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Accepted version. *Reproductive Toxicology*, Vol. 25, No. 1 (January 2008): 47-57. DOI. © 2008 Elsevier. Used with permission.

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Molecular Targets of 2,3,7,8-Tetrachlorodibenzo-P-Dioxin (TCDD) Within The Zebrafish Ovary: Insights into TCDD-Induced Endocrine Disruption and Reproductive Toxicity

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Abstract: TCDD is a reproductive toxicant and endocrine disruptor, yet the mechanisms by which it causes these reproductive alterations are not fully understood. In order to provide additional insight into the molecular mechanisms that underlie TCDD's reproductive toxicity, we assessed TCDD-induced transcriptional changes in the ovary as they relate to previously described impacts on serum estradiol concentrations and altered follicular development in zebrafish. *In-silico* computational approaches were used to correlate candidate regulatory motifs with observed changes in gene expression. Our data suggest that TCDD inhibits follicle maturation via attenuated gonadotropin responsiveness and/or depressed estradiol biosynthesis, and that interference of estrogen-regulated signal transduction may also contribute to TCDD's impacts on follicular development. TCDD may also alter ovarian function by disrupting various signaling pathways such as glucose and lipid metabolism, and regulation of transcription. Furthermore, events downstream from initial TCDD molecular-targets likely contribute to ovarian toxicity following chronic exposure to TCDD. Data presented here provide further insight into the mechanisms by which TCDD disrupts follicular development and reproduction in fish, and can be used to formulate new hypotheses regarding previously documented ovarian toxicity.

Keywords: TCDD, ovary, zebrafish, follicular development, microarray, endocrine disruptors

Introduction

2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is a persistent environmental contaminant that is a known reproductive toxicant and

endocrine disruptor in nearly all vertebrates. The effects of TCDD on reproduction and fertility have been studied extensively [1–3], and evidence suggests that TCDD compromises both ovarian function and follicular development. Female reproductive development is highly complex, and is synchronized by intricate and highly regulated signal transduction pathways that are integrated with the endocrine system. This complexity has made it particularly difficult to identify the molecular action of TCDD-induced ovarian toxicity. Although it is clear that TCDD impacts maturation and ovulation of ovarian follicles, as well as estradiol secretion [4–7], the mechanisms that underlie these reproductive toxicities are complicated and poorly understood.

It is generally accepted that TCDD toxicity is mediated by the aryl hydrocarbon receptor (AHR)-signaling cascade [8]. The ligand-bound AHR complex is translocated to the nucleus where it dimerizes with the aromatic hydrocarbon receptor nuclear translocator (ARNT) protein. This heteromeric complex binds to the aryl hydrocarbon-response element (AHRE) (TnGCGTG DNA motifs) located in the regulatory regions of several genes (*e.g.*, , *cyp1a1*) and can initiate or suppress gene transcription [9–11]. While it is thought that such transcriptional regulation mediates the toxicity of TCDD, specific roles of these gene changes in dioxin-induced toxicity are not understood. Additionally, some actions of TCDD may be AHR-independent and/or result from downstream transcriptional changes.

Evidence suggests that disruptions in female reproduction by TCDD are likely the result of a direct effect at the ovary [12–17]. Since the AHR is expressed in the ovary, TCDD could disrupt critical cellular signals that regulate follicular development and/or estradiol biosynthesis via AHR-mediated alterations in gene transcription, thereby contributing to the observed decrease in ovarian development and reduced reproductive capacity. Alternatively, TCDD could interfere with the hypothalamic-pituitary-gonadal (HPG) axis or estradiol metabolism. For example, TCDD could negatively regulate estrogen signaling by inducing oxidative metabolism of estrogens via the AHR-pathway, by suppressing the expression and/or efficacy of the estrogen receptors, or by inhibiting estradiol-regulated gene expression [18–21].

Since the basic features of the HPG axis and AHR-signaling pathways in fish are fundamentally similar to other vertebrates [22–24], fish are excellent model systems with which to investigate the effects of endocrine-disrupting chemicals on vertebrate reproductive function. The zebrafish has proven to be an effective system for investigation into the teratogenic effects of TCDD [25–27]. Zebrafish are highly prolific with rapid follicular development, and many of the receptors, enzymes, and peptide growth factors involved in follicular development have been characterized (see Ge 2005 for review); therefore, it is particularly suited for investigating TCDD's effects on the regulation of follicular development.

We have previously demonstrated that sublethal dietary exposure to TCDD alters follicular development, egg production, and serum 17 β estradiol concentrations in zebrafish [4]. Here we investigate the transcriptional events in the ovary that precede these previously described histomorphologic and physiologic alterations. We used quantitative RT-PCR to assess the effects on the expression of several candidate genes important in the regulation of follicle development, oocyte maturation, and vitellogenesis, and used cDNA microarray technology to evaluate altered gene expression profiles to identify other cellular pathways potentially impacted by TCDD-exposure. Additionally, we used a functional genomics approach to examine candidate regulatory motifs in relation to different expression profiles in an effort to better clarify potential mechanisms of toxicity following chronic exposure to TCDD.

Materials and Methods

Experimental animals

Adult female (AB strain, Zebrafish International Resource Center) and male zebrafish (golden longfin, Ekwil Farms) were housed separately and acclimated for several weeks prior to the initiation of experiments. Fish were maintained at 26–28°C on a 14-hour light and 10-hour dark cycle in a flow-through buffered, de-chlorinated water system and were spawned once weekly during the experiment.

TCDD exposure and RNA extraction

Trout chow yielding a final concentration of approximately 0, 10, 40, or 100 ng TCDD/g food (ppb) was prepared as previously described [28]. Females were fed brine shrimp nauplii daily, and contaminated trout chow diet 5 of 7 days per week. Fish were fed en masse to satiation, and based upon the average food consumed per fish, received an estimated dose of 0, 0.08, 0.32, or 0.80 ng TCDD/female/day. Based upon our previous work, fish accumulated approximately 0, 0.6, 3, and 14 ng TCDD/g fish after 15 days, and ovaries accumulated approximately 0.4, 2, and 5 ng TCDD/g ovary (body burdens were not measured in this study). Following dietary exposure, five females from each treatment group were euthanized and ovaries were extracted and frozen in liquid nitrogen. Total RNA was isolated from individual ovaries using Trizol reagent (Invitrogen) and purified using an RNeasy MinElute cleanup kit (Qiagen) according to manufacturer's instructions. Individual samples were analyzed by agarose gel electrophoresis to confirm the integrity of the 18S and 28S ribosomal RNAs, and quantified by UV spectrophotometry at 260 nm using a Nanodrop ND-1000 Spectrophotometer (Nanodrop Technologies).

Quantitative RT-PCR (QPCR)

QPCR was used to quantify selected gene transcripts important in both receptor- and non-receptor-mediated regulation of follicular development, as well as estradiol biosynthesis, included: luteinizing hormone receptor (*lhr*), follicle-stimulating hormone receptor (*fshr*), estrogen receptors (*esr1*, *esr2a*, *esr2b*), epidermal growth factor (*egf*), egf receptor (*egfr*), inhibins (*inhbba*, *inhbb*), steroidogenic acute regulatory protein (*star*), side chain cleavage enzyme (*cyp11a1*), and aromatase (*cyp19a1a*). cDNA was synthesized from 5 µg of total RNA from individual samples (n = 3 from each treatment group) using SuperscriptII reverse transcriptase (Invitrogen) and random hexamer primers following manufacturer's instructions. QPCR was performed using the Stratagene Mx3000 system and the Full Velocity SYBR Green QPCR Master Mix with the manufacturer's instructions (Stratagene) using gene-specific primers listed in [Table 1](#). Agarose gel electrophoresis and melting curve analysis confirmed that specific

products of expected size were amplified. All QPCR reactions were run in triplicate with negative (no template) controls. Relative gene expression data (fold-change) was calculated using the comparative quantification model [29] assuming 100% efficiency, using small nuclear ribonuclear protein D1 polypeptide (*snrpd1*) as the reference gene; *snrpd1* is important for mRNA processing, and expression was unaltered by TCDD exposure. QPCR on individual samples (n = 3 from each treatment group) was also used to verify microarray expression profiles. The gene-specific primers for these transcripts (cluster 4: *cyp1a1*; cluster 2: *sepp1a*, *lgals3l*, and *krt4*; cluster 1: *krml* and *vtg1*; cluster 3: *tfa*) are also listed also in [Table 1](#). The seven transcripts showed altered expression by at least 2-fold following exposure to at least one dose of TCDD, and were selected for microarray verification based upon their functional characterization, presence of candidate regulatory motifs, and to represent each of the clusters in gene expression (see details below and in [Table 2](#)).

Table 1. Primer sequences used for QPCR. Gene names are listed in the text and [Supplementary Tables](#).

Gene symbol	Sense Primer	Antisense Primer
<i>cyp1a1</i>	ACTGGTGCGACTGGTTAATATGAG	GTCTTCGCATGTGTTGATAAGAG
<i>cyp11a1</i>	CAGGTTTTCACTGGAATCGG	CTGGTTAAAGATGCCATCCC
<i>cyp19a1a</i>	ACTTCCAGAAAAATGTTCCGAGTC	TCTGAGGATAAGCTGCACGC
<i>egf</i>	GCATCCAGAGAATGAACCTCGACGG	TGATTTGTCCTGTTTGTGTGCCG
<i>egfr</i>	CTTACAAAGCCTGGAACGAAGAGCC	CCTGACACACTTTCTTTCCGGCG
<i>esr1</i>	TCCACATCCACACAGTAGGC	CTTTCTTGATCAGGGTGGGG
<i>esr2a</i>	AAGCTGCTGTGTCTGCTGGACTCGG	TCATGCAGTGCAGGTGGTCCATGCC
<i>esr2b</i>	GGTGAAGTGTGTCTTTCTGTGCCG	GTGTGATTTTTGGGGCTGGCC
<i>fshr</i>	AGCCGATTTGGATGCTTTAAAAGGC	TCAGACAGATGTCAGTGCACCTGGG
<i>inhbaa</i>	GCACATTCAGAAGCCGACTGCC	TAAAGTCCGTCTGCCGTGCGC
<i>inhbb</i>	CGAATTCGGTGGACAGACAAACGG	TCCGTTTATTATTAGGCTCGCGG
<i>krml2.2</i>	TATAAACTCAAGTGCAGAAAGGC	ACCAGCAAACAATCTTATGC
<i>krt4</i>	CAAAACCAAGTGCACCACCG	CATCTCCTCATTACAGGGG
<i>lgals3l</i>	GCTGTACAAGTGCATGTAAAGGG	CGTCTTTTATGCATGAAGCG
<i>lhr</i>	CAAAAAGGACGAGTCGCTGAAACGC	GCAGAAGAAAAACAAGAAGCAGGGC
<i>seppa1</i>	AAATCTGACTTTAACTGGTCCAGTG	ATGTTACATGACCTTTGCC
<i>snrpd1</i>	CGTCACGATTGAGTGAAGAATGGC	TGAGATCTTCATCTCCTCGGCC
<i>star</i>	ACCCACCTGTATTGTCATGCG	AATGGCTGCGTCTATACCCC
<i>tfa</i>	ATTAAGCACACTGTGGTCCGG	AGCATGAACTGGCACTTGGG
<i>vtg1</i>	GAGATTGAACTGACTGCAGCC	ATTCCACATGAACATAGGCC

Table 2. List of representative transcripts^a identified by microarray to be dysregulated greater than 2-fold in one or more treatment group. Presence of putative AHRE or ERE is noted. See Supplementary Tables 1–3 for complete gene list plus location of putative response elements.

Gene symbol	10 ppb	40 ppb	100 ppb	AHRE	ERE
Ovarian development					
<i>fabp3</i>	-2.92	-2.68	-4.14		
<i>tpte</i>	-1.91	-1.45	-2.60	*	
<i>tph1l</i>	-2.64	-1.53	1.19	*	
vtg1	-7.38	-1.62	-1.83	*	*
Detoxification/oxidative stress					
cyp1a	6.93	14.87	24.68	*	*
sepp1a	-1.71	-1.21	-2.48		
<i>serpina1</i>	29.44	1.51	3.07	*	*
Lipid metabolism					
<i>apoeb</i>	-1.83	-1.09	-4.12	*	
<i>apom</i>	6.16	1.04	1.32		
<i>lipf</i>	-2.06	-1.85	-2.30	*	*
Carbohydrate metabolism					
<i>ldha</i>	-1.78	-1.45	-2.59	*	*
<i>slc3a2</i>	-2.35	-1.68	-3.05		
Immune response/cellular repair					
<i>anxa1a</i>	-2.20	-3.36	-7.06	*	*
<i>cp</i>	24.49	1.06	2.16	*	
<i>fgb</i>	12.80	-1.82	-1.35	*	
<i>fgb</i>	5.66	1.43	1.61	*	*
<i>tfpib</i>	-1.54	-1.95	-5.66		
<i>timeless</i>	-2.92	1.88	1.07	*	
Structure					
krt4	-1.96	-2.93	-5.65	*	*
lgals3l	-1.89	-2.68	-2.56	*	
Signal transduction/transcription/regulation of cell cycle					
<i>rab5b</i>	2.45	1.34	2.13	*	*
<i>rad1</i>	-1.10	1.13	-2.16		
<i>rbp2a</i>	-2.98	-2.39	-4.54	*	*
<i>Igfbp1</i>	5.58	-1.38	-1.47	*	
<i>Junb</i>	-2.21	-1.88	-4.39	*	*
krm12.2	-2.59	-1.19	-2.41	*	*
<i>lztfl1</i>	-1.12	-1.12	-2.33	*	
<i>sp4</i>	1.51	2.32	1.96	*	
<i>ing3</i>	-2.29	1.17	-1.32		
<i>igfbp1</i>	5.58	-1.38	-1.47	*	
tfa	11.64	-2.09	-1.32	*	

Gene symbol 10 ppb 40 ppb 100 ppb AHRE ERE

ptena -2.32 1.51 1.38 *

^aGene symbols are from Affymetrix probe identifiers and are organized into general functional groups. Transcripts in bold were verified by QPCR.

Microarray hybridization and analysis

Differential ovarian gene expression was determined using the Affymetrix Zebrafish Genome Array, which represents approximately 14,900 transcripts. Experiments were designed to comply with MIAME guidelines [30]. In an effort to reduce variability, target synthesis using pooled RNA (of equal quantity and comparable quality from 5 females per treatment group) [31–33], biotin-labeling, hybridizations, and staining were performed using standard Affymetrix reagents and methods (<http://www.affymetrix.com/index.affx>). Pooled samples were run in duplicate such that a total of eight arrays were used.

Images were extracted from TIFF files using Microarray Suite Version 5.0 (Affymetrix). Raw data can be viewed at the National Center for Biotechnology Information Gene Expression Omnibus website (<http://www.ncbi.nlm.nih.gov/projects/geo/>); series record [GSE4859](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4859). Data were transformed and normalized using GeneSpring software (Agilent Technologies) and further analyzed using Bioconductor 1.6 [34]. Expressed data were obtained by selecting 8732 probes present in all eight chips. Differentially expressed probes were identified as those showing at least a 2-fold change in expression in both replicates of one or more of the treatment groups compared with control. The dysregulated transcripts were assigned to general functional groups based upon their Gene Ontology terms, or an annotated putative *H. sapiens* or *M. musculus* ortholog from Swiss-Prot (<http://us.expasy.org/sprot/>). The dysregulated transcripts were clustered using agglomerative hierarchical clustering [35] without performing mean centering of expression values, and using Ward's method for merging clusters.

In-silico Transcription Factor Analysis

Possible *cis*-acting AHRE (GCGTG) and ERE (AGGTCAnnnTGACCT) sequences were identified within the regulatory region of differentially expressed genes as well as candidate genes

determined by QPCR. The reference genes were 22877 RefSeq genes and Ensemble predictions mapped to the draft zebrafish genome, and the test sequences were RefSeqs overlapping with consensus sequences of differentially expressed Affymetrix probes. Of the dysregulated transcripts, 140 could be mapped to Ensemble genes and were used for subsequent analyses. The 5' regulatory sequences of the reference and dysregulated genes were modeled by the 5'-UTR of each RefSeq (5000 bp upstream sequences from the transcriptional start site). Regulatory sequences were acquired from the June 2004 draft assembly of the zebrafish genome using the University of California – Santa Cruz table browser [36] and were scanned for possible transcription factor binding sites using TFBS [37], JASPAR [38] for AHRE sequences at a 100% scoring threshold, and TRANSFAC Public 7.0 [39] for ERE sequences at an 80% scoring threshold. To compare control and differentially expressed sequences, the hypergeometric distribution in R 2.1.0 was used to describe the probability of drawing a sample the same size as the differentially expressed sequences from the control sample with the same or fewer transcription factor binding sites identified. A chi-squared test was used to determine if there was a location bias of transcription factor binding sites with respect to identified clusters. The starting position distributions of AHREs and EREs within a cluster were compared with the corresponding distributions in the entire Ensemble known gene collection. Distributions for a cluster significantly different ($p < 0.05$) from control suggested putative regulatory patterns.

Data analysis

Statistical analysis of QPCR data was performed using Sigma-Stat 2.0 (SPSS, Inc) and presented as means \pm standard error of the mean (SEM). Data were evaluated for homoscedasticity (Levene Median test) and one-way analysis of variance (ANOVA) was used to detect treatment-related effects on the expression of each candidate transcript. Where significant differences were indicated between treatment groups, and the data were homogeneous, pair-wise multiple comparisons were conducted using the Tukey test. When tests for homogeneous variance failed, the Kruskal-Wallis one way ANOVA on ranks was used, and significant differences were evaluated using the Dunn's test. Pearson's correlation was used to determine whether

changes in gene expression identified by microarray were correlated with changes in expression of the seven transcripts determined by QPCR. For all analyses, significant differences were identified at $p < 0.05$.

Results

Effects on the regulation of follicular development and estradiol biosynthesis

Dietary TCDD exposure suppressed the expression of all examined candidate transcripts that are important in both receptor- and non-receptor-mediated regulation of follicular development, as well as estradiol biosynthesis (Figure 1A). The candidate genes were down-regulated by at least 2-fold; overall changes in expression were not dose-dependent. Locations of putative AHREs and EREs within the regulatory region of the transcripts are illustrated in Figure 1B.

