3656.1	Carbon-nitrogen hydrolase	E	Amino acid transport, metabolism	YJL126W	
AN3657.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp44/Dis3	J	Translation, ribosomal structure, biogenesis	YOL021C	nucleolus cytoplasm nucleus
AN3658.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism	YKL221W	
AN3659.1	Adaptor protein Enigma and related PDZ-LIM proteins	TZ			
AN3660.1	Methyltransferase-like protein	R			
AN3661.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN3662.1	Alkaline ceramidase	I	Lipid transport, metabolism		
AN3663.1	Predicted mitochondrial carrier protein	C	Energy production, conversion	YDL119C	mitochondrion
AN3664.1	C-type lectin	TV			
AN3665.1	Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	P	Inorganic ion transport, metabolism	YGR125W	vacuole
AN3666.1	Predicted alpha-helical protein, potentially involved in replication/repair	L	Replication, recombination, repair	YDR013W	
AN3667.1	HMG-box transcription factor	K	Transcription		
AN3668.1	Chromatin remodeling protein, contains PHD Zn-finger	B	Chromatin structure, dynamics		
AN3669.1	Protein involved in cell differentiation/sexual development	R		YNL288W	cytoplasm
AN3671.1	predicted protein [Neurospora crassa]				
AN3673.1	Molecular chaperone Prefoldin, subunit 1	O	Posttranslational modification/turnover/chaperones		
AN3677.1	Asparagine synthase	E	Amino acid transport, metabolism	YML096W	cytoplasm
AN3678.1	Vacuolar assembly/sorting protein VPS9	U	Intracellular trafficking/secretion/transport		
AN3679.1	Reductases with broad range of substrate specificities	R			
AN3681.1	Uncharacterized membrane protein	S		YLR220W	vacuole
AN3682.1	hypothetical protein [Neurospora crassa]				
AN3683.1	hypothetical protein [Neurospora crassa]				
AN3685.1	Ngg1-interacting factor 3 protein NIF3L1	R			
AN3687.1	Alkyl hydroperoxide reductase/peroxiredoxin	O	Posttranslational modification/turnover/chaperones		
AN3688.1	Heat shock transcription factor	K	Transcription		
AN3689.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones	YKR017C	
AN3690.1	Mitochondrial carrier protein MRS3/4	C	Energy production, conversion	YJL133W	mitochondrion
AN3691.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones		
AN3692.1	Predicted membrane protein	S		YOL107W	Golgi early Golgi
AN3693.1	Beta-transducin family (WD-40 repeat) protein	B	Chromatin structure, dynamics		
AN3695.1	Isochorismate synthase	E	Amino acid transport, metabolism	YER090W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3696.1	Equilibrative nucleoside transporter protein	F	Nucleotide transport, metabolism		
AN3702.1	Leucyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YPL160W	cytoplasm
AN3705.1	Uncharacterized conserved protein	S			
AN3706.1	40s ribosomal protein s10	J	Translation, ribosomal structure, biogenesis		
AN3707.1	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	E	Amino acid transport, metabolism		
AN3708.1	Zinc-binding protein of the histidine triad (HIT) family	T	Signal transduction mechanisms	YDL125C	cytoplasm nucleus
AN3711.1	Ubiquitin-specific protease	O	Posttranslational modification/turnover/chaperones	YMR223W	nucleus
AN3712.1	Predicted hydrolase related to dienelactone hydrolase	R		YAL049C	cytoplasm
AN3714.1	hypothetical protein [Neurospora crassa]				
AN3715.1	Glycosylphosphatidylinositol anchor attachment protein GAA1	O	Posttranslational modification/turnover/chaperones		
AN3716.1	26S proteasome regulatory complex, subunit RPN9/PSMD13	O	Posttranslational modification/turnover/chaperones	YDR427W	nucleus
AN3717.1	Methyltransferases	H	Coenzyme transport, metabolism		
AN3719.1	Mitogen-activated protein kinase	T	Signal transduction mechanisms	YBL016W	cytoplasm nucleus
AN3720.1	Vesicle coat complex COPII, subunit SEC24/subunit SFB2	U	Intracellular trafficking/secretion/transport	YIL109C	ER to Golgi
AN3721.1	Kinesin-like protein	Z	Cytoskeleton		
AN3723.1	Uncharacterized conserved protein	S			
AN3724.1	unnamed protein product [Podospora anserina]				
AN3725.1	chaperone/heat shock protein [Emericella nidulans]			YFL014W	cytoplasm nucleus
AN3726.1	RAN guanine nucleotide release factor	T	Signal transduction mechanisms		
AN3727.1	Exo-beta-1,3-glucanase	G	Carbohydrate transport, metabolism	YGR279C	vacuole
AN3729.1	1,3-beta-glucan synthase/callose synthase catalytic subunit	M		YGR032W	
AN3730.1	beta (1-3) glucanosyltransferase Gel3p [Aspergillus fumigatus]			YMR307W	mitochondrion ER nuclear periphery
AN3731.1	SPRT-like metalloprotease	S			
AN3732.1	Coeffector of mDia Rho GTPase, regulates actin polymerization and cell adhesion turnover	TZ			
AN3733.1	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	G	Carbohydrate transport, metabolism	YLR057W	
AN3734.1	Integral membrane protein	R			
AN3735.1	GTPase-activating protein	R		YKL092C	cell periphery bud neck cytoplasm
AN3736.1					
AN3737.1	WD40 protein	S		YDL156W	cytoplasm nucleus
AN3738.1	Uncharacterized conserved protein	S		YLR201C	mitochondrion
AN3741.1	Alcohol dehydrogenase, class V	Q			
AN3742.1					
AN3743.1	RNA polymerase II, large subunit	K	Transcription		
AN3744.1	Mitochondrial ribosome small subunit component, mediator of apoptosis DAP3	J	Translation, ribosomal structure, biogenesis	YGL129C	mitochondrion
AN3745.1	Regulator of ribosome synthesis	J	Translation, ribosomal structure, biogenesis	YOR294W	
AN3746.1	Rac GTPase-activating protein BCR/ABR	T	Signal transduction mechanisms		
AN3747.1	Protein geranylgeranyltransferase type II, beta subunit	O	Posttranslational modification/turnover/chaperones	YPR176C	
AN3748.1	ATP phosphoribosyltransferase	E	Amino acid transport, metabolism	YER055C	
AN3749.1	Mismatch repair MSH3	L	Replication, recombination, repair	YCR092C	cytoplasm nucleus
AN3750.1	predicted protein [Neurospora crassa]				

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN3751.1	hypothetical protein [Neurospora crassa]				
AN3752.1	Uncharacterized conserved protein, contains TBC domain	TR			
AN3753.1	Telomerase catalytic subunit/reverse transcriptase TERT	LB			
AN3754.1	Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	T	Signal transduction mechanisms		
AN3755.1	Cyclin	R			
AN3756.1	20S proteasome, regulatory subunit beta type PSMB6/PSMB9/PRE3	O	Posttranslational modification/turnover/chaperones	YJL001W	nucleus
AN3757.1	Predicted alpha/beta hydrolase BEM46	R		YNL320W	
AN3758.1	Mitochondrial F1-ATPase assembly protein	O	Posttranslational modification/turnover/chaperones	YNL315C	mitochondrion
AN3759.1	Mitochondrial sulfhydryl oxidase involved in the biogenesis of cytosolic Fe/S proteins	O	Posttranslational modification/turnover/chaperones		
AN3760.1	Cell growth-regulating nucleolar protein	D	Cell cycle/division, chrom. partitioning		
AN3763.1	Predicted transporter (major facilitator superfamily)	R			
AN3765.1					
AN3766.1	Methyl-CpG binding transcription regulators	KB			
AN3767.1	Gamma-glutamyltransferase	E	Amino acid transport, metabolism		
AN3769.1	predicted protein [Neurospora crassa]				
AN3771.1	Predicted coiled-coil protein	R			
AN3772.1	Sideroflexin	R			
AN3776.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN3777.1	beta-1,6-glucanase [Verticillium fungicola]				
AN3778.1	Molybdopterin biosynthesis protein	H	Coenzyme transport, metabolism		
AN3779.1	Exopolyphosphatases and related proteins	C	Energy production, conversion	YHR201C	cytoplasm nucleus
AN3781.1	Na+/Pi symporter	P	Inorganic ion transport, metabolism		
AN3784.1	DNA excision repair protein XPA/XPAC/RAD14	L	Replication, recombination, repair	YMR201C	cytoplasm nucleus
AN3785.1	Chromatin assembly complex 1 subunit B/CAC2 (contains WD40 repeats)	BL			
AN3787.1	Peptide:N-glycanase	O	Posttranslational modification/turnover/chaperones	YPL096W	cytoplasm
AN3789.1	Predicted dioxygenase	R		YJR008W	cytoplasm nucleus
AN3790.1	mutanase [Penicillium purpurogenum]				
AN3791.1					
AN3793.1	Serine/threonine specific protein phosphatase PP1, catalytic subunit	TR			
AN3794.1	WD40 repeat protein	R			
AN3795.1	Cyclin B and related kinase-activating proteins	D	Cell cycle/division, chrom. partitioning		
AN3797.1	3'-5' DNA helicase	L	Replication, recombination, repair	YOL095C	
AN3798.1	Flavohemoprotein b5+b5R	C	Energy production, conversion		
AN3799.1	Fe2+/Zn2+ regulated transporter	P	Inorganic ion transport, metabolism		
AN3802.1	predicted protein [Neurospora crassa]				
AN3803.1	Translocase of outer mitochondrial membrane complex, subunit TOM37/Metaxin 1	U	Intracellular trafficking/secretion/transport		
AN3805.1	PEP phosphonomutase and related enzymes	G	Carbohydrate transport, metabolism		
AN3809.1	Amidases related to nicotinamidase	Q			
AN3810.1	Protein involved in transcription start site selection	K	Transcription	YNL222W	
AN3811.1	Transcription-coupled repair protein CSB/RAD26 (contains SNF2 family DNA-dependent ATPase domain)	KL			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3812.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	J	Translation, ribosomal structure, biogenesis	YGR195W	nucleolus nucleus
AN3813.1	Copper transporter	P	Inorganic ion transport, metabolism		
AN3814.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN3815.1	Dystonin, GAS (Growth-arrest-specific protein), and related proteins	Z	Cytoskeleton		
AN3817.1	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) reductase	I	Lipid transport, metabolism	YML075C	nuclear periphery
AN3818.1	predicted protein [Neurospora crassa]				
AN3819.1	hypothetical protein [Neurospora crassa]				
AN3821.1	Equilibrative nucleoside transporter protein	F	Nucleotide transport, metabolism		
AN3824.1	Phenylalanyl-tRNA synthetase, beta subunit	J	Translation, ribosomal structure, biogenesis	YFL022C	
AN3826.1	Major facilitator superfamily permease - Cdc91p	R		YLR459W	
AN3827.1	Protein required for normal rRNA processing	A	RNA processing, modification	YGR103W	nucleolus nucleus
AN3828.1					
AN3829.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion	YBR006W	cytoplasm
AN3830.1	Threonine/serine dehydratases	E	Amino acid transport, metabolism	YER086W	mitochondrion
AN3831.1	Uncharacterized protein, induced by hypoxia	R			
AN3832.1	Mitochondrial elongation factor	J	Translation, ribosomal structure, biogenesis	YLR069C	mitochondrion
AN3833.1	Predicted alpha/beta hydrolase	R			
AN3835.1	amyR [Emericella nidulans]				
AN3837.1	Beta-fructofuranosidase (invertase)	G	Carbohydrate transport, metabolism		
AN3838.1	unnamed protein product [Podospora anserina]			YOR118W	cytoplasm
AN3839.1	N-myristoyl transferase	I	Lipid transport, metabolism	YLR195C	cytoplasm
AN3840.1	Folylpolyglutamate synthase	H	Coenzyme transport, metabolism	YOR241W	cytoplasm
AN3841.1	Putative phosphoinositide phosphatase	I	Lipid transport, metabolism	YKL212W	vacuole ER
AN3842.1	GTPase Rab5/YPT51 and related small G protein superfamily GTPases	U	Intracellular trafficking/secretion/transport		
AN3843.1	Mitochondrial inner membrane protein (mitofilin)	M		YKR016W	mitochondrion
AN3844.1	predicted protein [Neurospora crassa]				
AN3846.1	Ornithine decarboxylase	E	Amino acid transport, metabolism	YKL184W	cytoplasm
AN3847.1	Cobalamin synthesis protein	H	Coenzyme transport, metabolism		
AN3849.1	2-hydroxychromene-2-carboxylate isomerase	Q			
AN3851.1	Putative N2,N2-dimethylguanosine tRNA methyltransferase	A	RNA processing, modification		
AN3852.1	predicted protein [Neurospora crassa]				
AN3853.1	Metalloendoprotease HMP1 (insulinase superfamily)	RO		YDR430C	mitochondrion
AN3855.1	Dioxygenases related to 2-nitropropane dioxygenase	R			
AN3861.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN3862.1	NADH-cytochrome b-5 reductase	HC			
AN3865.1	Methionyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YGR171C	mitochondrion
AN3866.1	Threonine/serine dehydratases	E	Amino acid transport, metabolism		
AN3867.1	Protein farnesyltransferase, alpha subunit/protein geranylgeranyltransferase type I, alpha subunit	O	Posttranslational modification/turnover/chaperones	YKL019W	vacuole
AN3868.1	predicted protein [Neurospora crassa]				
AN3869.1	Mevalonate kinase MVK/ERG12	I	Lipid transport, metabolism		
AN3873.1	Zinc-binding oxidoreductase	CR			
AN3874.1	hypothetical protein [Neurospora crassa]				
AN3877.1	hypothetical protein F9K20.18 [imported] - Arabidopsis thaliana				
AN3883.1	putative glucanase precursor [Schizosaccharomyces pombe]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN3888.1	Predicted transporter (major facilitator superfamily)	R		YBR293W	
AN3889.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN3890.1	Nucleotide excision repair complex XPC-HR23B, subunit XPC/DPB11	L	Replication, recombination, repair	YER162C	cytoplasm nucleus
AN3894.1	Aconitase/homoaconitase (aconitase superfamily)	CE		YJL200C	mitochondrion
AN3895.1	Predicted acyl-CoA transferases/carnitine dehydratase	C	Energy production, conversion		
AN3898.1	predicted protein [Neurospora crassa]				
AN3900.1	predicted protein [Neurospora crassa]				
AN3903.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN3904.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN3905.1	Phosphotyrosyl phosphatase activator	DT		YIL153W	cytoplasm nucleus
AN3907.1	Transcription initiation factor TFIID, subunit TAF1	K	Transcription	YGR274C	nucleus
AN3908.1	FKBP-type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN3909.1	Translesion DNA polymerase - REV1 deoxycytidyl transferase	L	Replication, recombination, repair		
AN3910.1	Origin recognition complex, subunit 1, and related proteins	L	Replication, recombination, repair		
AN3912.1	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q			
AN3913.1	Serine/threonine phosphatase 2C containing leucine-rich repeats, similar to SCN circadian oscillatory protein (SCOP)	T	Signal transduction mechanisms	YJL005W	
AN3914.1	Beta-glucanase/Beta-glucan synthetase	G	Carbohydrate transport, metabolism		
AN3915.1	Aquaporin (major intrinsic protein family)	G	Carbohydrate transport, metabolism		
AN3916.1	Ribulose kinase and related carbohydrate kinases	G	Carbohydrate transport, metabolism	YHL032C	mitochondrion
AN3918.1	Transferrin receptor and related proteins containing the protease-associated (PA) domain	OPR		YBR286W	
AN3919.1	Nuclear polyadenylated RNA binding protein	A	RNA processing, modification		
AN3920.1	Protoporphyrinogen oxidase	H	Coenzyme transport, metabolism	YER014W	mitochondrion
AN3921.1	Uncharacterized conserved protein	S			
AN3923.1	N-end rule pathway, recognition component UBR1	O	Posttranslational modification/turnover/chaperones		
AN3924.1	Transcription regulator XNP/ATRX, DEAD-box superfamily	K	Transcription		
AN3925.1	hypothetical protein (hypothetical protein B24P11.210 [imported] - Neurospora crassa)				
AN3926.1	WD40 repeat-containing protein	R			
AN3927.1	Sphingomyelinase family protein	T	Signal transduction mechanisms	YER019W	
AN3928.1	Protein involved in thiamine biosynthesis and DNA damage tolerance	R		YGR144W	
AN3929.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN3930.1	predicted protein [Neurospora crassa]				
AN3932.1	20S proteasome, regulatory subunit beta type PSMB5/PSMB8/PRE2	O	Posttranslational modification/turnover/chaperones	YPR103W	cytoplasm nucleus
AN3933.1	RNA polymerase I, second largest subunit	K	Transcription	YPR010C	nucleolus
AN3937.1	Uncharacterized conserved protein	S		YGR093W	nucleus
AN3938.1	DRIM (Down-regulated in metastasis)-like proteins	V	Defense mechanisms	YBL004W	nucleolus cytoplasm
AN3939.1	Cullins	D	Cell cycle/division, chrom. partitioning	YGR003W	cytoplasm nucleus
AN3940.1	Predicted alpha-helical protein, potentially involved in replication/repair	L	Replication, recombination, repair	YDR489W	

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN3941.1	M-phase inducer phosphatase	D	Cell cycle/division, chrom. partitioning		
AN3944.1	Predicted regulator of rRNA gene transcription (MYB-binding protein)	K	Transcription	YEL055C	nucleolus nucleus
AN3945.1	predicted protein [Neurospora crassa]				
AN3946.1	Mitotic checkpoint serine/threonine protein kinase	D	Cell cycle/division, chrom. partitioning	YGR188C	spindle pole microtubule nucleus
AN3948.1	Predicted integral membrane protein	S		YML038C	early Golgi
AN3951.1					
AN3952.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN3953.1	RNA-binding proteins	R			
AN3954.1	6-phosphogluconate dehydrogenase	G	Carbohydrate transport, metabolism	YHR183W	cytoplasm
AN3955.1	Uncharacterized conserved protein	S		YHR121W	cytoplasm nucleus
AN3957.1	Amidases	JIT			
AN3958.1	DNA alkylation damage repair protein	A	RNA processing, modification		
AN3963.1	Thioredoxin reductase	O	Posttranslational modification/turnover/chaperones		
AN3970.1	Kinesin (KAR3 subfamily)	Z	Cytoskeleton		
AN3971.1	Aldo/keto reductase family proteins	R			
AN3972.1	Oxoprolinase	E	Amino acid transport, metabolism	YKL215C	cytoplasm
AN3973.1	Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes	O	Posttranslational modification/turnover/chaperones	YBL064C	mitochondrion
AN3987.1	hypothetical protein [Streptomyces avermitilis MA-4680]				
AN3991.1	unsaturated glucuronylhydrolase [Bacteroides thetaiotaomicron VPI-5482]				
AN3999.1	E3 ubiquitin protein ligase	O	Posttranslational modification/turnover/chaperones		
AN4002.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN4003.1	Isocitrate/isopropylmalate dehydrogenase	CE			
AN4007.1	Succinyl-CoA:alpha-ketoacid-CoA transferase	C	Energy production, conversion		
AN4014.1	Vacuolar sorting protein VPS52/suppressor of actin Sac2	UZ			
AN4015.1	Translation initiation factor 5A (eIF-5A)	J	Translation, ribosomal structure, biogenesis	YEL034W	
AN4016.1	Ubiquitin/60s ribosomal protein L40 fusion	J	Translation, ribosomal structure, biogenesis	YKR094C	cytoplasm
AN4017.1	Uncharacterized conserved protein	S		YGL161C	cytoplasm
AN4018.1	Transferrin receptor and related proteins containing the protease-associated (PA) domain	OPR		YJR126C	
AN4019.1	Permease of the major facilitator superfamily	R			
AN4021.1	Zn finger protein	R			
AN4022.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin	B	Chromatin structure, dynamics		
AN4023.1	Uncharacterized conserved protein	S			
AN4024.1	hypothetical protein [Neurospora crassa]				
AN4025.1	Predicted acid phosphatase	R			
AN4026.1					
AN4028.1	Uncharacterized conserved protein	S			
AN4030.1	hypothetical protein [Neurospora crassa]				
AN4032.1	mRNA splicing factor ATP-dependent RNA helicase	A	RNA processing, modification	YKR086W	cytoplasm nucleus
AN4034.1	CCAAT-binding factor, subunit A (HAP3)	K	Transcription		
AN4035.1	ACETAMIDASE REGULATORY PROTEIN				
AN4036.1	Predicted GTPase activator protein	T	Signal transduction mechanisms		
AN4038.1	Translation initiation factor 5B (eIF-5B)	J	Translation, ribosomal structure, biogenesis		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4040.1	Tannase precursor				
AN4041.1					
AN4042.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI		YMR015C	ER
AN4043.1	Signal recognition particle, subunit Srp68	U	Intracellular trafficking/secretion/transport	YPL243W	cytoplasm
AN4044.1	DNA replication licensing factor, MCM3 component	L	Replication, recombination, repair		
AN4046.1	Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)	R		YGR110W	
AN4048.1	TatD-related DNase	L	Replication, recombination, repair	YMR262W	
AN4050.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion		
AN4051.1	predicted protein [Neurospora crassa]				
AN4052.1	Endoglucanase	G	Carbohydrate transport, metabolism	YLR300W	vacuole
AN4053.1	Nuclear transport receptor KAP120 (importin beta superfamily)	YU		YPL125W	cytoplasm nucleus
AN4055.1	acid phosphatase PHOa [Aspergillus fumigatus]				
AN4056.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN4057.1	mRNA capping enzyme, guanylyltransferase (alpha) subunit	A	RNA processing, modification		
AN4058.1	Dihydroxy-acid dehydratase	E	Amino acid transport, metabolism		
AN4060.1	40S ribosomal protein S19	J	Translation, ribosomal structure, biogenesis	YNL302C	cytoplasm
AN4062.1	predicted protein [Neurospora crassa]				
AN4064.1	Mitochondrial ADP/ATP carrier proteins	C	Energy production, conversion	YBL030C	
AN4065.1	KRR1-interacting protein involved in 40S ribosome biogenesis	J	Translation, ribosomal structure, biogenesis		
AN4066.1	Putative GTPase activating proteins (GAPs)	T	Signal transduction mechanisms		
AN4068.1	UDP-galactose transporter related protein	G	Carbohydrate transport, metabolism	YPL244C	
AN4070.1	Uncharacterized conserved protein	S			
AN4071.1	Predicted steroid reductase	I	Lipid transport, metabolism		
AN4072.1	FOG: Ankyrin repeat	R			
AN4073.1	40S ribosomal protein S12	J	Translation, ribosomal structure, biogenesis	YOR369C	
AN4074.1	Vacuolar import and degradation protein	U	Intracellular trafficking/secretion/transport		
AN4076.1	predicted protein [Neurospora crassa]				
AN4077.1	predicted protein [Neurospora crassa]				
AN4080.1	GTP-binding protein DRG1 (ODN superfamily)	T	Signal transduction mechanisms	YAL036C	cytoplasm
AN4082.1	Glycosyl transferase, family 8 - glycogenin	G	Carbohydrate transport, metabolism		
AN4085.1	Protein phosphatase 2A regulatory subunit A and related proteins	T	Signal transduction mechanisms	YAL016W	cytoplasm nucleus
AN4086.1	Phenylalanyl-tRNA synthetase beta subunit	J	Translation, ribosomal structure, biogenesis	YLR060W	cytoplasm
AN4087.1	40S ribosomal protein S3	J	Translation, ribosomal structure, biogenesis	YNL178W	
AN4088.1	predicted protein [Neurospora crassa]				
AN4089.1	Translation initiation factor 5B (eIF-5B)	J	Translation, ribosomal structure, biogenesis		
AN4090.1	Uncharacterized conserved protein	S			
AN4093.1	tRNA-specific adenosine deaminase 1	A	RNA processing, modification		
AN4094.1	Sterol reductase/lamin B receptor	IT		YNL280C	ER
AN4095.1	Cation-independent mannose-6-phosphate receptor CI-MPR	TU			
AN4096.1	hypothetical protein [Neurospora crassa]				
AN4098.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN4099.1	predicted protein [Neurospora crassa]				
AN4102.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN4104.1					
AN4105.1	Erythromycin esterase homolog	R			
AN4109.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4111.1	Probable taurine catabolism dioxygenase	Q			
AN4112.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN4120.1	Dioxygenases related to 2-nitropropane dioxygenase	R			
AN4124.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN4148.1	Predicted transporter (major facilitator superfamily)	R			
AN4150.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN4159.1	Glutamine synthetase	E	Amino acid transport, metabolism	YPR035W	cytoplasm
AN4160.1	predicted protein [Neurospora crassa]				
AN4161.1	Uncharacterized conserved protein	S		YMR114C	cytoplasm nucleus
AN4162.1	predicted protein [Neurospora crassa]				
AN4163.1	G protein beta subunit-like protein	T	Signal transduction mechanisms	YMR116C	
AN4166.1	WD40 protein DMR-N9	R			
AN4167.1	Predicted Ras related/Rac-GTP binding protein	V	Defense mechanisms	YAL048C	
AN4168.1	Uncharacterized conserved protein	S		YHR016C	
AN4169.1	hypothetical protein [Neurospora crassa]				
AN4170.1	Thioredoxin binding protein TBP-2/VDUP1	R		YFR022W	
AN4171.1	hypothetical protein [Neurospora crassa]			YNL047C	
AN4172.1	gp7 [Roseophage SIO1]				
AN4174.1	Glyoxalase	G	Carbohydrate transport, metabolism	YML004C	cytoplasm nucleus
AN4175.1	NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIT-4 [Neurospora crassa]				
AN4177.1	hypothetical protein [Neurospora crassa]				
AN4178.1	Predicted metal-binding protein	R		YER156C	cytoplasm nucleus
AN4179.1	Acetyl-CoA acetyltransferase	I	Lipid transport, metabolism		
AN4180.1	Predicted transporter (major facilitator superfamily)	R			
AN4182.1	Protein kinase PCTAIRE and related kinases	R		YBR160W	cytoplasm nucleus
AN4183.1	Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	OT			
AN4184.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN4186.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN4187.1	SNF2 family DNA-dependent ATPase domain-containing protein	K	Transcription	YPL082C	nucleus
AN4188.1	hypothetical protein (hypothetical protein 15E6.130 [imported] - Neurospora crassa emb|CAB88644.1| (AL353822) conserved hypothetical protein [Neurospora crassa])				
AN4189.1	Mitogen-activated protein kinase kinase (MAP2K)	T	Signal transduction mechanisms	YOR231W	
AN4192.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN4194.1	ARK protein kinase family	T	Signal transduction mechanisms		
AN4199.1					
AN4200.1	Leucine rich repeat proteins, some proteins contain F-box	R			
AN4201.1	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ			
AN4202.1	60S ribosomal protein L13a	J	Translation, ribosomal structure, biogenesis	YIL133C	cytoplasm
AN4204.1	Phosphoesterases	R			
AN4206.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN4207.1	Vesicle coat complex AP-1, gamma subunit	U	Intracellular trafficking/secretion/transport	YPR029C	
AN4208.1	Sterol O-acyltransferase/Diacylglycerol O-acyltransferase	I	Lipid transport, metabolism	YNR019W	ER

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4209.1	Predicted integral membrane protein	R			
AN4210.1	Signaling protein SWIFT and related BRCT domain proteins	KTDL			
AN4211.1	Integral membrane protein	R			
AN4214.1	Alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)	A	RNA processing, modification		
AN4215.1	Glutaredoxin and related proteins	O	Posttranslational modification/turnover/chaperones	YDR513W	nucleus
AN4216.1	conserved hypothetical protein [Neurospora crassa]				
AN4217.1	Threonine/serine dehydratases	E	Amino acid transport, metabolism	YCL064C	mitochondrion
AN4218.1	Translation elongation factor EF-1 alpha/Tu	J	Translation, ribosomal structure, biogenesis	YPR080W	cytoplasm
AN4219.1	RNA polymerase III subunit C11	K	Transcription	YDR045C	
AN4220.1	hypothetical protein [Neurospora crassa]			YGL242C	
AN4221.1	Uncharacterized conserved protein (tumor-rejection antigen MAGE in humans)	S			
AN4222.1	60S ribosomal protein L27	J	Translation, ribosomal structure, biogenesis	YHR010W	nucleolus cytoplasm
AN4223.1	Cytoskeleton-associated protein and related proteins	ZR			
AN4224.1	Uncharacterized conserved protein, contains TBC domain	TR		YJR116W	
AN4225.1	26S proteasome regulatory complex, subunit RPN6/PSMD11	O	Posttranslational modification/turnover/chaperones		
AN4226.1	Sof1-like rRNA processing protein (contains WD40 repeats)	A	RNA processing, modification	YLL011W	nucleolus
AN4227.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR		YDL114W	
AN4228.1	Cytosine deaminase and related metal-dependent hydrolases	FR			
AN4230.1	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I	Lipid transport, metabolism		
AN4231.1	Riboflavin synthase alpha chain	H	Coenzyme transport, metabolism	YBR256C	
AN4232.1	RNA-binding protein required for 60S ribosomal subunit biogenesis	J	Translation, ribosomal structure, biogenesis	YHR066W	nucleolus nucleus
AN4233.1	ATP-dependent RNA helicase	A	RNA processing, modification	YHR065C	
AN4234.1	Phosphoglucomutase/phosphomannomutase	G	Carbohydrate transport, metabolism	YEL058W	cytoplasm nucleus
AN4236.1	26S proteasome regulatory complex, ATPase RPT5	O	Posttranslational modification/turnover/chaperones	YOR117W	nucleus
AN4237.1	predicted protein [Neurospora crassa]				
AN4238.1	Ribosomal protein S6 kinase and related proteins	RT			
AN4239.1	hypothetical protein [Neurospora crassa]				
AN4240.1	Protein involved in glucose derepression and pre-vacuolar endosome protein sorting	U	Intracellular trafficking/secretion/transport	YLR025W	endosome
AN4241.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN4244.1	Spliceosome-associated coiled-coil protein	S			
AN4245.1	Ceramidases	T	Signal transduction mechanisms		
AN4247.1	predicted protein [Neurospora crassa]				
AN4248.1	predicted protein [Neurospora crassa]				
AN4250.1	Mitochondrial carnitine-acylcarnitine carrier protein	C	Energy production, conversion	YPR058W	
AN4251.1	Mitochondrial/chloroplast ribosomal protein S2	J	Translation, ribosomal structure, biogenesis		
AN4253.1	predicted protein [Neurospora crassa]				
AN4255.1	Hexokinase	G	Carbohydrate transport, metabolism		
AN4257.1	hypothetical protein [Streptomyces avermitilis MA-4680]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4258.1	Uridylate kinase/adenylate kinase	F	Nucleotide transport, metabolism	YKL024C	cytoplasm nucleus
AN4259.1	Uncharacterized conserved protein, contains PCI domain	R			
AN4261.1					
AN4262.1	Trehalose-6-phosphate synthase component TPS1 and related subunits	G	Carbohydrate transport, metabolism		
AN4263.1	FOG: Zn-finger	R			
AN4264.1	Cell division protein	D	Cell cycle/division, chrom. partitioning		
AN4265.1	Chromosome condensation complex Condensin, subunit H	BD			
AN4266.1	K+-dependent Na+:Ca2+ antiporter	P	Inorganic ion transport, metabolism		
AN4267.1	predicted protein [Neurospora crassa]				
AN4268.1	Dioxygenases related to 2-nitropropane dioxygenase	R			
AN4269.1	RNA polymerase, subunit L	K	Transcription	YOL005C	nucleus
AN4270.1	Synaptic vesicle protein EHS-1 and related EH domain proteins	TU			
AN4271.1	Leucine rich repeat proteins, some proteins contain F-box	R		YJR052W	cytoplasm nucleus
AN4273.1	predicted protein [Neurospora crassa]				
AN4274.1	Putative GTPase activating proteins (GAPs)	T	Signal transduction mechanisms		
AN4276.1	FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations	R			
AN4278.1	Phosphatidylinositol 4-kinase	T	Signal transduction mechanisms	YLR305C	
AN4280.1	Predicted mitochondrial carrier protein	C	Energy production, conversion		
AN4281.1	GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	TU		YFL038C	
AN4282.1	Puromycin-sensitive aminopeptidase and related aminopeptidases	EO			
AN4287.1	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE		YOR307C	ER
AN4290.1	Predicted translation initiation factor related to eIF-2B alpha/beta/delta subunits (CIG2/IDI2)	J	Translation, ribosomal structure, biogenesis	YPR118W	cytoplasm nucleus
AN4293.1	Nuclear pore complex, Nup133 component (sc Nup133)	YU		YKR082W	nuclear periphery
AN4294.1	(acyl-carrier-protein) S-malonyltransferase	I	Lipid transport, metabolism		
AN4295.1	Predicted member of the intramitochondrial sorting protein family	U	Intracellular trafficking/secretion/transport	YLR168C	mitochondrion
AN4297.1	NADH-ubiquinone oxidoreductase, NUFS7/PSST/20 kDa subunit	C	Energy production, conversion		
AN4298.1	U3 small nucleolar ribonucleoprotein (snoRNP) subunit - Mpp10p	A	RNA processing, modification		
AN4299.1	conserved hypothetical protein [Neurospora crassa]				
AN4302.1	hypothetical protein [Neurospora crassa]				
AN4303.1	Choline phosphate cytidylyltransferase/Predicted CDP-ethanolamine synthase	I	Lipid transport, metabolism	YGR007W	cytoplasm nucleus
AN4304.1	Glutaredoxin-related protein	O	Posttranslational modification/turnover/chaperones	YPL059W	mitochondrion
AN4305.1	Halotolerance protein HAL3 (contains flavoprotein domain)	PD			
AN4306.1	hypothetical protein ((AL451012) related to c-module-binding factor [Neurospora crassa])				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4307.1	Hypothetical ORF; Yil157cp [Saccharomyces cerevisiae]			YIL157C	mitochondrion
AN4308.1	Mitochondrial/chloroplast ribosomal protein L3	J	Translation, ribosomal structure, biogenesis	YGR220C	mitochondrion
AN4310.1	FOG: Ankyrin repeat	R		YGR233C	cytoplasm nucleus
AN4312.1	predicted protein [Neurospora crassa]				
AN4314.1	predicted protein [Neurospora crassa]				
AN4315.1	ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	EJ		YFR009W	cytoplasm
AN4316.1	Predicted transporter (major facilitator superfamily)	R			
AN4317.1	Vesicle coat complex COPII, subunit SEC13	U	Intracellular trafficking/secretion/transport	YLR208W	ER to Golgi
AN4318.1	peroxin [Yarrowia lipolytica]				
AN4321.1	Dipeptidyl peptidase III	R		YOL057W	cytoplasm nucleus
AN4322.1	Protein kinase	T	Signal transduction mechanisms	YGL083W	late Golgi
AN4323.1	Branched chain aminotransferase BCAT1, pyridoxal phosphate enzymes type IV superfamily	E	Amino acid transport, metabolism	YHR208W	
AN4324.1	predicted protein [Neurospora crassa]				
AN4326.1	Casein kinase II, beta subunit	TDK			
AN4327.1	Uncharacterized conserved protein, contains JmjC domain	BT			
AN4328.1	Amino acid transporters	E	Amino acid transport, metabolism	YBR132C	ER
AN4329.1	Putative steroid membrane receptor Hpr6.6/25-Dx	R			
AN4331.1	Structure-specific endonuclease ERCC1-XPF, ERCC1 component	L	Replication, recombination, repair		
AN4332.1	Protein transporter of the TRAM (translocating chain-associating membrane) superfamily	U	Intracellular trafficking/secretion/transport		
AN4333.1	predicted protein [Neurospora crassa]				
AN4334.1	hypothetical protein [Neurospora crassa]				
AN4336.1	Sorbitol dehydrogenase	Q			
AN4341.1					
AN4342.1	Tryptophan-rich basic nuclear protein	R			
AN4346.1	Nucleolar RNA-binding protein NIFK	R			
AN4349.1	Uncharacterized conserved protein, contains DENN and RUN domains	T	Signal transduction mechanisms		
AN4350.1	Pentafunctional AROM protein	E	Amino acid transport, metabolism		
AN4351.1	Predicted signal transduction protein	R		YOR275C	cytoplasm nucleus
AN4353.1	Peroxisomal 3-ketoacyl-CoA-thiolase P-44/SCP2	I	Lipid transport, metabolism		
AN4355.1	Pyrroline-5-carboxylate reductase	E	Amino acid transport, metabolism		
AN4358.1	Uncharacterized conserved protein	S			
AN4359.1	Znf1p [Gibberella moniliformis]				
AN4360.1	related to trfA protein [imported] - Neurospora crassa			YDR254W	microtubule
AN4361.1	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K	Transcription		
AN4362.1					
AN4364.1	Chitinase	M			
AN4365.1	DNA mismatch repair protein - MLH3 family	L	Replication, recombination, repair		
AN4367.1	Chitin synthase/hyaluronan synthase (glycosyltransferases)	M			
AN4369.1	Ras1 guanine nucleotide exchange factor	T	Signal transduction mechanisms		
AN4371.1					
AN4372.1	Endopolygalacturonase	M		YJR153W	
AN4375.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4376.1	Glutamate/leucine/phenylalanine/valine dehydrogenases	E	Amino acid transport, metabolism	YOR375C	cytoplasm nucleus
AN4377.1	predicted protein [Neurospora crassa]				
AN4378.1	Fucose permease	G	Carbohydrate transport, metabolism		
AN4380.1	Ribonucleotide reductase, alpha subunit	F	Nucleotide transport, metabolism	YER070W	
AN4382.1	Predicted panthothenate kinase/uridine kinase-related protein	FH		YFR007W	
AN4383.1	hypothetical protein [Neurospora crassa]				
AN4384.1	Folylpolyglutamate synthase	H	Coenzyme transport, metabolism	YMR113W	cytoplasm
AN4385.1	MEKK and related serine/threonine protein kinases	T	Signal transduction mechanisms		
AN4386.1	Predicted unusual protein kinase	R		YLR253W	mitochondrion
AN4387.1	Mitochondrial FAD carrier protein	C	Energy production, conversion	YIL006W	
AN4389.1	3-methyladenine DNA glycosidase	L	Replication, recombination, repair	YER142C	cytoplasm nucleus
AN4390.1	hypothetical protein [Neurospora crassa]			YBR078W	
AN4394.1					
AN4395.1	hypothetical protein [Neurospora crassa]			YEL036C	Golgi
AN4397.1	Acyl-CoA synthetase	I	Lipid transport, metabolism	YBR222C	cytoplasm
AN4398.1	mRNA splicing factor	A	RNA processing, modification		
AN4399.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YDL064W	cytoplasm nucleus
AN4401.1	Asparagine synthase (glutamine-hydrolyzing)	E	Amino acid transport, metabolism	YGR124W	cytoplasm
AN4402.1	Porin/voltage-dependent anion-selective channel protein	P	Inorganic ion transport, metabolism	YNL055C	mitochondrion cytoplasm
AN4405.1	Fatty acid desaturase	I	Lipid transport, metabolism		
AN4406.1	VAMP-associated protein involved in inositol metabolism	U	Intracellular trafficking/secretion/transport	YER120W	ER
AN4407.1	DNA repair and recombination protein RAD52/RAD22	L	Replication, recombination, repair		
AN4408.1	hypothetical protein [Magnaporthe grisea]				
AN4409.1	Ornithine carbamoyltransferase OTC/ARG3	E	Amino acid transport, metabolism	YJL088W	cytoplasm nucleus
AN4410.1	Uncharacterized conserved protein, contains WD40 repeat and BROMO domains	R			
AN4411.1	hypothetical protein ((AL513462) related to Sts1 protein [Neurospora crassa])				
AN4412.1	Nuclear exosomal RNA helicase MTR4, DEAD-box superfamily	A	RNA processing, modification	YJL050W	nucleolus nucleus
AN4413.1	IkappaB kinase complex, IKAP component	K	Transcription		
AN4414.1	Mevalonate pyrophosphate decarboxylase	I	Lipid transport, metabolism	YNR043W	cytoplasm
AN4415.1	Holocytochrome c synthase/heme-lyase	CO		YKL087C	
AN4416.1	SNARE protein PEP12/VAM3/Syntaxin 7/Syntaxin 17	U	Intracellular trafficking/secretion/transport	YOR036W	
AN4417.1	Uncharacterized conserved protein	S			
AN4418.1	predicted protein [Neurospora crassa]				
AN4419.1	Dual specificity phosphatase	V	Defense mechanisms	YIR026C	cytoplasm
AN4420.1	Acyl-CoA thioesterase	I	Lipid transport, metabolism		
AN4421.1	Glycolate oxidase	C	Energy production, conversion		
AN4422.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones		
AN4423.1					
AN4424.1	Glycolate oxidase	C	Energy production, conversion		
AN4425.1	TatD-related DNase	L	Replication, recombination, repair	YBL055C	cytoplasm
AN4426.1	Predicted protein tyrosine phosphatase	V	Defense mechanisms	YNL099C	cytoplasm
AN4428.1	Amino acid transporter protein	E	Amino acid transport, metabolism	YEL064C	
AN4430.1	Acetolactate synthase, small subunit	E	Amino acid transport, metabolism	YCL009C	mitochondrion

