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A high level of liver-specific expression of oncogenic Kras^{V12} drives robust liver tumorigenesis in transgenic zebrafish

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SUMMARY

Human liver cancer is one of the deadliest cancers worldwide, with hepatocellular carcinoma (HCC) being the most common type. Aberrant Ras signaling has been implicated in the development and progression of human HCC, but a complete understanding of the molecular mechanisms of this protein in hepatocarcinogenesis remains elusive. In this study, a stable in vivo liver cancer model using transgenic zebrafish was generated to elucidate Ras-driven tumorigenesis in HCC. Using the liver-specific *fabp10* (fatty acid binding protein 10) promoter, we overexpressed oncogenic *kras*^{V12} specifically in the transgenic zebrafish liver. Only a high level of *kras*^{V12} expression initiated liver tumorigenesis, which progressed from hyperplasia to benign and malignant tumors with activation of the Ras-Raf-MEK-ERK and Wnt–β-catenin pathways. Histological diagnosis of zebrafish tumors identified HCC as the main lesion. The tumors were invasive and transplantable, indicating malignancy of these HCC cells. Oncogenic *kras*^{V12} was also found to trigger p53-dependent senescence as a tumor suppressive barrier in the pre-neoplastic stage. Microarray analysis of zebrafish liver hyperplasia and HCC uncovered the deregulation of several stage-specific and common biological processes and signaling pathways responsible for *kras*^{V12}-driven liver tumorigenesis that recapitulated the molecular hallmarks of human liver cancer. Cross-species comparisons of cancer transcriptomes further defined a HCC-specific gene signature as well as a liver cancer progression gene signature that are evolutionarily conserved between human and zebrafish. Collectively, our study presents a comprehensive portrait of molecular mechanisms during progressive Ras-induced HCC. These observations indicate the validity of our transgenic zebrafish to model human liver cancer, and this model might act as a useful platform for drug screening and identifying new therapeutic targets.

INTRODUCTION

Hepatocellular carcinoma (HCC) ranks as the fifth most prevalent malignancy and the third leading cause of cancer mortalities worldwide (Villanueva et al., 2010). The neoplastic development of HCC is a complex multistage process, with hyperplastic nodules of regenerating hepatocytes in chronic inflammatory liver representing a potential first step towards HCC (Farazi and DePinho, 2006). Despite the availability of several therapies for HCC, understanding of its fundamental processes is rather limited and the ultimate clinical benefit remains negligible.

The Ras proto-oncogenes are central regulators of intracellular signal transduction pathways involved in malignant transformation. Approximately 7% of human liver cancers carry activating mutations in the *KRAS* oncogene, which is higher than the percentage that carry *HRAS* and *NRAS* mutations (Karnoub and Weinberg, 2008). Multiple lines of evidence have revealed the importance of extracellular signal-regulated kinase (ERK), downstream of Ras, during human hepatocarcinogenesis (Schmidt et al., 1997). Indeed, the core protein of hepatitis C virus has been shown to directly activate the Ras-Raf-MEK-ERK pathway in vitro (Hayashi et al., 2000). Although human HCC displays a low incidence of Ras mutations, activation of Ras signaling in the presence of wild-type Ras has been found in all human HCC when compared with non-neoplastic surrounding and normal livers (Calvisi et al., 2006). Many on-going clinical trials on anti-cancer drugs targeting Ras and its downstream signaling cascades in HCC are being conducted and so far the only drug approved for the treatment of advanced HCC is Sorafenib, a multi-target compound that blocks Ras-Raf-MEK-ERK and VEGF pathways (Llovet and Bruix, 2008; Villanueva et al., 2010). This demonstrates Ras signaling as an attractive target for liver cancer therapy.

Animal models have been widely used in biomedical research to understand the pathogenesis of cancer and as in vivo systems for testing new drug candidates. In recent years, several Hras-induced liver neoplasia in murine models have been reported. These models showed that *Hras* mutation solely caused hepatic dysplasia but was insufficient to induce HCC (Harada et al., 2004; Sandgren et al., 1989). Little evidence has determined whether liver tumorigenesis is dependent on the level of Ras activation. Moreover, the nature of Ras-induced mechanisms in liver cancer remains unclear. To date, no mouse models have intentionally utilized *Kras* as a driving

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oncogene to study liver tumorigenesis. Despite having a number of biological similarities to humans, the mouse is costly and unfeasible for large-scale studies (Sharpless and DePinho, 2006). The zebrafish (*Danio rerio*) is increasingly recognized as an alternative vertebrate model to study human diseases (Lieschke and Currie, 2007). It has been shown that histology and gene expression profiles of zebrafish tumors closely resemble those of humans (Lam et al., 2006; Lam and Gong, 2006; Langenau et al., 2007). Many strategies, including chemical carcinogens treatment, xenografts and transgenic approaches, have actively been applied to generate tumor models using zebrafish (Amatruda and Patton, 2008; Mizgirev and Revskoy, 2010; Spitsbergen and Kent, 2003). Over the past few years, the Ras oncogene has been used to drive tumorigenesis in several tissues, including muscle (Langenau et al., 2007), pancreas (Park et al., 2008), skin (Michailidou et al., 2009) and others (Le et al., 2007).

Motivated by these findings, we have generated a stable transgenic zebrafish model for HCC by overexpressing oncogenic *kras*^{V12} under the liver-specific *fabp10* promoter using the *Activator/Dissociation* (*Ac/Ds*) transposon system. We provide evidence that a high level of *kras*^{V12} expression is crucial in driving liver tumorigenesis from hyperplasia to carcinoma by deregulating several stage-specific and common pathways that demonstrate conservation between human and zebrafish liver cancer. Further analyses revealed two important gene signatures for HCC specificity and HCC progression.

RESULTS

Generation of *Tg(fabp10:EGFP-kras^{V12})* transgenic zebrafish

A plasmid construct was made to harbor a cDNA encoding a fusion protein of N-terminal enhanced green fluorescent protein (EGFP) and C-terminal zebrafish Kras^{V12} under control of the liver-specific *fabp10* promoter (Fig. 1A). The construct also contained *Ds* transposon sequences (Emelyanov et al., 2006) and was co-injected with synthesized *Ac* transposase mRNA into one-cell embryos. 1 month later, 25% of F_0 fish with EGFP fluorescence in the liver showed an enlarged abdomen, edema and died within 2 months. By contrast, siblings with no observable EGFP expression in the liver appeared normal and could carry the transgene insertions in germ cells. To obtain stable transgenic line, we crossed these normal F_0 fish with wild-type (WT) zebrafish and screened their offspring for EGFP expression in the liver. Two founders transmitted the transgene to their progenies (F_1).

In the F_1 generation of the two founders [F_1/Line I (F_1/I) and F_1/Line II (F_1/II)], EGFP expression could be detected from 3 days post-fertilization (dpf) (Fig. 1B). Higher intensity of EGFP fluorescence was observed in F_1/I than in F_1/II. As compared with *Tg(fabp10:dsRed)* fry that had normal liver morphology with liver-specific RFP expression (Korzh et al., 2008) (Fig. 1C,D), microscopic examination of the EGFP-positive F_1/I (*n*=196) at 7 dpf revealed that the majority of transgenic larvae had different degrees of liver enlargement (Fig. 1E,F), whereas 7% exhibited a smaller liver (Fig. 1G). In F_1/II (*n*=149), 63% of larvae showed enlarged liver and 3% had a smaller liver, whereas 34% showed no significant abnormalities that correlated with lower EGFP fluorescence. By juvenile to adult stage, fish with enlarged livers displayed abdominal swelling and progressive hemorrhages surrounding the abdominal walls (Fig. 1I,J). The health of fish with smaller livers worsened with time and most died by 1 month post-fertilization (mpf) (Fig. 1K). The effect of oncogenic *kras*^{V12} on liver development is shown in more detail in supplementary material Fig. S1.

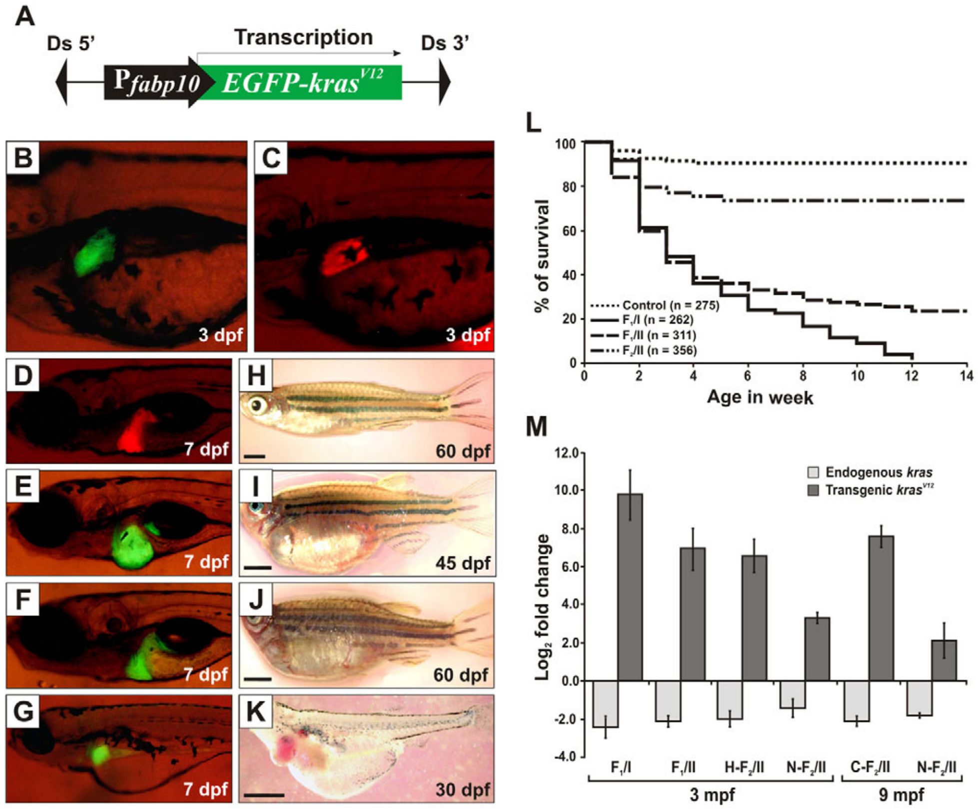


Fig. 1. Generation and characterization of *Tg(fabp10:EGFP-kras^{V12})* transgenic zebrafish. (A) Schematic diagram of the DNA construct used to generate *Tg(fabp10:EGFP-kras^{V12})* transgenic zebrafish. Ds, maize *Ds* transposon sequence. (B-G) Liver-specific expression of EGFP-Kras^{V12} in F_1 transgenic fry (B,E,F,G) as compared with the *Tg(fabp10:dsRFP; elaA:EGFP)* transgenic line expressing RFP in liver (Korzh et al., 2008) as normal control (C,D). (H-K) Gross observation of control fish (H) and F_1 *kras*^{V12} transgenic fish (I-K). Ages of the fish are indicated. Scale bars: 2 mm. (L) Kaplan-Meier survival curves of the *Tg(fabp10:EGFP-kras^{V12})* fish for three groups of heterozygous transgenic zebrafish from F_1/I (*n*=262), F_1/II (*n*=311), F_2/II (*n*=356) and WT siblings as control (*n*=275). (M) Determination of endogenous and transgenic *kras* expression levels by qRT-PCR. Log_2 fold changes for endogenous and transgenic *kras* mRNAs were calculated against an internal housekeeping gene (*β-actin*) using the C_T method. Histological analysis was performed to confirm their neoplastic stages before qRT-PCR (H, hyperplasia; C, carcinoma; N, normal liver). Results are presented as the mean ± s.d. and each bar represents five biological replicates.

A high level of Kras^{V12} expression led to early lethality and induced HCC

The Kaplan-Meier survival curves for heterozygous F_1 offspring (*n*=262, F_1/I; *n*=311, F_1/II) showed ~70% mortality by 30 dpf (Fig. 1L). Most of the fish that died before 30 dpf showed severe liver enlargement. By 90 days, 100% mortality was observed in F_1/I. By contrast, 24% of F_1/II transgenic fish survived by 90 dpf, thus enabling the maintenance of this line. Fish that survived past 90 days exhibited lower EGFP levels in the liver as compared with those that died before 90 days. F_2/II (*n*=356), which was obtained by outcrossing, showed mendelian 1:1 EGFP segregation, indicating a single transgene insertion.

Fig. 2A-C shows normal liver morphology and histology in WT zebrafish. Approximately 58% of F_1/I (*n*=12; all of which died at 65-90 dpf) showed macroscopic liver nodules. Histopathological analysis revealed that these fish had multiple large tumors with microscopic features of HCC (supplementary material Fig. S2). For line II, detailed histological progression of liver tumors was conducted with the F_2 generation. We found no tumor protrusion in the livers of 45 transgenic fish displaying swollen belly euthanized at 3 mpf (Fig. 2D). However, 16 fish (36%) displayed moderate liver hyperplasia (Fig. 2E,F). At the later stages, liver tumors in 12/54 (22%) F_2/II fish dissected at 6 mpf were observed, showing histopathological features of hepatocellular adenoma (Fig. 2G-I). By 9 mpf, malignant HCC appeared in 11/42 (26%) transgenics (Fig. 2J-L). These fish showed hemorrhage and swollen body upon death, with five of them showing invasions of tumor cells into blood vessels and internal organs (Fig. 2M-O).

We employed quantitative real-time PCR (qRT-PCR) to assess the levels of endogenous and transgenic *kras* transcripts in the transgenic livers. Samples were collected from six groups: 3-mpf F_1/I (carcinoma), 3-mpf F_1/II (hyperplasia), 3-mpf N-F_2/II (normal liver), 3-mpf H-F_2/II (hyperplasia), 9-mpf C-F_2/II (normal liver) and 9-mpf N-F_2/II (carcinoma) (Fig. 1M). After normalization against

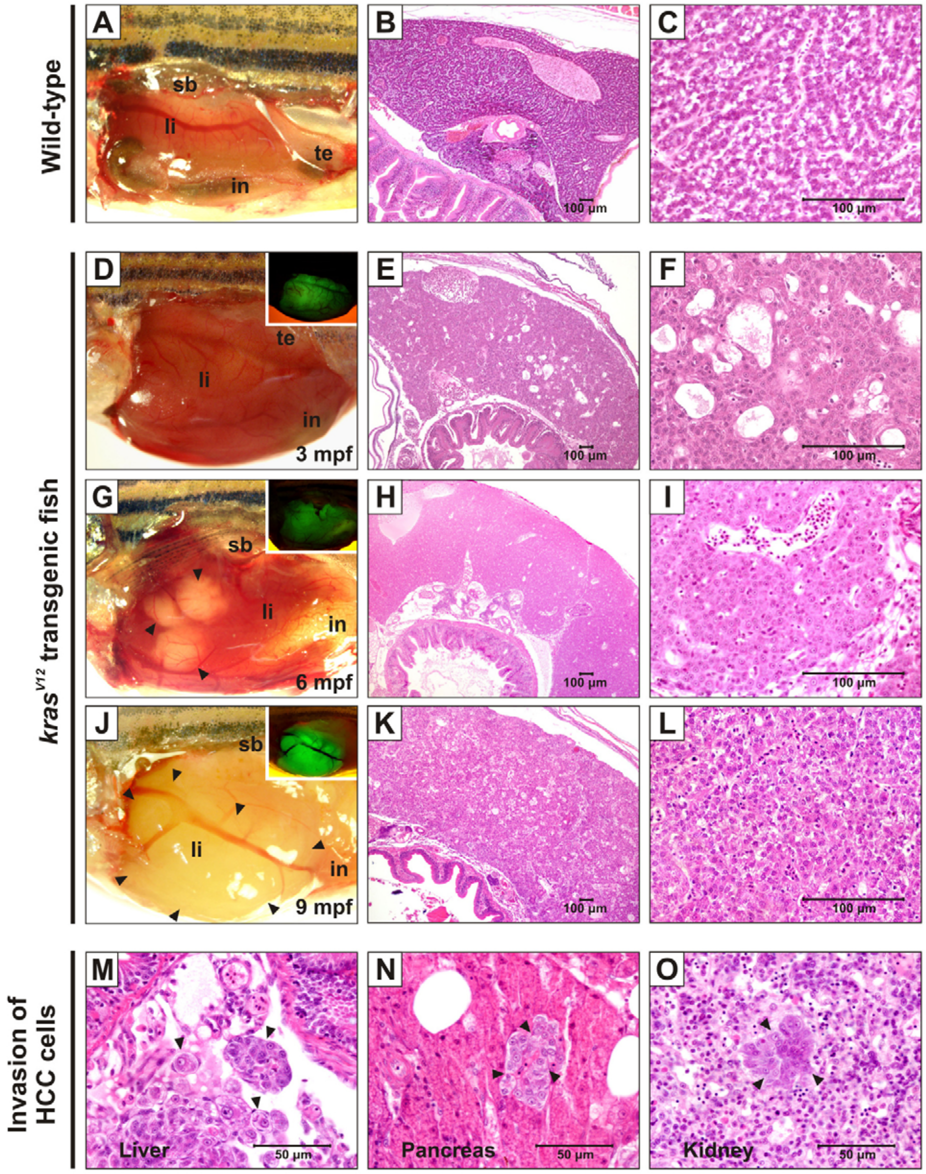


Fig. 2. Liver tumor progression in *kras*^{V12} transgenic zebrafish. Abbreviations: in, intestine; li, liver; sb, swimbladder; te, testis. (A-C) Gross morphology and histology of WT zebrafish showing normal liver and tissue architecture. (D-L) Gross morphology and histology of F_2/II *kras*^{V12} zebrafish. (D,G,I) Brightfield and fluorescence (insets) images displaying the progressive stages of liver tumors at 3, 6 and 9 mpf. Various tumor protrusions are indicated by arrowheads. Corresponding histological sections are shown in the same rows. Livers were observed at 3 mpf (D) and histological appearance revealed multifocal mild-to-moderate cystic degeneration (spongiosis hepatis) and diffused moderate hepatocellular hyperplasia (E,F). Many white nodules were developed in transgenic liver at 6 mpf (G) and their histology indicated hepatocellular adenoma containing vacuolated clear cells with increased cytoplasmic glycogen (H,I). Malignant tumors were visibly observed at around 9 mpf (J) and histological analysis confirmed that the tumor was HCC grade II-III (K,L). (M-O) Invasion of HCC cells (indicated by arrowheads) into blood vessels (M) and adjacent tissues, namely pancreas (N) and kidney (O).

β-actin, the expression levels of endogenous *kras* were consistent among these six groups, and were at similar levels as in matched WT controls (data not shown). By contrast, transgenic *kras*^{V12} was overexpressed in these groups. F_1/I had the highest level of *kras*^{V12} expression with $\log_2$ fold change over *β-actin* levels (9.85±2.69), as compared with the change over *β-actin* in F_1/II (6.95±2.24). In F_2/II, the levels of *kras*^{V12} transcript compared with *β-actin* transcript in transgenic fish undergoing tumorigenesis from hyperplasia (6.58±1.81) to carcinoma (7.60±1.21) were higher than their age-matched (3 and 9 mpf, respectively) transgenic siblings without liver lesions (3.26±0.65 and 2.12±1.88, respectively). These data demonstrated the threshold level of *kras*^{V12} to drive liver tumorigenesis because we consistently observed that only a high level of *kras*^{V12} expression leads to liver tumors from hyperplasia to carcinoma.

Transplantability of *kras*^{V12} liver tumors in WT recipients

Dissociated HCC cells pooled from four F_2/II transgenic zebrafish were injected intraperitoneally into 25 sublethally γ-irradiated WT adult zebrafish (~1×10^6 cells per recipient). At 7 days post-injection (dpi), we confirmed that all of the recipients exhibited EGFP fluorescence at the site of injection (Fig. 3A,D). Fluorescence intensified by 14 dpi and cells seemed to spread to adjacent tissues (Fig. 3B). At 60 dpi, the tumor cells distributed along the abdominal cavity and showed strong EGFP fluorescence at the abdominal region in seven of the recipients (Fig. 3E). By this time, the outgrowth of the tumor mass penetrated through the peritoneal cavity and/or abdominal wall (Fig. 3C,F), indicating capability of the *kras*^{V12} tumors for propagation and invasion in a new host.

Differential activation of ERK, JNK and p38 MAPK pathways during *kras*^{V12} liver tumorigenesis

The ERK pathway, one of the most-established mammalian mitogen-activated protein kinase (MAPK) pathways, is commonly activated downstream of Ras. To determine whether the ERK pathway is activated by overexpression of *kras*^{V12}, we conducted qRT-PCR to analyze the expression of various genes associated with this pathway.

Gene expression of the Raf kinases *braf* and *raf1*, and other upstream activators of the ERK pathway, namely *map2k1*, *map2k2*, *map4k2l* and *map4k5*, as well as the downstream *mapk1* and *mapk3*, were all upregulated in both hyperplastic liver (HL) and HCC, with higher expression levels in HCC than in HL (Fig. 4A). We also measured the transcript levels of other subfamilies of MAPKs. The level of *mapk8* (JNK1) was found to increase in both stages. Although an increase in *mapk12* (p38γ) and *mapk14a* (p38α) transcripts were observed in HL, their expressions became downregulated in HCC. A similar trend was observed in the transcript level of p38-regulated/activated protein kinase (PRAK; *mapkapk5*). The activation pattern of these three major MAPKs during liver tumorigenesis in our transgenic zebrafish model is consistent with those in human liver cancer and other HCC models (Fig. 4B).

We then determined the protein expression level of Kras in WT normal liver (N_{Wt}) and in F_2/II *kras*^{V12} transgenic zebrafish that had various liver morphologies, including normal liver (N_{Tg}), HL and HCC (Fig. 4C). Western blotting using anti-K-Ras (F234) revealed that total Kras was minimal in N_{Wt} but increasingly higher in N_{Tg}, HL and HCC. Immunoblotting with anti-K-Ras-2B (C19) confirmed that no Kras^{V12} protein could be detected in N_{Wt}. In N_{Tg}, Kras^{V12} protein was present at a much lower level as compared with HL and HCC. Because Ras signals through MEK and ERK proteins via phosphorylation, we showed that the levels of phospho-MEK1/2 and phospho-ERK1/2 proteins in N_{Tg} were similar to that in N_{Wt} but were visibly higher in HL and HCC. Indeed, immunohistochemistry of liver tumor sections showed apparently enhanced cytoplasmic and nuclear staining of phospho-MEK1/2 and phospho-ERK1/2 in HL, and this staining was intensified in HCC (Fig. 4D).

Activation of the Wnt–β-catenin pathway during *kras*^{V12} liver tumorigenesis

Of several signaling pathways frequently deregulated in HCC, the canonical Wnt pathway, with β-catenin as a crucial downstream component, is an important contributor to tumorigenesis (Farazi and DePinho, 2006). E-cadherin, which is a binding partner of β-catenin, also plays a critical role in liver tumorigenesis as a tumor and invasion suppressor (Wei et al., 2002). To verify activation of the Wnt–β-catenin pathway, we employed immunohistochemistry to examine the expression of β-catenin, E-cadherin and cellular proliferation marker Ki67 in *kras*^{V12} transgenic liver. β-catenin localized in the cell membrane in the WT liver (Fig. 5A). By

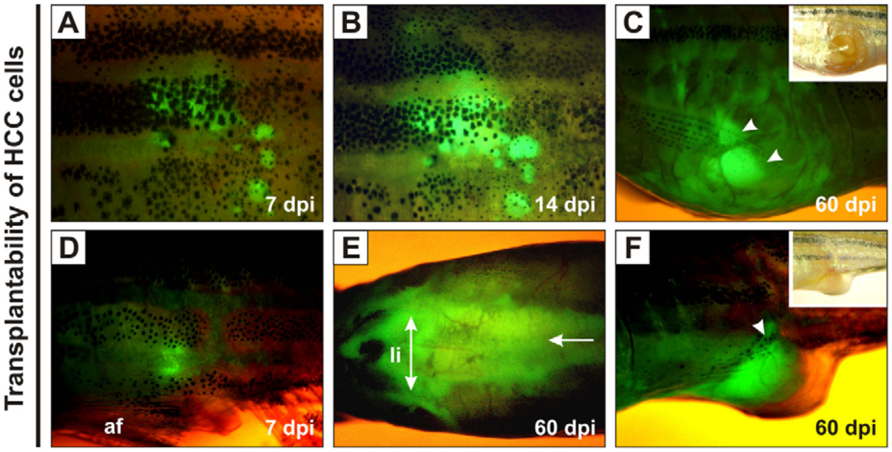
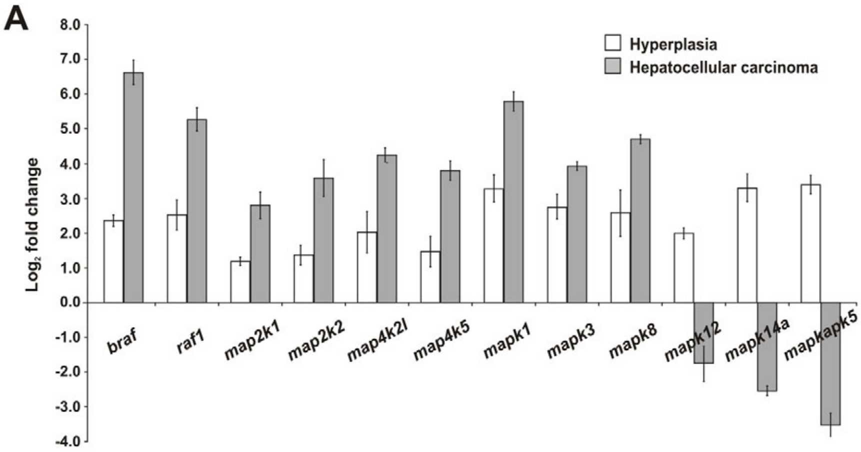


Fig. 3. Growth of transplanted *kras*^{V12} liver tumors in WT recipients. (A-F) EGFP-positive HCC cells were transplanted intraperitoneally into irradiated recipients. (A,D) EGFP fluorescence was observed near the sites of injection at 7 dpi. af, anal fin. (B) Transplanted cells proliferated by 14 dpi. (E) Extensive infiltration of tumor cells along the peritoneal cavity (arrow), especially in the region surrounding the liver (li; double-headed arrow), was observed at 60 dpi. (C,F) The outgrowth of EGFP-positive tumor mass (arrowheads) penetrated into the abdominal wall and/or peritoneal cavity at 60 dpi.



B

Gene		Protein	Activation status		
			kras^{V12} transgenic fish		Human & experimental HCCs
Zebrafish	Human		Hyperplasia	Carcinoma	
mapk3 *mapk1*	MAPK3 MAPK1	ERK1/p42 MAPK ERK2/p44 MAPK	Up	Up	Up [a]
mapk8	MAPK8	JNK1	Up	Up	Up [b]
mapk14a *mapk12*	MAPK14A MAPK12	p38α MAPK p38γ MAPK	Up	Down	Down [c]

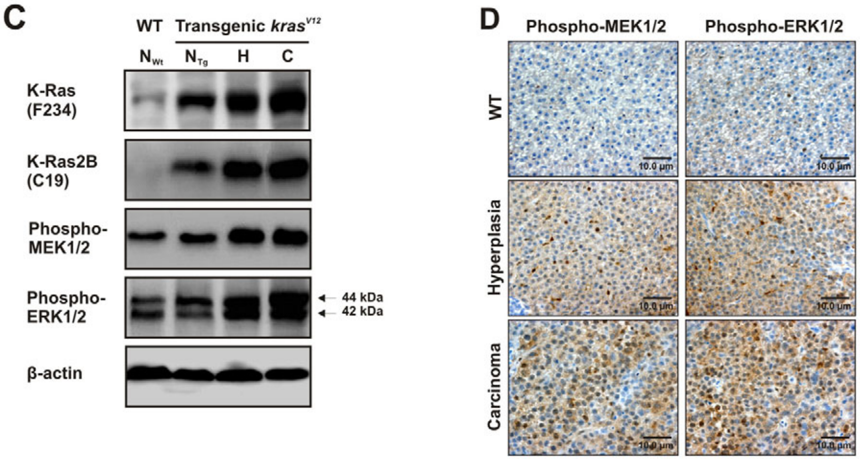


Fig. 4. Hyperactivation of the MAPK signaling pathway in *kras*^{V12} transgenic zebrafish. (A) Determination of expression levels of various kinase genes by qRT-PCR in liver hyperplasia (3 mpf) and carcinoma (9 mpf). The expression levels of these genes in each WT and transgenic liver sample were first measured and normalized with the expression level of *β-actin* (*n*=5 each). The $\log_2$ fold changes in expression in the transgenic samples as compared with matched WT sample are presented. (B) Comparison of MAPK family expression during liver tumorigenesis in *kras*^{V12} transgenic zebrafish, human liver cancer and other experimental models of HCC. [a](Schmidt et al., 1997); [b](Wurmbach et al., 2007; Chang et al., 2009); [c](Wurmbach et al., 2007). (C) Western blots of total proteins from WT normal liver (N$_{Wt}$) and *kras*^{V12} transgenic liver showing normal liver morphology (N$_{Tg}$), hyperplastic liver (H) or HCC (C) to detect total Kras (F234), Kras2B (C19) isoform, phospho-MEK1/2 and phospho-ERK1/2 (also known as phospho-p44/42 MAPK). Arrows: double bands of phospho-ERK1/2 (44 kDa and 42 kDa). β-actin, internal control for equal loading. (D) Immunohistochemical analysis of paraffin-embedded liver sections from WT (control; top row), 3-mpf transgenic (hyperplasia; middle row) and 9-mpf transgenic (carcinoma; bottom row) fish. Sections were stained with antibodies against phospho-MEK1/2 or phospho-ERK1/2. Scale bars: 10 μm.

contrast, mixed nuclear and membranous staining patterns of β-catenin were found in HL with a distinct nuclear pattern in HCC. Moreover, HCC showed no staining of E-cadherin, whereas HL retained similar E-cadherin staining in the cell membrane as in WT liver (Fig. 5B). There was little or no signal of Ki67 expression in WT liver, whereas nuclear staining of Ki67 was observed in HL and more so in HCC (Fig. 5C). These data indicated activation of the Wnt–β-catenin pathway as tumorigenesis progressed from HL to HCC in *kras*^{V12} transgenic fish.

Acceleration of liver tumor onset by loss of p53-mediated senescence in *kras*^{v12} transgenic zebrafish

Excessive activation of Ras signaling can induce DNA damage response (DDR) by DNA replication stress due to aberrant cell proliferation that could prompt the activation of p53-induced senescence as a barrier to tumor progression induced by Ras (DiMicco et al., 2006; Vousden and Prives, 2009). We performed the senescence-associated β-galactosidase (SA-βgal) assay on liver cryosections. Intense SA-βgal signals were observed only in HL at 3 mpf, whereas little signal was detected in HCC at 9 mpf (Fig. 6A). These observations suggested that the number of cells undergoing senescence increased in the pre-neoplastic lesions but subsided during progression to the carcinoma stage. Western blotting showed that endogenous p53 increased in HL but decreased in HCC (Fig. 6B). Importantly, p21 Waf1/Cip1, a direct transcriptional target of p53 whose activation leads to senescence, was elevated in HL but decreased in HCC. The level of phosphorylated MDM2 protein, the negative regulator of p53, was found to increase in both stages (Fig. 6B). Collectively, these observations verified the response of p53 in mediating senescence in HL, resulting in latent tumor development.

To find out whether loss of p53 could promote tumorigenesis, the homozygous *tp53*^{M214K} (*tp53*$^{-/-}$) mutant line (Berghmans et al., 2005) was crossed with *kras*^{V12} F_2/II to obtain heterozygous *tp53*$^{+/-}$ fish expressing *kras*^{V12} in the liver. This family was again crossed with the *tp53*$^{-/-}$ line to obtain mixed offspring with *tp53*$^{+/-}$ and

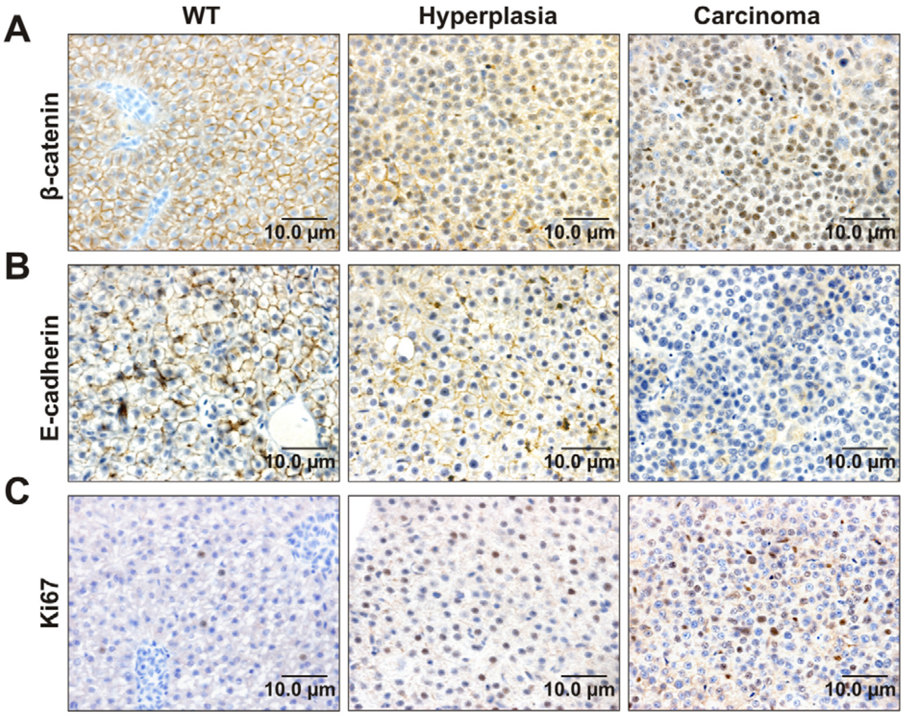


Fig. 5. Activation of the Wnt–β-catenin pathway during *kras*^{V12} liver tumorigenesis. Representative immunohistochemical liver sections from WT zebrafish as the control and *kras*^{V12} transgenic fish with liver hyperplasia and carcinoma are shown. (A) Immunohistochemistry for β-catenin showing an increasing nuclear localization of β-catenin during HCC progression. (B) Immunohistochemistry for E-cadherin showing loss of membranous E-cadherin expression during tumor growth. (C) Immunohistochemistry for Ki67 showing a high expression level of Ki67 in cell nuclei, which increased from hyperplasia to carcinoma.

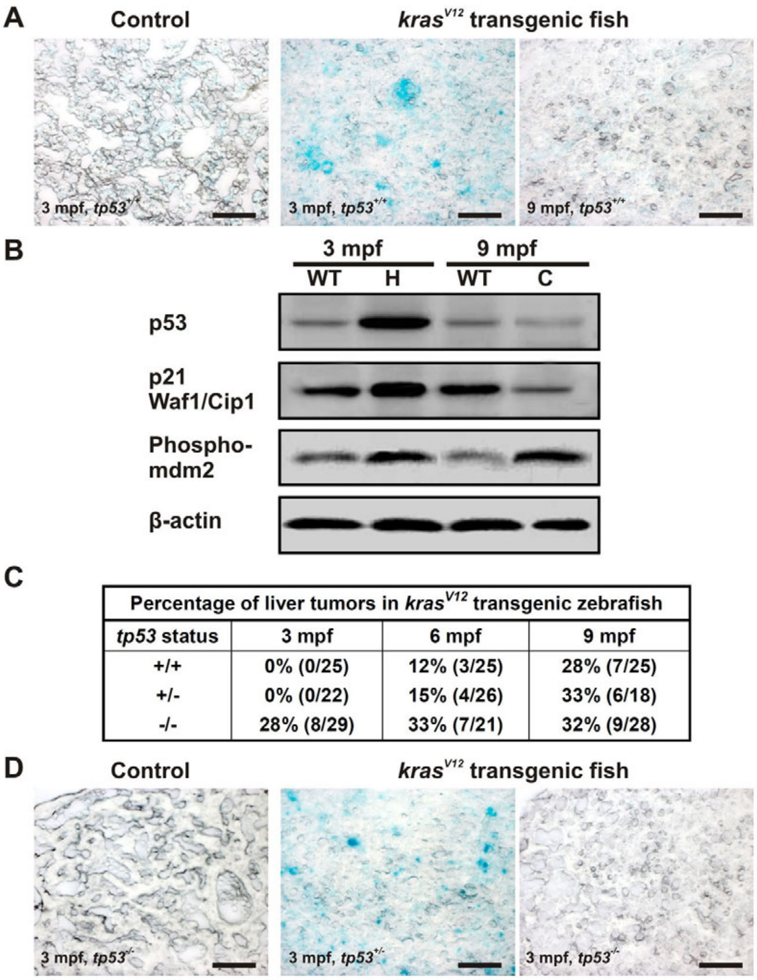
tp53$^{-/-}$ background. This cohort was randomly divided and maintained in three tanks. Each tank was sacrificed at 3, 6 and 9 mpf to screen for the presence of liver tumors (Fig. 6C). Liver morphology revealed that, at 3 mpf, 28% of the *tp53*$^{-/-}$ zebrafish showed tumor protrusions, with 63% of these having confirmed HCC. By contrast, no tumors were observed in the *tp53*$^{+/-}$ and *tp53*$^{+/+}$ siblings at 3 mpf. Notably, SA-βgal assay showed no senescence in transgenic *tp53*$^{-/-}$ fish, whereas strong signals were still detected in the transgenic fish with *tp53*$^{+/-}$ background (Fig. 6D). At 6 mpf, pre-neoplastic tumors were observed in the transgenic fish liver with *tp53*$^{+/+}$ and *tp53*$^{+/-}$ backgrounds (12% and 15%, respectively). At 9 mpf, liver tumor incidences in the *kras*^{V12} transgenics became similar, regardless of *tp53* status. No significant differences in the survival rates were noticed between these cohorts before 90 dpf. Thus, loss of p53 accelerated tumor onset but not the overall tumor incidence after 9 mpf.

Transcriptomic analyses of *kras*^{V12} liver tumorigenesis

Oligonucleotide microarray was conducted to investigate gene expression profiles in HL and HCC as outlined in supplementary material Fig. S3. By applying the selection criteria of ≥1.5 $\log_2$ fold change and $P \leq 0.01$ false discovery rate (FDR) adjustment, 1417 and 1564 differentially expressed genes having human homologs were obtained for HL and HCC, respectively (supplementary material Table S1). Because a biological process often involves a group of genes acting in concert, GSEA (Gene Set Enrichment Analysis) was used to compare predefined human gene sets from the Gene Ontology (GO) and KEGG of the Molecular Signature Database to gain biological insight into *kras*^{V12}-driven liver tumorigenesis. Overall, GSEA identified 42 and 151 significant human gene sets for zebrafish HL and HCC, respectively (supplementary material Table S2). Strikingly, activation of key signaling pathways was found in HL (p53) and HCC (TLR-NFκB, JAK-STAT, insulin-IGF and TGFβ), as well as in both HL and HCC (Raf-MEK-ERK, PI3K-AKT, Wnt–β-catenin, VEGF and complement cascade). GSEA also determined the genes within each significantly enriched human set that contributed most to the enrichment score in zebrafish HL and HCC. A total of 261 genes in the 42 hyperplasia gene sets and 598 genes in the 151 HCC gene sets were obtained (supplementary material Table S2). We then compared these genes with the differentially expressed zebrafish genes identified in supplementary material Table S1 to limit the results to only the significantly up- or downregulated genes. These genes are termed zebrafish enriched genes. Hence, 173 up- and 61 downregulated zebrafish enriched genes were found in HL, whereas there were 398 up- and 99 downregulated zebrafish enriched genes in HCC. By overlapping HL and HCC genes, we identified 128, 106 and 391 HL-specific, overlapping and HCC-specific enriched genes, respectively (supplementary material Table S3).

Identification of a HCC-specific signature and a liver cancer progression signature

To explore whether the zebrafish stage-specific and overlapping enriched genes in HL and HCC possess Ras signature, transcriptomic profiles of human mammary epithelial cells (HMECs) infected with activated oncogenes such as *β-catenin*, *E2F3*, *Myc*, *Ras* and *Src* (Bild et al., 2006) were used for cross-species GSEA. The upregulated zebrafish enriched genes were associated with signatures linked to oncogenic Ras but not the other oncogenes (Fig. 7A). Next, we questioned whether these zebrafish genes were conserved throughout human HCC progression, exclusively at a particular stage (cirrhosis, dysplasia and carcinoma) (Wurmbach et al., 2007) or involved in other human tumor types. Transcriptomic profiles from different



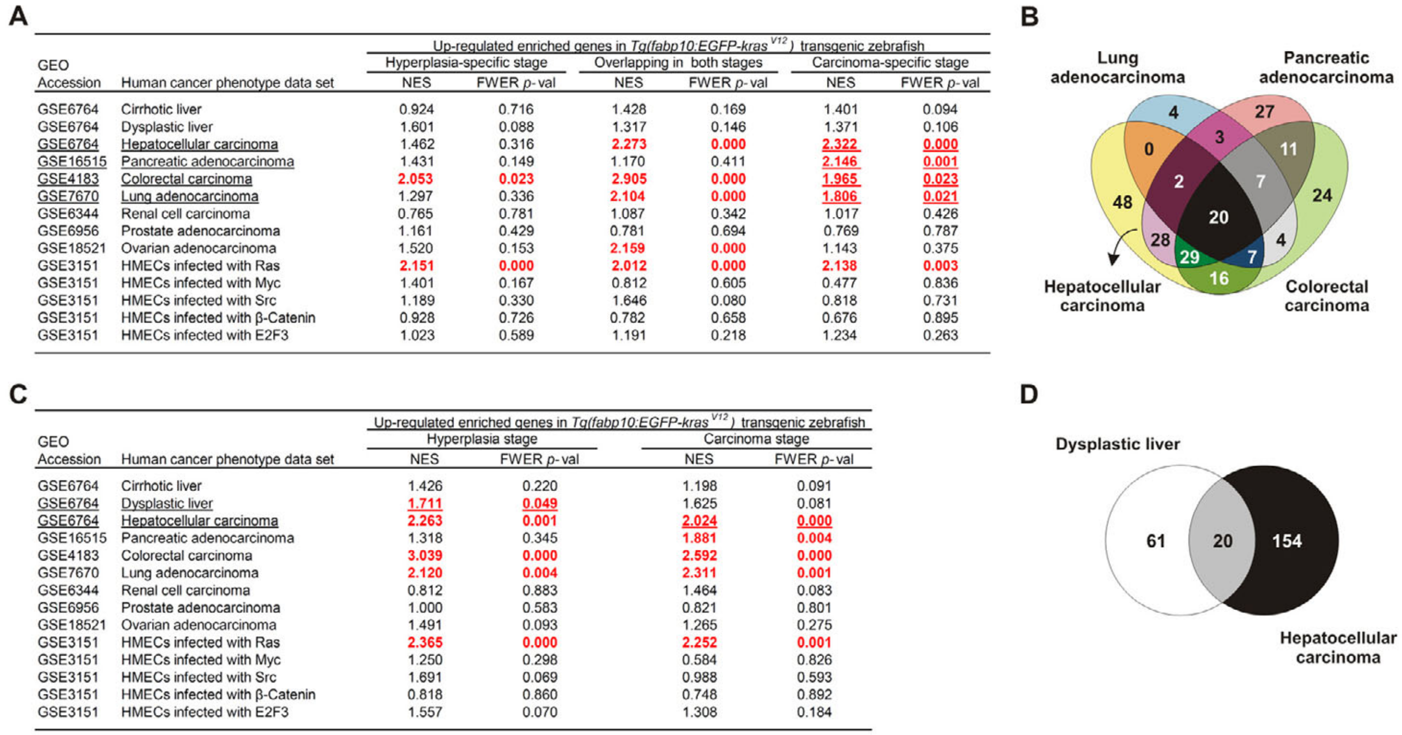
Percentage of liver tumors in $kras^{V12}$ transgenic zebrafish			
tp53 status	3 mpf	6 mpf	9 mpf
+/+	0% (0/25)	12% (3/25)	28% (7/25)
+/-	0% (0/22)	15% (4/26)	33% (6/18)
-/-	28% (8/29)	33% (7/21)	32% (9/28)

Fig. 6. $Kras^{V12}$-induced p53-dependent senescence in the pre-neoplastic liver. (A) Oncogenic $Kras^{V12}$-induced senescence at an early stage of liver tumor development. SA-βgal staining was performed on liver cryosections from 3- and 9-mpf $kras^{V12}$ transgenic and WT fish ($tp53^{+/+}$). (B) Western blots of total proteins from liver hyperplasia (H), carcinoma (C) and age-matched WT liver to evaluate the levels of tumor suppressor p53 together with its target, p21 Waf1/Cip1, and its regulator, phospho-MDM2, during tumorigenesis. β-actin, internal control for equal loading. (C) Acceleration of liver tumor onset in homozygous $tp53^{M214K}$ mutant transgenic fish. Percentages of tumors observed from $kras^{V12}$ transgenic fish with different p53 backgrounds at different time points are shown. (D) Suppression of senescence induced by oncogenic $kras^{V12}$ in $tp53^{-/-}$ background. SA-βgal staining was performed with four biological replicates in each group. Scale bars: 50 μm.

human cancers were used for the comparison. We found that the upregulated zebrafish HCC-specific enriched genes were associated with human liver, pancreatic, colorectal and lung tumors (Fig. 7A; supplementary material Table S4). Consistent with this, KRAS mutations are most frequently found in human tumors of pancreas, colon, lung and ovary (Karnoub and Weinberg, 2008). The fact that the upregulated zebrafish HCC-specific enriched genes matched to Ras signature might explain their association with these human tumor types. Next, we defined a HCC-specific gene signature (48 genes) from a subset of upregulated HCC-specific zebrafish enriched genes that were associated only with human HCC but not with the other tumor types (Fig. 7B; supplementary material Table S5).

Because each stage of $kras^{V12}$ liver tumorigenesis contains both stage-specific and overlapping enriched genes, cross-species analysis was again performed to assess whether HL zebrafish enriched genes, consisting of HL-specific and overlapping genes, showed any similarity with genes expressed in early human liver tumorigenesis. Indeed, the upregulated HL enriched genes were significantly associated with human dysplastic liver (Fig. 7C; supplementary material Table S6). Similarly, cross-species analysis of HCC-enriched genes revealed that these genes were significantly associated with human HCC (Fig. 7C; supplementary material Table S7). By overlapping the upregulated HL and HCC enriched genes shown in supplementary material Tables S6 and S7, we identified a liver cancer progression gene signature, which comprises 20 genes that remained upregulated throughout human and zebrafish HCC progression (Fig. 7D; supplementary material Table S8). By contrast, the zebrafish downregulated enriched genes were not related to any tumor types and oncogene status (data not shown). Similar observations were previously reported in several $Kras^{D12}$ transgenic models (Langenau et al., 2007; Sweet-Cordero et al., 2005), suggesting that the genes that are downregulated by Ras might be different between species and that Ras mostly upregulates gene expression.

To further validate the differentially expressed genes detected by microarray analyses, qRT-PCR was performed to confirm expression of 15 major genes in several individual lesions from each tumorigenesis stage and these tested genes belonged to several important signaling pathways and processes, including AKT (*akt2*), ERK (*mapk1*, *mapk3*, *mapk8*, *stmn1*), STAT (*stat3*), p53 (*mdm2*, *tp53*), TGFβ (*tgfb1*), WNT (*nlk*), angiogenesis (*angpt1*), cell cycle (*ccnb1, nbn, nfya*) and ribosome (*rpl19*). As shown in supplementary material Table S9, the qRT-PCR results closely paralleled the microarray data, thus confirming that liver lesions that looked similar at the histological level were also similar with respect to gene expression profiles.



GEO Accession	Human cancer phenotype data set	Up-regulated enriched genes in *Tg(fabp10:EGFP-kras*^{V12}*)* transgenic zebrafish: Hyperplasia-specific stage NES	FWER *p*-val	Overlapping in both stages NES	FWER *p*-val	Carcinoma-specific stage NES	FWER *p*-val
GSE6764	Cirrhotic liver	0.924	0.716	1.428	0.169	1.401	0.094
GSE6764	Dysplastic liver	1.601	0.088	1.317	0.146	1.371	0.106
GSE6764	Hepatocellular carcinoma	1.462	0.316	**2.273**	**0.000**	**2.322**	**0.000**
GSE16515	Pancreatic adenocarcinoma	1.431	0.149	1.170	0.411	**2.146**	**0.001**
GSE4183	Colorectal carcinoma	**2.053**	**0.023**	**2.905**	**0.000**	**1.965**	**0.023**
GSE7670	Lung adenocarcinoma	1.297	0.336	**2.104**	**0.000**	**1.806**	**0.021**
GSE6344	Renal cell carcinoma	0.765	0.781	1.087	0.342	1.017	0.426
GSE6956	Prostate adenocarcinoma	1.161	0.429	0.781	0.694	0.769	0.787
GSE18521	Ovarian adenocarcinoma	1.520	0.153	**2.159**	**0.000**	1.143	0.375
GSE3151	HMECs infected with Ras	**2.151**	**0.000**	**2.012**	**0.000**	**2.138**	**0.003**
GSE3151	HMECs infected with Myc	1.401	0.167	0.812	0.605	0.477	0.836
GSE3151	HMECs infected with Src	1.189	0.330	1.646	0.080	0.818	0.731
GSE3151	HMECs infected with β-Catenin	0.928	0.726	0.782	0.658	0.676	0.895
GSE3151	HMECs infected with E2F3	1.023	0.589	1.191	0.218	1.234	0.263

GEO Accession	Human cancer phenotype data set	Up-regulated enriched genes in *Tg(fabp10:EGFP-kras*^{V12}*)* transgenic zebrafish: Hyperplasia stage NES	FWER *p*-val	Carcinoma stage NES	FWER *p*-val
GSE6764	Cirrhotic liver	1.426	0.220	1.198	0.091
GSE6764	Dysplastic liver	**1.711**	**0.049**	1.625	0.081
GSE6764	Hepatocellular carcinoma	**2.263**	**0.001**	**2.024**	**0.000**
GSE16515	Pancreatic adenocarcinoma	1.318	0.345	**1.881**	**0.004**
GSE4183	Colorectal carcinoma	**3.039**	**0.000**	**2.592**	**0.000**
GSE7670	Lung adenocarcinoma	**2.120**	**0.004**	**2.311**	**0.001**
GSE6344	Renal cell carcinoma	0.812	0.883	1.464	0.083
GSE6956	Prostate adenocarcinoma	1.000	0.583	0.821	0.801
GSE18521	Ovarian adenocarcinoma	1.491	0.093	1.265	0.275
GSE3151	HMECs infected with Ras	**2.365**	**0.000**	**2.252**	**0.001**
GSE3151	HMECs infected with Myc	1.250	0.298	0.584	0.826
GSE3151	HMECs infected with Src	1.691	0.069	0.988	0.593
GSE3151	HMECs infected with β-Catenin	0.818	0.860	0.748	0.892
GSE3151	HMECs infected with E2F3	1.557	0.070	1.308	0.184

Fig. 7. GSEA identification of conserved gene signatures common between zebrafish and human HCC. (A) Cross-species GSEA comparisons of different human cancer transcriptomic profiles with zebrafish upregulated hyperplasia-specific, carcinoma-specific and overlapping enriched genes. Human cancer data sets were collected from the Gene Expression Omnibus (GEO) database and their access numbers are indicated. Positive normalized enrichment score (NES) indicated enrichment of the zebrafish enriched genes in the human tumor state. Results shown in red were statistically significant with family-wise error rate (FWER) *P*-value ≤0.05. Significantly matched human data sets are underlined and used for gene signature identification by overlapping the zebrafish upregulated carcinoma-specific enriched genes that were found associated with each human data set. (B) Venn diagram illustrating the identification of 48 genes specific to HCC in both human and zebrafish. The 48 genes are presented in supplementary material Table S5. Lists of zebrafish enriched genes in each significant human cancer data set used to identify HCC gene signature are shown in supplementary material Table S4. (C) The stage-specific and overlapping enriched genes in zebrafish hyperplasia and carcinoma used in cross-species GSEA comparisons with different human cancer transcriptomic profiles. (D) Venn diagram identification of 20 genes upregulated during tumor progression from hyperplasia/dysplasia to carcinoma in both zebrafish and human liver cancer. These genes are presented in supplementary material Table S8, representing the liver cancer progression gene signature. Lists of zebrafish enriched genes in each significant human cancer data set used to identify the gene signature are shown in supplementary material Tables S6 and S7.

DISCUSSION

A *kras*^{V12} transgenic zebrafish model for investigation of liver tumorigenesis

We have generated the first in vivo model of liver tumorigenesis driven by transgenic overexpression of oncogenic *kras*^{V12} in zebrafish. We provided evidence that the expression level of *kras*^{V12} is a crucial determinant of liver tumorigenesis through hyperactivation of the Ras-Raf-MEK-ERK pathway, because only the transgenic fish that exhibited higher *kras*^{V12} levels showed activation of ERK signaling and progression of liver tumor from hyperplasia to benign and invasive HCC. Although JNK and p38 MAPK were activated coordinately in HL, they were differently regulated in HCC, with the downregulation of p38 MAPK and upregulation of JNK. This is reminiscent of an earlier report that showed that hepatocyte-specific deletion of p38α promotes liver carcinogenesis with correlated activation of JNK (Hui et al., 2007). Furthermore, p38/PRAK could activate p53 in response to oncogenic Ras to mediate cellular senescence (Sun et al., 2007). Besides MAPKs, overexpression of Ras can initiate multiple signal transduction pathways implicated in tumorigenesis, as summarized in Fig. 8. We observed consistent activation of PI3K-AKT, VEGF and Wnt–β-catenin pathways as well as the complement cascade in zebrafish HL and HCC, underscoring the importance of these signaling pathways during liver tumorigenesis. It is also well known that complements act as pro-inflammatory factors as part of immune surveillance. Markiewski et al. suggested that a tumor-induced complement system could enhance tumor growth by modulation of the anti-cancer immune response (Markiewski et al., 2008). As such, our model confirms the role of complements in HCC development.

