Functional and evolutionary analysis of the CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN family

Running title: CASP-likes conservation in plants

Daniele Roppolo[1,5,]*, Brigitte Boeckmann[2], Alexandre Pfister[1], Emmanuel Boutet[2], Maria C. Rubio[1,3], Valérie Dénervaud-Tendon[1], Joop E. M. Vermeer[1], Jacqueline Gheyselinck[5], Ioannis Xenarios[2,4], Niko Geldner[1]

[1]Department of Plant Molecular Biology, University of Lausanne, Quartier Sorge, Lausanne, 1015, Switzerland

[2]Swiss Institute of Bioinformatics, Centre Médical Universitaire, 1211 Geneva 4, Switzerland

[3]Departamento de Nutrición Vegetal, Estación Experimental de Aula Dei, Consejo Superior de Investigaciones Científicas (CSIC), Apdo 13034, 50080 Zaragoza, Spain

[4]Vital-IT Group and University of Lausanne, Quartier Sorge, Bâtiment Génopode, 1015 Lausanne, Switzerland

[5]Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, Switzerland

Summary

How do local modifications of the cell wall take place? How is the plasma membrane organized to direct such modifications? The CASPL family described here is a genuine entry point to answer those questions.

Running head: CASP-like evolution

Corresponding author:

Daniele Roppolo
Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, Switzerland;
Telephone: +41 (0) 31 631 49 52; Email: daniele.roppolo@ips.unibe.ch

Research Areas:

Genes, Development and Evolution (primary)

Cell Biology (secondary)

DR and NG received funding from the Swiss National Science Foundation. NG received funding from the European Research Council.

ABSTRACT

CASPARIAN STRIP MEMBRANE DOMAIN PROTEINS (CASPs) are four-membrane-span proteins that mediate deposition of Casparian strips in the endodermis by recruiting the lignin polymerization machinery. CASPs show high stability in their membrane domain, which presents all landmarks of a membrane scaffold. Here, we characterize the large family of CASP-like (CASPL) proteins. CASPLs are present in all major divisions of land plants as well as in green algae. We show that CASPLs are able to integrate the CASP membrane domain when ectopically expressed in the endodermis, which suggests that CASPLs share with CASPs the propensity to form transmembrane scaffolds. A detailed mutagenesis analysis of CASP1 suggests that the propensity to form membrane scaffold is mediated by transmembrane domains. When we extended our phylogenetic analysis outside of the plant kingdom focusing on conservation in transmembrane domains, we identified CASPLs as homologous to MARVELs, some of which form membrane scaffolds. We show in *Arabidopsis thaliana* that CASPLs are expressed in a variety of tissues, where they may form membrane scaffold and direct local modification of the cell wall. Moreover, we identified the CASP first extracellular loop as a potential signature for Casparian strips: proteins carrying this signature are absent in plants lacking Casparian strips, an observation that may contribute to the study of root evolution.

INTRODUCTION

Biological membranes are conceptually simple structures that may be generated *in vitro* according to simple physicochemical principles. *In vivo*, however, membranes are highly complex and host a plethora of proteins that mediate transfer of molecules and communication across the membrane. Proteins may be trapped in membrane by their transmembrane domains, anchored by lipid tails or attach to membrane-integral proteins. A further level of complexity is seen when membrane proteins are not equally distributed, but occupy only a limited fraction of the available surface, i.e. they are polarly localized or they form small membrane subdomains in the micron range. The question of how membrane proteins are retained locally and prevented from diffusing freely is of high importance to cell biology. Polarly localized proteins may be retained in their respective domains by membrane fences; in such a situation, polarly localized proteins are mobile in their domains, but cannot diffuse through the tightly-packed scaffold proteins forming a molecular fence within the membrane. Membrane fences delimiting polar domains have been described in different organisms. For example, diffusion between membrane compartments is prevented in budding yeast at the level of the bud neck (Barral et al., 2000; Takizawa et al., 2000); in ciliated vertebrate cells, between ciliary and periciliary membranes (Hu et al., 2010); in epithelial cells, between apical and basolateral membranes (van Meer and Simons, 1986); in neurons, between axon and soma (Kobayashi et al., 1992; Winckler et al., 1999; Nakada et al., 2003); in spermatozoa, at the level of the annulus (Myles et al., 1984; Nehme et al., 1993). The existence of membrane scaffolds that prevent free protein diffusion has also been described in bacteria (Baldi and Barral, 2012; Schlimpert et al., 2012). In plants, we have shown the existence of a strict membrane fence in the root endodermis, where a median domain splits the cell in two lateral halves occupied by different sets of proteins (Alassimone et al., 2010). The situation in the plant endodermis is analogous to the separation of animal epithelia into apical and basolateral domains, and indeed a parallel between epithelia and endodermal cells has been drawn, despite the different origin of multicellularity in plants and animals (Grebe, 2011).

Protein complexes responsible for the formation of membrane fences have been identified. Septins are a family of proteins able to oligomerize and form filaments (Saarikangas and Barral, 2011); their role in the formation of membrane fences has been demonstrated in several organisms and cellular situations, including the yeast bud neck (Barral et al., 2000; Takizawa et al., 2000), animal cilia (Hu et al., 2010), mammalian spermatozoa (Ihara et al., 2005; Kissel et al., 2005; Kwitny et al., 2010). At the axonal initial segment of neurons, AnkyrinG is necessary to establish and maintain a membrane scaffold where different membrane proteins are immobilised and stabilised (Hedstrom et al., 2008; Sobotzik et al., 2009). In *Caulobacter crescentus*, the stalk proteins Stp form a complex that prevents diffusion between cell body and stalk, and in-between stalk compartments. Claudin and occludin are the main components of epithelial tight junctions (Furuse et al., 1993; Furuse et al., 1998). Occludins are four-membrane-span proteins and belong to the MARVEL protein family (Sánchez-Pulido et al., 2002), as do Tricellulin and MARVELD3 that are also tight-junction associated proteins (Furuse et al., 1993; Ikenouchi et al., 2005; Steed et al., 2009).

In contrast to the above-mentioned organisms, proteins defining membrane fences had long not been reported in plants. We have identified in A*rabidopsis thaliana* a family of membrane-span proteins that are exclusively expressed in the endodermis and that define the first reported membrane fence in plants (Roppolo et al., 2011). These CASPARIAN STRIP MEMBRANE DOMAIN PROTEINS (CASP1 to 5) are four-transmembrane proteins that localize at the root-shoot equatorial plane, splitting *de facto* the plasma membrane in two lateral domains and forming a median domain referred to as the Casparian strip membrane domain (CSD). CASPs initially localize all around the plasma membrane, then are quickly removed from lateral plasma membranes and remain localized exclusively at the CSD; here they show an extremely low turn-over, though they are eventually removed (Roppolo et al., 2011). The membrane proteins NIP5;1 and BOR1 are restricted from diffusing through the CSD and remain polarly localized in the outer and inner lateral membranes, respectively; a fluorescent lipophilic molecule, when integrated in the outer endodermal membrane is blocked at the level of the CSD and cannot diffuse into the inner membrane. Besides making a plasma membrane diffusion barrier, CASPs have an important role in directing the modification of the cell wall juxtaposing their membrane domain: by interacting with secreted peroxidases, they mediate the deposition of lignin and the building up of the Casparian strips (Roppolo et al., 2011; Naseer et al., 2012; Lee et al., 2013). The two CASPs activities - making membrane scaffolds and modification of the cell-wall - can be uncoupled: formation of the CASP domain is independent from the deposition of lignin, and interaction with peroxidases occurs outside the CSD when CASPs are ectopically expressed (Lee et al., 2013).

As CASPs are currently the only known proteins forming membrane fences in plants and because of their essential role in directing a local cell wall modification, we were interested in characterizing the repertoire of CASP-likes (CASPLs) in the plant kingdom. Our aim was to provide a molecular basis for the discovery of additional membrane domains in plants as well as to identify molecular players potentially involved in the modification of the cell wall. We extended our phylogenetic analysis outside of the plant kingdom and found conservation between CASPLs and the MARVEL protein family. Conserved residues are located in the transmembrane domains and we provide evidence suggesting that these domains may mediate CASP localization. We explore the potential use of the CASPL module in plants by investigating *CASPL* expression patterns and their ability to form membrane domains. Moreover, we related the appearance of the Casparian strips in the plant kingdom with the emergence of a CASP-specific signature that is not found in the genomes of plants lacking Casparian strips.

RESULTS

CASP-likes belong to the MARVEL protein family

In the attempt to understand the evolutionary history of the CASPs, we analysed sequenced plant genomes and EST databases for their repertoire of CASP homologs, that we termed CASP-likes (CASPLs). All in all, we annotated over 350 proteins from more than 50 plant species. *Arabidopsis thaliana* CASPs, AtCASPs, have four predicted transmembrane domains, with cytoplasmic N- and C-termini, variable N-terminus length, short C-terminus and short intracellular loop. Homologous plant proteins are conserved in the transmembrane domains (TMs), particularly the first (TM1) and the third (TM3): an arginine in TM1 and an aspartate in TM3 are present in the vast majority of CASPLs (Figure 1A; Supplemental Figure 1). Six proteins with sequence similarity were identified in green algae – *Chlorokybus atmophyticus* (Charophyte), *Ostreococcus tauri*, *Ostreococcus lucimarinus* and *Micromonas pusilla* (Chlorophyte) and Micromonas sp. (strain RCC299 / NOUM17) (Supplemental Table 3). Interestingly, *Chlorokybus* and *Micromonas* CASPLs are annotated in UniProtKB as carrying a MARVEL-like domain (IPR021128). Proteins carrying a MARVEL domain show high similarity in their transmembrane domains, but not necessarily in their extra- or intracellular exposed regions (Sánchez-Pulido et al., 2002). Conserved basic (R, H, K) and acidic (D, E) amino acids are present in TM1 and TM3 of MARVELs from stramenopiles and fungi, a situation that very much resembles conservation in TMs among CASPLs. CASPLs and MARVELs are predicted with high probability to be members of both families (Figure 1B; Supplemental Table 1), indicating that CASPL and MARVEL domains are likely to be homologous. Noticeable is furthermore the almost complementary taxonomic distribution of species with predicted CASPL (DUF588, PF04535) or MARVEL (PF01284) domains in opisthokonts and plants (Figure 1C; Supplemental Table 2), which led to the assumption that CASPLs could be the plant orthologs of the MARVEL family. Indeed, a reconstruction of the CASPL/MARVEL domain phylogeny places algae at the base of the plant clade when rooting with stramenopiles (Figure 1D; Supplemental Figure 2); however three genes in key positions of the CASPL/MARVEL domain phylogeny challenge this hypothesis by taking no stable position in the obtained trees (Figures 1D, 1E; Supplemental Figures 2-4). Thus, an origin of CASPLs by speciation seems as likely as an origin by gene duplication ancestral to the divergence of plants and animals.

Based on stable clades of the inferred gene phylogenies we classified the CASPL family into five groups, which all contain homologs from bryophytes, lycophytes or pteridophytes in addition to members from euphyllophytes such as conifers, dicotyledons, monocotyledons (Figure 1D and 1E; Supplemental Figures 3 and 4). Furthermore, subgroups are defined so that potential functionally-related homologs can be easily identified between species (Supplemental Table 3). Only a minor part of predicted proteins could not be stably attributed to any group. Figure 1A illustrates the model of evolution of the CASPL/MARVEL family and visualizes conserved sites within and between the five CASPL groups and MARVEL taxonomic groups. The two conserved charged residues as well as the two cysteines are present in four of the five CASPL subfamilies and MARVEL stramenopiles; members of CASPL group 4 possess a short extracellular loop 2, which lacks the two cysteines. Surprisingly, homologs from chlorophytes possess none of the conserved charged residues. Instead, we identify a glutamate four positions upstream of the conserved acidic amino acid, which is found also in MARVEL stramenopiles, many opisthokonts and in CASPL group 4, suggesting that both acidic residues in TM3 are likely an ancestral characteristic of this family.

Extracellular loops are dispensable for AtCASP1 localization at the CSD

To begin understanding how CASPs get localized, we exploited conservation in the CASPL family to identify potential residues necessary for AtCASP1 localization (Figure 2 and Supplemental Figure 5). We generated 14 AtCASP1-GFP variants, expressed them under the *AtCASP1* promoter, and compared their localization with a wild type AtCASP1-mCherry (Vermeer et al., 2014). Besides the transmembrane domains, conservation in CASPLs is found in the second extracellular loop (EL2). The EL1 is poorly conserved among CASPLs, even inside subgroups; however, AtCASPs present in their EL1 a stretch of 9 residues that is found highly-conserved in all spermatophytes (see below). We decided then to mutagenize residues in TM3 and EL2, and to delete either loop. When we mutagenized the MARVEL/CASPL conserved aspartate residue in TM3 (AtCASP1^{D134H}), we did not recover any lines in which fluorescence was visible, which suggests that this residue is essential for a correct protein folding (Supplemental table 4). In the EL2, mutations of residues conserved only in CASP subgroup (CASPL1A) did not affect the localization of AtCASP1 (A155S, H156D, N163D, Q170E; Supplemental Figure 5); in contrast, mutations in residues shared among most CASPLs affected to different extent AtCASP1 localization. C168S, F174V and C175S persisted longer than AtCASP1-mCherry at the lateral plasma membrane, although they started localizing at the CSD at the same time than wild type; G158S localized normally at the lateral plasma membrane, but its localization at the CSD was strongly delayed and signal there was extremely low (Supplemental Figure 5). W164G showed the strongest effect, being initially excluded from the CSD and almost undetectable later (Figure 2 and Supplemental Figure 5). Despite the fact that mutations in the EL2 affected AtCASP1 localization, when the entire EL2 (Δ158:175) was deleted, AtCASP1 was still able to localize at the CSD, although its signal faded out faster than wild type (Figure 2). Deletions of the EL1 (Δ72:80, Δ73:79, Δ74:78) did not affect localization at the CSD, although a longer persistence at the lateral membranes was observed and the exclusive enrichment at the CSD was delayed compared to AtCASP1-mCherry; the 9 aa deletion (Δ72:80) seemed less stable than wild-type at the CSD (Figure 2). In summary, this analysis shows that AtCASP1 extracellular loops are dispensable for localization at the CSD; single residue substitution in the EL2 affects AtCASP1 localization indicating that those residues contribute to, but are not essential for localization at CSD.

CASPs differ from CASP-like in their first extracellular loop

Although dispensable for the localization at the CSD, the conservation of the EL1 in euphyllophytes suggests a conserved function of this stretch (Figure 3A). To test if CASP homologs containing the EL1 stretch could be potential functional homologs of the AtCASPs, we cloned from *Lotus japonicus* a member of the family containing the 9 aa signature (ESLPFFTQF), and expressed it in Arabidopsis under the control of its own putative promoter. A 2 kb genomic fragment upstream the translational start codon of this Lotus gene was sufficient to drive expression in the endodermis of Arabidopsis roots, showing the ease of predicting potential CASP functional homologs following identity in the first extracellular loop (Figure 3B). A Lotus GFP translation fusion perfectly recapitulated the localization of the endogenous AtCASP1 at the CSD (Figure 3C), and the reporter reflected temporally and spatially the expression of the *AtCASP1* promoter. Therefore, this data suggests that the well-conserved EL1 serves some endodermis-specific function, and that conservation extends to regulatory elements. CASP homologs with this 9 aa signature are absent in *Physcomytrella patens* and *Selaginella moellendorffii* - which have no roots or roots of different evolutionary origin, respectively - while they are present in all roots of Casparian strip-bearing organisms (Raven and Edwards, 2001), for which we could extensively assess the genome (no genomes have been fully sequenced in the Moniliformopses). To extend further the correlation between presence of the CASP EL1 signature and appearance of Casparian strips, we analysed the genome of plants that have acquired parasitic behaviour and show extensively modified root anatomy. *Striga asiatica* is an obligate hemiparasite that does not have functional roots (Westwood et al., 2012); it belongs to the Orobanchaceae, a family of the Lamiales order containing plants that have evolved different parasitic behaviours (Westwood et al., 2010). In *Striga asiatica*, we could identify a single CASP homolog with a perfectly conserved EL1 signature; however, this protein is possibly non-functional, since it encodes a premature stop codon that prevents the complete translation of the fourth transmembrane domain (Sa in Figure 3D). In contrast to *S. asiatica*, we did find a potential functional allele in *Striga hermontica*, another obligate hemiparasite (Sh in Figure 3D). Functional alleles are also found in another member of the Orobanchaceae, *Triphysaria pusilla*, which is however a facultative hemiparasite (Tp in Figure 3D). The *S. asiatica* truncated allele is also found in *Mimulus guttatus*, where however we could identify 5 more potentially functional CASP homologs (Mg in Figure 3D). Mimulus belong to the same order as Striga (Lamiales) but shows normal root and non-parasitic life style. In the Lamiales, a complete loss of the EL1 stretch has happened in the carnivore plant *Utricularia gibba*, whose genome has been recently sequenced (Ibarra-Laclette et al., 2013). In correlation with the lack of true roots in this carnivore plant species, Ibarra-Laclette *et al*. (2013) reported the presence of a single CASP homolog (Ibarra-Laclette et al., 2013). We reassessed the *U. gibba* genome for

CASPLs and compared it to the genome of *M. guttatus*. *U. gibba* and *M. guttatus* genomes contain over 20 CASP homologs (Supplemental table 5); in Mimulus, 6 of them contain the EL1 signature, in 3 members perfectly conserved, in 3 showing a single residue divergence (Figure 3D). In contrast, the closest CASP homolog in Utricularia shows a clear divergence of the entire EL1: only two residues are identical to the AtCASP EL1 stretch (Ug in Figure 3D). The unique absence of conservation of the EL1 stretch in *U. gibba*, *P. patens* and *S. moellendorffii* correlates with the absence of Casparian strips in these species; in the Orobanchaceae with parasitic behaviour, potential CASP pseudogenization has occurred in *S. asiatica*. This correlation supports our hypothesis that the first extracellular loop bears residues necessary for the function of the CASPs in the deposition of the Casparian strips. For this reason, we named "CASP" all the members of the family that carry the AtCASP EL1 signature (E/QTLPPFFTQF, 2 aa substitution accepted, Supplemental Table 3), suggesting that they are functional homologs of the characterized CASPs in *A. thaliana*.

AtCASPLs from all groups localize in the endodermis as AtCASPs

To see if membrane domain formation may be a general feature in the CASPL family, we expressed several AtCASPLs in the endodermis, where they are not endogenously expressed. We evaluated then their ability to localize at the plasma membrane and at the CSD. Twenty-two AtCASPLs and AtCASP1, AtCASP2, AtCASP3, were expressed as N-terminal mCherry fusions under the control of the *AtCASP1* promoter (Supplemetary Table 6). As expected mCherry-AtCASPs localized correctly (Figure 4A). For nine *AtCASPLs*, we could not identify any lines expressing the transgene, or the expression was extremely weak; when expression was detectable, mCherry signal was mainly observed in the vacuole, suggesting that these AtCASPLs were quickly degraded (not shown). Twelve AtCASPLs were able to reach the plasma membrane, and nine of these showed a clear localization at the CSD (Figure 4A). Interestingly, the CSD-localized AtCASPLs represent all CASPL groups, which suggests that the propensity to form membrane domains is broadly conserved in CASPLs. As these CASPLs are not endogenously expressed in the endodermis (Brady et al., 2007; Birnbaum et al., 2008), their localization at the CSD may be caused by self-interaction, interaction with the endogenous AtCASPs, or interaction with other factors that mediate AtCASP localization and also recognize AtCASPLs. Because of the high divergence between CASPL groups, the comparison of the primary sequence of localized and non-localized

CASPLs does not give any useful information (Figure 4B). For example AtCASPL3A1, AtCASPL5A2 and AtCASPL4D1 do not contain in the second extracellular loop the W164 residue that when mutated prevents AtCASP1 localization, although they do localize at the CSD. When we limited the primary sequence analysis to AtCASPLs from group 1, we found two residues that differ between localized and non-localized AtCASPL1 (Figure 4B): localized AtCASPL1s and AtCASPs share the AtCASP1 L140 and F171 residues in TM3 and in EL2, respectively (position 61 and 76 in Figure 1A); AtCASPL1s excluded from the CSD but present at the lateral plasma membrane contain in the corresponding position a I (*vs* AtCASP1 L140; one methyl group missing) and Y (*vs* AtCASP1 F171; one extra hydroxyl group). These data points to a predominant role of TM3 and EL2 in the localization of AtCASPs. In addition, the global analysis presented here shows that CASPLs with very divergent extracellular loops can have similar behaviours in the endodermis.

AtCASPLs are expressed in a tissue-specific manner

AtCASPs are exclusively expressed in the endodermis, where Casparian strips are deposited. To see if other CASPLs have acquired tissue-specific function, we experimentally assessed the expression pattern of some *AtCASPLs* (Figure 5).

The closest CASPs' homolog, *AtCASPL1A1*, is expressed in the root endodermis at a late developmental stage, coinciding with the appearance of metaxylem vessels (Figure 5A). This area of the root is situated at around 25 cells far from the appearance of differentiated xylem vessel cells and Casparian strips. In 10-day-old roots, expression fades out in proximity to the hypocotyl, except in isolated endodermal cells that persist to express *AtCASPL1A1* (Figure 5A''). Expression is also reduced in endodermal cells overlaying lateral root primordia (Figure 5A'). No expression was detected in leaves or in the hypocotyl of 4-day-old seedlings.

In the root, *AtCASPL1D2* is exclusively expressed in the endodermis at a late development stage; no expression was detected in leaves or in the hypocotyl of 4-day-old seedlings. Interestingly and in contrast to *AtCASPL1A1*, *AtCASPL1D2* expression is strongly enhanced in endodermal cells overlaying lateral root primordia (Figure 5B'); when lateral roots have emerged, its expression is seen in a collar of endodermal cells at the base of the emerged root (not shown). *AtCASPL1D2* is also expressed in the floral organ abscission zone in cells that detach along with the shed organs (Figure 5B'' and 5B'''). Apart from *AtCASPL1D2*, *AtCASPL2A2* is reported to be expressed in the floral organ abscission zone (González-Carranza et al., 2012). *AtCASPL5C3* is expressed in the floral organ abscission zone as well, but its early expression in floral buds precedes the activation of the abscission zone and the expression of most of the genes known to be involved in floral organ shedding (Figure 5J). This suggests that AtCASPL5C3 has a different role than AtCASPL1D2 and AtCASPL2A2, and may be involved in the differentiation of precursors into mature abscission zone cells.

AtCASPLs are also found expressed in epidermal tissues. *AtCASPL4D1* is expressed in the root epidermis (Figure 5C); its expression begins in the root maturation zone and quickly declines. Expression was not detected in leaves or in the hypocotyl. *AtCASPL2A1* is by contrast expressed in the lateral root cap; it is also expressed in leaf epidermis (Figure 5D). In leaf, *AtCASPL5B1* is expressed exclusively in hair cells, both in differentiated trichomes and immature cells (Figure 5E). Apart from the above-mentioned *AtCASPLs* in the abscission zone, we have also found in the flower *AtCASPL1F1* expressed in the anther wall (Figure 5F).

We have identified three *AtCASPLs* expressed in the stele of the root. *AtCASPL5B2* is expressed in 4-day-old seedlings exclusively in the root meristematic zone and in young leaves (Figure 5H’ and 5H’’’); in 10-day-old roots expression is also detected in lateral root primordia (Figure 5H’’), and in the stele in proximity to the hypocotyl (not shown). In the strongest line, expression is detected in the stele all along the root. *AtCASPL5B3* is expressed in the root maturation zone (Figure 5I’), and in lateral root primordia (Figure 5I’’’). Longitudinal view and transversal sections show expression in two parallel files that we interpret as xylem pole pericycle cells (Figure 5I’ and 5I’’); this is consistent with later expression in lateral root primordia. We also detected *AtCASPL5B3* expression in leaves in files of cells parallel to the vasculature (Figure 5I’’’’). *AtCASPL1C1* is expressed in the root maturation zone; no expression was detected in leaves or hypocotyl (Figure 5G). This expression pattern is consistent among different transgenic lines, but it is not seen in all root tips. In a 10-day old plant, we could detect *AtCASPL1C1* expression in 5/42 tips of emerged lateral roots, which may reflect a very transient expression.

DISCUSSION

CASPLs are related to MARVEL

We thereby reveal that the MARVEL protein family until present experimentally described only in metazoan is related to plant CASP and their homologs, the CASPLs. Conservation is limited, but strikingly specific, at the level of the transmembrane domains and in the overall tetraspan protein structure; a putative cysteine bridge in the second extracellular loop is often present both in MARVELs and CASPLs. Besides the results presented here, an independent analysis classified CASPLs and MARVELs as members of the clan CL0396 (A. Bateman, PFAM (Bateman et al., 2004). Few MARVELs have been characterized in mammalian cell lines and model animals. Although a general function cannot be ascribed to this group of proteins, some common features emerge upon comparison of the available functional data: 1) MARVELs are integral membrane proteins, found either at the plasma membrane or in vesicle membranes; 2) when overexpressed, they tend to form lamellae in the smooth endoplasmic reticulum; 3) they are associated with membrane fusion events or membrane apposition; 4) they can occupy membrane subdomains. Among the characterized MARVELs are the tight junction-associated proteins Occludin, Tricellulin and MARVELD3 (Furuse et al., 1993; Ikenouchi et al., 2005; Steed et al., 2009); Synaptophysin, the most abundant protein in synaptic vesicle (Jahn et al., 1985; Wiedenmann and Franke, 1985); Singles Bar, necessary for myoblast membrane fusion in *Drosophila melanogaster* (Estrada et al., 2007). In a simple scenario, the last eukaryotic common ancestors possessed the MARVEL 4TM functional skeleton: transmembrane domains would be conserved during evolution, while extracellular loops would rather diverge in different eukaryotic divisions. The conservation in transmembrane domains may be necessary for interactions of CASPL/MARVEL within membranes. Indeed, the site-directed mutagenesis of AtCASP1 and the gene swap analysis presented here show that extracellular loops are dispensable for localization, pointing to a central role of transmembrane regions (note that apart from the N-terminus, which shows no conservation) intracellular regions are extremely short in the CASPL family). CASPL proteins may share the ability to undergo controlled polymerization of their transmembrane domains and thereby drive the formation of membrane scaffold microdomains in a variety of circumstances. Our hypothesis is supported by the few studies concerning the importance of the transmembrane domains of MARVELs: in synaptophysin, loss of the acid residues in TM1 prevents protein accumulation (Leube, 1995); in occludin, the transmembrane domain has been suggested to mediate dimerization (Yaffe et al., 2012); in MAL, the founder member of the family, transmembrane domain deletions prevent plasma membrane localization or formation of a correct microdomain (Magal et al., 2009).

For their expression in typical animal structures (e.g. epithelia, synapses), MARVEL family members have been used to trace the origin of “typical animal” and “typical multicellular” proteins. When the genome of a sponge was released Synaptogyrin, Synaptophysin and Occludin were considered holozoa-, metazoa-, vertebrate-specific, respectively (Srivastava et al., 2010). Our phylogenetic analysis now demonstrates a much more ancient origin of the MARVEL family, although do not challenge the idea that individual members may be associated with the appearance of specific structures.

CASPLs as membrane organizers and/or cell-wall modifiers

CASPs are the earliest known proteins localizing at the CSD and may be necessary for its formation. The ability of CASPLs from all groups to localize at the CSD when expressed in the endodermis supports the existence of a family module and prompts us to predict many yet-undiscovered plasma membrane domains in the formation of which CASPLs would be involved. Our expression analysis shows that *AtCASPLs* are expressed in a tissue-specific manner, which suggests that the CASPL module serves tissue-specific functions. An easy speculation is that CASPLs and CASPs perform similar, but specialized functions, that is 1) generation of membrane scaffolds and/or 2) recruitment of cell-wall modifying enzymes. Polar or local secondary cell wall modifications have been described in most tissues discussed above. For example, in anthers the endothecium cell wall thicken laterally, forming bar-like structures that are enriched in cellulose and lignin (Dawson et al., 1999); polar secretion of cell wall degrading enzyme is expected during abscission (Estornell et al., 2013). CASPLs may be involved in addressing different cell-wall modifying machineries in different tissues as well as in delimiting the region of the plasma membrane where such modifications must take place. CASPLs expressed in dividing cells may help establish cell polarity by ensuring asymmetric distribution of plasma membrane proteins, or contribute to callose deposition in plasmodesmata. Based on our results, we believe that CASPLs represents a genuine entry point to unravel membrane domains in plants and to uncover the mechanisms behind local modifications of the cell wall.

Evolution of CASPs, Casparian strips and the euphyllophyte root.

Roots have evolved independently in the Lycopodiopsida and the Euphyllophytes, the two groups of the tracheophytes (Raven and Edwards, 2001). Casparian strips are a typical feature of the euphyllophyte root, both in Spermatophytes and Moniliformopses. Casparian strip-like material has been sporadically reported in Lycopodiopsida; however, those structures should be considered at best analogous to Casparian strips, given the independent origin of roots in Lycopodiopsida and Euphyllophytes. We report here the conservation of the CASP EL1 in all spermatophyte genomes we could extensively assess; presence/absence in Moniliformopses could not be assessed because of the absence of fully-sequenced genomes in this group. Despite lack of evidence in the Moniliformopses, we proposed the CASP first extracellular loop as a signature for Casparian strips. How the CASP first extracellular loop would mediate Casparian strip deposition is a question that needs additional functional studies. Extracellular molecular players such as PER64 and ESB1 have recently been identified in the Casparian strips (Hosmani et al., 2013; Lee et al., 2013): CASP EL1 may be necessary to restrict the action of those players in the area of the cell-wall juxtaposing the CSD.

METHODS

Bioinformatics

Data Collection. Arabidopsis thaliana CASP1, CASP2, CASP3, CASP4, CASP5 protein sequences were used as template to identify related plant protein sequences in the UniProtKB with the BLAST tool available at www.uniprot.org. For organisms not present in UniProtKB, additional protein sequences have been deduced from nucleic acid sequences through BLAST tools available at http://blast.ncbi.nlm.nih.gov (e.g. *Adiantum capillus-veneris, Chlorokybus atmophyticus*, *Cucumis melo*, *Cynara cardunculus*, *Helianthus annuus*, *Lactuca saligna*, *Malus domestica*, *Marchantia polymorpha*, *Mimulus guttatus*, *Nicotiana tabacum*, *Osmunda lancea*, *Panicum virgatum*, *Picea glauca*, *Pinus taeda*, *Raphanus raphanistrum*, *Raphanus sativus*, *Striga hermonthica*, *Taraxacum kok-saghyz*, *Theobroma cacao*, *Triphysaria pusilla*, *Vigna unguiculata* and *Zea mays*) and with local BLAST on nucleic sequence sets (e.g. *Pteridium aquilinum* and *Ginkgo biloba*). All sequences have been annotated following gold standards of UniProtKB/Swiss-Prot and are publicly available at:
http://www.uniprot.org/uniprot/?query=family:(Casparian+strip+membrane+proteins+(CASP)+family).

Homology prediction. We collected 134 proteins with a predicted MARVEL domain from stramenopiles, selected fungi and opistokonts. A multiple sequence alignment (MSA) of CASPL and MARVEL-domain containing proteins was calculated with MAFFT (v7; option L-INS-I, gap opening penalty of 1.3, and a gap offset value of 0, BLOSUM30) (Katoh and Standley, 2014). The region homologous to the CASP domain was selected and realigned. The MSA was inspected and edited with JalViewLite (v2.6.1) (Waterhouse et al., 2009). From this alignment we obtained sub-datasets for plants (CASPL), algae, stramenopiles and ‘other’ MARVELs, which were used to scan the PfamA library v27.0 (Finn et al., 2014) and PDB v70 (30-Nov-2013) databases (Berman et al., 2003) with the profile Hidden Markov Model-based homology recognition search method HHpred (v) (Hildebrand et al., 2009) (Supplemental Table 1).

Phylogenetic analysis. Two data models were selected from the MSA, taking into account scores calculated with GUIDANCE (v1.3.1) (Penn et al., 2010). In order to keep a maximum number of aligned positions, we constructed a data model under less stringent conditions by masking MSA residues with low confidence. Alignment positions with a high number of gap positions and masked positions were subsequently removed. The second data model was selected manually and consisted only of the four transmembrane domains and the conserved adjacent regions as to optimize the analysis for deep nodes of the domain phylogeny. As outgroup, we retained sequences from stramenopiles and algae, all other MARVEL sequences were removed from the alignment. Finally, we reduced the sequence redundancy to 90%. Gene phylogenies were estimated by maximum likelihood (ML) from both data models, by bayesian inference (BI) analysis from the more stringently selected data model. The best fitting model of protein evolution according to ProtTest (v2.4) (Darriba et al., 2011) was determined for the CASPL dataset to be JTT+I+G+F under the AICc criterion. The maximum likelihood (ML) phylogeny was reconstructed with PhyML (v3.0) (Guindon et al., 2009), modelling among-site rate heterogeneity using a discrete gamma distribution of 8 categories and calculating non-parametric branch support by applying the approximate likelihood ratio test based on the Shimodaira-Hasegawa-like procedure (Anisimova and Gascuel, 2006). The bayesian analysis was performed with MrBayes (v3.2.0) (Ronquist et al., 2012) under the same evolutionary model as described above, in addition allowing rate variation across the tree. Two independent runs of four Metropolis-coupled MCMC chains were run for 5 million generations and the potential scale reduction factor (PSRF) approached a value of 1. A sample was taken every 1000 generations from the MCMC chains after a burn-in phase of 1 million generations. Phylogenetic trees were colorized according to the taxonomic classification of the species and the predicted protein subfamilies using Archaeopteryx (v0.957 beta) (www.phylosoft.org/archaeopteryx).

Sequence conservation logos. Sequence logos were constructed from the most stringent data model using the WebLogo3 server (weblogo.threeplusone.com). For CASPL group 1 we reduced the sequence redundancy above 90%, as this group was of special interest in this study and hence included in addition homologs from species other than those selected for the analysis of the superfamily. No redundancies were removed from the CASPL groups 2-5 and the MARVEL groups from algae, stramenopiles, fungi and ‘other’ opisthokonts.

Sequence analyses were performed on the Vital-IT High Performance Computing Center (www.vital-it.ch), mafft.cbrc.jp/alignment/server/ (MAFFT), and guidance.tau.ac.il (GUIDANCE).

Molecular cloning, PCR mutagenesis and transgenic lines

Classical cloning was used to generated GUS reporter lines (pCASPL:NLS-GUS); Gateway cloning for the generation of pCASP1:CASP1-mCherry, pLjCASP1:LjCASP1-GFP, and pCASP1:CASP1mutant-GFP; CRE-based recombination for the generation of swap lines (pCASP1:mCherry-CASPL). Transgenic lines were generated by floral dipping in *Arabidopsis thaliana* Col-0 background. Point mutations in CASP1 CDS have been generated by site-directed mutagenesis Additional details are available in Supplemental Table 4.

Staining and microscopy

For confocal microscopy, excitation and detection windows were set as follows: GFP 488 nm, 500–600 nm; mCherry 594 nm, 600–700 nm; GFP and mCherry 488 nm and 594 nm, 500–550 nm and 600–700 nm. For GUS staining, roots or flowers were stained in 10 mM EDTA, 0.1% Triton X-100, 2mM $K_4Fe(CN)_6$, 2 mM $K_3Fe(CN)_6$, 50 mM phosphate buffer pH 7.2, 4 mM X-Gluc. Incubation time was between 2h and 4h at 37 °C; samples were pre-incubated 1h at -20°C in 90% acetone, when this treatment increased staining efficiency. After staining, roots were cleared in 0.24 M HCL/20% methanol 15’ 57°C and then 7% NaOH/60% ethanol, and rehydrated according to Malamy and Benfey (Malamy and Benfey, 1997). For sections, stained samples were fixed in 4% paraformaldehyde overnight at 4°C, washed in PBS, dehydrated in a ethanol series (30%-100%), treated with Histoclear (25%-100%), included in Paraplast, sectioned with a microtome at 10-12 µM, dried overnight at 42°C and mounted in Merckoglas.

Accession numbers

UniProt Accession numbers are provided in Supplemental Table 3.

ACKNOWLEDGEMENT

DR acknowledges Prof. Cris Kuhlemeier for hosting his group.

Literature cited

Alassimone J, Naseer S, Geldner N (2010) A developmental framework for endodermal differentiation and polarity. Proc Natl Acad Sci U S A **107**: 5214–9

Anisimova M, Gascuel O (2006) Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol **55**: 539–52

Baldi S, Barral Y (2012) Bacterial border fence. Cell **151**: 1159–60

Barral Y, Mermall V, Mooseker MS, Snyder M (2000) Compartmentalization of the cell cortex by septins is required for maintenance of cell polarity in yeast. Mol Cell **5**: 841–51

Bateman A, Coin L, Durbin R, Finn RD, Hollich V, Griffiths-Jones S, Khanna A, Marshall M, Moxon S, Sonnhammer ELL, et al (2004) The Pfam protein families database. Nucleic Acids Res **32**: D138–41

Berman H, Henrick K, Nakamura H (2003) Announcing the worldwide Protein Data Bank. Nat Struct Biol **10**: 980

Birnbaum K, Shasha DE, Wang JY, Jung JW, Lambert GM, Galbraith DW, Benfey PN (2008) A Gene Expression Map of the Arabidopsis Root. Science (80-) **1956**: 10–15

Brady SM, Orlando DA, Lee J-Y, Wang JY, Koch J, Dinneny JR, Mace D, Ohler U, Benfey PN (2007) A high-resolution root spatiotemporal map reveals dominant expression patterns. Science (80-) **318**: 801–805

Darriba D, Taboada GL, Doallo R, Posada D (2011) ProtTest 3: fast selection of best-fit models of protein evolution. Bioinformatics **27**: 1164–5

Dawson J, Sozen E, Vizir I, Vav Waeyenberge S, Wilson ZA, Mulligan BJ (1999) Characterization and genetic mapping of a mutation (ms35) which prevents anther dehiscence in Arabidopsis thaliana by affecting secondary wall thickening in the endothecium. New Phytol **144**: 213–222

Estornell LH, Agustí J, Merelo P, Talón M, Tadeo FR (2013) Elucidating mechanisms underlying organ abscission. Plant Sci **199-200**: 48–60

Estrada B, Maeland AD, Gisselbrecht SS, Bloor JW, Brown NH, Michelson AM (2007) The MARVEL domain protein, Singles Bar, is required for progression past the pre-fusion complex stage of myoblast fusion. Dev Biol **307**: 328–39

Finn RD, Bateman A, Clements J, Coggill P, Eberhardt RY, Eddy SR, Heger A, Hetherington K, Holm L, Mistry J, et al (2014) Pfam: the protein families database. Nucleic Acids Res **42**: D222–30

Furuse M, Fujita K, Hiiragi T, Fujimoto K, Tsukita S (1998) Claudin-1 and -2: novel integral membrane proteins localizing at tight junctions with no sequence similarity to occludin. J Cell Biol **141**: 1539–50

Furuse M, Hirase T, Itoh M, Nagafuchi a, Yonemura S, Tsukita S (1993) Occludin: a novel integral membrane protein localizing at tight junctions. J Cell Biol **123**: 1777–88

González-Carranza ZH, Shahid AA, Zhang L, Liu Y, Ninsuwan U, Roberts JA (2012) A novel approach to dissect the abscission process in Arabidopsis. Plant Physiol **160**: 1342–56

Grebe M (2011) Unveiling the Casparian strip. Nature **473**: 294–295

Guindon S, Delsuc F, Dufayard J-F, Gascuel O (2009) Estimating maximum likelihood phylogenies with PhyML. Methods Mol Biol **537**: 113–37

Hedstrom KL, Ogawa Y, Rasband MN (2008) AnkyrinG is required for maintenance of the axon initial segment and neuronal polarity. J Cell Biol **183**: 635–40

Hildebrand A, Remmert M, Biegert A, Söding J (2009) Fast and accurate automatic structure prediction with HHpred. Proteins **77 Suppl 9**: 128–32

Hosmani PS, Kamiya T, Danku J, Naseer S, Geldner N, Guerinot M Lou, Salt DE (2013) Dirigent domain-containing protein is part of the machinery required for formation of the lignin-based Casparian strip in the root. Proc Natl Acad Sci U S A **110**: 14498–503

Hu Q, Milenkovic L, Jin H, Scott MP, Nachury M V, Spiliotis ET, Nelson WJ (2010) A septin diffusion barrier at the base of the primary cilium maintains ciliary membrane protein distribution. Science (80-) **329**: 436–9

Ibarra-Laclette E, Lyons E, Hernández-Guzmán G, Pérez-Torres CA, Carretero-Paulet L, Chang T-H, Lan T, Welch AJ, Juárez MJA, Simpson J, et al (2013) Architecture and evolution of a minute plant genome. Nature 1–6

Ihara M, Kinoshita A, Yamada S, Tanaka H, Tanigaki A, Kitano A, Goto M, Okubo K, Nishiyama H, Ogawa O, et al (2005) Cortical organization by the septin cytoskeleton is essential for structural and mechanical integrity of mammalian spermatozoa. Dev Cell **8**: 343–52

Ikenouchi J, Furuse M, Furuse K, Sasaki H, Tsukita S, Tsukita S (2005) Tricellulin constitutes a novel barrier at tricellular contacts of epithelial cells. J Cell Biol **171**: 939–45

Jahn R, Schiebler W, Ouimet C, Greengard P (1985) A 38,000-dalton membrane protein (p38) present in synaptic vesicles. PNAS **82**: 4137–41

Katoh K, Standley DM (2014) MAFFT: iterative refinement and additional methods. Methods Mol Biol **1079**: 131–46

Kissel H, Georgescu MM, Larisch S, Manova K, Hunnicutt GR, Steller H (2005) The Sept4 septin locus is required for sperm terminal differentiation in mice. Dev Cell **8**: 353–64

Kobayashi T, Storrie B, Simons K, Dotti CG (1992) A functional barrier to movement of lipids in polarized neurons. Nature **359**: 647–50

Kwitny S, Klaus A V, Hunnicutt GR (2010) The annulus of the mouse sperm tail is required to establish a membrane diffusion barrier that is engaged during the late steps of spermiogenesis. Biol Reprod **82**: 669–78

Lee Y, Rubio MC, Alassimone J, Geldner N (2013) A mechanism for localized lignin deposition in the endodermis. Cell **153**: 402–12

Leube RE (1995) The topogenic fate of the polytopic transmembrane proteins, synaptophysin and connexin, is determined by their membrane-spanning domains. J Cell Sci **108 (Pt 3**: 883–94

Magal LG, Yaffe Y, Shepshelovich J, Aranda JF, Marco C De, Gaus K, Alonso MA, Hirschberg K (2009) Clustering and Lateral Concentration of Raft Lipids by the MAL Protein. Mol Biol Evol **20**: 3751–3762

Malamy JE, Benfey PN (1997) Organization and cell differentiation in lateral roots of Arabidopsis thaliana. Development **124**: 33–44

Van Meer G, Simons K (1986) The function of tight junctions in maintaining differences in lipid composition between the apical and the basolateral cell surface domains of MDCK cells. EMBO J **5**: 1455–64

Myles DG, Primakoff P, Koppel DE (1984) A localized surface protein of guinea pig sperm exhibits free diffusion in its domain. J Cell Biol **98**: 1905–9

Nakada C, Ritchie K, Oba Y, Nakamura M, Hotta Y, Iino R, Kasai RS, Yamaguchi K, Fujiwara T, Kusumi A (2003) Accumulation of anchored proteins forms membrane diffusion barriers during neuronal polarization. Nat Cell Biol **5**: 626–32

Naseer S, Lee Y, Lapierre C, Franke R, Nawrath C, Geldner N (2012) Casparian strip diffusion barrier in Arabidopsis is made of a lignin polymer without suberin. PNAS **109**: 10101–6

Nehme CL, Cesario MM, Myles DG, Koppel DE, Bartles JR (1993) Breaching the diffusion barrier that compartmentalizes the transmembrane glycoprotein CE9 to the posterior-tail plasma membrane domain of the rat spermatozoon. J Cell Biol **120**: 687–94

Penn O, Privman E, Landan G, Graur D, Pupko T (2010) An alignment confidence score capturing robustness to guide tree uncertainty. Mol Biol Evol **27**: 1759–67

Raven J a, Edwards D (2001) Roots: evolutionary origins and biogeochemical significance. J Exp Bot **52**: 381–401

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol **61**: 539–42

Roppolo D, De Rybel B, Tendon VD, Pfister A, Alassimone J, Vermeer JEM, Yamazaki M, Stierhof Y-D, Beeckman T, Geldner N (2011) A novel protein family mediates Casparian strip formation in the endodermis. Nature **473**: 380–3

Saarikangas J, Barral Y (2011) The emerging functions of septins in metazoans. EMBO Rep **12**: 1118–26

Sánchez-Pulido L, Martín-Belmonte F, Valencia A, Alonso MA (2002) MARVEL: a conserved domain involved in membrane apposition events. Trends Biochem Sci **27**: 599–601

Schlimpert S, Klein EA, Briegel A, Hughes V, Kahnt J, Bolte K, Maier UG, Brun Y V, Jensen GJ, Gitai Z, et al (2012) General protein diffusion barriers create compartments within bacterial cells. Cell **151**: 1270–82

Sobotzik JM, Sie JM, Politi C, Del Turco D, Bennett V, Deller T, Schultz C (2009) AnkyrinG is required to maintain axo-dendritic polarity in vivo. PNAS **106**: 17564–9

Srivastava M, Simakov O, Chapman J, Fahey B, Gauthier ME a, Mitros T, Richards GS, Conaco C, Dacre M, Hellsten U, et al (2010) The Amphimedon queenslandica genome and the evolution of animal complexity. Nature **466**: 720–6

Steed E, Rodrigues NTL, Balda MS, Matter K (2009) Identification of MarvelD3 as a tight junction-associated transmembrane protein of the occludin family. BMC Cell Biol **10**: 95

Takizawa PA, DeRisi JL, Wilhelm JE, Vale RD (2000) Plasma membrane compartmentalization in yeast by messenger RNA transport and a septin diffusion barrier. Science (80-) **290**: 341–4

Vermeer JEM, von Wangenheim D, Barberon M, Lee Y, Stelzer EHK, Maizel A, Geldner N (2014) A spatial accommodation by neighboring cells is required for organ initiation in Arabidopsis. Science **343**: 178–83

Waterhouse AM, Procter JB, Martin DMA, Clamp M, Barton GJ (2009) Jalview Version 2--a multiple sequence alignment editor and analysis workbench. Bioinformatics **25**: 1189–91

Westwood JH, Claude W, Das M, Fernández-Aparicio M, Honaas A, Timko MP, Wafula EK, Wickett NJ, Yoder JI, Honaas LA (2012) The Parasitic Plant Genome Project: New Tools for Understanding the Biology of Orobanche and Striga. Weed Sci **60**: 295–306

Westwood JH, Yoder JI, Timko MP, DePamphilis CW (2010) The evolution of parasitism in plants. Trends Plant Sci **15**: 227–35

Wiedenmann B, Franke WW (1985) Identification and localization of synaptophysin, an integral membrane glycoprotein of Mr 38,000 characteristic of presynaptic vesicles. Cell **41**: 1017–28

Winckler B, Forscher P, Mellman I (1999) A diffusion barrier maintains distribution of membrane proteins in polarized neurons. Nature **397**: 698–701

Yaffe Y, Shepshelovitch J, Nevo-Yassaf I, Yeheskel A, Shmerling H, Kwiatek JM, Gaus K, Pasmanik-Chor M, Hirschberg K (2012) The MARVEL transmembrane motif of occludin mediates oligomerization and targeting to the basolateral surface in epithelia. J Cell Sci **125**: 3545–56

FIGURE LEGENDS

Figure 1. Evidence for a common origin of CASPLs and MARVELs. A. Sequence similarity and five conserved residues. Signature logos covering the four transmembrane domains and conserved adjacent regions of the CASPL/MARVEL domains have been constructed for the five plant groups, chlorophytes, stramenopiles and opisthokonts. Conserved residues are marked by an asterix. Yellow bars below logos correspond to the predicted transmembrane domains of CASP1 of *A. thaliana*; conserved regions of the extracellular loops (EL1, EL2) and of the intracellular loop (IL) are indicated. **B.** Homology prediction. CASPL and MARVEL domains are predicted to belong to both domain families with a probability of at least 97.3% (Supplemental Table 1). The cladogram presents a model of gene evolution for the analyzed CASPL/MARVEL groups. **C.** Taxonomic range for domain predictions. 99.5% of the CASPL domains are predicted in plant genes, 99.9% of MARVEL domains in genes from species of the animal lineage. **D.** Circular cladogram based on the maximum likelihood phylogeny of the CASPL and MARVEL domains. Genes from species in key positions of the CASPL/MARVEL domain phylogeny with no stable position in the tree are marked by triangles: two genes from the stramenopiles *Aureococcus anophagefferens* (UniProtKB F0YFA3 and F0Y3N5) and one gene from the rhodophyte *Cyanidioschyzon merolae* (UniProtKB: M1VAW8). Branch colors indicate taxonomic species groups. **E.** Circular cladogram of the CASPL family with MARVELs from stramenopiles and algae as outgroup, based on Bayesian inference analysis. The five CASPL subfamilies are marked by colors, stramenopiles and chlorophytes are colored as in 1D; unclassified genes are gray-colored.

Figure 2. Extracellular loops are dispensable for AtCASP1 localization.

The schematic shows deletions and mutagenized residues that affect or not localization (above and below, respectively). Documenting images are reported in Supplemental Figure 5. Mutations are annotated on a sequence logo of the CASPL1A subgroup to highlight conservation of the mutagenized residues. Pictures show representative images of AtCASP1 mutant-GFP/wt-cherry crosses (green and red labels, respectively). White numbers indicate position of the cell shown counted from the first elongating endodermal cell.

Figure 3. AtCASP first extracellular loop is conserved in euphyllophytes.

A) The EL1 of AtCASP1 is aligned to potential functional homologs. The 9 aa signature specific to AtCASPs and absent in AtCASPLs is highlighted in red. In the first position, E (red) or Q (green) are both found. Species abbreviations are as follow: At *Arabidopsis thaliana*, Al *Arabidopsis lyrata*; Rr *Raphanus raphanistrum*; Rs *Raphanus sativus*; Tc *Theobroma cacao*; Gm *Glycine max;* Lj *Lotus japonicus*; Mt *Medicago truncatula*; Vu *Vigna unguiculata*; Cm *Cucumis melo*; Rc *Ricinus communis*; Pt *Populus trichocarpa*; Md *Malus domestica*; Vv *Vitis vinifera*; Cs *Cynara scolymus*; Tk *Taraxacum kok-saghyz*; Ha *Helianthus annuus*; St *Solanum tuberosum*; Sd *Solanum demissum*; Nt *Nicotiana tabacum*; Osj *Oryza sativa* subsp. Japonica; Or *Oryza rufipogon*; Bd *Brachypodium distachyon*; Ta *Triticum aestivum*; Zm *Zea mays*, Pv *Panicum virgatum*; Sb *Sorghum bicolor*; Pta *Pinus taeda*; Pg *Picea glauca*. B and C) Expression of a *Lotus japonicus* potential AtCASP functional homolog (*LjCASP1*) in *A. thaliana*. The Lotus promoter drives expression exclusively in the endodermis (B) and LjCASP1-GFP localizes to the Casparian strip membrane domain (C). Pictures show confocal sections of a 5-day-old root. Rectangles in C highlight an endodermal cell. Abbreviations: ep epidermis, co cortex, en endodermis. Scale bars: 10 μm. D) AtCASP1 EL1 and TM4 are aligned to closest homologs from the Lamiales. *Mimulus guttatus* (Mg) and *Striga asiatica* (Sa) presents an AtCASP homolog potentially non-functional due to a premature stop codon (*) in TM4. *Utricularia gibba* (Ug) closest AtCASP homolog does not show conservation in the EL1 signature. *Striga hermontica* (Sh), *Triphysaria pusilla* (Tp) and *Mimulus guttatus* encode for potential functional AtCASP homologs. See also Supplementary Table 5.

Figure 4. AtCASPLs can localize at the CSD when expressed in the endodermis.

A) Root confocal sections of 5 day-old seedlings expressing mCherry-AtCASPLs under the control of the AtCASP1 promoter. Expression is seen only in endodermal files, where AtCASPLs are retained or excluded from the CSD (* marks exclusion). Scale bar: 5 µm. B) Alignment of AtCASPs and AtCASPLs that localize at the CSD (upper rectangles) or not (lower rectangles). Residues in blue are found in all CASPLs; residues in red are necessary for a correct localization of AtCASP1. The AtCASP first extracellular loop signature is highlighted in green. Yellow shadows show residues that are conserved in AtCASPL1s that localize at the CSD, but absent in AtCASPL1s that do not localize at the CSD. Note that conservation in extracellular loops is not an absolute requirement for localization at the CSD. See also Supplemental table 6.

Figure 5. AtCASPLs are expressed in different tissues.

A) *AtCASPL1A1* is expressed in the endodermis at late stages, initially in all cells (’), later only in isolated cells (’’); its expression is reduced in the endodermis overlaying lateral root primordia (’). B) *AtCASPL1D2* is expressed in late endodermis, particularly in cells overlaying lateral root primordia (’); it is also expressed in floral organ abscission zone (’’) on the side of the shed organ (’’). C) *AtCASPL4D1* is expressed in root epidermis from the maturation zone; its expression quickly declines. D’) *AtCASPL2A1* is expressed in the lateral root cap (’); D’’ shows a transversal section of the root tip; it is also expressed in leaves (not shown). E) *AtCASPL5B1* is expressed in immature and differentiated trichomes in leaves. F) *AtCASPL1F1* is expressed in anthers. G) *AtCASPL1C1* is expressed in the root maturation zone. H) *AtCASPL5B2* is expressed in dividing cells in the root (’), lateral root primordia (’’), leaves (’’’). I) *AtCASPL0B3* is expressed in root xylem pole pericycle (’), in lateral root primordia (’’’) and leaves (’’’’); I’’ shows a transversal section at the root tip. J) *AtCASPL5C3* is expressed early in floral organ abscission zone (’) and in rosette vestigial abscission zone (’’). All pictures represents whole mount stainings, except D’’ and I’’. Scale bars: 10 µm for A, B’, B’’, C, D, H’, H’’, I’’, I’’’, I’’’’, 100 µm for B’’’, E, F, H’’’, I’, J’; 500 µm for J’’.Supplemental material

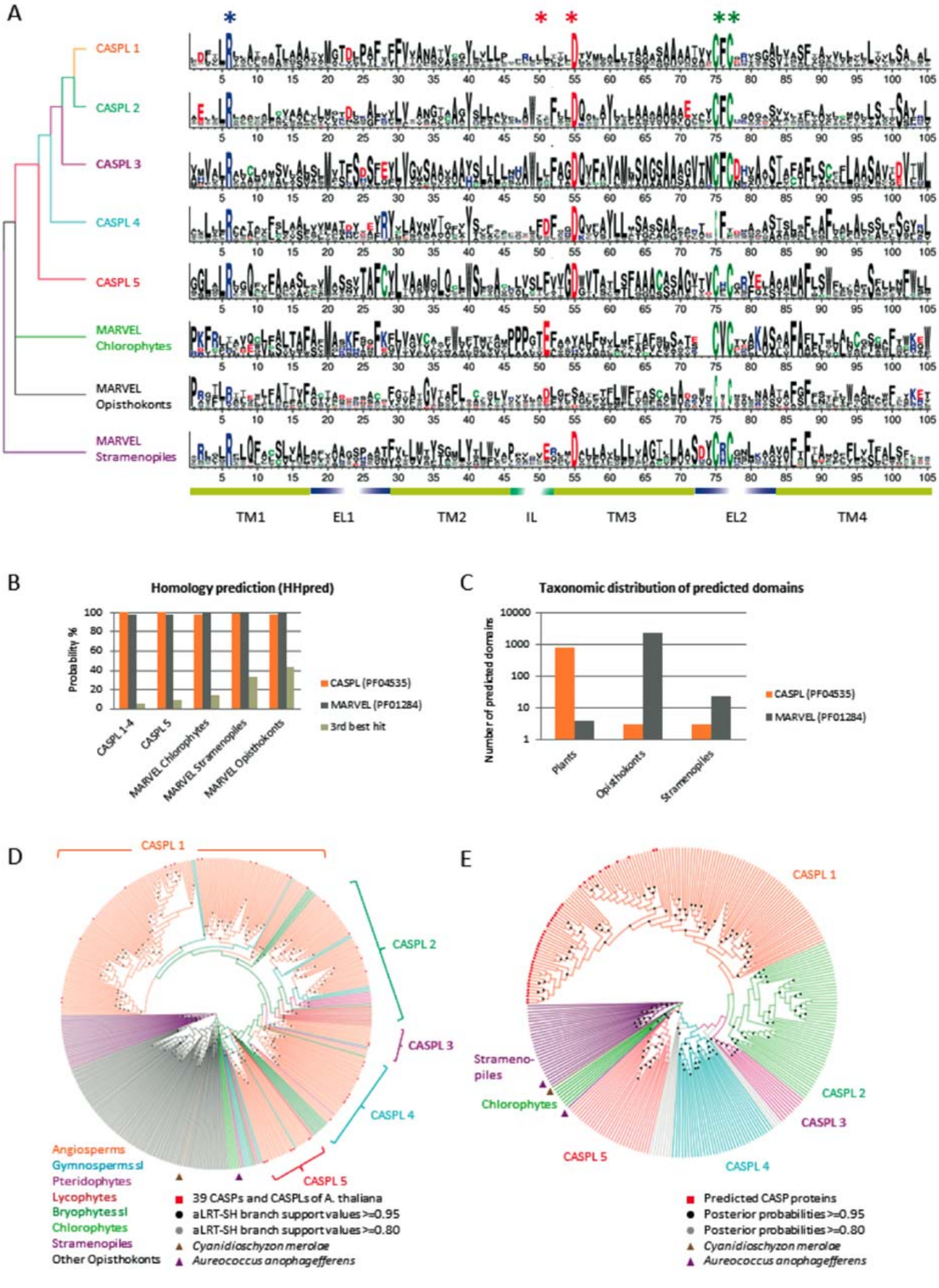
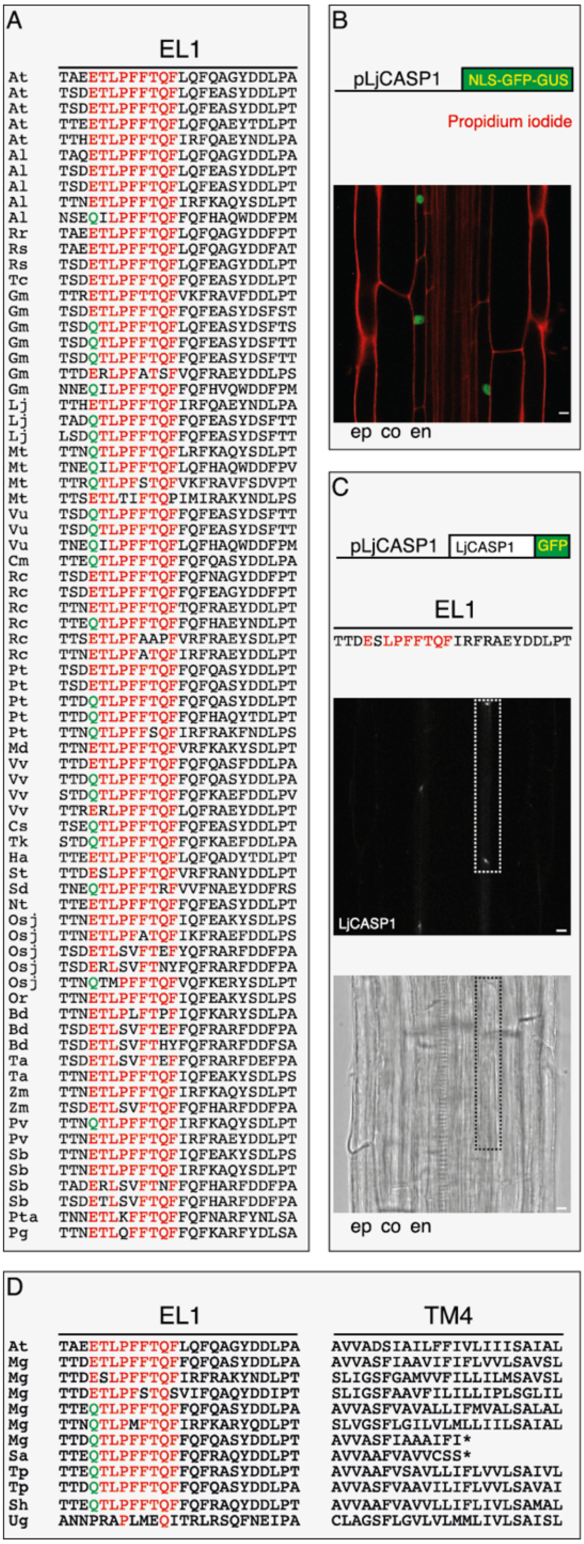


Figure 1. Evidence for a common origin of CASPLs and MARVELs. A. Sequence similarity and five conserved residues. Sequence logos covering the four transmembrane domains and conserved adjacent regions of the CASPL/MARVEL domains have been constructed for the five plant groups, chlorophytes, stramenopiles and opisthokonts. Conserved residues are marked by an asterix. Yellow bars below logos correspond to the predicted transmembrane domains of CASP1 fromA. thaliana, and the adjacent conserved regions of the assumed extracellular loops (EL1, EL2) and of the intracellular loop (IL) are indicated. The predicted relationship of the five CASPL groups and MARVEL taxonomic groups is shown as tree at the right of the sequence logos. The color code of the protein groups corresponds to that of Figure 1E. **B**. Homology prediction. CASPL and MARVEL domains are predicted to belong to both domain families with a probability of at least 97.3% (Supplemental Table 1). **C**. Taxonomic range for domain predictions. 99.5% of the CASPL domains are predicted in plant genes, 99.9% of MARVEL domains in genes from species of the animal lineage. **D**. Circular cladogram based on the maximum likelihood phylogeny of the CASPL and MARVEL domains. Genes from species in key positions of the CASPL/MARVEL domain phylogeny with no stable position in the tree are marked by triangles: two genes from the stramenopiles Aureococcus anophagefferens (UniProtKB F0YFA3 and F0Y3N5) and one gene from the rhodophyte Cyanidioschyzon merolae (UniProtKB: M1VAW8). Branch colors indicate taxonomic species groups. **E**. Circular cladogram of the CASPL phylogeny with MARVELs from stramenopiles and algae as outgroup, based on a Bayesian inference analysis. The five CASPL subfamilies are marked by colors, stramenopiles and chlorophytes are colored as in 1 D; unclassified genes are gray-colored.

Figure 2. **Extracellular loops are dispensable for AtCASP1 localization at the CSD.** Representative confocal images of AtCASP1-GFP mutant/wt-mCherry crosses (green and red labels, respectively). Numbers indicate position of the cell shown counted from he first elongating endodermal cell (the lower the number, the closer is the cell to the root apical meristem). White arrows point to the position of the Casparian strip membrane domain (CSD). The schematic summarizes the position of deletions and mutagenized residues that affect or not localization (above and below, respectively). Mutations are annotated on a sequence logo of the CASPL1A subgroup to highlight conservation of the mutagenized residues. Yellows strips indicate the position of the extracellular loops.



	EL1
At	TAEETLPFFTQFLQFQAGYDDLPA
At	TSDETLPFFTQFLQFEASYDDLPT
At	TSDETLPFFTQFLQFEASYDDLPT
At	TTEETLPFFTQFLQFQAEYTDLPT
At	TTHETLPFFTQFIRFQAEYNDLPA
Al	TAQETLPFFTQFLQFQAGYDDLPA
Al	TSDETLPFFTQFLQFEASYDDLPT
Al	TSDETLPFFTQFLQFEASYDDLPT
Al	TTNETLPFFTQFIRFKAQYSDLPT
Al	NSEQILPFFTQFFQFHAQWDDFPM
Rr	TAEETLPFFTQFLQFQAGYDDFPT
Rs	TAEETLPFFTQFLQFQAGYDDFAT
Rs	TSDETLPFFTQFLQFEAGYDDLPT
Tc	TSDETLPFFTQFFQFEASYDDLPT
Gm	TTRETLPFTTQFVKFRAVFDDLPT
Gm	TSDETLPFFTQFFQFEASYDSFST
Gm	TSDQTLPFFTQFLQFEASYDSFTS
Gm	TSDQTLPFFTQFFQFEASYDSFTT
Gm	TSDQTLPFFTQFFQFEASYDSFTT
Gm	TTDERLPFATSFVQFRAEYDDLPS
Gm	NNEQILPFFTQFFQFHVQWDDFPM
Lj	TTHETLPFFTQFIRFQAEYNDLPA
Lj	TADQTLPFFTQFFQFEASYDSFTT
Lj	LSDQTLPFFTQFFQFEASYDSFTT
Mt	TTNQTLPFFTQFLRFKAQYSDLPT
Mt	TNEQILPFFTQFLQFHAQWDDFPV
Mt	TTRQTLPFSTQFVKFRAVFSDVPT
Mt	TTSETLTIFTQPIMIRAKYNDLPS
Vu	TSDQTLPFFTQFFQFEASYDSFTT
Vu	TSDQTLPFFTQFFQFEASYDSFTT
Vu	TNEQILPFFTQFLQFHAQWDDFPM
Cm	TTEQTLPFFTQFFQFQASYDDLPA
Rc	TSDETLPFFTQFFQFNAGYDDFPT
Rc	TSDETLPFFTQFFQFEAGYDDFPT
Rc	TTNETLPFFTQFTQFRAEYDDLPT
Rc	TTEQTLPFFTQFFQFHAEYNDLPT
Rc	TTSETLPFAAPFVRFRAEYSDLPT
Rc	TTNETLPFATQFIRFRAEYDDLPT
Pt	TSDETLPFFTQFFQFQASYDDLPT
Pt	TSDETLPFFTQFFQFQASYDDLPT
Pt	TTDQTLPFFTQFFQFQASYDDLPT
Pt	TTDQTLPFFTQFFQFHAQYTDLPT
Pt	TTNQTLPFFSQFIRFRAKFNDLPS
Md	TTNETLPFFTQFVRFKAKYSDLPT
Vv	TTDETLPFFTQFFQFQASFDDLPA
Vv	TTDQTLPFFTQFFQFQASYDDLPA
Vv	STDQTLPFFTQFFQFKAEFDDLPV
Vv	TTRERLPFFTQFLQFRAEYDDLPT
Cs	TSEQTLPFFTQFFQFEASYDDLPT
Tk	STDQTLPFFTQFFQFKAEFDDLPA
Ha	TTEETLPFFTQFLQFQADYTDLPT
St	TTDESLPFFTQFVRFRANYDDLPT
Sd	TNEQTLPFFTRFVVFNAEYDDFRS
Nt	TTEETLPFFTQFFQFEASYDDLPT
Osj	TTNETLPFFTQFIQFEAKYSDLPS
Osj	TTNETLPFATQFIKFRAEFDDLPS
Osj	TSDETLSVFTEFYQFRARFDDFPA
Osj	TSDERLSVFTNYFQFRARFDDFPA
Osj	TTNQTMPFFTQFVQFKERYSDLPT
Or	TTNETLPFFTQFIQFEAKYSDLPS
Bd	TTNETLPLFTPFIQFKARYSDLPA
Bd	TSDETLSVFTEFFQFRARFDDFPA
Bd	TSDETLSVFTHYFQFRARFDDFSA
Ta	TSDETLSVFTEFFQFRARFDEFPA
Ta	TTNETLPFFTQFIQFEAKYSDLPS
Zm	TTNETLPFFTQFIRFKAQYSDLPT
Zm	TSDETLSVFTQFFQFHARFDDFPA
Pv	TTNQTLPFFTQFIRFKAQYSDLPT
Pv	TTNETLPFFTQFIRFRAEYDDLPT
Sb	TTNETLPFFTQFIQFEAKYSDLPS
Sb	TTNETLPFFTQFIRFKAQYSDLPT
Sb	TADERLSVFTNFFQFHARFDDFPA
Sb	TSDETLSVFTQFFQFHARFDDFPA
Pta	TNNETLKFFTQFFQFNARFYNLSA
Pg	TTNETLQFFTQFFQFKARFYDLSA

TTDESLPFFTQFIRFRAEYDDLPT

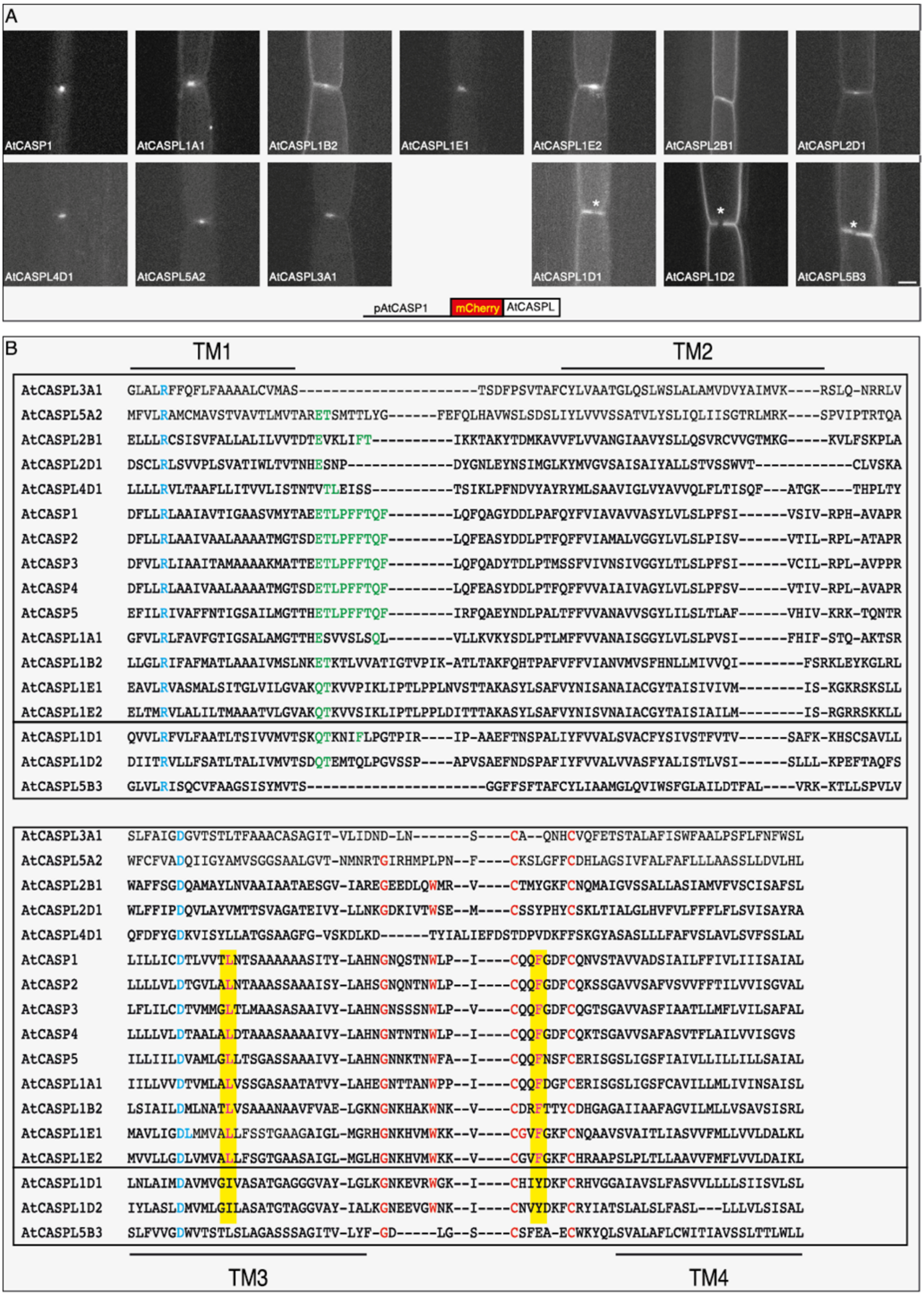
	EL1	TM4
At	TAEETLPFFTQFLQFQAGYDDLPA	AVVADSIAILFFIVLIIISAIAL
Mg	TTDETLPFFTQFFQFQASYDDLPA	AVVASFIAAVIFIFLVVLSAVSL
Mg	TTDESLPFFTQFIRFRAKYNDLPT	SLIGSFGAMVVFILLILMSAVSL
Mg	TTDETLPFSTQSVIFQAQYDDIPT	SLIGSFAAVFILILLIPLSGLIL
Mg	TTEQTLPFFTQFFQFQASYDDLPA	AVVASFVAVALLIFMVALSALAL
Mg	TTNQTLPMFTQFIRFKARYQDLPT	SLVGSFLGILVLMLLIILSAIAL
Mg	TTDQTLPFFTQFFQFQASYDDLPT	AVVASFIAAAIFI*
Sa	TTEQTLPFFTQFFQFRAQYDDLPT	AVVAAFVAVVCSS*
Tp	TTEQTLPFFTQFFQFRASYDDLPT	AVVAAFVSAVLLIFLVVLSAIVL
Tp	TTDQTLPFFTQFFQFQASYDDLPA	AVVASFVAAVILIFLVVLSAVAI
Sh	TTEQTLPFFTQFFQFRAQYDDLPT	AVVAAFVAVVLLIFLIVLSAMAL
Ug	ANNPRAPLMEQITRLRSQFNEIPA	CLAGSFLGVLVLMMLIVLSAISL

Figure 3. AtCASP first extracellular loop is conserved in euphyllophytes.

A) The EL1 of AtCASP1 is aligned to potential functional homologs. The 9 aa signature specific to AtCASPs and absent in AtCASPLs is highlighted in red. In the first position, E (red) or Q (green) are both found. Species abbreviations are as follow: At *Arabidopsis thaliana*, Al *Arabidopsis lyrata*; Rr *Raphanus raphanistrum*; Rs *Raphanus sativus*; Tc *Theobroma cacao*; Gm *Glycine max*; Lj *Lotus japonicus*; Mt *Medicago truncatula*; Vu *Vigna unguiculata*; Cm *Cucumis melo*; Rc *Ricinus communis*; Pt *Populus trichocarpa*; Md *Malus domestica*; Vv *Vitis vinifera*; Cs *Cynara scolymus*; Tk *Taraxacum kok-saghyz*; Ha *Helianthus annuus*; St *Solanum tuberosum*; Sd *Solanum demissum*; Nt *Nicotiana tabacum*; Osj *Oryza sativa* subsp. Japonica; Or *Oryza rufipogon*; Bd *Brachypodium distachyon*; Ta *Triticum aestivum*; Zm *Zea mays*, Pv *Panicum virgatum*; Sb *Sorghum bicolor*; Pta *Pinus taeda*; Pg *Picea glauca*.

B and C) Expression of a *Lotus japonicus* potential AtCASP functional homolog (LjCASP1) in A. thaliana. The Lotus promoter drives expression exclusively in the endodermis (B) and LjCASP1-GFP localizes to the Casparian strip membrane domain (C). Pictures show confocal sections of a 5-day-old root. Rectangles in C highlight an endodermal cell. Abbreviations: ep epidermis, co cortex, en endodermis. Scale bars: 10 µm.

D) AtCASP1 EL1 and TM4 are aligned to closest homologs from the Lamiales. *Mimulus guttatus* (Mg) and *Striga asiatica* (Sa) presents an AtCASP homolog potentially non-functional due to a premature stop codon (*) in TM4. *Utricularia gibba* (Ug) closest AtCASP homolog does not show conservation in the EL1 signature. *Striga hermontica* (Sh), *Triphysaria pusilla* (Tp) and *Mimulus guttatus* encode for potential functional AtCASP homologs. See also Supplementary Table 5.



```
AtCASPL3A1   GLALRFFQFLFAAAALCVMAS----------------------TSDFPSVTAFCYLVAATGLQSLWSLALAMVDVYAIMVK----RSLQ-NRRLV
AtCASPL5A2   MFVLRAMCMAVSTVAVTLMVTARETSMTTLYG------FEFQLHAVWSLSDSLIYLVVVSSATVLYSLIQLIISGTRLMRK----SPVIPTRTQA
AtCASPL2B1   ELLLRCSISVFALLALILVVTDTEVKLIFT----------IKKTAKYTDMKAVVFLVVANGIAAVYSLLQSVRCVVGTMKG-----KVLFSKPLA
AtCASPL2D1   DSCLRLSVVPLSVATIWLTVTNHESNP-------------DYGNLEYNSIMGLKYMVGVSAISAIYALLSTVSSWVT------------CLVSKA
AtCASPL4D1   LLLLRVLTAAFLLITVVLISTNTVTLEISS----------TSIKLPFNDVYAYRYMLSAAVIGLVYAVVQLFLTISQF---ATGK----THPLTY
AtCASP1      DFLLRLAAIAVTIGAASVMYTAEETLPFFTQF--------LQFQAGYDDLPAFQYFVIAVAVVASYLVLSLPFSI------VSIV-RPH-AVAPR
AtCASP2      DFLLRLAAIVAALAAAATMGTSDETLPFFTQF--------LQFEASYDDLPTFQFFVIAMALVGGYLVLSLPISV------VTIL-RPL-ATAPR
AtCASP3      DFVLRLIAAITAMAAAAKMATTEETLPFFTQF--------LQFQADYTDLPTMSSFVIVNSIVGGYLTLSLPFSI------VCIL-RPL-AVPPR
AtCASP4      DFLLRLAAIVAALAAAATMGTSDETLPFFTQF--------LQFEASYDDLPTFQFFVVAIAIVAGYLVLSLPFSV------VTIV-RPL-AVAPR
AtCASP5      EFILRIVAFFNTIGSAILMGTTHETLPFFTQF--------IRFQAEYNDLPALTFFVVANAVVSGYLILSLTLAF------VHIV-KRK-TQNTR
AtCASPL1A1   GFVLRLFAVFGTIGSALAMGTTHESVVSLSQL--------VLLKVKYSDLPTLMFFVVANAISGGYLVLSLPVSI------FHIF-STQ-AKTSR
AtCASPL1B2   LLGLRIFAFMATLAAAIVMSLNKETKTLVVATIGTVPIK-ATLTAKFQHTPAFVFFVIANVMVSFHNLLMIVVQI--------FSRKLEYKGLRL
AtCASPL1E1   EAVLRVASMALSITGLVILGVAKQTKVVPIKLIPTLPPLNVSTTAKASYLSAFVYNISANAIACGYTAISIVIVM--------IS-KGKRSKSLL
AtCASPL1E2   ELTMRVLALILTMAAATVLGVAKQTKVVSIKLIPTLPPLDITTTAKASYLSAFVYNISVNAIACGYTAISIAILM--------IS-RGRRSKKLL
AtCASPL1D1   QVVLRFVLFAATLTSIVVMVTSKQTKNIFLPGTPIR----IP-AAEFTNSPALIYFVVALSVACFYSIVSTFVTV------SAFK-KHSCSAVLL
AtCASPL1D2   DIITRVLLFSATLTALIVMVTSDQTEMTQLPGVSSP----APVSAEFNDSPAFIYFVVALVVASFYALISTLVSI------SLLL-KPEFTAQFS
AtCASPL5B3   GLVLRISQCVFAAGSISYMVTS----------------------GGFFSFTAFCYLIAAMGLQVIWSFGLAILDTFAL----VRK-KTLLSPVLV

AtCASPL3A1   SLFAIGDGVTSTLTFAAACASAGIT-VLIDND-LN-------S----CA--QNHCVQFETSTALAFISWFAALPSFLFNFWSL
AtCASPL5A2   WFCFVADQIIGYAMVSGGSAALGVT-NMNRTGIRHMPLPN--F----CKSLGFFCDHLAGSIVFALFAFLLLAASSLLDVLHL
AtCASPL2B1   WAFFSGDQAMAYLNVAAIAATAESGV-IAREGEEDLQWMR--V----CTMYGKFCNQMAIGVSSALLASIAMVFVSCISAFSL
AtCASPL2D1   WLFFIPDQVLAYVMTTSVAGATEIVY-LLNKGDKIVTWSE--M----CSSYPHYCSKLTIALGLHVFVLFFFLFLSVISAYRA
AtCASPL4D1   QFDFYGDKVISYLLATGSAAGFG-VSKDLKD------TYIALIEFDSTDPVDKFFSKGYASASLLLFAFVSLAVLSVFSSLAL
AtCASP1      LILLICDTLVVTLNTSAAAAAASITY-LAHNGNQSTNWLP--I----CQQFGDFCQNVSTAVVADSIAILFFIVLIIISAIAL
AtCASP2      LLLLVLDTGVLALNTAAASSAAAISY-LAHSGNQNTNWLP--I----CQQFGDFCQKSSGAVVSAFVSVVFFTILVVISGVAL
AtCASP3      LFLILCDTVMMGLTLMAASASAAIVY-LAHNGNSSSNWLP--V----CQQFGDFCQGTSGAVVASFIAATLLMFLVILSAFAL
AtCASP4      LLLLVLDTAALALDTAAASAAAAIVY-LAHNGNTNTNWLP--I----CQQFGDFCQKTSGAVVSAFASVTFLAILVVISGVS
AtCASP5      ILLIILDVAMLGLLTSGASSAAAIVY-LAHNGNNKTNWFA--I----CQQFNSFCERISGSLIGSFIAIVLLILLILLSAIAL
AtCASPL1A1   IILLVVDTVMLALVSSGASAATATVY-LAHEGNTTANWPP--I----CQQFDGFCERISGSLIGSFCAVILLMLIVINSAISL
AtCASPL1B2   LSIAILDMLNATLVSAAANAAVFVAE-LGKNGNKHAKWNK--V----CDRFTTYCDHGAGAIIAAFAGVILMLLVSAVSISRL
AtCASPL1E1   MAVLIGDLMMVALLFSSTGAAGAIGL-MGRHGNKHVMWKK--V----CGVFGKFCNQAAVSVAITLIASVVFMLLVVLDALKL
AtCASPL1E2   MVVLLGDLVMVALLFSGTGAASAIGL-MGLHGNKHVMWKK--V----CGVFGKFCHRAAPSLPLTLLAAVVFMFLVVLDAIKL
AtCASPL1D1   LNLAIMDAVMVGIVASATGAGGGVAY-LGLKGNKEVRWGK--I----CHIYDKFCRHVGGAIAVSLFASVVLLLLSIISVLSL
AtCASPL1D2   IYLASLDMVMLGILASATGTAGGVAY-IALKGNEEVGWNK--I----CNVYDKFCRYIATSLALSLFASL---LLLVLSISAL
AtCASPL5B3   SLFVVGDWVTSTLSLAGASSSAGITV-LYF-GD-----LG--S----CSFEA-ECWKYQLSVALAFLCWITIAVSSLTTLWLL
```

Figure 4. AtCASPLs can localize at the CSD when expressed in the endodermis.

A) Root confocal sections of 5 day-old seedlings expressing mCherry-AtCASPLs under the control of the AtCASP1 promoter. Expression is seen only in endodermal files, where AtCASPLs are retained or excluded from the CSD (* marks exclusion). Scale bar: 5 µm. B) Alignment of AtCASPs and AtCASPLs that localize at the CSD (upper rectangles) or not (lower rectangles). Residues in blue are found in all CASPLs; residues in red are necessary for a correct localization of AtCASP1. The AtCASP first extracellular loop signature is highlighted in green. Yellow shadows show residues that are conserved in AtCASPL1s that localize at the CSD, but absent in AtCASPL1s that do not localize at the CSD. Note that conservation in extracellular loops is not an absolute requirement for localization at the CSD. See also Supplemental table 6.

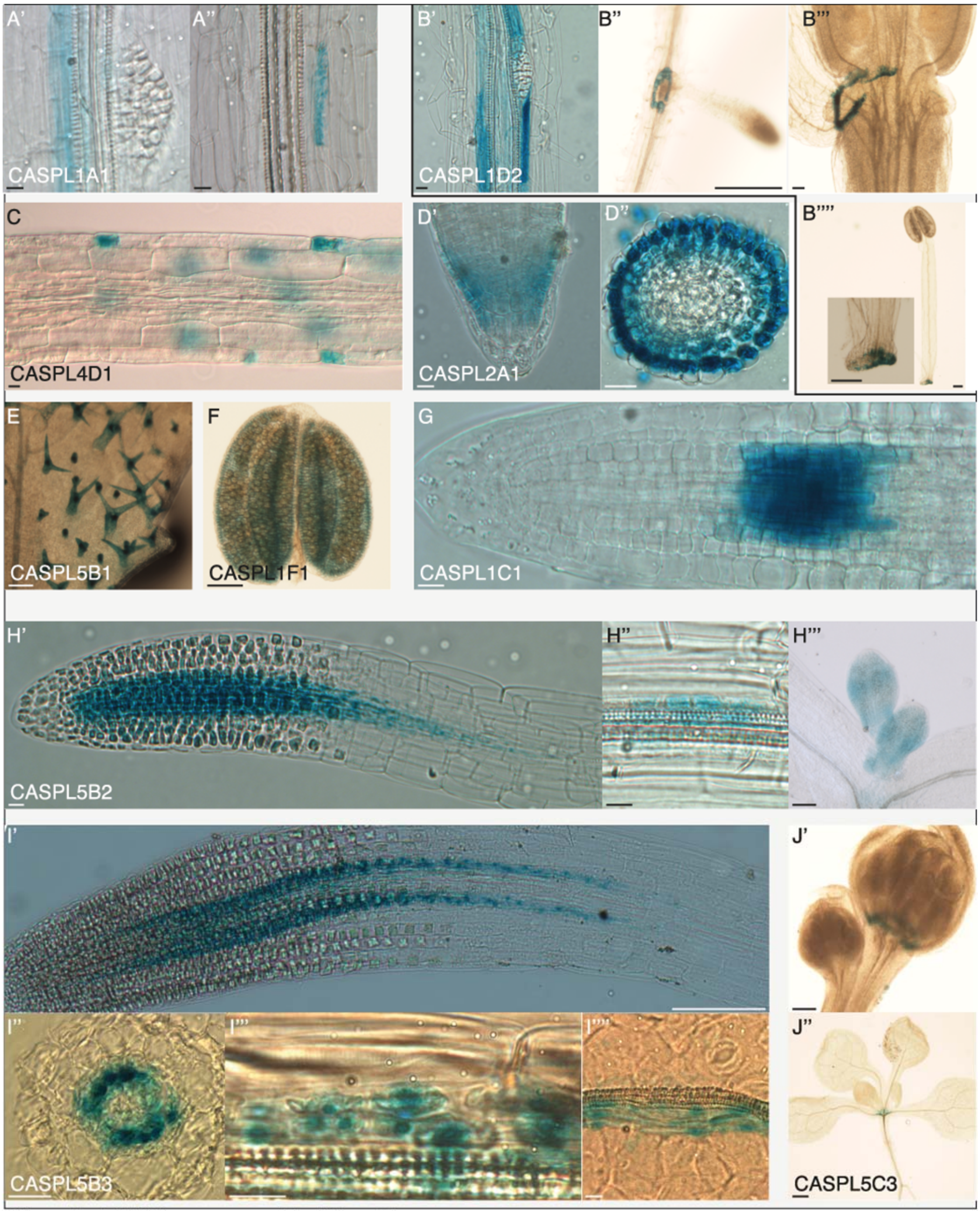


Figure 5. *AtCASPLs* are expressed in different tissues.