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4431.1	Predicted RNA-binding protein, contains KH domains	A	RNA processing, modification		
AN4433.1	FOG: PPR repeat	R			
AN4434.1	hypothetical protein B23I11.250 [imported] - Neurospora crassa			YIL093C	mitochondrion
AN4435.1	FOG: Leucine rich repeat	R			
AN4437.1	SOK1 kinase belonging to the STE20/SPS1/GC kinase family	T	Signal transduction mechanisms		
AN4439.1	predicted protein [Neurospora crassa]			YCL047C	
AN4440.1	predicted protein [Neurospora crassa]				
AN4441.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN4442.1	Ubiquitin fusion degradation protein-2	O	Posttranslational modification/turnover/chaperones	YDL190C	cytoplasm nucleus
AN4443.1	Methionine synthase II (cobalamin-independent)	E	Amino acid transport, metabolism	YER091C	cytoplasm
AN4445.1	DNA methyltransferase 1-associated protein-1	BK		YGR002C	nucleus
AN4446.1	emp24/gp25L/p24 family of membrane trafficking proteins	U	Intracellular trafficking/secretion/transport	YAR002C-A	vacuolar membrane
AN4447.1	Signal transduction histidine kinase	T	Signal transduction mechanisms		
AN4449.1	20S proteasome, regulatory subunit beta type PSMB3/PUP3	O	Posttranslational modification/turnover/chaperones	YER094C	
AN4453.1	Mitochondrial inheritance and actin cytoskeleton organization protein	Z	Cytoskeleton		
AN4456.1	U3 snoRNP-associated protein (contains WD40 repeats)	A	RNA processing, modification	YPR137W	nucleolus
AN4457.1	20S proteasome, regulatory subunit beta type PSMB2/PRE1	O	Posttranslational modification/turnover/chaperones	YER012W	
AN4458.1	Spindle pole body protein - Sad1p	Z	Cytoskeleton	YFR005C	cytoplasm nucleus
AN4459.1					
AN4460.1	WD40-repeat-containing subunit of the 18S rRNA processing complex	A	RNA processing, modification	YLR222C	nucleolus
AN4461.1	Transcriptional coactivator CAPER (RRM superfamily)	K	Transcription		
AN4462.1	Pyruvate carboxylase	C	Energy production, conversion	YBR218C	cytoplasm
AN4463.1	Vesicle coat protein clathrin, heavy chain	U	Intracellular trafficking/secretion/transport	YGL206C	late Golgi
AN4464.1	AICAR transformylase/IMP cyclohydrolase/methylglyoxal synthase	F	Nucleotide transport, metabolism	YMR120C	cytoplasm
AN4465.1	Putative growth response protein	T	Signal transduction mechanisms	YHR133C	nuclear periphery
AN4467.1	Peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones	YDR304C	vacuole
AN4469.1	Microtubule binding protein YTM1 (contains WD40 repeats)	Z	Cytoskeleton	YOR272W	nucleolus nucleus
AN4470.1	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	J	Translation, ribosomal structure, biogenesis	YER025W	cytoplasm
AN4471.1	WD40 repeat-containing protein	S		YKL021C	nucleolus nucleus
AN4472.1	Putative transcription factor HALR/MLL3, involved in embryonic development	R			
AN4473.1	Carboxylesterase and related proteins	R			
AN4475.1	60S ribosomal protein L11	J	Translation, ribosomal structure, biogenesis	YPR102C	cytoplasm
AN4477.1	Amino acid transporters	E	Amino acid transport, metabolism	YKL146W	ER
AN4478.1	Amino acid transporters	E	Amino acid transport, metabolism	YBR235W	
AN4479.1	FOG: HAMP domain	T	Signal transduction mechanisms		
AN4481.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism	YOL119C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4482.1	Synaptic vesicle transporter SV2 (major facilitator superfamily)	R			
AN4483.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	Signal transduction mechanisms	YLR248W	cytoplasm
AN4484.1	PHD finger protein	R			
AN4486.1	hypothetical protein [Neurospora crassa]			YLR451W	nucleus
AN4487.1	Serine carboxypeptidases	O	Posttranslational modification/turnover/chaperones		
AN4488.1	predicted protein [Neurospora crassa]				
AN4489.1	putative transcriptional activator protein [Schizosaccharomyces pombe]				
AN4490.1	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K	Transcription	YPL063W	mitochondrion
AN4491.1	predicted protein [Neurospora crassa]				
AN4492.1	26S proteasome regulatory complex, subunit RPN11	O	Posttranslational modification/turnover/chaperones	YFR004W	cytoplasm nucleus
AN4493.1	Histone deacetylase complex, catalytic component RPD3	B	Chromatin structure, dynamics		
AN4495.1	Cell division control protein/predicted DNA repair exonuclease	L	Replication, recombination, repair	YIL039W	ER
AN4496.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN4498.1	FOG: Low-complexity	S			
AN4501.1	Multifunctional chaperone (14-3-3 family)	O	Posttranslational modification/turnover/chaperones	YDR099W	cytoplasm nucleus
AN4504.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN4505.1	RNA-binding protein RBM8/Tsunagi (RRM superfamily)	R			
AN4506.1					
AN4508.1	Growth hormone-induced protein and related proteins	T	Signal transduction mechanisms		
AN4509.1	FOG: Immunoglobin and related proteins	RP			
AN4510.1	Leucine rich repeat proteins, some proteins contain F-box	R			
AN4511.1	predicted protein [Neurospora crassa]				
AN4513.1	Kinesin-like protein	Z	Cytoskeleton		
AN4514.1	Peptide methionine sulfoxide reductase	O	Posttranslational modification/turnover/chaperones		
AN4515.1	Beta-glucanase/Beta-glucan synthetase	G	Carbohydrate transport, metabolism	YEL040W	ER
AN4516.1	Alkaline phosphatase	P	Inorganic ion transport, metabolism		
AN4517.1	Heavy metal exporter HMT1, ABC superfamily	P	Inorganic ion transport, metabolism		
AN4519.1	FOG: Immunoglobin and related proteins	RP			
AN4520.1	Cactin	T	Signal transduction mechanisms		
AN4524.1	predicted protein [Neurospora crassa]				
AN4526.1	Purine-cytosine permease and related proteins	F	Nucleotide transport, metabolism		
AN4527.1	Transcription factor, Myb superfamily	K	Transcription		
AN4528.1	ER lumen protein retaining receptor	U	Intracellular trafficking/secretion/transport	YBL040C	ER
AN4529.1					
AN4530.1	Meiotic cell division protein Pelota/DOM34	J	Translation, ribosomal structure, biogenesis	YNL001W	cytoplasm
AN4531.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN4532.1	Protocatechuate 3,4-dioxygenase beta subunit	Q			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4533.1	Uncharacterized conserved protein, contains WD40 repeats	S			
AN4534.1	Uncharacterized conserved protein	S			
AN4535.1	F-box protein containing LRR	R			
AN4536.1	Serine/threonine protein kinase	RTKL			
AN4537.1	Ypt/Rab-specific GTPase-activating protein GYP6	U	Intracellular trafficking/secretion/transport		
AN4538.1	hypothetical protein [Neurospora crassa]				
AN4539.1	Predicted Yippee-type zinc-binding protein	R		YBL049W	
AN4540.1	Threonine dehydrogenase and related Zn-dependent dehydrogenases	ER			
AN4541.1	Predicted methyltransferase	R			
AN4543.1	Methyltransferases	R		YIL064W	cytoplasm
AN4544.1	Dual specificity phosphatase	V	Defense mechanisms		
AN4546.1	PolyC-binding proteins alphaCP-1 and related KH domain proteins	AR		YBR233W	cytoplasm
AN4547.1	Vesicle coat complex COPI, gamma subunit	U	Intracellular trafficking/secretion/transport	YNL287W	Golgi early Golgi
AN4548.1	Hypothetical ORF; Ydr306cp [Saccharomyces cerevisiae]				
AN4549.1	Predicted phosphatase	R			
AN4550.1	Aspartyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YLL018C	cytoplasm
AN4551.1	SNARE protein TLG1/Syntaxin 6	U	Intracellular trafficking/secretion/transport		
AN4553.1	Uncharacterized conserved protein	S			
AN4556.1	Predicted steroid reductase	R			
AN4557.1	AAA+-type ATPase containing the peptidase M41 domain	O	Posttranslational modification/turnover/chaperones	YMR089C	mitochondrion
AN4558.1	hypothetical protein [Neurospora crassa]				
AN4559.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN4560.1	60s ribosomal protein L30 isolog	J	Translation, ribosomal structure, biogenesis		
AN4561.1	Conserved phosducin-like protein	T	Signal transduction mechanisms	YOR281C	cytoplasm
AN4562.1	hypothetical protein [Neurospora crassa]				
AN4563.1	Casein kinase (serine/threonine/tyrosine protein kinase)	T	Signal transduction mechanisms	YPL204W	bud neck cytoplasm nucleus bud
AN4564.1	Kelch repeat-containing proteins	R			
AN4565.1	Unnamed protein	X			
AN4566.1	Chitin synthase/hyaluronan synthase (glycosyltransferases)	M		YNL192W	
AN4569.1	DMQ mono-oxygenase/Ubiquinone biosynthesis protein COQ7/CLK-1/CAT5	R			
AN4570.1	Paf1/RNA polymerase II complex, RTF1 component (involved in regulation of TATA box-binding protein)	K	Transcription	YGL244W	nucleus
AN4572.1	Predicted hydrolase (HAD superfamily)	R		YMR130W	
AN4574.1	Hypothetical ORF; Ypl277cp [Saccharomyces cerevisiae]				
AN4576.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN4577.1	Predicted acetamidase/formamidase	C	Energy production, conversion		
AN4578.1	transmembrane protein UsgS [Emericella nidulans]				
AN4579.1	predicted protein [Neurospora crassa]				
AN4580.1	Signal recognition particle, subunit Srp14	U	Intracellular trafficking/secretion/transport		
AN4581.1	Protein involved in high osmolarity signaling pathway	T	Signal transduction mechanisms		
AN4582.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4583.1	HSP90 co-chaperone CPR7/Cyclophilin	O	Posttranslational modification/turnover/chaperones	YLR216C	cytoplasm
AN4584.1	D-Tyr-tRNA (Tyr) deacylase	J	Translation, ribosomal structure, biogenesis	YDL219W	cytoplasm
AN4585.1	CCR4-NOT transcriptional regulation complex, NOT5 subunit	K	Transcription		
AN4590.1	Predicted transporter (major facilitator superfamily)	R			
AN4591.1	Phosphoglucomutase/phosphomannomutase	G	Carbohydrate transport, metabolism	YMR278W	cytoplasm nucleus
AN4592.1	Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	I	Lipid transport, metabolism		
AN4593.1	Transcription coactivator complex, P100 component	K	Transcription		
AN4594.1	40S ribosomal protein S20	J	Translation, ribosomal structure, biogenesis	YHL015W	
AN4597.1	Structural maintenance of chromosome protein 4 (chromosome condensation complex Condensin, subunit C)	BD		YLR086W	nucleus
AN4598.1	LST7 amino acid permease Golgi transport protein	UE			
AN4601.1	UDP-glucuronosyl and UDP-glucosyl transferase	GC			
AN4602.1	Molecular chaperone Prefoldin, subunit 3	O	Posttranslational modification/turnover/chaperones	YGR078C	cytoplasm
AN4603.1	Dihydroorotase and related enzymes	F	Nucleotide transport, metabolism	YIR027C	
AN4608.1	Predicted nucleoside-diphosphate-sugar epimerases	MG			
AN4611.1	Mitochondrial/chloroplast ribosomal protein S14/S29	J	Translation, ribosomal structure, biogenesis	YPR166C	
AN4612.1					
AN4613.1	Mitochondrial/chloroplast ribosome small subunit component	J	Translation, ribosomal structure, biogenesis		
AN4615.1	Cell cortex protein; Ydl222cp [Saccharomyces cerevisiae]			YML052W	
AN4616.1	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones	YHR064C	cytoplasm
AN4617.1	Exosomal 3'-5' exoribonuclease complex subunit Rrp40	J	Translation, ribosomal structure, biogenesis	YOL142W	nucleolus nucleus
AN4622.1					
AN4623.1	UDP-glucose:glycoprotein glucosyltransferase	G	Carbohydrate transport, metabolism		
AN4624.1	Predicted flavoprotein	R			
AN4631.1					
AN4632.1	FOG: FHA domain	T	Signal transduction mechanisms		
AN4633.1	Uncharacterized conserved protein	S		YPL098C	
AN4635.1	FOG: Leucine rich repeat	R			
AN4636.1	predicted protein [Neurospora crassa]				
AN4637.1	FOG: Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN4639.1	Guanine nucleotide binding protein MIP1	D	Cell cycle/division, chrom. partitioning		
AN4645.1	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport, metabolism		
AN4647.1	Peroxisomal phytanoyl-CoA hydroxylase	I	Lipid transport, metabolism		
AN4648.1	Conserved WD40 repeat-containing protein	S		YMR093W	nucleolus nucleus
AN4650.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN4651.1	RNA-binding protein SART3 (RRM superfamily)	A	RNA processing, modification		
AN4652.1	Mitochondrial/chloroplast ribosomal protein L22	J	Translation, ribosomal structure, biogenesis		
AN4653.1	Predicted phosphoglycerate mutase	G	Carbohydrate transport, metabolism	YKL128C	cytoplasm nucleus
AN4654.1					
AN4659.1	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ			
AN4663.1	Predicted spermine/spermidine synthase	E	Amino acid transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4667.1	Septin family protein (P-loop GTPase)	DZU		YJR076C	cell periphery bud neck
AN4670.1	FOG: WD40 repeat	R			
AN4672.1	Predicted PRP38-like splicing factor	S			
AN4673.1	predicted protein [Neurospora crassa]				
AN4674.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN4678.1	DNA polymerase iota/DNA damage inducible protein	L	Replication, recombination, repair	YDR419W	cytoplasm nucleus
AN4680.1	RNA polymerase II, large subunit	K	Transcription		
AN4683.1	Oligosaccharyltransferase, beta subunit	O	Posttranslational modification/turnover/chaperones	YEL002C	ER
AN4684.1	Triglyceride lipase-cholesterol esterase	I	Lipid transport, metabolism	YKL140W	
AN4687.1	3-Methylcrotonyl-CoA carboxylase, non-biotin containing subunit/Acetyl-CoA carboxylase carboxyl transferase, subunit beta	EI			
AN4688.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN4689.1					
AN4690.1	Acetyl/propionyl-CoA carboxylase, alpha subunit	I	Lipid transport, metabolism		
AN4691.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN4693.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN4694.1	PHD Zn-finger proteins	R		YPL181W	nucleus
AN4696.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN4699.1	predicted protein [Neurospora crassa]				
AN4700.1	Exo-beta-1,3-glucanase	G	Carbohydrate transport, metabolism		
AN4701.1					
AN4702.1	predicted protein [Neurospora crassa]				
AN4705.1	Uncharacterized conserved protein	S			
AN4706.1	Myosin class II heavy chain	Z	Cytoskeleton	YHR023W	bud neck
AN4707.1	mRNA splicing factor	A	RNA processing, modification		
AN4708.1	Conserved ATP/GTP binding protein	R		YMR097C	mitochondrion
AN4709.1	Phosphatidylinositol 3-kinase VPS34, involved in signal transduction	TU		YLR240W	endosome
AN4710.1	Uncharacterized conserved protein	S			
AN4711.1	predicted protein [Neurospora crassa]				
AN4712.1	hypothetical protein [Neurospora crassa]			YIL067C	vacuole
AN4714.1	Predicted dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	O	Posttranslational modification/turnover/chaperones	YKL027W	mitochondrion
AN4716.1	hypothetical protein [Neurospora crassa]			YJR075W	Golgi
AN4717.1	cAMP-dependent protein kinase catalytic subunit (PKA)	T	Signal transduction mechanisms		
AN4719.1	RhoGEF GTPase	T	Signal transduction mechanisms	YGR070W	
AN4721.1	DEAH-box RNA helicase	A	RNA processing, modification	YER013W	cytoplasm nucleus
AN4723.1	Mitochondrial RNA helicase SUV3, DEAD-box superfamily	A	RNA processing, modification	YPL029W	mitochondrion
AN4724.1	Vesicle trafficking protein Sec1	U	Intracellular trafficking/secretion/transport	YDR164C	bud neck cytoplasm bud
AN4725.1	Major histocompatibility complex protein BAT4, contains G-patch and ankyrin domains	R			
AN4726.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q		YNL181W	ER
AN4727.1	UDP-glucose 4-epimerase/UDP-sulfoquinovose synthase	M			
AN4728.1	Uncharacterized conserved protein	S			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4729.1	hypothetical protein [Neurospora crassa]				
AN4731.1	Proteasome maturation factor	O	Posttranslational modification/turnover/chaperones	YBR173C	cytoplasm nucleus
AN4732.1	predicted protein [Neurospora crassa]				
AN4733.1	Predicted small molecule transporter	U	Intracellular trafficking/secretion/transport		
AN4735.1	Anaphase-promoting complex (APC), subunit 5	DO			
AN4736.1	Apurinic/apyrimidinic endonuclease and related enzymes	L	Replication, recombination, repair		
AN4737.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN4740.1	complex I intermediate associated protein CIA30 homolog [Emericella nidulans]				
AN4742.1	Translation initiation factor 1 (eIF-1/SUI1)	J	Translation, ribosomal structure, biogenesis		
AN4743.1	Ras-related small GTPase, Rho type	R			
AN4751.1	Predicted DEAD-box-containing helicase	R			
AN4752.1	hypothetical protein [Neurospora crassa]				
AN4753.1	Mitochondrial protein Surfeit 1/SURF1/SHY1, required for expression of cytochrome oxidase	C	Energy production, conversion	YGR112W	mitochondrion
AN4754.1	Ubiquitin regulatory protein UBXD2, contains UAS and UBX domains	R			
AN4756.1	DNA-binding protein C1D involved in regulation of double-strand break repair	L	Replication, recombination, repair		
AN4757.1	Protein involved in ubiquinone biosynthesis	H	Coenzyme transport, metabolism	YDR204W	mitochondrion
AN4759.1	Guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport		
AN4761.1	Dolichyl-phosphate-mannose:protein O-mannosyl transferase	O	Posttranslational modification/turnover/chaperones	YDL095W	ER
AN4762.1	predicted protein [Neurospora crassa]				
AN4763.1	DHHC-type Zn-finger proteins	R			
AN4764.1	Putative transcription factor ASH1/LIN-59	K	Transcription		
AN4765.1	FOG: Immunoglobin and related proteins	RP			
AN4767.1	Scaffold/matrix specific factor hnRNP-U/SAF-A, contains SPRY domain	A	RNA processing, modification		
AN4768.1	predicted protein [Neurospora crassa]				
AN4769.1	ATP sulfurylase (sulfate adenylyltransferase)	P	Inorganic ion transport, metabolism	YJR010W	cytoplasm
AN4770.1	Phosphoadenosine phosphosulfate reductase	E	Amino acid transport, metabolism	YPR167C	
AN4771.1	WD40 repeat protein	R			
AN4774.1	Uroporphyrin III methyltransferase	H	Coenzyme transport, metabolism	YKR069W	
AN4775.1	26S proteasome regulatory complex, subunit RPN5/PSMD12	O	Posttranslational modification/turnover/chaperones	YDL147W	nucleus
AN4776.1	Phospholipase/carboxyhydrolase	E	Amino acid transport, metabolism		
AN4777.1	40s ribosomal protein S27	J	Translation, ribosomal structure, biogenesis	YHR021C	cytoplasm
AN4778.1	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferases	I	Lipid transport, metabolism	YHR123W	Golgi
AN4779.1	NIPSNAP1 protein	S			
AN4781.1	Lipoyltransferase	CH			
AN4782.1	Ras-related small GTPase, Rho type	R		YIL118W	
AN4783.1	COP9 signalosome, subunit CSN2	OT			
AN4784.1	Uncharacterized conserved protein	S			
AN4785.1	Unknown protein [Arabidopsis thaliana]			YPL248C	
AN4787.1	60S ribosomal protein L37	J	Translation, ribosomal structure, biogenesis	YLR185W	cytoplasm
AN4788.1	RNA splicing factor - Slu7p	A	RNA processing, modification		
AN4789.1	DNA polymerase zeta, catalytic subunit	L	Replication, recombination, repair	YPL167C	
AN4792.1	Proteins containing the FAD binding domain	C	Energy production, conversion		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4793.1	Aspartate-semialdehyde dehydrogenase	E	Amino acid transport, metabolism	YDR158W	cytoplasm nucleus
AN4794.1	40S ribosomal protein S4	J	Translation, ribosomal structure, biogenesis	YJR145C	cytoplasm
AN4797.1	hypothetical Myb-like DNA-binding protein [Schizosaccharomyces pombe]				
AN4798.1	Sorting nexin SNX11	U	Intracellular trafficking/secretion/transport		
AN4800.1	WD40 repeat-containing protein	R			
AN4802.1	60S ribosomal protein L21	J	Translation, ribosomal structure, biogenesis	YBR191W	cytoplasm
AN4803.1	Ribosomal protein S4	J	Translation, ribosomal structure, biogenesis	YBR189W	cytoplasm
AN4804.1	predicted protein [Neurospora crassa]				
AN4809.1	glutaminase A [Emericella nidulans]				
AN4810.1	Aminoacylase ACY1 and related metalloexopeptidases	E	Amino acid transport, metabolism		
AN4814.1	Predicted membrane protein	S			
AN4817.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R		YBR043C	cell periphery
AN4818.1	Signal transduction histidine kinase	T	Signal transduction mechanisms		
AN4819.1	Glutamine synthetase	E	Amino acid transport, metabolism		
AN4820.1	Aldehyde dehydrogenase	C	Energy production, conversion		
AN4821.1	TRANSCRIPTIONAL ACTIVATOR PROTEIN ACU-15				
AN4822.1	Isocitrate/isopropylmalate dehydrogenase	CE			
AN4824.1	Galactosyltransferases	G	Carbohydrate transport, metabolism		
AN4826.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN4829.1	Aldo/keto reductase family proteins	R			
AN4830.1	Uncharacterized conserved protein with similarity to phosphopantothenoylcysteine synthetase/decarboxylase	R		YIL083C	cytoplasm nucleus
AN4833.1	Esterase/lipase	I	Lipid transport, metabolism		
AN4834.1	hypothetical protein [Neurospora crassa]				
AN4836.1	Acetyl-CoA transporter	P	Inorganic ion transport, metabolism	YBR220C	
AN4839.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN4840.1	Thyroid hormone receptor-associated protein complex, subunit TRAP230	K	Transcription		
AN4841.1	Molybdopterin converting factor, large subunit	H	Coenzyme transport, metabolism		
AN4842.1	Putative cytochrome C oxidase assembly protein	C	Energy production, conversion	YBR037C	mitochondrion
AN4843.1	Alpha-amylase	G	Carbohydrate transport, metabolism	YJL221C	
AN4844.1	Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	GE			
AN4847.1	NAD-dependent aldehyde dehydrogenases	C	Energy production, conversion		
AN4850.1	RNA-binding protein RBM5 and related proteins, contain G-patch and RRM domains	R			
AN4851.1	predicted protein [Neurospora crassa]				
AN4852.1	glucan 1,3-beta-glucosidase GLUC78 precursor [Trichoderma atroviride]				
AN4854.1	hypothetical protein ((AL451015) conserved hypothetical protein [Neurospora crassa])				
AN4856.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN4857.1	Predicted unusual protein kinase	R			
AN4859.1	Plasma membrane H+-transporting ATPase	P	Inorganic ion transport, metabolism		
AN4860.1	Pectin methylesterase	G	Carbohydrate transport, metabolism		
AN4861.1	Transcription elongation factor TFIIS/Cofactor of enhancer-binding protein Sp1	K	Transcription	YGL043W	nucleus
AN4862.1	Ran GTPase-activating protein	AYT		YMR235C	cytoplasm
AN4864.1	Glucosyltransferase - Alg6p	GE		YOR002W	ER

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4866.1	Defense-related protein containing SCP domain	S			
AN4867.1	Gamma-tubulin complex, DGRIP91/SPC98 component	Z	Cytoskeleton		
AN4869.1	20S proteasome, regulatory subunit alpha type PSMA6/SCL1	O	Posttranslational modification/turnover/chaperones	YGL011C	cytoplasm nucleus
AN4870.1	predicted protein [Neurospora crassa]				
AN4871.1	Chitinase	G	Carbohydrate transport, metabolism	YDR371W	cytoplasm
AN4872.1	Ubiquitin/40S ribosomal protein S27a fusion	J	Translation, ribosomal structure, biogenesis	YLR167W	
AN4873.1	FOG: Zn-finger	R			
AN4874.1	Ribonuclease, T2 family	A	RNA processing, modification	YPL123C	
AN4875.1	Uncharacterized conserved protein	S		YDR282C	
AN4876.1	Vacuolar assembly/sorting protein VPS41	U	Intracellular trafficking/secretion/transport		
AN4878.1	Transcription factor	K	Transcription		
AN4880.1	Jacalin-like lectin domain-containing protein	R		YIL108W	cytoplasm
AN4881.1	predicted protein [Neurospora crassa]				
AN4883.1	ATP-dependent DNA ligase I	L	Replication, recombination, repair		
AN4884.1	ER to golgi transport protein/RAD50-interacting protein 1	UD			
AN4886.1	Subunit of cis-Golgi transport vesicle tethering complex - Sec34p	U	Intracellular trafficking/secretion/transport	YER157W	Golgi early Golgi
AN4887.1	MEKK and related serine/threonine protein kinases	T	Signal transduction mechanisms		
AN4888.1	Thiamine pyrophosphate-requiring enzyme	EH		YGR087C	cytoplasm
AN4890.1	Tomosyn and related SNARE-interacting proteins	U	Intracellular trafficking/secretion/transport	YBL106C	
AN4892.1	mRNA cleavage and polyadenylation factor I complex, subunit RNA14	A	RNA processing, modification		
AN4894.1	Histone acetyltransferase SAGA/ADA, catalytic subunit PCAF/GCN5 and related proteins	BK			
AN4895.1	hypothetical protein [Neurospora crassa]				
AN4896.1	Protein tyrosine phosphatase	T	Signal transduction mechanisms		
AN4898.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN4899.1	40 kDa farnesylated protein associated with peroxisomes	U	Intracellular trafficking/secretion/transport		
AN4900.1	RNA polymerase II, large subunit	K	Transcription		
AN4901.1	related to glutaminase A [MIPS] [Neurospora crassa]				
AN4902.1					
AN4903.1	ATP-dependent RNA helicase	A	RNA processing, modification	YHR169W	nucleolus nucleus
AN4904.1	Na+-independent Cl/HCO3 exchanger AE1 and related transporters (SLC4 family)	P	Inorganic ion transport, metabolism	YNL275W	
AN4905.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones		
AN4906.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ		YOR381W	
AN4908.1	Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondrial morphology/distribution, also found associated with eIF-3	R			
AN4912.1	hypothetical protein [Neurospora crassa]			YOR049C	
AN4913.1	Phosphoketolase	G	Carbohydrate transport, metabolism		
AN4914.1	Acetate kinase	C	Energy production, conversion		
AN4915.1	GTPase Rab5/YPT51 and related small G protein superfamily GTPases	U	Intracellular trafficking/secretion/transport	YOR089C	cytoplasm nucleus
AN4916.1	40S ribosomal protein S7	J	Translation, ribosomal structure, biogenesis	YOR096W	
AN4917.1	Dynactin, subunit p62	N			
AN4918.1	Predicted methyltransferase	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4919.1	Actin-related protein Arp2/3 complex, subunit ARPC5	Z	Cytoskeleton	YIL062C	actin
AN4920.1	Calcium transporting ATPase	P	Inorganic ion transport, metabolism		
AN4921.1	hypothetical protein [Trichodesmium erythraeum IMS101]				
AN4922.1	predicted protein [Neurospora crassa]				
AN4923.1	Hydroxymethylglutaryl-CoA synthase	I	Lipid transport, metabolism	YML126C	nucleus
AN4925.1	Transferrin receptor and related proteins containing the protease-associated (PA) domain	OPR			
AN4926.1	hypothetical protein [Neurospora crassa]				
AN4928.1	Transcription initiation factor TFIIB	K	Transcription	YPR086W	nucleus
AN4929.1	Drebrins and related actin binding proteins	Z	Cytoskeleton		
AN4931.1	predicted protein [Neurospora crassa]				
AN4932.1	Predicted membrane proteins, contain hemolysin III domain	RT		YOL002C	
AN4935.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN4936.1	U4/U6-associated splicing factor PRP4	A	RNA processing, modification		
AN4938.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN4939.1	Putative steroid membrane receptor Hpr6.6/25-Dx	R		YPL170W	ER cytoplasm
AN4940.1	hypothetical protein [Schizosaccharomyces pombe]			YML128C	ER
AN4941.1	hypothetical protein [Neurospora crassa]				
AN4943.1	Predicted splicing regulator, contains RRM, SWAP and RPR domains	R			
AN4945.1	hypothetical protein [Neurospora crassa]				
AN4946.1					
AN4947.1	Dolichol-phosphate mannosyltransferase	R		YPR183W	ER
AN4949.1	RNA polymerase III transcription factor (TF)III subunit; WD repeat protein [Schizosaccharomyces pombe]				
AN4951.1	Membrane coat complex Retromer, subunit VPS35	U	Intracellular trafficking/secretion/transport	YJL154C	vacuolar membrane endosome
AN4953.1	Ras-related small GTPase, Rho type	R		YNL090W	cytoplasm nucleus
AN4954.1	predicted protein [Neurospora crassa]				
AN4956.1	Thiamine pyrophosphate-requiring enzyme	EH		YMR108W	mitochondrion
AN4957.1	Galactokinase	G	Carbohydrate transport, metabolism	YBR020W	
AN4958.1	Uncharacterized conserved protein	S			
AN4959.1	Protein required for S-phase initiation or completion	D	Cell cycle/division, chrom. partitioning	YIL150C	cytoplasm nucleus
AN4960.1	predicted protein [Neurospora crassa]				
AN4965.1	Negative regulator of transcription	K	Transcription	YCR093W	cytoplasm
AN4966.1	Uncharacterized conserved protein	S			
AN4967.1	Predicted tubulin-tyrosine ligase	O	Posttranslational modification/turnover/chaperones	YBR094W	cytoplasm
AN4968.1	Peroxisomal membrane anchor protein (peroxin)	MOU			
AN4969.1	Centromere-associated protein HEC1	D	Cell cycle/division, chrom. partitioning	YIL144W	spindle pole
AN4971.1	C-type lectin	TV			
AN4972.1	Positive regulator of GAL genes; Gal4p [Saccharomyces cerevisiae]				
AN4973.1	predicted protein [Neurospora crassa]				
AN4974.1	Predicted methyltransferase	R			
AN4975.1	FAD-dependent oxidoreductase	R			
AN4976.1	TATA-box binding protein (TBP), component of TFIID and TFIIIB	K	Transcription	YER148W	nucleus
AN4977.1	Electron transfer flavoprotein ubiquinone oxidoreductase	C	Energy production, conversion	YOR356W	mitochondrion