Analysis of stage-specific liver lesions revealed the activation of DNA replication and damage elicited by excessive cell proliferation in HL only, which might result in oncogene-induced senescence (OIS). Replicative DNA damage triggered senescence through the p53 pathway. The increase of p53 then imparts its tumor suppressive effects through the induction of p21 to stall the cell cycle (Vousden and Prives, 2009). Nuclear transcription factor Y subunit α (*nfya*), previously proposed by Collado et al. as a marker that is specifically associated to OIS (Collado et al., 2005), was extremely up-regulated in *kras*^{V12} HL. Our list of enriched genes corresponding to HL as identified by GSEA (supplementary

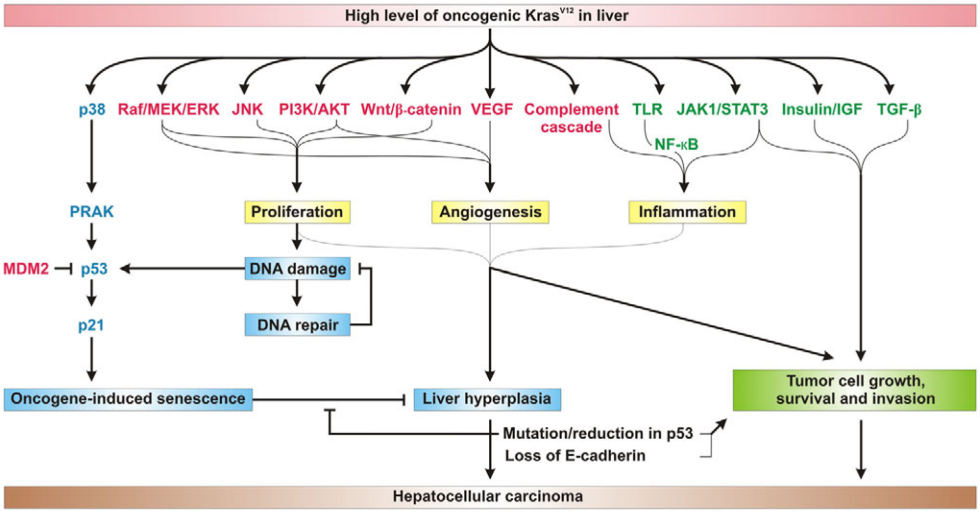


Fig. 8. Proposed mechanism of Ras-induced liver tumorigenesis in the transgenic zebrafish model. A high level of oncogenic Kras^{V12} in the zebrafish liver leads to the activation of several key signaling pathways implicated in liver tumorigenesis, showing signaling pathways significantly activated in HL (blue), in both HL and HCC (red) and in HCC (green), as determined by qRT-PCR, microarray and GSEA, and western blot and/or immunohistochemistry analyses in the present study. During early tumorigenesis, the Raf-MEK-ERK, JNK, PI3K-AKT and Wnt–β-catenin pathways drive proliferation, whereas Raf-MEK-ERK, PI3K-AKT and VEGF signaling induce angiogenesis and the complement cascade induces inflammation. Collectively, crosstalk among these signaling activates the three major processes, proliferation, angiogenesis and inflammation, leading to liver hyperplasia. Another mechanism upon overexpression of Kras^{V12} was the deregulation of p38 MAPK signaling. In hyperplasia, p38 MAPK was upregulated, leading to the activation of PRAK and subsequently p53, which then targets the downstream p21 to mediate cellular senescence. In addition, aberrant cell proliferation could also induce DNA damage, which might further prompt the upregulation of p53. Moreover, DNA damage triggers DNA repair, enabling hyperplastic cells to overcome such damage. Thus, oncogene-induced senescence acts as a p53-dependent tumor-suppressive mechanism in the pre-neoplastic stage to guard against tumor progression. Downregulation of p38 MAPK, together with a persistently high level of MDM2 that might eventually result in a reduction in p53, could also serve as alternative mechanisms for liver tumorigenesis to bypass senescence. In neoplastic stage, activation of JAK-STAT and TLR-NFκB pathways enhance the inflammatory process. Importantly, the consistent activation of proliferation, angiogenesis and inflammation with their involved pathways, together with activation of the JAK-STAT, insulin-IGF and TGFβ pathways, are essential for contribution to tumor cell growth, survival and invasion in HCC. Loss of the key tumor suppressors p53 and E-cadherin further characterizes malignant/invasive HCC in our model.

material Table S3) might thus yield new useful markers for the detection of senescence. Deleterious *TP53* mutations enhanced hepatocarcinogenesis, whereas restoration of *TP53* induced senescence that led to HCC regression (Takai et al., 2009; Xue et al., 2007). We have shown that *tp53* null mutation can accelerate HCC onset marked by the abrogation of OIS in *kras*^{V12} zebrafish. However, tumor incidence did not increase in *tp53*$^{-/-}$/*kras*^{V12} zebrafish. These observations support previous finding that *TP53* mutation is a late event in human HCC (Martin and Dufour, 2008). Moreover, HCC is rarely found in *tp53*$^{-/-}$ zebrafish and *Tp53* knockout mice alone (Berghmans et al., 2005; Donehower et al., 1992; Parant et al., 2010). Even in the absence of *tp53*, low expression of *kras*^{V12} seemed insufficient to initiate liver tumorigenesis (data not shown). This proposes that low levels of Ras require multiple mutations for neoplastic initiation in the liver.

In the sequence of events leading to HCC, we also observed the upregulation of two important transcription factors linking inflammation and cancer, namely NFκB and STAT3 (Mantovani et al., 2008). Both TLR, which is an essential upstream regulator of NFκB, and the JAK-STAT pathway were significantly activated only in *kras*^{V12} HCC. The synergistic activities of NFκB and STAT3, together with the complements, might play an important role in inflammation-mediated tumor growth. Consequently, inhibition of inflammation should be considered as a valuable strategy for HCC prevention. Furthermore, the emergence of JAK-STAT, IGF and TGFβ pathways in *kras*^{V12} HCC, and loss of E-cadherin, contributed to tumor cell growth, survival and invasion. This finding highlighted the significance of these pathways in HCC progression, which distinguishes them from the pathways that are activated in the early stage of *kras*^{V12} tumorigenesis.

Conserved gene expression signatures underlying liver tumorigenesis in humans and *kras*^{V12} transgenic zebrafish

Microarray analysis and GSEA uncovered two gene signatures, one being a HCC-specific signature and the other associated with a liver cancer progression signature. Both are upregulated in human and zebrafish liver cancer, underscoring the molecular conservation between species. Several genes in our gene signatures have been reported as prognostic markers for human HCC; for example, *ANGPT1* and *STMN1* in the HCC-specific signature, and *APOE* and *CCNB1* in the HCC progression signature (Torimura et al., 2004; Wong et al., 2008; Wurmbach et al., 2007; Yokoyama et al., 2006). Interestingly, a large family of ribosomal proteins contributed to the bulk of the HCC-specific signature. Previously, Lee et al. demonstrated a consistent elevation of ribosomal proteins in human and mouse liver cancers (Lee et al., 2004). Our study highlights the possibility that ribosomal proteins might serve as evolutionarily conserved markers in HCC. By contrast, several components of ERK signaling (*MAPK1*, *MAPK3*, *MAPKAPK2*, *MDM2*, *PRKCB1* and *YWHAB*), PI3K-AKT signaling (*PI3KCA*), Wnt signaling (*NLK*) and tumor invasion and/or metastasis (*DERL1*, *MMP14*, *RUVBL2* *SRC* and *THY1*) made up the majority of genes in the liver cancer progression signature. These genes might therefore likewise play an important role in HCC progression and could serve as markers of early liver tumorigenesis. Notably, the liver cancer progression signature comprises a group of genes participating in the cell cycle and in DNA damage and repair (*MCM5*, *NBN*, *RRM2* and *TK1*) that have not been previously reported in human HCC. The most prominent gene is *nibrin* (*NBN* or *NBS1*), a member of the DNA double-strand-break repair complex. *NBS1* was initially known as a putative tumor suppressor protecting genome stability. However, recent findings have suggested that NBS1 is also an oncoprotein because it is overexpressed in several human cancers and leads to cell proliferation and transformation (Chen et al., 2005; Hematulin et al., 2008). Some of the most critical regulated genes in these signatures have been confirmed by qRT-PCR from several individual lesions of transgenics (supplementary material Table S9). Further investigations of these genes should provide insights into liver tumorigenesis and probably provide new therapeutic targets for HCC.

In summary, our study presents the overall molecular mechanisms depicting Kras^{V12} liver tumorigenesis, which recapitulates many of the defined features of human liver cancer. This transgenic line might thus provide a novel model for understanding the multistep nature of HCC progression as well as crosstalk between Ras and different levels of other signaling pathways, which could enable the development of successful synergistic therapies against human liver cancer. Because HCC latency is relatively long and the penetrance of HCC phenotype in *kras*^{V12} transgenics is less than 30% even in 9-month-old fish, this transgenic line might not be practical for drug screening but it could be used for enhancer screens to identify mutations that accelerate the onset of Ras-induced HCC. The data obtained from this study is also a necessary and indispensable step towards establishment of novel and more efficient models, such as inducible transgenic models of liver cancer. Furthermore, the fluorescence-tagged liver tumors would enable live imaging of tumor progression and tumor-host interaction during transplantation; these are particularly suitable to the small and relatively transparent zebrafish system. Because early Ras activation has been shown to cause premature lethality and act in a dose-dependent manner to trigger cancer development, work is underway to apply the inducible gene expression systems (Emelyanov and Parinov, 2008) to control the induction time and expression level of transgene, which will then enhance the attributes of using transgenic zebrafish as a new platform for anti-cancer drug screening to target currently undruggable pathways or several other simultaneous pathways in HCC development.

METHODS

Fish maintenance

Zebrafish were maintained according to established protocols (Westerfield, 2000). All experiments involving animals were approved by the Institutional Animal Care and Use Committee (IACUC) of the National University of Singapore.

Generation of transgenic zebrafish using the *Ac/Ds* transposon system

Zebrafish *krasB* was amplified using reverse transcription PCR with the two primers kras1 (5′-GGAGCCAAGCGGCCGCATGACCGAATATAAGCTTGTG-3′) and kras2 (5′-GGAAGGAAGCGGCCGCTCACATTAATGCACATTTTGTTTTG-3′) containing the *Not*I restriction endonuclease excised sequence (underlined). The primers were designed based on the zgc:85725 cDNA sequence (GenBank BC078646; GI:50925043) (Strausberg et al., 2002). The amplified product was digested with *Not*I and cloned into the *Not*I site of the ET construct (Parinov et al., 2004) carrying a *TAA* stop codon after EGFP to terminate the translation of Kras. To produce the mutated (oncogenic) form of Kras^{V12} fused with EGFP, the *TAA* stop codon was removed, and glycine in position 12 of Kras^{V12} was replaced with valine using the QuikChange site-directed mutagenesis kit following manufacturer's instructions (Stratagene) and primers Forward: 5′-CTGTACAAGTTAAGCGGCGGCATGACCGAATATAAGCTTGTGGTCGTGGGAGCTGTAGGCG-3′ and Reverse: 5′-CGCCTACAGCTCCCACGACCACAAGCTTATATTCGGTCATGCCGCCGCTTAACTTGTACAG-3′. A 2.8-kb promoter of the *fabp10* gene (Her et al., 2003) was digested and subcloned into a 0.6-kb *miniDs* construct pMDS6 (Emelyanov et al., 2006) between the *Not*I and *Sac*II sites. The produced construct was then inserted with the fused *EGFP-kras*^{V12} sequence between the *Not*I and *Sac*II sites. As a result, the product transcribed from the *fabp10* promoter is a fusion protein of EGFP and Kras^{V12}. Transgenic zebrafish were generated using the *Ac/Ds* transposon system as described previously (Emelyanov et al., 2006).

RNA isolation and qRT-PCR

Total RNA was isolated using TriZOL reagent (Invitrogen) and reverse transcribed using the SuperScript II cDNA Synthesis Kit (Invitrogen). qRT-PCR was performed with cDNA as the template using the iQ Single-Color Real-Time PCR Detection System (Bio-Rad Laboratories). Primer sequences used for amplification are as follows: *β-actin* forward: 5′-CCACCTTAAATGGCCTAGCA-3′, reverse: 5′-CATTGTGAGGAGGGCAAAGT-3′; *kras (endogenous)* forward: 5′-GTCCAGACAGGCGGTATTGT-3′, reverse: 5′-GACGCAGTTGAGGGAGAAAG-3′; *kras*^{V12} forward: 5′-CGACCACTACCAGCAGAACA-3′, reverse: 5′-GCTTTTGCCTACGCCTACAG-3′; *akt2* forward: 5′-GAACACCTTCATGATCCGCT-3′, reverse: 5′-CTCTGGAGCTGGATTTGGAC-3′; *angpt1* forward: 5′-AACCCGAAGCCGACTTGTCC-3′, reverse: 5′-CGTCGGTCAGTTTTCGCGTC-3′; *braf* forward: 5′-AGCTTATGTCAGGGGCTTTG-3′, reverse: 5′-AGAGAGCGTGCCAATAACTC-3′; *ccnb1* forward: 5′-GGACTCAGACCAAGGGCCGC-3′, reverse: 5′-GCACAGCCGGAGGTCTCCAT-3′; *raf1* forward: 5′-ATGCCATACGTGTTCACAGC-3′, reverse: 5′-TCCCTTTGTGTACGGTTCCA-3′; *map2k1* forward: 5′-AAAGAGCAGACCTCAAGCAG-3′, reverse: 5′-TTCAGGAGGCAGTAGTTTGC-3′; *map2k2* forward: 5′-TGCCTCATAAAGAACCCTGC-3′, reverse: 5′-AGGCTTACAAGCATACAGGC-3′; *map4k2l* forward: 5′-TGATCTGGAGGACAAGGACC-3′, reverse: 5′-AGAAAGAGCTGCGTCTCTGC-3′; *map4k5* forward: 5′-AGGACAGTGTTCTGGCATTC-3′, reverse: 5′-ATACAAAGGCTCCAGCAGTG-3′; *mapk1* forward: 5′-GGATGATTTGCCCAAAGAGA-3′, reverse: 5′-GTCAGGTGAACGTTGAGGGT-3′;

mapk3 forward: 5′-GAGTCGGTGAAGGGACAAAA-3′, reverse: 5′-TGATCCCGATGATGTTCTCA-3′; *mapk8* forward: 5′-CTGCTGCAGATGACCATCCTTT-3′, reverse: 5′-ACAGAGCATATTTGAGGGGGCT-3′; *mapk12* forward: 5′-GTGAAATGACGGGCTACGTT-3′, reverse: 5′-AGACTGTAGCTTCGCTGTGA-3′; *mapk14a* forward: 5′-CCCGTGCAGTATCAGAACTT-3′, reverse: 5′-CAGACTTGTGGCAGGTGTAA-3′; *mapkapk5* forward: 5′-GACACAAGAACGATTTGCCC-3′, reverse: 5′-CTGGCTGATTCTGTGGAACA-3′; *mdm2* forward: 5′-AACTCCCAACACAACCTTCG-3′, reverse: 5′-GGGTCTCTTCCTGACTGCTG-3′; *nfya* forward: 5′-CGCGCCAAACTGGAGGCTGA-3′, reverse: 5′-TTTACCCCAGAGGCGGGGCA-3′; *nlk1* forward: 5′-GTGCCAAGTCCTGCTGAAAT-3′, reverse: 5′-AGTCGATTTGTGGAGGTTGG-3′; *rpl19* forward: 5′-CTTGCGCTGTGGCAAGAAGAA-3′, reverse: 5′-TTCTCGGGCATACGTGCGTT-3′; *stat3* forward: 5′-CTGAAACCTTGAGCGACACA-3′, reverse: 5′-AGCAGGTTGTGGAAGACCAG-3′; *stmn1* forward: 5′-CTCTGAAGGGCATACTTGGACCG-3′, reverse: 5′-CTGCTTCATGAGACTTGCGTCTC-3′; *tgfb1* forward: 5′-ATGATAGAATGGCTGCAGGG-3′, reverse: 5′-TGCAAGAGAGTTGCCATTTG-3′; *tp53* forward: 5′-GATGGTGAAGGACGAAGGAA-3′, reverse: 5′-ACAAAGGTCCCAGTGGAGTG-3′; *zgc:194152* forward: 5′-CTTCCTCTACCCGCATCGTCC-3′, reverse: 5′-AACTGGCACTGCTTTCACGC-3′. Reactions were run in triplicate for each sample. Gene expression levels in each WT or transgenic liver sample were normalized with the expression level of *β-actin* as the internal control. The $\log_2$ fold changes in expression in the transgenic sample as compared with the WT sample were then calculated using the C_T method (Schmittgen and Livak, 2008) following the formula: $\log_2$ fold change=–ΔΔCT=–[(C_T gene of interest–C_T *β-actin*)transgenic sample–(C_T gene of interest–C_T *β-actin*)WT sample]. For quantification of endogenous *kras* and transgenic *kras*^{V12} transcript levels, the $\log_2$ fold changes in expression were calculated using the formula: $\log_2$ fold change=–ΔCT=–[(C_T gene of interest–C_T *β-actin*)transgenic sample] (Schmittgen and Livak, 2008).

Gross morphology and histological analyses

Transgenic zebrafish were dissected to expose the abdominal area and then observed under the Nikon SMZ1600 stereomicroscope for gross liver morphology. Fish were then fixed in either Bouin's fixative (750 ml picric acid, 250 ml 37-40% formalin and 50 ml acetic acid) or 10% neutral buffered formalin (Sigma) for at least 2 days, dehydrated through a series of graded ethanol solutions, washed in clearing agent (Fisher Scientific) and embedded in paraffin blocks. Liver sections were stained with H&E for morphology analysis. Criteria for histological examination of zebrafish liver tumors were assessed as described previously (Lam et al., 2006).

Liver tumor transplantation

Adult WT zebrafish were γ-irradiated with 25 Grays and recovered for 2 days before transplantation. Liver tumors were aseptically dissected from 1-year-old *kras*^{V12} transgenic donors, washed twice with PBS and gently homogenized. Tumor cells were suspended in Hanks' balanced salt solution to a concentration of 1×10^6 cells per 10 μl. 10 μl of cell suspension was injected intraperitoneally using a 25-μl Hamilton syringe into immobilized previously irradiated recipients. Mock recipients were injected with 10 μl of Hanks' balanced salt solution.

Western blot analysis

Total proteins were isolated from samples using lysis buffer (10 mM Tris-HCl, pH 7.4, and 1% SDS) containing Complete Protease Inhibitor Cocktail (Roche). Protein concentrations were determined using the Bradford dye following the manufacturer's instructions (Bio-Rad Laboratories). 20 μg of proteins were loaded and separated in a 10% SDS-PAGE and transferred to PVDF membrane. Immunodetections were performed using the following antibodies: K-Ras (F234), which detects ubiquitously expressed K-Ras (Santa Cruz Biotechnology); K-Ras-2B (C19), which detects the C-terminus of the K-Ras-2B splice variant (Santa Cruz Biotechnology); anti-phospho-MEK1/2 (Ser217/221; Cell Signaling Technology); anti-phospho-ERK1/2 (p44/42 MAPK; Thr202/Tyr204; Cell Signaling Technology); anti-p53 (Cell Signaling Technology); anti-phospho-MDM2 (Cell Signaling Technology); anti-p21 Waf1/Cip1 (Santa Cruz Biotechnology); and anti-β-actin (Sigma). All antibodies were used at a working dilution of 1:1000. Signals were detected using chemiluminescence (Pierce Biotechnology) and exposure to X-ray film (Kodak).

Immunohistochemistry analysis

Immunostaining was performed on 5-μm sections of formalin-fixed and paraffin-embedded tissues. Sections were first boiled for antigen retrieval in 10 mM citrate buffer pH 6.0 for 10 minutes, treated with 3% hydrogen peroxide for 10 minutes at room temperature, and blocked using the SuperBlock Blocking Buffer (Pierce Biotechnology) for 30 minutes. Sections were then incubated in a humidified chamber at 4°C overnight with antibodies against phospho-MEK1/2 (Ser217/221; Cell Signaling Technology), phospho-ERK1/2 (Thr202/Tyr204; Cell Signaling Technology), β-catenin (Abcam), E-cadherin (Abcam) or Ki67 (Sigma) at working dilutions of 1:50 to 1:100. Next, sections were washed with PBS and incubated in either anti-mouse or anti-rabbit secondary antibody for 1 hour at room temperature. Signals indicating peroxidase activity were visualized using the Metal Enhanced DAB Substrate Kit (Pierce Biotechnology) following the manufacturer's instructions. The sections were then counterstained with hematoxylin, dehydrated and permanently mounted for microscopic examination.

Senescence-associated β-galactosidase assay

Liver cryosections of WT and transgenic zebrafish were prepared by fixing the tissues in 4% paraformaldehyde overnight at 4°C. After fixation, tissues were washed several times with PBS before incubating in 30% sucrose at 4°C overnight. Samples were then embedded and frozen at –20°C for 30 minutes, and sectioned into 10-μm thickness using Leica cryostat microtome. Sections were dried at 46°C for 2 hours and continued with the SA-βgal assay. SA-βgal expression was determined using the staining kit supplied by Cell Signaling Technology.

Zebrafish oligonucleotide microarray analyses

Microarray construction and hybridization were performed as described previously (Lam et al., 2006; Lam et al., 2009a; Lam et al., 2009b). Detailed workflow for microarray data and GSEA is presented in supplementary material Fig. S3.

TRANSLATIONAL IMPACT

Clinical issue

Human liver cancer, the most common of which is hepatocellular carcinoma (HCC), is a major cause of cancer death worldwide. Human HCCs have a complex molecular pathology, with heterogeneous morphology and genetics, but recent work has indicated that ubiquitous activation of the Ras-ERK pathway is present in nearly all HCCs. Thus, targeting Ras signaling has emerged as a potential strategy to treat advanced HCC. However, the mechanisms of Ras-induced liver tumorigenesis remain poorly understood, and in vivo models that enable investigations of the central role of Ras in liver cancer are lacking.

Results

In this paper, the authors establish a model of liver cancer by generating a transgenic zebrafish line, *Tg(fabp10:EGFP-kras*^{V12}*)*, that uses a strong hepatocyte-specific promoter to target oncogenic *kras*^{V12} expression to the liver. Fusing *kras*^{V12} to EGFP allows visualization of tumor development in zebrafish from early stages. The authors show that liver tumorigenesis in this system is driven only by a high level of *kras*^{V12} expression through activation of the ERK pathway, as well as by loss of E-cadherin expression and nuclear accumulation of β-catenin (indicating activation of canonical Wnt signaling). *kras*^{V12} transgenic tumors show progressive features from hyperplasia to invasive HCC, which is accompanied by a loss of the p53-dependent senescence response; the absence of p53 accelerates tumor onset. Microarrays and gene set enrichment analyses (GSEAs) of hyperplastic lesions and HCCs delineate several other pathways that are enriched during Ras-driven liver tumorigenesis. Finally, cross-species comparisons identify two conserved gene signatures accounting for HCC specificity and HCC progression in both zebrafish and human liver cancer.

Implications and future directions

This *kras*^{V12} transgenic zebrafish is the first in vivo model in which it is possible to address molecular mechanisms underlying Ras-driven liver tumorigenesis that recapitulates typical hallmarks of human HCC. The high incidence and consistent pattern of cancer in this model, coupled with low maintenance costs of zebrafish, allow systematic study of liver cancer progression from hyperplasia to carcinoma stages. Importantly, the two HCC gene signatures identified in this study might be useful as prognostic markers and/or potential therapeutic targets in human HCC. In addition, using this model to better understand crosstalk between Ras and other signaling pathways might contribute to the development of successful synergistic therapies for human liver cancer. This model provides a new platform that can be used for high-throughput screening of anti-cancer drugs to treat human liver cancer in the future.

Statistical analysis

Kaplan-Meier curves were computed using the survival distribution of each test group. The log-rank test was used to compare significant differences in death rates between the two transgenic lines. Statistical analysis was performed by a Student's t-test for direct comparisons between WT and transgenic groups. Based on Bonferroni's correction for multiple comparisons, P-values of <0.01 were considered statistically significant.

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COMPETING INTERESTS

The authors declare that they do not have any competing or financial interests.

AUTHOR CONTRIBUTIONS

A.T.N., A.E., S.P. and Z.G. conceived and designed the study. A.T.N., A.E. and C.H.V.K. performed the experiments. A.T.N., A.E., C.H.V.K., J.M.S., S.H.L., S.P. and Z.G. analyzed and interpreted the data. J.M.S., S.H.L. and S.M. supported techniques. A.T.N., A.E., C.H.V.K., S.P. and Z.G. wrote the manuscript. A.E., S.P. and Z.G. supervised the study.

SUPPLEMENTARY MATERIAL

Supplementary material for this article is available at http://dmm.biologists.org/lookup/suppl/doi:10.1242/dmm.007831/-/DC1

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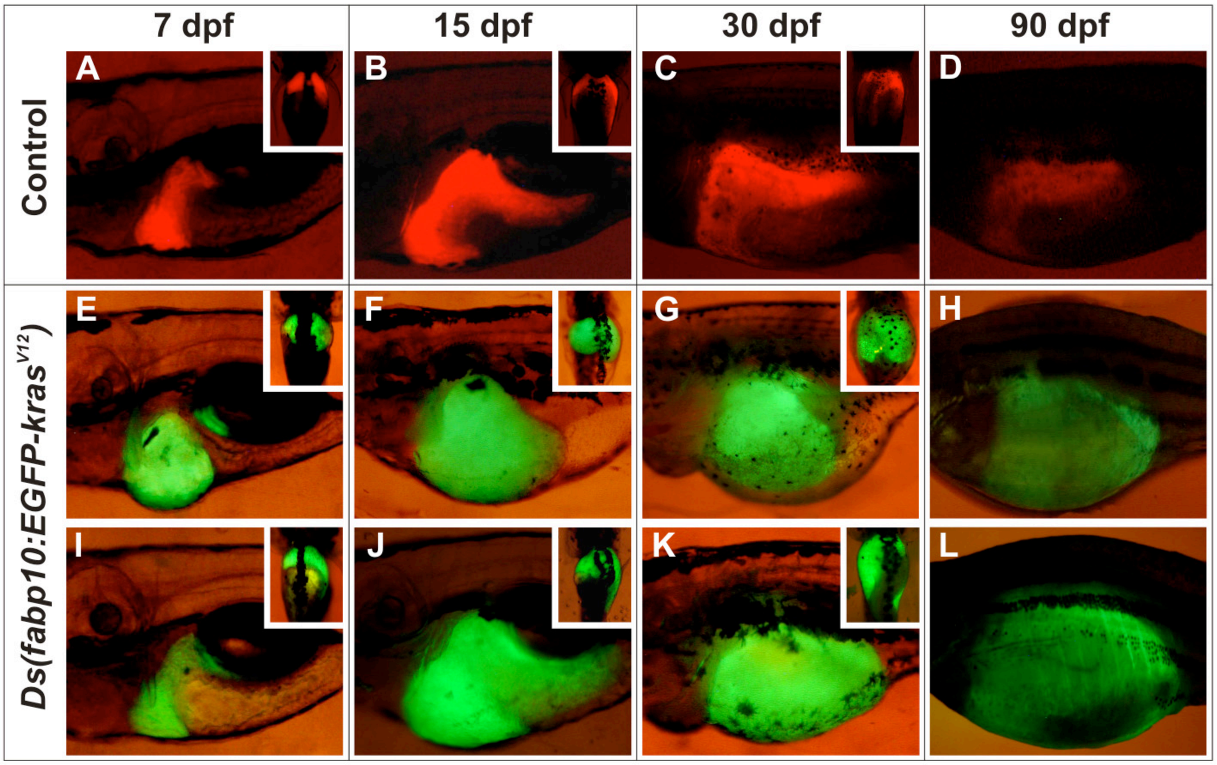

Fig. S1. Morphological development of liver in transgenic fish expressing *EGFP-kras*^{V12}. Comparison of liver morphogenesis between LiPan control [*Tg(fabp10:dsRFP; elaA:EGFP)*] zebrafish (A-D) and two representative cases of abnormal liver morphology distinguished by different degrees of liver enlargement/hyperplasia at the early stages (E-H and I-L) observed in the F_1/I *Tg(fabp10:EGFP-kras*^{V12}*)* zebrafish. Note that there were no obvious differences between these two cases at the later stages. (A,E,I) 7 dpf (day post-fertilization); (B,F,J) 15 dpf; (C,G,K) 30 dpf; (D,H,L) 90 dpf. All big images are lateral view whereas all insets are ventral view.

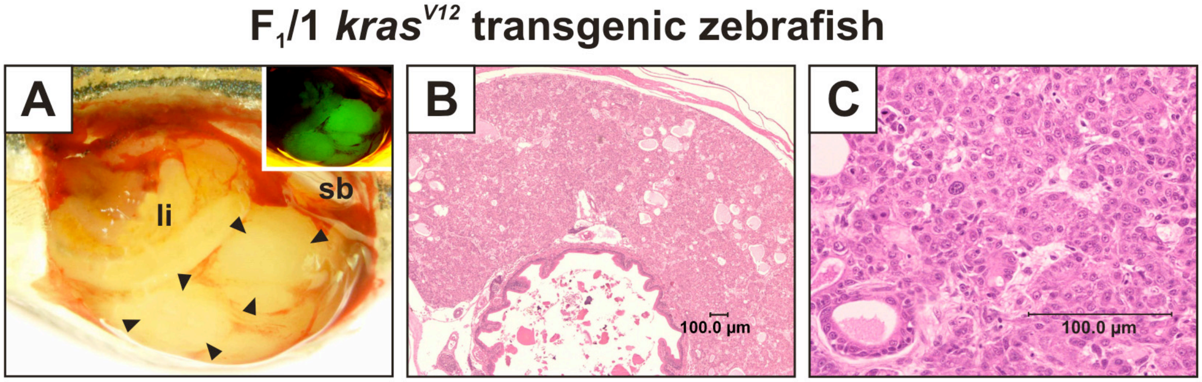

Fig. S2. Morphological and histological examination of liver tumor of F$_1$/I transgenic fish. (A) Liver from transgenic male fish of line F$_1$/I (84 dpf) displaying macroscopic tanned nodules. (B,C) Histological observations confirmed mixed carcinoma with hepatocellular component grade III.

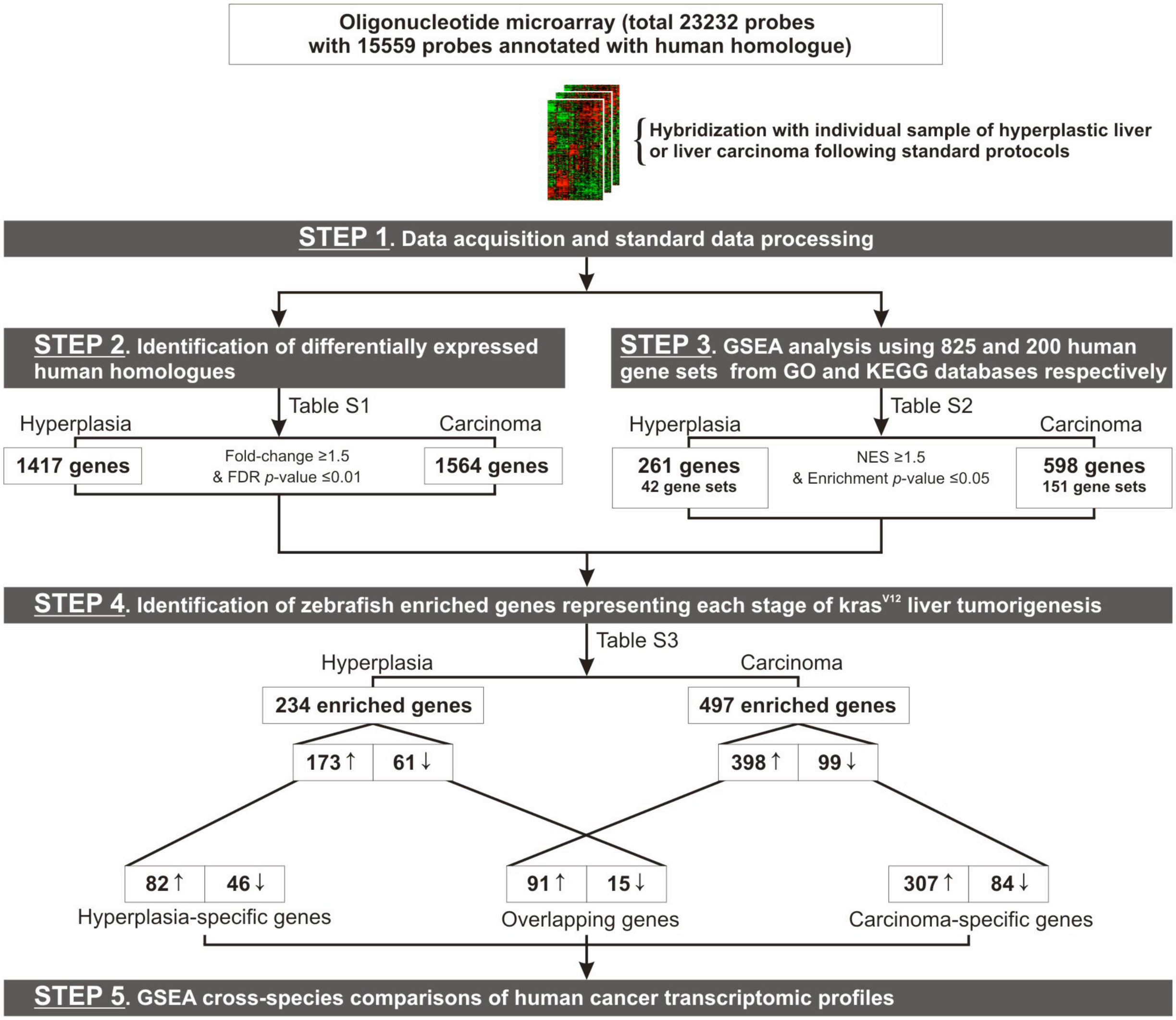

Fig. S3. Flowchart of microarray data analysis. Step 1: Data acquisition and standard data processing. Arrays were scanned for fluorescence signal detection using the GenePix 4000B Axon scanner (Molecular Devices, CA) and the generated images were analyzed using GenePix Pro® 4.0 image analysis software (Molecular Devices) to measure fluorescence signal intensities. All the arrays gave a mean signal-to-background ratio of more than 5 and >95% of the probes gave measurable signals. Microarray raw data were extracted and formatted to conform to the MIAME (Minimal Information About a Microarray Experiment) standards, and further subjected to Lowess normalization and transformation to $\log_2$ ratio using the R system software (http://www.R-project.org) (Lam et al., 2009a). Differences between the $\log_2$ ratios of transgenic and normal livers were calculated to obtain the fold-change values which indicate up- or down-regulation in gene expression. Statistical significance of the expression level was performed using Student's t-test to yield the p-value of each gene. The resulting p-values were then adjusted for Benjamini and Hochberg false discovery rate (FDR) to minimize the number of false positive genes that could be identified by chance. **Step 2:** Identification of differentially-expressed genes having human homologues. Zebrafish genes having human homologues and differentially expressed in hyperplasia and carcinoma were filtered using the selection criteria of fold-change ≥1.5 and FDR-adjusted p-value ≤0.01 as statistical cut-offs (supplementary material Table S1). **Step 3:** GSEA analysis using 825 and 200 predefined human gene sets from the GO and KEGG databases respectively. GSEA version 2.0.1 from the Broad Institute was used with predefined Gene Ontology (GO) and KEGG gene sets retrieved from the GSEA Molecular Signature Database (MSigDB v2.5). Detailed description of each gene set can be found at the MSigDB website (www.broad.mit.edu/gsea/msigdb/index.jsp). GSEA analysis was completed using phenotypic permutation with a weighted enrichment statistic and the Ratio_of_Classes metric to rank genes. One thousand permutations of the data were completed to obtain a false discovery rate (FDR) q-value (Subramanian et al., 2005). Human gene sets with normalized enrichment score (NES) ≥1.5, nominal (NOM) enrichment p-value ≤0.05 and FDR q-value ≤0.25 were considered significant (supplementary material Table S2). The genes within each significant human gene set that contributed maximally to the GSEA score in zebrafish hyperplasia and HCC were also identified. **Step 4:** Identification of zebrafish enriched genes representing each stage of $kras^{V12}$ liver tumorigenesis. The zebrafish differentially-expressed genes having human homologues which satisfied the statistical cut-offs in Step 2 and the genes obtained by GSEA analysis in Step 3 were then compared to identify the genes present in both steps. These genes were termed as zebrafish enriched genes. The enriched genes corresponding to each stage of kras^{V12} liver tumorigenesis were then overlapped to obtain the hyperplasia-specific enriched genes, carcinoma-specific enriched genes as well as overlapping enriched genes between two stages (supplementary material Table S3). Arrows indicate up- and down-regulated genes. **Step 5:** GSEA cross-species comparisons of human cancer transcriptomic profiles. Raw data files of different published human cancer data sets were obtained from the Gene Expression Omnibus (GEO) database. All of the retrieved data sets were generated using the Affymetrix GeneChip® platform. Probes with *P*-call values of <80% were then discarded across all samples to minimize variations from biological samples and identify only reliably measured genes. The lists of up- and down-regulated zebrafish enriched genes from Step 4 were used for GSEA cross-species comparison with these human cancer data sets. Statistical significance of the cross-species comparison was determined by the selection criteria of false discovery rate q-value (FDR q-value) ≤0.05 and family-wise error rate p-value (FWER p-value) ≤0.05.

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Table S1. Differentially expressed genes having human homologues in $kras^{V12}$ transgenic zebrafish in liver hyperplasia and carcinoma (log$_2$ fold-change ≥1.5; FDR-adjusted p-value ≤0.01). Data represent the mean log$_2$ fold-change differences of genes differentially expressed in HL (H, 3 months) and HCC (C, 9 months) when compared with age-matched wild-type normal livers. Genes whose average expression level differed by ≥1.5-fold in each age group after Student's t-test (FDR-adjusted p-value ≤0.01) and having human homologues were filtered. The GenBank accession number, gene name and gene symbols (zebrafish and human) of each gene are shown. The mean fold-changes indicating up- or down-regulation in gene expression at hyperplasia and carcinoma are also indicated.

GenBank	Gene name	Gene symbol		Fold-change	
		Zebrafish	Human	H	C
BI326782	Sim to alpha-2-macroglobulin	LOC100006925	A2M	4.23	2.84
AI957415	Weak sim to alpha-2-macroglobulin-like 1	sb:cb37	A2ML1	2.72	2.45
BM103155	Acetoacetyl-CoA synthetase	aacs	AACS	3.86	6.39
BC097202	LOC619247 sim to aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	zgc:114148	AASDHPPT	0.90	1.94
AW076835	ATP-binding cassette, sub-family A (ABC1), member 12	abca12	ABCA12	-2.35	-1.92
BI891029	Sim to ABCA3 | ATP-binding cassette, sub-family A (ABC1), member 3	BI891029	ABCA3	-1.77	-0.73
AW344325	Sim to ATP-binding cassette, sub-family B (MDR/TAP), member 1	im:7158730	ABCB1	-2.56	-2.24
AW019239	3' end of LOC571189: sim to sister of P-glycoprotein (ATP-binding cassette, sub-family B (MDR/TAP), member 11) and 3' to LOC571214: sim to Microtubule-associated serine/threonine-protein kinase 3	AW019239	ABCB11	3.96	3.46
AW279805	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	abcc2	ABCC2	1.41	3.15
BI672727	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	abcc4	ABCC4	-3.49	-0.50
AW019127	ATP-binding cassette, sub-family D (ALD), member 3a	abcd3a	ABCD3	4.18	3.40
BC047181	ATP-binding cassette, sub-family F (GCN20), member 2	abcf2	ABCF2	2.74	-2.39
BI671305	Abl-interactor 1	abi1a	ABI1	-1.24	2.44
BM072329	Amiloride binding protein 1 (amine oxidase (copper-containing))	abp1	ABP1	-2.00	-4.13
BC080266	LOC445477 sim to actin-binding Rho activating protein	zgc:92005	ABRA	-1.69	-0.86
AW466674	LOC553674 sim to acyl-Coenzyme A binding domain containing 5	zgc:112043	ACBD5	2.07	0.76
BM154186	3' end of aclyb | ATP citrate lyase b and 5' to klhl11 | kelch-like 11	BM154186	ACLY	1.71	-1.27
AI584333	3' end of acot11: acyl-CoA thioesterase 11 and 3' to CH211-215B16.4 sim to FAM151A | family with sequence similarity 151, member A	wu:fb92c04	ACOT11	1.50	1.53
AI882824	Acid phosphatase 5, tartrate resistant	acp5	ACP5	-4.20	-6.73
AI884128	Acyl-CoA synthetase long-chain family member 1	acsl1	ACSL1	-1.42	-3.06
AI558294	3' end of si:dkeyp-109h9.2: acyl-CoA synthetase long-chain family member 3 and 5' to si:dkeyp-109h9.3: potassium voltage-gated channel, Isk-related family, member 4	wu:fb78c09	ACSL3	-3.25	-0.90
AI721419	Acyl-CoA synthetase long-chain family member 4	acsl4	ACSL4	-1.61	2.36
BC081587	LOC447860 sim to acyl-CoA synthetase long-chain family member 5	zgc:92083	ACSL5	2.03	-4.91
AF180887	Actin, alpha 1, skeletal muscle	acta1	ACTC1	-2.03	0.73
BC071401	LOC415164 sim to actin, alpha, cardiac muscle 1	zgc:86725	ACTC1	-4.35	-1.86
AI588265	3' end of acvr1b | activin A receptor, type IB and 3' to dhh desert hedgehog	wu:fb98e08	ACVR1B	3.45	-1.88
BC045399	Aminoacylase 1	zgc:55605	ACY1	-1.24	-1.54
BC076532	Adenosine deaminase	ada	ADA	-0.20	-2.36
BM083001	Adenosine deaminase-like	adal	ADAL	-1.79	-0.80
BI851021	A disintegrin and metalloprotease domain 10b	adam10b	ADAM10	1.43	1.62
BC057428	A disintegrin and metalloproteinase domain 8a	adam8a	ADAM8	0.28	-2.04
AF329730	Adenylate cyclase activating polypeptide 1b	adcyap1b	ADCYAP1	-2.88	-1.11
AF399909	Alcohol dehydrogenase 5	adh5	ADH5	-2.15	1.77
BC055142	LOC393427 sim to ADH5: alcohol dehydrogenase 5 (class III), chi polypeptide	zgc:63568	ADH5	-0.47	-2.33
AI331606	3' end of adipoql2 | adiponectin, C1Q and collagen domain containing, like 2	LOC794315	ADIPOQ	1.04	-2.07
AI657574	Adenosine kinase a	adka	ADK	0.34	3.64
AW421018	3' end of adm2 adrenomedullin 2	AW421018	ADM2	0.55	1.89
BC078399	LOC445059 sim to ADP-ribosylarginine hydrolase	zgc:91926	ADPRH	3.46	2.16
AY048971	Adrenergic, alpha-2A-, receptor	adra2a	ADRA2A	1.61	2.09
BC092877	LOC550502 sim to adenylosuccinate synthase	zgc:110327	ADSS	-1.60	-2.25
BC070009	Adenylosuccinate synthase like 1	adssl1	ADSSL1	1.86	0.69
BM081849	Sim to AE binding protein 1	si:ch1073-459j12.1	AEBP1	-2.41	-1.09
AW422593	AE binding protein 2	aebp2	AEBP2	1.87	1.16
AF085218	Chico (sim to amino-terminal enhancer of split)	chico	AES	2.72	0.51
AW281869	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	agl	AGL	-1.52	-1.60
AW019740	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	agpat2	AGPAT1	-1.07	-1.83
BI884206	3' end of agpat3 | 1-acylglycerol-3-phosphate O-acyltransferase 3 and 5' to LOC564635	BI884206	AGPAT3	-1.01	3.99
AW019737	1-acylglycerol-3-phosphate O-acyltransferase 9	agpat9	AGPAT9	-1.77	0.53
AW233227	Anterior gradient homolog 2	agr2	AGR2	-4.47	-3.29
BG727310	Angiotensinogen	agt	AGT	0.95	6.48
AW019124	Alanine-glyoxylate aminotransferase	agxt	AGXT	0.49	6.18
BF717714	Alanine-glyoxylate aminotransferase, like	agxtl	AGXT	2.13	5.42
BI671185	S-adenosylhomocysteine hydrolase-like 1	ahcyl1	AHCYL1	-2.41	3.58
CD283124	Adenosylhomocysteinase	zgc:158222	AHCYL2	2.87	-1.81
Y08433	Aryl hydrocarbon receptor 1a	ahr1a	AHR	0.91	2.47
AF063446	Aryl hydrocarbon receptor 2	ahr2	AHR	0.06	2.62
AI496863	Alpha-2-HS-glycoprotein	ahsg	AHSG	4.03	5.06
BG305622	Programmed cell death 8 (apoptosis-inducing factor, mitochondrion-associated, 1)	pdcd8	AIFM1	-0.42	-1.77

BC075979	LOC436885 weak sim to AIFM3: apoptosis-inducing factor, mitochondrion-associated, 3	zgc:92275	AIFM3	2.37	2.24
AF274877	Aryl hydrocarbon receptor interacting protein	aip	AIP	-1.75	1.82
AW116492	Sim to A kinase (PRKA) anchor protein 13	LOC798734	AKAP13	4.20	1.31
BI982810	Weak sim to A kinase (PRKA) anchor protein 2	uo:ion006	AKAP2	2.14	2.80
BG302955	V-akt murine thymoma viral oncogene homolog 2, like	akt2l	AKT2	1.06	2.91
AF095747	Aminolevulinate, delta-, synthetase 2	alas2	ALAS2	-2.70	-0.08
L25273	Activated leukocyte cell adhesion molecule a	alcama	ALCAM	-1.76	1.51
AF339837	Aldehyde dehydrogenase 1 family, member A2	aldh1a2	ALDH1A2	-1.65	-2.25
AW344274	Sim to aldehyde dehydrogenase 2 family (mitochondrial)	wu:fb14d09	ALDH2	0.28	-2.42
AF254955	Aldehyde dehydrogenase 3 family, member D1	aldh3d1	ALDH3B1	0.16	-3.22
BI879264	Aldehyde dehydrogenase 7 family, member A1	aldh7a1	ALDH7A1	-2.39	-2.14
AI544950	Aldehyde dehydrogenase 9 family, member A1b	aldh9a1b	ALDH9A1	0.84	-4.07
AW116838	Aldolase a, fructose-bisphosphate, a	aldoaa	ALDOA	-4.07	-0.86
BM071225	Aldolase a, fructose-bisphosphate, b	aldoab	ALDOA	-3.61	-0.38
BG304331	Asparagine-linked glycosylation 9 homolog (S. cerevisiae, alpha- 1,2-mannosyltransferase)	alg9	ALG9	2.35	0.92
AW232270	Intergenic 3' to alk | anaplastic lymphoma kinase (Ki-1) and 3' to LOC100148741	AW232270	ALK	1.81	-1.18
CK865157	Intestinal alkaline phosphatase	zgc:110409	ALPI	-1.32	-1.95
BQ481034	Sim to alkaline phosphatase, liver/bone/kidney	LOC564254	ALPL	1.64	1.35
BG303733	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	als2cr8	ALS2CR8	-1.71	0.19
AI477606	Alpha-1-microglobulin/bikunin precursor, like	ambpl	AMBP	3.23	2.40
BM005224	Adenosylmethionine decarboxylase 1	amd1	AMD1	-2.23	2.40
BC063996	Adenosine monophosphate deaminase 1 (isoform M)	ampd1	AMPD1	2.30	1.33
BM103972	Amylase, alpha 2A; pancreatic	amy2a	AMY2A	1.61	-5.75
BC075900	LOC445049 sim to amylase, alpha 2A (pancreatic)	zgc:92137	AMY2A	2.73	2.95
AW280158	Sim to anaphase promoting complex subunit 1	AW280158	ANAPC1	-1.83	-1.20
BI878018	LOC558814 sim to anaphase promoting complex subunit 10	zgc:153242	ANAPC10	-0.47	-4.68
BM183990	Anaphase promoting complex subunit 5	anapc5	ANAPC5	-0.87	-2.14
AF379602	Angiopoietin 1	angpt1	ANGPT1	0.12	2.54
AB199647	Angiopoietin-like 1	angptl1	ANGPTL1	0.76	1.72
AB199648	Angiopoietin-like 2	angptl2	ANGPTL2	1.07	4.67
BQ169332	Angiopoietin-like 6	angptl6	ANGPTL2	1.14	2.51
BE201957	Angiopoietin-like 2b	zgc:194138	ANGPTL2	0.16	2.89
AF379604	Angiopoietin-like 3	angptl3	ANGPTL3	1.39	4.59
BE202096	LOC450053 sim to angiopoietin-like 7	zgc:101687	ANGPTL7	-2.83	-3.11
BI886030	Similar to Ankyrin repeat domain-containing protein 11 (Ankyrin repeat-containing cofactor 1)	LOC793422	ANKRD11	-1.60	0.86
BI673416	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	anp32b	ANP32B	-0.54	-2.19
AI545611	Sim to ANPEP | alanyl (membrane) aminopeptidase	LOC100006595	ANPEP	1.23	-2.21
AW128428	Annexin A1a	anxa1a	ANXA1	-3.68	1.21
AI331515	Annexin A1b	anxa1b	ANXA1	-5.29	-4.21
BI889370	Annexin A1c	anxa1c	ANXA1	-4.12	-1.96
BI889313	Annexin A11a	anxa11a	ANXA11	0.27	1.95
AI957567	Annexin A11b	anxa11b	ANXA11	0.67	2.21
BI885541	Annexin A13	anxa13	ANXA13	1.03	2.49
BI707699	LOC554118 sim to annexin A13	zgc:112421	ANXA13	-2.27	-1.78
AI883512	Annexin A2a	anxa2a	ANXA2	0.26	2.10
AW077600	LOC100000433 no homol 3' end of zgc:101785: LOC450032 sim to ANXA2: annexin A2	LOC100000433	ANXA2	-2.52	-4.05
BE557263	Annexin A4	anxa4	ANXA4	3.33	3.54
BC046873	Annexin A5	anxa5	ANXA5	2.53	-0.70
BI891593	Annexin A6	anxa6	ANXA6	2.48	-0.88
BM172690	Adaptor-related protein complex 2, beta 1 subunit	ap2b1	AP2B1	2.67	-0.52
BI473992	Sim to AP3B1 | adaptor-related protein complex 3, beta 1 subunit	LOC569016	AP3B1	-0.30	2.15
BI866388	Apoptotic protease activating factor 1	apaf1	APAF1	0.96	-2.16
AI793772	Apoptosis-inducing, TAF9-like domain 1	zgc:194319	APITD1	3.97	1.18
AJ245491	Weak sim to apolipoprotein A-I	xx:sd49	APOA1	3.86	3.68
Y13653	Apolipoprotein A-I (weak sim to APOA4)	apoa1	APOA4	-2.89	-5.72
AI477980	Apolipoprotein A-IV	apoa4	APOA4	1.94	-1.33
AW019803	Vitellogenin 6	vtg1	APOB	-4.32	-2.74
BM101644	LOC100148022 sim to apolipoprotein D	LOC100148022	APOD	-3.81	-4.95
AJ236882	Apolipoprotein Eb	apoeb	APOE	4.61	2.32
BI867505	Apolipoprotein M	apom	APOM	4.65	4.99
AW422269	Aquaporin 3	aqp3	AQP3	-6.34	-3.47
BG305916	3' end of LOC570191 sim to AQP9 | aquaporin 9 and 5' to lipc | lipase, hepatic	BG305916	AQP9	3.03	3.04
BI473712	Archain 1 like	arcn1l	ARCN1	2.14	2.45
BM005100	ADP-ribosylation factor 1 like	arf1l	ARF1	0.45	-2.05
BC075924	ADP-ribosylation factor 3a	arf3a	ARF3	-0.70	-2.70
BM036098	ADP-ribosylation factor GTPase activating protein 3	arfgap3	ARFGAP3	-3.16	-0.24
BG985689	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	arfip1	ARFIP1	-0.08	-2.60
AI641593	3' end of arfip2b | ADP-ribosylation factor interacting protein 2b and 5' to zgc:153126 sim to FHDC1 | FH2 domain containing 1	wu:fc17c06	ARFIP2	-0.53	-1.63
AW018735	Arginase, type II	arg2	ARG2	0.57	5.42
BI879861	Rho GTPase activating protein 12	arhgap12	ARHGAP12	1.87	3.84
AW826580	Rho GTPase activating protein 20	arhgap20	ARHGAP20	3.43	-1.16
CV576369	Intergenic 3' to DKEY-13N15.4 sim to ARHGAP25 | Rho GTPase activating protein 25 and 5' to si:dkey-13n15.5 sim to BMP10 | bone morphogenetic protein 10	CV576369	ARHGAP25	4.02	-0.20
BI671403	Rho GTPase activating protein 29a; wu:fj83g02	arhgap29a	ARHGAP29	1.59	1.39
BM187499	LOC557983 sim to Rho guanine nucleotide exchange factor (GEF) 1	zgc:136551	ARHGEF1	0.49	-1.68
BG883520	Rho guanine nucleotide exchange factor (GEF) 1	arhgef1	ARHGEF2	0.62	2.02
BE202058	Sim to Rho guanine nucleotide exchange factor (GEF) 4	LOC559017	ARHGEF4	-2.30	-1.11
BM571146	Intron of wu:fd16d01 weak sim to Rho guanine nucleotide exchange factor (GEF) 5	BM571146	ARHGEF5	4.55	0.34
BG305579	ADP-ribosylation factor-like 3, like 1	arl3l1	ARL3	0.63	-1.78
AW232572	ADP-ribosylation factor-like protein 3	si:ch211-208d15.4	ARL3	1.77	-0.30
BG308473	ADP-ribosylation factor-like 4, like	arl4l	ARL4A	-1.29	-1.69
AJ286835	ADP-ribosylation factor-like 4Cb	arl4cb	ARL4C	-2.65	-1.60
BC052766	ADP-ribosylation factor-like 8	arl8	ARL5B	-1.29	-2.18
BM035598	LOC767691 sim to arginine-rich, mutated in early stage tumors	zgc:153327	ARMET	4.19	1.30
AY707650	Aryl hydrocarbon receptor nuclear translocator	arnt	ARNT	1.78	0.90
AF144689	Aryl hydrocarbon receptor nuclear translocator-like 1a	arntl1a	ARNTL	2.81	1.60
AW173877	Actin related protein 2/3 complex, subunit 1A	arpc1a	ARPC1A	1.96	0.81
BE557608	LOC415190 sim to actin related protein 2/3 complex, subunit 1A, 41kDa	zgc:86896	ARPC1A	-2.33	-1.36
BI891122	Actin related protein 2/3 complex, subunit 2	arpc2	ARPC2	1.01	1.64
AW203061	Actin related protein 2/3 complex, subunit 5A	arpc5a	ARPC5	1.55	1.70
BI879038	CAMP-regulated phosphoprotein 19a	arpp19a	ARPP19	0.08	3.27
BI879707	Arrestin 3, retinal (X-arrestin), like	arr3l	ARR3	-2.11	-1.01
BI892004	Arrestin, beta 2	arrb2	ARRB2	1.09	3.26
BI876503	Arsenate resistance protein 2	ars2	ARS2	2.96	-0.27
BC083231	N-acylsphingosine amidohydrolase (acid ceramidase) 1	asah1	ASAH1	-0.21	-3.77
AB194413	N-acylsphingosine amidohydrolase 2	asah2	ASAH2	-2.03	-2.02
BM181758	Sim to ankyrin repeat and SOCS box-containing 3	BM181758	ASB3	0.01	-3.45
BM096034	Ankyrin repeat and SOCS box-containing 8	asb8	ASB8	0.33	-2.59
BC055218	Acetylserotonin O-methyltransferase-like	asmtl	ASMTL	-3.51	2.57
BE201971	Asparagine synthetase	asns	ASNS	0.96	2.55
BI672407	Weak sim to asparaginase homolog (S. cerevisiae)	LOC100006732	ASPG	-1.25	-1.59
AI877570	LOC100124594 sim to ASPG: asparaginase homolog	zgc:171644	ASPG	1.94	1.37
BI864195	Intron of asph: aspartate beta-hydroxylase	BI864195	ASPH	-2.73	-1.58
AW778181	Asp (abnormal spindle)-like, microcephaly associated (Drosophila)	aspm	ASPM	0.95	-4.15
BC081578	Argininosuccinate synthetase	ass	ASS1	-4.11	-1.72
BM184227	Ankyrin repeat, SAM and basic leucine zipper domain containing 1	asz1	ASZ1	-0.87	-4.16
BC081379	ATPase family, AAA domain containing 1a	atad1a	ATAD1	0.05	-2.05
BI534295	LOC565827 sim to ataxia, cerebellar, Cayman type homolog	si:dkey-49m19.1	ATCAY	2.19	-0.22
AW422298	Activating transcription factor 3	atf3	ATF3	1.33	2.01