A) *AtCASPL1A1* is expressed in the endodermis at late stages, initially in all cells (’), later only in isolated cells (”); its expression is reduced in the endodermis overlaying lateral root primordia (’).

B) *AtCASPL1D2* is expressed in late endodermis, particularly in cells overlaying lateral root primordia (’); expression persists at the base of emerged lateral roots (”); it is also expressed in floral organ abscission zone (’”) on the side of the shed organ (””).

C) *AtCASPL4D1* is expressed in root epidermis from the maturation zone; its expression quickly declines.

D’) *AtCASPL2A1* is expressed in the lateral root cap (’); D” shows a transversal section of the root tip; it is also expressed in leaves (not shown).

E) *AtCASPL5B1* is expressed in immature and differentiated trichomes in leaves.

F) *AtCASPL1F1* is expressed in anthers.

G) *AtCASPL1C1* is expressed in the root maturation zone.

H) *AtCASPL5B2* is expressed in dividing cells in the root (’), lateral root primordia (”), leaves (’”).

I) *AtCASPL5B3* is expressed in root xylem pole pericycle (’), in lateral root primordia (’”) and leaves (””); I” shows a transversal section at the root tip.

J) *AtCASPL5C3* is expressed early in floral organ abscission zone (’) and in rosette vestigial abscission zone (”).

All pictures represents whole mount stainings, except D” and I”. Scale bars: 10 µm for A, B’, B’”, C, D, H’, H”, I”, I’”, I””, 100 µm for B”, B””, E, F, H’”, I’, J’; 500 µm for J”.

Content:

- Supplemental Table 1. Homology prediction with HHpred for CASPL groups and MARVELs.
- Supplemental Table 2. Taxonomic distribution of species with predicted CASPL (DUF544) and MARVEL domains.
- Supplemental Table 3. Annotation of UniProtKB entries used for the phylogenetic analysis presented in Figure 1
- Supplemental Table 4. Transgenic lines
- Supplemental Table 5. CASPLs in *Mimulus guttatus* and *Utricularia Gibba*
- Supplementary Table 6. Localization of mCherry-AtCASPLs under the control of AtCASP1 promoter

- Supplemental Figure 1. Alignment of representative CASPL and MARVEL domains.
- Supplemental Figure 2. Maximum likelihood phylogeny of the CASPL/MARVEL domain, corresponding to Figure 1D.
- Supplemental Figure 3. Bayesian consensus phylogeny of the CASPL domain with MARVEL domains from algae and stramenopiles as outgroup, corresponding to Figure 1E.
- Supplemental Figure 4. Maximum likelihood phylogeny of the CASPL domain; the dataset is identical to the one in Figures 1E and Supplemental Figure 3.
- Supplemental Figure 5. Magnification of selected images presented in Figure 2.

- Dataset 1. Data model 1: CASPL/MARVEL domains (fasta format).
- Dataset 2. Data model 2: CASPL and outgroup (stramenopiles, algae) (fasta format).
- Dataset 3. ML CASPL/MARVEL domain phylogeny (NHX format) corresponding to Figures 1D and Supplemental Figure 2.
- Dataset 4. BI CASPL phylogeny (NHX format) corresponding to Figures 1E and Supplemental Figure 2.
- Dataset 5. ML CASPL phylogeny (NHX format), corresponding to Supplemental Figure 4.

Supplemental Table 1. Homology prediction with HHpred for CASPL groups and MARVELs (% probability).

	DUF588 (PF04535)	MARVEL (PF01284)	3rd best hit
Plant CASPL 1-4	**100**	97.5	4.5
Plant CASPL 5	**100**	97.3	9
Chlorophytes	97.9	**99.8**	13.9
Stramenopiles	98.7	**99.7**	33.2
Opisthokonts	97.9	**99.7**	43.2

Supplemental Table 2. Taxonomic distribution of species with predicted CASPL (DUF588) and MARVEL domains.

Number Species	Opisthokonta	Viridiplantae	Stramenopiles	Total
DUF588 (PF04535)	3	69	2	74
MARVEL (PF01284)	269	4	4	277

Number Predicted domains	Opisthokonta	Viridiplantae	Stramenopiles	Total
DUF588 (PF04535)	3	761	3	767
MARVEL (PF01284)	2165	4	22	2191

Pfam 27.0 (March 2013, 14831 families)

Supplementary Table 3. Annotation of UniProtKB entries used for the phylogenetic analysis presented in figure 1.

(U = unassigned)

Group(number); Subgroup (letter)	CASPL nomenclature	Species	UniProtAC ID	Additional ID and comments
0U	CaCASPL0U1	Chlorokybus atmophyticus	P0DI72	Annotated as Marvel
0U	CaCASPL0U2	Chlorokybus atmophyticus	P0DI73	Annotated as Marvel
0U	OtCASPL0U1	Ostreococcus tauri	Q00U99	Ot16g01510
0U	OlCASPL0U1	Ostreococcus lucimarinus	A4S8B7	
0U	MpCASPL0U1	Micromonas pusilla	C1N652	Annotated as Marvel
0U		Micromonas sp.	C1EI34	Annotated as Marvel
1A	RcCASP5	Ricinus communis	B9T4E6	
1A	VvCASP3	Vitis vinifera	A7PMY7	VIT_14s0108g01050
1A	PvCASP2	Panicum virgatum	P0DI34	
1A	SbCASP4	Sorghum bicolor	C5Y9U6	Sb06g018970
1A	OrCASP1	Oryza rufipogon	F2QA93	
1A	OsCASP5	Oryza sativa subsp. japonica	Q7XUV7	Os04g0460400 LOC_Os04g38690
1A	OsCASP6	Oryza sativa subsp. indica	A2XU91	
1A	OsCASP5	Oryza sativa subsp. japonica	Q6EP58	Os02g0578333 LOC_Os02g36845
1A	OsCASP5	Oryza sativa subsp. indica	B8AEC9	
1A	PvCASP1	Panicum virgatum	P0DI33	
1A	SbCASP3	Sorghum bicolor	C5Z7E3	Sb10g008220
1A	ZmCASP1	Zea mays	B6T959	
1A	TaCASP2	Triticum aestivum	P0DI42	
1A	OsCASP4	Oryza sativa subsp. japonica	Q6Z2U5	Os02g0743900 LOC_Os02g51010
1A	BdCASP3	Brachypodium distachyon	P0DI36	Bradi1g45110
1A	OsCASP3	Oryza sativa subsp. japonica	Q67X40	Os06g0231050 LOC_Os06g12500
1A	OsCASP3	Oryza sativa subsp. indica	A2YAZ1	
1A	StCASP1	Solanum tuberosum	P0DI44	
1A	MdCASP1	Malus domestica	P0DI54	
1A	PtCASP6	Populus trichocarpa	B9I534	
1A	AlCASP5	Arabidopsis lyrata	D7M7B3	
1A	AtCASP5	Arabidopsis thaliana	Q9LXF3	At5g15290
1A	LsCASP1	Lactuca sativa	P0DI59	
1A	MtCASP3	Medicago truncatula	G7L218	MTR_7g011090
1A	RcCASP4	Ricinus communis	B9S8Z3	
1A	AlCASP6	Arabidopsis lyrata	D7KBH3	
1A	AtCASPL1A1	Arabidopsis thaliana	Q9XI72	AT1G14160
1A	PtCASP5	Populus trichocarpa	B9HI87	
1A	MtCASP2	Medicago truncatula	G7JG80	MTR_4g081880
1A	LjCASP1	Lotus japonicus	P0DKC2	
1A	LjCASP2	Lotus japonicus	P0DI58	
1A	GmCASP6	Glycine max	C6T4A0	
1A	MtCASP1	Medicago truncatula	G7KGQ4	MTR_5g041900
1A	GmCASP5	Glycine max	C6T1G0	
1A	LsCASP1	Lactuca saligna	P0DI35	
1A	SdCASP1	Solanum demissum	Q60D27	
1A	SdCASP2	Solanum demissum	Q5NRN4	
1A	BdCASP2	Brachypodium distachyon	P0DI37	Bradi3g12975
1A	SbCASP2	Sorghum bicolor	C5YLC9	Sb07g000300
1A	OsCASP2	Oryza sativa subsp. japonica	Q6Z1Y7	Os08g0101900 LOC_Os08g01160
1A	OsCASP2	Oryza sativa subsp. indica	A2YQB8	
1A	BdCASP1	Brachypodium distachyon	P0DI38	Bradi5g15727
1A	TaCASP1	Triticum aestivum	E6Y2A0	
1A	OsCASP1	Oryza sativa subsp.	Q7XPU9	Os04g0684300

		japonica		LOC_Os04g58760
1A	OsCASP1	Oryza sativa subsp. indica	B8ART0	
1A	SbCASP1	Sorghum bicolor	C5YAP3	Sb06g033470
1A	ZmCASP2	Zea mays	B6U045	
1A	VvCASP1	Vitis vinifera	A7PP95	VIT_08s0007g02880
1A	CsCASP1	Cynara scolymus	P0DI62	
1A	TkCASP1	Taraxacum kok-saghyz	P0DI32	
1A	MgCASP3	Mimulus guttatus	P0DI53	
1A	TpCASP2	Triphysaria pusilla	P0DI30	
1A	VvCASP2	Vitis vinifera	A7QF77	VIT_06s0080g00840
1A	RcCASP3	Ricinus communis	B9SCX0	
1A	VuCASP3	Vigna unguiculata	P0DI41	
1A	GmCASP5	Glycine max	C6T4E0	
1A	MtCASP4	Medicago truncatula	G7IHF9	MTR_2g086740
1A	LjCASP3	Lotus japonicus	P0DI56	
1A	AlCASP3	Arabidopsis lyrata	D7LGW9	
1A	AtCASP3	Arabidopsis thaliana	Q9ZQI2	At2g27370
1A	PtCASP4	Populus trichocarpa	B9HQ42	
1A	HaCASP1	Helianthus annuus	P0DI60	
1A	CmCASP1	Cucumis melo	P0DI61	
1A	PtCASP3	Populus trichocarpa	B9IIR4	
1A	GmCASP4	Glycine max	C6TH93	
1A	LjCASP4	Lotus japonicus	P0DI55	
1A	VuCASP2	Vigna unguiculata	P0DI39	
1A	LjCASP5	Lotus japonicus	P0DI57	
1A	GmCASP3	Glycine max	C6T1K6	
1A	VuCASP1	Vigna unguiculata	P0DI40	
1A	GmCASP2	Glycine max	C6TFL9	
1A	GmCASP1	Glycine max	C6T2E7	
1A	RcCASP2	Ricinus communis	B9SX13	
1A	TcCASP1	Theobroma cacao	P0DI43	
1A	RcCASP1	Ricinus communis	B9SX12	
1A	AlCASP4	Arabidopsis lyrata	D7LZ50	
1A	AtCASP4	Arabidopsis thaliana	Q9FFZ7	At5g06200
1A	RsCASP2	Raphanus sativus	P0DI46	
1A	AlCASP2	Arabidopsis lyrata	D7LAP2	
1A	AtCASP2	Arabidopsis thaliana	Q9CAX3	At3g11550
1A	AlCASP1	Arabidopsis lyrata	D7LIN7	
1A	AtCASP1	Arabidopsis thaliana	Q9SIH4	At2g36100
1A	RrCASP1	Raphanus raphanistrum	P0DI49	
1A	RsCASP1	Raphanus sativus	P0DI45	
1A	PtCASP2	Populus trichocarpa	B9IIR5	
1A	PtCASP1	Populus trichocarpa	B9HBX2	
1A	MgCASP2	Mimulus guttatus	P0DI51	Premature stop codon, TM4 truncated
1A	MgCASP1	Mimulus guttatus	P0DI52	
1A	TpCASP1	Triphysaria pusilla	P0DI31	
1A	ShCASP1	Striga hermontica	P0DI63	
1A	NtCASP1	Nicotiana tabacum	P0DI50	
1A	PgCASP1	Picea glauca	P0DH81	
1A	PtCASP1	Pinus taeda	P0DH80	
1A	SaCASP1	Striga asiatica	Q1W3A5	Premature stop codon, TM4 truncated
1B	OsCASPL1B1	Oryza sativa subsp. indica	A2ZMM4	
1B	OsCASPL1B1	Oryza sativa subsp. indica	B8BMY7	
1B	OsCASPL1B1	Oryza sativa subsp. japonica	Q0ILZ7	Os12g0610800 LOC_Os12g41690
1B	SbCASPL1B1	Sorghum bicolor	C5YRU8	Sb08g021090
1B	ZmCASPL1B1	Zea mays	B6TUH4	
1B	GmCASPL1B1	Glycine max	C6TG62	
1B	PtCASPL1B1	Populus trichocarpa	B9I0U9	

1B	RcCASPL1B1	Ricinus communis	B9SV63	
1B	PtCASPL1B2	Populus trichocarpa	B9GIE4	
1B	AlCASPL1B1	Arabidopsis lyrata	D7MM00	
1B	AtCASPL1B1	Arabidopsis thaliana	Q9FI10	At5g44550
1B	AlCASPL1B2	Arabidopsis lyrata	D7MFJ8	
1B	AtCASPL1B2	Arabidopsis thaliana	Q9SUP0	At4g20390
1B	ZmCASPL1B2	Zea mays	A7QC16	
1C	PtCASPL1C1	Populus trichocarpa	B9IK21	
1C	ZmCASPL1C1	Zea mays	A7PJ32	
1C	OsCASPL1C1	Oryza sativa subsp. indica	A2WMK1	
1C	OsCASPL1C1	Oryza sativa subsp. japonica	Q9LI17	Os01g0237000 LOC_Os01g13560
1C	OsCASPL1C1	Oryza sativa subsp. indica	A2WMK7	
1C	OsCASPL1C2	Oryza sativa subsp. japonica	Q84UT5	Os05g0245300 LOC_Os05g15630
1C	OsCASPL1C2	Oryza sativa subsp. indica	A2Y2B7	
1C	SbCASPL1C1	Sorghum bicolor	C5YVA2	Sb09g008190
1C	ZmCASPL1C2	Zea mays	B6SZU6	
1C	AlCASPL1C1	Arabidopsis lyrata	D7M2M8	
1C	AtCASPL1C1	Arabidopsis thaliana	Q9ZT81	At4g03540
1C	AlCASPL1C2	Arabidopsis lyrata	D7KCH2	
1C	AtCASPL1C2	Arabidopsis thaliana	Q9LR57	At1g03700
1C	RcCASPL1C1	Ricinus communis	B9RW00	
1C	PtCASPL1C2	Populus trichocarpa	B9N2D0	
1C	PtCASPL1C3	Populus trichocarpa	B9N5U6	
1C	VvCASPL1C1	Vitis vinifera	A7R333	
1C	RcCASPL1C2	Ricinus communis	B9RZ92	
1C	PtCASPL1C2	Populus trichocarpa	B9N3F4	
1C	PtCASPL1C3	Populus trichocarpa	B9H2V1	
1D	MaCASPL1D1	Musa acuminata	Q1EPG6	
1D	OsCASPL1D1	Oryza sativa subsp. japonica	Q6YT98	Os07g0442900 LOC_Os07g26110
1D	SbCASPL1D1	Sorghum bicolor	C5X4A5	Sb02g009660
1D	ZmCASPL1D1	Zea mays	B6U361	
1D	InCASPL1D1	Ipomoea nil	A2PZE5	
1D	BvCASPL1D1	Beta vulgaris	D2KQI6	
1D	VvCASPL1D1	Vitis vinifera	A7NW79	VIT_05s0020g01830
1D	GmCASPL1D1	Glycine max	C6SXZ3	
1D	GmCASPL1D2	Glycine max	C6SVQ5	
1D	PtCASPL1D1	Populus trichocarpa	B9HMP5	
1D	RcCASPL1D1	Ricinus communis	B9RT03	
1D	AlCASPL1D1	Arabidopsis lyrata	D7MAF7	
1D	AtCASPL1D1	Arabidopsis thaliana	Q9FE29	AT4G15610
1D	AlCASPL1D2	Arabidopsis lyrata	D7L5G6	
1D	AtCASPL1D2	Arabidopsis thaliana	Q9SQU2	AT3G06390
1E	MaCASPL1E1	Musa acuminata	Q1EPG7	
1E	OsCASPL1E1	Oryza sativa subsp. japonica	Q9ARX2	Os01g0363300 LOC_Os01g26120
1E	OsCASPL1E1	Oryza sativa subsp. indica	B8A7Z5	
1E	SbCASPL1E1	Sorghum bicolor	C5XKI6	Sb03g014480
1E	ZmCASPL1E1	Zea mays	B4FAP1	
1E	PtCASPL1E1	Populus trichocarpa	B9HMP6	
1E	RcCASPL1E1	Ricinus communis	B9RT04	
1E	GmCASPL1E1	Glycine max	C6TBD0	
1E	GmCASPL1E2	Glycine max	C6SZP8	
1E	VvCASPL1E1	Vitis vinifera	A7PTY8	VIT_07s0104g01350
1E	VvCASPL1E2	Vitis vinifera	A7NW78	VIT_05s0020g01820
1E	AlCASPL1E1	Arabidopsis lyrata	D7MAF5	
1E	AtCASPL1E1	Arabidopsis thaliana	Q8L8Z1	At4g15630

1E	AlCASPL1E2	Arabidopsis lyrata	D7MAF6	
1E	AtCASPL1E2	Arabidopsis thaliana	O23413	At4g15620
1F	VvCASPL1F1	Vitis vinifera	A7PHN8	VIT_17s0000g00560
1F	RcCASPL1F1	Ricinus communis	B9RA90	
1F	PtCASPL1F1	Populus trichocarpa	B9IFI5	
1F	PtCASPL1F2	Populus trichocarpa	B9I3X5	
1F	AlCASPL1F1	Arabidopsis lyrata	D7MGK0	
1F	AtCASPL1F1	Arabidopsis thaliana	Q9M0L3	At4g25040
1F	RcCASPL1F2	Ricinus communis	B9RH17	
1F	PtCASPL1F3	Populus trichocarpa	B9GFG6	
1F	VvCASPL1F2	Vitis vinifera	A7PA04	VIT_14s0068g01400
1U	PsCASPL1U1	Picea sitchensis	A9P0A6	
1U	SbCASPL1U1	Sorghum bicolor	C5Y7C6	Sb05g025790
1U	OsCASPL1U1	Oryza sativa subsp. japonica	Q2R0D4	Os11g0649400 LOC_Os11g42940
1U	SbCASPL1U2	Sorghum bicolor	C5Y376	Sb05g019440
1U	OsCASPL1U2	Oryza sativa subsp. japonica	Q2R0D1	Os11g0649700 LOC_Os11g42970
1U	OsCASPL1U3	Oryza sativa subsp. japonica	Q2R0D2	Os11g0649600 LOC_Os11g42960
1U	SbCASPL1U3	Sorghum bicolor	C5Y7C7	Sb05g025800
1U	SbCASPL1U4	Sorghum bicolor	C5Y7C8	Sb05g025810
1U	PpCASPL1U1	Physcomitrella patens	A9TZ63	
1U	PpCASPL1U2	Physcomitrella patens	A9STS7	
1U	PpCASPL1U3	Physcomitrella patens	A9SEY7	
1U	PpCASPL1U4	Physcomitrella patens	A9TKY8	
1U	MpCASPL1U1	Marchantia polymorpha	P0DH83	
2A	AlCASPL2A1	Arabidopsis lyrata	D7KFC7	
2A	AtCASPL2A1	Arabidopsis thaliana	Q8VZQ3	At1g17200
2A	AlCASPL2A2	Arabidopsis lyrata	D7L342	
2A	AtCASPL2A2	Arabidopsis thaliana	Q9LUL1	At3g14380
2A	VvCASPL2A1	Vitis vinifera	A7QBZ2	VIT_01s0010g01870
2A	RcCASPL2A1	Ricinus communis	B9T3K6	
2A	PtCASPL2A1	Populus trichocarpa	B9I0G0	
2A	PtCASPL2A2	Populus trichocarpa	B9GHX8	
2A	GhCASPL2A1	Gossypium hirsutum	Q8W4Z5	
2A	GmCASPL2A1	Glycine max	C6SYW3	
2A	GmCASPL2A2	Glycine max	C6TCJ2	
2A	OsCASPL2A1	Oryza sativa subsp. japonica	Q0JEF7	Os04g0281900 LOC_Os04g21320
2A	OsCASPL2A1	Oryza sativa subsp. indica	B8ARW3	
2A	ZmCASPL2A1	Zea mays	B4FBQ7	
2A	SbCASPL2A1	Sorghum bicolor	C5YDQ9	Sb06g005640
2A	ZmCASPL2A2	Zea mays	B6SR79	
2A	PsCASPL2A1	Picea sitchensis	A9NMM6	
2A	PsCASPL2A2	Picea sitchensis	A9P1V1	
2A	PsCASPL2A3	Picea sitchensis	D5A972	
2B	PtCASPL2B1	Populus trichocarpa	B9IH36	
2B	PtCASPL2B2	Populus trichocarpa	B9HD38	
2B	RcCASPL2B1	Ricinus communis	B9SA89	
2B	VvCASPL2B1	Vitis vinifera	A7R385	
2B	AlCASPL2B1	Arabidopsis lyrata	D7M9V1	
2B	AtCASPL2B1	Arabidopsis thaliana	Q8L9B5	At4g16442
2B	ThCASPL2B1	Thellungiella halophila	E4MWF4	
2B	AlCASPL2B2	Arabidopsis lyrata	D7LIK3	
2B	AtCASPL2B2	Arabidopsis thaliana	Q8L924	At2g35760
2BC	PsCASPL2BC1	Picea sitchensis	D5A8E6	

2BC	PsCASPL2BC2	Picea sitchensis	B8LQF9	
2C	OsCASPL2C1	Oryza sativa subsp. japonica	Q67W83	Os06g0656300 LOC_Os06g44610
2C	SbCASPL2C1	Sorghum bicolor	C5Z782	Sb10g026120
2C	ZmCASPL2C1	Zea mays	B6U769	
2C	ZmCASPL2C2	Zea mays	B6TUB4	
2C	ZmCASPL2C3	Zea mays	B6SZA7	
2C	OsCASPL2C2	Oryza sativa subsp. japonica	Q6ETN2	Os02g0177700 LOC_Os02g08110
2C	SbCASPL2C2	Sorghum bicolor	C5XW97	Sb04g005230
2C	ZmCASPL2C4	Zea mays	B6U8R7	
2C	VvCASPL2C1	Vitis vinifera	A7Q6G6	VIT_11s0052g01140
2C	GmCASPL2C1	Glycine max	C6SZ04	
2C	AlCASPL2C1	Arabidopsis lyrata	D7MFW5	
2C	AtCASPL2C1	Arabidopsis thaliana	Q8L8U9	At4g25830
2C	GhCASPL2C1	Gossypium hirsutum	Q5K4H9	
2C	PtCASPL2C1	Populus trichocarpa	B9IM09	
2D	OsCASPL2D1	Oryza sativa subsp. japonica	Q6YW53	Os02g0219900 LOC_Os02g12760
2D	OsCASPL2D1	Oryza sativa subsp. indica	A2X2I0	
2D	SbCASPL2D1	Sorghum bicolor	C5XY39	Sb04g007720
2D	ZmCASPL2D1	Zea mays	B6TUW9	
2D	VvCASPL2D1	Vitis vinifera	A7P0P3	VIT_19s0090g00570
2D	GmCASPL2D1	Glycine max	C6T2J5	
2D	RcCASPL2D1	Ricinus communis	B9SV84	
2D	PtCASPL2D1	Populus trichocarpa	B9HTL5	
2D	AlCASPL2D1	Arabidopsis lyrata	D7MUY4	
2D	AtCASPL2D1	Arabidopsis thaliana	Q9FFT2	At5g54980
2U	OsCASPL2B-1	Oryza sativa subsp. japonica	Q0IN16	Os12g0514300 LOC_Os12g32970
2U	SbCASPL2U1	Sorghum bicolor	C5YP66	Sb08g016550
2U	ZmCASPL2U1	Zea mays	B6TGJ8	
2U	SbCASPL2U2	Sorghum bicolor	C5WUP3	Sb01g044070
2U	SmCASPL2U1	Selaginella moellendorffii	P0DH67	U-unassigned
2U	SmCASPL2U2	Selaginella moellendorffii	P0DH65	
2U	SmCASPL2U3	Selaginella moellendorffii	D8QNV6	
2U	SmCASPL2U4	Selaginella moellendorffii	D8SJ65	
2U	SmCASPL2U5	Selaginella moellendorffii	D8T829	
2U	SmCASPL2U6	Selaginella moellendorffii	D8T2C0	
2U	SmCASPL2U7	Selaginella moellendorffii	D8ST13	
2U	SmCASPL2U8	Selaginella moellendorffii	D8S6A8	
2U	SmCASPL2U9	Selaginella moellendorffii	P0DH63	
2U	SmCASPL2U10	Selaginella moellendorffii	P0DH61	
2U	SmCASPL2U11	Selaginella moellendorffii	D8ST12	
2U	MpCASPL2U1	Marchantia polymorpha	P0DH82	
2U	PaCASPL2U1	Pteridium aquilinum	P0DI24	
2U	PaCASPL2U2	Pteridium aquilinum	P0DI28	
2U	AcCASPL2U1	Adiantum capillus-veneris	P0DH84	
2U	PaCASPL2U3	Pteridium aquilinum	P0DI25	
2U	OlCASPL2U1	Osmunda lancea	P0DI21	
2U	OlCASPL2U2	Osmunda lancea	P0DI20	
3A	HvCASPL3A1	Hordeum vulgare	F2EL82	
3A	SbCASPL3A1	Sorghum bicolor	C5XIF2	Sb03g033320
3A	OsCASPL3A1	Oryza sativa subsp. japonica	Q5JM57	Os01g0725400 LOC_Os01g52610
3A	OsCASPL3A1	Oryza sativa subsp. indica	B8A927	
3A	VvCASPL3A1	Vitis vinifera	A7P756	VIT_09s0002g03780
3A	RcCASPL3A1	Ricinus communis	B9RQG7	

3A	PtCASPL3A1	Populus trichocarpa	B9GXD6	
3A	PtCASPL3A2	Populus trichocarpa	B9GGL4	
3A	AtCASPL3A1	Arabidopsis thaliana	Q3EB59	At3g16300
3A	AtCASPL3A2	Arabidopsis thaliana	Q1PFB8	At1g79780
3A	PcCASPL3A1	Picea sitchensis	A9NN43	
3A	PaCASPL3A1	Pteridium aquilinum	P0DI26	
4A	AtCASPL4A1	Arabidopsis thaliana	Q9FNE8	At5g40300
4A	AlCASPL4A1	Arabidopsis lyrata	D7MMW4	
4A	AtCASPL4A2	Arabidopsis thaliana	Q501G6	At5g62820
4A	AlCASPL4A2	Arabidopsis lyrata	D7LIR2	
4A	AtCASPL4A3	Arabidopsis thaliana	Q84WP5	At2g36330
4A	OsCASPL4A1	Oryza sativa subsp. indica	A3A2W2	Os02g0134500 LOC_Os02g04180
4A	SbCASPL4A1	Sorghum bicolor	C5XTX2	Sb04g002820
4A	ZmCASPL4A1	Zea mays	B6TWJ1	
4A	ZmCASPL4A2	Zea mays	C4JAF2	
4A	MtCASPL4A1	Medicago truncatula	O24088	
4A	AtCASPL4A4	Arabidopsis thaliana	Q3EA54	At4g11655
4B	HvCASPL4B1	Hordeum vulgare	F2E2E4	
4B	OsCASPL4B1	Oryza sativa subsp. japonica	Q84NQ7	Os07g0692200 LOC_Os07g49200
4B	HvCASPL4B2	Hordeum vulgare	F2D276	
4B	OsCASPL4B2	Oryza sativa subsp. japonica	Q10MR5	Os03g0298300 LOC_Os03g18680
4B	SbCASPL4B1	Sorghum bicolor	C5WNF5	Sb01g038100
4B	HvCASPL4B3	Hordeum vulgare	F2E5T1	
4B	OsCASPL4B3	Oryza sativa subsp. japonica	B9F6Z0	Os03g0817100 LOC_Os03g60250
4B	AlCASPL4B1	Arabidopsis lyrata	D7LBN4	
4B	AtCASPL4B1	Arabidopsis thaliana	Q8LE26	At2g38480
4B	OsCASPL4B4	Oryza sativa subsp. japonica	Q5W6M3	Os05g0344400 LOC_Os05g27790
4C	OsCASPL4C1	Oryza sativa subsp. japonica	Q2QNE3	Os12g0568700 LOC_Os12g38100
4C	RcCASPL4C1	Ricinus communis	B9SR15	
4C	PtCASPL4C1	Populus trichocarpa	B9HMF8	
4C	PtCASPL4C2	Populus trichocarpa	B9HTK2	
4C	AtCASPL4C1	Arabidopsis thaliana	Q9M2U0	At3g55390
4C	PpCASPL4C1	Physcomitrella patens	A9STU1	
4C	PpCASPL4C2	Physcomitrella patens	A9S848	
4C	PpCASPL4C3	Physcomitrella patens	A9T836	
4C	PaCASPL4C1	Pteridium aquilinum	P0DI23	
4D	SbCASPL4D1	Sorghum bicolor	C5Y494	Sb05g021340
4D	OsCASPL4D1	Oryza sativa subsp. japonica	Q2R2T4	Os11g0549625 LOC_Os11g34730
4D	GmCASPL4D1	Glycine max	C6T1Z6	
4D	CaCASPL4D1	Capsicum annuum	A1XGB4	
4D	RcCASPL4D1	Ricinus communis	B9SXY8	
4D	PtCASPL4D1	Populus trichocarpa	B9NBE5	
4D	AlCASPL4D1	Arabidopsis lyrata	D7LD60	
4D	AtCASPL4D1	Arabidopsis thaliana	Q8GWD5	At2g39530
4D	AlCASPL4D2	Arabidopsis lyrata	D7LD59	
4D	AtCASPL4D2	Arabidopsis thaliana	Q56X75	At2g39518
4U	SbCASPL4U1	Sorghum bicolor	C5XEK4	Sb03g029220
4U	ZmCASPL4U1	Zea mays	B6UBY6	
5A	PaCASPL5A1	Pteridium aquilinum	P0DI27	

5A	AtCASPL5A1	Arabidopsis thaliana	Q6NPF8	AT2G37200
5A	ZmCASPL5A1	Zea mays	P0DI67	
5A	ZmCASPL5A2	Zea mays	P0DI66	
5A	BdCASPL5A1	Brachypodium distachyon	P0DI68	
5A	OsCASPL5A1	Oryza sativa subsp. japonica	Q10Q78	Os03g0206600 LOC_Os03g10870
5A	ZmCASPL5A3	Zea mays	B4FNS3	
5A	OsCASPL5A2	Oryza sativa subsp. indica	A2Z669	
5A	OsCASPL5A2	Oryza sativa subsp. japonica	Q339M6	Os10g0343200 LOC_Os10g20250
5A	AtCASPL5A2	Arabidopsis thaliana	Q9SKN3	AT2G28370
5A	GbCASPL5A1	Ginkgo biloba	P0DI70	
5A	GbCASPL5A2	Ginkgo biloba	P0DI69	
5A	PcCASPL5A1	Pinus contorta	P0DI64	
5A	PsCASPL5A1	Picea sitchensis	A9NYX5	
5A	PpCASPL5A1	Physcomitrella patens	A9RLK6	
5A	PpCASPL5A2	Physcomitrella patens	A9RKK4	
5A	PaCASPL5A2	Pteridium aquilinum	P0DI22	
5A	SmCASPL5A1	Selaginella moellendorffii	D8QNI1	
5B	ZmCASPL5B1	Zea mays	B6TM88	
5B	OsCASPL5B1	Oryza sativa subsp. indica	B8AC36	
5B	OsCASPL5B1	Oryza sativa subsp. japonica	Q5N794	Os01g0847300 LOC_Os01g62850
5B	OsCASPL5B2	Oryza sativa subsp. indica	B8AYU8	
5B	OsCASPL5B2	Oryza sativa subsp. japonica	Q0DHM7	Os05g0456500 LOC_Os05g38250
5B	ZmCASPL5B2	Zea mays	B6TAX2	
5B	ZmCASPL5B3	Zea mays	B6T990	
5B	OsCASPL5B3	Oryza sativa subsp. indica	B8BD96	
5B	OsCASPL5B3	Oryza sativa subsp. japonica	Q6K478	Os09g0249400 LOC_Os09g07480
5B	AtCASPL5B1	Arabidopsis thaliana	Q9LZM5	AT5G02060
5B	AtCASPL5B2	Arabidopsis thaliana	Q945M8	AT3G53850
5B	AtCASPL5B3	Arabidopsis thaliana	Q8L7R5	At3G23200
5B	GbCASPL5B1	Ginkgo biloba	P0DI71	
5B	PcCASPL5B1	Picea sitchensis	D5ACW4	
5C	ZmCASPL5C1	Zea mays	B6U300	
5C	OsCASPL5C1	Oryza sativa subsp. indica	B8BPI2	
5C	OsCASPL5C1	Oryza sativa subsp. japonica	Q10EJ2	Os03g0767900 LOC_Os03g55870
5C	AtCASPL5C1	Arabidopsis thaliana	Q66GI1	AT4G37235
5C	AtCASPL5C2	Arabidopsis thaliana	P0CB17	AT3G50810
5C	AtCASPL5C3	Arabidopsis thaliana	Q3ECT8	AT1G49405
UU	PpCASPLUU-1	Physcomitrella patens	A9SG36	
UU	PpCASPLUU1	Physcomitrella patens	A9SU70	U-unassigned
UU	PpCASPLUU2	Physcomitrella patens	A9SHQ9	
UU	PpCASPLUU3	Physcomitrella patens	A9SG36	
UU	SmCASPLUU1	Selaginella moellendorffii	D8QQW9	
UU	SmCASPLUU2	Selaginella moellendorffii	D8R814	
UU	PpCASPLUU4	Physcomitrella patens	A9SB31	
UU	PpCASPLUU5	Physcomitrella patens	A9S1T8	
UU	PpCASPLUU6	Physcomitrella patens	A9RZ57	
UU	PpCASPLUU7	Physcomitrella patens	A9RJH1	
UU	SbCASPLUU-1	Sorghum bicolor	C5YHP6	Sb07g025950
UU	OsCASPLUU-1	Oryza sativa subsp. japonica	Q6Z1G3	Os08g0536200 LOC_Os08g42430
UU	OsCASPLUU-1	Oryza sativa subsp. indica	A2YXI1	

Supplemental Table 4. Transgenic lines used in this study

Transcriptional reporters.
Promoters of selected genes have been amplified, digested with KpnI and BamHI, and cloned upstream the NLS-GUS reporter coding sequence into pNDARO-30 (Genebank file below)

Gene	Primers used to amplify the promoter Forward Reverse	Number of transgenic lines showing the expression pattern reported in Figure 5
AtCASPL1A1 / AT1G14160	Attgcaggtacctggatcttttccactttactttg Attgcaggatcctttttgctctgtgactgtttac	6
AtCASPL1D2 / AT3G06390	Attgcaggtaccggaagctacgaaatctgctttc attgcaggatccagatgattctataactcttttgtgg	11
AtCASPL4D1 /AT2G39530	Attgcaggtacccttgttttctcgaaagag attgcaggatcctaaatcttcccgttaattaatcg	4
AtCASPL2A1 / AT1G17200	Attgcaggtaccccggattagcttcagtaaacca Attgcaggatcccttctagcttctttagttttctc	9
AtCASPL5B1 / AT5G02060	Attgcaggtaccataatgagataacaagaaatgg attgcaggatcctgatcagaacccaaaaacaaacac	4
AtCASPL1F1 / AT4G25040	Attgcaggtacctttggtgtttatgcatctc attgcaggatcctttttatttaaattcaagctttactc	33
AtCASPL5B2 / AT3G53850	Attgcaggtaccaaggcgcaacacagggattattggtg attgcaggatccttcaatcaataacgactcca	10
AtCASPL5B3 / AT3G23200	Attgcaggtacctttttgttaaggtattatgg attgcaggatccttctcttccacaagaaaccca	9
AtCASPL5C3 / AT1G49405	Attgcaggtaccaagaatcacattcacacatcag attgcaggatccccccagctttgcttgtg	10

```
LOCUS       pNDARO-030        8152 bp    DNA     circular     19-MAR-2009
SOURCE
  ORGANISM
COMMENT     This file is created by Vector NTI
            http://www.invitrogen.com/
COMMENT     VNTDATE|493216076|
COMMENT     VNTDBDATE|513192007|
COMMENT     LSOWNER|
COMMENT     VNTNAME|pNDARO-030|
COMMENT     VNTAUTHORNAME|Joop Vermeer|
FEATURES             Location/Qualifiers
     CDS             complement(5155..5967)
                     /vntifkey="4"
                     /label=Bacterial\Kan-R
     CDS             complement(7141..7689)
                     /vntifkey="4"
                     /label=BAR-R
     misc_feature    complement(4278..4302)
                     /vntifkey="21"
                     /label=RB
     misc_feature    6815..6846
                     /vntifkey="21"
                     /label=LB
     terminator      3975..4227
                     /vntifkey="43"
                     /label=NOS\terminator
     CDS             2042..2071
                     /vntifkey="4"
                     /label=NLS
     CDS             2093..3904
                     /vntifkey="4"
                     /label=GUS
     terminator      complement(106..129)
                     /vntifkey="43"
                     /label=SacB\terminator
     promoter        complement(1549..2011)
                     /vntifkey="30"
```

```
                     /label=SacB\promoter
     CDS             complement(130..1548)
                     /vntifkey="4"
                     /label=SacB
     primer          complement(2065..2080)
                     /vntifkey="27"
                     /label=oDR108
     primer          4013..4032
                     /vntifkey="27"
                     /label=oDR109
     primer          1..22
                     /vntifkey="27"
                     /label=oDR110
     misc_feature    46..96
                     /vntifkey="21"
                     /label=Arm-A
     misc_feature    complement(2042..2085)
                     /vntifkey="21"
                     /label=ArmB
     primer          complement(2244..2265)
                     /vntifkey="27"
                     /label=ng67
     primer          1899..1920
                     /vntifkey="27"
                     /label=oDR111
BASE COUNT     2059 a      1899 c      1997 g      2197 t
ORIGIN
        1 cgttgtaaaa cgacggccag tgagcgcgcg taatacgact cactataggg cgaattgggt
       61 accgggcccg acgtcgcatg ctcccggccg ccatggggcg cgccatcggc attttctttt
      121 gcgtttttat ttgttaactg ttaattgtcc ttgttcaagg atgctgtctt tgacaacaga
      181 tgttttcttg cctttgatgt tcagcaggaa gctaggcgca aacgttgatt gtttgtctgc
      241 gtagaatcct ctgtttgtca tatagcttgt aatcacgaca ttgtttcctt tcgcttgagg
      301 tacagcgaag tgtgagtaag taaaggttac atcgttagga tcaagatcca tttttaacac
      361 aaggccagtt ttgttcagcg gcttgtatgg gccagttaaa gaattagaaa cataaccaag
      421 catgtaaata tcgttagacg taatgccgtc aatcgtcatt tttgatccgc gggagtcagt
      481 gaacagatac catttgccgt tcattttaaa gacgttcgcg cgttcaattt catctgttac
      541 tgtgttagat gcaatcagcg gtttcatcac ttttttcagt gtgtaatcat cgtttagctc
      601 aatcataccg agagcgccgt ttgctaactc agccgtgcgt tttttatcgc tttgcagaag
      661 tttttgactt tcttgacgga agaatgatgt gcttttgcca tagtatgctt tgttaaataa
      721 agattcttcg ccttggtagc catcttcagt tccagtgttt gcttcaaata ctaagtattt
      781 gtggccttta tcttctacgt agtgaggatc tctcagcgta tggttgtcgc ctgagctgta
      841 gttgccttca tcgatgaact gctgtacatt ttgatacgtt tttccgtcac cgtcaaagat
      901 tgatttataa tcctctacac cgttgatgtt caaagagctg tctgatgctg atacgttaac
      961 ttgtgcagtt gtcagtgttt gtttgccgta atgtttaccg gagaaatcag tgtagaataa
     1021 acggattttt ccgtcagatg taaatgtggc tgaacctgac cattcttgtg tttggtcttt
     1081 taggatagaa tcatttgcat cgaatttgtc gctgtcttta aagacgcggc cagcgttttt
     1141 ccagctgtca atagaagttt cgccgacttt ttgatagaac atgtaaatcg atgtgtcatc
     1201 cgcattttta ggatctccgg ctaatgcaaa gacgatgtgg tagccgtgat agtttgcgac
     1261 agtgccgtca gcgttttgta atggccagct gtcccaaacg tccaggcctt ttgcagaaga
     1321 gatattttta attgtggacg aatcgaactc aggaacttga tatttttcat ttttttgctg
     1381 ttcagggatt tgcagcatat catggcgtgt aatatgggaa atgccgtatg tttccttata
     1441 tggcttttgg ttcgtttctt tcgcaaacgc ttgagttgcg cctcctgcca gcagtgcggt
     1501 agtaaaggtt aatactgttg cttgttttgc aaactttttg atgttcatcg ttcatgtctc
     1561 ctttttttatg tactgtgtta gcggtctgct tcttccagcc ctcctgtttg aagatggcaa
     1621 gttagttacg cacaataaaa aaagacctaa aatatgtaag ggtgacgcc aaagtataca
     1681 ctttgccctt tacacatttt aggtcttgcc tgctttatca gtaacaaacc cgcgcgattt
     1741 acttttcgac ctcattctat tagactctcg tttggattgc aactggtcta ttttcctctt
     1801 ttgtttgata gaaaatcata aaaggatttg cagactacgg gcctaaagaa ctaaaaaatc
     1861 tatctgtttc ttttcattct ctgtattttt tatagtttct gttgcatggg cataaagttg
     1921 cctttttaat cacaattcag aaaatatcat aatatctcat ttcactaaat aatagtgaac
     1981 ggcaggtata tgtgatgggt taaaaaggat cggcgcgcca ctagttctag aggatccaac
     2041 aatggctccc aagaagaaga gaaaggtaga tccccgggta ggtcagtccc ttatgttacg
     2101 tcctgtagaa accccaaccc gtgaaatcaa aaaactcgac ggcctgtggg cattcagtct
     2161 ggatcgcgaa aactgtggaa ttgatcagcg ttggtgggaa agcgcgttac aagaaagccg
     2221 ggcaattgct gtgccaggca gttttaacga tcagttcgcc gatgcagata ttcgtaatta
     2281 tgcgggcaac gtctggtatc agcgcgaagt ctttataccg aaaggttggg caggccagcg
```

```
2341 tatcgtgctg cgtttcgatg cggtcactca ttacggcaaa gtgtgggtca ataatcagga
2401 agtgatggag catcagggcg gctatacgcc atttgaagcc gatgtcacgc cgtatgttat
2461 tgccgggaaa agtgtacgta tcaccgtttg tgtgaacaac gaactgaact ggcagactat
2521 cccgccggga atggtgatta ccgacgaaaa cggcaagaaa aagcagtctt acttccatga
2581 tttctttaac tatgccggaa tccatcgcag cgtaatgctc tacaccacgc cgaacacctg
2641 ggtggacgat atcaccgtgg tgacgcatgt cgcgcaagac tgtaaccacg cgtctgttga
2701 ctggcaggtg gtggccaatg gtgatgtcag cgttgaactg cgtgatgcgg atcaacaggt
2761 ggttgcaact ggacaaggca ctagcgggac tttgcaagtg gtgaatccgc acctctggca
2821 accgggtgaa ggttatctct atgaactgtg cgtcacagcc aaaagccaga cagagtgtga
2881 tatctacccg cttcgcgtcg gcatccggtc agtggcagtg aagggcgaac agttcctgat
2941 taaccacaaa ccgttctact ttactggctt tggtcgtcat gaagatgcgg acttgcgtgg
3001 caaaggattc gataacgtgc tgatggtgca cgaccacgca ttaatggact ggattggggc
3061 caactcctac cgtacctcgc attaccctta cgctgaagag atgctcgact gggcagatga
3121 acatggcatc gtggtgattg atgaaactgc tgctgtcggc tttaacctct ctttaggcat
3181 tggtttcgaa gcgggcaaca agccgaaaga actgtacagc gaagaggcag tcaacgggga
3241 aactcagcaa gcgcacttac aggcgattaa agagctgata gcgcgtgaca aaaaccaccc
3301 aagcgtggtg atgtggagta ttgccaacga accggatacc cgtccgcaag gtgcacggga
3361 atatttcgcg ccactggcgg aagcaacgcg taaactcgac ccgacgcgtc cgatcacctg
3421 cgtcaatgta atgttctgcg acgctcacac cgataccatc agcgatctct ttgatgtgct
3481 gtgcctgaac cgttattacg gatggtatgt ccaaagcggc gatttggaaa cggcagagaa
3541 ggtactggaa aaagaacttc tggcctggca ggagaaactg catcagccga ttatcatcac
3601 cgaatacggc gtggatacgt tagccgggct gcactcaatg tacaccgaca tgtggagtga
3661 agagtatcag tgtgcatggc tggatatgta tcaccgcgtc tttgatcgcg tcagcgccgt
3721 cgtcggtgaa caggtatgga atttcgccga ttttgcgacc tcgcaaggca tattgcgcgt
3781 tggcggtaac aagaaaggga tcttcactcg cgaccgcaaa ccgaagtcgg cggcttttct
3841 gctgcaaaaa cgctggactg gcatgaactt cggtgaaaaa ccgcagcagg gaggcaaaca
3901 atgaatcaac aactctcctg gcgcaccatc gtcggctaca gcctcgggaa ttgctaccga
3961 gctcgaattt ccccgatcgt tcaaacattt ggcaataaag tttcttaaga ttgaatcctg
4021 ttgccggtct tgcgatgatt atcatataat ttctgttgaa ttacgttaag catgtaataa
4081 ttaacatgta atgcatgacg ttatttatga gatgggtttt tatgattaga gtcccgcaat
4141 tatacattta atacgcgata gaaaacaaaa tatagcgcgc aaactaggat aaattatcgc
4201 gcgcggtgtc atctatgtta ctagatcggg aattcgatat caagcttatc gataccgtcg
4261 acctcgaggg ggggccctga caggatatat tggcgggtaa actaagtcgc tgtatgtgtt
4321 tgtttgagat ctcatgtgag caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc
4381 gttgctggcg tttttccata ggctccgccc ccctgacgag catcacaaaa atcgacgctc
4441 aagtcagagg tggcgaaacc cgacaggact ataaagatac caggcgtttc cccctggaag
4501 ctccctcgtg cgctctcctg ttccgaccct gccgcttacc ggatacctgt ccgcctttct
4561 cccttcggga agcgtggcgc tttctcatag ctcacgctgt aggtatctca gttcggtgta
4621 ggtcgttcgc tccaagctgg gctgtgtgca cgaacccccc gttcagcccg accgctgcgc
4681 cttatccggt aactatcgtc ttgagtccaa cccggtaaga cacgacttat cgccactggc
4741 agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta cagagttctt
4801 gaagtggtgg cctaactacg gctacactag aagaacagta tttggtatct gcgctctgct
4861 gaagccagtt accttcggaa gaagagttgg tagctcttga tccggcaaac aaaccaccgc
4921 tggtagcggt ggtttttttg tttgcaagca gcagattacg cgcagaaaaa aaggatctca
4981 agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa actcacgtta
5041 agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt taaattaaaa
5101 atgaagtttt aaatcaatct aaagtatata tgtgtaacat tggtctagtg attagaaaaa
5161 ctcatcgagc atcaaatgaa actgcaattt attcatatca ggattatcaa taccatattt
5221 ttgaaaaagc cgtttctgta atgaaggaga aaactcaccg aggcagttcc ataggatggc
5281 aagatcctgg tatcggtctg cgattccgac tcgtccaaca tcaatacaac ctattaattt
5341 cccctcgtca aaaataaggt tatcaagtga gaaatcacca tgagtgacga ctgaatccgg
5401 tgagaatggc aaaagtttat gcatttcttt ccagacttgt tcaacaggcc agccattacg
5461 ctcgtcatca aaatcactcg catcaaccaa accgttattc attcgtgatt gcgcctgagc
5521 gagacgaaat acgcgatcgc tgttaaaagg acaattacaa acaggaatcg aatgcaaccg
5581 gcgcaggaac actgccagcg catcaacaat attttcacct gaatcaggat attcttctaa
5641 tacctggaat gctgttttcc ctgggatcgc agtggtgagt aaccatgcat catcaggagt
5701 acggataaaa tgcttgatgg tcggaagagg cataaattcc gtcagccagt ttagtctgac
5761 catctcatct gtaacatcat tggcaacgct acctttgcca tgtttcagaa acaactctgg
5821 cgcatcgggc ttcccataca atcggtagat tgtcgcacct gattgcccga cattatcgcg
5881 agcccattta tacccatata aatcagcatc catgttggaa tttaatcgcg gccttgagca
5941 agacgtttcc cgttgaatat ggctcataac accccttgta ttactgttta tgtaagcaga
6001 cagttttatt gttcatgatg atatattttt atcttgtgca atgtaacatc agagattttg
6061 agacacaacg tggctttgtt gaataaatcg aacttttgct gagttgaagg atcagatcac
6121 gcatcttccc gacaacgcag accgttccgt ggcaaagcaa aagttcaaaa tcaccaactg
6181 gtccacctac aacaaagctc tcatcaaccg tggctccctc actttctggc tggatgatgg
6241 ggcgattcag gcgatcccca tccaacagcc cgccgtcgag cgggcttttt tatccccgga
```

```
     6301 agcctgtgga tagagggtag ttatccacgt gaaaccgcta atgccccgca aagccttgat
     6361 tcacggggct ttccggcccg ctccaaaaac tatccacgtg aaatcgctaa tcagggtacg
     6421 tgaaatcgct aatcggagta cgtgaaatcg ctaataaggt cacgtgaaat cgctaatcaa
     6481 aaaggcacgt gagaacgcta atagcccttt cagatcaaca gcttgcaaac acccctcgct
     6541 ccggcaagta gttacagcaa gtagtatgtt caattagctt ttcaattatg aatatatata
     6601 tcaattattg gtcgcccttg gcttgtggac aatgcgctac gcgcaccggc tccgcccgtg
     6661 gacaaccgca agcggttgcc caccgtcgag cgcctttgcc cacaacccgg cggccggccg
     6721 caacagatcg ttttataaat tttttttttt gaaaaagaaa aagcccgaaa ggcggcaacc
     6781 tctcgggctt ctggatttcc gatccccgga attagatctt ggcaggatat attgtggtgt
     6841 aacgttatca gcttgcatgc cggtcgatct agtaacatag atgacaccgc gcgcgataat
     6901 ttatcctagt ttgcgcgcta tattttgttt tctatcgcgt attaaatgta taattgcggg
     6961 actctaatca taaaaaccca tctcataaat aacgtcatgc attacatgtt aattattaca
     7021 tgcttaacgt aattcaacag aaattatatg ataatcatcg caagaccggc aacaggattc
     7081 aatcttaaga aactttattg ccaaatgttt gaacgatctg cttgactcta ggggtcatca
     7141 gatttcggtg acgggcagga ccggacgggg cggcaccggc aggctgaagt ccagctgcca
     7201 gaaacccacg tcatgccagt tcccgtgctt gaagccggcc gcccgcagca tgccgcgggg
     7261 ggcatatccg agcgcctcgt gcatgcgcac gctcgggtcg ttgggcagcc cgatgacagc
     7321 gaccacgctc ttgaagccct gtgcctccag ggacttcagc aggtgggtgt agagcgtgga
     7381 gcccagtccc gtccgctggt ggcgggggga gacgtacacg gtcgactcgg ccgtccagtc
     7441 gtaggcgttg cgtgccttcc agggacccgc gtaggcgatg ccggcgacct cgccgtccac
     7501 ctcggcgacg agccagggat agcgctcccg cagacggacg aggtcgtccg tccactcctg
     7561 cggttcctgc ggctcggtac ggaagttgac cgtgcttgtc tcgatgtagt ggttgacgat
     7621 ggtgcagacc gccggcatgt ccgcctcggt ggcacggcgg atgtcggccg ggcgtcgttc
     7681 tgggctcatg gtagatcccc tcgatcgagt tgagagtgaa tatgagactc taattggata
     7741 ccgaggggaa tttatggaac gtcagtggag catttttgac aagaaatatt tgctagctga
     7801 tagtgacctt aggcgacttt tgaacgcgca ataatggttt ctgacgtatg tgcttagctc
     7861 attaaactcc agaaacccgc ggctcagtgg ctccttcaac gttgcggttc tgtcagttcc
     7921 aaacgtaaaa cggcttgtcc cgcgtcatcg gcgggggtca taacgtgact cccttaattc
     7981 tccgctcatg atcgataaca ttaacgctta caatttccat tcgccattca ggctgcgcaa
     8041 ctgttgggaa gggcgatcgg tgcgggcctc ttcgctatta cgccagctgg cgaaaggggg
     8101 atgtgctgca aggcgattaa gttgggtaac gccagggttt tcccagtcac ga
//
```

Translational reporters in the endodermis.

pCASP1:mCherry-CASPL lines were generated using a pUNI-based system. We introduced CASPL coding sequences into pNIGEL-23 (Genebank file below), either by Cre-mediated recombination using pUNI clones, or by classical cloning by digesting vector and PCR product with SfiI. Recombination was performed as in Geldner *et al.*, 2009.

Gene	pUNI Plasmid or PCR product
AtCASP1 / AT2G36100	U23399
AtCASP2 / AT3G11550	U63254
AtCASP3 / AT2G27370	U22823
AtCASPL1A1 / AT1G14160	U60216
AtCASPL1B2 / AT4G20390	U84839
AtCASPL1D1 / AT4G15610	U09043
AtCASPL1D2 / AT3G06390	U20765
AtCASPL1E1 / AT4G15630	U82194
AtCASPL1E2 / AT4G15620	U20479
AtCASPL2A1 / AT1G17200	C104840
AtCASPL2B1 / AT4G16442	U20698
AtCASPL2D1 / AT5G54980	U20296
AtCASPL3A1 / AT3G16300	5’- aattcggccgtcaaggccagaaggagatataaccATGGCGAAAGCAGCAGAGCA-3’ 5’- tcgacggcccatgaggccttagcggtggcgtgagagatg-3’
AtCASPL3A2 / AT1G79780	5’-aattcggccgtcaaggccagaaggagatataaccATGACGAGTAATGGAGAAGGGGGAGA-3’ 5’-tcgacggcccatgaggccctagggagtggagagcacaaggac-3’
AtCASPL4A1 / AT5G40300	U63732
AtCASPL4A2 / AT5G62820	U80035
AtCASPL4B1 / AT2G38480	U10032
AtCASPL4C1 / AT3G55390	U82201
AtCASPL4D1 / AT2G39530	U51086
AtCASPL5A1 / AT2G37200	C63176

AtCASPL5A2 / AT2G28370	U12460
AtCASPL5B1 / AT5G02060	S66993
AtCASPL5B2 / AT3G53850	U13495
AtCASPL5B3 / AT3G23200	U15935
AtCASPL5C1 / AT4G37235	S68175

```
LOCUS       pNIGEL23\pCASP1\mCherry        7067 bp    DNA     circular     22-DEC-2010
SOURCE
  ORGANISM
COMMENT     This file is created by Vector NTI
            http://www.invitrogen.com/
COMMENT     VNTDATE|574274682|
COMMENT     VNTDBDATE|574274908|
COMMENT     LSOWNER|
COMMENT     VNTNAME|pNIGEL23 pCASP1 mCherry|
COMMENT     VNTAUTHORNAME|Demo User|
FEATURES             Location/Qualifiers
     misc_feature    6865..6870
                     /vntifkey="21"
                     /label=HpaI/EcoRV
     misc_feature    complement(5544..6566)
                     /vntifkey="21"
                     /label=Hygromycin-Resistance
     promoter        complement(6567..6872)
                     /vntifkey="29"
                     /label=nos\promoter
     terminator      complement(5075..5540)
                     /vntifkey="43"
                     /label=nos\terminator
     misc_feature    5069..5074
                     /vntifkey="21"
                     /label=HpaI/EcoRV
     rep_origin      4529..5024
                     /vntifkey="33"
                     /label=Replication\origin\pSa
     primer_bind     1..20
                     /vntifkey="28"
                     /label=T7
     misc_feature    5040..5071
                     /vntifkey="21"
                     /label=LB
                     /note="Left T-DNA border"
     repeat_unit     1961..1994
                     /vntifkey="35"
                     /label=loxP
     CDS             complement(3325..4182)
                     /vntifkey="4"
                     /label=Ampicillin-Resistance
     primer_bind     complement(2054..2073)
                     /vntifkey="28"
                     /label=T3
     misc_feature    2445..2497
                     /vntifkey="21"
                     /label=RB
                     /note="right T-DNA border"
     CDS             34..1240
                     /vntifkey="4"
                     /label=CASP1-PR
     CDS             1247..1961
                     /vntifkey="4"
                     /label=mCherry
BASE COUNT     1898 a     1744 c     1648 g     1776 t        1 others
ORIGIN
        1 taatacgact cactataggg cgaattgggt accttaatct gcataaaagt gagtatgaga
       61 gagaagatta aatagatatc aatcctaact aatattcaag aaaacataat atagatcaat
      121 aaattgatga gagtaaaaac acaaagatgt ttagaaataa ttattgtcaa gactcaagtt
```

```
 181 tcttcaaaat atcaagaggc gcttggaata agacccttat tctacaatac atcaatctat
 241 atagagataa agactaagca taatttttaa aatagaaaaa atataaacgt aaataacact
 301 tttttgaggt aatactaaat tttctaaaca tgaaatgtta caaatccaca atatttccat
 361 ataaatttgt aaataatatt ttgttagata atgttaaatt ttctaaactg aaatattaac
 421 aaatccgcag tatttccatt attaaatctc gattttgttt caatgggaga tttgaatttt
 481 gaaccaaaaa aaaaaaaaaa gatttcatca agatatctag gggatattt tgctggaata
 541 tagctttgat gagaatattt atattttgta tctctgaaaa tcaagtttaa aggggaaatg
 601 attatgggtt gaaattttgc aatcaaaagc cctaatttgc aaaaactaca taagtttttt
 661 gtttgggctg gcgctatcgg atccttttag gcttacattt aacatctggt ccacttagaa
 721 agagtcacgt agtatatggt aattgtcaac ttgatttttc aagttaaaag aaatatgtat
 781 caaaatgact aaaaagtagt gaaatattat gtatctaatt tgtttattta ccaaattaat
 841 gctataaaaa tgttcaactg tacaattggc atggaataat atgaacataa atcatacatt
 901 attaagcact tttgcctacg aagggatacc aacttcatta gtttacattt tcttttgtgt
 961 tcaattgtta gctcaaaccc aattaagtgg ggaaagtaag aagcaacaac tcctcttccc
1021 ggacccctaa caaatcaact aaactcaata tcaaaccatt ttaaaagagc tcatcattaa
1081 ctagctacta attattctta atcaatcact gcttaataca aagcactata tatacacttg
1141 tatcttccat tagtttccca ccacaactac aaaacattcc aatacacaac acacaaagca
1201 cacacttttt ctttctttta aaccccaatt gcaagagaaa gaattcatgt tgagcaaggg
1261 cgaggaggat aacatggcca tcatcaagga gttcatgcgc ttcaaggtgc acatggaggg
1321 ctccgtgaac ggccacgagt tcgagatcga gggcgagggc gagggccgcc cctacgaggg
1381 cacccagacc gccaagctga aggtgaccaa gggtggcccc ctgcccttcg cctgggacat
1441 cctgtcccct cagttcatgt acggctccaa ggcctacgtg aagcaccccg ccgacatccc
1501 cgactacttg aagctgtcct tccccgaggg cttcaagtgg gagcgcgtga tgaacttcga
1561 ggacggcggc gtggtgaccg tgacccagga ctcctccctg caggacggcg agttcatcta
1621 caaggtgaag ctgcgcggca ccaacttccc ctccgacggc cccgtaatgc agaagaagac
1681 catgggctgg gaggcctcct ccgagcggat gtaccccgag gacggcgccc tgaagggcga
1741 gatcaagcag aggctgaagc tgaaggacgg cggccactac gacgctgagg tcaagaccac
1801 ctacaaggcc aagaagcccg tgcagctgcc cggcgcctac aacgtcaaca tcaagttgga
1861 catcacctcc cacaacgagg actacaccat cgtggaacag tacgaacgcg ccgagggccg
1921 ccactccacc ggcggcatgg acgagctgta caagcatatg ataacttcgt atagcataca
1981 ttatacgaag ttatcccggg ggatccacta gttctagagc ggccgccacc gcggtggagc
2041 tccagctttt gttcccttta gtgagggtta attccgagct tggcgtaatc atggtcatag
2101 ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg agccggaagh
2161 cataaagtgt aaagcctggg gtgcctaatg agtgagctaa ctcacattaa ttgcgttgcg
2221 ctcactgccc gctttccagt cgggaaacct gtcgtgccag ctgcattaat gaatcggcca
2281 acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc gcttcctcgc tcactgactc
2341 gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct cactcaaagg cggtaatacg
2401 gttatccaca gaatcagggg ataacgcagg aaagaacatg aaggccttga caggatatat
2461 tggcgggtaa actaagtcgc tgtatgtgtt tgtttgagat ctcatgtgag caaaaggcca
2521 gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc
2581 ccctgacgag catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact
2641 ataaagatac caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct
2701 gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc tttctcatag
2761 ctcacgctgt aggtatctca gttcggtgta ggtcgttcgc tccaagctgg gctgtgtgca
2821 cgaacccccc gttcagcccg accgctgcgc cttatccggt aactatcgtc ttgagtccaa
2881 cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc
2941 gaggtatgta ggcggtgcta cagagttctt gaagtggtgg cctaactacg gctacactag
3001 aagaacagta tttggtatct gcgctctgct gaagccagtt accttcggaa gaagagttgg
3061 tagctcttga tccggcaaac aaaccaccgc tggtagcggt ggtttttttg tttgcaagca
3121 gcagattacg cgcagaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc
3181 tgacgctcag tggaacgaaa actcacgtta agggattttg gtcatgagat tatcaaaaag
3241 gatcttcacc tagatccttt taaattaaaa atgaagtttt aaatcaatct aaagtatata
3301 tgagtaaact tggtctgaca gttaccaatg cttaatcagt gaggcaccta tctcagcgat
3361 ctgtctattt cgttcatcca tagttgcctg actccccgtc gtgtagataa ctacgatacg
3421 ggagggctta ccatctggcc ccagtgctgc aatgataccg cgagacccac gctcaccggc
3481 tccagattta tcagcaataa accagccagc cggaagggcc gagcgcagaa gtggtcctgc
3541 aactttatcc gcctccatcc agtctattaa ttgttgccgg gaagctagag taagtagttc
3601 gccagttaat agtttgcgca acgttgttgc cattgctaca ggcatcgtgg tgtcacgctc
3661 gtcgtttggt atggcttcat tcagctccgg ttcccaacga tcaaggcgag ttacatgatc
3721 ccccatgttg tgcaaaaaag cggttagctc cttcggtcct ccgatcgttg tcagaagtaa
3781 gttggccgca gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat
3841 gccatccgta agatgctttt ctgtgactgg tgagtactca accaagtcat tctgagaata
3901 gtgtatgcgg cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca
3961 tagcagaact ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag
4021 gatcttaccg ctgttgagat ccagttcgat gtaacccact cgtgcaccca actgatcttc
4081 agcatctttt actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc
```

```
     4141 aaaaaaggga ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata
     4201 ttattgaagc atttatcagg gttattgtct catgatgata tatttttatc ttgtgcaatg
     4261 taacatcaga gattttgaga cacaacgtgg ctttgttgaa taaatcgaac ttttgctgag
     4321 ttgaaggatc agatcacgca tcttcccgac aacgcagacc gttccgtggc aaagcaaaag
     4381 ttcaaaatca ccaactggtc cacctacaac aaagctctca tcaaccgtgg ctccctcact
     4441 ttctggctgg atgatggggc gattcaggcg atccccatcc aacagcccgc cgtcgagcgg
     4501 gcttttttat ccccggaagc ctgtggatag agggtagtta tccacgtgaa accgctaatg
     4561 ccccgcaaag ccttgattca cggggctttc cggcccgctc caaaaactat ccacgtgaaa
     4621 tcgctaatca gggtacgtga aatcgctaat cggagtacgt gaaatcgcta ataaggtcac
     4681 gtgaaatcgc taatcaaaaa ggcacgtgag aacgctaata gccctttcag atcaacagct
     4741 tgcaaacacc cctcgctccg gcaagtagtt acagcaagta gtatgttcaa ttagcttttc
     4801 aattatgaat atatatatca attattggtc gcccttggct tgtggacaat gcgctacgcg
     4861 caccggctcc gcccgtggac aaccgcaagc ggttgcccac cgtcgagcgc cagcgccttt
     4921 gcccacaacc cggcggccgg ccgcaacaga tcgttttata aatttttttt tttgaaaaag
     4981 aaaaagcccg aaaggcggca acctctcggg cttctggatt tccgatcccc ggaattagag
     5041 atcttggcag gatatattgt ggtgtaacgt tatcagcttg catgccggtc gatctagtaa
     5101 catagatgac accgcgcgcg ataatttatc ctagtttgcg cgctatattt tgttttctat
     5161 cgcgtattaa atgtataatt gcgggactct aatcataaaa acccatctca taaataacgt
     5221 catgcattac atgttaatta ttacatgctt aacgtaattc aacagaaatt atatgataat
     5281 catcgcaaga ccggcaacag gattcaatct taagaaactt tattgccaaa tgtttgaacg
     5341 atctgcttga ctctagggaa ttaattcctg aatcactgcg accggccctc ccgcgaccca
     5401 gccgagcgag cttagcgaac tgtggacgag aactgtgcca ccaagcgtaa ggccgttctc
     5461 tcgcatttgc cttgctaggc tcgcgcgagt tgctggctga ggcgttctcg aaatcagctc
     5521 ttgttcggtc ggcatctact ctattccttt gccctcggac gagtgctggg gcgtcggttt
     5581 ccactatcgg cgagtacttc tacacagcca tcggtccaga cggccgcgct tctgcgggcg
     5641 atttgtgtac gcccgacagt cccggctccg gatcggacga ttgcgtcgca tcgaccctgc
     5701 gcccaagctg catcatcgaa attgccgtca accaagctct gatagagttg gtcaagacca
     5761 atgcggagca tatacgcccg gagccttggc gatcctgcaa gctccggatg cctccgctcg
     5821 aagtagcgcg tctgctgctc catacaagcc aaccacggcc tccagaagaa gatgttggcg
     5881 acctcgtatt gggaatcccc gaacatcgcc tcgctccagt caatgaccgc tgttatgcgg
     5941 ccattgtccg tcaggacatt gttggagccg aaatccgcgt gcacgaggtg ccggacttcg
     6001 gggcagtcct cggcccaaag catcagctca tcgagagcct gcgcgacgga cgcactgacg
     6061 gtgtcgtcca tcacagtttg ccagtgatac acatggggat cagcaatcgc gcatatgaaa
     6121 tcacgccatg tagtgtattg accgattcct tgcggtccga atgggccgaa cccgctcgtc
     6181 tggctaagat cggccgcagc gatagcatcc atagcctccg cgaccggctg aagaacagcg
     6241 ggcagttcgg tttcaggcag gtcttgcaac gtgacaccct gtgcacggcg ggagatgcaa
     6301 taggtcaggc tctcgctgaa ctccccaatg tcaagcactt ccggaatcgg gagcgcggcc
     6361 gatgcaaagt gccgataaac ataacgatct ttgtagaaac catcggcgca gctatttacc
     6421 cgcaggacat atccacgccc tcctacatcg aagctgaaag cacgagattc ttcgccctcc
     6481 gagagctgca tcaggtcgga gacgctgtcg aacttttcga tcagaaactt ctcgacagac
     6541 gtcgcggtga gttcaggctt tttcataggg gggattcgag ttgagagtga atatgagact
     6601 ctaattggat accgagggga atttatggaa cgtcagtgga gcatttttga caagaaatat
     6661 ttgctagctg atagtgacct taggcgactt ttgaacgcgc aataatggtt tctgacgtat
     6721 gtgcttagct cattaaactc cagaaacccg cggctcagtg gctccttcaa cgttgcggtt
     6781 ctgtcagttc caaacgtaaa acggcttgtc ccgcgtcatc ggcgggggtc ataacgtgac
     6841 tcccttaatt ctccgctcat gatcgataac attaacgctt acaattaacg tttacaattt
     6901 cgcgccattc gccattcagg ctgcgcaact gttgggaagg gcgatcggtg cgggcctctt
     6961 cgctattacg ccagctggcg aaagggggat gtgctgcaag gcgattaagt tgggtaacgc
     7021 cagggttttc ccagtcacga cgttgtaaaa cgacggccag tgaattg
//
```

Mutagenesis

Site-directed mutagenesis was performed by overlapping PCR with mutated primers on root cDNA. The final PCR product was cloned into a pEntry vector, then recombined into AP067 (Genebank file below) by Gateway cloning. This backbone vector was generated by replacing the CASP1 CDS in pCASP1:CASP1genomic-GFP with a ccdB cassette (Roppolo et al., 2011). The mutated primer was used either with the forward primer 5'-acaagtttgtacaaaaaagcaggctctccaaccaccATGgcgaaagagtccaccacca-3' (containing attB1, the part specific to CASP1 is underlined) or the reverse primer 5'-tccgccaccaccaaccactttgtacaagaaagctgggtaatgcctcttgagggcgatggc-3' (containing attB2, the part specific to CASP1 without STOP is underlined). The two overlapping fragments containing the mutation of interest were used as a template in a third PCR using the attB1 and attB2 containing primers

Mutation	Forward mutated primer	Reverse mutated primer
D134H (GAT -> CAT)	5'-CTCATTTGCCATACTCTGGTC-3'	5'-GACCAGAGTATGGCAAATGAG-3'
A155S (GCA -> TCA)	5'-ACCTACCTTTCACACAACGGC-3'	5'-GCCGTTGTGTGAAAGGTAGGT-3'
H156D (CAC -> GAC)	5'-TACCTTGCAGACAACGGCAAC-3'	5'-GTTGCCGTTGTCTGCAAGGTA-3'
G158S (GGC -> AGC)	5'-GCACACAACAGCAACCAAAGC-3'	5'-GCTTTGGTTGCTGTTGTGTGC-3'
N163D (AAC -> GAC)	5'-CAAAGCACCGACTGGCTCCCT-3'	5'-AGGGAGCCAGTCGGTGCTTTG-3'
W164G (TGG -> GGG)	5'-AGCACCAACGGGCTCCCTATC-3'	5'-GATAGGGAGCCCGTTGGTGCT-3'
C168S (TGT -> AGT)	5'-CTCCCTATCAGTCAGCAGTTT-3'	5'-AAACTGCTGACTGATAGGGAG-3'
Q170E (CAG -> GAG)	5'-ATCTGTCAGGAGTTTGGAGAC-3'	5'-GTCTCCAAACTCCTGACAGAT-3'
F174V (TTC -> GTC)	5'-GGAGACGTCTGCCAGAACGT-3'	5'-ACGTTCTGGCAGACGTCTCC-3'
C175S (TGC -> AGC)	5'-GGAGACTTCAGCCAGAACG-3'	5'-CGTTCTGGCTGAAGTCTCC-3'
ΔEC2 G158-C175	5'-CACCTACCTTGCACACAACCAGAACGTTAGCACCGCGGTTGTG-3'	5'-CACAACCGCGGTGCTAACGTTCTGGTTGTGTGCAAGGTAGGTG-3'
ΔEC1 E72-F80	5'-CTGTCATGTACACCGCCGAGCTCCAGTTCCAAGCCGGTTAC-3'	5'-GTAACCGGCTTGGAACTGGAGCTCGGCGGTGTACATGACAG-3'
ΔEC1 T73-Q79	5'-CATGTACACCGCCGAGGAATTCCTCCAGTTCCAAGCCG-3'	5'-CGGCTTGGAACTGGAGGAATTCCTCGGCGGTGTACATG-3'
ΔEC1 L74-T78	5'-GTACACCGCCGAGGAAACTCAGTTCCTCCAGTTCCAAG-3'	5'-CTTGGAACTGGAGGAACTGAGTTTCCTCGGCGGTGTAC-3'

```
LOCUS       AP067\B4-pCASP1-R1-cassette-R2-GFP-B3       12732 bp    DNA      circular     24-SEP-2009
DEFINITION  attR1-attR2-attB3-attB4.
SOURCE
  ORGANISM
COMMENT     This file is created by Vector NTI
            http://www.invitrogen.com/
COMMENT     VNTDATE|530185395|
COMMENT     VNTDBDATE|530185395|
COMMENT     LSOWNER|
COMMENT     VNTNAME|AP067 B4-pCASP1-R1-cassette-R2-GFP-B3|
COMMENT     VNTAUTHORNAME|Geldner lab|
FEATURES             Location/Qualifiers
     misc_feature    12725..116
                     /vntifkey="21"
                     /label=attR1
     misc_feature    complement(2135..2258)
                     /vntifkey="21"
                     /label=attR2
     misc_feature    complement(2982..3002)
                     /vntifkey="21"
                     /label=attB3
     misc_feature    11497..11517
                     /vntifkey="21"
                     /label=attB4
     exon            2261..2980
                     /vntifkey="61"
                     /label=EGFP
     misc_marker     3343..4739
                     /vntifkey="22"
                     /label=Kan
     misc_signal     complement(4743..5075)
                     /vntifkey="87"
                     /label=LB
     misc_marker     5081..6330
                     /vntifkey="22"
                     /label=Sm/SpR
     misc_signal     complement(11234..11433)
                     /vntifkey="87"
                     /label=RB
     terminator      complement(3084..3309)
                     /vntifkey="43"
                     /label=T35S
     primer          3011..3026
                     /vntifkey="27"
                     /label=M13F
     primer          11461..11477
                     /vntifkey="27"
                     /label=M13\R
     misc_feature    11518..12724
```

```
                     /vntifkey="21"
                     /label=CASP1\promoter
     misc_feature    complement(1195..1854)
                     /vntifkey="21"
                     /label=Cm\(R)
     misc_feature    complement(545..850)
                     /vntifkey="21"
                     /label=ccdB
BASE COUNT     3076 a      3311 c      3174 g      3171 t
ORIGIN
        1 tacaaaaaag ctgaacgaga aacgtaaaat gatataaata tcaatatatt aaattagatt
       61 ttgcataaaa aacagactac ataatactgt aaaacacaac atatccagtc actatgaatc
      121 aactacttag atggtattag tgacctgtag tcgaccgaca gccttccaaa tgttcttcgg
      181 gtgatgctgc caacttagtc gaccgacagc cttccaaatg ttcttctcaa acggaatcgt
      241 cgtatccagc ctactcgcta ttgtcctcaa tgccgtatta aatcataaaa agaaataaga
      301 aaaagaggtg cgagcctctt ttttgtgtga caaaataaaa acatctacct attcatatac
      361 gctagtgtca tagtcctgaa aatcatctgc atcaagaaca atttcacaac tcttatactt
      421 ttctcttaca agtcgttcgg cttcatctgg attttcagcc tctatactta ctaaacgtga
      481 taaagtttct gtaatttcta ctgtatcgac ctgcagactg gctgtgtata agggagcctg
      541 acatttatat tccccagaac atcaggttaa tggcgttttt gatgtcattt tcgcggtggc
      601 tgagatcagc cacttcttcc ccgataacgg agaccggcac actggccata tcggtggtca
      661 tcatgcgcca gctttcatcc ccgatatgca ccaccgggta aagttcacgg gagactttat
      721 ctgacagcag acgtgcactg gccagggga tcaccatccg tcgcccgggc gtgtcaataa
      781 tatcactctg tacatccaca aacagacgat aacggctctc tcttttatag gtgtaaacct
      841 taaactgcat ttcaccagcc cctgttctcg tcagcaaaag agccgttcat ttcaataaac
      901 cgggcgacct cagccatccc ttcctgattt tccgctttcc agcgttcggc acgcagacga
      961 cgggcttcat tctgcatggt tgtgcttacc agaccggaga tattgacatc atatatgcct
     1021 tgagcaactg atagctgtcg ctgtcaactg tcactgtaat acgctgcttc atagcatacc
     1081 tctttttgac atacttcggg tatacatatc agtatatatt cttataccgc aaaaatcagc
     1141 gcgcaaatac gcatactgtt atctggcttt tagtaagccg gatccacgcg gcgtttacgc
     1201 cccgccctgc cactcatcgc agtactgttg taattcatta agcattctgc cgacatggaa
     1261 gccatcacag acggcatgat gaacctgaat cgccagcggc atcagcacct tgtcgccttg
     1321 cgtataatat ttgcccatgg tgaaaacggg ggcgaagaag ttgtccatat tggccacgtt
     1381 taaatcaaaa ctggtgaaac tcacccaggg attggctgag acgaaaaaca tattctcaat
     1441 aaacccttta gggaaatagg ccaggttttc accgtaacac gccacatctt gcgaatatat
     1501 gtgtagaaac tgccggaaat cgtcgtggta ttcactccag agcgatgaaa acgtttcagt
     1561 ttgctcatgg aaaacggtgt aacaagggtg aacactatcc catatcacca gctcaccgtc
     1621 tttcattgcc atacggaatt ccggatgagc attcatcagg cgggcaagaa tgtgaataaa
     1681 ggccggataa aacttgtgct tatttttctt tacggtcttt aaaaaggccg taatatccag
     1741 ctgaacggtc tggttatagg tacattgagc aactgactga aatgcctcaa aatgttcttt
     1801 acgatgccat tgggatatat caacggtggt atatccagtg atttttttct ccattttagc
     1861 ttccttagct cctgaaaatc tcgataactc aaaaaatacg cccggtagtg atcttatttc
     1921 attatggtga aagttggaac ctcttacgtg ccgatcaacg tctcattttc gccaaaagtt
     1981 ggcccagggc ttcccggtat caacagggac accaggattt atttattctg cgaagtgatc
     2041 ttccgtcaca ggtatttatt cggcgcaaag tgcgtcgggt gatgctgcca acttagtcga
     2101 ctacaggtca ctaataccat ctaagtagtt gattcatagt gactggatat gttgtgtttt
     2161 acagtattat gtagtctgtt ttttatgcaa aatctaattt aatatattga tatttatatc
     2221 attttacgtt tctcgttcag ctttcttgta caaagtgggg atggtgagca agggcgagga
     2281 gctgttcacc ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa
     2341 gttcagcgtg tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt
     2401 catctgcacc accggcaagc tgcccgtgcc ctggcccacc ctcgtgacca ccctgaccta
     2461 cggcgtgcag tgcttcagcc gctaccccga ccacatgaag cagcacgact tcttcaagtc
     2521 cgccatgccc gaaggctacg tccaggagcg caccatcttc ttcaaggacg acggcaacta
     2581 caagacccgc gccgaggtga agttcgaggg cgacaccctg gtgaaccgca tcgagctgaa
     2641 gggcatcgac ttcaaggagg acggcaacat cctggggcac aagctggagt acaactacaa
     2701 cagccacaac gtctatatca tggccgacaa gcagaagaac ggcatcaagg tgaacttcaa
     2761 gatccgccac aacatcgagg acggcagcgt gcagctcgcc gaccactacc agcagaacac
     2821 ccccatcggc gacggccccg tgctgctgcc cgacaaccac tacctgagca cccagtccgc
     2881 cctgagcaaa gaccccaacg agaagcgcga tcacatggtc ctgctggagt tcgtgaccgc
     2941 cgccgggatc actctcggca tggacgagct gtacaagtaa gcaactttat tatacatagt
     3001 tgataattca ctggccgtcg ttttacaacg tcgtgactgg gaaaacgatc taactgacta
     3061 gccgcggcca tggcggccgg gagcggccat gctagagtcc gcaaaaatca ccagtctctc
     3121 tctacaaatc tatctctctc tatttttctc cagaataatg tgtgagtagt tcccagataa
     3181 gggaattagg gttcttatag ggtttcgctc atgtgttgag catataagaa acccttagta
     3241 tgtatttgta tttgtaaaat acttctatca ataaaatttc taattcctaa aaccaaaatc
     3301 cagtgacctg caggtcgacc atatgggaga gctcgaatta tcatacatga gaattaaggg
     3361 agtcacgtta tgacccccgc cgatgacgcg ggacaagccg ttttacgttt ggaactgaca
     3421 gaaccgcaac gttgaaggag ccactcagcc gcgggtttct ggagtttaat gagctaagca
     3481 catacgtcag aaaccattat tgcgcgttca aaagtcgcct aaggtcacta tcagctagca
     3541 aatatttctt gtcaaaaatg ctccactgac gttccataaa ttcccctcgg tatccaatta
     3601 gagtctcata ttcactctca actcgatcga ggcatgattg aacaagatgg attgcacgca
     3661 ggttctccgg ccgcttgggt ggagaggcta ttcggctatg actgggcaca acagacaatc
     3721 ggctgctctg atgccgccgt gttccggctg tcagcgcagg ggcgcccggt tctttttgtc
     3781 aagaccgacc tgtccggtgc cctgaatgaa ctccaagacg aggcagcgcg gctatcgtgg
     3841 ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg ttgtcactga agcgggaagg
     3901 gactggctgc tattgggcga agtgccgggg caggatctcc tgtcatctca ccttgctcct
     3961 gccgagaaag tatccatcat ggctgatgca atgcggcggc tgcatacgct tgatccggct
     4021 acctgcccat tcgaccacca agcgaaacat cgcatcgagc gagcacgtac tcggatggaa
     4081 gccggtcttg tcgatcagga tgatctggac gaagagcatc aggggctcgc gccagccgaa
     4141 ctgttcgcca ggctcaaggc gcggatgccc gacggcgagg atctcgtcgt gacccacggc
     4201 gatgcctgct tgccgaatat catggtggaa aatggccgct tttctggatt catcgactgt
     4261 ggccggctgg gtgtggcgga ccgctatcag gacatagcgt tggctacccg tgatattgct
     4321 gaagagcttg gcggcgaatg ggctgaccgc ttcctcgtgc tttacggtat cgccgctccc
     4381 gattcgcagc gcatcgcctt ctatcgcctt cttgacgagt tcttctgagc gggactctgg
     4441 ggttcggact ctagctagag tcaagcagat cgttcaaaca tttggcaata aagtttctta
     4501 agattgaatc ctgttgccgg tcttgcgatg attatcatat aatttctgtt gaattacgtt
     4561 aagcatgtaa taattaacat gtaatgcatg acgttattta tgagatgggt ttttatgatt
     4621 agagtcccgc aattatacat ttaatacgcg atagaaaaca aaatatagcg cgcaaactag
```

```
4681 gataaattat cgcgcgcggt gtcatctatg ttactagatc gaccggcatg caagctgata
4741 attcaattcg gcgttaattc agtacattaa aaacgtccgc aatgtgttat taagttgtct
4801 aagcgtcaat ttgtttacac cacaatatat cctgccacca gccagccaac agctccccga
4861 ccggcagctc ggcacaaaat caccactcga tacaggcagc ccatcagtcc gggacggcgt
4921 cagcgggaga gccgttgtaa ggcggcagac tttgctcatg ttaccgatgc tattcggaag
4981 aacggcaact aagctgccgg gtttgaaaca cggatgatct cgcggagggt agcatgttga
5041 ttgtaacgat gacagagcgt tgctgcctgt gatcaattcg ggcacgaacc cagtggacat
5101 aagcctcgtt cggttcgtaa gctgtaatgc aagtagcgta actgccgtca cgcaactggt
5161 ccagaacctt gaccgaacgc agcggtggta acggcgcagt ggcggttttc atggcttctt
5221 gttatgacat gtttttttgg ggtacagtct atgcctcggg catccaagca gcaagcgcgt
5281 tacgccgtgg gtcgatgttt gatgttatgg agcagcaacg atgttacgca gcagggcagt
5341 cgccctaaaa caaagttaaa catcatgggg gaagcggtga tcgccgaagt atcgactcaa
5401 ctatcagagg tagttggcgt catcgagcgc catctcgaac cgacgttgct ggccgtacat
5461 ttgtacggct ccgcagtgga tggcggcctg aagccacaca gtgatattga tttgctggtt
5521 acggtgaccg taaggcttga tgaaacaacg cggcgagctt tgatcaacga ccttttggaa
5581 acttcggctt cccctggaga gagcgagatt ctccgcgctg tagaagtcac cattgttgtg
5641 cacgacgaca tcattccgtg gcgttatcca gctaagcgcg aactgcaatt tggagaatgg
5701 cagcgcaatg acattcttgc aggtatcttc gagccagcca cgatcgacat tgatctggct
5761 atcttgctga caaaagcaag agaacatagc gttgccttgg taggtccagc ggcggaggaa
5821 ctctttgatc cggttcctga acaggatcta tttgaggcgc taaatgaaac cttaacgcta
5881 tggaactcgc cgcccgactg ggctggcgat gagcgaaatg tagtgcttac gttgtcccgc
5941 atttggtaca gcgcagtaac cggcaaaatc gcgccgaagg atgtcgctgc cgactgggca
6001 atggagcgcc tgccggccca gtatcagccc gtcatacttg aagctagaca ggcttatctt
6061 ggacaagaag aagatcgctt ggcctcgcgc gcagatcagt tggaagaatt tgtccactac
6121 gtgaaaggcg agatcaccaa ggtagtcggc aaataatgtc tagctagaaa ttcgttcaag
6181 ccgacgccgc ttcgccggcg ttaactcaag cgattagatg cactaagcac ataattgctc
6241 acagccaaac tatcaggtca agtctgcttt tattattttt aagcgtgcat aataagccct
6301 acacaaattg ggagatatat catgcatgac caaaatccct taacgtgagt tttcgttcca
6361 ctgagcgtca gaccccgtag aaaagatcaa aggatcttct tgagatcctt tttttctgcg
6421 cgtaatctgc tgcttgcaaa caaaaaaacc accgctacca gcggtggttt gtttgccgga
6481 tcaagagcta ccaactcttt ttccgaaggt aactggcttc agcagagcgc agataccaaa
6541 tactgtcctt ctagtgtagc cgtagttagg ccaccacttc aagaactctg tagcaccgcc
6601 tacatacctc gctctgctaa tcctgttacc agtggctgct gccagtggcg ataagtcgtg
6661 tcttaccggg ttggactcaa gacgatagtt accggataag gcgcagcggt cgggctgaac
6721 ggggggttcg tgcacacagc ccagcttgga gcgaacgacc tacaccgaac tgagatacct
6781 acagcgtgag ctatgagaaa gcgccacgct tcccgaaggg agaaaggcgg acaggtatcc
6841 ggtaagcggc agggtcggaa caggagagcg cacgagggag cttccagggg gaaacgcctg
6901 gtatctttat agtcctgtcg ggtttcgcca cctctgactt gagcgtcgat ttttgtgatg
6961 ctcgtcaggg gggcggagcc tatggaaaaa cgccagcaac gcggcctttt tacggttcct
7021 ggccttttgc tggccttttg ctcacatgtt ctttcctgcg ttatcccctg attctgtgga
7081 taaccgtatt accgcctttg agtgagctga taccgctcgc cgcagccgaa cgaccgagcg
7141 cagcgagtca gtgagcgagg aagcggaaga gcgcctgatg cggtattttc tccttacgca
7201 tctgtgcggt atttcacacc gcatatggtg cactctcagt acaatctgct ctgatgccgc
7261 atagttaagc cagtatacac tccgctatcg ctacgtgact gggtcatggc tgcgccccga
7321 cacccgccaa cacccgctga cgcgccctga cgggcttgtc tgctcccggc atccgcttac
7381 agacaagctg tgaccgtctc cgggagctgc atgtgtcaga ggttttcacc gtcatcaccg
7441 aaacgcgcga ggcagggtgc cttgatgtgg gcgccggcgg tcgagtggcg acggcgcggc
7501 ttgtccgcgc cctggtagat tgcctggccg taggccagcc atttttgagc ggccagcggc
7561 cgcgataggc cgacgcgaag cggcggggcg tagggagcgc agcgaccgaa gggtaggcgc
7621 tttttgcagc tcttcggctg tgcgctggcc agacagttat gcacaggcca ggcgggtttt
7681 aagagtttta ataagtttta aagagtttta ggcggaaaaa tcgccttttt tctcttttat
7741 atcagtcact tacatgtgtg accggttccc aatgtacggc tttgggttcc caatgtacgg
7801 gttccggttc ccaatgtacg gctttgggtt cccaatgtac gtgctatcca caggaaagag
7861 accttttcga cctttttccc ctgctagggc aatttgccct agcatctgct ccgtacatta
7921 ggaaccggcg gatgcttcgc cctcgatcag gttgcggtag cgcatgacta ggatcgggcc
7981 agcctgcccc gcctcctcct tcaaatcgta ctccggcagg tcatttgacc cgatcagctt
8041 gcgcacggtg aaacagaact tcttgaactc tccggcgctg ccactgcgtt cgtagatcgt
8101 cttgaacaac catctggctt ctgccttgcc tgcggcgcgg cgtgccaggc ggtagagaaa
8161 acggccgatg ccgggatcga tcaaaaagta atcggggtga accgtcagca cgtccgggtt
8221 cttgccttct gtgatctcgc ggtacatcca atcagctagc tcgatctcga tgtactccgg
8281 ccgcccggtt tcgctcttta cgatcttgta gcggctaatc aaggcttcac cctcggatac
8341 cgtcaccagg cggccgttct tggccttctt cgtacgctgc atggcaacgt gcgtggtgtt
8401 taaccgaatg caggtttcta ccaggtcgtc tttctgcttt ccgccatcgg ctcgccggca
8461 gaacttgagt acgtccgcaa cgtgtggacg gaacacgcgg ccgggcttgt ctcccttccc
8521 ttcccggtat cggttcatgg attcggttag atgggaaacc gccatcagta ccaggtcgta
8581 atcccacaca ctggccatgc cggccggccc tgcggaaacc tctacgtgcc cgtctggaag
8641 ctcgtagcgg atcacctcgc cagctcgtcg gtcacgcttc gacagacgga aaacggccac
8701 gtccatgatg ctgcgactat cgcgggtgcc cacgtcatag agcatcggaa cgaaaaaatc
8761 tggttgctcg tcgcccttgg gcggcttcct aatcgacggc gcaccggctg ccggcggttg
8821 ccgggattct ttgcggattc gatcagcggc cgcttgccac gattcaccgg ggcgtgcttc
8881 tgcctcgatg cgttgccgct gggcggcctg cgcggccttc aacttctcca ccaggtcatc
8941 acccagcgcc gcgccgattt gtaccgggcc ggatggtttg cgaccgtcac gccgattcct
9001 cgggcttggg ggttccagtg ccattgcagg gccggcagac aacccagccg cttacgcctg
9061 gccaaccgcc cgttcctcca cacatggggc attccacggc gtcggtgcct ggttgttctt
9121 gattttccat gccgcctcct ttagccgcta aaattcatct actcatttat tcatttgctc
9181 atttactctg gtagctgcgc gatgtattca gatagcagct cggtaatggt cttgccttgg
9241 cgtaccgcgt acatcttcag cttggtgtga tcctccgccg gcaactgaaa gttgacccgc
9301 ttcatggctg gcgtgtctgc caggctggcc aacgttgcag ccttgctgct gcgtgcgctc
9361 ggacggccgg cacttagcgt gtttgtgctt ttgctcattt tctctttacc tcattaactc
9421 aaatgagttt tgatttaatt tcagcggcca gcgcctggac ctcgcgggca gcgtcgccct
9481 cgggttctga ttcaagaacg gttgtgccgg cggcggcagt gcctgggtag ctcacgcgct
9541 gcgtgatacg ggactcaaga atgggcagct cgtacccggc cagcgcctcg gcaacctcac
9601 cgccgatgcg cgtgcctttg atcgcccgcg acacgacaaa ggccgcttgt agccttccat
9661 ccgtgacctc aatgcgctgc ttaaccagct ccaccaggtc ggcggtggcc catatgtcgt
9721 aagggcttgg ctgcaccgga atcagcacga agtcggctgc cttgatcgcg gacacagcca
9781 agtccgccgc ctggggcgct ccgtcgatca ctacgaagtc gcgccggccg atggccttca
9841 cgtcgcggtc aatcgtcggg cggtcgatgc cgacaacggt tagcggttga tcttcccgca
9901 cggccgccca atcgcgggca ctgccctggg gatcggaatc gactaacaga acatcggccc
```

```
     9961 cggcgagttg cagggcgcgg gctagatggg ttgcgatggt cgtcttgcct gacccgcctt
    10021 tctggttaag tacagcgata accttcatgc gttccccttg cgtatttgtt tatttactca
    10081 tcgcatcata tacgcagcga ccgcatgacg caagctgttt tactcaaata cacatcacct
    10141 ttttagacgg cggcgctcgg tttcttcagc ggccaagctg gccggccagg ccgccagctt
    10201 ggcatcagac aaaccggcca ggatttcatg cagccgcacg gttgagacgt gcgcgggcgg
    10261 ctcgaacacg tacccggccg cgatcatctc cgcctcgatc tcttcggtaa tgaaaaacgg
    10321 ttcgtcctgg ccgtcctggt gcggtttcat gcttgttcct cttggcgttc attctcggcg
    10381 gccgccaggg cgtcggcctc ggtcaatgcg tcctcacgga aggcaccgcg ccgcctggcc
    10441 tcggtgggcg tcacttcctc gctgcgctca agtgcgcggt acagggtcga gcgatgcacg
    10501 ccaagcagtg cagccgcctc tttcacggtg cggccttcct ggtcgatcag ctcgcgggcg
    10561 tgcgcgatct gtgccggggt gagggtaggg cgggggccaa acttcacgcc tcgggccttg
    10621 gcggcctcgc gcccgctccg ggtgcggtcg atgattaggg aacgctcgaa ctcggcaatg
    10681 ccggcgaaca cggtcaacac catgcggccg gccggcgtgg tggtgtcggc ccacggctct
    10741 gccaggctac gcaggcccgc gccggcctcc tggatgcgct cggcaatgtc cagtaggtcg
    10801 cgggtgctgc gggccaggcg gtctagcctg gtcactgtca caacgtcgcc agggcgtagg
    10861 tggtcaagca tcctggccag ctccgggcgg tcgcgcctgg tgccggtgat cttctcggaa
    10921 aacagcttgg tgcagccggc cgcgtgcagt tcggcccgtt ggttggtcaa gtcctggtcg
    10981 tcggtgctga cgcgggcata gcccagcagg ccagcggcgg cgctcttgtt catggcgtaa
    11041 tgtctccggt tctagtcgca agtattctac tttatgcgac taaaacacgc gacaagaaaa
    11101 cgccaggaaa agggcagggc ggcagcctgt cgcgtaactt aggacttgtg cgacatgtcg
    11161 ttttcagaag acggctgcac tgaacgtcag aagccgactg cactatagca gcggaggggt
    11221 tggatcaaag tactttgatc ccgaggggaa ccctgtggtt ggcatgcaca tacaaatgga
    11281 cgaacggata aacctttca cgccctttta aatatccgtt attctaataa acgctctttt
    11341 ctcttaggtt tacccgccaa tatatcctgt caaacactga tagtttaaac tgaaggcggg
    11401 aaacgacaat ctgatccaag ctcaagctaa gcttgggccc gagcggataa caatttcaca
    11461 caggaaacag ctatgaccat gattacgcca agctatcaac tttgtataga aaagttgtta
    11521 atctgcataa aagtgagtat gagagagaag attaaataga tatcaatcct aactaatatt
    11581 caagaaaaca taatatagat caataaattg atgagagtaa aaacacaaag atgtttagaa
    11641 ataattattg tcaagactca agtttcttca aaatatcaag aggcgcttgg aataagaccc
    11701 ttattctaca atacatcaat ctatatagag ataaagacta agcataattt ttaaaataga
    11761 aaaaatataa acgtaaataa cactttttttg aggtaatact aaattttcta aacatgaaat
    11821 gttacaaatc cacaatattt ccatataaat ttgtaaataa tattttgtta gataatgtta
    11881 aattttctaa actgaaatat taacaaatcc gcagtatttc cattattaaa tctcgatttt
    11941 gtttcaatgg gagatttgaa ttttgaacca aaaaaaaaaa aaaagatttc atcaagatat
    12001 ctagggggat attttgctgg aatatagctt tgatgagaat atttatattt tgtatctctg
    12061 aaaatcaagt ttaaagggga aatgattatg ggttgaaatt ttgcaatcaa aagccctaat
    12121 ttgcaaaaac tacataagtt ttttgtttgg gctggcgcta tcggatcctt ttaggcttac
    12181 atttaacatc tggtccactt agaaagagtc acgtagtata tggtaattgt caacttgatt
    12241 tttcaagtta aaagaaatat gtatcaaaat gactaaaaag tagtgaaata ttatgtatct
    12301 aatttgttta tttaccaaat taatgctata aaaatgttca actgtacaat tggcatggaa
    12361 taatatgaac ataaatcata cattattaag cacttttgcc tacgaaggga taccaacttc
    12421 attagtttac attttctttt gtgttcaatt gttagctcaa acccaattaa gtggggaaag
    12481 taagaagcaa caactcctct tcccggaccc ctaacaaatc aactaaactc aatatcaaac
    12541 cattttaaaa gagctcatca ttaactagct actaattatt cttaatcaat cactgcttaa
    12601 tacaaagcac tatatataca cttgtatctt ccattagttt cccaccacaa ctacaaaaca
    12661 ttccaataca caacacacaa agcacacact ttttctttct tttaaacccc aattgcaaga
    12721 gaaacaagtt tg
//
```

