

Supplementary Information

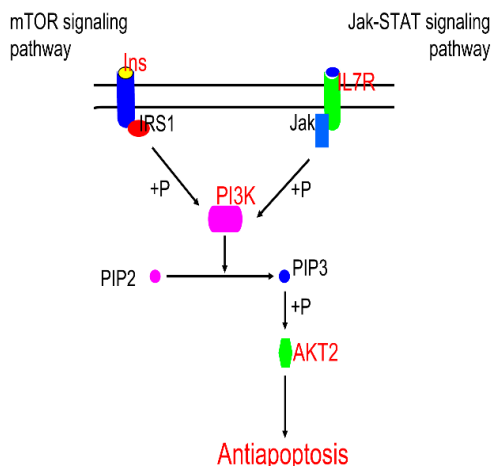


Figure S1. Diagram of putative PI3K–AKT network during Amur ide spawning migration. The *PI3K* and *AKT2* genes involved in the PI3K–AKT network and their expressions were up-regulated in SM, indicating that the PI3K–AKT is a strong candidate for apoptosis regulation and plays the critical roles on inhibition of apoptosis because of change of osmotic pressure during Amur ide spawning migration.

Table S1. Differential expressed genes identified by transcriptome comparison.

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|-------------|----------|--|
| comp99124_c0 | 56.67 | 0 | 37.78900814 | 3.65E-26 | adrenomedullin 2a precursor |
| comp102945_c4 | 19.5 | 0 | 37.10132625 | 4.23E-24 | PREDICTED: hypothetical protein LOC100333395 |
| comp102927_c7 | 12.6 | 0 | 35.03081174 | 6.28E-18 | Cideb protein |
| comp102325_c0 | 15.21 | 0 | 34.77221764 | 3.60E-17 | MHC class II antigen |
| comp102117_c5 | 16.92 | 0 | 34.5338489 | 1.80E-16 | starmaker |
| comp102025_c11 | 4.33 | 0 | 34.02053679 | 5.72E-15 | ATP-dependent RNA helicase DDX54 |
| comp102514_c3 | 3.68 | 0 | 33.96960035 | 7.93E-15 | ubiquitin carboxyl-terminal hydrolase 16 |
| comp102751_c15 | 9.11 | 0 | 33.79345644 | 2.61E-14 | PREDICTED: hypothetical protein LOC566559 isoform 1 |
| comp102456_c1 | 13.07 | 0 | 33.5835665 | 1.05E-13 | PREDICTED: urokinase plasminogen activator surface receptor-like |
| comp102333_c8 | 7.1 | 0 | 33.41925976 | 3.08E-13 | PREDICTED: GTPase IMAP family member 2-like |
| comp99484_c0 | 10.41 | 0 | 33.3858929 | 3.85E-13 | PREDICTED: mpv17-like protein-like |
| comp100385_c0 | 3.87 | 0 | 33.28605528 | 7.18E-13 | Thymidine phosphorylase |
| comp102998_c8 | 1 | 0 | 33.09450008 | 2.47E-12 | PREDICTED: hypothetical protein LOC100537129 |
| comp99539_c0 | 4.1 | 0 | 33.04307155 | 3.57E-12 | glia maturation factor beta |
| comp102831_c4 | 15 | 0 | 32.71952708 | 2.72E-11 | complement C3-H1 |
| comp102845_c1 | 9.86 | 0 | 32.64407485 | 4.36E-11 | uncharacterized protein LOC100006475 precursor |
| comp102924_c1 | 3.75 | 0 | 32.60690333 | 5.56E-11 | PREDICTED: uncharacterized protein LOC100889275 |
| comp102762_c2 | 1.39 | 0 | 32.34317329 | 2.99E-10 | influenza virus NS1A-binding protein homolog B |
| comp100080_c1 | 1.27 | 0 | 32.1678557 | 8.83E-10 | Zinc finger CCCH-type containing 14 |
| comp102296_c3 | 4.36 | 0 | 32.13915184 | 1.04E-09 | Uncharacterized protein |
| comp102351_c2 | 0.94 | 0 | 32.1288099 | 1.13E-09 | PREDICTED: hypothetical protein LOC100537969 |
| comp101989_c4 | 2.94 | 0 | 32.12229096 | 1.13E-09 | BET1 homolog |
| comp101544_c1 | 3.86 | 0 | 31.94454258 | 3.26E-09 | CD2 family receptor |
| comp102812_c4 | 6.25 | 0 | 31.8665226 | 5.26E-09 | Uncharacterized protein |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|-------------|----------|---|
| comp100941_c2 | 1.68 | 0 | 31.8415772 | 5.80E-09 | PREDICTED: magnesium transporter MRS2 homolog, mitochondrial-like |
| comp100775_c0 | 1.84 | 0 | 31.81292361 | 7.08E-09 | Family with sequence similarity 82, member A2 |
| comp102365_c3 | 4.67 | 0 | 31.78245833 | 8.67E-09 | polyprotein |
| comp102497_c3 | 5.09 | 0 | 31.77558036 | 8.67E-09 | PREDICTED: hypothetical protein LOC100007935 |
| comp101653_c0 | 1.22 | 0 | 31.6826713 | 1.47E-08 | complement C1q tumor necrosis factor-related protein 1 precursor |
| comp102571_c24 | 1.31 | 0 | 31.67795012 | 1.64E-08 | PREDICTED: protein FAM20A-like, partial |
| comp100076_c7 | 2.35 | 0 | 31.6010296 | 2.56E-08 | Ighmbp2l protein |
| comp102770_c0 | 0.84 | 0 | 31.51893121 | 4.09E-08 | PREDICTED: hypothetical protein LOC100538314 |
| comp100952_c3 | 3.64 | 0 | 31.49099552 | 4.62E-08 | PREDICTED: desmoglein-4-like |
| comp102578_c7 | 3.22 | 0 | 31.47082977 | 5.22E-08 | PREDICTED: complement C3 |
| comp102753_c2 | 0.43 | 0 | 31.45126377 | 5.90E-08 | Ugdh protein |
| comp101848_c2 | 0.71 | 0 | 31.31437987 | 1.28E-07 | PREDICTED: transmembrane protein 56-B |
| comp102866_c10 | 0.87 | 0 | 31.23303391 | 1.94E-07 | S-adenosylmethionine synthetase isoform type-2 |
| comp102134_c8 | 1.6 | 0 | 30.99688645 | 7.45E-07 | pyrroline-5-carboxylate reductase |
| comp101696_c1 | 1.35 | 0 | 30.81859709 | 1.72E-06 | ribonuclease P protein subunit p14 |
| comp102333_c9 | 3.61 | 0 | 30.81722375 | 1.72E-06 | uncharacterized protein LOC406638 |
| comp102898_c4 | 0.56 | 0 | 30.80133564 | 2.05E-06 | DNA replication licensing factor MCM5 |
| comp100708_c0 | 1.41 | 0 | 30.77540357 | 2.05E-06 | dnaJ homolog subfamily C member 15 |
| comp101267_c0 | 0.98 | 0 | 30.66063339 | 4.28E-06 | thymidine kinase 2, mitochondrial |
| comp101889_c0 | 1.02 | 0 | 30.61828384 | 5.19E-06 | AN1-type zinc finger protein 2B |
| comp102564_c2 | 0.5 | 0 | 30.60918662 | 5.19E-06 | signal transducer and activator of transcription 6, interleukin-4 induced |
| comp88163_c0 | 3.08 | 0 | 30.59483133 | 5.19E-06 | PREDICTED: hypothetical protein LOC100704550 |
| comp102369_c3 | 1.72 | 0 | 30.56650261 | 6.32E-06 | PREDICTED: TGF-beta receptor type-2-like |
| comp102539_c4 | 2.63 | 0 | 30.47061139 | 9.48E-06 | PREDICTED: hypothetical protein LOC560673 |
| comp102365_c2 | 2.54 | 0 | 30.37910264 | 1.45E-05 | protease/polymerase |
| comp102110_c2 | 0.3 | 0 | 30.32069364 | 2.25E-05 | p110 |
| comp95792_c0 | 2.67 | 0 | 30.28288732 | 2.25E-05 | PREDICTED: hypothetical protein LOC100537242 |
| comp102093_c0 | 0.52 | 0 | 30.25272535 | 2.82E-05 | uncharacterized protein LOC368688 |
| comp102630_c4 | 1.69 | 0 | 30.24559589 | 2.82E-05 | PREDICTED: hypothetical protein LOC100334801 |
| comp101797_c2 | 1.77 | 0 | 30.23226125 | 2.82E-05 | PREDICTED: hypothetical protein LOC569383 |
| comp102615_c8 | 0.39 | 0 | 30.17014366 | 4.53E-05 | midnolin |