AW420576	Sim to activating transcription factor 5	wu:fc14a10	ATF5	3.76	3.73
BM036484	3' end of atg4c | autophagy-related 4C	BM036484	ATG4C	-1.26	-2.15
BM183879	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	atic	ATIC	0.83	-3.92
AF286374	ATPase, Na+/K+ transporting, alpha 1a.2 polypeptide	atp1a1a.2	ATP1A1	0.37	-1.66
AY094620	ATPase, Na+/K+ transporting, alpha 1a.5 polypeptide	atp1a1a.5	ATP1A1	-0.74	-1.60
AY008375	ATPase, Na+/K+ transporting, alpha 1b polypeptide	atp1a1b	ATP1A1	-2.97	-1.05
BM172666	ATPase, Na+/K+ transporting, beta 1a polypeptide	atp1b1a	ATP1B1	-3.41	1.54
AF293369	ATPase, Na+/K+ transporting, beta 3b polypeptide	atp1b3b	ATP1B3	-1.21	-4.46
BM185985	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 like	atp2a1l	ATP2A1	-4.33	1.39
BI896301	Sim to ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	wu:cegs655	ATP2A1	-1.05	-3.26
BI891329	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2b	atp2a2b	ATP2A2	3.15	3.40
BI864494	ATPase, Ca++ transporting, plasma membrane 2	atp2b2	ATP2B2	-2.01	-1.32
BI980991	3' end of atp2b4: ATPase, Ca++ transporting, plasma membrane 4 and 3' to zgc:174320	BI980991	ATP2B4	-1.83	-0.81
AW342634	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A, like	atp6v1al	ATP6V1A	-0.89	2.78
BC045370	ATPase, H+ transporting, V1 subunit D	atp6v1d	ATP6V1D	2.45	1.23
BG883692	Sim to ATRX | alpha thalassemia/mental retardation syndrome X-linked	LOC568580	ATRX	1.76	1.15
AI957736	Aurora kinase B	aurkb	AURKB	-1.53	-0.99
BC067695	Serine/threonine kinase a (aurora kinase B)	stka	AURKB	-2.05	-5.45
AW076951	Oxytocin-like	oxtl	AVP	2.20	0.46
AB032263	Axin 2 (conductin, axil)	axin2	AXIN2	-0.12	-1.99
BF717552	Beta-2 microglobulin	zgc:64161	B2M	-3.71	-1.07
AF321830	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3-like	zgc:86586	B3GNT3	1.07	1.57
AF321829	Beta-3-galactosyltransferase (sim to UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7)	zgc:91787	B3GNT7	-2.93	-1.95
AW154318	Sim to BACE2 | beta-site APP-cleaving enzyme 2	wu:fi26d02	BACE2	1.63	0.54
BI867065	BCL2-antagonist of cell death	bad	BAD	-1.10	-1.77
AI721437	BCL2-associated athanogene 2	bag2	BAG2	-0.17	2.22
BM317353	Sim to BCL2-associated athanogene 2	BM317353	BAG2	-2.22	-1.15
AF239925	BMP and activin membrane-bound inhibitor (Xenopus laevis) homolog	bambi	BAMBI	1.05	2.23
BI891654	Bcl2-associated X protein, a	baxa	BAX	0.97	-2.32
BC049014	B-cell receptor-associated protein 31	bcap31	BCAP31	2.55	1.29
BE201801	Weak sim to breast cancer anti-estrogen resistance 3	LOC795201	BCAR3	1.35	1.68
BG308582	Branched chain aminotransferase 1, cytosolic	bcat1	BCAT1	-0.08	-2.36
BG305296	BRCA2 and CDKN1A interacting protein	bccip	BCCIP	0.28	-2.30
AF160641	Sim to B-cell CLL/lymphoma 11B (zinc finger protein)	si:dkey-7l12.1	BCL11B	3.28	1.53
AY695820	B-cell leukemia/lymphoma 2	bcl2	BCL2	1.49	2.34
AF317837	Bcl2-like	bcl2l	BCL2L1	-1.84	2.42
BI984364	BCL2-like 13 (apoptosis facilitator)	bcl2l13	BCL2L13	-1.87	-2.19
BM081091	Intergenic 3' to bcl6: B-cell CLL/lymphoma 6 (zinc finger protein 51) and 5' to LOC100150110: sim to polyprotein	BM081091	BCL6	-1.37	-2.51
AJ290391	Beta-carotene 15, 15-dioxygenase 2, like	bcdo2l	BCO2	0.10	2.00
BI670989	LOC560226 sim to breakpoint cluster region	DKEY-91M11.5	BCR	2.46	1.61
AI878399	3' end of LOC100002003 weak similar to B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB and 5' to zgc:101635	wu:fc57d05	BDP1	-1.53	0.73
AI497232	Betaine-homocysteine methyltransferase	bhmt	BHMT	-3.69	-3.51
AF442500	Baculoviral IAP repeat-containing 2	birc2	BIRC2	-0.62	2.64
AY057057	Baculoviral IAP repeat-containing 5a	birc5a	BIRC5	-1.15	3.11
AY057058	Baculoviral IAP repeat-containing 5B	birc5b	BIRC5	-0.73	1.89
BC095221	LOC553608 sim to transducin (beta)-like 1 X-linked receptor 1	zgc:110312	BL1XR1	2.98	1.29
AB038320	Bladder cancer associated protein	blcap	BLCAP	1.51	-2.43
BM104315	Basic leucine zipper nuclear factor 1	blzf1	BLZF1	-1.14	-2.36
AW059234	Bone morphogenetic protein 1a	bmp1a	BMP1	1.54	-1.44
NM_131342	Bone morphogenetic protein 4	bmp4	BMP4	-2.50	-0.98
BC054647	Bone morphogenetic protein 5	bmp5	BMP5	-2.88	-0.36
BG302761	Bone morphogenetic protein 8	bmp8	BMP8B	-1.80	-1.21
BC081626	Bone morphogenetic protein receptor, type IA,b	bmpr1ab	BMPR1A	-1.15	-2.25
AI878495	Sim to bone morphogenetic protein receptor, type IB	AI878495	BMPR1B	-0.93	-4.42
AI793560	Sim to basonuclin 1	LOC568786	BNC1	-1.69	-1.85
NM_201218	BCL2/adenovirus E1B interacting protein 2	bnip2	BNIP2	-2.62	1.97
AI477329	3' end of bnip3l2 | BCL2/adenovirus E1B interacting protein 3-like, 2 and 5' to LOC798555 sim to DPYSL2 | dihydropyrimidinase-like 2	AI477329	BNIP3L	1.01	2.46
AW420488	BCL2/adenovirus E1B interacting protein 3-like	bnip3l	BNIP3L	-0.59	2.24
BC078217	BCL2-related ovarian killer a	boka	BOK	0.36	-2.06
BC075949	LOC436903 sim to 2,3-bisphosphoglycerate mutase	zgc:92230	BPGM	-1.72	-3.19
BM156875	3'(2'), 5'-bisphosphate nucleotidase 1	bpnt1	BPNT1	-2.19	1.55
AW128614	Bromodomain containing 7	brd7	BRD7	1.48	1.53
BI710320	Intron of LOC564701 | similar to BR serine/threonine-protein kinase 2	BI710320	BRSK2	2.65	0.29
AW343700	3' end of brunol5; bruno-like 5, RNA binding protein and 3' end of zgc:66326 sim to RGMB; RGM domain family, member B	wu:fi48c05	BRUNOL5	-1.70	-1.74
BI878208	Basigin	bsg	BSG	0.43	2.05
BG306459	Basic transcription factor 3	btf3	BTF3	0.53	3.06
BC056691	B-cell translocation gene 1	btg1	BTG1	-2.63	-3.94
BM071805	B-cell translocation gene 4	btg4	BTG4	-5.02	-5.85
BE605308	Basic leucine zipper and W2 domains 1b	bzw1b	BZW2	-1.80	-3.11
BI983582	Sim to chromosome 11 open reading frame 9	BI983582	C11orf9	2.65	1.74
BI888368	LOC431737 sim to response gene to complement 32	zgc:91870	C13orf15	-2.22	-0.45
BI889079	LOC436753 sim to chromosome 19 open reading frame 10	zgc:92871	C19orf10	5.35	2.15
BI705710	Sim to core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	BI705710	C1GALT1	0.92	2.89
BM777196	3' end of zgc:165409; LOC797807: weak sim to C1orf25: chromosome 1 open reading frame 25 and 3' to LOC100002264: sim to BBS9: Bardet-Biedl syndrome 9	BM777196	C1orf25	1.97	0.76
BC096887	LOC560927 sim to complement component 1, s subcomponent	zgc:112309	C1S	3.35	1.90
BI705186	GC-rich sequence DNA-binding factor candidate	zgc:158234	C21orf66	-1.10	3.25
AI588354	3' end of DKEY-75L1.5 sim to C3 | complement component 3	AI588354	C3	1.80	2.87
AI722510	Complement component c3b	c3b	C3	0.95	4.95
AF047415	Complement component c3c	c3c	C3	5.65	6.12
AF047413	Complement component c3a	si:dkey-76b14.4	C3	1.30	1.92
BI708361	LOC641323 sim to chromosome 3 open reading frame 31	zgc:123195	C3orf31	3.43	0.79
BF717375	Complement component 8, gamma polypeptide	c8g	C8G	1.83	5.23
AW281891	Sim to chromosome 8 open reading frame 4	wu:fj58g06	C8orf4	2.23	1.25
CF594673	Complement component 9	c9	C9	2.66	4.21
AI723264	3' end of LOC557314 sim to C9orf89 and 3' to LOC100150223 similar to ninjurin 1	AI723264	C9orf89	1.70	0.64
BC095649	Adenylate kinase-like	zgc:112030	C9orf98	-1.52	-0.75
U55177	Carbonic anhydrase	cahz	CA2	-1.47	2.55
BF938524	Carbonic anhydrase VII	ca7	CA7	-0.82	-5.26
AW171091	Calcium binding protein 39, like 1	cab39l1	CAB39	1.68	0.68
BC085674	LOC492361 sim to calcium binding protein 39-like	zgc:92575	CAB39L	3.61	0.81
BI865668	Intron of cacna1ab | calcium channel, voltage-dependent, P/Q type, alpha 1A subunit, b	BI865668	CACNA1A	2.36	1.35
BI879509	Intron of LOC100151242 sim to CACNA1D | calcium channel, voltage-dependent, L type, alpha 1D subunit	BI879509	CACNA1D	0.70	2.46
AY528224	Calcium channel, voltage-dependent, L type, alpha 1D subunit	cacna1d	CACNA1D	0.65	2.49
AY495698	Calcium channel, voltage-dependent, L type, alpha 1S subunit	cacna1s	CACNA1S	-3.17	-1.66
BC057439	Calcium channel, voltage-dependent, gamma subunit 2	cacng2	CACNG2	-0.26	-2.74
AI721634	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	cad	CAD	-0.79	-2.25
BC076343	Calcitonin/calcitonin-related polypeptide, alpha	calca	CALCB	6.51	0.71
BI670912	Calmodulin 1b	calm1b	CALM2	1.42	2.60
AW128363	Calmodulin 2a (phosphorylase kinase, delta)	calm2a	CALM2	0.45	1.58
AI331854	Calmodulin 2b, (phosphorylase kinase, delta)	calm2b	CALM2	-0.74	-2.23
AF195882	Calreticulin	calr	CALR	3.47	2.60
NM_201465	Calreticulin like	calrl	CALR	3.64	3.80
BG302583	Calreticulin, like 2: sim to epidermal growth factor receptor pathway substrate 15	calrl2	CALR	3.07	3.53
BC093372	Calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	camk2a	CAMK2A	4.76	-1.91

BM070854	Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta 2	camk2d2	CAMK2D	2.22	2.17
AW232670	Calmegin	clgn	CANX	-1.45	1.63
BG727337	3' end of LOC570311 similar to calpain 10 and 5' to zgc:110542(sim to EIF4E2)	BG727337	CAPN10	3.89	-1.12
BC095045	Calpain 2, (m/II) large subunit b	capn2b	CAPN2	-2.65	-3.02
AI396726	Calpain 2, (m/II) large subunit, like	capn2l	CAPN2	-2.71	-1.86
AW281444	Calpain, small subunit 1	capns1	CAPNS1	-3.00	-2.34
BM181708	Caprin family member 2	caprin2	CAPRIN2	-3.02	-5.04
AI722206	Capping protein (actin filament) muscle Z-line, beta	capzb	CAPZB	2.62	0.37
BC056576	Calcium regulated heat stable protein 1	carhsp1	CARHSP1	0.12	-1.95
AW202784	Cysteinyl-tRNA synthetase	cars	CARS	1.16	2.67
AW115856	Sim to cysteinyl-tRNA synthetase 2, mitochondrial (putative)	si:ch211-198k9.5	CARS2	3.21	3.84
AW076882	Cancer susceptibility candidate 3 (metastatic lymph node 51)	casc3	CASC3	-1.17	2.68
AF252546	Calcium/calmodulin-dependent serine protein kinase	cask	CASK	2.55	2.35
AF233434	Caspase a	caspa	CASP1	-0.42	-2.08
AF327410	Caspase b	caspb	CASP1	-1.04	-2.07
AW466695	Caspase 3, apoptosis-related cysteine protease a	casp3a	CASP3	-1.43	-2.33
BC083437	Caspase 6, apoptosis-related cysteine peptidase, like 1	casp6l1	CASP6	-1.53	-2.38
AF273220	Caspase 8, apoptosis-related cysteine peptidase	casp8	CASP8	-1.90	-2.47
BI673444	CASP8 associated protein 2	casp8ap2	CASP8AP2	1.00	-1.79
AW116368	Calsequestrin-like	zgc:100957	CASQ1	-2.02	-2.16
BG308575	LOC559053 sim to Castor zinc finger 1	casz1	CASZ1	-1.20	-1.55
AF170069	Catalase	cat	CAT	-0.27	2.00
AW595386	Caveolin 1	cav1	CAV1	-0.63	2.99
AI666893	Cas-Br-M (murine) ecotropic retroviral transforming sequence	cbl	CBL	0.49	2.03
BE201648	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	cblb	CBLB	1.21	-1.54
BC092758	LOC550551 sim to chromobox homolog 7	zgc:110152	CBX7	3.44	0.84
BM102459	LOC795788 sim to chemokine (C-C motif) ligand 21	LOC795788	CCL21	-1.11	4.04
BM155325	Chemokine CCL-C10b (weak sim to chemokine (C-C motif) ligand 28/27/25)	LOC794616	CCL28	-2.21	-0.96
AF234784	Cyclin A2	ccna2	CCNA2	-0.77	5.68
AB040435	Cyclin B1	ccnb1	CCNB1	5.48	7.85
AW422010	Cyclin B2	ccnb2	CCNB2	1.61	4.85
BI886477	Cyclin B3	zgc:153369	CCNB3	-2.94	-1.07
X87581	Cyclin D1	ccnd1	CCND1	2.32	3.37
X83594	Cyclin E	ccne	CCNE1	1.29	3.71
BI672128	Cyclin F	ccnf	CCNF	-0.87	2.31
AI959372	Cyclin G1	ccng1	CCNG1	0.54	2.52
BE556826	Cyclin G2	ccng2	CCNG2	1.88	1.97
AW116346	Chaperonin containing TCP1, subunit 2 (beta)	cct2	CCT2	0.54	3.29
AI964352	Chaperonin containing TCP1, subunit 3 (gamma)	cct3	CCT3	-1.98	0.77
BG303560	Chaperonin containing TCP1, subunit 4 (delta)	cct4	CCT4	-1.84	2.56
AI964322	Chaperonin containing TCP1, subunit 5 (epsilon)	cct5	CCT5	1.95	0.73
BI888169	Chaperonin containing TCP1, subunit 6A (zeta 1)	cct6a	CCT6A	-0.44	1.55
BE557308	Chaperonin containing TCP1, subunit 7 (eta)	cct7	CCT7	-0.65	1.78
AW059098	Chaperonin containing TCP1, subunit 8 (theta)	cct8	CCT8	-1.33	1.57
BC076048	CD36 antigen	cd36	CD36	-1.47	-5.42
AW344023	Weak sim to CD44 | CD44 molecule (Indian blood group)	wu:fa99e04	CD44	-3.47	-3.41
AI436876	Intron of LOC100003927 weak sim to CD58 | CD58 molecule and 3' to of si:dkey-19a16.7 weak sim to LY9 | lymphocyte antigen 9	wu:fb34b02	CD58	-3.39	-2.94
AW019276	Cd63 antigen	cd63	CD63	-0.50	2.44
AF114830	Invariant chain-like protein 1	iclp1	CD74	-2.68	3.40
AF116539	Invariant chain-like protein 2	iclp2	CD74	-2.32	0.65
AI353506	CD9 antigen (p24)	cd9	CD9	2.70	4.61
BI888934	CD99 antigen-like 2	cd99l2	CD99L2	0.45	2.57
AI721645	Cell division cycle 2	cdc2	CDC2	0.97	2.34
AW116246	Cell division cycle 20 homolog	cdc20	CDC20	-0.51	5.55
AW059106	Intron of cdc23 | CDC23 (cell division cycle 23, yeast, homolog)	AW059106	CDC23	3.17	0.65
AF212941	Cdc25 (sim to cell division cycle 25 homolog A)	cdc25	CDC25A	1.54	3.56
BM037003	Cell division cycle 27	cdc27	CDC27	1.08	2.34
AY398322	Cell division cycle 42	cdc42	CDC42	1.28	1.56
AI964255	LOC558275 sim to CDC42 effector protein (Rho GTPase binding) 5	zgc:153966	CDC42	-0.74	2.35
BM184190	CDC42 effector protein (Rho GTPase binding) 4	cdc42ep4	CDC42EP4	0.63	2.80
BG303845	CDC42 small effector 1	cdc42se1	CDC42SE1	-1.93	-1.68
BI891546	Cell division cycle 45-like	cdc45l	CDC45L	1.36	3.37
AW171211	CDC5 cell division cycle 5-like (S. pombe)	cdc5l	CDC5L	0.44	2.20
AW165153	Cell division cycle 73, Paf1/RNA polymerase II complex component, homolog	cdc73	CDC73	0.57	2.05
BI704246	Cell division cycle associated 8-like	cdca8l	CDCA8	-0.15	-2.04
AW076614	3' end of LOC568392 sim to CDH1 | cadherin 1, type 1, E-cadherin and intron of LOC100150592 sim Tpase	AW076614	CDH1	1.31	4.37
U41419	Cadherin 11, osteoblast	cdh11	CDH11	-3.96	-0.72
AF428098	Cadherin 17, LI cadherin (liver-intestine)	cdh17	CDH17	0.38	-2.89
X67648	Cadherin 2, neuronal	cdh2	CDH2	2.90	5.35
AY496430	Cadherin 5 (vascular endothelium)	cdh5	CDH5	3.18	2.29
BI865765	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	cdipt	CDIPT	0.61	2.11
BC076283	LOC436788 sim to cyclin-dependent kinase 5, regulatory subunit 1 (p35)	zgc:92814	CDK5R1	-2.14	-1.95
BI886693	Cyclin-dependent kinase 8	cdk8	CDK8	2.20	3.36
AF398516	Cyclin-dependent kinase inhibitor 1b (p27, kip1)	cdkn1b	CDKN1B	-1.29	-2.13
BI884002	Cyclin-dependent kinase inhibitor 1b, like (p27, Kip1)	cdkn1bl	CDKN1B	-1.21	-2.03
AI957754	Transcribed locus sim to cysteine dioxygenase, type I	AI957754	CDO1	4.09	0.66
BC055505	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	cds2	CDS2	2.11	0.70
BG307558	Chromatin licensing and DNA replication factor 1	wu:fi38h09	CDT1	-1.28	-3.08
BI983420	CCAAT/enhancer binding protein (C/EBP), gamma	cebpg	CEBPG	-1.31	2.06
AF384217	Cat eye syndrome chromosome region, candidate 1a	cecr1a	CECR1	1.29	2.26
BC065350	LOC402927 sim to cat eye syndrome chromosome region, candidate 5	zgc:77375	CECR5	2.11	1.55
BM154534	Carboxyl ester lipase, tandem duplicate 1	cel.1	CEL	2.41	-0.66
AF003943	Carboxyl ester lipase, tandem duplicate 2	cel.2	CEL	-2.50	-1.41
AW115513	LOC554144 sim to elastase 1, pancreatic	zgc:112266	CELA1	-3.30	-2.97
AW019487	LOC445282 sim to elastase 1, pancreatic	zgc:92041	CELA1	-3.59	-2.97
BC085565	LOC445032 sim to elastase 1, pancreatic	zgc:92745	CELA1	-3.37	-2.65
BI705588	Elastase 2	ela2	CELA2A	-3.20	-0.11
AI558632	Elastase 3 like	ela3l	CELA2A	-3.75	-2.11
BQ260752	Sim to centromere protein F, 350/400ka (mitosin)	BQ260752	CENPF	2.91	-1.04
AB110416	Charon weak sim to Cerberus	cha	CER1	0.15	2.22
AF047412	Complement component bfb	bfb	CFB	1.82	4.28
U34662	Complement factor B	cfb	CFB	3.50	5.11
BF717453	LOC794927 weak sim to complement factor H	cfh	CFH	4.00	4.32
BC085367	LOC492777 weak sim to complement factor H	zgc:101554	CFH	5.39	3.62
BI887110	Cholesterol 25-hydroxylase	si:dkey-24l11.8	CH25H	-1.74	-1.70
AW128293	Chromatin assembly factor 1, subunit A (p150)	chaf1a	CHAF1A	-2.62	-4.35
BC085514	LOC492522 weak sim to coiled-coil-helix-coiled-coil-helix domain containing 3	zgc:103414	CHCHD3	2.59	-0.86
AI722567	Sim to chromodomain helicase DNA binding protein 7	LOC569471	CHD7	2.71	1.17
AW116064	LOC406323 sim to chitinase, acidic	zgc:56053	CHIA	-2.86	-6.47
BC054696	Chitinase domain containing 1	chid1	CHID1	2.10	2.20
AW019809	Choline kinase alpha (chka)	chka	CHKA	2.03	2.81
AW567276	3' end of chl1: camel and 5' end to LOC564085: sim to Dynein heavy chain 5, axonemal (Ciliary dynein heavy chain 5) (Axonemal beta dynein heavy chain 5)	wu:fk36h04	CHL1	-2.20	-1.71
BM172681	Putative breast adenocarcinoma marker	bc2	CHMP2A	-1.78	0.45
BI702909	Intron of chmp4c | chromatin modifying protein 4C	BI702909	CHMP4C	2.19	-0.49
AW420779	3' end of zgc:63904 sim to CHP | calcium binding protein P22 and 5' to khdrbs1a | KH domain containing, RNA binding, signal transduction associated 1a	AW420779	CHP	1.59	0.57
BC054566	LOC325361 sim to calcium binding protein P22	zgc:63904	CHP	-1.04	-1.51
AI558830	Choline phosphotransferase 1	chpt1	CHPT1	-0.57	2.24
AI477959	Intron of chpt1 | choline phosphotransferase 1	wu:fb49f01	CHPT1	1.92	-1.11

AA497144	Cholinergic receptor, nicotinic, delta polypeptide	chrnd	CHRND	-2.30	-0.59
AI667408	Carbohydrate (chondroitin) synthase 1	chys1	CHSY1	-2.76	-0.67
AI957909	CILP protein	CILP	CILP	-2.24	-0.66
BC049529	Creatine kinase, brain	ckb	CKB	-3.82	-0.51
AY036972	Creatine kinase, muscle a	ckma	CKM	-5.01	-1.01
BM005084	Cytoplasmic linker associated protein 2	clasp2	CLASP2	-2.64	0.11
AA566843	LOC565961 weak sim to chloride channel, calcium activated, family member 4	LOC565961	CLCA4	-1.94	-3.64
AI793436	Intron of wu:fb78c02:L sim to CLCN3: chloride channel 3	wu:fc47d12	CLCN3	2.79	2.81
AI667530	LOC393353 sim to chloride channel Ka	zgc:64141	CLCNKA	-2.68	1.49
AF359427	Claudin 10-like 1a	cldn10l1a	CLDN10	1.39	3.22
BC081634	Claudin 2	cldn2	CLDN14	1.28	1.98
BC054577	Claudin 15 like	cldn15l	CLDN15	-1.01	-1.93
BE606011	3' end of LOC567620 | similar to claudin 23 and 5' to LOC553515	BE606011	CLDN23	1.32	-1.86
BI888493	Weak sim to claudin 23	LOC553515	CLDN23	-2.24	-1.68
AF359434	Claudin h (sim to claudin 3)	cldnh	CLDN3	-2.58	0.41
AF359428	Claudin i	cldni	CLDN3	-5.66	-1.14
AF359423	Claudin a	cldna	CLDN4	-4.34	-1.15
AF359426	Claudin b	cldnb	CLDN4	-4.14	-0.48
AJ011789	Claudin d	cldnd	CLDN4	-8.73	-6.97
AF359425	Claudin e	cldne	CLDN4	-2.15	-0.20
AF359424	Claudin f	cldnf	CLDN4	-3.46	-0.88
AJ011790	LOC678651 sim to claudin 4	cldng	CLDN4	-5.27	-6.94
AF260240	Claudin 7	cldn7	CLDN7	-2.05	-0.54
BC075926	Claudin 7 like	zgc:92192	CLDN7	-0.95	-2.87
BE605983	LOC550497 sim to claudin 8	zgc:110333	CLDN8	-3.33	-2.62
BG883654	3' end of LOC568355 sim to C-type lectin domain family 11 member A precursor (Stem cell growth factor) (Lymphocyte secreted C-type lectin)	BG883654	CLEC11A	1.86	1.92
BI842255	Chloride intracellular channel 2	clic2	CLIC2	-2.14	2.30
AW420312	Sim to chloride intracellular channel 4	AW420312	CLIC4	-0.63	-1.63
BG305441	CDC-like kinase 4	clk4	CLK4	-0.51	2.37
AF133306	Clock	clock	CLOCK	1.34	3.80
AI396704	Intergenic 5' end to carm1 | coactivator-associated arginine methyltransferase 1 and 5'end to clpp: ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog	si:dkey-204f11.64	CLPP	-1.54	-0.99
BG728815	Clathrin, heavy polypeptide a (Hc)	cltca	CLTC	1.07	3.21
AW077466	Clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	clu	CLU	-1.73	-1.46
BC065587	Connector enhancer of kinase suppressor of Ras 1	cnksr1	CNKSR1	-1.25	-1.81
AW078462	Calponin 3, acidic	cnn3a	CNN3	1.23	3.72
BM036376	Similar to cyclin M2	LOC565702	CNNM2	-2.16	-1.48
BE201503	Sim to component of oligomeric golgi complex 3	im:7147618	COG3	-2.55	-0.53
AF192763	Collagen type XI alpha-2	col11a2	COL11A2	-1.75	-1.34
AI584441	Intron of LOC792499 | similar to collagen XIV and 5' to LOC792570 similar to zinc-fingers and homeoboxes 2	wu:fb93g03	COL14A1	-2.29	-2.44
BI671608	Im:7142837 sim to collagen, type XVI, alpha 1	im:7142837	COL16A1	-2.52	-3.32
BE605535	Sim to collagen, type XVII, alpha 1	wu:fk89a06	COL17A1	-2.80	-2.01
BM025541	Collagen type XVIII, alpha 1	col18a1	COL18A1	1.71	2.68
AJ318212	Collagen, type I, alpha 1	col1a1	COL1A1	-4.70	-3.25
AJ318214	Collagen, type I, alpha 3	col1a3	COL1A1	-4.28	-0.25
AJ318213	Collagen, type I, alpha 2	col1a2	COL1A2	-4.72	1.92
AI331578	LOC563353 sim to collagen, type XXI, alpha 1	si:ch211-106n13.3	COL21A1	6.92	2.36
BI879661	Collagen type II, alpha-1a	col2a1a	COL2A1	-3.02	-0.64
BI882313	Collagen type II, alpha-1b	col2a1b	COL2A1	-2.02	-1.65
AI601793	Collagen, type IV, alpha 5 (Alport syndrome)	col4a5	COL4A5	-2.40	-2.17
AL730406	Collagen, type IV, alpha 6	col4a6	COL4A6	2.67	-2.61
AW510261	LOC799369 sim to collagen, type V, alpha 1	col5a1	COL5A1	-2.24	-0.61
BE558113	Collagen, type VI, alpha 1	col6a1	COL6A1	-3.08	-2.01
BM184154	COMM domain containing 7	zgc:101056	COMMD7	1.62	0.42
AB040045	Zeta2-cop	copz2	COPZ2	0.57	3.15
BI885882	3' end of coronin, actin binding protein, 1C	BI885882	CORO1C	2.89	1.14
AW175342	Coronin, actin binding protein, 1C	coro1c	CORO1C	3.29	2.21
BG308803	LOC558987 sim to COX17 cytochrome c oxidase assembly homolog	LOC558987	COX17	2.47	-1.59
BI672330	LOC402880 sim to cytochrome c oxidase subunit IV isoform 1	LOC402880	COX4I1	0.50	-2.40
BI879411	LOC393776 sim to cytochrome c oxidase subunit IV isoform 1	zgc:73355	COX4I1	3.02	3.45
AF336125	Ceruloplasmin	cp	CP	4.05	5.55
BF717433	Carboxypeptidase A1 (pancreatic)	cpa1	CPA1	-3.17	-3.31
AF376130	Carboxypeptidase A5	cpa5	CPA1	-1.94	-3.62
AI667240	Carboxypeptidase B1 (tissue)	cpb1	CPB1	-3.13	-2.02
AB011681	Cytoplasmic polyadenylation element binding protein 1-like	zgc:194449	CPEB1	2.30	0.92
AF076918	Orb/CPEB-related RNA-binding protein	zorba	CPEB1	-2.44	-4.58
BG891864	Carboxypeptidase N, polypeptide 1	cpn1	CPN1	-0.98	4.04
AW078446	Copine I	cpne1	CPNE3	-3.01	2.20
AI793554	Cellular retinoic acid binding protein 2, a	crabp2a	CRABP2	-2.77	-1.83
BI846526	LOC449795 sim to Cysteine-rich protein 2	zgc:101840	CRIP2	2.24	-1.72
BI878977	LOC100124600 weak sim to CRP | C-reactive protein, pentraxin-related	zgc:171660	CRP	-1.71	-0.56
AB042249	Cryptochrome 1b (photolyase-like)	cry1b	CRY1	-0.47	-3.44
AW344177	Cryptochrome 2b	cry2b	CRY1	1.20	-1.90
AB042253	Cryptochrome 4	cry4	CRY1	-1.45	-2.09
BI983705	Cryptochrome 5	cry5	CRY2	-2.90	-1.59
AW116808	Cryptochrome DASH weak sim to cryptochrome 2 (photolyase-like)	cry-dash	CRY2	-0.71	-1.85
BC076518	Crystallin, alpha B, b	cryabb	CRYAB	-2.37	-1.15
BC090697	Crystallin, zeta (quinone reductase)	cryz	CRYZ	2.09	1.86
AI588190	Intergenic 3' to csad | cysteine sulfinic acid decarboxylase and 5' to zgc:153696 sim to ZNF740 | zinc finger protein 740	wu:fb97d04	CSAD	3.49	2.33
AW343922	Chromosome segregation 1-like (S. cerevisiae)	cse1l	CSE1L	-0.77	-2.19
AW171190	Casein kinase 2 alpha 1	ck2a1	CSNK2A1	0.80	4.35
AW116161	Casein kinase 2 alpha 2a	ck2a2a	CSNK2A2	1.52	0.96
S76877	Casein kinase 2 beta	ck2b	CSNK2B	-0.54	2.32
BI880158	3' end of csrnp1b | cysteine-serine-rich nuclear protein 1b and 3' to LOC556735 | similar to solute carrier organic anion transporter family, member 5A1	wu:fj66a01	CSRNP3	-0.70	1.83
CF595092	Cysteine and glycine-rich protein 2 binding protein	csrp2bp	CSRP2BP	1.10	2.29
BI846236	C-terminal binding protein 1	ctbp1	CTBP1	2.58	1.19
BC095870	LOC553744 sim to CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	zgc:113169	CTDSP1	1.71	1.10
BE693178	Connective tissue growth factor	ctgf	CTGF	-0.28	3.51
U41081	Catenin (cadherin-associated protein), beta 1	ctnnb1	CTNNB1	-1.20	1.90
BI891235	Catenin, beta 2	ctnnb2	CTNNB1	1.04	4.46
AB046866	Beta-catenin-interacting protein	icat	CTNNBIP1	1.12	-2.43
BI889539	Sim to catenin (cadherin-associated protein), delta 1	LOC556726	CTNND1	1.82	0.14
AW019526	LOC550419 sim to chymotrypsinogen B1	zgc:112160	CTRB1	-4.72	-4.11
BM101561	Chymotrypsinogen B1	ctrb1	CTRB2	-0.60	-3.53
BI476180	LOC793503 sim to chymotrypsin-like	LOC793503	CTRL	-3.35	-1.77
AJ278269	Nothepsin (sim to cathepsin E)	nots	CTSE	-4.16	-0.21
AI384696	Cathepsin K	ctsk	CTSK	-1.99	2.62
BI704278	Cathepsin L, a	ctsla	CTSL1	1.90	2.31
BC075887	Cathepsin L.1	ctsl.1	CTSL2	-1.95	-6.31
Y08321	Cathepsin L, 1 b	ctsl1b	CTSL2	-0.27	-1.69
BI672022	LOC641325 weak sim to cathepsin W	zgc:123103	CTSW	3.74	3.73
BC055600	Cortactin	cttn	CTTN	0.47	2.61
BM103906	CUE domain containing 2	cuedc2	CUEDC2	0.38	-3.33
AB032726	CUG triplet repeat, RNA-binding protein 1	cugbp1	CUGBP1	-2.09	-0.26
AF321194	CUG triplet repeat, RNA binding protein 2	cugbp2	CUGBP2	-1.45	2.88
BI888458	Cullin 3	cul3	CUL3	0.51	-3.93

BI886394	Cullin 5	cul5	CUL5	2.29	-0.46
BI878753	LOC556215 weak sim to CUB and zona pellucida-like domains 1	wu:fb66a12	CUZD1	-1.79	-4.22
AF268197	Coxsackie virus and adenovirus receptor	cxadr	CXADR	3.49	1.90
BG729476	3' end of cxcl12a | chemokine (C-X-C motif) ligand 12a (stromal cell-derived factor 1) and 5' to LOC560477	BG729476	CXCL12	-1.02	3.47
AI641124	Chemokine (C-X-C motif) ligand 12b (stromal cell-derived factor 1)	cxcl12b	CXCL12	-1.66	1.44
AY057095	Chemokine (C-X-C motif) receptor 4a	cxcr4a	CXCR4	-0.66	3.32
AW019729	Intergenic 3' to cyb5b | cytochrome b5 type B and 5' to dhx38 | DEAH (Asp-Glu-Ala-His) box polypeptide 38	wu:fd56d05	CYB5A	1.87	1.50
AW115575	Cytochrome P450, subfamily XIA, polypeptide 1	cyp11a1	CYP11A1	1.40	-5.43
AY281362	Cytochrome P450, family 17, subfamily A, polypeptide 1	cyp17a1	CYP17A1	0.52	-3.11
BM185037	LOC406641 sim to cytochrome P450, family 20, subfamily A, polypeptide 1	zgc:63986	CYP20A1	1.24	1.84
U68234	Cytochrome P450, subfamily XXVIA, polypeptide 1	cyp26a1	CYP26A1	0.30	-3.99
AI497370	Weak sim to cytochrome P450, family 2, subfamily C, polypeptide 8	zgc:136371	CYP2C8	3.24	1.72
AF248042	Cytochrome P450, family 2, subfamily J, polypeptide 28	cyp2j28	CYP2J2	1.60	-2.14
AF221128	NP_001036243 sim to cytochrome P450, family 2, subfamily J, polypeptide 2	zgc:162815	CYP2J2	-2.61	-2.13
BC071533	LOC415182 sim to cytochrome P450, family 2, subfamily J, polypeptide 2	zgc:86915	CYP2J2	2.31	-3.84
BG884091	Intron of LOC563369 sim to CYP2R1 | cytochrome P450, family 2, subfamily R, polypeptide 1	BG884091	CYP2R1	1.86	-0.23
BM185124	LOC402847 sim to cytochrome P450, family 2, subfamily U, polypeptide 1	LOC402847	CYP2U1	3.19	0.31
BC085438	Cytochrome P450, family 3, subfamily c, polypeptide 1 like, 2	cyp3c1l2	CYP3A4	-2.12	-4.14
BC095036	Cytochrome P450, family 46, subfamily A, polypeptide 1	cyp46a1	CYP46A1	-1.72	-3.88
BM185006	Sim to cytochrome P450, family 4, subfamily B, polypeptide 1	BM185006	CYP4B1	-4.46	-4.57
AW019701	LOC562008 sim to cytochrome P450, family 4, subfamily V, polypeptide 2	zgc:154042	CYP4V2	3.84	2.85
AW077854	Disabled homolog 2 (Drosophila)	dab2	DAB2	0.92	-4.50
AF427108	Dachshund a	dacha	DACH2	-3.50	-2.61
AY513131	Dapper homolog 2, antagonist of beta-catenin (xenopus)	dact2	DACT2	-1.41	-2.17
BM183249	Defender against cell death 1	dad1	DAD1	1.27	1.53
AF231127	Death associated protein 1a	dap1a	DAP	-0.28	-3.38
AF137535	Death-associated protein 6	daxx	DAXX	-2.06	-0.83
AB018191	Daz-like gene	dazl	DAZL	-4.42	-5.03
AI878520	3' end of LOC799835; sim to PRR7 protein and 3' end of LOC561153; sim to DBN1: drebrin 1	wu:fc60b09	DBN1	1.57	1.75
AI544627	3' end of LOC100148204 part sim to DBNL | drebrin-like and 3' to si:dkey-40c11.1 sim to RTKN | rhotekin	wu:fb76h05	DBNL	-1.48	-1.63
AI415831	LOC431748 sim to drebrin-like	zgc:91835	DBNL	-2.10	-1.48
BQ618302	3' end of LOC100151219 part sim to DBR1 | debranching enzyme homolog 1 and 3' to LOC572355 | sim to CHD9 | chromodomain helicase DNA binding protein 9	BQ618302	DBR1	3.20	-0.86
AF030285	Developing brain homeobox 1b	dbx1b	DBX1	4.94	3.08
BI846005	LOC563259 sim to doublecortin domain containing 2	zgc:123267	DCDC2	-2.22	-1.32
AW233222	Dachsous 1	dchs1	DCHS1	0.49	1.98
AJ344448	Decapping enzyme	dcp1a	DCP1A	-0.61	-2.40
AF280090	Dopachrome tautomerase	dct	DCT	2.96	0.38
AA494790	Dicarbonyl/L-xylulose reductase	dcxr	DCXR	0.86	2.17
AW184045	Dimethylarginine dimethylaminohydrolase 1	zgc:85829	DDAH1	-2.14	-0.83
AW116386	LOC393599 sim to damage-specific DNA binding protein 1, 127kDa	zgc:63840	DDB1	2.38	0.61
AI815343	LOC560581 sim to development and differentiation enhancing factor 2	zgc:158353	DDEF2	-1.96	-1.19
AW344255	DNA-damage inducible protein 2	ddi2	DDI2	1.73	-0.48
AW115990	3' end of brd8: bromodomain containing 8 and 3' end of im:7137886 sim to DDIT4L: DNA-damage-inducible transcript 4-like	AW115990	DDIT4L	-1.12	2.60
AW306107	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (DBP5 homolog, yeast)	ddx19	DDX19B	-1.77	-2.49
AI397119	Sim to DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	ddx20	DDX20	2.31	-1.84
BI890491	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39b	ddx39b	DDX39	-2.23	-1.86
BM184007	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	ddx41	DDX41	-2.49	-2.46
BG727249	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	ddx5	DDX5	-0.34	2.50
AI964375	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	ddx56	DDX56	3.12	0.37
AW422167	Degenerative spermatocyte homolog 2, lipid desaturase	degs2	DEGS2	-0.04	-3.03
AI667236	DEP domain containing 6	depdc6	DEPDC6	2.66	2.03
BC083220	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	dera	DERA	2.55	0.53
BM184284	Der1-like domain family, member 1	derl1	DERL1	2.27	1.83
AI601451	Intron of zgc:154009 : desmin	AI601451	DES	1.31	-1.94
BC067602	DNA fragmentation factor, beta polypeptide (caspase-activated DNase)	dffb	DFFB	0.40	-2.49
AI957604	3' end of dfna5: deafness, autosomal dominant 5	AI957604	DFNA5	0.92	3.08
BC055631	7-dehydrocholesterol reductase	dhcr7	DHCR7	0.21	6.20
BI708067	Dihydrodiol dehydrogenase (dimeric), like	dhdhl	DHDH	2.21	3.17
AY026507	Dihydrofolate reductase	dhfr	DHFR	-0.68	-3.24
AI721540	Dihydroorotate dehydrogenase	dhodh	DHODH	2.40	2.38
BI983608	LOC556393 sim to dehydrogenase/reductase (SDR family) member 12	zgc:153679	DHRS12	-2.91	-1.66
AW134000	Sim to diaphanous homolog 1	wu:fi40a06	DIAPH1	-7.31	-6.38
BM104245	3' end of dixdc1b: DIX domain containing 1b and 5' to ddx10: DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	BM104245	DIXDC1	-1.53	-1.03
BE605392	3' end of LOC566257 sim toDLC1 | deleted in liver cancer 1 and 3' to rars arginyl-tRNA synthetase	BE605392	DLC1	1.41	-1.50
BM184863	Discs, large (Drosophila) homolog 1	dlg1	DLG1	-2.22	2.57
BG883810	Intron of MGC162970 | similar to SAP102	BG883810	DLG3	4.18	-0.96
AI957667	Discs, large (Drosophila) homolog-associated protein 5	dlgap5	DLGAP5	0.37	-1.58
AF146429	DeltaC	dlc	DLL1	0.60	2.36
U67842	Distal-less homeobox gene 1a	dlx1a	DLX1	0.67	2.21
U67843	Distal-less homeobox gene 2b	dlx2b	DLX2	-2.82	-2.67
X65060	Dlx-3 (distal-less related homeobox-containing) gene	dlx3b	DLX3	2.64	3.83
U03876	Distal-less homeobox gene 5a	dlx5a	DLX5	2.15	-0.20
AI722479	3' end or last intron of LOC796779 | similar to deleted in malignant brain tumors 1 and 5' to si:dkey-14d8.21 weak sim to DMBT1 | deleted in malignant brain tumors 1	AI722479	DMBT1	-2.16	-1.74
BC083273	LOC450035 sim to doublesex and mab-3 related transcription factor 3	zgc:101766	DMRT3	1.78	-0.59
BI891737	LOC560838: DnaJ (Hsp40) homolog, subfamily A member	dnaja	DNAJA1	-0.42	3.34
AI497286	DnaJ (Hsp40) homolog, subfamily C, member 3	dnajc3	DNAJC3	-0.66	3.20
BC076354	DnaJ (Hsp40) homolog, subfamily C, member 5	dnajc5	DNAJC5	-2.08	-2.54
BI865944	DnaJ (Hsp40) homolog, subfamily C, member 7	dnajc7	DNAJC7	-1.81	0.79
AW019064	Deoxyribonuclease I-like 3	dnase1l3	DNASE1L3	2.82	1.43
BM172694	LOC393843 sim to DNASE1L3 | deoxyribonuclease I-like 3	zgc:77816	DNASE1L3	-1.90	-0.90
BC095578	Dead end	dnd	DND1	-2.26	-5.17
AI721310	Dynamin 1-like	dnm1l	DNM1L	-2.19	0.35
AB196917	DNA (cytosine-5-)-methyltransferase 6 (sim to DNA (cytosine-5-)-methyltransferase 3 alpha)	dnmt6	DNMT3A	1.85	-0.22
AB196915	DNA (cytosine-5-)-methyltransferase 4	dnmt4	DNMT3B	-0.19	-2.91
BG737918	DNA (cytosine-5-)-methyltransferase 5 (sim to DNA (cytosine-5-)-methyltransferase 3 beta)	dnmt5	DNMT3B	0.82	-3.35
AI931096	DNA (cytosine-5-)-methyltransferase 7 (sim to DNA (cytosine-5-)-methyltransferase 3 beta)	dnmt7	DNMT3B	-1.02	-2.57
BI887627	Deoxynucleotidyltransferase, terminal, interacting protein 2	dnttip2	DNTTIP2	1.12	1.80
AW202714	LOC393582 sim to dopey family member 2	zgc:63622	DOPEY2	2.13	1.18
BI983485	3' end of zgc:112231: sim to DPH3: DPH3, KTI11 homolog and 5' to zgc:92024: NCK adaptor protein 2	BI983485	DPH3	2.86	1.13
CK698755	Sim to DPH3 | DPH3, KTI11 homolog	zgc:112231	DPH3	-1.75	-1.34
BC085447	DPH5 homolog (S. cerevisiae)	dph5	DPH5	2.51	0.61
AW077909	Dipeptidylpeptidase 3	dpp3	DPP3	-2.33	-0.31
AW019791	Dihydropyrimidine dehydrogenase	dpyd	DPYD	5.17	3.17
AY333791	Dopamine receptor D2 like	drd2l	DRD2	3.38	0.04
AY750154	Dopamine receptor D4b	Drd4b	DRD4	2.57	-1.07
BE017474	Desmoglein 2	dsg2	DSG2	-3.41	-0.47
BI876262	Dentin sialophosphoprotein	BI876262	DSPP	-5.69	-5.67
BI884064	Dual serine/threonine and tyrosine protein kinase	dstyk	DSTYK	-0.19	4.50