Arabidopsis thaliana trasngenic lines with *Lotus japonicus* DNA
Gateway cloning was used to introduce the LjCASP1 promoter in a destination vector upstream of a NLS-GFP coding sequence, and to generate a pLjCASP1:LjCASP1-GFP translational repoter. Primers used are listed below.

LjCASP1	Forward primer (in bold Lj specific sequence)	Reverse primer
Promoter	ATTGCAGGTACC**ATGGCTGTAGTTTTGAGTACTTC**	ATTGCAGGTACC**TTTTATCTCAAATGAAGGAATTGTG**
Coding sequence	AAAAAGCAGGCTTA**ATGAAGTCAAGTCCTGCTG**	AGAAAGCTGGGTA**ACGTTTTGAGAGAACCAAAG**

Coding sequence of *LjCASP1*
atgaagtcaagtcctgctgagctaattagtgaggcaaagagttccacccaaaatagcaagatgaagag
ggcagtgtctgtgcttgatttcattctgaggctaattgcagttgttgccaccttagcaagtgccattg
caatgggaacaacggatgagtcacttcccttcttcactcagttcattcggttcagggctgagtatgat
gatcttcctactttgaggctttttgtagttgccagtgcatttgcaagcggctatctcattctttccct
accattatccatcttgcatatcacaaggagcagcgctcgaaggactagagttatcttgattatcttgg
atatggtaatgctaacttcattgacagctgcatcttctgcagcagcagctattgtttatttggctcac
aaggggaatgccaaagcaaattggtttgccttttgccaacagtatgactctttctgtgagcgcatatc
tggatctttgattggatccttcattgcaattccactgttcatcatgctgatccttttctctgctttgg
ttctctcaaaacgt

Protein sequence of LjCASP1
MKSSPAELISEAKSSTQNSKMKRAVSVLDFILRLIAVVATLASAIAMGTTDESLPFFTQFIRFRAEYD
DLPTLRLFVVASAFASGYLILSLPLSILHITRSSARRTRVILIIILDMVMLTSLTAASSAAAAIVYLAH
KGNAKANWFAFCQQYDSFCERISGSLIGSFIAIPLFIMLILFSALVLSKR

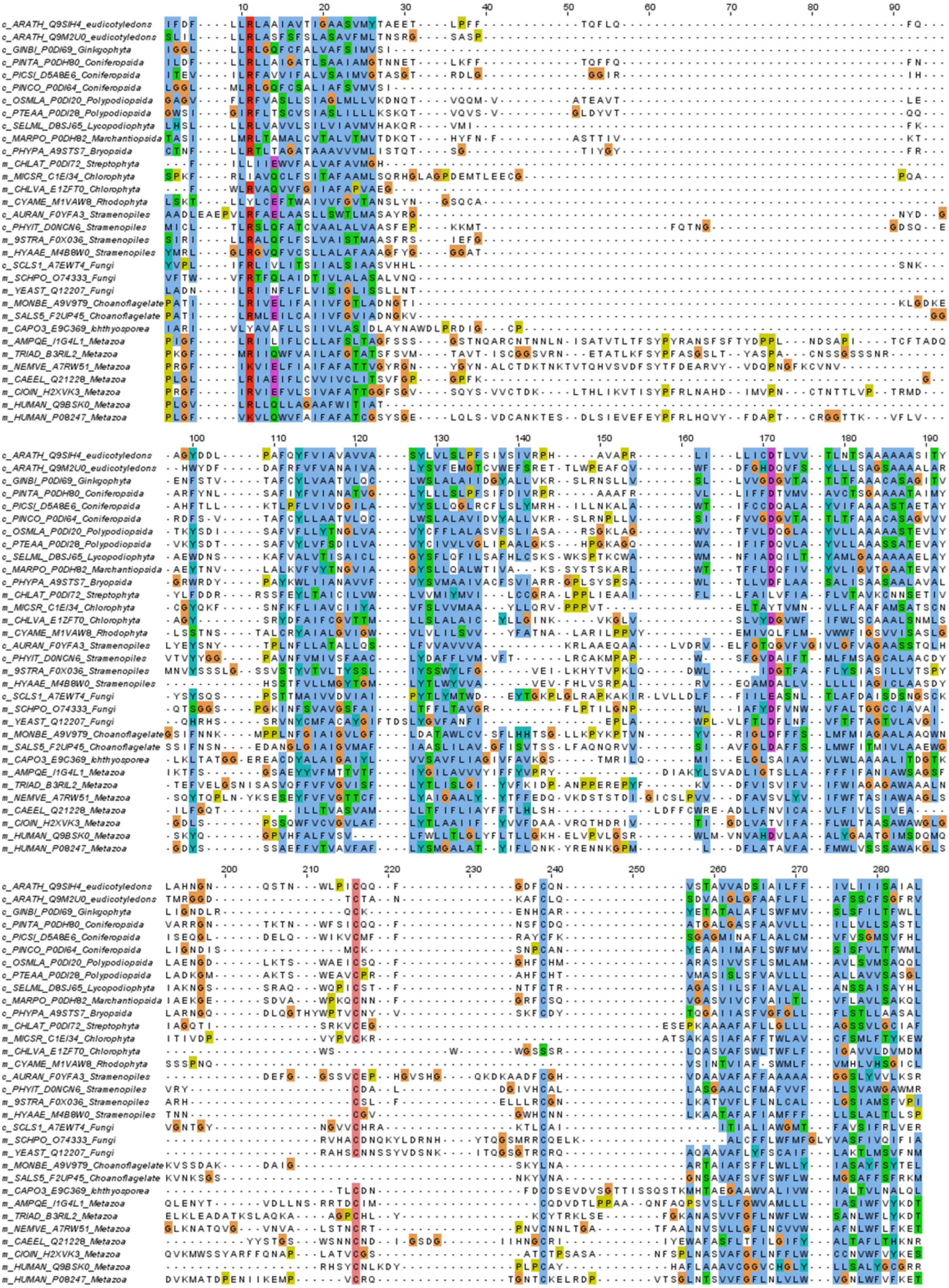
Supplemental Table 5. CASPLs in *Mimulus guttatus* and *Utricularia Gibba.* Nomenclature according to CoGe (www.genomevolution.org/CoGe). Attribution to groups was performed taking into consideration the group of the best AtCASPL homolog (best hit by blasting against the *A. thaliana* TAIR protein database). Red-highlighted gene names correspond to protein shown in Figure 3.

Arabidopsis thaliana		*Mimulus guttatus*	*Utricularia Gibba*
UniProt AC	CASPL nomenclature	CoGe nomenclature	
	39	22	21
Group 1	15	9	4
Q9SIH4	AtCASP1	mgf009756m	Scf00014.g2099.t1
Q9CAX3	AtCASP2	mgf002927m	Scf00007.g1335.t1
Q9ZQI2	AtCASP3	mgf006110m	Scf00093.g8119.t1
Q9FFZ7	AtCASP4	mgf006273m	Scf00544.g19275.t1
Q9LXF3	AtCASP5	mgf018947m	
Q9XI72	AtCASPL1A1	mgf000093m	
Q9FI10	AtCASPL1B1	mgf024243m	
Q9SUP0	AtCASPL1B2	mgf010649m	
Q9ZT81	AtCASPL1C1	mgf018769m	
Q9LR57	AtCASPL1C2		
Q9FE29	AtCASPL1D1		
Q9SQU2	AtCASPL1D2		
Q8L8Z1	AtCASPL1E1		
O23413	AtCASPL1E2		
Q9M0L3	AtCASPL1F1		
Group 2	6	5	5
Q8VZQ3	AtCASPL2A1	mgf002079m	Scf00331.g15634.t1
Q9LUL1	AtCASPL2A2	mgf013630m	Scf00133.g10042.t1
Q8L9B5	AtCASPL2B1	mgf008470m	Scf02954.g26077.t1
Q8L924	AtCASPL2B2	mgf010889m	Scf00018.g2583.t1
Q8L8U9	AtCASPL2C1	mgf010380m	Scf00208.g12616.t1
Q9FFT2	AtCASPL2D1		
Group3	2	1	1
Q3EB59	AtCASPL3A1	mgf005561m	Sc00907.g22639.t1
Q1PFB8	AtCASPL3A2		
Group4	8	3	3
Q9FNE8	AtCASPL4A1	mgf005818m	Scf00865.g22346.t1
Q501G6	AtCASPL4A2	mgf014579m	Scf00015.g2242.t1
Q84WP5	AtCASPL4A3	mgf004951m	Scf01120.g23809.t1
Q3EA54	AtCASPL4A4		
Q8LE26	AtCASPL4B1		
Q9M2U0	AtCASPL4C1		
Q8GWD5	AtCASPL4D1		
Q56X75	AtCASPL4D2		
Group 5	8	4	8
Q6NPF8	AtCASPL5A1	mgf009664m	Scf00129.g9844.t1
Q9SKN3	AtCASPL5A2	mgf012196m	Scf00873.g22404.t1
Q9LZM5	AtCASPL5B1	mgf025508m	Scf00105.g8744.t1
Q945M8	AtCASPL5B2	mgf003555m	Scf00077.g7165.t1
Q8L7R5	AtCASPL5B3		Scf00353.g16101.t1
Q66GI1	AtCASPL5C1		Scf00536.g19157.t1
P0CB17	AtCASPL5C2		Scf00063.g6361.t1
Q3ECT8	AtCASPL5C3		Scf00405.g17100.t1

Supplementary Table 6. Localization of mCherry-AtCASPLs under the control of AtCASP1 promoter (CSD = Casparian strip membrane domain)

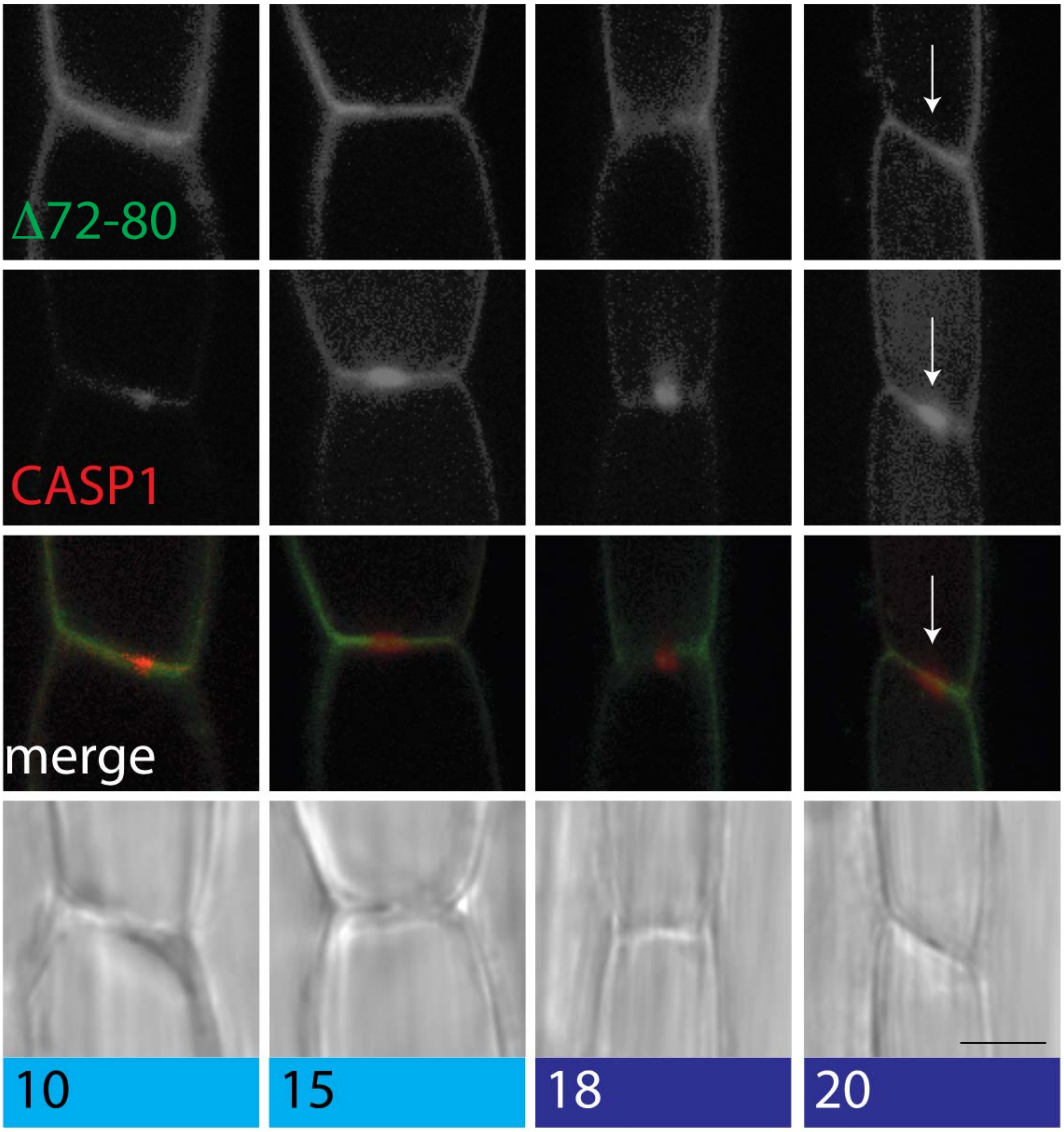
UniProt AC		Localization	
Group 1			
Q9SIH4	AtCASP1	CSD (2 lines)	No fluorescence (4 lines)
Q9CAX3	AtCASP2	CSD (1 line)	
Q9ZQI2	AtCASP3	CSD (1 line)	No fluorescence (9 lines)
Q9FFZ7	AtCASP4		
Q9LXF3	AtCASP5		
Q9XI72	AtCASPL1A1	CSD (2 lines)	No fluorescence (4 lines)
Q9FI10	AtCASPL1B1		
Q9SUP0	AtCASPL1B2	CSD (2 lines)	No fluorescence (13 lines)
Q9ZT81	AtCASPL1C1		
Q9LR57	AtCASPL1C2		
Q9FE29	AtCASPL1D1	Lateral plasma membranes (6 lines)	No fluorescence (2 lines)
Q9SQU2	AtCASPL1D2	Lateral plasma membranes (5 lines)	No fluorescence (5 lines)
Q8L8Z1	AtCASPL1E1	CSD (1 line)	No fluorescence (8 lines)
O23413	AtCASPL1E2	CSD (2 lines)	No fluorescence (10 lines)
Q9M0L3	AtCASPL1F1		
Group 2			
Q8VZQ3	AtCASPL2A1	Vacuole (2 lines)	No fluorescence (7 lines)
Q9LUL1	AtCASPL2A2		
Q8L9B5	AtCASPL2B1	CSD + lateral plasma membranes (3 lines)	No fluorescence (15 lines)
Q8L924	AtCASPL2B2		
Q8L8U9	AtCASPL2C1		
Q9FFT2	AtCASPL2D1	CSD	
Group3			
Q3EB59	AtCASPL3A1	CSD	
Q1PFB8	AtCASPL3A2	No expression (9 lines)	
Group4			
Q9FNE8	AtCASPL4A1	Weak, lateral plasma membranes and CSD (2 lines)	No fluorescence (5 lines)
Q501G6	AtCASPL4A2	Weak, cytoplasm (5 lines)	No fluorescence (2 lines)
Q84WP5	AtCASPL4A3		
Q3EA54	AtCASPL4A4		
Q8LE26	AtCASPL4B1	Vacuole (6 lines)	No fluorescence (13 lines)
Q9M2U0	AtCASPL4C1	Vacuole (1 line)	No fluorescence (8 lines)
Q8GWD5	AtCASPL4D1	CSD	
Q56X75	AtCASPL4D2		
Group50			
Q6NPF8	AtCASPL5A1	ER (3 lines)	No fluorescence (6 lines)
Q9SKN3	AtCASPL5A2	CSD	
Q9LZM5	AtCASPL5B1		No fluorescence (9 lines)
Q945M8	AtCASPL5B2	Vacuole (9 lines)	
Q8L7R5	AtCASPL5B3	Lateral plasma membranes	
Q66GI1	AtCASPL5C1	Vacuole (1 line)	No fluorescence (2 lines)
P0CB17	AtCASPL5C2		
Q3ECT8	AtCASPL5C3		

Supplemental Figure 1. Alignment of representative CASPL and MARVEL domains. The prefix of the sequence identifier indicates if a sequence was predicted to possess a CASPL (c_) or MARVEL (m_) domain.

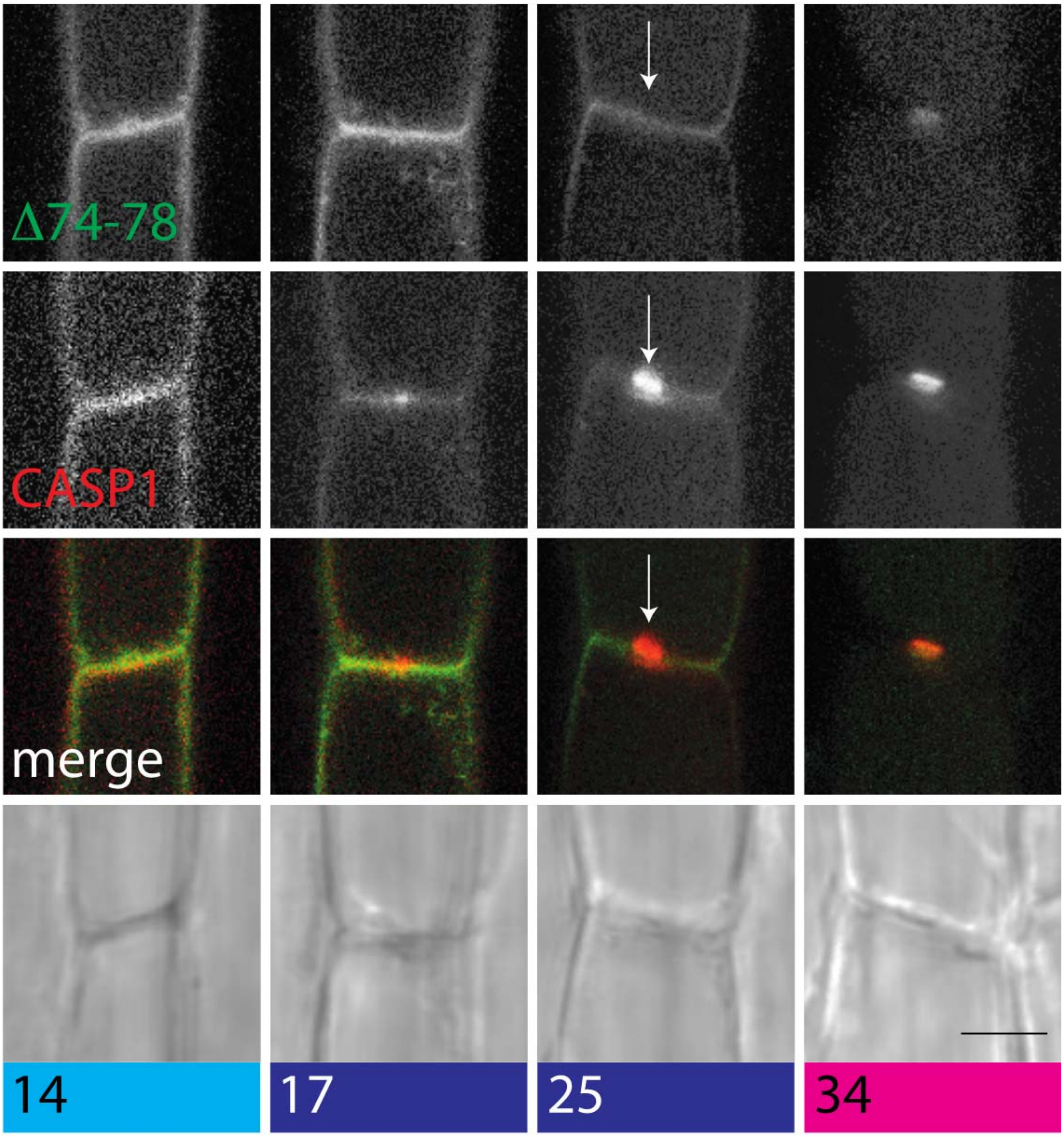


Supplemental Figure 2 related to Figure 2. **Extracelllar loops are dispensable for AtCASP1 localization at the CSD**.

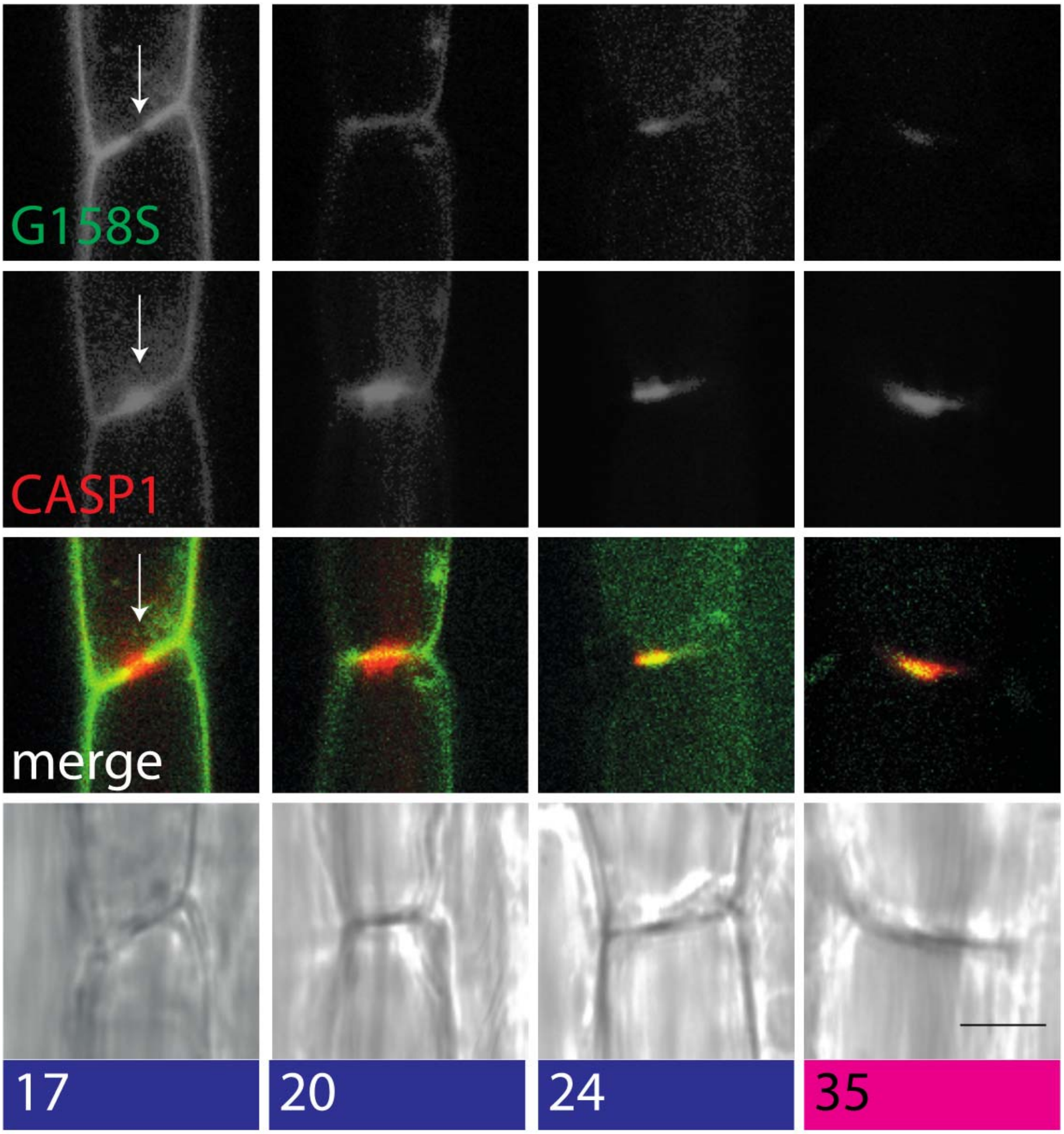
Representative confocal images of AtCASP1-GFP mutant/wt-mCherry crosses (green and red labels, respectively). Numbers indicate position of the cell shown counted from he first elongating endodermal cell (the lower the number, the closer is the cell to the root apical meristem). White arrows point to the position of the Casparian strip membrane domain (CSD). Scale bar:



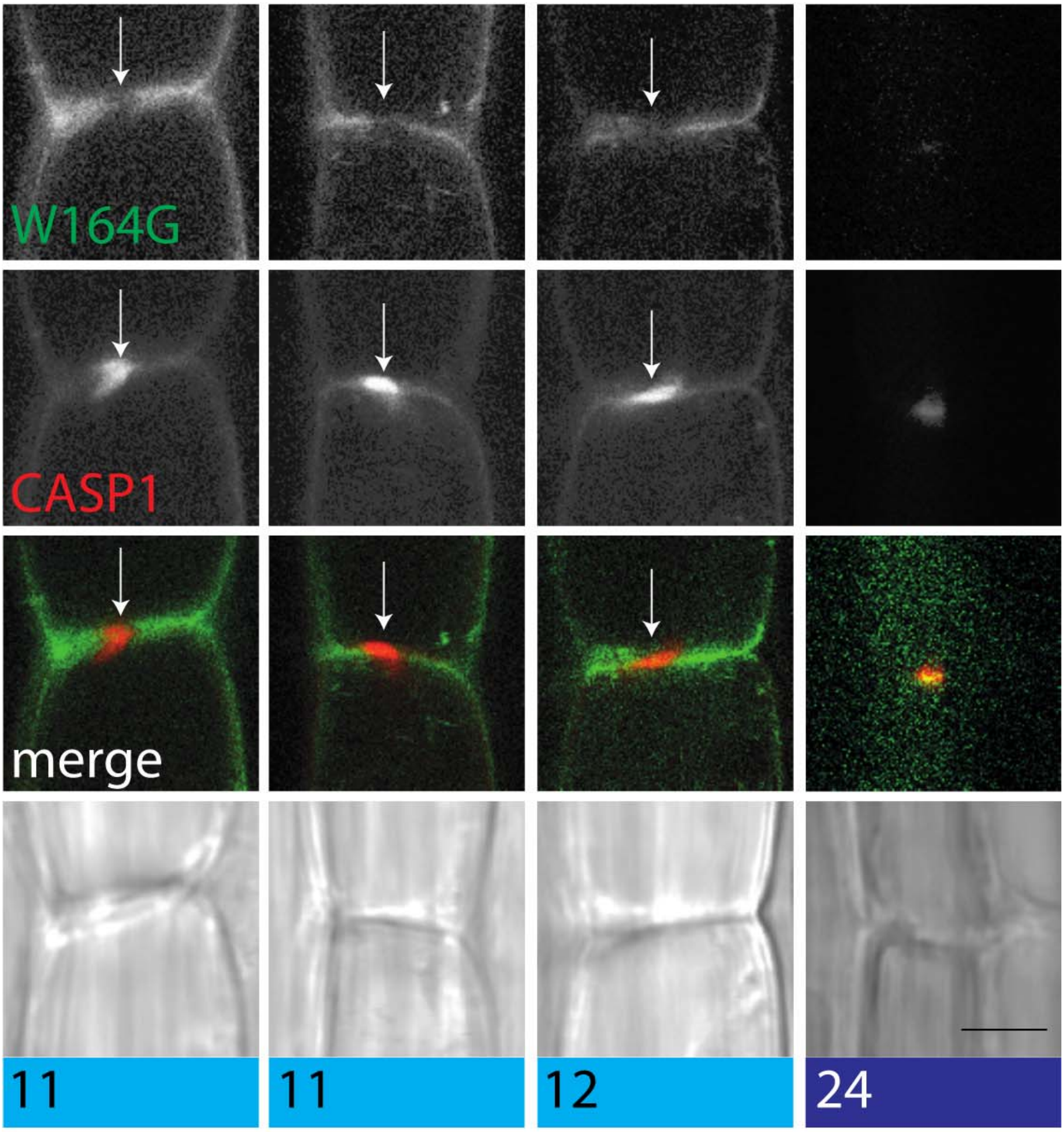
Deletion in the first extracellular loop of AtCASP1



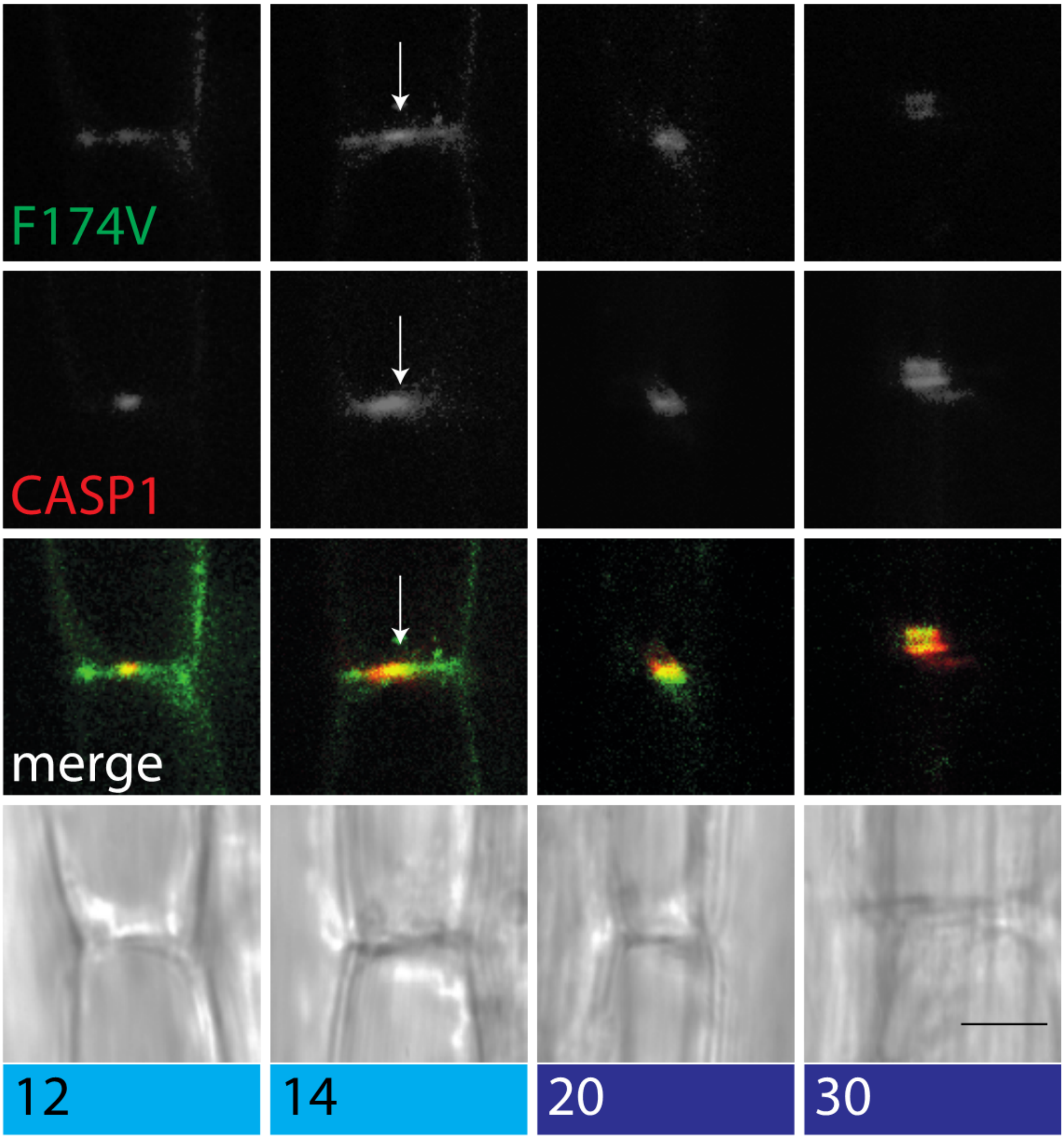
Deletion in the first extracellular loop of AtCASP1



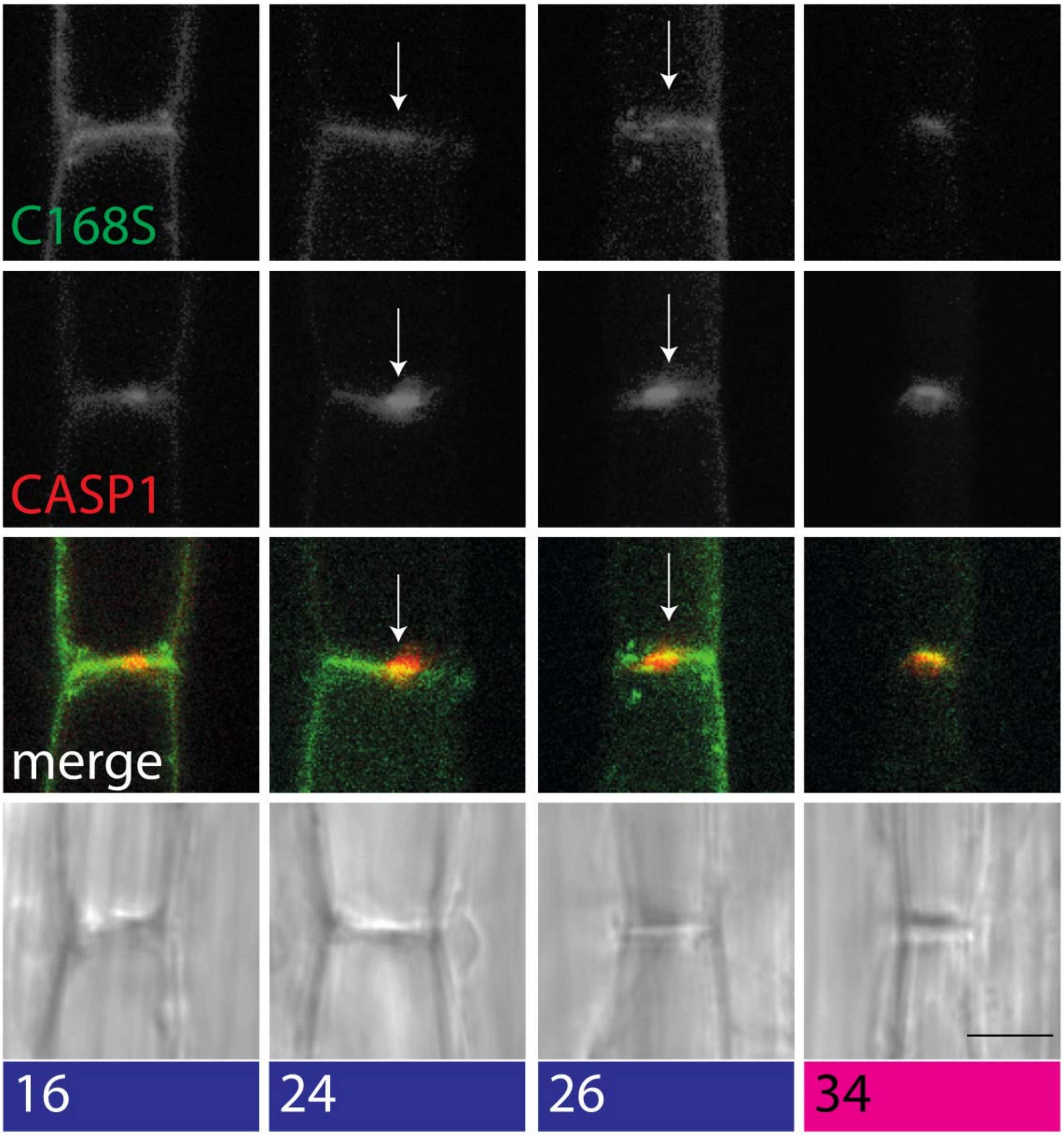
Mutation in the second exracellular loop of AtCASP1