| comp68714_c0 | 3.61 | 0 | 30.12534605 | 4.53E-05 | polymerase |
| comp95550_c0 | 2.66 | 0 | 30.12534605 | 4.53E-05 | predicted protein |
| comp102528_c7 | 0.4 | 0 | 30.09052649 | 5.79E-05 | PREDICTED: collagen alpha-1(XIII) chain |
| comp93184_c0 | 2.26 | 0 | 30.00986883 | 7.45E-05 | PREDICTED: serine incorporator 3-like |
| comp93876_c0 | 2.9 | 0 | 29.94846828 | 9.64E-05 | PREDICTED: hypothetical protein LOC100493142 |
| comp102994_c7 | 0.97 | 0 | 29.91932194 | 1.26E-04 | PREDICTED: protein NLRC3-like |
| comp102214_c4 | 2.16 | 0 | 29.89022784 | 1.26E-04 | PREDICTED: alpha-2-macroglobulin |
| comp93215_c1 | 2.38 | 0 | 29.88433795 | 1.26E-04 | pol-like protein ENS-3 |
| comp101788_c18 | 0.25 | 0 | 29.8457929 | 1.65E-04 | glycoprotein A repetitions predominant precursor |
| comp100654_c2 | 1.1 | 0 | 29.82749209 | 1.65E-04 | TPA_exp: putative tyrosine recombinase |
| comp102365_c1 | 2.27 | 0 | 29.67283384 | 2.91E-04 | gag-pol polyprotein |
| comp98009_c3 | 2.48 | 0 | 29.67283384 | 2.91E-04 | PREDICTED: hypothetical protein LOC100695311 |
| comp102646_c3 | 0.19 | 0 | 29.67207433 | 2.91E-04 | Lipin 1 |
| comp102073_c1 | 0.14 | 0 | 29.63045524 | 3.91E-04 | Si:dkey-102f14.5 |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|---------------|-----------|-----------|-------------|----------|--|
| comp102572_c6 | 3.36 | 0 | 29.59483133 | 3.91E-04 | complement C3-S |
| comp99185_c2 | 2.55 | 0 | 29.59483133 | 3.91E-04 | PREDICTED: hypothetical protein LOC100120441 |
| comp90720_c0 | 1.78 | 0 | 29.42490633 | 7.27E-04 | PREDICTED: tumor necrosis factor receptor superfamily member 11B |
| comp102296_c4 | 2.38 | 0 | 29.33179692 | 1.01E-03 | PREDICTED: immunoglobulin superfamily member 3-like |
| comp102842_c9 | 1.91 | 0 | 29.33179692 | 1.01E-03 | PREDICTED: retrotransposable element Tf2 155 kDa protein type 1-like |
| comp102826_c0 | 1.16 | 0 | 29.20206299 | 2.00E-03 | uncharacterized protein LOC550566 |
| comp100349_c1 | 2.56 | 0 | 29.12534605 | 2.00E-03 | Uncharacterized protein |
| comp102333_c6 | 1.93 | 0 | 29.12534605 | 2.00E-03 | PREDICTED: GTPase IMAP family member 8-like |
| comp68714_c1 | 2.01 | 0 | 29.12534605 | 2.00E-03 | gag-pol polyprotein |
| comp91271_c0 | 1.76 | 0 | 29.12534605 | 2.00E-03 | PREDICTED: RETRansposon-like family member (retr-1)-like |
| comp102672_c4 | 0.13 | 0 | 29.0594996 | 2.86E-03 | unnamed protein product |
| comp101324_c1 | 0.12 | 0 | 29.04196967 | 2.86E-03 | serine/threonine-protein kinase SIK1 |
| comp87594_c1 | 1.57 | 0 | 29.00986883 | 2.86E-03 | PREDICTED: serine/threonine-protein kinase TAO3-like isoform 1 |
| comp91133_c0 | 1.91 | 0 | 29.00986883 | 2.86E-03 | PREDICTED: uncharacterized protein K02A2.6-like |
| comp99329_c2 | 1.85 | 0 | 29.00986883 | 2.86E-03 | PREDICTED: hypothetical protein LOC100536880 |
| comp102761_c1 | 2.11 | 0 | 14.27128118 | 3.75E-12 | protein LSM14 homolog A |
| comp102185_c6 | 3.7 | 0 | 11.20599063 | 1.89E-12 | PREDICTED: SLIT-ROBO Rho GTPase-activating protein 3 |
| comp102031_c0 | 152.36 | 0.27 | 9.134886633 | 1.03E-21 | ornithine decarboxylase 1a |
| comp102721_c6 | 0.3 | 0 | 8.663682495 | 2.45E-06 | PREDICTED: copper-transporting ATPase 2 |
| comp102791_c0 | 1.54 | 0 | 8.50670801 | 5.57E-12 | complement C4-1 |
| comp102875_c2 | 19.83 | 0.08 | 7.870392595 | 3.41E-17 | PREDICTED: HHIP-like 1 |
| comp67791_c0 | 13.08 | 0.07 | 7.571655518 | 4.65E-13 | PREDICTED: SAM domain and HD domain-containing protein 1-like |
| comp102128_c0 | 0.65 | 0 | 7.525902929 | 1.45E-05 | tryptophanyl-tRNA synthetase, cytoplasmic |
| comp103038_c1 | 5.18 | 0.03 | 7.514501174 | 2.40E-12 | complement factor H-like 1 protein |
| comp102343_c2 | 5.63 | 0.06 | 6.589244915 | 4.22E-13 | novel transglutaminase family protein |
| comp102329_c0 | 0.66 | 0.01 | 6.546120426 | 6.32E-06 | PREDICTED: hypothetical protein LOC100701766 |
| comp102608_c5 | 1.37 | 0.02 | 6.40138073 | 7.11E-08 | PREDICTED: very long-chain acyl-CoA synthetase isoform 1 |
| comp103011_c3 | 10.38 | 0.14 | 6.230045058 | 3.30E-08 | Si:dkey-19a16.11 |
| comp102949_c3 | 0.98 | 0.02 | 5.963676365 | 5.30E-08 | PREDICTED: hypothetical protein LOC100008302 |
| comp102612_c3 | 1.91 | 0.03 | 5.916709147 | 7.19E-10 | PREDICTED: solute carrier organic anion transporter family member 1C1-like |
| comp101330_c3 | 17.22 | 0.33 | 5.691247748 | 2.33E-11 | short chain dehydrogenase/reductase family 16C, member 5b |
| comp102986_c4 | 0.59 | 0.01 | 5.647870838 | 8.44E-05 | cytochrome P450, family 2, subfamily P, polypeptide 9 |
| comp102860_c0 | 1.38 | 0.04 | 5.049164533 | 5.82E-07 | interleukin 13 receptor, alpha 1 precursor |
| comp102750_c4 | 33.55 | 1.03 | 5.026203033 | 3.25E-10 | PREDICTED: hypothetical protein LOC100334998 |
| comp54337_c0 | 2.53 | 0.1 | 4.605871234 | 4.88E-04 | hypothetical protein BRAFLDRAFT_201218 |
| comp93506_c1 | 2.13 | 0.1 | 4.342836828 | 1.33E-03 | PREDICTED: retrovirus polyprotein, putative-like |
| comp102203_c0 | 4.56 | 0.23 | 4.300823326 | 2.79E-06 | PREDICTED: hypothetical protein LOC100690401 |
| comp102753_c9 | 0.48 | 0.03 | 4.165792527 | 1.33E-03 | PREDICTED: nuclear factor 1 X-type |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | <i>p</i> -Value | Gene Name |
|----------------|--------------|--------------|-------------|-----------------|--|
| comp102036_c0 | 2.47 | 0.14 | 4.108371574 | 3.04E-03 | PREDICTED: hypothetical protein LOC100710874 |
| comp95589_c1 | 2.49 | 0.14 | 4.108371574 | 3.04E-03 | PREDICTED: ADM2 |
| comp96263_c2 | 2.16 | 0.13 | 4.108371574 | 3.04E-03 | PREDICTED: zinc finger protein 40 |
| comp103139_c0 | 1137.15 | 68.06 | 4.062422971 | 3.93E-08 | prostaglandin D2 synthase, brain precursor |
| comp102388_c8 | 7.08 | 0.43 | 4.051935629 | 2.46E-07 | ankyrin repeat and protein kinase domain-containing protein 1 |