BM104281	Denticleless homolog (Drosophila)	dtl	DTL	1.86	-2.84
BI888604	Dual specificity phosphatase 1	dusp1	DUSP1	0.73	2.33
BC078397	LOC445057 sim to dual specificity phosphatase 2	zgc:91929	DUSP2	-0.68	1.65
AI601685	Dual specificity phosphatase 5	dusp5	DUSP5	2.17	-1.99
BI706908	Dual specificity phosphatase 6	dusp6	DUSP6	3.53	-1.47
BE017477	DUTP pyrophosphatase	dut	DUT	0.59	-3.06
BM083964	Dishevelled, dsh homolog 2 (Drosophila)	dvl2	DVL2	0.51	-2.95
AW344179	Sim to ELL associated factor 1	AW344179	EAF1	2.16	-0.23
BI878159	Epithelial cell transforming sequence 2 oncogene	ect2	ECT2	2.41	4.72
BG303491	ER degradation enhancer, mannosidase alpha-like 1	edem1	EDEM1	-0.99	2.25
BI885824	Sim to endothelial differentiation-related factor 1	BI885824	EDF1	3.49	1.15
AB057355	Endothelin receptor type A	ednra	EDNRA	2.23	2.36
BC064291	Elongation factor 1-alpha	ef1a	EEF1A1	-3.31	2.56
BC075885	LOC436644 sim to eukaryotic translation elongation factor 1 alpha 2	zgc:92085	EEF1A2	-1.25	-1.59
BE557668	Eukaryotic translation elongation factor 1 beta 2	eef1b2	EEF1B2	2.91	2.49
CD606031	Eukaryotic translation elongation factor 2, like	eef2l	EEF2	3.17	-2.37
AW305495	LOC336168 sim to eukaryotic translation elongation factor 2	si:ch211-113n10.4	EEF2	-3.04	-1.01
BM036459	EF-hand domain (C-terminal) containing 1	efhc1	EFHC1	-1.91	3.56
Y09668	Ephrin A2	efna2	EFNA2	-2.17	-1.24
AF375224	Ephrin B1	efnb1	EFNB1	0.42	2.16
AF375226	Ephrin B2b	efnb2b	EFNB2	2.15	1.80
AY332224	Epidermal growth factor precursor	egf	EGF	-0.19	-2.06
BC076013	EGF-like-domain, multiple 6	egfl6	EGFL6	-1.40	-3.16
BG305741	3' end of egr1 | early growth response 1	BG305741	EGR1	3.18	5.26
AY070229	Early growth response 2a	egr2a	EGR2	1.72	3.46
X70322	Early growth response 2b	egr2b	EGR2	-1.81	-2.01
AI584583	EH-domain containing 3, like	ehd3l	EHD1	-2.01	-1.56
AF257517	Eukaryotic translation initiation factor 2, subunit 1 alpha	eif2s1	EIF2S1	-0.46	2.90
AI964258	Eukaryotic translation initiation factor 3, subunit C	eif3c	EIF3C	0.26	3.13
BG304333	Eukaryotic translation initiation factor 3, subunit 6	eif3ea	EIF3E	-0.42	2.26
AW232975	Sim to eukaryotic translation initiation factor 3, subunit F	LOC557270	EIF3F	1.02	1.65
AI477041	Eukaryotic translation initiation factor 3, subunit 6 interacting protein	eif3s6ip	EIF3L	0.45	2.43
BI876856	Eukaryotic translation initiation factor 4A, isoform 1B	eif4a1b	EIF4A1	-0.90	2.37
AW466697	Eukaryotic translation initiation factor 4A, isoform 2	eif4a2	EIF4A2	0.41	1.77
AF176316	Eukaryotic translation initiation factor 4e 1b	eif4e1b	EIF4E	-0.30	-4.10
BM154327	LOC492482 sim to eukaryotic translation initiation factor 4E binding	zgc:103720	EIF4EBP3	-4.61	-1.35
BM185252	Sim to eukaryotic translation initiation factor 4 gamma, 3	LOC568761	EIF4G3	-1.56	-0.72
U84615	ETS-related factor1	ef1	ELF1	-3.27	-0.23
AI666886	ELMO/CED-12 domain containing 2	elmod2	ELMOD2	1.70	1.32
BI866359	Intron of elovl1b | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1b	BI866359	ELOVL1	5.05	0.81
BG303052	ELOVL family member 5, elongation of long chain fatty acids (yeast)	elovl5	ELOVL5	3.48	3.12
BI876830	ELOVL family member 7, elongation of long chain fatty acids (yeast) b	elovl7b	ELOVL7	-1.93	-2.50
BI877696	Elongation of very long chain fatty acids-like	zgc:55879	ELOVL7	-2.70	-1.92
BE605325	Sim to epithelial membrane protein 2	BE605325	EMP2	-1.73	-2.32
BI845475	3' end of enah: enabled homolog and 5' end to lbr: lamin B receptor	BI845475	ENAH	-3.45	-2.55
BC090907	Enabled homolog (Drosophila)	enah	ENAH	-1.14	-1.54
BI704313	Ectodermal-neural cortex (with BTB-like domain)	enc1	ENC1	2.71	1.84
AI959507	Sim to ectonucleotide pyrophosphatase/phosphodiesterase 2	AI959507	ENPP2	2.96	2.95
AI721596	Weak sim to ectonucleotide pyrophosphatase/phosphodiesterase 3	AI721596	ENPP3	-1.63	-2.66
BC078419	Ectonucleoside triphosphate diphosphohydrolase 2 a.1	entpd2a.1	ENTPD2	-2.62	-2.42
AF329830	Eomesodermin homolog a	eomesa	EOMES	-1.19	-3.19
BI979933	Enhancer of polycomb homolog 2 (Drosophila)	epc2	EPC2	0.29	-2.11
AW077546	Ependymin	epd	EPDR1	-6.43	-3.81
BI840968	Intron of LOC100006306 sim to EPHA3 | EPH receptor A3	BI840968	EPHA3	1.79	-0.83
BC078252	Eph-like kinase 1	ek1	EPHA4	1.76	-3.08
AW154716	Eph receptor A4a	epha4a	EPHA4	0.38	-3.23
AF369381	Epha4b	epha4b	EPHA4	0.68	1.50
AW466558	Epoxide hydrolase 1, microsomal (xenobiotic)	ephx1	EPHX1	5.39	-0.93
AF349034	Myeloid-specific peroxidase	mpx	EPX	0.24	1.58
BC086811	V-ets erythroblastosis virus E26 oncogene like (avian)	erg	ERG	-1.10	-1.74
AW116232	ERGIC and golgi 3	ergic3	ERGIC3	-1.80	3.27
AI878797	3' end of erlin1 | ER lipid raft associated 1 and 3' to zgc:66426 calponin-homology and microtubule-associated protein	AI878797	ERLIN1	1.07	1.85
BC053166	ERO1-like	ero1l	ERO1LB	-1.84	-2.39
BG883231	LOC767700 sim to ERO1-like beta (S. cerevisiae)	zgc:153032	ERO1LB	2.14	2.17
BI890679	Thioredoxin domain containing 4 (endoplasmic reticulum)	txndc4	ERP44	2.05	2.11
AW128527	LOC798009 sim to ERBB receptor feedback inhibitor 1 (mitogen-inducible gene 6 protein)	zgc:162129	ERRFI1	2.77	3.23
AF349414	Estrogen receptor 2a	esr2a	ESR2	2.37	0.41
BG303774	Epithelial splicing regulatory protein 2	esrp2	ESRP1	-2.75	2.09
AW018801	LOC541449 sim to ethanolamine kinase 1	zgc:113516	ETNK1	1.61	3.09
BG985478	V-ets erythroblastosis virus E26 oncogene homolog 1a	ets1a	ETS1	-1.51	3.28
AI816689	Ets variant gene 5 (ets-related molecule)	etv5	ETV5	-2.07	-1.82
AI957816	LOC793139 envoplakin	evpl	EVPL	-3.77	-2.46
AI626478	Envoplakin	si:ch211-157f15.1	EVPL	-2.60	-1.80
AI477647	Exocyst complex component 1	exoc1	EXOC1	1.17	-2.46
BI878954	Exostoses (multiple) 1a	ext1a	EXT1	-1.73	-0.29
AY734456	Exostoses (multiple) 1b	ext1b	EXT1	2.00	2.46
BC081636	Eyes absent 2	zgc:92279	EYA2	-1.68	-2.00
BI476229	Ezrin	ezr	EZR	-1.26	-1.62
BC097035	Coagulation factor X ; LOC100150577	f10	F10	2.18	-3.86
AW115527	3' end of f2 | coagulation factor II (thrombin) and 5' to arhgap1 | Rho GTPase activating protein 1	AW115527	F2	2.63	-4.11
AY040345	Coagulation factor VII	f7	F7	2.84	-4.11
AI722559	Coagulation factor VIIi	f7i	F7	2.17	-3.66
BI843279	Coagulation factor IX	f9	F9	2.60	-3.87
BC076113	Fatty acid amide hydrolase 2a	faah2a	FAAH2	3.41	3.20
BI983434	Fatty acid amide hydrolase 2b	faah2b	FAAH2	-0.83	-1.55
BM185013	3' end of fabp2: fatty acid binding protein 2, intestinal and 3' to LOC558085 sim to USP53: ubiquitin specific peptidase 53	BM185013	FABP2	2.98	2.10
AF448057	Fatty acid binding protein 3, muscle and heart	fabp3	FABP3	2.03	3.40
CO931612	Fatty acid binding protein 6, ileal (gastrotropin)	fabp6	FABP6	-3.91	-4.29
AF309556	Fatty acid desaturase 2	fads2	FADS2	-3.42	5.07
BC095057	Fumarylacetoacetate hydrolase domain containing 1	fahd1	FAHD1	2.88	3.15
BM182806	Family with sequence similarity 125, member B	fam125bb	FAM125B	1.62	1.33
AY301038	Fanconi anemia, complementation group D2	fancd2	FANCD2	1.89	-1.44
BM096047	Fanconi anemia, complementation group L	fancl	FANCL	-2.12	0.16
BG883685	FERM, RhoGEF and pleckstrin domain protein 2	farp2	FARP2	-2.25	-0.52
AW058816	Phenylalanine-tRNA synthetase-like, alpha subunit	farsla	FARSA	3.04	0.61
AF469608	FAT tumor suppressor homolog 1	fat1	FAT1	-1.56	-2.96
BC083431	Fibulin 5	fbln5	FBLN5	1.35	2.05
AA494925	Fructose-1,6-bisphosphatase 1b	fbp1	FBP1	2.14	1.10
CK705086	Sim to FBXO11 | F-box protein 11	CK705086	FBXO11	2.22	3.12
BG303968	F-box protein 32	fbxo32	FBXO32	-0.60	-3.78
AW115660	LOC393403 weak sim to F-box protein 43	zgc:66488	FBXO43	-2.11	-2.91
BI885932	F-box protein 5	fbxo5	FBXO5	-1.38	-4.49
AY960873	F-box and WD-40 domain protein FBXW14	fbxw14	FBXW12	-0.50	-2.08
BC057409	F-box and WD-40 domain protein 5	fbxw5	FBXW5	-2.68	-2.77
AI957820	Flap structure-specific endonuclease 1	fen1	FEN1	-2.44	-2.21
AI883857	Fibrinogen alpha chain	fga	FGA	1.77	3.91
BI878927	Fibrinogen, B beta polypeptide	fgb	FGB	2.64	4.10

AF017370	Faciogenital dysplasia	fgd	FGD1	2.92	-0.37
AF544025	Fibroblast growth factor 10 a	fgf10a	FGF10	0.57	2.03
AB195468	Fibroblast growth factor 18b	fgf18b	FGF18	-0.73	1.66
AY753222	Fibroblast growth factor 23	fgf23	FGF23	-0.13	2.03
AF283555	Fibroblast growth factor 4	fgf4	FGF4	0.82	1.69
AB194699	Fibroblast growth factor 5	fgf5	FGF5	-0.30	4.59
AB194700	Fibroblast growth factor 6b	fgf6b	FGF6	-1.28	1.73
AF030560	Fibroblast growth factor 8a	fgf8a	FGF8	0.21	3.19
AB100171	Fibroblast growth factor 8 b	fgf8b	FGF8	-0.42	2.26
AF389400	Fibroblast growth factor receptor 1	fgfr1a	FGFR1	0.13	2.30
AW232332	FGFR1 oncogene partner 2	fgfr1op2	FGFR1OP2	-1.71	0.75
AB084105	Fibroblast growth factor receptor 2	fgfr2	FGFR2	0.25	1.68
U23839	Fibroblast growth factor receptor 4	fgfr4	FGFR4	3.08	5.06
BI878442	Fibrinogen gamma chain	fgg	FGG	1.79	4.45
BI983495	Fragile histidine triad gene	fhit	FHIT	-1.73	2.98
BI427744	FK506 binding protein 11	fkbp11	FKBP11	2.82	0.73
BI979906	LOC447939 sim to FK506-binding protein 2	zgc:101826	FKBP2	1.67	1.75
BI896312	Friend leukemia integration 1	fli1a	FLI1	-2.40	2.01
AY839950	Friend leukemia integration 1b	fli1b	FLI1	-0.54	2.59
AW777936	Flightless I homolog	flii	FLII	-3.79	-2.70
AA658587	Filamin B, beta (actin binding protein 278)	flnbl	FLNB	-0.66	-2.10
AI588460	Filamin C, gamma b (actin binding protein 280)	flncb	FLNC	0.46	2.50
BI885492	Flotillin 1b	flot1b	FLOT1	-1.90	-3.12
AW128244	Flotillin 2a	flot2a	FLOT2	1.50	2.95
AW076633	Intergenic 3' to flt1 | fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) and 5' to LOC566708 | similar to FMS-like tyrosine kinase 3	AW076633	FLT1	-1.35	-1.84
AF180354	Kinase insert domain receptor like (sim to fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	kdrl	FLT1	0.84	2.61
AI601469	Sim to feline leukemia virus subgroup C cellular receptor family, member 2	si:ch211-119b12.6	FLVCR2	0.95	1.86
BC096939	LOC449691 sim to fibromodulin	zgc:113456	FMOD	2.09	-0.88
BG302581	Fibronectin 1b	fn1b	FN1	2.44	-5.10
AF052250	Forkhead box A1	foxa1	FOXA1	2.40	4.21
AF052247	Forkhead box A	foxa	FOXA2	-1.15	-4.25
Z22762	Forkhead box A2	foxa2	FOXA2	3.82	2.78
AF052245	Forkhead box A3	foxa3	FOXA2	-0.26	3.82
NM_131729	Forkhead box C1b	foxc1b	FOXC1	-2.51	0.25
AF052251	Forkhead box D5	foxd5	FOXD4	4.36	-2.01
BF937564	LOC405850 sim to Forkhead box G1	zgc:85969	FOXG1	2.00	-0.51
AF263000	Forkhead box H1	foxh1	FOXH1	1.73	-2.85
AW076653	Forkhead box K2	foxk2	FOXK2	-2.16	-3.19
AW566603	Forkhead box Q1	foxq1	FOXQ1	-3.35	-1.47
BC058343	Folylpolyglutamate synthase	fpgs	FPGS	2.51	2.05
AI958047	Sim to FRAS1 related extracellular matrix protein 2	wu:fc90b05	FREM2	1.67	1.90
BC097220	LOC557352 sim to follistatin-like 3 (secreted glycoprotein)	zgc:114170	FSTL3	-1.72	-2.45
BI672329	3' end of zgc:92245 ;LOC792323 sim to ferritin, heavy polypeptide 1	BI672329	FTH1	2.34	1.32
BC081630	LOC447823 sim to ferritin, heavy polypeptide 1	zgc:92245	FTH1	-3.14	1.59
BC078236	LOC445165 sim to fucosidase, alpha-L- 1, tissue	zgc:101116	FUCA1	-3.83	1.24
AW115841	LOC394058; fusion (involved in t(12;16) in malignant liposarcoma)	fus	FUS	1.82	0.80
BC093307	LOC550469 sim to fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	zgc:112433	FUT9	-4.13	-2.88
BE605503	LOC664694 sim to fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	zgc:136963	FUT9	-3.55	-1.63
AW455046	FXYD domain containing ion transport regulator 1 (phospholemman)	LOC798940	FXYD1	2.90	3.93
BG307572	New protein weak sim toFYB: FYN binding protein (FYB-120/130)	BG307572	FYB	1.06	-1.59
CD604980	3' end of LOC796938 sim to FYB | FYN binding protein (FYB-120/130) and 3' to LOC797005 | similar to malignant fibrous histiocytoma amplified sequence 1	CD604980	FYB	1.84	-1.83
AF269145	FYN oncogene related to SRC, FGR, YES a	fyna	FYN	1.56	2.40
AF039411	Frizzled homolog 10	fzd10	FZD10	-1.10	-3.34
AF039410	Frizzled homolog 8b	fzd8b	FZD5	0.58	-3.66
AF336123	Frizzled homolog 7a	fzd7a	FZD7	1.03	-2.73
BC049397	Frizzled homolog 7b	fzd7b	FZD7	-1.23	-2.65
U49409	Frizzled homolog 8a	fzd8a	FZD8	3.04	1.36
CB361052	LOC100136843 no homology overlap with zgc:112970: LOC541543 weak sim to G2E3: G2/M-phase specific E3 ubiquitin ligase (partially)	zgc:174680	G2E3	-1.10	-1.57
AF257741	GA-binding protein transcription factor, alpha subunit	gabpa	GABPA	-2.18	1.38
BI671266	3' end of DKEYP-87A12.2 sim GABRD | gamma-aminobutyric acid (GABA) A receptor, delta and 5' to sult1st4 | sulfotransferase family 1, cytosolic sulfotransferase 4	BI671266	GABRD	1.90	-1.01
BE015653	Glutamate decarboxylase 1	gad1	GAD1	-1.31	3.50
BI672019	Growth arrest and DNA-damage-inducible, alpha	gadd45a	GADD45A	3.89	0.64
BF717630	Growth arrest and DNA-damage-inducible, beta	gadd45b	GADD45B	-0.90	3.13
BG306112	Growth arrest and DNA-damage-inducible, gamma	gadd45g	GADD45G	-1.30	2.04
BI880272	Intron of LOC559073 sim to to UDP-GalNAc:polypeptide, N-acetylgalactosaminyltransferase	BI880272	GALNT1	-1.74	-0.96
CK707391	3' end of si:dkey-162b3.1 sim to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	CK707391	GALNT2	1.99	2.29
BC090692	WD repeat domain 51B, like (sim to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4))	wdr51bl	GALNT4	-2.23	-1.12
BI896304	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	galnt7	GALNT7	-2.14	-1.30
BI672775	Sim to GANAB | glucosidase, alpha; neutral AB	LOC561509	GANAB	1.03	1.58
L27645	Growth associated protein 43	gap43	GAP43	0.20	-4.13
BC083506	Glyceraldehyde-3-phosphate dehydrogenase	gapdh	GAPDH	-1.64	-1.45
BM101651	Nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	nola1	GAR1	1.08	-3.25
AJ242515	GATA-binding protein 5	gata5	GATA5	4.04	1.40
AF191578	GATA-binding protein 6	gata6	GATA6	2.27	3.52
BM101878	3' end of DKEY-183C23.2: Golgi-specific brefeldin A-resistance factor 1 and 3' to zgc:114051: sim to H2AFY: H2A histone family, member Y	BM101878	GBF1	0.48	2.27
BM036082	Glycine C-acetyltransferase	gcat	GCAT	1.73	2.03
BG305473	Glutaryl-Coenzyme A dehydrogenase	gcdh	GCDH	1.28	2.45
BI985053	Glutaryl-Coenzyme A dehydrogenase, like	gcdhl	GCDH	3.47	1.98
AJ133697	Glucagon a	gcga	GCG	-0.53	4.81
BI981470	GTP cyclohydrolase I feedback regulator	gchfr	GCHFR	5.63	2.61
AW421330	LOC553701 sim to guanine deaminase	zgc:112282	GDA	1.79	2.54
AF411599	Growth differentiation factor 11	gdf11	GDF11	2.21	-2.54
U00931	Decapentaplegic and Vg-related 1 (sim to growth differentiation factor 3)	dvr1	GDF3	-4.01	-6.84
BI475848	Growth differentiation factor 6a	gdf6a	GDF6	-0.32	-2.07
AF113022	Growth/differentiation factor 7	gdf7	GDF7	0.73	2.74
AY833104	Growth differentiation factor 9	gdf9	GDF9	-0.21	-3.49
BI877998	GDP dissociation inhibitor 2	gdi2	GDI2	5.33	1.88
BE558157	Glycerophosphodiester phosphodiesterase domain containing 3	gdpd3	GDPD3	-2.40	-1.58
AW154507	Gem (nuclear organelle) associated protein 4	gemin4	GEMIN4	-2.16	-1.21
BQ093548	5' end of DKEY-222H21.13 sim to gamma-glutamyltransferase 1 (DKEY-222H21.13)	BQ093548	GGT1	4.72	2.12
AI723254	Weak sim to GTPase, IMAP family member 5	AI723254	GIMAP5	2.97	-0.37
AI959756	LOC503528 weak sim to GIN1: gypsy retrotransposon integrase 1	zgc:113436	GIN1	-1.93	-2.49
AF035481	Connexin 43	cx43	GJA1	2.48	0.52
BG303025	Connexin 28.9	cx28.9	GJA3	3.49	3.15
AF465751	Connexin 48.5	cx48.5	GJA3	-0.42	3.36
NM_212825	Connexin 33.8	cx33.8	GJB2	0.42	2.35
L46801	Connexin 43.4 (gap junction protein, gamma 1, 45kDa)	cx43.4	GJC1	-2.69	-4.30
BC081653	Connexin 47.1 (gap junction protein, gamma 1, 45kDa)	cx47.1	GJC1	2.43	-1.58
BF717767	LOC100136866 sim to glycerol kinase	zgc:172295	GK	2.08	0.55
BI840365	Galactosidase, beta 1-like	glb1l	GLB1	3.72	0.63
AY648848	GLE1 RNA export mediator-like	gle1l	GLE1	0.95	-2.17
AF085746	GLI-Kruppel family member GLI2a	gli2a	GLI2	-2.35	-0.25

BG303282	3' end of LOC565337: similar to glycolipid transfer protein domain containing and 3' end to atp1b2b:	BG303282	GLTPD1	3.01	2.51
BI704327	Sim to Glutamate-ammonia ligase (glutamine synthase) b	LOC798212	GLUL	-1.66	-4.20
BM184837	Glycerate kinase	zgc:153346	GLYCTK	4.60	1.55
BE605276	Glia maturation factor, beta	gmfb	GMFB	1.92	0.93
BM184447	Geminin, DNA replication inhibitor	gmnn	GMNN	-1.41	-4.30
BI885489	3' end of gmpr: guanosine monophosphate reductase and 3' to atxn1b: ataxin 1b	BI885489	GMPR	5.44	-1.18
AI958597	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	gnai1	GNAI1	-1.23	-4.05
AW116923	Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gnai2	GNAI2	-2.04	-3.08
BI983956	Guanine nucleotide binding protein (G protein) alpha v1	gnav1	GNAI2	4.94	0.62
BI318361	Guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	gnao1	GNAO1	-0.48	-2.42
AY050499	Guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	gnat1	GNAT1	-0.93	-2.95
BC076127	Guanine nucleotide binding protein (G protein), beta polypeptide 3, like	gnb3l	GNB3	-2.01	-3.05
AI558965	3' end of gnb5a | guanine nucleotide binding protein (G protein), beta 5a and 5' to ap4e1 | adaptor-related protein complex 4, epsilon 1 subunit	wu:fb78e09	GNB5	1.84	-0.96
BI883692	Guanine nucleotide binding protein (G protein), gamma 12	gng12	GNG12	2.70	0.70
BM005415	Guanine nucleotide binding protein (G protein), gamma 3	gng3	GNG3	-1.96	-1.71
BI879430	Guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	gngt1	GNGT1	-2.07	-3.25
BI318564	LOC797361 sim to guanine nucleotide binding protein-gamma transducing activity polypeptide 2	LOC797361	GNGT2	-1.60	-1.98
BC045323	Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID), b	gnsb	GNS	-0.11	2.03
BM183894	Glutamic-oxaloacetic transaminase 1, soluble	got1	GOT1	-1.37	-2.76
BG306810	Glycerol-3-phosphate dehydrogenase 1b	gpd1b	GPD1	-0.62	3.56
BC065340	G protein-coupled receptor 143	gpr143	GPR143	-3.25	-2.10
BE605485	G protein-coupled receptor 34 a	gpr34a	GPR34	2.35	4.98
BC054634	LOC791773 sim to G protein-coupled receptor 39	LOC791773	GPR39	2.63	0.27
AW595310	Sim to G protein-coupled receptor 44	LOC100000103	GPR44	-2.68	-1.77
AY619723	G-protein signaling modulator 1 (AGS3-like, C. elegans)	gpsm1	GPSM1	-0.10	2.63
CB890997	Glutamic pyruvate transaminase (alanine aminotransferase) 2	gpt2	GPT2	1.79	-0.49
AW232474	Glutathione peroxidase 1a	gpx1a	GPX1	3.78	3.52
BI896246	Glutathione peroxidase 4a	gpx4a	GPX4	2.87	2.50
BM036392	Glutathione peroxidase 4b	gpx4b	GPX4	2.54	2.69
BC095199	GRB2-related adaptor protein	grap	GRAP	-1.65	1.14
BI886875	Growth factor receptor-bound protein 2	grb2	GRB2	-0.29	2.11
AY427782	Gremlin 1 homolog, cysteine knot superfamily (Xenopus laevis)	grem1	GREM1	-2.93	-2.53
BI882203	3' end of grhl1 | grainyhead-like 1 and 5' to klf11b Kruppel-like factor 11b	BI882203	GRHL1	-3.44	-1.07
BE605668	LOC555744 sim to grainyhead-like 2	zgc:110324	GRHL2	-3.36	-1.43
AI477969	LOC795386 sim to grainyhead-like 3	sb:cb467	GRHL3	-2.51	-2.53
AF525742	Glutamate receptor, ionotropic, AMPA 1b	gria1b	GRIA1	-1.91	-2.66
AF273479	LOC553977 weak sim to Granulin 1	CH211-173P18.8	GRN	-4.58	0.79
BI865412	Sim to GrpE-like 2, mitochondrial (E. coli)	BI865412	GRPEL2	-3.02	0.55
AI957790	Growth hormone regulated TBC protein 1	grtp1	GRTP1	3.78	1.43
AB032265	Glycogen synthase kinase 3 beta	gsk3b	GSK3B	0.56	3.23
BG303563	Gelsolin b	gsnb	GSN	-0.75	-3.65
AW128619	G1 to S phase transition 1	gspt1	GSPT1	0.35	1.94
BF938011	Glutathione S-transferase, alpha-like	gstal	GSTA1	1.22	-2.37
BM071872	Glutathione S-transferase M	gstm	GSTM3	-0.56	-2.54
AF285098	Glutathione S-transferase pi	gstp1	GSTP1	-1.29	-1.77
BC096997	LOC573862 sim to glutathione transferase zeta 1	zgc:113898	GSTZ1	1.68	1.82
BM104296	Sim to general transcription factor IIA, 1, 19/37kDa	BM104296	GTF2A1	-0.73	-3.61
BG307533	General transcription factor IIA, 1	gtf2a1	GTF2A1	-0.87	-2.17
BI705646	General transcription factor IIE, polypeptide 2, beta	gtf2e2	GTF2E2	1.63	-0.15
BM103291	General transcription factor IIIC, polypeptide 5	gtf3c5	GTF3C5	1.30	3.01
AY850384	Guanylate cyclase activator 1d	guca1d	GUCA1A	2.59	-2.49
BI670894	LOC791705 sim to Guanylate kinase 1	guk1	GUK1	-2.74	-6.05
BI673452	Glycogenin 1	gyg1	GYG1	-4.07	-3.32
AW115892	LOC394155 sim to glycogen synthase 1 (muscle)	zgc:63701	GYS1	-2.57	-1.20
BC095660	Glycogen synthase 2	gys2	GYS2	0.86	4.27
AI667668	Sim to hyaluronan binding protein 2	LOC563048	HABP2	3.35	3.81
AW115528	2-hydroxyacyl-CoA lyase 1	hacl1	HACL1	1.49	1.90
AI959469	Hydroxyacylglutathione hydrolase	hagh	HAGH	0.70	2.98
AY130989	Hepcidin antimicrobial peptide 1; weak homol to HAMP; putative liver tumor regressor	hamp1	HAMP	3.08	0.23
AW777457	Hydroxyacid oxidase (glycolate oxidase) 1	hao1	HAO1	3.74	4.80
AI793901	Hyaluronan and proteoglycan link protein 1a	hapln1a	HAPLN1	1.66	-1.70
AI957786	Histidyl-tRNA synthetase	hars	HARS	1.79	1.40
U50380	Ba1 globin	ba1	HBE1	1.92	2.83
CN022310	LOC445037 sim to hemoglobin, gamma A	zgc:92880	HBG1	1.87	-0.66
BE693186	Hemoglobin alpha embryonic-1	hbae1	HBZ	-1.87	-3.67
BI704340	Histone deacetylase 1	hdac1	HDAC1	-1.83	1.31
AI667295	HECT domain containing 3	hectd3	HECTD3	1.81	2.63
AW154320	Helicase, lymphoid-specific	hells	HELLS	-0.37	-3.96
AF301264	Hairy-related 9	her9	HES1	-2.03	0.69
X97331	Hairy-related 3	her3	HES3	0.36	-1.72
AW117106	Hairy-related 4.1	CH73-21G5.4	HES5	3.11	-1.33
BC092915	Hairy-related 12	her12	HES5	1.02	-1.77
BM072241	LOC678530 sim to hairy and enhancer of split 5	zgc:136520	HES5	1.44	2.13
NM_194400	Hairy and enhancer of split 6 (Drosophila)	hes6	HES6	-1.81	-0.17
AY312568	Hairy-related 11 (sim to hairy and enhancer of split 7 (Drosophila))	her11	HES7	-1.09	-3.40
X95301	Hairy-related 5	her5	HES7	3.81	0.24
AF240772	Hairy and enhancer of split related-7	her7	HES7	0.47	-1.51
BG306318	Hexosaminidase A (alpha polypeptide)	hexa	HEXB	-0.02	2.13
CK707179	Weak sim to hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	CK707179	HEXDC	2.43	2.60
BG985516	Hairy/enhancer-of-split related with YRPW motif 1	hey1	HEY1	-2.65	0.81
BC093422	LOC550603 weak sim to major histocompatibility complex, class I-related	zgc:113060	MR1	1.30	1.75
AI626348	LOC571120 sim to hedgehog acyltransferase-like	zgc:154131	HHATL	-1.36	-1.70
AF131070	Hematopoietically expressed homeobox	hhex	HHEX	3.43	3.87
BM095392	3-hydroxyisobutyrate dehydrogenase	hibadhb	HIBADH	1.36	-2.24
BI476765	3-hydroxyisobutyryl-Coenzyme A hydrolase	hibch	HIBCH	2.41	0.88
AF111712	Hypermethylated in cancer 1 like	hic1l	HIC2	-1.02	-2.58
BI892416	Hypoxia induced gene 1 (sim to HIG1 domain family, member 1A)	hig1	HIGD1A	-1.21	-2.02
AW170846	Sim to huntingtin interacting protein 1	AW170846	HIP1	-3.74	-0.47
AI957899	LOC568076; HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	hira	HIRA	2.78	0.36
BI707054	LOC569609 weak sim to histidine acid phosphatase domain containing 1	LOC569609	HISPPD1	-2.08	-2.34
BI705577	Intron of mhc1uda | major histocompatibility complex class I UDA gene	BI705577	HLA-A	-0.85	-1.57
AW076914	Major histocompatibility complex class I UDA gene	mhc1uda	HLA-A	-3.93	-3.34
CV576541	Major histocompatibility complex class I ZE gene	mhc1ze	HLA-A	2.24	-1.25
NM_001004521	LOC368878 weak sim to major histocompatibility complex, class II, DP alpha 1	si:busm1-266f07.2	HLA-DPA1	-1.86	-1.92
L19450	LOC449802 sim to major histocompatibility complex, class II, DP alpha 1	zgc:92049	HLA-DPA1	-1.82	-1.58
L19449	Sim to major histocompatibility complex, class II, DQ alpha 1	L19449	HLA-DQA1	2.40	0.81
CN020335	LOC449802 weak sim to major histocompatibility complex, class II, DQ alpha 1	zgc:113912	HLA-DQA1	-2.48	-2.53
U08870	Major histocompatibility complex class II DAB gene	mhc2dab	HLA-DQB1	-3.07	-1.32
BI886388	LOC795095 sim to high-mobility group box 1	zgc:165618	HMGB1	-2.28	-1.01
AW777535	High-mobility group box 2	hmgb2	HMGB2	0.77	-2.24
CK703815	3' end of hmgcrb: 3-hydroxy-3-methylglutaryl-Coenzyme A reductase b	CK703815	HMGCR	2.27	0.96
BM036445	Hyaluronan mediated motility receptor	hmmr	HMMR	-3.46	-5.01
AI722432	Heme oxygenase (decycling) 1	hmox1	HMOX1	-0.64	2.63
AF288211	Homeo box (H6 family) 3	hmx3	HMX3	-2.92	-1.96
BG883304	Hepatocyte nuclear factor 4, alpha	hnf4a	HNF4A	0.08	3.47
BC066434	Heterogeneous nuclear ribonucleoprotein A0	hnrnpa0	HNRNPA0	-0.37	1.90
BC048898	Heterogeneous nuclear ribonucleoprotein A/B	hnrpab	HNRNPAB	-2.35	0.34
BI888859	Heterogeneous nuclear ribonucleoprotein D-like	hnrpdl	HNRNPD	0.12	1.73
BI880061	Heterogeneous nuclear ribonucleoprotein M	hnrnpm	HNRNPM	3.74	0.68

BI878475	Heterogeneous nuclear ribonucleoprotein R	hnrpr	HNRNPR	-1.50	0.49
AI793802	Homeodomain leucine zipper gene	homez	HOMEZ	3.78	0.95
AF071243	Homeo box A1a	hoxa1a	HOXA1	1.95	0.42
BC090761	Homeo box A13b	hoxa13b	HOXA13	-2.74	-2.84
AF307010	Homeo box A2b	hoxa2b	HOXA2	-3.27	-1.24
Y13944	Homeo box B3a	hoxb3a	HOXB3	0.23	2.02
NM_131537	Homeo box B5b	hoxb5b	HOXB5	0.08	-6.57
AY391430	Homeo box B9a	hoxb9a	HOXB9	2.25	5.40
NM_131122	Homeo box C4a	hoxc4a	HOXC4	-2.85	-3.15
NM_131126	Homeo box D9a	hoxd9a	HOXC9	-3.95	-4.70
X87750	Homeo box D10a	hoxd10a	HOXD10	2.17	-0.68
NM_131169	Homeo box D13a	hoxd13a	HOXD13	0.28	-4.01
Y14548	Homeo box D4a	hoxd4a	HOXD4	3.49	0.62
BG884044	Haptoglobin	hp	HP	3.84	6.10
BM035892	Hypoxanthine phosphoribosyltransferase 1, like	hprt1l	HPRT1	0.32	-2.87
AW116610	3' end of hpx ; hemopexin	AW116610	HPX	0.70	-2.66
BI880365	Heparan sulfate 6-O-sulfotransferase 1a	hs6st1a	HS6ST1	0.11	2.76
BG305366	Heat shock factor binding protein 1	hsbp1	HSBP1	2.82	0.33
BF717644	Hydroxysteroid (11-beta) dehydrogenase 3	hsd11b3	HSD11B1L	-0.29	3.49
BC083219	Hydroxysteroid (17-beta) dehydrogenase 10	hsd17b10	HSD17B10	1.30	-2.49
AW116075	Hydroxysteroid (17-beta) dehydrogenase 12a	hsd17b12a	HSD17B12	-1.42	-2.84
AI558603	Hydroxysteroid (17-beta) dehydrogenase 12b	hsd17b12b	HSD17B12	2.01	2.36
AF068773	Heat shock protein 90-alpha 1	hsp90a.1	HSP90AA1	0.28	2.17
AF068772	Heat shock protein 90kDa alpha (cytosolic), class B member 1	hsp90ab1	HSP90AB1	-0.66	2.13
AW116618	Heat shock protein 4, like	hspa4l	HSPA4	-1.69	3.79
BC052971	Heat shock 70kDa protein 5 (glucose-regulated protein)	hspa5	HSPA5	-0.37	2.57
AB062116	Heat shock cognate 70-kd protein like	hsp70l	HSPA8	-2.81	3.59
L77146	Heat shock protein 8	hspa8	HSPA8	-1.05	1.54
BM072378	Heat shock 70kDa protein 9 (mortalin)	hspa9	HSPA9	-0.90	2.31
AI878489	Heat shock protein, alpha-crystallin-related, b8	hspb8	HSPB8	1.54	1.74
BI896507	Heat shock 60kD protein 1 (chaperonin)	hspd1	HSPD1	2.68	1.68
AF273739	Heat shock 10kD protein 1 (chaperonin 10)	hspe1	HSPE1	-2.63	2.35
BQ074738	LOC791189 sim to hyaluronoglucosaminidase 1	zgc:158626	HYAL1	2.46	3.90
AW777557	3' end of LOC567869 sim to HYAL2: hyaluronoglucosaminidase 2 and 5' to zgc:136804: sim to HYAL1: hyaluronoglucosaminidase 1	AW777557	HYAL2	1.60	3.60
BI876732	Hypoxia up-regulated 1	hyou1	HYOU1	0.29	2.21
AF007414	Inhibitor of DNA binding 1	id1	ID1	0.22	2.59
BI880095	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein, b	id2b	ID2	-0.56	2.54
BI884399	3' end of idh3a | isocitrate dehydrogenase 3 (NAD+) alpha	BI884399	IDH3A	-0.48	2.36
BI890609	Interferon gamma inducible protein 30	ifi30	IFI30	-2.72	-2.35
AW018996	Weak sim to IFI44 | interferon-induced protein 44	wu:fd58b05	IFI44	-2.66	-2.72
BE605771	Sim to interferon induced transmembrane protein 5	wu:fa95e04	IFITM1	-3.38	-1.91
AB158361	Interferon, gamma 1-2	ifng1-2	IFNG	-1.35	-1.54
AF268051	Insulin-like growth factor 1 (somatomedin C)	igf1	IGF1	2.90	3.73
AF194333	Insulin-like growth factor 2a	igf2a	IGF2	0.63	2.07
AI878099	Intergenic 3' to igf2bp1 | insulin-like growth factor 2 mRNA binding protein 1 and 5' to wu:fb21f05 weak sim to ZWINT | ZW10 interactor	AI878099	IGF2BP1	-2.62	-2.17
AJ299409	Insulin-like growth factor binding protein 1	igfbp1	IGFBP1	0.71	5.40
AF198033	Insulin-like growth factor binding protein 2a	igfbp2a	IGFBP2	2.14	3.09
AJ299410	Insulin-like growth factor binding protein 3	igfbp3	IGFBP3	1.73	4.11
AB194243	Interleukin 15, like; weak sim	il15l	IL15	1.21	2.40
AW116942	3' end of LOC100149069 | similar to interleukin 16 and 5' to aqp10 | aquaporin 10	AW116942	IL16	-2.67	-1.75
AF364103	Interleukin 17 receptor D	il17rd	IL17RD	-1.00	-2.12
BI891114	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	imp4	IMP4	-2.11	-2.10
AW115597	IMP (inosine monophosphate) dehydrogenase 2	impdh2	IMPDH2	-3.21	0.37
CK704021	Inhibitor of growth family, member 5a	ing5a	ING5	-0.60	-1.84
X76051	Inhibin, beta B (activin)	inhbb	INHBB	0.32	2.52
BC045341	Insulin induced gene 1	insig1	INSIG1	1.37	3.69
BI474280	Insulin receptor a	insra	INSR	1.74	0.63
BI866892	Sim to integrator complex subunit 2	BI866892	INTS2	-1.61	-1.64
BI887357	Sim to integrator complex subunit 2	BI887357	INTS2	1.73	0.36
BM103255	Similar to Ran_GTP binding protein 5 (sim to importin 5)	LOC569455	IPO5	-2.29	0.39
BI710379	LOC553809 sim to interleukin-1 receptor-associated kinase 1 binding protein 1	zgc:112481	IRAK1BP1	-0.93	-1.91
BI326597	Interferon regulatory factor 11	irf11	IRF1	-1.90	-2.43
BC066724	Interferon regulatory factor 10	irf10	IRF4	-1.55	-1.91
AW567349	LOC562007 sim to immunoresponsive 1 homolog	zgc:154020	IRG1	-2.95	-3.68
CK015631	Iron-sulfur cluster assembly 1	isca1	ISCA1	-0.71	-1.66
D21135	Islet1	isl1	ISL1	-3.29	-1.11
AY423019	Islet1, like	isl1l	ISL1	0.63	3.54
BE557035	Sim to integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	LOC100151619	ITGA2	-1.42	-1.64
AI545475	Sim to integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	AI545475	ITGA3	-3.59	-3.00
AW595107	Intron of itga6b | integrin, alpha 6b	wu:fk35c01	ITGA6	-1.55	-1.35
CV576657	Muscle-specific beta 1 integrin binding protein 2	mibp2	ITGB1BP3	1.63	0.63
BE557429	Integrin, beta 4	itgb4	ITGB4	-1.90	-1.50
BI840469	3' end of itgb4 | integrin, beta 4 and 3' to zgc:194990 sim to TRIM39 | tripartite motif-containing 39	wu:fc35c01	ITGB4	-1.75	-3.37
BM095331	Inter-alpha (globulin) inhibitor H3	itih3	ITIH3	5.02	6.86
BC095235	LOC553614 sim to inter-alpha (globulin) inhibitor H3	zgc:110377	ITIH3	5.36	3.86
AW018989	LOC100003906 sim to inter-alpha (globulin) inhibitor H3	zgc:112265	ITIH3	3.31	3.64
BM104075	Integral membrane protein 2B a	itm2ba	ITM2B	1.07	2.82
BI839853	Integral membrane protein 2Bb	itm2bb	ITM2B	0.34	2.48
BE202129	LOC568010 sim to inositol 1,4,5-triphosphate receptor, type 3	LOC568010	ITPR3	-1.01	-2.30
BI839972	Influenza virus NS1A binding protein a	ivns1abpa	IVNS1ABP	3.16	0.55
AW344202	Influenza virus NS1A binding protein b	ivns1abpb	IVNS1ABP	-2.85	-3.90
AF229448	Jagged 1a	jag1a	JAG1	-1.36	2.08
AF229451	Jagged 1b	jag1b	JAG1	2.35	4.12
AF229449	Jagged 2	jag2	JAG2	-1.41	-2.11
U82980	Janus kinase 1	jak1	JAK1	0.14	2.88
AI584430	3' end of jak1 Janus kinase 1	wu:fb93e10	JAK1	1.66	1.08
AJ005690	Janus kinase 2a	jak2a	JAK2	-0.31	1.67
BI980014	Junctional adhesion molecule 3	jam3	JAM3	2.13	0.74
BI326453	Jun dimerization protein 2	zgc:92851	JDP2	-1.51	-1.31
BM095408	Jumonji domain containing 6	jmjd6	JMJD6	-1.00	-2.95
AA542460	JPH2 protein sim to junctophilin 2	zgc:162172	JPH2	-2.59	-1.06
BE605692	V-jun sarcoma virus 17 oncogene homolog (avian)	jun	JUN	0.42	2.09
BC053234	Jun B proto-oncogene	junb	JUNB	2.64	0.68
BE606155	Jun B proto-oncogene, like	junbl	JUNB	1.74	5.35
BI889237	K(lysine) acetyltransferase 5	zgc:92510	KAT5	-1.63	0.63
AI793533	Kelch repeat and BTB (POZ) domain containing 10	kbtbd10	KBTBD10	-0.88	-1.63
AA606074	3' end of LOC795942 | similar to potassium channel Kv1.1a and 5' to cat catalase	wu:fa27a01	KCNA1	-1.02	-1.76
AI657747	Similar to Kv3.3 potassium channel subunit	LOC559096	KCNC1	1.19	1.73
BC055133	Potassium inwardly-rectifying channel, subfamily J, member 1	kcnj1	KCNJ1	2.42	3.43
AW018995	3' end of zgc:123268 and 3' to LOC100000818 similar to cGMP-dependent protein kinase 1, beta isozyme (cGK 1 beta) (cGKI-beta)	si:dkey-121j17.5	KCNK2	-0.89	-1.53
BM102180	Potassium channel tetramerisation domain containing 12.1	kctd12.1	KCTD12	2.44	3.47
BM071271	Potassium channel tetramerisation domain containing 12.2	kctd12.2	KCTD12	-2.27	1.12
BM156084	LOC431771 sim to potassium channel tetramerisation domain containing 4	zgc:92463	KCTD4	3.56	1.95
AW567098	Potassium channel tetramerisation domain	zgc:77244	KCTD5	-1.59	-1.05
BC076416	Potassium channel tetramerisation domain containing 9	kctd9	KCTD9	-2.43	-2.35
BM154091	Potassium channel tetramerisation domain containing 9	zgc:113115	KCTD9	3.00	0.94
BI891150	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	kdelr2	KDELR2	-0.37	2.66
AW175431	Kelch-like ECH-associated protein 1a	keap1a	KEAP1	0.70	2.68

AW076648	Ketohexokinase	khk	KHK	1.89	-0.97
BI897419	Limb and neural patterns a (lunapark)	lnpa	KIAA1715	-2.36	-3.76
AF139990	Kinesin family member 23	kif23	KIF23	-3.65	-5.34
AL727928	Kinesin-associated protein 3	kifap3	KIFAP3	-1.68	-2.84
AF181248	Kinesin family member C1	kifc1	KIFC1	-2.44	-3.77
AI793626	KIN, antigenic determinant of recA protein homolog	kin	KIN	3.15	2.56
AY929068	Kit ligand a	kitlga	KITLG	-0.33	3.48
BI429411	Kruppel-like factor 12a	klf12a	KLF12	1.16	1.64
AW077452	3' end of zgc:111869 Kruppel-like factor 15 alternative spliced	AW077452	KLF15	2.83	0.88
AF392992	Kruppel-like factor 2a	klf2a	KLF2	-2.08	1.18
AF392995	Kruppel-like factor 2b	klf2b	KLF2	0.20	1.88
AF392993	Kruppel-like factor 3 (basic)	klf3	KLF3	-3.56	1.31
AF262978	Kruppel-like factor 4	klf4	KLF4	-3.57	-1.87
AF392996	Kruppel-like factor d	klfd	KLF4	-1.56	0.04
BI428467	Core promoter element binding protein	copeb	KLF6	-2.14	2.74
BE605860	3' end of si:ch211-208m1.2 sim to KLF8 | Kruppel-like factor 8 and 3' to zgc:136851 sim to KLF5 | Kruppel-like factor 5 (intestinal)	wu:fl22c07	KLF8	-3.48	-0.99
AI584555	Kelch-like 31 (Drosophila)	klhl31	KLHL31	4.59	-1.14
BM104473	Kynurenine 3-monooxygenase	kmo	KMO	1.48	3.53
BE200743	Intron of si:dkeyp-7c9.1 sim to KREMEN1: kringle containing transmembrane protein 1	wu:fk90e01	KREMEN1	1.42	1.71
AI477935	LOC550250 sim to KRT14 | keratin 14	zgc:110712	KRT14	1.57	-0.73
BE200701	NP_001107814 sim to keratin 15	si:dkeyp-113d7.4	KRT15	-1.52	-1.43
BC076059	Keratin 12	zgc:92533	KRT17	-4.03	-1.11
BE200731	Keratin, type 1, gene 19d	krt1-19d	KRT17	-3.87	-3.73
BC075874	LOC792173 sim to cytokeratin 17	zgc:92061	KRT17	-4.73	-4.94
BC045869	Keratin 18	krt18	KRT18	-0.42	3.08
AW018538	LOC553479 sim to keratin 18	si:ch211-133j6.3	KRT18	1.54	1.45
BG304957	Keratin-like (sim to keratin 18)	zgc:77517	KRT18	-2.02	-0.82
BE017931	Weak sim to keratin 19	wu:fk65c09	KRT19	-2.97	-3.06
AW076578	LOC436665 sim to keratin 19	zgc:92035	KRT19	-3.84	-1.44
AF134850	Keratin 4	krt4	KRT8	-2.86	-2.05
AF197909	Keratin 5	krt5	KRT8	-5.62	-1.05
BI704281	Keratin 8	krt8	KRT8	0.51	3.32
AI477659	LOC100009654 sim to keratin 8	zgc:158846	KRT8	-2.65	-4.16
BI877539	3-ketodihydrosphingosine reductase	kdsr	KSR	2.99	-1.25
BM081030	Intergenic 3' to si:ch211-240j18.3 and 5' to nos1 nitric oxide synthase 1 (neuronal)	BM081030	KSR2	2.14	0.43
AW019697	L-2-hydroxyglutarate dehydrogenase	l2hgdh	L2HGDH	1.85	-0.39
BG728552	Weak sim to laminin, alpha 4	BG728552	LAMA4	-0.15	-2.19
BI850028	Laminin, beta 1	lamb1	LAMB1	0.37	1.73
AF395739	LAG1 homolog, ceramide synthase 2 (S. cerevisiae)	lass2	LASS2	1.76	2.81
BM082387	LOC393492 sim to LBH | limb bud and heart development homolog	zgc:66337	LBH	-1.36	-2.44
AW566983	5' of zgc:136695; LOC678576; lymphocyte-specific protein tyrosine kinase	wu:fj94h02	LCK	-1.96	-2.48
AF157110	Lymphocyte cytosolic plastin 1	lcp1	LCP1	0.75	2.32
AF031378	LIM-domain binding factor 1a	ldb1a	LDB1	3.39	0.13
AF172089	Lefty1	lft1	LEFTY2	3.06	0.53
BM155827	Lectin, galactoside-binding, soluble, 1 (galectin 1)-like 1	lgals1l1	LGALS1	-2.64	0.41
AI958097	Lectin, galactoside-binding, soluble, 3 (galectin 3)-like	lgals3l	LGALS3	0.35	3.72
AW421190	Weak sim to lectin, galactoside-binding, soluble, 3 binding protein	AW421190	LGALS3BP	-2.07	-2.88
BI427732	LOC567193 weak sim to lectin, galactoside-binding, soluble, 4 (galectin 4)	LOC567193	LGALS4	-3.35	-1.54
NM_205622	Luteinizing hormone, beta polypeptide	lhb	LHB	-1.07	-2.17
AF001299	LIM homeobox 1b	lhx1b	LHX1	1.21	-3.86
L42547	LIM homeobox 5	lhx5	LHX5	1.50	0.43
BG303217	3' end of dkey-267j14.1; solute carrier family 44 member 5-B and 3' end of LOC799481: sim to LIM homeobox 8	BG303217	LHX8	1.16	1.75
BM023806	LIM homeobox 9	lhx9	LHX9	1.95	0.54
AW281831	DNA ligase (ATP) 1	si:dkeyp-35b8.5	LIG1	-1.06	-1.80
AF307846	LIM domain and actin binding 1	lima1	LIMA1	-1.92	-3.61
AW419601	Lin-7 homolog B (C. elegans)	lin7b	LIN7B	0.86	2.20
BM096032	Lipase, gastric (lysosomal acid, cholesterol esterase)	lipf	LIPA	3.10	-0.88
AW018709	Lipase, hepatic	lipc	LIPC	2.08	0.98
BM005190	Lipase, endothelial	lipg	LIPG	1.03	5.39
BC074085	Lipopolysaccharide-induced TNF factor	litaf	LITAF	-1.57	-2.07
AI497491	Wu:fb60g05 sim to lipopolysaccharide-induced TNF factor	wu:fb60g05	LITAF	-1.29	-2.93
AW175541	Lectin, mannose-binding, 1	lman1	LMAN1	1.90	2.61
BI889893	Limb region 1 like	lmbr1l	LMBR1L	-1.77	-0.31
BG985851	LIM domain only 4	lmo4	LMO4	1.56	1.13
BI981135	LIM domain only 4, like	lmo4l	LMO4	0.48	-3.81
BI866375	Ligand of numb-protein X 1	lnx1	LNX1	-1.12	-2.49
BG302899	Lysyl oxidase	lox	LOX	-2.67	-1.37
BI708370	Sim to lysophosphatidic acid receptor 1	BI708370	LPAR1	-2.42	-0.65
U57656	Lipoprotein lipase	lpl	LPL	3.55	2.60
AW343191	LOC553466 weak sim to leucine-rich alpha-2-glycoprotein 1	si:dkey-90m5.4	LRG1	2.36	2.56
AI882956	LOC559670 sim to leucine-rich repeats and guanylate kinase domain containing	si:ch211-234m22.1	LRGUK	1.79	0.85
BE017901	Sim to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	LOC565797	LRP1	2.16	2.22
BM023753	Sim to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	wu:fj39b01	LRP1	-1.62	2.93
AW077459	Intergenic 3' to lrp11: low density lipoprotein receptor-related protein 11 and 3' to pcmt: protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	AW077459	LRP11	2.64	-3.18
BI878642	Low density lipoprotein receptor-related protein associated protein 1	lrpap1	LRPAP1	-1.29	1.88
AW233607	Leucine-rich PPR-motif containing	lrpprc	LRPPRC	-2.51	-3.65
BE201896	Leucine rich repeat containing 17	lrrc17	LRRC17	1.06	4.90
AW116894	Leucine rich repeat containing 8 family, member A	lrrc8a	LRRC8A	2.49	0.82
BM186492	Sim to LSM3 homolog, U6 small nuclear RNA associated (S.cerevisiae)	BM186492	LSM3	2.02	1.39
BI878336	3' end of LOC100002518 | similar to lymphocyte antigen 75 and 3' to zgc:162904 sim to TSPAN3 | tetraspanin 3	BI878336	LY75	1.88	-0.56
NM_152974	Mab-21-like 1	mab21l1	MAB21L1	-1.28	-5.59
BC050170	MAD1 mitotic arrest deficient-like 1	mad1l1	MAD1L1	-1.73	-2.38
BI704353	Sim to MAD2L1 binding protein	LOC100148094	MAD2L1BP	-2.57	-1.41
AB006322	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	mafba	MAF	4.31	2.99
AB006324	V-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein L	mafl	MAFA	3.36	0.55
AB022286	Kreisler (mouse) maf-related leucine zipper homolog 2.2	krml2.2	MAFB	-0.09	2.03
AB006323	V-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog	maf	MAFB	2.40	4.79
AW058804	Membrane associated guanylate kinase, WW and PDZ domain containing 1	magi1	MAGI1	1.34	2.21
BE201746	Sim to mal, T-cell differentiation protein	BE201746	MAL	-3.19	-3.01
AI397375	Intron of wu:fj20e02 sim to MAN1A2 | mannosidase, alpha, class 1A, member 2	AI397375	MAN1A2	1.55	1.20
AL722241	Sim to microtubule-associated protein 1B	LOC100151220	MAP1B	2.01	0.90
BC066441	Mitogen-activated protein kinase kinase kinase 12	map3k12	MAP3K12	1.96	-3.40
BM182366	Very weak sim to MAP9 | microtubule-associated protein 9	si:ch73-34b5.1	MAP9	-0.50	-2.01
BI839722	Mitogen-activated protein kinase 1	mapk1	MAPK1	2.13	2.18
BI879418	Intron of mapk10 | mitogen-activated protein kinase 10	BI879418	MAPK10	1.95	-2.45
BC095227	Mitogen-activated protein kinase 15	mapk15	MAPK15	-1.85	-3.08
AB030902	Mitogen-activated protein kinase 3	mapk3	MAPK3	2.31	2.64
AB030900	Mitogen-activated protein kinase 8	mapk8	MAPK8	2.09	3.91
BG302813	Mitogen-activated protein kinase-activated protein kinase 2a	mapkapk2a	MAPKAPK2	2.10	2.35
AW175189	Microtubule-associated protein, RP/EB family, member 1, like	mapre1l	MAPRE1	0.69	2.67
AW826304	Intergenic 3' to LOC564520 weak sim to KIAA1267 and 3' to LOC100000342: sim to MAPT: microtubule-associated protein tau	AW826304	MAPT	2.93	-0.44
AI626282	3' end of mark2 | MAP/microtubule affinity-regulating kinase 2 and 3' to rcor2 | REST corepressor 2	wu:fc49e05	MARK2	-2.25	0.28
BI326616	Mannan-binding lectin serine peptidase 2	masp2	MASP2	4.62	2.66
AI959308	Methionine adenosyltransferase I, alpha	mat1a	MAT1A	4.05	4.15
BM154034	Myoglobin	mb	MB	-2.56	-0.27
BM036795	Methyl-CpG binding domain protein 3a	mbd3a	MBD3	2.36	0.29