Mutation in the second exracellular loop of AtCASP1



Mutation in the second exracellular loop of AtCASP1



Mutation in the second exracellular loop of AtCASP1

Dataset 1. Data model 1: 498 CASPL/MARVEL domains (fasta format).

```
>A2Y2B7_ORYSI
MNAVLRLAAAAAAATAAVVMVT--SRETTSF-----------FGIQMEAKYS--YTPSFIFFVVAYAVAAAYSLL-VLAV
PAGS--------------------------ALSRLALTTDVVLGMVLAGAVASAGAISD-IAKN-----GNSHA-G--WL
PV-CG--QIHA---------------YC----------NHVMAALIAGFVALAVHFVVV-MYSLHIV
>Q84UT5_ORYSJ
MNAVLRLAAAAAAATAAVVMVT--SRETTSF-----------FGIQMEAKYS--YTPSFIFFVVAYAVAAAYSLL-VLAV
PAGS--------------------------ALSRLALTTDVVLGMVLAGAVASAGAISD-IAKN-----GNSHA-G--WL
PV-CG--QIHA---------------YC----------NHVMAALIAGFVALAVHFVVV-MYSLHIV
>B6SZU6_MAIZE
ISAVLRLAAAGAAAAAAVIMVT--SHETTSL-----------FGIEMEAKYS--YTPSFVFFVVAFAVTFAYSLLAAVLV
RPGT--------------------------TASRLVLLSDVTVGMLLTGAVAATGAISQ-VGKS-----GNEHA-G--WL
PI-CA--QVQA---------------YC----------GHVMGALIAGFVSLLLYFLII-MYSLHAV
>C5YVA2_SORBI
ISAVLRLAAAGAAAAAAIIMVT--SHETTSF-----------FGIEMEAKYS--YTPSFVFFVVAFAVAFAYSLL-ALLA
RPGS--------------------------TASRLLLLSDVMVGMLLTGAVAATGAISQ-VGKS-----GNEHA-G--WL
PI-CA--QVQA---------------YC----------SHVMGALIAGFVSLLLYFLII-MYSLHAV
>Q9LR57_ARATH
GGLVLRFAAFCAALGAVIAMIT--SRERSSF-----------FVISLVAKYS--DLAAFKYFVIANAIVTVYSFL-VLFL
PKES--------------------------LLWKFVVVLDLMVTMLLTSSLSAAVAVAQ-VGKR-----GNANA-G--WL
PI-CG--QVPR---------------FC----------DQITGALIAGLVALVLYVFLL-IFSIHHV
>D7KCH2_ARALL
GGLVLRFAAFCAALGAVIAMIT--SRERSSF-----------FVISLVAKYS--DLAAFKYFVIANAIVTVYSFL-VLFL
PKES--------------------------LLWKFVVVLDLMVTMLLTSSLSAAVAVAQ-VGKR-----GNANA-G--WL
PI-CG--QVPR---------------FC----------DQITGALIAGLVALVLYVFLL-IFSIHHV
>D7M2M8_ARALL
GGLVLRLAAFGAALAALIVMIT--SRERASF-----------FAVSLEAKYT--DMAAFKYFVIANAVVSVYSFL-VLFL
PKES--------------------------LLWKFVVVLDLVMTMLLTSSLSAALAVAQ-VGKK-----GNANA-G--WL
PI-CG--QVPK---------------FC----------DQITGALIAGFVALVLYVLLL-LYSLHSV
>Q9ZT81_ARATH
GGLVLRLAAFGAALAALIVMIT--SRERASF-----------LAISLEAKYT--DMAAFKYFVIANAVVSVYSFL-VLFL
PKES--------------------------LLWKFVVVLDLVMTMLLTSSLSAALAVAQ-VGKK-----GNANA-G--WL
PI-CG--QVPK---------------FC----------DQITGALIAGFVALVLYVLLL-LYSLHAV
>B9N5U6_POPTR
LSLLLRLIAFGATLAAVIIMAT--SHEKGSF-----------FALSYEAKYS--DTPAFKYFVIANAIVTVYGFL-ALFI
PSES--------------------------PLWRLVLALDLVFTMLLISSISAALAVAQ-VGKK-----GNSSA-G--WL
PV-CG--QVTK---------------YC----------NQVTGALVAGFIAIITYIILL-LYSIYTF
>B9N2D0_POPTR
LSLLLRLIAVGATLAAVIIMAT--SHEKGTF-----------FAVSYEAKYT--DTPAFKYFVIANAIVTVYGFL-VLFH
PPGS--------------------------PLWRLVLALDLVFTMLLISSISAALAVAQ-VGKN-----GNSRA-G--WL
PV-CG--QVTK---------------YC----------NQVTGALVAGLIALITYIILL-LHSIYTF
>B9RW00_RICCO
FTLLLRLIAFGTALVAAIVMAT--SHESGSF-----------FTVSYEAKYS--DTPAFKYFVIVNAIVTVYSFL-ALFL
PSES--------------------------LLWRLVIVTDVVFTMLVTSSISAAVAVAQ-VGKK-----GNSHA-G--WL
PI-CG--QVPK---------------FC----------DQVTGALAAAFISLITYAILL-LYSIHTV
>A7PJ32_VITVI
CFLVLRLLAFGATLSAAIVMAT--SHERTTY-----------LSLSIEAKYS--HTPAFKYFVIANAIGSAYSLL-LLFL
PSHG--------------------------SLWPLVIASDVVITMFLTSSISAALSIAY-VGKK-----GNSYA-G--WL
PI-CD--QVPN---------------YC----------NHVTGALAAGFIGVVLYMVLL-QYSIYTK
>A7R333_VITVI
ITTLVRLLVLGAALSATIVMVT--SHDSAEV-----------LNLSFDAKYT--NARAFVYFAITNAIASGYSFI-ALFL
SFST--------------------------PLWHLVFLLDVFMTLLLTSSISVALAIAD-VGKK-----GNSHA-G--WL
PV-CG--QVPE---------------FC----------DHVTGALIAGFSAAVLYLVLL-LFSIHAV
>B9RZ92_RICCO
FSTILRFLALAATVVAVIVMIR--SHDSAIV-----------LNLTFSAKYN--NTPAFKYFVIAEGIASVYTII-VIFL
WSKG--------------------------LLGRLIVILDMVTTVLLTSSISAALAIAQ-VGKK-----GNSHA-G--WL
PV-CG--QVPK---------------FC----------DQAIIALVAGFVAAIVYFMLL-LCSLHAV
>B9H2V1_POPTR
FTNFLRLLALAATVVAIVFMVT--SHDSAQV-----------LNLTFTVKYS--NTPVFKYFVIAEAIAGGYIVI-SILL
SFKS--------------------------LFWRLLVILDMVTAVLLTSSISAALAIAQ-VGKK-----GNTHA-G--WL
PV-CE--QVPD---------------FC----------DQVTIALIAGFAAAIIYFVLL-LCSLYVV
>B9N3F4_POPTR
FTNTLRLLALAATVVAIVFMVT--SHDSAQV-----------LNLTFTAKYS--NTPAFKYLVIGEAIAGGYTVI-SILL
SFKG--------------------------LFWRLIVILDMVTTVLLTSSISAALAIAQ-VGKK-----GNTHA-G--WL
PI-CG--QVPD---------------FC----------DYVTIALIAGFAAAIIYFVLL-LCSLYVV
>A2WMK7_ORYSI
VAVVLRVAAAGAAAVAAVLMAM--SHDEVIV-----------YGMEVQAKFR--YTPSLVFFVAANAAVSACSLV-VLLV
PSSTSK------------------------LAARLLLMADVVLGMVLAGAFAAAGAMAE-LGKN-----GNSHA-G--WI
AI-CV--QVPL---------------FC----------DRVRSALVAGSATIVLYYLML-MYSIYTL
>Q9LI17_ORYSJ
VAVVLRVAAAGAAAVAAVLMAM--SHDEVIV-----------YGMEVQAKFR--YTPSLVFFVAANAAVSACSLV-VLLV
PSSTSK------------------------LAARLLLMADVVLGMVLAGAFAAAGAMAE-LGKN-----GNSHA-G--WI
AI-CV--QVPL---------------FC----------DRVRSALVAGSATIVLYYLML-MYSIYTL
>A2WMK1_ORYSI
```

```
VAVVLRVAAAGAAAVAAVLMAM--SHDEVIV-----------YGMEVQAKFR--YTPSLVFFVAANAAVSACSLV-VLLV
PSSTSK------------------------LAARLLLMADVVLGMVLAGALAAAGAMAE-LGKN-----GNSHA-G--WI
AI-CV--QVPL---------------FC----------DRVRSALVAGSATIVLYYLML-MYSIYTL
>B9IK21_POPTR
IVRGLRGLAFLATILATSFMAA--SHERA-X-----------FPFDYKADYT--DLMLFKAFLGANIAASLYSFF-FVC-
------------------XX--PKS-----LLWRLAIVLDVIMFGLLVAMDSAAIAAAY-LHKH-----GDSQA-F--WP
PI-CS--QVPT---------------YC----------YRVILAISIGFGGVFMFLLII-IISISVI
>D7LIN7_ARALL
FDFLLRLAAIGVTIGAASVMYT--AQETLPFFT---------QFLQFQAGYD--DLPAFQYFVIAVAIVASYLVL-SLPF
SIVT--------------IVRPLAV-----APRLILLIFDTLVVTLNTSAAAAAASIVY-LAHN-----GNQST-N--WL
PI-CQ--QFGD---------------FC----------QNVSTAVVAASIAILFFIVLI-IISAIAL
>Q9SIH4_ARATH
FDFLLRLAAIAVTIGAASVMYT--AEETLPFFT---------QFLQFQAGYD--DLPAFQYFVIAVAVVASYLVL-SLPF
SIVS--------------IVRPHAV-----APRLILLICDTLVVTLNTSAAAAAASITY-LAHN-----GNQST-N--WL
PI-CQ--QFGD---------------FC----------QNVSTAVVADSIAILFFIVLI-IISAIAL
>P0DI49_RAPRA
FDFLLRLAAIGITIGASSVMFT--AEETLPFFT---------QFLQFQAGYD--DFPTFQFFVIAIAIVASYLVL-SLPF
SIVT--------------IVRPLAV-----APRLILLISDTVVLTLTTAAAAAAASIVY-LAHN-----GNTNT-N--WL
PI-CQ--QFGD---------------FC----------QTASTAVVAASISVAFFVLLI-VISAIAL
>P0DI45_RAPSA
FDFLLRLAAIVTTITASSVMYT--AEETLPFFT---------QFLQFQAGYD--DFATFQFFVISIAMVASYLVL-SLPF
SIVS--------------IIRPLAA-----APRLILLISDTVVVTLTTAAAAAAAAIVY-LAHN-----GNPNT-N--WL
PI-CQ--QFGD---------------FC----------QAVSSAVVAASIAVVFFIILI-VISAISL
>P0DI55_LOTJA
VDFVLRLGAVAAALGAATTMAT--ADQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMALVGCYLVL-SLPL
SIVS--------------IIRPHAL-----GPKLFLIILDTVFLTLATASAASAAAVVY-VAHN-----GNQDS-N--WL
AI-CN--QFGD---------------FC----------AQTSGAVVSSLVAVVVFVLLI-VMSALAL
>C6TFL9_SOYBN
MDFILRLGAIAAALGAAATMGT--SDQTLPFFT---------QFLQFEASYD--SFTSFQFFVITMALVGGYLVL-SLPF
SFVA--------------IIRPHAA-----GPRLFLIILDTVFLTLTTASGASAAAIVY-LAHN-----GNQDS-N--WL
AI-CN--QFGD---------------FC----------AQTSSAVVSSFVAVVVLVLLV-VLSALAL
>P0DI39_VIGUN
MDFILRLGAIAAALGAAATMGT--SDQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMALVGGYLVL-SLPF
SVVA--------------IIRPHAV-----GPRLFLIILDTVFLTLATASAASAAAVVY-LAHN-----GDQDT-N--WL
AI-CN--QFGD---------------FC----------AQTSSAVVSSFVAVVVFVLLI-VMSALAM
>C6T2E7_SOYBN
MDFILRLGAIAAALGAAATMGT--SDQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMSLVGGYLVL-SLPF
SIVA--------------IVRPHAV-----GPRLFLIILDTAFLTLATAGGASAAAIVY-LAHN-----GDQDT-N--WL
AI-CN--QFGD---------------FC----------AQTSAAVVSSFVAVVVLVLLI-IMSALAI
>P0DI40_VIGUN
MDFILRLGGIAASLGAAATMGT--SDQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMALVAGYLVL-SLPF
SVVA--------------IIRPHAP-----GPRLFLIILDTVFLTLATASGASAAAIVY-LAHN-----GNQDS-N--WL
AI-CN--QFGD---------------FC----------AQTSGAVVASFVAVVILVLLV-IMSALAL
>C6T1K6_SOYBN
MDFILRLGAIAAAPGAAATMGT--SDQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMALVAGYLVL-SLPF
SIVV--------------IIRPHAV-----GPRLFLIILDTVFLTLATASGASAAAIVY-LAHN-----GNQDS-N--WL
AI-CN--QFGD---------------FC----------AQTSGAVVSSLVSVVIFVLLI-VMSALAL
>P0DI57_LOTJA
MDFILRLGAIAAALGAAATMGL--SDQTLPFFT---------QFFQFEASYD--SFTTFQFFVITMALVAGYLVL-SLPL
SIVA--------------VVRPHAA-----GPRLFLIILDTVFLTLATASGASAASIVY-LAHN-----GNQDT-N--WI
AI-CN--QFGD---------------FC----------AQTSGAVVSSLVAVLVFVLLI-VMSALVL
>C6TH93_SOYBN
LDFILRLGAITSALGAAATMAT--SDETLPFFT---------QFFQFEASYD--SFSTFQFFVIAMAFVGGYLVL-SLPF
SIVT--------------IIRPHAA-----GPRLFLIILDTVFLTLATSSAAAATAIVY-LAHN-----GNQDS-N--WL
AI-CN--QFGD---------------FC----------QEISGAVVASFVAVVLFVLLI-VMCAVAL
>D7LAP2_ARALL
FDFLLRLAAIVAALAAAATMGT--SDETLPFFT---------QFLQFEASYD--DLPTFQFFVIAMALVGGYLVL-SLPI
SVVT--------------ILRPLAT-----APRLLLLVLDTAVLALNTAAASSAAAISY-LAHS-----GNQNT-N--WL
PI-CQ--QFGD---------------FC----------QKSSGAVVSAFISVVFFTILV-VISGVAL
>Q9CAX3_ARATH
FDFLLRLAAIVAALAAAATMGT--SDETLPFFT---------QFLQFEASYD--DLPTFQFFVIAMALVGGYLVL-SLPI
SVVT--------------ILRPLAT-----APRLLLLVLDTGVLALNTAAASSAAAISY-LAHS-----GNQNT-N--WL
PI-CQ--QFGD---------------FC----------QKSSGAVVSAFVSVVFFTILV-VISGVAL
>D7LZ50_ARALL
FDFLLRLAAIVAALAAAATMGT--SDETLPFFT---------QFLQFEASYD--DLPTFQFFVVAIAIVTGYLVL-SLPF
SVVT--------------IVRPLAV-----APRLLLLVLDTAALALDTAAASAAAAIVY-LAHN-----GNTNT-N--WL
PI-CQ--QFGD---------------FC----------QKTSGAVVSAFASVTFLAILV-VISGVSL
>Q9FFZ7_ARATH
FDFLLRLAAIVAALAAAATMGT--SDETLPFFT---------QFLQFEASYD--DLPTFQFFVVAIAIVAGYLVL-SLPF
SVVT--------------IVRPLAV-----APRLLLLVLDTAALALDTAAASAAAAIVY-LAHN-----GNTNT-N--WL
PI-CQ--QFGD---------------FC----------QKTSGAVVSAFASVTFLAILV-VISGVSL
>P0DI46_RAPSA
FDFLLRLAAIVAASVAAGTMFT--SDETLPFFT---------QFLQFEAGYD--DLPTFQFFVIAMSLVSGYIVL-SLPI
SVVT--------------IVRPLAA-----APRLLLLVLDTAVMGLTMAAASSAAAISY-VAHN-----GNQNT-N--WL
PI-CQ--QFFD---------------FC----------QKTSGAVVSSFVAVVFFMILV-VLSGVAL
>B9IIR4_POPTR
FDLVLRLGAVVTALAAAATMGT--TDQTLPFFT---------QFFQFQASYD--DLPTFQFFVIAMAIVSGYLVL-SLPF
```

```
SIVA--------------IIRPHAT-----GPRLLLIILDTVALTLNTAAAAAAVAIVD-LAQN-----GNSSA-N--WL
GI-CQ--QFGD---------------FC----------QKASGAVVASFIAAGVLLFLI-VISALAL
>B9HBX2_POPTR
FDFILRLAAIATALAAAAMGT--SDETLPFFT---------QFFQFQASYD--DLPTFQFFVIAIAIVGGYLVL-SLPF
SIVA--------------IVRPHAV-----GPRLLLIILDAVALTLNTAAGAAAAAIVY-LAHN-----GNSNT-N--WL
AI-CQ--QYGD---------------FC----------QKVSGAVVASFITVVIFVFLI-VLSAFAL
>B9IIR5_POPTR
FDFILRLAAIATALAAAASMGT--SDETLPFFT---------QFFQFQASYD--DLPTFQFFVIAMAIVAGYLVL-SLPF
SIVA--------------IVRPHAA-----GPRLLLIILDTVALTLNTAAGAAAAAIVY-LAHN-----GNSST-N--WL
AI-CQ--QFGD---------------FC----------QKNSGAVVASFITVVIFVFLL-VLSAFAL
>P0DI43_THECC
FDFLLRLGAIIAALAAAATMGT--SDETLPFFT---------QFFQFEASYD--DLPTFMFFVIAMALIGGYLVL-SLPF
SIVT--------------IVRPHAV-----APRLLLFILDIVALTLTTAAGAAAAAIVY-LAHN-----GNPNT-N--WL
AI-CQ--QFGD---------------FC----------QEVSGAVVASFVTVVVLMSLV-LLSGVAL
>B9SX12_RICCO
FDFILRLGAVISALSAAATMGT--SDETLPFFT---------QFFQFEAGYD--DFPTFQFFVIAMGFVGGYLVL-SLPF
SVVA--------------IIRPHAV-----GIRLLLLILDTVALTLNTAAAAAAAAIVY-LAHN-----GNQSA-N--WL
AV-CQ--QFGD---------------FC----------QKVSGGVVASFVSVLVFLLLV-VMSAVAL
>B9SX13_RICCO
FDFILRLGAIAAALGAASTMGT--SDETLPFFT---------QFFQFNAGYD--DFPTFQFFVIAMAMVAGYLVL-SLPF
SIVS--------------ICRPHAA-----GPRILLFILDTVALTLNAAAGAAAADIVY-LAHN-----GNQTT-N--WL
AI-CL--QFGD---------------FC----------REVSGSVVASFASVVILMVLV-VMSGLAL
>P0DI61_CUCME
FDFVLRIGVLASALAAAAAMGT--SEQTLPFFT---------QFFQFEASYD--DLPTFQFFVVAMAVVAGYVVL-SIPF
SIVC--------------IIRPHAA-----GPRVLLLILDSVALTLNTAAAGAAAAVVS-LAHS-----GNSST-N--WL
AI-CN--QFGD---------------FC----------QQASGAVVGSFAAVLLFLLLI-LFSALSL
>P0DI30_TRIPD
FDFILRICALAAALAATATMGT--TDQTLPFFT---------QFFQFQASYD--DLPAFTFFVVANGIASGYLVL-SLPF
SIAT--------------IVRPHAA-----AIKLLLIIFDTVMVAFTAAAAAAAAAIVY-LAHN-----GNSKT-N--WF
AI-CQ--QFND---------------FC----------QRVSGAVVASFVAAVILIFLV-VLSAVAI
>P0DI53_MIMGU
FDFILRICALAAALAATATMGT--TDQTLPFFT---------QFFQFQASYD--DLPTFTFFVIANAIASGYLVL-SLPF
SIVA--------------IVRPHVT-----GVKLLLLILDTVLVAFTTAAAASAAAIVY-LAHN-----GNSNT-N--WF
AI-CQ--QFND---------------FC----------QRTSGAVVASFIAAAIFIFLV-VLSAVAL
>A7QF77_VITVI
FDFILRLSAIGAALAATTTMGT--TDQTLPFFT---------QFFQFQASYD--DLPAFSFFVIANAIASGYLFL-SLPF
SIVC--------------IVRPHAM-----GARLLLVICDTVMVALTIAAAAAAAAIVY-LAHN-----GNSNA-N--WV
AI-CQ--QFDD---------------FC----------QSVSGAVVASFIAAVLFMLMI-VLSAFSL
>A7PP95_VITVI
FDFLLRLAAIAATLAAATTMGT--TDETLPFFT---------QFFQFQASFD--DLPAFMFFVVATAIASGYLAL-SLPF
SLVS--------------IFRPHAQ-----GIRLLLIISDTVMLALTTAGAASATAIVY-LAHN-----GDSSA-N--WI
AI-CQ--QFTD---------------FC----------QSVSGAVVASFIAVVIFMLLV-MMSALAL
>Q1W3A5_STRAF
FDLILRISAATAALAATIVMGT--TEQTLPFFT---------QFFQFRAQYD--DLPTFTFFVVGMAIVTGYLIL-SVPL
SIVC--------------IARPVAI-----GPRFLLIVCDTVTAVLATSAAGSSAAIVY-LAHN-----GNSDA-N--WL
AI-CQ--QFND---------------FC----------QRVSGAVVAAFVAVVC-----------SS
>P0DI63_STRHE
FDLFLRISAATAALAATIVMGT--TEQTLPFFT---------QFFQFRAQYD--DLPTFTFFVVGMAIVTGYLIL-SVPF
SIVC--------------IARPVAI-----GPRFLLIVGDTLKAVLATSAAGSSAAIVY-LAHN-----GNSDA-N--WL
DI-CQ--QFND---------------FC----------QRVSGAVVAAFVAVVLLIFLI-VLSAMAL
>P0DI31_TRIPD
FDLILRISAATAALAATIVMGT--TEQTLPFFT---------QFFQFRASYD--DLPTFTFFVIAMAIVTGYLIL-SVPF
SIVC--------------IARPVVA-----APRILLILCDTLTVTLATSAAGASAAIVY-LAHN-----GXSDA-N--WL
AI-CQ--QFND---------------FC----------QRVSGAVVAAFVSAVLLIFLV-VLSAIVL
>P0DI52_MIMGU
FDLILRISAATAALAATITMGT--TEQTLPFFT---------QFFQFQASYD--DLPTFTFFVIAMSIVTGYLVL-SVPF
SIVC--------------IARPVAA-----APRLLLILCDTLAVTLNTSAAGASAAIVY-LAHN-----GNSDA-N--WL
AI-CQ--QFND---------------FC----------QRTSGAVVASFVAVVLLIFLV-VLSASAL
>P0DI50_TOBAC
FDLILRIAAFASALGAAVAMAT--TEETLPFFT---------QFFQFEASYD--DLPTFTFFVVAMAIVVAYLVL-SVPF
SIVC--------------IVRPHAV-----VPRLLLIIFDTVIIALTTGAAGSSAAIVY-LAHN-----GNQDA-N--WL
AI-CQ--QFGD---------------FC----------QRVSGAVVAAFVTVVILIFLV-VLSASAL
>P0DI51_MIMGU
FDLILRVSAATSALAATITMGT--TEQTLPFFT---------QFFQFQASYD--DLPAFTFFVIALSIVTGYLVL-SVPF
SVVC--------------IAQPLAA-----VPRLLLIVCDTLTVTLATAAASSSAAIVY-LAHN-----GNADA-N--WL
AI-CQ--QFGD---------------FC----------QRVSGGVVRGGGSAHIXXXET-LTDGVDV
>P0DI60_HELAN
IDFILRICAIAAALAAATAMGT--TSQQLPFFT---------QFFQFKADYN--DLPAFTFFVIANAMAGAYLVL-SLPF
SILC--------------IVRPHIL-----GARLMLLVFDTVAVPLVTAAASAAASIVY-LAHN-----GNSDA-N--WV
AI-CR--QFND---------------FC----------QRVSGAVVASFITALLFVVLV-AVSAVAL
>P0DI62_CYNCS
FDVVLRLAGIATALGAAIAMGS--TDQTLPFFT---------QFFQFKAEFD--DLPAFTFFVIANAITAAYLAL-TIPI
SIVC--------------IIRPHLV-----APRVLLIFLDTVMVALTTAAAGGTASIVY-LAHN-----GNSDA-N--WP
AI-CQ--QFND---------------XC----------QKVSGAVVASFLTVVVLMLLI-VLSAFAL
>P0DI32_TARKO
FDVVLRIAGIAAALGAVIAMGS--TDQTLPFFT---------QFFQFKAEFD--DLPVFTFFVIANAITAAYLAL-SIPI
SIVC--------------IIRPHLV-----GPRVLLTFLDTVMVGLTTAAAGGAASIVY-LAHN-----GNSDA-N--WP
```

```
AI-CQ--QFND---------------FC----------QEVSGAVVASFITVVVLMFLI-VLSAFSL
>B9SCX0_RICCO
FDFVVRLCAIATGLAATGIMGT--TEQTLPFFT---------QFFQFHAEYN--DLPTFMFFVFANGIASGYLIL-SLPF
SIVC--------------IVRPLAI-----VPRLLLIIFDTVVMALTIAAASAAAAIVY-LAHN-----GNSNA-N--WN
AI-CQ--QFND---------------FC----------QQTSTAVVASFITAAMLTFLI-VLSAFAL
>B9HQ42_POPTR
FDLTLRLSAIAAGFAATSLMAT--TDQTLPFFT---------QFFQFHAQYT--DLPTFLSFMIVNAITSGYLVL-SLPF
SIVC--------------IVRARAA-----GPRLLLIILDSVMMALTTSAASASAAIVY-LAHN-----GNSSS-N--WN
AF-CQ--QFNN---------------YC----------QQVSNAVVASFLAAALLLSLV-VLSAFAL
>D7LGW9_ARALL
FDFVLRLIAAITAMAAAAKMAT--TEETLPFFT---------QFLQFQAEYT--DLPTMSSFVIVNSIVGGYLTL-SLPF
SIVC--------------ILRPLAV-----PPRLFLIICDTAMMGLTMMAASASAAIVY-LAHN-----GNSSS-N--WL
PV-CQ--QFGD---------------FC----------QGTSGAVVASFIAATLLMFLV-ILSAFAL
>Q9ZQI2_ARATH
FDFVLRLIAAITAMAAAAKMAT--TEETLPFFT---------QFLQFQADYT--DLPTMSSFVIVNSIVGGYLTL-SLPF
SIVC--------------ILRPLAV-----PPRLFLILCDTVMMGLTLMAASASAAIVY-LAHN-----GNSSS-N--WL
PV-CQ--QFGD---------------FC----------QGTSGAVVASFIAATLLMFLV-ILSAFAL
>G7IHF9_MEDTR
LDFILRLGAIGAALGAAVIMGT--NEQILPFFT---------QFLQFHAQWD--DFPMFKFFVVANGAAAGFLIL-SLPF
SIVC--------------IVRPLAA-----GPRFLLVIVDLVLMALVVAAASSAAAVVY-LAHN-----GSQDA-N--WN
AI-CQ--QFTD---------------FC----------QGSSLAVVASFVASVFLACLV-VVSSVAL
>P0DI41_VIGUN
LDFILRLGAISSAIGAAAVMGN--NEQILPFFT---------QFFQFHVQWD--DFPMFQFFVFANGAAVVFLIL-SLPF
SIVC--------------IVRPFAV-----GPRLLLVIVDIFAMALVIAAASAAAAVVY-LAHN-----GSQDA-N--WI
AI-CQ--QYTD---------------FC----------QVTSQAVVASFVAAVFLICLI-VLSSVAL
>C6T4E0_SOYBN
LDFIIRLGAIGSALGAAAIMGN--SEQILPFFT---------QFFQFHAQWD--DFPMFQFFVFANGAAGGFLIL-SLPF
SIVC--------------IVRPYTV-----GPRLLLVILDILMMALVMAAASSAAAVVY-LAHN-----GSQDA-N--WI
AI-CQ--QFTD---------------FC----------QVTSEAVVASFVAAFLLICLI-VVSSVAL
>P0DI56_LOTJA
LDFILRLGAIGAAMGASILMGT--NEQILPFFT---------QFLQFHAQWD--DFPVFKLFVVLNALAGGFLIL-SLPL
SIVC--------------IVRPLAV-----GPRFLLLITDLVNMATVIAAASAAAAIVY-VAHN-----GSQDA-N--WI
AI-CQ--QFTD---------------FC----------QGTSEAVVVSFVAAVFLVCLI-VVSTLAL
>B6U045_MAIZE
LDLVLRVAAFGPALAAAIATGT--SDETLSVFT---------QFFQFHARFD--DFPALLFFMVANAIAAGYLVL-SLPF
SAVV--------------VLRPQAI-----GLRHLLLICDLIIAALLTAAAAAAAAIVD-LAHS-----GNQRA-N--WV
PI-CM--QFHG---------------FC----------QRTSGAVVASFLAVLVLLFLV-ILAAFTI
>C5YAP3_SORBI
LDFVLRVAAFGPALAAAIATGT--SDETLSVFT---------QFFQFHARFD--DFPALLFFMVANAIAAGYLVL-SLPF
SAVI--------------VLRPQAI-----GLRHLLLVCDMIIAALLTAAAAAAAAIVD-LAHS-----GNLRA-N--WV
PI-CM--QFHG---------------FC----------QRTSGAVVGSFLAVLVLLFLV-ILAAFAI
>P0DI38_BRADI
LDFLLRIAAFGPALAAAIATGT--SDETLSVFT---------EFFQFRARFD--DFPAFLFLMVANAIAAGYLVL-SLPF
SAVV--------------VLRPQAT-----GLRLLLLVCDTIMIGLLTAAAAAAAAIVE-LAHN-----GNERA-N--WV
AI-CM--QFHG---------------FC----------QRTSGAVVASFLSVFLFLLLV-VLAAFAI
>E6Y2A0_WHEAT
LDFLLRIAAFGPALAAAIATGT--SDETLSVFT---------EFFQFRARFD--EFPAFLFLMVASAIAAGYLLL-SLPF
SAVV--------------VLRPQTT-----VLRLLLLVCDTIMLGLLTAGAAAAAAIVD-LAHS-----GNERA-N--WV
PI-CM--QFHG---------------FC----------RRTSGAVVASFLSVFIFVLLV-VLAAFSI
>B8ART0_ORYSI
LDFILRIAAFGPALAAAISTGT--SDETLSVFT---------EFYQFRARFD--DFPAFLFFLVANAIVAGYLVL-SLPF
SAVL--------------VIRPQTI-----GLRLLLLVCDMIMAAMLTAAASAAAAIVD-LAHN-----GNLRA-N--WV
AI-CM--QFHG---------------FC----------QRTSGSVVASFLTVVILMFLV-ILAACSI
>Q7XPU9_ORYSJ
LDFILRIAAFGPALAAAISTGT--SDETLSVFT---------EFYQFRARFD--DFPAFLFFLVANAIVAGYLVL-SLPF
SAVL--------------VIRPQTI-----GLRLLLLVCDMIMAAMLTAAASAAAAIVD-LAHN-----GNLRA-N--WV
AI-CM--QFHG---------------FC----------QRTSGSVVASFLTVVILMFLV-ILAACSI
>C5YLC9_SORBI
IDFLLRVAAFGPTLAAAISTGT--ADERLSVFT---------NFFQFHARFD--DFPAFTFFLVANAVAAGYLVL-SLPF
SVVV--------------ILRPATG-----GVRLLLLLCDVLIMALLTAAGAAAAAIVY-VAHS-----GNRRA-N--WV
PI-CM--QFHG---------------FC----------QRTSGSVVATFLAVLVFIVLI-LMAACVI
>A2YQB8_ORYSI
IDFVLRVAAFGPTLAAAISIGT--SDERLSVFT---------NYFQFRARFD--DFPAFEFFIVANAIAAGYMVL-SLPF
SAAT--------------IMSSKAT-----GVKLLLLICDTIMVGLLTAAASAAAAMVY-VAHE-----GNLRA-N--WV
PI-CL--QFHG---------------FC----------QRTSGAVIASFLAVFVLMVLI-VMAAFTM
>Q6Z1Y7_ORYSJ
IDFVLRVAAFGPTLAAAISIGT--SDERLSVFT---------NYFQFRARFD--DFPAFEFFIVANAIAAGYMVL-SLPF
SAAT--------------IMSSKAT-----GVKLLLLICDTIMVGLLTAAASAAAAMVY-VAHE-----GNLRA-N--WV
PI-CL--QFHG---------------FC----------QRTSGAVIASFLAVFVLMVLI-VMAAFTM
>P0DI37_BRADI
LDLLLRVAAMGPTLAAAISTGT--SDETLSVFT---------HYFQFRARFD--DFSAFTFFMVANAVAAGYLLM-SLPF
SAFG--------------VIRPKAT-----SVRLLLLICDTIMVVLVTAAASAAAAIVY-VAHE-----GNRRA-N--WV
PI-CM--QFHG---------------FC----------KRTSGAVVASFLAVLIFILLV-FLGACAI
>B6T959_MAIZE
LDLILRFIAIIGTLASAIAMGT--TNETLPFFT---------QFIRFKAQYS--DLPTLTFFVVANSIVCAYLTL-SLPL
SIVH--------------IIRSRAK-----YSRLLLVVLDAAMLALVTPGASAAAAIVY-LAHK-----GNVRA-N--WL
AI-CQ--QFDS---------------FC----------ERISGCLIGSFGAMVMLVLLL-LLSAIAL
```

```
>C5Z7E3_SORBI
LDLILRFIAIIGTLASAIAMGT--TNETLPFFT---------QFIRFKAQYS--DLPTLTFFVVANSIVCAYLIL-SLPL
SIVH--------------IIRSRAK-----YSRLLLIFLDAAMLALVTAGASAAAAIVY-LAHK-----GNVRA-N--WL
AI-CQ--QFDS---------------FC----------ERISGSLIGSFGAMVMLILLI-LLSAIAL
>P0DI33_PANVG
LDLILRFIAIIGTLASAIAMGT--TNETLPFFT---------QFIRFKAQYS--DLPTLTFFVVANSIVCAYLIL-SLPL
SIVH--------------IIRSRAK-----FSRLLLIFLDAVMLALVTAGASAAAAIVY-LAHK-----GNVRA-N--WL
AI-CQ--QFDS---------------FC----------ERISGSLIGSFGAMVVLILLI-LLSAIAL
>A2YAZ1_ORYSI
LDVILRFVAIIGTLASAIAMGT--TNQTLPFFT---------QFIRFKAQYS--DLPTLTFFVVANSIVSAYLIL-SLPL
SIVH--------------VIRSRAK-----YSRLILIFFDAAMLALVTAGASAAAAIVY-LAHK-----GNARA-N--WL
AI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVVLVLLI-FLSAIAL
>Q67X40_ORYSJ
LDVILRFVAIIGTLASAIAMGT--TNQTLPFFT---------QFIRFKAQYS--DLPTLTFFVVANSIVSAYLIL-SLPL
SIVH--------------VIRSRAK-----YSRLILIFFDAAMLALVTAGASAAAAIVY-LAHK-----GNARA-N--WL
AI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVVLVLLI-FLSAIAL
>P0DI36_BRADI
LDLIFRVIAVIGTLASAIAMGT--TNQTMPFFT---------QFVQFKERYS--DLPTLTFFVVANSIASAYLII-SLPL
SIVH--------------IIRSRAK-----YSRLILIFFDVAMLALVTAAASAGAAIVY-LAHN-----GNVSA-N--WF
AI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVVLILLI-LLSAVAL
>P0DI42_WHEAT
LDLILRVIAVISTLASAIAMGT--TNETLPLFT---------PFIQFKARYS--DLPALTFFVVANSIVSAYLIL-SLPL
SIAH--------------IIRSGAK-----YSRLVLIIFDAAMLALVTAASSAATAIVY-LAHK-----GNVRA-N--WL
AI-CQ--QLDS---------------FC----------ERTSGSLVGSFGAMVLLILLI-LLSAMAL
>A2XU91_ORYSI
VDTFLRFIAIIGTIGSAIAMGT--TNETLPFFT---------QFIQFEAKYS--DLPSFTFFVAANAVVCTYLVL-SIPL
SIVH--------------ILRPRAR-----YSRLFLVFFDTAMLALLTAGASAAAAIVY-LAHK-----GNVRA-N--WF
SI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVLLVVLI-TLSAFAL
>Q7XUV7_ORYSJ
VDTFLRFIAIIGTIGSAIAMGT--TNETLPFFT---------QFIQFEAKYS--DLPSFTFFVAANAVVCTYLVL-SIPL
SIVH--------------ILRPRAR-----YSRLFLVFFDTAMLALLTAGASAAAAIVY-LAHK-----GNVRA-N--WF
SI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVLLVVLI-TLSAFAL
>F2QA93_ORYRU
VDTFLRFIAIIGTIGSAIAMGT--TNETLPFFT---------QFIQFEAKYS--DLPSFTFFVAANAVVCTYLVL-SIPL
SIVH--------------ILRPRAR-----YSRLFLVFFDTAMLALLTAGASAAAAIVY-LAHK-----GNVRA-N--WF
SI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVLLVVLI-TLSAFAL
>C5Y9U6_SORBI
ADVFLRFLSIVATIASAISMGT--TNETLPFFT---------QFIQFEAKYS--DLPSFTFFVAANAVVCTYLVL-SIPL
SIVH--------------IIRPRAR-----YSRLILVFFDAVMLALLTAGASAAAAIVY-LAHK-----GNVRA-N--WF
AI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVLLIVLI-FLSAFAL
>P0DI34_PANVG
ADVFLRFLAIVGTIASAISMGT--TNETLPFFT---------QFIQFEAKYS--DLPSFTFFVAANAVVCTYLVL-SIPL
SIVH--------------IVRPRAR-----YSRLVLVFFDAAMLTLLTAGASAAAAIVY-LAHK-----GNVRA-N--WF
AI-CQ--QFDS---------------FC----------ERISGSLIGSFAAMVLLIMLI-FLSAFAL
>Q6Z2U5_ORYSJ
ADLILRVVAVVAIVDSAIAMGT--TNQTLPFFT---------QFLRFKAQYS--DLPTLTLFVVANSAVTAYLVL-SIPL
SVVH--------------IIRSRAS-----YSRLVLIFLDSVMLALVAAVASASAAIVY-LAHK-----GNVRA-N--WF
AV-CQ--QFDS---------------FC----------ERISGPLIGSFAAMAVLLLLV-LLSAAAL
>B9I534_POPTR
LDFILRILAFIGTLGSAISMAT--TNETLPFFT---------QFIRFRAEYD--DLPTFTFFVVANGVVSAYLLF-SLPF
SIFN--------------IVRSKAQ-----NSRILLIILDTAMLGLLSAGASAAAAIVY-LAHQ-----GNVRT-N--WS
AI-CQ--QFNS---------------FC----------ERISGSLIGSFIGVVVFILLI-SLSAVAL
>B9T4E6_RICCO
LDFILRLVALVGTLASAILMGT--TNETLPFAT---------QFIRFRAEYD--DLPTFTFFVVANIVVSGYLLL-SLPL
SIVN--------------IVRSTAK-----NRRIILIIFDTAMLALLTAGASAAAAIVY-LAHK-----GNTRA-N--WF
AI-CQ--QFNS---------------FC----------ERISGSLIGSFVGVAVFILLI-LMSASAL
>A7PMY7_VITVI
LDFILRLITIIGTLGSAIAMGT--TNETLPFFT---------QFTQFRAEYD--DLPTFTFFVIANSIVSGYLVL-SLPM
SILH--------------IVRSGAR-----ASRIVLIFFDTAMLALLTAAASAASAIVY-LAHK-----GNAQA-N--WF
AI-CQ--QFKS---------------FC----------ERISGSLIGSFGGIILFILLV-LLSAVAL
>P0DI54_MALDO
LDFILRIVAFLGTLVSAVTMGT--TRERLPFFT---------QFLQFRAEYD--DLPTFTFFVVANSIVCAYLVF-SLAL
SVFH--------------IIRSNAK-----KSRIILIFFDTAMLALLTAGASAAAAIVY-LSHK-----GNAKA-N--WF
AI-CQ--QFNS---------------FC----------ERISGSLIGSFVGVVVFILLI-LLSAAAL
>P0DI44_SOLTU
LDLFIRIIAIIATLGSAIAMGT--TNETLPFFT---------QFVRFKAKYS--DLPTFTFFVVANAIVSAYLVL-SLGL
SIYH--------------IMRSRAQ-----ATRIALIFFDAAMLGLLTGGASASAAIVY-LAHK-----GNRKT-N--WF
PI-CQ--QYDS---------------FC----------HRTSGSLVGSFAGSVLIILLI-FLSAIAL
>P0DKC2_LOTJA
LDFILRLIAVVATLASAIAMGT--TDESLPFFT---------QFIRFRAEYD--DLPTLRLFVVASAFASGYLIL-SLPL
SILH--------------ITRSSAR-----RTRVILIILDMVMLTSLTAASSAAAAIVY-LAHK-----GNAKA-N--WF
AF-CQ--QYDS---------------FC----------ERISGSLIGSFIAIPLFIMLI-LFSALVL
>G7L218_MEDTR
LDFILRLIAIVATLASAIAMGT--TDESLPFFT---------QFVRFRANYD--DLPTLRFFVVASAIVSGYLIL-SLPL
SILH--------------IIRSSAG-----MTRVIFIILDTVMLGLLTAGSSAAASIVY-LAHK-----GNRKA-N--WF
AF-CQ--QYNS---------------FC----------ERISGSLIGSFIAIPLFIMLI-LLSALVL
>D7M7B3_ARALL
```

```
LEFILRIVAFFNTIGSAILMGT--THETLPFFT---------QFIRFQAEYN--DLPALTFFVVANAVVSGYLIM-SLTL
AFVH--------------IVKRKTQ-----NTRILLIVLDVAMLGLLSAGASSAAAIVY-LAHN-----GNNKT-N--WF
AI-CQ--QFNS---------------FC----------ERISGSLIGSFIAVVLLILLI-LLSAIAL
>Q9LXF3_ARATH
LEFILRIVAFFNTIGSAILMGT--THETLPFFT---------QFIRFQAEYN--DLPALTFFVVANAVVSGYLIL-SLTL
AFVH--------------IVKRKTQ-----NTRILLIILDVAMLGLLTSGASSAAAIVY-LAHN-----GNNKT-N--WF
AI-CQ--QFNS---------------FC----------ERISGSLIGSFIAIVLLILLI-LLSAIAL
>P0DI58_LOTJA
MDFILRIVAAIGTLGSALSTGT--TRETLPFTT---------QFVKFRAVFD--DLPTFVFFVTSNSIVCGYLVL-SLAL
SFFH--------------IIRSSAA-----KSRILLVFLDTVMFGLLTTGAAAAGTIVY-VSHY-----GNVNA-N--WF
PF-CG--QYNH---------------FC----------ERISGSLIGSFIAVVIFMIII-LMSAVSI
>C6T4A0_SOYBN
MDFILRIVAAIATLGSALGMGT--TRQTLPFST---------QFVKFRAVFS--DVPTFVFFVTSNSIVCGYLVL-SLVL
SFFH--------------IVRSAAV-----KSRVLQVFLDTVMYGLLTTGASAATAIVY-EAHY-----GNSNT-N--WF
PF-CR--QYNH---------------FC----------KQISGSLIGSFIAVVLFIILI-LMSAISI
>G7JG80_MEDTR
MDFILRIFAAMSTLGSALSMGT--AKQTMPFAT---------RFVRFKVSFH--DLPTFLFFVTANSIVCGYLAL-SLVL
SFFH--------------IVRTISV-----KSRILLVFLDTVMFGLLTSGASAAAAIVY-VAHY-----GNPSA-N--WF
PF-CQ--QYNS---------------FC----------GRISGSLVGSFIAVVIFMILI-LMSGISI
>C6T1G0_SOYBN
MDFILRIIAAVATLGSALAMGT--TNETLPFAT---------QFIKFRAEFD--DLPSLVFFVMANAVVCGYLVL-SLMI
SVFH--------------ILRSTPV-----KSRILLVALDTVMLSLVTASASAATSIVY-IAHN-----GNTGA-N--WF
AI-CQ--QYNN---------------FC----------ERISGSLIGSYIAVALFIILI-MLSLVAI
>G7KGQ4_MEDTR
MDFILRIIAGVATLASAVAMGT--TDERLPFAT---------SFVQFRAEYD--DLPSFVFFVLANSIVCGYLAL-SLIL
SILH--------------IVRSTAV-----KSRILLIVLDMVMMGLLAAAASAAASIVY-IAHY-----GNTQA-N--WF
PI-CQ--QYNS---------------FC----------ERISGSLIGSYIAVALFIIII-LLSQSAI
>B8AEC9_ORYSI
ADLVLRFVAIGGTAGSAIAMAT--TSETLPFAA---------PFVRFRAEYS--DLPTLMFFVVASSVVCAYLVL-SLPA
SVVH--------------VVRPGAR-----SSRAILAFLDTVMLALLTASASAAAAIVY-LAHR-----GSARA-N--WL
GI-CQ--QFTS---------------FC----------QRITASLVGSFAAAVVLVALV-FLSALSL
>Q6EP58_ORYSJ
ADLVLRFVAIGGTAGSAIAMAT--TSETLPFAA---------PFVRFRAEYS--DLPTLMFFVVASSVVCAYLVL-SLPA
SVVH--------------VVRPGAR-----SSRAILAFLDTVMLALLTASASAAAAIVY-LAHR-----GSARA-N--WL
GI-CQ--QFTS---------------FC----------QRITASLVGSFAAAVVLVALV-FLSALSL
>P0DI59_LACSA
LDFFLRPIAIVGTLASAIAMAT--TNQTLPFFS---------QFIRFRAKFN--DLPSFTFFVVASSIVSAYLIL-SLGF
SILH--------------IAKSNLV-----NSRVLLLLLDTAAMGLLMAGSAAATAIVQ-LAHK-----GNNKV-N--WF
AI-CQ--QYNS---------------FC----------KRVSGSLIGSYAGVVVLILLI-LLSGVAL
>Q5NRN4_SOLDE
FDLVLRIVALVGTLASAVAMGT--ADQALSFST---------QIVNFEAQYD--DIDAFKFFVVSNSITCVYLAL-SIPI
SIFH--------------IIRSRAG-----KSRVLLIVLDAIMLVFLTSGASAAAAIVY-LAHN-----GNTST-N--WF
SI-CQ--QYTD---------------FC----------QRSAGSLIGSFGAMALMVLLI-ILSSIAL
>Q60D27_SOLDE
FDLVLRIVALVGTLASAVAMGT--AGQALSFST---------QIVNFEAQYD--DIDAFKFFVVSNSITCVYLAL-SIPI
SIFH--------------IIRSRAG-----KSRVLLIVLDAIMLVFLTSGASAAAAIVY-LAHN-----GNTST-N--WF
SI-CQ--QYTD---------------FC----------QRSAGSLIGSFGAMALMVLLI-ILSSIAL
>P0DI35_LACSI
MDLVLRLVGIAGTLGAAIAMGT--NEQTLPFFT---------RFVVFNAEYD--DFRSFRLFVIVNAIVCAYFVL-TLPL
SIVH--------------IMRSAAR-----GSRILLIIMDTVMLALLTAGASAAASIVY-LAHN-----GNTST-N--WL
PV-CQ--QYGD---------------FC----------QGASGSLIGSFGAVVVFILII-LLGAIAL
>B9HI87_POPTR
ADLILRGVAAIGTFASALTMGT--TSETLTIFT---------QPIMIRAKYN--DLPSLTFFVIANSIVCGYLVL-SIPL
SISH--------------FIRREAR-----ITRIILVIFDTAMVELLTAGAAAATVVVY-LAHK-----GN--A-N--WL
AI-CQ--QFNN---------------FC----------ERISGSLIGSFASIIMIMLII-ITSAVAL
>B9S8Z3_RICCO
LDLVLRVFGAICTLGSAVAMGT--TSQTLPSSS---------QFFRFRAKYN--DLPMFMFFAIANSIVCAYLVL-SLRL
SIFH--------------IIRSAGI-----ITRIILVTFDMVMLVLLTCGASAATSIVY-LAHK-----GNASA-N--WL
PF-CV--RFSH---------------FC----------NRISGSLIGSFFSIIIFMLLV-ILSAVSQ
>D7KBH3_ARALL
LGFVLRLFAVFGTIGSALAMGT--THESVVSLS---------QLVLLKVKYS--DLPTLMFFVVANAIAGGYLVL-SLPV
SIFH--------------IFSTKAK-----TSRIILLVIDTVMLALVSSGASAATATVY-LAHE-----GNTTA-N--WP
PI-CQ--QFDG---------------FC----------ERISGSLIGSFCAVILLMLIV-INSAISL
>Q9XI72_ARATH
LGFVLRLFAVFGTIGSALAMGT--THESVVSLS---------QLVLLKVKYS--DLPTLMFFVVANAISGGYLVL-SLPV
SIFH--------------IFSTQAK-----TSRIILLVVDTVMLALVSSGASAATATVY-LAHE-----GNTTA-N--WP
PI-CQ--QFDG---------------FC----------ERISGSLIGSFCAVILLMLIV-INSAISL
>P0DH81_PICGL
LDFLLRLLAIGATLSAAITMGT--TNETLQFFT---------QFFQFKARFY--DLSAFIYFVIANAIVGGYLLL-SLPI
SILN--------------IVRPRAA-----SSRVFLIFFDTVMVAVCTSGAAAAVAILY-VARK-----GNSRT-N--WF
AI-CQ--RFNS---------------FC----------NQAIGAVSASFAGVVFLILLV-LLSASTL
>P0DH80_PINTA
LDFLLRLLAIGATLSAAIAMGT--NNETLKFFT---------QFFQFNARFY--NLSAFIYFVIANATVGLYLLL-SLPF
SIFD--------------IVRPRAA-----AFRVLLIFFDTVMVAVCTSGAAAATAIMY-VARR-----GNTKT-N--WF
SI-CQ--QFNS---------------FC----------DQATGALGASFAAVVLLILLV-LLSASTL
>D2KQI6_BETVM
VDVILRVLLLAASIASVVLMVT--SKQTEIIVS-------XXGSRPNAAKFQ--NSPAFIYLVAALSVAGLYSII-TALV
```

```
SL-S----YM--------XKPIVPP-----KLFWILLIHDVLLLGIVAAATGTAGGVGY-IGLK-----GNTHV-R--WG
KI-RN--VYDK---------------FC----------RHVGASIIVSLFAAAVLVLLV-FVNANSL
>B9RT03_RICCO
VDVGLRVFLFATTLTAIVVMST--AKQTELAPV---PGV-PGLRVPVEAKFN--HSPAFIYFVAALSVACLYSII-TTLA
SL-G----VI--------XKPIYAT-----KFLFYYALWDVLMLGIVAAATGAAGGVAY-IGLK-----GNSHT-R--WT
KI-CN--VYDT---------------FC----------KHVGSALAISLAASVVLVLLI-MLSVCSL
>B9HMP5_POPTR
VHVALRFLLFAASVTAVVVMVT--AKQTKIVPV---PGF-P-ISVPLEAKFS--DSPAFIYFISALSVAGLYGIL-TTLA
AI-S----IV--------XKPAYAT-----RFLLHFALLDVLMLGIVASATGAAGGVAY-VGLK-----GNSHV-R--WG
KV-CN--VYDK---------------FC----------QHVGSSIAVALFASVLLVLLT-MLSVFSI
>A7NW79_VITVI
LDVVLRILLLGSAVASVVVMVT--SVQTKLIAV---AGV-P-VLVSNKAKFQ--NSPAFIYFVAALSVVGLYSII-TTLA
SF-I----FI--------XKPSCST-----KTILHLAIWDVLMLGLAASATGTAGGVAY-VGLK-----GNSHV-G--WN
KV-CN--TYDK---------------FC----------RHVGGSIAVALFASILLVLLV-WLSLFTL
>C6SVQ5_SOYBN
FDVILRFLLFAASLVAVVVIVT--ANQTEVIRV-------P-QPVPWPAKFR--YSPAFVYFVAALSVTGLYSII-TTLA
SL-L----AS--------XKPALKT-----KLLLYFILWDALILGIIASATGTAGGVAY-LGLK-----GNRHVVG--WN
KI-CH--VYDK---------------FC----------RHVGASIAVALFGSVVTVLLI-WLSAYSI
>C6SXZ3_SOYBN
FDVILRFVLFAASLVAVVVIVT--GNQTEVILV-------P-QPVPWPAKFR--YTPAFVYFVAALSVTGLYSII-TTLA
SL-F----AS--------XKPALKT-----KLLPYFILWDALILGIIASATGTAGGVAY-LGLK-----GNSHVVG--WN
KI-CH--VYDK---------------FC----------RHVGASIAVALFGSIVTVLLI-WLSAYSI
>D7MAF7_ARALL
TQVVLRFVLFAATLTSIVVMVT--SKQTKNIFI---PGT-P-IRIP-AAKFT--NSPALIYFVVALSVACFYSIV-STFV
TV-S----AF--------XKHSCSA-----ILLLNLAIMDAVMVGIVASATGAGGGVAY-LGLK-----GNKEV-R--WG
KI-CN--IYDK---------------FC----------RHVGGAIAVSLFASVILLLLS-IISVLSL
>Q9FE29_ARATH
TQVVLRFVLFAATLTSIVVMVT--SKQTKNIFL---PGT-P-IRIP-AAEFT--NSPALIYFVVALSVACFYSIV-STFV
TV-S----AF--------XKHSCSA-----VLLLNLAIMDAVMVGIVASATGAGGGVAY-LGLK-----GNKEV-R--WG
KI-CH--IYDK---------------FC----------RHVGGAIAVSLFASVVLLLLS-IISVLSL
>D7L5G6_ARALL
IDVIIRVLLFSATLTALIVMVT--SDQTEKTQL---PGV-S-SPAPVSAEFN--DSPAFIFFVVALVVTSFYALM-STLV
SI-S----LL--------XKPEFTA-----RVSVYLASLDMVMLGILASATGTAGGVAY-IALK-----GNKEV-G--WN
KI-CN--VYDK---------------FC----------RYIATSLALSLFATLLLLVLS-ICSALS-
>Q9SQU2_ARATH
IDIITRVLLFSATLTALIVMVT--SDQTEMTQL---PGV-S-SPAPVSAEFN--DSPAFIYFVVALVVASFYALI-STLV
SI-S----LL--------XKPEFTA-----QFSIYLASLDMVMLGILASATGTAGGVAY-IALK-----GNEEV-G--WN
KI-CN--VYDK---------------FC----------RYIATSLALSLFASLLLLVLS-IWSALS-
>Q1EPG6_MUSAC
VDFGLRLLLLASAVSALVVLVT--SKQTESIPTSLPPPF-P-AFISRDAKFQ--HSPAFIYLLVALSVTCFYSII-TMVA
SF-A----AI--------XSPSSSP-----RMLFHLVLSDAVMAGVMASAAGTAGSVAY-LGLK-----GNSHV-N--WN
KV-CN--VYDK---------------FC----------RHVGSSAAVSLVASVLLVSLV-VLSSYSL
>B6U361_MAIZE
ADLALRVLLFAVTLSGLVVLAT--AEQTVRVPV---PQI-PGLVLSLPAKFK--DSPALIYLLVALCVTCFYSLL-STAF
TSLK----LL---------FGSSPS-----RTLFLLVLFDVFYAAIMASATGSAGGVAW-IGLK-----GNSHT-N--WN
KI-CN--IYGK---------------FC----------RHIGSSVFLGLIASVVLVLLT-ILNAHSL
>C5X4A5_SORBI
ADLALRALLFAVTLAGLIVLAT--AKQTVSIPV---PEI-PGLLVSRPAKFN--HSPALIYLLVAQCVTCFYSLL-TALT
SL-K----LI---------SGSSPT-----KTLFLLVLLDVLYAAIMASATGSAGGVAW-IGLK-----GNTHT-N--WT
KI-CN--IYGN---------------FC----------RHIGSSVFLGLVASVILVLLT-ILNAYCL
>Q6YT98_ORYSJ
ANLALRALLFAVSLSALVVLVT--AKQTVMVPF---XXR-PXILAPVPAKYT--HSPALIYLLAALCATCFYSLI-TAIS
SV-R----LL--------XSSACSA-----KTLFYLILLDVFYAAVMASATGTAGAVAW-VGLK-----GNSHT-R--WN
KI-CN--VYGK---------------FC----------RHIGSSTFLALIAAIVLVLLA-FLNAYSL
>A2PZE5_IPONI
TEAILRLLLLASLVVAVVVMVT--SKETELISVKLDPFP-P-FMLPLTAKFT--QSPAFIYFVAGLSVAGLYTII-STLA
SFYN----LL--------XKPGFCP-----ALVSHFIILDVVMLGIVGTATGAAGGVAY-IGLK-----GNSHV-G--WT
KV-CN--KYGK---------------LC----------THLGASLAVSFFAFIVLLLLI-ILSIHSL
>A9P0A6_PICSI
VDFSLRLLVIGSTFTAAIVMGT--NKQTAILP----------IVGPLSAKYQ--YSPAFVFFVIANAVACGYTLL-SLIF
SITG---------------XFTSTP-----LSVFLLSVTDLVMVALVSAGVSAAAAIAY-VGYK-----GNSHT-Q--WG
KV-CG--IYDR---------------FC----------HHGAGAIVASFVSLIIFMVLT-VMSTYSF
>B4FAP1_MAIZE
CSVALRVFVLAATLVSAVVMGV--DRQTSTIRITVTDAL-PPLEVPLTANWS--YSSAFVYFVVANAMVCLFSAA-ALAA
C---------------------RSR-----AAMVPVMVGDLLALALLYSAVGAAAEFGI-LGER-----GNSHV-R--WP
KV-CN--VYGR---------------FC----------ERAMAAVIVSLIAAFANLVLL-MLNILTI
>C5XKI6_SORBI
CSVALRVFVVASTLVSAVVMGV--DRQTRTIQITITDAL-PPLEVPLTANWS--YSSAFVYFVVANAMVCLFSAA-ALAA
C---------------------RSR-----AAMVPVMVGDLLALALLYSAVGAAAEFGI-LGER-----GNSHV-R--WA
KV-CN--VYGR---------------FC----------DRAMAAVIVSLIGAFANLVLL-MLNILTI
>Q9ARX2_ORYSJ
CCVVLRVFVLLGTLASAVVMAA--DRQSTTVQIAAGEELAPPLRVPVTAKWT--YSSAFVYFVVANAMVFAFSAA-ALAA
V---------------------RRR-----SAVVPVMVGDLVAMALLFSAVGAAAQFGL-LGER-----GNAHV-R--WA
KV-CD--VYGP---------------FC----------ERAMAAVVVALIAAFADLVLL-MLTILTI
>B8A7Z5_ORYSI
CCVALRVFVLLGTLASAVVMAA--DRQSTTVQIAAGEQLAPPLRVPVTAKWT--YSSAFVYFVVANAMVFAFSAA-ALAA
V---------------------RRR-----SAVVPVMVGDLVAMALLFSAVGAAAQFGL-LGER-----GNAHV-R--WA
```

```
KV-CD--VYGP---------------FC----------ERAMAAVVVALIAAFADLVLL-MLTILTI
>C6SZP8_SOYBN
SDLLLRLLAFTVTLVAAIVIAV--DKQTKVVPIQLSDSL-PPLDVPLTAKWH--QMSAIVYFLVTNAIACTYAVL-SLLL
ALVNRG----------------KSK-----GLWTLIAVLDAFMVALLFSGNGAAAAVGV-LGYK-----GNSHV-N--WN
KV-CN--VFGK---------------FC----------DQMAASIGVSLIGSLAFLLLV-IIPGVRL
>C6TBD0_SOYBN
CDLLLRLLAFTVTLVAAIVIAV--DKQTKLVPIQLSDSF-PPLNVPLTAKWH--QMSAFVYFLVTNAIACTYAAM-SLLL
ALVNRG----------------KSK-----GLWTLIAVLDTFMVALLFSGNGAAAAVGI-LGYK-----GNSHV-N--WN
KV-CN--VFGK---------------FC----------DQMAASIGVSLIGSLAFLLLV-VIPVVRL
>B9HMP6_POPTR
CDLLLRVLALVLTLAAAIVLGV--DKQTKVVPIKIVDTL-PAINLPVSAKWH--YLSAFTYSVASNAIACSYAAL-SLVL
AV-------------------XGKK-----GIMSIVIVLDLLMVAMLFSSNGAALAIGL-MGYQ-----GNSHV-R--WT
KV-CH--VFGR---------------FC----------NQVAVSISLSLLGSILFLLLV-GITSLRL
>B9RT04_RICCO
SFLVLRVLAFVLTSTAAIVHGV--NNQTETVPIQLTSSM-PPLYVPVVAKWH--YLSAFVFFVVSNAIACSYAAI-SVML
SF-------------------XGKK-----SMVPIILTLDLLMVALLFSSNGAATAIGV-MGYK-----GNSHV-K--WN
KV-CN--VFGK---------------FC----------NQVAASVVLSLIGSIVFVLLV-MLTAFRL
>A7NW78_VITVI
FDLVLRVVALALTLVAAVLLGV--DKQTKVVSLQLLPTL-PPMDVPVTAKWR--YLSAFVYFVVSNAIACSYAAL-SLLL
SV----------------XXSKGNK-----GLGLAITVMDLVMVALLFSSNGAAGAIGL-MGYE-----GNSRV-R--WG
KV-CN--VFGK---------------FC----------NQVAVALGLSFFGGLAFFLLV-VMAAFAL
>D7MAF6_ARALL
VELTMRVLALVLTMAAATVLGV--AKQTKVVSIKLIPAL-PPLDITTTAKAS--YLSAFVYNISANAIACGYTAI-SIAI
LM-------X--------XXGRRSK-----KLLMAVLLGDLVMVALLFSGTGAASAIGL-MGLQ-----GNKHV-M--WN
KV-CG--VFGK---------------FC----------HRAAPSLPLTFLAAVVFMFLV-VLDAIKL
>O23413_ARATH
VELTMRVLALILTMAAATVLGV--AKQTKVVSIKLIPTL-PPLDITTTAKAS--YLSAFVYNISVNAIACGYTAI-SIAI
LM-------X--------XXGRRSK-----KLLMVVLLGDLVMVALLFSGTGAASAIGL-MGLH-----GNKHV-M--WK
KV-CG--VFGK---------------FC----------HRAAPSLPLTLLAAVVFMFLV-VLDAIKL
>D7MAF5_ARALL
VEITMRVLALVLTMVAATVLGV--AKQTEVVPIKLIPTL-PPLNVATTAKAS--YLSAFVYNICANAIACGYTAI-SIMI
VI-------X--------XXGRRSK-----CLLMAVLIGDLMMVALLCSSTGAAGAIGL-MGRH-----GNKHV-M--WK
KV-CG--VFGK---------------FC----------NQAAVSVAITLIASVVFMLLV-VLDALKL
>Q8L8Z1_ARATH
LELTMRVLALVLTMVAATVLGV--AKQTKVVPIKLIPTL-PPLNVSTTAKAS--YLSAFVYNISANAIACGYTAI-SIVI
VM-------X--------XXGKRSK-----SLLMAVLIGDLMMVALLFSSTGAAGAIGL-MGRH-----GNKHV-M--WK
KV-CG--VFGK---------------FC----------NQAAVSVAITLIASVVFMLLV-VLDALKL
>A7PTY8_VITVI
SEFVLRILGLLLTLIAAVVAGV--DKQTKIIPLTLIKTL-PSLHVPVTAKWS--DMSAFVYLVVSNAIACSYAAI-SLVL
VT-------X--------XXXRGKG-----GRVLAVIVLDLHMVGLLFSANGAATAVGV-LGQY-----GNSHV-E--WK
KV-CN--VFDS---------------FC----------HHLVASLALSFLGSLSFLGLV-LLAILNL
>A7QC16_VITVI
IVLVLRVVAFLATASATIVMGL--NQETKTLLVGTIGTT-P-IRATLKAKFQ--HTPAFVFFVVANGLASVYNLV-MLGV
DV------XX--------RKLDCKG-----LRLVIISILDMVIVAVVAAGASSAAFMAE-LGKN-----GNSHA-K--WN
KI-CD--KFES---------------FC----------HQGGGALIPSFIALLLLFLIS-AISIITL
>B9GIE4_POPTR
VLLMLRVLAFFATAAATVVMGL--NKETKTLVVATVGST-P-IKASLTAKFQ--HTPAFVFFVIANGLASIHNLV-MIMG
DL------XX--------QKLDYKG-----LRLAMIAILDIMTVALVSGGVSAAAFMAE-LGKN-----GNSHA-R--WN
KI-CD--KFET---------------FC----------DHGGGALIASFAGLILMLIIS-VMSIIKL
>B9I0U9_POPTR
VLLMVRVVAFLATAAATLVMAL--NKETKTLVVATVGNT-P-IKVTLTAKFQ--HTPAFVFFVIANGMASFHNLL-MIMV
EL------XX--------QKLDYKG-----MRLAMVAILDMMTVALVSGGASAATFMAE-LGKN-----GNSHA-R--WD
KI-CD--KFET---------------FC----------DHGGAALIASSAGLILMMIIS-VMSIMKL
>B9SV63_RICCO
VLLMLRFVAFLATAAATIVMAA--NRETKTFVVATIGST-P-IKATVTAKFQ--HTPAFVFFVIANGMGSIHNLV-MIAG
DT------XX--------RKFDYKG-----LRWVTVAILDMLTAALISGGVNAAVFMAE-LGKN-----GNSHA-K--WN
KI-CD--RFGS---------------FC----------DHGGAAIIASFIGLLLMLVIS-IISIIKL
>D7MFJ8_ARALL
LLLGLRVFAFMATLAAAIVMSL--NKETKTLVVATIGTL-P-IKATLTAKFQ--DTPAFVFFVIANVMVSFHNLL-MIVL
QI------XX--------RKLEYKG-----VRLLSIAILDMLNATLVSAAANAAVFVAE-LGKN-----GNKHA-K--WN
KV-CD--RFAT---------------YC----------DHGAGALIAAFAGVILMLLVS-SVSISRL
>Q9SUP0_ARATH
LLLGLRIFAFMATLAAAIVMSL--NKETKTLVVATIGTV-P-IKATLTAKFQ--HTPAFVFFVIANVMVSFHNLL-MIVV
QI------XX--------RKLEYKG-----LRLLSIAILDMLNATLVSAAANAAVFVAE-LGKN-----GNKHA-K--WN
KV-CD--RFTT---------------YC----------DHGAGAIIAAFAGVILMLLVS-AVSISRL
>D7MM00_ARALL
ILLGLRLLAFSATLSAAIVMGL--NKETETFVVGKVGNT-P-IKATFTAKFD--HTPAFVFFVVANAMVSFHNLL-MIAL
QI------XX--------GKMEFTG-----FRLLSVAILDMLNVTLISAAANAAAFMAE-VGKN-----GNKHA-R--WD
KI-CD--RFAT---------------YC----------DHGAGALIAAFAGVILMLIIS-AASISRL
>Q9FI10_ARATH
ILLGLRLLAFSATLSAAIVMGL--NKETKTFIVGKVGNT-P-IQATFTAKFD--HTPAFVFFVVANAMVSFHNLL-MIAL
QI------XX--------GKMEFTG-----FRLLSVAILDMLNVTLISAAANAAAFMAE-VGKN-----GNKHA-R--WD
KI-CD--RFAT---------------YC----------DHGAGALIAAFAGVILMLIIS-AASISRL
>C6TG62_SOYBN
VILSLRVVAFFATASATLVMAF--NKQTKGMVVATIGTN-P-VTITLTAMFQ--HTPAFIFFVIVNAIASFYNLL-VIGV
EI------XX--------PQYDYKG-----LRLGLIAILDVMTMALAATGDGAATFMAE-LGRN-----GNSHA-R--WD
KI-CD--KFEA---------------YC----------NRGGVALVASFVGLILLLVVT-VMSITKL
```

```
>B6TUH4_MAIZE
QPVLLRAAAALAAAAAAAVMAL--DAQSYTAVVAIVGTR-P-LTQTFTAKFS--DTPAFVYFVIANAIAAAYNLL-VLLV
RRR-------------------RRT-----TAGLVVRMLDMVVMALLATGAAAAASMAE-LGRN-----GNARA-R--WN
PV-CD--RFGS---------------FC----------RRGGAALAASFVGVALMLALN-LLSAASG
>C5YRU8_SORBI
QPVVLRAAATLATAVAAAVMAL--NAQSYTAVVAIVGTR-P-LTQTFTTKFR--DTPAFVYFVIANAIAAVYNLV-MLLF
RCLIL-----------------RRR-----MAGLVVHMLDMVIMALLATGAATAAAMAE-LGKN-----GNVHA-R--WN
PI-CD--RFGS---------------FC----------SRGGVALASSFTGVALMLALN-LLSAASN
>A2ZMM4_ORYSI
QPV-VRACVFLATAVAAVIMGL--NKQSYTTVVAIVGTR-P-VTQTFTAKFK--DTPAFVFFVIANAIASGYNLM-VLVT
RRIL------------------QRR-----AQSLSVHLLDMVILTLLATGSATAASMAQ-LGKN-----GNLHA-R--WN
PI-CD--KFGS---------------FC----------NHGGIALMSSFIGVALMLALN-LLSAAAN
>B8BMY7_ORYSI
QPV-VRACVFLATAVAAVIMGL--NKQSYTTVVAIVGTR-P-VTQTFTAKFK--DTPAFVFFVIANAIASGYNLM-VLVT
RRIL------------------QRR-----AQSLSVHLLDMVILTLLATGSATAASMAQ-LGKN-----GNLHA-R--WN
PI-CD--KFGS---------------FC----------NHGGIALVSSFIGVALMLALN-LLSAAAN
>Q0ILZ7_ORYSJ
QPV-VRACVFLATAVAAVIMGL--NKQSYTTVVAIVGTR-P-VTQTFTAKFK--DTPAFVFFVIANAIASGYNLM-VLVT
RRIL------------------QRR-----AQSLSVHLLDMVILTLLATGSATAASMAQ-LGKN-----GNLHA-R--WN
PI-CD--KFGS---------------FC----------NHGGIALVSSFIGVALMLALN-LLSAAAN
>Q1EPG7_MUSAC
PGIILRIVAIVLTFISAVVMGA--ARQTTTVTGIDAETALL-TSITVTVKST--YSAAYVYFVVANVLVFFYSVV-SLVL
SMVN----------------XXRLT-----SMSLPFSIADLLMVVLLFSSNGAAAAISV-VAEK-----GQQNLXG--WD
KI-CN--LFGG---------------LC----------ARVNAAIVLSMLASVAYVILV-VFGMANL
>B9I3X5_POPTR
AQIFLRIVVIAASFASTWLMLT--NKQTIDI-----------GGFVLDANYS--YSPEFKFLSYANIVVGAFSFV-SLLF
LVLV--------------GRRSSNP-----TYYFILFLHDLALMSLVLGGCAAATVIGS-LGKY-----GNSHT-G--WM
QI-CD--HFGK---------------FC----------KRATTSVAFSYFSLVCLLILT-ITSASKS
>B9IFI5_POPTR
VQIFFRIVAIAASVASSWLMIT--SKQVIDI-----------GGIVLDARYS--YSPEFKFLAFTNIVVGCFSLL-SLLF
LVLV--------------VRQGSNP-----NHYFFLFLHDLAMMSLVVGGCAAATTVGF-LGKH-----GNSHT-G--WM
QI-CD--NFGK---------------FC----------NRAQTSVTISYLNLICLSILT-ITSASKS
>B9RA90_RICCO
AQICLRIVTIGATLAATWIMVT--DKQSITF-----------GDFVMVAKYN--YSSAFKFFVLANVIACACSVV-SLLF
LCAL--------------GRYSSNP-----GHVFLLFLHDLLMMSLVLAGCSAATAIGF-LGKY-----GNTKS-G--WM
PI-CD--QFGQ---------------FC----------NRGTISMMLSYLSMVCLLILT-VTSANKS
>A7PHN8_VITVI
AHICLRILTVTATLTAAWMMIT--SKQTVEV-----------YGIQVEAKYS--YSSAFKFFSYANAIACGCSVL-TLFP
AFSL--------------FYRGSTP-----MKFFFLFLHDLCMMSLVLAGCAAATAIGY-VGRY-----GNNHA-G--WM
AI-CD--QFDE---------------YC----------NRIRLSLMFSYLAFVFILMLT-IMSANKS
>A7PA04_VITVI
AQVVLRFFTLAFTGAAIAVMVT--AKETVEV-----------FSISFTVRYS--YLSAFKFLVGADAVVCGFSML-SLIF
VSIF--------------NK--GKS-----NHYFFLYFHDLILMVLSMSACAAATAVGY-VGRY-----GQDKA-A--WM
AV-CG--NVKM---------------FC----------DKALASILLSLIGFICLFLLT-IMAARNL
>B9RH17_RICCO
AQVIFRILAIAFAVASISAMVT--SDQNVIV-----------FGMDTAARYS--YSSAFRFLVGANAVVCGFSVL-SLIF
VCLM--------------SRREAIL-----EKNYYLFLHDMVMMVMMVSGCSAATAIGY-VGRY-----GEKEI-T--WT
AV-CD--FVGK---------------FC----------NQALVSIVLAYLALFCYVALT-TLAAHKL
>B9GFG6_POPTR
AQITLRFLAIAFTVTAIPVMIT--AKEPVSL-----------LGLAITPSYK--QSSAMKFLLGVNATVFAFTAL-SMLF
VWPL--------------RRSGSKP-----INYFFLHLHDMVMTLLLISGCAAATAVGY-LSQY-----GQPET-Y--WS
PI-CD--IVKK---------------FC----------HQMLISTVLSYLAFFCYLALN-ILSVHKL
>D7MGK0_ARALL
VQVSMRVLIIGAAMASMWVMIT--NREVASV-----------YGIAFEAKYS--YSSAFRYLVYAQIAVCAATLF-TLVW
ACLA--------------VRXX--------GLVFALFFFDLLTTLTAISAFSAAFAEGY-VGKY-----GNKQA-G--WL
PI-CG--YVHV---------------YC----------SRVTISLAMSFASFVLLFILT-VLTASSA
>Q9M0L3_ARATH
VQVSMRVLTIGAAMASMWVMIT--NREVASV-----------YGIAFEAKYS--YSSAFRYLVYAQIAVCAATLF-TLVW
ACLA--------------VRXX--------GLVFALFFFDLLTTLTAISAFSAAFAEGY-VGKY-----GNKQA-G--WL
PI-CG--YVHG---------------YC----------SRVTISLAMSFASFILLFILT-VLTASAA
>P0DH83_MARPO
TIALLRLLAFAATLSAFVTMIT--NKQKITI-----------GPFTRWSKWH--YSDAFMWFVVANCIAFIYLLF-AAIL
GLIS------------------HSP-----MLVKHLVILDLIVSYMLFSAASAATAVAY-IGKN-----GISQP-G--WT
AI-CG--VFER---------------YC----------HHVAGALVACFLGWLFLTIAV-FLGMRRS
>A9TKY8_PHYPA
LNFIVRLLTAMASAAALTTMVK--SNQ-------------------GPARWR--DFWAFKWFIIANAIVLTYSTL-AALA
SLLG--XXXX--------XXXLSST-----PLAWLTFLVDFLLANALMSAASTATAISW-VGRK-----GQPNA-G--WE
AQ-CV--AVGG---------------FC----------RRVLGALIASYIGWVLLALST-ILAATAI
>A9SEY7_PHYPA
LSLILRLLTLGATIAAIVAMLK--STQTVPT-----------LLGPHTARWK--DFPAFEWFVIGNSIVLVYAAL-GTLA
ACLSLF--XX--------XXXLSYT-----KTAWLTFLCDFICSCALISAGSTALGVAW-IGKH-----GQHSA----WN
AV-CP--TVDR---------------FC----------DYVQGALIATLCGFIFQALST-VIAASAL
>A9STS7_PHYPA
TNFLLRTLTAGATAAAVVVMLI--STQTSGT-----------IYGYFRGRWR--DYPAYKWLIIANAVVFVYSVM-AAIV
ACFSVI--XX--------XXXLSYS-----PSAWLTLLVDFLAASALISAASAALAVAL-LARN-----GQDLQ-GXXWP
TV-CN--YVSK---------------FC----------DYTQGAIIASFVGFGLLFLST-LLAASAL
>A9TZ63_PHYPA
```

```
LNLLLRLLQAFATAAAVIVMLL--ATQTEFT-----------RYGEVRGRWR--DYPAYKWFIIANAVVFVYALL-ATLV
ACCALI--XX--------XXXLSYS-----PSAWLTFLLDFVAASALMSAASAALAVAL-IARN-----GQNLQ-GXXWP
TF-CN--YVTR---------------FC----------DYAQGAIIASFCGFGLLALST-LLAASAL
>P0DH84_ADICA
WSMGVRLLTTLLCITSLILLLK--AKQTVRRALGL-------GYIAQTVKYS--DTSGFIYLVYINILVAAYGLI-VFVS
LIPS----AL--------XXXCSGK-----CSRWTIFVLDQVFAYVLLSAVSAATEVLY-LADK-----GMSKT-Q--WE
AL-CP--TYGF---------------FC----------HMVSASVAIGSVAVVLLAVLS-VSSAQSL
>P0DI28_PTEAA
WSIGIRFLTSCVSIASLILLLK--SKQTVQVSVGL-------DYVTQQVKYS--DTSAFVYLVFSDILVAVYCIV-VLVG
LIPA----AL--------XXXHPGK-----AGQWAIFIFDQVLAYVLLAAASSATEVAY-LADK-----GMAKT-S--WE
AV-CP--RFAH---------------FC----------HTVMASISLSFVAVLLLALLA-VVSASGL
>P0DI20_OSMLA
AGVFLRFVASLLSIAGLMLLVK--DNQTVQQMVAT-------EAVTLETKYS--DISAFVFLLYTNGLVAVYCFF-LALA
SVFSLIASXX------------SGK-----LAGWVTFVLDQGLAYVLLAAAAASTEVLY-LAEN-----GDLKT-S--WA
EI-CS--QFGH---------------FC----------HMARASIVVSFLSMLAMAVLS-VMSAQQL
>P0DI21_OSMLA
--MVLRIVASLLSIAALVLMAK--DKQVVYLNLAG-------EELTLEAKHS--YVEAFVYLVYSNGLVAIYCFL-LVFA
LVFRLIDKXX------------CGK-----SAAWIIFLLDQGLAYVLLAAAAASTEVAY-VAKR-----GNNKV-G--WS
EV-CS--TFGH---------------FC----------NLVGVSIVITFISVLAMATLS-VMSARRL
>P0DI25_PTEAA
MEVLLRVLAILLSIAGALVMAK--DKQDTFVMLGT-------VPVPLYARHS--YVEAFVFLVYANGIVAIYCFI-AVLL
SLLA------------------KSR-----VLAGLLFFMDQALAYLLLAAAAASTEVAY-IAKR-----GEKKL-V--WG
EV-CS--NFEH---------------FC----------NLVGVSLVLTFLSVLVLVTLA-ILSGKRL
>P0DI24_PTEAA
GELVLRCAATLVCMLSLMLLVR--DQQIAVQEVGV-------TSVTTQLRYS--SSTGLVYLVYANGLVALYCFV-VVLT
SSFN------------XXXXXRRNK-----SGAWALFVLDQVLACILLSAASAASEIAF-LVEK-----GAKKT-I--WD
SK-CI--VYGH---------------FC----------RMLEVSIATSFIAVIMLGSIC-VLSAKQL
>P0DH82_MARPO
ASILMRLTAMALCVTALVTMVT--DKQTHYFNFAS-------TTIVKTAEYT--NVLALKVFVYTNGVIAGYSLL-QALW
TIVA-------------XXXYSTSK-----ARLWTTFFLDQFIVYVLIGVTGAATEVAY-IAEK-----GESDV-A--WP
KQ-CN--NFGR---------------FC----------SQVGASVIVCFVAILTLVFLA-VLSAKQL
>Q8W4Z5_GOSHI
AETMLRLVPMALGVAALVVMLK--NSQSNDF---------------GSVSYS--DLGAFRYLVHANGICAGYSLL-SAII
AAVP----------------XPSTM-----PRAWTFFLLDQILTYVILGAAAVSTEVLY-LANK-----GDSAI-T--WS
AA-CG--TFAG---------------FC----------HKATIAVVITFVAVICYAVLS-LVSSYRL
>B9GHX8_POPTR
AETMLRLVPVALCVSALVVMLK--NTQTNDY---------------GSLSYS--DLGAFRYLVNANGICAGYSLL-SAVI
VAMP----------------XAWTM-----PQAWTFFLLDQVLTYVILAAGTVSTEVLY-LANK-----GDTSI-A--WS
AA-CV--SFGG---------------FC----------HKALISTVITFVAVIFYAALS-LVSSYKL
>B9I0G0_POPTR
AETMLRLVPMALCVSALVVMLK--NTQTNDY---------------GSLSYS--DLGAFRYLVHVNGICAGYSLL-SAVI
VAMP----------------XASTM-----PRAWAFFLLDQVLTYVILAAGTVSTEVLY-LASK-----GDTTI-T--WS
EA-CV--SFGG---------------FC----------HKALISIVITFVVVICYAALS-LLSSYKL
>B9T3K6_RICCO
AETVLRLVPMAFCISALVLMLK--NSQTNDF---------------GTLSYS--DLGAFRYLVHANGICAGYSLL-SAII
VAMP----------------XPSTM-----SRAWTFFFLDQVLTYVILAAAAVSVEALY-LARK-----GDIAI-T--WS
AA-CV--SFGG---------------FC----------HKAITSAVITFIVVVCYALLS-LVSSYKL
>A7QBZ2_VITVI
VETLLRLVPVALCTVSLVVMLK--NSQTNDF---------------GSLSYS--DLGAFRYLVHANGICAGYSLL-SAIF
TAMP----------------XPPTM-----SRAWTFFLLDQVLTYLILAAGAVSTEVVY-LAYK-----GDEAV-T--WS
DA-CS--SFGG---------------FC----------QKTTASISITFVTVLCYAVLS-LISSYKL
>C6TCJ2_SOYBN
AETFLRLFPVGLCVSALVLMLK--SSQQNEY---------------GSVDYS--DLGAFRYLVHANGICAGYSLF-SAVI
AAMP----------------XPSTI-----PRAWTFFLLDQVLTYIILAAGAVSTEVLY-LAEN-----GDAAT-T--WS
SA-CG--SFGR---------------FC----------HKVTASVAITFVAVFCYVLLS-LVSSYKL
>C6SYW3_SOYBN
VETFLRLFPIGLCVTALVIMLK--NSQENKY---------------GSVSYT--DLGAFRYLVHANGICAGYSLF-SAIF
VALP----------------XLSSV-----HIAWTFFVLDQVLTYIILSAGAASAEVLY-LAEK-----GNMAT-A--WS
SA-CR--SFGP---------------FC----------HKVTASTTITFVVVVFYVLLS-LISSYKL
>Q8VZQ3_ARATH
AETMLRLAPVGLCVAALVVMLK--DSETNEF---------------GSISYS--NLTAFRYLVHANGICAGYSLL-SAAI
AAMP----------------XSSTM-----PRVWTFFCLDQLLTYLVLAAGAVSAEVLY-LAYN-----GDSAI-T--WS
DA-CS--SYGG---------------FC----------HRATASVIITFFVVCFYIVLS-LISSYKL
>D7KFC7_ARALL
AETMLRLAPVGLCVAALVVMLK--DSETNEF---------------GSISYS--NLTAFRYLVHANGICAGYSLL-SAAI
AAMP----------------XSSTM-----PRVWTFFCLDQLLTYLVLAAGAVSAEVLY-LAYN-----GDSAI-T--WS
DA-CS--SYGG---------------FC----------HRATASVIITFFVVCFYILLS-LISSYKL
>B4FBQ7_MAIZE
VETLLRAAPLGLCVAAMTVMLR--NQQSNEY---------------GAVAYS--DLGGFKYLVYANGLCAAYSLV-SAFY
TAVP----------------XPATV-----SRSWLVFLLDQVFTYLILAAGAAAAELLY-LAYN-----GDKEV-T--WS
EA-CG--VFGS---------------FC----------RQARTSVAITFGTVLCFILLS-LISSYRL
>C5YDQ9_SORBI
VETLLRAAPLGLCVAAMTVMLR--DQQSNEY---------------GTVAYS--DLGGFKYLVYANGLCAAYSLV-SAFY
TAVP----------------XPATV-----SRSWVVFLLDQVFTYLILAAGAAAAELLY-LAYN-----GDKEV-T--WS
EA-CG--VFGS---------------FC----------RQARTSVAITFGTVLCFILLS-LISSYRL
>B6SR79_MAIZE
IETLLRAAPLVLCVAAMTLMLR--DQQSNEY---------------GTVAYS--DLGGFKYLVYANGLCAAYSLA-SAFY
```

```
TAVP----------------XPATV-----SRSWVVFLLDQVFTYLILAAGAAAAELLY-LAYN-----GDKEV-T--WS
EA-CG--VFGS---------------FC----------RQARISVAITFGAVLCFILLS-LLSSYRL
>B8ARW3_ORYSI
VETLLRAAPLGLCVAAMAIMLR--NSVTNEY---------------GTVSYS--DLGGFKYLVYANGLCAAYSLA-SAFY
IAVP----------------XPATL-----SRSWVVFLLDQVFTYLILAAGAASAELLY-LAYN-----GDKEV-T--WS
EA-CG--VFGG---------------FC----------RQARTSVAITFASVACYILLS-LISSYRL
>Q0JEF7_ORYSJ
VETLLRAAPLGLCVAAMAIMLR--NSVTNEY---------------GTVSYS--DLGGFKYLVYANGLCAAYSLA-SAFY
IAVP----------------XPATL-----SRSWVVFLLDQVFTYLILAAGAASAELLY-LAYN-----GDKEV-T--WS
EA-CG--VFGG---------------FC----------RQARTSVAITFASVACYILLS-LISSYRL
>D7L342_ARALL
VEAVLRVASMALSITGLVIMIK--NSISNDF---------------GSLSYS--NLGAFMYLVGANGVCAAYSLL-SALI
LALP----------------XPISK-----VQVRTLFLLDQVVTYVVLAAGAVSAETVY-LAYY-----GNIPI-T--WS
SA-CD--SYGI---------------FC----------HKALISVVFTFVVSLLYMLLS-LISSYRL
>Q9LUL1_ARATH
AEAVLRVASMALSITGLVIMIK--NSISNEF---------------GSVSYS--NIGAFMYLVSANGVCAAYSLL-SALI
LALP----------------XPISK-----VQVRTLFLLDQVVTYVVLAAGAVSAETVY-LAYY-----GNIPI-T--WS
SA-CD--SYGS---------------FC----------HNALISVVFTFVVSLLYMLLS-LISSYRL
>D5A972_PICSI
IEPALRFLPVGLCISALALMLK--SKEGNEN---------------GILEYK--HVGAFRYLAYANGICAAYSVL-STFN
SVVP----------------XSCSL-----SRAWFVFVFDQAFTYLMLGAGAVVTEVLY-LAYK-----GDEKI-T--WF
EI-CP--YYGR---------------FC----------NRVAASLVISFLALLCFIPLS-LISAYRV
>A9P1V1_PICSI
FETLFRLLPVGLCISALVLMLK--SEQSDQY---------------MQLDYS--NVDAFRCLAYANGICAGYSLI-SAFD
SMVP----------------XSHHI-----SRSWILFLLDQGITYLMLAGGAVATQVLY-VAYK-----GDEKA-T--WE
QI-CG--SYGR---------------FC----------NRAGASVIISFFALVCFLLLS-LLSAYRL
>A9NMM6_PICSI
FELLFRVTPLALCIAAMAIMLK--NKQSNQY---------------GALHYS--DVGGFKYLVYANGICAIYSIL-SLLG
SVLS--------------TGXDYSW-----TRAWIMFILDQALTYLILTAGVCGVEIMD-LAYQ-----GNEQV-S--WS
RV-CV--SYGK---------------FC----------NDARASVLITMAVLVCFMVLS-LLSAHRL
>D7MUY4_ARALL
IDSCLRLSVVPLSVATIWLTVT--NHESNPD--------------YGNLDYN--SIMGLKYMVGVSAISAIYALL-STIS
LWVT------------------CLV-----SKAWLFFVPDQVLAYVMTTSVAGATEIVY-LLNK-----GDKIV-T--WS
EM-CS--SYPH---------------YC----------SKLTIALGLHVFVLFFFLFLS-VISAYRA
>Q9FFT2_ARATH
IDSCLRLSVVPLSVATIWLTVT--NHESNPD--------------YGNLEYN--SIMGLKYMVGVSAISAIYALL-STVS
SWVT------------------CLV-----SKAWLFFIPDQVLAYVMTTSVAGATEIVY-LLNK-----GDKIV-T--WS
EM-CS--SYPH---------------YC----------SKLTIALGLHVFVLFFFLFLS-VISAYRA
>A7P0P3_VITVI
IDCSLRLCVIPLSVATIWLTVT--NQQDNSI--------------YGKLEFS--NLTGLKYMVCISGISAGYALV-AVVA
SWVR------------------CLV-----NKAWLFFVSDQIMAYLMVTSGAAVLEILY-LAYK-----GDRGV-S--WS
EA-CS--SYGR---------------FC----------SRVNLALALHALALCCFLVLA-VISAYRV
>B9HTL5_POPTR
LDFSLRLSVIPLSVATIWLTVT--NKQDNSI--------------YGYLKYS--DLTGLKYMVFISGICASYAFI-AAVS
TWIR------------------CIV-----TKTWLFFVSDQIVAYLMVTSGTAVLEILY-LAYN-----GDREV-S--WS
EA-CT--SYGK---------------FC----------YRMKLAVILHALALSCFIILA-VISAYRA
>B9SV84_RICCO
LDSSLRVSVIPLSAATIWLTVT--NHQDNSS--------------YGNLKYS--NIMGLKYMVCISAICASYAFV-AAVS
IWIK------------------CLV-----NKVWLFFVSDQIIAYLMVTSVAAAMEILY-IAYN-----GDQKV-T--WS
EA-CT--SYGK---------------FC----------NGMKTALILHALTLCFFIVLA-VISAYRA
>C6T2J5_SOYBN
FDSSLRLCAIPLSVATMWITVT--NKEDNSS--------------YGMLKYN--NLSALKYMVLVSALCACYALL-AAAC
SLVR------------------CFV-----SKAWIFFVSDQIVAYLAITSVAAVMEMYY-LAYN-----GAKED-S--WS
EA-CS--SYGS---------------FC----------SKVKLALILHTITFCCFFVIA-VISAFRA
>A2X2I0_ORYSI
AELGLRVCAVPLAVASVWEMAT--NKQVDET--------------YGEVRFS--DLSGFRYLVWINAITAAYSVA-SILL
SSCR------------------FIT-----RFDWLIFILDQASAYLLLTSASAAAEVVY-LARE-----GDREV-S--WG
EV-CS--YFGR---------------FC----------GAATVSVALNAAALLCFMALS-LISAFRV
>Q6YW53_ORYSJ
AELGLRVCAVPLAVASVWEMAT--NKQVDET--------------YGEVRFS--DLSGFRYLVWINAITAAYSVA-SILL
SSCR------------------FIT-----RFDWLIFLLDQASAYLLLTSASAAAEVVY-LARE-----GDREV-S--WG
EV-CS--YFGR---------------FC----------GAATVSVALNAAALLCFMALS-LISAFRV
>C5XY39_SORBI
PEMALRVCVVPLALASLWEMAT--NAQADDT--------------YGEVKFS--DLSGFSYLVGVNAVTAAYALV-SILL
SSLK------------------PLA-----RYDWVILVMDQASAYLLVTSASAAAELLQ-LARR-----GDREV-S--WG
EV-CS--YFGR---------------FC----------GKATVSLALHAAALACFVALA-LVSAFRV
>B6TUW9_MAIZE
PEMALRLCVVPLSLASLWEMAS--NAQADDT--------------YGEVKFS--DLSGFSYLVGVNAVTAAYAVA-SVLA
SSFK----------------XXLAA-----RYDWVVLVMDQASAYLLVTSASAAAELLQ-LARH-----GDRGV-S--WG
EA-CS--YFGR---------------FC----------GKATVSLALHAAALACFAALS-LVSAFRV
>D8T2C0_SELML
TDLMLRFAAFVCCTVTMVVLIT--DKQTSAIQVPGFNN----LTITKTVSFD--LAKAFVYLVSAAGIGAGYTLL-VLVL
SIIS----------------XXRSK-----AIAWFIFVFDQLITYVLLAAAAASTEVAY-MGAH-----APPEA-S--WL
KV-CS--LFGR---------------FC----------HQLGASLVTSLISTVLFAFSA-AISAYYL
>D8T829_SELML
TDLMLRFAAFVCCAVTMVVLIT--DKQTSAIQVPGFNN----LTITKTVSFD--LAKAFVYLVSAAGIGAGYTLL-VLVL
SIIS----------------XXRSK-----AIAWFIFVFDQLITYVLLAAAAASTEVAY-MGAH-----APPEA-S--WL
```

```
KV-CS--LFGR---------------FC----------HQLGASLVTSFISTVLFAFSA-AISAYYL
>D8SJ65_SELML
HSLLLRLVAVVLSILVIAVMVH--AKQRVMI---------------FKAEWD--NSKAFVALVTISAICLGYSFL-QFIL
SAFH----LCS------XXXXSPTK-----CWAWMNFIADQILTYAMLGAAAAAAELAY-IAKN-----GSSRA-Q--WQ
PI-CS--TFNT---------------FC----------TRAGASIILSFIAVLALANSS-AISAYHL
>D8QNV6_SELML
HSLLLRLVAVVVSILVIAVMVH--AKQRVMI---------------FKAEWD--NSKAFVALVAISAICLGYSFL-QFIL
SAFH----LCS------XXXXSPTK-----CWAWMNFIADQILTYAMLGAAAAAAELAY-IAKN-----GSSRA-Q--WQ
PI-CS--TFNT---------------FC----------TRAGASIILSFIAVLALANSS-AISAYHL
>P0DH65_SELML
VDFLVRIKAFAFCLAVIVLLKN--NVQTTVI---X-------PGIVLQAKYN--NTKAPVSLLVLASICCGYAFL-QAVV
SLLS----FIR------XXXXLNNT-----VLAWLTFLLDQVLTYLLLGSAAATAEAAY-IAKR-----GEDKV-Q--WK
AV-CG--PFKR---------------FC----------DHFAATVFLSFIAVIAFAVSA-AISAYYL
>P0DH67_SELML
VDFLVRIKAFAFCLAVIVLLKN--NVQTTVI---X-------PGIVLQAKYN--NTKAPVSLLVLASICCGYAFL-QAVV
SLLS----FIR------XXXXLNNT-----VLAWLTFLLDQVLTYLLLGSAAATAEAAY-IAKR-----GEDKV-Q--WK
AV-CG--PFKR---------------FC----------DHFAATVFLSFIAVIAFAVSA-AISAYYL
>E4MWF4_THEHA
TELILRCSVCALALVAAILIAT--DTQVKEI-----------FTIQKKAKYT--DMKALVFLVVVNGIAAAYSLL-HMVR
CVVG----MMK-------XXXLFSK-----PLAWAIFSGDQAIAYLTVAGVAAAAQSAA-FAKL-----GEPEL-Q--WM
KI-CT--IYGK---------------FC----------NQVGEGIATALLASIGMVLIS-SISAFAL
>D7LIK3_ARALL
TELILRSLVCAFALVAAILVAT--DVQVREI-----------FTIQKKAKFT--DMKALVFLVVINGIAAGYSLV-QAVC
CLVG----LMK-------XXXLLSE-----PLAWAIFFGDQAVAYLCVAGVAAAAQSAA-FAKL-----GQPEL-Q--WM
KI-CD--MYGK---------------FC----------NQVGEGIASALFACIGMVLIS-CISAFGV
>Q8L924_ARATH
TELILRCLVCVLALVAAILIAT--DVQVREI-----------FMIQKKAKFT--DMKALVLLVVVNGIAAGYSLV-QAVR
CVVG----LMK-------XXXLFSK-----PLAWAIFFGDQAVAYLCVAGVAAAAQSAA-FAKL-----GEPEL-Q--WM
KI-CN--MYGK---------------FC----------NQVGEGIASALFACIGMVLIS-CISAFGV
>B9SA89_RICCO
AELVLRCLICGLGVLAAVLVGT--DTQVKEI-----------FSIQKKARFT--DMKALVFLVIANGIAAAYSLL-QGVR
CVVG----MVR-------XXXLFSK-----PLAWAIFSGDQMMAYLTVAAVAAAAQSAV-FAKL-----GQPEL-Q--WM
KI-CN--MYGK---------------FC----------NQVGEGIASALLVSVSMVVLS-CISAFSL
>B9HD38_POPTR
AELVLRCVICALGVLAAVLVGT--DTQVKEI-----------FSIQKKARFT--DMKALVFLVVANGIAAAYSLV-QGVR
CVVG----MVK-------XXXLFSK-----PLAWVIFSGDQMMAYLTLSAVAAAVQSAS-FAKL-----GQPDL-Q--WM
KI-CN--MYGK---------------FC----------NQVGEGIASALLVSVSMVVLS-CISSFSL
>B9IH36_POPTR
AELVLRCVICCLGVLAAVLVGT--DTQVKEI-----------FSIQKKARFT--DMKALVFLVAANGIAAAYSFV-QGVR
CVVG----MVK-------XXXLFSK-----PLAWVIFSGDQMMAYLTMSAVAAAAQSSV-FAKL-----GQPDL-Q--WM
KI-CT--MYGK---------------FC----------NQVGEGIASALLVSVSMVVLS-CISAFSL
>A7R385_VITVI
AELVLRCVICGLGILAAVLVGT--DTQVKVI-----------FTIQKKAKFT--DMKALVFLVIANGIAAAYSLI-QGLR
CVVS----MVR-------XXXLFSK-----PLAWAIFSGDQVIAYLTLAAVAAAAQSSV-FGEF-----GQPEL-Q--WM
KI-CN--MYGK---------------FC----------NQVGEGIVSAVGVSLSMVILS-GISAFSL
>D7M9V1_ARALL
TELLLRCSISVFALLALILVVT--DTEVKLI-----------FTIKKTAKYT--DMKAVVFLVVANGIAAVYSLL-QSVR
CVVG----TMK-------XXXLFSK-----PLAWAFFSGDQAMAYLNVAAIAATAESGV-IARE-----GEEDL-Q--WM
RV-CN--MYGK---------------FC----------NQMAIGVSSALLASIAMVFVS-CISAFSL
>Q8L9B5_ARATH
TELLLRCSISVFALLALILVVT--DTEVKLI-----------FTIKKTAKYT--DMKAVVFLVVANGIAAVYSLL-QSVR
CVVG----TMK-------XXXLFSK-----PLAWAFFSGDQAMAYLNVAAIAATAESGV-IARE-----GEEDL-Q--WM
RV-CT--MYGK---------------FC----------NQMAIGVSSALLASIAMVFVS-CISAFSL
>B8LQF9_PICSI
GEVILRFAMIALALVAAVRVGT--DTQTRTI-----------FTIEKKAKYS--DMKALVFLVVMNGIVASYSLL-QGLR
CVLS----IYT-------XXXLTSK-----PLAWLIFALDQTMAYFSLAAAAAAAESAY-LAER-----GQTEF-Q--WM
KV-CI--FYEK---------------FC----------HQIGEGLVSTFLVSLSMATVS-GMSAYHL
>C5WUP3_SORBI
AELFMRCAACGLAVLAAALLGA--DRQTRTI-----------FSVEKTARFT--DMQSLVFLVIANGMAACYSLL-QGAR
CLVS----ILT-------XXXLINR-----PMAWAIFSCDQVMAYFTITAVAVAMEAAM-IGKY-----GSLQF-Q--WM
NT-CH--FYKR---------------FC----------AQAGGAVACAVAASLNMVGIS-LVSAFNL
>B6TGJ8_MAIZE
AEVALRAVLCGLGALAAALVAT--DTQTRTF-----------FSLQKKATYT--DMKAMVLLVAAAAAAAGYSLL-QAAR
CCCC----VAL---XXXXXXXXXXX-----LLAWCVFACDQALAYALLAAVVAALQASV-VAKQ-----GLPQL-Q--WM
AI-CA--LYGA---------------FC----------RQAGAGVACAVAAAVDAALLA-FLSAFNL
>C5YP66_SORBI
AEVALRALLCGLGALAAALVAT--DTQTRTF-----------FSLQKKASYT--DMKAMVFLVDAAAVAAGYSLL-QAAR
CCGG----GAMX-XXXXXXXXXXX------ALSWCVFSCDQALAYVLLAAVAAALQASV-VAKR-----GQPEL-Q--WM
GI-CA--LYGA---------------FC----------RQAGAGLATAVVAGLAAVLLA-FLSAFNL
>Q0IN16_ORYSJ
AEVALRCAVCALAALAAALVGT--GSQTRTF-----------FSLEKKARFT--DMKALVLLVAAHGAAAVYSLL-QLAR
CAAA----AA----XXXXXXXXXX------VVAWSVFSCDQAVAYALMAATAAALQSSV-VGKR-----GQPEL-Q--WM
PV-CG--LYGA---------------FC----------RRVGEGLAAAVAAGLAAVLLA-AVSAFNL
>D5A8E6_PICSI
TEVILRFAVVIFALVSAIMVGT--ASGTRDLG----------GGIRIHAHFT--LLKTLPFLVIVDGILAVYSLL-QGLR
CFLS----LYM-------XXXLLNK-----ALAWTIFCCDQALAYVIFAAAASTAETAY-ISEQ-----GLDEL-Q--WI
KV-CM--FFRA---------------YC----------FKSGAGMINAFLAALCMVFVS-GMSVFHL
```

```
>Q5K4H9_GOSHI
IEALIRLSTIVMLVLTACLIGL--DSQTKVIF-----------YVQKKASFK--DLRALVGLLYITSLAAAYNLL-QLCC
SSFS----AS--------XXXXXXX-XYA-YLAWLRYILDQAVVYAVFAGNLAALEHSF-LVLT-----GEENF-Q--WL
KW-CN--KYTR---------------FC----------TQIGGSLLCGFVASLLMFSIA-SISAFNL
>B9IM09_POPTR
IEAILRGIAILLLVSTACLVGL--DSQTKFV-----------IVYEKEVTYK--DLHALVVLVYVDAVAAAYNLL-QLCR
CSVS----AL--------XXXXXXX-XYR-YLSWACFVLDQLAAYTTFAAHSAALQHSV-LGIT-----GAKVF-Q--WM
KW-CN--RFTR---------------FC----------FQIGGALTCGYIASVLMVMIS-FISAFNL
>A7Q6G6_VITVI
AEAFLRLFAILVLVLTACLLGF--DTQTKLLF----------STIKKTATFR--DLGALQVVVYVDSVAAGYNLL-QLGR
GFIS----AK--------XXXXXXXXXYV-TLPWVCFLLDQAAVYTVFSANTAALQASI-IAVT-----GESSL-Q--WM
KV-CN--RYTR---------------FC----------IQVGGALLSGYLASLLMVLLS-SLSAFSL
>C6SZ04_SOYBN
GEVCLRVSAILVLVLTACLVAL--DTQTKVVF----------VSIEKKATYK--DLNALKILVYVTCAAAGYNLL-LLCK
HSIW----S----------RXXXXX-XYL-CMAWICFSLDQIAVYMTFAANTATMGAAV-LAIS-----GSEAF-Q--WL
KV-CD--KFTR---------------FC----------VEIGGALLCGYAASMLMALIS-TISAYKV
>D7MFW5_ARALL
TEVILRLCIVFFILLSSCLIGL--DSQTKEI-----------AYIHKKVSFR--YLLALEAELYINVVVAAYNLV-QIGL
GWYNVEQKXX--------------------NPKWFSYLLDQTAAYVVFAGTSAAAQHSL-LVVT-----GSREL-Q--WM
KW-CY--KFTR---------------FC----------FQMGSAIILNYIAAALMVLLS-SISAFNL
>Q8L8U9_ARATH
TEVILRLCIVFFLLLTSCLIGL--DSQTKEI-----------AYIHKNVSFR--YLLALEAELYIDVVVAAYNLV-QLGL
GWYNVEQKXX--------------------NPKWFSYLLDQTAAYVVFAGTSAAAQHSL-LVVT-----GSREL-Q--WM
KW-CY--KFTR---------------FC----------FQMGSAIILNYIAAALMVLLS-SISAFNL
>B6U8R7_MAIZE
AERVLRAACAAMAAAGALLLGF--SAQTKTV-----------LFIQKKAVPK--DVQALWVLIVAAAAAAAYHVA-QLAR
CFCME---XXXX-XXXXXXXXXLGR-----AVACASFLLDKGCAYMVFATTVAALQACF-VGLL-----GVDAL-Q--WS
KL-CN--IYTR---------------FC----------EQAAAGMVCSLLAAAGMAVLS-AFSARDL
>C5XW97_SORBI
TERVLRAACAAMAAAGALLLGF--SAETKTV-----------IFVQKKAVPK--DVQALWVLIVAAAAAAAYHAA-QLAR
CLCMD---XXX---XXXXXXXXLRR-----AVACATFLLDKGCAYMVLATTVAALQACF-VGLL-----GVEAL-Q--WS
KL-CN--IYTR---------------FC----------EQAAAGMVCSLVAAAGMAVLS-AFSARDL
>Q6ETN2_ORYSJ
AERLLRGGCVVMAATAALLLGF--SAETKTV-----------LFVRKTAVAK--DVQALWVLTVAAAAAAGYQFA-QLVR
CMYCSSSXXX------------XAM-----AVAWTSFLLDKGCAYVVFASTAAALQACM-VGLI-----GVEAL-Q--WS
KL-CN--IYTR---------------FC----------EQAAAGMLCSFLAAAGMAVLS-AFSARRL
>B6SZA7_MAIZE
AEGLLRGACAALAAAAALLVGL--STQTETV-----------LLVRKKATVK--DVQALWVLAMAAAAAAGYHLL-QLLK
CLYL----GRV---XXXXXXXRSSR-----ALAWTCLLLDKACAYTTFATTVAAAQACV-VALD-----GAHAV-Q--WT
KL-CN--IYTR---------------FC----------EQVAGSLVLGMLAAVGTAVLS-AASARNV
>B6TUB4_MAIZE
AEGLLRGACTALAAAAALLVGL--STQTETV-----------LLVRKKATVK--DVQALWVLAMAAAAAAGYHLL-QLLK
CLYL----GRV---XXXXXXXRSSR-----ALAWTCLLLDKACAYTTFATTVAAAQACV-VALD-----GAHAL-Q--WT
KL-CN--IYTR---------------FC----------EQVAGSLVLGMLAAVGTAVLS-AASARNV
>C5Z782_SORBI
AEGVLRGACAALAAAAALLVGL--STQTETV-----------LLVRKKATVK--DVQALWVLAMAAAAAAGYHLL-QLLK
CFYL----GRRX-XXXXXXXXRSSR-----ALAWTCLLLDKACAYTTFATTVAAAQACV-IALD-----GAHAL-Q--WT
KL-CN--IYTR---------------FC----------EQIAGSLVLGMLAAVGTAVLS-AASARNV
>B6U769_MAIZE
AEGLLRGACAALAAAAALLLGL--STQTETV-----------LLVRKKGTVK--DVQALWVLAMAAASAAGYHLL-QLLK
CLYL----GRG---XX--------R-----ALAWTCLLLDKACAYATFATTVAAAQACV-VALD-----GAHAL-Q--WT
KL-CN--IYTR---------------FC----------EQVAGSLVLGMLAAVGTAVLS-AASARNV
>Q67W83_ORYSJ
TEGLLRGACALLAAAAALLVGL--NTQTETV-----------LFIRKKATVK--DVQALWVLAMAAAAAAGYHLL-QLLR
CFYL----SRF---XXXXXX-XHRR-----AIAWLCFLLDKGCAYITFATTVAAAQACV-VALY-----GTHAL-Q--WT
KL-CN--IYTR---------------FC----------EQVAGSLVCAMLAAVGTALLS-VVSARNL
>D8ST12_SELML
SIILLRSFLLVLVIISEALMVT--DRETGSVPLPFFGLPRP-VFVTKTAKYE--LVTGLKFYVDALGVVIGYTVL-HLLF
NIGL----VA-----X-XXXXVDCK-----SVAWISFIADSMMGYLLLSGAAVATEIGY-LAEE-----GAPAV-L--WR
KV-CN--AFGY---------------FC----------TVYAISVVICFIAALVSFVVV-GISAYHL
>P0DH61_SELML
SIILLRSFLLVLVIISEALMVT--DRETGSVPLPFFGLPRP-VFVTKTAKYE--LVTGLKFYVDALGVVIGYTVL-HLLF
NIGL----VA-----X-XXXXVDCK-----SVAWISFIADSMMGYLLLSSAAVATEIGY-LAEE-----GAPAV-L--WR
KV-CN--AFGY---------------FC----------TVYAISVVICFIAALVSFVVV-GISAYHL
>P0DH63_SELML
SVLALRALTLVLLVIALALMVS--NKQTQSIPIKLPGMAST-IFLKKTATFS--QITGVQYYVGALSVAVAYMFF-QMLA
GLFT----ILTX------XXXVGSK-----SRAWVTFILDQLIAYLMVSAATVVAEVGY-IARR-----GETKV-G--WN
QV-CS--DFKH---------------YC----------FIYGFSLVNAFLATIAFLPVV-AVSAFHL
>D8S6A8_SELML
ALLLLRLAAMFLSLAALLITVL--NREDGFFSINVFGSPQP-ILAKATADFT--LVKGLKFFAGAMGIVAGYSFL-QLAI
AMAS----IF-----XXXXXXLGGK-----RMAWLCFVGDMTASHLCAAAAAVSAQLAY-LGKR-----GAPM-----WS
AV-CT--YFSH---------------YC----------LVFGLAVILAFLATLAALLVA-SISSYHL
>D8ST13_SELML
ALLLLRLAAMFLSLAALLITVL--NREDGFFSINVFGSPQP-ILTKATADFT--LVKGLKFFAGAMGIVAGYSFL-QLAI
AMAS----MF-----XXXXXXLGGK-----RMAWLCFVGDMTASHLCAAAAAVSAQLAY-LGKR-----GAPM-----WS
AV-CT--YFSH---------------YC----------LVFGLAVIFAFLATLAALLVA-SISSYHL
>C5XIF2_SORBI
```

```
VMVATRAVAMVMALLSMSLMVS--SKQRGILTIFG-------IEIPLDANWS--FSYSLQFLVAMSTASAAYSLA-QLLL
IAHK----AV--------XXXXXXXXX---RHAWLLFAGDQVFSLAMMSAGSAAAAVAN-LNRT-----GIRHT-A--LP
NF-CK--PLPR---------------FC----------DLSAVSIACAFLSCVFLAASA-VIDVIWL
>B8A927_ORYSI
VMVATRAVALVMAVLSMALMIS--AKQRGSLKIFG-------IEIPLYANWS--FSDSLEYLVGMSAVSAAYCLA-QLLL
TAHK----AV--------XXXXXXXXX---NYAWLLFTGDQIFAYAMMSAGSAAAAVAN-LNRT-----GIRHT-A--LP
NF-CK--PLPR---------------FC----------DLSAASIACAFLSCIFLAASA-VIDVIWL
>Q5JM57_ORYSJ
VMVATRAVALVMAVLSMALMIS--AKQRGSLKIFG-------IEIPLYANWS--FSDSLEYLVGMSAVSAAYCLA-QLLL
TAHK----AV--------XXXXXXXXX---NYAWLLFTGDQIFAYAMMSAGSAAAAVAN-LNRT-----GIRHT-A--LP
NF-CK--PLPR---------------FC----------DLSAASIACAFLSCIFLAASA-VIDVIWL
>F2EL82_HORVD
AMVAARAAALVMALLSVSLMVS--AKQRGTLAIFG-------IEIPLYAKWS--LSDSLQSLVGISAAAAAYSLA-QLLS
IAHT----AL--------XXXXXXXXX---RYAWMLLAGDQVFAYAMLSAGSAAAAVAN-LNRT-----GVRHT-A--LP
NF-CK--PLPR---------------FC----------DLSAASIACAFLGCAFLAASA-VIDVIWL
>A9NN43_PICSI
ANVGLRVLSLACSLVALVSMAS--NQESGVVTVFG-------FKLPVYSKWS--YSDSFEFLVGASAAAAAHSLL-QLLL
CGMK----MV--------XXXXXXXXX---NHAWLLFAGDQVFAYGMLAAASAAAGVTN-LNRT-----GFRHS-D--LP
NF-CK--PLHR---------------FC----------DKAAISIVFAFISSLILGGSA-VLDVFWL
>A7P756_VITVI
AHVVLRFVCLLTSVIALSLMAT--AKEAASISIYG-------FLLPVSSKWS--FSDSFEYLVGVSAAVAAHALL-QLII
SVSR----LL--------XXXXXXXXX---NHAWLIFAGDQAFAYAMLSAGSAASGVTN-LNRT-----GIRHS-P--LP
NF-CK--PLRS---------------FC----------DHVAASIAFTFFSCFLLATSA-ILDVIWL
>B9RQG7_RICCO
MHVILRLLCTITSVTAVSFMVT--AHQSSTVSIYG-------FMLPVRSKWS--FSHSFEYLVGVSAAVAAHSLL-QLLI
SMSR----LL--------XXXXXXXXX---SHAWLIFAGDQVFAYAMISAGAAASGVTN-LNRT-----GIQHT-A--LP
NF-CK--PLNY---------------FC----------NHVAVSIAFAFISCLLLAALA-VQEVIWL
>B9GGL4_POPTR
MNVLLRVLCMMTSVAALSSMVT--AQQSSTVSIYG-------FMLPIQSKWS--FSHSFEYVVGVSAVVAAHSLL-QLLI
SVSR----LL--------XXXXXXXXX---SHAWLVFAGDQVFAYAMISAGAAASGVTN-LNRT-----GIRHT-A--LP
NF-CK--PLQS---------------FC----------DHVAVSIFFTFLSCFLLAASA-VQEVIWL
>B9GXD6_POPTR
MHVLLRLLCIITSVAALSFMFT--AQQSSTISIYG-------FMLPVQSKWS--FSHSFEYLVGVSAAVAAHSLL-QLLI
SMSR----LL--------XXXXXXXXX---SHAWLIFAGDQVFAYAMISAGAAASGVTN-LNRT-----GIQHT-A--LP
NF-CK--PLQS---------------FC----------DHVAVSIFFTFTSCFLLAASA-VQEVIWL
>Q3EB59_ARATH
AMFVLRAMCMAVSTVAVTLMVT--ARETSMTTLYG-------FEFQLHAVWS--LSDSLIYLVVVSSATVLYSLI-QLII
SGTR----LM--------XXXXXXXXX---TQAWFCFVADQIIGYAMVSGGSAALGVTN-MNRT-----GIRHM-P--LP
NF-CK--SLGF---------------FC----------DHLAGSIVFALFAFLLLAASS-LLDVLHL
>Q1PFB8_ARATH
VQVALRGGCLAASATAMAVMLT--ATEEGVADIYG-------FKLTLSSNWS--FSPSYQYVVGACAGTVLYSLL-QLCL
GVYR----LV--------XXXXXXXXX---FQAWLCFTSDQLFCYLMMSAGSAGSGVTN-LNKT-----GIRHT-P--LP
DF-CK--TLSS---------------FC----------NHVALSLLLVFLSFIFLASSS-FFTVLVL
>P0DI26_PTEAA
VDIALRSAVVAFMVVSLSAMFT--STQHSEVHIIG-------FSIPVSLRWN--RSQPFEFLVVVELLICAYAFV-QFVY
QSVV----LA--------XX--XXXXX---RCIWVQLAADQVCAYLVLAAAAAAAGASR-TNKSGFQSLGMQNI-K--VP
GV-CI--VLDK---------------FC----------NRATIAIIFTLLAAGASGISV-TLDVYML
>P0DI23_PTEAA
ALLLLRLLTFAFSLASLVIMAT--NSATTTAT----------AGRHRTVNWV--DFDTYRYVLAACAIVCLYSFA-EIGL
GLWY--------------LLKGXXXMPES-MAHWFDFGHDQGFAYLIFSACSGATAVAH-NLRERHILIX--------GM
YG-CD--EANS---------------FC----------MKAEISIGLAFGAFLFIALSS-LLSGYRL
>A9S848_PHYPA
MLLLFRALTFSFSLAAVVVMGT--NRYRINP--------------QLKVSWY--DFEPYRYVLAVNAIICIYSFV-ETWL
AVYT--------------YLQGXXXLPEI-FQVWFDYGHDQGFAYLLFSANSAGVAMAQ-LLQSGNTLIX--------GA
YH-CT--EAGG---------------YC----------TQARVSIALGFVAFLFLALSS-LLTGLRV
>A9T836_PHYPA
IILIFRALTFSFSLTSVIVMGT--NRHRIDA--------------QSRVAWY--DFDPFRYVLAVNAIICIYSFV-EIWL
AVYT--------------YLKDXXXLPET-FQVWFDYGHDQGFAYLLFSANSAGIAMAQ-LLQSGNSLIX--------GA
YR-CS--DAGV---------------FC----------TQARASIGLGFGAFLFLALSS-LLTGLRV
>A9STU1_PHYPA
MLFVFRLLTFSFSLAAVLVMGT--NKQKIRS-----------APQYLEVAWH--DFDPFRYVFAVNAIICVYSFV-ETWL
AVYT--------------LSRGXXXLPET-FQVWFDYGHDQGFACLLFSANSVGIAMAQ-LLQSGSTLIX--------GQ
YY-CS--DAGA---------------YC----------TQARVSIAMGFGAFLFLALSS-FLTGLRV
>B9SR15_RICCO
LILVFRLSTFCFSLASSVFMLT--NP-----------------------TWY--HFDAFRYVFAANAIVAIYSLF-EMAA
SVWE--------------ISRGXXXFPEI-LQVWFDFGHDQVFAYLLLSADSAATALAK-TLKGGDT-------------
---CA--ASNA---------------FC----------VQSYIAIALGFAGFLFLGLSS-LLSGFRV
>B9HTK2_POPTR
LILVFRFAAFCFSLASAVFMLT--NSRGS-----------------DSLHWY--NFDAFRYVFAANAIVAIYSLF-EMAA
SVWE--------------ISRNXXXFPEI-CQVWFDFGHDQVFAYLLLSANTAGTELAR-TLKXX---------------
---CT--DNKA---------------FC----------VQSDIAIVLGFAGFLFLGISS-LFSGFRV
>B9HMF8_POPTR
LILVFRFSAFCFSLASAVFMLT--NSRGS-----------------DSFHWY--NFDAFRYVFAANAIVAVYSLF-EMTA
AVWE--------------ISRNXXXFPEV-CQVWFDFGHDQVFAYLLLSANSTGSEMAR-TMKXX---------------
---CT--DNKP---------------FC----------VQSDIAIALGFVGFLFLGVSS-LFSGFRV
>Q9M2U0_ARATH
LILLLRLASFSFSLASAVFMLT--NSRGS-----------------ASPHWY--DFDAFRFVFVANAIVALYSVF-EMGT
```

```
CVWE--------------FSREXXXWPEA-FQVWFDFGHDQVFSYLLLSAGSAAAALAR-TMRGGDT-------------
---CT--ANKA---------------FC----------LQSDVAIGLGFAAFLFLAFSS-CFSGFRV
>Q2QNE3_ORYSJ
VMLLLRLASLCFAVAAAAFAAT--DGAAL-------------------------RAAPFRFLLAANAIVAVYSAF-EVAA
AAWE--------------VAGGXXXLPEA-MQLWFDFGHDQGFGYMALAAAAAAAREAA---------------------
--TCGSHGGGT---------------AC----------VQGDIAVGLGFAGFAAVAAAA-AASGYRL
>A9RJH1_PHYPA
CSFGFRLSQIVLSLISIVVMCS--NSQRMHTP----------EVDFGTLKFN--HFQAYRYLIAVNVCVIFYSTL-QFTQ
LMYI--------------VILGXXXIPSIVISTWTTYGFDQLFTYLLLSASTSAGTIAN-ISYN-----GEMGVXX----
---CSRFDLAS---------------FC----------ARADAAVTLSFFTFLVMFSST-ALAVYRI
>A9RZ57_PHYPA
YSFAFRFSETVLSLIAIVVMCS--TRGSMRTD----------GVDFGTLKFN--HFQAYRYLVAVNVIVFVYSTF-QFIQ
LLYT--------------VILGXXXIPSIFISTWMTFGFDQLFLYLLLSASTSAATVAN-MSYT-----GEMGIXX----
---CSRFDVGS---------------FC----------SKADVAVTMSFFAVLAMLSST-ILAIYRI
>A9S1T8_PHYPA
FSLGLRVAEFVLSVIAFSLMAS--ADQ-------------------NGAVYS--TFTSYSFVLAVNVLVVFYTIG-QIIM
SVLL----LV--------XXXXPK----K-IYLFITFGCDQLSAFLLMAAGAAGASVAL-IINR-----GGVTD-A--YG
NG-C-----XXXXXT-------S---FC----------SHAQASVAFTFLSFFCMVISS-LLGVYSL
>A9SB31_PHYPA
LSLGLRVSEFVLSVIAFSLMAS--AEQ-------------------NGAVYS--TFTSYSFVLAINVLVALYAIG-QIIL
SVMP----LV--------XXXXPK----K-LYLFITFGCDQLSAFLLMAAGAAGASVAM-LINR-----KGVID-D--YG
SG-C-----XXXXXT-------V---FC----------AHAEASIAFTFLSFFCVMISS-YLGVYNL
>D8R814_SELML
AIVVLRVLQFIFSLIAFSVMAD--VLHDVQG-----------------------SIKSLSYTVAIGVLACAYALA-QLSF
SLWC----VI--------XXXXXXXXVTP-LYQYATFICDQMSTYFLISAASATATLID-VSGV----------------
---CG--SNGSGXX------------LC----------SRSTASVTFAFLAFLAFSASS-VLTGYYL
>D8QQW9_SELML
AIVVLRVLQFVFSLIAFSVMAD--LLHDVQG-----------------------SIKSLSYTVAIGVLACAYALA-QLSF
SLWC----VI--------XXXXXXXXVTP-LYQYATFICDQMSTYFLISAASATATLID-VSGV----------------
---CG--SNGSGXX------------LC----------SRSTASVTFAFLAFLAFSASS-VLTGYYL
>A9SHQ9_PHYPA
ISIVLRCLSIMFNVVSLGVIAS--NQGKSYFVVWRTX-----------------NSSNMQYLFAINVIVLVYCVV-QLIL
SIIN----LV--------XXXXXXXXPTQ-PASTITYICDQGLTYMLMAGFGAGVALQA-SVDK-----GESGMXX----
---CS--GANE---------------FC----------GKNKASAALSFLGFVCIALSA-NLNYLRL
>A9SU70_PHYPA
IVLSLRAAQIVFTVVGLGVMGS--LKHTSHGDY---------YYYYYDFSFT--QVDSYIGVLSLDVIVCLYAIV-QLVL
CFIQ----RS--------XXXXXXXXPTT-VAAKLTFVFDQVLAYALVATAGAAAGSAL-EIRK-----GTS--------
---C-----X-XXXT-------V---IC----------SKGEASVAMSFFAFAFLAATA-AVYSVRL
>F2E5T1_HORVD
ARLLLRAFAWLFSLLALVVMAT--DVHG----------------RGGAQDFS--TYPEYNYCLGMSIIALLYATA-QLVR
DAHR--------------LSX-XXXVXXXKAAAVVDFAGDQVVAYSLISGLSAAAPVTD-YMRQA--TDXX---------
--------------------------FN----------DSAAAAISLAFFAFLAISLSA-LISGYNL
>B9F6Z0_ORYSJ
ARLLLRAVAWLFSLLALVVMAS--NKHG----------------HGGAQDFD--NYPEYTYCLGISIIAVLYTTA-QVTR
DVHR--------------LSX-XXXIXXXKAAAVVDFAGDQVVAYLLMSALSAAAPVTD-YMRQA--ADXX---------
--------------------------FT----------DSAAAAISMAFLAFLAAGLSA-LVSGYNL
>F2D276_HORVD
CPLALHAAAAAFAFVALVLVAS--NQHG------------------XXMQFD--RYQEYMYLLAIAALAFAYSLA-QALR
HAHR--------------MRGGXXXIPAP-SARLFDFIADQVVAYLLMSALSAAIPITN-RMRTA--VIXX---------
--------------------------FT----------DATAAAISMAFLAFVALALSA-TVSGYKL
>C5WNF5_SORBI
SPLALHAAAAIFAFVALVLVAS--NQHG------------------XXMQFD--RYQEYRYLLAIASLALLYSLA-QAAR
HAHR--------------MRGGXXXVSSA-SARLLDFVGDQVVAYLLMSALSAAVPITN-RMRSA--VVXX---------
--------------------------FT----------DATAAAISMAFFSFVALALSA-VVSGYKL
>Q10MR5_ORYSJ
SPLALHAAAAAFAFVALVLVAS--NQHG------------------XXMEFD--RYQEYRYLLAIAALAFAYSLA-QALR
HALR--------------MRRGXXXVPTA-SGRLLDFASDQVVAYLLMSALSAATPITN-RMRSA--VIXX---------
--------------------------FT----------DTTAAAISMAFLAFVSLALSA-IVSGYKL
>F2E2E4_HORVD
IVLVLRAGAALLSFVAMALVAS--CRHG------------------XXMDFL--RYQEYRYLLGVSVVAFVYSAA-QALK
NFRR--------------RRRGXX------DASFLDFAGDQAVAYLLVTASAAALPITI-RMRSA--VVXX---------
--------------------------FT----------DAIAASIALGFLAFAALALSA-MLS----
>Q84NQ7_ORYSJ
IVLVLRAAAALLALVAMALVAS--CRHG------------------XXMEFT--RYQEYRYLLGVAVVASLYSAL-QAAR
TFRR--------------MRAGXXX-----AATFLDFAGDQAVGYLLITASSAALPITI-RMRSA--VVXX---------
--------------------------FT----------DVVAASISFAFLAFAALAFSA-LIAGFRL
>Q5W6M3_ORYSJ
SGSALRVAAWAFSLLAFVVMGA--NDHG------------------XXRQFE--HYEEYRYVVAIGVLAFIYTTL-QLVR
HGVR--------------LTGGXX-XQGK-VAVLVDFAGDQVTAYLLMSAVSAAIPITN-RMREG--ADXX---------
--------------------------FT----------DSSAASISMAFFAFLCLALSA-LVSGFKL
>Q8LE26_ARATH
ASPITRGICLLFSLIAFLIMVS--NKHG------------------XXRNFN--DYEEYRYVLAISIISTLYTAW-QTFA
HFSK------------------XXXFDRR-TSILVDFSGDQIVAYLLISAASSAIPLTN-IFREG--QDXX---------
--------------------------FT----------DSAASAISMAIFAFIALALSA-LFSGYKL
>D7LBN4_ARALL
ASPITRGICLLFSLLAFLIMVS--NKHG------------------XXRNFN--EYEEYRYVLAISIISTLYTAW-QTFA
HFSK------------------XXXFDRR-TSTLVDFSGDQIVAYLLISAASSAIPLTN-RFREG--QDXX---------
```

```
--------------------------FT----------DSAASAISMAIFAFVALALSA-LFSGYKL
>Q84WP5_ARATH
SALGFRLSEVVLALISFSIMAA--DKTK----------------GWSGDSFD--RYKEYRFCLSVNVVAFVYSSF-QACD
LAYH--------------LVKEXXXISHH-LRPLFEFIIDQVLAYLLMSASTAAVTRVD-DWVSNWGKDX----------
--------------------------FT----------EMASASIAMSFLAFLAFAFSS-LISGYNL
>D7LIR2_ARALL
VALGFRLSEVVLALISFSIMAA--DKTK----------------GWSGDSFD--RYKEYRFCLSVNVVAFIYASF-QACD
LAYH--------------LVKEXXXISHH-LRPLFEFIIDQVLAYLLMCASTAAVTRVD-DWVSNWGKDX----------
--------------------------FT----------EMASASIAMSFLTFLAFAFSS-LISGYNL
>D7MMW4_ARALL
TALGFRITEVILCVISFSIMAA--DKTQ----------------GWSGDSYD--RYKEYRYCLAVNVIAFVYSAF-EACD
AACY--------------MAKEXXXMNCG-FHDLFVFSMDQLLAYLLMSASSCAATRVD-DWVSNWGKDX----------
--------------------------FT----------QMATASIAVSFLAFGAFAVSA-LISSYRL
>Q501G6_ARATH
TALGFRITEVILCVISFSIMAA--DKTQ----------------GWSGDSYD--RYKEYRYCLAVNVIAFVYSAF-EACD
AACY--------------IAKEXXXINCG-FHDLFVFSMDQLLAYLLMSASSCAATRVD-DWVSNWGKDX----------
--------------------------FT----------QMATASIAVSFLAFGAFAVSA-LISSYRL
>Q9FNE8_ARATH
ALLGFRVIAFVSCLVSFSVMVS--DRDK----------------GWAHDSFY--NYKEFRFCLAANVIGFVYSGF-MICD
LVYL--------------LSTSXXXSRHN-LRHFLEFGLDQMLAYLLASASTSASIRVD-DWQSNWGADX----------
--------------------------FP----------DLARASVALSYVSFVAFAFCS-LASGYAL
>C5XTX2_SORBI
TALLARGAAAGLCLAALAVLAA--DTRK----------------GWARDSYS--NYTQFRYSEAVNVIGFIYSVF-QFVA
LVEL--------------MRRNXXXIPHP-KRDLFDFTMDQVLTYLLISSSSSATARVS-DLIDNWGSDX----------
--------------------------FP----------SMANGSIAISFLAFAVFAICS-LISAYNL
>C4JAF2_MAIZE
AALLARAAAAGLCLAALAVLAS--DTRR----------------GWARDSYS--NYAQFRYSEAVNVVGFLYSVF-QFVA
LAEL--------------MRRNXXXIPHP-KRDLFDFTMDQVVAYLLISSSSSATARAS-DLIENWGSDX----------
--------------------------FP----------SMANGSIAISFVAFVVFAICS-LISAYNL
>B6TWJ1_MAIZE
AALLARAAAAGXXLAALTVLAA--DTRR----------------GWARDSYS--NYAQFRYSEAVNVVGFLYSVF-QFVA
LAEL--------------MRRNXXXIPHP-KRGLFDFTMDQVLAYLLISSSSSATARAS-DLTENWGSDX----------
--------------------------FP----------NMANGSIAISFVAFVVFAICS-LISAYNL
>A3A2W2_ORYSJ
TALVARVAAALLCLAALAVLAA--DSRK----------------GFALDSYS--NYSQLRYSEAVNVIGFVYSVL-QFFV
LADL--------------MRRNXXXNPRR-KGDYFDFFMDQVLAYLLISSSSSATARVG-DWIDNWGSDX----------
--------------------------FP----------KMANSSIAISFMAFLVFAISA-LISAYNL
>C5XEK4_SORBI
LSVTLRLATAVLSLAAFSVIAS--ARTS----------------GWAGDYYA--HHLQYRYAVAVNVIVCAYSIA-QSFG
EIRR--------------LISPXXXFRSM-SSYYCSLFLDQALAYLLMSASSAAASRND-LWVSRFGTDX----------
--------------------------FN----------RKITSALWLSFIAFLMLALNA-LISTANL
>B6UBY6_MAIZE
LLLALRLATAVLSLAAFSVIAS--ARTS----------------GWAGDYYA--RHLQYRYAVAVNVIVFAYSVA-QSLG
KIRH--------------LVSPXXXFRTM-SSYYCSLFLDQVLAYLLMSASSAAASRND-LWVSRFGTDX----------
--------------------------FV----------RKITGALWLSFVAFLVLALNA-VISXANL
>O24088_MEDTR
ALLVIRVFAFVFCLIAFSVLGA--SEQRVLVSENLTNXXXXXXQTPYEFHWY--KWDEFRYSFAANVIGFVYSGL-QICH
LVMY--------------LITKXXXINPK-LQGYFNVAIDQTLAYILMSASSSAATAAH-LLKDYWLXXGAXX-------
--------------------------FI----------EMANASVSMSFLAFGAFALAS-LVSGIIL
>Q3EA54_ARATH
IGLVLRFITMVLCFVSALSLAV--NVQRPSKR----------HLTQNSSSFA--SYPELLYCFGVAVIGFVYTSL-QTFK
GVCD--------------ITHRXXXISEP-LSDYISFIFDQVICYLLVSSSSVAIAWIQHXXXXXXXX------------
--------------------------LR----------NNSIVSVSMSFSAFLVLTLSG-LLSGYKL
>Q56X75_ARATH
LLLLLRVLTGVFLVIALIILST--NSVTIVS-----------QGSALKFHFK--DVYAYRYMLSAAVIGLVYAVI-QLFF
TISE----FATG-XXXX-------------FNYQLDFYGDKLISYLVATGSAAGFGVTK-DLKDTFLALVXXXXTX----
-------PVDK---------------FF----------SKGYASASLLLFAFICLAVLS-VFSSFAM
>D7LD59_ARALL
SLLLLRVLTGVFLVIALIILST--NSVTIVS-----------QGSALKFHFK--DVYAYRYMLSAAVIGLLYAVI-QLFF
TISE----FATG-XXXX-------------FNYQLDFYGDKLISYLVATGSAAGFGVSK-DLKDAFIALVXXXXTX----
-------PVDK---------------FF----------SRGYASASLLLFSFICLAVLS-VFSSLAI
>Q8GWD5_ARATH
VLLLLRVLTAAFLLITVVLIST--NTVTLEI-----------SSTSIKLPFN--DVYAYRYMLSAAVIGLVYAVV-QLFL
TISQ----FATG-XXXX-------------LTYQFDFYGDKVISYLLATGSAAGFGVSK-DLKDTYIALIXXXXTX----
-------PVDK---------------FF----------SKGYASASLLLFAFVSLAVLS-VFSSLAL
>D7LD60_ARALL
VLLLLRVLTAAFLVITVVLIST--NTVTLEV-----------SSTSIKMRFN--DVYAYRYMLSAAVIGLLYAVV-QLFL
TISQ----FATG-XXXX-------------LNYQFNFYGDKIISYLLATGSAAGFGVSK-DLKETFLALIXXXXTX----
-------PVDK---------------FF----------SKGYASASLLLFAFVSLAVLS-VFSSLAL
>B9SXY8_RICCO
AALILRILTFIFLIASLVILTT--NTATLEL-----------DLVEVKVHFK--DVYAYRYMLATIVIGLAYTVL-QIAF
TLYY----VATGNXXXXXX-----------GNLAFDFFGDKVISYILVTGAAAGFASTK-DIKPVFSGSGXXXX------
--------------------------FI----------NKGYASASLLLIGFVCTAVLS-VFSSYAL
>B9NBE5_POPTR
TALFLRVLTFAFLMVSLVIMTT--NTGTIEI-----------GIDEFKVRSK--DFYSYRYMLAAIAFGLTYTIL-QIAL
TLNH----ISKRNXXXXXXX----------GNLVFDFYGDKVVSYILATGAAAAFGATK-ELKTQLAGLGXXX-------
--------------------------FF----------NKGYASASLLLLGFVCTAILS-VFSSYAL
```

```
>C6T1Z6_SOYBN
VLLLLRVLTFVFLLIALILIAI--VKQTD-------------XETGVEIKFN--DIYAYRYMISTIIIGFAYNLL-QMAL
SIFT----VVSGNXXXXXX-----------GGYLFDFFGDKIISYLLISGSAAGFGVTV-ELGRGVPSNX----------
--------------------------FM----------DKANASASLLLIAFLFTAVAS-TFTSFAL
>A1XGB4_CAPAN
VSLIVRILTLICLLISFIVIAT--NNQTVST-----------VAGDVKIKFK--DFYAYRYLIATVIIGMAYTLL-QIAF
SISL----LTTGNXXXXX------------GFLLFDFYGDKFISYFLVTGAAASFGMTQ-DLKQLEGSDXXXX-------
--------------------------FL----------NTSNAAASLCLIGFFFAVASS-IFSSYNL
>C5Y494_SORBI
AVLILRLLSLGLLAASLALIAA--DKLNVD------------SDPPQRYTFR--DVYAYRYVLAVAVIGCAYTLL-QLPL
AAVS----IIASGXXXXXXXXXXXX-----ALLVLVLLADVVFALLLATGAAAGFAFTY-DVKRYLDGQXXXXXXXXXXD
KLXXXXXX------------------FF----------DLAYAAAGLMLAAAACMALVI-MLSVYSL
>Q2R2T4_ORYSJ
AVLALRLLTLALLAASLAVIAA--DKLTLDFGG---------GLPPKKITFK--DVYAYRYVLAIAVIGCAYTLL-QIPF
VAVS----IAKRKXXXXXXX----------NVALFLIFADVIFALLVATGAGAGFGLTY-DAKSAFGGXXXXXXXXX---
--------------------------FF----------NMAYAAAGLMLLAAAAMALII-MLSIYSL
>A9SG36_PHYPA
ASIVLRLLTLIFAVVALAVLAS--NTGSFQVSTGS-------ATSVKTIKFT--ILSAFTYLFAVCGVVAVYSLL-LIIV
EMID----LA-------XXXXXTHT-----LVAIFVFVLDQTMAYVLISAASASANGVK-VSRDESNITGXX------XD
IS-C-----XXXXXD-------D---YC----------TKASASVAIAFIAFLFMAITA-GVSARRL
>C5YHP6_SORBI
TTVALRLLAFAASLAAAVVVAT--NRQERWG---------------ITVTFK--MFAVWEAFVAINFACAAYALLT----
----------------------XXXXXKL-VSKHWLHHMDQFTVNLQAASTAGAGAVGS-VAMWGNEPSX--------WY
AV-CR--LYRL---------------YC----------DRGAVSLALAFVAFVAFGVAS-SLSRYPR
>A2YXI1_ORYSI
VDVSLRLLAAATSLASAVVVAA--NHQQRWG---------------VRVDFT--LFQVWIGFVAVNLVCTVYAAAT----
----------------------XXXXXKA-MGRWWLHHADAVVVNLEAAATAGAGAIGS-IAMWGNEASX--------WY
AV-CR--LYRR---------------YC----------NAGAAALALSLAAVLLLGVAC-ARSRYPK
>Q6Z1G3_ORYSJ
VDVSLRLLAAATSLAAAVVVAA--NHQQRWG---------------IRVDFT--LFQVWIGFVAVNLVCTVYAAATX---
----------------------XXXXXKA-MGRWWLHHADAVVVNLEAAATAGAGAIGS-IAMWGNEASX--------WY
AV-CR--LYRR---------------YC----------NAGAAALALSLAAVLLLGVAC-ARSRYPK
>C5Y376_SORBI
VTLLLRLITLALALTSAVLMAT--ASECTIYGLDGAT--------ATTVTFK--DYQPFIYLVGSNIAATILEVA-AIYV
Q--XGKGDXXXX---XXXXX------------RVVLVVVDVAVQMLLYSATGAVFAA--------------XXXYXPQ-I
SA-C----XX--XXG-------H---FC----------EQVQRSKIISLAASLSAVLAA-VAKDVAL
>Q2R0D1_ORYSJ
VSLLLRLSTLALALTSAVVMAT--ASECTVVQLNGVV--------X-TITYK--DFPPFVYLVGFNIAAAMLEAA-AIYL
RLSTGGGDXXXX-XXXXXXX------------GILLVVIDVAVQALVYTATGGAFAA--------------XXXYXPQ-I
NA-C----XX--XXG-------R---FC----------GQVHQSKLLSFAGSAAVGLAV-VFRDVSL
>C5Y7C7_SORBI
VSIAGRIAGMGLAVAAAVLMST--ASQCTVY--XXXXXXXXXAARARTVTYS--DFPPFVFLVGAASIAAFLEAI-AIFL
VVWKKGKDXXXX-X--------------------LMPLLGVAVPALLYSATGAAFAAVS--------XXXXXXXNXKRXX
---CA--GSA--XXGXXXXXXXN---FC----------SQVHIAVYLSLAAAVAVSVAE-VVRGLGG
>Q2R0D2_ORYSJ
VNLALRIVVLGLAVAAAALMAT--ASQCTIFLYYGGP--------LHTITYK--DFGPFVYLVVASSIGAFMEAI-AIFL
TICKKKDGXXXX-X--------------------LLPLLDAAVPVLLYSATAAAFAAGD----------XXXXXVXKRXX
---C-----XXXXXG-------N---FC----------NQVHIAMYVSLAAGVALLVAE-IVKHWPD
>C5Y7C8_SORBI
VSLIFRVAGIGLAAVSAAAMLT--ASQCTVYADYGWR--------PRTVTYS--DFPAFVYLVAATAIATLLEAV-ALFL
SWSKKG---------XXXXX----------WRVLTMLLLGAVVPALLYTSAGAAFAVGW-E-----XXXXXXXXIXRR-F
SV-CR--SSV--XXG-------R---FC----------EHVHVSMWLALGAAVAVSFAE-FLTTFRW
>C5Y7C6_SORBI
LSLLFRIAALGLSLAAAIVMAT--ASQLVIGGGGGH------ESSSYSVSFG--QYNALRYFVAAGAISAVCSAA--XXL
FAVRADFTXXX-------------------VSLPLVPVLDAAAQGFLFSAAGAAFATRDVXXXXXXXXXXXXX-------
---CD--AAGA---------------FC----------GRVTVAAAVCAFAAVSVATAA-LASRDAG
>Q2R0D4_ORYSJ
VSLFFRIAVVGLSVAAAVVMAT--ASQAFPFNYGG------------AVSYT--KYPAFVYFVVAAVVSAVCSAA--XXL
SVVREA------------------------AAGWAVALLDVVTMGLLFSAAGAVFAVRR-MAPLXXXXXGADTVAGXWNG
EF-CH--AAGA---------------FC----------WRVTTSAIICAFAAAAVSVAV-LTKGARH
>P0DI68_BRADI
GGLGLRVAQFVFAGVALAVMAS--T-----------------------SDFP--SVTAFCYLVAATIMQCLWSFS-LAIV
DIYA----LLVK-RCLRNR-----------RAVCLFAIGDGITAALTFGAACSSAGITV-LIDN--------------DL
NI-CA---------E-------N---HC----------GSFKTATALAFMSWFALTPSF-LLNFWSM
>Q10Q78_ORYSJ
GGLGLRLAQFAFAAVALAVMAS--T-----------------------NDFP--SVTSFCFLVAAAILQCLWSFS-LAIV
DIYA----LLVK-RCLRNR-----------RAVCLFAIGDGITAALTFSAACASSGITV-LIDN--------------DL
DL-CS---------E-------N---HC----------ASFESATAMAFLSWFALSPSF-LLNFWSM
>B4FNS3_MAIZE
AGLGLRLAQAFFAAAALAVMAS--T-----------------------NDFP--SVSAFSYLVAAAILQCLWSLL-LAFV
DIYA----LLVK-RSLRNA-----------RAVCIFTIGDGITGTITLGAACASAGITV-LIGN--------------DL
NI-CA---------E-------N---HC----------ASFETATALAFISWFALAPSC-ILNFWSM
>A2Z669_ORYSI
GGLGLRLVQAFFAAAALAVMAS--T-----------------------DDFP--SVSAFCYLVAAAILQCLWSLS-LAVV
DIYA----LLVK-RSLRNP-----------QAVCIFTIGDGITGTLTLGAACASAGITV-LIGN--------------DL
NI-CA---------N-------N---HC----------ASFETATAMAFISWFALAPSC-VLNFWSM
>Q339M6_ORYSJ
```

```
GGLGLRLVQAFFAAAALAVMAS--T-----------------------DDFP--SVSAFCYLVAAAILQCLWSLS-LAVV
DIYA----LLVK-RSLRNP-----------QAVCIFTIGDGITGTLTLGAACASAGITV-LIGN--------------DL
NI-CA---------N-------N---HC----------ASFETATAMAFISWFALAPSC-VLNFWSM
>Q9SKN3_ARATH
LGLALRFFQFLFAAAALCVMAS--T-----------------------SDFP--SVTAFCYLVAATGLQSLWSLA-LAMV
DVYA----IMVK-RSLQNR-----------RLVSLFAIGDGVTSTLTFAAACASAGITV-LIDN--------------DL
NS-CA---------Q-------N---HC----------VQFETSTALAFISWFAALPSF-LFNFWSL
>P0DI69_GINBI
GGLLLRLGQFCFALVAFSIMVS--I-----------------------ENFS--TVTAFCYLVAATVLQCLWSLA-LAII
DGYA----LLVK-RSLRNS-----------LLVSLLVVGDGVTATLTFAAACASAGITV-LIGN--------------DL
RQ-CK---------E-------N---HC----------ARYETATALAFLSWFMVSLSF-ILTFWLL
>P0DI70_GINBI
GGLALRLGQFCFAVVAFSIMLS--T-----------------------DDFS--TVTAFCYLVAATVLQCLWSLA-LAVI
DGYA----LLVK-RSLRNS-----------LVVSLFVVGDGVTATLTFAAACASAGITV-LIGN--------------DL
RE-CD---------Q-------N---HC----------GKYETATAMAFLSWFMVSPSF-LLTFWLL
>P0DI64_PINCO
GGLMLRLGQFCSALIAFSVMVS--I-----------------------RDF---SVTAFCYLLAATVLQCLWSLA-LAVI
DVYA----LLVK-RSLRNP-----------LLVSIFVVGDGVTATLTFAAACASAGVVV-LIGN--------------DI
SM-CK---------S-------N---PC----------ANYEAAIIMAFLSWFMVSISF-VLTFWML
>A9NYX5_PICSI
GGLVLRLGQFCSALIAFSVMLS--V-----------------------RDF---SVTAFCYLVAATVLQCLWSLA-MAVI
DVYA----LLVK-RSLRNP-----------LLVSIFVVGDGVTATLTFAAACASAGVIV-LIGN--------------DI
AM-CK---------D-------N---PC----------ANYEAAIIMAFLSWFMVSISF-ILTFWLL
>P0DI27_PTEAA
GGLALRLGQLGFAVLSFSIMVS--T-----------------------PDFS--QVTAFCYLVAATVLQTLWSSI-TAVV
DIYA----LSVR-RSLHHS-----------LLVGLFAVGDGVTSTLTFAAACATAGITV-LIDN--------------DL
DE-CG---------Q-------N---HC----------GRFEAAAAMAFLSWIMAAPSF-LLAFWSF
>D8QNI1_SELML
GGLVLRSGQFACAVTALSIMIS--I-----------------------PDFS--SVTAFCYLVAAMALQLLWSVS-LAVV
DGYA----LLLR-RTLHNP-----------VLLSLLVIGDWVTSTLSLAAACSSAGITV-LIDS--------------DL
AQ-CA---------H-------N---HC----------GRYEAAVAMAFLTWFLVSLSF-FFSFWLL
>P0DI66_MAIZE
GGLGLRVLQLLFAAISLAVMSS--T-----------------------ADFA--SVSAFCYLITTTVLQCVWSLT-VAIV
DIYA----LLVK-RCLRNR-----------RAVTLFSIGDGITWLVSLSGACAAAGITV-LIDA--------------DL
IM-CS---------E-------N---PC----------ASFQTAVAMGFMCCFSLLPSF-LLNFYSI
>P0DI67_MAIZE
GGLGLRVLQLLFAAISLAVMSS--T-----------------------ADFA--SVSAFCYLITTTVLQCVWSLT-VAIV
DIYA----LLVK-RCLQNR-----------RAVTLFSIGDGITWLVSFSGACAAAGIPV-LIDA--------------DL
IM-CS---------E-------N---PC----------ASFQTAVAMGFMCCFSLLPSF-LLNFYSI
>A9RKK4_PHYPA
GGLALRFTQFGFSLISLCIMVS--I-----------------------AGFS--SVTAFCFLVATMVFQCIWSLC-LGAL
DIYA----LLTQ-RSFRNP-----------LIVSLFVVGDWVTSTMTFAGACAAAGITV-LIDN--------------DL
EQ-CG---------P-------N---HC----------GRFEAAAAMAFMSWTATTLSF-CLSFWLL
>A9RLK6_PHYPA
MGLALRFAQLGFALTALCIMVS--I-----------------------VGFS--SVTAFCFLVAAMVLQCIWSLC-LGVL
DCYA----LLTK-RSLRNS-----------LILSFFVVGDWITSTMTFAGACAAAGITV-LIDN--------------DL
NQ-CG---------P-------N---HC----------NRFEAAAAMAFMSWVITTISF-FLSFWIL
>P0DI22_PTEAA
GSLALRICQFSAAIVSFSVMIS--A-----------------------ANFS--SVTAFCFLVAAMVLQCMWSLS-VATI
EGYA----MLVG-RSLRDS-----------PLLSLFAVGDWVTAVITFAGACASAGIAV-LVGR--------------DI
HRGCD---------V-------N---FC----------GRYAAAAGMAFLSWLLISTSF-LFTFWLL
>P0DI71_GINBI
GGLALRVGQFLFAAAAIVIMVT--G-----------------------DEFT--NYTAFCYLVAAMSLQFLWSFM-LAIL
DTYA----LLIK-RGLRNS-----------VLLSLFVVGDWVTATLSLAAACSTAGVTV-LFDN--------------DL
NY-CG---------Q-------M---HC----------HRYQLSAAMAFLSWLLIGMSS-LLTFWLW
>D5ACW4_PICSI
GGLALRMGQFIFAAASVVIMVT--S-----------------------DEFI--NFTAFCYLAAAMALQFLWSFV-LATI
DVYA----LLIK-RGLPNS-----------ILLSLFVVGDWVTATLSLAAACSTAGITV-LFDK--------------DL
NY-CD---------Q-------M---HC----------RRYQLSATMAFFSWVLIAISS-LITLLLL
>Q6NPF8_ARATH
GGLILRLSQFVPALISVSVMVT--T-----------------------SDFR--SATAFCCLVLAVSLQSLWSLS-LFII
DAYA----LLVR-RSLRNH-----------SVVQCFTIGDGVTSTLTFAAASASAGITV-LIX---------------DL
GQ-CN---------V-------N---HC----------TRFETATAMAFISWFAVSPSF-ILNFWSL
>Q8L7R5_ARATH
TGLVLRISQCVFAAGSISYMVT--S-----------------------GGFF--SFTAFCYLIAAMGLQVIWSFG-LAIL
DTFA----LVRK-KTLLSP-----------VLVSLFVVGDWVTSTLSLAGASSSAGITV-LYFG--------------DL
GS-CS--F------E-------A---EC----------WKYQLSVALAFLCWITIAVSS-LTTLWLL
>Q945M8_ARATH
CGLLLRIGQCASAAASIGVMVS--A-----------------------KEFS--VHTAFCYLIASMGLQLLWSFG-LACL
DVYA----LRGK-KDLQNP-----------ILVSLFVVGDWVTAMLSLAAACSSAGVVV-LYEK--------------DI
KY-CN--TQS----Q-------Y---PC----------LRYEVAVALSFVTWIQIAVSS-HVTFWIL
>Q9LZM5_ARATH
SGLILRLGQCATAAASIGVMVS--S-----------------------YDFS--NYTAFCFLVASMGLQLIWSFG-LACL
DVYA----IRRK-SDLRSP-----------ILLSLFTVGDWVTALLALAAACSSAGVTV-LFTK--------------DT
EF-CR--QQP----A-------L---SC----------DRFQISVGLSFFNWFLAAISS-HTMFWIL
>B6T990_MAIZE
SGMALRLSQCVSAGASMGAMAT--A-----------------------YGFS--NYTAFCYLIASMGLQLLWSFG-LACL
```

```
DVYS----LKTK-RDLHNP-----------VLVSLFVVGDWVTAILSFAAASASAGVTI-LFER--------------DV
HF-CR--MYP----Q-------L---SC----------GRYALSVVLAFITWSFIATSA-VSMFWLL
>B8BD96_ORYSI
SGMSLRVSQCVFAGASVVAMAS--A-----------------------YGFS--NYTAFCYLIASMGLQLLWSFG-LACL
DIYS----LQTK-RDLHNP-----------VLVSLFVVGDWVTAILSFAAASASAGVTI-LFER--------------DV
HF-CR--MYP----Q-------L---SC----------GRYELSVILAFITWSFIATSA-VSMFWLL
>Q6K478_ORYSJ
SGMSLRVSQCVFAGASVVAMAS--A-----------------------YGFS--NYTAFCYLIASMGLQLLWSFG-LACL
DIYS----LQTK-RDLHNP-----------VLVSLFVVGDWVTAILSFAAASASAGVTI-LFER--------------DV
HF-CR--MYP----Q-------L---SC----------GRYELSVILAFITWSFIATSA-VSMFWLL
>B6TM88_MAIZE
GGLALRAGQFVFAAASICAMAS--A-----------------------PGFT--NYTAFCYLVASMGLQALWSLG-LGCL
DYYA----LTLR-RDLQQA-----------LLMSLFVVGDCVTAILSFAAACSAAGVVV-LFER--------------DA
YL-CR--RDP----Q-------L---PC----------GRFEVAAAFAFLCWTFSAASA-LVMSWLL
>B8AC36_ORYSI
SGLSLRVGQLVFAAASVCATAS--A-----------------------LGFA--AYTAFCYLIASMGLQALWSLG-LACL
DCYA----LKFK-KDLHSA-----------VLLSLFVVGDWVTAILSFAASCSAAGVVV-LFDR--------------DI
YA-CR---XP----Q-------L---PC----------GRFELAIACAFLSWAFSATSA-LVMFWLL
>Q5N794_ORYSJ
SGLSLRVGQLVFAAASVCATAS--A-----------------------LGFA--AYTAFCYLIASMGLQALWSLG-LACL
DCYA----LKFK-KDLHSA-----------VLLSLFVVGDWVTAILSFAASCSAAGVVV-LFDR--------------DI
YA-CR---XP----Q-------L---PC----------GRFELAIACAFLSWAFSATSA-LVMFWLL
>B6TAX2_MAIZE
GGLVLRVGQALFAAACIGVMGS--S-----------------------LGFA--SYTAFCYLIASMGLQMLWSFG-LACL
DGYA----IRAN-KDLTSP-----------ILLSLFVVGDWVTAILSFAASSSAAGVVI-LFQK--------------DV
LF-CR--RYP----Q-------L---PC----------GKYELATAFAFLSWALSATSA-LIMFWLL
>B8AYU8_ORYSI
GGLAMRVGQVAFAGASIGVMAS--G-----------------------AGFA--NYTAFCYLIASMGLQSLWSLG-LACL
DVYA----LTVK-RDLNNA-----------LLVSLFVIGDWVTALLSFAASCSAGGVMV-LFKR--------------DV
LF-CR--RYP----Q-------L---PC----------GRFELAVALAFLSWALSATSA-IIMFCLL
>Q0DHM7_ORYSJ
GGLAMRVGQVAFAGASIGVMAS--G-----------------------AGFA--NYTAFCYLIASMGLQSLWSLG-LACL
DVYA----LTVK-RDLNNA-----------LLVSLFVIGDWVTALLSFAASCSAGGVMV-LFKR--------------DV
LF-CR--RYP----Q-------L---PC----------GRFELAVALAFLSWALSATSA-IIMFCLL
>Q3ECT8_ARATH
ASLSLRLGQMVLAFGSLLFMTI--G-----------------------VRFY--QFTAFCYLVTIMSLAIPWNLT-LAMV
DIYC----VILQ-QPFQKP-----------RILLAISIGDWVVSVLALASASSAASVVD-ILRS--------------NE
SS-CP---------P-------T---IC----------NRYQFAATLAFLTWFLSLSSS-LFNLWLL
>B6U300_MAIZE
GSLGLRVGQAVFSSASLLFMSV--G-----------------------VEFF--SYTAFCFLVTIMGLVIPWSCT-LAMI
DVYS----VFVG-CPLRVP-----------GVMVIVVVGDCALSIVSFAAACSSAAVIDLLLQL--------------HG
SH-SS---------P-------T---FC----------GRYQLSAMMAFLSWLLMAASA-TFNLWFV
>B8BPI2_ORYSI
GSLGLRVEQAVFSSASLLFMSV--G-----------------------VEFF--SYTAFCFLVTIMGLVIPWSCT-LAMI
DVYS----ILVG-CPLRVP-----------GVMVIVVIGDWVLAILSLAAASSSAAVIDLLLQF--------------HG
SH-CS---------P-------R---FC----------GRYQLSAMMAFLSWFLTAASS-LFNLWFI
>Q10EJ2_ORYSJ
GSLGLRVGQAVFSSASLLFMSV--G-----------------------VEFF--SYTAFCFLVTIMGLVIPWSCT-LAMI
DVYS----ILVG-CPLRVP-----------GVMVIVVIGDWVLAILSLAAASSSAAVIDLLLQF--------------HG
SH-CS---------P-------R---FC----------GRYQLSAMMAFLSWFLTAASS-LFNLWFI
>P0CB17_ARATH
ASFALRFGQTIFSAASLIFMCF--D-----------------------FDFY--DFTTFCYLAMVMAIVTPWSIL-LALT
DTYS----VLVK-LLPQEL-----------RVLSIVFAGDFVLSFLSLGGACAVASATELLASA--------------DG
KI-CD---------G-------S---LC----------IQYQVSAALAFLCWFLLLASA-LFNFWSL
>Q66GI1_ARATH
SSFVLRLGQTLFSSASLLFMCFNDD-----------------------EDFY--AYTTFCYLVTVMGLVTPWSVT-LALM
EAYS----ILVK-KLPMQA-----------TVISVIVAGDFVLSFLSLGGACSTASVAVLLMDAXXX-------------
--------------------------QC----------DRYKLSATMAFLSSFLSFAST-FFNFCLL
>K3WS83_PYTUL
TRLALRFLQFASSLIVIVAFSS--AYAHLNQXXXXX------------------GSNDVTFAILMSFLGMVYGLFFL---
------------------XXXXXXXLCMR-XLLFCEQVMDFLMVLLLLIASIVLAVSDV---------------------
FQHCS--THHPKL-------------RC----------HDINVGVSFTFVSLAAFLATL-VLSCFAD
>K3WS84_PYTUL
LRLLLRFLQFAFSLIALITLSA--AFVASSYYGXXXXX----------------GSSPVIFTTLMTYTGFVYALWFL---
------------------XXXXXXXMCPR-XPLFYEQLMDFLMAVLLLIAAIVLLCSDY---------------------
VQNCS--VYGYML-------------RC----------RSIRTSVVFTFLAMASFLLTL-LLSFFDR
>G4ZSC0_PHYSP
SRSLLRFFDFALSLVALATVSR--AFVGASYYGXXXXX----------------GSRAATYTTLVTYTGMLVGLFFL---
------------------XXXXXXXFYPRPTPRFVEPLIDLILAAMLVVAGIVLVVSDY---------------------
VANCS--VYSYML-------------RC----------NELKTAVVFTFLASFSYFVTF-LFDCCES
>D0NLD9_PHYIT
SRALLRFLNFALSLVALATLSR--AFVGSSYYGXXXXX----------------GSRAATYATLMTYTGMLVGLFFL---
------------------XXXXXXXLFPRPTPRLIEQLLDLLLAALLVVAGIVLVASDY---------------------
VANCS--VYGYML-------------RC----------NQLKTAVVFTFLASLSYFVTF-LLDCCES
>H3HBC3_PHYRM
GRTLLRFLQFALALVALATISR--AFVGASYYGXXXXX----------------GSSAATYTQLVTYTSMLVGLFLF---
------------------XXXXXXXYFKRPTPRIVEQLMDLVLAAMLVVAGIVLVVSDY---------------------
```

```
VAHCS--VYGYML-------------RC----------NLLKTAVVFSFLTAAAHLASF-LLSSCED
>K3WS90_PYTUL
SSMMLRLLQCVGSLIAMSTVAA--GFHTSELSGNXXXX----------------GSHETNFMLLVAYSGMLYSGWYL---
------------------XXXXXXXCMPR-XRELFARVVDGVFALFFFCAAAALVASDY---------------------
VDACD--EYGXLL-------------QC----------NNLKTSVAFAFLTIVPFLLSF-ALTFVIS
>K3WS85_PYTUL
ARLGSRGLQFLFSLFALAFTVA--GFRSYENXXX--------------------GGSASTFTILMTYSAMMFSLWAL---
------------------XXXXXXXYVPR-XQVMTERVIDGVFAVVLLIAGIVLAMSDY---------------------
VEHCDYIXXXXXXXXX----------KC----------GNLKAGVVFTFLAMVAFLITF-GLNFLGI
>G4ZSC4_PHYSP
LRLGLRGLQFVCSLLAMSFAAA--GFYGXX------------------------ATHSSTFVLLMGYTGMLYTLWYV---
------------------XXXXXXXVANR-XALRLEQATDAALALALLVAGICLAASDY---------------------
TSNCGYGX------------------HC----------HNLKAATAFDFIAMFLFLVSL-GLTFVAA
>H3HBC4_PHYRM
LRLGLRGLQFFCSLLAMSFAAA--GFYSXX------------------------STHSSTFVLLMGYTGMLYTLWYV---
------------------XXXXXXXLANR-XAVRLEQATDALLAIVLLVAGICLAASDY---------------------
TSTCGYGX------------------HC----------HNLRAATAFDFIAMFFFLVSL-GLSFLGG
>D0NLE1_PHYIT
VRLGLRGLQLFCSLLAMSFAAA--GFYGXX------------------------STRSSTFVLLMGYTGMLYTLWYI---
------------------XXXXXXXLANR-XALRLEQGTDALLTLMLLIAGICLAASDY---------------------
TSNCGYGX------------------HC----------NNLRAATAFDFIAMFFFLVSL-GLTFVAG
>M4B8W0_HYAAE
MRLGLRGVQFVCSLLALAFAAA--GFYGXX------------------------ATHSSTFVLLMGYTGMLYTLWYV---
------------------XXXXXXXLVSR-XALRVEQAMDALLVLLLLIAGICLAASDY---------------------
TNNCGVGX------------------HC----------NNLKAATAFAFIAMFFFLLSL-ALTLLSP
>G4ZSC3_PHYSP
ANLALRCAQLLCCLLGLAFVAA--GXX---------------------------TFHSSNFVLLMNYTGMLYTLWFV---
------------------XXXXXXXFSTR-XSTRVEQGIDAVLAFVLLIGGICLAASDY---------------------
LEYCELVX------------------HC----------HNLKASVAFTFLAVFGFIATL-TLSILTT
>H3GGR0_PHYRM
TNLALRVAQLMSCLLGMSFVAA--GXX---------------------------TFHSSNFVLLMTYTGMLYTLWFV---
------------------XXXXXXXFSSR-XAPRVEQAIDAVLAFMLLVGGICLAASDY---------------------
LSYCELSX------------------HC----------HNLQAATAFTFIAMAFFLASL-SLSILAT
>F0X036_9STRA
IRILLRALQFLFSLVAISTMAA--SFRSIEFGMNVXXXXX--------------GSSVSTYVTVLTYSSLIYSSWYL---
------------------XXXXXXXH--XXXXKLQDWLIDGTFAFLYSIASILLVTSPY---------------------
ARHCS--LFELLL-------------RC----------GNLKATVVFLFLNLCALLGSI-AMSFVPI
>G5AEA0_PHYSP
VRCTGRTLQFACSVVALVCIVL--GYKHYYXXXX--------------------VEPKATYAILMAYSGVLYSLWHM---
------------------XXXXXXXLSRH-XTVGVERFMDVLIAVALLVAGILFATSAQ---------------------
VSDCS--TTNSEFTAY-XGSTLF---RC----------GSMNTGYVFTFIAVAMYVVTF-ALS----
>D0NMH8_PHYIT
VRCTGRTLQFGCSVVALVCIVL--GYKHYYXXXX--------------------LEPKATYAILMAYSGVLYSLWHM---
------------------XXXXXXXLSRH-XTVGVERFMDVLIAAGLLVAGILFASSKQ---------------------
VSDCS--TTNASFAVY-XGSTLF---RC----------GSMNTGYIFSFIAVALYLVTF-ALS----
>H3H3L9_PHYRM
VRCTGRTLQFACSVVALVCIVL--GYKHYYXXXX--------------------IEPKATYAILMAYSAVLYSLWHM---
------------------XXXXXXXLSRH-XTLGVERFMDVLVAAALLVAGILFATSAQ---------------------
VTDCS--SSNTAFETY-XGSTLF---RC----------GSMNTGYIFTFIAVALYLVTF-ALT----
>G5AE98_PHYSP
TRRCVLLLQFACCLVAFILFVA--SYKPYYXXXX--------------------VSPAATYVILMSYSGWLYALWHT---
------------------XXXXXXXLSRR-XKVGVERLMDLLVAVLLLVAGIIFAVSSQ---------------------
VTDCD--DTNAMLETYXXGTKLY---RC----------GSMDGGYIFAFVAVALYVITF-ALS----
>H3H3L4_PHYRM
TRRCVRLLQFSCSLVAFVLFVA--SYKPYYXXXX--------------------VSPAATYAILMAYSGWLYALWHI---
------------------XXXXXXXLSRR-XKVGVERLMDVLVAVLLLIAGIIFAVSSQ---------------------
VTDCD--DTNAMLETYXXGSTLY---RC----------GNMSVGYTFAFVAVALYAITF-ALS----
>G5AEA1_PHYSP
ARRGGRFVQFVLSLLTFISTVA--GYKHYFXXXX--------------------TSPVAMFMVLVSWSCILYTLFHL---
------------------XXXXXXXKSHR-XSAGIERFLDLLLAVLLLLFAILLAASHQ---------------------
VSDCD--TINAKYEADSGSLDGXNIYRC----------GSLTRAYVLAFIDCVFFLVTL-ALSFCGS
>H3H3L8_PHYRM
ARRGGRFIQFVLSLLIFVSTVA--GYKHYFXXXX--------------------TSPVAMFMVLVSWSCILYTLFQL---
------------------XXXXXXXKSRR-XSVGVERILDVLLAVLLLLFAILLAASHQ---------------------
VSDCD--TINSKYEADTGSLGGXNVYRC----------GSLTRAYVLAFIDCVFFLVTL-ALSFSGS
>D0NMH7_PHYIT
ARRGSRFIQFVLSLIIFISTVA--GYKHYFXXXX--------------------MSPVAMFMVLVSWSCVLYTLFHL---
------------------XXXXXXXKSHR-XSVSVERVVDLFLSALLLLFAILLAASHQ---------------------
VDHCD--TINAKYEADAGSLGGXSVYRC----------GSLTRAYVLAFIDCIFFLATF-ALSFGGS
>F0X038_9STRA
KHIIPRGLQLILSALALAFAAS--ASRRFINRRNGXXXXX--------------GSSELSFTLLVTYSTMLYALWHL---
--------------------XXXXXITDR-XRLSLLRLLDLIFLGFLFAAGLGLVLSDY---------------------
NRHCN--GYQXLL-------------HC----------GNIVASVVFTFLTMSPLLITL-ATSFSRT
>F0WMT2_9STRA
VRIVLRGSQVLLSLIAIFLLAG--SFPSQTLGNSNXXXXLXX---------------SSGFAVVLLYTSLLSSSWYF---
------------------XXXXXXX-XPNPIAPKYTVYADGAMTFLFLITGIALASSSY---------------------
VTHCD--DYEGFI-------------RC----------RVIKGAVALMFFLFFSFCGSAWIYTAVRY
```

```
>K3X3G8_PYTUL
ITLAMRVLQLASAVLALGFIAG--GFDGKDEVIPAPDGDGKKXXXXXXX-----GGPTVNFAMIVTYSAAIYAMLWI---
------------------XXXXXXXRVRV--PAHFSVALDSILTVMLLSAGCAVAASDY---------------------
VRYCS--ALTPYV-------------HC----------SSLKAGVAFCFLAFVAFLISV-AWGLWIL
>G4ZRP2_PHYSP
ISLTLRALQFATCAVALALVAA--SFEARKITLHVEGGAPQE--XXXXX-----GGPAVNFVLVVSFAAVLYGGFFL---
------------------XXXXXXXCASM--PAPWSFGVDAVFTMLFMSAGCALAACDY---------------------
VRYCD--ALGGVV-------------RC----------ALLASAAALCFMAFVSFLLSV-AWGAWMR
>H3GI99_PHYRM
ISLALRSLQLATCVVALALVAS--SFQPQTLSL-----DGHE--XXXXX-----GGPAVNFVLVVSFAACLYDGLFL---
------------------XXXXXXXCASM--PAPWSFGVDAVFTMLFMSAGCALAASDY---------------------
VRYCD--ALDGVV-------------HC----------ALLASGAALCFMAFVAFLLSV-AWGAWMR
>D0NCN6_PHYIT
ICLTLRSLQFATCVAALALVAA--SFEPKKMTFQTNGGDSQE--XXXXX-----GGPAVNFVMIVSFAACLYDAFFL---
------------------XXXXXXXCAKM--PAPWSFGVDAIFTMLFMSAGCALAACDY---------------------
VRYCD--ALDGIV-------------HC----------ALLASGAALCFMAFVVFLLSV-AWGAWMR
>Q5BAE2_EMENI
VMLLIRALQWASAVIVMGITSY--FISKGP------------------------RGQHIIYQEVISVLSVVFFLPAF---
----------------------XXXXMPN-MLSRFVFFIDVVFSYLWLTAFIFAAQDYN---------------------
WHNCYLNXXXXX--------------NC----------SRKKANESFIFLAFIFTFFGM-LLELYSL
>Q4WA14_ASPFU
--------------------------------------------------------------------------------
---------------------------PT-ALSKFVLAIDVIFSYLWLTAFIFAAQDYN---------------------
EQNCYFNXXXXX--------------GC----------SKKKANEAFIFLAFFFTFAGM-FLEIASL
>Q4WBB3_ASPFU
ASLVVRFMQWSSAVIVMGITSY--FINKWP------------------------HTQHTIYWEVISTMSVVFFLPAF---
----------------------XXXXMPT-RLSRFVLPIDVIFSYLWLTAFIFAAQDYN---------------------
WHNCAVNXXXXX--------------SC----------ALKKANESFIFLAL---------------
>C0NZ48_AJECG
LLFCTRLLQWCSAVIVMGIVAF--FLHRGP------------------------KGQHLKYEIVIAVLSVAFFLPGL---
----------------------XXXXIP--AVGKIAFPIDIIFSYLWLTSFIFTAQDYN---------------------
LGVCGLNXXXXX--------------RC----------SLKHALEAFTFLAFFGCLASA-MLEIYNL
>J3K1S1_COCIM
CLLLMRLLQWASAVIIVGIVSY--LINEGP------------------------KGAHLIYEEVIAVLSVAFFVPGL---
----------------------XXXXAP--AVGWLAFPIDLIFSYLWLTSFIFASQDYS--------------------X
GAVCSANXXXXX--------------GC----------AIKHASQSFIFIAFFCTMCSA-AMESWNL
>Q7S1V0_NEUCR
ILSLLNIFVWISSVIVLGIAAY--EIHQFKKYXDAX------------------PGARIVYILVIAVFTVAFFLLSF---
--------------------------XXX-XRPGYTLLFNLIFSYLWLVSVVFAAQSWSSXXXX----------------
--------------------------------------RKWHAMEAFTFIAFFGLFFNT-LYAWWQQ
>C0P0L7_AJECG
ISVILRIGEIGCAAVVAGIIGH--DLARFDDADSF-------------------PNGRWIYTIIVAGISILLGIIWL---
--------------------------IPF-SQSFTLWIGDLLLSFAWFAAFGVLVDVLK---------------------
KMDCG--GTFXWGHIXDXX-------VC----------SRWKAVEAFSFVSAILWLVST-IVGVWFT
>J3K9K9_COCIM
VSVFLRIGEIGFGAVVAGIIGS--YLHDFDGTDVW-------------------PQARWIYTEVVAGVSILLALLWL---
--------------------------LPF-SGSFFMWPTDLVLSFAWFAAFGLLVNALN---------------------
DLDCG--GVFXWGNIXGXX-------TC----------SRWKASEAFSFLSAIFWLVST-VVGIWFT
>Q4WUJ1_ASPFU
VSIVLRVAEIAFAAVVAGVIGY--YLHQFSDIDAW-------------------PQARWIYTEVVAGLSILLGLIWL---
--------------------------IPF-SSGFFSWPFDVVISFAWFAAFGILVDAIH---------------------
KLNCG--SIWXWHFNXXXXX------SC----------GRWKAAEAFSFLSAIVWLASA-LVGIWFT
>C8VAW4_EMENI
LSVILRIAEIGFGAVVAGIIGW--FLHRFGDLDIW-------------------PEARWIYTEVVAGISILFGIIWL---
--------------------------IPF-SSGFFTWPLDLLLSMAWFAAFGVQVDAND---------------------
RLNCG--SIWXWGSIXDXX-------YC----------GRWKAAQAFSFLSAIVWIVSA-LVGMWFT
>A7UWP7_NEUCR
ISIILRVAELAFASIVAALNGR--FLHAARGNSPW-------------------DLGRHIYTEVVAGLSILFAIVWL---
--------------------------FPF-SSSFIHWPMDLVISVMWFVSFGLLVNWLH---------------------
-XVCG--YVFXWDNVXXXXX------GC----------GEWKATVAFAFLSAICWLVSA-LVGLYWV
>I1S038_GIBZE
VSLVLRAAELVFAAIVAGVNGE--YLHNARGASSW-------------------QLGRFIYTEVVAALGMLFSLLLL---
--------------------------IPF-SSTFVHWPLDIFMSINWWIVFGLLVDLVG---------------------
-XSCG--RVFXWNNVHPVHGD-----QC----------GKTKAVIAFSFLSALLWLVSA-LVGFFWV
>C7YRL0_NECH7
VSLVLRAAELVFAAIVAGVNGE--YLHKSDGASAW-------------------QLGRFIYTEVVAALGILFSLLLL---
--------------------------IPF-SSTFIHWPLDIFMSINWWIVFGLLVDLIG---------------------
-XSCG--RVFXWGNVHPIHGD-----QC----------GKFKATIAFSFLSALLWLVSA-LVGFFWV
>A7EHU9_SCLS1
FNLLLRLGQLAFSTIVLGITSA--HLSRARSESGW-------------------TRKRFIYTEVTAALGLFFSLFFL---
--------------------------LPH-TWNFIHWPIDFLMFVMFMIAFGLLVDFIA---------------------
PSHCG--SAFXWFGRXGGX-------SC----------SRWKADVAFAFLASLFFLASF-LLGTFMH
>C7ZQE2_NECH7
ASVILRFLELACGAIVLGLLGR--FCYLVDEATNVS------------------VDGRIIYAMVVAGITIVYSILVF---
--------------------------APF-DILFMSFPFDFVLFIMWLVAFCLLETRTR---------------------
SHICS--AGWYYNYWGYYWGRFXRVXGC----------SQWRTVIAFSIIAWVLFIISS-ILGIYVF
>C7ZCW5_NECH7
```

```
CSVILRLGQIACATIVIGILAR--FSYVLTXXXXX-------------------EDGRLVYAMVVAGMSIVYSFLLC---
--------------------------PPF-RNLFLSFPCDFILFIMWLVAYCLLQTKSG---------------------
TNTCS--STWYRTYWGYYWGRYXRVXGC----------GQWRTVLAFSFIAWFAYLLSG-ILGIYVF
>Q4WUL4_ASPFU
LETILRFIQFVFGLTVIGLYGR--DLHDGDKXX---------------------APAKWVYAVVTAFLAVMTATV-Y---
-----------X-XXXXXXXXXXXXXXRA-RVQLPLFIWESVLCILWLTLFGIFGKMYIGXXXXXXXX------------
--------------------------------------TRMRHAVWVDLVNLGLWIVTM-GWVGLRW
>I1RH73_GIBZE
PRLVCRGLQFIFAIIACGFYGR--RVDKAEDGDYG-------------------FSPEWYFALTIAGLSAATSLIFV---
-----------X-XXXXXXXXXXXXXXKL-LKTYRAFAWDLILFITWLVAFGIFAGIFLGXXXXXXXXXXXX--------
--------------------------------------GPMKTAVWVDLVNSILWLTSG-VYGCIKT
>I1S431_GIBZE
SRALLRTLQCIFAVVVAVLYGL--DLQQATDNNVK-------------------PGSAWIYAEFVAGVSIILCVTHL---
--------------------------XXX-XAVWYWSLLDGLVCILWLSQFGVFASAYLGXXXXXXXXXXXXXXXX----
--------------------------------------GRMQSAVWVNFISMLLWLATT-IQGIMGC
>C7YJN8_NECH7
SRALFRTLQCLFALVVAILYGL--DLQKATSNHTK-------------------ADSKWVFAEFVAGVSMIVCIIHL---
--------------------------XXX-XTSCGWTVLDGMLSILWMAQFSVFASQFLGXXXXXXXXXXXXXX------
--------------------------------------SRMKAAVWINLISMLLWFATT-ILGTMRC
>P53279_YEAST
ADNLVRIINAVFLIISIGLISG--LIGTQTK-----------------------HSSRVNFCMFAAVYGLVTDSLYG---
--------------------XXXXXXTSL-TYPAILLVLDFLNFIFTFVAATALAVGIR---------------------
CHSCK--NKTXLEQNKIIQGSSS---RC----------HQSQAAVAFFYFSCFLFLIKV-TVATMGM
>Q12207_YEAST
ADNILRIINFLFLVISIGLISS--LLNTQHR-----------------------HSSRVNYCMFACAYGIFTDSLYG---
--------------------XXXXXXEPL-AWPLVLFTLDFLNFVFTFTAGTVLAVGIR---------------------
AHSCN--NSSXVDSNKITQGSGT---RC----------RQAQAAVAFLYFSCAIFLAKT-LMSVFNM
>Q5ANE3_CANAL
GDVILRAFNFVFLVIALGLTGS--LAATTITQ----------------------HNPQINFAVFAAAFGLLTSSFYG---
--------------------XXXXXXAAF-AWPVILFVFDFLNFVFTFAAATAIAAGIR---------------------
AHSCS--NQDXLDDNNIAQGSSG---RC----------RKAQASTAFLYFSTFIFIASA-IFSAISL
>Q753K0_ASHGO
LDNSLRAVNFVFLIIVLGLTGS--LIHGQRN-----------------------SHSRVNFGLFTAVFALVTDSFYS---
--------------------XXXXXXSAF-AWPIITIALDVLNLIFTFAAATALGQSIG---------------------
AHSCS--NRGXLDGNTISEQSTD---RC----------RKVQASSTFLFFSFFIFLAKA-VFSGLNI
>Q6CC67_YARLI
ADLILRGLIFMFAAIIMGLAGS--LASTHKKGH---------------------YNPQVSYAVFCGAWSALFGVFYP---
--------------------XXXXXXEAI-AFPIVILIIDFISWVLTLAGGAALATAIR---------------------
CHSCG--NMNXVNSNKVTQGSKG---RC----------RKAQATVAFLFFANFSFLATM-ILSAISV
>Q5AVJ7_EMENI
IQLGLRVWQFIWTLLVMALIGN--MIAQSFAX----------------------NPATINYTMFVAAFSMFTLFYLF---
--------------------XXXXXXDWA-IHPIILVTLDTLNMIFFLTSAIALAARLE---------------------
CHSCS--NQEXILNNEITNGSHNPEKRC----------REAQASTAFLWFAWAGYAASW-VISILQS
>Q4WIJ9_ASPFU
IQLGLRAWEFVFSLLVMALIGN--IIAMAFAX----------------------NPATINYSMFTATFSIISLFYLV---
--------------------XXXXXXNWA-IHPIIMIVLDVLNNIFFLTCAIALAARLE---------------------
CHSCS--NDEXTLHNEITNGAHNRQKRC----------REAQASVAFLWFAWAGYMAST-IISILMA
>C0NZJ7_AJECG
----------------MALVGN--MVADAFHX----------------------SSSTVNYILFVSAFSMLSLFYLF---
--------------------XXXXXXACL-IHPGFMFLVDLLNTIFIFCGAIAMPAKLR---------------------
VHSCR--NVMXTVTNSITRGSPRPEKRC----------REAQAVTAFLWFLWVMFLIST-ILSGLSM
>J3K6Y8_COCIM
LNLFLRALQVAFATIVMGLIGD--MLNDYDDX----------------------SQSTVNYVMFSVAFSLATLFYLI---
--------------------XXXXXXMFM-IHPVILFLVDLLNTLFIFCAAVALPSKLH---------------------
VPDCS--NDDXLRDNSITKKSRSLSKTC----------REAKASTAFLWFLWFTFLLTT-IFSGMTM
>A7EYJ0_SCLS1
AQIGLRSAQFVTVLISLALIAA--AIDIQRF-----------------------GNKSVNFAMFTTVVSMIVVLYGL---
---------------------XXXXXESL-AHTLILAIMDGAALLFNLLSGIILASYLH---------------------
VHSCS--NRRXVLTNQLTQGSTG---RC----------RELQAATAFIWFSFALFTASL-AVDLMKG
>Q0UPR7_PHANO
LITGLRAWQLICAILVVAFMAN--NIDRADNG----------------------THSIVNYSLFVGLWWLLSLIYFI---
---------------------XXXXXDKF-SIPIVDVAMDALSVLFSFCAAVALAAYLG---------------------
AHSCS--NRAXTTSNGVCNSSANTEQNC----------RQAQATCAFLWFGFAAFVATL-AINVMNG
>Q1K6H5_NEUCR
IPLILRFIQLIFLIILTGLIGN--VIALDVDASTT-------------------ARAAINFTMFVIALSWVVALFGL---
---------------------XXXXXQSV-AIPLVMLIFDAAATLFTVVAGIVLAAKLG---------------------
TPNCGNLXXXXYGHKWIAYGSADDAKRC----------REIQAGTVFMWLLLAAFSAAL-TLAIMSW
>I1RZW2_GIBZE
IQMILRATGLLMTLLLTALIGS--VISSNIDAIGS-------------------ATAAVNFIMFVAIVGWIVCIIGL---
---------------------XXXXXSAL-DKPLLQLPLDAIAVLFTFIGAIVLAAKLR---------------------
VVNCGEIXXXXLPTDWIAWGSANDEGRC----------RRLQASTVFIWFLFACVSGSL-FLTIRAA
>C7YRH9_NECH7
IKMVLRGFELLITLLLTAVTGN--VIASNIDAAGT-------------------ATAAVNFVMFVAAVCWIVSIIGL---
---------------------XXXXXSVL-DKPVAQLVLDGSVVLFTFIAAIVLAAKLR---------------------
VVDCGDIXXXXLPGDWIAWGSNSDQKRC----------RELQASTVFMWFLFGSFCGSL-FLTVRDV
>O74333_SCHPO
FTWVFRTFQLAIDTIVLALASA--LVNQQTSGX---------------------SPGKINFSVAVGSFAILTFFLTA---
```

```
--------------------XXXXXXTIL-GNPWLIAFYDFVNWVFALTGGCCIAVAIR---------------------
VHACD--NQKXLDRNHYTQGSMR---RC----------QELKALCFFLWFMFGLYVASF-IVQIFIA
>A7E5M8_SCLS1
KGYXXXX-----------------------------------------------SWSLIIYGSFCGGAAIIIAAIGV---
----------------------XXXXXXA-LQGTIMLILDGIASFILLTGGIAYAATIK---------------------
VGNCD--DFIXYVIXXXXXXXXXXXXRC----------RETQASTAFLWFTAACFIGSI-VIQFLGR
>Q5ATF8_EMENI
VNSIVRIFQAISAIIVLGISVD--LARGQDTRLQS-------------------VPPATGYAAFCGGFGTLVSFIGI---
----------------------XXXXXSS-LEGLITLSLDALSGVTMLASGIAYAVLLR---------------------
HTDCS--NAXXSEAXWXXXXXXXXXXRC----------ASAKADTAFMFTSFVACIGIV-GYSFFAR
>Q0V4R7_PHANO
ANWVCRAFQLLFGIVILGLSVT--LIRGHHWXX---------------------LPATLGYAAFLGGVTIIAALIGI---
----------------------XXXXXTF-LEGIVGMAIDVFAALLNIAGGIALAIKMR---------------------
GVTCN--IKDXDFDXXXXXXXXXXXXHC----------RESSADMVFMFLVAALFLVTA-GLAFLRK
>Q0V4R6_PHANO
SSSVLRGLQMLFGIVILGLSIT--LIKSQSKAWEGSAXXIXX------------PPTILPLAAAIGAISLAAAVFSL---
----------------------XXXXXDI-LREYIEMLVDVVVIMLNVVGGVIIAIKLQ---------------------
GMNCG--DTXXXXXXXXXXXXXXXXXRC----------KQSQTDSIFMFLTVAICFATM-LLTFLRM
>Q7S8H8_NEUCR
LCIGLRGLQILFGAVIVGLSAQ--FITAQKVGS---------------------AATTTQYSVFTGTYAILEGFLGI---
----------------------XXXXXSS-FPDIVVLGADAIGALVLLAGGIAWAVETR---------------------
GFSCTDPXXXXXXXXXXXXXXXXXXXSC----------KKGLADEVFQFLAFAVLVVLL-VVGWIRW
>Q5BA62_EMENI
----------------MLTHLL--PINTFRGHDDHVXXXIXXXXXXXX------VPAAWGFLMFCAAWTILVVVFHF---
--------------------XXXXXESRP-IIGYVGIVAEAVTVLAWLAGFIAVAVNVL--------------------X
TDACSSGXX-----------------SC----------AELKAATAFGAFEWLLFMVTA-TPAVLSF
>C0NHG7_AJECG
LNYALRALQLIFSIIIMGTDGY--AIHVFRGHTDYVXXXFXXXXXX--------VPNAWGFLLFCASWTVLIIIFHL---
--------------------XXXXXADRA-LIGYIRVAVEAVAVLSWLAGFIAVAVQIA---------------------
TDTCSTGXX-----------------SC----------GLLKVATVFGAFEWLLFMITA-AQTVILV
>C0P076_AJECG
IVMGLRGVQVVLAIIILGLTGW--AVNRTQG-----------------------YSDETNFLLFDAIWTFLVAVPFL---
--------------------XXXXXLQQF-AHKYALIAVEAITLLFWFAGFIAVAAILP--------------------X
SAACRHSX------------------VC----------KGLQAATVFGAFEWLLFVATT-VLVVVLP
>C8V3Q0_EMENI
LFYILRAVQAVFAVIVLGLTGH--AVNVTDGH----------------------WWDTINFMLFNGVWTLFIVVPYF---
--------------------XXXXXVPAI-AHRWVLVAVDTITMIFWFAGFIALAVDLG--------------------X
AHGCSKWX------------------PC----------RGLQAAAAFGAFNWVLFLVTT-VLNTMGA
>J3K8E6_COCIM
ISLAIRGVQALFGIIVLGLTAY--IASEG-------------------------SLESSNFLLFCGLWTAFIVVPYM---
-------------------XXXXXXAPVA-AHPFAIIGVDGVTMIFWFAGFIALGSKLP--------------------X
PRFCTTFX------------------AC----------RVLQAATVFGSFEWVLFVATL-ALAVLPV
>Q0UHA4_PHANO
IVLGLRGVQALFSIIVLGLTAY--LVDAYNGPGYNW------------------SPHSVNFMLFCSIWTLLAVAYLL---
--------------------XXXXXFPKA-AHKFAIGAVEFITMIFWFAAFVAVAVRWN---------------------
--------------------------SC------------GVAAIVFSAFLWLTFVATT-ILAALHI
>A7EF22_SCLS1
YTLPLRIVQAVFAIIVLGLMAY--AADDWSYXX---------------------SPDSVNFLVFASVWTLLALIYLI---
--------------------XXXXXFPSA-AHKFGILFAEAVTMIFWFAGFIAVAVMLN---------------------
NVGCGHSXXX----------------VC----------QASIAGDVFAAFLWLLFLATT-IMAALHV
>D5GKD3_TUBMM
PILLLRVTQGVLAFIVLGVAAY--VVDGYDG-----------------------AVDAANFLVFDSVWTFIALGYVV---
--------------------XXXXXFPNF-HNRWAVLGVEAITMVFWFAGFVALAAGID---------------------
RLRCDRXXXX----------------------------------LHLGLLNGLL------------X
>Q7S4F1_NEUCR
-----HMIATVFGLIELGLTCY--LVSPWXX-----------------------APGIYAFMLFSSVWTLLVLIYIA---
--------------------XXXXXFPKT-FQRTIALALEWITMIFWFAGSIALAVYFG---------------------
SPSCGADX------------------FC----------GCVEAATAFGFLLWVTFLFIV-IVDTMAT
>I1RTI0_GIBZE
IITIVHAVLAVFLIIELGLTAY--MVDFTDX----WXXX---------------SPASFAFLLFCTVWSILMLLYLA---
--------------------XXXXXAPRI-YHNMVALGILALTSLFWFAGATAVAAHIG---------------------
VPHCHGNX------------------QC----------QSTQAAVAFGYFIWAIFTGLT-IMEALAF
>C7ZDD4_NECH7
IITIIHAVLAIFLIIELGLTAY--VVDISNPRSWGWXXX---------------TPSSFSFMLFNSVWSILILFYLA---
--------------------XXXXXASRL-YHSVVALGLLAVTTIFWFAGSIAMAAKIG---------------------
VPNCHGSX------------------PC----------QSTQAAVAFGFFIWAIFTGLT-VMEGLAH
>F5H950_NEUCR
ILLPIRVFQATFSIVIIGLSGF--VAHWYNTNTAYL------------------PPSPISFLLFCGVYSLLSVLYLG---
--------------------XXXXXFPKT-ANPYAVLSLEITNLLFWLAGFASLSVFLS--------------------X
LLFCRGS-------------------VC----------GAARADVGIGACLFVSWIVTV-ALLARDA
>A7EEJ3_SCLS1
LLLPIRIAQAVFAIVVLGLSGY--VSHWYNTDTLTA------------------SPSQINFLVFVPVFTLISIVYLE---
--------------------XXXXXMSKA-SHPYIHLGVELLNVLFYFAGFIALSVFIG--------------------X
LLFCRGS-------------------VC----------GAARADAVFGAFSWLLWMGSS-AILALEM
>I1RCT8_GIBZE
AFISLRVLQLALSIASIGLSSY--VVHDYDRRSRGS------------------APSPFSYLLTSSIVSIVSVVYLT---
--------------------XXXXXVPRL-YHQYAGVVVEAVNAALYFAGFIAIAVFIG--------------------X
```

```
LIMCEGT-------------------VC----------SCARADAVVAAGQFTAWITTT-AFTAKEL
>C7YWL0_NECH7
VLISLRVLQLALSLASISLSSY--VINWFXXXXXX-------------------IPSPFNYLLVSSILSVFSLVYLE---
--------------------XXXXXAPRF-SQQYVAIGVESVNAALYFAGFIAIAIYIG--------------------X
LVFCEGA-------------------VC----------SSGRADAVVAAGQFTTWIATT-ILMAKDM
>Q0V428_PHANO
---------------------------------------------------------EVNFLIFAPSWTVLALGALI---
--------------------XXXXXXSSK-AAKVGLLVLEGLTMLYWFGGFVALAVFLS---------------------
DRICFGT-------------------VC----------DVARASTAISAVNWLMWAVTF-GFGVFQM
>A7ENZ3_SCLS1
PLLGLRIAQLVLAIIILGLSAY--GVYWL-------------------------VFDGDALTLASSVISIVICVYVI---
--------------------XXXXXAPAI-YNYWAVLGLDIIAVILWVVSFPVLASQIA-------------XXXXXXXX
XXSCG--YYYXX--------------SCSYKHKRGLGRGIMIATAALAGIQFVLFAITL-IILAINI
>A7EUN4_SCLS1
GATLLRLLQLIIALAILGMAAF--VVANA-------------------------AYSGAILATFVASLTTLVLLYTL---
--------------------XXXXXLTNI-FNNWAIALLDLLLTILWLATWITAAVQIR---------------XXXFXX
XXGCG--WF-----------------LCRRDLLEWEVETVFIAVAVLAAVEFVLFVISF-FYTLTHI
>Q6CD20_YARLI
YTVLTRYVQTGLSLLCWCLAIS--AVALIDGG----------------------YWSTDAYGIAVGILTFIWLAYVM---
--------------------XXXXXYPKY-ANGLAAVVGEVLINIFWFTSFIASAAQRG---------------------
PESCN--FRGXGNRXLKDXGX-----SC----------KVAKAYIAFAAITWLFFIFST-FFVIKTS
>P53747_YEAST
TFHVLRYFQLGLSVTNLLLASF--AIITNYK-----------------------VDRILRLSLAVSIISSVYFGI-----
--------------------------XXX-LPVLLIFVMEIVQTVLWFTAFVTLASKFG---------------------
SMSCS--SMPXGINXDYSG-------SC----------KIAKIDILPEAVLFILFLATT-YASYITV
>Q5AKB8_CANAL
VTYIIRGAQSVFCIVVLGLSAG--FLADVGY-----------------------NYDRVTFALVVSILNLIYFSYIL---
-------------------XXXXXXXKNF-SPSVIILVAEFIFFVFYLSAMGAIAAVIP---------------------
SGSCG--DYGXYSX------------AC----------SISKALIPFTLFNWLLFATSFGLFLGYSF
>Q5AKB6_CANAL
TASIIRGSQVVVTTIIFAVSIK--ALAVLGIYYD--------------------KSKPTFYITVVAALDIIYFCYTL---
-------------------XXXXXXXKNS-SPSIIPTASEFILYTLNLAASCISTINSP---------------------
TVLCDEFXXXXXXX------------LC----------HIHQCLHGFSVTNWVLFTISF-MMILYCT
>I1RLV3_GIBZE
WIVIIRGFQFLFSLIIVGLCGW--MIHDA-------------------------GLPENSLCIAIAVLSWIVILYSL---
------------------XXXXXXXLRSL-YHIIAVLCLDALMLVLWLAAWAATASRRA---------------XXVVXX
XXNCY--SDGXLIDSK----------NCSVFYKRDGENAILAAIAGLGALVWVLFIVTF-VWSLIMF
>C7YJD0_NECH7
WIMIIRGFQFLISLIIVGLCGR--MIHDA-------------------------YLDEEGFSLAVSILTWLAVAYVV---
------------------XXXXXXXLRGA-YHILAVLIVDGLLIIILWLAAWAATASRRS---------------XXVVXX
XXDCY--DDGXVVNSK----------SCDVVFKRAIHDAMLSSIAGLGALVWVLFIATF-VWTLLMF
>C8VBX0_EMENI
TKNLIHGLQGFLIFLGWALTIA--VFTKGGX-----------------------IDGRTAYYFALCWFSIPGLIYLV---
------------------XXXXXXXXRRF-GNVYAFATVDCLYVLLWFIAWVCIASYVA-QGKSEXXXXXXXXXXXXXXX
XXGCDNWXXXXXX-------------KC----------HVSTATCIMGVAIFILFLITA-WMSFRNV
>C7YUH0_NECH7
LKLGLHSFQVIFSFVAWCLQIG--VFNAKDAK----------------------VTGKNGWTFAVCFLSVPAWIFLI---
------------------XXXXXXXXRRF-AQPHAMLAVDALFTVMWLSAFATQASYNA-EG------------------
--SCG--K------------------AC----------GISKGVVGLGVLTTLLFAATT-FVSAFTL
>E3JZS8_PUCGT
SWISXXX-----------------------------------------------IRDRLRFLLFTSCWCLLFIPIYL---
----------------------XXXXXXX-XSVLSNVGFISLTWLFWLCGAASWTDALG--------------------X
TLHCG--DLFXRXXXXXXXXX-----YC----------GSLRAVQAFAWMIWLLFSAAL-LYISTVA
>A8N438_COPC7
ADTAVRRSIVLFSIIEMCIAAW--LTARYNSRHDYPXXX---------------VRARVRYILFCSVWTIVVGSLFL---
----------------------XXXXXXXXTSVAAHFIFLFVTFILWLAAAAAITSSLG--------------------X
GLSCSHQXXWA---------------YC----------GQLNAVEGFAWLIWILITFTL-IMVIIRG
>Q5KIU4_CRYNJ
VSTHIRRALLLFAIIEGCITAY--LVAQFNDDDTYPXXX---------------YRDRLKFLVFTSWWTVVFAAAYM---
----------------------XXXXXXX-XSIASHLAIWTVTWIFWLAAAASYTAALG--------------------X
GMRCSVSXXX----------------HC----------SSLVAAEAFAWIEWIIMTIFF-IFLLTIA
>Q07629_YEAST
FLTLLRFSQFASSVLVMSLLAY--AIHAYGNR----------------------GNKKTNFTLATGVISVFYLIA-----
----------------------XXXXPTL-IYIGMYFCAELIVCMLWLAAFVVLAKAQG---------------------
ERSCSNTXXXXXXXXXXXXXXXXXXXAC----------NSSQAAIAFSGLCFVLFLISV-ILLGINV
>A8N490_COPC7
IRTIIFGISLLFTLIALGTSAA--FIAFVDKGAKALXXXXXXXX----------VGSFAHLVLATSVITLISVPLLY---
------------------XXXXXXXXXXX-AQIFVELPSICIIWILWIASAGQTAQFEP-------------------XX
LTGCS--SSSXDFGXDSXDQGPT---TC----------HEGRAMMAFSFLNWLLFMSYAFILALYVF
>Q4WC24_ASPFU
IPSALLGVAFVFAVIELGLGGH--IASISTGSRKIPFYDPXXXXXXXXXXYS--VPGIVAFQIFTSVWTMLVSVA-----
--------XXXX-XXXXXXXXXXXXXXXX-IITGALGGAYFVTMVFWLACFADIATKLDEXXXXX---------------
--------------------------------------DYYNAVIAFAVLSWLVYFLHTHVLAILGI
>D5G7L5_TUBMM
ALLLLRISQLVLGATILGICAY--FAPNY-------------------------DDWLIPFDIVLSAFTLVWVAVVL---
----------------------XXXXASR-LLPLIVTMVDLVLAVFYIVSIAITADSYS-------------------XX
GNSCA--FLLSQPNMDEAAFR-----DC----------GELEAGFRVLITQTLTFLGAI-IWDGVVL
```

```
>E1ZFT0_CHLVA
PHFWLRVAQVVFGIIAFAPVAEGAXXXXXXXXXXXXXXXXXXXXXXXXXXXX--FSSKIRYTMFVGITGFIIAFFML---
--------------------XXXXXXXXX-ARGIIALVLDALWVVFWLAAAASMSDIVADXXXX----------------
--------------------------------------SNIKASCAFSWIAWFLWIGSL-VISVMDW
>E9CJG0_CAPO3
PRGFIRIIQLIFAIIAFAAAAS--EECGXXXXXXXXXX----------------EKDRFAFFIATGVIAFLFDLAIL---
--------XXXX-XXXXXXXX---------VTVMAELGFTALWSFFWLLASSLLADTVKDXXXXX---------------
--------------------------GCEP--------SSWQAAVVFGFINLICWVANI-YYLFKET
>C1L5K7_SCHJA
PRGFIKVIQMLIAISAFATTCD--------------------------------YSSAAQFYVFTGVLTMLYCAG-V---
--------XXXX-XXXXXX-----XXTDS-RFSKYEFIVSASIALLWFIASCAWADNVN--------------XXXXXXX
XXICN--XXXXXX-------------NCKATEQATY--GGLNASLIFGFTNVALWAAGL-WFIWKET
>K1RPP1_CRAGI
PKGFIKVIQWILAIFAFATTTS--------------------------------SRSSAEFYVFFGVMVFLYCIA-A---
--------XXXX-XXXXXX-----XXRSN-VWSIVDFVISAVITLLWLVSSSAWAQGLV-NLKY-XXXXXXXXXXXXX--
--TCS--XX-----------------NCVQTEFPNF--GSLNASVIFGFLNMLVWGGNL-WFLYKET
>D1LXF4_SACKO
PRGFIKFLEFILAIFAFATTAG--------------------------------PSSSAEYFVAVGVLAFLYCIV-A---
--------XXXX-XXXXXX-----XXDKD-LLPLGDFVMTCIFVLLWLTGSSAWAKGVT-DVKY-XXXXXXXXXXXX---
--ECS--LESV---------------TCTLVKSPSY--ATLNVSIVFGFLNMFVWAGNV-WFVYKET
>H3IJM3_STRPU
PRGFLRAIEF----------------------------------------------------------------------
-----------------------------------DLVFTGVFVLLFFISSCAWAAGLN-DVKY-XXXXXXXXXXXXXXX
--TCT--APX----------------TCESVTSPKY--SSLNFSVVFGFLNTIVWGGNM-WFIAKET
>E5S0X4_TRISP
EAGAXXXXXXXXXXXXXXXXXX------------------------------XXXXXXXXXXXXXXXXXXXXXXXXX---
--------XXXX-XXXXXXXXXXXXXXXX-XXEGADFVVTAVLAVFWFIASCAWASGVN----XXXXXXXXXXXXXXXXX
XXPCK--XXX----------------SCHFTPHWNY--AALNVSLIAGFACFFLFASNL-WFIWKET
>E9CAE7_CAPO3
PRVFLYIIVWFLAMISFGCVAG------------------------------SSWKSSGVFMVAIGVIVFIWAFV-M---
--------XXXX-XXXXXXXXXXXXX--------IELGVNIAMVFLFIIASAVWAKTVS-DIGDXXXXXXXXX-------
--------------------------------------TTWRAGAAFGFLSTFALLALA-VFIALSI
>E9CJ08_CAPO3
PTFILSALNWLFAIIVFGCIAD--------------------------------DDNACGYGIAIGVIAFIAASL-F---
--------XXXX-XXXXXX-----XXXQK-FLTLFTLGFSVLWTFLWFVGFCYLTDKWV-KFXXXXXXXXXXX-------
--------------------------------------NNAQAAIAFSFFSIITWAAFS-FLTLKKW
>K1QGZ9_CRAGI
PQVILRIASTLFAVIVFGCILG--------------------------------DPNACGYGTGIGIIAFLLCLG-F---
--------XXXD-XXXXXXXX---XXYRK-YVVLADLAISGLWTFLWFVGFCYMADAWR-RTXXXXXXXXXXXXXXX---
--------------------------------------DNIRAAIAFSFFSILSWGGIT-FFAVRRY
>H3HWE3_STRPU
PSVILRFISWVFAIIVFACISA--------------------------------DSGACGFGIFVGVIAFLACMV-F---
--------XXXD-XXXXXXXX---XXHRK-MAVMADLIFSGIWTFMYFVCFCYLTNKWV-GT-----XXXXXXXXXX---
--------------------------------------SSVQAAIAFSFFSIITWLAFM-KF-----
>E5SAH1_TRISP
PRCILRA---LFAIIVFGSISS--------------------------------SNFSCTFGNGLGILSFLMCIG-M---
--------XXXD-XXXXXXXX---XXTRK-RVVVGDLASSGIMTFLWFIAFCTLANKWS-SMXXXXXXXXXXXX------
----------------------------------------CEAAIAFSFFSTISWAGLA-FLGWKRY
>F2UP45_SALS5
PATILRMLEILCAIIVFGVIADNGXXXXXXXXXX--------------------NEDANGLGIAIGVMAFIAAS------
--------XXXX-XXXXXXXXXXXXXNQR-VVSIAVFGLDAFFSLMWFITMIVLAAEWG-KVXXXGXXXXX---------
--------------------------------------NAGNSAVAFSVFSWFLWMGSA-FFSFRKM
>A9V9T9_MONBE
PATILRIVELIFAIIVFGTLADNGXXXXXXXXXXXXXX----------------KMPPLNFGIAIGVLGFLDATAWL---
-----------X-XXXXXXXXXXXXXYKP-TVNYVRIGLDFFFSLMFMIAGAALAAQWN-KVXXXAXXXXXXX-------
--------------------------YL----------NAARTAIAFSFFLWLLYIASA-YFSYTEL
>J9FDD0_WUCBA
PAVILRIFALVVGLAQWIAVSR------------------------------ANSSSTCSFGSAMGFFAVLSSLG-L---
--------XXXX-XXXXXXXXXXXXX----RAVTTDMILSGLLTMLLFFRSHX---------------------------
--------------------------------------------IESFFMTTETFISPE-NIGYVRY
>E9C369_CAPO3
ARIVLYAVAFLLSIIVLASIDL--AYNAWDLPRDIGXXXXXXXX----------EREACDYALAIGAIYLVVSAVFL---
---------------XXXXXXXXXXXXMR-ILQMIELGLSAIAVVLWLAAAALITDGTK---------------------
-XLCD--NF-----------------DCDSEVDVSGTSTKMHTAEGAAWVALIVWIALT-VLNALQL
>S2JPE5_MUCC1
WRFWFRFVILLASIGHLGFAAG--------------------XYSGEDVPFY--TSACFYYLFAVAILSIIYSIY-HVFF
YCYR------------------XXXXKPK-MNRPIMFAIDLLMAVLWGIGVIVEVAKFR---------------------
---CT--DGG------------K---FC----------SFYNVSIFWGFLAFAAYILAV-FWDVWGA
>M1VAW8_CYAME
SKTLLYLCEFTWAIVVFGVTAN--SLYNGSQXXXXXXX----------------STALCRYAIALGVIGWVLVLILS---
--------XXXX-XXXXX--------XXI-LPPVYEMIVQLFLMVWWFIGSVVISASLGSXXXXX---------------
--------------------------------------VSINTVIAFSWMLFVMHLVHS-GICLWQW
>P0DI72_CHLAT
PRFILLIIEWVFALVAFAVMGH------------------------------DDRRSSFEYLTAICILVWLVVMIYM---
----------------------XXXXXXXALPPLIEAAIFLLFAILVFIAFLVTAVK-----------------------
---CNNSXXXXXXXXXXXXX------VCEGE-------SEPKAAAAFAFLLGLLLAGSS-VLGCIAF
>A4S8B7_OSTLU
```

```
PKFRALLVESLMALTTFSFMAK--QTEGLAGPELSTLNDCXEXXXX--------KFYQFKGVVGVYAGFWAYTVILI---
----------------------XXXXXXXAPPPGTEFASYALFTAAMATFVVMSITE-----------------------
---CA--SVVXSSDYY----------VCKNA-------DYSLVSLIFAAATIVLNCLTC-AFAWRQW
>Q00U99_OSTTA
RDYCFHNDLQVLSVTAFAFMAR--QTESLAGPEMETLNNCXVXXXX--------SFYQFKGVVGVYAAFWVYTVLLI---
----------------------XXXXXXXGPPPGTEFVVHALFTLCMIAFVSLSVIS-----------------------
---CT--STVXESDYS----------VCKNA-------AYAKASLVFAALVVVLNCATC-AFVFKQW
>C1N652_MICPC
PKFRLIAVQCLFALTAFATMAG--QNKNLAGPDAMTLEECXPXXXX--------KFAVFQFLVVICVTYWLFTMLWM---
----------------------XXXXXXXVPPAGTEFMIYAVFNVLILIAFSTSWTE-----------------------
---CN--ETIXDPTYP----------VCKRA-------TGAKASIAFAMFTWLALCVSM-MFTWKEW
>C1EI34_MICSR
PKFRLIAVQCLFSITAFAAMLS--QRHGLAGPDEMTLEECXPXXXX--------KFSNFKFLIAVCIIYAVFSLVVM---
----------------------XXXXXXXVPPPVTELTAYTVMNVLLFAAFAMSATS-----------------------
---CN--ITIXDPVYP----------VCKRA-------TSAKASIAFAFFTWLAVCFSM-LFTYKEW
>P0DI73_CHLAT
PKFRVTFAQWVCSLLMWSLMAS------------------------------YSKHGEFKFVVVFGLVMWGLASTYL---
--------------------XXXXXXXXX-LAPIVEFWANVAAGSLAFICLVLASAT-----------------------
---CN--RAVXEPQTK----------VCSGE-------LKPKASAAFAFLLLCAYGGLA-YLSWRTW
>F0YFA3_AURAN
AEPVLRFAELAASLLSWTLMAS--AYRGNYDGLYEYX-----------------NYTPLNFLLATALLQSLFVVA-----
--------XXXX-XXXXXXXXXXXXXXXX-XXXXXXX----VGIVLGFVAGAASSTQLX-----------------XXXX
XSVCE--PHGVSHGXXXXXXX-----FC----------GHVDAAVAFAFFAAAAAGGSLYVLKSRGL
>F0Y3N5_AURAN
EIPSIRLLMVVLSLLSFWVMAAAEXXXXXXXXXX--------------------FYPSLTFFVWVGVLSFVYTLGMA---
----------------------XXXXXXX-LRRQLETAGPPVLAWLTYTAAIAASATSTDLHXXXXXXXGXXXXXXXXXX
XXX-----------------------FC----------GHVVTATVFMYGLCAAYVGVV-VSSVYGG
>I1BYX0_RHIO9
---------------------------------X--------------------GKPAPNYTLFVAIISLPIPFF-L---
--------XXXX-XXXXXXXXXXXXXXFC-LKNRTNLIFCGFNSFLWATAGIATAVYAN--------------------X
ASACT--VDPXIQEXYGDSYVSXWGTQC----------NLAKVAAAFAWITCIIWLSTL-LCTLISF
>I1BH89_RHIO9
AKKVLHLVTLATTLLTICVVAPMIXXXXXXXXX---------------------GKPGPNYTLFVSIISLPIPFF-L---
--------XXXX-XXXXXXXXXXXXXXFC-LKNRTNLIFCGFNSFLWATAGIASAVYSN--------------------X
ASACT--VDSXLREXYGDDYVSXWGTQC----------NLSKVTAAFAWITCIIWLSTL-VCTVLSF
>D6RM15_COPC7
PVIVAHSTQIFFNFLAMACFASVAXXXXXXXXX---------------------PSGLSGFAIFVSIAGMLLSAF-M---
--------XXXX-XXXXXXXXXXXXXXLL-KEVRVSFILTGTGTALNLLIAFITIISAF--------------------X
QAGCK--DPEXDPNXEEXXXXXXXXXWC----------NTKKAGSFFFLFAFFAWTASL-VLLIMEW
>Q5KF55_CRYNJ
SHIILHSAAMFFTFIAVCTMGAVAXXXXXXXX----------------------VSGGTGFVLFLLLLSFSLTVI-L---
--------XXXX-XXXXXXXXXXXXXXFL-AQTRSTLILHAFGTFLMLLAAFIVTISAW--------------------T
EKGCK--NSSXDPHXDLXXXXXXXXXWC----------KTKKASAIFDWFSSIAWSILL-VLTIITF
>M7UBK4_BOTF1
VPLIFRLIVLITSMIALSIAAS--VHHLSNKYSYS-------------------QSPSTTMAIVVDVIAIPYTLYMT---
---------------XXXXXXXXXXXRAP-KAKIRLVLLDLFFIILEASNLTLAFDAIS-------------------XX
XXSCK--VGNXGYNGV----------VC----------HRAKTLCAIITIALLAWGMTF-AVSIFRL
>A7EWT4_SCLS1
VPLIFRLIVLITSIIALSIAAS--VHHLSNKYSYS-------------------QSPSTTMAIVVDVIAIPYTLYMT---
---------------XXXXXXXXXXXRAP-KAKIRLVLLDLFFIILEASNLTLAFDAIS-------------------XX
XXSCK--VGNXGYNGV----------VC----------HRAKTLCAIITIALIAWGMTF-AVSIFRL
>G2YUJ4_BOTF4
VPLIFRLIVLITSMIALSIAAS--VHHLSNKYSYS-------------------QSPSTTMAIVVDVIAIPYTLYMT---
---------------XXXXXXXXXXXRAP-KAKIRLVLLDLFFIILEASNLTLAFDAIS-------------------XX
XXSCK--VGNXGYNGV----------HC----------SRGE-------------------------
>Q5AKB5_CANAL
FTGFFRILQFIFNIICLALCAA-----------------------------X--FRPAKAFALGVSSANMIYNIYTL---
--------XXXX-XXXXX------------TFAVLILVAELAFPILYLTSCIILVVKTK-AXXXXXXXXXXXXXXXXXXX
XXXXX--XXXXXXXX-------L---VC----------SFWFGFTCFAFFKYTYXXXKS-LFEVYVF
>H3GEF8_PHYRM
IPMAVRVLTAVLAVIATGTAGS------------------------------FRSGNQVYFLMVIGALVVIAFTLRV---
--------XXXX-XXXXX----------X-PSPRALVMFDAVWMLFTFACAVAVAAAPV--------------------X
XXVCS--GVDXXXXXXXXXXXXF---KC----------SNIVTAIVTMFMASVCIVFDI-LFTTGAI
>Q7RY36_NEUCR
TFLVMRALQFAALIAVIGLSAN--FIDEFSTKSLG-------------------SPSELLGTLVVAVIAVIYVVISY---
--------------------------XXX-YDAMLPYLLSGILDGLLLIAFIVVASLLG------------------XXX
XXQCA--LMPXDPDANNFWTSXXFTXTC----------FETKAIWGLSIALCVLFAFSS-IVCVGLW
>H3ELT8_PRIPA
WRCIVKGAQLLLGAAILGLVLG--PMRATSLXXXX-------------------TTTRTEWQGVVVGXXXXXXXXXL---
--------XXXX-XXXXXXXXXXXXX--------VDAHASIVGFILYLLAACIESYYAX---------------------
---CY--PXXXPXLN-------L---VCHR--------XEWIIATILCFINVILYVIDF-ILAWMAG
```