| comp102817_c2 | 3.96 | 0.24 | 4.050835594 | 1.22E-05 | aig2-like domain-containing protein 1-b precursor |
| comp59020_c0 | 4.21 | 0.25 | 4.050656076 | 6.41E-05 | preprogalanin 2A |
| comp99861_c1 | 5.16 | 0.31 | 4.043556638 | 5.42E-07 | pleckstrin homology domain containing, family G (with RhoGef domain) member 5a (plekhg5a), transcript variant X1 |
| comp98319_c0 | 20.39 | 1.3 | 3.968152679 | 3.31E-07 | novel protein similar to vertebrate mitochondrial ribosomal protein S14 |
| comp102181_c0 | 2.6 | 0.17 | 3.944240476 | 6.51E-06 | Palmdelphin b |
| comp102842_c5 | 2.23 | 0.16 | 3.828263655 | 7.47E-04 | PREDICTED: retrotransposable element Tf2 155 kDa protein type 1-like |
| comp102643_c6 | 4.03 | 0.29 | 3.796561338 | 1.40E-05 | reverse transcriptase |
| comp97269_c0 | 2.52 | 0.18 | 3.775796235 | 9.21E-04 | Neuropilin 2b |
| comp102952_c8 | 2.78 | 0.22 | 3.664764923 | 1.42E-03 | PREDICTED: dnaJ homolog subfamily C member 16 |
| comp62047_c1 | 10.03 | 0.82 | 3.619677033 | 2.59E-06 | IFN-inducible and antiviral protein |
| comp102842_c2 | 4.2 | 0.34 | 3.605871234 | 3.80E-05 | PREDICTED: retrotransposable element Tf2 155 kDa protein type 1-like |
| comp102434_c7 | 0.89 | 0.07 | 3.600214508 | 8.98E-06 | testis-expressed sequence 2 protein |
| comp102527_c0 | 1.2 | 0.1 | 3.585144068 | 6.51E-05 | growth hormone receptor b |
| comp100295_c0 | 2.69 | 0.23 | 3.565229249 | 5.72E-04 | unnamed protein product |
| comp101835_c0 | 1 | 0.09 | 3.552639785 | 1.10E-04 | PREDICTED: toll-like receptor 5-like |
| comp93418_c0 | 3.28 | 0.28 | 3.539396284 | 1.96E-05 | YY1-associated factor 2 |
| comp102476_c2 | 2.55 | 0.22 | 3.521710786 | 6.82E-04 | PREDICTED: transmembrane protein 80-like |
| comp102279_c14 | 6.26 | 0.55 | 3.496879853 | 3.51E-06 | PREDICTED: protein phosphatase 1K, mitochondrial-like |
| comp94235_c1 | 1.85 | 0.17 | 3.480340352 | 2.81E-03 | PREDICTED: apolipoprotein B-100 |
| comp102262_c14 | 94.14 | 8.6 | 3.452010406 | 1.73E-06 | apoptosis-inducing factor, mitochondrion-associated 2 |
| comp102728_c3 | 7.29 | 0.67 | 3.445930321 | 6.77E-06 | PREDICTED: hypothetical protein LOC100004944 |
| comp102455_c10 | 4.38 | 0.42 | 3.394367128 | 1.16E-05 | PREDICTED: plectin-like |
| comp92134_c0 | 2.7 | 0.27 | 3.342836828 | 1.42E-03 | uncharacterized protein LOC768162 |
| comp70094_c0 | 5.78 | 0.58 | 3.316841619 | 1.33E-05 | PREDICTED: UMP-CMP kinase 2, mitochondrial, partial |
| comp70195_c1 | 6.91 | 0.7 | 3.293927227 | 9.91E-05 | interferon-inducible 58 kDa protein |
| comp100295_c4 | 3.84 | 0.39 | 3.288644267 | 3.68E-05 | PREDICTED: saecin |
| comp54916_c0 | 3.92 | 0.41 | 3.268836246 | 8.51E-04 | Meiosis expressed gene 1 homolog |
| comp101897_c0 | 0.78 | 0.08 | 3.203998194 | 1.18E-03 | required for meiotic nuclear division protein 1 homolog |
| comp70117_c0 | 3.18 | 0.36 | 3.15019175 | 1.39E-03 | protein phosphatase 1 regulatory subunit 3D |
| comp88493_c0 | 11.5 | 1.32 | 3.122446759 | 2.99E-05 | PREDICTED: hypothetical protein LOC794824 |
| comp102789_c0 | 3.53 | 0.41 | 3.110604345 | 2.85E-05 | relA-associated inhibitor |
| comp101244_c8 | 3.14 | 0.36 | 3.108371574 | 1.64E-03 | neuronal growth regulator 1 precursor |
| comp102716_c3 | 5.17 | 0.61 | 3.073571692 | 3.81E-05 | PREDICTED: protein FAM151B-like |
| comp70195_c0 | 7.93 | 0.95 | 3.059043862 | 5.29E-05 | interferon-inducible protein IFI58 |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|-------------|----------|---|
| comp59547_c0 | 9.01 | 1.09 | 3.054331734 | 3.41E-05 | IFN-regulatory factory 7 |
| comp102200_c2 | 9.08 | 1.1 | 3.038560751 | 2.20E-05 | PREDICTED: low-density lipoprotein receptor-related protein 1 |
| comp100925_c2 | 2.67 | 0.35 | 2.94240426 | 1.16E-04 | peroxisome proliferator-activated receptor delta b |
| comp94818_c1 | 6.64 | 0.87 | 2.935576679 | 7.86E-05 | PREDICTED: hypothetical protein LOC100704369 |
| comp102921_c0 | 3.65 | 0.49 | 2.897271329 | 1.08E-04 | UDP glucuronosyltransferase 5 family, polypeptide C1 |
| comp102450_c3 | 1.31 | 0.18 | 2.834712906 | 5.20E-04 | PREDICTED: inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1-like |
| comp100801_c4 | 3.41 | 0.48 | 2.828263655 | 1.43E-03 | Zgc:171445 protein |
| comp99570_c0 | 1.85 | 0.27 | 2.790523239 | 6.79E-04 | 3'-5' exoribonuclease 1 |
| comp102423_c4 | 3.6 | 0.52 | 2.786443479 | 8.77E-04 | Si:dkey-95h12.1 |
| comp102293_c8 | 1.76 | 0.26 | 2.782022898 | 5.03E-04 | PREDICTED: histone-lysine N-methyltransferase MLL3 |
| comp97178_c3 | 5.03 | 0.74 | 2.765069829 | 3.51E-04 | PREDICTED: peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein-like |
| comp99682_c0 | 7.94 | 1.19 | 2.73240364 | 4.10E-04 | Si:dkey-60b12.4 |
| comp100307_c2 | 3.11 | 0.48 | 2.693334075 | 1.95E-03 | Myxovirus (influenza) resistance A |
| comp102642_c0 | 6.26 | 1 | 2.651760005 | 3.85E-04 | Fibroblast growth factor receptor substrate 2a |
| comp102792_c7 | 0.78 | 0.12 | 2.644295994 | 1.42E-03 | formimidoyltransferase-cyclodeaminase |
| comp101642_c3 | 6.84 | 1.11 | 2.619902023 | 3.92E-04 | folliculin-interacting protein 2 |
| comp100801_c1 | 3.49 | 0.57 | 2.605871234 | 2.79E-03 | alpha-2-macroglobulin-like precursor |
| comp102641_c3 | 3.16 | 0.53 | 2.579052117 | 7.44E-04 | thyroid transcription factor 1-associated protein 26 homolog |
| comp102984_c4 | 2.86 | 0.48 | 2.578904186 | 2.55E-03 | tetratricopeptide repeat protein 12 |
| comp69638_c0 | 4.28 | 0.72 | 2.573449756 | 1.22E-03 | Cytokine inducible SH2-containing protein b |
| comp99986_c0 | 12.58 | 2.17 | 2.533978315 | 3.62E-04 | PREDICTED: hypothetical protein LOC100332522 |
| comp101958_c11 | 2.74 | 0.48 | 2.516001329 | 7.40E-04 | stromal membrane-associated protein 1 |
| comp102423_c1 | 2.71 | 0.48 | 2.492214452 | 2.66E-03 | PREDICTED: hypothetical protein LOC100702146 |