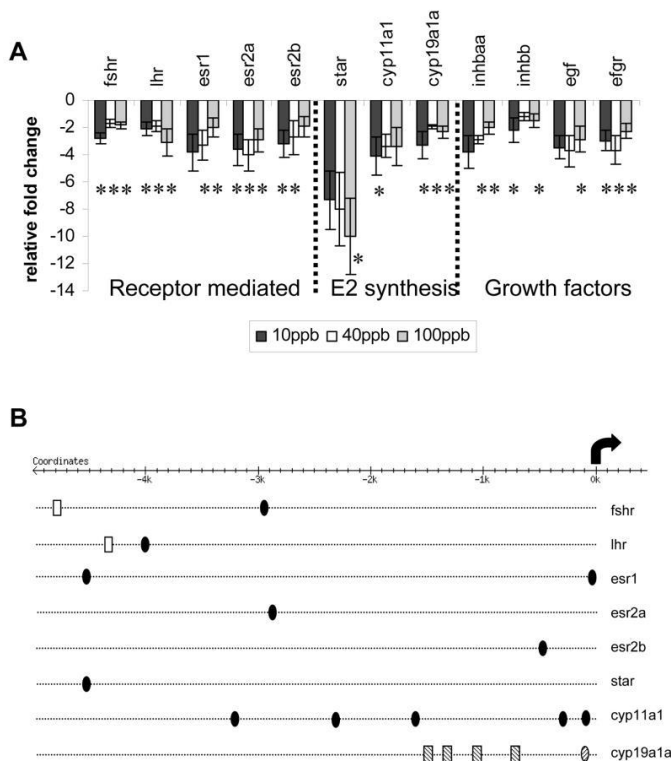


Figure 1. A. Fold changes in expression of several genes important for follicular development determined by QPCR; normalized to *snrpd1*. *Denotes significant changes in expression compared with control ($p < 0.05$); dose-dependent changes

were not observed. B. Location of putative AHREs (filled ovals, this study; lined ovals [86]; putative EREs (empty rectangles), and putative 1/2-EREs (lined rectangles [86]) within upstream regulatory regions. Arrow represents the transcriptional start site.

Effects of TCDD on Global Ovarian Gene Expression

Two hundred thirty-five probe sets (representing 229 unique transcripts) were identified as being either induced or suppressed greater than 2-fold following exposure to one or more TCDD concentration. Overall, more transcripts were suppressed than were induced with 37% (85/229), 7% (16/229), and 40% (92/229) of the transcripts down-regulated and 11% (25/229), 4% (9/229), and 11% (25/229) of the transcripts up-regulated in the 10, 40, and 100 ppb treatment groups, respectively. QPCR using individual samples verified microarray results for seven transcripts (Figure 2). The direction and fold-change values for samples from individual animals were correlated with changes in expression determined by microarray analysis of pooled samples for all seven genes ($p < 0.01$), demonstrating that our approach successfully identified changes in gene expression across treatment groups that could be validated with individual samples.

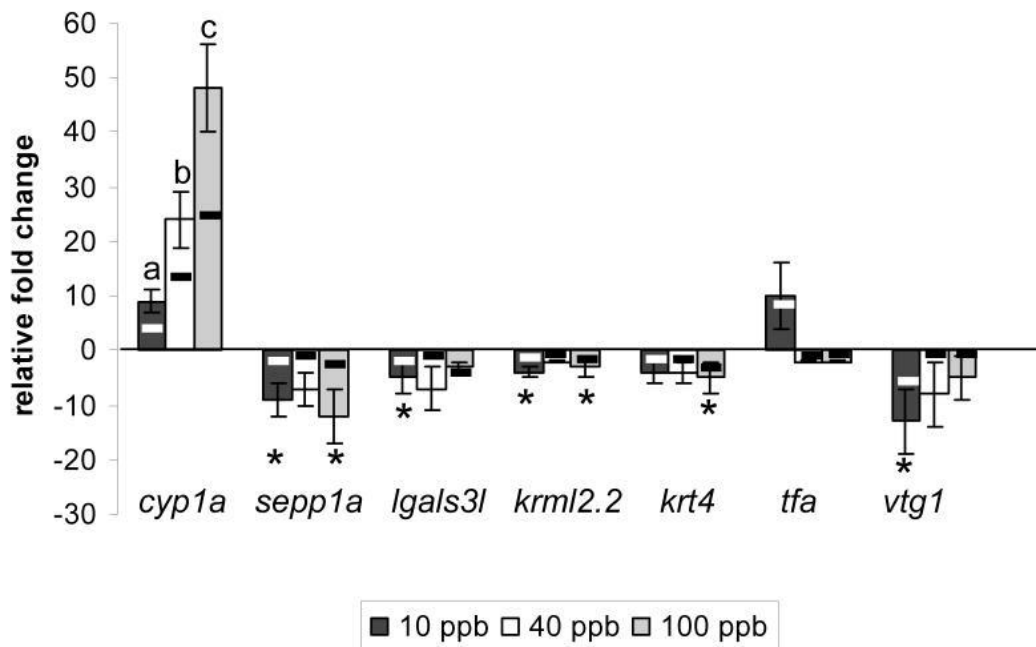


Figure 2. Validation of microarray results. Bars represent mean relative fold changes in gene expression determined by QPCR; normalized to *snrpd1*. Letters or * denote significant differences for that gene compared with control. Black and white lines

represent fold-changes in expression determined by array analysis. (Pearson's correlation, $p < 0.01$).

Differentially expressed transcripts with known functions (103/229) were assigned to general functional groups based upon the top three Gene Ontology (GO) functions and known biologic functions, and are important for signal transduction/transcription/regulation of the cell cycle, as well as for glucose and lipid metabolism, immune response/cellular repair, and structure (Table 2 and Figure 3). Hierarchical clustering grouped transcripts into one of five clusters (Figure 4A and Supplementary Table 1). On average, the 17 transcripts within the fifth cluster show minimal changes in gene expression across treatment groups and are therefore not shown in Figure 4 or discussed further (due to lack of statistical power). The majority of functionally annotated transcripts within clusters one and four regulate gene transcription or are important for signal transduction, while most functionally annotated transcripts within cluster two are important for maintaining structure, and those within cluster three play a role in immune function (see Figure 4A).

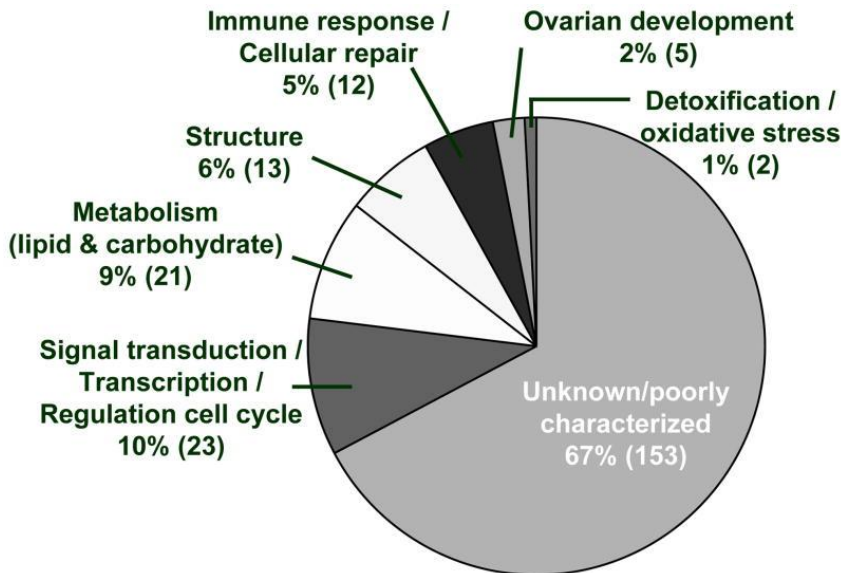


Figure 3. Proportion of dysregulated ovarian transcripts within each general functional group. The number in parentheses represents the number of transcripts out of 229 within each functional group.

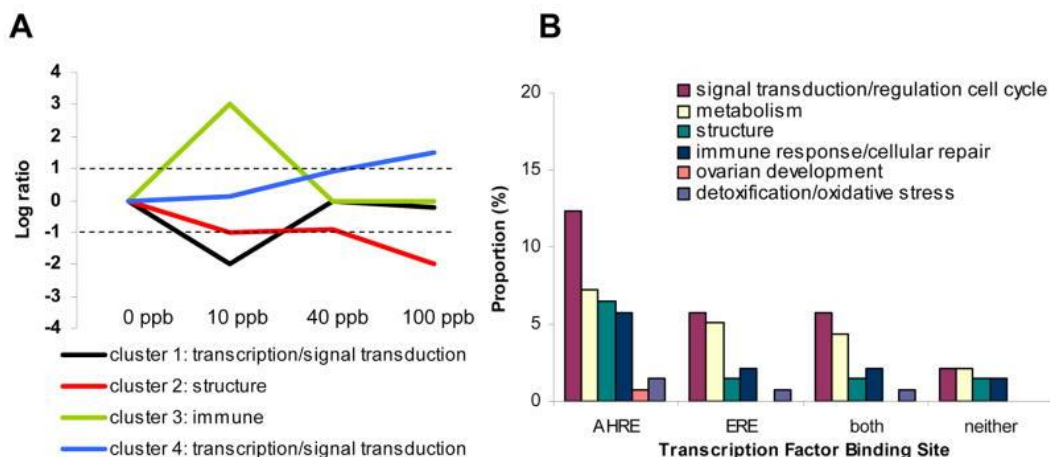


Figure 4. A. Gene expression (expressed as the log ratio compared with control) patterns of four hierarchical gene clusters including the primary functional group represented within each cluster. B. Proportion of dysregulated ovarian transcripts within each general functional group that contain putative AHREs, ERES, both or neither.

One hundred forty of the dysregulated transcripts were mapped to Ensemble genes, and 89% of these (125/140 corresponding to 113 unique transcripts) were found to have putative AHREs in the regulatory region of the gene (Figure 4B, Supplementary Tables 1 and 2), compared with 92% of the reference genes (21046/22877). Using hypergeometric distribution to calculate the probability of finding only 125 or fewer genes out of 140 that were drawn from 22877, our data suggest differentially expressed transcripts are not enriched for putative AHREs in ($p = 0.14$). Estimated probability density curves shown in Figure 5A illustrate the potential location bias of putative AHREs for each cluster along with the location of putative AHREs for all genes in the zebrafish genome for comparison. Upstream regions of genes within cluster 2 have putative AHRE distributions that are significantly different ($p = 2.9 \times 10^{-12}$) from those of the control gene set, with AHREs distributed 3000 – 4000 bp and 1500 bp upstream of the transcriptional start site (TSS). In cluster 3, AHREs tend to be further upstream (~ 3500 bp) from the TSS than control ($p = 2.0 \times 10^{-7}$), and in cluster 4, AHREs tend to be concentrated within 2000 bp upstream of the TSS ($p = 0.01$). Of the 113 unique transcripts that contain putative AHREs, 16% were upregulated and 51% were downregulated across treatment groups; many function as transcription factors and regulate the cell cycle (Figure 5).

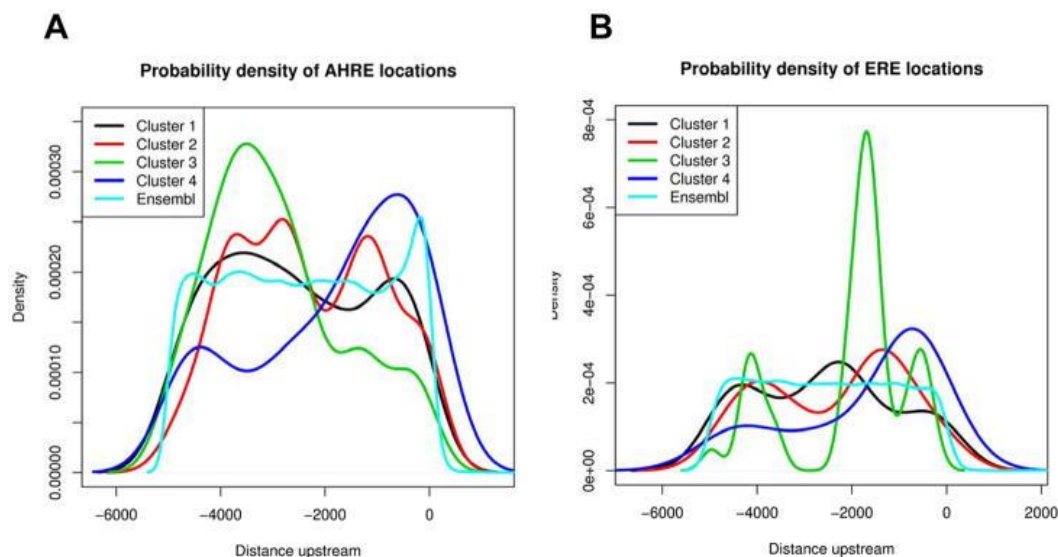


Figure 5. Probability density curves illustrate the potential location bias of putative AHREs (A) and EREs (B) with respect to the translational start site for the transcripts within each hierarchical cluster compared with reference. Note: Probability density curves represent the probability distribution in terms of integrals, illustrated as a line depicting the relative frequency that each response element is represented at that location.

Approximately 49% of the mapped dysregulated probes (68/140 corresponding to 58 unique transcripts) were found to have putative EREs in the regulatory region of the gene ([Figure 4B](#), [Supplementary Tables 1](#) and [3](#)); 17% of these transcripts were upregulated and 55% were downregulated across treatment groups. Forty-two percent of the reference genes (9608/22877) contained putative EREs in the regulatory region; differentially expressed genes contained putative EREs at a much higher rate than would be expected ($p = 0.05$). Estimated probability density curves shown in [Figure 5B](#) illustrate the potential location bias of putative EREs for each cluster. In cluster 1, EREs tend to be centered around 2000 bp from the TSS ($p = 3.0 \times 10^{-7}$). In cluster 3, EREs are largely concentrated at about 1800–2000 bp upstream of the TSS ($p = 8.2 \times 10^{-7}$) and in cluster 4, EREs tend to be concentrated within 2000 bp upstream ($p = 0.02$). Many of these transcripts function in carbohydrate and lipid metabolism, or regulation of transcription or the cell cycle ([Figure 4B](#)).

Approximately 41% of the dysregulated probes contain both putative AHRE and ERE in the regulatory region ([Figure 4B](#), [Supplementary Table 1](#)); approximately 20% of these transcripts were upregulated, while the majority of the transcripts (51%) were

downregulated across treatment groups. Approximately 40% of the reference genes (9039/22877) contain putative AHREs and EREs in the regulatory region; the dysregulated transcripts were not significantly enriched for both AHREs and EREs ($p = 0.35$). As with those with putative EREs, many of these transcripts are important for carbohydrate and lipid metabolism or function as transcription factors and regulate the cell cycle ([Figure 4B](#)).

Discussion

TCDD has been shown to perturb the regulation of vertebrate follicular development and ovulation, as well as steroidogenesis in the ovary [[3-6](#); [40](#)]. Regulation of these processes is complex, integrating receptor-mediated hormonal signals from the pituitary with locally produced factors to form an intimate regulatory network within and between follicles. This poses a challenge for identifying the molecular mechanisms that regulate TCDD's reproductive toxicity. Furthermore, the sometimes subtle secondary and tertiary effects on gene expression following chronic dioxin exposure can be difficult to ascertain and to correlate with observed toxicities. This study represents one of the first attempts to characterize the effects on ovarian gene expression following exposure of fish to chronic, sublethal concentrations of TCDD. Using a candidate-gene approach in conjunction with a genomics approach, we have identified several novel dioxin-responsive genes that with further study may better clarify TCDD's ovarian toxicity.

Effects on the regulation of follicular development and estradiol biosynthesis

All of the candidate genes selected for QPCR analysis (those important for receptor- and non-receptor mediated regulation of follicular development and estradiol biosynthesis) show peak expression in follicles that are in the mid-to-late stages of vitellogenesis, and should therefore be highly expressed in whole ovary of cycling females under normal conditions [[41-44](#)]. Gonadotropins are important regulators of follicular development, and in zebrafish, have been shown to induce the expression of several other genes important for oocyte development [[41](#); [45](#)]. Suppression of

both gonadotropin receptors suggests that impaired follicular development may be the result of this suppression. Similar effects on ovarian gonadotropin receptor expression have been shown in mammals [6;46–48] and others suggest that TCDD's anovulatory effects are likely mediated directly at the ovary in an AHR-dependent manner [49;50]. Collectively, this suggests that TCDD primarily acts at the ovary to suppress expression of gonadotropin receptors.

Exposure to TCDD also downregulates the expression of several genes important in estradiol biosynthesis (*star*, *cyp11a1*, and *cyp19a1a*), and likely contributes to the previously observed reduced serum estradiol concentrations [4]. While it has been proposed that reduced estradiol concentrations following exposure to TCDD may result from suppression of aromatase activity, the mechanism by which TCDD disrupts ovarian steroidogenesis is not clear. Baba et al [51] show that exposure to DMBA, an AHR agonist, is correlated with increased estradiol concentrations and increased aromatase expression, while others suggest that the target of TCDD-induced suppression of estradiol is upstream of aromatase in the steroidogenic pathway [52]. However, other *in vitro* and *in vivo* studies demonstrate that exposure to TCDD decreases the expression and activity of aromatase, and is correlated with decreased estradiol concentrations [53–55]. While our data support findings in mammalian systems that suggest TCDD-induced reductions in serum estradiol may result from diminished aromatase expression/activity, impairing estradiol biosynthesis, we cannot rule out *star* and *cyp11a1* as potential targets. Others have demonstrated that expression of *star* and *cyp11a1* is suppressed in the interregal gland following exposure to β NF, lending support for these transcripts as other potential targets for endocrine disruption by AHR-ligands [56].

While not as well characterized in fish, estradiol also plays a role in regulating follicle development and ovulation via ERs in the ovary. Three forms of the ER (*esr1*, *esr2a*, *esr2b*) are expressed in the zebrafish ovary, and all are capable of initiating transcription of genes [57;58]. Here we show that all three forms of the ER are downregulated following chronic exposure to TCDD, as has been demonstrated for mammals [59;60]. By suppressing the expression of ERs in the ovary, follicles may be unable to respond to estrogen signaling and/or induce the transcription of estrogen-responsive genes

important for ovarian development [61–64]. Our array data further support this hypothesis in that more than half of transcripts with putative EREs were downregulated in the ovaries of TCDD-treated fish.

Finally, while follicular development is primarily controlled by gonadotropin hormones, various local factors released from granulosa and theca cells as well as from oocytes, also mediate gonadotropin signaling. Peptide growth factors such as inhibins and follistatins potentiate the action of gonadotropins and maturation-inducing steroid in the induction of final oocyte maturation [44]. Activin β A (Inhbaa) promotes ovary and follicle growth, whereas activin β B (Inhbb) exerts a tonic role throughout follicle development, and becomes critical at the late stage of oocytes maturation and/or ovulation [65]. Epidermal growth factor enhances the rate of oocyte maturation via gonadotropin signaling, inhibits apoptosis, stimulates follicle cell proliferation, and plays a role in controlling follicle survival and steroidogenesis [66;67]. TCDD exposure suppressed the expression of both forms of *inhibin*, as well as *egf* and its receptor, although not significantly at all doses, suggesting that impacts further upstream (e.g., expression of gonadotropin receptors) may have a greater impact on follicular development.

Effects of TCDD on Global Ovarian Gene Expression

While our microarray experimental design does not allow us to make direct conclusions about the mechanisms that underlie TCDD's ovarian toxicity, we are still able to offer valuable insights into additional cellular pathways and signal cascades that are altered by chronic exposure to TCDD. TCDD disrupts several integrated cellular pathways (including structure, glucose and lipid metabolism, immune response, and regulation of transcription) reaffirming the complexity of TCDD toxicity and identifying several new avenues for further study. For example, chronic exposure to 10 ppb TCDD shows a trend for greater alterations in the expression of genes important for transcription/signal transduction (cluster 1) and immune response genes (cluster 3) compared to chronic exposure to 40 and 100 ppb TCDD. Exposure to 10 ppb TCDD for 15 days resulted in reduced estradiol concentrations in zebrafish, but follicular development, overall egg production and spawn success were not altered; follicular

development, egg production and spawn success was reduced following exposure to 40 and 100 ppb TCDD for 15 days [4]. Therefore, the roles that such cellular pathways play in the modulation by TCDD of follicular development and reproductive success by TCDD warrants further study.