Dataset 2. Data model 2: CASPL and outgroup (stramenopiles, algae) (fasta format).

```
>A2Y2B7_ORYSI
MNAVLRLAAAAAAATAAVVMVTYTPSFIFFVVAYAVAAAYSLLLAALSRLALTTDVVLGMVLAGAVASAGAI
SDCYCNHVMAALIAGFVALAVHFVVVMYSLHIV
>B6SZU6_MAIZE
ISAVLRLAAAGAAAAAAVIMVTYTPSFVFFVVAFAVTFAYSLLVLTASRLVLLSDVTVGMLLTGAVAATGAI
SQCYCGHVMGALIAGFVSLLLYFLIIMYSLHAV
>Q9LR57_ARATH
GGLVLRFAAFCAALGAVIAMITDLAAFKYFVIANAIVTVYSFLLFLLWKFVVVLDLMVTMLLTSSLSAAVAV
AQCFCDQITGALIAGLVALVLYVFLLIFSIHHV
>D7M2M8_ARALL
GGLVLRLAAFGAALAALIVMITDMAAFKYFVIANAVVSVYSFLLFLLWKFVVVLDLVMTMLLTSSLSAALAV
AQCFCDQITGALIAGFVALVLYVLLLLYSLHSV
>B9N5U6_POPTR
LSLLLRLIAFGATLAAVIIMATDTPAFKYFVIANAIVTVYGFLLFPLWRLVLALDLVFTMLLISSISAALAV
AQCYCNQVTGALVAGFIAIITYIILLLYSIYTF
>B9RW00_RICCO
FTLLLRLIAFGTALVAAIVMATDTPAFKYFVIVNAIVTVYSFLLFLLWRLVIVTDVVFTMLVTSSISAAVAV
AQCFCDQVTGALAAAFISLITYAILLLYSIHTV
>A7PJ32_VITVI
CFLVLRLLAFGATLSAAIVMATHTPAFKYFVIANAIGSAYSLLLFSLWPLVIASDVVITMFLTSSISAALSI
AYCYCNHVTGALAAGFIGVVLYMVLLQYSIYTK
>A7R333_VITVI
ITTLVRLLVLGAALSATIVMVTNARAFVYFAITNAIASGYSFILFPLWHLVFLLDVFMTLLLTSSISVALAI
ADCFCDHVTGALIAGFSAAVLYLVLLLFSIHAV
>B9RZ92_RICCO
FSTILRFLALAATVVAVIVMIRNTPAFKYFVIAEGIASVYTIIIFLLGRLIVILDMVTTVLLTSSISAALAI
AQCFCDQAIIALVAGFVAAIVYFMLLLCSLHAV
>B9H2V1_POPTR
FTNFLRLLALAATVVAIVFMVTNTPVFKYFVIAEAIAGGYIVIILLFWRLLVILDMVTAVLLTSSISAALAI
AQCFCDQVTIALIAGFAAAIIYFVLLLCSLYVV
>A2WMK7_ORYSI
VAVVLRVAAAGAAAVAAVLMAMYTPSLVFFVAANAAVSACSLVLLLAARLLLMADVVLGMVLAGAFAAAGAM
AECFCDRVRSALVAGSATIVLYYLMLMYSIYTL
>D7LIN7_ARALL
FDFLLRLAAIGVTIGAASVMYTDLPAFQYFVIAVAIVASYLVLLPAPRLILLIFDTLVVTLNTSAAAAAASI
VYCFCQNVSTAVVAASIAILFFIVLIIISAIAL
>P0DI49_RAPRA
FDFLLRLAAIGITIGASSVMFTDFPTFQFFVIAIAIVASYLVLLPAPRLILLISDTVVLTLTTAAAAAAASI
VYCFCQTASTAVVAASISVAFFVLLIVISAIAL
>P0DI45_RAPSA
FDFLLRLAAIVTTITASSVMYTDFATFQFFVISIAMVASYLVLLPAPRLILLISDTVVVTLTTAAAAAAAAI
VYCFCQAVSSAVVAASIAVVFFIILIVISAISL
>P0DI55_LOTJA
VDFVLRLGAVAAALGAATTMATSFTTFQFFVITMALVGCYLVLLPGPKLFLIILDTVFLTLATASAASAAAV
VYCFCAQTSGAVVSSLVAVVVFVLLIVMSALAL
>C6TFL9_SOYBN
MDFILRLGAIAAALGAAATMGTSFTSFQFFVITMALVGGYLVLLPGPRLFLIILDTVFLTLTTASGASAAAI
VYCFCAQTSSAVVSSFVAVVVLVLLVVLSALAL
>C6TH93_SOYBN
LDFILRLGAITSALGAAATMATSFSTFQFFVIAMAFVGGYLVLLPGPRLFLIILDTVFLTLATSSAAAATAI
VYCFCQEISGAVVASFVAVVLFVLLIVMCAVAL
>D7LAP2_ARALL
FDFLLRLAAIVAALAAAATMGTDLPTFQFFVIAMALVGGYLVLLPAPRLLLLVLDTAVLALNTAAASSAAAI
SYCFCQKSSGAVVSAFISVVFFTILVVISGVAL
>D7LZ50_ARALL
FDFLLRLAAIVAALAAAATMGTDLPTFQFFVVAIAIVTGYLVLLPAPRLLLLVLDTAALALDTAAASAAAAI
VYCFCQKTSGAVVSAFASVTFLAILVVISGVSL
>P0DI46_RAPSA
FDFLLRLAAIVAASVAAGTMFTDLPTFQFFVIAMSLVSGYIVLLPAPRLLLLVLDTAVMGLTMAAASSAAAI
SYCFCQKTSGAVVSSFVAVVFFMILVVLSGVAL
>B9IIR4_POPTR
FDLVLRLGAVVTALAAAATMGTDLPTFQFFVIAMAIVSGYLVLLPGPRLLLIILDTVALTLNTAAAAAAVAI
VDCFCQKASGAVVASFIAAGVLLFLIVISALAL
>B9HBX2_POPTR
FDFILRLAAIATALAAAAAMGTDLPTFQFFVIAIAIVGGYLVLLPGPRLLLIILDAVALTLNTAAGAAAAAI
VYCFCQKVSGAVVASFITVVIFVFLIVLSAFAL
>P0DI43_THECC
FDFLLRLGAIIAALAAAATMGTDLPTFMFFVIAMALIGGYLVLLPAPRLLLFILDIVALTLTTAAGAAAAAI
VYCFCQEVSGAVVASFVTVVVLMSLVLLSGVAL
>B9SX12_RICCO
FDFILRLGAVISALSAAATMGTDFPTFQFFVIAMGFVGGYLVLLPGIRLLLLILDTVALTLNTAAAAAAAAI
VYCFCQKVSGGVVASFVSVLVFLLLVVMSAVAL
>B9SX13_RICCO
```

```
FDFILRLGAIAAALGAASTMGTDFPTFQFFVIAMAMVAGYLVLLPGPRILLFILDTVALTLNAAAGAAAADI
VYCFCREVSGSVVASFASVVILMVLVVMSGLAL
>P0DI61_CUCME
FDFVLRIGVLASALAAAAAMGTDLPTFQFFVVAMAVVAGYVVLIPGPRVLLLILDSVALTLNTAAAGAAAAV
VSCFCQQASGAVVGSFAAVLLFLLLILFSALSL
>P0DI30_TRIPD
FDFILRICALAAALAATATMGTDLPAFTFFVVANGIASGYLVLLPAIKLLLIIFDTVMVAFTAAAAAAAAAI
VYCFCQRVSGAVVASFVAAVILIFLVVLSAVAI
>P0DI53_MIMGU
FDFILRICALAAALAATATMGTDLPTFTFFVIANAIASGYLVLLPGVKLLLLILDTVLVAFTTAAAASAAAI
VYCFCQRTSGAVVASFIAAAIFIFLVVLSAVAL
>A7QF77_VITVI
FDFILRLSAIGAALAATTTMGTDLPAFSFFVIANAIASGYLFLLPGARLLLVICDTVMVALTIAAAAAAAAI
VYCFCQSVSGAVVASFIAAVLFMLMIVLSAFSL
>A7PP95_VITVI
FDFLLRLAAIAATLAAATTMGTDLPAFMFFVVATAIASGYLALLPGIRLLLIISDTVMLALTTAGAASATAI
VYCFCQSVSGAVVASFIAVVIFMLLVMMSALAL
>Q1W3A5_STRAF
FDLILRISAATAALAATIVMGTDLPTFTFFVVGMAIVTGYLILVPGPRFLLIVCDTVTAVLATSAAGSSAAI
VYCFCQRVSGAVVAAFVAVVC----------SS
>P0DI31_TRIPD
FDLILRISAATAALAATIVMGTDLPTFTFFVIAMAIVTGYLILVPAPRILLILCDTLTVTLATSAAGASAAI
VYCFCQRVSGAVVAAFVSAVLLIFLVVLSAIVL
>P0DI52_MIMGU
FDLILRISAATAALAATITMGTDLPTFTFFVIAMSIVTGYLVLVPAPRLLLILCDTLAVTLNTSAAGASAAI
VYCFCQRTSGAVVASFVAVVLLIFLVVLSASAL
>P0DI50_TOBAC
FDLILRIAAFASALGAAVAMATDLPTFTFFVVAMAIVVAYLVLVPVPRLLLIIFDTVIIALTTGAAGSSAAI
VYCFCQRVSGAVVAAFVTVVILIFLVVLSASAL
>P0DI51_MIMGU
FDLILRVSAATSALAATITMGTDLPAFTFFVIALSIVTGYLVLVPVPRLLLIVCDTLTVTLATAAASSSAAI
VYCFCQRVSGGVVXXXXXXXXXXXXXXXXXXXX
>P0DI60_HELAN
IDFILRICAIAAALAAATAMGTDLPAFTFFVIANAMAGAYLVLLPGARLMLLVFDTVAVPLVTAAASAAASI
VYCFCQRVSGAVVASFITALLFVVLVAVSAVAL
>P0DI62_CYNCS
FDVVLRLAGIATALGAAIAMGSDLPAFTFFVIANAITAAYLALIPAPRVLLIFLDTVMVALTTAAAGGTASI
VYCXCQKVSGAVVASFLTVVVLMLLIVLSAFAL
>P0DI32_TARKO
FDVVLRIAGIAAALGAVIAMGSDLPVFTFFVIANAITAAYLALIPGPRVLLTFLDTVMVGLTTAAAGGAASI
VYCFCQEVSGAVVASFITVVVLMFLIVLSAFSL
>B9SCX0_RICCO
FDFVVRLCAIATGLAATGIMGTDLPTFMFFVFANGIASGYLILLPVPRLLLIIFDTVVMALTIAAASAAAAI
VYCFCQQTSTAVVASFITAAMLTFLIVLSAFAL
>B9HQ42_POPTR
FDLTLRLSAIAAGFAATSLMATDLPTFLSFMIVNAITSGYLVLLPGPRLLLIIILDSVMMALTTSAASASAAI
VYCYCQQVSNAVVASFLAAALLLSLVVLSAFAL
>D7LGW9_ARALL
FDFVLRLIAAITAMAAAAKMATDLPTMSSFVIVNSIVGGYLTLLPPPRLFLIICDTAMMGLTMMAASASAAI
VYCFCQGTSGAVVASFIAATLLMFLVILSAFAL
>G7IHF9_MEDTR
LDFILRLGAIGAALGAAVIMGTDFPMFKFFVVANGAAAGFLILLPGPRFLLVIVDLVLMALVVAAASSAAAV
VYCFCQGSSLAVVASFVASVFLACLVVVSSVAL
>P0DI41_VIGUN
LDFILRLGAISSAIGAAAVMGNDFPMFQFFVFANGAAVVFLILLPGPRLLLVIVDIFAMALVIAAASAAAAV
VYCFCQVTSQAVVASFVAAVFLICLIVLSSVAL
>C6T4E0_SOYBN
LDFIIRLGAIGSALGAAAIMGNDFPMFQFFVFANGAAGGFLILLPGPRLLLVILDILMMALVMAAASSAAAV
VYCFCQVTSEAVVASFVAAFLLICLIVVSSVAL
>P0DI56_LOTJA
LDFILRLGAIGAAMGASILMGTDFPVFKLFVVLNALAGGFLILLPGPRFLLLITDLVNMATVIAAASAAAAI
VYCFCQGTSEAVVVSFVAAVFLVCLIVVSTLAL
>B6U045_MAIZE
LDLVLRVAAFGPALAAAIATGTDFPALLFFMVANAIAAGYLVLLPGLRHLLLICDLIIAALLTAAAAAAAAI
VDCFCQRTSGAVVASFLAVLVLLFLVILAAFTI
>P0DI38_BRADI
LDFLLRIAAFGPALAAAIATGTDFPAFLFLMVANAIAAGYLVLLPGLRLLLLVCDTIMIGLLTAAAAAAAAI
VECFCQRTSGAVVASFLSVFLFLLLVVLAAFAI
>E6Y2A0_WHEAT
LDFLLRIAAFGPALAAAIATGTEFPAFLFLMVASAIAAGYLLLLPVLRLLLLVCDTIMLGLLTAGAAAAAAI
VDCFCRRTSGAVVASFLSVFIFVLLVVLAAFSI
>B8ART0_ORYSI
LDFILRIAAFGPALAAAISTGTDFPAFLFFLVANAIVAGYLVLLPGLRLLLLVCDMIMAAMLTAAASAAAAI
VDCFCQRTSGSVVASFLTVVILMFLVILAACSI
>C5YLC9_SORBI
IDFLLRVAAFGPTLAAAISTGTDFPAFTFFLVANAVAAGYLVLLPGVRLLLLLCDVLIMALLTAAGAAAAAI
VYCFCQRTSGSVVATFLAVLVFIVLILMAACVI
```

```
>A2YQB8_ORYSI
IDFVLRVAAFGPTLAAAISIGTDFPAFEFFIVANAIAAGYMVLLPGVKLLLLICDTIMVGLLTAAASAAAAM
VYCFCQRTSGAVIASFLAVFVLMVLIVMAAFTM
>P0DI37_BRADI
LDLLLRVAAMGPTLAAAISTGTDFSAFTFFMVANAVAAGYLLMLPSVRLLLLICDTIMVVLVTAAASAAAAI
VYCFCKRTSGAVVASFLAVLIFILLVFLGACAI
>B6T959_MAIZE
LDLILRFIAIIGTLASAIAMGTDLPTLTFFVVANSIVCAYLTLLPYSRLLLVVLDAAMLALVTPGASAAAAI
VYCFCERISGCLIGSFGAMVMLVLLLLLSAIAL
>P0DI36_BRADI
LDLIFRVIAVIGTLASAIAMGTDLPTLTFFVVANSIASAYLIILPYSRLILIFFDVAMLALVTAAASAGAAI
VYCFCERISGSLIGSFAAMVVLILLILLSAVAL
>P0DI42_WHEAT
LDLILRVIAVISTLASAIAMGTDLPALTFFVVANSIVSAYLILLPYSRLVLIIFDAAMLALVTAASSAATAI
VYCFCERTSGSLVGSFGAMVLLILLILLSAMAL
>A2XU91_ORYSI
VDTFLRFIAIIGTIGSAIAMGTDLPSFTFFVAANAVVCTYLVLIPYSRLFLVFFDTAMLALLTAGASAAAAI
VYCFCERISGSLIGSFAAMVLLVVLITLSAFAL
>C5Y9U6_SORBI
ADVFLRFLSIVATIASAISMGTDLPSFTFFVAANAVVCTYLVLIPYSRLILVFFDAVMLALLTAGASAAAAI
VYCFCERISGSLIGSFAAMVLLIVLIFLSAFAL
>Q6Z2U5_ORYSJ
ADLILRVVAVVAIVDSAIAMGTDLPTLTLFVVANSAVTAYLVLIPYSRLVLIFLDSVMLALVAAVASASAAI
VYCFCERISGPLIGSFAAMAVLLLLVLLSAAAL
>B9I534_POPTR
LDFILRILAFIGTLGSAISMATDLPTFTFFVVANGVVSAYLLFLPNSRILLIILDTAMLGLLSAGASAAAAI
VYCFCERISGSLIGSFIGVVVFILLISLSAVAL
>B9T4E6_RICCO
LDFILRLVALVGTLASAILMGTDLPTFTFFVVANIVVSGYLLLLPNRRIILIIFDTAMLALLTAGASAAAAI
VYCFCERISGSLIGSFVGVAVFILLILMSASAL
>A7PMY7_VITVI
LDFILRLITIIGTLGSAIAMGTDLPTFTFFVIANSIVSGYLVLLPASRIVLIFFDTAMLALLTAAASAASAI
VYCFCERISGSLIGSFGGIILFILLVLLSAVAL
>P0DI54_MALDO
LDFILRIVAFLGTLVSAVTMGTDLPTFTFFVVANSIVCAYLVFLAKSRIILIFFDTAMLALLTAGASAAAAI
VYCFCERISGSLIGSFVGVVVFILLILLSAAAL
>P0DI44_SOLTU
LDLFIRIIAIIATLGSAIAMGTDLPTFTFFVVANAIVSAYLVLLGATRIALIFFDAAMLGLLTGGASASAAI
VYCFCHRTSGSLVGSFAGSVLIILLIFLSAIAL
>P0DKC2_LOTJA
LDFILRLIAVVATLASAIAMGTDLPTLRLFVVASAFASGYLILLPRTRVILIIILDMVMLTSLTAASSAAAAI
VYCFCERISGSLIGSFIAIPLFIMLILFSALVL
>G7L218_MEDTR
LDFILRLIAIVATLASAIAMGTDLPTLRFFVVASAIVSGYLILLPMTRVIFIILDTVMLGLLTAGSSAAASI
VYCFCERISGSLIGSFIAIPLFIMLILLSALVL
>D7M7B3_ARALL
LEFILRIVAFFNTIGSAILMGTDLPALTFFVVANAVVSGYLIMLTNTRILLIVLDVAMLGLLSAGASSAAAI
VYCFCERISGSLIGSFIAVVLLILLILLSAIAL
>P0DI58_LOTJA
MDFILRIVAAIGTLGSALSTGTDLPTFVFFVTSNSIVCGYLVLLAKSRILLVFLDTVMFGLLTTGAAAAGTI
VYCFCERISGSLIGSFIAVVIFMIIILMSAVSI
>C6T4A0_SOYBN
MDFILRIVAAIATLGSALGMGTDVPTFVFFVTSNSIVCGYLVLLVKSRVLQVFLDTVMYGLLTTGASAATAI
VYCFCKQISGSLIGSFIAVVLFIILILMSAISI
>G7JG80_MEDTR
MDFILRIFAAMSTLGSALSMGTDLPTFLFFVTANSIVCGYLALLVKSRILLVFLDTVMFGLLTSGASAAAAI
VYCFCGRISGSLVGSFIAVVIFMILILMSGISI
>C6T1G0_SOYBN
MDFILRIIAAVATLGSALAMGTDLPSLVFFVMANAVVCGYLVLLMKSRILLVALDTVMLSLVTASASAATSI
VYCFCERISGSLIGSYIAVALFIILIMLSLVAI
>G7KGQ4_MEDTR
MDFILRIIAGVATLASAVAMGTDLPSFVFFVLANSIVCGYLALLIKSRILLIVLDMVMMGLLAAAASAAASI
VYCFCERISGSLIGSYIAVALFIIIILLSQSAI
>B8AEC9_ORYSI
ADLVLRFVAIGGTAGSAIAMATDLPTLMFFVVASSVVCAYLVLLPSSRAILAFLDTVMLALLTASASAAAAI
VYCFCQRITASLVGSFAAAVVLVALVFLSALSL
>P0DI59_LACSA
LDFFLRPIAIVGTLASAIAMATDLPSFTFFVVASSIVSAYLILLGNSRVLLLLLDTAAMGLLMAGSAAATAI
VQCFCKRVSGSLIGSYAGVVVLILLILLSGVAL
>Q5NRN4_SOLDE
FDLVLRIVALVGTLASAVAMGTDIDAFKFFVVSNSITCVYLALIPKSRVLLIVLDAIMLVFLTSGASAAAAI
VYCFCQRSAGSLIGSFGAMALMVLLIILSSIAL
>P0DI35_LACSI
MDLVLRLVGIAGTLGAAIAMGTDFRSFRLFVIVNAIVCAYFVLLPGSRILLIIMDTVMLALLTAGASAAASI
VYCFCQGASGSLIGSFGAVVVFILIIILLGAIAL
>B9HI87_POPTR
ADLILRGVAAIGTFASALTMGTDLPSLTFFVIANSIVCGYLVLIPITRIILVIFDTAMVELLTAGAAAATVV
```

```
VYCFCERISGSLIGSFASIIMIMLIIITSAVAL
>B9S8Z3_RICCO
LDLVLRVFGAICTLGSAVAMGTDLPMFMFFAIANSIVCAYLVLLRITRIILVTFDMVMLVLLTCGASAATSI
VYCFCNRISGSLIGSFFSIIIFMLLVILSAVSQ
>D7KBH3_ARALL
LGFVLRLFAVFGTIGSALAMGTDLPTLMFFVVANAIAGGYLVLLPTSRIILLVIDTVMLALVSSGASAATAT
VYCFCERISGSLIGSFCAVILLMLIVINSAISL
>P0DH81_PICGL
LDFLLRLLAIGATLSAAITMGTDLSAFIYFVIANAIVGGYLLLLPSSRVFLIFFDTVMVAVCTSGAAAAVAI
LYCFCNQAIGAVSASFAGVVFLILLVLLSASTL
>P0DH80_PINTA
LDFLLRLLAIGATLSAAIAMGTNLSAFIYFVIANATVGLYLLLLPAFRVLLIFFDTVMVAVCTSGAAAATAI
MYCFCDQATGALGASFAAVVLLILLVLLSASTL
>D2KQI6_BETVM
VDVILRVLLLAASIASVVLMVTNSPAFIYLVAALSVAGLYSIIALKLFWILLIHDVLLLGIVAAATGTAGGV
GYRFCRHVGASIIVSLFAAAVLVLLVFVNANSL
>B9RT03_RICCO
VDVGLRVFLFATTLTAIVVMSTHSPAFIYFVAALSVACLYSIITLKFLFYYALWDVLMLGIVAAATGAAGGV
AYCFCKHVGSALAISLAASVVLVLLIMLSVCSL
>B9HMP5_POPTR
VHVALRFLLFAASVTAVVVMVTDSPAFIYFISALSVAGLYGILTLRFLLHFALLDVLMLGIVASATGAAGGV
AYCFCQHVGSSIAVALFASVLLVLLTMLSVFSI
>A7NW79_VITVI
LDVVLRILLLGSAVASVVVMVTNSPAFIYFVAALSVVGLYSIITLKTILHLAIWDVLMLGLAASATGTAGGV
AYCFCRHVGGSIAVALFASILLVLLVWLSLFTL
>C6SVQ5_SOYBN
FDVILRFLLFAASLVAVVVIVTYSPAFVYFVAALSVTGLYSIITLKLLLYFILWDALILGIIASATGTAGGV
AYCFCRHVGASIAVALFGSVVTVLLIWLSAYSI
>D7MAF7_ARALL
TQVVLRFVLFAATLTSIVVMVTNSPALIYFVVALSVACFYSIVTFILLLNLAIMDAVMVGIVASATGAGGGV
AYCFCRHVGGAIAVSLFASVILLLLSIISVLSL
>D7L5G6_ARALL
IDVIIRVLLFSATLTALIVMVTDSPAFIFFVVALVVTSFYALMTLRVSVYLASLDMVMLGILASATGTAGGV
AYCFCRYIATSLALSLFATLLLLVLSICSALS-
>Q1EPG6_MUSAC
VDFGLRLLLLASAVSALVVLVTHSPAFIYLLVALSVTCFYSIIMVRMLFHLVLSDAVMAGVMASAAGTAGSV
AYCFCRHVGSSAAVSLVASVLLVSLVVLSSYSL
>B6U361_MAIZE
ADLALRVLLFAVTLSGLVVLATDSPALIYLLVALCVTCFYSLLTARTLFLLVLFDVFYAAIMASATGSAGGV
AWCFCRHIGSSVFLGLIASVVLVLLTILNAHSL
>C5X4A5_SORBI
ADLALRALLFAVTLAGLIVLATHSPALIYLLVAQCVTCFYSLLALKTLFLLVLLDVLYAAIMASATGSAGGV
AWCFCRHIGSSVFLGLVASVILVLLTILNAYCL
>Q6YT98_ORYSJ
ANLALRALLFAVSLSALVVLVTHSPALIYLLAALCATCFYSLIAIKTLFYLILLDVFYAAVMASATGTAGAV
AWCFCRHIGSSTFLALIAAIVLVLLAFLNAYSL
>A2PZE5_IPONI
TEAILRLLLLASLVVAVVVMVTQSPAFIYFVAGLSVAGLYTIITLALVSHFIILDVVMLGIVGTATGAAGGV
AYCLCTHLGASLAVSFFAFIVLLLLIILSIHSL
>A9P0A6_PICSI
VDFSLRLLVIGSTFTAAIVMGTYSPAFVFFVIANAVACGYTLLLILSVFLLSVTDLVMVALVSAGVSAAAAI
AYCFCHHGAGAIVASFVSLIIFMVLTVMSTYSF
>B4FAP1_MAIZE
CSVALRVFVLAATLVSAVVMGVYSSAFVYFVVANAMVCLFSAALAAAMVPVMVGDLLALALLYSAVGAAAEF
GICFCERAMAAVIVSLIAAFANLVLLMLNILTI
>Q9ARX2_ORYSJ
CCVVLRVFVLLGTLASAVVMAAYSSAFVYFVVANAMVFAFSAALASAVVPVMVGDLVAMALLFSAVGAAAQF
GLCFCERAMAAVVVALIAAFADLVLLMLTILTI
>C6SZP8_SOYBN
SDLLLRLLAFTVTLVAAIVIAVQMSAIVYFLVTNAIACTYAVLLLGLWTLIAVLDAFMVALLFSGNGAAAAV
GVCFCDQMAASIGVSLIGSLAFLLLVIIPGVRL
>B9HMP6_POPTR
CDLLLRVLALVLTLAAAIVLGVYLSAFTYSVASNAIACSYAALLVGIMSIVIVLDLLMVAMLFSSNGAALAI
GLCFCNQVAVSISLSLLGSILFLLLVGITSLRL
>B9RT04_RICCO
SFLVLRVLAFVLTSTAAIVHGVYLSAFVFFVVSNAIACSYAAIVMSMVPIILTLDLLMVALLFSSNGAATAI
GVCFCNQVAASVVLSLIGSIVFVLLVMLTAFRL
>A7NW78_VITVI
FDLVLRVVALALTLVAAVLLGVYLSAFVYFVVSNAIACSYAALLLGLGLAITVMDLVMVALLFSSNGAAGAI
GLCFCNQVAVALGLSFFGGLAFFLLVVMAAFAL
>D7MAF6_ARALL
VELTMRVLALVLTMAAATVLGVYLSAFVYNISANAIACGYTAIIAKLLMAVLLGDLVMVALLFSGTGAASAI
GLCFCHRAAPSLPLTFLAAVVFMFLVVLDAIKL
>D7MAF5_ARALL
VEITMRVLALVLTMVAATVLGVYLSAFVYNICANAIACGYTAIIMCLLMAVLIGDLMMVALLCSSTGAAGAI
GLCFCNQAAVSVAITLIASVVFMLLVVLDALKL
>A7PTY8_VITVI
```

```
SEFVLRILGLLLTLIAAVVAGVDMSAFVYLVVSNAIACSYAAILVGRVLAVIVLDLHMVGLLFSANGAATAV
GVCFCHHLVASLALSFLGSLSFLGLVLLAILNL
>A7QC16_VITVI
IVLVLRVVAFLATASATIVMGLHTPAFVFFVVANGLASVYNLVLGLRLVIISILDMVIVAVVAAGASSAAFM
AECFCHQGGGALIPSFIALLLLFLISAISIITL
>B9GIE4_POPTR
VLLMLRVLAFFATAAATVVMGLHTPAFVFFVIANGLASIHNLVIMLRLAMIAILDIMTVALVSGGVSAAAFM
AECFCDHGGGALIASFAGLILMLIISVMSIIKL
>B9I0U9_POPTR
VLLMVRVVAFLATAAATLVMALHTPAFVFFVIANGMASFHNLLIMMRLAMVAILDMMTVALVSGGASAATFM
AECFCDHGGAALIASSAGLILMMIISVMSIMKL
>B9SV63_RICCO
VLLMLRFVAFLATAAATIVMAAHTPAFVFFVIANGMGSIHNLVIALRWVTVAILDMLTAALISGGVNAAVFM
AECFCDHGGAAIIASFIGLLLMLVISIISIIKL
>D7MFJ8_ARALL
LLLGLRVFAFMATLAAAIVMSLDTPAFVFFVIANVMVSFHNLLIVVRLLSIAILDMLNATLVSAAANAAVFV
AECYCDHGAGALIAAFAGVILMLLVSSVSISRL
>D7MM00_ARALL
ILLGLRLLAFSATLSAAIVMGLHTPAFVFFVVANAMVSFHNLLIAFRLLSVAILDMLNVTLISAAANAAAFM
AECYCDHGAGALIAAFAGVILMLIISAASISRL
>C6TG62_SOYBN
VILSLRVVAFFATASATLVMAFHTPAFIFFVIVNAIASFYNLLIGLRLGLIAILDVMTMALAATGDGAATFM
AECYCNRGGVALVASFVGLILLLVVTVMSITKL
>B6TUH4_MAIZE
QPVLLRAAAALAAAAAAAVMALDTPAFVYFVIANAIAAAYNLLLLTAGLVVRMLDMVVMALLATGAAAAASM
AECFCRRGGAALAASFVGVALMLALNLLSAASG
>C5YRU8_SORBI
QPVVLRAAATLATAVAAAVMALDTPAFVYFVIANAIAAVYNLVLLMAGLVVHMLDMVIMALLATGAATAAAM
AECFCSRGGVALASSFTGVALMLALNLLSAASN
>A2ZMM4_ORYSI
QPV-VRACVFLATAVAAVIMGLDTPAFVFFVIANAIASGYNLMLVAQSLSVHLLDMVILTLLATGSATAASM
AQCFCNHGGIALMSSFIGVALMLALNLLSAAAN
>Q1EPG7_MUSAC
PGIILRIVAIVLTFISAVVMGAYSAAYVYFVVANVLVFFYSVVLVSMSLPFSIADLLMVVLLFSSNGAAAAI
SVCLCARVNAAIVLSMLASVAYVILVVFGMANL
>B9I3X5_POPTR
AQIFLRIVVIAASFASTWLMLTYSPEFKFLSYANIVVGAFSFVLLTYYFILFLHDLALMSLVLGGCAAATVI
GSCFCKRATTSVAFSYFSLVCLLILTITSASKS
>B9IFI5_POPTR
VQIFFRIVAIAASVASSWLMITYSPEFKFLAFTNIVVGCFSLLLLNHYFFLFLHDLAMMSLVVGGCAAATTV
GFCFCNRAQTSVTISYLNLICLSILTITSASKS
>B9RA90_RICCO
AQICLRIVTIGATLAATWIMVTYSSAFKFFVLANVIACACSVVLLGHVFLLFLHDLLMMSLVLAGCSAATAI
GFCFCNRGTISMMLSYLSMVCLLILTVTSANKS
>A7PHN8_VITVI
AHICLRILTVTATLTAAWMMITYSSAFKFFSYANAIACGCSVLLFMKFFFLFLHDLCMMSLVLAGCAAATAI
GYCYCNRIRLSLMFSYLAFVFILMLTIMSANKS
>A7PA04_VITVI
AQVVLRFFTLAFTGAAIAVMVTYLSAFKFLVGADAVVCGFSMLLINHYFFLYFHDLILMVLSMSACAAATAV
GYCFCDKALASILLSLIGFICLFLLTIMAARNL
>B9RH17_RICCO
AQVIFRILAIAFAVASISAMVTYSSAFRFLVGANAVVCGFSVLLIEKNYYLFLHDMVMMVMMVSGCSAATAI
GYCFCNQALVSIVLAYLALFCYVALTTLAAHKL
>B9GFG6_POPTR
AQITLRFLAIAFTVTAIPVMITQSSAMKFLLGVNATVFAFTALMLINYFFLHLHDMVMTLLLISGCAAATAV
GYCFCHQMLISTVLSYLAFFCYLALNILSVHKL
>D7MGK0_ARALL
VQVSMRVLIIGAAMASMWVMITYSSAFRYLVYAQIAVCAATLFLVGLVFALFFFDLLTTLTAISAFSAAFAE
GYCYCSRVTISLAMSFASFVLLFILTVLTASSA
>P0DH83_MARPO
TIALLRLLAFAATLSAFVTMITYSDAFMWFVVANCIAFIYLLFAIMLVKHLVILDLIVSYMLFSAASAATAV
AYCYCHHVAGALVACFLGWLFLTIAVFLGMRRS
>A9TKY8_PHYPA
LNFIVRLLTAMASAAALTTMVKDFWAFKWFIIANAIVLTYSTLALPLAWLTFLVDFLLANALMSAASTATAI
SWCFCRRVLGALIASYIGWVLLALSTILAATAI
>A9SEY7_PHYPA
LSLILRLLTLGATIAAIVAMLKDFPAFEWFVIGNSIVLVYAALTLKTAWLTFLCDFICSCALISAGSTALGV
AWCFCDYVQGALIATLCGFIFQALSTVIAASAL
>A9STS7_PHYPA
TNFLLRTLTAGATAAAVVVMLIDYPAYKWLIIANAVVFVYSVMAIPSAWLTLLVDFLAASALISAASAALAV
ALCFCDYTQGAIIASFVGFGLLFLSTLLAASAL
>A9TZ63_PHYPA
LNLLLRLLQAFATAAAVIVMLLDYPAYKWFIIANAVVFVYALLTLPSAWLTFLLDFVAASALMSAASAALAV
ALCFCDYAQGAIIASFCGFGLLALSTLLAASAL
>P0DH84_ADICA
WSMGVRLLTTLLCITSLILLLKDTSGFIYLVYINILVAAYGLIFVCSRWTIFVLDQVFAYVLLSAVSAATEV
LYCFCHMVSASVAIGSVAVVLLAVLSVSSAQSL
```

```
>P0DI28_PTEAA
WSIGIRFLTSCVSIASLILLLKDTSAFVYLVFSDILVAVYCIVLVAGQWAIFIFDQVLAYVLLAAASSATEV
AYCFCHTVMASISLSFVAVLLLALLAVVSASGL
>P0DI20_OSMLA
AGVFLRFVASLLSIAGLMLLVKDISAFVFLLYTNGLVAVYCFFALLAGWVTFVLDQGLAYVLLAAAAASTEV
LYCFCHMARASIVVSFLSMLAMAVLSVMSAQQL
>P0DI21_OSMLA
--MVLRIVASLLSIAALVLMAKYVEAFVYLVYSNGLVAIYCFLVFSAAWIIFLLDQGLAYVLLAAAAASTEV
AYCFCNLVGVSIVITFISVLAMATLSVMSARRL
>P0DI25_PTEAA
MEVLLRVLAILLSIAGALVMAKYVEAFVFLVYANGIVAIYCFIVLVLAGLLFFMDQALAYLLLAAAAASTEV
AYCFCNLVGVSLVLTFLSVLVLVTLAILSGKRL
>P0DI24_PTEAA
GELVLRCAATLVCMLSLMLLVRSSTGLVYLVYANGLVALYCFVVLSGAWALFVLDQVLACILLSAASAASEI
AFCFCRMLEVSIATSFIAVIMLGSICVLSAKQL
>P0DH82_MARPO
ASILMRLTAMALCVTALVTMVTNVLALKVFVYTNGVIAGYSLLALARLWTTFFLDQFIVYVLIGVTGAATEV
AYCFCSQVGASVIVCFVAILTLVFLAVLSAKQL
>Q8W4Z5_GOSHI
AETMLRLVPMALGVAALVVMLKDLGAFRYLVHANGICAGYSLLAIPRAWTFFLLDQILTYVILGAAAVSTEV
LYCFCHKATIAVVITFVAVICYAVLSLVSSYRL
>B9GHX8_POPTR
AETMLRLVPVALCVSALVVMLKDLGAFRYLVNANGICAGYSLLAVPQAWTFFLLDQVLTYVILAAGTVSTEV
LYCFCHKALISTVITFVAVIFYAALSLVSSYKL
>B9T3K6_RICCO
AETVLRLVPMAFCISALVLMLKDLGAFRYLVHANGICAGYSLLAISRAWTFFFLDQVLTYVILAAAAVSVEA
LYCFCHKAITSAVITFIVVVCYALLSLVSSYKL
>A7QBZ2_VITVI
VETLLRLVPVALCTVSLVVMLKDLGAFRYLVHANGICAGYSLLAISRAWTFFLLDQVLTYLILAAGAVSTEV
VYCFCQKTTASISITFVTVLCYAVLSLISSYKL
>C6TCJ2_SOYBN
AETFLRLFPVGLCVSALVLMLKDLGAFRYLVHANGICAGYSLFAVPRAWTFFLLDQVLTYIILAAGAVSTEV
LYCFCHKVTASVAITFVAVFCYVLLSLVSSYKL
>C6SYW3_SOYBN
VETFLRLFPIGLCVTALVIMLKDLGAFRYLVHANGICAGYSLFAIHIAWTFFVLDQVLTYIILSAGAASAEV
LYCFCHKVTASTTITFVVVVFYVLLSLISSYKL
>Q8VZQ3_ARATH
AETMLRLAPVGLCVAALVVMLKNLTAFRYLVHANGICAGYSLLAAPRVWTFFCLDQLLTYLVLAAGAVSAEV
LYCFCHRATASVIITFFVVCFYIVLSLISSYKL
>B4FBQ7_MAIZE
VETLLRAAPLGLCVAAMTVMLRDLGGFKYLVYANGLCAAYSLVAFSRSWLVFLLDQVFTYLILAAGAAAAEL
LYCFCRQARTSVAITFGTVLCFILLSLISSYRL
>D7L342_ARALL
VEAVLRVASMALSITGLVIMIKNLGAFMYLVGANGVCAAYSLLALVQVRTLFLLDQVVTYVVLAAGAVSAET
VYCFCHKALISVVFTFVVSLLYMLLSLISSYRL
>D5A972_PICSI
IEPALRFLPVGLCISALALMLKHVGAFRYLAYANGICAAYSVLTFSRAWFVFVFDQAFTYLMLGAGAVVTEV
LYCFCNRVAASLVISFLALLCFIPLSLISAYRV
>A9P1V1_PICSI
FETLFRLLPVGLCISALVLMLKNVDAFRCLAYANGICAGYSLIAFSRSWILFLLDQGITYLMLAGGAVATQV
LYCFCNRAGASVIISFFALVCFLLLSLLSAYRL
>A9NMM6_PICSI
FELLFRVTPLALCIAAMAIMLKDVGGFKYLVYANGICAIYSILLLTRAWIMFILDQALTYLILTAGVCGVEI
MDCFCNDARASVLITMAVLVCFMVLSLLSAHRL
>D7MUY4_ARALL
IDSCLRLSVVPLSVATIWLTVTSIMGLKYMVGVSAISAIYALLTISKAWLFFVPDQVLAYVMTTSVAGATEI
VYCYCSKLTIALGLHVFVLFFFLFLSVISAYRA
>A7P0P3_VITVI
IDCSLRLCVIPLSVATIWLTVTNLTGLKYMVCISGISAGYALVVVNKAWLFFVSDQIMAYLMVTSGAAVLEI
LYCFCSRVNLALALHALALCCFLVLAVISAYRV
>B9HTL5_POPTR
LDFSLRLSVIPLSVATIWLTVTDLTGLKYMVFISGICASYAFIAVTKTWLFFVSDQIVAYLMVTSGTAVLEI
LYCFCYRMKLAVILHALALSCFIILAVISAYRA
>B9SV84_RICCO
LDSSLRVSVIPLSAATIWLTVTNIMGLKYMVCISAICASYAFVAVNKVWLFFVSDQIIAYLMVTSVAAAMEI
LYCFCNGMKTALILHALTLCFFIVLAVISAYRA
>C6T2J5_SOYBN
FDSSLRLCAIPLSVATMWITVTNLSALKYMVLVSALCACYALLAASKAWIFFVSDQIVAYLAITSVAAVMEM
YYCFCSKVKLALILHTITFCCFFVIAVISAFRA
>A2X2I0_ORYSI
AELGLRVCAVPLAVASVWEMATDLSGFRYLVWINAITAAYSVAILRFDWLIFILDQASAYLLLTSASAAAEV
VYCFCGAATVSVALNAAALLCFMALSLISAFRV
>C5XY39_SORBI
PEMALRVCVVPLALASLWEMATDLSGFSYLVGVNAVTAAYALVILRYDWVILVMDQASAYLLVTSASAAAEL
LQCFCGKATVSLALHAAALACFVALALVSAFRV
>D8T2C0_SELML
TDLMLRFAAFVCCTVTMVVLITLAKAFVYLVSAAGIGAGYTLLLVAIAWFIFVFDQLITYVLLAAAAASTEV
```

```
AYCFCHQLGASLVTSLISTVLFAFSAAISAYYL
>D8SJ65_SELML
HSLLLRLVAVVLSILVIAVMVHNSKAFVALVTISAICLGYSFLFICWAWMNFIADQILTYAMLGAAAAAAEL
AYCFCTRAGASIILSFIAVLALANSSAISAYHL
>P0DH65_SELML
VDFLVRIKAFAFCLAVIVLLKNNTKAPVSLLVLASICCGYAFLAVVLAWLTFLLDQVLTYLLLGSAAATAEA
AYCFCDHFAATVFLSFIAVIAFAVSAAISAYYL
>E4MWF4_THEHA
TELILRCSVCALALVAAILIATDMKALVFLVVVNGIAAAYSLLMVPLAWAIFSGDQAIAYLTVAGVAAAAQS
AACFCNQVGEGIATALLASIGMVLISSISAFAL
>D7LIK3_ARALL
TELILRSLVCAFALVAAILVATDMKALVFLVVINGIAAGYSLVAVPLAWAIFFGDQAVAYLCVAGVAAAAQS
AACFCNQVGEGIASALFACIGMVLISCISAFGV
>B9SA89_RICCO
AELVLRCLICGLGVLAAVLVGTDMKALVFLVIANGIAAAYSLLGVPLAWAIFSGDQMMAYLTVAAVAAAAQS
AVCFCNQVGEGIASALLVSVSMVVLSCISAFSL
>A7R385_VITVI
AELVLRCVICGLGILAAVLVGTDMKALVFLVIANGIAAAYSLIGLPLAWAIFSGDQVIAYLTLAAVAAAAQS
SVCFCNQVGEGIVSAVGVSLSMVILSGISAFSL
>D7M9V1_ARALL
TELLLRCSISVFALLALILVVTDMKAVVFLVVANGIAAVYSLLSVPLAWAFFSGDQAMAYLNVAAIAATAES
GVCFCNQMAIGVSSALLASIAMVFVSCISAFSL
>B8LQF9_PICSI
GEVILRFAMIALALVAAVRVGTDMKALVFLVVMNGIVASYSLLGLPLAWLIFALDQTMAYFSLAAAAAAAES
AYCFCHQIGEGLVSTFLVSLSMATVSGMSAYHL
>C5WUP3_SORBI
AELFMRCAACGLAVLAAALLGADMQSLVFLVIANGMAACYSLLGAPMAWAIFSCDQVMAYFTITAVAVAMEA
AMCFCAQAGGAVACAVAASLNMVGISLVSAFNL
>B6TGJ8_MAIZE
AEVALRAVLCGLGALAAALVATDMKAMVLLVAAAAAAAGYSLLAALLAWCVFACDQALAYALLAAVVAALQA
SVCFCRQAGAGVACAVAAAVDAALLAFLSAFNL
>C5YP66_SORBI
AEVALRALLCGLGALAAALVATDMKAMVFLVDAAAVAAGYSLLAAALSWCVFSCDQALAYVLLAAVAAALQA
SVCFCRQAGAGLATAVVAGLAAVLLAFLSAFNL
>Q0IN16_ORYSJ
AEVALRCAVCALAALAAALVGTDMKALVLLVAAHGAAAVYSLLLAVVAWSVFSCDQAVAYALMAATAAALQS
SVCFCRRVGEGLAAAVAAGLAAVLLAAVSAFNL
>D5A8E6_PICSI
TEVILRFAVVIFALVSAIMVGTLLKTLPFLVIVDGILAVYSLLGLALAWTIFCCDQALAYVIFAAAASTAET
AYCYCFKSGAGMINAFLAALCMVFVSGMSVFHL
>Q5K4H9_GOSHI
IEALIRLSTIVMLVLTACLIGLDLRALVGLLYITSLAAAYNLLLCYLAWLRYILDQAVVYAVFAGNLAALEH
SFCFCTQIGGSLLCGFVASLLMFSIASISAFNL
>B9IM09_POPTR
IEAILRGIAILLLVSTACLVGLDLHALVVLVYVDAVAAAYNLLLCYLSWACFVLDQLAAYTTFAAHSAALQH
SVCFCFQIGGALTCGYIASVLMVMISFISAFNL
>A7Q6G6_VITVI
AEAFLRLFAILVLVLTACLLGFDLGALQVVVYVDSVAAGYNLLLGTLPWVCFLLDQAAVYTVFSANTAALQA
SICFCIQVGGALLSGYLASLLMVLLSSLSAFSL
>C6SZ04_SOYBN
GEVCLRVSAILVLVLTACLVALDLNALKILVYVTCAAAGYNLLLCCMAWICFSLDQIAVYMTFAANTATMGA
AVCFCVEIGGALLCGYAASMLMALISTISAYKV
>D7MFW5_ARALL
TEVILRLCIVFFILLSSCLIGLYLLALEAELYINVVVAAYNLVIGNPKWFSYLLDQTAAYVVFAGTSAAAQH
SLCFCFQMGSAIILNYIAAALMVLLSSISAFNL
>B6U8R7_MAIZE
AERVLRAACAAMAAAGALLLGFDVQALWVLIVAAAAAAAYHVALAAVACASFLLDKGCAYMVFATTVAALQA
CFCFCEQAAAGMVCSLLAAAGMAVLSAFSARDL
>Q6ETN2_ORYSJ
AERLLRGGCVVMAATAALLLGFDVQALWVLTVAAAAAAGYQFALVAVAWTSFLLDKGCAYVVFASTAAALQA
CMCFCEQAAAGMLCSFLAAAGMAVLSAFSARRL
>B6SZA7_MAIZE
AEGLLRGACAALAAAAALLVGLDVQALWVLAMAAAAAAGYHLLLLALAWTCLLLDKACAYTTFATTVAAAQA
CVCFCEQVAGSLVLGMLAAVGTAVLSAASARNV
>Q67W83_ORYSJ
TEGLLRGACALLAAAAALLVGLDVQALWVLAMAAAAAAGYHLLLLAIAWLCFLLDKGCAYITFATTVAAAQA
CVCFCEQVAGSLVCAMLAAVGTALLSVVSARNL
>D8ST12_SELML
SIILLRSFLLVLVIISEALMVTLVTGLKFYVDALGVVIGYTVLLLSVAWISFIADSMMGYLLLSGAAVATEI
GYCFCTVYAISVVICFIAALVSFVVVGISAYHL
>P0DH63_SELML
SVLALRALTLVLLVIALALMVSQITGVQYYVGALSVAVAYMFFMLSRAWVTFILDQLIAYLMVSAATVVAEV
GYCYCFIYGFSLVNAFLATIAFLPVVAVSAFHL
>D8S6A8_SELML
ALLLLRLAAMFLSLAALLITVLLVKGLKFFAGAMGIVAGYSFLLARMAWLCFVGDMTASHLCAAAAAVSAQL
AYCYCLVFGLAVILAFLATLAALLVASISSYHL
>C5XIF2_SORBI
```

```
VMVATRAVAMVMALLSMSLMVSFSYSLQFLVAMSTASAAYSLALLRHAWLLFAGDQVFSLAMMSAGSAAAAV
ANCFCDLSAVSIACAFLSCVFLAASAVIDVIWL
>B8A927_ORYSI
VMVATRAVALVMAVLSMALMISFSDSLEYLVGMSAVSAAYCLALLNYAWLLFTGDQIFAYAMMSAGSAAAAV
ANCFCDLSAASIACAFLSCIFLAASAVIDVIWL
>F2EL82_HORVD
AMVAARAAALVMALLSVSLMVSLSDSLQSLVGISAAAAAYSLALLRYAWMLLAGDQVFAYAMLSAGSAAAAV
ANCFCDLSAASIACAFLGCAFLAASAVIDVIWL
>A9NN43_PICSI
ANVGLRVLSLACSLVALVSMASYSDSFEFLVGASAAAAAHSLLLLNHAWLLFAGDQVFAYGMLAAASAAAGV
TNCFCDKAAISIVFAFISSLILGGSAVLDVFWL
>A7P756_VITVI
AHVVLRFVCLLTSVIALSLMATFSDSFEYLVGVSAAVAAHALLLINHAWLIFAGDQAFAYAMLSAGSAASGV
TNCFCDHVAASIAFTFFSCFLLATSAILDVIWL
>B9RQG7_RICCO
MHVILRLLCTITSVTAVSFMVTFSHSFEYLVGVSAAVAAHSLLLLSHAWLIFAGDQVFAYAMISAGAAASGV
TNCFCNHVAVSIAFAFISCLLLAALAVQEVIWL
>B9GGL4_POPTR
MNVLLRVLCMMTSVAALSSMVTFSHSFEYVVGVSAVVAAHSLLLLSHAWLVFAGDQVFAYAMISAGAAASGV
TNCFCDHVAVSIFFTFLSCFLLAASAVQEVIWL
>Q3EB59_ARATH
AMFVLRAMCMAVSTVAVTLMVTLSDSLIYLVVVSSATVLYSLILITQAWFCFVADQIIGYAMVSGGSAALGV
TNCFCDHLAGSIVFALFAFLLLAASSLLDVLHL
>Q1PFB8_ARATH
VQVALRGGCLAASATAMAVMLTFSPSYQYVVGACAGTVLYSLLLCFQAWLCFTSDQLFCYLMMSAGSAGSGV
TNCFCNHVALSLLLVFLSFIFLASSSFFTVLVL
>P0DI26_PTEAA
VDIALRSAVVAFMVVSLSAMFTRSQPFEFLVVVELLICAYAFVFVRCIWVQLAADQVCAYLVLAAAAAAAGA
SRCFCNRATIAIIFTLLAAGASGISVTLDVYML
>P0DI23_PTEAA
ALLLLRLLTFAFSLASLVIMATDFDTYRYVLAACAIVCLYSFAIGMAHWFDFGHDQGFAYLIFSACSGATAV
AHCFCMKAEISIGLAFGAFLFIALSSLLSGYRL
>A9S848_PHYPA
MLLLFRALTFSFSLAAVVVMGTDFEPYRYVLAVNAIICIYSFVTWFQVWFDYGHDQGFAYLLFSANSAGVAM
AQCYCTQARVSIALGFVAFLFLALSSLLTGLRV
>A9T836_PHYPA
IILIFRALTFSFSLTSVIVMGTDFDPFRYVLAVNAIICIYSFVIWFQVWFDYGHDQGFAYLLFSANSAGIAM
AQCFCTQARASIGLGFGAFLFLALSSLLTGLRV
>A9STU1_PHYPA
MLFVFRLLTFSFSLAAVLVMGTDFDPFRYVFAVNAIICVYSFVTWFQVWFDYGHDQGFACLLFSANSVGIAM
AQCYCTQARVSIAMGFGAFLFLALSSFLTGLRV
>B9SR15_RICCO
LILVFRLSTFCFSLASSVFMLTHFDAFRYVFAANAIVAIYSLFMALQVWFDFGHDQVFAYLLLSADSAATAL
AKCFCVQSYIAIALGFAGFLFLGLSSLLSGFRV
>B9HTK2_POPTR
LILVFRFAAFCFSLASAVFMLTNFDAFRYVFAANAIVAIYSLFMACQVWFDFGHDQVFAYLLLSANTAGTEL
ARCFCVQSDIAIVLGFAGFLFLGISSLFSGFRV
>Q9M2U0_ARATH
LILLLRLASFSFSLASAVFMLTDFDAFRFVFVANAIVALYSVFMGFQVWFDFGHDQVFSYLLLSAGSAAAAL
ARCFCLQSDVAIGLGFAAFLFLAFSSCFSGFRV
>Q2QNE3_ORYSJ
VMLLLRLASLCFAVAAAAFAATRAAPFRFLLAANAIVAVYSAFVAMQLWFDFGHDQGFGYMALAAAAAAARE
AACACVQGDIAVGLGFAGFAAVAAAAAASGYRL
>A9RJH1_PHYPA
CSFGFRLSQIVLSLISIVVMCSHFQAYRYLIAVNVCVIFYSTLFTISTWTTYGFDQLFTYLLLSASTSAGTI
ANCFCARADAAVTLSFFTFLVMFSSTALAVYRI
>A9RZ57_PHYPA
YSFAFRFSETVLSLIAIVVMCSHFQAYRYLVAVNVIVFVYSTFFIISTWMTFGFDQLFLYLLLSASTSAATV
ANCFCSKADVAVTMSFFAVLAMLSSTILAIYRI
>A9S1T8_PHYPA
FSLGLRVAEFVLSVIAFSLMASTFTSYSFVLAVNVLVVFYTIGIIIYLFITFGCDQLSAFLLMAAGAAGASV
ALCFCSHAQASVAFTFLSFFCMVISSLLGVYSL
>A9SB31_PHYPA
LSLGLRVSEFVLSVIAFSLMASTFTSYSFVLAINVLVALYAIGIILYLFITFGCDQLSAFLLMAAGAAGASV
AMCFCAHAEASIAFTFLSFFCVMISSYLGVYNL
>D8R814_SELML
AIVVLRVLQFIFSLIAFSVMADSIKSLSYTVAIGVLACAYALALSLYQYATFICDQMSTYFLISAASATATL
IDCLCSRSTASVTFAFLAFLAFSASSVLTGYYL
>A9SHQ9_PHYPA
ISIVLRCLSIMFNVVSLGVIASNSSNMQYLFAINVIVLVYCVVLIPASTITYICDQGLTYMLMAGFGAGVAL
QACFCGKNKASAALSFLGFVCIALSANLNYLRL
>A9SU70_PHYPA
IVLSLRAAQIVFTVVGLGVMGSQVDSYIGVLSLDVIVCLYAIVLVVAAKLTFVFDQVLAYALVATAGAAAGS
ALCICSKGEASVAMSFFAFAFLAATAAVYSVRL
>F2E5T1_HORVD
ARLLLRAFAWLFSLLALVVMATTYPEYNYCLGMSIIALLYATALVAAAVVDFAGDQVVAYSLISGLSAAAPV
TD-FNDSAAAAISLAFFAFLAISLSALISGYNL
```

```
>B9F6Z0_ORYSJ
ARLLLRAVAWLFSLLALVVMASNYPEYTYCLGISIIAVLYTTAVTAAAVVDFAGDQVVAYLLMSALSAAAPV
TD-FTDSAAAAISMAFLAFLAAGLSALVSGYNL
>F2D276_HORVD
CPLALHAAAAAFAFVALVLVASRYQEYMYLLAIAALAFAYSLAALSARLFDFIADQVVAYLLMSALSAAIPI
TN-FTDATAAAISMAFLAFVALALSATVSGYKL
>C5WNF5_SORBI
SPLALHAAAAIFAFVALVLVASRYQEYRYLLAIASLALLYSLAAASARLLDFVGDQVVAYLLMSALSAAVPI
TN-FTDATAAAISMAFFSFVALALSAVVSGYKL
>F2E2E4_HORVD
IVLVLRAGAALLSFVAMALVASRYQEYRYLLGVSVVAFVYSAAALDASFLDFAGDQAVAYLLVTASAAALPI
TI-FTDAIAASIALGFLAFAALALSAMLS----
>Q84NQ7_ORYSJ
IVLVLRAAAALLALVAMALVASRYQEYRYLLGVAVVASLYSALAAAATFLDFAGDQAVGYLLITASSAALPI
TI-FTDVVAASISFAFLAFAALAFSALIAGFRL
>Q5W6M3_ORYSJ
SGSALRVAAWAFSLLAFVVMGAHYEEYRYVVAIGVLAFIYTTLLVVAVLVDFAGDQVTAYLLMSAVSAAIPI
TN-FTDSSAASISMAFFAFLCLALSALVSGFKL
>Q8LE26_ARATH
ASPITRGICLLFSLIAFLIMVSDYEEYRYVLAISIISTLYTAWTFTSILVDFSGDQIVAYLLISAASSAIPL
TN-FTDSAASAISMAIFAFIALALSALFSGYKL
>Q84WP5_ARATH
SALGFRLSEVVLALISFSIMAARYKEYRFCLSVNVVAFVYSSFACLRPLFEFIIDQVLAYLLMSASTAAVTR
VD-FTEMASASIAMSFLAFLAFAFSSLISGYNL
>D7MMW4_ARALL
TALGFRITEVILCVISFSIMAARYKEYRYCLAVNVIAFVYSAFACFHDLFVFSMDQLLAYLLMSASSCAATR
VD-FTQMATASIAVSFLAFGAFAVSALISSYRL
>Q9FNE8_ARATH
ALLGFRVIAFVSCLVSFSVMVSNYKEFRFCLAANVIGFVYSGFICLRHFLEFGLDQMLAYLLASASTSASIR
VD-FPDLARASVALSYVSFVAFAFCSLASGYAL
>C5XTX2_SORBI
TALLARGAAAGLCLAALAVLAANYTQFRYSEAVNVIGFIYSVFFVKRDLFDFTMDQVLTYLLISSSSSATAR
VS-FPSMANGSIAISFLAFAVFAICSLISAYNL
>C4JAF2_MAIZE
AALLARAAAAGLCLAALAVLASNYAQFRYSEAVNVVGFLYSVFFVKRDLFDFTMDQVVAYLLISSSSSATAR
AS-FPSMANGSIAISFVAFVVFAICSLISAYNL
>A3A2W2_ORYSJ
TALVARVAAALLCLAALAVLAANYSQLRYSEAVNVIGFVYSVLFFKGDYFDFFMDQVLAYLLISSSSSATAR
VG-FPKMANSSIAISFMAFLVFAISALISAYNL
>C5XEK4_SORBI
LSVTLRLATAVLSLAAFSVIASHHLQYRYAVAVNVIVCAYSIASFSSYYCSLFLDQALAYLLMSASSAAASR
ND-FNRKITSALWLSFIAFLMLALNALISTANL
>B6UBY6_MAIZE
LLLALRLATAVLSLAAFSVIASRHLQYRYAVAVNVIVFAYSVASLSSYYCSLFLDQVLAYLLMSASSAAASR
ND-FVRKITGALWLSFVAFLVLALNAVISXANL
>O24088_MEDTR
ALLVIRVFAFVFCLIAFSVLGAKWDEFRYSFAANVIGFVYSGLICLQGYFNVAIDQTLAYILMSASSSAATA
AH-FIEMANASVSMSFLAFGAFALASLVSGIIL
>Q3EA54_ARATH
IGLVLRFITMVLCFVSALSLAVSYPELLYCFGVAVIGFVYTSLTFLSDYISFIFDQVICYLLVSSSSVAIAW
IQ-LRNNSIVSVSMSFSAFLVLTLSGLLSGYKL
>Q56X75_ARATH
LLLLLRVLTGVFLVIALIILSTDVYAYRYMLSAAVIGLVYAVILFFNYQLDFYGDKLISYLVATGSAAGFGV
TK-FFSKGYASASLLLFAFICLAVLSVFSSFAM
>Q8GWD5_ARATH
VLLLLRVLTAAFLLITVVLISTDVYAYRYMLSAAVIGLVYAVVLFLTYQFDFYGDKVISYLLATGSAAGFGV
SK-FFSKGYASASLLLFAFVSLAVLSVFSSLAL
>B9SXY8_RICCO
AALILRILTFIFLIASLVILTTDVYAYRYMLATIVIGLAYTVLIAGNLAFDFFGDKVISYILVTGAAAGFAS
TK-FINKGYASASLLLIGFVCTAVLSVFSSYAL
>B9NBE5_POPTR
TALFLRVLTFAFLMVSLVIMTTDFYSYRYMLAAIAFGLTYTILIAGNLVFDFYGDKVVSYILATGAAAAFGA
TK-FFNKGYASASLLLLGFVCTAILSVFSSYAL
>C6T1Z6_SOYBN
VLLLLRVLTFVFLLIALILIAIDIYAYRYMISTIIIGFAYNLLMAGGYLFDFFGDKIISYLLISGSAAGFGV
TV-FMDKANASASLLLIAFLFTAVASTFTSFAL
>A1XGB4_CAPAN
VSLIVRILTLICLLISFIVIATDFYAYRYLIATVIIGMAYTLLIAGFLLFDFYGDKFISYFLVTGAAASFGM
TQ-FLNTSNAAASLCLIGFFFAVASSIFSSYNL
>C5Y494_SORBI
AVLILRLLSLGLLAASLALIAADVYAYRYVLAVAVIGCAYTLLLPALLVLVLLADVVFALLLATGAAAGFAF
TYRFFDLAYAAAGLMLAAAACMALVIMLSVYSL
>Q2R2T4_ORYSJ
AVLALRLLTLALLAASLAVIAADVYAYRYVLAIAVIGCAYTLLIPNVALFLIFADVIFALLVATGAGAGFGL
TY-FFNMAYAAAGLMLLAAAAMALIIMLSIYSL
>A9SG36_PHYPA
ASIVLRLLTLIFAVVALAVLASILSAFTYLFAVCGVVAVYSLLIIILVAIFVFVLDQTMAYVLISAASASANG
```

```
VKCYCTKASASVAIAFIAFLFMAITAGVSARRL
>C5YHP6_SORBI
TTVALRLLAFAASLAAAVVVATMFAVWEAFVAINFACAAYALLAVVSKHWLHHMDQFTVNLQAASTAGAGAV
GSCYCDRGAVSLALAFVAFVAFGVASSLSRYPR
>A2YXI1_ORYSI
VDVSLRLLAAATSLASAVVVAALFQVWIGFVAVNLVCTVYAAAAAMGRWWLHHADAVVVNLEAAATAGAGAI
GSCYCNAGAAALALSLAAVLLLGVACARSRYPK
>C5Y376_SORBI
VTLLLRLITLALALTSAVLMATDYQPFIYLVGSNIAATILEVAIY--RVVLVVVDVAVQMLLYSATGAVFAA
--CFCEQVQRSKIISLAASLSAVLAAVAKDVAL
>Q2R0D1_ORYSJ
VSLLLRLSTLALALTSAVVMATDFPPFVYLVGFNIAAAMLEAAIY--GILLVVIDVAVQALVYTATGGAFAA
--CFCGQVHQSKLLSFAGSAAVGLAVVFRDVSL
>C5Y7C7_SORBI
VSIAGRIAGMGLAVAAAVLMSTDFPPFVFLVGAASIAAFLEAIIF----LMPLLGVAVPALLYSATGAAFAA
VSCFCSQVHIAVYLSLAAAVAVSVAEVVRGLGG
>Q2R0D2_ORYSJ
VNLALRIVVLGLAVAAAALMATDFGPFVYLVVASSIGAFMEAIIF----LLPLLDAAVPVLLYSATAAAFAA
GDCFCNQVHIAMYVSLAAGVALLVAEIVKHWPD
>C5Y7C8_SORBI
VSLIFRVAGIGLAAVSAAAMLTDFPAFVYLVAATAIATLLEAVLFWRVLTMLLLGAVVPALLYTSAGAAFAV
GWCFCEHVHVSMWLALGAAVAVSFAEFLTTFRW
>C5Y7C6_SORBI
LSLLFRIAALGLSLAAAIVMATQYNALRYFVAAGAISAVCSAAALVSLPLVPVLDAAAQGFLFSAAGAAFAT
RDCFCGRVTVAAAVCAFAAVSVATAALASRDAG
>Q2R0D4_ORYSJ
VSLFFRIAVVGLSVAAAVVMATKYPAFVYFVVAAVVSAVCSAAALAAGWAVALLDVVTMGLLFSAAGAVFAV
RRCFCWRVTTSAIICAFAAAAVSVAVLTKGARH
>P0DI68_BRADI
GGLGLRVAQFVFAGVALAVMASSVTAFCYLVAATIMQCLWSFSAIRAVCLFAIGDGITAALTFGAACSSAGI
TVCHCGSFKTATALAFMSWFALTPSFLLNFWSM
>Q10Q78_ORYSJ
GGLGLRLAQFAFAAVALAVMASSVTSFCFLVAAAILQCLWSFSAIRAVCLFAIGDGITAALTFSAACASSGI
TVCHCASFESATAMAFLSWFALSPSFLLNFWSM
>B4FNS3_MAIZE
AGLGLRLAQAFFAAAALAVMASSVSAFSYLVAAAILQCLWSLLAFRAVCIFTIGDGITGTITLGAACASAGI
TVCHCASFETATALAFISWFALAPSCILNFWSM
>Q9SKN3_ARATH
LGLALRFFQFLFAAAALCVMASSVTAFCYLVAATGLQSLWSLAAMRLVSLFAIGDGVTSTLTFAAACASAGI
TVCHCVQFETSTALAFISWFAALPSFLFNFWSL
>P0DI69_GINBI
GGLLLRLGQFCFALVAFSIMVSTVTAFCYLVAATVLQCLWSLAAILLVSLLVVGDGVTATLTFAAACASAGI
TVCHCARYETATALAFLSWFMVSLSFILTFWLL
>P0DI70_GINBI
GGLALRLGQFCFAVVAFSIMLSTVTAFCYLVAATVLQCLWSLAAVLVVSLFVVGDGVTATLTFAAACASAGI
TVCHCGKYETATAMAFLSWFMVSPSFLLTFWLL
>P0DI64_PINCO
GGLMLRLGQFCSALIAFSVMVSSVTAFCYLLAATVLQCLWSLAAVLLVSIFVVGDGVTATLTFAAACASAGV
VVCPCANYEAAIIMAFLSWFMVSISFVLTFWML
>P0DI27_PTEAA
GGLALRLGQLGFAVLSFSIMVSQVTAFCYLVAATVLQTLWSSIAVLLVGLFAVGDGVTSTLTFAAACATAGI
TVCHCGRFEAAAAMAFLSWIMAAPSFLLAFWSF
>D8QNI1_SELML
GGLVLRSGQFACAVTALSIMISSVTAFCYLVAAMALQLLWSVSAVVLLSLLVIGDWVTSTLSLAAACSSAGI
TVCHCGRYEAAVAMAFLTWFLVSLSFFFSFWLL
>P0DI66_MAIZE
GGLGLRVLQLLFAAISLAVMSSSVSAFCYLITTTVLQCVWSLTAIRAVTLFSIGDGITWLVSLSGACAAAGI
TVCPCASFQTAVAMGFMCCFSLLPSFLLNFYSI
>A9RKK4_PHYPA
GGLALRFTQFGFSLISLCIMVSSVTAFCFLVATMVFQCIWSLCGALIVSLFVVGDWVTSTMTFAGACAAAGI
TVCHCGRFEAAAAMAFMSWTATTLSFCLSFWLL
>A9RLK6_PHYPA
MGLALRFAQLGFALTALCIMVSSVTAFCFLVAAMVLQCIWSLCGVLILSFFVVGDWITSTMTFAGACAAAGI
TVCHCNRFEAAAAMAFMSWVITTISFFLSFWIL
>P0DI22_PTEAA
GSLALRICQFSAAIVSFSVMISSVTAFCFLVAAMVLQCMWSLSATPLLSLFAVGDWVTAVITFAGACASAGI
AVCFCGRYAAAAGMAFLSWLLISTSFLFTFWLL
>P0DI71_GINBI
GGLALRVGQFLFAAAAIVIMVTNYTAFCYLVAAMSLQFLWSFMAIVLLSLFVVGDWVTATLSLAAACSTAGV
TVCHCHRYQLSAAMAFLSWLLIGMSSLLTFWLW
>D5ACW4_PICSI
GGLALRMGQFIFAAASVVIMVTNFTAFCYLAAAMALQFLWSFVATILLSLFVVGDWVTATLSLAAACSTAGI
TVCHCRRYQLSATMAFFSWVLIAISSLITLLLL
>Q6NPF8_ARATH
GGLILRLSQFVPALISVSVMVTSATAFCCLVLAVSLQSLWSLSFISVVQCFTIGDGVTSTLTFAAASASAGI
TVCHCTRFETATAMAFISWFAVSPSFILNFWSL
>Q8L7R5_ARATH
```

```
TGLVLRISQCVFAAGSISYMVTSFTAFCYLIAAMGLQVIWSFGAIVLVSLFVVGDWVTSTLSLAGASSSAGI
TVCECWKYQLSVALAFLCWITIAVSSLTTLWLL
>Q945M8_ARATH
CGLLLRIGQCASAAASIGVMVSVHTAFCYLIASMGLQLLWSFGACILVSLFVVGDWVTAMLSLAAACSSAGV
VVCPCLRYEVAVALSFVTWIQIAVSSHVTFWIL
>Q9LZM5_ARATH
SGLILRLGQCATAAASIGVMVSNYTAFCFLVASMGLQLIWSFGACILLSLFTVGDWVTALLALAAACSSAGV
TVCSCDRFQISVGLSFFNWFLAAISSHTMFWIL
>B6T990_MAIZE
SGMALRLSQCVSAGASMGAMATNYTAFCYLIASMGLQLLWSFGACVLVSLFVVGDWVTAILSFAAASASAGV
TICSCGRYALSVVLAFITWSFIATSAVSMFWLL
>B6TM88_MAIZE
GGLALRAGQFVFAAASICAMASNYTAFCYLVASMGLQALWSLGGCLLMSLFVVGDCVTAILSFAAACSAAGV
VVCPCGRFEVAAAFAFLCWTFSAASALVMSWLL
>B8AC36_ORYSI
SGLSLRVGQLVFAAASVCATASAYTAFCYLIASMGLQALWSLGACVLLSLFVVGDWVTAILSFAASCSAAGV
VVCPCGRFELAIACAFLSWAFSATSALVMFWLL
>B6TAX2_MAIZE
GGLVLRVGQALFAAACIGVMGSSYTAFCYLIASMGLQMLWSFGACILLSLFVVGDWVTAILSFAASSSAAGV
VICPCGKYELATAFAFLSWALSATSALIMFWLL
>B8AYU8_ORYSI
GGLAMRVGQVAFAGASIGVMASNYTAFCYLIASMGLQSLWSLGACLLVSLFVIGDWVTALLSFAASCSAGGV
MVCPCGRFELAVALAFLSWALSATSAIIMFCLL
>Q3ECT8_ARATH
ASLSLRLGQMVLAFGSLLFMTIQFTAFCYLVTIMSLAIPWNLTAMRILLAISIGDWVVSVLALASASSAASV
VDCICNRYQFAATLAFLTWFLSLSSSLFNLWLL
>B6U300_MAIZE
GSLGLRVGQAVFSSASLLFMSVSYTAFCFLVTIMGLVIPWSCTAMGVMVIVVVGDCALSIVSFAAACSSAAV
IDSFCGRYQLSAMMAFLSWLLMAASATFNLWFV
>B8BPI2_ORYSI
GSLGLRVEQAVFSSASLLFMSVSYTAFCFLVTIMGLVIPWSCTAMGVMVIVVIGDWVLAILSLAAASSSAAV
IDCFCGRYQLSAMMAFLSWFLTAASSLFNLWFI
>P0CB17_ARATH
ASFALRFGQTIFSAASLIFMCFDFTTFCYLAMVMAIVTPWSILALRVLSIVFAGDFVLSFLSLGGACAVASA
TECLCIQYQVSAALAFLCWFLLLASALFNFWSL
>Q66GI1_ARATH
SSFVLRLGQTLFSSASLLFMCFAYTTFCYLVTVMGLVTPWSVTALTVISVIVAGDFVLSFLSLGGACSTASV
AV-QCDRYKLSATMAFLSSFLSFASTFFNFCLL
>K3WS83_PYTUL
TRLALRFLQFASSLIVIVAFSSGSNDVTFAILMSFLGMVYGLFVFPLLFCEQVMDFLMVLLLLIASIVLAVS
DVCRCHDINVGVSFTFVSLAAFLATLVLSCFAD
>K3WS84_PYTUL
LRLLLRFLQFAFSLIALITLSAGSSPVIFTTLMTYTGFVYALWIFPPLFYEQLMDFLMAVLLLIAAIVLLCS
DYCRCRSIRTSVVFTFLAMASFLLTLLLSFFDR
>G4ZSC0_PHYSP
SRSLLRFFDFALSLVALATVSRGSRAATYTTLVTYTGMLVGLFLVTPRFVEPLIDLILAAMLVVAGIVLVVS
DYCRCNELKTAVVFTFLASFSYFVTFLFDCCES
>D0NLD9_PHYIT
SRALLRFLNFALSLVALATLSRGSRAATYATLMTYTGMLVGLFLFTPRLIEQLLDLLLAALLVVAGIVLVAS
DYCRCNQLKTAVVFTFLASLSYFVTFLLDCCES
>H3HBC3_PHYRM
GRTLLRFLQFALALVALATISRGSSAATYTQLVTYTSMLVGLFLFTPRIVEQLMDLVLAAMLVVAGIVLVVS
DYCRCNLLKTAVVFSFLTAAAHLASFLLSSCED
>K3WS90_PYTUL
SSMMLRLLQCVGSLIAMSTVAAGSHETNFMLLVAYSGMLYSGWGVPRELFARVVDGVFALFFFCAAAALVAS
DYCQCNNLKTSVAFAFLTIVPFLLSFALTFVIS
>K3WS85_PYTUL
ARLGSRGLQFLFSLFALAFTVAGGSASTFTILMTYSAMMFSLWAAPQVMTERVIDGVFAVVLLIAGIVLAMS
DYCKCGNLKAGVVFTFLAMVAFLITFGLNFLGI
>G4ZSC4_PHYSP
LRLGLRGLQFVCSLLAMSFAAAATHSSTFVLLMGYTGMLYTLWVAPALRLEQATDAALALALLVAGICLAAS
DYCHCHNLKAATAFDFIAMFLFLVSLGLTFVAA
>H3HBC4_PHYRM
LRLGLRGLQFFCSLLAMSFAAASTHSSTFVLLMGYTGMLYTLWVCPAVRLEQATDALLAIVLLVAGICLAAS
DYCHCHNLRAATAFDFIAMFFFLVSLGLSFLGG
>D0NLE1_PHYIT
VRLGLRGLQLFCSLLAMSFAAASTRSSTFVLLMGYTGMLYTLWVAPALRLEQGTDALLTLMLLIAGICLAAS
DYCHCNNLRAATAFDFIAMFFFLVSLGLTFVAG
>M4B8W0_HYAAE
MRLGLRGVQFVCSLLALAFAAAATHSSTFVLLMGYTGMLYTLWVAPALRVEQAMDALLVLLLLIAGICLAAS
DYCHCNNLKAATAFAFIAMFFFLLSLALTLLSP
>G4ZSC3_PHYSP
ANLALRCAQLLCCLLGLAFVAATFHSSNFVLLMNYTGMLYTLWGALSTRVEQGIDAVLAFVLLIGGICLAAS
DYCHCHNLKASVAFTFLAVFGFIATLTLSILTT
>H3GGR0_PHYRM
TNLALRVAQLMSCLLGMSFVAATFHSSNFVLLMTYTGMLYTLWVALAPRVEQAIDAVLAFMLLVGGICLAAS
DYCHCHNLQAATAFTFIAMAFFLASLSLSILAT
```

```
>F0X036_9STRA
IRILLRALQFLFSLVAISTMAAGSSVSTYVTVLTYSSLIYSSWFGVPKLQDWLIDGTFAFLYSIASILLVTS
PYCRCGNLKATVVFLFLNLCALLGSIAMSFVPI
>G5AEA0_PHYSP
VRCTGRTLQFACSVVALVCIVLVEPKATYAILMAYSGVLYSLWVAPTVGVERFMDVLIAVALLVAGILFATS
AQCRCGSMNTGYVFTFIAVAMYVVTFALS----
>G5AE98_PHYSP
TRRCVLLLQFACCLVAFILFVAVSPAATYVILMSYSGWLYALWVAPKVGVERLMDLLVAVLLLVAGIIFAVS
SQCRCGSMDGGYIFAFVAVALYVITFALS----
>H3H3L4_PHYRM
TRRCVRLLQFSCSLVAFVLFVAVSPAATYAILMAYSGWLYALWVAPKVGVERLMDVLVAVLLLIAGIIFAVS
SQCRCGNMSVGYTFAFVAVALYAITFALS----
>G5AEA1_PHYSP
ARRGGRFVQFVLSLLTFISTVATSPVAMFMVLVSWSCILYTLFVVPSAGIERFLDLLLAVLLLLFAILLAAS
HQCRCGSLTRAYVLAFIDCVFFLVTLALSFCGS
>D0NMH7_PHYIT
ARRGSRFIQFVLSLIIFISTVAMSPVAMFMVLVSWSCVLYTLFVVPSVSVERVVDLFLSALLLLFAILLAAS
HQCRCGSLTRAYVLAFIDCIFFLATFALSFGGS
>F0X038_9STRA
KHIIPRGLQLILSALALAFAASGSSELSFTLLVTYSTMLYALWFTPRLSLLRLLDLIFLGFLFAAGLGLVLS
DYCHCGNIVASVVFTFLTMSPLLITLATSFSRT
>F0WMT2_9STRA
VRIVLRGSQVLLSLIAIFLLAG---SSGFAVVLLYTSLLSSSWAYIAPKYTVYADGAMTFLFLITGIALASS
SYCRCRVIKGAVALMFFLFFSFCGSAWTSYKSY
>K3X3G8_PYTUL
ITLAMRVLQLASAVLALGFIAGGGPTVNFAMIVTYSAAIYAMLAF-PAHFSVALDSILTVMLLSAGCAVAAS
DYCHCSSLKAGVAFCFLAFVAFLISVAWGLWIL
>G4ZRP2_PHYSP
ISLTLRALQFATCAVALALVAAGGPAVNFVLVVSFAAVLYGGFLL-PAPWSFGVDAVFTMLFMSAGCALAAC
DYCRCALLASAAALCFMAFVSFLLSVAWGAWMR
>H3GI99_PHYRM
ISLALRSLQLATCVVALALVASGGPAVNFVLVVSFAACLYDGLLL-PAPWSFGVDAVFTMLFMSAGCALAAS
DYCHCALLASGAALCFMAFVAFLLSVAWGAWMR
>D0NCN6_PHYIT
ICLTLRSLQFATCVAALALVAAGGPAVNFVMIVSFAACLYDAFVM-PAPWSFGVDAIFTMLFMSAGCALAAC
DYCHCALLASGAALCFMAFVVFLLSVAWGAWMR
>M1VAW8_CYAME
SKTLLYLCEFTWAIVVFGVTANSTALCRYAIALGVIGWVLVLIVVLPPVYEMIVQLFLMVWWFIGSVVISAS
LG---VSINTVIAFSWMLFVMHLVHSGICLWQW
>P0DI72_CHLAT
PRFILLIIEWVFALVAFAVMGHRRSSFEYLTAICILVWLVVMIVILPPLIEAAIFLLFAILVFIAFLVTAVK
--CVCSEPKAAAAFAFLLGLLLAGSSVLGCIAF
>A4S8B7_OSTLU
PKFRALLVESLMALTTFSFMAKKFYQFKGVVGVYAGFWAYTVIAMPPPGTEFASYALFTAAMATFVVMSITE
--CVCDYSLVSLIFAAATIVLNCLTCAFAWRQW
>Q00U99_OSTTA
RDYCFHNDLQVLSVTAFAFMARSFYQFKGVVGVYAAFWVYTVLGLPPPGTEFVVHALFTLCMIAFVSLSVIS
--CVCAYAKASLVFAALVVVLNCATCAFVFKQW
>C1N652_MICPC
PKFRLIAVQCLFALTAFATMAGKFAVFQFLVVICVTYWLFTMLGMPPAGTEFMIYAVFNVLILIAFSTSWTE
--CVCTGAKASIAFAMFTWLALCVSMMFTWKEW
>C1EI34_MICSR
PKFRLIAVQCLFSITAFAAMLSKFSNFKFLIAVCIIYAVFSLVAAPPPVTELTAYTVMNVLLFAAFAMSATS
--CVCTSAKASIAFAFFTWLAVCFSMLFTYKEW
>P0DI73_CHLAT
PKFRVTFAQWVCSLLMWSLMASKHGEFKFVVVFGLVMWGLASTVYLAPIVEFWANVAAGSLAFICLVLASAT
--CVCLKPKASAAFAFLLLCAYGGLAYLSWRTW
>F0YFA3_AURAN
AEPVLRFAELAASLLSWTLMASNYTPLNFLLATALLQSLFVVAVVFGTQGVF----VGIVLGFVAGAASSTQ
LHCFCGHVDAAVAFAFFAAAAAGGSLYVVLKXX
>F0Y3N5_AURAN
XXXXXXXLMVVLSLLSFWVMAAFYPSLTFFVWVGVLSFVYTLGVGLRRQLETAGPPVLAWLTYTAAIAASAT
ST-FCGHVVTATVFMYGLCAAYVGVVVSSVYGG
>H3GEF8_PHYRM
IPMAVRVLTAVLAVIATGTAGSSGNQVYFLMVIGALVVIAFTLLVPSPRALVMFDAVWMLFTFACAVAVAAA
PVCKCSNIVTAIVTMFMASVCIVFDILFTTGAI
>E1ZFT0_CHLVA
PHFWLRVAQVVFGIIAFAPVAEFSSKIRYTMFVGITGFIIAFFVAARGIIALVLDALWVVFWLAAAASMSDI
VA---SNIKASCAFSWIAWFLWIGSLVISVMDW
```