| comp102794_c4 | 6.18 | 1.1 | 2.489761023 | 9.66E-04 | Si:ch211-182e10.4 |
| comp101584_c0 | 7.63 | 1.38 | 2.461854403 | 6.15E-04 | probable ribosome biogenesis protein NEP1 |
| comp95531_c0 | 1.69 | 0.31 | 2.456224697 | 2.56E-03 | enolase superfamily 1 |
| comp100778_c2 | 7.65 | 1.41 | 2.43855899 | 6.23E-04 | PREDICTED: uncharacterized protein C6orf150-like |
| comp89409_c2 | 6.49 | 1.2 | 2.435946232 | 2.97E-03 | E3 ubiquitin-protein ligase parkin |
| comp102504_c1 | 7.76 | 1.44 | 2.424652053 | 5.91E-04 | uncharacterized protein LOC692330 |
| comp100578_c1 | 7.81 | 1.46 | 2.421908399 | 6.26E-04 | PREDICTED: probable G-protein coupled receptor-like |
| comp99726_c0 | 2.9 | 0.54 | 2.418950984 | 1.19E-03 | PREDICTED: protein FAM83C-like |
| comp100876_c14 | 10.48 | 1.97 | 2.411192795 | 7.86E-04 | PREDICTED: hypothetical protein LOC100707133 |
| comp88384_c0 | 2.87 | 0.54 | 2.400997934 | 1.92E-03 | Replication factor C (activator 1) 3 |
| comp89473_c0 | 4.71 | 0.9 | 2.394367128 | 1.76E-03 | Transmembrane protein 170A |
| comp102423_c3 | 4.28 | 0.81 | 2.393462901 | 1.43E-03 | PREDICTED: hypothetical protein LOC100703585 |
| comp100309_c0 | 5.05 | 0.96 | 2.39216454 | 1.70E-03 | Rhesus blood group, C glycoprotein a |
| comp100390_c1 | 3.22 | 0.1 | 2.39216454 | 1.70E-03 | LysM, putative peptidoglycan-binding, domain containing 1 |
| comp97714_c1 | 4.14 | 0.79 | 2.380804678 | 2.81E-03 | Sox9a protein |
| comp102725_c1 | 4.37 | 0.86 | 2.352041382 | 1.35E-03 | PREDICTED: hypothetical protein LOC100005456 |
| comp102181_c5 | 5.15 | 1.02 | 2.334066618 | 1.65E-03 | Uncharacterized protein |
| comp102087_c6 | 2.39 | 0.5 | 2.253017148 | 1.68E-03 | suppressor of cytokine signaling 3b |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|--------------|--------------|--------------|----------|---|
| comp102600_c16 | 4.19 | 0.89 | 2.24035387 | 2.40E-03 | PREDICTED: protein jagged-2-like |
| comp102818_c3 | 6.69 | 1.44 | 2.211343688 | 1.49E-03 | conserved hypothetical protein |
| comp101730_c0 | 1.74 | 0.38 | 2.207041996 | 2.99E-03 | nuclear factor, interleukin 3 regulated, member 6 |
| comp102454_c1 | 2.54 | 0.55 | 2.194850964 | 2.41E-03 | ovarian TNF receptor |
| comp102149_c0 | 1753.31 | 384.13 | 2.190412697 | 1.32E-03 | PREDICTED: hypothetical protein LOC556125 |
| comp69987_c0 | 6.11 | 1.35 | 2.182719163 | 2.56E-03 | tether containing UBX domain for GLUT4 |
| comp103013_c11 | 10.8 | 2.42 | 2.15545804 | 1.77E-03 | Myeloid cell leukemia sequence 1b |
| comp102484_c6 | 5.73 | 1.29 | 2.153057175 | 2.37E-03 | cholesteryl ester transfer protein precursor |
| comp101798_c0 | 22.53 | 5.14 | 2.133004444 | 1.85E-03 | hydroxymethylglutaryl-CoA synthase, cytoplasmic |
| comp101939_c4 | 169.91 | 40.48 | 2.069303681 | 2.32E-03 | Ceruloplasmin |
| comp69666_c0 | 308.35 | 75.27 | 2.034382341 | 2.72E-03 | Sepp1a protein |
| comp103171_c0 | 195.29 | 796 | -2.027156846 | 2.81E-03 | novel elastase protein (zgc:637440) |
| comp68911_c0 | 765.1 | 3125.68 | -2.030452641 | 2.76E-03 | Try protein |
| comp103180_c0 | 163.6 | 671.79 | -2.037874358 | 2.69E-03 | PREDICTED: syncollin-like |
| comp102210_c0 | 500.1 | 2087.51 | -2.061493791 | 2.40E-03 | pancreatic elastase precursor |
| comp62899_c0 | 174.73 | 753.77 | -2.109004544 | 1.94E-03 | six-cysteine containing astacin protease 3 precursor |
| comp61984_c0 | 1.63 | 7.04 | -2.113256505 | 2.80E-03 | Uncharacterized protein |
| comp71713_c0 | 12.89 | 56.21 | -2.124195595 | 1.87E-03 | glucokinase |
| comp115558_c0 | 2.87 | 12.53 | -2.126989962 | 3.07E-03 | fep15 selenoprotein precursor |
| comp102032_c6 | 1.09 | 4.79 | -2.136963066 | 2.19E-03 | PREDICTED: c-Jun-amino-terminal kinase-interacting protein 4-like |
| comp102458_c14 | 6.85 | 30.38 | -2.149483538 | 1.76E-03 | steroid hormone receptor ERR1 |
| comp102451_c3 | 6.6 | 29.44 | -2.156706265 | 1.64E-03 | putative hexokinase HKDC1 |
| comp62088_c0 | 10.95 | 48.83 | -2.15730424 | 1.90E-03 | PREDICTED: elastase inhibitor-like |
| comp100340_c0 | 4.94 | 22.06 | -2.158703255 | 1.77E-03 | squalene synthase |
| comp103030_c2 | 0.79 | 3.55 | -2.165308674 | 2.09E-03 | HEAT repeat-containing protein 1 |
| comp102715_c4 | 1.39 | 6.23 | -2.169065254 | 1.98E-03 | PREDICTED: im:7147678 |
| comp64707_c0 | 4.5 | 20.54 | -2.189875445 | 1.56E-03 | probable phosphatase phospho1 |
| comp102051_c0 | 8.66 | 40.14 | -2.212896955 | 1.30E-03 | glutathione S-transferase theta-like |
| comp100511_c0 | 18.78 | 87.63 | -2.222350104 | 1.21E-03 | poly(U)-specific endoribonuclease-A precursor |
| comp102431_c0 | 5.5 | 26.35 | -2.259400273 | 1.11E-03 | PREDICTED: hypothetical protein LOC557984 |
| comp103680_c0 | 39.68 | 192.49 | -2.278226163 | 9.08E-04 | Si:dkey-14d8.7 protein |
| comp102458_c8 | 3.97 | 19.3 | -2.280260802 | 1.36E-03 | estrogen-related receptor alpha |
| comp101902_c0 | 6.28 | 30.99 | -2.30267668 | 9.04E-04 | DNase I |
| comp102936_c9 | 2.41 | 11.91 | -2.304175853 | 8.63E-04 | malic enzyme 1, NADP(+)-dependent, cytosolic |
| comp102546_c1 | 0.43 | 2.14 | -2.311099788 | 1.55E-03 | Interleukin enhancer binding factor 3b |
| comp71193_c0 | 0.81 | 4.06 | -2.322499089 | 1.35E-03 | protein phosphatase 1 regulatory subunit 3B |
| comp100850_c0 | 351.26 | 1763.83 | -2.328081045 | 6.85E-04 | chymotrypsin B1 precursor |
| comp103032_c0 | 0.97 | 4.89 | -2.332728222 | 2.51E-03 | PREDICTED: EMILIN-3 |
| comp100683_c0 | 0.26 | 1.33 | -2.346273655 | 2.47E-03 | cysteinyl-tRNA synthetase, cytoplasmic |
| comp102908_c10 | 1.01 | 5.19 | -2.361560904 | 3.02E-03 | Si:dkeyp-2c8.3 |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|--------------|--------------|--------------|----------|---|
| comp102905_c13 | 2.48 | 12.78 | -2.36442847 | 7.85E-04 | mitochondrial 39S ribosomal protein l16 |