Following chronic exposure to TCDD, we show that transcripts such as keratins (*krt 4, 8, and 18*), collagens (*col1a2, col5a2l*), lectins (*lgals3l* and *lgals1l2*), and actins (*acta2*) necessary for maintaining structural integrity were suppressed. We verified the expression profiles for two of these transcripts (*krt 4* and *lgals3l*); expression profiles for similar transcripts (cluster 2) suggest a trend for a dose-dependent suppression of structure-related transcripts. TCDD has also been shown to impact the expression of genes important for maintaining and metabolizing the extracellular matrix in the regenerating fin of zebrafish [68] and in the liver of medaka [69]. Since TCDD exposure is associated with wasting-syndrome, decreased ovarian somatic index, and inhibited regenerative growth of the fin and liver, the impacts of TCDD on the expression of structural proteins warrants further consideration as an integral component of the sublethal toxic response to TCDD.

Many of the ovarian transcripts disrupted by TCDD are important for regulation of the cell cycle and signal transduction. Genes such as *cyp1a1* (cluster 4) show a trend for a dose-dependent increase in their suppression, while others such as the large Maf protein *krm12.2* (cluster 1) are downregulated following chronic exposure to 10 ppb TCDD but not 40 or 100 ppb TCDD. Most of the genes within cluster 4 (15/17) have putative AHREs, and *cyp1a1* is known to be induced by exposure to TCDD in an AHRE-mediated manner; therefore, investigation into whether the expression of such transcripts is induced by TCDD in an AHRE-mediated manner warrants further study. Large Maf proteins such as *krm12.2* are important for regulation of cell differentiation. While the function of large Maf proteins in fish ovarian development is not known, *krm12.2* plays a role in the differentiation of cell lineages in developing embryos [70], and large Maf proteins have been shown to be key regulators of gonad morphogenesis in *Drosophila* [71]. Expression of another gene, *tfa* (cluster 3) is also increased following chronic exposure to 10 ppb TCDD. In mammals, transferrins have an inhibitory effect on FSH-

induced differentiation of granulosa cells [72;73]. Alterations in such transcripts may account for observed alterations in follicular development, and warrant further investigation. Similar impacts on the expression of transcripts important for signal transduction and regulation of cellular differentiation have been noted by others to occur in embryonic heart and regenerating tail of zebrafish [68;74;75] as well as liver, brain, and testis of medaka [76]. While the specific transcriptional profiles within these different tissue types following exposure to TCDD reflect tissue-specific targets of TCDD, overall impacts on the regulation of important signaling molecules and transcription factors likely constitute a common denominator in TCDD's toxicity.

Our work also identifies several novel pathways by which chronic exposure to TCDD may alter ovarian development. For example, both glucose and lipid metabolism may be altered in the ovary as a result of TCDD exposure. Since glucose and lipids play active roles in oogenesis and egg quality in fish [77], perhaps TCDD-induced disruption of these pathways contributes to the observed impacts on ovarian development [4] as well as offspring survival [28]; this hypothesis warrants further consideration. Several genes important for immune response also appear altered by TCDD exposure. Alterations in the expression of transcripts involved in immune function could induce an inflammatory response, negatively impacting steroidogenesis and follicular development [78], or perhaps interfere with normal ovarian development by restricting the removal of apoptotic cells or cellular debris [79]. Such transcriptional changes could also reflect responses from immune cells as the result of tissue repair, as suggested by Volz et al. [69]. Additional studies are necessary to elucidate the impacts of altered immune response on ovarian development in fishes.

Insights into the mechanisms of TCDD-induced ovarian toxicity

In-silico analysis of the regulatory region of dysregulated transcripts have enabled us to further support hypotheses regarding the mechanisms by which chronic exposure to TCDD induces ovarian toxicity and to identify new avenues for continued research into

TCDD's sublethal toxic response in the ovary. The AHR-pathway remains active in zebrafish ovary following chronic exposure to TCDD, evidenced by increased *cyp1a1* expression compared with control. While AHR-mediated changes in gene expression likely contribute to TCDD-induced ovarian toxicity, dysregulated transcripts identified by microarray do not appear to be enriched for AHREs compared with reference genes. While we cannot be sure which of these AHREs are functional, others have reported similar findings in that not all TCDD-induced changes in gene expression could be correlated with the presence of AHREs either by promoter analysis or determination of AHR-dependence [69;80;81]. Collectively, these studies suggest that TCDD-induced histopathologic alterations likely involve changes in the expression of genes downstream from initial AHRE-activated transcription in addition to direct AHRE-mediated changes in gene expression (e.g., by altering the expression of transcription factors and signaling proteins via the AHRE, leading to an alteration in the expression of their target genes in a tissue-specific manner).

Our data also suggest that impacts on the expression of estradiol-regulated genes may also be important for TCDD-induced ovarian toxicity. Several propose that interactions between AHR and ER pathways are inhibitory, and that AHR-ligands could suppress expression of genes via the AHRE [19;82;83]. While dysregulated transcripts identified by microarray are enriched for putative EREs, presence of both AHRE and ERE was not different than for reference genes; therefore no conclusions regarding potential interaction/interference between the two signaling pathways can be drawn from these data. Others suggest that when estrogen is present, AHR ligands can attenuate estrogen signaling at an ERE site, and that while the AHR is involved, the mechanism of action is independent from AHRE-mediated signaling [20;84;85]. Our findings here lend support to this hypothesis. Putative EREs were identified in the promoter regions of *lhr*, *fshr*, and *cyp19a1a*, of which only *cyp19a1a* has been demonstrated to be estrogen responsive in zebrafish [84]. Further, dysregulated transcripts identified by microarray appear to be enriched for EREs compared with reference genes. Collectively these studies suggest that the antiestrogenic actions of TCDD at the ovary entail multiple and perhaps gene/promoter-specific molecular mechanisms involving ER/AHR cross-talk, and warrant further study.

Conclusions

Environmental compounds that disrupt hormone signaling can exert a profound effect on reproduction. Our data suggest that TCDD inhibits expression of key genes that regulate follicular development and estradiol biosynthesis, and provide further evidence for a mechanistic link for impairment of reproduction in fish exposed to TCDD. Suppression of all of the candidate genes in this study following chronic exposure to TCDD is consistent with previously described reductions in serum 17 β estradiol concentrations and attenuated follicular development [4], and suggests that TCDD inhibits the transition of pre-vitellogenic follicles to vitellogenic follicles via attenuated gonadotropin responsiveness and/or reduced estradiol biosynthesis. Overall lack of a dose response suggests that the ovary is highly sensitive to TCDD, and that accumulations of less than 1 ng TCDD/g female are sufficient to reduce reproductive capacity of female zebrafish. Furthermore, TCDD appears to impact several integrated cellular pathways, illustrating the complex and profound effects it has on the reproductive system. Our data also suggest that ovarian toxicities following chronic exposure to TCDD result from downstream effects of AHR-mediated signal transduction pathways, or from feedback reactions to cellular changes induced by TCDD. Further examination of the relationships among altered structural integrity, glucose and lipid metabolism, immune response, and regulation of transcription in response to ovarian toxicity will better clarify the mechanisms by which TCDD exerts its reproductive toxicity, particularly its low-dose, long-term effects.

Acknowledgments: We gratefully acknowledge Lisa Meyer for her technical assistance. Research was supported in part by: USEPA (TKH, GRO MA916290), UWM Institute of Environmental Health (TKH/RJH), Greater Milwaukee Foundation Shaw Scientist Award (MJC), National Institute of Biomedical Imaging and Bioengineering (MJH, R01EB001421), and the UWM Marine and Freshwater Biomedical Center (P30ES004184).

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Supplementary Table 1. Summary of cluster analysis and transcription factor analysis (unique transcripts)

Cluster	Affy ID	Symbol	Description	10ppb	40ppb	100ppb	AHRE	ERE
1	Dr.8215.1.A1_at	sox21a	SRY-box containing gene 21a	-2.33	-1.32	-1.00	Y	Y
1	Dr.7110.1.S1_at	zgc:77614	zgc:77059	-3.04	-2.42	-7.29	Y	Y
1	Dr.6147.1.A1_at	zgc:77150	zgc:76913	-2.95	-1.70	-4.17	Y	Y
1	Dr.2978.1.S1_at	vg3	vitellogenin 3, phosvitinless	-6.65	-1.67	-1.79	Y	Y
1	Dr.25593.2.A1_at	wu:fa56g11	wu:fa56g11	-3.90	-1.03	-1.20	Y	Y
1	Dr.25285.1.S1_at	zgc:73223	zgc:73223	-2.47	-1.15	-1.11	Y	Y
1	Dr.25009.4.A1_at	wu:fb59c05	wu:fb59c05	-7.93	-1.73	-2.05	Y	Y
			Kreisler (mouse) maf-related leucine zipper					
1	Dr.23470.1.S1_s_at	krml2.2	homolog 2.2	-3.67	-1.02	-2.68	Y	Y
1	Dr.18893.1.S1_at	im:7138745	im:7138745	-2.73	-1.06	1.01	Y	Y
1	Dr.16681.1.A1_at		NA	-2.17	1.07	1.47	Y	Y
1	Dr.11971.1.A1_at	zgc:92317	zgc:91877	-2.34	-1.06	-1.46	Y	Y
1	Dr.921.1.A1_at	timeless	timeless homolog (Drosophila)	-2.92	1.88	1.07	Y	
1	Dr.8090.1.A1_at	ndrg1l	N-myc downstream regulated gene 1, like procollagen-lysine 1, 2-oxoglutarate 5-	-3.58	1.33	-1.93	Y	
			dioxygenase 1					
1	Dr.7688.1.A1_at	plod1		-2.24	1.00	-1.43	Y	
1	Dr.25774.1.S1_at		NA	-3.06	-1.59	-1.94	Y	
1	Dr.25498.1.S1_at	bzw1	basic leucine zipper and W2 domains 1	-2.15	1.43	1.18	Y	
1	Dr.25009.6.A1_a_at	vg1	vitellogenin 1	-7.38	-1.62	-1.83	Y	
1	Dr.24920.1.S1_at		NA	-2.56	-1.13	-1.36	Y	
1	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog,	-3.84	1.86	-1.83	Y	
1	Dr.20140.1.A1_at	E2F4	NA	-2.60	-1.64	-1.50	Y	
1	Dr.1991.1.A1_s_at	zgc:66417	zgc:66417	-7.09	-1.19	-5.92	Y	
1	Dr.195.1.S2_at	ck2a1	casein kinase 2 alpha 1	-3.29	-1.04	-1.86	Y	
1	Dr.18466.1.A1_at		NA	-2.23	1.03	-1.56	Y	
1	Dr.17776.1.A1_at	tph1l	tryptophan hydroxylase 1, like	-2.64	-1.53	1.19	Y	
1	Dr.17113.1.A1_a_at	ptena	phosphatase and tensin homolog A	-2.32	1.51	1.38	Y	
1	Dr.13994.2.A1_a_at	zgc:101086	zgc:101086	-2.37	-1.20	-1.67	Y	
1	Dr.13775.1.S1_at		NA	-3.60	-1.20	-1.50	Y	
1	Dr.12714.1.A1_at		NA	-5.65	-1.56	-1.01	Y	
1	Dr.10170.1.A1_at		NA	-2.38	-1.23	-1.64	Y	
1	Dr.4412.13.A1_x_at	wu:fa56g11	wu:fa56g11	-2.92	1.16	-1.13		Y
1	Dr.16504.1.A1_at		NA	-2.60	-1.33	-1.90		Y
1	Dr.16380.1.A1_at	zgc:92068	zgc:86738	-2.45	-1.26	-1.18		Y
1	Dr.4412.12.A1_at	wu:fa56g11	wu:fa56g11	-3.55	-1.05	-1.32		
1	Dr.25593.1.S1_at	wu:fa56g11	wu:fa56g11	-2.80	1.30	1.06		
1	Dr.13096.2.S1_at	zgc:86738	zgc:77882	-3.95	1.18	-1.89		
2	Dr.9682.1.A1_at		NA	-4.11	-4.33	-3.91	Y	Y

Supplementary Table 1 (cont.). Summary of cluster analysis and transcription factor analysis (unique transcripts)

Cluster	Affy ID	Symbol	Description	10ppb	40ppb	100ppb	AHRE	ERE
2	Dr.956.1.S1_at	wu:fa92g05	wu:fa92g05	-1.17	-1.36	-2.22	Y	Y
2	Dr.913.1.S1_at	zgc:63909	zgc:63909	-2.60	-1.62	-2.69	Y	Y
2	Dr.8723.1.S1_at	zgc:92903	zgc:92068	-1.21	-1.61	-3.77	Y	Y
2	Dr.7626.1.A1_at	zgc:73257	zgc:73257	-2.25	-1.15	-2.18	Y	Y
2	Dr.7236.1.A1_at	wu:fc31g04	wu:fc31g04	-2.90	-1.25	-2.87	Y	Y
2	Dr.5853.1.A1_at	zgc:77059	zgc:76953	-2.38	-1.03	-1.02	Y	Y
2	Dr.4387.1.S1_at	krt4	keratin 4	-1.96	-2.93	-5.65	Y	Y
2	Dr.4249.1.S1_at	lipf	lipase, gastric	-2.06	-1.85	-2.30	Y	Y
2	Dr.4212.1.S1_at	ldha	lactate dehydrogenase A4	-1.78	-1.45	-2.59	Y	Y
2	Dr.25155.1.S1_s_at	ba1	ba1 globin	-1.11	1.22	-2.50	Y	Y
2	Dr.24233.1.S1_at	fn1b	fibronectin 1b	-1.03	-1.57	-2.69	Y	Y
2	Dr.24122.1.A1_at	zgc:77882	zgc:77614	-2.49	-2.05	-2.06	Y	Y
2	Dr.20722.1.S1_at	zgc:56454	zgc:56454	-2.14	-1.43	-2.95	Y	Y
2	Dr.16206.1.A1_s_at	wu:fo83d04	NA	1.26	1.65	1.23	Y	Y
2	Dr.1619.1.A1_at	wu:fb83a09	wu:fb83a09	-3.44	-1.98	-2.03	Y	Y
2	Dr.15054.1.S1_at	rbp2a	retinol binding protein 2a, cellular	-2.98	-2.39	-4.54	Y	Y
2	Dr.13689.1.S1_at	zgc:66449	zgc:66449	-2.65	-1.76	-1.90	Y	Y
2	Dr.1260.1.S1_at	anxa2a	annexin A2a	-2.42	-2.92	-4.84	Y	Y
2	Dr.12575.1.S1_at	dcp1a	decapping enzyme	-1.12	-1.10	-2.16	Y	Y
2	Dr.10326.1.S1_at	junb	jun B proto-oncogene	-2.21	-1.88	-4.39	Y	Y
2	Dr.890.1.S1_at	zgc:77517	zgc:77150	-2.69	-1.18	-1.53	Y	
2	Dr.8045.1.S1_at	prtfdc1	phosphoribosyl transferase domain containing	-1.44	-1.12	-3.05	Y	
2	Dr.59.1.S1_at	anxa1a	annexin A1a	-2.20	-3.36	-7.06	Y	
2	Dr.3628.1.S1_at	rap1b	RAS related protein 1b	-1.79	-1.41	-2.40	Y	
2	Dr.3512.1.A1_at		NA	-1.86	-1.34	-2.26	Y	
2	Dr.3459.1.S1_at	cd163	Cd63 antigen	-2.04	-1.47	-3.70	Y	
2	Dr.3180.1.A1_at	zgc:76913	zgc:76908	-1.84	-2.40	-2.50	Y	
2	Dr.2363.1.S1_at	tagln2	transgelin 2	-2.93	-2.27	-2.21	Y	
2	Dr.20815.3.A1_at	lgals3l	lectin, galactoside-binding, soluble, 3 (galectin 3)-like	-1.89	-2.68	-2.56	Y	
2	Dr.20277.1.A1_at	acta2	actin, alpha 2, smooth muscle, aorta	-1.83	-1.27	-2.65	Y	
2	Dr.18135.1.A1_at	wu:fl63a03	wu:fl63a03	-1.07	1.07	-4.01	Y	
2	Dr.17850.1.S1_at	zgc:56592	zgc:56592	-2.61	-2.05	-3.41	Y	
2	Dr.15930.1.A1_at		NA	-1.51	-1.03	-2.18	Y	
2	Dr.15856.1.A1_at		NA	-2.66	-1.10	-2.12	Y	
2	Dr.14748.1.S1_at	zgc:63985	zgc:63985	-1.54	-1.52	-2.65	Y	
2	Dr.14041.1.S1_at	zgc:103597	zgc:103597	-2.65	-1.91	-1.97	Y	
2	Dr.1377.1.A1_at	col1a2	collagen, type I, alpha 2	-2.47	-1.44	-2.56	Y	

Supplementary Table 1 (cont.). Summary of cluster analysis and transcription factor analysis (unique transcripts)