Dataset 3. CASPL/MARVEL domain phylogeny (NHX format) corresponding to Figures 1D and Supplemental Figure 2

```
(((((((((((((((((((B9IK21_POPTR:1.2465654785[&&NHX:C=255.102.51],(A7PJ32_VITVI:0.2524028553[&&
NHX:C=255.102.51],((A7R333_VITVI:0.250338306[&&NHX:C=255.102.51],(B9RZ92_RICCO:0.1445976513[&&
NHX:C=255.102.51],(B9H2V1_POPTR:0.0633341903[&&NHX:C=255.102.51],B9N3F4_POPTR:0.0331740353[&&N
HX:C=255.102.51])0.9790000000:0.1301195863[&&NHX:C=255.102.51])0.9890000000:0.2384414748[&&NHX
:C=255.102.51])0.9760000000:0.192419341[&&NHX:C=255.102.51],((((Q9LR57_ARATH:1.0E-
10[&&NHX:C=255.102.51],D7KCH2_ARALL:1.0E-
10[&&NHX:C=255.102.51])1.0000000000:0.1697800056[&&NHX:C=255.102.51],(Q9ZT81_ARATH:0.017302922
4[&&NHX:C=255.102.51],D7M2M8_ARALL:0.0059171949[&&NHX:C=255.102.51])0.7830000000:0.027461595[&
&NHX:C=255.102.51])0.9960000000:0.2277834822[&&NHX:C=255.102.51],(B9RW00_RICCO:0.1276325598[&&
NHX:C=255.102.51],(B9N5U6_POPTR:0.0205962324[&&NHX:C=255.102.51],B9N2D0_POPTR:0.0852954015[&&N
HX:C=255.102.51])0.9910000000:0.1458508967[&&NHX:C=255.102.51])0.9080000000:0.0799282974[&&NHX
:C=255.102.51])0.7110000000:0.0560069383[&&NHX:C=255.102.51],((A2WMK1_ORYSI:5.024E-
7[&&NHX:C=255.102.51],(A2WMK7_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q9LI17_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.7570000000:0.0068749481[&&NHX:C=255.102.51])1.0000000000:0.5531963037
[&&NHX:C=255.102.51],((A2Y2B7_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q84UT5_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9960000000:0.2591288622[&&NHX:C=255.102.51],(B6SZU6_MAIZE:0.047508283
7[&&NHX:C=255.102.51],C5YVA2_SORBI:0.0195210451[&&NHX:C=255.102.51])0.9640000000:0.1632424021[
&&NHX:C=255.102.51])0.8270000000:0.0983890266[&&NHX:C=255.102.51])1.0000000000:0.4714445479[&&
NHX:C=255.102.51])0.0860000000:0.0328958187[&&NHX:C=255.102.51])0.8450000000:0.0635901144[&&NH
X:C=255.102.51])0.6470000000:0.0673729872[&&NHX:C=255.102.51])0.9800000000:0.3862749485[&&NHX:
C=255.102.51],(((((((P0DI54_MALDO:0.1328920261[&&NHX:C=255.102.51],(P0DI44_SOLTU:0.2283226338[
&&NHX:C=255.102.51],(((P0DI33_PANVG:0.0135995387[&&NHX:C=255.102.51],(B6T959_MAIZE:0.048348149
3[&&NHX:C=255.102.51],C5Z7E3_SORBI:2.2E-
7[&&NHX:C=255.102.51])0.7530000000:0.0066504799[&&NHX:C=255.102.51])0.9090000000:0.0230464502[
&&NHX:C=255.102.51],((A2YAZ1_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q67X40_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9590000000:0.0410282919[&&NHX:C=255.102.51],(Q6Z2U5_ORYSJ:0.217954746
6[&&NHX:C=255.102.51],(P0DI42_WHEAT:0.1232927251[&&NHX:C=255.102.51],P0DI36_BRADI:0.0771445265
[&&NHX:C=255.102.51])0.7880000000:0.0150772393[&&NHX:C=255.102.51])0.8770000000:0.024508078[&&
NHX:C=255.102.51])0.7610000000:0.0136933566[&&NHX:C=255.102.51])0.9140000000:0.050251504[&&NHX
:C=255.102.51],((B8AEC9_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q6EP58_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])1.0000000000:0.3566405034[&&NHX:C=255.102.51],((F2QA93_ORYRU:4.237E-
7[&&NHX:C=255.102.51],(Q7XUV7_ORYSJ:1.0E-10[&&NHX:C=255.102.51],A2XU91_ORYSI:2.0E-
10[&&NHX:C=255.102.51])0.0000000000:1.0E-
10[&&NHX:C=255.102.51])0.9430000000:0.0492390617[&&NHX:C=255.102.51],(C5Y9U6_SORBI:0.022406535
6[&&NHX:C=255.102.51],P0DI34_PANVG:0.0258195419[&&NHX:C=255.102.51])0.8920000000:0.0378804774[
&&NHX:C=255.102.51])0.9830000000:0.0991572591[&&NHX:C=255.102.51])0.7040000000:0.0473314188[&&
NHX:C=255.102.51])0.9250000000:0.0568339766[&&NHX:C=255.102.51])0.9460000000:0.0727617769[&&NH
X:C=255.102.51])0.8020000000:0.0162614043[&&NHX:C=255.102.51],((B9S8Z3_RICCO:0.3093563245[&&NH
X:C=255.102.51],(B9HI87_POPTR:0.2671396882[&&NHX:C=255.102.51],(D7KBH3_ARALL:5.03E-
7[&&NHX:C=255.102.51],Q9XI72_ARATH:0.0195529152[&&NHX:C=255.102.51])1.0000000000:0.3990804723[
&&NHX:C=255.102.51])0.4070000000:0.0502523405[&&NHX:C=255.102.51])0.9500000000:0.1130375001[&&
NHX:C=255.102.51],(((G7JG80_MEDTR:0.1851302674[&&NHX:C=255.102.51],(C6T4A0_SOYBN:0.117017966[&
&NHX:C=255.102.51],P0DI58_LOTJA:0.0968737619[&&NHX:C=255.102.51])0.1480000000:0.032004333[&&NH
X:C=255.102.51])0.9840000000:0.136935485[&&NHX:C=255.102.51],(C6T1G0_SOYBN:0.138289461[&&NHX:C
=255.102.51],G7KGQ4_MEDTR:0.1554225917[&&NHX:C=255.102.51])0.7130000000:0.060349273[&&NHX:C=25
5.102.51])0.9800000000:0.1287753789[&&NHX:C=255.102.51],(P0DI35_LACSI:0.2648319952[&&NHX:C=255
.102.51],(Q5NRN4_SOLDE:2.852E-
7[&&NHX:C=255.102.51],Q60D27_SOLDE:0.0064519059[&&NHX:C=255.102.51])1.0000000000:0.3494314563[
&&NHX:C=255.102.51])0.9550000000:0.1183353723[&&NHX:C=255.102.51])0.8570000000:0.0559846192[&&
NHX:C=255.102.51])0.8850000000:0.0521698974[&&NHX:C=255.102.51])0.3290000000:0.0287786976[&&NH
X:C=255.102.51],A7PMY7_VITVI:0.1476526666[&&NHX:C=255.102.51])0.0000000000:6.36216E-
5[&&NHX:C=255.102.51],((B9I534_POPTR:0.1117268076[&&NHX:C=255.102.51],(D7M7B3_ARALL:0.01933016
[&&NHX:C=255.102.51],Q9LXF3_ARATH:0.0143277688[&&NHX:C=255.102.51])1.0000000000:0.219505688[&&
NHX:C=255.102.51])0.8820000000:0.056811864[&&NHX:C=255.102.51],(P0DI59_LACSA:0.2958505594[&&NH
X:C=255.102.51],(P0DKC2_LOTJA:0.0885732527[&&NHX:C=255.102.51],G7L218_MEDTR:0.0445109335[&&NHX
:C=255.102.51])0.9980000000:0.1652178676[&&NHX:C=255.102.51])0.8390000000:0.0405584132[&&NHX:C
=255.102.51])0.2650000000:0.0270177845[&&NHX:C=255.102.51])0.8710000000:0.047076038[&&NHX:C=25
5.102.51],B9T4E6_RICCO:0.0885187172[&&NHX:C=255.102.51])0.9940000000:0.215804867[&&NHX:C=255.1
02.51],((((P0DI38_BRADI:0.0263053973[&&NHX:C=255.102.51],E6Y2A0_WHEAT:0.0797387164[&&NHX:C=255
.102.51])0.9040000000:0.0547506918[&&NHX:C=255.102.51],((B8ART0_ORYSI:1.0E-
10[&&NHX:C=255.102.51],Q7XPU9_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9950000000:0.123151216[&&NHX:C=255.102.51],(B6U045_MAIZE:0.0337802405
[&&NHX:C=255.102.51],C5YAP3_SORBI:0.0155395621[&&NHX:C=255.102.51])0.9430000000:0.0682034109[&
&NHX:C=255.102.51])0.7810000000:0.0532379332[&&NHX:C=255.102.51])0.9060000000:0.0660598479[&&N
HX:C=255.102.51],(P0DI37_BRADI:0.1431243148[&&NHX:C=255.102.51],(C5YLC9_SORBI:0.1773176701[&&N
HX:C=255.102.51],(A2YQB8_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q6Z1Y7_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9990000000:0.1736657914[&&NHX:C=255.102.51])0.5320000000:0.0470005072
[&&NHX:C=255.102.51])0.8090000000:0.0492938211[&&NHX:C=255.102.51])1.0000000000:0.2902050939[&
&NHX:C=255.102.51],(A7PP95_VITVI:0.1595746769[&&NHX:C=255.102.51],(A7QF77_VITVI:0.0957566759[&
&NHX:C=255.102.51],((P0DI60_HELAN:0.2230622585[&&NHX:C=255.102.51],(P0DI62_CYNCS:0.0371768901[
&&NHX:C=255.102.51],P0DI32_TARKO:0.0528042105[&&NHX:C=255.102.51])1.0000000000:0.2041950084[&&
```

```
NHX:C=255.102.51])0.6980000000:0.0661143081[&&NHX:C=255.102.51],((P0DI30_TRIPD:0.0785801282[&&
NHX:C=255.102.51],P0DI53_MIMGU:0.0612985335[&&NHX:C=255.102.51])0.9770000000:0.0924745592[&&NH
X:C=255.102.51],(((D7LGW9_ARALL:0.0064552657[&&NHX:C=255.102.51],Q9ZQI2_ARATH:0.0207784891[&&N
HX:C=255.102.51])1.0000000000:0.3123627094[&&NHX:C=255.102.51],(((P0DI41_VIGUN:0.0824425187[&&
NHX:C=255.102.51],C6T4E0_SOYBN:0.0649354729[&&NHX:C=255.102.51])0.9030000000:0.0516482904[&&NH
X:C=255.102.51],(G7IHF9_MEDTR:0.0793603272[&&NHX:C=255.102.51],P0DI56_LOTJA:0.1538463273[&&NHX
:C=255.102.51])0.7820000000:0.0392735167[&&NHX:C=255.102.51])1.0000000000:0.2970287321[&&NHX:C
=255.102.51],(B9SCX0_RICCO:0.0936504519[&&NHX:C=255.102.51],B9HQ42_POPTR:0.2672731087[&&NHX:C=
255.102.51])0.5860000000:0.0536083613[&&NHX:C=255.102.51])0.0140000000:0.016985474[&&NHX:C=255
.102.51])0.8420000000:0.0849790261[&&NHX:C=255.102.51],((B9IIR4_POPTR:0.1295095246[&&NHX:C=255
.102.51],((B9HBX2_POPTR:0.0263425521[&&NHX:C=255.102.51],B9IIR5_POPTR:0.0386660355[&&NHX:C=255
.102.51])0.8830000000:0.0335296383[&&NHX:C=255.102.51],(P0DI61_CUCME:0.2682827449[&&NHX:C=255.
102.51],((C6TH93_SOYBN:0.0693000101[&&NHX:C=255.102.51],((C6TFL9_SOYBN:0.0440177533[&&NHX:C=25
5.102.51],P0DI40_VIGUN:0.0538050454[&&NHX:C=255.102.51])0.7700000000:0.019525131[&&NHX:C=255.1
02.51],((P0DI39_VIGUN:0.0262061663[&&NHX:C=255.102.51],C6T2E7_SOYBN:0.0519798376[&&NHX:C=255.1
02.51])0.8930000000:0.0244222179[&&NHX:C=255.102.51],(P0DI55_LOTJA:0.0988327311[&&NHX:C=255.10
2.51],(C6T1K6_SOYBN:0.0275488867[&&NHX:C=255.102.51],P0DI57_LOTJA:0.0694499919[&&NHX:C=255.102
.51])0.6910000000:0.0066676891[&&NHX:C=255.102.51])0.7620000000:0.0069119254[&&NHX:C=255.102.5
1])0.0000000000:1.1142E-
6[&&NHX:C=255.102.51])0.9730000000:0.0845102208[&&NHX:C=255.102.51])0.9850000000:0.1119083141[
&&NHX:C=255.102.51],(B9SX12_RICCO:0.1150129119[&&NHX:C=255.102.51],((P0DI43_THECC:0.0984477972
[&&NHX:C=255.102.51],B9SX13_RICCO:0.1555679502[&&NHX:C=255.102.51])0.8160000000:0.0328963302[&
&NHX:C=255.102.51],(((D7LZ50_ARALL:0.0066641104[&&NHX:C=255.102.51],Q9FFZ7_ARATH:3.756E-
7[&&NHX:C=255.102.51])0.9880000000:0.0785324709[&&NHX:C=255.102.51],(P0DI46_RAPSA:0.134078655[
&&NHX:C=255.102.51],(D7LAP2_ARALL:0.0064112666[&&NHX:C=255.102.51],Q9CAX3_ARATH:0.0070399581[&
&NHX:C=255.102.51])0.8960000000:0.0302461121[&&NHX:C=255.102.51])0.9060000000:0.0378245223[&&N
HX:C=255.102.51])0.8330000000:0.0596870549[&&NHX:C=255.102.51],((D7LIN7_ARALL:0.0089207991[&&N
HX:C=255.102.51],Q9SIH4_ARATH:0.0461324445[&&NHX:C=255.102.51])0.9730000000:0.0873261441[&&NHX
:C=255.102.51],(P0DI49_RAPRA:0.0510053515[&&NHX:C=255.102.51],P0DI45_RAPSA:0.1015464082[&&NHX:
C=255.102.51])0.0530000000:0.035104194[&&NHX:C=255.102.51])1.0000000000:0.2157764064[&&NHX:C=2
55.102.51])0.9550000000:0.0805912048[&&NHX:C=255.102.51])0.7740000000:0.0281989614[&&NHX:C=255
.102.51])0.1540000000:0.0291307166[&&NHX:C=255.102.51])0.0490000000:0.0353045126[&&NHX:C=255.1
02.51])0.3630000000:0.0378830316[&&NHX:C=255.102.51])0.8310000000:0.0363063239[&&NHX:C=255.102
.51])0.9630000000:0.0783301715[&&NHX:C=255.102.51],(P0DI50_TOBAC:0.1438463807[&&NHX:C=255.102.
51],(P0DI51_MIMGU:0.2414750139[&&NHX:C=255.102.51],(P0DI52_MIMGU:0.0295605189[&&NHX:C=255.102.
51],(P0DI31_TRIPD:0.0339679683[&&NHX:C=255.102.51],(Q1W3A5_STRAF:0.0363029928[&&NHX:C=255.102.
51],P0DI63_STRHE:0.0316660821[&&NHX:C=255.102.51])0.9890000000:0.0824905532[&&NHX:C=255.102.51
])0.8630000000:0.0390799964[&&NHX:C=255.102.51])0.2540000000:0.0282540059[&&NHX:C=255.102.51])
0.9370000000:0.0852814727[&&NHX:C=255.102.51])0.9900000000:0.111447666[&&NHX:C=255.102.51])0.8
070000000:0.038273489[&&NHX:C=255.102.51])0.0000000000:0.0011016255[&&NHX:C=255.102.51])0.7620
000000:0.0333552917[&&NHX:C=255.102.51])0.1900000000:0.0101476407[&&NHX:C=255.102.51])0.899000
0000:0.0644113713[&&NHX:C=255.102.51])0.9050000000:0.0724683515[&&NHX:C=255.102.51])0.95800000
00:0.1346044475[&&NHX:C=255.102.51])0.8600000000:0.0834089559[&&NHX:C=255.102.51],(P0DH81_PICG
L:0.0588597743[&&NHX:C=0.153.153],P0DH80_PINTA:0.1431718391[&&NHX:C=0.153.153])0.9850000000:0.
2028627849[&&NHX:C=0.153.153])0.9980000000:0.4959592817[&&NHX:C=0.153.153])0.8890000000:0.1940
172532[&&NHX:C=0.102.0],(((((D7L5G6_ARALL:0.0514078898[&&NHX:C=255.102.51],Q9SQU2_ARATH:0.0291
925969[&&NHX:C=255.102.51])1.0000000000:0.4160589582[&&NHX:C=255.102.51],(D7MAF7_ARALL:7.518E-
7[&&NHX:C=255.102.51],Q9FE29_ARATH:0.0314831133[&&NHX:C=255.102.51])0.9970000000:0.3029981927[
&&NHX:C=255.102.51])0.7350000000:0.06302503[&&NHX:C=255.102.51],((A2PZE5_IPONI:0.4693607222[&&
NHX:C=255.102.51],((B9RT03_RICCO:0.2181308121[&&NHX:C=255.102.51],B9HMP5_POPTR:0.2050856791[&&
NHX:C=255.102.51])0.7100000000:0.0847208292[&&NHX:C=255.102.51],((C6SVQ5_SOYBN:0.0121852568[&&
NHX:C=255.102.51],C6SXZ3_SOYBN:0.0434895481[&&NHX:C=255.102.51])1.0000000000:0.3014871008[&&NH
X:C=255.102.51],(D2KQI6_BETVM:0.3313395551[&&NHX:C=255.102.51],A7NW79_VITVI:0.2537385409[&&NHX
:C=255.102.51])0.6010000000:0.0687095063[&&NHX:C=255.102.51])0.1410000000:0.0348451074[&&NHX:C
=255.102.51])0.0000000000:0.0307902996[&&NHX:C=255.102.51])0.7700000000:0.0652403304[&&NHX:C=2
55.102.51],(Q1EPG6_MUSAC:0.2868227197[&&NHX:C=255.102.51],(Q6YT98_ORYSJ:0.2287100937[&&NHX:C=2
55.102.51],(B6U361_MAIZE:0.1432606972[&&NHX:C=255.102.51],C5X4A5_SORBI:0.0972504396[&&NHX:C=25
5.102.51])0.9480000000:0.1027201728[&&NHX:C=255.102.51])0.9980000000:0.2530587953[&&NHX:C=255.
102.51])0.9900000000:0.1817054372[&&NHX:C=255.102.51])0.0000000000:0.0213689963[&&NHX:C=255.10
2.51])0.9990000000:0.4916117385[&&NHX:C=255.102.51],((((C5Y376_SORBI:0.2656475887[&&NHX:C=255.
102.51],Q2R0D1_ORYSJ:0.247597593[&&NHX:C=255.102.51])0.9920000000:0.5424971297[&&NHX:C=255.102
.51],(Q2R0D2_ORYSJ:0.3029455136[&&NHX:C=255.102.51],(C5Y7C8_SORBI:0.5835808277[&&NHX:C=255.102
.51],C5Y7C7_SORBI:0.1673237817[&&NHX:C=255.102.51])0.8090000000:0.1227163588[&&NHX:C=255.102.5
1])0.7770000000:0.1928975733[&&NHX:C=255.102.51])0.8000000000:0.3433883636[&&NHX:C=255.102.51]
,(Q2R0D4_ORYSJ:0.3307563731[&&NHX:C=255.102.51],C5Y7C6_SORBI:0.5492466405[&&NHX:C=255.102.51])
0.9630000000:0.5689643224[&&NHX:C=255.102.51])0.9960000000:1.1242777317[&&NHX:C=255.102.51],((
(C6SZP8_SOYBN:0.057961209[&&NHX:C=255.102.51],C6TBD0_SOYBN:0.016971904[&&NHX:C=255.102.51])0.9
970000000:0.2674132732[&&NHX:C=255.102.51],(B9RT04_RICCO:0.2339756185[&&NHX:C=255.102.51],(B9H
MP6_POPTR:0.2269129508[&&NHX:C=255.102.51],(A7NW78_VITVI:0.2531699067[&&NHX:C=255.102.51],(A7P
TY8_VITVI:0.4278399574[&&NHX:C=255.102.51],(Q8L8Z1_ARATH:2.5357E-
6[&&NHX:C=255.102.51],(D7MAF5_ARALL:0.0509154287[&&NHX:C=255.102.51],(D7MAF6_ARALL:0.027966854
5[&&NHX:C=255.102.51],O23413_ARATH:0.0170727559[&&NHX:C=255.102.51])1.0000000000:0.1659020128[
&&NHX:C=255.102.51])0.0000000000:0.0136310697[&&NHX:C=255.102.51])1.0000000000:0.3887994451[&&
NHX:C=255.102.51])0.3830000000:0.0551915117[&&NHX:C=255.102.51])0.5600000000:0.0565604577[&&NH
X:C=255.102.51])0.8570000000:0.0666600133[&&NHX:C=255.102.51])0.8940000000:0.0979235623[&&NHX:
C=255.102.51])0.8280000000:0.0968983547[&&NHX:C=255.102.51],(Q1EPG7_MUSAC:0.757482079[&&NHX:C=
255.102.51],(C5XKI6_SORBI:1.177E-
```

```
6[&&NHX:C=255.102.51],(B4FAP1_MAIZE:0.0151473459[&&NHX:C=255.102.51],(Q9ARX2_ORYSJ:0.012961060
3[&&NHX:C=255.102.51],B8A7Z5_ORYSI:4.3388E-
6[&&NHX:C=255.102.51])1.0000000000:0.2883351227[&&NHX:C=255.102.51])0.7770000000:0.0374924022[
&&NHX:C=255.102.51])0.9990000000:0.5324827481[&&NHX:C=255.102.51])0.8400000000:0.164300873[&&N
HX:C=255.102.51])0.8880000000:0.197486921[&&NHX:C=255.102.51])0.8400000000:0.1345186671[&&NHX:
C=255.102.51])0.9520000000:0.1812346775[&&NHX:C=255.102.51],((((Q0ILZ7_ORYSJ:1.66E-
7[&&NHX:C=255.102.51],(B8BMY7_ORYSI:8.3E-
8[&&NHX:C=255.102.51],A2ZMM4_ORYSI:0.0064282483[&&NHX:C=255.102.51])0.0000000000:8.3E-
8[&&NHX:C=255.102.51])0.9370000000:0.1377199606[&&NHX:C=255.102.51],(B6TUH4_MAIZE:0.1622581137
[&&NHX:C=255.102.51],C5YRU8_SORBI:0.0484463302[&&NHX:C=255.102.51])0.9540000000:0.1561735773[&
&NHX:C=255.102.51])0.9990000000:0.5204185817[&&NHX:C=255.102.51],(A7QC16_VITVI:0.1925822851[&&
NHX:C=255.102.51],((B9GIE4_POPTR:0.0515728005[&&NHX:C=255.102.51],(B9I0U9_POPTR:0.03348449[&&N
HX:C=255.102.51],C6TG62_SOYBN:0.3875322907[&&NHX:C=255.102.51])0.9590000000:0.0735511762[&&NHX
:C=255.102.51])0.8580000000:0.051340557[&&NHX:C=255.102.51],(B9SV63_RICCO:0.1703302563[&&NHX:C
=255.102.51],((D7MFJ8_ARALL:0.0330216572[&&NHX:C=255.102.51],Q9SUP0_ARATH:0.0197159193[&&NHX:C
=255.102.51])0.9270000000:0.0822426758[&&NHX:C=255.102.51],(D7MM00_ARALL:0.0073213918[&&NHX:C=
255.102.51],Q9FI10_ARATH:0.0120518067[&&NHX:C=255.102.51])0.9950000000:0.1764023098[&&NHX:C=25
5.102.51])0.9970000000:0.2400885606[&&NHX:C=255.102.51])0.4870000000:0.0386317414[&&NHX:C=255.
102.51])0.7980000000:0.0915927392[&&NHX:C=255.102.51])0.8980000000:0.1829095451[&&NHX:C=255.10
2.51])0.9970000000:0.5565163712[&&NHX:C=255.102.51],A9P0A6_PICSI:0.4350220894[&&NHX:C=0.153.15
3])0.7070000000:0.1072225172[&&NHX:C=0.153.153])0.8760000000:0.1219833906[&&NHX:C=0.153.153])0
.7390000000:0.0681565409[&&NHX:C=0.102.0],((A7PA04_VITVI:0.4577389046[&&NHX:C=255.102.51],(B9R
H17_RICCO:0.3980954649[&&NHX:C=255.102.51],B9GFG6_POPTR:0.5365376413[&&NHX:C=255.102.51])0.754
0000000:0.1003853695[&&NHX:C=255.102.51])0.9830000000:0.3159538688[&&NHX:C=255.102.51],((B9RA9
0_RICCO:0.2309745076[&&NHX:C=255.102.51],(B9I3X5_POPTR:0.1174881359[&&NHX:C=255.102.51],B9IFI5
_POPTR:0.1986539651[&&NHX:C=255.102.51])0.9940000000:0.2771137333[&&NHX:C=255.102.51])0.942000
0000:0.1649692068[&&NHX:C=255.102.51],(A7PHN8_VITVI:0.3646837528[&&NHX:C=255.102.51],(D7MGK0_A
RALL:0.0293515345[&&NHX:C=255.102.51],Q9M0L3_ARATH:1.8682E-
6[&&NHX:C=255.102.51])1.0000000000:0.8880655658[&&NHX:C=255.102.51])0.0000000000:0.0144298852[
&&NHX:C=255.102.51])0.8470000000:0.1295704503[&&NHX:C=255.102.51])0.9980000000:0.6216438151[&&
NHX:C=255.102.51])0.8510000000:0.1510370816[&&NHX:C=0.102.0],(P0DH83_MARPO:0.8189228439[&&NHX:
C=0.102.0],(A9TKY8_PHYPA:0.4271205768[&&NHX:C=0.102.0],(A9SEY7_PHYPA:0.3627383734[&&NHX:C=0.10
2.0],(A9STS7_PHYPA:0.1902900436[&&NHX:C=0.102.0],A9TZ63_PHYPA:0.1262065891[&&NHX:C=0.102.0])0.
9870000000:0.3230217707[&&NHX:C=0.102.0])0.8830000000:0.1685289112[&&NHX:C=0.102.0])0.99200000
00:0.5411783949[&&NHX:C=0.102.0])0.8700000000:0.1590362639[&&NHX:C=0.102.0])0.9910000000:0.281
6855906[&&NHX:C=0.102.0],((((((A7R385_VITVI:0.0621117793[&&NHX:C=255.102.51],(B9SA89_RICCO:0.
0057354279[&&NHX:C=255.102.51],((B9HD38_POPTR:0.0261293362[&&NHX:C=255.102.51],B9IH36_POPTR:0.
0390110488[&&NHX:C=255.102.51])0.9120000000:0.0361089684[&&NHX:C=255.102.51],((D7M9V1_ARALL:2.
206E-
7[&&NHX:C=255.102.51],Q8L9B5_ARATH:0.006714025[&&NHX:C=255.102.51])1.0000000000:0.2973611995[&
&NHX:C=255.102.51],(E4MWF4_THEHA:0.0554180971[&&NHX:C=255.102.51],(D7LIK3_ARALL:0.0749007598[&
&NHX:C=255.102.51],Q8L924_ARATH:0.0204509672[&&NHX:C=255.102.51])0.9920000000:0.1040031462[&&N
HX:C=255.102.51])0.9130000000:0.0631299441[&&NHX:C=255.102.51])0.9870000000:0.1411249959[&&NHX
:C=255.102.51])0.2590000000:0.0200659213[&&NHX:C=255.102.51])0.9590000000:0.092808498[&&NHX:C=
255.102.51])0.7970000000:0.1565919944[&&NHX:C=255.102.51],((Q0IN16_ORYSJ:0.1712005611[&&NHX:C=
255.102.51],(B6TGJ8_MAIZE:0.1569923195[&&NHX:C=255.102.51],C5YP66_SORBI:0.0675867669[&&NHX:C=2
55.102.51])0.9890000000:0.2210037124[&&NHX:C=255.102.51])0.9990000000:0.3265329201[&&NHX:C=255
.102.51],(C5WUP3_SORBI:0.3979822734[&&NHX:C=255.102.51],(((Q6ETN2_ORYSJ:0.1710732849[&&NHX:C=2
55.102.51],(B6U8R7_MAIZE:0.02029994[&&NHX:C=255.102.51],C5XW97_SORBI:0.0711771811[&&NHX:C=255.
102.51])0.9470000000:0.1366516904[&&NHX:C=255.102.51])0.9910000000:0.2848533015[&&NHX:C=255.10
2.51],(Q67W83_ORYSJ:0.076403785[&&NHX:C=255.102.51],(C5Z782_SORBI:0.0301299812[&&NHX:C=255.102
.51],(B6SZA7_MAIZE:0.0071299617[&&NHX:C=255.102.51],(B6TUB4_MAIZE:0.0071210142[&&NHX:C=255.102
.51],B6U769_MAIZE:0.0383627313[&&NHX:C=255.102.51])0.0000000000:2.449E-
7[&&NHX:C=255.102.51])0.7640000000:0.006896512[&&NHX:C=255.102.51])0.9640000000:0.1181893446[&
&NHX:C=255.102.51])0.8450000000:0.0798164409[&&NHX:C=255.102.51])0.9980000000:0.5913103377[&&N
HX:C=255.102.51],(A7Q6G6_VITVI:0.2999731863[&&NHX:C=255.102.51],(C6SZ04_SOYBN:0.4118148979[&&N
HX:C=255.102.51],(B9IM09_POPTR:0.2748442678[&&NHX:C=255.102.51],(Q5K4H9_GOSHI:0.2683235312[&&N
HX:C=255.102.51],(D7MFW5_ARALL:0.0303998571[&&NHX:C=255.102.51],Q8L8U9_ARATH:0.0070764711[&&NH
X:C=255.102.51])1.0000000000:0.6591954305[&&NHX:C=255.102.51])0.9410000000:0.1918839691[&&NHX:
C=255.102.51])0.8930000000:0.0898839722[&&NHX:C=255.102.51])0.5240000000:0.0602300907[&&NHX:C=
255.102.51])0.9750000000:0.3203288281[&&NHX:C=255.102.51])0.9940000000:0.5071826023[&&NHX:C=25
5.102.51])0.1750000000:0.0845921213[&&NHX:C=255.102.51])0.8240000000:0.0775672971[&&NHX:C=255.
102.51])0.9700000000:0.2341833393[&&NHX:C=255.102.51],(B8LQF9_PICSI:0.1533711291[&&NHX:C=0.153
.153],D5A8E6_PICSI:0.7800175716[&&NHX:C=0.153.153])0.0040000000:0.071204848[&&NHX:C=0.153.153]
)1.0000000000:0.5538089569[&&NHX:C=0.153.153],((((A7P0P3_VITVI:0.0821958072[&&NHX:C=255.102.5
1],(B9HTL5_POPTR:0.1288168938[&&NHX:C=255.102.51],(C6T2J5_SOYBN:0.3501614898[&&NHX:C=255.102.5
1],(B9SV84_RICCO:0.0894524716[&&NHX:C=255.102.51],(D7MUY4_ARALL:0.0292193661[&&NHX:C=255.102.5
1],Q9FFT2_ARATH:2.0861E-
6[&&NHX:C=255.102.51])1.0000000000:0.516407514[&&NHX:C=255.102.51])0.8730000000:0.0818846664[&
&NHX:C=255.102.51])0.7330000000:0.0521789651[&&NHX:C=255.102.51])0.8890000000:0.1031047516[&&N
HX:C=255.102.51])0.9830000000:0.4242088796[&&NHX:C=255.102.51],((A2X2I0_ORYSI:5.787E-
7[&&NHX:C=255.102.51],Q6YW53_ORYSJ:0.0077905427[&&NHX:C=255.102.51])0.9380000000:0.149258522[&
&NHX:C=255.102.51],(C5XY39_SORBI:0.0223275667[&&NHX:C=255.102.51],B6TUW9_MAIZE:0.1146489749[&&
NHX:C=255.102.51])0.9600000000:0.2200089454[&&NHX:C=255.102.51])0.9910000000:0.5031883751[&&NH
X:C=255.102.51])0.9880000000:0.4310342699[&&NHX:C=255.102.51],(((((((((D7L342_ARALL:0.0141281
895[&&NHX:C=255.102.51],Q9LUL1_ARATH:0.0363653345[&&NHX:C=255.102.51])1.0000000000:0.495775301
8[&&NHX:C=255.102.51],B9T3K6_RICCO:0.1062870406[&&NHX:C=255.102.51])0.7090000000:0.0290296366[
```

```
&&NHX:C=255.102.51],(B9GHX8_POPTR:0.0650937676[&&NHX:C=255.102.51],B9I0G0_POPTR:0.0429789002[&
&NHX:C=255.102.51])0.9520000000:0.0569615431[&&NHX:C=255.102.51])0.8890000000:0.0390280788[&&N
HX:C=255.102.51],Q8W4Z5_GOSHI:0.1015984002[&&NHX:C=255.102.51])0.9270000000:0.056997455[&&NHX:
C=255.102.51],(C6TCJ2_SOYBN:0.0588429214[&&NHX:C=255.102.51],C6SYW3_SOYBN:0.2455757303[&&NHX:C
=255.102.51])0.9850000000:0.1156642257[&&NHX:C=255.102.51])0.8250000000:0.0360946906[&&NHX:C=2
55.102.51],(Q8VZQ3_ARATH:0.0072392527[&&NHX:C=255.102.51],D7KFC7_ARALL:7.614E-
7[&&NHX:C=255.102.51])1.0000000000:0.1933890799[&&NHX:C=255.102.51])0.8750000000:0.0639988139[
&&NHX:C=255.102.51],A7QBZ2_VITVI:0.1276510779[&&NHX:C=255.102.51])0.9370000000:0.1353187843[&&
NHX:C=255.102.51],((B8ARW3_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q0JEF7_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.8850000000:0.0566292581[&&NHX:C=255.102.51],(B4FBQ7_MAIZE:0.015129121
4[&&NHX:C=255.102.51],(B6SR79_MAIZE:0.0547758777[&&NHX:C=255.102.51],C5YDQ9_SORBI:2.378E-
7[&&NHX:C=255.102.51])0.7670000000:0.0077497788[&&NHX:C=255.102.51])0.9170000000:0.0671285117[
&&NHX:C=255.102.51])0.9870000000:0.2657227879[&&NHX:C=255.102.51])0.9710000000:0.2483427858[&&
NHX:C=255.102.51],(A9P1V1_PICSI:0.3281202133[&&NHX:C=0.153.153],D5A972_PICSI:0.316169872[&&NHX
:C=0.153.153])0.8810000000:0.1377505373[&&NHX:C=0.153.153])0.0000000000:0.0614206598[&&NHX:C=0
.153.153],A9NMM6_PICSI:0.5556137217[&&NHX:C=0.153.153])0.8100000000:0.1156931092[&&NHX:C=0.153
.153])0.9710000000:0.3294795415[&&NHX:C=0.153.153],((P0DI24_PTEAA:0.6584711946[&&NHX:C=255.0.2
04],(P0DH84_ADICA:0.3095144828[&&NHX:C=255.0.204],P0DI28_PTEAA:0.2660669876[&&NHX:C=255.0.204]
)0.9880000000:0.3217037472[&&NHX:C=255.0.204])0.9130000000:0.1791678181[&&NHX:C=255.0.204],(P0
DI20_OSMLA:0.2722645144[&&NHX:C=255.0.204],(P0DI25_PTEAA:0.642984568[&&NHX:C=255.0.204],P0DI21
_OSMLA:0.0865339282[&&NHX:C=255.0.204])0.9890000000:0.2509623966[&&NHX:C=255.0.204])0.11500000
00:0.0885597424[&&NHX:C=255.0.204])0.9940000000:0.3466597583[&&NHX:C=255.0.204])0.8460000000:0
.1233522577[&&NHX:C=255.0.204],P0DH82_MARPO:0.6634286301[&&NHX:C=0.102.0])0.8520000000:0.12870
08292[&&NHX:C=0.102.0])0.0000000000:0.0270751258[&&NHX:C=0.102.0],((D8ST12_SELML:0.0061836644[
&&NHX:C=204.0.0],P0DH61_SELML:7.278E-
7[&&NHX:C=204.0.0])0.9990000000:0.5339045455[&&NHX:C=204.0.0],(P0DH63_SELML:0.6357724158[&&NHX
:C=204.0.0],(D8S6A8_SELML:1.3068E-
6[&&NHX:C=204.0.0],D8ST13_SELML:0.019797114[&&NHX:C=204.0.0])1.0000000000:0.8650509794[&&NHX:C
=204.0.0])0.0950000000:0.1343044476[&&NHX:C=204.0.0])0.9960000000:0.4839885786[&&NHX:C=204.0.0
])0.6120000000:0.0904567005[&&NHX:C=0.102.0],(D8T2C0_SELML:0.0128938823[&&NHX:C=204.0.0],D8T82
9_SELML:2.0301E-
6[&&NHX:C=204.0.0])1.0000000000:0.5888766123[&&NHX:C=204.0.0])0.9490000000:0.2547107054[&&NHX:
C=0.102.0],((P0DH65_SELML:1.0E-10[&&NHX:C=204.0.0],P0DH67_SELML:1.0E-
10[&&NHX:C=204.0.0])0.9990000000:0.6150298296[&&NHX:C=204.0.0],(D8SJ65_SELML:0.0031943693[&&NH
X:C=204.0.0],D8QNV6_SELML:0.0109378003[&&NHX:C=204.0.0])0.9990000000:0.5864708843[&&NHX:C=204.
0.0])0.9160000000:0.219749997[&&NHX:C=204.0.0])0.9200000000:0.1884352642[&&NHX:C=0.102.0])0.74
00000000:0.0885231457[&&NHX:C=0.102.0],(((((B8A927_ORYSI:1.0E-
10[&&NHX:C=255.102.51],Q5JM57_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9330000000:0.0642350888[&&NHX:C=255.102.51],(F2EL82_HORVD:0.151696053
3[&&NHX:C=255.102.51],C5XIF2_SORBI:0.084251172[&&NHX:C=255.102.51])0.7520000000:0.0390787409[&
&NHX:C=255.102.51])1.0000000000:0.369921443[&&NHX:C=255.102.51],((A7P756_VITVI:0.1309476397[&&
NHX:C=255.102.51],(B9GGL4_POPTR:0.0562204657[&&NHX:C=255.102.51],(B9GXD6_POPTR:0.0166208122[&&
NHX:C=255.102.51],B9RQG7_RICCO:0.1012299676[&&NHX:C=255.102.51])0.3420000000:0.0324460108[&&NH
X:C=255.102.51])0.9970000000:0.1599198094[&&NHX:C=255.102.51])0.7780000000:0.1006307381[&&NHX:
C=255.102.51],(Q1PFB8_ARATH:0.564120633[&&NHX:C=255.102.51],Q3EB59_ARATH:0.4710156324[&&NHX:C=
255.102.51])0.9060000000:0.169759743[&&NHX:C=255.102.51])0.4710000000:0.1058493429[&&NHX:C=255
.102.51])0.8230000000:0.1326499441[&&NHX:C=255.102.51],A9NN43_PICSI:0.2578595237[&&NHX:C=0.153
.153])0.9580000000:0.4517297229[&&NHX:C=0.153.153],P0DI26_PTEAA:1.1481291214[&&NHX:C=255.0.204
])0.9770000000:0.5045072549[&&NHX:C=255.0.204])0.5700000000:0.1661104583[&&NHX:C=0.102.0],(C5Y
HP6_SORBI:0.26262444[&&NHX:C=255.102.51],(A2YXI1_ORYSI:0.0167978292[&&NHX:C=255.102.51],Q6Z1G3
_ORYSJ:5.006E-
7[&&NHX:C=255.102.51])0.9640000000:0.383231063[&&NHX:C=255.102.51])1.0000000000:1.4210915767[&
&NHX:C=255.102.51])0.7520000000:0.2165051673[&&NHX:C=0.102.0],A9SG36_PHYPA:1.001908391[&&NHX:C
=0.102.0])0.7310000000:0.1566342729[&&NHX:C=0.102.0],(((C6T1Z6_SOYBN:0.3630719468[&&NHX:C=255.
102.51],(A1XGB4_CAPAN:0.3844115138[&&NHX:C=255.102.51],((((Q56X75_ARATH:3.4406E-
6[&&NHX:C=255.102.51],D7LD59_ARALL:0.0681404956[&&NHX:C=255.102.51])0.9550000000:0.177142471[&
&NHX:C=255.102.51],(Q8GWD5_ARATH:0.046015519[&&NHX:C=255.102.51],D7LD60_ARALL:0.0350639026[&&N
HX:C=255.102.51])0.9330000000:0.1098527566[&&NHX:C=255.102.51])1.0000000000:0.4376176262[&&NHX
:C=255.102.51],(B9NBE5_POPTR:0.3037040615[&&NHX:C=255.102.51],B9SXY8_RICCO:0.1793918559[&&NHX:
C=255.102.51])0.5380000000:0.0753033124[&&NHX:C=255.102.51])0.7330000000:0.0846739666[&&NHX:C=
255.102.51],(C5Y494_SORBI:0.3624340925[&&NHX:C=255.102.51],Q2R2T4_ORYSJ:0.1337204342[&&NHX:C=2
55.102.51])1.0000000000:0.9537571634[&&NHX:C=255.102.51])0.9490000000:0.2492713825[&&NHX:C=255
.102.51])0.7540000000:0.1153908435[&&NHX:C=255.102.51])0.9990000000:0.7099647501[&&NHX:C=255.1
02.51],(((Q5W6M3_ORYSJ:0.3176072581[&&NHX:C=255.102.51],(Q8LE26_ARATH:0.0399086373[&&NHX:C=255
.102.51],D7LBN4_ARALL:0.0055530683[&&NHX:C=255.102.51])1.0000000000:0.5434478094[&&NHX:C=255.1
02.51])0.5360000000:0.0533973384[&&NHX:C=255.102.51],((F2E5T1_HORVD:0.2437361198[&&NHX:C=255.1
02.51],B9F6Z0_ORYSJ:0.0129487611[&&NHX:C=255.102.51])0.9930000000:0.2681622827[&&NHX:C=255.102
.51],((C5WNF5_SORBI:0.0705844552[&&NHX:C=255.102.51],(F2D276_HORVD:0.0852417648[&&NHX:C=255.10
2.51],Q10MR5_ORYSJ:0.0811994461[&&NHX:C=255.102.51])0.4620000000:0.0516190063[&&NHX:C=255.102.
51])0.9030000000:0.1306619167[&&NHX:C=255.102.51],(F2E2E4_HORVD:0.1776869537[&&NHX:C=255.102.5
1],Q84NQ7_ORYSJ:0.1391852676[&&NHX:C=255.102.51])0.9950000000:0.3589358968[&&NHX:C=255.102.51]
)0.9940000000:0.3356004925[&&NHX:C=255.102.51])0.3220000000:0.0699660754[&&NHX:C=255.102.51])0
.9960000000:0.5565740806[&&NHX:C=255.102.51],(Q3EA54_ARATH:1.0626366772[&&NHX:C=255.102.51],(O
24088_MEDTR:0.729812591[&&NHX:C=255.102.51],((Q9FNE8_ARATH:0.5956107024[&&NHX:C=255.102.51],((
D7MMW4_ARALL:0.0132453621[&&NHX:C=255.102.51],Q501G6_ARATH:0.0030561384[&&NHX:C=255.102.51])1.
0000000000:0.287547105[&&NHX:C=255.102.51],(Q84WP5_ARATH:4.414E-
7[&&NHX:C=255.102.51],D7LIR2_ARALL:0.0423104153[&&NHX:C=255.102.51])0.9320000000:0.1241697077[
```

```
&&NHX:C=255.102.51])0.8930000000:0.1474975025[&&NHX:C=255.102.51])0.4320000000:0.1044970918[&&
NHX:C=255.102.51],((C5XEK4_SORBI:0.0991630981[&&NHX:C=255.102.51],B6UBY6_MAIZE:0.0466360093[&&
NHX:C=255.102.51])1.0000000000:1.0333835383[&&NHX:C=255.102.51],(A3A2W2_ORYSJ:0.1293234595[&&N
HX:C=255.102.51],(C5XTX2_SORBI:0.0294319123[&&NHX:C=255.102.51],(C4JAF2_MAIZE:0.0162149039[&&N
HX:C=255.102.51],B6TWJ1_MAIZE:0.0322246102[&&NHX:C=255.102.51])0.9550000000:0.0719861457[&&NHX
:C=255.102.51])0.9540000000:0.1407845864[&&NHX:C=255.102.51])0.9780000000:0.3316567721[&&NHX:C
=255.102.51])0.8760000000:0.209533997[&&NHX:C=255.102.51])0.9410000000:0.2731575101[&&NHX:C=25
5.102.51])0.8700000000:0.2482248898[&&NHX:C=255.102.51])0.8110000000:0.1471709197[&&NHX:C=255.
102.51])0.9090000000:0.266035022[&&NHX:C=255.102.51])0.8540000000:0.1406536636[&&NHX:C=255.102
.51],(P0DI23_PTEAA:0.3638873724[&&NHX:C=255.0.204],((Q2QNE3_ORYSJ:0.9428141977[&&NHX:C=255.102
.51],(B9SR15_RICCO:0.074691175[&&NHX:C=255.102.51],(Q9M2U0_ARATH:0.2996117551[&&NHX:C=255.102.
51],(B9HTK2_POPTR:0.0224581133[&&NHX:C=255.102.51],B9HMF8_POPTR:0.1083352348[&&NHX:C=255.102.5
1])0.8840000000:0.0680202795[&&NHX:C=255.102.51])0.0010000000:0.0701202488[&&NHX:C=255.102.51]
)0.8390000000:0.1472347211[&&NHX:C=255.102.51])0.9710000000:0.3526664429[&&NHX:C=255.102.51],(
A9T836_PHYPA:0.0694824656[&&NHX:C=0.102.0],(A9STU1_PHYPA:0.2077811896[&&NHX:C=0.102.0],A9S848_
PHYPA:0.098334149[&&NHX:C=0.102.0])0.7210000000:0.0766995392[&&NHX:C=0.102.0])0.9910000000:0.3
312385978[&&NHX:C=0.102.0])0.8290000000:0.1830123458[&&NHX:C=0.102.0])0.9910000000:0.605675619
5[&&NHX:C=0.102.0])0.7540000000:0.1458874824[&&NHX:C=0.102.0])0.7480000000:0.1365257702[&&NHX:
C=0.102.0],(A9RJH1_PHYPA:0.144233994[&&NHX:C=0.102.0],A9RZ57_PHYPA:0.1983721791[&&NHX:C=0.102.
0])1.0000000000:0.7851441577[&&NHX:C=0.102.0])0.8000000000:0.1718889715[&&NHX:C=0.102.0],(A9SU
70_PHYPA:1.0771605802[&&NHX:C=0.102.0],A9SHQ9_PHYPA:0.8838275394[&&NHX:C=0.102.0])0.7480000000
:0.1917828493[&&NHX:C=0.102.0])0.9190000000:0.3533671743[&&NHX:C=0.102.0],(A9S1T8_PHYPA:0.0807
52982[&&NHX:C=0.102.0],A9SB31_PHYPA:0.1378828635[&&NHX:C=0.102.0])0.9930000000:0.6680333666[&&
NHX:C=0.102.0])0.8100000000:0.1933673809[&&NHX:C=0.102.0],(D8QQW9_SELML:0.0159598724[&&NHX:C=2
04.0.0],D8R814_SELML:1.9118E-
6[&&NHX:C=204.0.0])0.9980000000:0.8315833293[&&NHX:C=204.0.0])0.8960000000:0.3684200386[&&NHX:
C=0.102.0],(F0YFA3_AURAN:1.2342213798[&&NHX:C=153.0.153],(((Q6NPF8_ARATH:0.3049818107[&&NHX:C=
255.102.51],(Q9SKN3_ARATH:0.2034978869[&&NHX:C=255.102.51],((B4FNS3_MAIZE:0.0639494914[&&NHX:C
=255.102.51],(A2Z669_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q339M6_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.8860000000:0.0413847487[&&NHX:C=255.102.51])0.9980000000:0.1431754634
[&&NHX:C=255.102.51],(P0DI68_BRADI:0.0765290038[&&NHX:C=255.102.51],(Q10Q78_ORYSJ:0.0909245817
[&&NHX:C=255.102.51],(P0DI66_MAIZE:0.0075352311[&&NHX:C=255.102.51],P0DI67_MAIZE:0.0166329733[
&&NHX:C=255.102.51])1.0000000000:0.4161146669[&&NHX:C=255.102.51])0.0000000000:0.0125170583[&&
NHX:C=255.102.51])0.7860000000:0.0348516736[&&NHX:C=255.102.51])0.9860000000:0.138997991[&&NHX
:C=255.102.51])0.8340000000:0.0614569886[&&NHX:C=255.102.51])0.9600000000:0.1289344536[&&NHX:C
=255.102.51],P0DI27_PTEAA:0.2598296224[&&NHX:C=0.153.153])0.0000000000:2.0608E-
6[&&NHX:C=0.153.153],((((((P0CB17_ARATH:0.480216568[&&NHX:C=255.102.51],Q66GI1_ARATH:0.1885479
959[&&NHX:C=255.102.51])0.9850000000:0.3430090516[&&NHX:C=255.102.51],(Q3ECT8_ARATH:0.58073784
04[&&NHX:C=255.102.51],(B6U300_MAIZE:0.1182995195[&&NHX:C=255.102.51],(B8BPI2_ORYSI:0.00803909
11[&&NHX:C=255.102.51],Q10EJ2_ORYSJ:3.222E-
7[&&NHX:C=255.102.51])0.7850000000:0.027586577[&&NHX:C=255.102.51])0.9630000000:0.2251065687[&
&NHX:C=255.102.51])0.8580000000:0.1428583832[&&NHX:C=255.102.51])0.9990000000:0.5864058797[&&N
HX:C=255.102.51],((((((B6TM88_MAIZE:0.2334576406[&&NHX:C=255.102.51],(B8AC36_ORYSI:1.0E-
10[&&NHX:C=255.102.51],Q5N794_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9790000000:0.1322448852[&&NHX:C=255.102.51])0.9010000000:0.0960439346
[&&NHX:C=255.102.51],(B8AYU8_ORYSI:1.0E-10[&&NHX:C=255.102.51],Q0DHM7_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.9990000000:0.1739821266[&&NHX:C=255.102.51])0.6560000000:0.0578273945
[&&NHX:C=255.102.51],B6TAX2_MAIZE:0.1990825852[&&NHX:C=255.102.51])0.9470000000:0.1309625401[&
&NHX:C=255.102.51],(B6T990_MAIZE:0.0458306984[&&NHX:C=255.102.51],(B8BD96_ORYSI:1.0E-
10[&&NHX:C=255.102.51],Q6K478_ORYSJ:1.0E-
10[&&NHX:C=255.102.51])0.8570000000:0.0383167599[&&NHX:C=255.102.51])0.9910000000:0.199656502[
&&NHX:C=255.102.51])0.9190000000:0.1262775291[&&NHX:C=255.102.51],(Q945M8_ARATH:0.259457159[&&
NHX:C=255.102.51],Q9LZM5_ARATH:0.3126877661[&&NHX:C=255.102.51])0.5400000000:0.0998269712[&&NH
X:C=255.102.51])0.9560000000:0.1966915287[&&NHX:C=255.102.51],Q8L7R5_ARATH:0.4660679344[&&NHX:
C=255.102.51])0.8910000000:0.1329239421[&&NHX:C=255.102.51],(P0DI71_GINBI:0.1189429955[&&NHX:C
=0.153.153],D5ACW4_PICSI:0.1565595833[&&NHX:C=0.153.153])0.8580000000:0.1045504787[&&NHX:C=0.1
53.153])0.7730000000:0.0785308795[&&NHX:C=0.102.0])0.9560000000:0.2331033471[&&NHX:C=0.102.0],
D8QNI1_SELML:0.2543912249[&&NHX:C=204.0.0])0.9010000000:0.0941443561[&&NHX:C=0.102.0],(P0DI22_
PTEAA:0.4113812185[&&NHX:C=255.0.204],(A9RKK4_PHYPA:0.137219608[&&NHX:C=0.102.0],A9RLK6_PHYPA:
0.1013502833[&&NHX:C=0.102.0])0.9980000000:0.2845910863[&&NHX:C=0.102.0])0.0200000000:0.034985
5794[&&NHX:C=0.102.0])0.9170000000:0.071173304[&&NHX:C=0.102.0],(P0DI70_GINBI:0.0386405264[&&N
HX:C=0.153.153],(P0DI69_GINBI:0.0395702192[&&NHX:C=0.153.153],(P0DI64_PINCO:0.0475859041[&&NHX
:C=0.153.153],A9NYX5_PICSI:0.0369442012[&&NHX:C=0.153.153])0.9990000000:0.2060688529[&&NHX:C=0
.153.153])0.9590000000:0.0792820537[&&NHX:C=0.153.153])0.9180000000:0.0758550083[&&NHX:C=0.153
.153])0.8400000000:0.039665901[&&NHX:C=0.102.0])0.9830000000:1.0359801188[&&NHX:C=0.102.0])0.8
320000000:0.3605052248[&&NHX:C=0.102.0])0.1290000000:0.1611562656[&&NHX:C=0.102.0],F0Y3N5_AURA
N:2.0301072217[&&NHX:C=153.0.153])0.8250000000:0.3570840661[&&NHX:C=0.102.0],(P0DI73_CHLAT:1.3
440643597[&&NHX:C=0.255.0],(P0DI72_CHLAT:0.7596787761[&&NHX:C=0.255.0],(C1EI34_MICSR:0.2170069
893[&&NHX:C=0.255.0],(C1N652_MICPC:0.2005289465[&&NHX:C=0.255.0],(A4S8B7_OSTLU:0.3041322708[&&
NHX:C=0.255.0],Q00U99_OSTTA:0.4199310783[&&NHX:C=0.255.0])1.0000000000:1.012298227[&&NHX:C=0.2
55.0])0.7880000000:0.1231202662[&&NHX:C=0.255.0])0.9900000000:0.7599833541[&&NHX:C=0.255.0])0.
2210000000:0.0886311845[&&NHX:C=0.255.0])0.9580000000:0.4736744275[&&NHX:C=0.255.0])0.84700000
00:0.2171104292[&&NHX:C=0.255.0],(((((F2UP45_SALS5:0.3385148984[&&NHX:C=51.51.51],A9V9T9_MONBE
:0.7708454274[&&NHX:C=51.51.51])0.8330000000:0.3957538001[&&NHX:C=51.51.51],(E9CJ08_CAPO3:0.24
04775858[&&NHX:C=51.51.51],(H3HWE3_STRPU:0.4338577596[&&NHX:C=51.51.51],(K1QGZ9_CRAGI:0.314788
5145[&&NHX:C=51.51.51],(E5SAH1_TRISP:0.2309742039[&&NHX:C=51.51.51],J9FDD0_WUCBA:1.8432397997[
&&NHX:C=51.51.51])0.9170000000:0.533301568[&&NHX:C=51.51.51])0.8310000000:0.1966583619[&&NHX:C
```

```
=51.51.51])0.9410000000:0.2944926893[&&NHX:C=51.51.51])0.9580000000:0.563083561[&&NHX:C=51.51.
51])0.8470000000:0.4041783468[&&NHX:C=51.51.51],(E9CAE7_CAPO3:1.1778502439[&&NHX:C=51.51.51],(
E9CJG0_CAPO3:0.5626094966[&&NHX:C=51.51.51],(H3IJM3_STRPU:0.3126205078[&&NHX:C=51.51.51],((K1R
PP1_CRAGI:0.2824917207[&&NHX:C=51.51.51],(C1L5K7_SCHJA:0.40595245[&&NHX:C=51.51.51],E5S0X4_TRI
SP:0.819022014[&&NHX:C=51.51.51])0.9140000000:0.3764174322[&&NHX:C=51.51.51])0.8840000000:0.23
52070877[&&NHX:C=51.51.51],D1LXF4_SACKO:0.3951710961[&&NHX:C=51.51.51])0.0000000000:0.12134887
99[&&NHX:C=51.51.51])0.9740000000:0.6244162474[&&NHX:C=51.51.51])0.2690000000:0.3193898738[&&N
HX:C=51.51.51])0.9300000000:0.421174168[&&NHX:C=51.51.51])0.8550000000:0.2830936486[&&NHX:C=51
.51.51],(E9C369_CAPO3:1.6610857326[&&NHX:C=51.51.51],((A7EWT4_SCLS1:0.0010525642[&&NHX:C=51.51
.51],(M7UBK4_BOTF1:8.202E-
7[&&NHX:C=51.51.51],G2YUJ4_BOTF4:0.0420248627[&&NHX:C=51.51.51]):0.0154755836[&&NHX:C=51.51.51
])0.0000000000:2.3854293201[&&NHX:C=51.51.51],(E1ZFT0_CHLVA:0.7557537048[&&NHX:C=51.51.51],((I
1BYX0_RHIO9:0.0860722622[&&NHX:C=51.51.51],I1BH89_RHIO9:0.0704917817[&&NHX:C=51.51.51])0.98900
00000:1.6854334588[&&NHX:C=51.51.51],(D6RM15_COPC7:0.862702193[&&NHX:C=51.51.51],Q5KF55_CRYNJ:
0.6222768225[&&NHX:C=51.51.51])0.3100000000:0.5419109259[&&NHX:C=51.51.51])0.9360000000:0.7384
280517[&&NHX:C=51.51.51])0.6460000000:0.1101963652[&&NHX:C=51.51.51])1.0000000000:0.3430412849
[&&NHX:C=51.51.51])0.2820000000:0.1322849755[&&NHX:C=51.51.51])0.6760000000:0.1609033807[&&NHX
:C=51.51.51],((A8N490_COPC7:2.1092419086[&&NHX:C=51.51.51],M1VAW8_CYAME:1.497784794[&&NHX:C=51
.51.51])0.3290000000:0.1921487649[&&NHX:C=51.51.51],(Q7RY36_NEUCR:1.9482166675[&&NHX:C=51.51.5
1],(((((C7ZQE2_NECH7:0.2582904977[&&NHX:C=51.51.51],C7ZCW5_NECH7:0.3734852967[&&NHX:C=51.51.51
])0.9930000000:0.7475349849[&&NHX:C=51.51.51],(((Q4WUJ1_ASPFU:0.1477083336[&&NHX:C=51.51.51],(
C8VAW4_EMENI:0.2081826559[&&NHX:C=51.51.51],(C0P0L7_AJECG:0.3248260471[&&NHX:C=51.51.51],J3K9K
9_COCIM:0.2045872196[&&NHX:C=51.51.51])0.9600000000:0.156995447[&&NHX:C=51.51.51])0.0810000000
:0.0716166174[&&NHX:C=51.51.51])0.9560000000:0.3104229115[&&NHX:C=51.51.51],(A7UWP7_NEUCR:0.30
97586661[&&NHX:C=51.51.51],(A7EHU9_SCLS1:1.0229472861[&&NHX:C=51.51.51],(I1S038_GIBZE:0.074952
3841[&&NHX:C=51.51.51],C7YRL0_NECH7:0.0275185242[&&NHX:C=51.51.51])0.9340000000:0.2133864358[&
&NHX:C=51.51.51])0.8740000000:0.1581772704[&&NHX:C=51.51.51])0.9210000000:0.2304459899[&&NHX:C
=51.51.51])0.8420000000:0.3996099392[&&NHX:C=51.51.51],((I1S431_GIBZE:0.24753302[&&NHX:C=51.51
.51],C7YJN8_NECH7:0.3030287771[&&NHX:C=51.51.51])0.9660000000:0.6119724814[&&NHX:C=51.51.51],(
Q4WUL4_ASPFU:1.2349873294[&&NHX:C=51.51.51],I1RH73_GIBZE:0.9876933406[&&NHX:C=51.51.51])0.5920
000000:0.198976601[&&NHX:C=51.51.51])0.9740000000:0.8022056458[&&NHX:C=51.51.51])0.9130000000:
0.3677769455[&&NHX:C=51.51.51])0.8120000000:0.3431355739[&&NHX:C=51.51.51],(D5G7L5_TUBMM:2.288
899949[&&NHX:C=51.51.51],(Q7S1V0_NEUCR:0.8840319976[&&NHX:C=51.51.51],((Q4WA14_ASPFU:0.1717216
695[&&NHX:C=51.51.51],(Q4WBB3_ASPFU:0.2909942736[&&NHX:C=51.51.51],Q5BAE2_EMENI:0.1088278173[&
&NHX:C=51.51.51])0.4210000000:0.0899508691[&&NHX:C=51.51.51])0.8600000000:0.2051499095[&&NHX:C
=51.51.51],(J3K1S1_COCIM:0.3552412857[&&NHX:C=51.51.51],C0NZ48_AJECG:0.3424389586[&&NHX:C=51.5
1.51])0.1580000000:0.2169443923[&&NHX:C=51.51.51])0.8990000000:0.4587512794[&&NHX:C=51.51.51])
0.8830000000:0.5682033004[&&NHX:C=51.51.51])0.7110000000:0.3095232393[&&NHX:C=51.51.51])0.7880
000000:0.3465032483[&&NHX:C=51.51.51],((Q5AKB5_CANAL:1.5759920053[&&NHX:C=51.51.51],(Q5AKB8_CA
NAL:0.3858294664[&&NHX:C=51.51.51],(Q5AKB6_CANAL:0.9598152234[&&NHX:C=51.51.51],H3ELT8_PRIPA:2
.6342037625[&&NHX:C=51.51.51])0.7510000000:0.659970404[&&NHX:C=51.51.51])0.8970000000:0.530096
4384[&&NHX:C=51.51.51])0.8900000000:0.5692742495[&&NHX:C=51.51.51],S2JPE5_MUCC1:1.901150223[&&
NHX:C=51.51.51])0.6190000000:0.1117537294[&&NHX:C=51.51.51])0.8390000000:0.2416883085[&&NHX:C=
51.51.51],((P53747_YEAST:1.5407538374[&&NHX:C=51.51.51],Q07629_YEAST:0.9022948245[&&NHX:C=51.5
1.51])0.8100000000:0.2913430572[&&NHX:C=51.51.51],((((C8V3Q0_EMENI:0.5149857705[&&NHX:C=51.51.
51],((J3K8E6_COCIM:0.5709816186[&&NHX:C=51.51.51],(C0P076_AJECG:0.4756425742[&&NHX:C=51.51.51]
,(Q5BA62_EMENI:0.4375792435[&&NHX:C=51.51.51],C0NHG7_AJECG:0.1967352096[&&NHX:C=51.51.51])1.00
00000000:0.8570621379[&&NHX:C=51.51.51])0.8150000000:0.1464968227[&&NHX:C=51.51.51])0.86200000
00:0.0913830497[&&NHX:C=51.51.51],(Q4WC24_ASPFU:0.9130946304[&&NHX:C=51.51.51],(A8N438_COPC7:0
.4435079693[&&NHX:C=51.51.51],(Q5KIU4_CRYNJ:0.5145408892[&&NHX:C=51.51.51],E3JZS8_PUCGT:0.8383
829675[&&NHX:C=51.51.51])0.8930000000:0.3852066446[&&NHX:C=51.51.51])0.9970000000:1.1754526811
[&&NHX:C=51.51.51])0.8900000000:0.6114072605[&&NHX:C=51.51.51])0.0000000000:1.9357E-
6[&&NHX:C=51.51.51])0.9020000000:0.1666564107[&&NHX:C=51.51.51],((Q0V428_PHANO:1.2412383004[&&
NHX:C=51.51.51],(A7EEJ3_SCLS1:0.2603931332[&&NHX:C=51.51.51],(F5H950_NEUCR:0.4595154554[&&NHX:
C=51.51.51],(I1RCT8_GIBZE:0.2796975478[&&NHX:C=51.51.51],C7YWL0_NECH7:0.1960996309[&&NHX:C=51.
51.51])1.0000000000:0.8107217418[&&NHX:C=51.51.51])0.5660000000:0.1743351723[&&NHX:C=51.51.51]
)0.9470000000:0.477531319[&&NHX:C=51.51.51])0.8790000000:0.3083857044[&&NHX:C=51.51.51],(D5GKD
3_TUBMM:0.8913295804[&&NHX:C=51.51.51],((Q0UHA4_PHANO:0.3273775567[&&NHX:C=51.51.51],A7EF22_SC
LS1:0.388490689[&&NHX:C=51.51.51])0.8730000000:0.1348624487[&&NHX:C=51.51.51],(Q7S4F1_NEUCR:0.
6800535001[&&NHX:C=51.51.51],(I1RTI0_GIBZE:0.2542657697[&&NHX:C=51.51.51],C7ZDD4_NECH7:0.10672
76032[&&NHX:C=51.51.51])0.9740000000:0.5612406013[&&NHX:C=51.51.51])0.9810000000:0.4628860405[
&&NHX:C=51.51.51])0.6100000000:0.0377625393[&&NHX:C=51.51.51])0.6210000000:0.0374964452[&&NHX:
C=51.51.51])0.8600000000:0.1914136182[&&NHX:C=51.51.51])0.9390000000:0.334069317[&&NHX:C=51.51
.51],((Q0UPR7_PHANO:0.9273546031[&&NHX:C=51.51.51],(Q5AVJ7_EMENI:0.0981412011[&&NHX:C=51.51.51
],Q4WIJ9_ASPFU:0.2444293896[&&NHX:C=51.51.51])0.9590000000:0.3215601657[&&NHX:C=51.51.51])0.07
10000000:0.1848146222[&&NHX:C=51.51.51],((C0NZJ7_AJECG:0.3308864647[&&NHX:C=51.51.51],J3K6Y8_C
OCIM:0.484345155[&&NHX:C=51.51.51])0.9750000000:0.2595809875[&&NHX:C=51.51.51],(((A7EYJ0_SCLS1
:0.9285542371[&&NHX:C=51.51.51],(Q1K6H5_NEUCR:0.4500216261[&&NHX:C=51.51.51],(I1RZW2_GIBZE:0.2
323190398[&&NHX:C=51.51.51],C7YRH9_NECH7:0.1920594613[&&NHX:C=51.51.51])0.9910000000:0.4796388
497[&&NHX:C=51.51.51])0.9180000000:0.3061376074[&&NHX:C=51.51.51])0.9210000000:0.3209002705[&&
NHX:C=51.51.51],(A7E5M8_SCLS1:1.0848999946[&&NHX:C=51.51.51],(Q5ATF8_EMENI:0.9162490283[&&NHX:
C=51.51.51],(Q7S8H8_NEUCR:1.2651253118[&&NHX:C=51.51.51],(Q0V4R7_PHANO:0.4552707407[&&NHX:C=51
.51.51],Q0V4R6_PHANO:0.9231267962[&&NHX:C=51.51.51])0.8900000000:0.3595615855[&&NHX:C=51.51.51
])0.6550000000:0.1244426022[&&NHX:C=51.51.51])0.5490000000:0.240225664[&&NHX:C=51.51.51])0.940
0000000:0.4552198144[&&NHX:C=51.51.51])0.8570000000:0.1602135838[&&NHX:C=51.51.51],(O74333_SCH
PO:1.3112491113[&&NHX:C=51.51.51],(H3GEF8_PHYRM:2.3475158948[&&NHX:C=51.51.51],(Q6CC67_YARLI:0
.6030174196[&&NHX:C=51.51.51],(Q5ANE3_CANAL:0.2342736894[&&NHX:C=51.51.51],(Q753K0_ASHGO:0.525
```

```
4880356[&&NHX:C=51.51.51],(P53279_YEAST:0.3827619903[&&NHX:C=51.51.51],Q12207_YEAST:0.25064232
13[&&NHX:C=51.51.51])0.9790000000:0.2680962127[&&NHX:C=51.51.51])0.8860000000:0.1255249014[&&N
HX:C=51.51.51])0.9370000000:0.2622597687[&&NHX:C=51.51.51])0.6220000000:0.1134616558[&&NHX:C=5
1.51.51])0.4230000000:0.2082427737[&&NHX:C=51.51.51])0.8690000000:0.1948924217[&&NHX:C=51.51.5
1])0.9040000000:0.161802022[&&NHX:C=51.51.51])0.0090000000:0.0264017709[&&NHX:C=51.51.51])0.98
80000000:0.5100582621[&&NHX:C=51.51.51])0.9150000000:0.3010538172[&&NHX:C=51.51.51],((Q6CD20_Y
ARLI:1.573858096[&&NHX:C=51.51.51],(C7YUH0_NECH7:0.4912764322[&&NHX:C=51.51.51],C8VBX0_EMENI:1
.4662401752[&&NHX:C=51.51.51])0.9670000000:0.7503908629[&&NHX:C=51.51.51])0.8160000000:0.23624
84696[&&NHX:C=51.51.51],((I1RLV3_GIBZE:0.3303900223[&&NHX:C=51.51.51],C7YJD0_NECH7:0.258147032
3[&&NHX:C=51.51.51])0.9850000000:0.8838898876[&&NHX:C=51.51.51],(A7ENZ3_SCLS1:0.8840316071[&&N
HX:C=51.51.51],A7EUN4_SCLS1:1.4252614741[&&NHX:C=51.51.51])0.6150000000:0.4317105952[&&NHX:C=5
1.51.51])0.9090000000:0.5080463528[&&NHX:C=51.51.51])0.6760000000:0.114546208[&&NHX:C=51.51.51
])0.8210000000:0.191540972[&&NHX:C=51.51.51])0.8320000000:0.2248033694[&&NHX:C=51.51.51])0.691
0000000:0.1233587621[&&NHX:C=51.51.51])0.8510000000:0.3019933788[&&NHX:C=51.51.51])0.783000000
0:0.1995081045[&&NHX:C=51.51.51])0.8620000000:0.0654811892[&&NHX:C=51.51.51])0.6090000000:0.46
51293058[&&NHX:C=102.0.102],(((((M4B8W0_HYAAE:0.1664644162[&&NHX:C=102.0.102],(G4ZSC4_PHYSP:0.
0545110897[&&NHX:C=102.0.102],(D0NLE1_PHYIT:0.0932087493[&&NHX:C=102.0.102],H3HBC4_PHYRM:0.089
334746[&&NHX:C=102.0.102])0.8410000000:0.0442959527[&&NHX:C=102.0.102])0.8540000000:0.08675551
55[&&NHX:C=102.0.102])0.9530000000:0.2257346228[&&NHX:C=102.0.102],(G4ZSC3_PHYSP:0.2845052378[
&&NHX:C=102.0.102],H3GGR0_PHYRM:0.0557664971[&&NHX:C=102.0.102])0.9650000000:0.2793438828[&&NH
X:C=102.0.102])0.9840000000:0.4331281336[&&NHX:C=102.0.102],(K3WS90_PYTUL:0.565763735[&&NHX:C=
102.0.102],(K3X3G8_PYTUL:0.4266246351[&&NHX:C=102.0.102],(D0NCN6_PHYIT:0.0362930603[&&NHX:C=10
2.0.102],(G4ZRP2_PHYSP:0.1325957748[&&NHX:C=102.0.102],H3GI99_PHYRM:0.1103059445[&&NHX:C=102.0
.102])0.4720000000:0.0766460283[&&NHX:C=102.0.102])0.9750000000:0.6188217155[&&NHX:C=102.0.102
])1.0000000000:1.0407713543[&&NHX:C=102.0.102])0.0820000000:0.1412952535[&&NHX:C=102.0.102])0.
8590000000:0.1318508935[&&NHX:C=102.0.102],(((H3HBC3_PHYRM:0.2238486051[&&NHX:C=102.0.102],(G4
ZSC0_PHYSP:0.1104462475[&&NHX:C=102.0.102],D0NLD9_PHYIT:0.0856597054[&&NHX:C=102.0.102])0.7340
000000:0.0834286325[&&NHX:C=102.0.102])0.9780000000:0.29564338[&&NHX:C=102.0.102],(K3WS83_PYTU
L:0.7613957169[&&NHX:C=102.0.102],K3WS84_PYTUL:0.2017944734[&&NHX:C=102.0.102])0.3290000000:0.
1226885462[&&NHX:C=102.0.102])0.9980000000:0.4814829148[&&NHX:C=102.0.102],(F0X038_9STRA:0.983
5704155[&&NHX:C=102.0.102],(K3WS85_PYTUL:0.2917716236[&&NHX:C=102.0.102],((H3H3L8_PHYRM:0.0165
068371[&&NHX:C=102.0.102],(D0NMH7_PHYIT:0.1635672194[&&NHX:C=102.0.102],G5AEA1_PHYSP:0.0739156
474[&&NHX:C=102.0.102])0.6740000000:0.0347529087[&&NHX:C=102.0.102])0.9980000000:0.7008747987[
&&NHX:C=102.0.102],((H3H3L9_PHYRM:0.0633321719[&&NHX:C=102.0.102],(G5AEA0_PHYSP:0.0593487727[&
&NHX:C=102.0.102],D0NMH8_PHYIT:0.0821256145[&&NHX:C=102.0.102])0.4480000000:0.0325146768[&&NHX
:C=102.0.102])0.9790000000:0.2707089786[&&NHX:C=102.0.102],(G5AE98_PHYSP:0.1196229984[&&NHX:C=
102.0.102],H3H3L4_PHYRM:0.0395827445[&&NHX:C=102.0.102])0.9690000000:0.1992150299[&&NHX:C=102.
0.102])0.5870000000:0.1772632321[&&NHX:C=102.0.102])1.0000000000:0.7119079715[&&NHX:C=102.0.10
2])0.0000000000:0.0279137579[&&NHX:C=102.0.102])0.8370000000:0.1633653529[&&NHX:C=102.0.102])0
.7880000000:0.1131429556[&&NHX:C=102.0.102])0.6350000000:0.2172129631[&&NHX:C=102.0.102],(F0WM
T2_9STRA:1.114510982[&&NHX:C=102.0.102],F0X036_9STRA:0.6065750253[&&NHX:C=102.0.102])0.8120000
000:0.2457656955[&&NHX:C=102.0.102])0.9980000000:0.4651293058[&&NHX:C=102.0.102])
```