AF227738	Hexose-binding lectin 3	hbl3	MBL2	-1.23	-3.47
BI533325	Sim to Myelin basic protein	sb:cb183	MBP	-3.29	-1.60
CK705161	Melanoma cell adhesion molecule b	mcamb	MCAM	2.32	1.26
BI864114	Intergenic 3' to LOC100151023 weak sim to MCF2L | MCF.2 cell line derived transforming sequence-like and 5' to ect2 | epithelial cell transforming sequence 2 oncogene	BI864114	MCF2L	3.53	3.85
AW115626	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	mcm2	MCM2	2.35	2.32
BI889166	Minichromosome maintenance complex component 3	mcm3	MCM3	1.71	3.04
AW115871	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae), like	mcm3l	MCM3	0.63	4.88
AW174245	MCM4 minichromosome maintenance deficient 4, mitotin (S. cerevisiae)	mcm4	MCM4	0.55	3.70
AW058902	MCM5 minichromosome maintenance deficient 5 (S. cerevisiae)	mcm5	MCM5	3.09	2.95
AI883326	MCM6 minichromosome maintenance deficient 6, mitotin (S. cerevisiae)	mcm6	MCM6	-0.23	3.69
AW777430	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	mcm7	MCM7	-0.87	3.74
BC044140	Mucolipin 2	mcoln2	MCOLN2	1.41	2.41
BC091973	LOC541484 sim to MyoD family inhibitor domain containing	zgc:113363	MDFIC	3.33	0.43
BE605537	Malate dehydrogenase 1a, NAD (soluble)	mdh1a	MDH1	-0.39	-1.68
AW826477	Malate dehydrogenase 1b, NAD (soluble)	mdh1b	MDH1	-1.32	-2.81
BG305824	Mitochondrial malate dehydrogenase	zgc:64133	MDH2	-1.62	-1.35
AF149802	Midkine-related growth factor	mdka	MDK	-0.36	3.89
AF010255	Transformed 3T3 cell double minute 2 homolog	mdm2	MDM2	5.66	3.07
BI881716	Transformed 3T3 cell double minute 4 homolog	BI881716	MDM4	1.17	2.29
CV486371	Mediator complex subunit 29	med29	MED29	-0.41	-2.79
BI981180	Thyroid hormone receptor associated protein 6	thrap6	MED30	0.65	2.68
AW165313	Sim to mediator complex subunit 7	AW165313	MED7	-2.21	-1.74
U66568	Myocyte enhancer factor 2a	mef2a	MEF2A	-1.14	2.53
U66569	Myocyte enhancer factor 2ca	mef2ca	MEF2C	0.88	2.27
AI588147	Intergenic 3' to mef2d | myocyte enhancer factor 2d and 3' to nes nestin	AI588147	MEF2D	-1.66	-1.04
AW128332	Maternal embryonic leucine zipper kinase	melk	MELK	0.85	4.32
AB055680	Met proto-oncogene (hepatocyte growth factor receptor)	met	MET	2.47	3.82
AW231999	Sim to microfibrillar-associated protein 4	LOC555289	MFAP4	-3.12	-0.80
BF717537	Microfibrillar-associated protein 4	mfap4	MFAP4	-2.77	-2.96
AI544976	Major facilitator superfamily domain containing 2ab	mfsd2ab	MFSD2A	1.12	2.17
AW165058	MAX gene associated	mga	MGA	2.22	0.90
AW115530	Similar to maltase-glucoamylase	LOC100148922	MGAM	-2.45	-3.78
BC074045	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	mgat4b	MGAT4B	2.30	2.69
BI864451	LOC777616 sim to mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	zgc:154054	MGAT4B	-1.18	-2.17
AI957809	3' end of zgc:101663 : alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase C and 5' to LOC100001596 | similar to thyrotropin beta subunit	wu:fd06c04	MGAT4C	-0.30	-2.26
BI883744	Sim to MGAT5 | mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	zgc:136939	MGAT5	3.44	-0.34
AI667631	Sim to meningioma expressed antigen 5 (hyaluronidase)	LOC571547	MGEA5	-1.93	-1.78
BI880123	Matrix Gla protein	mgp	MGP	-3.26	-1.70
BC074022	LOC431762 sim to microsomal glutathione S-transferase 1	zgc:92357	MGST1	2.87	0.53
BI983132	Flavoprotein oxidoreductase MICAL3	mical3	MICAL3	-0.08	2.67
U27121	Gastrulation specific protein (Mid1 interacting protein 1)	g12	MID1IP1	-4.45	-1.56
BC093343	MID1 interacting protein 1	mid1ip1	MID1IP1	-1.89	-4.36
DQ003080	Major intrinsic protein of lens fiber 2	mip2	MIP	-0.97	-2.82
BI705604	MAP kinase interacting serine/threonine kinase 1	mknk1	MKNK1	0.56	-1.53
BI839784	MAP kinase-interacting serine/threonine kinase 2b	mknk2b	MKNK2	1.11	3.35
BI888915	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	mllt10	MLLT10	-1.98	-0.83
AW305943	Matrix metalloproteinase 13	mmp13	MMP13	-1.13	-1.58
BM081219	Matrix metalloproteinase 14 (membrane-inserted) alpha	mmp14a	MMP14	1.93	2.09
BM182277	Matrix metalloproteinase 2	mmp2	MMP2	-3.26	-0.29
BM156872	MOB1, Mps One Binder kinase activator-like 1A (yeast)	mobkl1a	MOBKL1A	1.29	2.20
BI475827	3' end of mocs1 | molybdenum cofactor synthesis step-1 and 5' to insm1b insulinoma-associated 1b	BI475827	MOCS1	-2.70	-1.40
AB032727	V-mos Moloney murine sarcoma viral oncogene homolog	mos	MOS	-3.32	-5.36
BC081598	Mannose-P-dolichol utilization defect 1a	mpdu1a	MPDU1	2.67	1.81
BI883872	LOC445224 sim to M-phase phosphoprotein 6	zgc:100960	MPHOSPH6	-0.91	-1.68
BM154669	Sim to myosin phosphatase Rho interacting protein	im:7154419	MPRIP	1.65	2.05
BC055143	MpV17 transgene, murine homolog, glomerulosclerosis	mpv17	MPV17	-2.99	-0.32
Z46777	Major histocompatibility complex class I UBA gene	mhc1uba	MR1	-5.11	-2.69
AI477589	Major histocompatibility complex class I UEA gene	mhc1uea	MR1	-3.66	-2.78
AF137534	Major histocompatibility complex class I UFA gene	mhc1ufa	MR1	-3.46	-2.51
BC056726	Major histocompatibility complex class I UXA2 gene	mhc1uxa2	MR1	-1.43	-3.64
BC053202	Meiotic recombination 11 homolog A (S. cerevisiae)	mre11a	MRE11A	1.85	-0.28
BC049041	Mitochondrial ribosomal protein L14	mrpl14	MRPL14	-0.41	-2.20
AI601311	Mitochondrial ribosomal protein L15	mrpl15	MRPL15	-1.40	-2.61
CD605616	Sim to mitochondrial ribosomal protein S31	si:ch211-114c12.1	MRPS31	-2.45	-1.78
AF412833	MutS homolog 2 (E. coli) (mutS homolog 2, colon cancer, nonpolyposis type 1)	msh2	MSH2	2.36	-2.26
AF412834	MutS homolog 6 (E. coli)	msh6	MSH6	2.15	0.41
AW076848	LOC573213 sim to mesothelin	LOC573213	MSLN	-2.22	-2.50
CV485301	Sim to MSRA | methionine sulfoxide reductase A	im:7149628	MSRA	-0.70	2.26
AF370035	Macrophage stimulating 1 (hepatocyte growth factor-like)	mst1	MST1	2.23	-3.01
U16310	Muscle segment homeobox A	msxa	MSX2	3.23	-1.35
AW567292	Muscle segment homeobox C	msxc	MSX2	-1.79	-1.80
AW115744	Metastasis associated family, member 3	mta3	MTA3	1.60	-1.23
AF458116	Metal-regulatory transcription factor 1	mtf1	MTF1	2.49	0.60
BG303602	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent)	mthfd1	MTHFD1	4.10	1.55
AW422831	Sim to MTRR | 5-methyltetrahydrofolate-homocysteine methyltransferase reductase	LOC560667	MTRR	-1.52	1.29
AI974191	LOC692303 sim to microsomal triglyceride transfer protein	zgc:136353	MTTP	3.24	0.94
AI626485	3' end of LOC100150694 | similar to platelet-derived growth factor or 3' of LOC100150536 sim to MTUS1 | microtubule associated tumor suppressor 1	AI626485	MTUS1	-1.70	-2.27
AW175351	Sim to mucin 2, oligomeric mucus/gel-forming	LOC572172	MUC2	-3.40	-1.83
BI672148	LOC572175 weak sim to mucin 2, oligomeric mucus/gel-forming	LOC572175	MUC2	-2.45	-1.68
AI641080	3' end of murc | muscle-related coiled-coil protein or 3' end of of LOC571423 sim to DNAH5 | dynein, axonemal, heavy chain 5	AI641080	MURC	-1.04	-1.72
AW184499	Major vault protein	mvp	MVP	2.02	-2.67
AW421176	Intron of mxc | myxovirus (influenza virus) resistance C	AW421176	MX1	1.53	-1.00
BM181722	MAX dimerization protein 3	mxd3	MXD3	0.22	-3.36
BG884411	Transcription factor cmyb	LOC100000853	MYB	-2.38	-0.75
BC085629	Myosin binding protein C, slow type	mybpc1	MYBPC1	-1.65	-2.62
BC074055	LOC393530 sim to myosin binding protein C, slow type	zgc:66097	MYBPC1	-2.18	-2.46
AI794621	LOC541384 sim to myosin binding protein C, fast type	zgc:110761	MYBPC2	-3.54	-2.53
BM104128	LOC692317 sim to myosin binding protein C, fast type	zgc:136545	MYBPC2	1.60	-1.50
AW454173	Myosin binding protein C, cardiac	mybpc3	MYBPC3	-1.73	-1.71
BM103298	MYC binding protein 2; esrom	mycbp2	MYCBP2	0.47	2.33
AW115849	V-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) b	mycl1b	MYCL1	2.88	2.43
AI721479	V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	mycn	MYCN	-1.22	-2.51
BI890420	Myelin expression factor 2	myef2	MYEF2	3.50	0.61
BI886767	Myosin, heavy polypeptide 10, non-muscle	myh10	MYH10	2.12	1.57
AF180893	Myosin, heavy polypeptide 1, skeletal muscle	myhz1	MYH2	-4.62	-0.57
AW343155	LOC100002040	LOC100002040	MYH4	-2.50	-2.36
AY921650	Myosin heavy chain 4	myhc4	MYH4	-5.29	-2.21
AF165817	Myosin, heavy polypeptide 2, fast muscle specific	myhz2	MYH4	-6.63	-0.76
BF158199	LOC100008376 sim to myosin, heavy chain 4, skeletal muscle	wu:fd14a01	MYH4	-4.02	-1.70
BM095209	Sim to myosin, heavy chain 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)	BM095209	MYH6	-3.67	-1.40
BC096949	Ventricular myosin heavy chain	vmhc	MYH7	3.63	0.58
AW281681	LOC336165 sim to myosin, light chain 1, alkali; skeletal, fast	zgc:77231	MYL1	-3.80	-1.79

BG985673	Myosin light chain 2 like	zgc:110679	MYL2	-4.01	-2.18
AF114428	Myosin, light polypeptide 7, regulatory	myl7	MYL7	-4.62	-2.06
AI626776	Myosin, light polypeptide 9, regulatory	myl9	MYL9	-2.25	0.72
BM181653	Myosin regulatory light chain interacting protein	mylip	MYLIP	-3.67	-3.41
AI106316	3' end of mylk4: myosin light chain kinase family, member 4 and 5' to gmds: GDP-mannose 4,6-dehydratase	AI106316	MYLK4	0.84	-1.86
AI477343	Myosin XVIII-like 1	myo18l1	MYO18A	0.09	1.72
AW058877	Myosin IE	myo1e	MYO1E	-1.63	0.45
BI867099	LOC393609 sim to myosin IE	zgc:64042	MYO1E	-2.17	-1.81
AA495066	3' end of LOC573741 | similar to myoskeleton and 3' to zgc:101640 phosphatidylinositol transfer protein, cytoplasmic 1	wu:fa05e12	MYOCD	-2.59	-1.52
BC065451	Myozenin 1	zgc:77785	MYOZ1	-2.11	-2.32
BC085365	LOC492779 sim to N-acetylneuraminic acid synthase (sialic acid synthase)	zgc:101549	NANS	-1.01	-2.75
BI877937	NMDA receptor-regulated gene 1a	narg1a	NARG1	3.20	-1.11
BI880972	NMDA receptor-regulated gene 1b	narg1b	NARG1	2.98	-0.49
AL716141	3' end of zgc:162648 (sim to NAT8L: N-acetyltransferase 8-like (GCN5-related, putative) and 3' end to poln: DNA polymerase nu	wu:fb94h12	NAT8L	-1.47	-2.98
BI888811	Nibrin	zgc:194152	NBN	2.15	2.05
BI880074	Intergenic 3' to ncam1 | neural cell adhesion molecule 1 and 5' to zbtb16 | zinc finger and BTB domain containing 16	BI880074	NCAM1	-2.26	-1.72
AY029402	Neural cell adhesion molecule 1	ncam1	NCAM1	-1.09	2.91
AY029401	Neural cell adhesion molecule 3	ncam3	NCAM1	0.29	1.94
BI705634	Neural cell adhesion molecule 2	zgc:152904	NCAM2	0.77	-1.98
BI879542	Neutrophil cytosolic factor 1	ncf1	NCF1	-1.05	-2.79
BI889900	Sim to NCK interacting protein with SH3 domain	BI889900	NCKIPSD	0.74	1.92
AI601734	Intron of si:ch211-216l23.2; LOC565061 weak sim to nuclear receptor coactivator 5	AI601734	NCOA5	0.64	1.67
AW171396	Intergenic 3' to LOC5646645' to ncoa6: nuclear receptor coactivator 6	wu:fi41a10	NCOA6	-2.03	-1.86
BG305349	Nuclear receptor co-repressor 1	ncor1	NCOR1	-0.44	1.55
BC055168	Neuronal calcium sensor 1a	ncs1a	NCS1	5.37	0.22
AY751744	Nicastrin	ncstn	NCSTN	3.28	0.98
AI722423	Kinetochore associated 2-like	kntc2l	NDC80	2.42	0.33
BI840930	Nedd4 family interacting protein 1	ndfip1	NDFIP1	3.71	0.68
BE202095	Necdin-like 2	ndnl2	NDNL2	1.50	0.45
BM184118	NADPH dependent diflavin oxidoreductase 1	ndor1	NDOR1	4.53	-0.61
BI880439	Intron of N-myc downstream regulated family member 3b	BI880439	NDRG3	3.54	3.12
BM182832	N-myc downstream regulated family member 3a	ndrg3a	NDRG3	-1.74	2.84
BM185338	N-myc downstream regulated family member 3b	ndrg3b	NDRG3	-0.96	2.40
BI840924	Sim to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	wu:fa55f06	NDUFA4	-1.71	-4.04
AI884287	NADH dehydrogenase (ubiquinone) flavoprotein 1	ndufv1	NDUFV1	-1.57	-1.30
BC095287	LOC553536 sim NECAP endocytosis associated 2	zgc:110468	NECAP2	-2.78	0.55
BG729199	Neural precursor cell expressed, developmentally down-regulated 8	nedd8l	NEDD8	1.75	1.33
BC095779	LOC553718 sim to neurofilament, medium polypeptide	zgc:112359	NEFM	-1.84	-0.96
AI477081	Intergenic 3' to negr1 | neuronal growth regulator 1 and 5' to zranb2 zinc finger, RAN-binding domain containing 2	wu:fb55d11	NEGR1	2.37	0.77
BM184173	NIMA (never in mitosis gene a)-related kinase 2	nek2	NEK2	1.75	-3.62
BC090546	Neuron derived neurotrophic factor	nenf	NENF	2.90	0.76
AI667315	Neogenin 1	neo1	NEO1	-2.42	-0.19
BM025913	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	nfatc2ip	NFATC2IP	-3.26	0.22
BI845682	Intron of nfia | nuclear factor I/A	BI845682	NFIA	1.43	2.64
BC080210	Nuclear factor, interleukin 3 regulated	nfil3	NFIL3	3.16	0.48
BM026051	Sim to nuclear factor, interleukin 3 regulated	si:dkey-52h23.1	NFIL3	2.54	1.03
AI397155	3' end of LOC100000812 sim to NFIL3 | nuclear factor, interleukin 3 regulated and 5' to DKEY-172O19.3	wu:fb15g03	NFIL3	-1.74	-0.40
BM102747	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	nfkb2	NFKB2	2.32	2.06
AW232219	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha a	nfkbiaa	NFKBIA	1.68	0.38
AA495045	3 end of zgc:92567 : nuclear transcription factor Y, alpha like and 5' to ahcyl1: S-adenosylhomocysteine hydrolase-like 1	AA495045	NFYA	6.56	1.74
AI884272	NHP2 ribonucleoprotein homolog	nhp2	NHP2	-0.93	-2.12
AW019573	Nidogen 1a	nid1a	NID1	4.04	1.15
BC083262	LOC450042 sim to non imprinted in Prader-Willi/Angelman syndrome 1	nipa1	NIPA1	2.22	1.16
AW594957	Ichthyin sim to NIPA-like domain containing 4	zgc:91960	NIPAL4	3.19	2.19
AI957936	Natural killer-tumor recognition sequence	nktr	NKTR	2.00	3.54
AB067731	Posterior neuron-specific homeobox	pnx	NKX1-2	-3.14	-1.55
AF321112	NK2 homeobox 1b	nkx2.1b	NKX2-1	3.76	-0.18
AF253054	NK2 homeobox 1a	nkx2.1a	NKX2-4	1.12	2.45
U66572	NK2 transcription factor related 5	nkx2.5	NKX2-5	2.88	0.60
BI842967	LOC555375 sim to NK3 homeobox 1	LOC555375	NKX3-1	-2.13	-1.93
AY225416	NK3 homeobox 2	nkx3.2	NKX3-2	-0.56	-3.87
BC076337	NK6 transcription factor related, locus 1	nkx6.1	NKX6-1	1.06	2.42
BI879886	Sim to neuroligin 4, X-linked	LOC561122	NLGN4X	-1.39	-1.58
BG304985	Nemo like kinase b	nlk1	NLK	2.16	2.35
BM026055	Weak sim to NLRP12 | NLR family, pyrin domain containing 12	si:ch211-278p9.4	NLRP12	-1.55	-0.50
AF201764	Non-metastatic cells 2, protein (NM23B) expressed in	nme2	NME2	2.54	1.55
BM181863	Non-metastatic cells 4, protein expressed in	nme4	NME4	1.64	4.01
BI672359	LOC436789 sim to non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	zgc:92812	NME5	-1.73	-1.77
AW076762	LOC792676 weak sim to N-myc (and STAT) interactor	nmi	NMI	1.99	-0.16
AW232713	3' end of nmnat2 | nicotinamide nucleotide adenylyltransferase 2 and 3' to DKEY-161L11.81 sim to LAMC2 | laminin, gamma 2	wu:fj24h11	NMNAT2	1.54	2.70
BI889170	Sim to NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	wu:fc27e05	NOB1	1.97	2.00
AF056327	Nodal-related 1	ndr1	NODAL	2.55	1.67
AF002219	Nodal-related 2; cyclop	ndr2	NODAL	3.11	0.67
AF159147	Noggin 1	nog1	NOG	4.83	4.48
BM034958	LOC613021 sim to nucleolar protein 8	si:ch211-103f16.2	NOL8	-1.10	-2.35
BI430378	Nitric oxide synthase 2a, inducible	nos2a	NOS2	-2.45	-0.79
BI846489	Intergenic 5' UTR of notchl | notch homolog, like and 5' to LOC569402 sim to TAP1 | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	BI846489	NOTCH1	1.78	2.14
X69088	Notch homolog 1a	notch1a	NOTCH1	0.64	-1.79
U57973	Notch homolog 1b	notch1b	NOTCH1	1.40	1.87
Y10354	Notch homolog 2	notch2	NOTCH2	-2.01	1.53
BE201310	LOC100002182 sim to Notch homolog 2	LOC100002182	NOTCH2	4.75	4.33
U57975	Notch homolog 3 (more sim to NOTCH2)	notch3	NOTCH3	0.18	1.84
AI942978	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	npl	NPL	1.77	2.32
BI476714	Nuclear protein localization 4 homolog (S. cerevisiae)	nploc4	NPLOC4	-2.86	0.70
BI890458	LOC553507 sim to nucleophosmin (nucleolar phosphoprotein B23, numatrin)	LOC553507	NPM1	2.63	1.79
BG307975	Sim to neuroplastin	BG307975	NPTN	1.50	-0.55
BI892036	Nuclear receptor subfamily 0, group B, member 2a	nr0b2a	NR0B2	-1.54	-2.65
CD605447	Nuclear receptor subfamily 1, group d, member 1	nr1d1	NR1D1	-1.64	-2.96
AF342941	Nuclear receptor subfamily 1, group D, member 2	nr1d2a	NR1D2	-0.62	3.45
BG308431	Nuclear receptor subfamily 1, group D, member 2b	nr1d2b	NR1D2	-2.44	1.03
AW826882	Sim to nuclear receptor subfamily 2, group E, member 3	zgc:103631	NR2E3	-1.01	-1.50
X70299	Nuclear receptor subfamily 2, group F, member 1	nr2f1	NR2F1	0.32	2.28
BI706217	Intergenic 5' to zgc:92034: sim to ARRDC3: arrestin domain containing 3 and 5' to nr2f1b: nuclear receptor subfamily 2, group F, member 1b	BI706217	NR2F2	1.54	0.99
S80986	Nuclear receptor subfamily 2, group F, member 2	nr2f2	NR2F2	1.40	2.45
U93458	Nuclear receptor subfamily 2, group F, member 5	nr2f5	NR2F2	3.09	1.07
AF014926	Nuclear receptor subfamily 5, group A, member 2	nr5a2	NR5A2	2.45	4.82
U62619	Neuroblastoma RAS viral (v-ras) oncogene homolog	nras	NRAS	-2.64	-0.55
BG985738	Neuropilin 2b	nrp2b	NRP2	-2.09	1.56
BI476369	Neurexin 2a	nrxn2a	NRXN2	1.76	0.44
AI793467	5'-nucleotidase, cytosolic III	zgc:66117	NT5C3	-1.91	-0.81

AW343382	5'-nucleotidase, ecto (CD73)	nt5e	NTE5E	-2.63	-0.89
AF002717	Netrin 1a	ntn1a	NTN1	1.16	1.92
AW077469	Intergenic 3' to si:ch211-220b11.1 sim to NTRK2 | neurotrophic tyrosine kinase, receptor, type 2 and 3' to kcmf1 potassium channel modulatory factor 1	AW077469	NTRK2	-2.19	-0.53
BM187002	3' end of LOC561496 sim to NUAK1 | NUAK family, SNF1-like kinase, 1 and 5' to LOC567795 weak sim to MUPCDH | mucin-like protocadherin	BM187002	NUAK1	2.22	0.93
BC049486	Nudix (nucleoside diphosphate linked moiety X)-type motif 1	nudt1	NUDT1	-1.14	-5.40
AW420858	Intergenic 3' to nudt4 | nudix (nucleoside diphosphate linked moiety X)-type motif 4 and 5' to CH211-204P6.5 sim to EEA1 | early endosome antigen 1	wu:fj88a02	NUDT4	3.08	-0.97
BI982971	Nudix (nucleoside diphosphate linked moiety X)-type motif 9	nudt9	NUDT9	-0.37	-4.43
AI477432	Nucleoporin 107	nup107	NUP107	2.43	1.66
AW170971	Nucleoporin 155	AW170971	NUP155	-3.29	-0.73
BI891507	Nucleoporin-like 2	zgc:77724	NUPL2	1.91	-1.16
BF717555	Nuclear protein, transcriptional regulator, 1 (candidate of metastasis 1)	nupr1	NUPR1	1.71	3.29
BI979960	3' end of zgc:92136 nogo-B receptor precursor and 3' to LOC793494 similar to Na-K-Cl cotransporter	BI979960	NUS1	1.16	1.54
BM184045	Nucleolar and spindle associated protein 1	nusap1	NUSAP1	-0.46	-5.20
BM181739	Similar to otoconin 90	LOC793660	OC90	-1.50	-1.69
AW116260	Occludin	ocln	OCLN	-2.55	-0.80
AI558633	Sim to opioid growth factor receptor	AI558633	OGFR	-2.85	-3.03
AW019131	Sim to opioid growth factor receptor	AW019131	OGFR	-3.11	-2.89
BM071771	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) 1	ogt.1	OGT	-3.07	0.62
BF717452	Weak sim to OLFM4 | olfactomedin 4	LOC569381	OLFM4	-2.17	-3.46
BG727373	Sim to 5-oxoprolinase (ATP-hydrolysing)	LOC100151110	OPLAH	3.19	1.32
AF109371	Opsin 1 (cone pigments), long-wave-sensitive, 1	opn1lw1	OPN1LW	-3.28	-0.52
AB035276	Vertebrate ancient long opsin a	valopa	OPN1LW	2.99	0.29
BC076120	Opsin 1 (cone pigments), long-wave-sensitive, 2	opn1lw2	OPN1MW	-3.13	-0.06
AW059358	Similar to multiple tissue opsin	LOC100000053	OPN3	-1.60	-1.70
AJ001596	Opioid receptor, delta 1	oprd1	OPRD1	-2.27	0.37
AF285173	Opioid receptor, kappa 1	oprk1	OPRK1	2.12	0.76
AF012746	Odorant receptor, family C, subfamily 103, member 5	or103-1	OR2AT4	2.68	-2.03
BG303377	Origin recognition complex, subunit 3-like (yeast)	orc3l	ORC3L	4.12	-1.03
NM_212671	Origin recognition complex, subunit 6 homolog-like (yeast)	orc6l	ORC6L	-1.91	-5.99
BI865590	Amplified in osteosarcoma	os9	OS9	1.53	1.38
BM025945	LOC100003104 weak sim to OSBP: oxysterol binding protein or intron of CNKSR2: connector enhancer of kinase suppressor of Ras 2 or 5' to wu:fa18f11 sim to C1orf198	LOC100003104	OSBP	-1.14	-1.70
BM184075	Oxysterol binding protein-like 7	osbpl7	OSBPL6	-2.01	-6.36
AI959376	LOC447807 weak sim to organic solute transporter alpha	zgc:92111	OSTalpha	1.45	2.19
AI641585	LOC393239 sim to oligosaccharyltransferase complex subunit	zgc:56559	OSTC	2.07	1.33
AF071496	Orthopedia homolog b	otpb	OTP	-2.02	-2.20
U14591	Orthodenticle homolog 1	otx1	OTX1	-0.44	-4.50
BI670964	Cone-rod homeobox	crx	OTX2	-2.93	-1.82
U14592	Orthodenticle homolog 2	otx2	OTX2	-0.96	-2.78
AW154676	Sim to 3-oxoacid CoA transferase 1	AW154676	OXCT1	2.84	1.96
AW280053	3-oxoacid CoA transferase 1a	oxct1a	OXCT1	-4.50	-2.05
AF317643	Purinergic receptor P2X, ligand-gated ion channel, 4a	p2rx4a	P2RX4	-0.64	-2.82
AI477493	Proliferation-associated 2G4, a	pa2g4a	PA2G4	-0.48	2.03
AI588301	Proliferation-associated 2G4 ,b	pa2g4b	PA2G4	0.16	2.71
BG891950	Poly A binding protein, cytoplasmic 1 b	pabpc1b	PABPC1	0.21	-2.05
AI964234	Poly(A) binding protein, cytoplasmic 4 (inducible form)	pabpc4	PABPC4	-0.70	-3.19
AW059111	Protein kinase C and casein kinase substrate in neurons 1	pacsin1	PACSIN1	-1.59	1.24
AI384268	wu:fb12c09 weak sim to pleckstrin homology-like domain, family B, member 2 or 3' end of LOC100149252 weak sim to PAFAH1B2 | platelet-activating factor acetylhydrolase, isoform Ib, subunit 2 (30kDa)	wu:fb12c09	PAFAH1B2	-1.92	-2.12
AW421213	Phenylalanine hydroxylase	pah	PAH	3.15	6.15
CD605405	Sim to PAPD5 | PAP associated domain containing 5	LOC568678	PAPD5	1.80	-0.89
BI673488	Poly(A) polymerase gamma	papolg	PAPOLG	-1.36	-2.13
AI384140	3'-phosphoadenosine 5'-phosphosulfate synthase 2	papss2	PAPSS2	-0.25	4.41
AI353121	3' end of si:dkey-259k14.2 sim to PARG | poly (ADP-ribose) glycohydrolase and 3' to si:ch211-229p19.3 sim to OGDH | oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	AI353121	PARG	0.61	-2.20
NM_001002872	Parvin, alpha a	parvaa	PARVA	0.71	2.05
BI708864	Parvin, beta	parvb	PARVB	-0.34	1.86
AF014366	Paired box gene 3a	pax3a	PAX3	1.31	3.44
AF072548	Paired box gene 5	pax5	PAX5	0.30	2.06
X63183	Paired box gene 6a	pax6a	PAX6	0.59	2.11
AW420720	Pyruvate carboxylase	pc	PC	3.02	1.77
BI896470	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	pcbd1	PCBD1	2.70	2.82
AF043902	Protocadherin 10a	pcdh10a	PCDH10	2.54	0.57
AY772390	Protocadherin 15a	pcdh15a	PCDH15	2.34	2.17
AY772391	Protocadherin 15b	pcdh15b	PCDH15	1.73	0.26
AW232442	3' end of pcdh18b | protocadherin 18b	wu:fj19f12	PCDH18	-0.55	-1.70
BI673679	Intron of wu:fc83e05 sim to PCDH19: protocadherin 19	BI673679	PCDH19	-1.72	-1.14
AY576979	Protocadherin 1 alpha 4	pcdh1a4	PCDHA2	-2.19	-0.66
AB075940	Protocadherin 2 alpha b 12	pcdh2ab12	PCDHA3	-1.87	-0.27
BI866262	3' ed of pcdh2ac | protocadherin 2 alpha c and 5' to pcdh2g1 | protocadherin 2 gamma 1	BI866262	PCDHAC2	-0.76	-1.64
AB075939	LOC791897 sim to protocadherin alpha subfamily C, 2	pcdh2ab6	PCDHAC2	0.39	-2.49
AY583022	Protocadherin 2 gamma 10	pcdh2g10	PCDHGA10	-2.01	-2.92
AY583051	Protocadherin 2 gamma 3	pcdh2g3	PCDHGA10	-1.57	-2.53
AY583048	Protocadherin 1 gamma b 9	pcdh2g29	PCDHGA11	-6.00	-4.24
AY576963	Protocadherin 1 gamma 32	pcdh1g32	PCDHGC5	-1.19	-2.18
BG727092	Phosphoenolpyruvate carboxykinase 1 (soluble)	pck1	PCK1	-3.39	6.05
AW116521	LOC327176 sim to protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	zgc:123165	PCMTD1	-0.56	-1.50
AF140608	Proliferating cell nuclear antigen	pcna	PCNA	2.54	0.83
BI671284	3' end of zgc:103434; phosphate cytidylyltransferase 2, ethanolamine and 5' to CH1073-467M9.4; sim to guanine nucleotide binding protein (G protein) family	BI671284	PCYT2	1.58	0.73
BI880387	LOC100007784 sim to phosducin	LOC100007784	PDC	1.66	-2.73
BG306678	Phosducin 1	pdc1	PDC	2.15	-0.74
AI883967	Programmed cell death 11	pdcd11	PDCD11	-0.40	-2.35
BC054132	Programmed cell death 2	pdcd2	PDCD2	-0.17	-2.00
BM181817	Programmed cell death 4a	pdcd4a	PDCD4	-0.28	-1.93
BM071298	Programmed cell death 6	pdcd6	PDCD6	-0.66	-1.83
BI889956	Programmed cell death 7	pdcd7	PDCD7	-1.21	-2.02
BI879847	Phosphodiesterase 6G, cGMP-specific, rod, gamma	pde6g	PDE6G	-3.27	-1.45
BC095757	Sim to phosphodiesterase 6G, cGMP-specific, rod, gamma	zgc:112320	PDE6G	-1.36	-2.18
BG307503	Sim to phosphodiesterase 8B	BG307503	PDE8B	3.80	-1.34
AF200951	Platelet derived growth factor receptor alpha	pdgfra	PDGFRA	3.62	1.70
BC076185	Pyruvate dehydrogenase E1 alpha 1	zgc:92705	PDHA1	-0.43	-1.51
BG305862	Pyruvate dehydrogenase (lipoamide) beta	pdhb	PDHB	-1.61	0.34
AI667512	Protein disulfide isomerase family A, member 3	pdia3	PDIA3	2.21	-1.66
BC077131	Protein disulfide-isomerase A3	zgc:100906	PDIA3	1.64	-0.67
BG304294	LOC791995 sim to PDIA3 | protein disulfide isomerase family A, member 3	zgc:77086	PDIA3	-1.13	2.25
AI585024	Intron of pdia5 protein disulfide isomerase family A, member 5	AI585024	PDIA5	1.86	0.46
AW232485	Pyruvate dehydrogenase kinase 4	si:rp71-57j15.4	PDK2	3.00	2.77
BC095249	PDZ and LIM domain 3a	pdlim3a	PDLIM3	1.75	-0.93
BM154358	PDZ and LIM domain 7	pdlim7	PDLIM7	-7.97	-1.72
BC055193	Yippee-like 5 (sim to pyruvate dehydrogenase phosphatase regulatory subunit)	ypel5	PDPR	0.62	3.11
AF036325	Pancreatic and duodenal homeobox 1	pdx1	PDX1	-0.24	4.14
BM185817	Pyridoxal (pyridoxine, vitamin B6) kinase a	pdxka	PDXK	-0.72	-1.69

BC085468	LOC492499 sim to pyridoxal (pyridoxine, vitamin B6) kinase	zgc:101900	PDXK	1.74	1.08
AY309090	Prodynorphin	pdyn	PDYN	5.09	0.90
AA658595	PDZ domain containing 1 like	pdzk1l	PDZK1	-3.84	-4.74
BC076531	LOC436918 sim to peroxisomal D3,D2-enoyl-CoA isomerase	zgc:92030	PECI	1.96	0.66
AI721587	Sim to proline, glutamate and leucine rich protein 1	LOC100003680	PELP1	3.92	0.77
BI709646	Period homolog 4	per4	PER1	-1.02	-2.63
BI890045	PERP, TP53 apoptosis effector	perp	PERP	-3.37	1.41
BI891290	LOC393485 sim to prefoldin subunit 6	zgc:66282	PFDN6	2.41	0.54
AW115515	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	pfkfb3	PFKFB3	-3.22	-0.60
BI845214	LOC550259 sim to phosphofructokinase, liver	zgc:110298	PFKL	2.35	2.00
BC081652	Phosphofructokinase, muscle	pfkm	PFKM	-4.39	-2.83
BI888926	LOC799355 sim to profilin 2	LOC799355	PFN2	-3.08	-0.39
AI353357	Phosphoglycerate mutase 2 (muscle)	pgam2	PGAM2	-5.22	-2.85
AI331440	Sim to PGAP1 | post-GPI attachment to proteins 1	si:dkey-191g15.7	PGAP1	1.58	1.65
BI883476	Per1-like domain containing 1 precursor; post-GPI attachment to proteins 3	zgc:171485	PGAP3	-0.89	2.71
BI880695	Prohibitin	phb	PHB	-1.18	-1.83
AW154457	PHD finger protein 6	phf6	PHF6	0.28	-3.32
AB010103	Dharma (weak sim to paired-like homeobox 2b)	dharma	PHOX2B	1.18	2.30
BF158382	PHD and ring finger domains 1	phrf1	PHRF1	-0.97	1.78
BM183976	Phytanoyl-CoA hydroxylase	phyh	PHYH	2.48	1.75
BC085396	LOC492804 sim to phytanoyl-CoA dioxygenase domain containing 1	zgc:101639	PHYHD1	2.50	1.10
BG883236	3' end of pi4kb | phosphatidylinositol 4-kinase, catalytic, beta and 5' to zgc:64042 sim to MYO1E | myosin IE	BG883236	PI4KB	-3.10	0.73
BI704177	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide	pi4kb	PI4KB	1.28	2.22
BM182311	Protein inhibitor of activated STAT, 4 -like	pias4l	PIAS4	-0.17	-3.10
AW279624	Weak sim to phosphatidylinositol binding clathrin assembly protein	LOC100005187	PICALM	3.45	3.22
BC065590	Phosphatidylinositol glycan, class F	pigf	PIGF	1.65	1.12
AI878774	Phosphatidylinositol glycan, class P	pigp	PIGP	-2.56	0.38
AI588435	LOC571356 sim to phosphoinositide-3-kinase, class 2, alpha polypeptide	si:dkey-24l11.7	PIK3C2A	0.72	2.20
BQ078437	Sim to PIK3C2B | phosphoinositide-3-kinase, class 2, beta polypeptide	im:7150469	PIK3C2B	1.22	3.17
BM025885	LOC561737 sim to phosphoinositide 3-kinase catalytic subunit	LOC561737	PIK3CA	2.24	1.95
BI706734	Sim to phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	LOC557176	PIK3R1	0.68	2.72
BM317287	Weak sim to PIM1 | pim-1 oncogene	LOC100148646	PIM1	-1.41	-1.83
BI672275	Weak sim to PIM1 | pim-1 oncogene	LOC571281	PIM1	1.51	1.63
BI475851	Intergenic 3' to pim1 | pim-1 oncogene and 5' to DKEY-83K24.4	BI475851	PIM2	3.01	0.61
BQ618300	3' end of LOC564787 | similar to Serine/threonine-protein kinase Pim-3 and 3' to rab3a | RAB3A, member RAS oncogene family	BQ618300	PIM3	-1.01	-1.54
BI705891	Protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	pin1	PIN1	0.74	3.26
BI672331	Piwi-like 1 (Drosophila)	piwil1	PIWIL1	-0.44	-2.11
AI667249	Pyruvate kinase, liver and RBC	pklr	PKLR	2.51	4.48
BI891882	Pyruvate kinase, muscle a	pkm2a	PKM2	-2.03	-1.45
AW077091	Plakophilin 3	pkp3	PKP3	-3.05	-2.26
BI881145	Plakophilin-like (sim to plakophilin 3)	zgc:136656	PKP3	-4.06	-1.62
AI877926	Phospholipase A2, group XV	pla2g15	PLA2G15	2.77	2.23
BM036485	LOC436896 sim to phospholipase A2, group XVI	zgc:92249	PLA2G16	-1.18	-1.80
BI475847	Pleomorphic adenoma gene X (plagx)	plagx	PLAG1	-0.34	2.43
AF186476	Pleiomorphic adenoma gene-like 2	plagl2	PLAGL2	1.28	-2.57
BG892360	LOC565641 weak sim to plasminogen activator, urokinase receptor	LOC565641	PLAUR	-1.19	-2.50
AW466858	LOC337489 sim to phospholipase C, delta 1	AW466858	PLCD1	-1.39	-3.49
BC061706	Pleckstrin	plek	PLEK	5.32	2.44
BI326382	Intron of plekha8: pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	BI326382	PLEKHA8	1.24	2.01
BM071184	Pleckstrin homology domain containing, family F (with FYVE domain) member 1	plekhf1	PLEKHF1	-2.98	-1.80
AY654285	Quattro (sim to pleckstrin homology domain containing, family G (with RhoGef domain) member 4B)	quo	PLEKHG4B	2.12	0.86
BC059801	Plasminogen	plg	PLG	3.85	5.18
BC096807	Perilipin 2	plin2	PLIN2	2.32	2.35
AW116681	Sim to polo-like kinase 1 (Drosophila)	AW116681	PLK1	-4.16	-5.88
BG303034	Polo-like kinase 3 (Drosophila)	plk3	PLK3	-1.08	-2.64
BG307977	LOC799067 sim to phospholamban	LOC799067	PLN	-3.22	-1.48
AI974140	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 3	plod3	PLOD3	-2.03	0.99
AI497382	3' end of plrg1 | pleiotropic regulator 1 and 3' to fgg | fibrinogen, gamma polypeptide	AI497382	PLRG1	2.66	-0.71
BM181765	LOC445125 sim to phospholipid transfer protein	zgc:100903	PLTP	3.29	3.77
BI878456	Plexin D1	plxnd1	PLXND1	0.70	4.30
BI672438	LOC553216 sim to peptidase M20 domain containing 1	zgc:123113	PM20D1	-1.71	-2.20
BI866970	Phosphomannomutase 2	pmm2	PMM2	-1.00	2.63
BI475826	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	pms1	PMS1	-1.24	-1.71
AI444539	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	pms2	PMS2	1.02	-2.52
BE605389	Nucleoside phosphorylase	np	PNP	0.85	4.10
AW077814	Pyridoxine 5'-phosphate oxidase	pnpo	PNPO	3.08	-0.20
AA495158	Polymerase (DNA directed), alpha 1	pola1	POLA1	4.25	0.83
AW344260	Polymerase (DNA directed), alpha 2	pola2	POLA2	2.66	0.59
BI891643	Polymerase (DNA directed), beta	polb	POLB	2.58	2.18
BC045410	Polymerase (DNA directed), delta 2, regulatory subunit	pold2	POLD2	2.82	1.10
BM182566	LOC100006179 sim to polymerase (DNA directed), epsilon 2 (p59 subunit)	LOC100006179	POLE2	1.72	2.07
AI793653	Polymerase (DNA directed), eta	zgc:136881	POLH	0.60	1.69
BI844059	Polymerase (RNA) III (DNA directed) polypeptide E	polr3e	POLR3E	-2.08	0.31
AY648756	Polymerase (RNA) III (DNA directed) polypeptide F	polr3f	POLR3F	0.74	-2.11
BG303768	POM121 membrane glycoprotein (rat)	pom121	POM121C	-3.99	-0.54
AY135148	Proopiomelanocortin a (adrenocorticotropin/ beta-lipotropin/alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/beta-endorphin)	pomca	POMC	-2.44	-0.46
BC095793	LOC554122 sim to paraoxonase 2	zgc:112374	PON2	2.10	0.79
BI983321	Processing of precursor 4, ribonuclease P/MRP subunit	pop4	POP4	-1.16	1.60
BC091467	Processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	pop5	POP5	-2.37	-1.73
AW203110	Sim to periostin, osteoblast specific factor	LOC567379	POSTN	-2.09	-0.37
AF395831	POU domain, class 4, transcription factor 2	pou4f2	POU4F2	-2.02	-3.04
X84224	POU domain, class 5, transcription factor 1 (OCT-4)	pou5f1	POU5F1	-1.27	-5.14
BI879231	Peter pan homolog (Drosophila)	ppan	PPAN	-1.07	-3.08
AF342937	Peroxisome proliferator-activated receptor delta a	pparda	PPARD	0.47	1.99
AF342938	Peroxisome proliferator-activated receptor delta b	ppardb	PPARD	2.21	1.30
AW567464	Peptidylprolyl isomerase A (cyclophilin A)	ppia	PPIA	-2.02	-1.68
BI897492	Peptidylprolyl isomerase B (cyclophilin B)	ppib	PPIB	0.32	2.84
BI887309	Peptidyl-prolyl isomerase G (cyclophilin G)	ppig	PPIG	0.43	-2.04
BI841405	3' end of ppil1: peptidylprolyl isomerase (cyclophilin)-like 1 and 3' end of slc6a11 | solute carrier family 6 (neurotransmitter transporter, GABA), member 11(more sim to member 13)	BI841405	PPIL1	-1.42	-1.63
BI890287	Periplakin	ppl	PPL	-5.31	-2.30
BG303651	Protein phosphatase 1D magnesium-dependent, delta isoform (WIP1)	ppm1d	PPM1D	-3.60	-3.14
AW202926	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	ppm1g	PPM1G	3.20	-0.60
AW232124	Protein phosphatase 1, catalytic subunit, beta isoform, like	ppp1cbl	PPP1CB	-0.87	3.15
BM184537	Sim to protein phosphatase 1, regulatory (inhibitor) subunit 12A	LOC571837	PPP1R12A	-2.49	0.59
BI890937	LOC393783 sim to protein phosphatase 1, regulatory (inhibitor) subunit 14A	zgc:73377	PPP1R14A	-0.66	1.72
BG305445	Protein phosphatase 1, regulatory (inhibitor) subunit 14B	ppp1r14b	PPP1R14B	0.74	2.27
BI876166	LOC571470 weak sim protein phosphatase 1, regulatory (inhibitor) subunit 15B	si:ch211-107o23.1	PPP1R15B	1.86	2.67
BI886169	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	zgc:73259	PPP1R3C	1.23	3.17
BF157490	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (m0re simmilr to PPP2R1B)	ppp2r1a	PPP2R1A	-1.75	0.88
AI878244	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	ppp2r1a	PPP2R1B	-2.11	0.89
BM072366	PPPDE peptidase domain containing 2a	pppde2a	PPPDE2	1.45	2.55
BI865895	3' end of ppt1 | palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	BI865895	PPT1	-1.65	0.96
BI889958	Protein regulator of cytokinesis 1	prc1	PRC1	-0.27	-5.27

AI461323	PR domain containing 12	zgc:101606	PRDM12	0.53	1.50
AA605696	Peroxiredoxin 6	prdx6	PRDX6	-2.01	-1.69
AI588696	Prickle homolog 1 (Drosophila) b	prickle1b	PRICKLE1	-1.62	-1.43
AW174526	cAMP-dependent protein kinase catalytic subunit	zgc:91856	PRKACA	2.57	0.73
BC054603	Protein kinase C, beta 1, like	prkcb1l	PRKCB	2.02	-0.33
BM181735	Protein kinase C, beta b	prkcbb	PRKCB1	4.40	2.68
AW116649	Protein kinase C substrate 80K-H	prkcsh	PRKCSH	2.06	1.10
AI601576	Intron of LOC556339 sim to PRKG2: protein kinase, cGMP-dependent, type II	AI601576	PRKG2	6.19	0.27
BC092358	Prolactin	prl	PRL	1.60	2.30
BI475857	3' end of prlra: prolactin receptor a and 5' end to zgc:158706; LOC572528 sim to ARID5A: AT rich interactive domain 5A (MRF1-like)	wu:fj65c07	PRLR	-1.88	-2.45
BI891684	Protein arginine methyltransferase 1	prmt1	PRMT1	-1.08	-2.29
BC053182	Protein C (inactivator of coagulation factors Va and VIIIa)	proc	PROC	3.70	2.36
AI476972	LOC436664 sim to proline dehydrogenase (oxidase) 2	zgc:92040	PRODH2	2.33	1.60
BE693164	3' end of prop1 | paired-like homeodomain transcription factor prop1 and 3' to mcfd2 | multiple coagulation factor deficiency 2	BE693164	PROP1	2.52	1.38
AY032595	Prospero-related homeobox gene 1	prox1	PROX1	1.54	3.71
AF210644	Retinal degradation slow 4	rds4	PRPH2	-1.54	-0.53
BE015655	LOC791604 sim to retinal degeneration slow protein	zgc:73336	PRPH2	1.50	-0.74
AJ297822	Trypsin	try	PRSS1	-4.15	-0.58
BF717729	LOC474322 sim to protease, serine, 3 (mesotrypsin)	zgc:92590	PRSS3	-3.99	-3.02
BC077104	LOC554458 weak sim to protease, serine, 36	zgc:100868	PRSS36	-1.67	-2.27
AW202972	LOC100101646 weak sim to protease, serine, 36	zgc:165423	PRSS36	-3.38	-1.11
AI477424	Proteasome (prosome, macropain) subunit, alpha type, 2	psma2	PSMA2	-2.21	-0.53
AF155581	Proteasome (prosome, macropain) subunit, beta type, 7	psmb7	PSMB7	-3.63	1.14
AF032390	Proteasome (prosome, macropain) subunit, beta type, 8	psmb8	PSMB8	1.98	0.19
AW019161	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	psmd10	PSMD10	0.23	-2.32
AI641775	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	psmd2	PSMD2	2.43	-0.31
BI839952	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	psmd3	PSMD3	-0.31	2.40
AI793350	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	psmd4	PSMD4	-1.61	1.58
AW419901	Paraspeckle component 1	pspc1	PSPC1	4.53	1.02
BI888210	Polypyrimidine tract binding protein 1	ptbp1	PTBP1	-1.83	-0.97
BI867303	Sim to prostaglandin E synthase 2	BI867303	PTGES2	-2.20	-1.04
AW077232	3' end of im:6903726 sim to PTGR2 | prostaglandin reductase 2 and 3' to zgc:77419 sim to TMEM62 | transmembrane protein 62	wu:fj33d06	PTGR2	1.36	-2.43
AF132082	Parathyroid hormone 2 receptor	pth2r	PTH2R	-0.47	4.07
NM_194376	Prothymosin, alpha a	ptmaa	PTMA	-0.51	2.41
BG304253	Intron of wu:fc14a08 sim to PTP4A3 | protein tyrosine phosphatase type IVA, member 3	BG304253	PTP4A3	-1.58	-1.26
BI843539	Intergenic 5' to zgc:77752: LOC393862 and 3' to zgc:77650 sim to ARF5	BI843539	PTPDC1	-3.27	-3.79
BC055174	Protein tyrosine phosphatase-like A domain containing 1	ptplad1	PTPLAD1	3.12	0.97
AW421037	Intergenic 3' to zgc:113105 sim to PTPN18 | protein tyrosine phosphatase, non-receptor type 18 and 5' to plxna3 plexin A3	wu:fj78f12	PTPN18	-2.04	-0.38
AW116344	Protein tyrosine phosphatase, non-receptor type 2, like	ptpn2l	PTPN2	-1.90	0.73
BI889244	Sim to PTPN9 | protein tyrosine phosphatase, non-receptor type 9	LOC560176	PTPN9	1.60	-1.10
AW594810	Weak sim to PTPRC | protein tyrosine phosphatase, receptor type, C (partially)	AW594810	PTPRC	0.65	1.62
BI840692	LOC100148757 weak sim to protein tyrosine phosphatase, receptor type, D	LOC100148757	PTPRD	-3.83	-3.30
BG305324	Sim to PTPRE: protein tyrosine phosphatase, receptor type, E	LOC569164	PTPRE	0.54	1.54
BI880896	3' end of ptprq | protein tyrosine phosphatase, receptor type, Q and 3' to LOC555340 sim to IQSEC3 | IQ motif and Sec7 domain 3	BI880896	PTPRQ	1.41	1.76
AJ311886	Protein tyrosine phosphatase, receptor type, S	ptprs	PTPRS	1.25	3.87
AI330860	LOC336776 weak sim to pentraxin-related gene, rapidly induced by IL-1 beta	si:ch211-272f3.3	PTX3	-1.52	-1.57
BI878946	PWP2 periodic tryptophan protein homolog (yeast)	pwp2h	PWP2	0.91	-2.53
BI673753	Paxillin	pxn	PXN	3.89	-4.05
AF231013	PYD and CARD domain containing	pycard	PYCARD	-1.73	-1.27
AW058876	Pyrroline-5-carboxylate reductase 1	pycr1	PYCR1	-2.12	-1.48
AI884070	Intergenic 3' to pygb | phosphorylase, glycogen; brain and 3' to abhd12 abhydrolase domain containing 12	AI884070	PYGB	2.35	-1.02
AW115768	Glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	qrsl1	QRSL1	-1.44	-2.27
AI793834	LOC386994 sim to RAB11A, member RAS oncogene family	zgc:63565	RAB11A	-2.35	-1.11
BQ616271	3' end of rab14l: RAB14, member RAS oncogene family, like and 3' of LOC100000720: similar to v-abl Abelson murine leukemia viral oncogene homolog 1	BQ616271	RAB14	-0.69	-1.57
AW175399	RAB14, member RAS oncogene family	rab14	RAB14	1.46	1.57
AI496921	RAB1A, member RAS oncogene family	rab1a	RAB1A	-1.84	2.41
BI891631	RAB25, member RAS oncogene family	rab25	RAB25	-2.41	-2.62
AW058859	RAB28, member RAS oncogene family	rab28	RAB28	1.05	2.37
BC049531	RAB32, member RAS oncogene family	rab32	RAB32	-0.27	2.81
BI982099	RAB3C, member RAS oncogene family	rab3c	RAB3C	1.47	-1.75
AI585084	RAB3 GTPase activating protein subunit 2 (non-catalytic)	rab3gap2	RAB3GAP2	0.30	2.51
BC076375	LOC436797 sim to RAB40B, member RAS oncogene family	zgc:92926	RAB40B	-2.62	-0.76
BI892446	RAB5A, member RAS oncogene family like	rab5al	RAB5A	1.53	1.85
BI884413	RAB5B, member RAS oncogene family	rab5b	RAB5B	1.64	2.74
BI705589	RAB6A, member RAS oncogene family	rab6a	RAB6A	2.14	3.29
BM103996	Kelch repeat-containing protein (weak sim to Rab9 effector protein with kelch motifs)	krcp	RABEPK	-2.30	-3.79
BF156891	RAB guanine nucleotide exchange factor (GEF) 1	rabgef1	RABGEF1	0.74	2.71
AI793816	RAB interacting factor	rabif	RABIF	-0.60	2.34
BI867235	RAB, member of RAS oncogene family-like 3	rabl3	RABL3	2.53	3.09
BI889437	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	rac1	RAC1	-0.86	2.41
BI890225	Ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	rac3	RAC3	1.58	2.04
BI980132	Rac GTPase-activating protein 1	racgap1	RACGAP1	2.62	3.29
AW184428	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	rad51	RAD51	2.18	-1.90
DQ021477	RAD52 homolog (S. cerevisiae)	rad52	RAD52	1.61	-1.59
BI881477	RAS related protein 1b	rap1b	RAP1B	0.31	2.51
AI793909	3' end of zgc:175180; RAP1 GTPase activating protein and 3' to spsb1; splA/ryanodine receptor domain and SOCS box containing 1	wu:fb95f11	RAP1GAP	-1.84	-3.31
BI474934	LOC100144557 sim to RAP1 GTPase activating protein	zgc:175180	RAP1GAP	-1.87	-1.56
BI671914	RAP2B, member of RAS oncogene family	rap2b	RAP2B	0.15	2.67
AW420252	RAP2C, member of RAS oncogene family	rap2c	RAP2C	-1.59	2.45
AW115989	Sim to arginyl-tRNA synthetase 2, mitochondrial	AW115989	RARS2	-2.12	-0.96
AW115682	RasGEF domain family, member 1Ba	rasgef1ba	RASGEF1B	-2.47	1.96
AA497284	Ras-like family 11 member A	zgc:110179	RASL11A	2.89	0.89
BI879607	Intergenic 3' or intron of rbbp6l: retinoblastoma binding protein 6-like or intron	BI879607	RBBP6	0.88	1.59
CD605211	RanBP-type and C3HC4-type zinc finger containing 1	zgc:91964	RBCK1	-1.78	1.66
BC071473	Ribokinase	rbks	RBKS	1.96	0.95
AW281574	Retinoblastoma-like 1 (p107)	rbl1	RBL1	-0.88	-1.96
BC051781	RNA binding motif protein 28	rbm28	RBM28	2.88	0.89
AW175474	RNA-binding region (RNP1, RRM) containing 1	rbm38	RBM38	1.66	4.05
AI878421	RNA binding motif protein 4.1	rbm4.1	RBM4	-2.69	-0.89
AW165263	RNA binding motif protein 5	rbm5	RBM5	1.72	2.42
AY395732	Retinol binding protein 1b, cellular	rbp1b	RBP1	-2.18	-4.56
AF448140	Retinol binding protein 2a, cellular	rbp2a	RBP2	-0.32	-2.13
X85957	Sim to interphotoreceptor retinol-binding protein	irbp	RBP3	-2.85	-0.78
CN505126	Retinol binding protein 4, like	rbp4l	RBP4	0.11	2.32
BI878598	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	rcbtb1	RCBTB1	0.45	-2.26
BI983343	Regulator of chromosome condensation 1	rcc1	RCC1	1.53	2.79
BI890056	Retinol dehydrogenase 10	rdh10b	RDH10	-1.84	-2.96
BI672318	Retinol dehydrogenase 1, like (all trans)	rdh1l	RDH16	3.28	3.41
AW019030	Epidermal retinal dehydrogenase 2	rdhe2	RDHE2	3.70	1.86
BI891332	Radixin	rdx	RDX	2.10	2.69
AY163839	V-rel reticuloendotheliosis viral oncogene homolog A	rela	RELA	0.35	2.74
BG883859	RELT tumor necrosis factor receptor	relt	RELT	-2.55	-1.01
AY167037	Renin	ren	REN	-0.78	-2.42