Cluster	Affy ID	Symbol	Description	10ppb	40ppb	100ppb	AHRE	ERE
2	Dr.1372.1.S1_at	krt18	keratin 18	-1.43	-1.76	-3.09	Y	
2	Dr.1361.1.S1_at	wu:fa98f12	wu:fa98f12	-1.91	-2.41	-4.90	Y	
2	Dr.1282.1.S1_at	krt8	keratin 8	-1.45	-1.89	-3.02	Y	
2	Dr.1246.1.S1_at	apoeb	apolipoprotein Eb	-1.83	-1.09	-4.12	Y	
2	Dr.12106.1.S1_at	lztfl1	leucine zipper transcription factor-like 1	-1.12	-1.12	-2.33	Y	
2	Dr.1201.1.S1_at	zgc:56142	zgc:56142	-2.46	-1.92	-3.71	Y	
2	Dr.11609.1.S1_at	LOC402847		-1.62	-1.54	-2.86	Y	
2	Dr.11348.1.S1_at	zgc:86724	zgc:77517	-3.04	-2.42	-7.29	Y	
2	Dr.10879.1.A1_at	wu:fe14f11	wu:fe14f11	-1.82	-1.12	-2.38	Y	
2	Dr.10314.1.S1_a_at	mmp13	matrix metalloproteinase 13	1.20	1.60	-2.51	Y	
2	AFFX-Dr-GAPDH-3_at						Y	
2	Dr.4048.1.S1_at		NA	-2.15	-1.26	-3.36		Y
2	Dr.2973.1.A1_at		NA	-1.49	-2.39	-1.77		Y
2	Dr.24341.1.S1_at	zgc:76953	zgc:76908	-1.54	-1.10	-2.39		Y
2	Dr.1411.1.S1_at	hbaa1	hemoglobin alpha adult-1	-1.10	1.27	-2.64		Y
			Kreisler (mouse) maf-related leucine zipper					
2	Dr.8198.1.A1_at	krml2	homolog 2	-2.59	-1.19	-2.41		
2	Dr.5809.1.A1_at	wu:fb11g12	wu:fb11g12	-2.30	-1.57	-7.28		
2	Dr.5513.1.S1_at	slc3a2	solute carrier family 3, member 2	-2.35	-1.68	-3.05		
2	Dr.23469.1.S1_s_at	wu:fj17g12	wu:fj17g12	-2.30	-2.50	-2.56		
2	Dr.18880.1.A1_at		NA	-2.05	-1.26	-2.13		
2	Dr.16206.1.A1_at	wu:fo83d04	wu:fo83d04	-1.22	-1.06	-6.09		
2	Dr.13510.1.S1_at	actr10	actin-related protein 10 homolog (S. cerevisiae)	-1.80	-1.23	-2.29		
2	Dr.12498.1.S1_at	rad1	RAD1 homolog (S. pombe)	-1.10	1.13	-2.16		
2	Dr.1194.1.S1_at	zgc:76908	zgc:76908	-2.34	-1.85	-3.53		
3	Dr.8390.1.S1_at	zgc:55420	zgc:55420	3.84	-1.12	1.13	Y	Y
3	Dr.728.4.S1_at	fgb	fibrinogen, B beta polypeptide	5.66	1.43	1.61	Y	Y
3	Dr.6550.1.A1_at	LOC407646		3.05	1.42	-1.09	Y	Y
3	Dr.4797.1.S1_at		NA	8.50	-1.19	1.20	Y	Y
3	Dr.3581.1.S1_at	ctrb1	chymotrypsinogen B1	2.58	1.84	-2.41	Y	Y
3	Dr.3025.3.S1_at	wu:fa04f09	wu:fa04f09	17.52	1.37	2.04	Y	Y
3	Dr.25379.1.S1_at	sb:cb37	sb:cb37	5.19	1.73	1.80	Y	Y
3	Dr.2426.1.S1_at	zgc:66321	zgc:66321	5.00	-1.34	-1.29	Y	Y
			serine (or cysteine) proteinase inhibitor, clade A					
3	Dr.1605.1.S1_at	serpina1	(alpha-1 antiproteinase, antitrypsin), member 1	29.44	1.51	3.07	Y	Y
3	Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1	5.58	-1.38	-1.47	Y	
3	Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide	12.80	-1.82	-1.35	Y	
3	Dr.4907.1.S1_at	fgg	fibrinogen, gamma polypeptide	12.96	-1.66	-1.12	Y	

Supplementary Table 1 (cont.). Summary of cluster analysis and transcription factor analysis (unique transcripts)

Cluster	Affy ID	Symbol	Description	10ppb	40ppb	100ppb	AHRE	ERE
3	Dr.3613.1.S1_at	cp	ceruloplasmin	24.49	1.06	2.16	Y	
3	Dr.20270.1.S1_at	wu:fi20c07	wu:fi20c07	12.95	-1.13	1.33	Y	
3	Dr.1889.2.A1_a_at	tfa	transferrin-a	11.64	-2.09	-1.32	Y	
3	Dr.5562.1.S1_at	si:ch211-219i10.1	si:ch211-219i10.1	16.55	1.24	1.12		
3	Dr.1889.1.S1_at	tfa	transferrin-a	9.49	-2.25	-1.42		
4	Dr.7806.1.A1_at		NA	-2.44	1.04	2.65	Y	Y
4	Dr.26469.1.S1_at	sp4	sp4 transcription factor	1.51	2.32	1.96	Y	Y
4	Dr.16524.1.S1_at	wu:fc12b04	wu:fc12b04	1.85	2.39	2.05	Y	Y
4	Dr.13972.1.S1_at	zgc:64114	zgc:64114	1.19	2.45	4.16	Y	Y
4	Dr.13182.1.A1_at	rab5b	RAB5B, member RAS oncogene family	2.45	1.34	2.13	Y	Y
4	Dr.12833.1.A1_at	zgc:64213	zgc:64213	-1.62	1.18	3.28	Y	Y
4	Dr.1192.1.S1_at	wu:fb11h03	wu:fb11h03	-1.60	-1.17	3.48	Y	Y
4	Dr.9478.1.S1_at	cyp1a	cytochrome P450, family 1, subfamily A	6.93	14.87	24.68	Y	
4	Dr.9450.1.A1_at	zgc:63724	zgc:63724	-1.46	1.74	3.59	Y	
4	Dr.19990.1.S1_at	zgc:66101	zgc:66101	1.57	1.55	2.43	Y	
4	Dr.19877.1.S1_at	zgc:66133	zgc:66133	1.72	2.17	3.31	Y	
4	Dr.17662.1.S1_at		NA	1.88	3.38	1.62	Y	
4	Dr.15418.1.S1_at	wu:fc23f06	wu:fc23f06	1.26	1.27	3.01	Y	
4	AFFX-Dr-acta1-5_x_at						Y	
4	Dr.24858.1.S1_at	zgc:110540	zgc:110540	1.37	2.56	1.97		
4	Dr.15555.1.S1_at		NA	1.48	2.58	2.72		
4	Dr.1192.1.S1_a_at	wu:fb11h03	wu:fb11h03	-2.96	-1.56	2.95		
5	Dr.26139.1.A1_x_at	NA	NA	1.36	2.17	-1.07	Y	Y
5	Dr.25378.1.A1_at	zgc:110540	zgc:110540	1.64	2.32	1.48	Y	Y
5	Dr.24249.1.S1_at	zc3hdc5	zinc finger CCCH type domain containing 5	1.60	1.54	1.02	Y	Y
5	Dr.5002.1.A1_at	NA	NA	1.74	2.33	1.78	Y	
5	Dr.25086.1.A1_at	NA	NA	1.43	1.30	1.03	Y	
5	Dr.1368.7.S1_at	zgc:86724	zgc:86724	1.26	1.38	1.30	Y	

Supplementary Table 2. Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000000935	ENSDART0000001053	Dr.24249.1.S1_at	zc3hd5	zinc finger CCCH type domain containing 5 [Source:RefSeq_peptide;Acc:NP_956530]	-4874	-4869	-1	agcgtg
ENSDARG00000000935	ENSDART0000001053	Dr.24249.1.S1_at	zc3hd5	zinc finger CCCH type domain containing 5 [Source:RefSeq_peptide;Acc:NP_956530]	-2211	-2206	-1	tcgctg
ENSDARG00000000935	ENSDART0000001053	Dr.24249.1.S1_at	zc3hd5	zinc finger CCCH type domain containing 5 [Source:RefSeq_peptide;Acc:NP_956530]	210	215	-1	tcgctg
ENSDARG00000000935	ENSDART0000001053	Dr.24249.1.S1_at	zc3hd5	zinc finger CCCH type domain containing 5 [Source:RefSeq_peptide;Acc:NP_956530]	748	753	-1	agcgtg
ENSDARG00000001953	ENSDART00000003247	Dr.7626.1.A1_at,Dr.7626.2.S1_at	NP_998562.1	zgc:73257 [Source:RefSeq_peptide;Acc:NP_998562]	-1683	-1678	-1	tcgctg
ENSDARG00000001953	ENSDART00000003247	Dr.7626.1.A1_at,Dr.7626.2.S1_at	NP_998562.1	zgc:73257 [Source:RefSeq_peptide;Acc:NP_998562]	-1087	-1082	-1	ggcgtg
ENSDARG00000001953	ENSDART00000003247	Dr.7626.1.A1_at,Dr.7626.2.S1_at	NP_998562.1	zgc:73257 [Source:RefSeq_peptide;Acc:NP_998562]	-862	-857	-1	agcgtg
ENSDARG00000001953	ENSDART00000003247	Dr.7626.1.A1_at,Dr.7626.2.S1_at	NP_998562.1	zgc:73257 [Source:RefSeq_peptide;Acc:NP_998562]	-347	-342	1	tcgctg
ENSDARG00000002082	ENSDART00000005010	Dr.195.1.S1_at,Dr.195.1.S2_at,Dr.195.1.S1_at	ck2a1	casein kinase 2 alpha 1 [Source:RefSeq_peptide;Acc:NP_571327]	-983	-978	1	agcgtg
ENSDARG00000002082	ENSDART00000005010	Dr.195.1.S1_at,Dr.195.1.S2_at,Dr.195.1.S1_at	ck2a1	casein kinase 2 alpha 1 [Source:RefSeq_peptide;Acc:NP_571327]	-941	-936	1	cgcgtg
ENSDARG00000002082	ENSDART00000005010	Dr.195.1.S1_at,Dr.195.1.S2_at,Dr.195.1.S1_at	ck2a1	casein kinase 2 alpha 1 [Source:RefSeq_peptide;Acc:NP_571327]	-846	-841	-1	tcgctg
ENSDARG00000002082	ENSDART00000005010	Dr.195.1.S1_at,Dr.195.1.S2_at,Dr.195.1.S1_at	ck2a1	casein kinase 2 alpha 1 [Source:RefSeq_peptide;Acc:NP_571327]	-726	-721	1	ggcgtg
ENSDARG00000002082	ENSDART00000005010	Dr.195.1.S1_at,Dr.195.1.S2_at,Dr.195.1.S1_at	ck2a1	casein kinase 2 alpha 1 [Source:RefSeq_peptide;Acc:NP_571327]	-553	-548	1	ggcgtg
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-248	-243	1	ggcgtg
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-215	-210	1	agcgtg
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-248	-243	1	ggcgtg
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-215	-210	1	agcgtg
ENSDARG00000003216	ENSDART00000011967	Dr.1260.1.S1_at	annexin A2a (anxa2a), mRNA [Source:RefSeq_dna;Acc:NM_181761]	-3672	-3667	-1	agcgtg	
ENSDARG00000003323	ENSDART00000017567	Dr.12575.1.S1_at	dcp1a	decapping enzyme [Source:RefSeq_peptide;Acc:NP_878313]	-2628	-2623	-1	tcgctg
ENSDARG00000003323	ENSDART00000017567	Dr.12575.1.S1_at	dcp1a	decapping enzyme [Source:RefSeq_peptide;Acc:NP_878313]	-2299	-2294	-1	ggcgtg
ENSDARG00000003323	ENSDART00000017567	Dr.12575.1.S1_at	dcp1a	decapping enzyme [Source:RefSeq_peptide;Acc:NP_878313]	-170	-165	1	agcgtg
ENSDARG00000004060	ENSDART00000026017	Dr.3180.1.A1_at	zgc:76913	Unknown (protein for MGC:76913) [Source:RefSeq_peptide;Acc:NP_997844]	-1103	-1098	-1	tcgctg
ENSDARG00000004296	ENSDART00000027026	Dr.2426.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	-3749	-3744	1	tcgctg
ENSDARG00000004296	ENSDART00000027026	Dr.2426.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	-3743	-3738	1	tcgctg
ENSDARG00000004296	ENSDART00000027026	Dr.2426.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	-3737	-3732	1	tcgctg
ENSDARG00000004296	ENSDART00000027026	Dr.2426.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	-3725	-3720	1	tcgctg
ENSDARG00000004296	ENSDART00000027026	Dr.2426.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	30	35	1	tcgctg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-3691	-3686	1	tcgctg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-3596	-3591	1	agcgtg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-855	-850	-1	tcgctg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-844	-839	1	ggcgtg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-820	-815	-1	agcgtg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-791	-786	1	ggcgtg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-532	-527	-1	ggcgtg
ENSDARG00000005186	ENSDART00000002285	Dr.26469.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-383	-378	-1	agcgtg
ENSDARG00000006074	ENSDART00000002186	Dr.15856.1.A1_at,Dr.13404.1.A1_at	NP_956234.1	uridine monophosphate kinase [Source:RefSeq_peptide;Acc:NP_956234]	-3203	-3198	1	tcgctg
ENSDARG00000006526	ENSDART00000017312	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-2209	-2204	1	ggcgtg
ENSDARG00000006526	ENSDART00000017312	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-2163	-2158	-1	ggcgtg
ENSDARG00000006526	ENSDART00000017312	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1504	-1499	-1	tcgctg
ENSDARG00000006526	ENSDART00000017312	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-4430	-4425	1	ggcgtg
ENSDARG00000006526	ENSDART00000017312	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-4387	-4382	-1	agcgtg
ENSDARG00000006526	ENSDART00000023692	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-2223	-2218	1	agcgtg
ENSDARG00000006526	ENSDART00000023692	Dr.24233.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1263	-1258	1	tcgctg
ENSDARG00000007219	ENSDART00000005791	Dr.25774.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-2349	-2344	-1	agcgtg
ENSDARG00000007219	ENSDART00000005791	Dr.25774.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1147	-1142	-1	agcgtg
ENSDARG00000007219	ENSDART00000005791	Dr.25774.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-817	-812	-1	agcgtg
ENSDARG00000007481	ENSDART00000058261	Dr.5002.1.A1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-12	-7	1	cgcgtg
ENSDARG00000008867	ENSDART00000042250	Dr.3628.1.S1_at	rap1b	RAS related protein 1b [Source:RefSeq_peptide;Acc:NP_955827]	-3595	-3590	-1	cgcgtg
ENSDARG00000008867	ENSDART00000042250	Dr.3628.1.S1_at	rap1b	RAS related protein 1b [Source:RefSeq_peptide;Acc:NP_955827]	-1533	-1528	-1	tcgctg
ENSDARG00000008867	ENSDART00000042250	Dr.3628.1.S1_at	rap1b	RAS related protein 1b [Source:RefSeq_peptide;Acc:NP_955827]	-234	-229	-1	agcgtg
ENSDARG00000008895	ENSDART00000055048	Dr.1619.1.A1_at,Dr.1619.1.A1_at,Dr.1619.1.A1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-1617	-1612	1	cgcgtg
ENSDARG00000008969	ENSDART00000011701	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-3590	-3585	1	agcgtg
ENSDARG00000008969	ENSDART00000011701	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-3263	-3258	1	ggcgtg
ENSDARG00000008969	ENSDART00000011701	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-2312	-2307	-1	tcgctg
ENSDARG00000008969	ENSDART00000011701	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-2219	-2214	-1	cgcgtg
ENSDARG00000008969	ENSDART00000041987	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-311	-306	-1	tcgctg
ENSDARG00000008969	ENSDART00000041987	Dr.5462.1.S1_at,Dr.5462.1.S1_at	fgb	fibrinogen, B beta polypeptide [Source:RefSeq_peptide;Acc:NP_997939]	-178	-173	1	tcgctg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1352	-1347	-1	cgcgtg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1350	-1345	1	cgcgtg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1280	-1275	1	agcgtg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1352	-1347	-1	cgcgtg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1350	-1345	1	cgcgtg
ENSDARG00000009483	ENSDART00000009889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-1280	-1275	1	agcgtg
ENSDARG00000010312	ENSDART00000010537	Dr.3613.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-3990	-3985	-1	tcgctg
ENSDARG00000010312	ENSDART00000010537	Dr.3613.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1870	-1865	-1	ggcgtg
ENSDARG00000010312	ENSDART00000010537	Dr.3613.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1737	-1732	1	ggcgtg
ENSDARG00000010312	ENSDART00000010537	Dr.3613.1.S1_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-125	-120	1	tcgctg
ENSDARG00000010420	ENSDART00000049420	Dr.8090.1.A1_at	ndrg1l	N-myc downstream regulated gene 1, like [Source:RefSeq_peptide;Acc:NP_956986]	-3038	-3033	1	agcgtg
ENSDARG00000010420	ENSDART00000049420	Dr.8090.1.A1_at	ndrg1l	N-myc downstream regulated gene 1, like [Source:RefSeq_peptide;Acc:NP_956986]	-2860	-2855	-1	agcgtg
ENSDARG00000010481	ENSDART00000013575	Dr.25498.1.S1_at	NP_956002.1	basic leucine zipper and W2 domains 1 [Source:RefSeq_peptide;Acc:NP_956002]	-2137	-2132	-1	ggcgtg
ENSDARG00000010481	ENSDART00000013575	Dr.25498.1.S1_at	NP_956002.1	basic leucine zipper and W2 domains 1 [Source:RefSeq_peptide;Acc:NP_956002]	-1647	-1642	1	tcgctg
ENSDARG00000011312	ENSDART00000008698	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-3610	-3605	-1	agcgtg
ENSDARG00000011312	ENSDART00000008698	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-3392	-3387	-1	agcgtg
ENSDARG00000011312	ENSDART00000008698	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-3025	-3020	-1	agcgtg
ENSDARG00000011312	ENSDART00000008698	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-2651	-2646	-1	agcgtg
ENSDARG00000011312	ENSDART00000008698	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1477	-1472	-1	agcgtg
ENSDARG00000011683	ENSDART00000013454	Dr.8045.1.S1_at	NP_955812.2	HHPG protein [Source:RefSeq_peptide;Acc:NP_955812]	-1022	-97	-1	ggcgtg
ENSDARG00000012395	ENSDART00000005436	Dr.10314.1.S1_a_at	mmp13	matrix metalloproteinase 13 [Source:RefSeq_peptide;Acc:NP_958911]	-2663	-2658	-1	tcgctg
ENSDARG00000012395	ENSDART00000005436	Dr.10314.1.S1_a_at	mmp13	matrix metalloproteinase 13 [Source:RefSeq_peptide;Acc:NP_958911]	-2528	-2523	1	ggcgtg
ENSDARG00000012395	ENSDART00000005436	Dr.10314.1.S1_a_at	mmp13	matrix metalloproteinase 13 [Source:RefSeq_peptide;Acc:NP_958911]	-2276	-2271	-1	cgcgtg
ENSDARG00000012395	ENSDART00000005436	Dr.10314.1.S1_a_at	mmp13	matrix metalloproteinase 13 [Source:RefSeq_peptide;Acc:NP_958911]	-2020	-20		