Dataset 4. CASPL phylogeny (NHX format) corresponding to Figures 1E and Supplemental Figure 3

```
(((((((((((((((((((((((((((((D7LIN7_ARALL:0.09539173298238836[&&NHX:C=255.102.51],P0DI49_RAPRA
:0.0505428898963617[&&NHX:C=255.102.51])0.563:0.03522819820258207[&&NHX:C=255.102.51],P0DI45_R
APSA:0.0596086087511346[&&NHX:C=255.102.51])1.000:0.1725558782227109[&&NHX:D=Y:C=255.102.51],(
(D7LAP2_ARALL:0.01533160097118793[&&NHX:C=255.102.51],P0DI46_RAPSA:0.1125895260608164[&&NHX:C=
255.102.51])0.985:0.03169125359408159[&&NHX:D=Y:C=255.102.51],D7LZ50_ARALL:0.07268362752987566
[&&NHX:C=255.102.51])1.000:0.0928073842785 4134[&&NHX:D=Y:C=255.102.51])0.517:0.058190923088878
49[&&NHX:C=255.102.51],(((P0DI55_LOTJA:0.0599129499359446 5[&&NHX:C=255.102.51],C6TFL9_SOYBN:0.
0553675918179787 3[&&NHX:C=255.102.51])1.000:0.07140289899399707[&&NHX:D=Y:C=255.102.51],C6TH93
_SOYBN:0.0585900589929667 9[&&NHX:C=255.102.51])1.000:0.1092789811626284[&&NHX:D=Y:C=255.102.51
],((P0DI43_THECC:0.09084979035851402[&&NHX:C=255.102.51],B9SX13_RICCO:0.102512175194675 4[&&NHX
:C=255.102.51])0.942:0.04055797771704586[&&NHX:D=N:C=255.102.51],B9SX12_RICCO:0.07492658655135
936[&&NHX:C=255.102.51])0.188:0.0178862831829324[&&NHX:C=255.102.51])0.418:0.0478890166234912 9
[&&NHX:C=255.102.51])0.245:0.0357936850985431 9[&&NHX:C=255.102.51],(B9IIR4_POPTR:0.07859759543
909059[&&NHX:C=255.102.51],P0DI61_CUCME:0.2077189685010031[&&NHX:C=255.102.51])0.662:0.0369051
0547565876[&&NHX:C=255.102.51])0.419:0.0257512048052781 8[&&NHX:C=255.102.51],B9HBX2_POPTR:0.04
17776390936502[&&NHX:C=255.102.51])0.996:0.0646036301293870 4[&&NHX:D=Y:C=255.102.51],((((Q1W3A
5_STRAF:0.0888030791906395 3[&&NHX:C=255.102.51],P0DI31_TRIPD:0.0414919859299245 4[&&NHX:C=255.1
02.51])0.452:0.0277155931425067 6[&&NHX:C=255.102.51],(P0DI52_MIMGU:0.036068945081253 7[&&NHX:C=
255.102.51],P0DI51_MIMGU:0.08075365163571246[&&NHX:C=255.102.51])0.357:0.0179427904093037 8[&&N
HX:C=255.102.51])0.993:0.0902043550666159 6[&&NHX:D=Y:C=255.102.51],P0DI50_TOBAC:0.088533376893
70584[&&NHX:C=255.102.51])0.992:0.0899059879462029 8[&&NHX:D=Y:C=255.102.51],(P0DI62_CYNCS:0.03
57831123754335 9[&&NHX:C=255.102.51],P0DI32_TARKO:0.0534982768638775 8[&&NHX:C=255.102.51])1.000
:0.143885001771427 2[&&NHX:D=Y:C=255.102.51])0.717:0.0553069156119047 1[&&NHX:C=255.102.51])0.32
3:0.0183390046400565 3[&&NHX:C=255.102.51],(((P0DI30_TRIPD:0.0562775080256791 9[&&NHX:C=255.102.
51],P0DI53_MIMGU:0.049007731578663[&&NHX:C=255.102.51])0.992:0.0451704483525393 9[&&NHX:D=Y:C=2
55.102.51],P0DI60_HELAN:0.1586006744636458[&&NHX:C=255.102.51])0.908:0.0345286609221640 4[&&NHX
:D=N:C=255.102.51],(A7QF77_VITVI:0.0845391728610290 2[&&NHX:C=255.102.51],((B9SCX0_RICCO:0.1048
539627404477[&&NHX:C=255.102.51],((G7IHF9_MEDTR:0.0668079471877927 2[&&NHX:C=255.102.51],P0DI56
_LOTJA:0.1438542637098998[&&NHX:C=255.102.51])0.657:0.0471459429802613 3[&&NHX:C=255.102.51],(P
0DI41_VIGUN:0.0716905329647672 3[&&NHX:C=255.102.51],C6T4E0_SOYBN:0.0496893116125403 5[&&NHX:C=2
55.102.51])0.958:0.0556485700437731 2[&&NHX:D=Y:C=255.102.51])1.000:0.234525910846291 2[&&NHX:D=
Y:C=255.102.51])0.649:0.0426058778703479 5[&&NHX:C=255.102.51],(B9HQ42_POPTR:0.165377280189497[
&&NHX:C=255.102.51],D7LGW9_ARALL:0.2070096535505175[&&NHX:C=255.102.51])0.740:0.05322395499201
694[&&NHX:C=255.102.51])0.996:0.0632096506360499 8[&&NHX:D=Y:C=255.102.51])0.291:0.022152828417
29956[&&NHX:C=255.102.51])0.420:0.0272291085739796 5[&&NHX:C=255.102.51])0.653:0.03345901747044
213[&&NHX:C=255.102.51],A7PP95_VITVI:0.1052240330555715[&&NHX:C=255.102.51])0.726:0.0441630191
130994[&&NHX:C=255.102.51],(((B6U045_MAIZE:0.0695237561610756 2[&&NHX:C=255.102.51],B8ART0_ORYS
I:0.083547597217398 4[&&NHX:C=255.102.51])0.964:0.0412441052749598 8[&&NHX:D=Y:C=255.102.51],(P0
DI38_BRADI:0.0212333813754961 4[&&NHX:C=255.102.51],E6Y2A0_WHEAT:0.0687903674624104 2[&&NHX:C=25
5.102.51])1.000:0.0595795486244689 4[&&NHX:D=Y:C=255.102.51])0.999:0.0515118827309898 5[&&NHX:D=
Y:C=255.102.51],((C5YLC9_SORBI:0.109776680265727[&&NHX:C=255.102.51],P0DI37_BRADI:0.1101045105
323271[&&NHX:C=255.102.51])0.646:0.0301895184366225[&&NHX:C=255.102.51],A2YQB8_ORYSI:0.1232714
170474622[&&NHX:C=255.102.51])0.397:0.0203328892468679 4[&&NHX:C=255.102.51])1.000:0.1928790718
437724[&&NHX:D=Y:C=255.102.51])0.973:0.0733579252494888[&&NHX:D=Y:C=255.102.51],(((((((((B6T95
9_MAIZE:0.0697548021628227[&&NHX:C=255.102.51],((P0DI36_BRADI:0.0393290742168846 7[&&NHX:C=255.
102.51],Q6Z2U5_ORYSJ:0.1715955661154068[&&NHX:C=255.102.51])0.441:0.0109174544056587 7[&&NHX:C=
255.102.51],P0DI42_WHEAT:0.0728587428750777 2[&&NHX:C=255.102.51])0.971:0.0355992025404139 3[&&N
HX:D=Y:C=255.102.51])0.594:0.0329742525404968 9[&&NHX:C=255.102.51],((A2XU91_ORYSI:0.0350058657
4800581[&&NHX:C=255.102.51],C5Y9U6_SORBI:0.0654968403237071 6[&&NHX:C=255.102.51])1.000:0.07698
824113584442[&&NHX:D=Y:C=255.102.51],B8AEC9_ORYSI:0.2087132893838256[&&NHX:C=255.102.51])0.819
:0.0495535433837905 4[&&NHX:D=N:C=255.102.51])0.503:0.0432102007155708 4[&&NHX:C=255.102.51],Q5N
RN4_SOLDE:0.2593435135339724[&&NHX:C=255.102.51])0.534:0.0450101450275204 1[&&NHX:C=255.102.51]
,(P0DI44_SOLTU:0.1357534183757059[&&NHX:C=255.102.51],P0DI59_LACSA:0.201386759423412 5[&&NHX:C=
255.102.51])0.759:0.0404226280874446 7[&&NHX:C=255.102.51])0.249:0.0203221808375451 1[&&NHX:C=25
5.102.51],(((B9I534_POPTR:0.0507840131228980 1[&&NHX:C=255.102.51],D7M7B3_ARALL:0.1401953180588
81[&&NHX:C=255.102.51])0.802:0.0466447829895922 4[&&NHX:D=N:C=255.102.51],B9T4E6_RICCO:0.077710
68758712338[&&NHX:C=255.102.51])0.671:0.0380143146484164 4[&&NHX:C=255.102.51],P0DI54_MALDO:0.0
64009929391365[&&NHX:C=255.102.51])0.497:0.0332024430854307 6[&&NHX:C=255.102.51])0.160:0.02450
788979702096[&&NHX:C=255.102.51],A7PMY7_VITVI:0.0731190090689004 4[&&NHX:C=255.102.51])0.374:0.
0290963542438088 3[&&NHX:C=255.102.51],((B9HI87_POPTR:0.1702150928628599[&&NHX:C=255.102.51],B9
S8Z3_RICCO:0.1773508593518612[&&NHX:C=255.102.51])0.437:0.0630418042448578 5[&&NHX:C=255.102.51
],D7KBH3_ARALL:0.186328323520407 6[&&NHX:C=255.102.51])0.824:0.0698221433309529 2[&&NHX:D=N:C=25
5.102.51])0.247:0.0251978126689011 8[&&NHX:C=255.102.51],((P0DKC2_LOTJA:0.0675271693123440 7[&&N
HX:C=255.102.51],G7L218_MEDTR:0.0231998408602321 1[&&NHX:C=255.102.51])1.000:0.1236865149496225
[&&NHX:D=Y:C=255.102.51],(((P0DI58_LOTJA:0.0563903992092253 6[&&NHX:C=255.102.51],G7JG80_MEDTR:
0.0677540571561042 9[&&NHX:C=255.102.51])0.574:0.0190155537170478 4[&&NHX:C=255.102.51],C6T4A0_S
OYBN:0.0649416394900880 2[&&NHX:C=255.102.51])1.000:0.0749381466280386[&&NHX:D=Y:C=255.102.51],
(C6T1G0_SOYBN:0.0767860716645009 4[&&NHX:C=255.102.51],G7KGQ4_MEDTR:0.0927633960611419 6[&&NHX:C
=255.102.51])0.997:0.0556201608826709 2[&&NHX:D=Y:C=255.102.51])1.000:0.0946325212156079 3[&&NHX
:D=Y:C=255.102.51])0.426:0.0378123593981324[&&NHX:C=255.102.51])0.721:0.0552185337369955 3[&&NH
X:C=255.102.51],P0DI35_LACSI:0.1637071461731535[&&NHX:C=255.102.51])1.000:0.1067923885915768[&
&NHX:D=Y:C=255.102.51])0.967:0.0819865566053503 3[&&NHX:D=Y:C=255.102.51],(P0DH81_PICGL:0.05030
92942161984[&&NHX:C=255.102.51],P0DH80_PINTA:0.0576799418219402 4[&&NHX:C=255.102.51])1.000:0.1
62667117211436 8[&&NHX:D=Y:C=255.102.51])1.000:0.1810558840241884[&&NHX:D=Y:C=255.102.51],A9P0A
```

```
6_PICSI:0.186091517863786[&&NHX:C=255.102.51])0.683:0.0590845030082016 4[&&NHX:C=255.102.51],((
A7QC16_VITVI:0.1342418605525494[&&NHX:C=255.102.51],((((B9GIE4_POPTR:0.03949032785200249[&&NHX
:C=255.102.51],B9SV63_RICCO:0.1328817774827361[&&NHX:C=255.102.51])0.422:0.0210216090706600l[&
&NHX:C=255.102.51],B9I0U9_POPTR:0.04802840238362862[&&NHX:C=255.102.51])0.403:0.02840303296933
148[&&NHX:C=255.102.51],(D7MFJ8_ARALL:0.09687638502370793[&&NHX:C=255.102.51],D7MM00_ARALL:0.0
504304299147104[&&NHX:C=255.102.51])1.000:0.1926526421238034[&&NHX:D=Y:C=255.102.51])0.458:0.0
516767897553260 9[&&NHX:C=255.102.51],C6TG62_SOYBN:0.2132315468234128[&&NHX:C=255.102.51])0.954
:0.08443946112151389[&&NHX:D=Y:C=255.102.51])0.998:0.1303107462467442[&&NHX:D=Y:C=255.102.51],
((B6TUH4_MAIZE:0.08236358851608372[&&NHX:C=255.102.51],C5YRU8_SORBI:0.0231330981798021[&&NHX:C
=255.102.51])0.981:0.08737857790213957[&&NHX:D=Y:C=255.102.51],A2ZMM4_ORYSI:0.114242396513753 9
[&&NHX:C=255.102.51])1.000:0.2403083730065255[&&NHX:D=Y:C=255.102.51])1.000:0.2287443995536675
[&&NHX:D=Y:C=255.102.51])0.486:0.04746501939574754[&&NHX:C=255.102.51],(((((Q9LR57_ARATH:0.094
8725821760911[&&NHX:C=255.102.51],D7M2M8_ARALL:0.02207765604650024[&&NHX:C=255.102.51])1.000:0
.1165255479473229[&&NHX:D=Y:C=255.102.51],(B9N5U6_POPTR:0.08924069920136254[&&NHX:C=255.102.51
],B9RW00_RICCO:0.09193152008257927[&&NHX:C=255.102.51])0.991:0.04775844425297254[&&NHX:D=Y:C=2
55.102.51])0.929:0.04276643473991325[&&NHX:D=N:C=255.102.51],(A7R333_VITVI:0.191891482386896 8[
&&NHX:C=255.102.51],(B9RZ92_RICCO:0.06685050103742768[&&NHX:C=255.102.51],B9H2V1_POPTR:0.11743
50186501003[&&NHX:C=255.102.51])1.000:0.1617693616262969[&&NHX:D=Y:C=255.102.51])0.699:0.05642
614917324153[&&NHX:C=255.102.51])0.661:0.03794679031876665[&&NHX:C=255.102.51],A7PJ32_VITVI:0.
148238099065133 2[&&NHX:C=255.102.51])0.933:0.06507235716172806[&&NHX:D=N:C=255.102.51],((A2Y2B
7_ORYSI:0.1421853405851285[&&NHX:C=255.102.51],B6SZU6_MAIZE:0.1157339732186806[&&NHX:C=255.102
.51]):0.08008005687879392[&&NHX:C=255.102.51],A2WMK7_ORYSI:0.233286787437905[&&NHX:C=255.102.5
1])0.981:0.2166596539232351[&&NHX:D=Y:C=255.102.51])1.000:0.1136918594504625[&&NHX:D=Y:C=255.1
02.51])0.999:0.05131208169090086[&&NHX:D=Y:C=255.102.51],(P0DH83_MARPO:0.3554640367930859[&&NH
X:C=255.102.51],(A9TKY8_PHYPA:0.1899872720445504[&&NHX:C=255.102.51],(A9SEY7_PHYPA:0.214451419
8600978[&&NHX:C=255.102.51],(A9STS7_PHYPA:0.1067339357898235[&&NHX:C=255.102.51],A9TZ63_PHYPA:
0.0419860265599587[&&NHX:C=255.102.51])1.000:0.09777287648462259[&&NHX:D=Y:C=255.102.51])0.918
:0.07004509874574498[&&NHX:D=N:C=255.102.51])1.000:0.2697681526650188[&&NHX:D=Y:C=255.102.51])
0.981:0.1072209257713331[&&NHX:D=Y:C=255.102.51])0.473:0.08548549862503538[&&NHX:C=255.102.51]
,((((((((D2KQI6_BETVM:0.1821607879462184[&&NHX:C=255.102.51],A7NW79_VITVI:0.1175612187334706[
&&NHX:C=255.102.51])0.901:0.04506328329146399[&&NHX:D=N:C=255.102.51],C6SVQ5_SOYBN:0.116214503
8049531[&&NHX:C=255.102.51])0.858:0.03185433598879533[&&NHX:D=N:C=255.102.51],A2PZE5_IPONI:0.2
18878642217809 3[&&NHX:C=255.102.51])0.498:0.02721974816572218[&&NHX:C=255.102.51],B9HMP5_POPTR
:0.1003899393684136[&&NHX:C=255.102.51])0.824:0.03277260245774929[&&NHX:D=N:C=255.102.51],B9RT
03_RICCO:0.1111459760633266[&&NHX:C=255.102.51])0.983:0.04995689036147107[&&NHX:D=Y:C=255.102.
51],D7MAF7_ARALL:0.1413159048910667[&&NHX:C=255.102.51])0.578:0.0363422810192581[&&NHX:C=255.1
02.51],D7L5G6_ARALL:0.2369290999153358[&&NHX:C=255.102.51])0.366:0.04045407456225369[&&NHX:C=2
55.102.51],(Q1EPG6_MUSAC:0.1259311240117835[&&NHX:C=255.102.51],((B6U361_MAIZE:0.0416754401902
6068[&&NHX:C=255.102.51],C5X4A5_SORBI:0.05450808477415363[&&NHX:C=255.102.51])0.998:0.04969818
209755414[&&NHX:D=Y:C=255.102.51],Q6YT98_ORYSJ:0.0897667142714236[&&NHX:C=255.102.51])1.000:0.
137665222364409 4[&&NHX:D=Y:C=255.102.51])0.999:0.09287968490952872[&&NHX:D=Y:C=255.102.51])1.0
00:0.2512580259393917[&&NHX:D=Y:C=255.102.51],((((B4FAP1_MAIZE:0.04378889016156055[&&NHX:C=255
.102.51],Q9ARX2_ORYSJ:0.09196631591852696[&&NHX:C=255.102.51])1.000:0.3178393815004146[&&NHX:D
=Y:C=255.102.51],Q1EPG7_MUSAC:0.2671483058910404[&&NHX:C=255.102.51])0.917:0.1000668519715339[
&&NHX:D=N:C=255.102.51],((((C6SZP8_SOYBN:0.2559474169073139[&&NHX:C=255.102.51],B9HMP6_POPTR:0
.1361069449510431[&&NHX:C=255.102.51])0.228:0.02453865139086179[&&NHX:C=255.102.51],(A7NW78_VI
TVI:0.1486085706904947[&&NHX:C=255.102.51],A7PTY8_VITVI:0.2271150514178161[&&NHX:C=255.102.51]
)0.419:0.03407859551060753[&&NHX:C=255.102.51])0.249:0.03611775422403238[&&NHX:C=255.102.51],B
9RT04_RICCO:0.1144290395567515[&&NHX:C=255.102.51])0.400:0.04504623040872165[&&NHX:C=255.102.5
1],(D7MAF6_ARALL:0.1128349131095968[&&NHX:C=255.102.51],D7MAF5_ARALL:0.04261386216372608[&&NHX
:C=255.102.51])1.000:0.2286338531924544[&&NHX:D=Y:C=255.102.51])0.994:0.1085003916836402[&&NHX
:D=Y:C=255.102.51])0.940:0.0917542234022878 4[&&NHX:D=N:C=255.102.51],(((C5Y376_SORBI:0.1753093
866069584[&&NHX:C=255.102.51],Q2R0D1_ORYSJ:0.1018942833646043[&&NHX:C=255.102.51])1.000:0.2563
672382152787[&&NHX:D=Y:C=255.102.51],((C5Y7C7_SORBI:0.0874637156871183[&&NHX:C=255.102.51],Q2R
0D2_ORYSJ:0.1696576099847486[&&NHX:C=255.102.51])0.523:0.07324498400505097[&&NHX:C=255.102.51]
,C5Y7C8_SORBI:0.3206998677385703[&&NHX:C=255.102.51])0.664:0.1093916471117985[&&NHX:C=255.102.
51])1.000:0.1672517907281832[&&NHX:D=Y:C=255.102.51],(C5Y7C6_SORBI:0.239669363321576[&&NHX:C=2
55.102.51],Q2R0D4_ORYSJ:0.1628185035944385[&&NHX:C=255.102.51])1.000:0.2383133815300889[&&NHX:
D=Y:C=255.102.51])1.000:0.2659253265944309[&&NHX:D=Y:C=255.102.51])0.941:0.0965012897694696 2[&
&NHX:D=N:C=255.102.51])0.629:0.0650323079097482[&&NHX:C=255.102.51])0.672:0.1171404070687886[&
&NHX:C=255.102.51],((((B9I3X5_POPTR:0.09723849879845409[&&NHX:C=255.102.51],B9IFI5_POPTR:0.099
3016245614278[&&NHX:C=255.102.51])1.000:0.1328508691750004[&&NHX:D=Y:C=255.102.51],((B9RA90_RI
CCO:0.07970621978005006[&&NHX:C=255.102.51],A7PHN8_VITVI:0.1809279299327342[&&NHX:C=255.102.51
])0.761:0.06378409847710453[&&NHX:C=255.102.51],D7MGK0_ARALL:0.4660086525865495[&&NHX:C=255.10
2.51])0.485:0.04912590113376313[&&NHX:C=255.102.51])0.994:0.1424936322491019[&&NHX:D=Y:C=255.1
02.51],(B9RH17_RICCO:0.1482571827507792[&&NHX:C=255.102.51],B9GFG6_POPTR:0.1966015415486028[&&
NHX:C=255.102.51])0.907:0.04983946813537535[&&NHX:D=N:C=255.102.51])0.445:0.03607300685266827[
&&NHX:C=255.102.51],A7PA04_VITVI:0.1973300981516986[&&NHX:C=255.102.51])1.000:0.18633999263304
94[&&NHX:D=Y:C=255.102.51])0.909:0.06800796631957058[&&NHX:D=N:C=255.102.51],(((((((P0DH84_ADI
CA:0.1739685493132664[&&NHX:C=102.255.102],P0DI28_PTEAA:0.1659579701531219[&&NHX:C=102.255.102
])1.000:0.1377601382941764[&&NHX:D=Y:C=102.255.102],P0DI24_PTEAA:0.2955331808674594[&&NHX:C=10
2.255.102])0.984:0.06762968369057615[&&NHX:D=Y:C=102.255.102],(P0DI20_OSMLA:0.1622567921941403
[&&NHX:C=102.255.102],(P0DI21_OSMLA:0.01687983938324497[&&NHX:C=102.255.102],P0DI25_PTEAA:0.25
52460680030351[&&NHX:C=102.255.102])1.000:0.09677890500262963[&&NHX:D=Y:C=102.255.102])0.989:0
.05180178824763126[&&NHX:D=Y:C=102.255.102])1.000:0.1162079308699777[&&NHX:D=Y:C=102.255.102],
((D8T2C0_SELML:0.2554842640163954[&&NHX:C=102.255.102],(D8SJ65_SELML:0.2552056742750133[&&NHX:
C=102.255.102],P0DH65_SELML:0.3122869522211832[&&NHX:C=102.255.102])0.988:0.1349177203655499[&
```

```
&NHX:D=Y:C=102.255.102])0.889:0.0852685285295225 7[&&NHX:D=N:C=102.255.102],(((((((E4MWF4_THEHA
:0.0336613913600073 6[&&NHX:C=102.255.102],D7LIK3_ARALL:0.08923358439911663[&&NHX:C=102.255.102
])0.999:0.0596287368402623 2[&&NHX:D=Y:C=102.255.102],D7M9V1_ARALL:0.1650170443844348[&&NHX:C=1
02.255.102])0.801:0.04694602058710794[&&NHX:D=N:C=102.255.102],(B9SA89_RICCO:0.016150753758671
79[&&NHX:C=102.255.102],A7R385_VITVI:0.08127335961710501[&&NHX:C=102.255.102])0.853:0.05200316
856754714[&&NHX:D=N:C=102.255.102])0.488:0.04134534892055201[&&NHX:C=102.255.102],(C5WUP3_SORB
I:0.221678819536915 3[&&NHX:C=102.255.102],(((B6TGJ8_MAIZE:0.06711432611257989[&&NHX:C=102.255.
102],C5YP66_SORBI:0.05347746599502162[&&NHX:C=102.255.102])1.000:0.1313099621779434[&&NHX:D=Y:
C=102.255.102],Q0IN16_ORYSJ:0.07861431214051932[&&NHX:C=102.255.102])0.998:0.1290737258478955[
&&NHX:D=Y:C=102.255.102],((((Q5K4H9_GOSHI:0.2131591704446975[&&NHX:C=102.255.102],D7MFW5_ARALL
:0.4191198033921451[&&NHX:C=102.255.102])0.809:0.0727547696583922[&&NHX:D=N:C=102.255.102],B9I
M09_POPTR:0.117394060107901 6[&&NHX:C=102.255.102])0.776:0.05671928661838356[&&NHX:C=102.255.10
2],(A7Q6G6_VITVI:0.158278372793017[&&NHX:C=102.255.102],C6SZ04_SOYBN:0.2494516568458654[&&NHX:
C=102.255.102])0.739:0.05064438248322338[&&NHX:C=102.255.102])1.000:0.2304524078959499[&&NHX:D
=Y:C=102.255.102],((B6U8R7_MAIZE:0.0788166700499474[&&NHX:C=102.255.102],Q6ETN2_ORYSJ:0.088499
58066087332[&&NHX:C=102.255.102])1.000:0.1581998314548887[&&NHX:D=Y:C=102.255.102],(B6SZA7_MAI
ZE:0.0578446820840781 7[&&NHX:C=102.255.102],Q67W83_ORYSJ:0.04183886210026011[&&NHX:C=102.255.1
02])0.920:0.05392875847202837[&&NHX:D=N:C=102.255.102])1.000:0.3182972548317443[&&NHX:D=Y:C=10
2.255.102])1.000:0.1997353662059654[&&NHX:D=Y:C=102.255.102])0.848:0.09967657584796626[&&NHX:D
=N:C=102.255.102])0.867:0.0804494265933987 1[&&NHX:D=N:C=102.255.102])0.993:0.161823184140641 5[
&&NHX:D=Y:C=102.255.102],D5A8E6_PICSI:0.3206397655602619[&&NHX:C=102.255.102])0.404:0.02850578
563420838[&&NHX:C=102.255.102],B8LQF9_PICSI:0.1061887710405551[&&NHX:C=102.255.102])1.000:0.23
33492873037159[&&NHX:D=Y:C=102.255.102],((D8ST12_SELML:0.2362753981776577[&&NHX:C=102.255.102]
,P0DH63_SELML:0.3044155407090396[&&NHX:C=102.255.102])0.989:0.1348628135764205[&&NHX:D=Y:C=102
.255.102],D8S6A8_SELML:0.3921125412390281[&&NHX:C=102.255.102])1.000:0.2095836371192813[&&NHX:
D=Y:C=102.255.102])0.411:0.04102458556511644[&&NHX:C=102.255.102])0.912:0.0667217900008413 3[&&
NHX:D=N:C=102.255.102])0.623:0.04197695288440512[&&NHX:C=102.255.102],P0DH82_MARPO:0.344193367
6288908[&&NHX:C=102.255.102])0.523:0.03670144894353147[&&NHX:C=102.255.102],(((((((Q8W4Z5_GOSH
I:0.04179177664870909[&&NHX:C=102.255.102],B9T3K6_RICCO:0.0929833888779824[&&NHX:C=102.255.102
])0.501:0.01603573278515974[&&NHX:C=102.255.102],(B9GHX8_POPTR:0.04272949524161317[&&NHX:C=102
.255.102],D7L342_ARALL:0.2970415843403169[&&NHX:C=102.255.102])0.597:0.03331655164067022[&&NHX
:C=102.255.102])0.936:0.0333242448760941[&&NHX:D=N:C=102.255.102],(C6TCJ2_SOYBN:0.020302234767
20082[&&NHX:C=102.255.102],C6SYW3_SOYBN:0.1098245228560519[&&NHX:C=102.255.102])0.999:0.060309
10037955253[&&NHX:D=Y:C=102.255.102])0.346:0.01976141934120004[&&NHX:C=102.255.102],Q8VZQ3_ARA
TH:0.1225170356557472[&&NHX:C=102.255.102])0.419:0.02461853264304696[&&NHX:C=102.255.102],A7QB
Z2_VITVI:0.08231245179662462[&&NHX:C=102.255.102])0.999:0.1047850263454173[&&NHX:D=Y:C=102.255
.102],(B4FBQ7_MAIZE:0.1406276562099149[&&NHX:C=102.255.102],A9NMM6_PICSI:0.2940772513144406[&&
NHX:C=102.255.102])0.870:0.07532077455150209[&&NHX:D=N:C=102.255.102])0.674:0.0461956093030617
[&&NHX:C=102.255.102],(D5A972_PICSI:0.1543646550075995[&&NHX:C=102.255.102],A9P1V1_PICSI:0.125
1786522648246[&&NHX:C=102.255.102])0.977:0.08015198268834156[&&NHX:D=Y:C=102.255.102])1.000:0.
1525765145959023[&&NHX:D=Y:C=102.255.102])0.680:0.06230741743926636[&&NHX:C=102.255.102],(((((
D7MUY4_ARALL:0.2627515399804743[&&NHX:C=102.255.102],B9SV84_RICCO:0.04762115610972616[&&NHX:C=
102.255.102])0.946:0.0437023726155966[&&NHX:D=N:C=102.255.102],C6T2J5_SOYBN:0.2005349482652697
[&&NHX:C=102.255.102])0.900:0.03360620438119051[&&NHX:D=N:C=102.255.102],B9HTL5_POPTR:0.084208
07581277191[&&NHX:C=102.255.102])0.927:0.0697039161648549 4[&&NHX:D=N:C=102.255.102],A7P0P3_VIT
VI:0.01500394902369891[&&NHX:C=102.255.102])1.000:0.296238066305915[&&NHX:D=Y:C=102.255.102],(
A2X2I0_ORYSI:0.08385249414393742[&&NHX:C=102.255.102],C5XY39_SORBI:0.1363632429127019[&&NHX:C=
102.255.102])1.000:0.2041414516311602[&&NHX:D=Y:C=102.255.102])1.000:0.2130438759142225[&&NHX:
D=Y:C=102.255.102])1.000:0.146817452181253[&&NHX:D=Y:C=102.255.102])0.840:0.0580220560484199[&
&NHX:D=N:C=102.255.102],((((((C5XIF2_SORBI:0.0558658850692[&&NHX:C=255.51.204],F2EL82_HORVD:0.
08938646220817818[&&NHX:C=255.51.204])0.872:0.03118774533338891[&&NHX:D=N:C=255.51.204],B8A927
_ORYSI:0.04576641816642504[&&NHX:C=255.51.204])1.000:0.1875393186214991[&&NHX:D=Y:C=255.51.204
],(Q3EB59_ARATH:0.2466756739290061[&&NHX:C=255.51.204],Q1PFB8_ARATH:0.3453924873699567[&&NHX:C
=255.51.204])0.998:0.1078811900823557[&&NHX:D=Y:C=255.51.204])0.587:0.04784773803368497[&&NHX:
C=255.51.204],(A7P756_VITVI:0.0788404965195487[&&NHX:C=255.51.204],(B9RQG7_RICCO:0.05388360249
157656[&&NHX:C=255.51.204],B9GGL4_POPTR:0.06396338901561753[&&NHX:C=255.51.204])1.000:0.078834
36362113276[&&NHX:D=Y:C=255.51.204])0.690:0.03849719257544212[&&NHX:C=255.51.204])0.999:0.1195
65687382500 5[&&NHX:D=Y:C=255.51.204],A9NN43_PICSI:0.09841760420330573[&&NHX:C=255.51.204])1.00
0:0.1791968557733754[&&NHX:D=Y:C=255.51.204],P0DI26_PTEAA:0.502821725114724[&&NHX:C=255.51.204
])0.999:0.1333587510380902[&&NHX:D=Y:C=255.51.204])0.826:0.06589170274043848[&&NHX:D=N:C=255.5
1.204],(C5YHP6_SORBI:0.1116230517480649[&&NHX:C=204.204.204],A2YXI1_ORYSI:0.2687886347564923[&
&NHX:C=204.204.204])1.000:0.5189442468255848[&&NHX:D=Y:C=204.204.204])0.780:0.0810593236667758
2[&&NHX:C=255.51.204],A9SG36_PHYPA:0.3260704481571756[&&NHX:C=204.204.204])0.867:0.03867765678
928044[&&NHX:D=N:C=255.51.204],(((P0DI23_PTEAA:0.107081003253869 9[&&NHX:C=0.255.255],(((A9S848
_PHYPA:0.03499008183858193[&&NHX:C=0.255.255],A9STU1_PHYPA:0.0675289903810756[&&NHX:C=0.255.25
5])0.994:0.0432771460066462 8[&&NHX:D=Y:C=0.255.255],A9T836_PHYPA:0.02659125139031788[&&NHX:C=0
.255.255])1.000:0.1356557268821084[&&NHX:D=Y:C=0.255.255],((B9SR15_RICCO:0.04947596053057473[&
&NHX:C=0.255.255],B9HTK2_POPTR:0.05997394160530193[&&NHX:C=0.255.255])0.918:0.047054726277332 4
1[&&NHX:D=N:C=0.255.255],(Q9M2U0_ARATH:0.08016360440947963[&&NHX:C=0.255.255],Q2QNE3_ORYSJ:0.4
673615310572691[&&NHX:C=0.255.255])0.445:0.05882150533862011[&&NHX:C=0.255.255])1.000:0.152849
233485882[&&NHX:D=Y:C=0.255.255])0.992:0.1021886651966466[&&NHX:D=Y:C=0.255.255])1.000:0.19763
43969899302[&&NHX:D=Y:C=0.255.255],((((Q56X75_ARATH:0.07578987372054583[&&NHX:C=0.255.255],Q8G
WD5_ARATH:0.06825417038682206[&&NHX:C=0.255.255])1.000:0.1775939281627868[&&NHX:D=Y:C=0.255.25
5],(B9SXY8_RICCO:0.06357432585476183[&&NHX:C=0.255.255],B9NBE5_POPTR:0.1086919626220913[&&NHX:
C=0.255.255])0.929:0.06135427965475688[&&NHX:D=N:C=0.255.255])0.514:0.04615314581473149[&&NHX:
C=0.255.255],(C6T1Z6_SOYBN:0.1700650031392501[&&NHX:C=0.255.255],A1XGB4_CAPAN:0.22378308549452
7[&&NHX:C=0.255.255])0.805:0.0788379120906923 8[&&NHX:D=N:C=0.255.255])0.884:0.1356276017898696
```

```
[&&NHX:D=N:C=0.255.255],(C5Y494_SORBI:0.1153767333492138[&&NHX:C=0.255.255],Q2R2T4_ORYSJ:0.079
97823959812983[&&NHX:C=0.255.255])1.000:0.322045084085643[&&NHX:D=Y:C=0.255.255])1.000:0.33356
25697182424[&&NHX:D=Y:C=0.255.255])0.702:0.0701181163895289 9[&&NHX:C=0.255.255],(((((F2E5T1_HO
RVD:0.1036873350890881[&&NHX:C=0.255.255],B9F6Z0_ORYSJ:0.02673356173000307[&&NHX:C=0.255.255])
1.000:0.1318898056248713[&&NHX:D=Y:C=0.255.255],((F2D276_HORVD:0.06951294764781996[&&NHX:C=0.2
55.255],C5WNF5_SORBI:0.03344065402702497[&&NHX:C=0.255.255])0.999:0.09191154469549576[&&NHX:D=
Y:C=0.255.255],(F2E2E4_HORVD:0.07989999382532148[&&NHX:C=0.255.255],Q84NQ7_ORYSJ:0.08355282959
578121[&&NHX:C=0.255.255])1.000:0.1738276101497755[&&NHX:D=Y:C=0.255.255])0.996:0.132908209175
7224[&&NHX:D=Y:C=0.255.255])0.584:0.03984028382912026[&&NHX:C=0.255.255],Q8LE26_ARATH:0.243350
374314963[&&NHX:C=0.255.255])0.625:0.05281109509547804[&&NHX:C=0.255.255],Q5W6M3_ORYSJ:0.13723
2469149316[&&NHX:C=0.255.255])1.000:0.1891312839669923[&&NHX:D=Y:C=0.255.255],((((((Q84WP5_ARA
TH:0.0930397336720152[&&NHX:C=0.255.255],D7MMW4_ARALL:0.1267215555032997[&&NHX:C=0.255.255])0.
992:0.07818367432755319[&&NHX:D=Y:C=0.255.255],Q9FNE8_ARATH:0.2397433376899379[&&NHX:C=0.255.2
55])0.597:0.06723676819164719[&&NHX:C=0.255.255],O24088_MEDTR:0.2493911468446454[&&NHX:C=0.255
.255])0.768:0.06871543704227968[&&NHX:C=0.255.255],((C5XTX2_SORBI:0.02063241433466136[&&NHX:C=
0.255.255],C4JAF2_MAIZE:0.05341545207808479[&&NHX:C=0.255.255])1.000:0.1007555904415777[&&NHX:
D=Y:C=0.255.255],A3A2W2_ORYSJ:0.03121083456145672[&&NHX:C=0.255.255])1.000:0.1681771470480945[
&&NHX:D=Y:C=0.255.255])0.334:0.05808972087841118[&&NHX:C=0.255.255],Q3EA54_ARATH:0.47442169468
18169[&&NHX:C=0.255.255])0.594:0.08353986058212377[&&NHX:C=0.255.255],(C5XEK4_SORBI:0.04831341
231638401[&&NHX:C=0.255.255],B6UBY6_MAIZE:0.04094847744352206[&&NHX:C=0.255.255])1.000:0.36593
44569468522[&&NHX:D=Y:C=0.255.255])0.974:0.103275116245624 5[&&NHX:D=Y:C=0.255.255])0.998:0.124
6160068129221[&&NHX:D=Y:C=0.255.255])0.738:0.05749568797364905[&&NHX:C=0.255.255])0.319:0.0415
2108452403007[&&NHX:C=0.255.255],(A9RJH1_PHYPA:0.1162824491682775[&&NHX:C=204.204.204],A9RZ57_
PHYPA:0.06414691929946467[&&NHX:C=204.204.204])1.000:0.327715840221199[&&NHX:D=Y:C=204.204.204
])0.434:0.06186913752563414[&&NHX:C=0.255.255],(A9SHQ9_PHYPA:0.389708953577483[&&NHX:C=204.204
.204],A9SU70_PHYPA:0.3837681978726167[&&NHX:C=204.204.204])0.911:0.1028964365473066[&&NHX:D=N:
C=204.204.204])0.664:0.1100933318580707[&&NHX:C=0.255.255],((A9S1T8_PHYPA:0.05507024639952742[
&&NHX:C=204.204.204],A9SB31_PHYPA:0.04540322996575667[&&NHX:C=204.204.204])1.000:0.27257392011
24885[&&NHX:D=Y:C=204.204.204],D8R814_SELML:0.3277574348867359[&&NHX:C=204.204.204])0.434:0.05
634071352994122[&&NHX:C=204.204.204])0.948:0.1444084422001705[&&NHX:D=N:C=0.255.255],((((((((
(P0DI68_BRADI:0.05885416746758015[&&NHX:C=255.102.102],Q10Q78_ORYSJ:0.0527701577459593[&&NHX:C
=255.102.102])0.554:0.01956507946454566[&&NHX:C=255.102.102],(B4FNS3_MAIZE:0.1296032224328521[
&&NHX:C=255.102.102],P0DI66_MAIZE:0.2549228962701768[&&NHX:C=255.102.102])0.465:0.029022167270
09015[&&NHX:C=255.102.102])0.936:0.09490739416074001[&&NHX:D=N:C=255.102.102],Q9SKN3_ARATH:0.1
224704952726755[&&NHX:C=255.102.102])0.518:0.02350840873609024[&&NHX:C=255.102.102],Q6NPF8_ARA
TH:0.1776847425346983[&&NHX:C=255.102.102])0.912:0.09126211095206345[&&NHX:D=N:C=255.102.102],
P0DI27_PTEAA:0.1242454145779809[&&NHX:C=255.102.102])0.702:0.03286451443088446[&&NHX:C=255.102
.102],((D8QNI1_SELML:0.1056008775216827[&&NHX:C=255.102.102],(((P0DI71_GINBI:0.070489477920710
75[&&NHX:C=255.102.102],D5ACW4_PICSI:0.09236185274014402[&&NHX:C=255.102.102])0.876:0.04965280
933801158[&&NHX:D=N:C=255.102.102],(Q8L7R5_ARATH:0.17031875303788[&&NHX:C=255.102.102],((Q945M
8_ARATH:0.1159392614391147[&&NHX:C=255.102.102],Q9LZM5_ARATH:0.1495360969196085[&&NHX:C=255.10
2.102])0.999:0.07085496856910643[&&NHX:D=Y:C=255.102.102],(B6T990_MAIZE:0.1577911706257066[&&N
HX:C=255.102.102],(((B6TM88_MAIZE:0.1036411228303186[&&NHX:C=255.102.102],B8AC36_ORYSI:0.06229
643550983699[&&NHX:C=255.102.102])0.997:0.04325623263871971[&&NHX:D=Y:C=255.102.102],B8AYU8_OR
YSI:0.09814894221153979[&&NHX:C=255.102.102])0.866:0.03399518858064556[&&NHX:D=N:C=255.102.102
],B6TAX2_MAIZE:0.08118697674823931[&&NHX:C=255.102.102])1.000:0.09687531732689278[&&NHX:D=Y:C=
255.102.102])0.962:0.05737988860714173[&&NHX:D=Y:C=255.102.102])0.999:0.07662543357819285[&&NH
X:D=Y:C=255.102.102])0.986:0.0679009739125465[&&NHX:D=Y:C=255.102.102])0.505:0.038945520250393
35[&&NHX:C=255.102.102],((Q3ECT8_ARATH:0.2779835220410002[&&NHX:C=255.102.102],(B6U300_MAIZE:0
.07255184843605804[&&NHX:C=255.102.102],B8BPI2_ORYSI:0.02435875314946069[&&NHX:C=255.102.102])
1.000:0.1218718958269117[&&NHX:D=Y:C=255.102.102])0.661:0.05701083089989112[&&NHX:C=255.102.10
2],(P0CB17_ARATH:0.2433070283225115[&&NHX:C=255.102.102],Q66GI1_ARATH:0.1048752216438073[&&NHX
:C=255.102.102])1.000:0.1510293088356907[&&NHX:D=Y:C=255.102.102])1.000:0.3153594153406317[&&N
HX:D=Y:C=255.102.102])1.000:0.1205116468747745[&&NHX:D=Y:C=255.102.102])1.000:0.06783056692156
429[&&NHX:D=Y:C=255.102.102],((A9RKK4_PHYPA:0.07037858282378126[&&NHX:C=255.102.102],A9RLK6_PH
YPA:0.073387041352751[&&NHX:C=255.102.102])1.000:0.160495161807142[&&NHX:D=Y:C=255.102.102],P0
DI22_PTEAA:0.1675746161423391[&&NHX:C=255.102.102])0.852:0.03678739203441336[&&NHX:D=N:C=255.1
02.102])0.993:0.05913144934695941[&&NHX:D=Y:C=255.102.102])0.477:0.02413631498427063[&&NHX:C=2
55.102.102],P0DI70_GINBI:0.0244316613426712[&&NHX:C=255.102.102])0.769:0.03348464978755218[&&N
HX:C=255.102.102],P0DI69_GINBI:0.02703772828426053[&&NHX:C=255.102.102])0.740:0.06928727855361
05[&&NHX:C=255.102.102],P0DI64_PINCO:0.06101173697579768[&&NHX:C=255.102.102])1.000:0.44738964
04961268[&&NHX:D=Y:C=255.102.102],F0YFA3_AURAN:0.606715020681373[&&NHX:C=255.102.102])0.453:0.
1105267238537225[&&NHX:C=255.102.102])0.961:0.08426584426390618[&&NHX:D=Y:C=255.102.102],(((M1
VAW8_CYAME:0.6564237468769378[&&NHX:C=0.255.0],E1ZFT0_CHLVA:0.5311007755864446[&&NHX:C=0.255.0
])0.962:0.172354845842493[&&NHX:D=Y:C=0.255.0],((P0DI72_CHLAT:0.3876403882953819[&&NHX:C=0.255
.0],(((A4S8B7_OSTLU:0.209284283686427[&&NHX:C=0.255.0],Q00U99_OSTTA:0.3026911443469376[&&NHX:C
=0.255.0])1.000:0.50691881799988[&&NHX:D=Y:C=0.255.0],C1N652_MICPC:0.1371606116615071[&&NHX:C=
0.255.0])0.831:0.08430886551100075[&&NHX:D=N:C=0.255.0],C1EI34_MICSR:0.1570576511791437[&&NHX:
C=0.255.0])1.000:0.2893908574372987[&&NHX:D=Y:C=0.255.0])0.508:0.05618691581703339[&&NHX:C=0.2
55.0],P0DI73_CHLAT:0.616923692233222[&&NHX:C=0.255.0])0.989:0.1487037801473663[&&NHX:D=Y:C=0.2
55.0])0.859:0.1279160504486529[&&NHX:D=N:C=0.255.0],F0Y3N5_AURAN:0.6814596367623876[&&NHX:C=0.
255.0])0.332:0.1033088642151874[&&NHX:C=0.255.0])0.308:0.05445593490541635[&&NHX:C=0.255.0],((
(((((((K3WS83_PYTUL:0.3048664759370477[&&NHX:C=102.0.102],K3WS84_PYTUL:0.1285148473688423[&&NH
X:C=102.0.102])0.912:0.08957235144892527[&&NHX:D=N:C=102.0.102],((G4ZSC0_PHYSP:0.0724098236317
3999[&&NHX:C=102.0.102],D0NLD9_PHYIT:0.04970474898003588[&&NHX:C=102.0.102])0.971:0.0614807640
0123758[&&NHX:D=Y:C=102.0.102],H3HBC3_PHYRM:0.1163461281759063[&&NHX:C=102.0.102])1.000:0.2214
025829884504[&&NHX:D=Y:C=102.0.102])0.994:0.10953697673076[&&NHX:D=Y:C=102.0.102],((G5AEA0_PHY
```

```
SP:0.154019410085212[&&NHX:C=102.0.102],(G5AE98_PHYSP:0.06016674325971208[&&NHX:C=102.0.102],H
3H3L4_PHYRM:0.04270291537116668[&&NHX:C=102.0.102])0.992:0.09188581717583676[&&NHX:D=Y:C=102.0
.102])0.984:0.1211799874293367[&&NHX:D=Y:C=102.0.102],(G5AEA1_PHYSP:0.03545969006509938[&&NHX:
C=102.0.102],D0NMH7_PHYIT:0.09088291583090258[&&NHX:C=102.0.102])1.000:0.3289776011476696[&&NH
X:D=Y:C=102.0.102])1.000:0.1986709136535166[&&NHX:D=Y:C=102.0.102])0.982:0.10477620374008[&&NH
X:D=Y:C=102.0.102],K3WS85_PYTUL:0.1646443629429002[&&NHX:C=102.0.102])0.662:0.0669304393282065
3[&&NHX:C=102.0.102],(F0X036_9STRA:0.2413148955477843[&&NHX:C=102.0.102],F0WMT2_9STRA:0.572409
149273856[&&NHX:C=102.0.102])0.997:0.2192891635344509[&&NHX:D=Y:C=102.0.102])0.349:0.051947295
95221442[&&NHX:C=102.0.102],(((G4ZSC4_PHYSP:0.02920754489485669[&&NHX:C=102.0.102],(H3HBC4_PHY
RM:0.04808447429888062[&&NHX:C=102.0.102],D0NLE1_PHYIT:0.05200869547440674[&&NHX:C=102.0.102])
0.986:0.03063459023734787[&&NHX:D=Y:C=102.0.102])0.993:0.05206426784903122[&&NHX:D=Y:C=102.0.1
02],M4B8W0_HYAAE:0.0670125035702955[&&NHX:C=102.0.102])0.917:0.05897653872527362[&&NHX:D=N:C=1
02.0.102],(G4ZSC3_PHYSP:0.1352933680905037[&&NHX:C=102.0.102],H3GGR0_PHYRM:0.04183184845834263
[&&NHX:C=102.0.102])1.000:0.1426890130145191[&&NHX:D=Y:C=102.0.102])1.000:0.2060769872318302[&
&NHX:D=Y:C=102.0.102])0.431:0.07307299965830313[&&NHX:C=102.0.102],(K3WS90_PYTUL:0.31746619200
89544[&&NHX:C=102.0.102],F0X038_9STRA:0.4048792018771983[&&NHX:C=102.0.102])0.489:0.0871332877
0831517[&&NHX:C=102.0.102])0.966:0.1309684742392311[&&NHX:D=Y:C=102.0.102],(K3X3G8_PYTUL:0.151
1544464732626[&&NHX:C=102.0.102],((G4ZRP2_PHYSP:0.05077331432088555[&&NHX:C=102.0.102],D0NCN6_
PHYIT:0.05015670898457823[&&NHX:C=102.0.102])0.623:0.0308102325708841[&&NHX:C=102.0.102],H3GI9
9_PHYRM:0.01913946853019549[&&NHX:C=102.0.102])1.000:0.2781520383188036[&&NHX:D=Y:C=102.0.102]
)1.000:0.2468997149657672[&&NHX:D=Y:C=102.0.102])0.993:0.2088036434129358[&&NHX:D=Y:C=102.0.10
2],H3GEF8_PHYRM:0.8235349535690903[&&NHX:C=102.0.102])0.527:0.05445593490541635[&&NHX:C=102.0.
102])[&&NHX:C=102.0.102]
```