BM156937	3' end of renbp renin binding protein and 3' to si:ch211-218o21.2 sim to KDM5C | lysine (K)-specific demethylase 5C	BM156937	RENBP	0.68	-2.39
AF007949	Receptor tyrosine kinase	ret1	RET	1.60	-1.06
BI673663	Small fragment nuclease; sim to REXO2 | REX2, RNA exonuclease 2 homolog	smfn	REXO2	-0.09	-2.39
BI890048	Replication factor C (activator 1) 3	rfc3	RFC3	3.73	-0.67
AY648755	Replication factor C (activator 1) 5	rfc5	RFC5	2.58	-0.74
BC067339	LOC405832 sim to ring finger and FYVE-like domain containing 1	zgc:77828	RFFL	-1.88	-0.89
BG727567	3' end of rfx1b | regulatory factor X, 1b and 3' to wu:fc06c01 sim to DCAF15 | DDB1 and CUL4 associated factor 15	BG727567	RFX1	-2.34	-1.26
AI721391	Regulatory factor X, 2 (influences HLA class II expression)	rfx2	RFX2	-1.81	-1.07
BC091800	RGM domain family, member A	rgma	RGMA	0.18	-2.45
BG305908	3' end of rgr: retinal G protein coupled receptor	BG305908	RGR	-1.61	-2.20
AW127926	Regulator of G-protein signalling 14	rgs14	RGS14	-1.89	-2.48
AI883982	LOC445235 sim to regulator of G-protein signaling 3	zgc:100933	RGS3	-2.18	-1.93
AW282047	Rhesus blood group-associated glycoprotein	rhag	RHAG	-2.10	-1.58
AF209468	Rh50-like protein (Rh family, C glycoprotein)	rh50	RHCG	2.32	3.45
BC066492	Rhesus blood group, C glycoprotein	rhcg	RHCG	2.34	2.55
BI888792	Ras homolog gene family, member Ab	rhoab	RHOA	0.83	1.92
AW115884	Ras homolog gene family, member T1a	rhot1a	RHOT1	-0.33	1.53
BM186358	Ras homolog gene family, member T2	rhot2	RHOT2	-6.80	-2.24
AY314756	Ras homolog gene family, member V (more similar to RHOU | ras homolog gene family, member U)	rhov	RHOU	1.68	-0.29
BI981058	Regulating synaptic membrane exocytosis 2	rims2	RIMS1	-2.82	1.25
BM101597	Receptor-interacting serine-threonine kinase 4	ripk4	RIPK4	-1.64	-0.27
BI891065	Retinaldehyde binding protein 1b	rlbp1b	RLBP1	0.35	1.63
BI476474	Relaxin 3	rln3	RLN3	-1.09	5.45
BF717998	Ribonuclease like 2	rnasel2	RNASE2	-2.05	-2.41
NM_212854	Rho family GTPase 1	rnd1	RND1	1.03	2.28
BC076009	Rho family GTPase 3b	rnd3b	RND3	-2.39	1.25
BM035975	LOC619251 sim to ring finger protein 11	zgc:114095	RNF11	2.02	1.39
BI475873	Sim to ring finger protein 19A	LOC557995	RNF19A	1.96	0.65
AW305541	Ring finger protein 2	rnf2	RNF2	-1.51	2.45
AI942512	LOC678565 sim to ribonuclease/angiogenin inhibitor 1	zgc:136791	RNH1	-2.55	-2.56
BQ092666	RNA-binding region (RNP1, RRM) containing 3	rnpc3	RNPC3	1.92	-1.15
AF337035	Roundabout homolog 2	robo2	ROBO2	1.82	4.12
AF295804	Rho-associated, coiled-coil containing protein kinase 2a	rock2a	ROCK2	1.79	2.54
BI846960	RAR-related orphan receptor A, paralog b	rorab	RORA	-1.11	-1.66
AI477564	Ribosomal protein L10	rpl10	RPL10	1.84	3.35
BI891769	Ribosomal protein L10a	rpl10a	RPL10A	-1.72	3.60
AF385081	Ribosomal protein L13	rpl13	RPL13	0.99	2.64
BM153976	Ribosomal protein L13a	rpl13a	RPL13A	0.82	2.60
BI891434	Ribosomal protein L18a	rpl18a	RPL18	0.78	3.57
BI886167	Ribosomal protein L19	rpl19	RPL19	1.20	2.81
BI707410	Ribosomal protein L23a	rpl23a	RPL23A	-0.29	3.03
CN014167	Ribosomal protein L26	rpl26	RPL26	0.17	1.80
BI890906	Ribosomal protein L28-like	rpl28l	RPL28	0.11	3.30
BI710147	Ribosomal protein L30	rpl30	RPL30	0.42	3.12
BI887366	Ribosomal protein L34	rpl34	RPL34	1.86	2.07
BM096077	Ribosomal protein L35	rpl35	RPL35	0.31	2.63
BI891138	Ribosomal protein L35a	rpl35a	RPL35A	3.21	1.59
AI106421	Ribosomal protein L36	rpl36	RPL36	0.18	3.31
AI353168	Ribosomal protein L36A	rpl36a	RPL36AL	0.96	1.63
CF595288	Ribosomal protein L4	rpl4	RPL4	-0.54	1.89
AI964289	Ribosomal protein L5b	rpl5b	RPL5	0.29	3.83
BG305988	Ribosomal protein L7	rpl7	RPL7	1.85	2.84
AI964218	Ribosomal protein L7a	rpl7a	RPL7A	0.45	1.68
AW128744	Ribosomal protein L8	rpl8	RPL8	1.03	2.40
BI890218	Ribosomal protein L9	rpl9	RPL9	-0.55	3.18
AF134852	Ribosomal protein, large, P0	rplp0	RPLP0	-1.03	2.26
AI330989	Ribosomal protein, large, P1	rplp1	RPLP1	-1.08	2.49
AI965225	Ribophorin I	rpn1	RPN1	1.06	1.95
AI793600	Sim to ribophorin II	AI793600	RPN2	-0.58	1.82
BI842921	Ribosomal protein S10	rps10	RPS10	1.65	2.46
BI892430	Ribosomal protein S11	rps11	RPS11	1.93	2.86
BM070699	Ribosomal protein S12	rps12	RPS12	1.00	2.43
AI722592	Ribosomal protein S14	rps14	RPS14	1.59	2.49
BM183474	Ribosomal protein S15	rps15	RPS15	-0.27	2.95
BM104738	Ribosomal protein S15a	rps15a	RPS15A	1.72	2.37
AF210641	Ribosomal protein S18	rps18	RPS18	1.32	2.74
AW076723	Ribosomal protein S2	rps2	RPS2	-0.53	2.13
AW232284	Ribosomal protein S21	rps21	RPS21	0.12	2.55
BI318094	Ribosomal protein S25	rps25	RPS25	-0.24	2.43
BF717296	Ribosomal protein S26	rps26	RPS26	-0.36	1.89
BM156154	Ribosomal protein S26, like	rps26l	RPS26	-0.34	2.89
BM155568	Ribosomal protein S29	rps29	RPS29	1.27	3.50
AA606173	Ribosomal protein S3	rps3	RPS3	0.66	4.33
AI558833	Ribosomal protein S3A	rps3a	RPS3A	-1.05	1.92
AI964239	Ribosomal protein S4, X-linked	rps4x	RPS4X	-0.32	1.99
BE017895	Ribosomal protein S5	rps5	RPS5	-0.85	2.35
AI478010	Ribosomal protein S7	rps7	RPS7	1.01	1.90
BI889445	Ribosomal protein S8	rps8	RPS8	-0.52	2.18
AI964216	Ribosomal protein S9	rps9	RPS9	-0.50	3.01
AI384355	Ribosomal protein SA	rpsa	RPSA	-0.86	2.72
BM156813	Related RAS viral (r-ras) oncogene homolog	rras	RRAS	-1.80	0.35
BI672948	LOC100144565 sim to ribosome binding protein 1	zgc:171356	RRBP1	1.58	0.75
AI667289	Sim to ras responsive element binding protein 1	wu:fc38g07	RREB1	-2.01	0.85
U57964	Ribonucleotide reductase M1 polypeptide	rrm1	RRM1	0.60	2.61
BI866879	Ribonucleotide reductase M2 polypeptide	rrm2	RRM2	2.02	4.17
CK702787	Sim to remodeling and spacing factor 1	CK702787	RSF1	-1.69	-1.69
BI983061	Reticulon 1 a	rtn1a	RTN1	-2.32	0.75
BE201762	Reticulon 3	rtn3	RTN3	0.62	2.26
BC081614	Reticulon 4a	rtn4a	RTN4	-2.77	-3.73
BG305505	3' end of LOC100004523 similar to reticulon 4 receptor-like 1	BG305505	RTN4RL1	4.45	2.49
AY263332	Reticulon 4 receptor-like 2 a	rtn4rl2a	RTN4RL2	1.24	2.79
AY263334	Reticulon 4 receptor-like 2b	rtn4rl2b	RTN4RL2	0.38	-2.92
BG303457	Rap2 interacting protein (RUN domain containing 3A)	rap2ip	RUNDC3A	-2.36	3.97
AB043787	Runt-related transcription factor 1	runx1	RUNX1	1.22	2.21
BG308524	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	LOC563252	RUNX1T1	-1.93	-0.84
AY382181	Runt-related transcription factor 2b	runx2b	RUNX2	-1.61	1.32
AW153781	RuvB-like 2 (E. coli)	ruvbl2	RUVBL2	2.11	2.52
AI878606	3' end of LOC100007598 sim to RXFP3 | relaxin/insulin-like family peptide receptor 3 and 5' to LOC100007476 similar to uveal autoantigen with coiled-coil domains and ankyrin repeats	wu:fc62e05	RXFP3	2.50	-1.01
U29942	Retinoid x receptor, beta a	rxrab	RXRA	2.42	2.14
AI958589	3' end of ryr1a | ryanodine receptor 1a (skeletal)	wu:fa97h07	RYR3	-2.34	-1.78
BM104515	S100 calcium binding protein A1	s100a1	S100A1	-4.27	-4.30
CK872210	LOC449788 sim to S100 calcium binding protein A10a	s100a10a	S100A1	-2.39	-2.17
BC080247	S100 calcium binding protein S	s100s	S100A1	3.39	-1.06
AW202804	S100 calcium binding protein U	s100u	S100A1	-1.93	-1.75
AW595487	Ictacalcin 2 sim to S100 calcium binding protein A4	icn2	S100A4	-4.26	2.32
BG985836	Sal-like 1a	sall1a	SALL1	1.86	2.29
BC090729	Sim to Sin3A-associated protein, 18kDa	LOC794620	SAP18	-2.25	-2.22

AW128723	Sap30-like	sap30l	SAP30L	-1.53	0.68
BG304241	Spindle assembly 6 homolog (C. elegans)	sass6	SASS6	0.46	-4.61
AW078366	Secretory carrier membrane protein 2	scamp2	SCAMP2	1.95	2.33
BI886699	Secretory carrier membrane protein 2 like	scamp2l	SCAMP2	0.38	-4.09
BC085533	Secretory carrier membrane protein 3	zgc:103488	SCAMP3	1.59	0.71
BC065670	Secretory carrier membrane protein 5	scamp5	SCAMP5	-2.19	1.28
BE202194	Scavenger receptor class B, member 1	scarb1	SCARB1	-1.28	-3.17
BC095851	Sim to stearoyl-CoA desaturase 4 isoform a	zgc:112951	SCD	4.10	0.96
BC090478	Sec1 family domain containing 2	scfd2	SCFD2	0.93	2.07
AW117001	Scinderin like b	scinlb	SCIN	-1.96	1.80
AW154574	Serine carboxypeptidase 1	scpep1	SCPEP1	-1.14	-1.90
BG305416	Sim to SCY1-like 1 (S. cerevisiae)	wu:fk36e11	SCYL1	3.23	0.57
AW019206	3' end of si:ch211-244b2.1 sim to SCYL2 | SCY1-like 2 and 3' to si:ch211-244b2.3 weak sim to ZC3HAV1 | zinc finger CCCH-type, antiviral 1	wu:fd50f01	SCYL2	1.69	1.16
AI959694	Syndecan 4	sdc4	SDC4	-1.04	2.40
BI886016	Syndecan binding protein (syntenin)	sdcbp	SDCBP	2.45	1.95
AW232790	3' end of zgc:163000 : succinate dehydrogenase assembly factor 2, mitochondrial precursor	AW232790	SDHAF2	-1.74	-0.92
BI702979	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	sdhb	SDHB	-1.59	-1.23
BI671139	LOC402824 sim to serum deprivation response protein	LOC402824	SDPR	-3.16	1.03
AF466189	OG9 homeobox gene/mezzo	og9x	SEBOX	3.74	0.85
AI883266	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	sec22a	SEC22A	2.05	0.89
BG302794	Sec31p homolog (yeast)	sec31p	SEC31A	0.93	4.20
AY029527	Sec61 alpha like 1	sec61al1	SEC61A1	0.27	2.53
BC081491	Selenoprotein K	zgc:103591	SELK	0.90	1.78
BI889650	Selenoprotein T, 1b	selt1b	SELT	-1.40	-2.50
AF083382	Semaphorin 3ab	sema3ab	SEMA3A	-2.53	1.37
AL721402	Intergenic 3' to sema3gb | semaphorin 3gb and 3' to wasb | Wiskott-Aldrich syndrome (eczema-thrombocytopenia) b	AL721402	SEMA3F	-1.20	-1.62
AY766120	Semaphorin 3ga	sema3ga	SEMA3F	2.08	0.47
AY766121	Semaphorin 3gb	sema3gb	SEMA3F	-3.41	-0.31
AF073289	Semaphorin 4e (sim to sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D)	sema4e	SEMA4D	-2.24	-2.01
BI843214	LOC571373 weak sim to SENP7: SUMO1/sentrin specific peptidase 7 [Homo sapiens]	LOC571373	SENP7	2.03	-0.95
AF322071	Selenoprotein P, plasma, 1a	sepp1a	SEPP1	-1.79	-3.56
AF322072	Selenoprotein P, plasma, 1b	sepp1b	SEPP1	-2.35	-3.01
BE606074	Septin 6	sept6	SEPT6	3.39	3.75
BF717472	Selenoprotein X, 1	sepx1	SEPX1	0.27	-2.26
NM_199727	Serine incorporator 1 (Tumor differentially expressed 2)	serinc1	SERINC1	-0.06	1.96
AW116276	LOC569338 sim to serine incorporator 1	si:ch211-232d9.2	SERINC1	-5.11	-4.82
AW018949	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	serpina1	SERPINA1	1.88	4.54
AW018965	LOC556938 sim to serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	zgc:113828	SERPINA1	4.66	4.20
BC083441	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7	serpina7	SERPINA7	3.51	3.70
BF717503	Serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1	serpinc1	SERPINC1	2.47	5.08
BG799195	Serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1	serpind1	SERPIND1	-0.61	2.72
BM184276	Serpin peptidase inhibitor, clade F , member 2, like	serpinf2l	SERPINF2	4.91	3.01
BC067135	SERTA domain containing 2	sertad2	SERTAD2	2.29	-1.34
AI964822	Weak sim to SETD8 | SET domain containing (lysine methyltransferase) 8	LOC100003868	SETD8	2.89	-1.50
BI886759	SET domain, bifurcated 2	setdb2	SETDB2	1.22	1.95
BC066392	Splicing factor 3a, subunit 1	sf3a1	SF3A1	-0.77	-2.05
AB055672	Secreted frizzled-related protein 5	sfrp5	SFRP5	-0.45	-3.24
BI890669	Splicing factor, arginine/serine-rich 2	sfrs2	SFRS2	1.82	2.18
BM072333	Splicing factor, arginine/serine-rich 6b	sfrs6b	SFRS6	-3.10	2.26
BC053226	SFT2 domain containing 1	sft2d1	SFT2D1	0.83	2.66
BI673509	LOC503601 sim to SFT2 domain containing 1	zgc:110788	SFT2D1	-1.94	-2.65
BI673466	Serum/glucocorticoid regulated kinase 1	sgk1	SGK1	1.24	4.61
BI670851	LOC768159 sim to serum/glucocorticoid regulated kinase 1	zgc:154030	SGK1	-1.52	-0.72
AI544889	LOC559050 sim to serum/glucocorticoid regulated kinase 1	zgc:154065	SGK1	0.99	1.73
AW281658	SH3-domain binding protein 5 (BTK-associated)	sh3bp5	SH3BP5	1.12	-2.65
BI983776	SH3-domain GRB2-like 3	sh3gl3	SH3GL3	-1.63	-0.49
BM154195	SH3-domain GRB2-like 3-like	zgc:158742	SH3GL3	0.53	-1.55
AA658631	Sim to SH3 and multiple ankyrin repeat domains 3	AA658631	SHANK3	-1.83	-2.10
AW019651	Sex hormone binding globulin	shbg	SHBG	5.97	4.60
L27585	Sonic hedgehog a	shha	SHH	2.56	4.09
U30710	Sonic hedgehog b (twh; twhh)	shhb	SHH	2.64	3.44
BE605465	Sim to SHROOM2 | shroom family member 2	LOC571333	SHROOM2	1.75	-1.17
BI885759	Shroom family member 4	shroom4	SHROOM4	1.54	1.98
BI886779	Seven in absentia homolog 1 (Drosophila)	siah1	SIAH1	-2.30	-2.35
BG729183	3' end of siah2l seven in absentia homolog 2 (Drosophila)-like and 3' to rbmx2 | RNA binding motif protein, X-linked 2	BG729183	SIAH2	2.89	0.43
BI983651	Sigma non-opioid intracellular receptor 1	sigmar1	SIGMAR1	0.97	-2.21
AW076688	Silver homolog (mouse) a	silva	SILV	-0.53	-3.95
BM072610	Sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	sirt3	SIRT3	2.16	-0.53
AB045623	Sine oculis homeobox homolog 4.2	six4.2	SIX4	-0.45	2.63
AW420324	Src kinase associated phosphoprotein 2	skap2	SKAP2	2.00	0.14
AF060117	Nuclear oncoprotein skia (v-ski sarcoma viral oncogene homolog (avian))	skia	SKI	-0.89	2.05
AI545551	Intron of Superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (skiv2l)	AI545551	SKIV2L	0.78	2.24
AW019603	Sim to solute carrier family 13 (sodium-dependent citrate transporter), member 5	si:ch211-221p4.4	SLC13A5	3.86	2.12
AW165069	LOC326634 sim to solute carrier family 14 (urea transporter), member 2	zgc:136632	SLC14A2	-3.26	-2.85
AW018970	Solute carrier family 15 (oligopeptide transporter), member 1	slc15a1	SLC15A1	-2.24	-3.68
AW154070	Solute carrier family 15 (H+/peptide transporter), member 2	slc15a2	SLC15A2	-2.09	-2.42
AW184640	LOC449947 sim to solute carrier family 16, member 12 (monocarboxylic acid transporter 12)	zgc:110441	SLC16A12	-1.49	-2.32
BI985003	LOC574425 sim to solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	zgc:114041	SLC16A13	-1.74	-2.01
AW116414	Solute carrier family 16 (monocarboxylic acid transporters), member 3	slc16a3	SLC16A3	-3.70	-4.64
AW232016	Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6a	slc17a6l	SLC17A6	0.37	1.78
AW059376	3' end of slc17a9b | solute carrier family 17, member 9b	AW059376	SLC17A9	2.90	1.55
BG729177	3' end of slc17a9b: solute carrier family 17, member 9b	BG729177	SLC17A9	6.42	2.41
BI840114	LOC555979 sim to solute carrier family 22, member 23	zgc:171831	SLC22A23	-5.76	0.76
BI865582	Solute carrier family 22, member 7-like	zgc:63958	SLC22A7	-1.39	-2.41
BM095990	Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	slc25a1	SLC25A1	-0.35	-2.69
BC045395	Solute carrier family 25 (mitochondrial carrier, brain), member 14	slc25a14	SLC25A14	2.69	-1.22
AI942949	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	slc25a20	SLC25A20	0.17	3.13
BC066404	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	slc25a25	SLC25A25	-1.04	-2.74
BC096793	Solute carrier family 25, member 26	slc25a26	SLC25A26	-2.27	-1.57
BG306043	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3, like	slc25a3l	SLC25A3	-1.35	3.17
AW174196	Solute carrier family 25, member 32a	slc25a32a	SLC25A32	2.85	2.25
CK702997	3' end of slc25a36b | solute carrier family 25, member 36b and 5' to LOC558375 sim to to Tripartite motif-containing protein 16	CK702997	SLC25A36	1.54	1.26
AA605664	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	slc25a4	SLC25A4	-4.06	-2.16
AI883208	LOC436633 sim to solute carrier family 25, member 40	zgc:92520	SLC25A40	1.57	0.56
AW127912	Solute carrier family 25 alpha, member 5	slc25a5	SLC25A5	-0.56	2.55
BG799220	Sim to solute carrier family 27 (fatty acid transporter), member 1	zgc:153860	SLC27A1	0.56	4.41
AI477656	Solute carrier family 2 (facilitated glucose transporter), member 5(pseudo)	slc2a5	SLC2A5	4.62	2.52
BC049409	Solute carrier family 2 (facilitated glucose transporter), member 8-like	slc2a8l	SLC2A8	2.85	-1.62
AB055665	Solute carrier family 2 (facilitated glucose transporter), member 15a	slc2a15a	SLC2A9	1.68	5.93
AI522773	Solute carrier family 30 (zinc transporter), member 6	slc30a6	SLC30A6	-1.13	-4.76
BC055208	Solute carrier family 33 (acetyl-CoA transporter), member 1	slc33a1	SLC33A1	4.62	0.45

AW343846	Solute carrier family 34 (sodium phosphate), member 2b	slc34a2b	SLC34A2	1.21	2.84
BC057491	Solute carrier family 35, member A5	slc35a5	SLC35A5	2.25	-0.22
AW115742	Solute carrier family 35, member B1	slc35b1	SLC35B1	-2.86	-0.96
BM183463	Solute carrier family 37 (glycerol-3-phosphate transporter), member 2	slc37a2	SLC37A2	-1.51	2.66
BI877883	Solute carrier family 38, member 3	slc38a3	SLC38A3	-2.50	-1.08
BC096946	Solute carrier family 38, member 4	slc38a4	SLC38A4	2.73	-2.31
BM184056	Solute carrier family 39 (zinc transporter), member 3	slc39a3	SLC39A1	2.02	0.62
BC090821	Solute carrier family 39 (zinc transporter), member 9	slc39a9	SLC39A9	1.71	0.78
AI641064	LOC790938 weak sim to solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	zgc:158423	SLC3A2	-0.78	-1.60
AW019543	Solute carrier family 41, member 1	slc41a1	SLC41A1	4.18	1.99
AW117094	3' end of zgc:103664 : solute carrier family 43, member 2 and 5' to LOC566188 sim to INPP5J | inositol polyphosphate-5-phosphatase J	wu:fi32b04	SLC43A2	-3.56	-3.85
AW115724	Choline transporter-like protein 2 sim to SLC44A2: solute carrier family 44, member 2	zgc:63569	SLC44A2	-3.28	-2.74
AI477964	Intron of slc4a2a solute carrier family 4, anion exchanger, member 2a	AI477964	SLC4A2	2.48	0.86
BC058316	Solute carrier family 5 (sodium/glucose cotransporter), member 1	slc5a1	SLC5A1	-2.39	-4.16
BI472731	LOC692318 sim to SLC6A1 | solute carrier family 6 (neurotransmitter transporter, GABA), member 1	zgc:136569	SLC6A1	-0.81	1.65
BC059804	Solute carrier family 6 (neurotransmitter transporter), member 19	slc6a19	SLC6A19	-3.18	-0.74
AW019145	LOC553256 sim to solute carrier family 6 (neutral amino acid transporter), member 19	zgc:162095	SLC6A19	-2.36	-3.12
AW076663	3' end of slc7a4 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	AW076663	SLC7A4	-1.78	-1.82
BQ284787	Solute carrier family 8 (sodium/calcium exchanger), member 4b	slc8a4b	SLC8A1	-0.46	2.02
AF127920	MAD homolog 5 (Drosophila)	smad5	SMAD5	-1.67	-2.26
BI841943	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	smad7	SMAD7	-0.30	2.25
BI704195	MAD homolog 9 (Drosophila)	smad9	SMAD9	3.87	-0.45
AW154421	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	smarca2	SMARCA2	0.94	2.44
BE016502	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	smarca4	SMARCA4	1.64	-0.42
BI980217	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	smarce1	SMARCE1	-2.81	1.36
BC044141	Structural maintenance of chromosomes 2	smc2	SMC2	-3.20	-2.08
AF083557	Survival motor neuron 1	smn1	SMN1	-2.12	-0.10
AF096509	Smoothened homolog (Drosophila)	smo	SMO	2.02	-1.89
BI844024	Sim to SPARC related modular calcium binding 1	LOC795519	SMOC1	0.83	2.45
AJ009864	Spermine synthase	sms	SMS	-2.74	1.16
AI437336	WW domain containing E3 ubiquitin protein ligase 1 (SMAD specific E3 ubiquitin protein ligase 1)	wwp1	SMURF1	3.86	0.92
AI601278	SET and MYND domain containing 1 a	smyd1a	SMYD1	-4.25	-1.84
AF091594	Synaptosome-associated protein 25 b	snap25b	SNAP25	2.74	-0.25
AI353581	LOC796145 sim to synaptosomal-associated protein, 91kDa homolog	LOC796145	SNAP91	-1.42	-1.52
AW420768	LOC567959 sim to SNAP-associated protein	si:dkey-222b8.2	SNAPIN	1.63	1.50
BI671665	Intron of LOC100001856 similar to Sushi, nidogen and EGF-like domain-containing protein 1 precursor (Insulin-responsive sequence DNA-binding protein 1) (IRE-BP1)	BI671665	SNED1	-1.82	-1.37
BI842571	SNF related kinase	snrk	SNRK	1.61	-0.36
BI885984	Small nuclear ribonucleoprotein polypeptide C	snrpc	SNRPC	-0.93	-2.10
BM037469	Small nuclear ribonucleoprotein D3 polypeptide	snrpd3	SNRPD3	-1.59	-2.47
BG304285	Sim to SNW domain containing 1	BG304285	SNW1	-2.46	0.68
BF157344	Sim to sorting nexin 12	snx12	SNX12	-1.31	2.11
BC090713	Sorting nexin 13	zgc:113125	SNX13	-1.61	-0.45
BG728207	LOC555448 sim to Sorting nexin 8	snx8	SNX8	-0.36	-2.79
BC091825	Sorting nexin 9	snx9	SNX9	-3.50	0.43
BG303759	3' end of socs2 suppressor of cytokine signaling 2	BG303759	SOCS2	1.55	0.85
Y12236	Superoxide dismutase 1, soluble	sod1	SOD1	2.45	2.10
AI721653	LOC792544 part sim to SON DNA binding protein	wu:fc30f01	SON	3.13	0.30
BI983463	Sim to SORL1 | sortilin-related receptor, L(DLR class) A	LOC567650	SORL1	0.90	-2.59
U85091	SRY-box containing gene 11b	sox11b	SOX11	-1.99	-3.24
AF101266	SRY-box containing gene 21a	sox21a	SOX14	-1.89	-2.50
AB071895	SRY-box containing gene 32	sox32	SOX17	-3.33	0.55
X79821	SRY-box containing gene 19a	sox19a	SOX2	-2.27	-2.02
AW059068	SRY-box containing gene 19b	sox19b	SOX2	-1.78	-2.07
BI980800	SRY-box containing gene 2	sox2	SOX2	-2.29	-0.48
BG985680	SRY-box containing gene 3	sox3	SOX3	-1.97	-1.74
AW344031	SRY-box containing gene 8	sox8	SOX8	0.63	2.23
AI641094	Sp1 transcription factor	sp1	SP1	1.16	6.47
BC093591	LOC550611 weak sim to SP100 nuclear antigen	zgc:113411	SP100	-1.86	-0.51
BC065349	LOC402928 sim to Sp6 transcription factor	zgc:77358	SP6	-2.54	-1.18
BI473004	Signal peptidase complex subunit 1 homolog	spcs1	SPCS1	1.57	1.45
AI793770	Signal peptidase complex subunit 2 homolog (S. cerevisiae)	spcs2	SPCS2	1.20	1.94
AW019444	3' end of spcs2 | signal peptidase complex subunit 2 homolog and 3' to defbl3 defensin, beta-like 3	wu:fe11f09	SPCS2	1.75	1.58
AI721702	SPEG complex locus	speg	SPEG	2.37	-1.57
AI544644	Sim to SPG20 | spastic paraplegia 20 (Troyer syndrome)	LOC791952	SPG20	-3.06	-1.47
AF371368	Sprouty (Drosophila) homolog 4	spry4	SPRY4	4.97	4.55
AI883714	Sim to SPTLC2: serine palmitoyltransferase, long chain base subunit 2	zgc:175221	SPTLC2	3.14	0.79
BI884972	V-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	src	SRC	2.44	2.76
BI889953	LOC100037309 sim to sterol regulatory element binding transcription factor 2	zgc:158371	SREBF2	-1.43	1.62
BI885993	Signal recognition particle 54	srp54	SRP54	1.58	2.83
AF164472	Intron sim to serine/arginine repetitive matrix 1	AF164472	SRRM1	1.29	2.32
AF164483	Serine/arginine repetitive matrix 1	srrm1	SRRM1	1.84	4.16
AF364084	Signal sequence receptor, beta	ssr2	SSR2	-0.39	2.43
BM104604	Signal sequence receptor, gamma	ssr3	SSR3	4.40	1.60
BI888470	Structure specific recognition protein 1a	ssrp1a	SSRP1	-0.08	-2.04
AJ238017	Somatostatin 2	sst2	SST	0.28	-2.25
AW174328	Suppression of tumorigenicity 14 (colon carcinoma) a	st14a	ST14	-2.42	-1.83
BM082738	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	st3gal1	ST3GAL2	-0.87	-5.25
AW116215	ST3 beta-galactoside alpha-2,3-sialyltransferase 2, like	st3gal2l	ST3GAL2	0.86	2.82
BM182555	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	st6gal1	ST6GAL1	-1.05	-1.72
BG799048	Beta-galactosamide alpha-2,6-sialyltransferase 2	st6gal2	ST6GAL2	-0.60	2.41
BM184316	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	st8sia2	ST8SIA2	0.90	-3.36
AI584415	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	stam	STAM	1.95	1.33
AF220435	Steroidogenic acute regulatory protein	star	STAR	-3.48	-1.08
AJ005693	Signal transduction and activation of transcription 3	stat3	STAT3	-1.06	2.53
BI879876	Intron of stat5.1 | signal transducer and activator of transcription 5.1	BI879876	STAT5B	2.22	1.99
AI884184	3' end of stat5.1 signal transducer and activator of transcription 5.1	wu:fc75a07	STAT5B	0.90	1.84
AW115780	Staufen, RNA binding protein, homolog 2 (Drosophila)	stau2	STAU2	0.43	3.07
CD605508	Stromal interaction molecule 1	si:dkey-24p1.5	STIM1	1.32	-2.83
BM156040	3' end of stk38l | serine/threonine kinase 38 like and 5' to pion | pigeon homolog	BM156040	STK38L	2.01	1.22
BI891936	Stathmin 1a	stmn1a	STMN1	-1.30	3.93
AW184525	Integral membrane protein 1 (STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	itm1	STT3A	2.50	2.73
BC062862	Syntaxin 11b.1	stx11b.1	STX11	-1.11	-2.39
AI721420	Syntaxin binding protein 6 (amisyn)	stxbp6	STXBP6	-2.63	0.26
BC078355	Suppressor of defective silencing 3 homolog (SDS3, S. cerevisiae)	suds3	SUDS3	3.20	-0.78
NM_183348	Sulfotransferase family 1, cytosolic sulfotransferase 3	sult1st3	SULT1A1	2.65	-3.11
AW174510	Sulfotransferase family, cytosolic sulfotransferase 6	sult1st6	SULT1C2	1.11	-2.43
BC056283	SMT3 suppressor of mif two 3 homolog 1 (yeast)	sumo1	SUMO1	1.72	0.87
AW233541	Weak sim to SUN2 | Sad1 and UNC84 domain containing 2	LOC796761	SUN2	1.83	-0.36
BM156926	Surfeit 6-like	surf6l	SURF6	-1.24	-2.69
AI721414	Suppressor of zeste 12 homolog b	suz12b	SUZ12	-1.51	0.69
AW018950	LOC559122 weak sim to SVEP1 sushi, von Willebrand factor type A, EGF and pentraxin	LOC559122	SVEP1	-1.39	-1.73

	domain containing 1				
AI641697	Sim to supervillin	im:7142403	SVIL	-1.35	-2.18
BG302925	LOC100001855 sim to supervillin	LOC100001855	SVIL	-1.00	-3.85
BM182436	LOC393645 sim to SWAP-70 protein	zgc:63599	SWAP70	3.43	0.80
AA566708	LOC568900 sim to syncollin	LOC568900	SYCN	-2.35	-2.76
BI534277	LOC570672 sim to synapsin I	DKEY-90N12.3	SYN1	1.49	1.76
BI981168	Purkinje cell protein 4b sim to synapsin II	pcp4b	SYN2	1.45	-2.84
BI980133	3' end of syncripl | synaptotagmin binding, cytoplasmic RNA interacting protein, like and 3' to si:dkey-3h2.3 weak sim to NLRC3 | NLR family, CARD domain containing 3	wu:fj32a12	SYNCRIP	-2.30	0.65
BE201590	Weak sim to SYNE2 spectrin repeat containing, nuclear envelope 2	si:dkey-274c14.3	SYNE2	0.57	1.53
AI723329	Intergenic 3' to synj1 | synaptojanin 1 and 5' to slc9a6b | solute carrier family 9 (sodium/hydrogen exchanger), member 6b	AI723329	SYNJ1	2.24	0.81
BI844823	Synaptoporin	synpr	SYNPR	-2.98	-2.10
BI670974	Synaptophysin b	sypb	SYP	2.63	-0.77
AW174543	Synaptotagmin IV	syt4	SYT4	0.91	-3.09
BE200811	Synovial apoptosis inhibitor 1, synoviolin	syvn1	SYVN1	3.05	1.36
S57147	No tail	ntl	T	-1.03	-5.22
BI705624	Transforming, acidic coiled-coil containing protein 3	tacc3	TACC3	-1.05	-4.29
BI671845	Transcriptional adapter 1-like protein	zgc:85851	TADA1	-1.32	2.00
BC055562	Transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	tada2b	TADA2B	4.56	0.91
AW154429	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	taf5l	TAF5L	-3.59	-2.80
AI353492	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor	taf8	TAF8	-2.20	-0.95
BI673379	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	taf9	TAF9	0.88	-2.07
BI867933	LOC415208 sim to TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	zgc:86811	TAF9	-4.41	1.00
BI896473	Transaldolase 1	taldo1	TALDO1	2.20	2.63
BM026665	3' end of LOC798408 sim to TAOK3 | TAO kinase 3 and 3' to pbp | phosphatidylethanolamine binding protein	BM026665	TAOK3	-2.71	-1.37
AF032394	ATP-binding cassette, sub-family B (MDR/TAP), member 3 like 1	abcb3l1	TAP2	-3.10	-2.57
AI641018	Threonyl-tRNA synthetase	zgc:92586	TARS	2.33	2.30
AI522688	Tyrosine aminotransferase	tat	TAT	4.01	5.93
BI983522	LOC554092 sim to TBC1 domain family, member 17	zgc:110443	TBC1D17	1.79	1.81
BI672484	3' end of si:ch211-199c19.3 sim to TBC1D9: TBC1 domain family, member 9 (with GRAM domain) and 5' to ucp4: uncoupling protein 4	BI672484	TBC1D9	-2.04	0.73
BM025937	Tubulin cofactor a	tbca	TBCA	3.14	0.33
BM184246	Tubulin folding cofactor B	tbcb	TBCB	0.75	2.13
BI984755	Tubulin-specific chaperone c-like	tbccl	TBCC	-0.70	-3.41
AW232076	Tubulin-specific chaperone d	tbcd	TBCD	1.83	1.13
BM184129	TATA box binding protein	tbp	TBP	2.65	1.34
BM095827	T-box 15	tbx15	TBX15	-0.72	-4.07
AF179405	T-box 2b	tbx2b	TBX2	0.44	3.27
AY398422	Thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	tbxas1	TBXAS1	-2.59	4.75
BC046074	Transcription elongation factor A (SII), 2	tcea2	TCEA2	-0.22	-2.32
AJ006310	Paraxis (transcription factor 15 (basic helix-loop-helix))	par1	TCF15	2.55	-4.84
AY825026	Transcription factor 7 (T-cell specific, HMG-box)	tcf7	TCF7	0.24	3.34
AF136455	Transcription factor 7-like 2 (T-cell specific, HMG-box)	tcf7l2	TCF7L2	-0.95	2.46
AW019798	Transcobalamin II	si:ch211-102c2.6	TCN2	0.69	-1.53
AI957669	Intergenic 3' to zgc:171784 : TEA domain family member 3 and 5' to LOC797914 | similar to sphingomyelin phosphodiesterase 2	wu:fc96g12	TEAD3	-1.73	-1.33
U43671	Thyrotroph embryonic factor	tef	TEF	-4.47	-0.26
BI842909	LOC553686 sim to thyrotrophic embryonic factor	zgc:112180	TEF	-3.03	-1.50
BI704253	Transferrin-a	tfa	TF	0.84	3.58
AI722745	Transcription factor AP-2 alpha	tfap2a	TFAP2A	1.40	-1.50
AW117076	Transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	tfap2c	TFAP2C	-2.12	-1.48
BM187021	Intron of si:ch211-210c8.8 sim to TFCP2 | transcription factor CP2	BM187021	TFCP2	2.73	1.08
BI980047	Sim to transcription factor CP2	wu:fc10e04	TFCP2	1.70	0.90
BI867054	Transcription factor Dp-1, like	tfdp1l	TFDP1	1.47	2.06
AI974139	Transcription factor Dp-2 (E2F dimerization partner 2)	tfdp2	TFDP2	-1.61	2.43
AY649365	Transferrin receptor 2	tfr2	TFR2	2.00	3.20
AW566567	Transforming growth factor, beta 1	tgfb1	TGFB1	0.41	1.88
AY338730	Transforming growth factor, beta 2	tgfb2	TGFB2	0.62	2.27
AY614705	Transforming growth factor, beta 3	tgfb3	TGFB3	-0.39	1.79
AW018635	Transforming growth factor, beta-induced	tgfbi	TGFBI	0.99	1.70
AW203007	Transforming growth factor, beta receptor II	tgfbr2	TGFBR2	-0.38	2.24
AW305396	3' end of DKEY-101K6.5: sim to TGFBR2: TGF-beta type II receptor and 3' end to DKEY-101K6.4: sim to OSBPL11: oxysterol binding protein-like 11	wu:fj64g10	TGFBR2	3.14	2.87
BG306444	Sim to transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	BG306444	TGM1	-1.92	-1.70
AF075384	Tyrosine hydroxylase	th	TH	0.39	2.62
BI888350	THO complex 3	thoc3	THOC3	-0.46	-2.24
BM181792	Thy-1 cell surface antigen (weak)	thy1	THY1	2.28	3.33
AI477343	TGFB1-induced anti-apoptotic factor 1	tiaf1	TIAF1	0.09	1.72
AW344036	TIA1 cytotoxic granule-associated RNA binding protein-like 1	tial1	TIAL1	2.38	2.23
AF053633	Endothelium-specific receptor tyrosine kinase 1 (sim to tyrosine kinase with immunoglobulin-like and EGF-like domains 1)	tie1	TIE1	1.41	2.29
AI965244	Sim to timeless homolog (Drosophila)	AI965244	TIMELESS	1.55	0.39
BE605781	Translocase of inner mitochondrial membrane 17 homolog A (yeast)	timm17a	TIMM17A	-2.35	0.83
AI332057	Tissue inhibitor of metalloproteinase 2	timp2	TIMP2	-3.97	0.50
AW171093	TERF1 (TRF1)-interacting nuclear factor 2 (weak sim)	tinf2	TINF2	1.99	2.45
BI885944	Sim to tight junction protein 3 (zona occludens 3)	BI885944	TJP3	-1.82	-0.61
BC044148	Thymidine kinase 1, soluble	tk1	TK1	2.80	2.76
BM095334	Groucho 2 (sim to transducin-like enhancer of split 3 (E(sp1) homolog)	gro2	TLE3	-1.91	-2.67
BI885570	Sim to talin 2; 3' end of tln1	BI885570	TLN1	1.71	2.68
BG304206	Toll-like receptor 3	tlr3	TLR3	0.71	2.98
AI965294	Intron of tlr7 | toll-like receptor 7	wu:fc89c06	TLR7	3.86	-0.55
AF398519	T-cell leukemia, homeobox 3b	tlx3b	TLX3	3.18	0.94
AI877509	Transmembrane emp24 protein transport domain containing 1b; interleukin 1 receptor-like 1 ligand	tmed1b	TMED1	-2.04	-1.10
BI672201	Transmembrane emp24 domain-containing protein 10	zgc:85681	TMED10	1.67	1.04
BM035946	Transmembrane emp24 protein transport domain containing 3	tmed3	TMED3	1.47	2.60
AW344170	Transmembrane emp24 protein transport domain containing 9	tmed9	TMED9	-1.72	0.93
BI880791	LOC402976 sim to transmembrane protein 27	LOC402976	TMEM27	-2.73	-2.22
BI428441	Transmembrane protein 37	tmem37	TMEM37	-0.45	-2.43
AW128379	Transmembrane protein 38A	tmem38a	TMEM38A	-3.97	-2.62
BC045460	LOC393145 sim to transmembrane protein 38B	zgc:55815	TMEM38B	2.87	0.89
AW116654	Thymopoietin	tmpo	TMPO	1.92	2.34
AW058840	LOC553624 sim to thymopoietin	zgc:110551	TMPO	-1.83	-1.44
BI878819	Sim to transmembrane protease, serine 13	LOC559754	TMPRSS13	-2.01	-0.80
BG729678	Transmembrane protease, serine 4b	tmprss4b	TMPRSS4	-1.90	-1.87
U14940	Tenascin C	tnc	TNC	2.68	0.27
BM096075	Weak sim to TNFAIP2 | tumor necrosis factor, alpha-induced protein 2	DKEY-183C23.1	TNFAIP2	1.62	1.52
BC053238	Tumor necrosis factor, alpha-induced protein 8, like	tnfaip8l	TNFAIP8	-1.38	-1.72
AF250042	Tumor necrosis factor receptor superfamily, member a	tnfrsfa	TNFRSF14	-1.45	-3.26
AA658585	3' end of tnfrsf21 | tumor necrosis factor receptor superfamily, member 21 and 5' to LOC799325 : weak sim to GPR110 | G protein-coupled receptor 110	AA658585	TNFRSF21	-1.49	-1.84
BE201526	3' end of zgc:136557 : tumor necrosis factor receptor superfamily, member 9 and 5' to zgc:162431 weak sim to CCDC50 | coiled-coil domain containing 50	BE201526	TNFRSF9	1.63	1.15
AF250041	Tumor necrosis factor (ligand) superfamily, member 10 like	tnfsf10l	TNFSF10	-1.23	-2.25
BC090312	Tumor necrosis factor (ligand) superfamily, member 10 like 4 (weak sim to tumor necrosis factor (ligand) superfamily, member 10)	tnfsf10l4	TNFSF10	-3.23	-1.89
BM156764	TNFAIP3 interacting protein 1	tnip1	TNIP1	-0.58	1.50
AW343766	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	tnks	TNKS	2.87	1.48

BC071546	LOC415175 sim to troponin C type 1 (slow)	zgc:86932	TNNC1	-1.70	-1.26
BC047857	Troponin I, skeletal, fast 2a.2	tnni2a.2	TNNI2	-2.72	-2.52
AI964276	Troponin I, skeletal, fast 2a.4	tnni2a.4	TNNI2	-2.29	-1.33
AI617763	Troponin I, skeletal, fast 2b.2	tnni2b.2	TNNI2	-4.42	-3.12
BE693169	Troponin T3b, skeletal, fast	tnnt3b	TNNT3	-7.69	0.57
BI705660	Target of myb1 (chicken)	tom1	TOM1	2.64	2.61
BI671327	3' end of tomm70a | translocase of outer mitochondrial membrane 70 homolog A and 5' to tbc1d23 | TBC1 domain family, member 23	wu:fc56c01	TOMM70A	-1.42	-2.27
BM156751	Topoisomerase (DNA) II alpha	top2a	TOP2A	-1.31	-4.24
BI867046	Sim to TOPORS | topoisomerase I binding, arginine/serine-rich	si:ch211-145b13.4	TOPORS	0.96	1.71
BC062843	LOC393830 sim to torsin family 1, member A (torsin A)	zgc:77727	TOR1A	0.89	-2.16
BM183866	LOC565062 sim to torsin family 1, member B (torsin B)	LOC565062	TOR1B	-1.57	-0.86
U60804	Tumor protein p53	tp53	TP53	2.47	-3.54
AI626138	Tumor protein p53 binding protein, 2	tp53bp2	TP53BP2	2.15	-2.34
BM005448	Weak sim to tumor protein p53 inducible nuclear protein 1	LOC555795	TP53INP1	0.44	-1.94
AF412283	Tumor protein p63	tp63	TP63	-3.09	2.80
BI890917	Trophoblast glycoprotein-like	tpbgl	TPBG	0.81	2.29
BI882446	Tumor protein D52-like 2	tpd52l2	TPD52L2	2.00	2.08
BG303492	Tryptophan hydroxylase 1b	tph1b	TPH1	0.85	-3.45
AF387820	Triosephosphate isomerase 1a	tpi1a	TPI1	-4.17	-6.12
AI588611	Tropomyosin 1 (alpha)	tpm1	TPM1	-4.86	-1.70
AF180892	Alpha-tropomyosin	tpma	TPM1	-3.35	-1.88
AW455045	Tropomyosin 4	tpm4	TPM4	-2.07	0.79
AW344264	Translocated promoter region (to activated MET oncogene) (nuclear pore complex-associated protein TPR)	tpr	TPR	3.28	4.94
AF204241	Tyrosylprotein sulfotransferase 1	tpst1	TPST1	0.27	2.77
AF288217	Translationally controlled tumor protein	tctp	TPT1	-1.70	2.49
BI672829	Weak sim to Targeting protein for Xklp2 (Restricted expression proliferation-associated protein 100) (p100) (Differentially expressed in cancerous and non-cancerous lung cells 2) (DIL-2) (Protein fls353) (Hepatocellular carcinoma-associated antigen 519)	sinup	TPX2	-2.00	-3.47
BM026054	Transcribed locus Repeats in BACs sim to T cell receptor alpha locus	BM026054	TRA@	-1.55	-2.29
NM_131607	Tnfrsf1a-associated via death domain	tradd	TRADD	-0.72	-2.12
AI667210	Tnf receptor-associated factor 2b	traf2b	TRAF2	1.77	-0.40
BI709770	TRAF-interacting protein	traip	TRAIP	-0.93	-2.97
AW281809	3' end of LOC100001887 sim to TRAK1 | trafficking protein, kinesin binding 1 and ' to zgc:110712 Krt14 or Krt20	AW281809	TRAK1	-2.23	-1.12
AW116159	Translocating chain-associating membrane protein 1	tram1	TRAM1	3.37	2.24
BC083391	Trafficking protein particle complex 6b	trappc6b	TRAPPC6B	-3.36	-1.19
BC068383	Trafficking protein particle complex 6b-like	trappc6bl	TRAPPC6B	4.12	-2.48
AB196920	tRNA aspartic acid methyltransferase 1	trdmt1	TRDMT1	-1.90	-2.96
BI891984	LOC565972 weak sim to tripartite motif-containing 16	si:dkey-7b17.2	TRIM16	-1.74	-1.37
BI867009	LOC692298 weak sim to tripartite motif-containing 16	zgc:136585	TRIM16	-2.14	-0.93
AW059436	Weak sim to Tripartite motif-containing protein 35 (Hemopoietic lineage switch protein 5)	LOC799694	TRIM35	-2.37	-1.77
BC091879	LOC541547 weak sim to tripartite motif-containing 35	zgc:113250	TRIM35	-1.59	-1.84
BC049414	LOC394070 sim to tripartite motif-containing 54	zgc:56376	TRIM54	-2.96	-1.73
AY677196	Transient receptor potential cation channel, subfamily A, member 1a	trpa1a	TRPA1	4.29	4.41
AA497276	Transient receptor potential cation channel, subfamily C, member 4 associated protein b	trpc4apb	TRPC4AP	3.20	-1.06
AY974804	Transient receptor potential cation channel, subfamily C, member 2	trpc2	TRPC7	1.85	2.21
BQ092359	Intergenic 3' to LOC792324 sim to ASCC1 | activating signal cointegrator 1 complex subunit 1 and 5' to LOC799255 sim to gag-like protein probably intron of TRPS1 | trichorhinophalangeal syndrome I	BQ092359	TRPS1	2.16	-0.57
BC095056	LOC553550 sim to tRNA splicing endonuclease 54 homolog (S. cerevisiae)	zgc:109927	TSEN54	-0.52	-2.28
AW203163	Tetraspan 2	zgc:110586	TSPAN2	-1.33	-1.96
BM183928	Sarcoma amplified sequence; sim to TSPAN31: tetraspanin 31	sas	TSPAN31	1.16	2.28
BM024328	Tetraspanin 7b	tspan7b	TSPAN7	-2.06	-1.23
AI666975	Tissue specific transplantation	zgc:100864	TSTA3	-2.98	-1.73
BI878949	Titin a	ttna	TTN	-3.82	4.85
AI354069	Titin-like	ttnl	TTN	-2.44	-0.97
BM025895	Tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency)	ttpa	TTPA	4.58	2.25
BI889398	Weak sim to transthyretin	LOC570474	TTR	2.27	2.55
CN173753	Transthyretin (prealbumin, amyloidosis type I)	ttr	TTR	7.17	5.38
BM036121	Traf and tnf receptor associated protein	ttrap	TTRAP	0.56	-2.21
AI204734	Sim to Danio rerio cDNA clone IMAGE:7137547 contain repeat 5' end to sim to TUBA1A	AI204734	TUBA1A	3.30	1.07
BI673660	Tubulin, alpha 7 like	tuba7l	TUBA1A	-2.96	-2.29
BE017692	Tubulin, alpha 8 like 2	tuba8l2	TUBA1B	-1.90	3.65
BI982778	LOC767746 sim to beta-tubulin	zgc:153426	TUBB	-4.31	-2.32
BI883931	3' end of tubd1: tubulin, delta 1	BI883931	TUBD1	1.45	1.68
BI980399	Tumor suppressor candidate 4	tusc4	TUSC4	5.98	4.67
BC074070	Twinfilin, actin-binding protein, homolog 1b	twf1b	TWF1	3.34	-0.85
CN317747	Thioredoxin domain containing 17	txndc17	TXNDC17	2.63	-1.64
AI793730	Thioredoxin domain containing 5	txndc5	TXNDC5	0.17	2.06
AY005804	Thymidylate synthase	tyms	TYMS	-1.66	-3.28
AI958574	Intergenic 3' to LOC565006 sim to UACA | uveal autoantigen with coiled-coil domains and ankyrin repeats and 5' to go2: groucho 2	AI958574	UACA	0.80	1.84
BQ074792	Sim to ubiquitin-like modifier activating enzyme 1	LOC100001302	UBA1	4.02	-1.07
AI959564	Ubiquitin-like modifier activating enzyme 1	uba1	UBA1	2.74	-2.54
AW116617	Sim to ubiquitin-like modifier activating enzyme 2	AW116617	UBA2	-2.89	-2.22
BI984826	Ubiquitin-like modifier activating enzyme 5	uba5	UBA5	2.15	2.18
BG302714	Intergenic 3' to si:dkey-1o2.1 sim to UBAC1 | UBA domain containing 1 and 5' to DKEY-56D12.1 sim to MSH3 | mutS homolog 3	BG302714	UBAC1	-2.14	-0.70
BI866338	LOC777766 sim to ubiquitin C	zgc:153686	UBC	2.38	2.35
BM072375	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	ube2d2	UBE2D2	-0.16	1.89
BI879262	Ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	ube2e3	UBE2E3	0.12	1.57
BM181650	Ubiquitin-conjugating enzyme E2G 1	ube2g1	UBE2G1	-1.18	3.74
AW175187	Ubiquitin-conjugating enzyme E2G 2	ube2g2	UBE2G1	2.28	1.65
AW154232	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	ube2h	UBE2H	1.38	3.71
AI641713	Ubiquitin-conjugating enzyme E2L 3	ube2l3	UBE2L3	-0.26	3.12
BC095212	Ubiquitin-conjugating enzyme E2Q (putative) 1	ube2q1	UBE2Q2	1.84	2.76
AI204792	Intron of zgc:114060 ubiquitin-conjugating enzyme E2S	AI204792	UBE2S	0.90	-1.60
BF938814	Ubiquitin protein ligase E3C	ube3c	UBE3C	1.76	0.39
BI877821	Ataxin-1 ubiquitin-like interacting protein	ubin	UBQLN1	0.18	2.53
BM185181	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	uchl1	UCHL1	-3.14	-4.60
AJ243250	Uncoupling protein 2	ucp2	UCP2	-2.28	0.43
BC053173	Uncoupling protein 2, like	ucp2l	UCP2	-4.76	-2.43
BF156623	Uncoupling protein 4	ucp4	UCP3	2.59	4.96
BC078313	LOC445225 sim to UEV and lactate/malate dehyrogenase domains	zgc:100959	UEVLD	-2.01	0.95
BC076020	Ubiquitin fusion degradation 1-like	ufd1l	UFD1L	-0.37	-1.96
AW116285	Ubiquitin-fold modifier 1	ubfm1	UFM1	-2.13	-1.72
BF717454	UDP glucuronosyltransferase 1 family a, b	ugt1ab	UGT1A6	1.46	-2.07
AI522542	Intron of zgc:153634 sim to UGT2A1 | UDP glucuronosyltransferase 2 family, polypeptide A1	AI522542	UGT2A1	2.86	-0.68
AI545978	LOC550352 sim to UDP glucuronosyltransferase 2 family, polypeptide A1	zgc:112491	UGT2A1	7.97	2.42
AW127886	LOC767756 Sim to UDP glucuronosyltransferase	zgc:153634	UGT2A1	1.48	-2.26
BM104057	Uracil-DNA glycosylase	ung	UNG	0.32	-5.60
BI888708	Signal peptide peptidase 3	sppl3	UNQ1887	-1.90	-0.35
AI544884	Ureidopropionase, beta	upb1	UPB1	1.57	4.42
BC044525	Uridine phosphorylase 2	upp2	UPP2	-3.24	2.39
AI437412	Ubiquinol-cytochrome c reductase core protein II	zgc:92453	UQCRC2	-1.54	-0.87
AW420002	LOC556744 sim to UROC1 urocanase domain containing 1	zgc:194768	UROC1	2.45	-0.60
AW466607	Ubiquitin specific protease 11-like	DKEY-181C21.2	USP11	1.62	-1.74
BG303320	3' end of LOC558397: sim to Ubiquitin carboxyl-terminal hydrolase 13 (Ubiquitin thioesterase 13) (Ubiquitin-specific-processing protease 13) (Deubiquitinating enzyme 13)	BG303320	USP13	-2.32	-1.53