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN4978.1	Alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)	A	RNA processing, modification		
AN4979.1	Dihydroneopterin aldolase	H	Coenzyme transport, metabolism		
AN4980.1	Ribosomal protein S6 kinase and related proteins	RT		YBR028C	cytoplasm
AN4983.1	hypothetical protein [Neurospora crassa]				
AN4984.1	Cyclin	R			
AN4985.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN4986.1	hypothetical protein [Neurospora crassa]				
AN4987.1	cAMP-dependent protein kinase types I and II, regulatory subunit	T	Signal transduction mechanisms	YIL033C	cytoplasm nucleus
AN4988.1	Protein involved in Snf1 protein kinase complex assembly	G	Carbohydrate transport, metabolism		
AN4990.1	Uncharacterized membrane protein	S			
AN4991.1	aureobasidin-resistance protein; AurA [Aspergillus nidulans]			YKL004W	early Golgi
AN4992.1	Lecithin:cholesterol acyltransferase (LCAT)/Acyl-ceramide synthase	I	Lipid transport, metabolism	YNR008W	
AN4993.1	N-acetyltransferase	R		YPR051W	cytoplasm nucleus
AN4996.1	predicted protein [Neurospora crassa]				
AN4997.1	Phosphatidylinositol transfer protein SEC14 and related proteins	I	Lipid transport, metabolism	YMR079W	cytoplasm nucleus
AN4998.1	Ras GTPase-activating protein family - IQGAP	T	Signal transduction mechanisms		
AN5001.1	Exosome 3'-5' exoribonuclease complex, subunit PM/SCL-100 (Rrp6)	J	Translation, ribosomal structure, biogenesis		
AN5003.1	FOG: Zn-finger	R			
AN5005.1	predicted protein [Neurospora crassa]				
AN5006.1	Mismatch repair ATPase MSH2 (MutS family)	L	Replication, recombination, repair		
AN5008.1	Cytochrome c oxidase, subunit VIb/COX12	C	Energy production, conversion	YMR244C-A	cytoplasm nucleus
AN5009.1	FOG: RRM domain	R			
AN5010.1	HAT (Half-A-TPR) repeat-containing protein	R		YDR449C	nucleolus
AN5011.1	FGF receptor activating protein 1	T	Signal transduction mechanisms	YCR017C	ER
AN5013.1	3'-5' exonuclease	L	Replication, recombination, repair		
AN5014.1	60S ribosomal protein L22	J	Translation, ribosomal structure, biogenesis	YLR061W	cytoplasm
AN5015.1	General stress protein	R			
AN5019.1	Methionine synthase II (cobalamin-independent)	E	Amino acid transport, metabolism		
AN5020.1	GTP-binding ADP-ribosylation factor Arf6 (dArf3)	U	Intracellular trafficking/secretion/transport		
AN5021.1	Glycosyltransferase	M			
AN5022.1	Dynactin, subunit p25	Z	Cytoskeleton		
AN5025.1	Amine oxidase	Q		YMR020W	
AN5026.1	PHD finger protein AF10	R			
AN5027.1	Uncharacterized conserved protein	S		YEL023C	
AN5028.1	Peroxidase/oxygenase	R			
AN5048.1	Transcription factor, contains HOX domain	R			
AN5049.1	Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	P	Inorganic ion transport, metabolism		
AN5050.1	Predicted transporter (major facilitator superfamily)	R			
AN5052.1					
AN5057.1	Protein tyrosine phosphatase CDC14	V	Defense mechanisms	YFR028C	nucleolus
AN5067.1	Predicted transporter (major facilitator superfamily)	R			
AN5068.1	hypothetical protein [Aspergillus fumigatus]				
AN5069.1	hypothetical protein [Neurospora crassa]				
AN5085.1	SpoC1-C1C protein - Emericella nidulans				
AN5098.1	Splicing factor 3b, subunit 2	A	RNA processing, modification		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5099.1	hypothetical protein [Neurospora crassa]				
AN5100.1	Cell cycle control protein	DKT		YCR094W	late Golgi
AN5101.1	hypothetical protein [Neurospora crassa]				
AN5102.1	Global transcriptional regulator, cell division control protein	E	Amino acid transport, metabolism	YGL207W	nucleus
AN5103.1	Mitochondrial carrier protein	C	Energy production, conversion		
AN5105.1	Dolichyl-phosphate-mannose:protein O-mannosyl transferase	O	Posttranslational modification/turnover/chaperones	YAL023C	ER
AN5106.1	GTPase Rab2, small G protein superfamily	U	Intracellular trafficking/secretion/transport		
AN5107.1	Choline transporter-like protein	I	Lipid transport, metabolism		
AN5108.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN5109.1	Aldo/keto reductase family proteins	R		YDL124W	cytoplasm nucleus
AN5110.1	Uncharacterized conserved protein (YdiU family)	S		YPL222W	mitochondrion
AN5111.1	E3 ubiquitin ligase interacting with arginine methyltransferase	O	Posttranslational modification/turnover/chaperones		
AN5113.1	Peroxisomal biogenesis protein (peroxin 16)	U	Intracellular trafficking/secretion/transport		
AN5114.1	Ribonuclease HI	L	Replication, recombination, repair	YNL072W	cytoplasm nucleus
AN5115.1	Heterochromatin-associated protein HP1 and related CHROMO domain proteins	B	Chromatin structure, dynamics		
AN5116.1	Alpha-tubulin folding cofactor B	O	Posttranslational modification/turnover/chaperones	YNL148C	
AN5118.1	related to DRPLA protein [imported] - Neurospora crassa				
AN5119.1	Predicted methyltransferase	R		YML014W	cytoplasm
AN5121.1	26S proteasome regulatory complex, subunit RPN8/PSMD7	O	Posttranslational modification/turnover/chaperones	YOR261C	cytoplasm nucleus
AN5122.1	Adenylate kinase	F	Nucleotide transport, metabolism	YDR226W	cytoplasm nucleus
AN5123.1	Dimeric dihydrodiol dehydrogenase	GQ			
AN5124.1	mRNA cleavage and polyadenylation factor I/II complex, subunit Pcf11	A	RNA processing, modification		
AN5126.1	ATPase involved in DNA repair	L	Replication, recombination, repair		
AN5127.1	V-SNARE	U	Intracellular trafficking/secretion/transport		
AN5129.1	Molecular chaperones HSP70/HSC70, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones	YLL024C	cytoplasm nucleus
AN5130.1	Coproporphyrinogen III oxidase CPO/HEM13	H	Coenzyme transport, metabolism	YDR044W	cytoplasm nucleus
AN5131.1	Microtubule-associated anchor protein involved in autophagy and membrane trafficking	Z	Cytoskeleton	YBL078C	
AN5134.1	Glutamate synthase	E	Amino acid transport, metabolism	YDL171C	
AN5137.1	Cytochrome P450	Q		YMR302C	mitochondrion
AN5138.1	Dihydroxyacid dehydratase/phosphogluconate dehydratase	EG			
AN5139.1	WD40 repeat protein	R		YPR135W	nucleus
AN5140.1	Permease of the major facilitator superfamily	R			
AN5141.1	Superfamily II DNA and RNA helicases	LKJ			
AN5143.1	Protein involved in vacuolar polyphosphate accumulation, contains SPX domain	P	Inorganic ion transport, metabolism	YFL004W	ER
AN5144.1	Fructose-6-phosphate 2-kinase/fructose-2,6-biphosphatase	G	Carbohydrate transport, metabolism		
AN5145.1	hypothetical protein [Neurospora crassa]				
AN5146.1	Glycolate oxidase	C	Energy production, conversion		
AN5148.1	Manganese superoxide dismutase	P	Inorganic ion transport, metabolism	YJR101W	mitochondrion
AN5149.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5150.1	GPI transamidase complex, GPI17/PIG-S component, involved in glycosylphosphatidylinositol anchor biosynthesis	MO		YDR434W	ER
AN5151.1	Predicted membrane proteins, contain hemolysin III domain	RT			
AN5152.1	predicted protein [Neurospora crassa]				
AN5154.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN5155.1	Subunit of tRNA-specific adenosine-34 deaminase	A	RNA processing, modification		
AN5156.1	Cyclin	R			
AN5157.1	Proteins containing armadillo/beta-catenin-like repeat	R			
AN5158.1	Predicted kinase	R			
AN5162.1	Pyruvate dehydrogenase E1, alpha subunit	C	Energy production, conversion	YER178W	mitochondrion
AN5163.1	von Willebrand factor and related coagulation proteins	WV			
AN5164.1	Ribosomal protein S4 and related proteins	J	Translation, ribosomal structure, biogenesis		
AN5165.1	hypothetical protein [Neurospora crassa]				
AN5166.1	CDP-diacylglycerol synthase	I	Lipid transport, metabolism	YBR029C	
AN5167.1	hypothetical protein [Neurospora crassa]				
AN5169.1	hypothetical protein [Neurospora crassa]				
AN5175.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN5176.1	1,4-beta-D-glucan-cellobiohydrolyase [Aspergillus nidulans]				
AN5177.1	WD40 repeat protein	R		YPR169W	nucleolus nucleus
AN5178.1	Alcohol dehydrogenase, class IV	C	Energy production, conversion	YGL256W	mitochondrion
AN5179.1	Diphthamide biosynthesis protein	J	Translation, ribosomal structure, biogenesis	YKL191W	cytoplasm
AN5181.1	Nuclear distribution protein NUDC	T	Signal transduction mechanisms		
AN5182.1	predicted protein [Neurospora crassa]				
AN5184.1	Sterol reductase/lamin B receptor	IT			
AN5185.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN5186.1	Ubiquitin-specific protease	O	Posttranslational modification/turnover/chaperones		
AN5188.1	Ribonuclease H	L	Replication, recombination, repair	YMR234W	cytoplasm nucleus
AN5191.1	Uncharacterized conserved protein	S			
AN5192.1	Very long-chain acyl-CoA synthetase/fatty acid transporter	I	Lipid transport, metabolism	YBR041W	lipid particle
AN5194.1	Transporter, ABC superfamily (Breast cancer resistance protein)	Q		YCR011C	ER
AN5195.1	ER vesicle integral membrane protein involved in establishing cell polarity, signaling and protein degradation	OUT		YGL054C	vacuole ER
AN5196.1	mRNA splicing factor	S		YDR364C	cytoplasm nucleus
AN5197.1	FOG: RCC1 domain	S			
AN5198.1	Predicted transporter (major facilitator superfamily)	R			
AN5199.1	Putative methionine aminopeptidase	O	Posttranslational modification/turnover/chaperones	YLR244C	cytoplasm nucleus
AN5200.1	Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	CR		YBL098W	mitochondrion
AN5203.1	Ribosomal protein S8	J	Translation, ribosomal structure, biogenesis	YMR158W	
AN5205.1	FOG: Immunoglobin and related proteins	RP			
AN5206.1	Isocitrate dehydrogenase, alpha subunit	E	Amino acid transport, metabolism	YIL094C	mitochondrion
AN5207.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5208.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN5209.1	predicted protein [Neurospora crassa]				
AN5210.1	Pyruvate kinase	G	Carbohydrate transport, metabolism	YAL038W	cytoplasm
AN5213.1	conserved hypothetical protein [Neurospora crassa]				
AN5215.1	WD-repeat protein WDR6, WD repeat superfamily	R		YPL183C	cytoplasm
AN5216.1	5'-3' exonuclease	L	Replication, recombination, repair	YGR258C	cytoplasm nucleus
AN5217.1	hypothetical protein [Neurospora crassa]			YGR086C	
AN5218.1	Activating transcription factor 4	K	Transcription		
AN5220.1	von Willebrand factor and related coagulation proteins	WV			
AN5221.1	FOG: Immunoglobin and related proteins	RP			
AN5222.1	40S ribosomal protein S11	J	Translation, ribosomal structure, biogenesis	YDR025W	cytoplasm
AN5224.1	Clathrin assembly protein AP180 and related proteins, contain ENTH domain	TU			
AN5225.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN5226.1	Predicted membrane protein	S			
AN5228.1	NADH:flavin oxidoreductase/12-oxophytodienoate reductase	CR		YHR179W	cytoplasm nucleus
AN5230.1	predicted protein [Neurospora crassa]				
AN5231.1	hypothetical protein [Neurospora crassa]				
AN5232.1	predicted protein [Neurospora crassa]				
AN5234.1	Alcohol dehydrogenase, class IV	C	Energy production, conversion		
AN5235.1	Transcription-coupled repair protein CSA, contains WD40 domain	KL			
AN5236.1	Predicted membrane protein	S			
AN5267.1	Poly(3-hydroxybutyrate) depolymerase	Q			
AN5273.1	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport, metabolism		
AN5284.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN5285.1	hypothetical protein [Neurospora crassa]				
AN5296.1	Sensory transduction histidine kinase	T	Signal transduction mechanisms		
AN5307.1	NADH-dehydrogenase (ubiquinone)	C	Energy production, conversion		
AN5311.1	hypothetical protein [Neurospora crassa]				
AN5317.1	hypothetical protein [Burkholderia fungorum]				
AN5318.1	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q			
AN5321.1	Acetylcholinesterase/Butyrylcholinesterase	T	Signal transduction mechanisms		
AN5323.1	Predicted transporter (major facilitator superfamily)	R			
AN5324.1	Chitinase	G	Carbohydrate transport, metabolism		
AN5328.1	Protocatechuate 3,4-dioxygenase beta subunit	Q			
AN5330.1	Histone acetyltransferase HPA2 and related acetyltransferases	KR			
AN5333.1	hypothetical protein [Microbulbifer degradans 2-40]				
AN5335.1	Cytochrome P450 CYP2 subfamily	Q			
AN5336.1	5' nucleotidase	F	Nucleotide transport, metabolism		
AN5337.1	Transcription-associated recombination protein - Thp1p	D	Cell cycle/division, chrom. partitioning		
AN5338.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN5339.1	predicted protein [Neurospora crassa]				
AN5340.1	Protein involved in rRNA processing	A	RNA processing, modification	YER127W	
AN5343.1	Kinesin (SMY1 subfamily)	Z	Cytoskeleton		
AN5344.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YGL058W	cytoplasm nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5346.1	Beta-1,4-mannosyltransferase	O	Posttranslational modification/turnover/chaperones	YBR110W	ER
AN5351.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones		
AN5353.1	Uncharacterized conserved protein	S			
AN5356.1	Mitochondrial carnitine-acylcarnitine carrier protein	C	Energy production, conversion	YOR100C	
AN5367.1	hypothetical protein [Neurospora crassa]				
AN5370.1	Permeases of the major facilitator superfamily	GEPR			
AN5375.1	predicted protein [Neurospora crassa]				
AN5376.1	Dienelactone hydrolase and related enzymes	Q			
AN5378.1	Predicted transporter (major facilitator superfamily)	R		YEL065W	vacuole
AN5387.1	Uncharacterized protein conserved in bacteria	S			
AN5390.1					
AN5399.1	predicted protein [Neurospora crassa]				
AN5400.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN5401.1	probable DNA-binding protein [Pirellula sp.]				
AN5402.1	Intracellular membrane-bound Ca2+-independent phospholipase A2	I	Lipid transport, metabolism		
AN5403.1	Uncharacterized conserved protein	S			
AN5404.1	Reticulon	U	Intracellular trafficking/secretion/transport	YDR233C	cell periphery ER
AN5405.1	predicted protein [Neurospora crassa]				
AN5406.1	DNA topoisomerase type II	B	Chromatin structure, dynamics	YNL088W	nucleus
AN5407.1	Predicted GTPase activator NB4S/EVI5 (contains TBC domain)/Calmodulin-binding protein Pollux (contains PTB and TBC domains)	R			
AN5410.1					
AN5422.1	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms		
AN5436.1	Predicted signaling-associated protein (contains a PDZ domain)	R		YNL123W	nucleus
AN5438.1	Hsp90 co-chaperone CNS1 (contains TPR repeats)	O	Posttranslational modification/turnover/chaperones	YBR155W	cytoplasm
AN5440.1	Catalase (peroxidase I)	P	Inorganic ion transport, metabolism	YKR066C	mitochondrion
AN5441.1	Ribosomal protein S18	J	Translation, ribosomal structure, biogenesis	YML026C	cytoplasm
AN5442.1	Serine carboxypeptidases (lysosomal cathepsin A)	OE		YMR297W	vacuole
AN5443.1	Predicted exosome subunit	J	Translation, ribosomal structure, biogenesis	YLR022C	cytoplasm nucleus
AN5445.1					
AN5447.1	Glutamate decarboxylase/sphingosine phosphate lyase	E	Amino acid transport, metabolism	YMR250W	cytoplasm
AN5448.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN5449.1	Arylsulfatase A and related enzymes	P	Inorganic ion transport, metabolism		
AN5450.1	Endosomal membrane proteins, EMP70	U	Intracellular trafficking/secretion/transport	YLR083C	vacuole
AN5452.1	Splicing factor 3b, subunit 3	A	RNA processing, modification		
AN5453.1	predicted protein [Neurospora crassa]				
AN5455.1	Uncharacterized conserved protein	S		YJL109C	nucleolus
AN5456.1	Uncharacterized conserved protein	S			
AN5457.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ			
AN5480.1	predicted protein [Neurospora crassa]			YHR087W	cytoplasm nucleus
AN5481.1	predicted protein [Neurospora crassa]				
AN5482.1	GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein superfamily	U	Intracellular trafficking/secretion/transport	YLR293C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5483.1	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL			
AN5484.1	2-enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/Peroxisomal 3-ketoacyl-CoA-thiolase, sterol-binding domain and related enzymes	I	Lipid transport, metabolism		
AN5485.1	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	YU			
AN5486.1	Carbon-nitrogen hydrolase	E	Amino acid transport, metabolism	YLR351C	mitochondrion cytoplasm
AN5489.1	Pinin (desmosome-associated protein)	Z	Cytoskeleton		
AN5491.1	Cytoplasm to vacuole targeting protein	U	Intracellular trafficking/secretion/transport		
AN5492.1	Adenine deaminase/adenosine deaminase	F	Nucleotide transport, metabolism		
AN5493.1	Concentrative Na+-nucleoside cotransporter CNT1/CNT2	FP			
AN5494.1	Checkpoint kinase and related serine/threonine protein kinases	D	Cell cycle/division, chrom. partitioning	YBR274W	cytoplasm
AN5495.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YOR339C	
AN5496.1	predicted protein [Neurospora crassa]				
AN5497.1	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H	Coenzyme transport, metabolism	YDR487C	cytoplasm nucleus
AN5498.1	Transcription initiation factor IIE, beta subunit	K	Transcription	YKR062W	nucleus
AN5499.1	Uncharacterized conserved coiled-coil protein	S		YKR095W	nuclear periphery
AN5501.1	Esterase/lipase	I	Lipid transport, metabolism		
AN5512.1	Magnesium-dependent phosphatase	R		YER134C	cytoplasm nucleus
AN5513.1	predicted protein [Neurospora crassa]				
AN5514.1	DNA/RNA helicase MER3/SLH1, DEAD-box superfamily	A	RNA processing, modification	YGL251C	
AN5515.1	Predicted UDP-galactose transporter	G	Carbohydrate transport, metabolism		
AN5516.1	HORMA domain	B	Chromatin structure, dynamics		
AN5517.1	Cdc4 and related F-box and WD-40 proteins	R			
AN5518.1	Predicted GTPase	R			
AN5519.1	Clathrin adaptor complex, small subunit	U	Intracellular trafficking/secretion/transport	YJL024C	early Golgi
AN5520.1	60S ribosomal protein L7A	J	Translation, ribosomal structure, biogenesis	YLL045C	cytoplasm
AN5522.1	predicted protein [Neurospora crassa]				
AN5523.1	Trehalose-6-phosphate synthase component TPS1 and related subunits	G	Carbohydrate transport, metabolism	YBR126C	cytoplasm
AN5524.1	Glyoxylase	R			
AN5525.1	Aconitase/homoaconitase (aconitase superfamily)	CE		YLR304C	
AN5527.1	DNA repair protein, SNF2 family	L	Replication, recombination, repair		
AN5528.1	Mitochondrial Fe/S cluster exporter, ABC superfamily	U	Intracellular trafficking/secretion/transport	YMR301C	mitochondrion
AN5529.1	NDR and related serine/threonine kinases	R		YNL161W	bud neck cytoplasm
AN5530.1	Splicing factor 3a, subunit 2	A	RNA processing, modification	YDL043C	nucleus
AN5531.1	Beta-tubulin folding cofactor E	O	Posttranslational modification/turnover/chaperones	YER007W	
AN5532.1	Spliceosomal protein FBP21	A	RNA processing, modification		
AN5533.1	Cell division protein	D	Cell cycle/division, chrom. partitioning		
AN5534.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	Energy production, conversion	YNL274C	cytoplasm nucleus
AN5535.1	Uncharacterized conserved protein	S			
AN5536.1	GTPase XAB1, interacts with DNA repair protein XPA	L	Replication, recombination, repair	YJR072C	cytoplasm
AN5537.1	Purine nucleoside permease	F	Nucleotide transport, metabolism		
AN5549.1	Inorganic phosphate transporter	P	Inorganic ion transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5552.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR			
AN5557.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN5558.1	Subtilisin-related protease/Vacuolar protease B	O	Posttranslational modification/turnover/chaperones	YEL060C	cytoplasm
AN5559.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN5563.1	Aldo/keto reductase family proteins	R		YBR149W	cytoplasm nucleus
AN5564.1	Predicted phosphatase	R			
AN5566.1	GMP synthase	F	Nucleotide transport, metabolism	YMR217W	
AN5567.1	Uncharacterized conserved protein	S			
AN5568.1	conserved hypothetical protein [Neurospora crassa]				
AN5569.1	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit TFB1	KL		YDR311W	nucleus
AN5570.1	Chromatin remodeling protein, contains PHD Zn-finger	B	Chromatin structure, dynamics		
AN5571.1	2-oxoglutarate dehydrogenase, E1 subunit	G	Carbohydrate transport, metabolism	YIL125W	mitochondrion
AN5573.1	predicted protein [Neurospora crassa]				
AN5574.1	Uncharacterized conserved protein	S			
AN5575.1	hypothetical protein (hypothetical protein B24M22.240 [imported] - Neurospora crassa)				
AN5576.1					
AN5577.1	Manganese superoxide dismutase	P	Inorganic ion transport, metabolism	YHR008C	mitochondrion
AN5578.1	Tuftelin-interacting protein TIP39, contains G-patch domain	A	RNA processing, modification		
AN5579.1	Vacuolar protein sorting-associated protein	U	Intracellular trafficking/secretion/transport	YLL040C	endosome cytoplasm
AN5580.1	predicted protein [Neurospora crassa]				
AN5585.1	3-keto sterol reductase	I	Lipid transport, metabolism	YLR100W	lipid particle
AN5586.1	GDP-mannose pyrophosphorylase/mannose-1-phosphate guanylyltransferase	M		YDL055C	cytoplasm
AN5588.1	AAA+-type ATPase containing the peptidase M41 domain	O	Posttranslational modification/turnover/chaperones	YPR024W	mitochondrion
AN5589.1	Ribulose kinase and related carbohydrate kinases	G	Carbohydrate transport, metabolism		
AN5591.1	Aspartate/tyrosine/aromatic aminotransferase	E	Amino acid transport, metabolism		
AN5592.1	Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	T	Signal transduction mechanisms		
AN5593.1	Beta-TrCP (transducin repeats containing)/Slimb proteins	S			
AN5595.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN5596.1	Permease of the major facilitator superfamily	R			
AN5599.1	hypothetical protein [Neurospora crassa]			YBL011W	ER
AN5600.1	Cis-prenyltransferase	I	Lipid transport, metabolism		
AN5601.1	Lysine-ketoglutarate reductase/saccharopine dehydrogenase	E	Amino acid transport, metabolism	YNR050C	cytoplasm
AN5602.1	Uncharacterized conserved protein	S		YDR214W	cytoplasm
AN5603.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN5604.1	Fructose-1,6-bisphosphatase	G	Carbohydrate transport, metabolism	YLR377C	
AN5606.1	Vacuolar H+-ATPase V0 sector, subunit a	C	Energy production, conversion	YOR270C	vacuolar membrane
AN5607.1	Uncharacterized conserved protein	S		YFL007W	cytoplasm nucleus
AN5610.1	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	Q		YBR115C	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5611.1	Predicted carbonic anhydrase involved in protection against oxidative damage	P	Inorganic ion transport, metabolism	YNL036W	cytoplasm nucleus
AN5612.1	predicted protein [Neurospora crassa]				
AN5613.1	Xanthine dehydrogenase	F	Nucleotide transport, metabolism		
AN5614.1	hypothetical protein [Neurospora crassa]			YNL279W	vacuole
AN5616.1	Kynurenine aminotransferase, glutamine transaminase K	E	Amino acid transport, metabolism	YJL060W	mitochondrion cytoplasm
AN5617.1	ATPase related to the helicase subunit of the Holliday junction resolvase	L	Replication, recombination, repair	YNL218W	cytoplasm nucleus
AN5618.1	Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	ZD		YOR257W	
AN5619.1	Meltrins, fertilins and related Zn-dependent metalloproteinases of the ADAMs family	O	Posttranslational modification/turnover/chaperones		
AN5624.1	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain	R			
AN5625.1	Histone acetyltransferase (MYST family)	B	Chromatin structure, dynamics		
AN5626.1	Acyl-CoA synthetase	I	Lipid transport, metabolism	YLR153C	nucleus
AN5627.1	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	YU			
AN5629.1	NADH:ubiquinone oxidoreductase, NDUFV1/51kDa subunit	C	Energy production, conversion		
AN5630.1	N-methyltransferase	R			
AN5631.1	SAP family cell cycle dependent phosphatase-associated protein	D	Cell cycle/division, chrom. partitioning		
AN5632.1	Protein involved in vacuolar protein sorting	U	Intracellular trafficking/secretion/transport	YDR486C	vacuolar membrane
AN5633.1	Mn2+ and Fe2+ transporters of the NRAMP family	P	Inorganic ion transport, metabolism	YHR050W	
AN5634.1	Isocitrate lyase	C	Energy production, conversion	YER065C	
AN5635.1	Neutral trehalase	G	Carbohydrate transport, metabolism	YDR001C	cytoplasm
AN5637.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN5638.1	OTU (ovarian tumor)-like cysteine protease	TO		YHL013C	cytoplasm
AN5640.1	Histone acetyltransferase (MYST family)	B	Chromatin structure, dynamics		
AN5641.1	Clathrin-associated protein medium chain	U	Intracellular trafficking/secretion/transport		
AN5642.1	predicted protein [Neurospora crassa]				
AN5643.1	Chromatin remodeling complex WSTF-ISWI, small subunit	K	Transcription	YOR304W	nucleus
AN5644.1	Aldehyde dehydrogenase	C	Energy production, conversion	YMR110C	endosome lipid particle
AN5646.1	3-oxoacyl CoA thiolase	I	Lipid transport, metabolism	YIL160C	
AN5648.1	Uncharacterized conserved protein	S			
AN5653.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN5656.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN5657.1	predicted protein [Neurospora crassa]				
AN5658.1	Gamma-glutamyltransferase	E	Amino acid transport, metabolism	YLR299W	
AN5659.1	FOG: Zn-finger	R			
AN5660.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN5661.1	H/ACA small nucleolar RNP component GAR1	J	Translation, ribosomal structure, biogenesis		
AN5662.1	Threonyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YIL078W	cytoplasm
AN5663.1	Galactosyltransferases	G	Carbohydrate transport, metabolism		
AN5667.1	Uncharacterized conserved protein	S			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5668.1	Golgi-associated protein/Nedd4 WW domain-binding protein	R			
AN5669.1	Succinyl-CoA:alpha-ketoacid-CoA transferase	C	Energy production, conversion		
AN5671.1	unnamed protein product [Podospora anserina]				
AN5672.1	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	MR			
AN5673.1	hypothetical protein [Neurospora crassa]				
AN5674.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN5675.1	Predicted ubiquitin regulatory protein, contains UAS and UBX domains	O	Posttranslational modification/turnover/chaperones	YDR330W	cytoplasm nucleus
AN5676.1	Pre-initiation complex, subunit CDC6, AAA+ superfamily ATPase	LD		YJL194W	cytoplasm nucleus
AN5678.1	Amino acid transporters	E	Amino acid transport, metabolism	YKR039W	vacuole
AN5679.1	U6 snRNA-associated Sm-like protein	A	RNA processing, modification		
AN5681.1	Predicted E3 ubiquitin ligase, integral peroxisomal membrane protein	O	Posttranslational modification/turnover/chaperones	YDR265W	peroxisome
AN5682.1	Predicted small molecule transporter	U	Intracellular trafficking/secretion/transport		
AN5685.1	Uncharacterized conserved protein	S			
AN5686.1	Actin filament-coating protein tropomyosin	Z	Cytoskeleton	YNL079C	
AN5687.1	predicted protein [Neurospora crassa]				
AN5688.1	Cyclopropane fatty acid synthase and related methyltransferases	M			
AN5690.1	Copper amine oxidase	Q			
AN5692.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		YLR324W	peroxisome
AN5693.1	Uncharacterized conserved protein	S		YJL104W	mitochondrion
AN5694.1	DNA polymerase sigma	L	Replication, recombination, repair		
AN5697.1	Protein kinase C substrate, 80 KD protein, heavy chain	T	Signal transduction mechanisms		
AN5698.1	3-oxoacyl CoA thiolase	I	Lipid transport, metabolism		
AN5701.1	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	E	Amino acid transport, metabolism	YBR249C	cytoplasm nucleus
AN5702.1	Uncharacterized conserved protein	S			
AN5705.1	Golgi protein	U	Intracellular trafficking/secretion/transport	YDR372C	cytoplasm nucleus
AN5706.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			
AN5710.1	Cytosolic sorting protein GGA2/TOM1	U	Intracellular trafficking/secretion/transport	YHR108W	late Golgi
AN5711.1	Uncharacterized conserved protein	S			
AN5713.1	Chaperonin complex component, TCP-1 eta subunit (CCT7)	O	Posttranslational modification/turnover/chaperones	YJL111W	
AN5714.1					
AN5715.1	40s ribosomal protein S26	J	Translation, ribosomal structure, biogenesis	YER131W	cytoplasm
AN5716.1	FOG: CBS domain	R			
AN5717.1	Karyopherin (importin) beta 3	YU		YMR308C	cytoplasm nucleus
AN5719.1	60s acidic ribosomal protein P1	J	Translation, ribosomal structure, biogenesis	YDL130W	cytoplasm
AN5720.1	Predicted membrane protein	S		YOL092W	vacuolar membrane
AN5721.1	Uncharacterized conserved protein	S			
AN5722.1	Protein phosphatase 2C/pyruvate dehydrogenase (lipoamide) phosphatase	T	Signal transduction mechanisms	YOR090C	
AN5724.1	Inner membrane protein translocase involved in respiratory chain assembly	OU			
AN5725.1	Glycosyltransferase	M		YNL048W	ER
AN5726.1	FOG: Zn-finger	R			

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN5727.1	Arabinogalactan endo-1,4-beta-galactosidase	G	Carbohydrate transport, metabolism		
AN5728.1	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	T	Signal transduction mechanisms		
AN5730.1	predicted protein [Neurospora crassa]				
AN5731.1	Chorismate synthase	E	Amino acid transport, metabolism	YGL148W	cytoplasm
AN5732.1	Lipoate-protein ligase A	H	Coenzyme transport, metabolism	YJL046W	
AN5733.1	Uncharacterized protein conserved in bacteria	S			
AN5734.1	Predicted transporter (major facilitator superfamily)	R			
AN5737.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN5740.1	Ras-related small GTPase, Rho type	R		YPR165W	
AN5741.1	predicted protein [Neurospora crassa]				
AN5742.1	Fucose permease	G	Carbohydrate transport, metabolism		
AN5743.1	Ca2+ transporting ATPase	P	Inorganic ion transport, metabolism		
AN5744.1	Multifunctional chaperone (14-3-3 family)	O	Posttranslational modification/turnover/chaperones		
AN5745.1	Translation initiation factor eIF3, p35 subunit	J	Translation, ribosomal structure, biogenesis		
AN5746.1	Enolase	G	Carbohydrate transport, metabolism	YGR254W	cytoplasm
AN5747.1	26S proteasome regulatory complex, ATPase RPT4	O	Posttranslational modification/turnover/chaperones	YOR259C	nucleus
AN5748.1	1, 2-alpha-mannosidase	G	Carbohydrate transport, metabolism	YJR131W	ER
AN5749.1	Aminoacylase ACY1 and related metalloexopeptidases	E	Amino acid transport, metabolism		
AN5750.1	predicted protein [Neurospora crassa]				
AN5751.1	Polynucleotide kinase 3' phosphatase	L	Replication, recombination, repair		
AN5752.1	subunit of RNA polymerase II holoenzyme/mediator complex; Srb5p [Saccharomyces cerevisiae]				
AN5753.1					
AN5755.1	hypothetical protein (related to a-agglutinin core protein AGA1 [imported] - Neurospora crassa)				
AN5757.1	Casein kinase (serine/threonine/tyrosine protein kinase)	T	Signal transduction mechanisms	YER123W	vacuole
AN5758.1	Guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport	YNL206C	nucleus
AN5759.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN5760.1	Protein geranylgeranyltransferase Type I, beta subunit	O	Posttranslational modification/turnover/chaperones	YGL155W	cytoplasm nucleus
AN5761.1					
AN5763.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN5767.1	predicted protein [Neurospora crassa]				
AN5768.1	hypothetical protein ((AL451013) conserved hypothetical protein [Neurospora crassa])			YKL051W	cell periphery
AN5769.1	Prenylated rab acceptor 1	U	Intracellular trafficking/secretion/transport		
AN5770.1	Zuotin and related molecular chaperones (DnaJ superfamily), contains DNA-binding domains	O	Posttranslational modification/turnover/chaperones		
AN5771.1	predicted protein [Neurospora crassa]				
AN5772.1	Phosphomannomutase	I	Lipid transport, metabolism		
AN5773.1	DEAD box-containing helicase-like transcription factor/DNA repair protein	L	Replication, recombination, repair		
AN5774.1	Uncharacterized conserved protein	S			
AN5776.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN5777.1	Predicted lipase	I	Lipid transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5778.1	Actin-related protein Arp2/3 complex, subunit ARPC1/p41-ARC	Z	Cytoskeleton	YBR234C	actin
AN5781.1	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)	O	Posttranslational modification/turnover/chaperones		
AN5782.1	Predicted fumarylacetoacetate hydralase	R			
AN5783.1	20S proteasome, regulatory subunit beta type PSMB4/PRE4	O	Posttranslational modification/turnover/chaperones		
AN5784.1	20S proteasome, regulatory subunit beta type PSMB1/PRE7	O	Posttranslational modification/turnover/chaperones	YBL041W	
AN5785.1	Predicted RNA-binding protein Pno1p interacting with Nob1p and involved in 26S proteasome assembly	O	Posttranslational modification/turnover/chaperones	YOR145C	
AN5786.1	hypothetical protein [Neurospora crassa]			YHR194W	nucleus
AN5787.1	Rac GTPase-activating protein BCR/ABR	T	Signal transduction mechanisms		
AN5789.1	Predicted protein carboxyl methylase	R		YCR047C	cytoplasm nucleus
AN5790.1	Isocitrate dehydrogenase, gamma subunit	E	Amino acid transport, metabolism	YNL037C	mitochondrion
AN5799.1	Gamma-glutamyl phosphate reductase	E	Amino acid transport, metabolism	YOR323C	cytoplasm nucleus
AN5800.1	60s ribosomal protein L18	J	Translation, ribosomal structure, biogenesis	YOL120C	
AN5801.1	Mitochondrial solute carrier protein	C	Energy production, conversion	YPR011C	mitochondrion
AN5803.1	Ca2+-binding actin-bundling protein (fimbrin/plastin), EF-Hand protein superfamily	Z	Cytoskeleton	YDR129C	actin
AN5804.1	Phosphatidic acid-preferring phospholipase A1, contains DDHD domain	IU		YOR022C	mitochondrion
AN5805.1	HGG motif-containing thioesterase	R			
AN5806.1	Transcriptional coactivator	K	Transcription		
AN5807.1	predicted protein [Neurospora crassa]				
AN5808.1	predicted protein [Neurospora crassa]				
AN5810.1	Putative metallopeptidase	R		YFR006W	cytoplasm
AN5811.1	predicted protein [Neurospora crassa]				
AN5812.1	Bifunctional leukotriene A4 hydrolase/aminopeptidase LTA4H	IOVE		YNL045W	cytoplasm nucleus
AN5814.1	Uncharacterized conserved protein	S		YPR040W	cytoplasm nucleus
AN5815.1	Serine/threonine protein kinase	D	Cell cycle/division, chrom. partitioning	YPL209C	microtubule
AN5817.1	Gamma-glutamyl kinase	E	Amino acid transport, metabolism	YDR300C	cytoplasm
AN5819.1	Signal recognition particle receptor, beta subunit (small G protein superfamily)	U	Intracellular trafficking/secretion/transport	YKL154W	ER
AN5820.1	Cystathionine beta-synthase and related enzymes	E	Amino acid transport, metabolism	YGR155W	cytoplasm
AN5821.1	Ca2+/H+ antiporter VCX1 and related proteins	P	Inorganic ion transport, metabolism		
AN5822.1	Cyclin-dependent kinase WEE1	D	Cell cycle/division, chrom. partitioning		
AN5823.1	Lysine/ornithine N-monooxygenase	Q			
AN5824.1	Ankyrin repeat and DHHC-type Zn-finger domain containing proteins	R			
AN5825.1	Cyclin	R			
AN5827.1	mRNA splicing factor ATP-dependent RNA helicase	A	RNA processing, modification		
AN5828.1	Cytochrome b5	C	Energy production, conversion		
AN5829.1	Microtubule-associated proteins	Z	Cytoskeleton		
AN5830.1	Predicted hydrolase (HAD superfamily)	R			
AN5832.1	Ras-related GTPase	R			
AN5833.1	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	I	Lipid transport, metabolism		
AN5835.1	Glycine/serine hydroxymethyltransferase	E	Amino acid transport, metabolism		
AN5836.1	RNA polymerase II, large subunit	K	Transcription		
AN5837.1	Cytochrome P450	Q			
AN5838.1	NADP/FAD dependent oxidoreductase	C	Energy production, conversion		