Dataset 5. ML CASPL phylogeny (NHX format), corresponding to Supplemental Figure 4.

```
(((((((((((((((((P0DH82_MARPO:0.5724083308[&&NHX:C=204.204.204],((P0DI20_OSMLA:0.2643009836[&&
NHX:C=204.204.204],(P0DI25_PTEAA:0.4264462169[&&NHX:C=204.204.204],P0DI21_OSMLA:0.0030344027[&
&NHX:C=204.204.204])0.9550000000:0.1658874664[&&NHX:C=204.204.204])0.6850000000:0.0835774776[&
&NHX:C=204.204.204],(P0DI24_PTEAA:0.4726220997[&&NHX:C=204.204.204],(P0DH84_ADICA:0.2520193485
[&&NHX:C=204.204.204],P0DI28_PTEAA:0.282911651[&&NHX:C=204.204.204])0.9560000000:0.2404147513[
&&NHX:C=204.204.204])0.8860000000:0.1294247126[&&NHX:C=204.204.204])0.9730000000:0.2389442836[
&&NHX:C=204.204.204])0.4370000000:0.0550679005[&&NHX:C=204.204.204],(((A9NMM6_PICSI:0.50653613
04[&&NHX:C=204.204.204],B4FBQ7_MAIZE:0.2053917364[&&NHX:C=204.204.204])0.8370000000:0.11711976
[&&NHX:C=204.204.204],((D5A972_PICSI:0.2525150182[&&NHX:C=204.204.204],A9P1V1_PICSI:0.19880499
75[&&NHX:C=204.204.204])0.9090000000:0.1473914344[&&NHX:C=204.204.204],(Q8VZQ3_ARATH:0.1957549
457[&&NHX:C=204.204.204],((A7QBZ2_VITVI:0.1367595559[&&NHX:C=204.204.204],((Q8W4Z5_GOSHI:0.058
0375019[&&NHX:C=204.204.204],B9T3K6_RICCO:0.152416928[&&NHX:C=204.204.204])0.7610000000:0.0162
536811[&&NHX:C=204.204.204],(D7L342_ARALL:0.4641447487[&&NHX:C=204.204.204],B9GHX8_POPTR:0.034
9876405[&&NHX:C=204.204.204])0.8840000000:0.0476963796[&&NHX:C=204.204.204])0.8670000000:0.043
8219939[&&NHX:C=204.204.204])0.4630000000:0.0227504296[&&NHX:C=204.204.204],(C6TCJ2_SOYBN:0.02
31535933[&&NHX:C=204.204.204],C6SYW3_SOYBN:0.1630104915[&&NHX:C=204.204.204])0.9590000000:0.08
87684088[&&NHX:C=204.204.204])0.0000000000:3.12122E-
5[&&NHX:C=204.204.204])0.9470000000:0.1816800933[&&NHX:C=204.204.204])0.0260000000:0.054549899
3[&&NHX:C=204.204.204])0.6380000000:0.1930490596[&&NHX:C=204.204.204],((A7P0P3_VITVI:7.0704E-
6[&&NHX:C=204.204.204],(B9HTL5_POPTR:0.1188840602[&&NHX:C=204.204.204],(C6T2J5_SOYBN:0.3075550
152[&&NHX:C=204.204.204],(D7MUY4_ARALL:0.4006283206[&&NHX:C=204.204.204],B9SV84_RICCO:0.057584
1876[&&NHX:C=204.204.204])0.9030000000:0.0622836338[&&NHX:C=204.204.204])0.8370000000:0.049713
4251[&&NHX:C=204.204.204])0.8190000000:0.1279215937[&&NHX:C=204.204.204])0.9820000000:0.466578
1997[&&NHX:C=204.204.204],(A2X2I0_ORYSI:0.140234068[&&NHX:C=204.204.204],C5XY39_SORBI:0.214652
4811[&&NHX:C=204.204.204])0.9500000000:0.3905853265[&&NHX:C=204.204.204])0.9860000000:0.529726
123[&&NHX:C=204.204.204])0.6830000000:0.1276075326[&&NHX:C=204.204.204])0.8650000000:0.0937887
631[&&NHX:C=204.204.204],((B8LQF9_PICSI:0.1707643065[&&NHX:C=204.204.204],(D5A8E6_PICSI:0.5284
906386[&&NHX:C=204.204.204],(D7M9V1_ARALL:0.2369620684[&&NHX:C=204.204.204],((E4MWF4_THEHA:0.0
459083104[&&NHX:C=204.204.204],D7LIK3_ARALL:0.1294245694[&&NHX:C=204.204.204])0.9240000000:0.0
964057391[&&NHX:C=204.204.204],(B9SA89_RICCO:6.64426E-
5[&&NHX:C=204.204.204],(A7R385_VITVI:0.0653654713[&&NHX:C=204.204.204],((Q0IN16_ORYSJ:0.174881
7969[&&NHX:C=204.204.204],(B6TGJ8_MAIZE:0.1207657859[&&NHX:C=204.204.204],C5YP66_SORBI:0.06446
0247[&&NHX:C=204.204.204])0.9640000000:0.1859980533[&&NHX:C=204.204.204])0.9730000000:0.281462
3809[&&NHX:C=204.204.204],(C5WUP3_SORBI:0.2725804703[&&NHX:C=204.204.204],(((B6SZA7_MAIZE:0.08
85184265[&&NHX:C=204.204.204],Q67W83_ORYSJ:0.0591879793[&&NHX:C=204.204.204])0.2880000000:0.04
20413737[&&NHX:C=204.204.204],(B6U8R7_MAIZE:0.1285123959[&&NHX:C=204.204.204],Q6ETN2_ORYSJ:0.1
260404541[&&NHX:C=204.204.204])0.9900000000:0.288483504[&&NHX:C=204.204.204])0.9980000000:0.60
99771894[&&NHX:C=204.204.204],((C6SZ04_SOYBN:0.3576881881[&&NHX:C=204.204.204],A7Q6G6_VITVI:0.
2608375546[&&NHX:C=204.204.204])0.7090000000:0.0487931151[&&NHX:C=204.204.204],(B9IM09_POPTR:0
.1745901483[&&NHX:C=204.204.204],(Q5K4H9_GOSHI:0.3005605154[&&NHX:C=204.204.204],D7MFW5_ARALL:
0.6768773903[&&NHX:C=204.204.204])0.8960000000:0.1397211457[&&NHX:C=204.204.204])0.6020000000:
0.0701526958[&&NHX:C=204.204.204])0.9510000000:0.3438226164[&&NHX:C=204.204.204])0.9870000000:
0.5023973169[&&NHX:C=204.204.204])0.2550000000:0.1102762937[&&NHX:C=204.204.204])0.9110000000:
0.1396315323[&&NHX:C=204.204.204])0.6990000000:0.0827379198[&&NHX:C=204.204.204])0.9830000000:
0.1372439282[&&NHX:C=204.204.204])0.6550000000:0.0184619163[&&NHX:C=204.204.204])0.9870000000:
0.3047283468[&&NHX:C=204.204.204])0.0000000000:0.0052661633[&&NHX:C=204.204.204])0.9940000000:
0.5257079069[&&NHX:C=204.204.204],(D8S6A8_SELML:0.7343369534[&&NHX:C=204.204.204],(D8ST12_SELM
L:0.3945344732[&&NHX:C=204.204.204],P0DH63_SELML:0.4831249956[&&NHX:C=204.204.204])0.850000000
0:0.2089356773[&&NHX:C=204.204.204])0.9850000000:0.405609229[&&NHX:C=204.204.204])0.2900000000
:0.0594943176[&&NHX:C=204.204.204])0.6450000000:0.1192867427[&&NHX:C=204.204.204],(D8T2C0_SELM
L:0.4762219522[&&NHX:C=204.204.204],(D8SJ65_SELML:0.3714895787[&&NHX:C=204.204.204],P0DH65_SEL
ML:0.5909726099[&&NHX:C=204.204.204])0.8370000000:0.2410786372[&&NHX:C=204.204.204])0.21000000
00:0.0768909379[&&NHX:C=204.204.204])0.9720000000:0.3267206529[&&NHX:C=204.204.204],((A7PA04_V
ITVI:0.3118089041[&&NHX:C=204.204.204],((B9RH17_RICCO:0.249114361[&&NHX:C=204.204.204],B9GFG6_
POPTR:0.3650171968[&&NHX:C=204.204.204])0.8160000000:0.0844491125[&&NHX:C=204.204.204],((B9I3X
5_POPTR:0.1676532144[&&NHX:C=204.204.204],B9IFI5_POPTR:0.1479866647[&&NHX:C=204.204.204])0.979
0000000:0.2448516895[&&NHX:C=204.204.204],(D7MGK0_ARALL:0.8233617134[&&NHX:C=204.204.204],(A7P
HN8_VITVI:0.2971520601[&&NHX:C=204.204.204],B9RA90_RICCO:0.1358177189[&&NHX:C=204.204.204])0.2
570000000:0.0733921596[&&NHX:C=204.204.204])0.6670000000:0.0491395351[&&NHX:C=204.204.204])0.9
800000000:0.3010877161[&&NHX:C=204.204.204])0.6630000000:0.0578115811[&&NHX:C=204.204.204])0.9
960000000:0.4751196163[&&NHX:C=204.204.204],((P0DH83_MARPO:0.7182233294[&&NHX:C=204.204.204],(
A9TKY8_PHYPA:0.3085081656[&&NHX:C=204.204.204],(A9SEY7_PHYPA:0.3538738422[&&NHX:C=204.204.204]
,(A9STS7_PHYPA:0.1767314582[&&NHX:C=204.204.204],A9TZ63_PHYPA:0.0585821803[&&NHX:C=204.204.204
])0.9280000000:0.1583458551[&&NHX:C=204.204.204])0.7810000000:0.1263717578[&&NHX:C=204.204.204
])0.9680000000:0.4048299664[&&NHX:C=204.204.204])0.8240000000:0.1183066565[&&NHX:C=204.204.204
],((A7PJ32_VITVI:0.1981875859[&&NHX:C=204.204.204],(((Q9LR57_ARATH:0.1469772014[&&NHX:C=204.20
4.204],D7M2M8_ARALL:0.0299562754[&&NHX:C=204.204.204])0.9950000000:0.2143958111[&&NHX:C=204.20
4.204],(B9RW00_RICCO:0.1464271104[&&NHX:C=204.204.204],B9N5U6_POPTR:0.1254452542[&&NHX:C=204.2
04.204])0.8220000000:0.0579136685[&&NHX:C=204.204.204])0.9070000000:0.0865823601[&&NHX:C=204.2
04.204],((B9RZ92_RICCO:0.1060804027[&&NHX:C=204.204.204],B9H2V1_POPTR:0.1793065803[&&NHX:C=204
.204.204])0.9880000000:0.2787966491[&&NHX:C=204.204.204],(A7R333_VITVI:0.265469441[&&NHX:C=204
.204.204],(A2WMK7_ORYSI:0.4505378363[&&NHX:C=204.204.204],(A2Y2B7_ORYSI:0.2543079121[&&NHX:C=2
04.204.204],B6SZU6_MAIZE:0.1593925027[&&NHX:C=204.204.204])0.8100000000:0.083003724[&&NHX:C=20
```

```
4.204.204])0.9990000000:0.4684865211[&&NHX:C=204.204.204])0.0860000000:0.033460755[&&NHX:C=204
.204.204])0.2040000000:0.0546360609[&&NHX:C=204.204.204])0.8410000000:0.0821457211[&&NHX:C=204
.204.204])0.9990000000:0.319459276[&&NHX:C=204.204.204],((((D7MAF7_ARALL:0.2307820526[&&NHX:C=
204.204.204],(B9RT03_RICCO:0.1874200004[&&NHX:C=204.204.204],(B9HMP5_POPTR:0.1659022174[&&NHX:
C=204.204.204],(A2PZE5_IPONI:0.3499691096[&&NHX:C=204.204.204],(C6SVQ5_SOYBN:0.1876080756[&&NH
X:C=204.204.204],(A7NW79_VITVI:0.1818893419[&&NHX:C=204.204.204],D2KQI6_BETVM:0.2710184825[&&N
HX:C=204.204.204])0.7880000000:0.0639956945[&&NHX:C=204.204.204])0.6240000000:0.0347842726[&&N
HX:C=204.204.204])0.2860000000:0.0207441685[&&NHX:C=204.204.204])0.4440000000:0.0382560846[&&N
HX:C=204.204.204])0.9140000000:0.0796195495[&&NHX:C=204.204.204])0.1620000000:0.02209877[&&NHX
:C=204.204.204],(D7L5G6_ARALL:0.4156191145[&&NHX:C=204.204.204],(Q1EPG6_MUSAC:0.2135217231[&&N
HX:C=204.204.204],(Q6YT98_ORYSJ:0.1493642136[&&NHX:C=204.204.204],(B6U361_MAIZE:0.0612288338[&
&NHX:C=204.204.204],C5X4A5_SORBI:0.0787640664[&&NHX:C=204.204.204])0.8980000000:0.0686402551[&
&NHX:C=204.204.204])0.9930000000:0.2177788847[&&NHX:C=204.204.204])0.9420000000:0.1391159953[&
&NHX:C=204.204.204])0.3130000000:0.0440230741[&&NHX:C=204.204.204])0.9950000000:0.5203419194[&
&NHX:C=204.204.204],(((C5Y7C6_SORBI:0.3750304271[&&NHX:C=204.204.204],Q2R0D4_ORYSJ:0.292343268
9[&&NHX:C=204.204.204])0.9540000000:0.4685445545[&&NHX:C=204.204.204],((C5Y376_SORBI:0.2401044
806[&&NHX:C=204.204.204],Q2R0D1_ORYSJ:0.2054057886[&&NHX:C=204.204.204])0.9530000000:0.3699440
548[&&NHX:C=204.204.204],(Q2R0D2_ORYSJ:0.2481870919[&&NHX:C=204.204.204],(C5Y7C7_SORBI:0.12612
44957[&&NHX:C=204.204.204],C5Y7C8_SORBI:0.6048981492[&&NHX:C=204.204.204])0.7750000000:0.07998
1637[&&NHX:C=204.204.204])0.8760000000:0.2230155245[&&NHX:C=204.204.204])0.5980000000:0.263029
842[&&NHX:C=204.204.204])0.9860000000:0.731407064[&&NHX:C=204.204.204],((B9RT04_RICCO:0.139751
637[&&NHX:C=204.204.204],(C6SZP8_SOYBN:0.4373728401[&&NHX:C=204.204.204],(B9HMP6_POPTR:0.21844
47204[&&NHX:C=204.204.204],(A7NW78_VITVI:0.2321316212[&&NHX:C=204.204.204],(A7PTY8_VITVI:0.366
4323928[&&NHX:C=204.204.204],(D7MAF6_ARALL:0.1461267444[&&NHX:C=204.204.204],D7MAF5_ARALL:0.07
70295999[&&NHX:C=204.204.204])1.0000000000:0.3860216369[&&NHX:C=204.204.204])0.0730000000:0.01
57266711[&&NHX:C=204.204.204])0.8410000000:0.077859838[&&NHX:C=204.204.204])0.2720000000:0.033
1683027[&&NHX:C=204.204.204])0.2860000000:0.0408790845[&&NHX:C=204.204.204])0.8160000000:0.094
550609[&&NHX:C=204.204.204],(Q1EPG7_MUSAC:0.398020956[&&NHX:C=204.204.204],(B4FAP1_MAIZE:0.041
7702292[&&NHX:C=204.204.204],Q9ARX2_ORYSJ:0.1587586771[&&NHX:C=204.204.204])0.9970000000:0.596
8893727[&&NHX:C=204.204.204])0.9360000000:0.2501478534[&&NHX:C=204.204.204])0.8630000000:0.171
1832957[&&NHX:C=204.204.204])0.8640000000:0.1692037587[&&NHX:C=204.204.204])0.8890000000:0.156
757206[&&NHX:C=204.204.204],((A9P0A6_PICSI:0.2616283122[&&NHX:C=204.204.204],((A2ZMM4_ORYSI:0.
1401646728[&&NHX:C=204.204.204],(B6TUH4_MAIZE:0.1326219564[&&NHX:C=204.204.204],C5YRU8_SORBI:0
.0324996057[&&NHX:C=204.204.204])0.9350000000:0.1789564426[&&NHX:C=204.204.204])0.9890000000:0
.4596341449[&&NHX:C=204.204.204],(A7QC16_VITVI:0.1988309174[&&NHX:C=204.204.204],(C6TG62_SOYBN
:0.2841446417[&&NHX:C=204.204.204],((D7MFJ8_ARALL:0.149943162[&&NHX:C=204.204.204],D7MM00_ARAL
L:0.0585978754[&&NHX:C=204.204.204])0.9990000000:0.2949463446[&&NHX:C=204.204.204],(B9I0U9_POP
TR:0.0891130932[&&NHX:C=204.204.204],(B9GIE4_POPTR:0.0449855419[&&NHX:C=204.204.204],B9SV63_RI
CCO:0.2151343978[&&NHX:C=204.204.204])0.3610000000:0.0278297018[&&NHX:C=204.204.204])0.7010000
000:0.0278820461[&&NHX:C=204.204.204])0.8200000000:0.0765910626[&&NHX:C=204.204.204])0.7970000
000:0.084337365[&&NHX:C=204.204.204])0.8590000000:0.1621752557[&&NHX:C=204.204.204])0.98500000
00:0.4287498775[&&NHX:C=204.204.204])0.7660000000:0.1032344557[&&NHX:C=204.204.204],((P0DH81_P
ICGL:0.0362092216[&&NHX:C=204.204.204],P0DH80_PINTA:0.1179861107[&&NHX:C=204.204.204])0.990000
0000:0.2635750807[&&NHX:C=204.204.204],((((C5YLC9_SORBI:0.1644922235[&&NHX:C=204.204.204],P0DI
37_BRADI:0.1347250617[&&NHX:C=204.204.204])0.8590000000:0.0403101261[&&NHX:C=204.204.204],(A2Y
QB8_ORYSI:0.1635438881[&&NHX:C=204.204.204],((P0DI38_BRADI:0.0274871967[&&NHX:C=204.204.204],E
6Y2A0_WHEAT:0.0898369043[&&NHX:C=204.204.204])0.9150000000:0.0854185326[&&NHX:C=204.204.204],(
B8ART0_ORYSI:0.1010737533[&&NHX:C=204.204.204],B6U045_MAIZE:0.1064067628[&&NHX:C=204.204.204])
0.7130000000:0.053480251[&&NHX:C=204.204.204])0.9050000000:0.0731600524[&&NHX:C=204.204.204])0
.0000000000:1.487E-
6[&&NHX:C=204.204.204])0.9990000000:0.2190760588[&&NHX:C=204.204.204],(A7PP95_VITVI:0.15320850
35[&&NHX:C=204.204.204],(A7QF77_VITVI:0.0997247865[&&NHX:C=204.204.204],((P0DI60_HELAN:0.21787
88992[&&NHX:C=204.204.204],(P0DI30_TRIPD:0.0732226523[&&NHX:C=204.204.204],P0DI53_MIMGU:0.0635
698517[&&NHX:C=204.204.204])0.9030000000:0.0574869642[&&NHX:C=204.204.204])0.5690000000:0.0415
214082[&&NHX:C=204.204.204],(((D7LGW9_ARALL:0.2827836697[&&NHX:C=204.204.204],B9HQ42_POPTR:0.2
075422753[&&NHX:C=204.204.204])0.5620000000:0.0637709311[&&NHX:C=204.204.204],(B9SCX0_RICCO:0.
1098372956[&&NHX:C=204.204.204],((P0DI41_VIGUN:0.0940448099[&&NHX:C=204.204.204],C6T4E0_SOYBN:
0.0558423461[&&NHX:C=204.204.204])0.7740000000:0.0414403562[&&NHX:C=204.204.204],(G7IHF9_MEDTR
:0.0822043364[&&NHX:C=204.204.204],P0DI56_LOTJA:0.196731594[&&NHX:C=204.204.204])0.7930000000:
0.0657726334[&&NHX:C=204.204.204])1.0000000000:0.3227787097[&&NHX:C=204.204.204])0.8170000000:
0.0570603214[&&NHX:C=204.204.204])0.8390000000:0.0567277246[&&NHX:C=204.204.204],((P0DI62_CYNC
S:0.0380882987[&&NHX:C=204.204.204],P0DI32_TARKO:0.0721857304[&&NHX:C=204.204.204])0.998000000
0:0.208341406[&&NHX:C=204.204.204],((B9HBX2_POPTR:0.05220859[&&NHX:C=204.204.204],(((B9SX12_RI
CCO:0.1048967714[&&NHX:C=204.204.204],((C6TH93_SOYBN:0.0701652884[&&NHX:C=204.204.204],(P0DI55
_LOTJA:0.0796393039[&&NHX:C=204.204.204],C6TFL9_SOYBN:0.0685105083[&&NHX:C=204.204.204])0.9590
000000:0.0969015001[&&NHX:C=204.204.204])0.9800000000:0.1217542491[&&NHX:C=204.204.204],(P0DI4
3_THECC:0.1344736239[&&NHX:C=204.204.204],B9SX13_RICCO:0.1219254786[&&NHX:C=204.204.204])0.896
0000000:0.0529979475[&&NHX:C=204.204.204])0.7520000000:0.0146456519[&&NHX:C=204.204.204])0.845
0000000:0.050946366[&&NHX:C=204.204.204],((D7LIN7_ARALL:0.1008878064[&&NHX:C=204.204.204],(P0D
I45_RAPSA:0.0977539626[&&NHX:C=204.204.204],P0DI49_RAPRA:0.0561633891[&&NHX:C=204.204.204])0.2
590000000:0.0447214637[&&NHX:C=204.204.204])0.9930000000:0.2253715668[&&NHX:C=204.204.204],(D7
LZ50_ARALL:0.0988988339[&&NHX:C=204.204.204],(D7LAP2_ARALL:0.0117652685[&&NHX:C=204.204.204],P
0DI46_RAPSA:0.1547196081[&&NHX:C=204.204.204])0.8790000000:0.0360577355[&&NHX:C=204.204.204])0
.9490000000:0.1040700404[&&NHX:C=204.204.204])0.8100000000:0.0713820222[&&NHX:C=204.204.204])0
.4170000000:0.0405587427[&&NHX:C=204.204.204],(P0DI61_CUCME:0.301189257[&&NHX:C=204.204.204],B
9IIR4_POPTR:0.0919878357[&&NHX:C=204.204.204])0.1000000000:0.0430722785[&&NHX:C=204.204.204])0
.3590000000:0.0304647892[&&NHX:C=204.204.204])0.9460000000:0.0909750128[&&NHX:C=204.204.204],(
```

```
P0DI50_TOBAC:0.1282363615[&&NHX:C=204.204.204],(P0DI51_MIMGU:0.0805768369[&&NHX:C=204.204.204]
,(P0DI52_MIMGU:0.0376808021[&&NHX:C=204.204.204],(Q1W3A5_STRAF:0.1235954787[&&NHX:C=204.204.20
4],P0DI31_TRIPD:0.0406785862[&&NHX:C=204.204.204])0.3970000000:0.0405570199[&&NHX:C=204.204.20
4])0.5090000000:0.0311163752[&&NHX:C=204.204.204])0.9220000000:0.103413176[&&NHX:C=204.204.204
])0.9710000000:0.1439105576[&&NHX:C=204.204.204])0.1070000000:0.0294331145[&&NHX:C=204.204.204
])0.7320000000:0.0397186711[&&NHX:C=204.204.204])0.8820000000:0.0465334877[&&NHX:C=204.204.204
])0.7120000000:0.0197748019[&&NHX:C=204.204.204])0.7560000000:0.0553451309[&&NHX:C=204.204.204
])0.7600000000:0.0406493145[&&NHX:C=204.204.204])0.5580000000:0.022800207[&&NHX:C=204.204.204]
,((P0DKC2_LOTJA:0.0830292134[&&NHX:C=204.204.204],G7L218_MEDTR:0.0316051624[&&NHX:C=204.204.20
4])0.9580000000:0.1399882994[&&NHX:C=204.204.204],((((B9S8Z3_RICCO:0.2480566392[&&NHX:C=204.20
4.204],(D7KBH3_ARALL:0.2460143648[&&NHX:C=204.204.204],B9HI87_POPTR:0.235763766[&&NHX:C=204.20
4.204])0.1130000000:0.037087264[&&NHX:C=204.204.204])0.8170000000:0.0689479507[&&NHX:C=204.204
.204],((C6T4A0_SOYBN:0.0766078099[&&NHX:C=204.204.204],(G7JG80_MEDTR:0.0932029517[&&NHX:C=204.
204.204],P0DI58_LOTJA:0.0634862672[&&NHX:C=204.204.204])0.2640000000:0.0188220279[&&NHX:C=204.
204.204])0.9160000000:0.0769385062[&&NHX:C=204.204.204],(C6T1G0_SOYBN:0.0884987718[&&NHX:C=204
.204.204],G7KGQ4_MEDTR:0.1330580857[&&NHX:C=204.204.204])0.9270000000:0.0901673545[&&NHX:C=204
.204.204])0.9530000000:0.1137699715[&&NHX:C=204.204.204])0.8160000000:0.0499033293[&&NHX:C=204
.204.204],(((B8AEC9_ORYSI:0.2699012082[&&NHX:C=204.204.204],(A2XU91_ORYSI:0.0483054364[&&NHX:C
=204.204.204],C5Y9U6_SORBI:0.0768168918[&&NHX:C=204.204.204])0.9170000000:0.0892208168[&&NHX:C
=204.204.204])0.9020000000:0.0874454981[&&NHX:C=204.204.204],(B6T959_MAIZE:0.09837506[&&NHX:C=
204.204.204],(P0DI42_WHEAT:0.0757977346[&&NHX:C=204.204.204],(Q6Z2U5_ORYSJ:0.2455800533[&&NHX:
C=204.204.204],P0DI36_BRADI:0.046799048[&&NHX:C=204.204.204])0.7770000000:0.0277311041[&&NHX:C
=204.204.204])0.8870000000:0.0416037543[&&NHX:C=204.204.204])0.9020000000:0.0566255333[&&NHX:C
=204.204.204])0.8160000000:0.0380346507[&&NHX:C=204.204.204],(Q5NRN4_SOLDE:0.3226744773[&&NHX:
C=204.204.204],P0DI35_LACSI:0.2489940582[&&NHX:C=204.204.204])0.4970000000:0.0572365161[&&NHX:
C=204.204.204])0.8590000000:0.0399187434[&&NHX:C=204.204.204])0.7640000000:0.0101934034[&&NHX:
C=204.204.204],((B9T4E6_RICCO:0.1180658954[&&NHX:C=204.204.204],(P0DI59_LACSA:0.3033855987[&&N
HX:C=204.204.204],(B9I534_POPTR:0.0676229125[&&NHX:C=204.204.204],D7M7B3_ARALL:0.1909529404[&&
NHX:C=204.204.204])0.5740000000:0.0401113969[&&NHX:C=204.204.204])0.3530000000:0.0311284851[&&
NHX:C=204.204.204])0.7720000000:0.0249169061[&&NHX:C=204.204.204],(P0DI54_MALDO:0.1121379232[&
&NHX:C=204.204.204],(A7PMY7_VITVI:0.0846232407[&&NHX:C=204.204.204],P0DI44_SOLTU:0.2272884261[
&&NHX:C=204.204.204])0.7330000000:0.0225095069[&&NHX:C=204.204.204])0.1020000000:0.0101076842[
&&NHX:C=204.204.204])0.8590000000:0.0218719265[&&NHX:C=204.204.204])0.8190000000:0.0575850986[
&&NHX:C=204.204.204])0.9880000000:0.2306448625[&&NHX:C=204.204.204])0.7750000000:0.1165360008[
&&NHX:C=204.204.204])0.9830000000:0.258369866[&&NHX:C=204.204.204])0.7340000000:0.0483431687[&
&NHX:C=204.204.204])0.7890000000:0.0734635349[&&NHX:C=204.204.204])0.8970000000:0.1801336986[&
&NHX:C=204.204.204])0.8810000000:0.2520100062[&&NHX:C=204.204.204])0.3970000000:0.0881977533[&
&NHX:C=204.204.204])0.8220000000:0.1326267055[&&NHX:C=204.204.204],(P0DI26_PTEAA:1.0268873548[
&&NHX:C=204.204.204],(A9NN43_PICSI:0.1595866516[&&NHX:C=204.204.204],((B9RQG7_RICCO:0.07996027
25[&&NHX:C=204.204.204],B9GGL4_POPTR:0.0943592317[&&NHX:C=204.204.204])0.9550000000:0.12558323
79[&&NHX:C=204.204.204],(((B8A927_ORYSI:0.0606784473[&&NHX:C=204.204.204],(F2EL82_HORVD:0.1401
671754[&&NHX:C=204.204.204],C5XIF2_SORBI:0.075873482[&&NHX:C=204.204.204])0.8480000000:0.04523
22[&&NHX:C=204.204.204])1.0000000000:0.3114883037[&&NHX:C=204.204.204],(Q3EB59_ARATH:0.4106969
065[&&NHX:C=204.204.204],Q1PFB8_ARATH:0.5638667982[&&NHX:C=204.204.204])0.8980000000:0.1908054
502[&&NHX:C=204.204.204])0.8180000000:0.0872217074[&&NHX:C=204.204.204],A7P756_VITVI:0.1146129
988[&&NHX:C=204.204.204])0.0000000000:0.0090180148[&&NHX:C=204.204.204])0.9560000000:0.2568523
508[&&NHX:C=204.204.204])0.9400000000:0.341237074[&&NHX:C=204.204.204])0.8990000000:0.30006355
69[&&NHX:C=204.204.204])0.2560000000:0.1380854571[&&NHX:C=204.204.204],(C5YHP6_SORBI:0.2235336
465[&&NHX:C=204.204.204],A2YXI1_ORYSI:0.464008406[&&NHX:C=204.204.204])1.0000000000:1.26197608
16[&&NHX:C=204.204.204])0.7490000000:0.1302922101[&&NHX:C=204.204.204],((A1XGB4_CAPAN:0.288594
7322[&&NHX:C=204.204.204],(C6T1Z6_SOYBN:0.2798694287[&&NHX:C=204.204.204],(((Q56X75_ARATH:0.10
50955926[&&NHX:C=204.204.204],Q8GWD5_ARATH:0.1058948987[&&NHX:C=204.204.204])0.9970000000:0.31
17513226[&&NHX:C=204.204.204],(B9NBE5_POPTR:0.1700847806[&&NHX:C=204.204.204],B9SXY8_RICCO:0.0
934944483[&&NHX:C=204.204.204])0.8060000000:0.0810914103[&&NHX:C=204.204.204])0.0000000000:0.0
118293838[&&NHX:C=204.204.204],(C5Y494_SORBI:0.1953348639[&&NHX:C=204.204.204],Q2R2T4_ORYSJ:0.
1103614069[&&NHX:C=204.204.204])1.0000000000:0.8206608545[&&NHX:C=204.204.204])0.9320000000:0.
1582576483[&&NHX:C=204.204.204])0.6860000000:0.0427455083[&&NHX:C=204.204.204])1.0000000000:0.
8367421538[&&NHX:C=204.204.204],(P0DI23_PTEAA:0.1627796279[&&NHX:C=204.204.204],((A9T836_PHYPA
:0.0253731614[&&NHX:C=204.204.204],(A9S848_PHYPA:0.0526399042[&&NHX:C=204.204.204],A9STU1_PHYP
A:0.103261841[&&NHX:C=204.204.204])0.9180000000:0.0724800166[&&NHX:C=204.204.204])0.9760000000
:0.218116521[&&NHX:C=204.204.204],(Q2QNE3_ORYSJ:0.7921248919[&&NHX:C=204.204.204],(Q9M2U0_ARAT
H:0.1735367301[&&NHX:C=204.204.204],(B9SR15_RICCO:0.0777523724[&&NHX:C=204.204.204],B9HTK2_POP
TR:0.0915700386[&&NHX:C=204.204.204])0.8400000000:0.0684047344[&&NHX:C=204.204.204])0.30300000
00:0.0997806675[&&NHX:C=204.204.204])0.9240000000:0.2057745465[&&NHX:C=204.204.204])0.92200000
00:0.1801895175[&&NHX:C=204.204.204])0.9180000000:0.338362563[&&NHX:C=204.204.204])0.822000000
0:0.1650169687[&&NHX:C=204.204.204])0.3940000000:0.0831571765[&&NHX:C=204.204.204],(A9SG36_PHY
PA:0.6564205159[&&NHX:C=204.204.204],(A9SHQ9_PHYPA:0.7892490417[&&NHX:C=204.204.204],A9SU70_PH
YPA:0.7518962285[&&NHX:C=204.204.204])0.7460000000:0.1798275752[&&NHX:C=204.204.204])0.0190000
000:0.183285713[&&NHX:C=204.204.204])0.6660000000:0.0669993254[&&NHX:C=204.204.204],(A9RJH1_PH
YPA:0.2100588713[&&NHX:C=204.204.204],A9RZ57_PHYPA:0.0808776112[&&NHX:C=204.204.204])0.9990000
000:0.5289722709[&&NHX:C=204.204.204])0.8580000000:0.1284478031[&&NHX:C=204.204.204],((C5XEK4_
SORBI:0.0391083068[&&NHX:C=204.204.204],B6UBY6_MAIZE:0.0954724731[&&NHX:C=204.204.204])1.00000
00000:0.6643667923[&&NHX:C=204.204.204],(((Q84WP5_ARATH:0.1475274105[&&NHX:C=204.204.204],D7MM
W4_ARALL:0.1939654035[&&NHX:C=204.204.204])0.0110000000:0.0534093039[&&NHX:C=204.204.204],(Q9F
NE8_ARATH:0.4204530469[&&NHX:C=204.204.204],(Q3EA54_ARATH:0.9985082621[&&NHX:C=204.204.204],(O
24088_MEDTR:0.4409619582[&&NHX:C=204.204.204],(A3A2W2_ORYSJ:0.0946136318[&&NHX:C=204.204.204],
(C5XTX2_SORBI:0.0232297006[&&NHX:C=204.204.204],C4JAF2_MAIZE:0.0830588549[&&NHX:C=204.204.204]
```

```
)0.9260000000:0.1129906577[&&NHX:C=204.204.204])0.9990000000:0.3498576327[&&NHX:C=204.204.204]
)0.0000000000:0.0230023728[&&NHX:C=204.204.204])0.8150000000:0.0913655275[&&NHX:C=204.204.204]
)0.7060000000:0.1049708219[&&NHX:C=204.204.204])0.9370000000:0.2636177058[&&NHX:C=204.204.204]
,((F2E5T1_HORVD:0.1797339345[&&NHX:C=204.204.204],B9F6Z0_ORYSJ:0.0244258054[&&NHX:C=204.204.20
4])0.9720000000:0.2129342839[&&NHX:C=204.204.204],(((F2D276_HORVD:0.1138183195[&&NHX:C=204.204
.204],C5WNF5_SORBI:0.0421295599[&&NHX:C=204.204.204])0.9240000000:0.1539953161[&&NHX:C=204.204
.204],(F2E2E4_HORVD:0.1227473407[&&NHX:C=204.204.204],Q84NQ7_ORYSJ:0.1358309987[&&NHX:C=204.20
4.204])0.9900000000:0.30632322[&&NHX:C=204.204.204])0.9620000000:0.2036419823[&&NHX:C=204.204.
204],(Q8LE26_ARATH:0.4073498797[&&NHX:C=204.204.204],Q5W6M3_ORYSJ:0.2391813624[&&NHX:C=204.204
.204])0.7790000000:0.0583770684[&&NHX:C=204.204.204])0.5850000000:0.0569280462[&&NHX:C=204.204
.204])0.9740000000:0.4198223962[&&NHX:C=204.204.204])0.2030000000:0.162535295[&&NHX:C=204.204.
204])0.8910000000:0.1821292921[&&NHX:C=204.204.204])0.9320000000:0.2625927238[&&NHX:C=204.204.
204],(A9S1T8_PHYPA:0.1057692699[&&NHX:C=204.204.204],A9SB31_PHYPA:0.0393461979[&&NHX:C=204.204
.204])0.9890000000:0.4529334873[&&NHX:C=204.204.204])0.0000000000:0.1321587367[&&NHX:C=204.204
.204],D8R814_SELML:0.5518380113[&&NHX:C=204.204.204])0.9490000000:0.471967627[&&NHX:C=204.204.
204],(((P0DI27_PTEAA:0.1824337537[&&NHX:C=204.204.204],(Q6NPF8_ARATH:0.2579744309[&&NHX:C=204.
204.204],(Q9SKN3_ARATH:0.1976385286[&&NHX:C=204.204.204],((Q10Q78_ORYSJ:0.0763470646[&&NHX:C=2
04.204.204],P0DI68_BRADI:0.0845108877[&&NHX:C=204.204.204])0.7480000000:0.0231652318[&&NHX:C=2
04.204.204],(P0DI66_MAIZE:0.38238972[&&NHX:C=204.204.204],B4FNS3_MAIZE:0.183890185[&&NHX:C=204
.204.204])0.3350000000:0.0315760789[&&NHX:C=204.204.204])0.9870000000:0.1327381296[&&NHX:C=204
.204.204])0.3100000000:0.0266287721[&&NHX:C=204.204.204])0.9480000000:0.1222134901[&&NHX:C=204
.204.204])0.0000000000:4.3497E-
6[&&NHX:C=204.204.204],((P0DI70_GINBI:0.0306315972[&&NHX:C=204.204.204],(P0DI69_GINBI:0.031570
1869[&&NHX:C=204.204.204],P0DI64_PINCO:0.1792347315[&&NHX:C=204.204.204])0.9130000000:0.050257
0205[&&NHX:C=204.204.204])0.8210000000:0.0432560928[&&NHX:C=204.204.204],((P0DI22_PTEAA:0.2531
645182[&&NHX:C=204.204.204],(A9RKK4_PHYPA:0.0898828458[&&NHX:C=204.204.204],A9RLK6_PHYPA:0.105
3412163[&&NHX:C=204.204.204])0.9970000000:0.2399965578[&&NHX:C=204.204.204])0.7780000000:0.044
9995254[&&NHX:C=204.204.204],(D8QNI1_SELML:0.1548118058[&&NHX:C=204.204.204],(((P0DI71_GINBI:0
.0970767577[&&NHX:C=204.204.204],D5ACW4_PICSI:0.1296496278[&&NHX:C=204.204.204])0.8870000000:0
.0788684287[&&NHX:C=204.204.204],(Q8L7R5_ARATH:0.2362196266[&&NHX:C=204.204.204],((Q945M8_ARAT
H:0.1606992283[&&NHX:C=204.204.204],Q9LZM5_ARATH:0.2172982704[&&NHX:C=204.204.204])0.822000000
0:0.0953210494[&&NHX:C=204.204.204],(B6T990_MAIZE:0.2284484802[&&NHX:C=204.204.204],(B6TAX2_MA
IZE:0.1104397067[&&NHX:C=204.204.204],(B8AYU8_ORYSI:0.1327700858[&&NHX:C=204.204.204],(B6TM88_
MAIZE:0.1470691359[&&NHX:C=204.204.204],B8AC36_ORYSI:0.085474674[&&NHX:C=204.204.204])0.860000
0000:0.0541259476[&&NHX:C=204.204.204])0.6970000000:0.040697777[&&NHX:C=204.204.204])0.9510000
000:0.1214418933[&&NHX:C=204.204.204])0.5900000000:0.0636814811[&&NHX:C=204.204.204])0.9190000
000:0.1112057107[&&NHX:C=204.204.204])0.8870000000:0.08972193[&&NHX:C=204.204.204])0.000000000
0:0.0272335532[&&NHX:C=204.204.204],((B6U300_MAIZE:0.1026537815[&&NHX:C=204.204.204],B8BPI2_OR
YSI:0.0324467721[&&NHX:C=204.204.204])0.9150000000:0.1556020495[&&NHX:C=204.204.204],(Q3ECT8_A
RATH:0.4037861596[&&NHX:C=204.204.204],(P0CB17_ARATH:0.3591532527[&&NHX:C=204.204.204],Q66GI1_
ARATH:0.1514823419[&&NHX:C=204.204.204])0.9830000000:0.2451079692[&&NHX:C=204.204.204])0.00000
00000:0.0656601747[&&NHX:C=204.204.204])1.0000000000:0.5262296665[&&NHX:C=204.204.204])0.96500
00000:0.1945581845[&&NHX:C=204.204.204])0.9340000000:0.1050067648[&&NHX:C=204.204.204])0.91100
00000:0.083254107[&&NHX:C=204.204.204])0.7900000000:0.0275495581[&&NHX:C=204.204.204])0.988000
0000:0.9300112929[&&NHX:C=204.204.204],F0YFA3_AURAN:1.177454178[&&NHX:C=102.0.204])0.178000000
0:0.1476866683[&&NHX:C=204.204.204])0.7540000000:0.1983340042[&&NHX:C=204.204.204],F0Y3N5_AURA
N:1.4849931912[&&NHX:C=102.0.204])0.7770000000:0.2656007784[&&NHX:C=204.204.204],((E1ZFT0_CHLV
A:1.1440265764[&&NHX:C=0.255.0],M1VAW8_CYAME:1.3476137691[&&NHX:C=102.51.0])0.8670000000:0.347
9926338[&&NHX:C=0.255.0],(P0DI73_CHLAT:1.1599848064[&&NHX:C=0.255.0],(P0DI72_CHLAT:0.856821589
6[&&NHX:C=0.255.0],(C1EI34_MICSR:0.2286144106[&&NHX:C=0.255.0],(C1N652_MICPC:0.1881111788[&&NH
X:C=0.255.0],(A4S8B7_OSTLU:0.2877817006[&&NHX:C=0.255.0],Q00U99_OSTTA:0.4850337175[&&NHX:C=0.2
55.0])1.0000000000:0.8738711042[&&NHX:C=0.255.0])0.8300000000:0.1593574653[&&NHX:C=0.255.0])0.
9640000000:0.4651011056[&&NHX:C=0.255.0])0.5670000000:0.0919602093[&&NHX:C=0.255.0])0.90100000
00:0.3041769626[&&NHX:C=0.255.0])0.6250000000:0.263125652[&&NHX:C=0.255.0])0.7650000000:0.1670
8745945[&&NHX:C=0.255.0],(H3GEF8_PHYRM:2.1908331232[&&NHX:C=102.0.204],((F0X036_9STRA:0.478855
4689[&&NHX:C=102.0.204],F0WMT2_9STRA:1.0577456706[&&NHX:C=102.0.204])0.6530000000:0.1385848646
[&&NHX:C=102.0.204],((K3WS85_PYTUL:0.2749531425[&&NHX:C=102.0.204],(F0X038_9STRA:0.757162585[&
&NHX:C=102.0.204],(((G5AEA1_PHYSP:0.0257102165[&&NHX:C=102.0.204],D0NMH7_PHYIT:0.1569600422[&&
NHX:C=102.0.204])1.0000000000:0.604904315[&&NHX:C=102.0.204],(G5AEA0_PHYSP:0.2276465334[&&NHX:
C=102.0.204],(G5AE98_PHYSP:0.0954926753[&&NHX:C=102.0.204],H3H3L4_PHYRM:0.0487281617[&&NHX:C=1
02.0.204])0.9150000000:0.1594227133[&&NHX:C=102.0.204])0.5050000000:0.151654323[&&NHX:C=102.0.
204])0.9620000000:0.34737192[&&NHX:C=102.0.204],((H3HBC3_PHYRM:0.1812840018[&&NHX:C=102.0.204]
,(G4ZSC0_PHYSP:0.1046832024[&&NHX:C=102.0.204],D0NLD9_PHYIT:0.0782151945[&&NHX:C=102.0.204])0.
8420000000:0.0873814607[&&NHX:C=102.0.204])0.9860000000:0.3459364176[&&NHX:C=102.0.204],(K3WS8
4_PYTUL:0.2049086898[&&NHX:C=102.0.204],K3WS83_PYTUL:0.4910520627[&&NHX:C=102.0.204])0.1150000
000:0.1190482007[&&NHX:C=102.0.204])0.9470000000:0.2404943945[&&NHX:C=102.0.204])0.7580000000:
0.1048443149[&&NHX:C=102.0.204])0.4160000000:0.0424477531[&&NHX:C=102.0.204])0.8940000000:0.16
45723609[&&NHX:C=102.0.204],(((M4B8W0_HYAAE:0.1235778878[&&NHX:C=102.0.204],(G4ZSC4_PHYSP:0.04
09388372[&&NHX:C=102.0.204],(D0NLE1_PHYIT:0.0754260496[&&NHX:C=102.0.204],H3HBC4_PHYRM:0.07445
39768[&&NHX:C=102.0.204])0.8190000000:0.0427154922[&&NHX:C=102.0.204])0.8220000000:0.062701388
5[&&NHX:C=102.0.204])0.9290000000:0.1350728969[&&NHX:C=102.0.204],(G4ZSC3_PHYSP:0.2368605598[&
&NHX:C=102.0.204],H3GGR0_PHYRM:0.0505684801[&&NHX:C=102.0.204])0.9760000000:0.2003503545[&&NHX
:C=102.0.204])0.9740000000:0.27098359[&&NHX:C=102.0.204],(K3WS90_PYTUL:0.5694452134[&&NHX:C=10
2.0.204],(K3X3G8_PYTUL:0.2196499663[&&NHX:C=102.0.204],(H3GI99_PHYRM:3.3812E-
6[&&NHX:C=102.0.204],(G4ZRP2_PHYSP:0.0709235896[&&NHX:C=102.0.204],D0NCN6_PHYIT:0.0895809396[&
&NHX:C=102.0.204]):0.051663502[&&NHX:C=102.0.204])0.0460000000:0.5228465009[&&NHX:C=102.0.204]
)0.9850000000:0.7855163973[&&NHX:C=102.0.204])0.9990000000:0.1490509889[&&NHX:C=102.0.204])0.7
```

```
730000000:0.1216650341[&&NHX:C=102.0.204])0.8690000000:0.2508009516[&&NHX:C=102.0.204])0.85000
00000:0.4393284957[&&NHX:C=102.0.204])0.3370000000:0.16708745945[&&NHX:C=102.0.204])[&&NHX:C=1
02.0.204]
```