| comp102530_c7 | 4.94 | 25.53 | -2.371096909 | 6.38E-04 | heparin cofactor 2 precursor |
| comp97270_c0 | 0.61 | 3.16 | -2.381189711 | 1.30E-03 | PREDICTED: hypothetical protein LOC100001663 |
| comp89363_c0 | 0.34 | 1.8 | -2.415246436 | 2.94E-03 | dehydrodolichyl diphosphate synthase |
| comp102127_c8 | 0.75 | 4.11 | -2.446715728 | 1.43E-03 | novel protein similar to vertebrate COMM domain containing 9 (COMMD9) |
| comp102950_c1 | 0.47 | 2.59 | -2.449201757 | 7.86E-04 | Chloride channel 2 |
| comp103123_c0 | 218.85 | 1200.42 | -2.455500558 | 3.65E-04 | Amylase, alpha 2A; pancreatic |
| comp101235_c1 | 62.8 | 345.94 | -2.461718237 | 3.53E-04 | PREDICTED: fatty acid synthase-like |
| comp103032_c10 | 0.78 | 4.31 | -2.475517093 | 1.85E-03 | Elastin microfibril interfacier 3a |
| comp97726_c1 | 1.23 | 6.88 | -2.486051256 | 1.20E-03 | Proteasome (prosome, macropain) subunit, beta type, 10 |
| comp89158_c1 | 0.95 | 5.38 | -2.502653223 | 6.86E-04 | PREDICTED: calmegin-like |
| comp102176_c10 | 3.82 | 0 | -2.517647961 | 7.75E-04 | PREDICTED: hypothetical protein LOC100535924 |
| comp101289_c0 | 0.28 | 1.59 | -2.521283793 | 1.31E-03 | interleukin 7 receptor precursor |
| comp66504_c0 | 0.89 | 5.13 | -2.523411783 | 1.88E-03 | PREDICTED: microfibril-associated glycoprotein 4-like |
| comp103534_c0 | 49.79 | 289.66 | -2.54028155 | 2.44E-04 | chymotrypsin-like precursor |
| comp88432_c0 | 1.54 | 9.21 | -2.576653805 | 4.17E-04 | Fgf19 protein |
| comp102964_c0 | 2.19 | 13.19 | -2.587761059 | 2.38E-04 | uncharacterized protein LOC553197 |
| comp102615_c10 | 61.75 | 377.48 | -2.611993436 | 1.66E-04 | Cpb1 protein, partial |
| comp102803_c0 | 62.54 | 384.35 | -2.61967196 | 1.59E-04 | Cel.2 protein |
| comp94017_c3 | 0.56 | 3.47 | -2.622947457 | 2.47E-03 | uncharacterized protein LOC393586 |
| comp102620_c7 | 0.27 | 1.65 | -2.631568212 | 1.83E-03 | protein SSXT |
| comp101599_c0 | 0.24 | 1.49 | -2.657404962 | 6.98E-04 | PREDICTED: dihydroxyacetone phosphate acyltransferase-like |
| comp93327_c1 | 26.79 | 171.69 | -2.680027069 | 1.21E-04 | Hsp90a.2 protein |
| comp100272_c0 | 0.44 | 2.84 | -2.691603817 | 5.21E-04 | PREDICTED: tyrosine-protein kinase BAZ1B |
| comp100350_c0 | 0.63 | 4.12 | -2.719089046 | 2.83E-04 | protein phosphatase 1, regulatory (inhibitor) subunit 14Ab |
| comp93327_c0 | 34.06 | 224.4 | -2.7198656 | 9.86E-05 | heat shock protein 90, alpha (cytosolic), class A member 1, tandem duplicate 2 |
| comp93706_c0 | 0.35 | 2.35 | -2.752897531 | 8.63E-04 | Transcription elongation factor, mitochondrial |
| comp93536_c0 | 0.58 | 3.95 | -2.756698846 | 1.84E-03 | PREDICTED: hypothetical protein LOC100150934 |
| comp101238_c1 | 0.39 | 2.63 | -2.764894846 | 6.72E-04 | suppressor of G2 allele of SKP1 homolog |
| comp101398_c0 | 0.44 | 3.15 | -2.827367831 | 2.22E-04 | PREDICTED: nucleotide exchange factor SIL1-like |
| comp102173_c5 | 2.47 | 17.76 | -2.848157098 | 5.31E-05 | PREDICTED: nodal modulator 1 |
| comp100723_c0 | 0.04 | 0.31 | -2.851233082 | 2.76E-03 | G/T mismatch-specific thymine DNA glycosylase |
| comp93327_c2 | 5.29 | 39.98 | -2.919385021 | 7.45E-05 | PREDICTED: heat shock protein HSP 90-alpha-like |
| comp101217_c0 | 0.68 | 5.19 | -2.923949713 | 1.37E-04 | PREDICTED: uncharacterized protein LOC575262 |
| comp100319_c0 | 0.28 | 2.14 | -2.925292273 | 2.25E-04 | PREDICTED: hypothetical protein LOC558212 |
| comp101669_c0 | 0.12 | 0.93 | -2.932418175 | 1.31E-03 | PREDICTED: e3 ubiquitin/ISG15 ligase TRIM25 |
| comp69063_c0 | 0.46 | 3.55 | -2.942565391 | 1.82E-03 | uncharacterized protein LOC793030 precursor |
| comp101051_c0 | 0.69 | 5.42 | -2.973769627 | 1.32E-04 | ubiquitin C-terminal hydrolase L1 |
| comp100438_c0 | 3.38 | 26.77 | -2.985973242 | 2.49E-05 | Ddx5 protein |
| comp102982_c3 | 0.12 | 1.03 | -3.050368681 | 3.45E-04 | replication protein A 70 kDa DNA-binding subunit |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|--------------|----------|---|
| comp69999_c1 | 0.38 | 3.15 | -3.054379394 | 4.97E-04 | polyadenylate-binding protein 4 |
| comp102748_c0 | 1.97 | 17.5 | -3.15481999 | 1.19E-05 | DnaJ (Hsp40) homolog, subfamily B, member 1 |
| comp102507_c0 | 0.46 | 4.1 | -3.162359597 | 1.91E-05 | ER degradation-enhancing alpha-mannosidase-like 1 |
| comp91343_c0 | 0.29 | 2.66 | -3.201483688 | 2.55E-03 | GTP binding protein 1, like |
| comp102526_c5 | 0.68 | 6.3 | -3.211687468 | 2.25E-05 | guanylate binding protein 4 |
| comp89910_c0 | 1.34 | 13.12 | -3.286315718 | 1.05E-05 | mid1-interacting protein 1-like |
| comp103002_c6 | 0.42 | 4.11 | -3.301019362 | 2.31E-04 | PREDICTED: hypothetical protein LOC100498431 |
| comp99919_c0 | 0.19 | 1.89 | -3.301019362 | 1.72E-03 | Zinc finger protein 503 |
| comp102119_c5 | 0.38 | 3.77 | -3.303455661 | 1.49E-05 | PREDICTED: plexin-C1 |
| comp102659_c8 | 0.66 | 6.67 | -3.347015692 | 1.18E-05 | PREDICTED: receptor-type tyrosine-protein phosphatase zeta |
| comp102832_c7 | 25.17 | 257.08 | -3.352569943 | 2.82E-06 | PREDICTED: maltase-glucoamylase, intestinal |
| comp100688_c0 | 0.36 | 3.83 | -3.394128766 | 1.18E-03 | gamma-glutamyl cyclotransferase a |
| comp102786_c1 | 0.91 | 9.64 | -3.411500326 | 3.38E-06 | PREDICTED: lon protease homolog, mitochondrial |
| comp102401_c0 | 0.3 | 3.35 | -3.462783801 | 6.81E-06 | PREDICTED: baculoviral IAP repeat-containing protein 6 |
| comp102538_c1 | 0.19 | 2.17 | -3.502653223 | 2.81E-03 | PREDICTED: phosphofurin acidic cluster sorting protein 2-like |
| comp93835_c1 | 0.23 | 2.56 | -3.502653223 | 8.70E-05 | conserved hypothetical protein |
| comp97468_c1 | 0.28 | 3.24 | -3.533680119 | 2.56E-04 | superoxide dismutase-like |
| comp101358_c1 | 0.23 | 2.78 | -3.622947457 | 1.77E-03 | tripartite motif containing 35 |
| comp99683_c0 | 0.2 | 2.5 | -3.644269245 | 2.28E-05 | cleavage and polyadenylation specificity factor subunit 6 |