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN5839.1	ATP-dependent RNA helicase A	A	RNA processing, modification		
AN5840.1	Protein containing adaptin N-terminal region	J	Translation, ribosomal structure, biogenesis	YGL195W	cytoplasm
AN5846.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN5848.1	unnamed protein product [Podospora anserina]				
AN5849.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN5850.1	Hydroxysteroid 17-beta dehydrogenase 11	Q			
AN5856.1	Mg2+ and Co2+ transporters	P	Inorganic ion transport, metabolism		
AN5857.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN5860.1	Predicted transporter (major facilitator superfamily)	R			
AN5861.1	17 beta-hydroxysteroid dehydrogenase type 3, HSD17B3	I	Lipid transport, metabolism	YBR159W	ER
AN5862.1	Predicted membrane protein	S		YER044C	ER
AN5864.1	Predicted transporter (major facilitator superfamily)	R			
AN5865.1	GTP-binding protein CRFG/NOG1 (ODN superfamily)	R		YPL093W	nucleus
AN5866.1	Arylalkylamine N-acetyltransferase	R		YDR071C	cytoplasm
AN5867.1	Acetylglutamate kinase/acetylglutamate synthase	E	Amino acid transport, metabolism		
AN5868.1	Predicted membrane protein	S			
AN5869.1	Lysophosphatidic acid acyltransferase endophilin/SH3GL, involved in synaptic vesicle formation	IT			
AN5870.1	hypothetical protein [Neurospora crassa]				
AN5871.1	Predicted RNA methylase involved in rRNA processing	A	RNA processing, modification		
AN5872.1	20S proteasome, regulatory subunit alpha type PSMA5/PUP2	O	Posttranslational modification/turnover/chaperones	YGR253C	cytoplasm nucleus
AN5873.1	Gamma-tubulin complex, DGRIP84/SPC97 component	Z	Cytoskeleton	YHR172W	spindle pole
AN5875.1	rRNA processing protein	JD		YCL059C	nucleolus cytoplasm
AN5876.1	Permeases of the major facilitator superfamily	R			
AN5877.1	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	IQ			
AN5878.1	3-oxoacyl CoA thiolase	I	Lipid transport, metabolism		
AN5879.1	Uncharacterized conserved protein, contains ML domain	R		YDL046W	vacuole
AN5880.1	Vacuolar H+-ATPase V1 sector, subunit F	C	Energy production, conversion	YGR020C	vacuolar membrane
AN5881.1	predicted protein [Neurospora crassa]				
AN5882.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN5883.1	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport, metabolism	YGL125W	cytoplasm nucleus
AN5884.1	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F	Nucleotide transport, metabolism	YML106W	cytoplasm nucleus
AN5885.1	Glycogen synthase	G	Carbohydrate transport, metabolism		
AN5886.1	3-isopropylmalate dehydratase (aconitase superfamily)	E	Amino acid transport, metabolism	YGL009C	cytoplasm nucleus
AN5887.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	C	Energy production, conversion	YNL331C	
AN5888.1	Glycosyltransferase	G	Carbohydrate transport, metabolism	YBR243C	
AN5890.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN5891.1	PHD Zn-finger proteins	R			
AN5892.1	Origin recognition complex, subunit 4	L	Replication, recombination, repair		
AN5893.1	G protein signaling regulators	T	Signal transduction mechanisms		
AN5894.1	RNA polymerase II assessory factor Cdc73p	K	Transcription	YLR418C	nucleus
AN5895.1	RAB proteins geranylgeranyltransferase component A (RAB escort protein)	O	Posttranslational modification/turnover/chaperones	YER136W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5899.1	Structural maintenance of chromosome protein 2 (chromosome condensation complex Condensin, subunit E)	BD		YFR031C	cytoplasm nucleus
AN5900.1	E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN5901.1	Uncharacterized conserved protein	S			
AN5902.1	Alpha-1,2 glucosyltransferase/transcriptional activator	OKIT		YGR227W	
AN5903.1	Tyrosyl-DNA phosphodiesterase	L	Replication, recombination, repair	YBR223C	cytoplasm nucleus
AN5906.1	Chaperone-dependent E3 ubiquitin protein ligase (contains TPR repeats)	O	Posttranslational modification/turnover/chaperones		
AN5908.1	Triosephosphate isomerase	G	Carbohydrate transport, metabolism		
AN5909.1	Dihydroorotate dehydrogenase	F	Nucleotide transport, metabolism		
AN5910.1	Putative RNA polymerase II regulator	K	Transcription		
AN5911.1	Actin-related protein	Z	Cytoskeleton		
AN5912.1	GTP-binding ADP-ribosylation factor-like protein ARL1	U	Intracellular trafficking/secretion/transport	YBR164C	early Golgi
AN5913.1	Alcohol dehydrogenase, class V	Q			
AN5914.1	S-adenosylmethionine:diacylglycerol 3-amino-3-carboxypropyl transferase	I	Lipid transport, metabolism		
AN5915.1	Golgi proteins involved in ER retention (RER)	U	Intracellular trafficking/secretion/transport	YCL001W	
AN5916.1	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport, metabolism		
AN5917.1	Predicted transporter (major facilitator superfamily)	R		YGR289C	
AN5918.1	Catalase	P	Inorganic ion transport, metabolism	YDR256C	
AN5920.1	Vacuolar assembly/sorting protein VPS9	U	Intracellular trafficking/secretion/transport		
AN5922.1	5'-phosphoribosylglycinamide formyltransferase	G	Carbohydrate transport, metabolism		
AN5924.1	predicted protein [Neurospora crassa]				
AN5925.1	Predicted ATP-dependent RNA helicase	A	RNA processing, modification	YDR291W	nucleus
AN5929.1	Calcium-responsive transcription coactivator	K	Transcription		
AN5930.1	predicted protein [Neurospora crassa]				
AN5931.1	ATP-dependent RNA helicase	A	RNA processing, modification	YNL112W	cytoplasm nucleus
AN5932.1	DNA polymerase alpha, catalytic subunit	L	Replication, recombination, repair	YNL102W	nucleus
AN5934.1	FOG: RCC1 domain	S			
AN5935.1	Permeases of the major facilitator superfamily	GEPR			
AN5938.1	Predicted dehydrogenase	G	Carbohydrate transport, metabolism		
AN5940.1	Uncharacterized conserved protein	S			
AN5950.1	Vesicle coat complex AP-1/AP-2/AP-4, beta subunit	U	Intracellular trafficking/secretion/transport	YJR005W	cell periphery bud neck
AN5951.1	Predicted membrane protein	S			
AN5952.1	L-kynurenine hydrolase	E	Amino acid transport, metabolism		
AN5954.1	RNA polymerase I-associated factor - PAF67	JK			
AN5955.1	NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIRA				
AN5957.1	Branched chain aminotransferase BCAT1, pyridoxal phosphate enzymes type IV superfamily	E	Amino acid transport, metabolism		
AN5958.1	Protein required for meiosis	D	Cell cycle/division, chrom. partitioning		
AN5959.1	Prephenate dehydrogenase (NADP+)	E	Amino acid transport, metabolism	YBR166C	cytoplasm
AN5960.1	40S ribosomal protein S14	J	Translation, ribosomal structure, biogenesis	YJL191W	nucleolus cytoplasm nucleus
AN5966.1	FOG: Zn-finger	R			
AN5968.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN5970.1	Thioredoxin/protein disulfide isomerase	O	Posttranslational modification/turnover/chaperones		
AN5971.1	NADH:ubiquinone oxidoreductase, NDUFA5/B13 subunit	C	Energy production, conversion		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN5972.1	Vesicle coat complex COPI, beta' subunit	U	Intracellular trafficking/secretion/transport	YGL137W	Golgi early Golgi
AN5973.1	Ribosomal protein S6 kinase and related proteins	RT		YKL126W	cytoplasm
AN5975.1	Mannitol-1-phosphate/altronate dehydrogenases	G	Carbohydrate transport, metabolism		
AN5977.1	Flavonol reductase/cinnamoyl-CoA reductase	V	Defense mechanisms	YGL157W	cytoplasm nucleus
AN5979.1	40S ribosomal protein S17	J	Translation, ribosomal structure, biogenesis	YML024W	cytoplasm
AN5980.1	predicted protein [Neurospora crassa]				
AN5982.1	DNA-dependent protein kinase	L	Replication, recombination, repair	YKL203C	
AN5983.1	Uncharacterized conserved protein	S			
AN5985.1	Aldehyde reductase	R			
AN5986.1	Aldo/keto reductase family proteins	R		YOR120W	cytoplasm nucleus
AN5988.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN5989.1	Predicted dehydrogenase	G	Carbohydrate transport, metabolism		
AN5990.1	Acyl-CoA synthetase	I	Lipid transport, metabolism		
AN5991.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones		
AN5992.1	DNA replication licensing factor, MCM7 component	L	Replication, recombination, repair	YBR202W	cytoplasm nucleus
AN5994.1	Predicted sugar kinase	G	Carbohydrate transport, metabolism	YKL151C	cytoplasm
AN5995.1	Carbonic anhydrase	R			
AN5996.1	60S acidic ribosomal protein P2	J	Translation, ribosomal structure, biogenesis	YDR382W	cytoplasm
AN5997.1	40S ribosomal protein S15	J	Translation, ribosomal structure, biogenesis	YOL040C	
AN5998.1	Predicted histone tail methylase containing SET domain	B	Chromatin structure, dynamics		
AN5999.1	Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	R		YJR109C	cytoplasm
AN6003.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN6004.1	hypothetical protein [Neurospora crassa]				
AN6006.1	Nuclear transport receptor RANBP7/RANBP8 (importin beta superfamily)	YU		YJR132W	cytoplasm nucleus
AN6009.1	WD40-like repeat containing protein	R			
AN6010.1	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	O	Posttranslational modification/turnover/chaperones	YJR045C	
AN6012.1	Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	K	Transcription		
AN6014.1	Acyl-CoA synthetase	I	Lipid transport, metabolism	YOR317W	ER
AN6015.1	related to meiosis-specific protein NDT80 [MIPS] [Neurospora crassa]				
AN6017.1	Translation initiation factor 3, subunit g (eIF-3g)	J	Translation, ribosomal structure, biogenesis	YER056C	vacuole
AN6031.1	Dioxygenases related to 2-nitropropane dioxygenase	R			
AN6032.1	Dihydropteroate synthase/7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase/Dihydroneopterin aldolase	H	Coenzyme transport, metabolism		
AN6033.1	Predicted GTPase-activating protein	T	Signal transduction mechanisms	YER122C	Golgi early Golgi
AN6034.1					
AN6035.1	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	MR			
AN6036.1	U1 snRNP complex, subunit SNU71 and related PWI-motif proteins	A	RNA processing, modification		
AN6037.1	Glucose-6-phosphate isomerase	G	Carbohydrate transport, metabolism	YBR196C	cytoplasm
AN6038.1	predicted protein [Neurospora crassa]				
AN6039.1	predicted protein [Neurospora crassa]				
AN6041.1	Uncharacterized conserved protein	S			
AN6045.1	Copper chaperone for superoxide dismutase	P	Inorganic ion transport, metabolism	YMR038C	cytoplasm nucleus

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6046.1	Sorbin and SH3 domain-containing protein	T	Signal transduction mechanisms		
AN6047.1	predicted protein [Neurospora crassa]				
AN6048.1	Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT2/GOT1	E	Amino acid transport, metabolism	YLR027C	
AN6049.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN6050.1					
AN6051.1	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q			
AN6053.1	Predicted mechanosensitive ion channel	M			
AN6054.1	Mitochondrial genome maintenance protein MGM101, mitochondrial precursor			YJR144W	
AN6055.1	Biotin holocarboxylase synthetase/biotin-protein ligase	H	Coenzyme transport, metabolism	YDL141W	cytoplasm nucleus
AN6057.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN6058.1	Uncharacterized conserved protein	S			
AN6059.1	HVA22/DP1 gene product-related proteins	V	Defense mechanisms		
AN6061.1	hypothetical protein [Schizosaccharomyces pombe]				
AN6064.1	Isoamyl acetate-hydrolyzing esterase	I	Lipid transport, metabolism	YOR126C	
AN6067.1	Translation initiation factor 5 (eIF-5)	J	Translation, ribosomal structure, biogenesis	YPR041W	cytoplasm
AN6068.1	Uncharacterized conserved protein	S		YKL033W	cytoplasm
AN6069.1	ATP-dependent DNA ligase I	L	Replication, recombination, repair	YDL164C	mitochondrion nucleus
AN6070.1	DNA replication licensing factor, MCM4 component	L	Replication, recombination, repair	YPR019W	cytoplasm nucleus
AN6071.1	Uncharacterized conserved protein	R			
AN6072.1	Guanidinoacetate methyltransferase and related proteins	E	Amino acid transport, metabolism	YDR465C	cytoplasm nucleus
AN6073.1	Prohibitin-like protein	O	Posttranslational modification/turnover/chaperones	YGR231C	mitochondrion
AN6074.1	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A	RNA processing, modification	YGL044C	
AN6075.1	Phenylalanine and histidine ammonia-lyase	Q			
AN6076.1	DEAD box-containing helicase-like transcription factor/DNA repair protein	L	Replication, recombination, repair		
AN6078.1	Adenine deaminase/adenosine deaminase	F	Nucleotide transport, metabolism	YNL141W	cytoplasm nucleus
AN6079.1	Predicted RNA-binding protein	R			
AN6080.1	Vesicle coat complex COPI, zeta subunit	U	Intracellular trafficking/secretion/transport	YPL010W	
AN6081.1	Cytoskeleton-associated protein and related proteins	ZR			
AN6082.1	60S ribosomal protein L30	J	Translation, ribosomal structure, biogenesis	YGL030W	
AN6083.1	60s ribosomal protein L10	J	Translation, ribosomal structure, biogenesis	YLR075W	cytoplasm
AN6084.1	predicted protein [Neurospora crassa]				
AN6085.1	DEAH-box RNA helicase	A	RNA processing, modification	YKL078W	nucleolus
AN6086.1	F-box protein FBX9	R			
AN6087.1	Mitochondrial carrier protein CGI-69	C	Energy production, conversion	YGR257C	mitochondrion
AN6089.1	Mitochondrial chaperonin, Cpn60/Hsp60p	O	Posttranslational modification/turnover/chaperones	YLR259C	mitochondrion
AN6090.1	Glucose-repressible protein and related proteins	R			
AN6091.1	predicted protein [Neurospora crassa]				
AN6093.1	Poly(3-hydroxybutyrate) depolymerase	Q			
AN6095.1	Permeases of the major facilitator superfamily	GEPR			
AN6102.1	hypothetical protein [Neurospora crassa]				
AN6104.1	Polyadenylate-binding protein (RRM superfamily)	AJ			
AN6107.1	Cl- channel CLC-3 and related proteins (CLC superfamily)	P	Inorganic ion transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6108.1	dihydrofolate reductase [Coprinopsis cinerea]				
AN6110.1	Uncharacterized conserved protein	S			
AN6111.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp45	J	Translation, ribosomal structure, biogenesis	YDR280W	nucleolus nucleus
AN6112.1	P-type ATPase	R		YAL026C	late Golgi early Golgi
AN6114.1	DNA polymerase IV (family X)	L	Replication, recombination, repair		
AN6115.1	High-affinity nickel permease	P	Inorganic ion transport, metabolism		
AN6116.1					
AN6118.1	Amino acid transporters	E	Amino acid transport, metabolism	YPL265W	vacuole cell periphery
AN6119.1	Zinc carboxypeptidase	S		YHR132C	vacuole
AN6120.1	Guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport		
AN6122.1	Zinc transporter and related ZIP domain-containing proteins	P	Inorganic ion transport, metabolism		
AN6123.1	Uncharacterized conserved protein	S			
AN6124.1	Amidases related to nicotinamidase	Q			
AN6126.1	Acetyl-CoA carboxylase	I	Lipid transport, metabolism	YNR016C	cytoplasm
AN6132.1	predicted protein [Neurospora crassa]				
AN6136.1	Protein involved in mRNA turnover and stability	A	RNA processing, modification		
AN6138.1	DNA-binding cell division cycle control protein	D	Cell cycle/division, chrom. partitioning		
AN6139.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	I	Lipid transport, metabolism	YDL052C	ER
AN6140.1	NpgA protein [Emericella nidulans]				
AN6141.1	Imidazoleglycerol-phosphate synthase subunit H-like	H	Coenzyme transport, metabolism	YMR095C	cytoplasm
AN6143.1	hypothetical protein [Neurospora crassa]				
AN6147.1	Histone tail methylase	B	Chromatin structure, dynamics		
AN6148.1	Acetylcholinesterase/Butyrylcholinesterase	T	Signal transduction mechanisms		
AN6149.1	ATP-dependent RNA helicase	A	RNA processing, modification	YGL064C	mitochondrion
AN6150.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN6151.1	PEP phosphonomutase and related enzymes	G	Carbohydrate transport, metabolism		
AN6157.1	Uridine 5'- monophosphate synthase/orotate phosphoribosyltransferase	F	Nucleotide transport, metabolism	YEL021W	
AN6159.1	Sterol O-acyltransferase/Diacylglycerol O-acyltransferase	I	Lipid transport, metabolism		
AN6160.1	Polyadenylation factor I complex, subunit PFS2	A	RNA processing, modification	YNL317W	nucleus
AN6162.1	Farnesyl cysteine-carboxyl methyltransferase	O	Posttranslational modification/turnover/chaperones		
AN6165.1	Pseudouridylate synthase	J	Translation, ribosomal structure, biogenesis	YPL212C	nucleus
AN6166.1	Transcription initiation factor IIE, alpha subunit	K	Transcription	YKL028W	nucleus
AN6167.1	NADH:flavin oxidoreductases, Old Yellow Enzyme family	C	Energy production, conversion		
AN6168.1	NADP+-dependent malic enzyme	C	Energy production, conversion		
AN6169.1	hypothetical protein [Neurospora crassa]				
AN6170.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones	YMR214W	
AN6171.1	U3 small nucleolar ribonucleoprotein (snoRNP) component	A	RNA processing, modification	YHR148W	
AN6172.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN6173.1	Hypothetical ORF; Ylr278cp [Saccharomyces cerevisiae]				
AN6176.1	predicted protein [Neurospora crassa]				
AN6177.1	Flotillins	UZ			
AN6180.1	predicted protein [Neurospora crassa]				
AN6182.1	Galactose-1-phosphate uridylyltransferase	C	Energy production, conversion	YBR018C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6186.1	Nucleotide excision repair complex XPC-HR23B, subunit XPC/DPB11	L	Replication, recombination, repair		
AN6188.1	Predicted hydrolases of HD superfamily	R		YGL101W	cytoplasm nucleus
AN6190.1	Cell cycle-associated protein	D	Cell cycle/division, chrom. partitioning		
AN6191.1	Cobalamin synthesis protein	H	Coenzyme transport, metabolism	YNR029C	cytoplasm
AN6192.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN6193.1	Mitochondrial ATP-dependent protease PIM1/LON	O	Posttranslational modification/turnover/chaperones	YBL022C	mitochondrion
AN6194.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN6195.1	FOG: Zn-finger	R			
AN6196.1					
AN6197.1	WD40 repeat-containing protein	S		YOR269W	cytoplasm nucleus
AN6198.1	unknown [Aspergillus oryzae]				
AN6200.1	Uncharacterized conserved protein	S		YPL012W	cytoplasm nucleus
AN6202.1	60S ribosomal protein L3 and related proteins	J	Translation, ribosomal structure, biogenesis	YOR063W	cytoplasm
AN6203.1	putative protein [Neurospora crassa]				
AN6204.1	cell wall beta-glucan assembly; Kre6p [Saccharomyces cerevisiae]				
AN6206.1					
AN6207.1	Dehydrogenase kinase	T	Signal transduction mechanisms		
AN6208.1					
AN6211.1	Lysophospholipase	I	Lipid transport, metabolism		
AN6213.1	Small nuclear ribonucleoprotein (snRNP)	A	RNA processing, modification		
AN6214.1	Histone acetyltransferase type b catalytic subunit	B	Chromatin structure, dynamics	YPL001W	
AN6216.1	ZIP-like zinc transporter proteins	U	Intracellular trafficking/secretion/transport		
AN6217.1	Cdc4 and related F-box and WD-40 proteins	R		YFL009W	
AN6218.1	unnamed protein product [Podospora anserina]				
AN6219.1	Mitochondrial phosphate carrier protein	C	Energy production, conversion		
AN6221.1	GATA-4/5/6 transcription factors	K	Transcription	YKR034W	
AN6222.1	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL			
AN6223.1	RNA polymerase II holoenzyme and mediator subcomplex, subunit SURB7/SRB7	K	Transcription		
AN6224.1	predicted protein [Neurospora crassa]				
AN6226.1	Predicted metal-dependent hydrolase with the TIM-barrel fold	R			
AN6228.1	GYF domain containing proteins	R			
AN6229.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			
AN6230.1	Medusa [Emericella nidulans]				
AN6231.1	Tryptophan synthase beta chain	E	Amino acid transport, metabolism	YGL026C	cytoplasm nucleus
AN6232.1	Vacuolar H+-ATPase V1 sector, subunit B	C	Energy production, conversion	YBR127C	vacuolar membrane
AN6233.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN6234.1	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure, biogenesis		
AN6235.1	Enoyl-CoA hydratase/carnithine racemase	I	Lipid transport, metabolism		
AN6236.1	Non-ribosomal peptide synthetase modules and related proteins	Q			
AN6237.1	Multidrug/pheromone exporter, ABC superfamily	Q			
AN6238.1	Predicted transporter (major facilitator superfamily)	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6239.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN6240.1	predicted protein [Neurospora crassa]				
AN6241.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN6243.1	MAPK related serine/threonine protein kinase	T	Signal transduction mechanisms		
AN6244.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp42	J	Translation, ribosomal structure, biogenesis	YDL111C	nucleolus cytoplasm nucleus
AN6245.1	predicted protein [Neurospora crassa]				
AN6247.1	predicted protein [Neurospora crassa]				
AN6248.1	Molecular chaperone of the GrpE family	O	Posttranslational modification/turnover/chaperones	YOR232W	cytoplasm
AN6249.1	Calcineurin-mediated signaling pathway inhibitor DSCR1	TR			
AN6250.1	Arginyl-tRNA-protein transferase	O	Posttranslational modification/turnover/chaperones		
AN6251.1	Diadenosine and diphosphoinositol polyphosphate phosphohydrolase	T	Signal transduction mechanisms	YOR163W	cytoplasm nucleus
AN6252.1	RNA polymerase II, subunit POLR2C/RPB3	K	Transcription	YIL021W	nucleus
AN6253.1	Phenylalanyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YPR047W	mitochondrion
AN6254.1	Mitochondrial oxoglutarate/malate carrier proteins	C	Energy production, conversion	YLR348C	mitochondrion
AN6256.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN6257.1	Vesicle coat complex COPII, subunit SEC31	U	Intracellular trafficking/secretion/transport	YDL195W	ER to Golgi
AN6258.1	Peroxisomal membrane anchor protein (peroxin)	MOU			
AN6261.1	hypothetical protein ((AL355933) conserved hypothetical protein [Neurospora crassa])				
AN6262.1	predicted protein [Neurospora crassa]				
AN6263.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones		
AN6265.1	WD40-repeat-containing subunit of the 18S rRNA processing complex	A	RNA processing, modification	YER082C	
AN6266.1	Uncharacterized conserved protein	S		YDL060W	cytoplasm nucleus
AN6267.1	Protein required for fusion of vesicles in vesicular transport, alpha-SNAP	U	Intracellular trafficking/secretion/transport	YBL050W	
AN6268.1	Uncharacterized conserved protein	S			
AN6269.1	Membrane component of ER protein translocation complex	U	Intracellular trafficking/secretion/transport		
AN6271.1	predicted protein [Neurospora crassa]				
AN6272.1	Ferredoxin/adrenodoxin reductase	F	Nucleotide transport, metabolism	YDR376W	mitochondrion
AN6273.1	Allergen Asp f 15 precursor (Asp f 13)				
AN6274.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN6275.1	predicted protein [Neurospora crassa]				
AN6277.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN6279.1	Carnitine O-acyltransferase CRAT	I	Lipid transport, metabolism	YML042W	
AN6280.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN6282.1	Isopropylmalate/homocitrate/citramalate synthases	E	Amino acid transport, metabolism		
AN6286.1	Glucosidase I	G	Carbohydrate transport, metabolism	YMR196W	cytoplasm
AN6287.1	Mitochondrial F1F0-ATP synthase, subunit OSCP/ATP5	C	Energy production, conversion	YDR298C	mitochondrion
AN6288.1	Cell cycle-associated protein Mob1-1	D	Cell cycle/division, chrom. partitioning	YIL106W	spindle pole cytoplasm
AN6289.1	Uncharacterized conserved protein	S		YDR137W	early Golgi

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6290.1	hypothetical protein (hypothetical protein B5O22.190 [imported] - Neurospora crassa)				
AN6291.1	WD40 repeat protein	S			
AN6293.1	hypothetical protein B23I11.340 [imported] - Neurospora crassa			YPL133C	cytoplasm nucleus
AN6295.1	predicted protein [Neurospora crassa]				
AN6298.1	hypothetical protein [Neurospora crassa]				
AN6299.1	Uncharacterized conserved protein	S			
AN6300.1	Replication factor C, subunit RFC3	DL		YBR087W	nucleus
AN6302.1	Mitochondrial ribosomal protein L16	J	Translation, ribosomal structure, biogenesis	YBL038W	mitochondrion
AN6303.1	Replication factor C, subunit RFC1 (large subunit)	L	Replication, recombination, repair	YOR217W	nucleus
AN6304.1	Stress-activated MAP kinase-interacting protein, Sin1p	T	Signal transduction mechanisms		
AN6305.1	cAMP-dependent protein kinase catalytic subunit (PKA)	T	Signal transduction mechanisms	YPL203W	nucleus
AN6307.1	Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	U	Intracellular trafficking/secretion/transport	YKR044W	cytoplasm
AN6308.1	predicted protein [Neurospora crassa]				
AN6309.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN6310.1	AAA ATPase containing von Willebrand factor type A (vWA) domain	R			
AN6311.1	Cl- channel CLC-3 and related proteins (CLC superfamily)	P	Inorganic ion transport, metabolism		
AN6312.1	predicted protein [Neurospora crassa]				
AN6313.1	Uncharacterized conserved protein	S			
AN6318.1	Chitin synthase/hyaluronan synthase (glycosyltransferases)	M			
AN6323.1	Microtubule-associated protein dynactin DCTN1/Glued	DZ			
AN6325.1	Haloacid dehalogenase-like hydrolase	R		YGL224C	
AN6326.1	Vigilin	I	Lipid transport, metabolism		
AN6327.1	von Willebrand factor and related coagulation proteins	WV			
AN6328.1	Predicted seven transmembrane receptor - rhodopsin family	T	Signal transduction mechanisms		
AN6329.1	Uncharacterized conserved protein	S			
AN6330.1	Elongation factor 2	J	Translation, ribosomal structure, biogenesis	YOR133W	cytoplasm
AN6331.1	Proteins containing the RNA recognition motif	R			
AN6334.1	GTP-binding protein AARP2 involved in 40S ribosome biogenesis	J	Translation, ribosomal structure, biogenesis		
AN6336.1	Dehydrogenase kinase	T	Signal transduction mechanisms		
AN6338.1	Aromatic amino acid aminotransferase and related proteins	E	Amino acid transport, metabolism	YGL202W	cytoplasm
AN6339.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN6340.1	Kinesin (KAR3 subfamily)	Z	Cytoskeleton	YPR141C	spindle pole microtubule nucleus
AN6341.1	Actin-binding protein Coronin, contains WD40 repeats	Z	Cytoskeleton		
AN6343.1	Class 2 transcription repressor NC2, alpha subunit (DRAP1)	K	Transcription		
AN6345.1	Predicted phosphate acyltransferase, contains PlsC domain	I	Lipid transport, metabolism	YPR139C	
AN6346.1	Dihydroxy-acid dehydratase	E	Amino acid transport, metabolism	YJR016C	mitochondrion
AN6347.1	Serine/threonine protein kinase	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6348.1	Mitochondrial import inner membrane translocase, subunit TIM23	U	Intracellular trafficking/secretion/transport	YNR017W	mitochondrion
AN6349.1	Cell cycle-associated protein	D	Cell cycle/division, chrom. partitioning		
AN6351.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport	YDL113C	endosome
AN6352.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN6354.1	Ubiquitin C-terminal hydrolase	O	Posttranslational modification/turnover/chaperones		
AN6359.1	Cdc4 and related F-box and WD-40 proteins	R		YIL046W	cytoplasm nucleus
AN6360.1	hypothetical protein [Neurospora crassa]				
AN6361.1	Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1	R			
AN6362.1	predicted protein [Neurospora crassa]				
AN6363.1	Serine/threonine protein kinase involved in cell cycle control	TD		YOR119C	
AN6364.1	Structural maintenance of chromosome protein 3 (sister chromatid cohesion complex Cohesin, subunit SMC3)	D	Cell cycle/division, chrom. partitioning	YJL074C	nucleus
AN6365.1	Hypothetical ORF; Ypl067cp [Saccharomyces cerevisiae]				
AN6366.1	NADH-cytochrome b-5 reductase	HC		YIL043C	ER
AN6367.1	Phosphatidylinositol-4-phosphate 5-kinase and related FYVE finger-containing proteins	T	Signal transduction mechanisms		
AN6368.1	Arginyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YDR341C	
AN6369.1	Transporter, ABC superfamily (Breast cancer resistance protein)	Q			
AN6371.1	hypothetical protein [Neurospora crassa]				
AN6372.1					
AN6374.1	RNA helicase	A	RNA processing, modification	YLR276C	
AN6375.1	Phosphate acyltransferase	I	Lipid transport, metabolism		
AN6383.1	Carboxylesterase type B	I	Lipid transport, metabolism		
AN6387.1	Vesicular amine transporter	U	Intracellular trafficking/secretion/transport		
AN6389.1	Carboxylesterase and related proteins	R			
AN6390.1	Homogentisate 1,2-dioxygenase	E	Amino acid transport, metabolism		
AN6391.1	Serine/threonine protein phosphatase 2A, catalytic subunit	T	Signal transduction mechanisms	YDL134C	cytoplasm nucleus
AN6394.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN6396.1	putative regulatory protein; zinc finger [Schizosaccharomyces pombe]				
AN6398.1	Nucleoside-diphosphate-sugar epimerases	MG			
AN6409.1	hypothetical protein [Neurospora crassa]				
AN6410.1	Endoglucanase	G	Carbohydrate transport, metabolism		
AN6412.1	Vesicular amine transporter	U	Intracellular trafficking/secretion/transport		
AN6420.1	Pirin-related protein	R			
AN6421.1	Hypothetical 25.2 kDa protein in SNZ3-COS4 intergenic region and in SNZ2-COS1 intergenic region				
AN6422.1	predicted protein [Neurospora crassa]				
AN6423.1	Uncharacterized protein conserved in bacteria	S			
AN6433.1	Acyl-CoA:diacylglycerol acyltransferase (DGAT)	I	Lipid transport, metabolism		
AN6438.1	Dipeptidyl aminopeptidase	O	Posttranslational modification/turnover/chaperones		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6442.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN6443.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q		YGR281W	cell periphery
AN6445.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN6452.1	Sexual differentiation process protein ISP4	T	Signal transduction mechanisms		
AN6462.1	Metal-dependent amidase/aminoacylase/carboxypeptidase	R			
AN6466.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN6472.1	Predicted glycosyl hydrolase	G	Carbohydrate transport, metabolism		
AN6477.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN6487.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones	YLR121C	mitochondrion
AN6492.1	CCAAT-binding factor, subunit C (HAP5)	K	Transcription		
AN6493.1	Exocyst complex, subunit SEC15	U	Intracellular trafficking/secretion/transport	YGL233W	cell periphery bud neck cytoplasm
AN6494.1	Protein Mei2, essential for commitment to meiosis, and related proteins	D	Cell cycle/division, chrom. partitioning		
AN6499.1	NAD-dependent malate dehydrogenase	C	Energy production, conversion		
AN6500.1	60S ribosomal protein L28	J	Translation, ribosomal structure, biogenesis		
AN6501.1	Splicing factor 3b, subunit 4	A	RNA processing, modification	YOR319W	nucleus
AN6502.1	Mitochondrial FAD carrier protein	C	Energy production, conversion	YIL134W	
AN6503.1	FOG: Zn-finger	R			
AN6505.1	WD40 repeat-containing protein	R			
AN6506.1	Sterol C5 desaturase	I	Lipid transport, metabolism	YLR056W	ER
AN6507.1	Nuclear cap-binding complex, subunit NCBP1/CBP80	A	RNA processing, modification	YMR125W	nucleus
AN6508.1	Glycogen synthase kinase-3	G	Carbohydrate transport, metabolism	YMR139W	cytoplasm
AN6510.1	Translocase of outer mitochondrial membrane complex, subunit TOM40	U	Intracellular trafficking/secretion/transport	YMR203W	
AN6511.1	RNA polymerase II elongator complex, subunit ELP2, WD repeat superfamily	BK			
AN6512.1	Predicted ABC-type transport, ATPase component/CCR4 associated factor	RK		YFL028C	cytoplasm nucleus
AN6513.1	tRNA delta(2)-isopentenylpyrophosphate transferase	J	Translation, ribosomal structure, biogenesis	YOR274W	cytoplasm nucleus
AN6514.1	Nuclear 5'-3' exoribonuclease-interacting protein, Rai1p	L	Replication, recombination, repair	YGL246C	nucleus
AN6515.1	Uncharacterized conserved protein	S		YOR164C	cytoplasm
AN6517.1	Replication factor C, subunit RFC2	L	Replication, recombination, repair	YOL094C	nucleus
AN6520.1	NADH-cytochrome b-5 reductase	HC			
AN6521.1	Aconitase/homoaconitase (aconitase superfamily)	CE		YDR234W	mitochondrion
AN6522.1	Mitochondrial GTPase	J	Translation, ribosomal structure, biogenesis	YMR023C	mitochondrion cytoplasm
AN6524.1	predicted protein [Neurospora crassa]				
AN6525.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	Energy production, conversion	YOR388C	
AN6526.1	Leucyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YLR382C	mitochondrion
AN6527.1	hypothetical protein ((AL451018) related to sucrose cleavage protein [Neurospora crassa])				
AN6528.1	Prenyl protein protease	O	Posttranslational modification/turnover/chaperones	YMR274C	
AN6529.1	Chitinase	M			
AN6530.1	Predicted membrane protein	S		YOR175C	ER
AN6531.1	Vacuolar sorting protein VPS45/Stt10 (Sec1 family)	U	Intracellular trafficking/secretion/transport	YGL095C	late Golgi early Golgi