Supplementary Table 2 (cont.). Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000013481	ENSDART00000007454	Dr.17662.1.S1_at	bty	bloodthirsty (bty), mRNA [Source:RefSeq_dna;Acc:NM_001020475]	-1542	-1537	-1	tcgctg
ENSDARG00000013613	ENSDART00000018408	Dr.16504.1.A1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-1875	-1870	-1	cgctgt
ENSDARG00000013613	ENSDART00000018408	Dr.16504.1.A1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-1475	-1470	-1	tcgctg
ENSDARG00000013613	ENSDART00000018408	Dr.16504.1.A1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-1422	-1417	-1	agcgtg
ENSDARG00000013646	ENSDART00000019664	Dr.1605.1.S1_at	serpina1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:RefSeq_peptide;Acc:NP_001013277]	-4808	-4803	-1	agcgtg
ENSDARG00000014209	ENSDART00000023208	Dr.15930.1.A1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-3248	-3243	-1	agcgtg
ENSDARG00000014209	ENSDART00000023208	Dr.15930.1.A1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-2763	-2758	-1	agcgtg
ENSDARG00000014209	ENSDART00000023208	Dr.15930.1.A1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-4258	-4253	-1	ggcgtg
ENSDARG00000014429	ENSDART00000017280	Dr.4907.1.S1_at	fgg	fibrinogen gamma polypeptide [Source:RefSeq_peptide;Acc:NP_998219]	-4836	-4831	1	cgctgt
ENSDARG00000014629	ENSDART00000020883	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4912	-4907	-1	tcgctg
ENSDARG00000014629	ENSDART00000020883	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4071	-4066	-1	agcgtg
ENSDARG00000014629	ENSDART00000049779	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4912	-4907	-1	tcgctg
ENSDARG00000014629	ENSDART00000049779	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4071	-4066	-1	agcgtg
ENSDARG00000014629	ENSDART00000066174	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4912	-4907	-1	tcgctg
ENSDARG00000014629	ENSDART00000066174	Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at,Dr.921.1.A1_at,DrAffx.2.64.S1_at			-4071	-4066	-1	agcgtg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-3978	-3973	-1	tcgctg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-3265	-3260	-1	tcgctg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-2732	-2727	-1	tcgctg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1510	-1505	1	cgctgt
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1468	-1463	-1	cgctgt
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1419	-1414	-1	cgctgt
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1375	-1370	1	tcgctg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1229	-1224	1	cgctgt
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-1076	-1071	-1	cgctgt
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-229	-224	-1	agcgtg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-220	-215	-1	agcgtg
ENSDARG00000014947	ENSDART00000026576	Dr.8587.1.A1_at,Dr.8587.1.A2_at	igfbp1	insulin-like growth factor binding protein 1 [Source:RefSeq_peptide;Acc:NP_775390]	-72	-67	-1	agcgtg
ENSDARG00000015866	ENSDART00000019110	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-3239	-3234	-1	tcgctg
ENSDARG00000015866	ENSDART00000019110	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-401	-396	1	cgctgt
ENSDARG00000015866	ENSDART00000058963	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-3537	-3532	-1	tcgctg
ENSDARG00000015866	ENSDART00000058963	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-699	-694	1	cgctgt
ENSDARG00000015866	ENSDART00000058964	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-3239	-3234	-1	tcgctg
ENSDARG00000015866	ENSDART00000058964	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at			-401	-396	1	cgctgt
ENSDARG00000016059	ENSDART00000021065	Dr.13182.1.A1_at	rab5b	RAB5B, member RAS oncogene family [Source:RefSeq_peptide;Acc:NP_998050]	-3042	-3037	-1	tcgctg
ENSDARG00000016059	ENSDART00000021065	Dr.13182.1.A1_at	rab5b	RAB5B, member RAS oncogene family [Source:RefSeq_peptide;Acc:NP_998050]	-2041	-2036	1	agcgtg
ENSDARG00000016059	ENSDART00000021065	Dr.13182.1.A1_at	rab5b	RAB5B, member RAS oncogene family [Source:RefSeq_peptide;Acc:NP_998050]	-672	-667	1	agcgtg
ENSDARG00000016059	ENSDART00000021065	Dr.13182.1.A1_at	rab5b	RAB5B, member RAS oncogene family [Source:RefSeq_peptide;Acc:NP_998050]	-4468	-4463	1	agcgtg
ENSDARG00000016448	ENSDART00000014979	Dr.2978.1.S1_at	vg3	Vitellogenin 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9DFT9]	-1530	-1525	-1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-3533	-3528	1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-3351	-3346	1	agcgtg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-2761	-2756	-1	cgctgt
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-2765	-2750	-1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-4965	-4960	-1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-3533	-3528	1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-3351	-3346	1	agcgtg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-2761	-2756	-1	cgctgt
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-2765	-2750	-1	tcgctg
ENSDARG00000016771	ENSDART00000003845	Dr.1889.2.A1_a_at,Dr.1889.1.S1_at	tfa	transferrin-a [Source:RefSeq_peptide;Acc:NP_001015057]	-4965	-4960	-1	tcgctg
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3552	-3547	1	cgctgt
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-2451	-2446	-1	tcgctg
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-1138	-1133	-1	tcgctg
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3552	-3547	1	cgctgt
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-2451	-2446	-1	tcgctg
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-1138	-1133	-1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3793	-3788	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3785	-3780	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3587	-3582	-1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3364	-3359	1	ggcgtg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2980	-2975	1	agcgtg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2502	-2497	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1174	-1169	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2596	-2591	1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4243	-4238	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4239	-4234	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4053	-4048	-1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3793	-3788	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3785	-3780	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3587	-3582	-1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-3364	-3359	1	ggcgtg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2980	-2975	1	agcgtg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2502	-2497	1	tcgctg
ENSDARG00000017619	ENSDART00000026842	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1174	-1169	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-2596	-2591	1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4243	-4238	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4239	-4234	-1	tcgctg
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-4053	-4048	-1	tcgctg
ENSDARG00000017624	ENSDART00000012644	Dr.4387.1.S1_at	krt4	keratin 4 [Source:RefSeq_peptide;Acc:NP_571584]	-1874	-1869	1	tcgctg
ENSDARG00000017624	ENSDART00000012644	Dr.4387.1.S1_at	krt4	keratin 4 [Source:RefSeq_peptide;Acc:NP_571584]	-1435	-1430	-1	tcgctg
ENSDARG00000017624	ENSDART00000012644	Dr.4387.1.S1_at	krt4	keratin 4 [Source:RefSeq_peptide;Acc:NP_571584]	-9	-4	-1	tcgctg
ENSDARG00000018404	ENSDART00000020750	Dr.1372.1.S1_at	krt18	keratin 18 [Source:RefSeq_peptide;Acc:NP_848524]	-2408	-2403	1	ggcgtg
ENSDARG00000018404	ENSDART00000020750	Dr.1372.1.S1_at	krt18	keratin 18 [Source:RefSeq_peptide;Acc:NP_848524]	-4641	-4636	-1	cgctgt

Supplementary Table 2 (cont.). Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence	
ENSDARG00000018529	ENSDART00000020541	Dr.4249.1.S1_at	lipf	lipase, gastric [Source:RefSeq_peptide;Acc:NP_998569]		0	5	-1	agcgtg
ENSDARG00000018921	ENSDART00000023006	Dr.9450.1.A1_at	NP_956912.1	hypothetical protein LOC393590 [Source:RefSeq_peptide;Acc:NP_956912]	-1589	-1584	1	tcgctg	
ENSDARG00000018921	ENSDART00000023006	Dr.9450.1.A1_at	NP_956912.1	hypothetical protein LOC393590 [Source:RefSeq_peptide;Acc:NP_956912]	-1563	-1558	1	tcgctg	
ENSDARG00000018921	ENSDART00000023006	Dr.9450.1.A1_at	NP_956912.1	hypothetical protein LOC393590 [Source:RefSeq_peptide;Acc:NP_956912]	-1559	-1554	1	tcgctg	
ENSDARG00000018921	ENSDART00000023006	Dr.9450.1.A1_at	NP_956912.1	hypothetical protein LOC393590 [Source:RefSeq_peptide;Acc:NP_956912]	25	30	-1	cgctgt	
ENSDARG00000019057	ENSDART00000032224	Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at,Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at,Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at,Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at			-3377	-3372	-1	tcgctg	
ENSDARG00000019057	ENSDART00000048630	Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at,Dr.18039.1.S1_at,Dr.11348.1.S1_x_at,Dr.11348.1.S1_at			-3377	-3372	-1	tcgctg	
ENSDARG00000019057	ENSDART00000050015	Dr.11348.1.S1_at			-3377	-3372	-1	tcgctg	
ENSDARG00000019302	ENSDART0000007649	Dr.25285.1.S1_at,Dr.11211.1.S1_at	zgc:73223	hypothetical protein MGC73223 [Source:RefSeq_peptide;Acc:NP_957126]	-3810	-3805	1	agcgtg	
ENSDARG00000019302	ENSDART0000007649	Dr.25285.1.S1_at,Dr.11211.1.S1_at	zgc:73223	hypothetical protein MGC73223 [Source:RefSeq_peptide;Acc:NP_957126]	-2001	-1996	1	tcgctg	
ENSDARG00000019302	ENSDART0000007649	Dr.25285.1.S1_at,Dr.11211.1.S1_at	zgc:73223	hypothetical protein MGC73223 [Source:RefSeq_peptide;Acc:NP_957126]	-348	-343	-1	tcgctg	
ENSDARG00000019302	ENSDART0000007649	Dr.25285.1.S1_at,Dr.11211.1.S1_at	zgc:73223	hypothetical protein MGC73223 [Source:RefSeq_peptide;Acc:NP_957126]	-4447	-4442	1	tcgctg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-3963	-3958	-1	agcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-2701	-2696	-1	ggcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-4704	-4699	-1	agcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1423	-1418	-1	agcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1407	-1402	1	ggcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1232	-1227	-1	tcgctg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1189	-1184	-1	tcgctg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1139	-1134	-1	tcgctg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1084	-1079	-1	cgctgt	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1056	-1051	-1	cgctgt	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-1016	-1011	-1	cgctgt	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-623	-618	1	cgctgt	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-159	-154	-1	tcgctg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-4337	-4332	-1	agcgtg	
ENSDARG00000019469	ENSDART00000011211	Dr.24253.1.S1_at	stk3	serine/threonine kinase 3 (STE20 homolog, yeast) [Source:RefSeq_peptide;Acc:NP_955966]	-4922	-4917	-1	agcgtg	
ENSDARG00000019862	ENSDART00000009054	Dr.913.1.S1_at	zgc:63909	tropomyosin 4 isoform 2 [Source:RefSeq_peptide;Acc:NP_998323]	-3027	-3022	1	tcgctg	
ENSDARG00000019862	ENSDART00000009054	Dr.913.1.S1_at	zgc:63909	tropomyosin 4 isoform 2 [Source:RefSeq_peptide;Acc:NP_998323]	-2322	-2317	1	agcgtg	
ENSDARG00000019862	ENSDART00000009054	Dr.913.1.S1_at	zgc:63909	tropomyosin 4 isoform 2 [Source:RefSeq_peptide;Acc:NP_998323]	-1865	-1860	1	agcgtg	
ENSDARG00000020007	ENSDART00000042990	Dr.1377.1.A1_at,Dr.23532.1.A1_at,Dr.5521.1.S1_at	col1a2	collagen, type I, alpha 2 [Source:RefSeq_peptide;Acc:NP_892013]	-3691	-3686	-1	cgctgt	
ENSDARG00000020007	ENSDART00000042990	Dr.1377.1.A1_at,Dr.23532.1.A1_at,Dr.5521.1.S1_at	col1a2	collagen, type I, alpha 2 [Source:RefSeq_peptide;Acc:NP_892013]	-2964	-2959	1	cgctgt	
ENSDARG00000020007	ENSDART00000042990	Dr.1377.1.A1_at,Dr.23532.1.A1_at,Dr.5521.1.S1_at	col1a2	collagen, type I, alpha 2 [Source:RefSeq_peptide;Acc:NP_892013]	-2808	-2803	1	tcgctg	
ENSDARG00000020007	ENSDART00000042990	Dr.1377.1.A1_at,Dr.23532.1.A1_at,Dr.5521.1.S1_at	col1a2	collagen, type I, alpha 2 [Source:RefSeq_peptide;Acc:NP_892013]	-909	-904	-1	tcgctg	
ENSDARG00000020007	ENSDART00000042990	Dr.1377.1.A1_at,Dr.23532.1.A1_at,Dr.5521.1.S1_at	col1a2	collagen, type I, alpha 2 [Source:RefSeq_peptide;Acc:NP_892013]	-234	-229	-1	cgctgt	
ENSDARG00000020190	ENSDART00000003437	Dr.25086.1.A1_at			6	11	-1	tcgctg	
ENSDARG00000020190	ENSDART00000003437	Dr.25086.1.A1_at			-2407	-2402	-1	agcgtg	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at			-4030	-4025	1	ggcgtg	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at			-3871	-3866	-1	tcgctg	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at			-3757	-3752	1	agcgtg	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at			-4843	-4838	-1	ggcgtg	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at			-1953	-1948	1	tcgctg	
ENSDARG00000020893	ENSDART00000004693	Dr.17850.1.S1_at	zgc:56592	zgc:56592 [Source:RefSeq_peptide;Acc:NP_998573]	-1091	-1086	1	ggcgtg	
ENSDARG00000020893	ENSDART00000004693	Dr.17850.1.S1_at	zgc:56592	zgc:56592 [Source:RefSeq_peptide;Acc:NP_998573]	-1911	-1906	1	ggcgtg	
ENSDARG00000021443	ENSDART00000014168	Dr.24122.1.A1_at	NP_955943.1	CCCH zinc finger protein C3H-2 [Source:RefSeq_peptide;Acc:NP_955943]	-4527	-4522	-1	cgctgt	
ENSDARG00000021443	ENSDART00000014168	Dr.24122.1.A1_at	NP_955943.1	CCCH zinc finger protein C3H-2 [Source:RefSeq_peptide;Acc:NP_955943]	-3319	-3314	1	cgctgt	
ENSDARG00000022295	ENSDART00000029465	Dr.15418.1.S1_at	wu:fc23f06	transcription factor 2 like protein [Source:RefSeq_peptide;Acc:NP_919353]	-71	-66	1	ggcgtg	
ENSDARG00000022295	ENSDART00000029465	Dr.15418.1.S1_at	wu:fc23f06	transcription factor 2 like protein [Source:RefSeq_peptide;Acc:NP_919353]	-4671	-4666	1	ggcgtg	
ENSDARG00000022767	ENSDART00000028709	Dr.5662.1.S1_at	Q5BLC2_BRARE	Novel protein similar to vertebrate apolipoprotein B (Including Ag(X) antigen) (APOB). [Source:Uniprot/SPTREMBL;Acc:Q5TZ29]	-152	-147	1	agcgtg	
ENSDARG00000022767	ENSDART00000028709	Dr.5662.1.S1_at	Q5BLC2_BRARE	Novel protein similar to vertebrate apolipoprotein B (Including Ag(X) antigen) (APOB). [Source:Uniprot/SPTREMBL;Acc:Q5TZ29]	-2584	-2579	-1	tcgctg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-780	-775	1	tcgctg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-3618	-3613	1	agcgtg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-3588	-3583	-1	agcgtg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-2611	-2606	-1	agcgtg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-2515	-2510	-1	tcgctg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-4711	-4706	1	tcgctg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-1933	-1928	1	tcgctg	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-1521	-1516	1	cgctgt	
ENSDARG00000023820	ENSDART00000038657	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-162	-157	-1	tcgctg	
ENSDARG00000024407	ENSDART00000033943	Dr.16681.1.A1_at	mamd1	Novel protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q7ZZ84]	-2931	-2926	1	tcgctg	
ENSDARG00000024407	ENSDART00000033943	Dr.16681.1.A1_at	mamd1	Novel protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q7ZZ84]	-2240	-2235	-1	tcgctg	
ENSDARG00000024480	ENSDART00000034117	Dr.3512.1.A1_at	Q6NWE8_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6NWE8]	-1626	-1621	1	agcgtg	
ENSDARG00000024480	ENSDART00000034117	Dr.3512.1.A1_at	Q6NWE8_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6NWE8]	-1593	-1588	-1	tcgctg	
ENSDARG00000024480	ENSDART00000034117	Dr.3512.1.A1_at	Q6NWE8_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6NWE8]	-1573	-1568	-1	tcgctg	
ENSDARG00000024480	ENSDART00000034117	Dr.3512.1.A1_at	Q6NWE8_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6NWE8]	-1569	-1564	-1	tcgctg	
ENSDARG00000024480	ENSDART00000034117	Dr.3512.1.A1_at	Q6NWE8_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6NWE8]	-1565	-1560	-1	tcgctg	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-3817	-3812	-1	agcgtg	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-3698	-3693	-1	agcgtg	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-2476	-2471	-1	cgctgt	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-4576	-4571	1	ggcgtg	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-4314	-4309	1	agcgtg	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.1.A1_at,Dr.3025.3.S1_at			-4209	-4204	1	tcgctg	