| comp102656_c0 | 0.22 | 2.82 | -3.648951473 | 8.99E-06 | PREDICTED: hypothetical protein LOC100698500 |
| comp60482_c0 | 0.23 | 3.17 | -3.786446189 | 9.21E-04 | IGF |
| comp89158_c0 | 0.4 | 5.6 | -3.792817277 | 2.45E-05 | Si:ch211-274f20.2 |
| comp102529_c8 | 1.33 | 18.57 | -3.80445941 | 4.26E-07 | trans-2,3-enoyl-CoA reductase |
| comp115872_c0 | 0.99 | 14.84 | -3.907198349 | 3.32E-06 | metallothionein B-like |
| comp101706_c1 | 0.28 | 4.36 | -3.964637478 | 4.73E-07 | protein NipSnap homolog 2 |
| comp102184_c1 | 3.91 | 61.24 | -3.969076109 | 8.08E-08 | PREDICTED: maltase-glucoamylase, intestinal-like |
| comp102942_c7 | 0.15 | 2.59 | -4.112257718 | 2.61E-05 | PREDICTED: hypothetical protein LOC100692678 |
| comp89027_c0 | 0.39 | 6.92 | -4.151318735 | 4.48E-08 | PREDICTED: uncharacterized protein LOC763830, partial |
| comp98089_c0 | 6.06 | 112.25 | -4.21203887 | 2.32E-08 | apolipoprotein D-like precursor |
| comp92587_c0 | 0.1 | 1.82 | -4.22701878 | 2.29E-03 | Solute carrier family 28 |
| comp98365_c5 | 0.11 | 2.25 | -4.301019362 | 1.74E-03 | growth hormone receptor |
| comp102403_c1 | 0.06 | 1.3 | -4.35459414 | 1.34E-05 | ELMO/CED-12 domain containing 2 precursor |
| comp70923_c2 | 0.14 | 2.83 | -4.37140869 | 1.33E-03 | PREDICTED: erythroid differentiation-related factor 1-like |
| comp102628_c2 | 2.38 | 49.59 | -4.382899911 | 6.70E-09 | heat shock 70 kDa protein |
| comp101759_c0 | 0.04 | 0.82 | -4.430485567 | 1.13E-04 | PREDICTED: probable ergosterol biosynthetic protein 28-like |
| comp101274_c13 | 0.12 | 2.67 | -4.506120051 | 2.20E-05 | PREDICTED: hypothetical protein LOC560266 |
| comp96421_c3 | 0.19 | 4.48 | -4.546775776 | 1.85E-07 | uncharacterized protein LOC567731 precursor |
| comp101181_c0 | 0.23 | 6.66 | -4.847549117 | 1.40E-09 | PREDICTED: vitellogenin |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|--------------|--------------|--------------|----------|--|
| comp83201_c0 | 0.34 | 10.07 | -4.885981863 | 1.04E-08 | Retinoic acid receptor responder protein 3 |
| comp94015_c0 | 0.12 | 4.28 | -5.188544633 | 9.85E-07 | PREDICTED: UHRF1-binding protein 1-like |
| comp93355_c3 | 0.07 | 2.59 | -5.264493486 | 2.69E-05 | unnamed protein product |
| comp101279_c2 | 0.22 | 8.49 | -5.267673548 | 2.45E-10 | rho-related gtp-binding protein rhoc |
| comp100318_c1 | 0.05 | 2.26 | -5.438522886 | 1.14E-05 | myosin heavy chain |
| comp101504_c1 | 0.03 | 1.67 | -5.740474884 | 5.79E-07 | SRF6-like |
| comp69517_c0 | 0.59 | 31.7 | -5.752345744 | 2.92E-12 | aspartyl-tRNA synthetase, cytoplasmic |
| comp102814_c2 | 0.03 | 1.62 | -5.759816224 | 4.03E-07 | putative L-aspartate dehydrogenase |
| comp102544_c0 | 0.01 | 1.3 | -6.504942325 | 4.54E-07 | PREDICTED: phosphatidylinositol 3-kinase regulatory subunit alpha isoform 1 |
| comp101847_c9 | 0.19 | 21.71 | -6.861734316 | 3.85E-09 | Cytochrome P450, family 2, subfamily K, polypeptide 6 |
| comp102894_c4 | 0.08 | 10.92 | -7.025669634 | 9.43E-14 | PREDICTED: hypothetical protein LOC100710859 |
| comp99707_c1 | 0.15 | 20.31 | -7.087615724 | 9.61E-10 | hypothetical protein SERLA73DRAFT_67379 |
| comp70577_c0 | 0.1 | 15.4 | -7.212710944 | 4.29E-12 | PREDICTED: hypothetical protein LOC100333953 |
| comp102199_c0 | 0.36 | 56.41 | -7.292632585 | 3.12E-16 | carboxypeptidase A precursor |
| comp101826_c2 | 0.02 | 3.35 | -7.696151222 | 9.81E-13 | serine/threonine-protein kinase Sgk1 |
| comp102799_c4 | 0 | 0.96 | -11.03233839 | 1.65E-04 | zgc:123060 (ZFIN) |
| comp102863_c0 | 0 | 2.03 | -13.08221512 | 1.12E-11 | BSD domain containing 1 |
| comp102301_c13 | 0 | 2.19 | -29.10443731 | 2.86E-03 | probable E3 ubiquitin-protein ligase MYCBP2 |
| comp56672_c0 | 0 | 1.93 | -29.10443731 | 2.86E-03 | dnaJ homolog subfamily C member 17 |
| comp68552_c0 | 0 | 1.78 | -29.10443731 | 2.86E-03 | uncharacterized protein LOC563088 |
| comp92255_c2 | 0 | 1.86 | -29.10443731 | 2.86E-03 | novel protein similar to vertebrate IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) |
| comp96783_c2 | 0 | 1.75 | -29.10443731 | 2.86E-03 | myosin light chain kinase 3 |
| comp99266_c0 | 0 | 1.75 | -29.10443731 | 2.86E-03 | PREDICTED: early endosome antigen 1 |
| comp101708_c0 | 0 | 0.41 | -29.11659337 | 2.00E-03 | solute carrier family 25 member 47-B |
| comp102975_c0 | 0 | 0.3 | -29.21032165 | 2.00E-03 | cysteine and histidine-rich domain-containing protein 1 |
| comp90049_c0 | 0 | 1.72 | -29.21135252 | 2.00E-03 | si:dkeyp-52c3.2 |
| comp95917_c1 | 0 | 1.71 | -29.21135252 | 2.00E-03 | PREDICTED: trinucleotide repeat-containing gene 6B protein |
| comp96313_c2 | 0 | 2.12 | -29.21135252 | 2.00E-03 | putative transcription factor COE1 |
| comp101498_c2 | 0 | 0.74 | -29.32238383 | 1.01E-03 | uncharacterized protein LOC100037365 |
| comp80071_c2 | 0 | 2.94 | -29.40399759 | 1.01E-03 | gamma-glutamylcyclotransferase precursor |
| comp102784_c0 | 0 | 0.99 | -29.44751709 | 7.27E-04 | Transposable element Tcb1 transposase |
| comp98627_c2 | 0 | 1.31 | -29.46922522 | 7.27E-04 | Zgc:110391 protein, partial |
| comp71302_c0 | 0 | 2.37 | -29.49146044 | 7.27E-04 | zgc:101901 |
| comp98392_c1 | 0 | 1.83 | -29.49146044 | 7.27E-04 | Zinc finger, BED-type containing 1 |
| comp97430_c0 | 0 | 1.09 | -29.50497524 | 5.30E-04 | Salt-inducible kinase 2a |
| comp100878_c0 | 0 | 0.73 | -29.54967505 | 5.30E-04 | PREDICTED: hypothetical protein LOC100693263 |
| comp96436_c0 | 0 | 2.39 | -29.57392226 | 5.30E-04 | ORF2-encoded protein |
| comp98885_c2 | 0 | 1.62 | -29.5811181 | 5.30E-04 | PREDICTED: sorbin and SH3 domain-containing protein 2 |
| comp102854_c2 | 0 | 0.08 | -29.63050612 | 3.91E-04 | E3 ubiquitin-protein ligase HECTD1 |