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6532.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN6533.1	Targeting complex (TRAPP) subunit	U	Intracellular trafficking/secretion/transport		
AN6534.1	Mannosyltransferase OCH1 and related enzymes	M		YBR161W	vacuole
AN6536.1	Imidazoleglycerol-phosphate dehydratase	E	Amino acid transport, metabolism	YOR202W	
AN6538.1	LRR-containing protein	S			
AN6540.1	related to PET127 [Neurospora crassa]				
AN6541.1	Glycinamide ribonucleotide synthetase (GARS)/Aminoimidazole ribonucleotide synthetase (AIRS)	F	Nucleotide transport, metabolism	YGL234W	cytoplasm
AN6542.1	Actin and related proteins	Z	Cytoskeleton	YFL039C	
AN6543.1	Armadillo/beta-catenin-like repeat-containing protein	O	Posttranslational modification/turnover/chaperones	YBR101C	cytoplasm
AN6544.1	Predicted membrane protein	S		YOL129W	vacuolar membrane
AN6546.1	Leptin receptor gene-related protein	T	Signal transduction mechanisms	YJR044C	endosome
AN6547.1	20S proteasome, regulatory subunit alpha type PSMA1/PRE5	O	Posttranslational modification/turnover/chaperones	YMR314W	cytoplasm nucleus
AN6548.1	Predicted Rossmann fold nucleotide-binding protein	R		YJL055W	cytoplasm nucleus
AN6549.1	RNA polymerase II transcriptional regulation mediator	K	Transcription		
AN6550.1	Para-aminobenzoate (PABA) synthase ABZ1	J	Translation, ribosomal structure, biogenesis	YNR033W	cytoplasm
AN6551.1	hypothetical protein ((AL451018) putative protein [Neurospora crassa])				
AN6553.1	Serine/threonine protein kinase	T	Signal transduction mechanisms		
AN6555.1	Alpha/beta hydrolase	R		YMR210W	
AN6558.1	DNA-directed RNA polymerase, subunit L	K	Transcription	YNL113W	nucleolus
AN6560.1	Microtubule-associated protein TAU	Z	Cytoskeleton		
AN6561.1	Uncharacterized conserved protein	S		YOR287C	
AN6562.1	TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	K	Transcription		
AN6563.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones	YPL048W	cytoplasm
AN6564.1	Mitochondrial/chloroplast ribosomal protein S9	J	Translation, ribosomal structure, biogenesis	YBR146W	
AN6566.1	Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	T	Signal transduction mechanisms	YKL190W	cytoplasm
AN6567.1	Polycomb enhancer protein, EPC	K	Transcription		
AN6568.1	Uncharacterized conserved protein	S		YDR257C	nucleus
AN6569.1	Predicted metalloprotease with chaperone activity (RNAse H/HSP70 fold)	O	Posttranslational modification/turnover/chaperones	YKR038C	cytoplasm nucleus
AN6570.1	Protein involved in Snf1 protein kinase complex assembly	G	Carbohydrate transport, metabolism		
AN6571.1	Ttp1p			YBR015C	Golgi
AN6572.1	ABC (ATP binding cassette) 1 protein	R			
AN6574.1	E3 ubiquitin ligase involved in syntaxin degradation	O	Posttranslational modification/turnover/chaperones		
AN6577.1	NAD/FAD-utilizing protein possibly involved in translation	J	Translation, ribosomal structure, biogenesis	YGL236C	
AN6578.1	Gluconate transport-inducing protein	TG			
AN6579.1	TonB protein [Pantoea agglomerans]				
AN6581.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN6587.1	Translational repressor Pumilio/PUF3 and related RNA-binding proteins (Puf superfamily)	J	Translation, ribosomal structure, biogenesis		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6588.1					
AN6589.1	Glycosylphosphatidylinositol anchor synthesis protein	T	Signal transduction mechanisms	YLL031C	ER
AN6591.1	Nuclear export receptor CSE1/CAS (importin beta superfamily)	YU		YGL238W	cytoplasm nucleus
AN6594.1	Uncharacterized conserved protein	S		YLR215C	cytoplasm
AN6596.1	predicted protein [Neurospora crassa]				
AN6597.1	Protein kinase PITSLRE and related kinases	R			
AN6598.1	Uncharacterized conserved protein	S			
AN6599.1	Uncharacterized conserved protein	S		YGR021W	mitochondrion
AN6600.1	hypothetical protein ((AL513463) conserved hypothetical protein [Neurospora crassa])				
AN6601.1	Transmembrane protein	R			
AN6604.1	hypothetical protein [Neurospora crassa]				
AN6608.1	hypothetical protein [Neurospora crassa]				
AN6609.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN6611.1	Uncharacterized conserved protein	S		YNL127W	
AN6612.1	RNA-binding nuclear protein (MAK16) containing a distinct C4 Zn-finger	A	RNA processing, modification		
AN6614.1	P-type ATPase	P	Inorganic ion transport, metabolism	YIL048W	early Golgi
AN6615.1	Regucalcin gene promoter region-related protein (RGPR)	K	Transcription		
AN6618.1	Ypt/Rab-specific GTPase-activating protein GYP7 and related proteins	T	Signal transduction mechanisms	YDL234C	cytoplasm
AN6623.1	Permease of the major facilitator superfamily	R			
AN6624.1	FOG: TPR repeat	R			
AN6625.1					
AN6626.1	Peroxisomal membrane protein MPV17 and related proteins	R			
AN6627.1	Signal recognition particle receptor, alpha subunit	U	Intracellular trafficking/secretion/transport	YDR292C	
AN6628.1	Predicted membrane protein	S		YNL263C	
AN6629.1	60S ribosomal protein L14	J	Translation, ribosomal structure, biogenesis	YKL006W	cytoplasm
AN6630.1	Transcription factor containing NAC and TS-N domains	K	Transcription	YHR193C	cytoplasm
AN6631.1	Mitochondrial F1F0-ATP synthase, subunit d/ATP7	C	Energy production, conversion	YKL016C	mitochondrion
AN6634.1					
AN6636.1	Betaine aldehyde dehydrogenase	C	Energy production, conversion	YHR039C	ER
AN6637.1	Glutamine phosphoribosylpyrophosphate amidotransferase	F	Nucleotide transport, metabolism		
AN6638.1	Site-specific DNA methylase	L	Replication, recombination, repair		
AN6639.1	Uncharacterized protein involved in propionate catabolism	R		YPR002W	mitochondrion cytoplasm
AN6640.1	Metal-dependent amidase/aminoacylase/carboxypeptidase	R			
AN6642.1	Ca2+ transporting ATPase	P	Inorganic ion transport, metabolism	YDR039C	cell periphery
AN6644.1	Acetylornithine aminotransferase	E	Amino acid transport, metabolism		
AN6645.1	7-keto-8-aminopelargonate synthetase and related enzymes	H	Coenzyme transport, metabolism		
AN6649.1	Very long-chain acyl-CoA synthetase/fatty acid transporter	I	Lipid transport, metabolism		
AN6650.1	Citrate synthase	C	Energy production, conversion		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6651.1	ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	EJ		YPL226W	cytoplasm
AN6652.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN6653.1	Malate synthase	C	Energy production, conversion	YIR031C	
AN6654.1	Glutamine synthetase	E	Amino acid transport, metabolism		
AN6655.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN6658.1	Amine oxidase	Q			
AN6669.1	Predicted transporter (major facilitator superfamily)	R			
AN6672.1					
AN6673.1	putative large secreted protein [Streptomyces coelicolor A3(2)]				
AN6675.1	PHD finger protein BR140/LIN-49	R			
AN6678.1	Uncharacterized conserved protein	S			
AN6679.1	40S ribosomal protein S13	J	Translation, ribosomal structure, biogenesis	YDR064W	
AN6680.1	predicted protein [Neurospora crassa]				
AN6681.1	Splicing factor U2AF, large subunit (RRM superfamily)	A	RNA processing, modification		
AN6682.1	8-oxoguanine DNA glycosylase	L	Replication, recombination, repair	YML060W	nucleus
AN6684.1	hypothetical protein [Neurospora crassa]				
AN6685.1	Large exoproteins involved in heme utilization or adhesion	U	Intracellular trafficking/secretion/transport	YLR084C	cell periphery bud neck
AN6687.1	Nucleosome-binding factor SPN, POB3 subunit	KLB		YML069W	nucleus
AN6688.1	Septin family protein (P-loop GTPase)	DZU		YLR314C	
AN6690.1	Predicted mitochondrial carrier protein	C	Energy production, conversion	YMR166C	mitochondrion
AN6694.1	DNA replication checkpoint protein CHL12/CTF18	DL			
AN6695.1	Nonsense-mediated mRNA decay 2 protein	A	RNA processing, modification	YHR077C	cytoplasm
AN6696.1	hypothetical protein [Neurospora crassa]				
AN6697.1	hypothetical protein [Neurospora crassa]			YJL116C	
AN6698.1	Uncharacterized conserved protein	S			
AN6700.1	ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	EJ		YNL014W	
AN6702.1	Negative regulator of COPII vesicle formation	U	Intracellular trafficking/secretion/transport	YFL025C	ER
AN6703.1	Permeases of the major facilitator superfamily	GEPR		YKL217W	
AN6705.1	Chromatin remodeling factor subunit and related transcription factors	B	Chromatin structure, dynamics		
AN6707.1	DNA or RNA helicases of superfamily II	KL			
AN6708.1	Dihydrolipoamide acetyltransferase	C	Energy production, conversion	YNL071W	mitochondrion
AN6709.1	Guanine nucleotide exchange factor	U	Intracellular trafficking/secretion/transport	YDR170C	late Golgi
AN6711.1	Ribose-phosphate pyrophosphokinase	FE			
AN6712.1	Phospholipase D1	I	Lipid transport, metabolism		
AN6714.1	Uncharacterized conserved protein, contains TPR repeats	R		YNL313C	cytoplasm nucleus
AN6715.1	hypothetical protein [Neurospora crassa]				
AN6716.1	predicted protein [Neurospora crassa]				
AN6717.1	NAD-dependent malate dehydrogenase	C	Energy production, conversion	YKL085W	mitochondrion
AN6718.1	ATPases of the AAA+ class	O	Posttranslational modification/turnover/chaperones		
AN6720.1	Fructose-6-phosphate 2-kinase/fructose-2,6-biphosphatase	G	Carbohydrate transport, metabolism		

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN6721.1	Predicted metal-dependent hydrolase with the TIM-barrel fold	R			
AN6722.1	Predicted transporter (major facilitator superfamily)	R			
AN6723.1	Predicted metal-dependent hydrolase of the TIM-barrel fold	R			
AN6725.1	Protein involved in mRNA turnover and stability	A	RNA processing, modification		
AN6726.1	20S proteasome, regulatory subunit alpha type PSMA2/PRE8	O	Posttranslational modification/turnover/chaperones	YML092C	nucleus
AN6728.1	DNA repair protein RAD51/RHP55	L	Replication, recombination, repair		
AN6729.1	Uncharacterized Fe-S protein	R			
AN6730.1	Xanthine/uracil permeases	F	Nucleotide transport, metabolism		
AN6731.1	Fatty acid desaturase	I	Lipid transport, metabolism	YGL055W	ER
AN6732.1	Calmodulin and related proteins (EF-Hand superfamily)	T	Signal transduction mechanisms		
AN6733.1	FOG: Zn-finger	R			
AN6735.1	Small nuclear ribonucleoprotein E	A	RNA processing, modification	YOR159C	
AN6738.1	Nuclear pore complex, Nup155 component (D Nup154, sc Nup157/Nup170)	YU		YBL079W	nuclear periphery
AN6740.1					
AN6741.1	DNA damage inducible protein	L	Replication, recombination, repair	YER143W	cytoplasm
AN6743.1	Predicted acyl esterases	R			
AN6746.1	Uncharacterized conserved protein	S			
AN6752.1	Acyl-CoA oxidase	I	Lipid transport, metabolism	YGL205W	
AN6753.1	NADH:flavin oxidoreductase/12-oxophytodienoate reductase	CR			
AN6755.1	Very-long-chain acyl-CoA dehydrogenase	I	Lipid transport, metabolism		
AN6761.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN6774.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN6776.1	Predicted hydrolase related to dienelactone hydrolase	R			
AN6779.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q			
AN6780.1					
AN6792.1	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate reductase	C	Energy production, conversion		
AN6793.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN6795.1	antigenic cell wall protein MP1 [Aspergillus flavus]				
AN6809.1	Phosphatidylinositol transfer protein SEC14 and related proteins	I	Lipid transport, metabolism		
AN6815.1	Atrazine chlorohydrolase/guanine deaminase	FQ		YDL238C	cytoplasm
AN6817.1	Putative NADP-dependent oxidoreductases	R			
AN6818.1	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	Q			
AN6820.1	Signal transduction histidine kinase	T	Signal transduction mechanisms		
AN6823.1	hypothetical protein ((AL513443) hypothetical protein [Neurospora crassa])				
AN6824.1	Predicted sugar kinase	G	Carbohydrate transport, metabolism	YJR049C	cytoplasm nucleus
AN6825.1	Transport protein particle (TRAPP) complex subunit	U	Intracellular trafficking/secretion/transport		
AN6826.1	Microfibrillar-associated protein MFAP1	Z	Cytoskeleton		
AN6828.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6836.1	Acetyltransferase (isoleucine patch superfamily)	R			
AN6840.1	Glyoxylase	R			
AN6841.1	Mitochondrial inner membrane protease, subunit IMP1	O	Posttranslational modification/turnover/chaperones	YMR150C	
AN6842.1	Phosphatidylethanolamine binding protein	R		YDR322W	mitochondrion
AN6843.1	Mitochondrial/chloroplast ribosomal protein L4	J	Translation, ribosomal structure, biogenesis	YML025C	mitochondrion
AN6844.1	Enoyl-CoA hydratase	I	Lipid transport, metabolism	YDR036C	mitochondrion
AN6845.1	Iron transporter	P	Inorganic ion transport, metabolism		
AN6846.1	predicted protein [Neurospora crassa]				
AN6847.1	Arylsulfatase A and related enzymes	P	Inorganic ion transport, metabolism		
AN6848.1	Permeases of the major facilitator superfamily	GEPR			
AN6851.1	5'-AMP-activated protein kinase, gamma subunit	C	Energy production, conversion		
AN6853.1	Phosphatidylinositol transfer protein PDR16 and related proteins	I	Lipid transport, metabolism	YNL231C	lipid particle
AN6854.1	predicted protein [Neurospora crassa]				
AN6855.1	DNA polymerase alpha-primase complex, polymerase-associated subunit B	L	Replication, recombination, repair	YBL035C	nucleus
AN6856.1	predicted protein [Neurospora crassa]				
AN6857.1	hypothetical protein [Neurospora crassa]			YJL186W	
AN6858.1	predicted protein [Neurospora crassa]				
AN6859.1	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains	AK			
AN6861.1	predicted protein [Neurospora crassa]				
AN6863.1	Kinesin-like protein	Z	Cytoskeleton	YKL079W	cytoplasm bud
AN6864.1	Translation initiation factor 2B, delta subunit (eIF-2Bdelta/GCD2)	J	Translation, ribosomal structure, biogenesis		
AN6865.1	Isoamyl acetate-hydrolyzing esterase and related enzymes	R		YDR361C	cytoplasm nucleus
AN6866.1	Chorismate mutase	E	Amino acid transport, metabolism	YPR060C	cytoplasm nucleus
AN6869.1	Arginase family protein	E	Amino acid transport, metabolism		
AN6870.1	Uncharacterized membrane protein, predicted efflux pump	R			
AN6874.1	Glycosyltransferase	M		YGL065C	ER
AN6875.1	Kinesin-like protein	Z	Cytoskeleton		
AN6878.1	conserved hypothetical protein [Neurospora crassa]				
AN6879.1	Permeases of the major facilitator superfamily	GEPR			
AN6880.1	Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	KIT			
AN6881.1	predicted protein [Neurospora crassa]				
AN6883.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN6884.1	hypothetical protein [Neurospora crassa]				
AN6886.1	PalH [Emericella nidulans]				
AN6887.1					
AN6888.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones		
AN6889.1	hypothetical protein [Neurospora crassa]				
AN6890.1	UV radiation resistance associated protein	R			
AN6891.1	predicted protein [Neurospora crassa]				
AN6892.1	Serine/threonine protein phosphatase	T	Signal transduction mechanisms		
AN6893.1	Uncharacterized conserved protein	S		YEL015W	
AN6894.1	Cyclophilin type, U box-containing peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN6895.1	DNA helicase PIF1/RRM3	D	Cell cycle/division, chrom. partitioning		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN6896.1	Nucleotide excision repair factor NEF2, RAD4/CUT5 component	L	Replication, recombination, repair		
AN6898.1	Vacuolar assembly/sorting protein DID4	U	Intracellular trafficking/secretion/transport	YKL002W	endosome
AN6899.1	repetitive proline rich protein [Oryza sativa]				
AN6900.1	Triosephosphate isomerase	G	Carbohydrate transport, metabolism	YDR050C	cytoplasm nucleus
AN6901.1	mitochondrial protein [Emericella nidulans]			YAL010C	mitochondrion
AN6902.1	Protein involved in mRNA turnover	A	RNA processing, modification	YKL009W	nucleolus nucleus
AN6904.1	Mitochondrial/chloroplast ribosomal protein 36a	J	Translation, ribosomal structure, biogenesis	YPR100W	mitochondrion
AN6906.1	mRNA splicing factor	R		YLL036C	nucleus
AN6907.1	Translation elongation factor 2/ribosome biogenesis protein RIA1 and related proteins	J	Translation, ribosomal structure, biogenesis		
AN6908.1	FOG: FHA domain	T	Signal transduction mechanisms		
AN6909.1	Predicted membrane protein	S			
AN6911.1	Vacuolar assembly/sorting protein VPS16	U	Intracellular trafficking/secretion/transport	YPL045W	vacuolar membrane
AN6912.1	predicted protein [Neurospora crassa]				
AN6913.1	Ubiquitin-specific protease	O	Posttranslational modification/turnover/chaperones		
AN6914.1	Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	ZD			
AN6915.1	Uncharacterized conserved protein	S			
AN6920.1	Vacuolar sorting protein VPS24	U	Intracellular trafficking/secretion/transport	YKL041W	endosome
AN6921.1	HSP90 co-chaperone p23	O	Posttranslational modification/turnover/chaperones		
AN6922.1	Uncharacterized conserved protein, contains CCCH-type Zn-finger	R		YOR091W	cytoplasm
AN6923.1	Predicted transporter (major facilitator superfamily)	R			
AN6925.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN6933.1	NADP+-dependent malic enzyme	C	Energy production, conversion	YKL029C	mitochondrion
AN6934.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN6939.1	Predicted nucleic-acid-binding protein, contains PIN domain	R			
AN6941.1					
AN6959.1	Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7	DKL			
AN7060.1	Tyrosinase (Monophenol monooxygenase)				
AN7068.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN7084.1	Polyketide synthase modules and related proteins	Q			
AN7087.1	hypothetical protein [Nostoc punctiforme]				
AN7114.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ			
AN7115.1	Uncharacterized protein conserved in bacteria	S			
AN7140.1	Predicted amino acid aldolase or racemase	E	Amino acid transport, metabolism		
AN7156.1	Predicted dehydrogenases and related proteins	R			
AN7175.1	SAM-dependent methyltransferases	QR			
AN7187.1	D-aspartate oxidase	E	Amino acid transport, metabolism		
AN7188.1	Sexual differentiation process protein ISP4	T	Signal transduction mechanisms		
AN7189.1	hypothetical protein [Neurospora crassa]				
AN7192.1	predicted protein [Neurospora crassa]				
AN7193.1	Aldo/keto reductase family proteins	R			
AN7194.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7201.1	Predicted protease	O	Posttranslational modification/turnover/chaperones		
AN7202.1	Amidases related to nicotinamidase	Q			
AN7204.1	Fatty acid desaturase	I	Lipid transport, metabolism		
AN7208.1	hypothetical protein [Neurospora crassa]				
AN7211.1	C-8,7 sterol isomerase	I	Lipid transport, metabolism		
AN7220.1					
AN7222.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN7228.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN7229.1	Arylsulfatase A and related enzymes	P	Inorganic ion transport, metabolism		
AN7230.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN7231.1	Hydrolytic enzymes of the alpha/beta hydrolase fold	OR			
AN7232.1	hypothetical protein [Neurospora crassa]				
AN7233.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN7240.1	Fucose permease	G	Carbohydrate transport, metabolism		
AN7248.1	predicted protein [Neurospora crassa]				
AN7249.1	Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	U	Intracellular trafficking/secretion/transport		
AN7250.1	Na+/H+ antiporter	P	Inorganic ion transport, metabolism		
AN7252.1	Adenylate cyclase, family 3 (some proteins contain HAMP domain)	T	Signal transduction mechanisms		
AN7254.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones	YDL126C	cytoplasm nucleus
AN7256.1	25D9-5p [Aspergillus fumigatus]				
AN7258.1	Peroxisomal membrane protein MPV17 and related proteins	R			
AN7259.1	Uncharacterized conserved protein	S		YLR128W	
AN7260.1	Protein involved in the nuclear export of pre-ribosomes	JU		YLR002C	nucleolus nucleus
AN7261.1	Uncharacterized conserved protein	S			
AN7273.1	predicted protein [Neurospora crassa]				
AN7275.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN7279.1	hypothetical protein [Streptomyces avermitilis MA-4680]				
AN7284.1	Mitochondrial ribosomal protein L17	J	Translation, ribosomal structure, biogenesis		
AN7285.1	predicted protein [Neurospora crassa]				
AN7287.1	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	Energy production, conversion	YJR095W	
AN7289.1	Protein tyrosine kinase 9/actin monomer-binding protein	W		YGR080W	actin
AN7291.1	Translation initiation factor 5B (eIF-5B)	J	Translation, ribosomal structure, biogenesis		
AN7292.1	Soluble epoxide hydrolase	I	Lipid transport, metabolism		
AN7293.1	Uncharacterized conserved protein	S			
AN7294.1	PHD Zn-finger protein	R			
AN7295.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN7296.1	Sister chromatid cohesion complex Cohesin, subunit PDS5	D	Cell cycle/division, chrom. partitioning	YMR076C	nucleus
AN7298.1	Metal-dependent hydrolase	R			
AN7299.1	Metallopeptidase	R			
AN7300.1	PHD Zn-finger protein	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7301.1	Glucosyltransferase - Alg8p	K	Transcription	YOR067C	
AN7302.1	Mannose lectin ERGIC-53, involved in glycoprotein traffic	U	Intracellular trafficking/secretion/transport	YLR080W	vacuole
AN7303.1	Chromatin remodeling complex WSTF-ISWI, large subunit (contains heterochromatin localization, PHD and BROMO domains)	B	Chromatin structure, dynamics		
AN7304.1	Mitochondrial solute carrier protein	C	Energy production, conversion	YHR002W	
AN7305.1	TBP-binding protein, activator of basal transcription (contains rrm motif)	K	Transcription	YNR054C	nucleolus cytoplasm
AN7306.1	Predicted E3 ubiquitin ligase involved in peroxisome organization	O	Posttranslational modification/turnover/chaperones		
AN7307.1	Uncharacterized conserved protein	S			
AN7309.1	Postreplication repair protein RAD18	L	Replication, recombination, repair	YCR066W	
AN7310.1	Uncharacterized conserved protein	S		YJL049W	
AN7311.1	Protein with predicted involvement in meiosis (GSG1)	D	Cell cycle/division, chrom. partitioning	YDR108W	cytoplasm
AN7312.1	tRNA nucleotidyltransferase/poly(A) polymerase	J	Translation, ribosomal structure, biogenesis		
AN7313.1	hypothetical protein [Neurospora crassa]				
AN7314.1	Putative phosphoinositide phosphatase	I	Lipid transport, metabolism	YNL325C	
AN7320.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN7324.1	Glycine/D-amino acid oxidases (deaminating)	E	Amino acid transport, metabolism		
AN7325.1	DNA polymerase delta, catalytic subunit	L	Replication, recombination, repair	YDL102W	nucleus
AN7328.1	hypothetical protein [Neurospora crassa]				
AN7331.1	Cyanate lyase	P	Inorganic ion transport, metabolism		
AN7332.1	hypothetical protein [Neurospora crassa]				
AN7335.1	35% identity with Ybp1p, which is required for the oxidative stress response to peroxides via the the Yap1p transcription factor; Ybp2p [Saccharomyces cerevisiae]				
AN7337.1	Predicted DHHC-type Zn-finger protein	R			
AN7341.1	predicted protein [Neurospora crassa]				
AN7348.1	Uncharacterized conserved protein	S			
AN7350.1	FOG: RRM domain	R			
AN7352.1	E3 ubiquitin ligase involved in syntaxin degradation	O	Posttranslational modification/turnover/chaperones		
AN7353.1	Predicted dehydrogenases and related proteins	R		YMR315W	cytoplasm nucleus
AN7354.1	60S ribosomal protein L32	J	Translation, ribosomal structure, biogenesis	YBL092W	
AN7355.1	RNA pseudouridylate synthases	A	RNA processing, modification		
AN7356.1	Predicted thioesterase	R			
AN7358.1	Dihydroxyacid dehydratase/phosphogluconate dehydratase	EG			
AN7359.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN7360.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN7361.1	Glutamyl-tRNA synthetase (mitochondrial)	J	Translation, ribosomal structure, biogenesis	YOL033W	mitochondrion
AN7363.1	Nucleoside phosphorylase	F	Nucleotide transport, metabolism		
AN7366.1	hypothetical protein PCZA361.15 - Amycolatopsis orientalis				
AN7367.1	Carbon-nitrogen hydrolase	E	Amino acid transport, metabolism		
AN7377.1	predicted protein [Neurospora crassa]				
AN7382.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN7387.1	Pyrroline-5-carboxylate reductase	E	Amino acid transport, metabolism		
AN7388.1	Catalase (peroxidase I)	P	Inorganic ion transport, metabolism		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7392.1	Amino acid transporters	E	Amino acid transport, metabolism	YGL077C	cell periphery bud
AN7395.1	hypothetical protein [Neurospora crassa]				
AN7396.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN7401.1	Beta-1,4-xylanase	G	Carbohydrate transport, metabolism		
AN7402.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO		YIL099W	
AN7403.1	hypothetical protein [Neurospora crassa]				
AN7404.1					
AN7407.1	Carboxylesterase type B	I	Lipid transport, metabolism		
AN7418.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN7422.1	Ubiquitin-specific protease UBP14	O	Posttranslational modification/turnover/chaperones	YBR058C	cytoplasm nucleus
AN7423.1	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins	L	Replication, recombination, repair	YAR007C	nucleus
AN7424.1	ATP-dependent RNA helicase	A	RNA processing, modification	YGL078C	nucleolus nucleus
AN7428.1	Ubiquitin activating E1 enzyme-like protein	H	Coenzyme transport, metabolism	YHR171W	
AN7430.1	Glutamine amidotransferase/cyclase	E	Amino acid transport, metabolism	YBR248C	cytoplasm nucleus
AN7431.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones	YKL059C	nucleus
AN7433.1	hypothetical protein [Neurospora crassa]				
AN7435.1	Uracil DNA glycosylase	L	Replication, recombination, repair	YML021C	cytoplasm nucleus
AN7436.1	Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)	O	Posttranslational modification/turnover/chaperones	YCL043C	vacuole
AN7437.1	Permeases of the major facilitator superfamily	R		YCL038C	
AN7438.1	Thyroid hormone receptor-associated coactivator complex component (TRAP170)	K	Transcription		
AN7439.1	DNA polymerase epsilon, subunit B	L	Replication, recombination, repair	YPR175W	cytoplasm nucleus
AN7440.1	Cell cycle-regulated histone H1-binding protein	BD			
AN7441.1	Actin-related protein - Arp4p/Act3p	Z	Cytoskeleton		
AN7443.1	hypothetical protein [Neurospora crassa]				
AN7447.1	HAT repeat protein	A	RNA processing, modification	YBR055C	cytoplasm nucleus
AN7448.1	WD40 repeat stress protein/actin interacting protein	Z	Cytoskeleton		
AN7450.1	complex I intermediate-associated protein CIA84 precursor [Neurospora crassa]				
AN7451.1	Glutamate/leucine/phenylalanine/valine dehydrogenases	E	Amino acid transport, metabolism	YDL215C	cytoplasm
AN7454.1	hypothetical protein [Neurospora crassa]				
AN7455.1	F-box protein JEMMA and related proteins with JmjC, PHD, F-box and LRR domains	B	Chromatin structure, dynamics		
AN7458.1	WD40 repeat protein	R		YJL069C	nucleolus
AN7459.1	Hexokinase	G	Carbohydrate transport, metabolism	YGL253W	cytoplasm
AN7461.1	NAD-dependent histone deacetylases and class I sirtuins (SIR2 family)	BK		YPL015C	cytoplasm
AN7462.1	Golgi transport complex COD1 protein	U	Intracellular trafficking/secretion/transport	YPR105C	early Golgi
AN7463.1	Ammonia permease	P	Inorganic ion transport, metabolism	YPR138C	cell periphery
AN7464.1	Ca2+ transporting ATPase	P	Inorganic ion transport, metabolism	YGL167C	ER
AN7465.1	Sister chromatid cohesion complex Cohesin, subunit RAD21/SCC1	D	Cell cycle/division, chrom. partitioning	YDL003W	cytoplasm nucleus
AN7466.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN7468.1	Gluconate transport-inducing protein	TG			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7469.1	Riboflavin kinase	H	Coenzyme transport, metabolism	YDR236C	cytoplasm
AN7470.1					
AN7471.1	Predicted carbohydrate kinase, contains PfkB domain	R			
AN7472.1	Oligosaccharyltransferase, alpha subunit (ribophorin I)	O	Posttranslational modification/turnover/chaperones	YJL002C	ER
AN7473.1	mRNA capping enzyme, guanylyltransferase (alpha) subunit	A	RNA processing, modification		
AN7474.1	RNA-binding protein (contains RRM and Pumilio-like repeats)	R			
AN7475.1	DNA-binding protein YL1 and related proteins	R			
AN7476.1					
AN7479.1	Asparaginyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YHR019C	
AN7480.1	FOG: RRM domain	R			
AN7481.1	Sister chromatid cohesion complex Cohesin, subunit PDS5	D	Cell cycle/division, chrom. partitioning		
AN7483.1	hypothetical protein [Neurospora crassa]				
AN7484.1	Uncharacterized conserved protein	S			
AN7485.1	Predicted transporter (major facilitator superfamily)	R			
AN7487.1	Ras-related small GTPase, Rho type	R		YLR229C	
AN7488.1	Arginase family protein	E	Amino acid transport, metabolism		
AN7489.1	3-oxoacyl-(acyl-carrier-protein) synthase (I and II)	IQ		YER061C	mitochondrion
AN7490.1	Transcriptional activator, adenine-specific DNA methyltransferase	KT			
AN7491.1	Ubiquitin C-terminal hydrolase UCHL1	O	Posttranslational modification/turnover/chaperones	YJR099W	
AN7492.1	Uncharacterized conserved protein	S		YLR270W	cytoplasm nucleus
AN7493.1	predicted protein [Neurospora crassa]				
AN7494.1	Cellular protein (glioma tumor suppressor candidate region gene 2)	R			
AN7495.1	mRNA splicing protein CDC5 (Myb superfamily)	AD			
AN7496.1	FOG: Immunoglobin and related proteins	RP			
AN7497.1	NADH:ubiquinone oxidoreductase, NDUFS4/18 kDa subunit	C	Energy production, conversion		
AN7498.1	HEAT repeat-containing protein	R		YJR070C	cytoplasm nucleus
AN7500.1	NADH-dehydrogenase (ubiquinone)	C	Energy production, conversion		
AN7501.1	LisH motif-containing protein	Z	Cytoskeleton		
AN7502.1	Armadillo/beta-Catenin/plakoglobin	TZ		YNR012W	cytoplasm nucleus
AN7503.1	Uncharacterized conserved protein	S		YDR365C	nucleolus nucleus
AN7504.1	predicted protein [Neurospora crassa]				
AN7505.1	Alpha-glucosidases, family 31 of glycosyl hydrolases	G	Carbohydrate transport, metabolism		
AN7508.1	hypothetical protein [Neurospora crassa]				
AN7511.1	beta (1-3) glucanosyltransferase Gel3p [Aspergillus fumigatus]				
AN7512.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN7513.1	Transcriptional activator FOSB/c-Fos and related bZIP transcription factors	K	Transcription		
AN7514.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN7517.1	hypothetical protein ((AL513466) hypothetical protein [Neurospora crassa])				
AN7521.1	Carboxylesterase type B	I	Lipid transport, metabolism		
AN7524.1	Arylacetamide deacetylase	V	Defense mechanisms		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7525.1	ATPases involved in chromosome partitioning	D	Cell cycle/division, chrom. partitioning		
AN7526.1	Apoptosis antagonizing transcription factor/protein transport protein	KU		YDR299W	nucleolus
AN7527.1	Zinc-binding oxidoreductase	CR			
AN7529.1	Metal-dependent amidase/aminoacylase/carboxypeptidase	R			
AN7533.1	KEKE-like motif-containing transcription regulator (Rlr1)/suppressor of sin4	K	Transcription		
AN7534.1	putative mannosyltransferase [Paracoccidioides brasiliensis]				
AN7535.1	hypothetical protein [Neurospora crassa]				
AN7537.1	Ribosomal protein S6 kinase and related proteins	RT			
AN7538.1	Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KL			
AN7540.1	Translation initiation factor 3, subunit d (eIF-3d)	J	Translation, ribosomal structure, biogenesis		
AN7541.1	Cutinase precursor (Cutin hydrolase) (L1)				
AN7542.1	predicted protein [Neurospora crassa]				
AN7543.1	hypothetical protein [Podospora anserina]				
AN7544.1	C2H2 Zn-finger protein	R			
AN7545.1	CCAAT-binding factor, subunit B (HAP2)	K	Transcription		
AN7548.1	Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	R			
AN7549.1	AAA+-type ATPase	O	Posttranslational modification/turnover/chaperones		
AN7550.1	Type I phosphodiesterase/nucleotide pyrophosphatase	R		YCR026C	
AN7553.1	Upstream transcription factor 2/L-myc-2 protein	K	Transcription		
AN7554.1	Predicted component of NuA3 histone acetyltransferase complex	B	Chromatin structure, dynamics	YER049W	nucleus
AN7558.1					
AN7559.1	Transcription initiation factor TFIID, subunit TAF7	K	Transcription		
AN7560.1	PalC [Emericella nidulans]				
AN7562.1	Subunit of Golgi mannosyltransferase complex	GM		YDR245W	Golgi
AN7563.1	Serine/threonine protein kinase Chk2 and related proteins	D	Cell cycle/division, chrom. partitioning		
AN7564.1	Threonine aldolase	E	Amino acid transport, metabolism	YEL046C	cytoplasm nucleus
AN7565.1					
AN7566.1	3'-5' exonuclease	L	Replication, recombination, repair	YGR276C	
AN7567.1	Glutaredoxin-related protein	O	Posttranslational modification/turnover/chaperones	YDR098C	cytoplasm nucleus
AN7568.1	Gamma-butyrobetaine,2-oxoglutarate dioxygenase	I	Lipid transport, metabolism		
AN7569.1	Mitochondrial solute carrier protein	C	Energy production, conversion	YGR096W	mitochondrion
AN7570.1	Alpha tubulin	Z	Cytoskeleton		
AN7571.1	Predicted mechanosensitive ion channel	M			
AN7572.1	NDR and related serine/threonine kinases	R			
AN7576.1	Adaptor protein Enigma and related PDZ-LIM proteins	TZ		YDL240W	cell periphery bud neck cytoplasm
AN7577.1	Ubiquitin-conjugating enzyme	O	Posttranslational modification/turnover/chaperones		
AN7578.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN7579.1	26S proteasome regulatory complex, subunit RPN10/PSMD4	O	Posttranslational modification/turnover/chaperones	YHR200W	cytoplasm nucleus
AN7580.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7581.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN7583.1	Transcriptional regulator	K	Transcription		
AN7587.1	FOG: Low-complexity	S			
AN7588.1	D-ribulose-5-phosphate 3-epimerase	G	Carbohydrate transport, metabolism	YJL121C	cytoplasm nucleus
AN7589.1	Predicted hydrolase involved in interstrand cross-link repair	L	Replication, recombination, repair		
AN7590.1	Reductases with broad range of substrate specificities	R			
AN7591.1	Permeases of the major facilitator superfamily	R			
AN7594.1	Uncharacterized conserved protein	S			
AN7597.1	Sexual differentiation process protein ISP4	T	Signal transduction mechanisms	YJL212C	ER
AN7600.1	Sulfite reductase (ferredoxin)	P	Inorganic ion transport, metabolism	YJR137C	cytoplasm
AN7601.1	hypothetical protein [Neurospora crassa]				
AN7603.1	Vacuolar H+-ATPase V0 sector, subunit c''	C	Energy production, conversion	YHR026W	vacuole ER
AN7604.1	Phosphatidic acid-preferring phospholipase A1, contains DDHD domain	IU			
AN7605.1	predicted protein [Neurospora crassa]				
AN7606.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN7607.1					
AN7608.1	RNA Polymerase C (III) 37 kDa subunit	K	Transcription		
AN7609.1	Mitochondrial/chloroplast DNA-directed RNA polymerase RPO41, provides primers for DNA replication-initiation	KL		YFL036W	
AN7610.1	putative transcription factor [Emericella nidulans]				
AN7620.1	Uncharacterized conserved protein	S			
AN7621.1	Predicted oxidoreductase	C	Energy production, conversion		
AN7622.1	hypothetical protein [Nostoc punctiforme]				
AN7623.1	hypothetical protein [Neurospora crassa]				
AN7624.1	Alpha-D-galactosidase (melibiase)	G	Carbohydrate transport, metabolism		
AN7625.1	Myo-inositol-1-phosphate synthase	I	Lipid transport, metabolism	YJL153C	cytoplasm
AN7626.1	Adaptor protein Enigma and related PDZ-LIM proteins	TZ			
AN7628.1	mRNA deadenylase subunit	A	RNA processing, modification		
AN7629.1	predicted protein [Neurospora crassa]				
AN7630.1	Angio-associated migratory cell protein (contains WD40 repeats)	S			
AN7632.1	Alcohol dehydrogenase, class III	Q		YDL168W	cytoplasm
AN7633.1	Malate/L-lactate dehydrogenases	C	Energy production, conversion		
AN7636.1	Zinc-binding oxidoreductase	CR			
AN7639.1	Endo-beta-mannanase	G	Carbohydrate transport, metabolism		
AN7641.1	Copper amine oxidase	Q			
AN7646.1	Pectate lyase	G	Carbohydrate transport, metabolism		
AN7648.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN7649.1	Mitochondrial import inner membrane translocase, subunit TIM9	U	Intracellular trafficking/secretion/transport	YEL020W-A	
AN7650.1	Rho GTPase-activating protein	TZ			
AN7651.1	hypothetical protein FLJ35107 [Homo sapiens]				
AN7652.1	DNA helicase	L	Replication, recombination, repair	YKL017C	cytoplasm
AN7657.1	GEL1 protein [Aspergillus fumigatus]			YOL030W	ER nucleus
AN7658.1	Cdc42-interacting protein CIP4	Z	Cytoskeleton		
AN7659.1	ATP-dependent RNA helicase	A	RNA processing, modification	YOR046C	nuclear periphery