Supplementary Table 2 (cont.). Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-4658	-4653	1	tcgctg
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-166	-161	-1	tcgctg
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-136	-131	1	tcgctg
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-4658	-4653	1	tcgctg
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-166	-161	-1	tcgctg
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb1h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-136	-131	1	tcgctg
ENSDARG00000027669	ENSDART00000035274	Dr.1991.1.A1_s_at	zgc:66417	hypothetical protein LOC387303 [Source:RefSeq_peptide;Acc:NP_956419]	-2874	-2869	1	tcgctg
ENSDARG00000027669	ENSDART00000035274	Dr.1991.1.A1_s_at	zgc:66417	hypothetical protein LOC387303 [Source:RefSeq_peptide;Acc:NP_956419]	-129	-124	-1	ggcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-3372	-3367	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-2691	-2686	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-1910	-1905	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4427	-4422	1	cgcggtg
ENSDARG00000027924	ENSDART00000047994	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4195	-4190	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-3372	-3367	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-2691	-2686	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-1910	-1905	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4427	-4422	1	cgcggtg
ENSDARG00000027924	ENSDART00000047994	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4195	-4190	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-3372	-3367	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-2691	-2686	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-1910	-1905	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4427	-4422	1	cgcggtg
ENSDARG00000027924	ENSDART00000047994	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4195	-4190	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-3372	-3367	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-2691	-2686	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-1910	-1905	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4427	-4422	1	cgcggtg
ENSDARG00000027924	ENSDART00000047994	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4195	-4190	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-3372	-3367	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-2691	-2686	-1	agcgtg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-1910	-1905	1	tcgctg
ENSDARG00000027924	ENSDART00000024900	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4427	-4422	1	cgcggtg
ENSDARG00000027924	ENSDART00000047994	593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25			-4195	-4190	1	tcgctg
ENSDARG00000028618	ENSDART00000028260	Dr.890.1.S1_at	zgc:77517	hypothetical protein LOC393540 [Source:RefSeq_peptide;Acc:NP_956862]	-4195	-4190	1	tcgctg
ENSDARG00000028618	ENSDART00000028260	Dr.890.1.S1_at	zgc:77517	hypothetical protein LOC393540 [Source:RefSeq_peptide;Acc:NP_956862]	-3818	-3813	-1	tcgctg
ENSDARG00000028784	ENSDART00000044410	Dr.12714.1.A1_at			-102	-97	1	cgcggtg
ENSDARG00000029086	ENSDART00000041921	Dr.1282.1.S1_at	kr18	keratin 8 [Source:RefSeq_peptide;Acc:NP_956374]	-551	-546	-1	agcgtg
ENSDARG00000030236	ENSDART00000011928	Dr.1368.7.S1_at	zgc:91877	hypothetical protein LOC337397 [Source:RefSeq_peptide;Acc:NP_997941]	-3387	-3382	-1	cgcggtg
ENSDARG00000030236	ENSDART00000011928	Dr.1368.7.S1_at	zgc:91877	hypothetical protein LOC337397 [Source:RefSeq_peptide;Acc:NP_997941]	-1028	-1023	-1	tcgctg
ENSDARG00000030662	ENSDART00000048550	Dr.9682.1.A1_at			77	82	-1	agcgtg
ENSDARG00000030662	ENSDART00000048550	Dr.9682.1.A1_at			-3682	-3677	1	tcgctg
ENSDARG00000030662	ENSDART00000048550	Dr.9682.1.A1_at			-1444	-1439	1	cgcggtg
ENSDARG00000030662	ENSDART00000048550	Dr.9682.1.A1_at			-301	-296	-1	tcgctg
ENSDARG00000030662	ENSDART00000048550	Dr.9682.1.A1_at			-4904	-4899	-1	agcgtg
ENSDARG00000031664	ENSDART00000049339	Dr.8215.1.A1_at	sox21a	SRY-box 21 [Source:RefSeq_peptide;Acc:NP_571361]	-2414	-2409	1	agcgtg
ENSDARG00000031664	ENSDART00000049339	Dr.8215.1.A1_at	sox21a	SRY-box 21 [Source:RefSeq_peptide;Acc:NP_571361]	-311	-306	-1	ggcgtg
ENSDARG00000031664	ENSDART00000049339	Dr.8215.1.A1_at	sox21a	SRY-box 21 [Source:RefSeq_peptide;Acc:NP_571361]	-213	-208	1	cgcggtg
ENSDARG00000031854	ENSDART00000043418	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-4616	-4611	-1	tcgctg
ENSDARG00000031854	ENSDART00000043418	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-769	-764	1	cgcggtg
ENSDARG00000031854	ENSDART00000043418	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-545	-540	-1	ggcgtg
ENSDARG00000031854	ENSDART00000050805	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-4616	-4611	-1	tcgctg
ENSDARG00000031854	ENSDART00000050805	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-769	-764	1	cgcggtg
ENSDARG00000031854	ENSDART00000050805	Dr.7688.1.A1_at,Dr.7688.1.A1_at			-545	-540	-1	ggcgtg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-3386	-3381	-1	cgcggtg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-2983	-2978	1	ggcgtg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-2703	-2698	-1	tcgctg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-2417	-2412	-1	tcgctg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-2381	-2376	1	tcgctg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-1870	-1865	1	tcgctg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-4407	-4402	-1	ggcgtg
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-4306	-4301	1	cgcggtg
ENSDARG00000033949	ENSDART00000045135	Dr.18466.1.A1_at	NP_001017680.1	hypothetical protein LOC550375 [Source:RefSeq_peptide;Acc:NP_001017680]	-3737	-3732	1	tcgctg
ENSDARG00000033949	ENSDART00000045135	Dr.18466.1.A1_at	NP_001017680.1	hypothetical protein LOC550375 [Source:RefSeq_peptide;Acc:NP_001017680]	-1464	-1459	1	agcgtg
ENSDARG00000034351	ENSDART00000043771	Dr.23631.1.S1_at	tagln2	transgelin 2 [Source:RefSeq_peptide;Acc:NP_963870]	-1492	-1487	1	agcgtg
ENSDARG00000035160	ENSDART00000050933	Dr.13775.1.S1_at			-40	-35	1	agcgtg
ENSDARG00000035666	ENSDART00000051733	Dr.4797.1.S1_at	Q6DGW1_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6DGW1]	-3118	-3113	-1	ggcgtg
ENSDARG00000035666	ENSDART00000051733	Dr.4797.1.S1_at	Q6DGW1_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6DGW1]	-3045	-3040	1	agcgtg
ENSDARG00000035666	ENSDART00000051733	Dr.4797.1.S1_at	Q6DGW1_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6DGW1]	-1406	-1401	1	ggcgtg
ENSDARG00000035666	ENSDART00000051733	Dr.4797.1.S1_at	Q6DGW1_BRARE	Hypothetical protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6DGW1]	-859	-854	1	tcgctg
ENSDARG00000035743	ENSDART00000051853	Dr.14748.1.S1_at	zgc:63985	Unknown (protein for MGC:63985) [Source:RefSeq_peptide;Acc:NP_956252]	-1043	-1038	1	agcgtg
ENSDARG00000036082	ENSDART00000052385	Dr.15819.1.A1_at,Dr.17776.1.A1_at	NP_001001843.1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-3632	-3627	1	tcgctg
ENSDARG00000036082	ENSDART00000052385	Dr.15819.1.A1_at,Dr.17776.1.A1_at	NP_001001843.1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-1852	-1847	1	agcgtg
ENSDARG00000036082	ENSDART00000052385	Dr.15819.1.A1_at,Dr.17776.1.A1_at	NP_001001843.1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-1701	-1696	-1	agcgtg

Supplementary Table 2 (cont.). Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG0000036082	ENSDART0000052385	Dr.15819.1.A1_at,Dr.17776.1.A1_at	NP_001001843.1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-240	-235	-1	agcgtg
ENSDARG0000036082	ENSDART0000052385	Dr.15819.1.A1_at,Dr.17776.1.A1_at	NP_001001843.1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-56	-51	1	cgcggt
ENSDARG0000036470	ENSDART0000052991	Dr.10326.1.S1_at	junb	jun B proto-oncogene [Source:RefSeq_peptide;Acc:NP_998721]	-66	-61	-1	ggcggt
ENSDARG0000036481	ENSDART0000053001	Dr.6550.1.A1_at	Q6PG35_BRARE	LOC407646 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6PG35]	-4651	-4646	-1	tcgctg
ENSDARG0000036517	ENSDART0000053070	Dr.14111.1.S1_at	si:xx-by187g17.1	Novel protein similar to zebrafish hemoglobin alpha-adult 1 (Hbaa1). [Source:Uniprot/SPTREMBL;Acc:Q6ZM17]	-2107	-2102	-1	tcgctg
ENSDARG0000036517	ENSDART0000053070	Dr.14111.1.S1_at	si:xx-by187g17.1	Novel protein similar to zebrafish hemoglobin alpha-adult 1 (Hbaa1). [Source:Uniprot/SPTREMBL;Acc:Q6ZM17]	-4658	-4651	1	tcgctg
ENSDARG0000036518	ENSDART0000043748	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-3361	-3356	1	tcgctg
ENSDARG0000036518	ENSDART0000043748	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-1341	-1336	-1	tcgctg
ENSDARG0000036518	ENSDART0000043748	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-4481	-4476	-1	tcgctg
ENSDARG0000036519	ENSDART0000053072	Dr.14111.1.S1_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-2950	-2945	1	cgcggt
ENSDARG0000036521	ENSDART0000053073	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-3811	-3806	1	tcgctg
ENSDARG0000036521	ENSDART0000053073	Dr.25155.1.S1_s_at	ba2	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-1332	-1327	-1	tcgctg
ENSDARG0000036527	ENSDART0000053078	Dr.14111.1.S1_at	si:xx-by187g17.1	hemoglobin alpha adult-1 (hbaa1), mRNA [Source:RefSeq_dna;Acc:NM_131257]	-2104	-2099	-1	tcgctg
ENSDARG0000036527	ENSDART0000053078	Dr.14111.1.S1_at	si:xx-by187g17.1	hemoglobin alpha adult-1 (hbaa1), mRNA [Source:RefSeq_dna;Acc:NM_131257]	-4653	-4678	1	tcgctg
ENSDARG0000036528	ENSDART0000053080	Dr.8723.1.S1_at	NP_001002461.1	zgc:92903 [Source:RefSeq_peptide;Acc:NP_001002461]	-1100	-1095	-1	agcgtg
ENSDARG0000036528	ENSDART0000053080	Dr.8723.1.S1_at	NP_001002461.1	zgc:92903 [Source:RefSeq_peptide;Acc:NP_001002461]	-48	-43	1	tcgctg
ENSDARG0000036529	ENSDART0000053081	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-3358	-3353	1	tcgctg
ENSDARG0000036529	ENSDART0000053081	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-1341	-1336	-1	tcgctg
ENSDARG0000036529	ENSDART0000053081	Dr.25155.1.S1_s_at	ba2l	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-4476	-4471	-1	tcgctg
ENSDARG0000036531	ENSDART0000053083	Dr.14111.1.S1_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-2943	-2938	1	cgcggt
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3938	-3933	-1	cgcggt
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3823	-3818	-1	tcgctg
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3765	-3760	1	ggcggt
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3350	-3345	1	agcgtg
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4669	-4664	1	agcgtg
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4994	-4989	-1	ggcggt
ENSDARG0000036533	ENSDART0000053086	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4937	-4932	-1	ggcggt
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3902	-3897	-1	cgcggt
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3787	-3782	-1	tcgctg
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3729	-3724	1	ggcggt
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-3314	-3309	1	agcgtg
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4633	-4628	1	agcgtg
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4958	-4953	-1	ggcggt
ENSDARG0000036533	ENSDART0000053087	Dr.10170.1.A1_at,Dr.10170.1.A1_at	Dr.10170.1.A1_at		-4901	-4896	-1	ggcggt
ENSDARG0000036535	ENSDART0000042396	Dr.25155.1.S1_s_at	ba2	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-3804	-3799	1	tcgctg
ENSDARG0000036535	ENSDART0000042396	Dr.25155.1.S1_s_at	ba2	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-1325	-1320	-1	tcgctg
ENSDARG0000037281	ENSDART0000054230	Dr.4907.1.S1_at	NP_998219.1	fibrinogen gamma polypeptide [Source:RefSeq_peptide;Acc:NP_998219]	-4801	-4796	1	cgcggt
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-3332	-3327	1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-4700	-4695	-1	cgcggt
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-1223	-1218	-1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-1219	-1214	-1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-1203	-1198	-1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-1199	-1194	-1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-578	-573	-1	tcgctg
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-351	-346	1	ggcggt
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-243	-238	-1	cgcggt
ENSDARG0000037618	ENSDART0000054788	Dr.13972.1.S1_at	zgc:64114	hypothetical protein LOC378866 [Source:RefSeq_peptide;Acc:NP_956401]	-30	-25	-1	tcgctg
ENSDARG0000038321	ENSDART0000055897	Dr.9682.1.A1_at			-3855	-3850	1	tcgctg
ENSDARG0000038321	ENSDART0000055897	Dr.9682.1.A1_at			-1979	-1974	-1	ggcggt
ENSDARG0000038321	ENSDART0000055897	Dr.9682.1.A1_at			-346	-341	-1	tcgctg
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-4477	-4472	1	agcgtg
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-1704	-1699	1	agcgtg
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-4665	-4660	1	ggcggt
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-1420	-1415	1	ggcggt
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-1399	-1394	-1	ggcggt
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-1221	-1216	1	tcgctg
ENSDARG0000038622	ENSDART0000056382	Dr.20270.1.S1_at			-1057	-1052	-1	tcgctg
ENSDARG0000038812	ENSDART0000056679	Dr.20140.1.A1_at	NP_991178.1	E2F transcription factor 4, p107/p130-binding [Source:RefSeq_peptide;Acc:NP_991178]	-3847	-3842	1	ggcggt
ENSDARG0000038813	ENSDART0000056680	Dr.20140.1.A1_at	NP_991178.1	E2F transcription factor 4, p107/p130-binding [Source:RefSeq_peptide;Acc:NP_991178]	-3732	-3727	1	ggcggt
ENSDARG0000039027	ENSDART0000056969	Dr.4797.1.S1_at,Dr.4797.1.S1_at			-2978	-2973	-1	agcgtg
ENSDARG0000039027	ENSDART0000056969	Dr.4797.1.S1_at,Dr.4797.1.S1_at			-862	-857	-1	tcgctg
ENSDARG0000039027	ENSDART0000056969	Dr.4797.1.S1_at,Dr.4797.1.S1_at			-540	-535	1	ggcggt
ENSDARG0000039027	ENSDART0000056969	Dr.4797.1.S1_at,Dr.4797.1.S1_at			-4068	-4063	-1	agcgtg
ENSDARG0000039728	ENSDART0000037346	Dr.3581.1.S1_at,Dr.3581.1.S1_a_at	ctrb1	chymotrypsinogen B1 [Source:RefSeq_peptide;Acc:NP_997783]	-4839	-4834	-1	ggcggt
ENSDARG0000039747	ENSDART0000058095	Dr.4797.1.S1_at			-2916	-2911	-1	ggcggt
ENSDARG0000039747	ENSDART0000058095	Dr.4797.1.S1_at			-2797	-2792	1	agcgtg
ENSDARG0000039747	ENSDART0000058095	Dr.4797.1.S1_at			-2399	-2394	1	agcgtg
ENSDARG0000039747	ENSDART0000058095	Dr.4797.1.S1_at			-1967	-1962	-1	tcgctg
ENSDARG0000039841	ENSDART0000058272	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2848	-2843	1	tcgctg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-3815	-3810	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-2730	-2725	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-1064	-1059	1	tcgctg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-3815	-3810	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-2730	-2725	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-1064	-1059	1	tcgctg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-3815	-3810	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-2730	-2725	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-1064	-1059	1	tcgctg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-3815	-3810	1	agcgtg
ENSDARG0000039914	ENSDART0000058384	AFFX-Dr-GAPDH-3_at,AFFX-Dr-GAPDH-M_at,Dr.1194.1.S1_at,AFFX-Dr-GAPDH-5_at	zgc:76908	glyceraldehyde 3-phosphate dehydrogenase [Source:RefSeq_peptide;Acc:NP_998259]	-2730	-2725	1	agcgtg

Supplementary Table 2 (cont.). Location of putative AHRES

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2312	-2307	-1	tcgctg
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2072	-2067	-1	agcgtg
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-4585	-4580	1	agcgtg
ENSDARG00000041685	ENSDART0000006984	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-3122	-3117	-1	tcgctg
ENSDARG00000041685	ENSDART0000006984	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2882	-2877	-1	agcgtg
ENSDARG00000041685	ENSDART0000006984	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-629	-624	-1	ggcgtg
ENSDARG00000041685	ENSDART00000061093	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-3476	-3471	1	ggcgtg
ENSDARG00000041685	ENSDART00000061093	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-3106	-3101	-1	tcgctg
ENSDARG00000041685	ENSDART00000061093	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2371	-2366	-1	ggcgtg
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2312	-2307	-1	tcgctg
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-2072	-2067	-1	agcgtg
ENSDARG00000041685	ENSDART00000061098	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.16397.1.A1_at,Dr.3025.2.S1_at,Dr.3025.3.S1_at			-4585	-4580	1	agcgtg
ENSDARG00000041769	ENSDART00000061219	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-1147	-1142	1	agcgtg
ENSDARG00000041769	ENSDART00000061219	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-593	-588	1	tcgctg
ENSDARG00000041769	ENSDART00000061219	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-11	-6	1	cgctgt
ENSDARG00000041774	ENSDART00000061223	Dr.25009.6.A1_a_at			-3462	-3457	1	tcgctg
ENSDARG00000041774	ENSDART00000061223	Dr.25009.6.A1_a_at			-3163	-3158	-1	tcgctg
ENSDARG00000041774	ENSDART00000061223	Dr.25009.6.A1_a_at			-2354	-2349	1	tcgctg
ENSDARG00000041813	ENSDART00000061279	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-1147	-1142	1	agcgtg
ENSDARG00000041813	ENSDART00000061279	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-593	-588	1	tcgctg
ENSDARG00000041813	ENSDART00000061279	Dr.7806.1.A1_at	NP_001014360.1	hypothetical protein LOC541525 [Source:RefSeq_peptide;Acc:NP_001014360]	-11	-6	1	cgctgt
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-3994	-3989	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-3121	-3116	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-3028	-3023	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-2933	-2928	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-2886	-2881	-1	ggcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-2842	-2837	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-2749	-2744	-1	tcgctg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1985	-1980	1	ggcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1912	-1907	-1	cgctgt
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1723	-1718	1	agcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1616	-1611	1	cgctgt
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1309	-1304	-1	agcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1225	-1220	1	agcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-1129	-1124	-1	agcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-204	-199	1	ggcgtg
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-4007	-4002	-1	cgctgt
ENSDARG00000041997	ENSDART00000061544	Dr.12106.1.S1_at	NP_955881.1	leucine zipper transcription factor-like 1 [Source:RefSeq_peptide;Acc:NP_955881]	-4005	-4000	1	cgctgt
ENSDARG00000042035	ENSDART00000061601	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2073	-2068	1	tcgctg
ENSDARG00000042035	ENSDART00000061601	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-1107	-1102	1	agcgtg
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-3478	-3473	1	cgctgt
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2685	-2680	-1	agcgtg
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-1952	-1947	-1	agcgtg
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-4240	-4235	-1	cgctgt
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-4141	-4136	1	ggcgtg
ENSDARG00000042036	ENSDART00000061605	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-4030	-4025	-1	tcgctg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-3458	-3453	1	cgctgt
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-3452	-3447	-1	cgctgt
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-3296	-3291	-1	agcgtg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-3099	-3094	1	tcgctg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-4806	-4801	-1	agcgtg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-2894	-2889	-1	agcgtg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-2740	-2735	-1	agcgtg
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at			-1791	-1786	1	tcgctg
ENSDARG00000042046	ENSDART00000061618	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-1760	-1755	1	tcgctg
ENSDARG00000042050	ENSDART00000061623	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-3571	-3566	-1	ggcgtg
ENSDARG00000042050	ENSDART00000061623	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-1913	-1908	-1	agcgtg
ENSDARG00000042102	ENSDART00000061707	Dr.13689.1.S1_at	zgc:66449	Unknown (protein for MGC:66449) [Source:RefSeq_peptide;Acc:NP_956095]	-2802	-2797	-1	cgctgt
ENSDARG00000042391	ENSDART00000062156	Dr.14748.1.S1_at	zgc:63985	zgc:63985 (zgc:63985), mRNA [Source:RefSeq_dna;Acc:NM_199958]	-1900	-1895	-1	tcgctg
ENSDARG00000042391	ENSDART00000062156	Dr.14748.1.S1_at	zgc:63985	zgc:63985 (zgc:63985), mRNA [Source:RefSeq_dna;Acc:NM_199958]	-1043	-1038	1	agcgtg
ENSDARG00000043218	ENSDART00000063453	Dr.15054.1.S1_at	rbp2a	retinol binding protein 2a, cellular [Source:RefSeq_peptide;Acc:NP_694549]	-2638	-2633	1	ggcgtg
ENSDARG00000043218	ENSDART00000063453	Dr.15054.1.S1_at	rbp2a	retinol binding protein 2a, cellular [Source:RefSeq_peptide;Acc:NP_694549]	-2352	-2347	1	cgctgt
ENSDARG00000043218	ENSDART00000063453	Dr.15054.1.S1_at	rbp2a	retinol binding protein 2a, cellular [Source:RefSeq_peptide;Acc:NP_694549]	-1487	-1482	1	tcgctg
ENSDARG00000043218	ENSDART00000063453	Dr.15054.1.S1_at	rbp2a	retinol binding protein 2a, cellular [Source:RefSeq_peptide;Acc:NP_694549]	-4225	-4220	1	agcgtg
ENSDARG00000043320	ENSDART00000063596	Dr.14268.1.A1_at,Dr.18893.1.S1_at			-4981	-4976	1	tcgctg
ENSDARG00000043320	ENSDART00000063596	Dr.14268.1.A1_at,Dr.18893.1.S1_at			-557	-552	1	ggcgtg
ENSDARG00000043320	ENSDART00000063596	Dr.14268.1.A1_at,Dr.18893.1.S1_at			-251	-246	1	agcgtg
ENSDARG00000043592	ENSDART00000064008	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-734	-729	-1	cgctgt
ENSDARG00000043592	ENSDART00000064008	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-561	-556	-1	agcgtg
ENSDARG00000043592	ENSDART00000064008	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-527	-522	-1	tcgctg
ENSDARG00000043592	ENSDART00000064010	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-533	-528	-1	cgctgt
ENSDARG00000043592	ENSDART00000064010	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-360	-355	-1	agcgtg
ENSDARG00000043592	ENSDART00000064010	Dr.17113.1.A1_a_at,Dr.3889.1.A1_at,Dr.17113.1.A1_a_at,Dr.3889.1.A1_at	ptena	phosphatase and tensin-like protein A [Source:RefSeq_peptide;Acc:NP_957002]	-326	-321	-1	tcgctg
ENSDARG00000043618	ENSDART00000064041	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2734	-2729	-1	cgctgt