	(Isopeptidase T-3) (ISOT-3)				
BI878085	Ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	usp14	USP14	-0.70	2.22
BI880724	LOC494031 sim to ubiquitin specific peptidase 2	zgc:92134	USP2	-2.27	0.53
BI880068	Ubiquitin specific peptidase 24;LOC100149597	usp24	USP24	-0.39	2.55
BI887079	Ubiquitin specific protease 9 (usp9)	usp9	USP9X	0.39	2.41
AI964232	Sim to UTP20 | UTP20, small subunit (SSU) processome component, homolog	im:7159098	UTP20	-1.73	0.71
AY279079	Vang-like 1 (van gogh, Drosophila)	vangl1	VANGL1	1.14	1.95
AA606013	VAMP (vesicle-associated membrane protein)-associated protein A	vapa	VAPA	1.69	2.48
BI673936	Intron of wu:fk86g11sim to VAV3 | vav 3 guanine nucleotide exchange factor and 5' to sh3glb1 SH3-domain GRB2-like endophilin B1	BI673936	VAV3	1.68	-1.24
BE201171	Vav 3 guanine nucleotide exchange factor	wu:fk86g11	VAV3	1.76	2.58
BG303991	Intergenic 3' to sc:d0202 and 5' to LOC100003052	BG303991	VCAM1	6.63	2.05
AW344246	Vascular cell adhesion molecule 1-like	zgc:158875	VCAM1	1.92	3.08
BI892394	Voltage-dependent anion channel 2	vdac2	VDAC2	-1.85	-1.21
AF466147	Vascular endothelial growth factor c	vegfc	VEGFC	-0.29	2.24
AF069994	Vimentin	vim	VIM	-2.23	-0.76
AI626761	Sim to vitamin K epoxide reductase complex, subunit 1-like	wu:fc03a11	VKORC1L1	3.36	2.71
BI705594	Very low density lipoprotein receptor	vldlr	VLDLR	2.15	-5.03
BC049319	Vaccinia related kinase 2	vrk2	VRK2	2.64	0.31
AI331200	LOC796658 weak sim to VTCN1 | V-set domain containing T cell activation inhibitor 1	si:dkey-169i5.4	VTCN1	-0.77	-1.52
BC095724	Vitronectin a	vtna	VTN	3.11	2.60
BM096343	Vitronectin b	vtnb	VTN	3.22	4.14
BI890241	WD repeat domain 33	wdr33	WDR33	3.76	0.32
BI886163	LOC393506 sim to WD repeat domain 77	zgc:65780	WDR77	-1.78	-0.46
AI959228	WD repeat domain containing 82	wdr82	WDR82	-0.72	-1.86
AI957865	Wolf-Hirschhorn syndrome candidate 1	whsc1	WHSC1	-3.25	-3.62
AF122925	Wnt inhibitory factor 1	wif1	WIF1	0.62	-2.16
BC053306	WD repeat domain, phosphoinositide interacting 1	wipi1	WIPI1	1.99	-0.49
BC066432	Wingless-type MMTV integration site family, member 16	wnt16	WNT16	2.71	1.73
AF544026	Wingless-type MMTV integration site family, member 2B	wnt2b	WNT2B	0.23	1.82
AF139536	Wingless-type MMTV integration site family, member 4b	wnt4b	WNT4	0.93	2.22
U10869	Wingless-type MMTV integration site family, member 8a	wnt8a	WNT8A	0.27	-2.00
AI397280	Intergenic 3' to wnt9a | wingless-type MMTV integration site family, member 9A and 3' to keap1a kelch-like ECH-associated protein 1a	wu:fb09c09	WNT9A	-1.08	-2.50
X85735	Wilms tumor 1a	wt1a	WT1	1.70	2.09
BM104374	WW domain containing oxidoreductase	wwox	WWOX	1.32	1.70
BG728392	Cardiomyopathy associated 1 (weak sim to xin actin-binding repeat containing 2)	cmya1	XIRP2	0.85	-2.06
BQ260844	Xeroderma pigmentosum, complementation group C	xpc	XPC	2.90	-2.36
AA497185	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	xpnpep1	XPNPEP1	2.01	0.82
BI704306	5'-3' exoribonuclease 2	xrn2	XRN2	0.96	-2.38
BE201596	Yes-associated protein 1	si:ch211-181p1.5	YAP1	-1.94	1.02
AF093129	Y box binding protein 1	ybx1	YBX1	-2.20	1.18
BC076436	YEATS domain containing 4	yeats4	YEATS4	0.65	2.57
AW127946	Sim to YME1L1 | YME1-like 1	LOC793098	YME1L1	1.79	-0.37
BM171814	Yippee-like 3	ypel3	YPEL3	1.71	-2.93
BC053247	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide 2	ywhab2	YWHAB	1.60	2.33
BM024808	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide 2	ywhag2	YWHAG	-1.66	-1.52
AW202701	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, iota polypeptide	ywhai	YWHAZ	-2.79	-1.69
BI890446	YY1 transcription factor a	yy1a	YY1	-2.39	1.31
BI982056	LOC560615 sim to similar to Zinc finger and BTB domain containing 16	LOC560615	ZBTB16	-1.19	-2.22
BI706995	Sim to ZBTB17 | zinc finger and BTB domain containing 17	LOC564967	ZBTB17	0.55	-1.98
AI626609	Zinc finger and BTB domain containing 2b	zbtb2b	ZBTB2	-2.47	-1.84
AW116298	Zinc finger, DHHC-type containing 13	zdhhc13	ZDHHC13	-1.15	2.26
AJ249490	Cth1 (sim to zinc finger protein 36, C3H type-like 2)	cth1	ZFP36L2	-0.84	-5.76
AI723133	Zinc finger, FYVE domain containing 26	zfyve26	ZFYVE26	-1.72	-0.78
AW510252	Weak sim to ZHX2 | zinc fingers and homeoboxes 2	wu:fk11d03	ZHX2	-1.88	-0.41
AI641415	Zinc finger protein Zic6 (sim to Zic family member 1 (odd-paired homolog, Drosophila))	zic6	ZIC1	0.54	-2.43
BE693149	Sim to Zic family member 2 (odd-paired homolog, Drosophila)	BE693149	ZIC2	-1.14	-1.86
BM182229	Zic family member 5 (odd-paired homolog, Drosophila)	zic5	ZIC5	-2.93	-2.03
BI890247	Zinc metallopeptidase (STE24 homolog, S. cerevisiae)	zmpste24	ZMPSTE24	1.32	2.13
BC091788	LOC100126120 sim to zinc finger protein 235	zgc:173726	ZNF235	2.80	1.87
BM072263	3' end of si:ch211-221n23.1 sim to ZNF238: zinc finger protein 238 and 5' to LOC560549: sim to AKT3 | v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	BM072263	ZNF238	-1.77	-2.13
BE200843	Weak sim to ZNF551 | zinc finger protein 551 (partially)	si:ch211-106h4.12	ZNF551	-1.63	-1.91
CK706206	Sim to zinc finger protein 567	LOC568921	ZNF567	2.96	-0.75
AF157109	Draculin sim to zinc finger protein 569	drl	ZNF569	-2.48	-0.19
BC092159	LOC548342 sim to zinc finger protein 569	zgc:113209	ZNF569	-1.99	1.62
CV487580	Sim to ZNF585B | zinc finger protein 585B	LOC799404	ZNF585B	3.28	1.07
BC096910	LOC569258 sim to ZNF678 | zinc finger protein 678	zgc:113372	ZNF678	-1.50	1.26
AF222996	Zinc finger protein 703	znf703	ZNF703	-1.33	-2.49
AI884171	Sim to zinc finger protein 708	wu:fc74g06	ZNF708	1.54	1.32
AI545215	Intergenic 3' to CH211-255F4.8 sim to ZNF729 | zinc finger protein 729 and 5' to CH211-255F4.12 sim to ZNF135 | zinc finger protein 135	AI545215	ZNF729	2.10	0.63
BI880278	LOC564210 sim to zinc finger protein 76 (expressed in testis)	zgc:153635	ZNF76	2.14	0.76
BC092919	Zinc finger-like gene 2a	znfl2a	ZNF778	-2.22	-5.43
BI980550	LOC503597: sim to ZNF782: zinc finger protein 782	zgc:110821	ZNF782	2.77	0.71
AI957416	Intron of si:ch211-215c3.2 sim to ZNF827 | zinc finger protein 827	AI957416	ZNF827	-1.76	1.25

Table S2. Statistically enriched human gene sets (NES ≥1.5, nominal enrichment p-value ≤0.05 and FDR q-value ≤0.25) representing biological processes and pathways in zebrafish liver hyperplasia and carcinoma identified by GSEA. The up- or down-regulated activity of a gene set is defined respectively by positive or negative values of NES. The list of genes in each significantly enriched gene set that contributed most to the enrichment results in hyperplasia and carcinoma are also listed. Within these gene lists, genes having $\log_2$ fold-change ≥1.5 and FDR-adjusted p-value ≤0.01 are underlined and these are termed as zebrafish enriched genes.

Zebrafish liver hyperplasia (3 months)		**Enriched GO gene sets (NES ≥1.5, NOM *p*-value ≤0.05 and FDR *q*-value ≤0.25) in zebrafish liver hyperplasia (3 months)**	**Enriched gene lists**
	Up-regulated	BLOOD_COAGULATION	F10, F2, F7, F9, LMAN1, PLG, PROC
		CELL_CYCLE_ARREST_GO_0007050	CUL5, GADD45A, NBN, NOTCH2, PPM1G, TP53
		CHEMICAL_HOMEOSTASIS	AIFM3, ANGPTL3, APOA1, APOA4, APOE, BAX, BCL2, CALCB, CALR, CLCN3, CP, DERL1, EDNRA, NPC2, RHCG, SLC40A1, SOD1, SRI, TFR2, THY1
		COAGULATION	F10, F2, F7, F9, LMAN1, PLG, PROC
		DNA_METABOLIC_PROCESS	BAX, DDB1, GADD45A, IGF1, KIN, MCM2, MCM3, MCM5, MRE11A, MSH2, MSH6, NBN, ORC3L, POLA1, POLB, POLD2, POLE2, RAD51, RAD52, RFC3, RUVBL2, SOD1, SUMO1, TINF2, TP53, XPC
		DNA_REPAIR	DDB1, GADD45A, MRE11A, MSH2, MSH6, NBN, POLA1, POLE2, RAD51, RAD52, RFC3, RUVBL2, SOD1, SUMO1, TP53, XPC
		DNA_REPLICATION	IGF1, KIN, MCM2, MCM3, MCM5, MRE11A, MSH2, MSH6, NBN, ORC3L, POLA1, POLB, POLD2, POLE2, RAD51, RFC3
		ESTABLISHMENT_OF_LOCALIZATION	ABCB11, ABCD3, AGXT, AHSG, APOA1, APOA4, APOE, AQP9, ARCN1, AVP, BAX, C3orf31, CALR, CEL, CHKA, COX17, DERL1, DPH3, EDNRA, F2
		HEMOSTASIS	F10, F2, F7, F9, LMAN1, PLG, PROC
		HOMEOSTATIC_PROCESS	AIFM3, APOA1, APOA4, APOE, BAX, BCL2, CALCB, CALR, CLCN3, CP, DERL1, EDNRA, GPX1, LDB1, MAFB, PCDH15, RHCG, SLC40A1, SOD1, SRI, TFR2, THY1
		IMMUNE_SYSTEM_PROCESS	APOA1, APOA4, AQP9, CTSW, FYN, LDB1, NFIL3, NOTCH2, MAFB, OPRK1
		LIPID_METABOLIC_PROCESS	ACAD8, ACADS, ACAT2, ACOX3, ANGPTL3, APOA1, APOA4, CEL, CHKA, CYP11A1, CYP2J2, ECHS1, EDF1, GPX4, HACL1, HAO1, HSD11B2, LPL, MTTP, NPC2, NR2F2, PECI, PI4KB, PLTP, PPARD
		LIPID_TRANSPORT	ABCD3, ANGPTL3, APOA1, APOA4, APOE, CHKA, GOT2, NPC2, PPARD
		NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	AHSG, F2, PROC, SOD1, THY1
		REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	APOE, FGD1, MAPT, ROBO1, ROBO2, THY1
		REGULATION_OF_BODY_FLUID_LEVELS	CEL, F10, F2, F7, F9, LMAN1, PLG, PROC
		REGULATION_OF_RNA_METABOLIC_PROCESS	ARNTL, ATF5, CALR, EDF1, ESR2, GATA6, HIRA, HSBP1, JUNB, LDB1, MAFA, MDFIC, MDM2, MTF1, NARG1, NEUROG1, NFKB2, NFYA, NKX2-5, NME2, NOTCH2
		REGULATION_OF_TRANSCRIPTION__DNA_DEPENDENT	ARNTL, ATF5, CALR, EDF1, ESR2, GATA6, HIRA, HSBP1, JUNB, LDB1, MAFA, MDFIC, MDM2, MTF1, NARG1, NEUROG1, NFKB2, NFYA, NKX2-5, NME2, NOTCH2, NR2F2
		RESPONSE_TO_DNA_DAMAGE_STIMULUS	DDB1, GADD45A, MRE11A, MSH2, MSH6, NBN, POLA1, POLE2, RAD51, RAD52, RFC3, RUVBL2, SOD1, SUMO1, TP53, XPC
		RESPONSE_TO_ORGANIC_SUBSTANCE	AQP9, BCL2, GOT2, MAFA, SOD1
		RESPONSE_TO_WOUNDING	AHSG, CDO1, F10, F2, F7, F9, LMAN1, NMI, PLG, PROC, RTN4RL1, SOD1
		WOUND_HEALING	F10, F2, F7, F9, LMAN1, PLG, PROC, RTN4RL1

	Down-regulated	CALCIUM_INDEPENDENT_CELL_CELL_ADHESION	CLDN23, CLDN3, CLDN4, CLDN7, CLDN8
		DEVELOPMENTAL_MATURATION	FARP2, KRT19, MYH11, MYOZ1, TTN
		FATTY_ACID_BIOSYNTHETIC_PROCESS	CD74, FADS2, PTGDS, PTGES3, PTGS1
		Enriched KEGG gene sets (NES ≥1.5, NOM *p*-value ≤0.05 and FDR *q*-value ≤0.25) in zebrafish liver hyperplasia	**Enriched gene lists**
	Up-regulated	HSA00230_PURINE_METABOLISM	ADK, ADSSL1, AK5, GDA, NME2, NME4, PDE8B, POLA1, POLA2, POLD2, POLE2, RFC5, RRM2
		HSA00240_PYRIMIDINE_METABOLISM	DCTD, DHODH, DPYD, NME2, NME4, NP, POLA1, POLA2, POLD2, POLE2, RFC5, RRM2, RRM2B, TK1, UPB1
		HSA00480_GLUTATHIONE_METABOLISM	GGT1, GPX1, GPX4, MGST1, OPLAH
		HSA00561_GLYCEROLIPID_METABOLISM	CEL, GK, LIPA, LIPC, LPL
		HSA03030_DNA_POLYMERASE	POLA1, POLA2, POLB, POLD2, POLE2, RFC5
		HSA03320_PPAR_SIGNALING_PATHWAY	ACSL5, APOA1, FABP2, FABP3, GK, LPL, PLTP, PPARD, RXRA, UBC
		HSA04010_MAPK_SIGNALING_PATHWAY	BRAF, DUSP5, DUSP6, FGFR4, GADD45A, GADD45B, GNG12, MAP3K12, MAPK1, MAPK3, MAPK8, MAPKAPK2, MAPT, NFKB2, NLK, PDGFRA, PRKACA, PRKCB1, TP53
		HSA04012_ERBB_SIGNALING_PATHWAY	BRAF, CAMK2A, CAMK2D, MAPK1, MAPK3, MAPK8, PIK3CA, PRKCB1, SRC
		HSA04110_CELL_CYCLE	CCNB1, CCNB2, CCND1, CDC25A, GADD45A, GADD45B, MCM2, MCM3, MCM5, MDM2, ORC3L, PCNA, SMAD4, TFDP1, TP53, YWHAB
		HSA04115_P53_SIGNALING_PATHWAY	BAX, CCNB1, CCNB2, CCND1, CCNG2, GADD45A, GADD45B, IGF1, IGFBP3, MDM2, RRM2, RRM2B, TP53
		HSA04150_MTOR_SIGNALING_PATHWAY	BRAF, CAB39, IGF1, MAPK1, MAPK3, PIK3CA
		HSA04310_WNT_SIGNALING_PATHWAY	CAMK2A, CAMK2D, CCND1, CTBP1, FZD8, MAPK8, NLK, PPARD, PRICKLE1, PRKACA, PRKCB1, TP53, WNT16
		HSA04370_VEGF_SIGNALING_PATHWAY	MAPK1, MAPK3, MAPKAPK2, PIK3CA, PRKCB1, PXN, SRC
		HSA04540_GAP_JUNCTION	DRD2, MAPK1, MAPK3, PDGFRA, PRKACA, PRKCB1, PRKG2, SRC, TUBA1A
		HSA04610_COMPLEMENT_AND_COAGULATION_CASCADES	A2M, C1S, C3, C8G, C9, CFB, CFH, F10, F2, F7, F9, FGA, FGB, FGG, MASP2, PLG, PROC, SERPINA1, SERPINC1, SERPINF2
		HSA04720_LONG_TERM_POTENTIATION	BRAF, CAMK2A, CAMK2D, MAPK1, MAPK3, PRKACA, PRKCB1
		HSA04730_LONG_TERM_DEPRESSION	BRAF, IGF1, MAPK1, MAPK3, PRKCB1, PRKG2
		HSA04912_GNRH_SIGNALING_PATHWAY	CAMK2A, CAMK2D, MAPK1, MAPK3, MAPK8, MMP14, PRKACA, PRKCB1, SRC
	Down-regulated	HSA00010_GLYCOLYSIS_AND_GLUCONEOGENESIS	ADH5, ALDH7A1, ALDOA, BPGM, GAPDH, PDHB, PFKM, PGAM2, PKM2, TPI1
		HSA00330_ARGININE_AND_PROLINE_METABOLISM	ASS1, CKB, CKM, GOT1, NOS1, PYCR1, RARS2
		HSA01430_CELL_COMMUNICATION	COL11A2, COL17A1, COL1A1, COL1A2, COL2A1, COL5A1, COL6A1, DSG2, GJC1, ITGB4, KRT15, KRT17, KRT18, KRT19, KRT8, VIM
		HSA04530_TIGHT_JUNCTION	CLDN23, CLDN3, CLDN4, CLDN7, CLDN8, GNAI2, MYH2, MYH4, MYH6, MYL2, MYL7, MYL9, NRAS, OCLN, PPP2R1A, PPP2R1B, RRAS, TJP3
Zebrafish HCC (9 months)		**Enriched GO gene sets (NES ≥1.5, NOM *p*-value ≤0.05 and FDR *q*-value ≤0.25) in zebrafish HCC (9 months)**	**Enriched gene lists**
	Up-regulated	ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	ADRA2A, ARHGEF2, ARPC5, CDC42, CXCL12, DBN1, DLG1, RAC1, RAC3, RACGAP1, RHOA, RND1, SCIN, TTN
		ACTIN_FILAMENT_BASED_PROCESS	ADRA2A, ARHGEF2, ARPC5, CDC42, CXCL12, DBN1, DLG1, MYH10, RAC1, RAC3, RACGAP1, RHOA, RND1, SCIN, TTN
		AMINO_ACID_AND_DERIVATIVE_METABOLIC_PROCESS	AARS, ASMTL, DHPS, ETNK1, FPGS, GAD1, GGT1, GSTZ1, HGD, MAT1A, MSRA, PAH, SMS, TGFB2, WARS, YARS
		AMINO_ACID_METABOLIC_PROCESS	AARS, ALDH18A1, CDO1, FPGS, GAD1, GCLM, GGT1, GSTZ1, HGD, KARS, MAT1A, MSRA, PAH, SMS, WARS, YARS
		ANGIOGENESIS	ANGPT1, ANGPTL3, C1GALT1, CANX, PLG, RUNX1, SHH, TGFB2, THY1
		ANTI_APOPTOSIS	ANXA4, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CDC2, DAD1, GPX1, HSPA9, NOTCH2, NPM1, RELA, TIAF1, TPT1, TXNDC5

		BIOSYNTHETIC_PROCESS	ADK, ALG5, ALG8, APOA1, ASMTL, CD74, CHPT1, CTPS, DHCR7, EEF1A1, EIF3C, EIF3E, EIF3F, EIF4A2, ETNK1, EXT1, FADS2, GALNT2, GCHFR, GYS2, HS6ST1, HSP90AA1, HSP90AB1, INHBB
		CARBOHYDRATE_BIOSYNTHETIC_PROCESS	EXT1, GYS2, HS6ST1, MPDU1, PMM2
		CARBOXYLIC_ACID_METABOLIC_PROCESS	AGXT, CD74, FADS2, HACL1, HAO1, IGF1
		CATION_HOMEOSTASIS	BCL2, CALR, CLCN3, CP, CXCL12, CXCR4, EDNRA, FTH1, SOD1, TFR2, THY1
		CELL_CELL_SIGNALING	AGT, APOE, CCL21, CD9, EFNB1, EFNB2, FGF18, FGF4, FGF5, FGF6, GAD1, GCHFR, GJA3, GJB2, GRB2, IL15, INHBB, MAPK1, MBP
		CELL_CYCLE_CHECKPOINT_GO_0000075	BIRC5, CCNA2, CCNG2, CDC45L, NBN, TGFB1
		CELL_PROLIFERATION_GO_0008283	ABI1, ADRA2A, ARHGEF2, CD74, CDC25A, CDC27, CLEC11A, COL18A1, CTBP1, DLG1, FABP3, FGF10, FGF18, FGF4, FGF5, FGF6, FLT1, FTH1, GCG, GPX1, IGF1, IL15
		CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	ABI1, ADRA2A, AGT, APOA1, APOE, BIRC2, BSG, C3, CBL, CXCL12, CXCR4, EDNRA, ENPP2, FGF5, FGFR4, FYN, GCG
		CELLULAR_BIOSYNTHETIC_PROCESS	ADK, ASMTL, CD74, EEF1A1, EIF3C, EIF3E, EIF3F, EIF4A2, ETNK1, EXT1, FADS2, GCHFR, HS6ST1, HSP90AA1, HSP90AB1, INHBB, PAH, PMM2, RPL13, RPL18, RPL19, RPL23A, RPL26, RPL28, RPL30
		CELLULAR_CATION_HOMEOSTASIS	BCL2, CALR, CLCN3, CP, CXCL12, CXCR4, EDNRA, FTH1, SOD1, TFR2, THY1
		CELLULAR_HOMEOSTASIS	AIFM3, BCL2, BCL2L1, CALR, CLCN3, CP, CXCL12, CXCR4, EDNRA, FTH1, GPX1, PCDH15, RHCG, RHOT1, SOD1, TFR2, THY1
		CELLULAR_LIPID_METABOLIC_PROCESS	APOA1, APOM, CD74, CHPT1, DHCR7, ETNK1, FADS2, GPX4, HACL1, HAO1, LPL, PI4KB, PIK3C2A, PIK3R1, SERINC1, SHH, SOD1, WWOX
		CELLULAR_LOCALIZATION	AGXT, AP3B1, APOA1, APOE, ARCN1, BCL2, BCL2L1, BIRC5, CALR, CANX, CD74, CDH1, DERL1, DOPEY2, ERGIC3, GBF1, GOSR2, GSK3B, HSP90AA1, KDELR2, KRT18, LMAN1, MYH10, NCKIPSD, NPM1, NUP107, PDIA3, PDIA4, PEX3, RAB14
		CELLULAR_PROTEIN_CATABOLIC_PROCESS	CDC20, DERL1, EDEM1, RNF11, SYVN1, UBE2D2, UBE2G1, UBE2H, UBE2L3
		CHEMICAL_HOMEOSTASIS	AIFM3, ANGPTL3, APOA1, APOE, BCL2, BCL2L1, CALR, CAV1, CLCN3, CP, CXCL12, CXCR4, DERL1, EDNRA, FTH1, RHCG, SOD1, TFR2, THY1
		CYTOKINE_PRODUCTION	APOA1, INHBB, SOD1, TGFB2, TLR3
		DEFENSE_RESPONSE	AHSG, BCL2, BNIP3L, CCL21, CXCR4, HP, INHBB, RAC1, RELA, TGFB1, TIAL1, TLR3
		EPITHELIAL_TO_MESENCHYMAL_TRANSITION	CTNNB1, S100A4, TGFB1, TGFB2, TGFB3
		ESTABLISHMENT_OF_CELLULAR_LOCALIZATION	AGXT, AP3B1, APOA1, APOE, ARCN1, BCL2, BCL2L1, BIRC5, CALR, CANX, CD74, CDH1, DERL1, DOPEY2, ERGIC3, GBF1, GOSR2, GSK3B, HSP90AA1, KDELR2, KRT18, LMAN1, MYH10, NCKIPSD, NPM1, NUP107, PDIA3, PDIA4, PEX3, RAB14, RAB3GAP2, RHOT1
		ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	AGXT, AIP, ANGPTL3, AP3B1, APOA1, ARCN1, CALR, CANX, CD74, CDH1, DERL1, GSK3B, KDELR2, NCKIPSD, NPM1, PDIA3, PEX3, RAB3GAP2, SNAPIN, SSR2, TGFB1, TPR, TRAM1
		G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	ADRA2A, APOA1, APOE, C3, CXCL12, CXCR4, EDNRA, ENPP2, GCG, GPR34
		GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	APOM, GPX4, GSK3B, GYS2, ISL1, PDX1, SLC25A3
		GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	APOA1, DPM1, PI4KB, PIGF, PIK3C2A, PIK3R1, SERINC1
		GOLGI_VESICLE_TRANSPORT	COPB2, COPZ1, DOPEY2, ERGIC3, GBF1, GOLGA5, GOSR2, KRT18, LMAN1, LMAN2L, RAB14, RER1, SCAMP3, SEC22A, TMED10, ZW10
		HOMEOSTATIC_PROCESS	AIFM3, ANGPTL3, APOA1, APOE, BCL2, BCL2L1, CALR, CAV1, CLCN3, CP, CXCL12, CXCR4, DERL1, EDNRA, FTH1, GPX1, MAFB, PCDH15, RHCG, RHOT1, SOD1, TFR2, THY1
		IMMUNE_RESPONSE	ANXA11, APOA1, AQP9, BCL2, BNIP3L, CCL21, CD74, CTSW, CXCL12, CXCR4, FTH1, FYN, IL15, MBP, MR1, NFIL3, PAX5, TCF7, TGFB1, TGFB2, THY1, VTN
		IMMUNE_SYSTEM_PROCESS	ANXA11, APOA1, AQP9, BCL2, BNIP3L, CCL21, CD74, CDC42, CTSW, CXCL12, CXCR4, FTH1, FYN, IL15, MAFB, MBP, NFIL3, NOTCH2
		INTRACELLULAR_PROTEIN_TRANSPORT	AGXT, AP3B1, ARCN1, CALR, CD74, CDH1, DERL1, GSK3B, KDELR2, NCKIPSD, NPM1, PDIA3, PEX3, RAB3GAP2, SNAPIN, SSR2, TGFB1, TPR, TRAM1
		INTRACELLULAR_TRANSPORT	AGXT, ANP32A, AP3B1, AP3M1, APOE, APPBP2, ARCN1, BCL2, BCL2L1, CALR, CD74, CDH1, COPZ1, CRYAA, DERL1, DOPEY2, ERGIC3, GBF1, GOSR2, GSK3B, HSP90AA1, KDELR2, KHDRBS1, KIF1B, KRT18, LMAN1, MTX2, MYH10, NCKIPSD, NPM1, NUP107, PDIA3, PEX3, RAB14, RAB3GAP2, RHOT1, RPL11, SEC22A, SNAPIN, SSR2, STARD3, TGFB1, TIMM17A, TMED10, TOM1

		ION_HOMEOSTASIS	AIFM3, BCL2, BCL2L1, CALR, CLCN3, CP, CXCL12, CXCR4, EDNRA, FTH1, RHCG, SOD1, TFR2, THY1
		ION_TRANSPORT	CACNA1D, FXYD1, KCNC1, KCNJ1, RHCG, SGK1, SLC34A2, SLC8A1, TRPA1, UCP3
		LIPID_BIOSYNTHETIC_PROCESS	APOA1, CD74, CHPT1, DHCR7, ETNK1, FADS2, PI4KB, PIK3C2A, SOD1
		LIPID_TRANSPORT	ABCD3, ANGPTL3, APOA1, APOE, CAV1, CHKA
		MACROMOLECULE_BIOSYNTHETIC_PROCESS	AARS, ALG1, ALG5, ALG8, APOA1, CEBPG, DHPS, DPM1, EEF1A1, EIF2B1, EIF2S3, EIF3C, EIF3E, EIF3F, EIF4A2, EXT1, GALNT2, GYS2, HS6ST1, INHBB, MGAT4B, MPDU1, NACA, PIGF, PMM2, RPL11, RPL13, RPL18, RPL19, RPL23A, RPL26, RPL28, RPL30, RPL34, RPL35
		MACROMOLECULE_LOCALIZATION	AGXT, AIP, ANGPTL3, AP3B1, APOA1, ARCN1, BIRC5, CALR, CANX, CD74, CDH1, DERL1, GSK3B, KDELR2, NCKIPSD, NPM1, NUP107, PDIA3, PEX3, RAB3GAP2, SNAPIN, SSR2, TGFB1, TPR, TRAM1
		MEMBRANE_LIPID_METABOLIC_PROCESS	APOA1, APOM, CHPT1, ETNK1, GPX4, LPL, PI4KB, PIK3C2A, PIK3R1, SERINC1
		MEMBRANE_ORGANIZATION_AND_BIOGENESIS	AGRN, AHSG, BCL2, BCL2L1, CBL, CD9, CORO1C, GOSR2, PI4KB, PICALM, RABIF, RAC1, SOD1, VAPA
		MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	AGXT, CD74, FADS2, HACL1, HAO1, IGF1
		MONOVALENT_INORGANIC_CATION_TRANSPORT	KCNC1, KCNJ1, SGK1, SLC8A1, UCP3
		MULTI_ORGANISM_PROCESS	AGT, BCL2, BNIP3L, C9, CXCL12, CXCR4, DERL1, FLT1, MAFF, PPARD, SOD1, TGFB1, TLR3, TNIP1
		NEGATIVE_REGULATION_OF_APOPTOSIS	ANXA4, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CD74, CDC2, DAD1, GPX1, GSK3B, HSPA9, KRT18, MAPK8, NME2, NOTCH2, NPM1, PIM1, PROC, RELA, SOD1, TIAF1, TPT1, TXNDC5
		NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	ABI1, ADAM10, AHSG, AMBP, ANXA4, APOA1, ARHGEF2, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CD74, CDC2, CDC42, CDC45L, COL18A1, CTBP1, DAD1, DLG1, FABP3, FTH1
		NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	AHSG, ANXA4, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CD74, CDC2, DAD1, GPX1, GSK3B, HSPA9, KRT18, MAFB, MAPK8, NME2, NOTCH1, NOTCH2, NPM1, PIM1, PLG, PROC, RELA, SHH, SOD1, THY1, TIAF1, TPT1, TXNDC5
		NEGATIVE_REGULATION_OF_METABOLIC_PROCESS	ARHGEF2, CDC42, CDC45L, ID1, ID2, IGFBP3, INHBB, KLF12, MAPRE1, MDM2, MDM4, PA2G4, SOD1, STAT3, TBX2, TGFB1, TP63
		NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	AHSG, PROC, SOD1, TGFB2, THY1
		NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH	ANXA4, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CD74, CDC2, DAD1, GPX1, GSK3B, HSPA9, KRT18, MAPK8, NME2, NOTCH2, NPM1, PIM1, PROC, RELA, SOD1, TIAF1, TPT1, TXNDC5
		NITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	ASMTL, ETNK1, GCHFR, HSP90AA1, HSP90AB1, PAH, TGFB2
		ORGAN_MORPHOGENESIS	ANGPTL3, C1GALT1, CANX, COL18A1, FGF10, FLI1, LAMB1, NKX6-1, NOTCH2, PAX3, PAX5, PAX6, PDX1, PLG, PROX1, RUNX1, SHH, SOD1, TGFB1, TGFB2, TGFB3, THY1
		ORGANIC_ACID_METABOLIC_PROCESS	AGXT, CD74, FADS2, FPGS, GAD1, GGT1, GSTZ1, HACL1, HAO1, IGF1, MAT1A, MSRA, PAH
		PHOSPHOINOSITIDE_METABOLIC_PROCESS	DPM1, PI4KB, PIGF, PIK3C2A, PIK3R1
		PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	APOA1, CHPT1, DPM1, ETNK1, PI4KB, PIGF, PIK3C2A
		PHOSPHOLIPID_METABOLIC_PROCESS	APOA1, CHPT1, ETNK1, GPX4, LPL, PI4KB, PIK3C2A, PIK3R1, SERINC1
		PHOSPHORYLATION	ABI1, ADAM10, BCR, CCND1, CSNK2A1, CTBP1, GLYCTK, GSK3B, IGFBP3, MAPK3, MAPK8, MAPKAPK2, MCM7, MKNK2, MOBKL1A, PIK3R1, PRKCB1, PIM1, ROCK2
		POSITIVE_REGULATION_OF_CELL_PROLIFERATION	ADRA2A, CLEC11A, FGF10, FGF18, FGF4, FLT1, IGF1, IL15, LAMB1, NME2, TBX2, TGFB2, TGFBR2, TSPAN31
		POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	AHSG, CBL, CDC42, CDC42EP4, ROBO2
		POSITIVE_REGULATION_OF_CELLULAR_PROCESS	ADRA2A, AHSG, AIFM3, ANGPTL3, APOE, ARNTL, ASNS, BIRC2, BIRC5, BNIP3L, CBL, CCND1, CDC42, CDC42EP4, CDH1, CLEC11A, CLOCK, ECT2, EGR1, FGF10, FGF18, FGF4 FLT1
		POST_TRANSLATIONAL_PROTEIN_MODIFICATION	ABI1, ADAM10, BCR, CBL, CCND1, CSNK2A1, CTBP1, GAD1, GLYCTK, GSK3B, IGFBP3, MAPK3, MAPK8, MAPKAPK2, MDM2, MKNK2, MOBKL1A
		PROTEIN_AMINO_ACID_PHOSPHORYLATION	ABI1, ADAM10, BCR, CCND1, CSNK2A1, CTBP1, GLYCTK, GSK3B, IGFBP3, MAPK3, MAPK8, MAPKAPK2, MKNK2, MOBKL1A, PIM1, PRKCB1, ROCK2, SGK1, TGFB1
		PROTEIN_FOLDING	AIP, BAG2, CCT4, CCT6A, CCT7, DNAJA1, HSP90AA1, HSPE1, LMAN1, LRPAP1, RUVBL2

		PROTEIN_KINASE_CASCADE	ADRA2A, AMBP, BIRC2, CXCR4, ECT2, FGFR1, FYN, GADD45G, HMOX1, MAPK8, MAPKAPK2, MKNK2, NLK, RELA, RHOA, SOD1, SRC, STAT3, STAT5B
		PROTEIN_LOCALIZATION	AGXT, AIP, ANGPTL3, AP3B1, APOA1, ARCN1, BIRC5, CALR, CANX, CD74, CDH1, DERL1, GSK3B, KDELR2, NCKIPSD, NPM1, PDIA3, PEX3, RAB3GAP2, SNAPIN, SSR2, TGFB1, TPR, TRAM1
		PROTEIN_METABOLIC_PROCESS	ABI1, ADAM10, ADPRH, AGRN, AIP, AKT2, ALG5, ALG8, ANGPTL3, APOA1, APOE, ARHGEF2, BAG2, BCR, CBL, CCND1, CCT4, CCT6A, CCT7, CD74, CD9, CDC20, CDC42, CLDN14, CSNK2A1, CTBP1, CTSK, CXCL12
		PROTEIN_MODIFICATION_PROCESS	ABI1, ADAM10, ADPRH, AKT2, ALG5, ALG8, BCR, CBL, CCND1, CSNK2A1, CTBP1, FBXO11, GAD1, GALNT2, GLYCTK, GSK3B, IGFBP3
		PROTEIN_TARGETING	AGXT, CALR, CDH1, GSK3B, NCKIPSD, PDIA3, SSR2, TGFB1, TPR, TRAM1
		PROTEIN_TRANSPORT	AGXT, AIP, ANGPTL3, AP3B1, ARCN1, CALR, CD74, CDH1, DERL1, GSK3B, KDELR2, NCKIPSD, NPM1, PDIA3, PEX3, RAB3GAP2, SNAPIN, SSR2, TGFB1, TPR, TRAM1
		RAS_PROTEIN_SIGNAL_TRANSDUCTION	ADRA2A, APOA1, APOE, ARHGAP29, GNB1, GRAP, GRB2, IGF1, NOTCH2, RAC1, RHOA
		REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	CDO1, CDC42, CDC42EP4, ROBO2, THY1
		REGULATION_OF_APOPTOSIS	AIFM3, ANXA4, APOE, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CALR, CD74, CDC2, DAD1, GPX1, GSK3B, HSPA9, HSPD1, IGFBP3, KRT18, MAPK1, MAPK8, NME2, NOTCH2, NPM1, PIM1, PLG
		REGULATION_OF_CELL_DIFFERENTIATION	IGFBP3, MAFB, NME2, NOTCH1, NOTCH2, RUNX1, SCIN, SHH, TGFB2
		REGULATION_OF_CELL_MIGRATION	ANGPTL3, LAMB1, PLG, SHH, THY1
		REGULATION_OF_CELL_PROLIFERATION	ABI1, ADRA2A, ARHGEF2, CLEC11A, COL18A1, CTBP1, FABP3, FGF10, FGF18, FGF4, FLT1, FTH1, GPX1, IGF1, IL15, LAMB1, MDM2, MDM4, NME2, NOTCH2, NPM1, PLG, SCIN
		REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	AHSG, APOE, ARHGEF2, CBL, CDC42, CDC42EP4, CXCL12, EIF3C, EIF3E, EIF3F, EIF4A2, MAPRE1, RAC1, ROBO2, THY1
		REGULATION_OF_CELLULAR_METABOLIC_PROCESS	AHR, ANGPTL3, ARHGEF2, ARNTL, ATF5, BRD7, CALR, CCND1, CDC45L, CLOCK, CXCL12, EGR1, EIF3C, EIF3E, EIF3F, EIF4A2, GATA6
		REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS	ANGPTL3, ARHGEF2, CCND1, CXCL12, EIF3C, EIF3E, EIF3F, EIF4A2, IGFBP3, INHBB, MAPRE1, SHH, TGFB1, TLR3
		REGULATION_OF_DEVELOPMENTAL_PROCESS	AHSG, AIFM3, ANGPTL3, ANXA4, APOE, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CALR, CD74, CDC2, CDC42, CDC42EP4, DAD1, GPX1, GSK3B, HSPA9, HSPD1, IGFBP3, KRT18, MAFB
		REGULATION_OF_METABOLIC_PROCESS	AHR, ANGPTL3, ARHGEF2, ARNTL, ATF5, BRD7, CALR, CCND1, CDC42, CDC45L, CLOCK, CXCL12, EGR1, EIF3C, EIF3E, EIF3F, EIF4A2, GATA6
		REGULATION_OF_MITOTIC_CELL_CYCLE	ASNS, BIRC5, DLG1, RCC1, TGFB1
		REGULATION_OF_MOLECULAR_FUNCTION	ADRA2A, AIFM3, ANGPTL3, BCL2, BIRC5, CCND1, CCNG1, CDC25A, CXCR4, EDNRA, GADD45G, GPX1, ID1, ID2, NPM1
		REGULATION_OF_PROGRAMMED_CELL_DEATH	AIFM3, ANXA4, APOE, ASNS, BCL2, BCL2L1, BIRC5, BNIP2, BNIP3L, CALR, CD74, CDC2, DAD1, GPX1, GSK3B, HSPA9, HSPD1, IGFBP3, KRT18, MAPK1, MAPK8, NME2, NOTCH2, NPM1, PIM1, PLG
		REGULATION_OF_PROTEIN_METABOLIC_PROCESS	ANGPTL3, ARHGEF2, CCND1, CDC42, CXCL12, EIF3C, EIF3E, EIF3F, EIF4A2, IGFBP3, INHBB, MAPRE1, MDM2, MDM4, SHH, TGFB1, TLR3
		REGULATION_OF_TRANSFERASE_ACTIVITY	ADRA2A, CCND1, CCNG1, CDC25A, CXCR4, GADD45G, SERINC1, SOD1, THY1
		RESPONSE_TO_ORGANIC_SUBSTANCE	AQP9, BCL2, GYS2, RELA, SOD1
		RHO_PROTEIN_SIGNAL_TRANSDUCTION	ADRA2A, APOA1, APOE, ARHGAP29, RAC1, RHOA
		SECRETION	APOA1, AQP9, CANX, CLCNKA, COPZ1, DOPEY2, ERGIC3, GBF1, GOSR2, INHBB, KCNJ1, KRT18, LMAN1, PDIA4, RAB14, RIMS1, SCIN, SNAPIN, TMED10
		SIGNAL_TRANSDUCTION	ABI1, ADAM10, ADRA2A, AGRN, AGT, AIFM3, ALCAM, AMBP, ANGPT1, ANXA4, APOA1, APOE, ARHGAP29, BCAR3, BCL2L1, BIRC2, BSG, C3, CBL, CCNA2, CD74
		SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	ADRA2A, APOA1, APOE, ARHGAP29, GNB1, GRAP, GRB2, IGF1, NOTCH2, PTPLAD1, RAC1, RHOA, RUNDC3A, VAV3
		SULFUR_METABOLIC_PROCESS	CDO1, CHST5, EXT1, GCLM, GPX1, HS6ST1, MSRA, SMS, SOD1, TPST1

		TRANSLATION	AARS, CEBPG, DHPS, EEF1A1, EIF2B1, EIF2S3, EIF3C, EIF3E, EIF3F, EIF4A2, INHBB, NACA, RPL11, RPL13, RPL18, RPL19, RPL23A, RPL26, RPL28, RPL30, RPL34, RPL35, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPS10, RPS11, RPS12, RPS2, RPS3, RPS3A, RPS5, RPS9, TLR3, TNIP1, WARS, YARS
		TRANSPORT	ABCB11, ABCC2, ABCD3, AGXT, AHSG, AIP, ANGPTL3, AP3B1, APOA1, APOE, AQP9, ARCN1, BCL2, BCL2L1, CACNA1D, CALR, CAV1, CBL, CD74, CDH1, CHKA, CORO1C, CPNE3, DERL1, EDNRA, ERGIC3, FXYD1, GBF1, GJB2
		TRNA_METABOLIC_PROCESS	AARS, KARS, POP4, SARS, SSB, WARS, YARS
		VASCULATURE_DEVELOPMENT	ANGPTL3, C1GALT1, CANX, PLG, RUNX1, SHH, TGFB2, THY1
		VESICLE_MEDIATED_TRANSPORT	AHSG, CBL, COPZ1, CORO1C, CPNE3, DOPEY2, ERGIC3, GBF1, GOSR2, KRT18, LMAN1, LRPAP1, PI4KB, PICALM, PPT1, RAB14, RAB1A, RAC1, RIMS1, SCIN, SEC22A, SEC23B, TMED10, TOM1, VPS33B
	Down-regulated	APOPTOTIC_NUCLEAR_CHANGES	AIFM1, BAX, CASP3, DFFB, TOP2A
		APOPTOTIC_PROGRAM	AIFM1, APAF1, BAD, BAX, CASP3, CASP8, CASP8AP2, DFFB, F2, LCK, TOP2A, TP53
		CASPASE_ACTIVATION	APAF1, BAX, CASP8AP2, F2, LCK, TP53
		CELL_CYCLE_ARREST_GO_0007050	BTG4, CDKN1B, CUL3, CUL5, PPM1G, TP53
		CELL_DEVELOPMENT	AIFM1, ANXA1, APAF1, BAD, BAX, BCL6, BOK, BTG1, BTG4, CASP3, CASP6, CASP8, CASP8AP2, CDK5R1, CDKN1B, CSE1L, CUL3, CUL5, DAZL, DDX41, DFFB, F2, GADD45B, GSTM3, GSTP1
		CELL_STRUCTURE_DISASSEMBLY_DURING_APOPTOSIS	CHAF1A, DFFB, HELLS, MAP3K12, MSH2, NUSAP1, PHB, RSF1, TOP2A
		CHROMOSOME_SEGREGATION	ARL8B, CENPF, NUSAP1, SRPK1, TOP2A
		COVALENT_CHROMATIN_MODIFICATION	HELLS, HTATIP, MAP3K12, MYST3, PHB
		DNA_METABOLIC_PROCESS	AIFM1, BAX, CDT1, DFFB, DNMT3B, DUT, EGF, FEN1, GMNN, HELLS, HMGB2, MSH2, NOL8, PMS1, PMS2, RAD51, RAD52, TOP2A, TP53, UNG, XPC
		DNA_PACKAGING	CHAF1A, DFFB, HELLS, NAP1L1, NUSAP1, RSF1, TOP2A
		DNA_REPAIR	FEN1, HMGB2, MSH2, PMS1, PMS2, RAD51, RAD52, TP53, UNG, XPC
		GROWTH	BCL6, BMPR1B, CAPRIN2, CDKN1B, ING5, RTN4RL2, TP53, XRN2
		INDUCTION_OF_APOPTOSIS_BY_EXTRACELLULAR_SIGNALS	BAX, CASP8AP2, DAXX, PDCD6, SST
		INDUCTION_OF_APOPTOSIS_BY_INTRACELLULAR_SIGNALS	AIFM1, BAX, CUL3, CUL5, TP53
		MICROTUBULE_BASED_PROCESS	GSN, KIF23, KIFAP3, LIMA1, LRPPRC, MID1IP1, NUSAP1, PRC1, RHOT2
		NEGATIVE_REGULATION_OF_CELL_CYCLE	BTG4, CDKN1B, CUL3, CUL5, GMNN, PPM1G, TP53
		NEGATIVE_REGULATION_OF_GROWTH	BCL6, CAPRIN2, CDKN1B, ING5, SERTAD2, TP53
		NUCLEAR_ORGANIZATION_AND_BIOGENESIS	AIFM1, BAX, CASP3, DFFB, TOP2A
		POSITIVE_REGULATION_OF_CASPASE_ACTIVITY	APAF1, BAX, CASP8AP2, F2, LCK, TP53
		POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	AIFM1, BAX, BCL6, BMPR1B, BOK, BTG1, CASP3, CASP6, CASP8AP2, CDK5R1, CDKN1B, CUL3, CUL5, LCK, PDCD6, PDCD7, SST, TNFSF10, TOP2A, TP53, TP53BP2, TRADD, TRAIP
		POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	APAF1, BAX, CASP8AP2, F2, LCK, TNNT2, TP53
		RESPONSE_TO_HORMONE_STIMULUS	GATA3, GSTM3, KRT19, NCOA6, PDCD7
		RESPONSE_TO_OXIDATIVE_STRESS	ANGPTL7, APOA4, NUDT1, PRDX6, SEPP1
		Enriched KEGG gene sets (NES ≥1.5, NOM *p*-value ≤0.05 and FDR *q*-value ≤0.25) in zebrafish HCC (9 months)	**Enriched gene lists**
	Up-regulated	HSA00240_PYRIMIDINE_METABOLISM	CTPS, DHODH, DPYD, ENTPD6, NME2, NME4, POLD2, RRM1, RRM2, TK1, TXNRD1, UPB1, UPP2
		HSA00564_GLYCEROPHOSPHOLIPID_METABOLISM	AGPAT3, CDIPT, CHKA, CHPT1, ETNK1, GPD1
		HSA00970_AMINOACYL_TRNA_BIOSYNTHESIS	AARS, CARS, CARS2, EPRS, FARSA, HARS, KARS, QARS, SARS, TARS, WARS, YARS
		HSA03010_RIBOSOME	RPL10A, RPL13, RPL13A, RPL18, RPL19, RPL23A, RPL26, RPL28, RPL30, RPL34, RPL35, RPL35A, RPL36AL, RPL7, RPL8, RPL9, RPS10, RPS11, RPS12, RPS15A, RPS18, RPS2, RPS21, RPS24, RPS25, RPS26, RPS29, RPS3, RPS3A, RPS5, RPS7, RPS8, RPS9, RPSA
		HSA04010_MAPK_SIGNALING_PATHWAY	AKT2, ARRB2, CACNA1D, CDC42, DUSP1, DUSP2, FGF10, FGF18, FGF23, FGF4, FGF5, FGF6, FGF8, FGFR1, FGFR2, FGFR4, FLNC, GADD45G, GRB2, JUN, MAPK1, MAPK3, MAPK8, MAPKAPK2, MEF2C, MKNK2, NLK, PDGFRA, PRKCB1, RAC1, RAC3, RAP1B, STMN1, TGFB1, TGFB2, TGFB3, TGFBR2
		HSA04012_ERBB_SIGNALING_PATHWAY	AKT2, CAMK2D, CBL, GRB2, GSK3B, JUN, MAPK1, MAPK3, MAPK8, PIK3CA, PIK3R1, PRKCB1, SRC, STAT5B
		HSA04060_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	CCL21, CXCL12, CXCR4, FLT1, IL15, INHBB, KITLG, MET, PDGFRA, PRL, TGFB1, TGFB2, TGFB3, TGFBR2

		HSA04110_CELL_CYCLE	CCNA2, CCNB1, CCNB2, CCND1, CCNE1, CDC2, CDC20, CDC25A, CDC27, CDC45L, GADD45G, GSK3B, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, MDM2, TFDP1, TGFB1, TGFB2, TGFB3, YWHAB
		HSA04150_MTOR_SIGNALING_PATHWAY	AKT2, IGF1, MAPK1, MAPK3, PIK3CA, PIK3R1, VEGFC
		HSA04310_WNT_SIGNALING_PATHWAY	CAMK2D, CCND1, CER1, CSNK2A1, CSNK2B, CTBP1, CTNNB1, FZD8, GSK3B, JUN, MAPK8, NLK, PPARD, PRKCB1, RAC1, RAC3, RHOA, ROCK2, TCF7, TCF7L2, VANGL1, WNT16, WNT2B, WNT4
		HSA04350_TGF_BETA_SIGNALING_PATHWAY	GDF7, ID1, ID2, INHBB, MAPK1, MAPK3, NODAL, NOG, RHOA, ROCK2, SMAD7, SP1, TFDP1, TGFB1, TGFB2, TGFB3, TGFBR2
		HSA04370_VEGF_SIGNALING_PATHWAY	AKT2, CDC42, MAPK1, MAPK3, MAPKAPK2, PIK3CA, PIK3R1, PRKCB1, RAC1, RAC3, SRC
		HSA04510_FOCAL_ADHESION	AKT2, BCL2, BIRC2, CAV1, CCND1, CDC42, COL1A2, CTNNB1, FLNC, FLT1, FYN, GRB2, GSK3B, IGF1, JUN, LAMB1, MAPK1, MAPK3, MAPK8, MET, PARVA, PARVB, PDGFRA, PIK3CA, PIK3R1, PPP1CB, PRKCB1, RAC1, RAC3, RAP1B, RHOA, ROCK2, SRC, TLN1, VAV3, VEGFC, VTN
		HSA04520_ADHERENS_JUNCTION	CDC42, CDH1, CSNK2A1, CSNK2B, CTNNB1, FGFR1, FYN, MAPK1, MAPK3, MET, NLK, RAC1, RAC3, RHOA, SRC, TCF7, TCF7L2, TGFBR2
		HSA04610_COMPLEMENT_AND_COAGULATION_CASCADES	A2M, C1S, C3, C8G, C9, CFB, CFH, FGA, FGB, FGG, MASP2, PLG, PROC, SERPINA1, SERPINC1, SERPIND1, SERPINF2
		HSA04620_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	AKT2, CHUK, FOS, JUN, MAPK1, MAPK3, MAPK8, MYD88, PIK3CA, PIK3R1, PIK3R3, RAC1, RELA, STAT1, TLR3
		HSA04630_JAK_STAT_SIGNALING_PATHWAY	AKT2, BCL2L1, CBL, CCND1, GRB2, IL15, JAK1, PIK3CA, PIK3R1, PIM1, PRL, SPRY4, STAM, STAT3, STAT5B
		HSA04660_T_CELL_RECEPTOR_SIGNALING_PATHWAY	AKT2, CBL, CDC42, FYN, GRB2, JUN, PIK3CA, PIK3R1, RHOA, VAV3
		HSA04662_B_CELL_RECEPTOR_SIGNALING_PATHWAY	AKT2, GSK3B, JUN, PIK3CA, PIK3R1, PRKCB1, RAC1, RAC3, VAV3
		HSA04664_FC_EPSILON_RI_SIGNALING_PATHWAY	AKT2, FYN, GRB2, MAPK1, MAPK3, MAPK8, PIK3CA, PIK3R1, PRKCB1, RAC1, RAC3, VAV3
		HSA04810_REGULATION_OF_ACTIN_CYTOSKELETON	ARPC2, ARPC5, CDC42, FGF10, FGF18, FGF23, FGF4, FGF5, FGF6, FGF8, FGFR1, FGFR2, FGFR4, ITGA5, MAPK1, MAPK3, MYH10, PDGFRA, PIK3CA, PIK3R1, PPP1CB, RAC1, RAC3, RDX, RHOA, ROCK2, SCIN, VAV3
		HSA04910_INSULIN_SIGNALING_PATHWAY	AKT2, CALM2, CBL, FLOT2, GRB2, GSK3B, GYS2, MAPK1, MAPK3, MAPK8, MKNK2, PCK1, PFKL, PIK3CA, PIK3R1, PKLR, PPP1CB, PPP1R3C
		HSA04912_GNRH_SIGNALING_PATHWAY	CACNA1D, CALM2, CAMK2D, CDC42, GRB2, JUN, MAPK1, MAPK3, MAPK8, MMP14, PRKCB1, SRC
	Down-regulated	HSA00010_GLYCOLYSIS_AND_GLUCONEOGENESIS	ADH5, ALDH2, ALDH7A1, ALDH9A1, ALDOC, BPGM, GAPDH, HK2, LDHA, PDHA1, PFKM, PGAM2, PKM2, TPI1
		HSA00071_FATTY_ACID_METABOLISM	ACSL1, ACSL5, ADH5, ALDH2, ALDH7A1, ALDH9A1, CPT2, HADHB
		HSA04210_APOPTOSIS	AIFM1, APAF1, BAD, BAX, CAPN2, CASP3, CASP6, CASP8, CHP, DFFB, TNFSF10, TP53, TRADD
		HSA04512_ECM_RECEPTOR_INTERACTION	CD36, COL1A1, COL11A2, COL2A1, COL4A6, COL6A1, FN1, HMMR, ITGA2, ITGA3, ITGB4, LAMA4

Table S3. Stage-specific and overlapping enriched genes in zebrafish liver hyperplasia and carcinoma. By comparing the enriched genes (supplementary material Table S2) between hyperplasia and carcinoma, we obtained stage-specific and overlapping enriched genes which were similarly regulated in both stages. The gene symbol and gene name of each gene (human homologue) are shown.