| comp101583_c0 | 0 | 0.89 | -29.63972465 | 3.91E-04 | PREDICTED: hypothetical protein LOC100697633 |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|--------------|----------|--|
| comp102412_c2 | 0 | 3.61 | -29.65192511 | 3.91E-04 | PREDICTED: microfibril-associated glycoprotein 4 |
| comp56282_c0 | 0 | 2.26 | -29.65192511 | 3.91E-04 | invariant chain like protein 1 |
| comp93358_c0 | 0 | 1.8 | -29.65192511 | 3.91E-04 | probable alpha-ketoglutarate-dependent dioxygenase ABH6 |
| comp102966_c5 | 0 | 0.25 | -29.67676733 | 2.91E-04 | RAC-alpha serine/threonine-protein kinase |
| comp102570_c4 | 0 | 0.39 | -29.7601414 | 2.18E-04 | isobutyryl-CoA dehydrogenase, mitochondrial |
| comp102114_c11 | 0 | 0.48 | -29.80521846 | 1.65E-04 | PREDICTED: cell death activator CIDE-A-like |
| comp98762_c1 | 0 | 1.37 | -29.83026235 | 1.65E-04 | Wilms tumor suppressor protein 1b |
| comp89799_c0 | 0 | 1.05 | -29.93818373 | 9.64E-05 | transcription elongation factor B polypeptide 1 |
| comp102835_c2 | 0 | 0.87 | -29.95551361 | 9.64E-05 | PREDICTED: band 4.1-like protein 2-like, partial |
| comp102865_c13 | 0 | 0.88 | -29.97446053 | 9.64E-05 | PREDICTED: centromere protein V |
| comp91465_c0 | 0 | 3.39 | -29.9889601 | 9.64E-05 | zona pellucida glycoprotein 2.1 |
| comp97205_c0 | 0 | 2.55 | -29.9889601 | 9.64E-05 | PREDICTED: transposon TX1 uncharacterized 149 kDa protein-like |
| comp90899_c1 | 0 | 2.78 | -30.04785378 | 7.45E-05 | PREDICTED: hypothetical protein LOC568313 |
| comp97112_c0 | 0 | 0.46 | -30.06335135 | 5.79E-05 | Aldehyde dehydrogenase 9 family, member A1b |
| comp102593_c7 | 0 | 3.9 | -30.10443731 | 5.79E-05 | hypothetical protein MYCTH_2071514 |
| comp98392_c0 | 0 | 2.37 | -30.1588851 | 4.53E-05 | PREDICTED: hypothetical protein LOC100700880 |
| comp102406_c2 | 0 | 0.97 | -30.28076009 | 2.25E-05 | MAP7 domain-containing protein 1 |
| comp102473_c3 | 0 | 1.13 | -30.29005993 | 2.25E-05 | PREDICTED: wolframin |
| comp102583_c12 | 0 | 1.74 | -30.30220595 | 2.25E-05 | PREDICTED: leukocyte elastase inhibitor isoform 1 |
| comp99076_c1 | 0 | 1.86 | -30.31088819 | 2.25E-05 | uncharacterized protein LOC791929 |
| comp99905_c1 | 0 | 2.96 | -30.31088819 | 2.25E-05 | PREDICTED: suppressor of tumorigenicity 14 protein homolog |
| comp93835_c2 | 0 | 2.98 | -30.3581939 | 1.80E-05 | PREDICTED: uncharacterized protein LOC100890688 |
| comp89898_c0 | 0 | 1.09 | -30.3931366 | 1.45E-05 | PREDICTED: hypothetical protein LOC100534830 |
| comp103011_c7 | 0 | 2.82 | -30.40399759 | 1.45E-05 | PREDICTED: hypothetical protein LOC553357 |
| comp95528_c0 | 0 | 2.95 | -30.40399759 | 1.45E-05 | MHC class II invariant chain Ii |
| comp101618_c7 | 0 | 0.41 | -30.43035504 | 1.17E-05 | oxysterol binding protein-like 3a |
| comp92178_c1 | 0 | 1.28 | -30.50623579 | 7.72E-06 | integrator complex subunit 10 |
| comp102522_c0 | 0 | 0.7 | -30.56023239 | 6.32E-06 | uncharacterized protein LOC100141491 precursor |
| comp102274_c0 | 0 | 0.44 | -30.56346532 | 6.32E-06 | PREDICTED: protein FAM13A isoform 1 |
| comp102156_c16 | 0 | 1.63 | -30.58271224 | 6.32E-06 | PREDICTED: oxysterol-binding protein-related protein 10-like, partial |
| comp102014_c2 | 0 | 0.3 | -30.5957971 | 5.19E-06 | protein transport protein Sec24C |
| comp102006_c3 | 0 | 3.44 | -30.59658632 | 5.19E-06 | PREDICTED: hypothetical protein LOC100332181 |
| comp99707_c0 | 0 | 7.65 | -30.79631502 | 2.05E-06 | Zgc:158463 |
| comp101827_c2 | 0 | 0.59 | -30.80794696 | 1.72E-06 | Eukaryotic translation initiation factor 5 |
| comp100128_c4 | 0 | 0.74 | -30.84627763 | 1.45E-06 | fat storage-inducing transmembrane protein 2 |
| comp97699_c1 | 0 | 3.06 | -30.86342921 | 1.45E-06 | Zgc:174680 |
| comp102379_c11 | 0 | 0.93 | -30.88264589 | 1.22E-06 | Tryptophan 2,3-dioxygenase a |
| comp99142_c1 | 0 | 0.88 | -30.88974642 | 1.22E-06 | NEDD8 |
| comp60157_c0 | 0 | 3.5 | -30.89585069 | 1.22E-06 | uncharacterized protein LOC100327252 precursor |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|-----------|-----------|--------------|----------|--|
| comp102058_c22 | 0 | 1.12 | -30.96562922 | 8.76E-07 | PREDICTED: ribosomal protein S6 kinase beta-1-like |
| comp102551_c5 | 0 | 0.68 | -30.98233254 | 7.45E-07 | predicted protein |
| comp96828_c2 | 0 | 2.49 | -31.04785378 | 5.43E-07 | PREDICTED: protein transport protein Sec31A |
| comp99967_c1 | 0 | 1.43 | -31.13382224 | 3.45E-07 | PREDICTED: pleckstrin homology domain-containing family G member 5 |
| comp102593_c18 | 0 | 8.46 | -31.1588851 | 2.97E-07 | hypothetical protein PABG_06807 |
| comp102492_c1 | 0 | 1.21 | -31.17983829 | 2.57E-07 | PREDICTED: collagen alpha-1(XII) chain-like |
| comp93355_c6 | 0 | 3.41 | -31.18535731 | 2.57E-07 | PREDICTED: LOW QUALITY PROTEIN: wu:f104e06 |
| comp92949_c0 | 0 | 2.55 | -31.23688761 | 1.94E-07 | PREDICTED: hypothetical protein LOC100537292 |
| comp101409_c1 | 0 | 2.02 | -31.57872358 | 2.87E-08 | DNA damage-inducible transcript 4 protein |
| comp102519_c6 | 0 | 1.73 | -31.63243151 | 2.04E-08 | PREDICTED: hypothetical protein LOC100538074 |
| comp101021_c0 | 0 | 5.2 | -31.75396434 | 9.62E-09 | PREDICTED: urokinase plasminogen activator surface receptor-like |
| comp88529_c1 | 0 | 2.22 | -31.75714442 | 9.62E-09 | gap junction beta-6 protein |
| comp102665_c1 | 0 | 0.64 | -31.81525434 | 7.08E-09 | PREDICTED: protein cordon-bleu |
| comp102794_c5 | 0 | 1.06 | -31.8563624 | 5.80E-09 | abhydrolase domain-containing protein 4 |
| comp89370_c0 | 0 | 4.99 | -31.86277329 | 5.26E-09 | UPF0542 protein C5orf43 homolog |
| comp102887_c12 | 0 | 1.05 | -31.91669856 | 3.94E-09 | PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1-like |
| comp102620_c6 | 0 | 1.34 | -31.93272518 | 3.58E-09 | nucleolysin TIAR |
| comp101302_c0 | 0 | 13.32 | -32.01870744 | 2.07E-09 | cytochrome oxidase subunit I (mitochondrion) |