Supplementary Table 2 (cont.). Location of putative AHREs

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000043618	ENSDART00000064041	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2732	-2727	1	cgcggt
ENSDARG00000043618	ENSDART00000064044	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2734	-2729	-1	cgcggt
ENSDARG00000043618	ENSDART00000064044	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2732	-2727	1	cgcggt
ENSDARG00000043670	ENSDART00000024462	Dr.1605.1.S1_at	NM_001013259.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 1 (serpin1), mRNA [Source:RefSeq_dna;Acc:NM_001013259]	-4819	-4814	1	agcggtg
ENSDARG00000043670	ENSDART00000024462	Dr.1605.1.S1_at	NM_001013259.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 1 (serpin1), mRNA [Source:RefSeq_dna;Acc:NM_001013259]	-4143	-4138	1	agcggtg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-3071	-3066	-1	tcgctg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-2789	-2784	1	cgcggt
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-2454	-2449	-1	ggcggtg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-1360	-1355	1	ggcggtg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-942	-937	-1	cgcggtg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-105	-100	-1	cgcggtg
ENSDARG00000043692	ENSDART00000064157	Dr.19877.1.S1_at	zgc:66133	hypothetical protein LOC393468 [Source:RefSeq_peptide;Acc:NP_956790]	-16	-11	-1	cgcggtg
ENSDARG00000043960	ENSDART00000064542	Dr.6147.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-3939	-3934	-1	agcggtg
ENSDARG00000043960	ENSDART00000064542	Dr.6147.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-4689	-4684	1	cgcggtg
ENSDARG00000043960	ENSDART00000064542	Dr.6147.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-552	-547	1	tcgctg
ENSDARG00000043960	ENSDART00000064542	Dr.6147.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-4539	-4534	1	tcgctg
ENSDARG00000043990	ENSDART00000064579	Dr.7806.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-138	-133	1	tcgctg
ENSDARG00000043997	ENSDART00000064586	Dr.11609.1.S1_at	Q7SZD0_BRARE	LOC402847 protein (Fragment) [Source:UniProt/SPTREMBL;Acc:Q7SZD0]	-2929	-2924	-1	agcggtg
ENSDARG00000043997	ENSDART00000064586	Dr.11609.1.S1_at	Q7SZD0_BRARE	LOC402847 protein (Fragment) [Source:UniProt/SPTREMBL;Acc:Q7SZD0]	-600	-595	-1	tcgctg
ENSDARG00000043997	ENSDART00000064586	Dr.11609.1.S1_at	Q7SZD0_BRARE	LOC402847 protein (Fragment) [Source:UniProt/SPTREMBL;Acc:Q7SZD0]	-552	-547	-1	tcgctg
ENSDARG00000043997	ENSDART00000064586	Dr.11609.1.S1_at	Q7SZD0_BRARE	LOC402847 protein (Fragment) [Source:UniProt/SPTREMBL;Acc:Q7SZD0]	-67	-62	1	ggcggtg
ENSDARG00000044001	ENSDART00000064597	Dr.20815.3.A1_at	NP_999858.1	chimera galectin Gal3 [Source:RefSeq_peptide;Acc:NP_999858]	-3720	-3715	-1	tcgctg
ENSDARG00000044001	ENSDART00000064597	Dr.20815.3.A1_at	NP_999858.1	chimera galectin Gal3 [Source:RefSeq_peptide;Acc:NP_999858]	-371	-366	-1	tcgctg
ENSDARG00000044002	ENSDART00000064591	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-3995	-3990	-1	tcgctg
ENSDARG00000044002	ENSDART00000064591	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-4812	-4807	-1	agcggtg
ENSDARG00000044002	ENSDART00000064591	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-4972	-4967	-1	tcgctg
ENSDARG00000044002	ENSDART00000064591	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-1517	-1512	1	tcgctg
ENSDARG00000044002	ENSDART00000064596	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-439	-434	-1	tcgctg
ENSDARG00000044002	ENSDART00000064596	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-1653	-1648	-1	ggcggtg
ENSDARG00000044002	ENSDART00000064596	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-1300	-1295	-1	tcgctg
ENSDARG00000044002	ENSDART00000064596	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-1140	-1135	-1	agcggtg
ENSDARG00000044002	ENSDART00000064596	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-323	-318	-1	tcgctg
ENSDARG00000044101	ENSDART00000064753	Dr.18135.1.A1_at	zgc:92568	zgc:92568 [Source:RefSeq_peptide;Acc:NP_001005937]	-4881	-4876	1	ggcggtg
ENSDARG00000044101	ENSDART00000064753	Dr.18135.1.A1_at	zgc:92568	zgc:92568 [Source:RefSeq_peptide;Acc:NP_001005937]	-475	-470	1	agcggtg
ENSDARG00000044125	ENSDART00000064789	Dr.8723.1.S1_at	zgc:92903	zgc:92903 [Source:RefSeq_peptide;Acc:NP_001002461]	-1108	-1103	-1	agcggtg
ENSDARG00000044125	ENSDART00000064789	Dr.8723.1.S1_at	zgc:92903	zgc:92903 [Source:RefSeq_peptide;Acc:NP_001002461]	-48	-43	1	tcgctg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-3256	-3251	-1	agcggtg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-1753	-1748	-1	tcgctg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-76	-71	1	ggcggtg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-43	-38	1	agcggtg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-3256	-3251	-1	agcggtg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-1753	-1748	-1	tcgctg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-76	-71	1	ggcggtg
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	kmlm2.2	Kreisler (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-43	-38	1	agcggtg
ENSDARG00000044613	ENSDART00000014927	Dr.14041.1.S1_at	NP_001005976.1	hypothetical protein LOC449803 [Source:RefSeq_peptide;Acc:NP_001005976]	-3600	-3595	1	ggcggtg
ENSDARG00000044613	ENSDART00000014927	Dr.14041.1.S1_at	NP_001005976.1	hypothetical protein LOC449803 [Source:RefSeq_peptide;Acc:NP_001005976]	-3377	-3372	1	cgcggtg
ENSDARG00000044613	ENSDART00000014927	Dr.14041.1.S1_at	NP_001005976.1	hypothetical protein LOC449803 [Source:RefSeq_peptide;Acc:NP_001005976]	-58	-53	-1	tcgctg
ENSDARG00000044613	ENSDART00000014927	Dr.14041.1.S1_at	NP_001005976.1	hypothetical protein LOC449803 [Source:RefSeq_peptide;Acc:NP_001005976]	-39	-34	1	agcggtg
ENSDARG00000044625	ENSDART00000065562	Dr.14268.1.A1_at,Dr.18893.1.S1_at	zgc:92226	hypothetical protein LOC492341 [Source:RefSeq_peptide;Acc:NP_001007308]	-4982	-4977	1	tcgctg
ENSDARG00000044625	ENSDART00000065562	Dr.14268.1.A1_at,Dr.18893.1.S1_at	zgc:92226	hypothetical protein LOC492341 [Source:RefSeq_peptide;Acc:NP_001007308]	-251	-246	1	agcggtg
ENSDARG00000044936	ENSDART00000066051	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-3792	-3787	1	tcgctg
ENSDARG00000044936	ENSDART00000066051	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-3267	-3262	1	cgcggtg
ENSDARG00000044936	ENSDART00000066051	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-4066	-4061	1	tcgctg
ENSDARG00000044975	ENSDART00000030103	Dr.1361.1.S1_at			-3650	-3645	1	cgcggtg
ENSDARG00000044975	ENSDART00000030103	Dr.1361.1.S1_at			-2276	-2271	1	agcggtg
ENSDARG00000044975	ENSDART00000030103	Dr.1361.1.S1_at			-1621	-1616	-1	ggcggtg
ENSDARG00000044975	ENSDART00000030103	Dr.1361.1.S1_at			-4656	-4651	-1	tcgctg
ENSDARG00000044975	ENSDART00000030103	Dr.1361.1.S1_at			-50	-45	1	agcggtg
ENSDARG00000044983	ENSDART00000066126	Dr.7110.1.S1_at			-3372	-3367	1	agcggtg
ENSDARG00000045180	ENSDART00000066430	Dr.20277.1.A1_at	NP_997785.1	actin, alpha 2, smooth muscle, aorta [Source:RefSeq_peptide;Acc:NP_997785]	-2999	-2994	1	agcggtg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-3672	-3667	1	tcgctg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-3639	-3634	-1	cgcggtg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-3033	-3028	-1	agcggtg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-1880	-1875	1	ggcggtg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-294	-289	-1	tcgctg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-22	-17	-1	ggcggtg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-4498	-4493	-1	tcgctg
ENSDARG00000045407	ENSDART00000066773	Dr.10879.1.A1_at	NP_001018414.1	hypothetical protein LOC553602 [Source:RefSeq_peptide;Acc:NP_001018414]	-3212	-3207	-1	tcgctg
ENSDARG00000045407	ENSDART00000066773	Dr.10879.1.A1_at	NP_001018414.1	hypothetical protein LOC553602 [Source:RefSeq_peptide;Acc:NP_001018414]	-877	-872	1	agcggtg
ENSDARG00000045407	ENSDART00000066773	Dr.10879.1.A1_at	NP_001018414.1	hypothetical protein LOC553602 [Source:RefSeq_peptide;Acc:NP_001018414]	-100	-95	-1	agcggtg
ENSDARG00000045567	ENSDART00000067004	Dr.13994.1.S1_x_at,Dr.13994.2.A1_a_at,Dr.13994.1.S1_at,Dr.13994.2.A1_x_at,Dr.2819.1.A1_at	zgc:101086	hypothetical protein LOC445172 [Source:RefSeq_peptide;Acc:NP_001003566]	-2856	-2851	-1	tcgctg
ENSDARG00000045567	ENSDART00000067004	Dr.13994.1.S1_x_at,Dr.13994.2.A1_a_at,Dr.13994.1.S1_at,Dr.13994.2.A1_x_at,Dr.2819.1.A1_at	zgc:101086	hypothetical protein LOC445172 [Source:RefSeq_peptide;Acc:NP_001003566]	-2844	-2839	-1	agcggtg
ENSDARG00000045567	ENSDART00000067004	Dr.13994.1.S1_x_at,Dr.13994.2.A1_a_at,Dr.13994.1.S1_at,Dr.13994.2.A1_x_at,Dr.2819.1.A1_at	zgc:101086	hypothetical protein LOC445172 [Source:RefSeq_peptide;Acc:NP_001003566]				
ENSDARG00000045585	ENSDART00000067027	Dr.13689.1.S1_at	zgc:66449	Unknown (protein for MGC:66449) [Source:RefSeq_peptide;Acc:NP_956095]	-2742	-2737	-1	ggcggtg
ENSDARG00000045585	ENSDART00000067027	Dr.13689.1.S1_at	zgc:66449	Unknown (protein for MGC:66449) [Source:RefSeq_peptide;Acc:NP_956095]	-2806	-2801	-1	cgcggtg
ENSDARG00000045678	ENSDART00000067159	Dr.15819.1.A1_at,Dr.17776.1.A1_at	tpH1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-4153	-4148	-1	tcgctg
ENSDARG00000045678	ENSDART00000067159	Dr.15819.1.A1_at,Dr.17776.1.A1_at	tpH1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-3633	-3628	1	tcgctg
ENSDARG00000045678	ENSDART00000067159	Dr.15819.1.A1_at,Dr.17776.1.A1_at	tpH1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-1855	-1850	1	agcggtg
ENSDARG00000045678	ENSDART00000067159	Dr.15819.1.A1_at,Dr.17776.1.A1_at	tpH1	tryptophan hydroxylase 1, like [Source:RefSeq_peptide;Acc:NP_001001843]	-1704	-1699	-1	agcggtg
ENSDARG000								

Supplementary Table 3. Location of putative EREs	Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000000935	ENSDART00000001053	Dr.24249.1.S1_at	zcd3dc5	zinc finger CCH type domain containing 5 [Source:RefSeq_peptide;Acc:NP_956530]	-2575	-2557	1	aaagttaactgtgacctt	
ENSDARG00000001953	ENSDART00000003247	Dr.7626.1.A1_at,Dr.7626.2.S1_at,Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	NP_998562.1	zgc:73257 [Source:RefSeq_peptide;Acc:NP_998562] Kreisl (mouse) maf-related leucine zipper homolog 2.2	135	153	1	aaagcctctgtgacctgc	
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	[Source:RefSeq_peptide;Acc:NP_571917] Kreisl (mouse) maf-related leucine zipper homolog 2.2	-1337	-1319	-1	tcacgcaactgtgaccaac	
ENSDARG00000002667	ENSDART00000003004	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	krml2.2	[Source:RefSeq_peptide;Acc:NP_571917]	-1337	-1319	-1	tcacgcaactgtgaccaac	
ENSDARG00000003323	ENSDART00000017567	Dr.12575.1.S1_at	dcp1a	decapping enzyme [Source:RefSeq_peptide;Acc:NP_878313]	-1949	-1931	1	tcagggaccatgaccoga	
ENSDARG00000003323	ENSDART00000017567	Dr.12575.1.S1_at	dcp1a	decapping enzyme [Source:RefSeq_peptide;Acc:NP_878313]	-381	-363	1	gtgagtaaacatgacctga	
ENSDARG00000004296	ENSDART00000027026	Dr.26469.1.S1_at	zgc:66321	similar to alpha-1-microglobulin/bikunin precursor [Source:RefSeq_peptide;Acc:NP_957412]	-4061	-4043	-1	atagtglaaatgacctca	
ENSDARG00000005186	ENSDART00000022285	Dr.24233.1.S1_at	NP_956418.1	sp4 transcription factor [Source:RefSeq_peptide;Acc:NP_956418]	-1496	-1478	1	tgacctgactgtgaccgct	
ENSDARG00000006526	ENSDART00000017312	Dr.4412.13.A1_x_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-1176	-1158	-1	tccagttactatgacctt	
ENSDARG00000008835	ENSDART00000021286	Dr.4412.13.A1_x_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-3795	-3777	1	caagttgtacgtgacctca	
ENSDARG00000008835	ENSDART00000021286	Dr.4412.13.A1_x_at	fn1b	fibronectin 1b (fn1b), mRNA [Source:RefSeq_dna;Acc:NM_001013261]	-613	-595	1	gaagggcacggtgacctt	
ENSDARG00000008895	ENSDART00000040312	Dr.1619.1.A1_at,Dr.1619.1.A1_at,Dr.1619.1.A1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-3866	-3848	1	caacatcacctgaccaga	
ENSDARG00000008895	ENSDART00000044775	Dr.1619.1.A1_at,Dr.1619.1.A1_at,Dr.1619.1.A1_at	zgc:110540	deoxycytidine kinase [Source:RefSeq_peptide;Acc:NP_001014374]	-3872	-3854	1	caacatcacctgaccaga	
ENSDARG00000009483	ENSDART00000099889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	wu:fc12b04	protein-glutamine gamma-glutamyltransferase [Source:RefSeq_peptide;Acc:NP_997821]	-2635	-2617	1	tcagttcatttgcattag	
ENSDARG00000009483	ENSDART00000099889	Dr.25378.1.A1_at,Dr.24858.1.S1_at	wu:fc12b04	protein-glutamine gamma-glutamyltransferase [Source:RefSeq_peptide;Acc:NP_997821]	-2635	-2617	1	tcagttcatttgcattag	
ENSDARG00000013454	ENSDART00000019328	Dr.16524.1.S1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-4284	-4266	1	ggaagccgctgtgacctga	
ENSDARG00000013613	ENSDART00000018408	Dr.16504.1.A1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-2201	-2183	1	atgagttcgttgcacctg	
ENSDARG00000013613	ENSDART00000018408	Dr.16504.1.A1_at	zgc:112421	hypothetical protein LOC554118 [Source:RefSeq_peptide;Acc:NP_001019585]	-2201	-2183	1	atgagttcgttgcacctg	
ENSDARG00000013646	ENSDART00000019664	Dr.15930.1.A1_at	serpina1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:RefSeq_peptide;Acc:NP_001013277]	-267	-249	-1	ttatgggacctgacctt	
ENSDARG00000014209	ENSDART00000023208	Dr.15930.1.A1_at	serpina1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:RefSeq_peptide;Acc:NP_001013277]	-1492	-1474	-1	tttttttactgtgacctga	
ENSDARG00000015866	ENSDART00000019110	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-1647	-1629	-1	gctattatttgcacctga	
ENSDARG00000015866	ENSDART00000058963	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-1945	-1927	-1	gctattatttgcacctga	
ENSDARG00000015866	ENSDART00000058963	Dr.728.4.S1_at,Dr.728.4.S1_at,Dr.728.4.S1_at	NP_001017836.1	hypothetical protein LOC550534 [Source:RefSeq_peptide;Acc:NP_001017836]	-1647	-1629	-1	gctattatttgcacctga	
ENSDARG00000016448	ENSDART00000014979	Dr.2978.1.S1_at	vg3	Vitellogenin 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9DFT9]	-386	-368	-1	acaggtcaatgtgacctg	
ENSDARG00000016448	ENSDART00000014979	Dr.2978.1.S1_at	vg3	Vitellogenin 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9DFT9]	-386	-368	-1	acaggtcaatgtgacctg	
ENSDARG00000016448	ENSDART00000014979	Dr.2978.1.S1_at	vg3	Vitellogenin 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9DFT9]	-4076	-4058	-1	actaataatttgcacctga	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3275	-3257	1	acaggttaaagtgacctt	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3275	-3257	1	acaggttaaagtgacctt	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-2166	-2148	1	acagggcaacactaacccaa	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-175	-157	1	acagggcaacactaacccaa	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3275	-3257	1	acagggcaacactaacccaa	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-3275	-3257	1	acagggcaacactaacccaa	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-2166	-2148	1	acagggcaacactaacccaa	
ENSDARG00000016825	ENSDART00000050238	Dr.25009.6.A1_a_at,Dr.25009.1.S1_a_at	NP_739573.1	vitellogenin 1 [Source:RefSeq_peptide;Acc:NP_739573]	-175	-157	1	acagggcaacactaacccaa	
ENSDARG00000017289	ENSDART00000047865	Dr.25331.1.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25331.1.S1_at,Dr.25379.1.S1_at	t,Dr.3025.3.S1_at		-1425	-1407	1	tgagttctaaagtgacctg	
ENSDARG00000017289	ENSDART00000050670	Dr.25331.1.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25331.1.S1_at,Dr.25379.1.S1_at	t,Dr.3025.3.S1_at		-1728	-1710	1	tgagttctaaagtgacctg	
ENSDARG00000017289	ENSDART00000047865	Dr.25331.1.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25331.1.S1_at,Dr.25379.1.S1_at	t,Dr.3025.3.S1_at		-1425	-1407	1	tgagttctaaagtgacctg	
ENSDARG00000017289	ENSDART00000050670	Dr.25331.1.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25331.1.S1_at,Dr.25379.1.S1_at	t,Dr.3025.3.S1_at		-1728	-1710	1	tgagttctaaagtgacctg	
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-503	-485	-1	tcaggacactgtgacctt	
ENSDARG00000017619	ENSDART00000038499	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-503	-485	-1	tcaggacactgtgacctt	
ENSDARG00000017624	ENSDART00000012644	Dr.4387.1.S1_at	krt4	keratin 4 [Source:RefSeq_peptide;Acc:NP_571584]	-937	-919	-1	ataggtgtgtgaccttaa	
ENSDARG00000018529	ENSDART00000020254	Dr.4249.1.S1_at	lipf	lipase, gastric [Source:RefSeq_peptide;Acc:NP_998569]	-1057	-1039	-1	tgatgtggcgtgacctgt	
ENSDARG00000019302	ENSDART0000007649	Dr.25285.1.S1_at,Dr.11211.1.S1_at	zgc:73223	hypothetical protein MGC73223 [Source:RefSeq_peptide;Acc:NP_957126]	29	47	-1	accaggaatgacctt	
ENSDARG00000019862	ENSDART00000090954	Dr.913.1.S1_at	zgc:63909	tropomyosin 4 isoform 2 [Source:RefSeq_peptide;Acc:NP_998323]	-4507	-4489	-1	tcaggagaatgaccacaa	
ENSDARG00000020485	ENSDART00000011573	Dr.10314.1.S1_a_at	NP_955943.1	CCCH zinc finger protein C3H-2 [Source:RefSeq_peptide;Acc:NP_955943]	-1349	-1331	-1	tcgggtgtgtgacctga	
ENSDARG00000021443	ENSDART00000014168	Dr.24122.1.A1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-1795	-1777	-1	tccagttactatgacctt	
ENSDARG00000023820	ENSDART00000038857	Dr.8390.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-3604	-3586	1	gcagcacacactgaccac	
ENSDARG00000023963	ENSDART00000036075	Dr.913.1.S1_at	zgc:55420	hypothetical protein LOC406828 [Source:RefSeq_peptide;Acc:NP_998672]	-4731	-4713	1	tcaggagaatgaccacaa	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	r,3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-2075	-2057	-1	caaagtgtctctgaccac	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	r,3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-4197	-4179	-1	gtagattttgtgaccgga	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	r,3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-2075	-2057	-1	caaagtgtctctgaccac	
ENSDARG00000024892	ENSDART00000033228	Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at	r,3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at		-4197	-4179	-1	gtagattttgtgaccgga	
ENSDARG00000025400	ENSDART00000044869	Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at	at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at		-4281	-4263	1	aaagtgcagtgtgaccggg	
ENSDARG00000025400	ENSDART00000046418	Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at	at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at		-4281	-4263	1	aaagtgcagtgtgaccggg	
ENSDARG00000025400	ENSDART00000061150	Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at	at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at		-4380	-4362	1	aaagtgcagtgtgaccggg	
ENSDARG00000025400	ENSDART00000061161	Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at	at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at		-4281	-4263	1	aaagtgcagtgtgaccggg	
ENSDARG00000025400	ENSDART00000061165	Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at	at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at,Dr.25009.4.A1_at		-4281	-4263	1	aaagtgcagtgtgaccggg	
ENSDARG00000026039	ENSDART00000038200	Dr.9478.1.S1_at	cyp1a	cytochrome P450, family 1, subfamily A [Source:RefSeq_peptide;Acc:NP_571954]	-4819	-4801	1	aaagttcaactgtgacctt	
ENSDARG00000026090	ENSDART00000035302	Dr.12833.1.A1_at	zgc:64213	hypothetical protein LOC393393 [Source:RefSeq_peptide;Acc:NP_956715]	-36	-18	-1	ctagataaactgaccgga	
ENSDARG00000026680	ENSDART00000036600	Dr.26139.1.A1_at,Dr.26139.1.A1_x_at	slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14 [Source:RefSeq_peptide;Acc:NP_956458]	-774	-756	-1	tcaattcaactgaccgga	
ENSDARG00000026680	ENSDART00000036600	Dr.26139.1.A1_at,Dr.26139.1.A1_x_at	slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14 [Source:RefSeq_peptide;Acc:NP_956458]	-774	-756	-1	tcaattcaactgaccgga	
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb11h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-740	-722	-1	ttatgtcaactgaccacaa	
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb11h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-669	-651	1	ataagttcaactgaccacaa	
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb11h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-740	-722	-1	ttatgtcaactgaccacaa	
ENSDARG00000027088	ENSDART00000039267	Dr.1192.1.S1_at,Dr.1192.1.S1_a_at	wu:fb11h03	prostaglandin D2 synthase [Source:RefSeq_peptide;Acc:NP_998799]	-669	-651	1	ataagttcaactgaccacaa	
ENSDARG00000027924	ENSDART00000051147	Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25593.1.S1_at	at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at		-2247	-2229	-1	taaaatcggttgcacctt	
ENSDARG00000027924	ENSDART00000051147	Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25593.1.S1_at	at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at		-4561	-4543	-1	caagttgtacgtgacctca	
ENSDARG00000027924	ENSDART00000051147	Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25593.1.S1_at	at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at		-2247	-2229	-1	taaaatcggttgcacctt	