ACSL5	Acyl-CoA synthetase long-chain family member 5
ADSSL1	Adenylosuccinate synthase like 1
APOA4	Apolipoprotein A-IV
AVP	Arginine vasopressin
C3orf31	Chromosome 3 open reading frame 31
CAB39	Calcium binding protein 39
CALCB	Calcitonin-related polypeptide beta
CAMK2A	Calcium/calmodulin-dependent protein kinase II alpha
CDO1	Cysteine dioxygenase, type I
CEL	Carboxyl ester lipase (bile salt-stimulated lipase)
COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)
CTBP1	C-terminal binding protein 1
CUL5	Cullin 5
CYP2J2	Cytochrome P450, family 2, subfamily J, polypeptide 2
DDB1	Damage-specific DNA binding protein 1, 127kDa
DRD2	Dopamine receptor D2
DUSP5	Dual specificity phosphatase 5
DUSP6	Dual specificity phosphatase 6
EDF1	Endothelial differentiation-related factor 1
ESR2	Estrogen receptor 2 (ER beta)
F10	Coagulation factor X
F2	Coagulation factor II (thrombin)
F7	Coagulation factor VII (serum prothrombin conversion accelerator)
F9	Coagulation factor IX
FABP2	Fatty acid binding protein 2, intestinal
FGD1	FYVE, RhoGEF and PH domain containing 1
FZD8	Frizzled homolog 8 (Drosophila)
GADD45A	Growth arrest and DNA-damage-inducible, alpha
GDA	Guanine deaminase
GK	Glycerol kinase
GNG12	Guanine nucleotide binding protein (G protein), gamma 12
HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)
HSBP1	Heat shock factor binding protein 1
JUNB	Jun B proto-oncogene
KIN	KIN, antigenic determinant of recA protein homolog (mouse)
LDB1	LIM domain binding 1
LIPA	Lipase A, lysosomal acid, cholesterol esterase
LIPC	Lipase, hepatic
MAFA	v-Maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)
MAP3K12	Mitogen-activated protein kinase kinase kinase 12
MAPT	Microtubule-associated protein tau
MDFIC	MyoD family inhibitor domain containing
MGST1	Microsomal glutathione S-transferase 1
MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
MSH2	MutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
MSH6	MutS homolog 6 (E. coli)
MTF1	Metal-regulatory transcription factor 1
MTTP	Microsomal triglyceride transfer protein
NARG1	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
NFIL3	Nuclear factor, interleukin 3 regulated
NFKB2	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
NFYA	Nuclear transcription factor Y, alpha
NKX2-5	NK2 transcription factor related, locus 5 (Drosophila)
NMI	N-myc (and STAT) interactor
NR2F2	Nuclear receptor subfamily 2, group F, member 2

Table S4. Lists of up-regulated carcinoma-specific zebrafish enriched genes in different human cancer data sets. The up-regulated HCC-specific zebrafish enriched genes were significantly enriched (FDR q-value ≤0.05 and FWER p-value ≤0.05) in human hepatocellular carcinoma (GSE6764), human pancreatic adenocarcinoma (GSE16515), human colorectal carcinoma (GSE4183) and human lung adenocarcinoma (GSE7670). GSEA identified the genes from this gene list which contributed maximally to the GSEA scores of corresponding human cancer transcriptomic profiles.

Human cancer	**No.**	**Gene Symbol**	**Gene Name**
Human hepatocellular carcinoma (GSE6764)	1	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
	2	ABI1	Abl-interactor 1
	3	ADAM10	ADAM metallopeptidase domain 10
	4	AHR	Aryl hydrocarbon receptor
	5	AIP	Aryl hydrocarbon receptor interacting protein
	6	ALCAM	Activated leukocyte cell adhesion molecule
	7	ANGPT1	Angiopoietin 1
	8	ANXA11	Annexin A11
	9	AP3B1	Adaptor-related protein complex 3, beta 1 subunit
	10	APOM	Apolipoprotein M
	11	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2
	12	ARPC2	Actin related protein 2/3 complex, subunit 2, 34kDa
	13	ARPC5	Actin related protein 2/3 complex, subunit 5, 16kDa
	14	ARRB2	Arrestin, beta 2
	15	ASNS	Asparagine synthetase (glutamine-hydrolyzing)
	16	BAG2	BCL2-associated athanogene 2
	17	BCR	Breakpoint cluster region
	18	BIRC5	Baculoviral IAP repeat-containing 5
	19	BRD7	Bromodomain containing 7
	20	BSG	Basigin (Ok blood group)
	21	C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
	22	CACNA1D	Calcium channel, voltage-dependent, L type, alpha 1D subunit
	23	CANX	Calnexin
	24	CAV1	Caveolin 1, caveolae protein, 22kDa
	25	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence
	26	CCL21	Chemokine (C-C motif) ligand 21
	27	CCNA2	Cyclin A2
	28	CCNE1	Cyclin E1
	29	CCT4	Chaperonin containing TCP1, subunit 4 (delta)

30	CCT6A	Chaperonin containing TCP1, subunit 6A (zeta 1)
31	CCT7	Chaperonin containing TCP1, subunit 7 (eta)
32	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
33	CD9	CD9 molecule
34	CDC2	Cyclin-dependent kinase 1
35	CDC20	Cell division cycle 20 homolog (S. cerevisiae)
36	CDC27	Cell division cycle 27 homolog (S. cerevisiae)
37	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
38	CDC45L	Cell division cycle 45 homolog (S. cerevisiae)
39	CDIPT	CDP-diacylglycerol—inositol 3-phosphatidyltransferase
40	COL1A2	Collagen, type XVIII, alpha 1
41	CORO1C	Coronin, actin binding protein, 1C
42	CPNE3	Copine III
43	CSNK2A1	Casein kinase 2, alpha 1 polypeptide
44	CSNK2B	Casein kinase 2, beta polypeptide
45	CTNNB1	Catenin (cadherin-associated protein), beta 1, 88kDa
46	CTSK	Cathepsin K
47	CXCR4	Chemokine (C-X-C motif) receptor 4
48	DBN1	Drebrin 1
49	DLG1	Discs, large homolog 1 (Drosophila)
50	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
51	DUSP2	Dual specificity phosphatase 2
52	ECT2	Epithelial cell transforming sequence 2 oncogene
53	EIF4A2	Eukaryotic translation initiation factor 4A2
54	ENPP2	Ectonucleotide pyrophosphatase/phosphodiesterase 2
55	ERGIC3	ERGIC and golgi 3
56	EXT1	Exostosin 1
57	FBXO11	F-box protein 11
58	FLNC	Filamin C, gamma
59	FTH1	Ferritin, heavy polypeptide 1
60	GAD1	Glutamate decarboxylase 1 (brain, 67kDa)
61	GBF1	Golgi brefeldin A resistant guanine nucleotide exchange factor 1
62	GPR34	G protein-coupled receptor 34
63	GRB2	Growth factor receptor-bound protein 2
64	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1
65	HSP90AA1	Heat shock protein 90kDa alpha (cytosolic), class A member 1
66	HSPD1	Heat shock 60kDa protein 1 (chaperonin)
67	IL15	Interleukin 15
68	KITLG	KIT ligand
69	KRT18	Keratin 18
70	LAMB1	Laminin, beta 1
71	LRPAP1	Low density lipoprotein receptor-related protein associated protein 1
72	MAPRE1	Microtubule-associated protein, RP/EB family, member 1
73	MCM4	Minichromosome maintenance complex component 4
74	MCM6	Minichromosome maintenance complex component 6
75	MCM7	Minichromosome maintenance complex component 7
76	MDM4	Mdm4 p53 binding protein homolog (mouse)
77	MET	Met proto-oncogene (hepatocyte growth factor receptor)
78	MOBKL1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)

79	MR1	Major histocompatibility complex, class I-related
80	MYH10	Myosin, heavy chain 10, non-muscle
81	NCKIPSD	NCK interacting protein with SH3 domain
82	NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
83	NUP107	Nucleoporin 107kDa
84	PA2G4	Proliferation-associated 2G4, 38kDa
85	PARVB	Parvin, beta
86	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide
87	POP4	Processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
88	PPP1CB	Protein phosphatase 1, catalytic subunit, beta isozyme
89	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)
90	RABIF	RAB interacting factor
91	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
92	RAC3	Ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
93	RACGAP1	Rac GTPase activating protein 1
94	RCC1	Regulator of chromosome condensation 1
95	RELA	v-Rel reticuloendotheliosis viral oncogene homolog A (avian)
96	RHOA	Ras homolog gene family, member A
97	RHOT1	Ras homolog gene family, member T1
98	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
99	RPL10A	Ribosomal protein L10a
100	RPL13	Ribosomal protein L13
101	RPL18	Ribosomal protein L18
102	RPL19	Ribosomal protein L19
103	RPL23A	Ribosomal protein L23a
104	RPL28	Ribosomal protein L28
105	RPL30	Ribosomal protein L30
106	RPL35	Ribosomal protein L35
107	RPL35A	Ribosomal protein L35a
108	RPL4	Ribosomal protein L4
109	RPL5	Ribosomal protein L5
110	RPL7	Ribosomal protein L7
111	RPL7A	Ribosomal protein L7a
112	RPL8	Ribosomal protein L8
113	RPL9	Ribosomal protein L9
114	RPS10	Ribosomal protein S10
115	RPS12	Ribosomal protein S11
116	RPS18	Ribosomal protein S18
117	RPS2	Ribosomal protein S2
118	RPS21	Ribosomal protein S21
119	RPS3	Ribosomal protein S3
120	RPS5	Ribosomal protein S5
121	RPS7	Ribosomal protein S7
122	RPS8	Ribosomal protein S8
123	RRM1	Ribonucleotide reductase M1
124	RUNX1	Runt-related transcription factor 1
125	S100A4	S100 calcium binding protein A4
126	SCIN	Scinderin

	127	SLC25A3	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
	128	SP1	Sp1 transcription factor
	129	SSR2	Signal sequence receptor, beta (translocon-associated protein beta)
	130	STAT5B	Signal transducer and activator of transcription 5B
	131	STMN1	Stathmin 1
	132	TBX2	T-box 2
	133	TCF7	Transcription factor 7 (T-cell specific, HMG-box)
	134	TFDP1	Transcription factor Dp-1
	135	TGFB1	Transforming growth factor, beta 1
	136	TGFB2	Transforming growth factor, beta 2
	137	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1
	138	TLN1	Talin 1
	139	TOM1	Target of myb1 (chicken)
	140	TPR	Translocated promoter region (to activated MET oncogene)
	141	TRPA1	Transient receptor potential cation channel, subfamily A, member 1
	142	TTN	Titin
	143	TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)
	144	UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
	145	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
	146	VANGL1	Vang-like 1 (van gogh, Drosophila)
	147	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
	148	VAV3	Vav 3 guanine nucleotide exchange factor
	149	VEGFC	Vascular endothelial growth factor C
	150	WNT4	Wingless-type MMTV integration site family, member 4
Human pancreatic adenocarcinoma (GSE16515)	1	ABI1	Abl-interactor 1
	2	ADAM10	ADAM metallopeptidase domain 10
	3	AHR	Aryl hydrocarbon receptor
	4	AIP	Aryl hydrocarbon receptor interacting protein
	5	ANXA11	Annexin A11
	6	ANXA4	Annexin A4
	7	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2
	8	ARPC2	Actin related protein 2/3 complex, subunit 2, 34kDa
	9	ARPC5	Actin related protein 2/3 complex, subunit 5, 16kDa
	10	BCAR3	Breast cancer anti-estrogen resistance 3
	11	BCL2L1	BCL2-like 1
	12	BCR	Breakpoint cluster region
	13	BIRC2	Baculoviral IAP repeat-containing 2
	14	BIRC5	Baculoviral IAP repeat-containing 5
	15	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
	16	BRD7	Bromodomain containing 7
	17	BSG	Basigin (Ok blood group)
	18	C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
	19	CALM2	Calmodulin 2 (phosphorylase kinase, delta)
	20	CARS	Cysteinyl-tRNA synthetase
	21	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence
	22	CCNA2	Cyclin A2
	23	CCNE1	Cyclin E1

24	CCT6A	Chaperonin containing TCP1, subunit 6A (zeta 1)
25	CCT7	Chaperonin containing TCP1, subunit 7 (eta)
26	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
27	CD9	CD9 molecule
28	CDC2	Cyclin-dependent kinase 1
29	CDC20	Cell division cycle 20 homolog (S. cerevisiae)
30	CDC27	Cell division cycle 27 homolog (S. cerevisiae)
31	CDC42	Cell division cycle 42 (GTP binding protein, 25kDa)
32	CDC45L	Cell division cycle 45 homolog (S. cerevisiae)
33	CDH1	Cadherin 1, type 1, E-cadherin (epithelial)
34	CHPT1	Choline phosphotransferase 1
35	CLOCK	Collagen, type I, alpha 2
36	COL18A1	Clock homolog (mouse)
37	COL1A2	Collagen, type XVIII, alpha 1
38	CORO1C	Coronin, actin binding protein, 1C
39	CSNK2A1	Casein kinase 2, alpha 1 polypeptide
40	CSNK2B	Casein kinase 2, beta polypeptide
41	CTNNB1	Catenin (cadherin-associated protein), beta 1, 88kDa
42	CTSK	Cathepsin K
43	CXCR4	Chemokine (C-X-C motif) receptor 4
44	DAD1	Defender against cell death 1
45	DBN1	Drebrin 1
46	DHCR7	7-Dehydrocholesterol reductase
47	DLG1	Discs, large homolog 1 (Drosophila)
48	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
49	DUSP2	Dual specificity phosphatase 2
50	ECT2	Epithelial cell transforming sequence 2 oncogene
51	EFNB1	Ephrin-B1
52	EFNB2	Ephrin-B2
53	ETNK1	Ethanolamine kinase 1
54	EXT1	Exostosin 1
55	FGF18	Fibroblast growth factor 18
56	FLOT2	Flotillin 2
57	FPGS	Folylpolyglutamate synthase
58	FTH1	Ferritin, heavy polypeptide 1
59	GAD1	Glutamate decarboxylase 1 (brain, 67kDa)
60	GCHFR	GTP cyclohydrolase I feedback regulator
61	GJB2	Gap junction protein, beta 2, 26kDa
62	GRB2	Growth factor receptor-bound protein 2
63	GSK3B	Glycogen synthase kinase 3 beta
64	HP	Haptoglobin
65	HSP90AA1	Heat shock protein 90kDa alpha (cytosolic), class A member 1
66	HSPD1	Heat shock 60kDa protein 1 (chaperonin)
67	HSPE1	Heat shock 10kDa protein 1 (chaperonin 10)
68	ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
69	IL15	Interleukin 15
70	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
71	KITLG	KIT ligand
72	KRT18	Keratin 18

73	LRP1	Low density lipoprotein receptor-related protein 1
74	MAPRE1	Microtubule-associated protein, RP/EB family, member 1
75	MCM4	Minichromosome maintenance complex component 4
76	MCM6	Minichromosome maintenance complex component 6
77	MCM7	Minichromosome maintenance complex component 7
78	MET	Met proto-oncogene (hepatocyte growth factor receptor)
79	MGAT4B	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B
80	NCKIPSD	NCK interacting protein with SH3 domain
81	NOG	Noggin
82	NUP107	Nucleoporin 107kDa
83	PA2G4	Proliferation-associated 2G4, 38kDa
84	PARVA	Parvin, alpha
85	PARVB	Parvin, beta
86	PDIA3	Protein disulfide isomerase family A, member 3
87	PFKL	Phosphofructokinase, liver
88	PICALM	Phosphatidylinositol binding clathrin assembly protein
89	PIM1	Pim-1 oncogene
90	PMM2	Phosphomannomutase 2
91	POP4	Processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
92	PPP1R3C	Protein phosphatase 1, regulatory (inhibitor) subunit 3C
93	RAB14	RAB14, member RAS oncogene family
94	RAB1A	RAB1A, member RAS oncogene family
95	RABIF	RAB interacting factor
96	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
97	RACGAP1	Rac GTPase activating protein 1
98	RCC1	Regulator of chromosome condensation 1
99	RELA	v-Rel reticuloendotheliosis viral oncogene homolog A (avian)
100	RHOA	Ras homolog gene family, member A
101	RND1	Rho family GTPase 1
102	RPL28	Ribosomal protein L28
103	RRM1	Ribonucleotide reductase M1
104	RUNX1	Runt-related transcription factor 1
105	S100A4	S100 calcium binding protein A4
106	SCIN	Scinderin
107	SHH	Sonic hedgehog
108	SMAD7	SMAD family member 7
109	SP1	Sp1 transcription factor
110	SPRY4	Sprouty homolog 4 (Drosophila)
111	TARS	Threonyl-tRNA synthetase
112	TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)
113	TFDP1	Transcription factor Dp-1
114	TGFB1	Transforming growth factor, beta 1
115	TGFB2	Transforming growth factor, beta 2
116	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1
117	TLN1	Talin 1
118	TLR3	Toll-like receptor 3
119	TNIP1	TNFAIP3 interacting protein 1
120	TOM1	Target of myb1 (chicken)
121	TPR	Translocated promoter region (to activated MET oncogene)

	122	TRPA1	Transient receptor potential cation channel, subfamily A, member 1
	123	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
	124	UBE2L3	Ubiquitin-conjugating enzyme E2L 3
	125	VANGL1	Vang-like 1 (van gogh, Drosophila)
	126	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
	127	VEGFC	Vascular endothelial growth factor C
Human colorectal carcinoma (GSE4183)	1	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
	2	ADAM10	ADAM metallopeptidase domain 10
	3	AGT	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
	4	AHR	Aryl hydrocarbon receptor
	5	AKT2	v-Akt murine thymoma viral oncogene homolog 2
	6	ALCAM	Activated leukocyte cell adhesion molecule
	7	AP3B1	Adaptor-related protein complex 3, beta 1 subunit
	8	ASNS	Asparagine synthetase (glutamine-hydrolyzing)
	9	BAG2	BCL2-associated athanogene 2
	10	BCL2L1	BCL2-like 1
	11	BCR	Breakpoint cluster region
	12	BIRC5	Baculoviral IAP repeat-containing 5
	13	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
	14	BRD7	Bromodomain containing 7
	15	C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
	16	CANX	Calnexin
	17	CARS	Cysteinyl-tRNA synthetase
	18	CAV1	Caveolin 1, caveolae protein, 22kDa
	19	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence
	20	CCNA2	Cyclin A2
	21	CCNE1	Cyclin E1
	22	CCT4	Chaperonin containing TCP1, subunit 4 (delta)
	23	CCT6A	Chaperonin containing TCP1, subunit 6A (zeta 1)
	24	CCT7	Chaperonin containing TCP1, subunit 7 (eta)
	25	CDC2	Cyclin-dependent kinase 1
	26	CDC20	Cell division cycle 20 homolog (S. cerevisiae)
	27	CDC27	Cell division cycle 27 homolog (S. cerevisiae)
	28	CDC45L	Cell division cycle 45 homolog (S. cerevisiae)
	29	CLEC11A	C-type lectin domain family 11, member A
	30	COL18A1	Clock homolog (mouse)
	31	COL1A2	Collagen, type XVIII, alpha 1
	32	CORO1C	Coronin, actin binding protein, 1C
	33	CPNE3	Copine III
	34	CSNK2B	Casein kinase 2, beta polypeptide
	35	CTNNB1	Catenin (cadherin-associated protein), beta 1, 88kDa
	36	CTSK	Cathepsin K
	37	CXCR4	Chemokine (C-X-C motif) receptor 4
	38	DAD1	Defender against cell death 1
	39	DBN1	Drebrin 1

40	DHCR7	7-Dehydrocholesterol reductase
41	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
42	DUSP1	Dual specificity phosphatase 1
43	DUSP2	Dual specificity phosphatase 2
44	ECT2	Epithelial cell transforming sequence 2 oncogene
45	EDEM1	ER degradation enhancer, mannosidase alpha-like 1
46	EGR1	Early growth response 1
47	ENPP2	Ectonucleotide pyrophosphatase/phosphodiesterase 2
48	ERGIC3	ERGIC and golgi 3
49	FADS2	Fatty acid desaturase 2
50	FGFR1	Fibroblast growth factor receptor 1
51	FLI1	Friend leukemia virus integration 1
52	FLNC	Filamin C, gamma
53	FLT1	Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
54	FPGS	Folylpolyglutamate synthase
55	GAD1	Glutamate decarboxylase 1 (brain, 67kDa)
56	GADD45B	Growth arrest and DNA-damage-inducible, beta
57	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
58	GCHFR	GTP cyclohydrolase I feedback regulator
59	GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)
60	GSK3B	Glycogen synthase kinase 3 beta
61	HSPD1	Heat shock 60kDa protein 1 (chaperonin)
62	HSPE1	Heat shock 10kDa protein 1 (chaperonin 10)
63	INHBB	Inhibin, beta B
64	JAK1	Janus kinase 1
65	JUN	Jun proto-oncogene
66	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
67	LAMB1	Laminin, beta 1
68	LRPAP1	Low density lipoprotein receptor-related protein associated protein 1
69	MAPRE1	Microtubule-associated protein, RP/EB family, member 1
70	MCM4	Minichromosome maintenance complex component 4
71	MCM6	Minichromosome maintenance complex component 6
72	MCM7	Minichromosome maintenance complex component 7
73	MET	Met proto-oncogene (hepatocyte growth factor receptor)
74	MYH10	Myosin, heavy chain 10, non-muscle
75	NODAL	Nodal homolog (mouse)
76	NUP107	Nucleoporin 107kDa
77	PA2G4	Proliferation-associated 2G4, 38kDa
78	PAH	Phenylalanine hydroxylase
79	PARVA	Parvin, alpha
80	PARVB	Parvin, beta
81	PDIA3	Protein disulfide isomerase family A, member 3
82	PIK3C2A	Phosphoinositide-3-kinase, class 2, alpha polypeptide
83	PIM1	Pim-1 oncogene
84	PMM2	Phosphomannomutase 2
85	POP4	Processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
86	PROX1	Prospero homeobox 1

	87	RAC3	Ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
	88	RACGAP1	Rac GTPase activating protein 1
	89	RCC1	Regulator of chromosome condensation 1
	90	RDX	Radixin
	91	RHOA	Ras homolog gene family, member A
	92	RND1	Rho family GTPase 1
	93	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
	94	RPL35A	Ribosomal protein L35a
	95	RRM1	Ribonucleotide reductase M1
	96	RTN4RL2	Reticulon 4 receptor-like 2
	97	RUNX1	Runt-related transcription factor 1
	98	S100A4	S100 calcium binding protein A4
	99	SERPIND1	Serpin peptidase inhibitor, clade D (heparin cofactor), member 1
	100	SHH	Sonic hedgehog
	101	SLC8A1	Solute carrier family 8 (sodium/calcium exchanger), member 1
	102	SSR2	Signal sequence receptor, beta (translocon-associated protein beta)
	103	STAT3	Signal transducer and activator of transcription 3 (acute-phase response factor)
	104	TARS	Threonyl-tRNA synthetase
	105	TCF7	Transcription factor 7 (T-cell specific, HMG-box)
	106	TFDP1	Transcription factor Dp-1
	107	TGFB1	Transforming growth factor, beta 1
	108	TGFB2	Transforming growth factor, beta 2
	109	TGFB3	Transforming growth factor, beta 3
	110	TGFBR2	Transforming growth factor, beta receptor II (70/80kDa)
	111	TLN1	Talin 1
	112	TRPA1	Transient receptor potential cation channel, subfamily A, member 1
	113	TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)
	114	VANGL1	Vang-like 1 (van gogh, Drosophila)
	115	VEGFC	Vascular endothelial growth factor C
	116	VTN	Vitronectin
	117	WNT4	Wingless-type MMTV integration site family, member 4
	118	WWOX	WW domain containing oxidoreductase
Human lung adenocarcinoma (GSE7670)	1	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
	2	AGT	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
	3	AHR	Aryl hydrocarbon receptor
	4	ASNS	Asparagine synthetase (glutamine-hydrolyzing)
	5	BIRC5	Baculoviral IAP repeat-containing 5
	6	C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
	7	CANX	Calnexin
	8	CCNA2	Cyclin A2
	9	CCNE1	Cyclin E1
	10	CCT6A	Chaperonin containing TCP1, subunit 6A (zeta 1)
	11	CDC2	Cyclin-dependent kinase 1
	12	CDC20	Cell division cycle 20 homolog (S. cerevisiae)
	13	CDC45L	Cell division cycle 45 homolog (S. cerevisiae)
	14	CDH1	Cadherin 1, type 1, E-cadherin (epithelial)
	15	COL18A1	Clock homolog (mouse)

16	COL1A2	Collagen, type XVIII, alpha 1
17	CTSK	Cathepsin K
18	ECT2	Epithelial cell transforming sequence 2 oncogene
19	ERGIC3	ERGIC and golgi 3
20	FPGS	Folylpolyglutamate synthase
21	GAD1	Glutamate decarboxylase 1 (brain, 67kDa)
22	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
23	GCG	Glucagon
24	GSTZ1	Glutathione transferase zeta 1
25	HP	Haptoglobin
26	HSPD1	Heat shock 60kDa protein 1 (chaperonin)
27	HSPE1	Heat shock 10kDa protein 1 (chaperonin 10)
28	INHBB	Inhibin, beta B
29	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
30	KRT18	Keratin 18
31	MCM4	Minichromosome maintenance complex component 4
32	MCM6	Minichromosome maintenance complex component 6
33	MET	Met proto-oncogene (hepatocyte growth factor receptor)
34	MGAT4B	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B
35	PAX3	Paired box 3
36	PDIA3	Protein disulfide isomerase family A, member 3
37	PMM2	Phosphomannomutase 2
38	RACGAP1	Rac GTPase activating protein 1
39	RUNX1	Runt-related transcription factor 1
40	SERPIND1	Serpin peptidase inhibitor, clade D (heparin cofactor), member 1
41	SSR2	Signal sequence receptor, beta (translocon-associated protein beta)
42	TARS	Threonyl-tRNA synthetase
43	TFDP1	Transcription factor Dp-1
44	TSPAN31	Tetraspanin 31
45	TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)
46	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
47	WNT4	Wingless-type MMTV integration site family, member 4

Table S5. Potential HCC-specific gene signature restricted only to human HCC. Comparison of genes within the up-regulated HCC-specific zebrafish enriched genes (supplementary material Table S4) as identified by GSEA cross-species analysis of different human tumor data sets yielded a subset list of 48 genes. These genes were enriched only in human HCC.

No.	Gene Symbol	Gene Name
1	ANGPT1	Angiopoietin 1
2	APOM	Apolipoprotein M
3	ARRB2	Arrestin, beta 2
4	CACNA1D	Calcium channel, voltage-dependent, L type, alpha 1D subunit
5	CCL21	Chemokine (C-C motif) ligand 21
6	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
7	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
8	EIF4A2	Eukaryotic translation initiation factor 4A2
9	FBXO11	F-box protein 11
10	GBF1	Golgi brefeldin A resistant guanine nucleotide exchange factor 1
11	GPR34	G protein-coupled receptor 34
12	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1
13	MDM4	Mdm4 p53 binding protein homolog (mouse)
14	MOBKL1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)
15	MR1	Major histocompatibility complex, class I-related
16	NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
17	PPP1CB	Protein phosphatase 1, catalytic subunit, beta isozyme
18	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)
19	RHOT1	Ras homolog gene family, member T1
20	RPL10A	Ribosomal protein L10a
21	RPL13	Ribosomal protein L13
22	RPL18	Ribosomal protein L18
23	RPL19	Ribosomal protein L19
24	RPL23A	Ribosomal protein L23a
25	RPL30	Ribosomal protein L30
26	RPL35	Ribosomal protein L35
27	RPL4	Ribosomal protein L4
28	RPL5	Ribosomal protein L5
29	RPL7	Ribosomal protein L7
30	RPL7A	Ribosomal protein L7a
31	RPL8	Ribosomal protein L8
32	RPL9	Ribosomal protein L9
33	RPS10	Ribosomal protein S10
34	RPS11	Ribosomal protein S11
35	RPS18	Ribosomal protein S18
36	RPS2	Ribosomal protein S2
37	RPS21	Ribosomal protein S21
38	RPS3	Ribosomal protein S3
39	RPS5	Ribosomal protein S5

40	RPS7	Ribosomal protein S7
41	RPS8	Ribosomal protein S8
42	SLC25A3	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
43	STAT5B	Signal transducer and activator of transcription 5B
44	STMN1	Stathmin 1
45	TBX2	T-box 2
46	TTN	Titin
47	UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
48	VAV3	Vav 3 guanine nucleotide exchange factor

Table S6. Lists of up-regulated hyperplasia zebrafish enriched genes in human dysplastic liver data sets. The hyperplasia up-regulated zebrafish enriched genes, comprising of hyperplasia-specific and overlapping enriched genes in both stages, were significantly associated with human dysplastic liver (GSE6764) (FDR q-value ≤0.05 and FWER p-value ≤0.05). GSEA identified the genes from this gene list which contributed maximally to the GSEA scores of human dysplastic liver transcriptomic profiles.

Zebrafish up-regulated hyperplasia enriched genes in human dysplastic liver (GSE6764)		
No.	Gene Symbol	Gene Name
1	A2M	Alpha-2-macroglobulin
2	ADSSL1	Adenylosuccinate synthase like 1
3	AGXT	Alanine-glyoxylate aminotransferase
4	AHSG	Alpha-2-HS-glycoprotein
5	APOA1	Apolipoprotein A-I
6	APOE	Apolipoprotein E
7	AVP	Arginine vasopressin
8	C1S	Complement component 1, s subcomponent
9	C8G	Complement component 8, gamma polypeptide
10	CAB39	Calcium binding protein 39
11	CALR	Calreticulin
12	CCNB1	Cyclin B1
13	CCND1	Cyclin D1
14	CDC25A	Cell division cycle 25 homolog A (S. pombe)
15	CDO1	Cysteine dioxygenase, type I
16	CFB	Complement factor B
17	CFH	Complement factor H
18	CP	Ceruloplasmin (ferroxidase)
19	CTBP1	C-terminal binding protein 1
20	CYP2J2	Cytochrome P450, family 2, subfamily J, polypeptide 2
21	DERL1	Der1-like domain family, member 1
22	DUSP5	Dual specificity phosphatase 5
23	DUSP6	Dual specificity phosphatase 6
24	EDF1	Endothelial differentiation-related factor 1
25	F10	Coagulation factor X
26	F7	Coagulation factor II (thrombin)
27	FGA	Fibrinogen alpha chain
28	FGD1	FYVE, RhoGEF and PH domain containing 1
29	FYN	FYN oncogene related to SRC, FGR, YES
30	GADD45A	Growth arrest and DNA-damage-inducible, alpha
31	GATA6	GATA binding protein 6
32	GDA	Guanine deaminase

33	GGT1	Gamma-glutamyltransferase 1
34	GK	Glycerol kinase
35	GPX1	Glutathione peroxidase 1
36	IGF1	Insulin-like growth factor 1 (somatomedin C)
37	LDB1	LIM domain binding 1
38	LIPA	Lipase A, lysosomal acid, cholesterol esterase
39	MAFB	v-Maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
40	MAP3K12	Mitogen-activated protein kinase kinase kinase 12
41	MAPK1	Mitogen-activated protein kinase 1
42	MAPK3	Mitogen-activated protein kinase 3
43	MAPKAPK2	Mitogen-activated protein kinase-activated protein kinase 2
44	MBP	Myelin basic protein
45	MCM5	Minichromosome maintenance complex component 5
46	MDM2	Mdm2 p53 binding protein homolog (mouse)
47	MGST1	Microsomal glutathione S-transferase 1
48	MMP14	Matrix metallopeptidase 14 (membrane-inserted)
49	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
50	NARG1	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
51	NBN	Nibrin
52	NFIL3	Nuclear factor, interleukin 3 regulated
53	NFKB2	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
54	NFYA	Nuclear transcription factor Y, alpha
55	NLK	Nemo-like kinase
56	NMI	N-myc (and STAT) interactor
57	PCNA	Proliferating cell nuclear antigen
58	PDE8B	Phosphodiesterase 8B
59	PDGFRA	Platelet-derived growth factor receptor, alpha polypeptide
60	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
61	PLG	Plasminogen
62	POLB	Polymerase (DNA directed), beta
63	PPARD	Peroxisome proliferator-activated receptor delta
64	PPM1G	Protein phosphatase, Mg2+/Mn2+ dependent, 1G
65	PRKACA	Protein kinase, cAMP-dependent, catalytic, alpha
66	PRKCB1	Protein kinase C, beta
67	PXN	Paxillin
68	ROBO2	Roundabout, axon guidance receptor, homolog 2 (Drosophila)
69	RRM2	Ribonucleotide reductase M2
70	RTN4RL1	Reticulon 4 receptor-like 1
71	RUVBL2	RuvB-like 2 (E. coli)
72	SERPINA1	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
73	SERPINC1	Serpin peptidase inhibitor, clade C (antithrombin), member 1
74	SRC	v-Src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
75	THY1	Thy-1 cell surface antigen
76	TINF2	TERF1 (TRF1)-interacting nuclear factor 2
77	TK1	Thymidine kinase 1, soluble
78	UBC	Ubiquitin C
79	WNT16	Wingless-type MMTV integration site family, member 16
80	XPC	Xeroderma pigmentosum, complementation group C
81	YWHAB	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,

	beta polypeptide

Table S7. Lists of up-regulated HCC zebrafish enriched genes in human HCC data sets. The HCC up-regulated zebrafish enriched genes, comprising of carcinoma-specific and overlapping enriched genes in both stages, were significantly associated with human HCC (GSE6764) (FDR q-value ≤0.05 and FWER p-value ≤0.05). GSEA identified the genes from this gene list which contributed maximally to the GSEA score of human HCC transcriptomic profiles.

Zebrafish up-regulated HCC enriched genes in human hepatocellular carcinoma (GSE6764)		
No.	Gene Symbol	Gene Name
1	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
2	ABI1	Abl-interactor 1
3	ADAM10	ADAM metallopeptidase domain 10
4	AHR	Aryl hydrocarbon receptor
5	AIP	Aryl hydrocarbon receptor interacting protein
6	ALCAM	Activated leukocyte cell adhesion molecule
7	ANGPT1	Angiopoietin 1
8	ANXA11	Annexin A11
9	AP3B1	Adaptor-related protein complex 3, beta 1 subunit
10	APOE	Apolipoprotein E
11	APOM	Apolipoprotein M
12	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2
13	ARPC2	Actin related protein 2/3 complex, subunit 2, 34kDa
14	ARPC5	Actin related protein 2/3 complex, subunit 5, 16kDa
15	ARRB2	Arrestin, beta 2
16	ASNS	Asparagine synthetase (glutamine-hydrolyzing)
17	BAG2	BCL2-associated athanogene 2
18	BCR	Breakpoint cluster region
19	BIRC5	Baculoviral IAP repeat-containing 5
20	BRD7	Bromodomain containing 7
21	BSG	Basigin (Ok blood group)
22	C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
23	CACNA1D	Calcium channel, voltage-dependent, L type, alpha 1D subunit
24	CANX	Calnexin
25	CAV1	Caveolin 1, caveolae protein, 22kDa
26	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence
27	CCL21	Chemokine (C-C motif) ligand 21
28	CCNA2	Cyclin A2
29	CCNB1	Cyclin B1
30	CCNB2	Cyclin B2
31	CCNE1	Cyclin E1

32	CCNG2	Cyclin G2
33	CCT4	Chaperonin containing TCP1, subunit 4 (delta)
34	CCT6A	Chaperonin containing TCP1, subunit 6A (zeta 1)
35	CCT7	Chaperonin containing TCP1, subunit 7 (eta)
36	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
37	CD9	CD9 molecule
38	CDC2	Cyclin-dependent kinase 1
39	CDC20	Cell division cycle 20 homolog (S. cerevisiae)
40	CDC25A	Cell division cycle 25 homolog A (S. pombe)
41	CDC27	Cell division cycle 27 homolog (S. cerevisiae)
42	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
43	CDC45L	Cell division cycle 45 homolog (S. cerevisiae)
44	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
45	CHKA	Choline kinase alpha
46	COL1A2	Collagen, type I, alpha 2
47	CORO1C	Coronin, actin binding protein, 1C
48	CPNE3	Copine III
49	CSNK2A1	Casein kinase 2, alpha 1 polypeptide
50	CSNK2B	Casein kinase 2, beta polypeptide
51	CTNNB1	Catenin (cadherin-associated protein), beta 1, 88kDa
52	CTSK	Cathepsin K
53	CXCR4	Chemokine (C-X-C motif) receptor 4
54	DBN1	Drebrin 1
55	DERL1	Der1-like domain family, member 1
56	DLG1	Discs, large homolog 1 (Drosophila)
57	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
58	DUSP2	Dual specificity phosphatase 2
59	ECT2	Epithelial cell transforming sequence 2 oncogene
60	EDNRA	Endothelin receptor type A
61	EIF4A2	Eukaryotic translation initiation factor 4A2
62	ENPP2	Ectonucleotide pyrophosphatase/phosphodiesterase 2
63	ERGIC3	ERGIC and golgi 3
64	EXT1	Exostosin 1
65	FBXO11	F-box protein 11
66	FGFR4	Fibroblast growth factor receptor 4
67	FLNC	Filamin C, gamma
68	FTH1	Ferritin, heavy polypeptide 1
69	GAD1	Glutamate decarboxylase 1 (brain, 67kDa)
70	GBF1	Golgi brefeldin A resistant guanine nucleotide exchange factor 1
71	GPR34	G protein-coupled receptor 34
72	GRB2	Growth factor receptor-bound protein 2
73	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1
74	HSP90AA1	Heat shock protein 90kDa alpha (cytosolic), class A member 1
75	HSPD1	Heat shock 60kDa protein 1 (chaperonin)
76	IL15	Interleukin 15
77	KITLG	KIT ligand
78	KRT18	Keratin 18
79	LAMB1	Laminin, beta 1
80	LPL	Lipoprotein lipase
81	MAPK1	Mitogen-activated protein kinase 1

82	MAPK3	Mitogen-activated protein kinase 3
83	MAPKAPK2	Mitogen-activated protein kinase-activated protein kinase 2
84	MAPRE1	Microtubule-associated protein, RP/EB family, member 1
85	MCM2	Minichromosome maintenance complex component 2
86	MCM3	Minichromosome maintenance complex component 3
87	MCM4	Minichromosome maintenance complex component 4
88	MCM5	Minichromosome maintenance complex component 5
89	MCM6	Minichromosome maintenance complex component 6
90	MCM7	Minichromosome maintenance complex component 7
91	MDM2	Mdm2 p53 binding protein homolog (mouse)
92	MDM4	Mdm4 p53 binding protein homolog (mouse)
93	MET	Met proto-oncogene (hepatocyte growth factor receptor)
94	MMP14	Matrix metallopeptidase 14 (membrane-inserted)
95	MOBKL1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)
96	MR1	Major histocompatibility complex, class I-related
97	NBN	Nibrin
98	NCKIPSD	NCK interacting protein with SH3 domain
99	NLK	Nemo-like kinase
100	NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
101	NUP107	Nucleoporin 107kDa
102	PA2G4	Proliferation-associated 2G4, 38kDa
103	PARVB	Parvin, beta
104	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
105	PLTP	Phospholipid transfer protein
106	POLE2	Polymerase (DNA directed), epsilon 2 (p59 subunit)
107	POP4	Processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)
108	PPP1CB	Protein phosphatase 1, catalytic subunit, beta isozyme
109	PRKCB1	Protein kinase C, beta
110	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)
111	RABIF	RAB interacting factor
112	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
113	RAC3	Ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
114	RACGAP1	Rac GTPase activating protein 1
115	RCC1	Regulator of chromosome condensation 1
116	RELA	v-Rel reticuloendotheliosis viral oncogene homolog A (avian)
117	RHOA	Ras homolog gene family, member A
118	RHOT1	Ras homolog gene family, member T1
119	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
120	RPL10A	Ribosomal protein L10a
121	RPL13	Ribosomal protein L13
122	RPL18	Ribosomal protein L18
123	RPL19	Ribosomal protein L19
124	RPL23A	Ribosomal protein L23a
125	RPL28	Ribosomal protein L28
126	RPL30	Ribosomal protein L30
127	RPL35	Ribosomal protein L35
128	RPL4	Ribosomal protein L4
129	RPL5	Ribosomal protein L5
130	RPL7	Ribosomal protein L7

131	RPL7A	Ribosomal protein L7a
132	RPL8	Ribosomal protein L8
133	RPL9	Ribosomal protein L9
134	RPS10	Ribosomal protein S10
135	RPS18	Ribosomal protein S18
136	RPS2	Ribosomal protein S2
137	RPS21	Ribosomal protein S21
138	RPS3	Ribosomal protein S3
139	RPS5	Ribosomal protein S5
140	RPS7	Ribosomal protein S7
141	RPS8	Ribosomal protein S8
142	RRM1	Ribonucleotide reductase M1
143	RRM2	Ribonucleotide reductase M2
144	RUNX1	Runt-related transcription factor 1
145	RUVBL2	RuvB-like 2 (E. coli)
146	S100A4	S100 calcium binding protein A4
147	SCIN	Scinderin
148	SLC25A3	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
149	SP1	Sp1 transcription factor
150	SRC	v-Src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
151	SSR2	Signal sequence receptor, beta (translocon-associated protein beta)
152	STAT5B	Signal transducer and activator of transcription 5B
153	STMN1	Stathmin 1
154	TBX2	T-box 2
155	TCF7	Transcription factor 7 (T-cell specific, HMG-box)
156	TGFB2	Transforming growth factor, beta 2
157	THY1	Thy-1 cell surface antigen
158	TIAL1	TGFB1-induced anti-apoptotic factor 1
159	TK1	Thymidine kinase 1, soluble
160	TLN1	Talin 1
161	TOM1	Target of myb1 (chicken)
162	TPR	Translocated promoter region (to activated MET oncogene)
163	TRAM1	Translocation associated membrane protein 1
164	TRPA1	Transient receptor potential cation channel, subfamily A, member 1
165	TTN	Titin
166	TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)
167	UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
168	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
169	VANGL1	Vang-like 1 (van gogh, Drosophila)
170	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
171	VAV3	Vav 3 guanine nucleotide exchange factor
172	VEGFC	Vascular endothelial growth factor C
173	WNT4	Wingless-type MMTV integration site family, member 4
174	YWHAB	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide

Table S8. Liver cancer progression-associated gene signature. Identification of 20 genes from the zebrafish up-regulated enriched genes in both hyperplasia and carcinoma stages which remained up-regulated throughout human HCC progression from dysplasia (supplementary material Table S6) to carcinoma (supplementary material Table S7). These genes represent potential biological markers associated with liver cancer progression.

No.	Gene Symbol	Gene Name
1	APOE	Apolipoprotein E
2	CCNB1	Cyclin B1
3	CDC25A	Cell division cycle 25 homolog A (S. pombe)
4	DERL1	Der1-like domain family, member 1
5	MAPK1	Mitogen-activated protein kinase 1
6	MAPK3	Mitogen-activated protein kinase 3
7	MAPKAPK2	Mitogen-activated protein kinase-activated protein kinase 2
8	MCM5	Minichromosome maintenance complex component 5
9	MDM2	Mdm2 p53 binding protein homolog (mouse)
10	MMP14	Matrix metallopeptidase 14 (membrane-inserted)
11	NBN	Nibrin
12	NLK	Nemo-like kinase
13	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
14	PRKCB1	Protein kinase C, beta
15	RRM2	Ribonucleotide reductase M2
16	RUVBL2	RuvB-like 2 (E. coli)
17	SRC	v-Src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
18	THY1	Thy-1 cell surface antigen
19	TK1	Thymidine kinase 1, soluble
20	YWHAB	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide

Table S9: Validation of differential gene expression by quantitative real-time PCR. Individual lesions from each liver tumorigenesis stage (hyperplastic liver, HL; hepatocellular carcinoma, HCC) were examined for the expression level of the selected genes. The $\log_2$ fold change obtained from microarray data and RT-PCR for the genes validated are as shown in the table.

No.	**Gene symbol**		**Gene name**	**Log$_2$ fold change**							
				Microarray		Quantitative real-ti**me PCR**					
	Zebrafish	Human		HL	HCC	HL1	HL2	HL3	HCC1	HCC2	HCC3
1	*akt2l*	*AKT2*	V-akt murine thymoma viral oncogene homolog 2, like	1.06	2.91	3.54	2.95	2.78	6.75	5.46	6.03
2	*angpt1*	*ANGPT1*	Angiopoietin 1	0.12	2.54	0.26	0.73	0.23	1.58	2.34	1.87
3	*ccnb1*	*CCNB1*	Cyclin B1	5.48	7.85	5.11	4.12	4.09	9.67	9.46	8.23
4	*mapk1*	*MAPK1*	Mitogen-activated protein kinase 1	2.13	2.18	3.28	2.54	4.45	5.79	6.78	6.92
5	*mapk3*	*MAPK3*	Mitogen-activated protein kinase 3	2.31	2.64	2.73	1.12	3.67	3.92	4.65	3.75
6	*mapk8*	*MAPK8*	Mitogen-activated protein kinase 8	2.09	3.91	2.58	2.56	2.91	4.71	3.56	4.42
7	*mdm2*	*MDM2*	Transformed 3T3 cell double minute 2 homolog	5.66	3.07	2.91	3.40	3.66	3.64	4.07	4.54
8	*nfya*	*NFYA*	Nuclear transcription factor Y, alpha	6.56	1.74	4.83	5.13	5.76	0.47	0.56	0.91
9	*nlk1*	*NLK*	Nemo like kinase b	2.16	2.35	1.02	2.34	2.61	1.64	1.07	1.13
10	*rpl19*	*RPL19*	Ribosomal protein 19	1.20	2.81	2.98	1.45	2.76	4.78	4.75	4.12
11	*stat3*	*STAT3*	Signal transduction and activation of transcription 3	-1.06	2.53	-0.67	-1.05	0.12	3.76	3.21	2.65
12	*stmn1a*	*STMN1*	Stathmin 1a	-1.30	3.93	-0.59	-0.33	-0.67	4.76	4.12	5.23
13	*tgfb1*	*TGFB1*	Transforming growth factor, beta 1	0.41	1.88	0.79	0.04	-0.32	3.40	2.11	2.18
14	*tp53*	*TP53*	Tumor protein p53	2.47	-3.54	3.55	2.76	4.29	-0.18	-1.12	-1.56
15	*zgc:194152*	*NBN*	Nibrin	2.15	2.05	1.54	2.25	2.71	3.76	1.10	1.75