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7660.1	Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	H	Coenzyme transport, metabolism		
AN7661.1	Predicted DNA-binding protein	K	Transcription		
AN7663.1	Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	C	Energy production, conversion		
AN7664.1	Ca2+ transporting ATPase	P	Inorganic ion transport, metabolism		
AN7666.1	Predicted sugar kinase	G	Carbohydrate transport, metabolism		
AN7671.1	Mitochondrial carrier protein	C	Energy production, conversion		
AN7672.1	hypothetical protein [Neurospora crassa]			YPL050C	Golgi
AN7673.1	Putative zinc transporter	P	Inorganic ion transport, metabolism	YIL023C	
AN7676.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q			
AN7677.1	hypothetical protein [Neurospora crassa]			YDR479C	cytoplasm
AN7678.1	Dual-specificity tyrosine-phosphorylation regulated kinase	R			
AN7679.1	COPII vesicle protein	U	Intracellular trafficking/secretion/transport	YML067C	ER
AN7680.1	Myosin class II heavy chain	Z	Cytoskeleton		
AN7681.1	Mod5 protein sorting/negative effector of RNA Pol III synthesis	K	Transcription		
AN7683.1	involved in secretion of proteins that lack classical secretory signal sequences; Nce102p [Saccharomyces cerevisiae]			YPR149W	
AN7684.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN7687.1	Translocase of outer mitochondrial membrane complex, subunit TOM70/TOM72	U	Intracellular trafficking/secretion/transport	YNL121C	mitochondrion
AN7688.1	Protein similar to predicted member of the intramitochondrial sorting protein family	U	Intracellular trafficking/secretion/transport		
AN7690.1					
AN7696.1	predicted protein [Neurospora crassa]				
AN7697.1	Sensory transduction histidine kinase	T	Signal transduction mechanisms		
AN7698.1	Myosin class I heavy chain	Z	Cytoskeleton	YER118C	cell periphery bud neck cytoplasm
AN7699.1	predicted protein [Neurospora crassa]				
AN7700.1	FOG: RRM domain	R			
AN7701.1	Mitochondrial/chloroplast ribosomal protein S16	J	Translation, ribosomal structure, biogenesis	YPL013C	mitochondrion
AN7704.1	Phospholipase A2-activating protein (contains WD40 repeats)	I	Lipid transport, metabolism	YKL213C	cytoplasm nucleus
AN7705.1	Serine/threonine kinase receptor-associated protein	I	Lipid transport, metabolism		
AN7706.1	RRM motif-containing protein	A	RNA processing, modification		
AN7707.1	Ca2+-binding actin-bundling protein (actinin), alpha chain (EF-Hand protein superfamily)	Z	Cytoskeleton		
AN7708.1	Aldo/keto reductases, related to diketogulonate reductase	R			
AN7709.1	Initiator tRNA phosphoribosyl-transferase	A	RNA processing, modification	YMR283C	cytoplasm
AN7710.1	Predicted phosphatase/phosphohexomutase	R			
AN7711.1	Nucleoside diphosphate-sugar hydrolase of the MutT (NUDIX) family	L	Replication, recombination, repair	YBR111C	cytoplasm nucleus
AN7714.1	predicted protein [Neurospora crassa]				
AN7715.1	Glycosyltransferase	R		YPL227C	ER
AN7717.1	predicted protein [Neurospora crassa]				
AN7718.1	Protein involved in autophagocytosis during starvation	R			
AN7719.1	Cyclin L	R			
AN7720.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7721.1	Transport protein Sec61, alpha subunit	UO		YLR378C	ER
AN7722.1	Putative glutamate/ornithine acetyltransferase	E	Amino acid transport, metabolism	YMR062C	mitochondrion
AN7723.1	Origin recognition complex, subunit 2	L	Replication, recombination, repair	YBR060C	cytoplasm nucleus
AN7724.1	predicted protein [Neurospora crassa]				
AN7725.1	Stationary phase-induced protein, SOR/SNZ family	H	Coenzyme transport, metabolism	YFL059W	
AN7726.1	Nuclear protein export factor	UD			
AN7727.1	predicted protein [Neurospora crassa]				
AN7729.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q		YDR135C	vacuolar membrane
AN7730.1	Xaa-Pro aminopeptidase	E	Amino acid transport, metabolism		
AN7731.1	Nuclear transport receptor LGL2 (importin beta superfamily)	YU			
AN7732.1	predicted protein [Neurospora crassa]				
AN7733.1	Carbon-nitrogen hydrolase	E	Amino acid transport, metabolism	YJR062C	mitochondrion
AN7736.1	Ankyrin repeat protein	R		YDR049W	cytoplasm
AN7737.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	T	Signal transduction mechanisms		
AN7739.1	predicted protein [Neurospora crassa]				
AN7741.1	Adaptor complexes medium subunit family	U	Intracellular trafficking/secretion/transport	YOL062C	cell periphery bud neck
AN7742.1	Single-stranded DNA-binding protein	L	Replication, recombination, repair	YCR028C-A	mitochondrion
AN7745.1	Inositol polyphosphate 5-phosphatase and related proteins	U	Intracellular trafficking/secretion/transport		
AN7746.1	Decapping enzyme complex component DCP1	KA			
AN7747.1	Uncharacterized conserved protein	S			
AN7748.1	S-M checkpoint control protein CID1 and related nucleotidyltransferases	D	Cell cycle/division, chrom. partitioning		
AN7749.1	Nuclear pore complex, Nup214/CAN component	YU			
AN7750.1	Protein predicted to be involved in carbohydrate metabolism	G	Carbohydrate transport, metabolism		
AN7751.1	Squalene monooxygenase	I	Lipid transport, metabolism		
AN7752.1	Protoheme ferro-lyase (ferrochelatase)	H	Coenzyme transport, metabolism	YOR176W	mitochondrion
AN7754.1	predicted protein [Neurospora crassa]				
AN7755.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN7757.1	FOG: Low-complexity	S			
AN7758.1	SAM-dependent methyltransferases	QR			
AN7759.1	von Willebrand factor and related coagulation proteins	WV			
AN7760.1	Amphiphysin	U	Intracellular trafficking/secretion/transport		
AN7762.1	RNA 3'-terminal phosphate cyclase	A	RNA processing, modification		
AN7763.1	Pyruvate carboxylase	C	Energy production, conversion		
AN7770.1	Reductases with broad range of substrate specificities	R		YNL202W	
AN7771.1	predicted protein [Neurospora crassa]				
AN7772.1	Cytochrome P450 CYP3/CYP5/CYP6/CYP9 subfamilies	Q			
AN7773.1	Cytochrome P450 CYP3/CYP5/CYP6/CYP9 subfamilies	Q			
AN7774.1	hypothetical protein [Neurospora crassa]				
AN7777.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN7781.1	hypothetical protein [Neurospora crassa]				
AN7782.1	Alkylated DNA repair protein	L	Replication, recombination, repair		
AN7783.1	RhoGEF GTPase	T	Signal transduction mechanisms		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN7784.1	GTPase-activating protein VRP	R		YGR100W	cytoplasm
AN7785.1					
AN7786.1	predicted protein [Neurospora crassa]				
AN7797.1	Tellurite resistance protein and related permeases	P	Inorganic ion transport, metabolism		
AN7801.1	Predicted hydrolase of the alpha/beta superfamily	R			
AN7836.1	cystein rich protein [Metarhizium anisopliae]				
AN7844.1	Acyl-CoA thioesterase	I	Lipid transport, metabolism		
AN7888.1	hypothetical protein [Neurospora crassa]				
AN7895.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			
AN7905.1	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases	I	Lipid transport, metabolism		
AN7918.1	haloacid dehalogenase, type II [Brucella suis 1330]				
AN7939.1	Uncharacterized conserved protein	S			
AN7943.1	Arylacetamide deacetylase	V	Defense mechanisms		
AN7950.1	Cellobiohydrolase A (1,4-beta-cellobiosidase A)	G	Carbohydrate transport, metabolism		
AN7959.1	hypothetical protein [Neurospora crassa]				
AN7962.1	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	GO			
AN7967.1	Purine-cytosine permease and related proteins	F	Nucleotide transport, metabolism		
AN7993.1	Vacuolar sorting protein VPS45	U	Intracellular trafficking/secretion/transport	YDR027C	early Golgi
AN7994.1	DNA replication licensing factor, MCM5 component	L	Replication, recombination, repair	YLR274W	
AN7995.1	Ribokinase	G	Carbohydrate transport, metabolism	YCR036W	cytoplasm nucleus
AN7996.1	hypothetical protein ((AL513410) hypothetical protein [Neurospora crassa])				
AN7997.1	RNA polymerase III transcription factor (TF)IIIC subunit	K	Transcription		
AN8000.1	Histone acetyltransferase SAGA, TRRAP/TRA1 component, PI-3 kinase superfamily	TBLD		YHR099W	
AN8001.1	Uncharacterized conserved protein	S		YKL095W	nucleus
AN8002.1	Anaphase-promoting complex (APC), Cdc16 subunit	DO		YKL022C	nucleus
AN8003.1	Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	R			
AN8004.1	Cytochrome P450	Q			
AN8007.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN8009.1	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	P	Inorganic ion transport, metabolism	YDL244W	
AN8010.1	Glycogen synthase	G	Carbohydrate transport, metabolism	YFR015C	cytoplasm
AN8012.1	Polyprenyl synthetase	H	Coenzyme transport, metabolism	YJL167W	
AN8013.1	Anaphase-promoting complex (APC), Cdc23 subunit	DO		YHR166C	nucleus
AN8015.1	Splicing factor 3a, subunit 3	A	RNA processing, modification	YDL030W	nucleus
AN8016.1	Predicted ATP-dependent RNA helicase FAL1, involved in rRNA maturation, DEAD-box superfamily	J	Translation, ribosomal structure, biogenesis	YDR021W	nucleolus nucleus
AN8018.1	Predicted membrane protein	S			
AN8019.1	FOG: Ankyrin repeat	R			
AN8020.1	conserved hypothetical protein [Neurospora crassa]				
AN8023.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR		YKR001C	endosome cytoplasm
AN8024.1	Carbon-nitrogen hydrolase	E	Amino acid transport, metabolism		
AN8026.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN8028.1	Soluble epoxide hydrolase	I	Lipid transport, metabolism		
AN8029.1	Na+/K+ transporter	P	Inorganic ion transport, metabolism	YKR050W	
AN8031.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8032.1	C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	IE			
AN8033.1	Proteins containing the FAD binding domain	C	Energy production, conversion		
AN8034.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN8035.1	Heat shock transcription factor	K	Transcription		
AN8036.1	Aldo/keto reductase family proteins	R			
AN8038.1	mRNA cleavage and polyadenylation factor I complex, subunit RNA15	A	RNA processing, modification		
AN8039.1	Histone 2A	B	Chromatin structure, dynamics	YOL012C	nucleus
AN8040.1	Protein involved in inorganic phosphate transport	P	Inorganic ion transport, metabolism	YBR106W	ER
AN8041.1	Glyceraldehyde 3-phosphate dehydrogenase	G	Carbohydrate transport, metabolism	YGR192C	cytoplasm nucleus
AN8042.1	Histone deacetylase complex, catalytic component HDA1	B	Chromatin structure, dynamics	YNL021W	nucleus
AN8043.1	hypothetical protein [Neurospora crassa]				
AN8044.1	N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	O	Posttranslational modification/turnover/chaperones	YLR389C	
AN8045.1	mRNA cleavage factor I subunit	A	RNA processing, modification		
AN8046.1	Predicted lipase	I	Lipid transport, metabolism	YJR107W	
AN8047.1	Similar to bacterial dephospho-CoA kinase	H	Coenzyme transport, metabolism		
AN8048.1	predicted protein [Neurospora crassa]				
AN8049.1	NADH:ubiquinone oxidoreductase, NDUFS6/13 kDa subunit	C	Energy production, conversion		
AN8050.1	Uncharacterized conserved protein	S			
AN8051.1	predicted protein [Neurospora crassa]				
AN8053.1	Inositol polyphosphate 5-phosphatase and related proteins	U	Intracellular trafficking/secretion/transport		
AN8054.1	20S proteasome, regulatory subunit alpha type PSMA7/PRE6	O	Posttranslational modification/turnover/chaperones	YOL038W	cytoplasm nucleus
AN8055.1	RNA-binding Ran Zn-finger protein and related proteins	R			
AN8056.1	Chromosome condensation complex Condensin, subunit G	BD		YDR325W	nucleolus nucleus
AN8057.1	Cysteine synthase	E	Amino acid transport, metabolism		
AN8058.1	Sulfite oxidase, molybdopterin-binding component	C	Energy production, conversion		
AN8059.1	Mitochondrial import inner membrane translocase, subunit TIM22	U	Intracellular trafficking/secretion/transport	YDL217C	
AN8060.1	Putative NADH-flavin reductase	R			
AN8061.1	Peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN8063.1	hypothetical protein [Neurospora crassa]				
AN8064.1	Replication factor C, subunit RFC5	L	Replication, recombination, repair	YNL290W	nucleus
AN8065.1	Actin-related protein Arp2/3 complex, subunit ARPC3	Z	Cytoskeleton	YLR370C	actin
AN8066.1	tRNA(1-methyladenosine) methyltransferase, subunit GCD10	J	Translation, ribosomal structure, biogenesis	YNL062C	nucleus
AN8067.1	Uncharacterized conserved protein	S			
AN8068.1	Endoglucanase	G	Carbohydrate transport, metabolism		
AN8069.1	Uncharacterized conserved protein	R			
AN8070.1	N-acetylglucosaminyltransferase complex, subunit PIG-P, required for phosphatidylinositol biosynthesis	S			
AN8071.1	Cell-cycle nuclear protein, contains WD-40 repeats	D	Cell cycle/division, chrom. partitioning		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8072.1	hypothetical protein B13N20.140 [imported] - Neurospora crassa				
AN8073.1	tRNA and rRNA cytosine-C5-methylase (nucleolar protein NOL1/NOP2)	A	RNA processing, modification		
AN8074.1	Ubiquitin carboxyl-terminal hydrolase	O	Posttranslational modification/turnover/chaperones		
AN8075.1	Deoxyhypusine synthase	O	Posttranslational modification/turnover/chaperones	YHR068W	cytoplasm
AN8076.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN8077.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN8078.1	Cytochrome P450 CYP2 subfamily	Q			
AN8079.1	predicted protein [Neurospora crassa]				
AN8083.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R		YLL028W	cell periphery ER bud
AN8089.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN8095.1	Permeases of the major facilitator superfamily	GEPR			
AN8099.1	Thermophilic glucose-6-phosphate isomerase and related metalloenzymes	GR			
AN8100.1	Kef-type K+ transport systems, membrane components	P	Inorganic ion transport, metabolism		
AN8102.1	Aspartyl protease	O	Posttranslational modification/turnover/chaperones		
AN8103.1	predicted protein [Neurospora crassa]				
AN8104.1	hypothetical protein [Neurospora crassa]				
AN8105.1	Non-ribosomal peptide synthetase modules and related proteins	Q			
AN8116.1	FOG: Zn-finger	R			
AN8117.1	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme	I	Lipid transport, metabolism	YLR372W	ER
AN8119.1	Glycolipid 2-alpha-mannosyltransferase (alpha-1,2-mannosyltransferase)	G	Carbohydrate transport, metabolism		
AN8120.1	Uncharacterized conserved protein	S			
AN8121.1	Phosphoribosylformylglycinamidine synthase	F	Nucleotide transport, metabolism	YGR061C	cytoplasm
AN8122.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R		YPR156C	cell periphery
AN8126.1	Predicted sugar phosphate isomerase	R			
AN8127.1	Uncharacterized conserved protein	S			
AN8129.1					
AN8144.1	predicted protein [Neurospora crassa]				
AN8145.1	Uncharacterized conserved protein	S		YML079W	cytoplasm nucleus
AN8152.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN8162.1	Predicted NAD/FAD-binding protein	R			
AN8163.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN8164.1	predicted protein [Neurospora crassa]				
AN8165.1	rRNA adenine N-6-methyltransferase	A	RNA processing, modification		
AN8167.1	hypothetical protein [Neurospora crassa]				
AN8168.1	Predicted nucleoside-diphosphate-sugar epimerases	MG			
AN8169.1	Asparaginase	E	Amino acid transport, metabolism		
AN8170.1	DNA replication factor/protein phosphatase inhibitor SET/SPR-2	L	Replication, recombination, repair		

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN8171.1	SNARE protein TLG1/Syntaxin 6	U	Intracellular trafficking/secretion/transport		
AN8172.1	Aromatic amino acid aminotransferase and related proteins	E	Amino acid transport, metabolism		
AN8173.1	Uncharacterized conserved protein	S		YCR059C	cytoplasm nucleus
AN8176.1	Ribosomal protein RPL1/RPL2/RL4L4	A	RNA processing, modification	YDR012W	cytoplasm
AN8179.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones		
AN8180.1	mRNA splicing factor/probable chromatin binding snw family nuclear protein	AB			
AN8181.1	predicted protein [Neurospora crassa]				
AN8182.1	Septin family protein (P-loop GTPase)	DZU		YHR107C	cell periphery bud neck
AN8183.1	WD40-repeat-containing subunit of the 18S rRNA processing complex	A	RNA processing, modification	YCR057C	nucleolus
AN8184.1	Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	Q			
AN8185.1	5'-3' exonuclease XRN1/KEM1/SEP1 involved in DNA strand exchange and mRNA turnover	LD		YGL173C	cytoplasm
AN8187.1	Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1	B	Chromatin structure, dynamics	YEL056W	
AN8189.1	predicted protein [Neurospora crassa]				
AN8191.1	Predicted mRNA cap-binding protein related to eIF-4E	J	Translation, ribosomal structure, biogenesis		
AN8194.1	emp24/gp25L/p24 family of membrane trafficking proteins	U	Intracellular trafficking/secretion/transport	YDL018C	ER
AN8197.1	FOG: Ankyrin repeat	R			
AN8200.1	hypothetical protein ((AL513466) putative protein [Neurospora crassa])				
AN8201.1	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 3'-5' helicase subunit SSL2	KL		YIL143C	nucleus
AN8202.1					
AN8203.1	Predicted NAD synthase, contains CN hydrolase domain	HR		YHR074W	cytoplasm nucleus
AN8204.1	NADH pyrophosphatase I of the Nudix family of hydrolases	L	Replication, recombination, repair	YGL067W	cytoplasm nucleus
AN8206.1	Flavin-containing monooxygenase	Q		YHR176W	
AN8208.1	ER-Golgi vesicle-tethering protein p115	U	Intracellular trafficking/secretion/transport		
AN8210.1	TGc (transglutaminase/protease-like) domain-containing protein involved in cytokinesis	D	Cell cycle/division, chrom. partitioning		
AN8211.1	DNA-binding protein jumonji/RBP2/SMCY, contains JmjC domain	R			
AN8212.1	GIY-YIG type nuclease	R			
AN8213.1	Thymidylate kinase/adenylate kinase	F	Nucleotide transport, metabolism	YJR057W	cytoplasm
AN8214.1	Queuine-tRNA ribosyltransferase	A	RNA processing, modification		
AN8215.1	5,10-methylenetetrahydrofolate reductase	E	Amino acid transport, metabolism	YPL023C	
AN8216.1	Nucleoside diphosphate kinase	F	Nucleotide transport, metabolism	YKL067W	cytoplasm nucleus
AN8217.1	Glucosidase II catalytic (alpha) subunit and related enzymes, glycosyl hydrolase family 31	GMO			
AN8218.1	Thioredoxin reductase	O	Posttranslational modification/turnover/chaperones		
AN8224.1	Glutamyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YGL245W	cytoplasm
AN8225.1	Ribosomal protein L1	J	Translation, ribosomal structure, biogenesis	YDR116C	mitochondrion
AN8226.1	Low density lipoprotein receptor	U	Intracellular trafficking/secretion/transport		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8227.1					
AN8228.1	Predicted ATPase, nucleotide-binding	D	Cell cycle/division, chrom. partitioning		
AN8229.1	Inner membrane protein translocase involved in respiratory chain assembly	OU		YER154W	mitochondrion
AN8231.1	S-adenosylmethionine decarboxylase	T	Signal transduction mechanisms	YOL052C	cytoplasm nucleus
AN8232.1	Transcription initiation factor TFIID, subunit TAF6 (also component of histone acetyltransferase SAGA)	K	Transcription	YGL112C	nucleus
AN8233.1	Phosphatidylinositol transfer protein SEC14 and related proteins	I	Lipid transport, metabolism	YJL145W	cytoplasm
AN8234.1	predicted protein [Neurospora crassa]				
AN8235.1	predicted protein [Neurospora crassa]				
AN8236.1	Putative growth response protein	T	Signal transduction mechanisms		
AN8237.1	predicted protein [Neurospora crassa]				
AN8242.1	Arylacetamide deacetylase	V	Defense mechanisms		
AN8244.1	Uncharacterized conserved coiled-coil protein	S			
AN8246.1	Signal recognition particle, subunit Srp54	U	Intracellular trafficking/secretion/transport	YPR088C	
AN8247.1	Uncharacterized conserved protein	S			
AN8248.1	hypothetical protein ((AL513410) conserved hypothetical protein [Neurospora crassa])			YDR470C	
AN8251.1	putative transcriptional activator [Aspergillus nidulans]				
AN8252.1	Aminopeptidase I zinc metalloprotease (M18)	E	Amino acid transport, metabolism		
AN8253.1	Predicted RNA-binding protein Nob1p involved in 26S proteasome assembly	O	Posttranslational modification/turnover/chaperones	YOR056C	cytoplasm
AN8255.1	tRNA splicing endonuclease SEN2	J	Translation, ribosomal structure, biogenesis		
AN8256.1	Mitochondrial ribosomal protein MRP7 (L2)	J	Translation, ribosomal structure, biogenesis		
AN8257.1	Phospholipid scramblase	M			
AN8258.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YMR022W	ER
AN8260.1	Oxidosqualene-lanosterol cyclase and related proteins	I	Lipid transport, metabolism	YHR072W	lipid particle
AN8261.1	Protein kinase PCTAIRE and related kinases	R			
AN8262.1	related to G protein coupled receptor like protein [Neurospora crassa]				
AN8264.1	hypothetical protein [Schizosaccharomyces pombe]				
AN8268.1	RasGAP SH3 binding protein rasputin, contains NTF2 and RRM domains	T	Signal transduction mechanisms		
AN8269.1	Molecular chaperone (HSP90 family)	O	Posttranslational modification/turnover/chaperones		
AN8271.1	SWI-SNF chromatin-remodeling complex protein	B	Chromatin structure, dynamics		
AN8272.1	RNA polymerase III (C) subunit	K	Transcription		
AN8273.1	Ubiquinol cytochrome c reductase, subunit QCR2	C	Energy production, conversion	YPR191W	mitochondrion
AN8274.1	Mitochondrial tricarboxylate/dicarboxylate carrier proteins	C	Energy production, conversion	YMR241W	mitochondrion
AN8275.1	Citrate synthase	C	Energy production, conversion	YNR001C	mitochondrion
AN8276.1	RNA polymerase II C-terminal domain-binding protein RA4, contains RPR and RRM domains	AK			
AN8277.1	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport, metabolism	YLR303W	
AN8280.1	Long-chain acyl-CoA synthetases (AMP-forming)	I	Lipid transport, metabolism	YER015W	
AN8282.1	hypothetical protein ((AL390189) conserved hypothetical protein [Neurospora crassa])				
AN8283.1	Cytochrome P450	Q			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8284.1	hypothetical protein [Neurospora crassa]				
AN8285.1	Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7	DKL		YDL108W	nucleus
AN8286.1	Kinesin-like protein	Z	Cytoskeleton		
AN8287.1	Acyl-CoA:diacylglycerol acyltransferase (DGAT)	I	Lipid transport, metabolism		
AN8288.1	Inositol-1,4,5-triphosphate 5-phosphatase (synaptojanin), INP51/INP52/INP53 family	U	Intracellular trafficking/secretion/transport	YOR109W	
AN8291.1	Vesicle coat complex AP-3, delta subunit	U	Intracellular trafficking/secretion/transport	YPL195W	early Golgi
AN8293.1	WD repeat protein	R		YLR409C	nucleus
AN8312.1	Neutral protease II precursor (Deuterolysin) (NPII)				
AN8317.1	Proteins containing the FAD binding domain	C	Energy production, conversion	YDL174C	mitochondrion
AN8329.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN8333.1	PhiA protein [Emericella nidulans]				
AN8339.1	Uncharacterized conserved protein	S			
AN8343.1	FKBP-type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones	YDR519W	ER
AN8344.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN8346.1	Sulfide:quinone oxidoreductase/flavo-binding protein	C	Energy production, conversion		
AN8354.1	hypothetical protein [Neurospora crassa]				
AN8355.1	hypothetical protein [Neurospora crassa]				
AN8359.1	Monoamine oxidase	E	Amino acid transport, metabolism		
AN8361.1	hypothetical protein (hypothetical protein 1A9.40 [imported] - Neurospora crassa)				
AN8363.1	Multiple inositol polyphosphate phosphatase	R			
AN8369.1	Glycosyltransferase	M			
AN8389.1	GLP_587_13681_12494 [Giardia lamblia ATCC 50803]				
AN8392.1	Alpha-galactosidase	G	Carbohydrate transport, metabolism		
AN8396.1	Thiamine pyrophosphate-requiring enzyme	EH			
AN8400.1	Permeases of the major facilitator superfamily	GEPR			
AN8401.1	Beta-glucosidase-related glycosidases	G	Carbohydrate transport, metabolism		
AN8402.1					
AN8404.1	Phosphatidylethanolamine binding protein	R		YLR178C	cytoplasm nucleus
AN8405.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN8406.1	Threonine dehydrogenase and related Zn-dependent dehydrogenases	ER			
AN8412.1	Polyketide synthase modules and related proteins	Q			
AN8415.1	Acyl-CoA dehydrogenases	I	Lipid transport, metabolism		
AN8417.1	Hydantoin racemase	E	Amino acid transport, metabolism		
AN8421.1	hypothetical protein ((AL442164) conserved hypothetical protein [Neurospora crassa])			YKL046C	ER bud
AN8430.1	Kelch repeat-containing proteins	R			
AN8443.1	predicted protein [Neurospora crassa]				
AN8444.1	Glycosyltransferases, probably involved in cell wall biogenesis	M			
AN8445.1	Predicted aminopeptidases	R			
AN8449.1	Sulfite oxidase, molybdopterin-binding component	C	Energy production, conversion		
AN8450.1	NAD-dependent histone deacetylases and class I sirtuins (SIR2 family)	BK			
AN8454.1	Copper amine oxidase	Q			
AN8467.1	Predicted transporter (major facilitator superfamily)	R			

A. nidulans locus	**A. nidulans locus description**	**COG category**	**COG description**	**S. cerevisiae BBH**	**GO cellular location for yeast gene**
AN8477.1	Beta-xylosidase	G	Carbohydrate transport, metabolism		
AN8478.1	bll1370 [Bradyrhizobium japonicum]				
AN8482.1	putative dimethyl-allyl-tryptophan-synthase [Claviceps purpurea]				
AN8488.1	SNARE protein YKT6, synaptobrevin/VAMP syperfamily	U	Intracellular trafficking/secretion/transport	YKL196C	
AN8489.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN8491.1	Ribosome biogenesis protein NIP7	J	Translation, ribosomal structure, biogenesis	YPL211W	nucleolus nucleus
AN8495.1	Uncharacterized conserved protein	S			
AN8496.1	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	G	Carbohydrate transport, metabolism		
AN8499.1	Predicted transporter (major facilitator superfamily)	R			
AN8502.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN8512.1	predicted protein [Neurospora crassa]				
AN8521.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN8523.1	predicted protein [Neurospora crassa]				
AN8528.1	Beta-lactamase class C and other penicillin binding proteins	V	Defense mechanisms		
AN8534.1	Permeases	R			
AN8539.1	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure, biogenesis		
AN8540.1	Predicted transporter (major facilitator superfamily)	R			
AN8546.1	Phospholipase C	M			
AN8547.1	Choline dehydrogenase and related flavoproteins	E	Amino acid transport, metabolism		
AN8552.1	Sorbitol dehydrogenase	Q			
AN8553.1	Catalase	P	Inorganic ion transport, metabolism		
AN8558.1	hypothetical protein [Streptomyces avermitilis MA-4680]				
AN8559.1	Branched chain alpha-keto acid dehydrogenase E1, beta subunit	C	Energy production, conversion		
AN8562.1	FOG: Ankyrin repeat	R			
AN8565.1	Homoserine acetyltransferase	E	Amino acid transport, metabolism		
AN8566.1	Protocatechuate 3,4-dioxygenase beta subunit	Q			
AN8583.1	Flavonol reductase/cinnamoyl-CoA reductase	V	Defense mechanisms		
AN8587.1	Glycolate oxidase	C	Energy production, conversion		
AN8591.1	hypothetical protein [Neurospora crassa]				
AN8594.1	Probable taurine catabolism dioxygenase	Q			
AN8596.1	amyR [Emericella nidulans]				
AN8597.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	C	Energy production, conversion		
AN8600.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN8601.1	predicted protein [Neurospora crassa]				
AN8604.1	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure, biogenesis	YIR042C	
AN8605.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones	YDR155C	cytoplasm nucleus
AN8613.1	predicted protein [Neurospora crassa]				
AN8614.1	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S			
AN8621.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8622.1	Phosphodiesterase/alkaline phosphatase D	P	Inorganic ion transport, metabolism		
AN8628.1	Zn-dependent alcohol dehydrogenases	R			
AN8629.1	Uncharacterized conserved protein	S			
AN8637.1	Catalase	P	Inorganic ion transport, metabolism		
AN8639.1	Trehalose-6-phosphate synthase component TPS1 and related subunits	G	Carbohydrate transport, metabolism		
AN8651.1	Zinc-binding oxidoreductase	CR		YNL134C	cytoplasm nucleus
AN8652.1					
AN8653.1	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	J	Translation, ribosomal structure, biogenesis		
AN8654.1	Dimethylglycine dehydrogenase precursor	E	Amino acid transport, metabolism		
AN8655.1	hypothetical protein [Neurospora crassa]				
AN8656.1	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	PR			
AN8657.1	FAD-dependent oxidoreductase	R			
AN8660.1	Flavin-containing monooxygenase	Q			
AN8663.1	FOG: Zn-finger	R			
AN8664.1	Predicted hydrolase related to dienelactone hydrolase	R			
AN8666.1	von Willebrand factor and related coagulation proteins	WV			
AN8667.1	GATA-4/5/6 transcription factors	K	Transcription		
AN8668.1	Uncharacterized conserved protein	S			
AN8669.1	predicted protein [Neurospora crassa]				
AN8670.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN8671.1	tRNA-splicing endonuclease positive effector (SEN1)	A	RNA processing, modification		
AN8672.1	P-type ATPase	R		YER166W	late Golgi
AN8674.1	Vacuolar H+-ATPase V1 sector, subunit E	C	Energy production, conversion	YOR332W	vacuolar membrane
AN8675.1	Uncharacterized conserved protein	S			
AN8676.1	Regulator of arginine metabolism and related MADS box-containing transcription factors	K	Transcription		
AN8677.1	Galactosyltransferases	G	Carbohydrate transport, metabolism		
AN8679.1	RAB proteins geranylgeranyltransferase component A (RAB escort protein)	O	Posttranslational modification/turnover/chaperones		
AN8680.1	Cyclophilin type peptidyl-prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN8682.1	Exosomal 3'-5' exoribonuclease complex, subunit Rrp43	J	Translation, ribosomal structure, biogenesis		
AN8683.1	Ferric reductase, NADH/NADPH oxidase and related proteins	PQ			
AN8684.1	Predicted N-acetyltransferase	R			
AN8686.1	PTAC beta [Aspergillus nidulans]				
AN8687.1	Activating signal cointegrator 1	K	Transcription		
AN8689.1	Hexokinase	G	Carbohydrate transport, metabolism	YCL040W	cytoplasm
AN8690.1	predicted protein [Neurospora crassa]				
AN8691.1	Ribonucleases P/MRP protein subunit	A	RNA processing, modification	YNL221C	cytoplasm nucleus
AN8692.1	Peroxiredoxin	O	Posttranslational modification/turnover/chaperones	YLR109W	cytoplasm nucleus
AN8693.1	Serine/threonine protein kinase	D	Cell cycle/division, chrom. partitioning		
AN8695.1	Uncharacterized conserved protein	S			
AN8696.1	Uncharacterized conserved protein	S		YGL050W	
AN8697.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8698.1	Actin-related protein Arp2/3 complex, subunit ARPC4	Z	Cytoskeleton	YKL013C	actin
AN8699.1	Ubiquitin-specific protease	O	Posttranslational modification/turnover/chaperones	YFR010W	cytoplasm nucleus
AN8700.1	Permeases of the major facilitator superfamily	GEPR			
AN8701.1	Conserved WD40 repeat-containing protein	S		YDR128W	vacuolar membrane
AN8702.1	Ubiquitin-protein ligase	O	Posttranslational modification/turnover/chaperones	YDR092W	cytoplasm
AN8704.1	60s ribosomal protein L24	J	Translation, ribosomal structure, biogenesis		
AN8706.1	Glucosamine-phosphate N-acetyltransferase	M			
AN8707.1	Fumarase	C	Energy production, conversion	YPL262W	mitochondrion cytoplasm
AN8709.1	Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT2/GOT1	E	Amino acid transport, metabolism		
AN8710.1	FOG: Low-complexity	S			
AN8712.1	Translation initiation factor 1A (eIF-1A)	J	Translation, ribosomal structure, biogenesis	YMR260C	cytoplasm
AN8713.1	Structure-specific endonuclease ERCC1-XPF, catalytic component XPF/ERCC4	L	Replication, recombination, repair	YPL022W	nucleus
AN8715.1	Actin regulatory protein (Wiskott-Aldrich syndrome protein)	TZ			
AN8716.1	Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	CR			
AN8717.1	DNA-binding centromere protein B (CENP-B)	BD			
AN8720.1	Phosphoglycerate mutase	G	Carbohydrate transport, metabolism	YKR043C	cytoplasm nucleus
AN8721.1	Uncharacterized conserved protein	S		YPL030W	cytoplasm
AN8722.1	ATP-dependent RNA helicase	A	RNA processing, modification	YDL084W	nucleus
AN8723.1	predicted protein [Neurospora crassa]				
AN8724.1	C-type lectin	TV			
AN8726.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN8727.1	integral membrane protein [Magnaporthe grisea]				
AN8731.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Q			
AN8735.1	Amidases related to nicotinamidase	Q			
AN8741.1	FOG: Zn-finger	R			
AN8742.1	Structural maintenance of chromosome protein SMC5/Spr18, SMC superfamily	BDL		YOL034W	cytoplasm nucleus
AN8743.1	Predicted lipase/calmodulin-binding heat-shock protein	IOT			
AN8744.1	Glycolate oxidase	C	Energy production, conversion		
AN8745.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN8746.1	RNA polymerase II general transcription factor BTF3 and related proteins	K	Transcription	YPL037C	cytoplasm
AN8748.1	Lysophospholipase	I	Lipid transport, metabolism	YLR118C	cytoplasm nucleus
AN8750.1	predicted protein [Neurospora crassa]				
AN8751.1	NDR and related serine/threonine kinases	R		YGR092W	bud neck cytoplasm
AN8753.1	hypothetical protein ((AL389901) hypothetical protein [Neurospora crassa])				
AN8755.1	Isocitrate lyase	C	Energy production, conversion	YPR006C	mitochondrion
AN8756.1	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	HC			
AN8757.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN8758.1	hypothetical protein [Neurospora crassa]				
AN8759.1	15-hydroxyprostaglandin dehydrogenase and related dehydrogenases	IR			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8761.1	Endopolygalacturonase	M			
AN8763.1	NADH:ubiquinone oxidoreductase NDUFA2/B8 subunit	C	Energy production, conversion		
AN8764.1	Uncharacterized conserved protein	S			
AN8765.1	Extracellular protein SEL-1 and related proteins	MOT			
AN8766.1	predicted protein [Neurospora crassa]			YGR174C	mitochondrion
AN8767.1	Ankyrin	M			
AN8769.1	Synaptobrevin/VAMP-like protein	U	Intracellular trafficking/secretion/transport	YOR327C	vacuole
AN8771.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN8780.1	Predicted metalloprotease with chaperone activity (RNAse H/HSP70 fold)	O	Posttranslational modification/turnover/chaperones	YDL104C	mitochondrion
AN8782.1	Esterase D	R		YJL068C	cytoplasm
AN8783.1	Regulator of spindle pole body duplication	D	Cell cycle/division, chrom. partitioning		
AN8784.1	predicted protein [Neurospora crassa]				
AN8785.1	Mitochondrial aspartate/glutamate carrier protein Aralar/Citrin (contains EF-hand Ca2+-binding domains)	C	Energy production, conversion		
AN8787.1	Nuclear mRNA export factor receptor LOS1/Exportin-t (importin beta superfamily)	YUJ		YKL205W	nuclear periphery
AN8790.1	Sugar (pentulose and hexulose) kinases	G	Carbohydrate transport, metabolism	YGR194C	cytoplasm
AN8791.1	Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	P	Inorganic ion transport, metabolism	YPL224C	
AN8793.1	Succinate dehydrogenase, cytochrome b subunit	G	Carbohydrate transport, metabolism	YMR118C	
AN8794.1	predicted protein [Neurospora crassa]				
AN8795.1	Adaptor complexes medium subunit family	U	Intracellular trafficking/secretion/transport		
AN8796.1	GTP-binding protein	T	Signal transduction mechanisms	YML121W	vacuolar membrane
AN8797.1	hypothetical protein ((AL513442) conserved hypothetical protein [Neurospora crassa])				
AN8798.1	Auxilin-like protein and related proteins containing DnaJ domain	R			
AN8799.1	tRNA(1-methyladenosine) methyltransferase, subunit GCD14	J	Translation, ribosomal structure, biogenesis	YJL125C	nucleus
AN8801.1	Dioxygenases related to 2-nitropropane dioxygenase	R			
AN8804.1	hypothetical proline-rich protein; possible coiled-coil region [Schizosaccharomyces pombe]				
AN8805.1	FOG: Ankyrin repeat	R		YPL239W	cytoplasm
AN8806.1	Ceramide glucosyltransferase	IM			
AN8807.1	Uncharacterized conserved protein	S		YLL002W	nucleus
AN8808.1	Hypothetical ORF; Ydl237wp [Saccharomyces cerevisiae]			YDL237W	
AN8809.1	Proteins containing regions of low-complexity	R			
AN8810.1	predicted protein [Neurospora crassa]			YHR045W	ER
AN8811.1					
AN8812.1	Lipid exporter ABCA1 and related proteins, ABC superfamily	IR			
AN8814.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN8815.1	Predicted nucleoside-diphosphate-sugar epimerases	MG			
AN8817.1	CLOCK-CONTROLLED PROTEIN 8 (ccg-8) [Neurospora crassa]				
AN8819.1	Reductases with broad range of substrate specificities	R			
AN8820.1	Serine-threonine phosphatase 2B, catalytic subunit	R		YML057W	cytoplasm