| comp102816_c11 | 0 | 1.63 | -32.06363678 | 1.59E-09 | Activated leukocyte cell adhesion molecule |
| comp100712_c0 | 0 | 2.99 | -32.11659337 | 1.13E-09 | protein IMPACT |
| comp102652_c1 | 0 | 1.45 | -32.1837826 | 7.51E-10 | mucolipin-2 |
| comp100875_c0 | 0 | 1.45 | -32.30908369 | 3.47E-10 | CD2-associated protein |
| comp102883_c1 | 0 | 1.23 | -32.33556247 | 2.99E-10 | complement receptor-like protein precursor |
| comp102724_c0 | 0 | 1.13 | -32.3398109 | 2.99E-10 | PREDICTED: transcriptional repressor NF-X1-like |
| comp102106_c0 | 0 | 2.77 | -32.34381185 | 2.99E-10 | Rnu3ip2 protein |
| comp102866_c2 | 0 | 2.14 | -32.35259844 | 2.78E-10 | PREDICTED: ankyrin repeat and SAM domain-containing protein 1A-like |
| comp102450_c7 | 0 | 1.79 | -32.3909773 | 2.24E-10 | 45 kDa calcium-binding protein precursor |
| comp102566_c14 | 0 | 3.23 | -32.4246998 | 1.81E-10 | uncharacterized protein LOC559970 |
| comp101818_c1 | 0 | 1.45 | -32.46198932 | 1.38E-10 | uncharacterized protein LOC564531 |
| comp102593_c22 | 0 | 14.52 | -32.47008678 | 1.29E-10 | hypothetical protein AN5245.2 |
| comp96751_c0 | 0 | 1.26 | -32.49833924 | 1.13E-10 | PREDICTED: pantothenate kinase 4-like |
| comp102462_c1 | 0 | 1.41 | -32.56548223 | 7.15E-11 | PREDICTED: protein sidekick-1 |
| comp126569_c0 | 0 | 6.74 | -32.62316611 | 5.23E-11 | ATP synthase F0 subunit 6 (mitochondrion) |
| comp102651_c0 | 0 | 3.18 | -32.66336425 | 3.86E-11 | PREDICTED: si:ch211-197g15.7 |
| comp101847_c3 | 0 | 20.27 | -32.82185011 | 1.47E-11 | uncharacterized protein LOC100170784 |
| comp98419_c0 | 0 | 6.87 | -32.82185011 | 1.47E-11 | cytochrome b |
| comp99666_c0 | 0 | 4.89 | -32.89504897 | 9.12E-12 | COP9 signalosome complex subunit 4 |
| comp89974_c0 | 0 | 7.01 | -32.9984715 | 4.76E-12 | ATPase, H ⁺ transporting, V1 subunit F |

Table S1. *Cont.*

| Gene ID | RSEM (FW) | RSEM (SM) | Fold Change | p-Value | Gene Name |
|----------------|--------------|--------------|--------------|----------|---|
| comp101806_c1 | 0 | 4.16 | -33.00532269 | 4.54E-12 | PREDICTED: FAST kinase domain-containing protein 5-like |
| comp125637_c0 | 0 | 12.37 | -33.06220908 | 3.11E-12 | cytochrome oxidase subunit II |
| comp100614_c4 | 0 | 3.71 | -33.07217346 | 2.97E-12 | Protein tyrosine phosphatase, receptor type, C |
| comp102940_c2 | 0 | 1.83 | -33.2955383 | 6.90E-13 | UHRF1-binding protein 1-like |
| comp102395_c1 | 0 | 5.76 | -33.31130891 | 6.12E-13 | PREDICTED: zinc-binding protein A33-like |
| comp102593_c16 | 0 | 15.14 | -33.44839171 | 2.48E-13 | transcript antisense to ribosomal RNA protein |
| comp102514_c1 | 0 | 5.67 | -33.50739032 | 1.68E-13 | Uncharacterized protein |
| comp99321_c0 | 0 | 4.59 | -33.59238863 | 9.79E-14 | V-fos FBJ murine osteosarcoma viral oncogene homolog |
| comp99121_c0 | 0 | 15.98 | -33.7482935 | 3.50E-14 | Cytochrome c oxidase III, mitochondria |
| comp102592_c0 | 0 | 2.32 | -33.77202381 | 2.93E-14 | G protein-coupled receptor 56 precursor |
| comp102167_c10 | 0 | 4.32 | -34.00881024 | 6.16E-15 | novel protein similar to vertebrate gliacolin (C1Q) |
| comp101302_c1 | 0 | 20.44 | -34.05145602 | 4.59E-15 | cytochrome oxidase subunit I (mitochondrion) |
| comp102901_c1 | 0 | 3.82 | -34.13215621 | 2.67E-15 | PREDICTED: Hypothetical protein LOC100004401 |
| comp99594_c0 | 0 | 4.24 | -34.13548634 | 2.61E-15 | phosphatidylinositide phosphatase SAC1-B |
| comp101702_c0 | 0 | 20.99 | -34.19516048 | 1.78E-15 | Ependymin |
| comp97193_c3 | 0 | 6.41 | -34.43074233 | 3.66E-16 | acyl-CoA-binding domain-containing protein 5A |
| comp102884_c12 | 0 | 7.05 | -34.52532389 | 1.94E-16 | E3 ubiquitin-protein ligase LRSAM1 |
| comp102221_c5 | 0 | 5.19 | -34.5539225 | 1.57E-16 | G protein-coupled receptor 161 |
| comp102354_c4 | 0 | 14.11 | -34.77152155 | 3.65E-17 | DDB1- and CUL4-associated factor 13 |
| comp70508_c0 | 0 | 9.82 | -34.84278945 | 2.23E-17 | β -centractin |
| comp99354_c0 | 0 | 14.7 | -35.45492096 | 3.46E-19 | casein kinase 2 α 1 |
| comp102644_c2 | 0 | 29.27 | -36.0859036 | 4.61E-21 | Golgi transport 1 homolog B |

Table S2. Primers used for qRT-PCR validation.

| Gene ID | Gene Name | Primers Sequences | |
|----------------|----------------|-----------------------|-----------------------|
| | | Sense 5'–3' | Anti-Sense 5'–3' |
| comp103013_c11 | MCL1b | TCACACGGTTCTACTGTGTG | CATCATGTTCCGATCCTTCC |
| comp102279_c14 | PPM1K | TCAGCTATCGCAGATGACCG | GTGAAGATGCCTGGCTAACG |
| comp102791_c0 | C4 | AGGCACTGAACAGCAGATAG | TGCTTCCTCTAGATTGCCAC |
| comp102564_c2 | STAT6 | TTCAGAACTGCCGACAAACG | GAAGAAGCTGCAAACGCTTC |
| comp93418_c0 | YAF2 | GGAAGTGACAGTGGGAGATC | GTGAGACTCTCCGTTGAGTG |
| comp101330_c3 | SDR16C5 | TGAAGCGTGAGGTTGGTGAC | GATGAGTCCAGCAGAACTCG |
| comp102898_c4 | MCM5 | GGTCGTGATGGTCTTTGATG | GAGCAGCAGACCATCTCTAT |
| comp89409_c2 | Park2 | AGAACGGTGGCTGTATGCAC | CCCATTGGTTCCATTCCCTG |
| comp102628_c2 | Hap70 | AAGAGAACCCTCTCCTCCAG | GCTTTCTCCACAGGCTCAAG |
| comp102986_c4 | Cyp2p9 | GGTGAAGAGAAAGTGAAGCGC | GATCACTTCCTGGATGCTGAG |
| comp102087_c6 | Soes3b | ATGAGGCAGCTGGTCCCGTT | GGAGACCTCTTCGAAGGTCC |
| comp102484_c6 | CETP | GACATCTCTGTGACCTCTTC | CATTAAGGAGTCAAGGAGCG |
| comp60482_c0 | IGF | GTCAGCCACCTCAGTTTCCT | TCCAGTGTGAACGCTAACGC |
| comp102814_c2 | ASPDH | AGTGGAGGTGTGTCATCCAC | CCACCCATAATGCACCACT |
| comp101847_c9 | Cyp2k6 | TTGACACAACCTCAGCCTGTG | TAAGCTCGTCTGACCATGTG |
| comp102544_c0 | PIK3 | AACCAGGGATGTGTGCTGGT | TCAGGGACAGCAGCAAACCT |
| comp99124_c0 | Adm2a | AACATGAGGCTCTCCCTGTG | GGCGCTAATCTGCTCAAAGG |
| comp102572_c6 | C3c | AATCCTTGACACCACCCGC | CGAGCAGCACATGGCTGATT |
| comp98419_c0 | Cytb | GGGAGAACAGTGCTAGTAGT | AACCATCATCCACCTGCTGT |
| comp102860_c0 | IL13RA1 | GGCTTGTGAGGCACATTGTT | ATCTCTTCCACCACAGAGT |
| Reference | β -actin | TGCAAAGCCGGATTTCGCTGG | AGTTGGTGACAATACCGTGC |