Supplementary Table 3 (cont.). Location of putative EREs

Gene ID	Transcript ID	Affy IDs	Symbol	Description	Start	End	Strand	Sequence
ENSDARG00000027924	ENSDART00000051147	Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at			-4561	-4543	-1	caagttgacgtgacccta
ENSDARG00000027924	ENSDART00000051147	Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25593.2.A1_at,Dr.25593.1.S1_at,Dr.4412.12.A1_at,Dr.25527.1.A1_x_at,Dr.25527.1.A1_at			-2247	-2229	-1	taaaatcggttgacctt
ENSDARG00000027924	ENSDART00000051147	Dr.1282.1.S1_at	krb8	keratin 8 [Source:RefSeq_peptide;Acc:NP_956374]	-4561	-4543	-1	caagttgacgtgacccta
ENSDARG00000029086	ENSDART00000011928	Dr.1368.7.S1_at	zgc:91877	hypothetical protein LOC337397 [Source:RefSeq_peptide;Acc:NP_997941]	-218	-200	-1	glaattcaatgaccaga
ENSDARG00000030236	ENSDART00000048550	Dr.9682.1.A1_at			-3947	-3929	-1	gccattcaacgtgaccga
ENSDARG00000031664	ENSDART00000049339	Dr.8215.1.A1_at	sox21a	SRY-box 21 [Source:RefSeq_peptide;Acc:NP_571361]	-1860	-1842	-1	gcacgtgctgacgtgct
ENSDARG00000033735	ENSDART00000049874	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-4888	-4870	1	ctggagcaacctgaccct
ENSDARG00000033735	ENSDART00000049874	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-3790	-3772	-1	aaagcaactgtgacctag
ENSDARG00000033735	ENSDART00000050898	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-2927	-2909	-1	tgagcctatgagaccac
ENSDARG00000033735	ENSDART00000050898	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-1290	-1272	-1	tgatgtaactgtgacctt
ENSDARG00000033735	ENSDART00000050898	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-3845	-3827	-1	aaagcaactgtgacctag
ENSDARG00000033735	ENSDART00000050898	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-2982	-2964	-1	tgagcctatgagaccac
ENSDARG00000033735	ENSDART00000050898	Dr.2973.1.A1_at,Dr.2973.1.A1_at	Q4Z8P3_BRARE	Neutrophil cytosolic factor 1. [Source:Uniprot/SPTREMBL;Acc:Q4Z8P3]	-1345	-1327	-1	tgatgtaactgtgacctt
ENSDARG00000033770	ENSDART00000011961	Dr.25009.6.A1_a_at	vg1	Vitellogenin 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8JH36]	-179	-161	1	gcagggcaactgacctaa
ENSDARG00000035160	ENSDART00000050933	Dr.13775.1.S1_at			-2271	-2253	-1	ttggtaacctgacctgc
ENSDARG00000035743	ENSDART00000051853	Dr.14748.1.S1_at	zgc:63985	Unknown (protein for MGC:63985) [Source:RefSeq_peptide;Acc:NP_956252]	-4293	-4275	-1	acaatgagctctgacctg
ENSDARG00000036481	ENSDART00000053001	Dr.6550.1.A1_at	Q6PG35_BRARE	LOC407646 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q6PG35]	-806	-788	-1	aaatggaaattgacctc
ENSDARG00000036517	ENSDART00000053070	Dr.1411.1.S1_at						
ENSDARG00000036519	ENSDART00000053072	Dr.1411.1.S1_at	si:xx-by187g17.1	[Source:Uniprot/SPTREMBL;Acc:Q6ZM17]	-1684	-1646	1	tcocgggggtgaccttc
ENSDARG00000036519	ENSDART00000053072	Dr.1411.1.S1_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-3250	-3232	1	acaattcacttgacctt
ENSDARG00000036521	ENSDART00000053073	Dr.25155.1.S1_s_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-1642	-1624	1	tcocgggggtgaccttc
ENSDARG00000036527	ENSDART00000053078	Dr.1411.1.S1_at	ba2	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-4287	-4249	-1	tcocgggggtgaccttc
ENSDARG00000036528	ENSDART00000053080	Dr.8723.1.S1_at	NP_001002461.1	hemoglobin alpha adult-1 (hbaa1), mRNA [Source:RefSeq_dna;Acc:NM_131257]	-1684	-1646	1	tcocgggggtgaccttc
ENSDARG00000036531	ENSDART00000053083	Dr.1411.1.S1_at	zgc:92903	[Source:RefSeq_peptide;Acc:NP_001002461]	-273	-255	1	taagtcacttgacctgc
ENSDARG00000036531	ENSDART00000053083	Dr.1411.1.S1_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-3243	-3225	1	acaattcacttgacctt
ENSDARG00000036535	ENSDART00000042396	Dr.1411.1.S1_at	hbaa1	Hemoglobin alpha chain (Alpha globin aa1). [Source:Uniprot/SWISSPROT;Acc:Q90487]	-1636	-1618	1	tcocgggggtgaccttc
ENSDARG00000036535	ENSDART00000042396	Dr.25155.1.S1_s_at	ba2	Hemoglobin beta-1 chain (BetaA1 globin). [Source:Uniprot/SWISSPROT;Acc:Q90486]	-4257	-4239	-1	tcocgggggtgaccttc
ENSDARG00000036776	ENSDART00000053399	Dr.16380.1.A1_at	NP_001004540.1	aldehyde dehydrogenase 8 family, member A1 [Source:RefSeq_peptide;Acc:NP_001004540]	-2837	-2819	1	acaactctttgacctgt
ENSDARG00000036776	ENSDART00000053399	Dr.16380.1.A1_at	NP_001004540.1	aldehyde dehydrogenase 8 family, member A1 [Source:RefSeq_peptide;Acc:NP_001004540]	-549	-531	-1	ataagctacaatgacctaa
ENSDARG00000036893	ENSDART00000053567	Dr.16206.1.A1_at,Dr.16206.1.A1_s_at			-3911	-3893	-1	taaaagtattgaccctaa
ENSDARG00000036893	ENSDART00000053567	Dr.16206.1.A1_at,Dr.16206.1.A1_s_at			-1045	-1027	-1	acagaaagtgtgaccacaa
ENSDARG00000036893	ENSDART00000053567	Dr.16206.1.A1_at,Dr.16206.1.A1_s_at			-3911	-3893	-1	taaaagtattgaccctaa
ENSDARG00000036893	ENSDART00000053567	Dr.16206.1.A1_at,Dr.16206.1.A1_s_at			-1045	-1027	-1	acagaaagtgtgaccacaa
ENSDARG00000039027	ENSDART00000056969	Dr.4797.1.S1_at,Dr.4797.1.S1_at	zgc:76953	hypothetical protein LOC406625 [Source:RefSeq_peptide;Acc:NP_999924]	-3691	-3673	-1	ataagtaacttgaccttc
ENSDARG00000039150	ENSDART00000057192	Dr.24341.1.S1_at	ctrb1	chymotrypsinogen B1 [Source:RefSeq_peptide;Acc:NP_997783]	-4485	-4467	-1	gcgaataattgaccttc
ENSDARG00000039728	ENSDART00000037346	Dr.3581.1.S1_at,Dr.3581.1.S1_a_at			-3957	-3939	-1	ttgttaactctgaccttc
ENSDARG00000039747	ENSDART00000058095	Dr.4797.1.S1_at			-908	-890	-1	tcagtcttaattgacctt
ENSDARG00000040251	ENSDART00000011497	Dr.4048.1.S1_at	zgc:110367	hypothetical protein LOC550475 [Source:RefSeq_peptide;Acc:NP_001017778]	-3906	-3888	1	ttaggtttattgacctt
ENSDARG00000040251	ENSDART00000011497	Dr.4048.1.S1_at	zgc:110367	hypothetical protein LOC550475 [Source:RefSeq_peptide;Acc:NP_001017778]	-3370	-3352	-1	agcattgacctgaccac
ENSDARG00000040251	ENSDART00000011497	Dr.4048.1.S1_at	zgc:110367	hypothetical protein LOC550475 [Source:RefSeq_peptide;Acc:NP_001017778]	-2569	-2551	-1	ccagttgacctgaccac
ENSDARG00000040251	ENSDART00000011497	Dr.4048.1.S1_at	zgc:110367	hypothetical protein LOC550475 [Source:RefSeq_peptide;Acc:NP_001017778]	-1128	-1110	-1	ctggaacacctgacctt
ENSDARG00000040295	ENSDART00000058965	Dr.1246.1.S1_at	apoeb	Apolipoprotein Eb precursor (Apo-Eb). [Source:Uniprot/SWISSPROT;Acc:O42364]	-1366	-1348	1	aaagtaattgaccttc
ENSDARG00000040527	ENSDART00000059311	Dr.20722.1.S1_at	NP_956583.1	similar to yolk sac gene 2 [Source:RefSeq_peptide;Acc:NP_956583]	-3077	-3059	-1	aaagtaattgaccttc
ENSDARG00000040528	ENSDART00000059314	Dr.5853.1.A1_at	zgc:77059	hypothetical protein LOC405809 [Source:RefSeq_peptide;Acc:NP_998038]	-4761	-4743	-1	tcatgatcatgaccttc
ENSDARG00000040856	ENSDART00000059886	Dr.4212.1.S1_at	ldha	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A). [Source:Uniprot/SWISSPROT;Acc:Q9PVK5]	-404	-386	-1	atlagcaglattgacctt
ENSDARG00000041639	ENSDART00000044076	Dr.25379.1.S1_at,Dr.23812.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.23812.1.A1_a_t,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1784	-1766	1	agagatcacatgaccacaa
ENSDARG00000041639	ENSDART00000044076	Dr.25379.1.S1_at,Dr.23812.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.23812.1.A1_a_t,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1603	-1585	-1	tcctgacctgaccttc
ENSDARG00000041639	ENSDART00000044076	Dr.25379.1.S1_at,Dr.23812.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.23812.1.A1_a_t,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1784	-1766	1	agagatcacatgaccacaa
ENSDARG00000041639	ENSDART00000044076	Dr.25379.1.S1_at,Dr.23812.1.A1_at,Dr.25379.1.S1_at,Dr.3025.3.S1_at,Dr.23812.1.A1_a_t,Dr.25379.1.S1_at,Dr.3025.3.S1_at			-1603	-1585	-1	tcctgacctgaccttc
ENSDARG00000041639	ENSDART00000061043	Dr.25331.1.S1_at,Dr.25379.1.S1_at,Dr.25331.1.S1_at,Dr.25379.1.S1_at			-4961	-4943	-1	caaagtctctgaccctag
ENSDARG00000041774	ENSDART00000061223	Dr.25009.6.A1_a_at			-1168	-1150	-1	acagtgaactgaccacaa
ENSDARG00000041774	ENSDART00000061223	Dr.25009.6.A1_a_at			-190	-172	-1	aaagccagggtgaccttc
ENSDARG00000042035	ENSDART00000061601	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2474	-2456	-1	aacgcaaaactctgacctt
ENSDARG00000042040	ENSDART00000061613	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2186	-2168	-1	aacgcaaaactctgacctt
ENSDARG00000042046	ENSDART00000061618	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2155	-2137	-1	aacgcaaaactctgacctt
ENSDARG00000042391	ENSDART00000062156	Dr.14748.1.S1_at	zgc:63985	zgc:63985 (zgc:63985), mRNA [Source:RefSeq_dna;Acc:NM_199958]	-4265	-4247	-1	acagtgaactctgacctt
ENSDARG00000043618	ENSDART00000064041	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2063	-2045	-1	ctggagcaacctgacctt
ENSDARG00000043618	ENSDART00000064044	Dr.7236.1.A1_at,Dr.7236.1.A1_at			-2063	-2045	-1	ctggagcaacctgacctt
ENSDARG00000043670	ENSDART00000024462	Dr.1605.1.S1_at						
ENSDARG00000043960	ENSDART00000064542	Dr.6147.1.A1_at	NM_001013259.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (serpina1), mRNA [Source:RefSeq_dna;Acc:NM_001013259]	-688	-670	1	atgatttaacatgacctaa
ENSDARG00000043990	ENSDART00000064579	Dr.7806.1.A1_at	zgc:77150	hypothetical protein LOC406587 [Source:RefSeq_peptide;Acc:NP_999913]	-831	-813	-1	tcacccctctgaccttc
ENSDARG00000044002	ENSDART00000064591	Dr.11609.1.S1_at,Dr.11609.1.S1_at	NP_001002187.1	hypothetical protein LOC431734 [Source:RefSeq_peptide;Acc:NP_001002187]	-4078	-4060	-1	tgccgattctgaccttc
ENSDARG00000044125	ENSDART00000064789	Dr.8723.1.S1_at	zgc:92903	[Source:RefSeq_peptide;Acc:NP_001002461]	-2977	-2959	-1	caagtattttgaccttc
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	Kreisl2	Kreisl2 (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-273	-255	1	taagtcacttgacctgc
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	Kreisl2	Kreisl2 (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-1466	-1448	-1	tcagcaactctgaccac
ENSDARG00000044176	ENSDART00000064858	Dr.23470.1.S1_s_at,Dr.8198.1.A1_at	Kreisl2	Kreisl2 (mouse) maf-related leucine zipper homolog 2.2 [Source:RefSeq_peptide;Acc:NP_571917]	-1466	-1448	-1	tcagcaactctgaccac
ENSDARG00000044613	ENSDART00000014927	Dr.14041.1.S1_at	NP_001005976.1	hypothetical protein LOC449803 [Source:RefSeq_peptide;Acc:NP_001005976]	-4747	-4729	1	aaagcaaaattgaccttc
ENSDARG00000044936	ENSDART00000066051	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-2318	-2300	-1	gcagatctgaccttc
ENSDARG00000044936	ENSDART00000066051	Dr.7110.1.S1_at	zgc:77614	hypothetical protein LOC393868 [Source:RefSeq_peptide;Acc:NP_957188]	-4494	-4476	-1	actggacattgaccagg
ENSDARG00000045230	ENSDART00000066506	Dr.956.1.S1_at	NP_001002695.1	zgc:92631 [Source:RefSeq_peptide;Acc:NP_001002695]	-68	-50	1	tcgttcaattgaccttc