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8821.1	hypothetical protein ((AL513444) hypothetical protein [Neurospora crassa])				
AN8822.1	Lysophospholipase	I	Lipid transport, metabolism		
AN8823.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN8824.1	Translation initiation factor 6 (eIF-6)	J	Translation, ribosomal structure, biogenesis	YPR016C	nucleolus nucleus
AN8825.1	Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	U	Intracellular trafficking/secretion/transport		
AN8827.1	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	T	Signal transduction mechanisms	YGL179C	
AN8828.1	Transport protein particle (TRAPP) complex subunit	U	Intracellular trafficking/secretion/transport	YML077W	
AN8829.1	predicted protein [Neurospora crassa]				
AN8830.1	Checkpoint kinase and related serine/threonine protein kinases	D	Cell cycle/division, chrom. partitioning	YCR008W	
AN8831.1	Amphiphysin	U	Intracellular trafficking/secretion/transport	YCR009C	actin cytoplasm
AN8832.1	Peptidyl-tRNA hydrolase	J	Translation, ribosomal structure, biogenesis		
AN8834.1	Ribosome biogenesis protein RPF1, contains IMP4 domain	A	RNA processing, modification		
AN8835.1	Glycyl-tRNA synthetase and related class II tRNA synthetase	J	Translation, ribosomal structure, biogenesis		
AN8836.1	p21-activated serine/threonine protein kinase	T	Signal transduction mechanisms		
AN8837.1	Predicted sugar kinase	G	Carbohydrate transport, metabolism	YPL188W	mitochondrion
AN8838.1	TPR-containing nuclear phosphoprotein that regulates K(+) uptake	P	Inorganic ion transport, metabolism	YOL145C	nucleus
AN8839.1	predicted protein [Neurospora crassa]				
AN8841.1	Nuclear protein ES2	R			
AN8843.1	Homoserine kinase	E	Amino acid transport, metabolism	YHR025W	
AN8844.1	SCF ubiquitin ligase, Rbx1 component	O	Posttranslational modification/turnover/chaperones	YOL133W	
AN8845.1	predicted protein [Neurospora crassa]				
AN8846.1	Protein involved in beta-1,3-glucan synthesis	G	Carbohydrate transport, metabolism	YGR229C	late Golgi
AN8847.1	ATP binding protein	OC			
AN8848.1	Nucleotide-sugar transporter VRG4/SQV-7	GOU		YGL225W	Golgi early Golgi
AN8849.1	Uncharacterized conserved protein	S		YIL096C	nucleolus nucleus
AN8850.1	Uncharacterized conserved protein	S			
AN8851.1	Pseudouridine synthase	J	Translation, ribosomal structure, biogenesis	YLR175W	nucleolus
AN8853.1	Peptide chain release factor 1 (eRF1)	J	Translation, ribosomal structure, biogenesis	YBR143C	cytoplasm
AN8855.1	hypothetical protein [Neurospora crassa]			YBR141C	nucleolus
AN8857.1	G10 protein/predicted nuclear transcription regulator	K	Transcription	YCR063W	nucleus
AN8858.1	Transcription factor of the Forkhead/HNF3 family	K	Transcription		
AN8859.1	Aspartate kinase	E	Amino acid transport, metabolism	YER052C	cytoplasm
AN8860.1	Predicted nucleotide kinase/nuclear protein involved oxidative stress response	F	Nucleotide transport, metabolism	YDL166C	cytoplasm nucleus
AN8862.1	Myosin class V heavy chain	Z	Cytoskeleton	YOR326W	cell periphery bud neck cytoplasm bud
AN8863.1	Nucleosome assembly protein NAP-1	BD		YKR048C	cytoplasm
AN8866.1	D-3-phosphoglycerate dehydrogenase, D-isomer-specific 2-hydroxy acid dehydrogenase superfamily	E	Amino acid transport, metabolism	YIL074C	cytoplasm
AN8867.1	Seryl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YDR023W	cytoplasm
AN8868.1	Ras-related GTPase	R		YCR027C	cytoplasm
AN8869.1	Armadillo/beta-Catenin/plakoglobin	TZ		YHR128W	
AN8870.1	40S ribosomal protein S3A	J	Translation, ribosomal structure, biogenesis	YML063W	cytoplasm
AN8872.1	Adenosine monophosphate deaminase	F	Nucleotide transport, metabolism	YML035C	cytoplasm
AN8873.1	Drebrins and related actin binding proteins	Z	Cytoskeleton		

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN8874.1	Vacuolar sorting protein VPS1, dynamin, and related proteins	UR		YLL001W	mitochondrion
AN8875.1	UDP-N-acetylglucosamine transporter	G	Carbohydrate transport, metabolism		
AN8877.1	Regulator of Rac1, required for phagocytosis and cell migration	T	Signal transduction mechanisms		
AN8878.1	Predicted undecaprenyl diphosphate synthase	I	Lipid transport, metabolism	YDL193W	ER
AN8879.1	Exocyst subunit - Sec10p	U	Intracellular trafficking/secretion/transport		
AN8880.1	Sortilin and related receptors	R		YBL017C	endosome
AN8881.1	Mitochondrial carnitine-acylcarnitine carrier protein	C	Energy production, conversion	YOR130C	mitochondrion
AN8884.1	hypothetical protein [Neurospora crassa]				
AN8885.1	QUINIC ACID UTILIZATION ACTIVATOR				
AN8886.1	Pentafunctional AROM protein	E	Amino acid transport, metabolism		
AN8887.1	Glycosyl transferase, family 8 - glycogenin	G	Carbohydrate transport, metabolism		
AN8891.1	Endopolygalacturonase	M			
AN8892.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN8894.1	hypothetical protein [Neurospora crassa]				
AN8895.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN8896.1	Hydroxysteroid 17-beta dehydrogenase 11	Q			
AN8897.1	Esterase/lipase	I	Lipid transport, metabolism		
AN8898.1	Predicted flavoprotein involved in K+ transport	P	Inorganic ion transport, metabolism		
AN8899.1	1-aminocyclopropane-1-carboxylate deaminase	E	Amino acid transport, metabolism		
AN8900.1	Acetylcholinesterase/Butyrylcholinesterase	T	Signal transduction mechanisms		
AN8903.1	H+/oligopeptide symporter	E	Amino acid transport, metabolism		
AN8906.1					
AN8907.1	C-4 sterol methyl oxidase	I	Lipid transport, metabolism		
AN8908.1	putative lipoprotein [Streptomyces coelicolor A3(2)]				
AN8927.1	unknown [Fusarium sporotrichioides]				
AN8928.1	Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	Q			
AN8931.1	Uncharacterized conserved protein	S			
AN8932.1	Predicted TIM-barrel enzyme, possibly a dioxygenase	R			
AN8941.1	Na+/K+ ATPase, alpha subunit	P	Inorganic ion transport, metabolism		
AN8943.1	hypothetical protein [Neurospora crassa]				
AN8945.1	methyltransferase [Gibberella zeae]				
AN8946.1	GAS-1 homologue [Candida glabrata]				
AN8956.1	Na+/Pi symporter	P	Inorganic ion transport, metabolism	YBR296C	ER
AN8957.1	Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	Q			
AN8959.1	Peripheral-type benzodiazepine receptor and related proteins	T	Signal transduction mechanisms		
AN8968.1	hypothetical protein [Neurospora crassa]				
AN8973.1	hypothetical protein [Neurospora crassa]				
AN8978.1	regulatory protein alcR - Emericella nidulans				
AN8979.1	Alcohol dehydrogenase, class V	Q		YMR083W	mitochondrion
AN8982.1	FAD-dependent oxidoreductase	R			
AN8983.1	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	R			
AN8989.1	Lactoylglutathione lyase and related lyases	E	Amino acid transport, metabolism		
AN8990.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN8992.1					
AN9000.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		

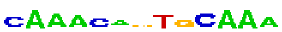
A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN9002.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN9004.1	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	C	Energy production, conversion		
AN9007.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN9008.1	Bacteriophytochrome (light-regulated signal transduction histidine kinase)	T	Signal transduction mechanisms		
AN9010.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism	YGR260W	ER
AN9012.1	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	EM			
AN9013.1	unnamed protein product [Saccharomyces cerevisiae]				
AN9014.1	Glycolate oxidase	C	Energy production, conversion		
AN9021.1					
AN9031.1	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	Q			
AN9032.1	hypothetical protein [Neurospora crassa]				
AN9034.1	Aldehyde dehydrogenase	C	Energy production, conversion		
AN9037.1	Anaerobic dehydrogenases, typically selenocysteine-containing	C	Energy production, conversion		
AN9038.1	Molybdopterin biosynthesis enzyme	H	Coenzyme transport, metabolism		
AN9039.1	Phosphatidylserine decarboxylase	I	Lipid transport, metabolism		
AN9054.1					
AN9057.1	predicted protein [Neurospora crassa]				
AN9060.1	Molecular chaperone (DnaJ superfamily)	O	Posttranslational modification/turnover/chaperones	YNL227C	cytoplasm
AN9062.1	F1-ATP synthase assembly protein	C	Energy production, conversion	YJL180C	cytoplasm
AN9063.1	Oxysterol-binding protein	I	Lipid transport, metabolism	YDL019C	
AN9064.1	Sorbitol dehydrogenase	Q		YJR159W	
AN9065.1	hypothetical protein [Neurospora crassa]			YLR203C	mitochondrion
AN9066.1	Proteins containing the FAD binding domain	C	Energy production, conversion		
AN9067.1	FOG: RRM domain	R			
AN9070.1	SPRY domain-containing proteins	R			
AN9072.1	GTPase Rab4, small G protein superfamily	U	Intracellular trafficking/secretion/transport		
AN9075.1	NADPH:quinone reductase and related Zn-dependent oxidoreductases	CR			
AN9076.1					
AN9078.1	predicted protein [Neurospora crassa]				
AN9079.1	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain	R		YOR296W	cytoplasm
AN9083.1	Adenine phosphoribosyl transferases	F	Nucleotide transport, metabolism	YML022W	cytoplasm nucleus
AN9085.1	U5 snRNP-specific protein-like factor and related proteins	A	RNA processing, modification		
AN9086.1	Transport protein particle (TRAPP) complex subunit	U	Intracellular trafficking/secretion/transport	YKR068C	late Golgi
AN9087.1	Calcium-responsive transcription coactivator	K	Transcription		
AN9089.1	predicted protein [Neurospora crassa]				
AN9090.1	FOG: RRM domain	R		YHR086W	cytoplasm nucleus
AN9092.1	Meiotic recombination protein Dmc1	DL			
AN9094.1	UDP-N-acetylglucosamine pyrophosphorylase	M		YDL103C	cytoplasm nucleus
AN9095.1	Predicted peptidyl prolyl cis-trans isomerase	O	Posttranslational modification/turnover/chaperones		
AN9096.1					

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN9099.1	SPRY domain-containing proteins	R			
AN9101.1	DnaJ-class molecular chaperone	O	Posttranslational modification/turnover/chaperones		
AN9102.1	DNA-dependent RNA polymerase I	K	Transcription		
AN9103.1	Monodehydroascorbate/ferredoxin reductase	R			
AN9104.1	Nucleolar GTPase/ATPase p130	Y	Nuclear structure		
AN9108.1	predicted protein [Neurospora crassa]				
AN9109.1	hypothetical protein [Neurospora crassa]				
AN9110.1	involved in sterol uptake; Upc2p [Saccharomyces cerevisiae]				
AN9112.1	Alcohol dehydrogenase, class V	Q			
AN9113.1	TPR repeat-containing protein	R			
AN9116.1	Nicotinic acid phosphoribosyltransferase	H	Coenzyme transport, metabolism	YOR209C	cytoplasm nucleus
AN9117.1	CUTINASE TRANSCRIPTION FACTOR 1 BETA				
AN9119.1	Uncharacterized conserved protein	S			
AN9120.1	RNA polymerase II, second largest subunit	K	Transcription	YOR151C	cytoplasm nucleus
AN9121.1	ESDC [Aspergillus nidulans]				
AN9122.1	probable lipase/esterase [Pirellula sp.]				
AN9124.1	Molecular co-chaperone STI1	O	Posttranslational modification/turnover/chaperones	YOR027W	cytoplasm
AN9125.1	RNA polymerase III, subunit C34	K	Transcription	YNR003C	
AN9126.1	Chromatin remodeling protein, contains PHD Zn-finger	B	Chromatin structure, dynamics		
AN9127.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN9130.1	Carboxylesterase type B	I	Lipid transport, metabolism		
AN9133.1	Tellurite resistance protein and related permeases	P	Inorganic ion transport, metabolism	YPL092W	
AN9135.1	Synaptic vesicle transporter SV2 (major facilitator superfamily)	R			
AN9138.1	Amidases	JIT			
AN9140.1	Hypothetical ORF; Ymr221cp [Saccharomyces cerevisiae]			YMR221C	vacuole
AN9142.1	predicted protein [Neurospora crassa]				
AN9143.1	hypothetical protein [Neurospora crassa]				
AN9144.1	Cystathionine beta-lyases/cystathionine gamma-synthases	E	Amino acid transport, metabolism		
AN9146.1	hypothetical protein [Neurospora crassa]				
AN9147.1	von Willebrand factor and related coagulation proteins	WV			
AN9148.1	UDP-glucose pyrophosphorylase	G	Carbohydrate transport, metabolism	YKL035W	cytoplasm
AN9149.1	Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A, contains C2 domain	R		YOR086C	cell periphery
AN9151.1	Exoribonuclease R	K	Transcription		
AN9157.1	Glutaminyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YOR168W	cytoplasm
AN9158.1	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	IQR			
AN9159.1	oxidoreductase [Penicillium citrinum]				
AN9163.1	predicted protein [Neurospora crassa]				
AN9166.1	hypothetical protein [Neurospora crassa]				
AN9168.1	Predicted transporter (major facilitator superfamily)	R		YDR536W	
AN9171.1	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	R			
AN9172.1	UDP-glucose/GDP-mannose dehydrogenase	GT			

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN9173.1	Permeases of the major facilitator superfamily	GEPR			
AN9174.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN9181.1	hypothetical protein [Neurospora crassa]				
AN9183.1	Beta-glucosidase, lactase phlorizinhydrolase, and related proteins	G	Carbohydrate transport, metabolism		
AN9186.1	Purple acid phosphatase	G	Carbohydrate transport, metabolism		
AN9192.1	hypothetical protein [Oryza sativa (japonica cultivar-group)]				
AN9194.1	Predicted nucleoside-diphosphate-sugar epimerases	MG			
AN9195.1	L-asparaginase II	E	Amino acid transport, metabolism		
AN9200.1	hypothetical protein [Neurospora crassa]				
AN9204.1	Acetyltransferases, including N-acetylases of ribosomal proteins	J	Translation, ribosomal structure, biogenesis		
AN9274.1	PEP2 [Nectria haematococca]				
AN9286.1	Alpha-glucuronidase	G	Carbohydrate transport, metabolism		
AN9287.1	Lysophospholipase L1 and related esterases	E	Amino acid transport, metabolism		
AN9291.1	Permeases of the major facilitator superfamily	GEPR			
AN9297.1	Myosin-crossreactive antigen	S			
AN9303.1	related to 7alpha-cephem-methoxylase P8 chain [Neurospora crassa]				
AN9304.1	Glutathione S-transferase	O	Posttranslational modification/turnover/chaperones		
AN9305.1					
AN9307.1	Uncharacterized protein conserved in bacteria	S			
AN9308.1	FAD/FMN-containing dehydrogenases	C	Energy production, conversion		
AN9311.1	conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
AN9314.1	ent-kaurene synthase - fungus (Gibberella fujikuroi)				
AN9315.1	Monodehydroascorbate/ferredoxin reductase	R			
AN9317.1	Asparagine synthase (glutamine-hydrolyzing)	E	Amino acid transport, metabolism		
AN9333.1	Monocarboxylate transporter	G	Carbohydrate transport, metabolism		
AN9339.1	Catalase	P	Inorganic ion transport, metabolism		
AN9340.1	Acid trehalase	G	Carbohydrate transport, metabolism	YPR026W	
AN9342.1	Multidrug/pheromone exporter, ABC superfamily	Q			
AN9356.1	Possible oxidoreductase	R			
AN9357.1	Predicted dehydrogenase	Q		YIR035C	cytoplasm
AN9358.1	Class 2 transcription repressor NC2, beta subunit (Dr1)	K	Transcription	YDR397C	nucleus
AN9359.1	Actin and related proteins	Z	Cytoskeleton	YMR033W	
AN9360.1	Protein containing a U1-type Zn-finger and implicated in RNA splicing or processing	A	RNA processing, modification		
AN9361.1	Chitinase	M			
AN9362.1	U2 snRNP splicing factor, small subunit, and related proteins	A	RNA processing, modification		
AN9370.1	Predicted transporter (major facilitator superfamily)	R		YOR378W	
AN9374.1	hypothetical protein [Neurospora crassa]				
AN9377.1	Allergen Asp f 4				
AN9383.1	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins	R			
AN9384.1	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	QI			
AN9392.1	Permease of the major facilitator superfamily	G	Carbohydrate transport, metabolism		
AN9393.1	Permeases of the major facilitator superfamily	GEPR		YJR124C	

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN9394.1	Succinyl-CoA:alpha-ketoacid-CoA transferase	C	Energy production, conversion		
AN9398.1	Cell adhesion complex protein bystin	W		YBR247C	nucleolus cytoplasm nucleus
AN9399.1	Histone H3 (Lys4) methyltransferase complex, subunit CPS60/ASH2/BRE2	BK		YLR015W	nucleus
AN9401.1	Zn2+-binding dehydrogenase (nuclear receptor binding factor-1)	KC		YBR026C	mitochondrion
AN9402.1	5' nucleotidase	F	Nucleotide transport, metabolism	YHR202W	vacuole
AN9403.1	Pyruvate dehydrogenase E1, beta subunit	C	Energy production, conversion	YBR221C	mitochondrion
AN9404.1	hypothetical protein [Neurospora crassa]				
AN9405.1	predicted protein [Neurospora crassa]			YOR228C	mitochondrion
AN9406.1	tRNA methyltransferase	J	Translation, ribosomal structure, biogenesis	YDR120C	nuclear periphery nucleus
AN9407.1	3-oxoacyl-[acyl-carrier protein] reductase	I	Lipid transport, metabolism	YPL231W	cytoplasm
AN9408.1	Enoyl reductase domain of yeast-type FAS1	I	Lipid transport, metabolism	YKL182W	cytoplasm
AN9409.1	Uncharacterized conserved protein	S		YGR187C	cytoplasm
AN9410.1	Predicted alpha/beta hydrolase	R		YDR444W	cytoplasm
AN9411.1	NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit	C	Energy production, conversion		
AN9412.1	hypothetical protein [Neurospora crassa]				
AN9413.1	cytokinesis inhibitor byr4 related protein [imported] - Neurospora crassa				
AN9419.1	Alanyl-tRNA synthetase	J	Translation, ribosomal structure, biogenesis	YOR335C	cytoplasm
AN9421.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN9434.1	Predicted Zn2+-dependent endopeptidase, insulinase superfamily	O	Posttranslational modification/turnover/chaperones	YOL098C	cytoplasm
AN9436.1	RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 5'-3' helicase subunit RAD3	KL		YER171W	cytoplasm nucleus
AN9437.1	Predicted E3 ubiquitin ligase	O	Posttranslational modification/turnover/chaperones		
AN9446.1	Pantothenate kinase PanK and related proteins	H	Coenzyme transport, metabolism	YDR531W	cytoplasm nucleus
AN9448.1	predicted protein [Neurospora crassa]				
AN9451.1	predicted protein [Neurospora crassa]				
AN9460.1	Signal peptidase complex subunit	U	Intracellular trafficking/secretion/transport	YLR066W	ER
AN9461.1	Dehydrogenase kinase	T	Signal transduction mechanisms	YGL059W	mitochondrion
AN9463.1	Ras GTPase-activating protein family - IQGAP	T	Signal transduction mechanisms	YPL242C	bud neck
AN9464.1	Glutaredoxin and related proteins	O	Posttranslational modification/turnover/chaperones		
AN9465.1	60S ribosomal protein L9	J	Translation, ribosomal structure, biogenesis	YNL067W	cytoplasm
AN9466.1	hypothetical protein [Neurospora crassa]			YGR266W	ER
AN9467.1	Serine/threonine protein phosphatase 2A, regulatory subunit	T	Signal transduction mechanisms	YOR014W	cytoplasm nucleus
AN9468.1	40S ribosomal protein S16	J	Translation, ribosomal structure, biogenesis	YMR143W	cytoplasm
AN9469.1	Mitochondrial/chloroplast ribosomal protein L13	J	Translation, ribosomal structure, biogenesis	YOR150W	mitochondrion
AN9470.1	Uricase (urate oxidase)	Q			
AN9471.1	Cytosine deaminase FCY1 and related enzymes	F	Nucleotide transport, metabolism		
AN9472.1	Vesicular amine transporter	U	Intracellular trafficking/secretion/transport		
AN9473.1	predicted protein [Neurospora crassa]				
AN9474.1	Voltage-gated shaker-like K+ channel, subunit beta/KCNAB	C	Energy production, conversion	YPL088W	
AN9480.1	Splicing coactivator SRm160/300, subunit SRm300	A	RNA processing, modification		
AN9481.1	Chloride ion current inducer protein	P	Inorganic ion transport, metabolism		
AN9482.1	predicted protein [Neurospora crassa]				

A. nidulans locus	A. nidulans locus description	COG category	COG description	S. cerevisiae BBH	GO cellular location for yeast gene
AN9483.1	predicted protein [Neurospora crassa]				
AN9485.1	hypothetical serine-rich secreted protein [Schizosaccharomyces pombe]				
AN9486.1	Lipoate synthase	H	Coenzyme transport, metabolism	YOR196C	mitochondrion
AN9489.1					
AN9490.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN9491.1	Tumor differentially expressed (TDE) protein	S			
AN9492.1	FOG: Zn-finger	R			
AN9496.1	C-8,7 sterol isomerase	I	Lipid transport, metabolism		
AN9497.1	Predicted haloacid-halidohydrolase and related hydrolases	R			
AN9498.1	TPR repeat-containing protein	R			
AN9500.1	Cyclin	R			
AN9503.1					
AN9504.1	Ras GTPase activating protein RasGAP/neurofibromin	V	Defense mechanisms		
AN9506.1	Amino acid transporters	E	Amino acid transport, metabolism		
AN9509.1	Putative nucleic acid-binding protein Hcc-1/proliferation associated cytokine-inducible protein, contains SAP domain	D	Cell cycle/division, chrom. partitioning		
AN9511.1	Methylase	R			
AN9512.1	hypothetical protein [Neurospora crassa]				
AN9514.1	Phosphoglycerate dehydrogenase and related dehydrogenases	HE			
AN9515.1	predicted protein [Neurospora crassa]				
AN9518.1	Predicted hydrolase (HAD superfamily)	R			
AN9521.1	Ca2+-binding protein, EF-Hand protein superfamily	T	Signal transduction mechanisms		
AN9522.1	Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	I	Lipid transport, metabolism		
AN9523.1	predicted protein [Neurospora crassa]				
AN9526.1	SNARE protein SED5/Syntaxin 5	U	Intracellular trafficking/secretion/transport	YLR026C	
AN9527.1	Uncharacterized conserved protein, contains double-stranded beta-helix domain	S		YMR009W	cytoplasm nucleus
AN9528.1	hypothetical protein ((AF238480) maintaining mitochondrial morphology protein MMM1 [Neurospora crassa])			YLL006W	mitochondrion
AN9533.1					
AN9538.1	FOG: Zn-finger	R			

ID	Conpat Consensus	Similar sequence	# 5' Sites	# 3' Sites	5' /3' Bias?	% Aligned	Strand Bias?	Enriched in COG categories (# genes in category)	Enriched in cell location (# genes in category)
1821		bHLH	115	8	up[3]	35%	yes[3]	J:Translation, ribosomal structure, biogenesis (16)[1]	nucleus (22)
1622		areA/gln3	25	3	up[1]	60%			nucleus (8)
234			46	11	up[2]	35%		A:RNA processing, modification (8)	
1934		bHLH	36	3	up[3]	47%	yes[1]	I:Lipid transport, metabolism (10)[2]	
1710		puf	5	20	down[1]	30%	yes[3]		
896			14	2	up	43%	yes		
1602			34	0	up[3]	50%			nucleolus (4)
1879			24	1	up[2]	63%	yes		
1132			14	2	up	36%	yes[3]		
2683			27	1	up[3]	48%	yes[1]		
2223			5	16	down	63%	yes[3]		
1291		yAP1	21	1	up[2]	62%	yes		
992			1	21	down[3]	86%	yes[3]		
2611			0	17	down[3]	59%			
1739			9	0	up	44%	yes[1]	J:Translation, ribosomal structure, biogenesis (4)	
418			33	1	up[3]	45%			
2077		puf	1	9	down	56%	yes		mitochondrion (4)[1]
973			74	6	up[3]	36%	yes[1]	A:RNA processing, modification (12)[1]	nucleolus (8)[2]
2488			37	4	up[3]	38%	yes[2]	T:Signal transduction mechanisms (11)[2]	cytoplasm (13)[1]
1144		puf	2	11	down	36%	yes[3]		mitochondrion (6)[3]
1635			13	1	up	69%	yes[3]	J:Translation, ribosomal structure, biogenesis (8)[3]	cytoplasm (8)[2]
1940			2	19	down[2]	47%	yes[3]	D:Cell cycle/division, chrom. partitioning (5)[1]	
2199		bHLH	40	3	up[3]	30%			
1426			14	1	up	50%		C:Energy production, conversion (5)[1]	
2525		stuA/mbp1	18	1	up[1]	39%	yes	Replication, recombination, repair (10)[3]	nucleus (8)[1]
813		yATF-B	11	1	up	45%			
1650			11	0	up	73%		J:Translation, ribosomal structure, biogenesis (4)	nucleolus (4)[2]
2093			44	5	up[3]	30%	yes[3]	I:Lipid transport, metabolism (8)	
1998			25	1	up[3]	40%	yes	I:Lipid transport, metabolism (7)[1]	peroxisome (2)[1]
2497			0	8	down	100%	yes[2]		
751			25	2	up[2]	40%			
2483		cpcA/gcn4	19	4	up	26%		E:Amino acid transport, metabolism (7)[1] J:Translation, ribosomal structure, biogenesis (7)[2]	cytoplasm (12)[3]
2249			36	0	up[3]	25%		A:RNA processing, modification (7) J:Translation, ribosomal structure, biogenesis (13)[3]	nucleolus (8)[3], nucleus (12)[1]
1059			12	1	up	92%			
2451			0	10	down[1]	80%			cell periphery (2)

Similar sequence determined comparing pattern with known factors in yeast and Aspergillus via CompareACE (score cutoff 0.85)
Pvalues indicated by superscript: [1]pvalue < 1e-3, [2]pvalue < 1e-4, [3]pvalue < 1e-5

§S5. Transposable Elements

A number of unusual features were also observed in *Aspergillus* TEs. First, in *A. fumigatus*, one subfamily of I-1_AF non-LTR retrotransposons has a unique target-site, and was found in long terminal repeats of the Afut2 *Gypsy*-like LTR retrotransposon. Second, the *Aspergillus Helitrons* have 5’-TT and CTTG-3’ termini, which differ from the canonical 5’-TC and CTRR-3’ termini[70]. Moreover, Aspergillus *Helitrons* do not contain 3’ palindromic structures, which are present in other eukaryotes[70,71], indicating that 3’ palindromes are not essential for rolling-circle transpositions. Third, all three genomes possess unusual *Mariners*, 7-9 kb in length, that encode a conserved protein of unknown function in addition to a transposase. Finally, we identified families of SINE elements derived from the 5’-half of 5S rRNA containing an internal pol III promoter. They are the first examples of SINE elements present in fungi. Moreover, such 5s RNA derived SINE elements have been found previously in the zebrafish genome only.

Table §S5.1: Major superfamilies of transposable elements identified in the aspergillus genomes

Species	Percentage of all TEs and repetitive elements in the assembly	Percentage of different classes among all transposable and repetitive elements						
		Non-LTR retrotransposons	LTR retrotransposons		DNA transposons			
		I	Gypsy	Copia	*Mariner*	*MuDR*	*hAT*	*Helitron*
A. nidulans	3.0	19	22	14	20	12†	5†	2
A. fumigatus	2.9	15	55	4	25	-	-	-
A. oryzae	1.4	20	31	-	49	<<1	-	-

[†] Putative classification based on hallmarks of nonautonomous elements DNA9-1_AN, DNA9-2_AN, DNA9-3_AN, and DNA9-4_AN (MuDR superfamily) and hAT-N1_AN, and hAT-N2_AN (hAT superfamily). There are no MuDR and hAT transposases detectable in the aspergillus genomes.

§S6. Assembly and Genetic Map Integration

§S6.1. Chromosome Size Estimates and Comparison to Assembly

Chromosome	Estimated Size†	Assembly Size	Estimated Coverage
I	3.8	3.67	96.6%
II	4.2	3.94	93.8%
III	3.5	3.39	96.9%
IV	2.9	2.81	96.9%
V	3.8	2.22	58.4%
VI	3.5	3.34	95.4%
VII	4.5	4.41	98.0%
VIII	5	4.85	97.0%
Unlinked		1.43	
Total	**31.2**	**30.06**	**96.3%**

†Chromosome estimated sizes taken from Brody, H., J. Griffith, et al. (1991). "Chromosome-specific recombinant DNA libraries from the fungus Aspergillus nidulans." Nucleic Acids Res 19(11): 3105-9.

§S6.2. Genetic Map Description and Integration

Around 260 known genetic markers, which have associated sequences, exist for *Aspergillus nidulans*[4,5]. These 260 genetic markers were filtered to a set of 196 unambiguous sequences with accessions in GenBank. Of these 196 markers, 103 are ordered on the linkage group map whereas the remaining 93 are unordered. The file of genetic markers is available for download at http://www.broad.mit.edu/cgi-bin/annotation/aspergillus/download_license.cgi .

These markers were compared to the current assembly using BLASTN. Where these matches were unique, were of high quality, and contained most or all the gene, we assigned a marker position in one of our contigs. A total of 187 markers were placed uniquely within the assembly and only 14 of the markers showed discrepancies (see below). We used the 187 unique marker alignments to correlate contigs with linkage groups, creating the correlated genetic maps displayed here.

- 28.5 Mb (18 supercontigs) of the 30 Mb assembly or 95% of the assembly, are anchored to the genetic map.
- 26.8 Mb (12 supercontigs) or 89% of the assembly are ordered and oriented.
- 1.7 Mb can only be placed on a linkage group without specifying order or orientation

More detail is available at http://www.broad.mit.edu/annotation/fungi/aspergillus/markers.html.

§S6.3. Discrepancies between Assembly and Genetic Map

There are a few cases where marker order on the linkage group map conflicts with the locations of markers in supercontigs. The discrepancies may be due to:

1. Errors in assembly of sequence into contigs or supercontigs

2. Errors in order of markers on the linkage group map
3. Correct but incomplete assembly data: for example, one supercontig may lie within a gap between contigs in another supercontig

The following discrepancies were noted and corrected when related to an error in assembly (see also (http://www.gla.ac.uk/Acad/IBLS/molgen/aspergillus/). *All discrepancies that could be associated with errors in the assembly were corrected prior to analysis.* The order and orientation of contigs within supercontigs in this corrected assembly used for analysis is provided below.

1. **Re-orient Supercontig 9, on LG IV**: uvsH and bimD map distally while uvsB is centromere-proximal
2. **Supercontig 15 should be on LG VI not LG IV**: Supercontig 15 is shown as relating to linkage group IV on the basis of the pacA marker. However the clone labelled "pacA" has been found to encode a suppressor of pacA, and has been renamed "suApacA". SuApacA maps on VI, as does cnxG, located in contig 169. Telomeric repeats located at the end of contig 170 determine that supercontig 15 is the short left arm of linkage group VI, with contig 170 distal to contig 169.
3. **Supercontig 14 should be on LG VII**: The alcA gene is genetically mapped to the short left arm of linkage group VII, and therefore locating supercontig 14 to that position (orientation unknown).
4. **Supercontig 16 should be on LG VIII**: supercontig 16 probably relates to the right arm of linkage group VIII, on the basis of a tentative identification of AN9403.1 as "pdhA" (encoding a pyruvate dehydrogenase subunit).
5. **Telomeric simple repeats** are found at:
    - the start of contig 1.134: LG II left end.
    - as stated in item 2, 1.170 (supercontig 15) is clearly the LEFT arm of VI because cnxG (meiotically at the left end of VI) locates to 1.169.
    - the start of contig 1.1: right end of LG VIII.
    - on unattached contigs 1.200 and 1.216

§S6.4. *A. nidulans* Assembly Contig Order and Orientation

The following provides the order and orientation of contigs within supercontigs in the corrected *A. nidulans* assembly used for analysis. Supercontigs are ordered from the end of one arm of each chromosome to the end of the other arm although the selection of which arm to start from was arbitrary for each chromosome.

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
7	108	352786	-1	1
7	107	444822	-1	1
7	106	67855	-1	1
7	105	277183	-1	1
7	104	297769	-1	1
7	103	69272	-1	1
7	102	132643	-1	1
7	101	209568	-1	1
7	100	337251	-1	1

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
7	99	2005	-1	1
8	109	233950	1	1
8	110	298245	1	1
8	111	62418	1	1
8	112	353724	1	1
8	113	316066	1	1
8	114	25936	1	1
8	115	127320	1	1
8	116	56802	1	1
36	194	8226	1	1
11	134	78670	1	2
11	135	301041	1	2
11	136	31127	1	2
11	137	32282	1	2
11	138	39791	1	2
11	139	347029	1	2
11	140	26834	1	2
11	141	203328	1	2
11	142	43730	1	2
11	143	30509	1	2
11	144	72448	1	2
11	145	176570	1	2
4	71	8494	-1	2
4	70	41226	-1	2
4	69	80995	-1	2
4	68	250663	-1	2
4	67	254221	-1	2
4	66	88283	-1	2
4	65	278071	-1	2
4	64	203363	-1	2
4	63	41959	-1	2
4	62	201480	-1	2
4	61	865047	-1	2
4	60	68571	-1	2
4	59	177453	-1	2
5	86	112247	-1	3
5	85	34531	-1	3
5	84	621812	-1	3
5	83	55015	-1	3
5	82	44985	-1	3
5	81	156263	-1	3
5	80	335440	-1	3
5	79	209053	-1	3
5	78	353456	-1	3
5	77	132523	-1	3
5	76	153210	-1	3
5	75	213493	-1	3
5	74	12387	-1	3
5	73	3923	-1	3

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
5	72	17816	-1	3
13	163	91924	-1	3
13	162	65002	-1	3
13	161	266267	-1	3
13	160	146980	-1	3
13	159	58286	-1	3
13	158	283337	-1	3
26	183	10603	1	3
56	214	6579	1	3
9	128	280307	-1	4
9	127	138927	-1	4
9	126	40772	-1	4
9	125	32723	-1	4
9	124	55685	-1	4
9	123	128436	-1	4
9	122	214949	-1	4
9	121	13722	-1	4
9	120	3924	-1	4
9	119	137987	-1	4
9	118	105880	-1	4
9	117	274575	-1	4
10	129	627835	1	4
10	130	308583	1	4
10	131	116788	1	4
10	132	254738	1	4
10	133	81213	1	4
58	216	6436	1	5
6	87	12990	1	5
6	88	183820	1	5
6	89	282268	1	5
6	90	3363	1	5
6	91	6778	1	5
6	92	62660	1	5
6	93	340023	1	5
6	94	523724	1	5
6	95	103820	1	5
6	96	98894	1	5
6	97	24746	1	5
6	98	565485	1	5
15	170	216503	-1	6
15	169	351151	-1	6
3	58	83422	-1	6
3	57	28094	-1	6
3	56	45063	-1	6
3	55	492661	-1	6
3	54	183474	-1	6
3	53	51172	-1	6
3	52	82934	-1	6
3	51	1114266	-1	6

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
3	50	47652	-1	6
3	49	206454	-1	6
3	48	95913	-1	6
3	47	137873	-1	6
3	46	103482	-1	6
3	45	83158	-1	6
3	44	17771	-1	6
14	168	229305	-1	7
14	167	41972	-1	7
14	166	41526	-1	7
14	165	114598	-1	7
14	164	150254	-1	7
2	22	276296	1	7
2	23	67024	1	7
2	24	43525	1	7
2	25	229102	1	7
2	26	389371	1	7
2	27	113764	1	7
2	28	98898	1	7
2	29	525887	1	7
2	30	89802	1	7
2	31	2490	1	7
2	32	435990	1	7
2	33	2149	1	7
2	34	177275	1	7
2	35	84073	1	7
2	36	96901	1	7
2	37	75346	1	7
2	38	233386	1	7
2	39	240080	1	7
2	40	150763	1	7
2	41	64302	1	7
2	42	99573	1	7
2	43	338545	1	7
16	171	24092	1	8
16	172	523550	1	8
16	173	11633	1	8
1	21	2196	-1	8
1	20	21570	-1	8
1	19	71437	-1	8
1	18	175793	-1	8
1	17	347844	-1	8
1	16	451587	-1	8
1	15	178329	-1	8
1	14	364334	-1	8
1	13	249512	-1	8
1	12	174100	-1	8
1	11	61200	-1	8
1	10	175166	-1	8

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
1	9	14258	-1	8
1	8	49390	-1	8
1	7	773302	-1	8
1	6	266891	-1	8
1	5	450355	-1	8
1	4	155056	-1	8
1	3	127977	-1	8
1	2	168814	-1	8
1	1	10851	-1	8
12	146	11447	1	0
12	147	5126	1	0
12	148	4102	1	0
12	149	38673	1	0
12	150	109819	1	0
12	151	72894	1	0
12	152	53749	1	0
12	153	403022	1	0
12	154	34335	1	0
12	155	40523	1	0
12	156	11675	1	0
12	157	136262	1	0
17	174	26679	1	0
18	175	19880	1	0
19	176	15731	1	0
20	177	14522	1	0
21	178	12319	1	0
22	179	11756	1	0
23	180	11235	1	0
24	181	10660	1	0
25	182	10620	1	0
27	184	2754	1	0
27	185	7835	1	0
28	186	10198	1	0
29	187	10087	1	0
30	188	10072	1	0
31	189	10019	1	0
32	190	9210	1	0
33	191	9200	1	0
34	192	9030	1	0
35	193	8744	1	0
37	195	8077	1	0
38	196	8076	1	0
39	197	7797	1	0
40	198	7688	1	0
41	199	7686	1	0
42	200	7501	1	0
43	201	7389	1	0
44	202	7303	1	0
45	203	7055	1	0

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
46	204	6994	1	0
47	205	6930	1	0
48	206	6924	1	0
49	207	6880	1	0
50	208	6838	1	0
51	209	6773	1	0
52	210	6735	1	0
53	211	6721	1	0
54	212	6710	1	0
55	213	6639	1	0
57	215	6468	1	0
59	217	2295	1	0
59	218	4089	1	0
60	219	6367	1	0
61	220	6090	1	0
62	221	5785	1	0
63	222	5781	1	0
64	223	5626	1	0
65	224	5623	1	0
66	225	5462	1	0
67	226	5454	1	0
68	227	5437	1	0
69	228	5427	1	0
70	229	5381	1	0
71	230	5336	1	0
72	231	5185	1	0
73	232	5001	1	0
74	233	4981	1	0
75	234	4876	1	0
76	235	4760	1	0
77	236	4673	1	0
78	237	4650	1	0
79	238	4644	1	0
80	239	4316	1	0
81	240	3963	1	0
82	241	3865	1	0
83	242	3786	1	0
84	243	3623	1	0
85	244	3100	1	0
86	245	3093	1	0
87	246	3023	1	0
88	247	2515	1	0
89	248	2259	1	0

§S8. Peroxisomes

Table §S8.1 Enzymes involved in fatty acid beta-oxidation in *Aspergillus* species[a]

PUTATIVE FUNCTION	*A. nidulans*	*A. fumigatus*	*A. oryzae*
Mitochondrial[b]			
acyl-CoA dehydrogenase	AN0824.2	70.m15426	20092.m00067
enoyl-CoA hydratase	AN5916.2[d]	72.m19960	20177.m00746
hydroxyacyl-CoA dehydrogenase	AN7008.2	89.m02079	20119.m00087
ketoacyl-CoA thiolase	AN4179.2[d]	69.m15561	20170.m00460
Lon protease[e]	AN6193.2	72.m19291	20145.m00253
Peroxisomal[c]			
acyl-CoA oxidase	AN6765.2 AN6752.2	65.m07221 65.m07222	20158.m00219 20176.m00510 20081.m00050
acyl-CoA dehydrogenase	AN2264.2 AN6595.2	71.m15905	20132.m00109
multifunctional enzyme	AN7111.2[d]	89.m02027	20153.m00196
ketoacyl-CoA thiolase	AN5646.2 AN1050.2 AN5878.2	58.m07559 70.m15207 72.m19253	20138.m00141 20149.m00282 20082.m00061
Lon protease[e]	AN0122.2	71.m15403	20148.m00233

Notes

[a] The genes shown represent a minimal set. There are additional probable orthologs for most classes of enzyme. Of particular interest is the finding of a large number of enoyl-CoA hydratases (PFAM00378-15 in *A.oryzae*, 10 in *A.fumigatus* and 12 in *A.nidulans* with either mitochondrial or peroxisomal locations predicted) and hydroxyacyl-CoA dehydrogenases (PFAM02737

and 00725 – 5 in *A.oryzae*,3 in *A,fumigatus* and 4 in *A.nidulans* none of which have predicted peroxisomal targetting.

[b] Assignment of proteins to mitochondria was based on TargetP (http://www.cbs.dtu.dk/services/TargetP/ Olof Emanuelsson, Henrik Nielsen, Søren Brunak, and Gunnar von Heijne: "Predicting subcellular localization of proteins based on their N-terminal amino acid sequence", J. Mol. Biol. 300, 1005-1016 (2000) and PSORT II (http://psort.nibb.ac.jp/).

[c] Peroxisomal location was based on the presence of a C-terminal PTS-1 consensus of the form(S/A R/K L/M) or a PTS-2 consensensus (R/K L/V/I X5 H/Q L/A/F/I). The PTS-2 consensus was only found in the ketoacyl-CoA thiolases.

[d] Inactivation of AN5916.2 and AN7111.2 has been shown to affect fatty acid utilisation (Maggio- Hall and Keller (ref 77 in previous version) and a mutation in AN4179.2 results in loss of growth on short chain fatty acids (M.J.Hynes, unpublished).

[e] *Saccharomyces cerevisiae* contains a mitochondrial Lon protease (Pim1/Lon1) but lacks a peroxisomal enzyme.

§S9. Hyphal Growth

Table §S9.1. Rho GTPases in *Aspergillus fumigatus*, *Aspergillus nidulans* and *Aspergillus oryzae*

	Comments	*A. fumigatus*	*A. nidulans*	*A. oryzae*
Cdc42	designated *modA* in *A. nidulans*,Genbank	57.m05868	10129.m00259	20124.m00121
BSpCdc42[a]		2.4e-87	5.5e-88	1.3e-86
BAnCdc42		5.3e-99	1.9e-103	1.2e-99
Rac	No Rac in Sc or Sp	59.m09236	10080.m00194	20164.m00289
BPmCflB		2.5e-99	1.2e-87	1.2e-87
BAnRac		1.1e-100	2.0e-106	5.4e-90
Rho1/5	designated *RhoA* in *A. nidulans*,Genbank	69.m14857	10098.m00327	20178.m00433
BSpRho1		1.8e-82	5.1e-85	3.3e-83
BSpRho5		5.5e-81	3.3e-83	1.6e-81
BSpRho3		6.3e-48	4.3e-49	4.9e-48
BAnRho1/5		5.3e-99	2.4e-103	3.3e-97
Rho2		59.m08858	10084.m00301	20125.m00098
BSpRho2		2.5e-60	1.2e-71	1.8e-73
BAnRho2		1.1e-77	3.0e-103	8.0e-96
Rho3		59.m09201	10081.m00065	20166.m00259
BSpRho3		5.7e-47	7.4e-61	2.1e-47
BAnRho3		1.6e-67	5.1e-101	1.4e-68
Rho4		71.m15175	10047.m00059	20150.m00290
BSpRho4		1.4e-66	2.9e-66	7.8e-66
BAnRho4		6.8e-122	2.2e-139	1.5e-101
Rho6				20154.m00241
BSpRho1				1.5e-37
BScRho1				4.6e-38
BAoRho6		Rho1/5: 5.3e-41	Rac: 3.1e-33	5.6e-111

[a]B denotes BLASTP query sequence, hits with lowest e values shown

Sc, *S. cerevisiae*; Sp, *S. pombe*; Pm, *P. marneffei*; An, *A. nidulans*

Table §S9.2 Rho GEFs in *Aspergillus fumigatus*, *Aspergillus nidulans* and *Aspergillus oryzae*

	A. fumigatus	***A. nidulans***	***A. oryzae***
Scd1 (Cdc24)	58.m07516	10096.m00053	20165.m00196
BSpScd1	4.6e-55	8.4e-63	1.9e-71
BScCdc24	3.9e-46	8.1e-47	5.5e-46
BAnScd1	0	0	0
Rgf1/2 (Rom1/2)	71.m15707	10080.m00170	20148.m00145
BSpRgf1	1.6e-245	1.1e-237	7.7e-233
BSpRgf2	4.4e-206	3.6e-201	6.5e-202
BScRom1	3.6e-126	3.8e-118	1.8e-124
BScRom2	1.3e-169	1.3e-165	8.3e-168
BAnRgf1/2	0	0	0
Rgf3	71.m15816	10132.m00137	20123.m00134
BSpRgf3	5.7e-108	2.9e-109	5.7e-66
AnBRgf3	0	0	0
Gef1/3	65.m07373	10061.m00505	20146.m00208
BSpGef1	1.9e-18	3.2e-12	2.1e-11
BSpGef3	1.1e-14	9.0e-19	1.3e-13
BAnGef1/3	0	0	0
Gef2	71.m15388	10004.m00063	20148.m00240
BSpGef2	0.00050	3.1e-08	5.0e-09
BAnGef2	4.2e-285	0	0

[a]B denotes BLASTP query sequence, hits with lowest e values shown
Sc, *S. cerevisiae*; Sp, *S. pombe*; An, *A. nidulans.*

§S10. Gene Prediction Protocol and Accuracy Estimation

§S10.1. Gene Prediction Protocol

Gene structures were predicted using a combination of FGENESH, FGENESH+, and GENEWISE. Both FGENESH and FGENESH+ are gene prediction programs acquired from Softberry.com and GENEWISE is part of the WISE2 package developed by Ewan Birney and is available from the Sanger Center.

Both FGENESH and FGENESH+ utilize a statistical model of gene structure that require training on each organism for accurate prediction. FGENESH+ additionally combines a protein sequence with the statistical model to improve accuracy. We acquired these programs already trained by Softberry on *Aspergillus nidulans* sequences.

GENEWISE (as we ran it), splices and aligns a protein sequence with genomic sequence to predict a gene structure. Although GENEWISE does utilize some species-specific parameters, most notably for intron nucleotide statistics and splice site consensus sequences, these can be set to non-species specific defaults. In this case, GENEWISE essentially produces the best local alignment of a protein assuming that introns start at GT and end at AG most of the time and in some cases this results a full alignment of the protein to the genome. Since we are interested in predicting complete gene structures, we post-processed GENEWISE incomplete protein alignments by moving the first and last exon upstream or downstream to the nearest start and stop codons respectively. If a stop codon was encountered upstream of a gene before a start could be found, the gene call was not used.

Briefly, these three gene callers were combined in the following manner:

1. FGENESH was run on the entire genomic sequence to provide an initial set of predicted genes. Each FGENESH predicted was put into a set of EVIDENCE_GENES.
2. The genome was also searched against the non-redundant protein database using BLASTX
3. Regions of the genome with blastx homology spanning over 80% of a protein (when sub-alignments are stitched together in a consistent fashion) were considered "Homologous Gene Regions" (HGRs).
4. HGRs were clustered into groups of HGRs that all implicated the same gene structure (most often representing groups of essentially orthologous proteins).
5. For each cluster of HGRs, the protein showing the most sequence similarity to the genome was passed to both FGENESH and GENEWISE to produce 2 gene predictions, if the protein had >80% amino acid identity to the translated genome (cumulative across sub-alignments).
6. If the protein used in the previous had >90% amino acid identity to the translated genome (cumulative across sub-alignments), then the GENEWISE call, if valid, was favored over the FGENESH+ call, and was used as the EVIDENCE_GENE for the HGR (see below for the reason why) and added to the set of EVIDENCE_GENES. If this protein had >80% but less than 90% amino acid identity to the translated genome (cumulative across

sub-alignments), then the FGENESH+ call, if valid, was favored over the GENEWISE call, and was used as the EVIDENCE_GENE for the HGR and added to the set of EVIDENCE_GENES.

7. When EVIDENCE_GENES overlapped in their exons, the EVIDENCE_GENE with the least amount of homology support (as measured by the sequence similarity of the protein used to make the call or zero for FGENESH calls) was removed from the set of EVIDENCE_GENES.
8. All remaining EVIDENCE_GENES were then called as our official ANNOTATED_GENES and passed to the next step of gene calling for Gene Naming.

Additional information is available
http://www.broad.mit.edu/annotation/fungi/aspergillus/gene_finding.html

§S10.2. Accuracy Estimation

The accuracy of our gene prediction protocol was assessed by comparing predicted to overlapping EST alignments (aligned using est2genome). Alignments of individual ESTs were grouped into *EST clusters* corresponding to sets of ESTs predicting the identical gene structure at a particular locus.

Table §S10.1 – Estimated Gene Prediction Accuracy

Category	Number	Percentage
Genes	9541	
EST Clusters		
EST Clusters Not Overlapping Genes	946	20%
Genes Overlapping EST Clusters	3143	33%
Genes w/No Discrepancies Relative to EST Alignments	2183	69%
Genes hitting multiple EST clusters	563	
Genes w/Discrepancies		
Genes w/Missing Exons	119	4%
Genes w/Wrong Exons	35	1%
Genes w/Splice Junction Difference	907	29%
Nucleotide level statistics relative to EST alignments (Burset and Guigo 1996)		
AC (Approximate Correlation)	0.76	
ACP (Average Conditional Probability)	0.88	
CC (Correlation Coefficient)	0.76	
Sensitivity	0.94	
Specificity	0.98	

§S11 Genes Implicated In Sexual Reproduction in Fungi

Table §S11.1 provides a list of 215 genes that are implicated in sexual reproduction in fungi. In all cases, if a gene is present in A. nidulans, it is present in all three fungi.

Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
Mating Process				
MAT1 (matB)	Mating-type (alpha-box domain transcriptional activator)	AN2755.2	-	20164.m00251*
MAT2 (matA)	Mating-type (HMG-box transcriptional activator)	AN4734.2	59.m09249	-
ppgA (MFa1, MFa2)	Pheromone precursor (alpha-factor like)	AN5791.2	69.m14805	20086.m00080*
ppgB (MFa1, MFa2)	Pheromone precursor (for a-factor like)	Ambiguous	Ambiguous	Ambiguous
(KEX1)	Carboxypeptidase alpha-factor processing	AN1384.2	70.m14837	20080.m00038*
KexB (KEX2)	Endoprotease for alpha-factor processing	AN3583.2	58.m07381	20179.m00626
(STE13)	Dipeptidyl aminopeptidase alpha-factor processing	AN2946.2	59.m09093	20174.m00466*
(STE23)	Dipeptidyl aminopeptidase for a-factor processing	AN8044.2*	53.m03900*	20129.m0021*
(RCE1)	CAAX prenyl protease a-factor C-terminal processing	AN6528.2	62.m03116	20107.m00091*
(STE24)	CAAX prenyl protease	Yes**	58.m07859	20142.m00264*
(RAM1/STE16)	CAAX-farnesyltransferase beta subunit; a-factor modification	AN2002.2	58.m07610	20138.m00208*
(RAM2)	CAAX-farnesyltransferase alpha subunit	AN3867.2	58.m07839	20142.m00239*
(STE14)	CAAX-prenyl cysteine carboxymethyltransferase	AN6162.2	72.m19009	20177.m00422*
atrD (STE6)	ATP-dependent efflux pump for a-factor like pheromone	AN2300.2	58.m08958	20136.m00137*
Mating Signalling				
preB (STE 2)	Pheromone Receptor (for alpha-factor like pheromone)	AN2520.2	59.m08468	20123.m00180*
preA (STE 3)	Pheromone Receptor (for a-factor like pheromone)	AN7743.2	71.m15771	20162.m00356*
fadA (GPA1)	Alpha-subunit G protein	AN0651.2	70.m15256	20180.m01174
sfaD (STE 4)	Beta-subunit G protein	AN0081.2	71.m15359	20148.m002796*
(STE5)	Scaffold protein	-	-	-
(STE18)	Gamma-subunit G protein	AN2742.2 *	54.m06689	20175.m00541*
(STE20)	Serine/threonine protein kinase MKKKK	AN2067.2*	57.m05766	20178.m00629*
steC (STE11)	Serine/threonine protein kinase MKKK	AN2269.2	71.m15914	20132.m00123*
(STE7)	Serine/threonine protein kinase MKK	AN3422.2*	59.m09275	20164.m00222*
mpkB (FUS3)	Mitogen-activated protein kinase	AN3719.2	69.m15727	20178.m00764*
steA (Ste12)	Transcriptional Activator. Homeodomain DNA binding	AN2290.2	71.m15938*	20132.m00151*
(FAR1)	Cell cycle arrest in G1/various other roles	-	-	-
(STE50)	Pheromone adaptation feedback response	AN7252.2 *	72.m19797	20134.m00115*
(DIG1/RST1)	Transcription factor, interacts ste12 pheromone response	-	-	-
(DIG2/RST2)	Transcription factor, interacts ste12 pheromone response	-	-	-

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Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
Fruiting Body Development				
veA	Velvet activator induces sexual reproduction *A.nidulans*	AN1052.2	70.m15191*	20173.m00346*
NsdD	GATA-transcription factor	AN3152.2	59.m08512*	20010.m00003*
CsnD	Signalosome subunit 4, regulation of sexual development	AN1539.2	55.m03058*	20171.m00527*
CsnE	Signalosome subunit 5, regulation of sexual development	AN2129.2	72.m19712*	20115.m00100*
rosA	Binuclear zinc transcription factor	AN5170.2	69.m14866	20084.m00028
mutA	Mutanase, cell wall turnover during sexual development	AN7349.2	57.m05694*	20150.m00367*
stuA	APSES-transcription factor	AN5836.2	72.m19916*	20177.m00377*
medA	Transcription factor	AN6230.2	72.m19977*	20141.m00193*
prot1[††]	Cys6-Zn2 transcriptional activator	AN1848.2*	58.m07662*	20129.m00151*
Nc mat A-2	mating type TF; conserved amphipathic helix	No	No	No
Nc mat A-3	mating type HMG box TF	No	No	No
Nc asd-1	ascus development; rhamnogalacuronase B	AN7135.2	89.m02015	20153.m00219
Nc asd-4	ascus development; GATA-Zn finger transcription factor	areB	72.m19434	20141.m00163
Nc mei-3 (Sc RAD52)	meiosis defective;	uvsC	uvsC	uvsC
Um rum1	repressor of b mating type regulated genes	AN8211.2	53.m03763	20147.m00252
Um umc1	MADS-box TF, modulator of pheromone-inducible gene expression	AN8676.2	62.m03394	20152.m00250
Pa cro1 (Sc SHE4)	regulator of myosin function;required for syncytial to cellular transition	AN0135.2	71.m15419	20158.m00313
Budding and Fisson Yeast Genes involved in Mating, Karyogamy and Meiosis				
Sc BIM1	microtubule-binding protein	AN2862.2	59.m08708	20175.m00472
Sc BNI1	formin	AN6523.2	62.m03112	20107.m00085
Sc CDC31	spindle pole body component	AN5618.2*	58.m07543*	20138.m00126*
Sc CSM1	mediates accurate chromosome segregation during Meiosis I	No	No	No
Sc CSM3	mediates accurate chromosome segregation during meiosis	No	No	No
Sc DIT1	sporulation-specific enzyme required for spore wall maturation	AN2705.2	67.m02885	20137.m00125
Sc HO	endonuclease, mating type switching	No	No	No
Sc IDS2	modulator of Ime2 activity	No	No	No
Sc IME1	master transcriptional regulator of meiosis	No	No	No
Sc IME2	inducer of meiosis, S/T kinase	AN6243.2	72.m19414	20141.m00207
Sc IME4	mRNA N6-adenosine methyltransferase, IME1 regulation	No	No	No
Sc KAR1	required for karyogamy	No	No	No
Sc KAR3	kinesin-like motor required for karyogamy	AN6340.2	72.m19518	20135.m00123
Sc KAR4	TF required for mating and meiosis	No	No	No

§S11 Genes Implicated In Sexual Reproduction in Fungi

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Gene	**Function**	***A.nidulans***	***A.fumigatus***	***A.oryzae***
Sc KAR5	nuclear membrane fusion during karyogamy	ambiguous	ambiguous	No
Sc KAR9	cytoplasmic microtubule orientation during karyogamy	No	No	No
Sc MUM2	essential for meiotic DNA replication	No	No	No
Sc MUS81	Holliday junction resolvase	AN3118.2	59.m08619	20140.m00135
Sc NAM8/MRE2	RNA binding protein required for meiotic recombination	AN9090.2	66.m04770	20169.m00407
Sc NDT80	meiosis-specific transcriptional activator	AN6015.2*	72.m19128*	20177.m00637*
Sc REC102	chromosome synapsis during meiotic recombination	No	No	No
Sc RIM4	RNA-binding protein, early and middle sporulation gene expression	No	No	No
Sc RME1	Zn finger transcriptonal repressor of IME1	No	No	No
Sc STE6	ABC transporter required fo a-factor transport	AN2300.2	58.m08958	20136.m00137
Sc SPO1	meiosis-specific phospholipase B	No	No	No
Sc SPO11	required for synaptonemal complex formation	AN8259.2	53.m03702	20147.m00194
Sc SPO13	meiosis specific protein required for Meiosis I and II	No	No	No
Sc SST2	RGS protein, regulates desensitization to alpha-factor	flbA	72.m19237	20082.m00044
Sc SPO22	meiosis-specific phospholipase A2	No	No	No
Sc SUM1	transcriptional repressor of middle sporulation-specific genes	No	No	No
Sc UME3/SSN8	C-type cyclin	AN2172.2	72.m19668	20180.m00841
Sc UME6	C6 Zn finger regulator of early meiotic genes	No	No	No
Sp atf21	bZip TF, involved in regulation of meiosis	AN6849.2*	59.m09396*	20175.m00406*
Sp bgs1	1,3-beta-glucan synthase subunit, Sp Mei4 target gene	AN3729.2	69.m15386	20179.m00743
Sp byr1	homologue of Sc STE7			
Sp byr2	homolouge of Sc STE11			
Sp dhc1	dynein heavy chain, homologue of Sc DYN1	nudA	71.m15397	10004.m0006
Sp fus1	homologue of Sc BNI1			
Sp gpa1	GTP binding (alpha-1 subunit) involved in conjugation	AN3090.2	59.m08656	20171.m00394
Sp hsk1	homologue of Sc CDC7, Dbf4-dependent kinase	AN3450.2	59.m09313	20102.m00075
Sp isp5	amino acid permease involved in sexual differentiation	AN5678.2	65.m07404	20146.m00246
Sp isp6	serine protease involved in sexual differentiation	AN0238.2	71.m15644	20121.m00147
Sp lid2	homologue of Um rum1, Sc ECM5			
Sp ume3	homologue of Sc UME3			
Sp mam1	abc transporter for m-factor pheromone, homologue of Sc STE6			
Sp mam2	pheromone p-factor receptor, homologue of Sc STE2			
Sp mam4	M-factor farnesyl cysteine carboxyl methyltransferase	AN6162.2	72.m19009	20177.m00422
Sp map1	MADS-box domain TF, pheromone receptor activator	AN8676.2*	62.m03394*	20152.m00250*

§S11 Genes Implicated In Sexual Reproduction in Fungi

Table §S11.1 provides a list of 215 genes that are implicated in sexual reproduction in fungi. In all cases, if a gene is present in A. nidulans, it is present in all three fungi.

Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
Sp map2	P-factor pheromone	No	No	No
Sp map3	pheromone M-factor receptor, homologue of Sc STE3			
Sp mat1-Mc	mating-type M-specific polypeptide Mc, HMG-box TF	AN1962.2*	58.m09001*	20138.m00150*
Sp mat1-Mi	mating-type M-specific polypeptide Mi	No	No	No
Sp mat1-Pc	mating-type P-specific polypeptide Pc, HMG-box TF	No	No	No
Sp mat1-Pi	mating-type P-specific polypeptide Pi, homeodomain TF	No	No	No
Sp mde3	homologue of Sc IME2, Sp Mei4 target gene	AN6243.2	72.m19414	20141.m00207
Sp mde5	kelch repeat protein, Sp Mei4 target gene	No	No	No
Sp mde6	ketch repeat protein, Sp Mei4 target gene	No	No	No
Sp mde7	RNA-binding protein involved in meiosis, Sp Mei4 target	AN7700.2	71.m15729	20162.m00295
Sp mfm1,mfm2,mfm3	M-factor pheromone precursor	No	No	No
Sp mei2	RNA-binding protein involved in meiosis	AN6494.2*	62.m03081*	20059.m00031*
Sp mei3	meiosis inducing protein, inactivates Sp Ran1	No	No	No
Sp mei4	fork head domain TF, meiotic regulator	AN8858.2*	71.m15996*	20108.m00079*
Sp mes1	meiosis II protein, Sp Mei4 target gene	No	No	No
Sp meu1	Sp Mei4 target gene	apsB	62.m03168	20174.m00436
Sp meu14	involved in Meiosis II nuclear division, Sp Mei4 target gene	AN3931.2	69.m14916	20174.m00532
Sp mus81	homologue of Sc MUS81			
Sp pkl1	homologue of Sc KAR3			
Sp rad22	DNA repair protein	radC	58.m08972	20110.m00135
Sp ran1/pat1	serine/threonine protein kinase, negative regulator of meiosis	AN4935.2	59.m08839	20175.m00321
Sp rec6	meiotic recombination protein	No	No	No
Sp rec8	cohesin complex (meiotic), homologue of Sc REC8	No	No	No
Sp rec10	sister chromatid cohesion	No	No	No
Sp rec11	sister chromatid cohesion	No	No	No
Sp rec12	homologue of Sc SPO11			
Sp rec15	meiotic recombination protein	No	No	No
Sp rem1	meiotic B-type cyclin	AN2137.2	72.m19703	20180.m00780
Sp rep1	regulator of pre-meiotic DNA replication	No	No	No
Sp rgs1	homologue of Sc SST2			
Sp rhp51	homologue of Sc RAD51//52, Nc mei-3	uvsC	uvsC	uvsC
Sp spk1	homologue of Sc FUS3	mpkB	69.m15727	20178.m00764
Sp spo6	homologue of Sc DBF4, required for orign of replication firing	nimO	69.m15647	20161.m00192
Sp ssm4	dynactin complex, homologue of Sc NIP100	AN6323.2	72.m19441	20141.m00154
Sp ste4	SAM domain, similar to Sc STE50	AN7252.2	72.m19797	20134.m00115

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Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
Sp ste6	GEF involved in conjugation; related to Sc CDC25	AN2130.2	72.m19711	20115.m00099
Sp ste7	meiotic suppressor protein	No	No	No
Sp ste11	HMG-box TF, target of pheromone signaling	AN3667.2*	58.m07428*	20179.m00464*
Sp spn5	septin, Sp Mei4 target gene	sepB	65.m07502	20176.m00407
Sp spn7	septin, Sp Mei4 target gene	AN4667.2	71.m15708	20176.m00407
Sp sxa2	serine carboxypeptidase, degrades extracellular P-factor	AN2555.2	57.m05650	20156.m00343
Sp tht1	homologue of Sc KAR5			

Core Meiotic Transcriptome Conserved in S. *cerevisiae* and *S. pombe*

Anaphase-promoting complex				
Sc CDC27/ Sp nuc2	APC component	bimA	72.m19026	20177.m00440
Sc APC4/ Sp cut20	APC component	AN0905.2	70.m15514	ambiguous
Sc CDC16/ Sp cut9	APC component	AN8002.2	53.m03844	20159.m00191
Sc APC1/ Sp cut4	APC component	AN2772.2	59.m09271	20164.m00226
Sc APC5/ Sp apc5	APC component	AN4735.2	59.m09246	20164.m00254
Sc CDC23/ Sp cut23	APC component	AN8013.2	53.m03861	20159.m00208
Sc CDC26/ Sp hcn1	APC component	No	No	No
Sc HCT1/ Sp ste9	APC regulator	AN2965.2	59.m09050	20174.m00432
Sc CDC20/ Sp mfr1	APC regulator	AN2965.2	59.m09050	20174.m00432
Sc AMA1/ Sp slp1	APC regulator	AN0814.2	70.m15414	20125.m00181
Septins				
Sc CDC10/ Sp spn2	septin	AN1394.2	70.m14828	20070.m00026
Sc CDC3/ Sp spn5	septin	sepB	65.m07502	20176.m00407
Sc SPR3/ Sp spn6	sporulation regulated septin	AN8182.2	53.m03797	20147.m00293
Sc SPR28/ Sp spn7	sporulation regulated septin	AN4667.2	71.m15708	20148.m00144
Cell cycle regulators				
Sc CDC14/ Sp clp1	protein phosphatase	AN5057.2	59.m08669	20175.m00513
Sc CDC5/ Sp plo1	polo kinase	AN1560.2	55.m03076	20176.m00605
Sc CLB1/ Sp cig2	B-type cyclin	nimE	58.m07451	20165.m00281
Sc CLB3/ Sp cdc13	B-type cyclin	AN2137.2	72.m19703	20180.m00780
Sc CLB4/ Sp cig1	B-type cyclin			
Sc CLB5	B-type cyclin			
Sc CLB6	B-type cyclin			
Recombination/chromosome cohesion				
Sc REC114/ Sp rec7	meiotic recombination protein	No	No	No

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Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
Sc DMC1/ Sp dmc1	DNA-binding helix-hairpin-helix protein, DNA strand exchange	AN9092.2	66.m04768	20169.m00401
Sc MND1/ Sp mcp7	recombinatino and meioic nuclear division, interacts with Hop2	AN1843.2	58.m07668	20129.m00169
Sc HOP2/ Sp meu13	prevents synapsis between nonhomologous chromosomes	No	No	No
Sc SMC3/ Sp smc3	cohesin	AN6364.2	72.m19496	20116.m00127
Sc REC8/ Sp rec8	cohesin complex (meiotic)	No	No	No
Chromosome segregation				
Sc STU1/ Sp dis1	spindle pole body component	AN5521.2	69.m15719	20178.m00784
Sc TID3/ Sp ncd10	chromosome segregation, kinetochore-associated Ndc80 complex	AN4969.2	59.m08873	20125.m00127
Sc UBC11/ Sp ubc11	ubiquitin-conjugating enzyme, chromosome segregation in Sp	AN5495.2	69.m15458	20178.m00805
DNA repair				
Sc RAD23/ Sp rhp23	DNA excision-repair, NEF2 subunit	AN2304.2	71.m15953	20108.m00125
Sc EXO1/ Sp exo1	DNA repair, recombination	AN3035.2	59.m08982	20174.m00347
Sc HRR25/ Sp hhp1	casein kinase involved in DNA repair and chromsome segregation	AN4563.2	57.m05554	20158.m00387
Other genes in the conserved meiotic core program				
Sc HUL4/ SPBP87.27	hect domain E3 ubiquitin-protein ligase	AN0444.2	54.m06635	20175.m00618
Sc LEE1/ Sp scp3	Zn finger transcription factor, unknown function	AN3447.2	59.m09478	20102.m00073
Sc ENA2/ Sp cta3	P-type ATPase sodium pump	AN6642.2, AN1628.2	62.m03239, 58.m07687	20132.m00104, 20136.m00211
Sc PMC1/ SPBC839.06	vacuolar ATPase Ca2+ pump	AN1189.2	70.m15033	20168.m00440
Sc CMK2/ Sp cmk1	calmodulin-dependent protein kinase	AN3065.2, AN2412.2	59.m08933, 72.m19463	20174.m00277, 20073.m00030
Sc CHS1/ Sp chs1	chitin synthase, pheromone inducible	AN4566.2	57.m05488	20153.m00320
Sc ISA1/ SPCC645.03C	mitochondrial matrix protein, iron metabolism	AN1974.2	58.m07579	20138.m00166
Sc HTZ1/ Sp pht1	histone H2AZ varient	AN8039.2	53.m03907	20167.m00250
Sc AUT7/ SPBP8B7.24C	required for autophagic vesicle delivery to vacuole in Sc	AN5131.2	54.m06897	20128.m00130
Sc BAG7/ SPBC557.01	Rho-GAP	AN7650.2	57.m05408	20105.m00070
Sc ROM2/ SPAC1006.06	Rho-GEF	AN4719.2	71.m15707	10080.m00170
Sc RAS2/ Sp ras1	Ras	AN0182.2	71.m16065	20158.m00254
Sc GNA1/ Sp gna1	glucosamine acetyl transferase involved in cell cycle progression	AN8706.2	62.m03363	20152.m00287
Sc SGA1/ Sp meu17	sporulation-specific glucosamylase, Sp Mei4 target gene	AN8904.2	57.m05372	20130.m00115, 20178.m00683
Sc CLG1/ SPBC1D7.03	cyclin-like protein interacts with Sc Pho85	AN4984.2	59.m08886	20125.m00144
Sc CYB2/ SPAB1A11.03	cytochrome-c oxidoreductase	AN3901.2	89.m01949|	20115.m00086
Sc ECM4/ SPCC1281.07C	glutathione-S-transferase domain, unknown function	AN5831.2	72.m19666	20097.m00066
Sc TOS7/ SPCC1739.10	unknown function in yeasts, putative membrane component of	palI	59.m09122	20164.m00305

§S11 Genes Implicated In Sexual Reproduction in Fungi

Table §S11.1 provides a list of 215 genes that are implicated in sexual reproduction in fungi. In all cases, if a gene is present in A. nidulans, it is present in all three fungi.

Gene	Function	*A.nidulans*	*A.fumigatus*	*A.oryzae*
	signal transduction pathways for pH regulation in *A. nidulans*			
Sc ARN2/ SPCC61.01C	ARN family of transporters for siderophore-iron chelates	AN5378.2	65.m07225	20176.m00502
Sc GTT1/ SPAC688.04C	ER associated glutathione S-transferase	AN0629.2	70.m15652	20155.m00295
Sc RIB5/ SPCC1450.13C	riboflavin synthase, alpha subunit	AN4231.2	54.m06785	20071.m00045
Sc CHO1/ SPCC1442.12	phosphatidylserine synthase	AN5661.2	58.m08891	20179.m00714
Sc XKS1/ SPCPJ732.02C	xyulose kinase	AN8790.2	71.m15584	20113.m00155
Sc PCT1/ SPCC1827.02C	CTP:phosphocholine cytidylyltransferase	AN1357.2	70.m14873	20074.m00033
Sc ELC1/ SPBC1861.07	transcription elongation factor	No	69.m15210	20101.m00073
Sc SYF2/ SPBC3E7.13C	splicesome component	AN1861.2	58.m07654	20129.m00143
Sc PGM2/ SPBC32F12.10	phosphoglucomutase	AN2867.2	59.m08711	20175.m00469
Sc RKI1/ Sp ppi	ribose-5-phosphate isomerase	AN2440.2	69.m15218	20101.m00084
Sc SUR4/ SPAC1B2.03C	long chain fatty acid elongation enzyme	AN8117.2	53.m03827	20159.m00172
Sc PIB1/ SPBC36B7.05C	RING-type ubiquitin ligase, FYVE finger domain	AN0627.2*	70.m15658*	20174.m00539*, 20093.m00096*
Sc PIN3/ Sp csh3	SH3-domain protein	AN2995.2	59.m09437	20174.m00392
Sc SSO2/ Sp sso1	syntaxin	AN3416.2	66.m04618	20041.m00017
Sc FBP1/ Sp fbp1	fructose-1,6-biphosphatase	AN5604.2	58.m07528	20138.m00109
Sc GLG1/ SPBC4C3.08	self-glucosylating initiator of glycogen synthesis	AN4082.2	54.m06723	No
Sc ARE2/ SPAC13G7.05	acyl-CoA:sterol acyltransferase	AN4208.2	54.m06767	20068.m00041
Sc GDI1/ Sp gdi1	secretory pathway regulator	AN5895.2	72.m19235	20082.m00039
Sc PDC1/ SPAC3H8.01	pyruvate decarboxylase	AN4888.2	59.m08784	20175.m00382
Sc OXR1/ SPAC8C9.16C	unknown function	AN3004.2	59.m09010	20174.m00378
Sc KGD1// SPBC3H7.03C	mitochondrial alpha-ketoglutarate dehydrogenase complex	AN5571.2	58.m07497	20165.m00219
Sc DAP1/ SPAC26H5.15	Sc damage response, related to mammalian membrane progesterone	AN4939.2	59.m08843	20175.m00316

* homology limited to functional domain
**present but missing in official annotation
Sc=Saccharomycese cerevisiae; Sp=Schizosaccharomyces pombe; Nc=Neurospora crassa; Um=Ustilago maydis; Pa=Podospora anserina

§S12. Two Predicted TPP Riboswitches

Based on conservation, we identified three TPP binding riboswitches[1], one of which has not been described in Aspergillus. Riboswitches are regulatory elements found in untranslated regions of mRNA which fold to bind target metabolites leading to altered gene expression[1-3]. A TPP riboswitch, which binds thiamin pyrophosphate and regulates genes involved in thiamine biosynthesis, was previously identified in the 5' UTR of the *A. oryzae thi4*[1]. We find this element conserved upstream of thi4 in *A. fumigatus* and *A. nidulans*. We also find an element recently shown to be present upstream of orthologous NMT1 thiamine biosynthesis genes (AN8009, 53.m03858, AO70322000058)[4], corresponding to the known *N. crassa* NMT1 riboswitch[1]. A third element was found conserved upstream of orthologous purine-cytosine permease genes (AN4526, 53.m05980, AO70321000134). This element has not been previously characterized in any organism, although evidence linking purine influx to thiamine biosynthesis has been reported[5,6].

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§S13 Aspergillus nidulans Comparative Map