**Table S4.** List of differentially expressed genes that could be manually assigned into major functional groups. Up-regulated genes are in red, while down-regulated genes are in blue font.

| Mannually annotated group   | Probe Set ID                                   | Gene description  | Fold change      |
|---|--|---|------------------|
| Cell death/growth/differentiation                                     | Gga.5710.2.S1_a_at                             | HtrA serine peptidase 3   | 16.757           |
| Cell death/growth/differentiation                                     | Gga.5164.1.S2_at                               | BCL2-related protein A1   | 13.157           |
| Cell death/growth/differentiation                                     | Gga.2582.1.S1_at<br>Gga.1247.1.S2 at           | transforming growth factor, beta-induced, 68kDa   | 13.131<br>11.957 |
| Cell death/growth/differentiation Cell death/growth/differentiation   | Gga.744.1.S1 at                                | B6.1 GATA binding protein 3   | 9.192            |
| Cell death/growth/differentiation                                     | Gga.3179.1.S2 at                               | brain abundant, membrane attached signal protein 1  | 8.359            |
| Cell death/growth/differentiation                                     | GgaAffx.12413.1.S1 at                          | RNA binding motif protein 38  | 6.574            |
| Cell death/growth/differentiation                                     | Gga.5164.1.S1_at                               | BCL2-related protein A1   | 5.638            |
| Cell death/growth/differentiation                                     | Gga.11726.1.S1_a_at                            | Growth arrest and DNA-damage-inducible, gamma   | 5.443            |
| Cell death/growth/differentiation                                     | GgaAffx.21663.1.S1_s_at                        | hepatoma-derived growth factor, related protein 3   | 5.272            |
| Cell death/growth/differentiation                                     | Gga.7539.1.S1_at                               | forkhead box L2   | 4.678<br>4.173   |
| Cell death/growth/differentiation Cell death/growth/differentiation   | Gga.4328.1.S1_at<br>Gga.9179.1.S1_at           | insulin-like growth factor binding protein 7 death-associated protein kinase 1  | 3.825            |
| Cell death/growth/differentiation                                     | GgaAffx.12808.1.S1 s at                        | shisa homolog 5 (Xenopus laevis)  | 3.553            |
| Cell death/growth/differentiation                                     | Gga.4720.3.S1_a_at                             | coiled-coil domain containing 21  | 3.546            |
| Cell death/growth/differentiation                                     | Gga.7709.1.S1_at                               | death-associated protein kinase 1   | 3.509            |
| Cell death/growth/differentiation                                     | Gga.4176.1.S1_at                               | eukaryotic translation initiation factor 5A2  | 3.219            |
| Cell death/growth/differentiation                                     | Gga.2628.1.S1_s_at                             | cyclin D2   | 0.482            |
| Cell death/growth/differentiation                                     | Gga.1325.1.S1_at                               | MAD1 mitotic arrest deficient-like 1 (yeast)  | 0.453            |
| Cell death/growth/differentiation Cell death/growth/differentiation   | GgaAffx.4278.2.S1_s_at<br>Gga.2554.1.A1 at     | transforming growth factor, beta receptor associated protein 1 transforming growth factor, beta 3                       | 0.448<br>0.399   |
| Cell death/growth/differentiation                                     | Gga.10930.1.S1 at                              | BCL2-like 13 (apoptosis facilitator)  | 0.396            |
| Cell death/growth/differentiation                                     | GgaAffx.10239.1.S1 at                          | optic atrophy 1 (autosomal dominant)  | 0.395            |
| Cell death/growth/differentiation                                     | GgaAffx.24127.1.S1_at                          | fibroblast growth factor receptor 1   | 0.372            |
| Cell death/growth/differentiation                                     | GgaAffx.25789.4.S1_s_at                        | fibroblast growth factor 1 (acidic)   | 0.283            |
| Cell death/growth/differentiation                                     | GgaAffx.4984.1.S1_at                           | cell division cycle 2, G1 to S and G2 to M  | 0.258            |
| Cell death/growth/differentiation                                     | GgaAffx.10104.2.S1_s_at                        | Gametocyte specific factor 1  | 0.245            |
| Chaperonin/HSP Chaperonin/HSP   | GgaAffx.4144.1.S1_s_at<br>GgaAffx.5862.1.S1_at | DnaJ (Hsp40) homolog, subfamily A, member 4<br>t-complex 1  | 0.491<br>0.462   |
| Chaperonin/HSP  | GgaAffx.4681.1.S1 at                           | t-complex 11 (mouse)-like 2   | 0.391            |
| Chaperonin/HSP  | GgaAffx.193.1.S1 at                            | DnaJ (Hsp40) homolog, subfamily C, member 11  | 0.387            |
| Chaperonin/HSP  | GgaAffx.6430.1.S1_at                           | chaperonin containing TCP1, subunit 2 (beta)  | 0.379            |
| Cytoskeletal components/regulation                                    |  | caldesmon 1   | 29.979           |
| Cytoskeletal components/regulation                                    |  | myosin, light chain kinase  | 23.408           |
| Cytoskeletal components/regulation                                    |  | caldesmon 1   | 16.044           |
| Cytoskeletal components/regulation Cytoskeletal components/regulation |  | caldesmon 1 myosin IF   | 14.532<br>10.163 |
| Cytoskeletal components/regulation                                    |  | actin related protein 2/3 complex, subunit 1B, 41kDa  | 8.429            |
| Cytoskeletal components/regulation                                    |  | centrosomal protein 170kDa  | 8.138            |
| Cytoskeletal components/regulation                                    |  | calponin 2  | 7.683            |
| Cytoskeletal components/regulation                                    |  | Kinesin light chain 1   | 6.638            |
| Cytoskeletal components/regulation                                    |  | actin related protein 2/3 complex, subunit 1B, 41kDa  | 6.556            |
| Cytoskeletal components/regulation                                    |  | ARP3 actin-related protein 3 homolog B (yeast)  | 5.890            |
| Cytoskeletal components/regulation                                    |  | Kinesin light chain 1  Dynein, light chain, Tctex-type 1  | 5.404<br>4.778   |
| Cytoskeletal components/regulation                                    |  | transgelin  | 4.369            |
| Cytoskeletal components/regulation                                    |  | tubulin, alpha 1c   | 3.717            |
| Cytoskeletal components/regulation                                    |  | similar to kinesin, putative  | 3.638            |
| Cytoskeletal components/regulation                                    |  | cytoskeleton associated protein 5   | 3.501            |
| Cytoskeletal components/regulation                                    |  | tubulin, beta 6   | 3.342            |
| Cytoskeletal components/regulation                                    |  | Kinesin family member 5C  | 3.211            |
| Cytoskeletal components/regulation                                    |  | myosin regulatory light chain interacting protein  Myosin VI  | 3.056<br>0.488   |
| Cytoskeletal components/regulation                                    |  | tubulin folding cofactor E  | 0.458            |
| Cytoskeletal components/regulation                                    |  | microtubule-associated protein 4  | 0.442            |
| Cytoskeletal components/regulation                                    |  | microtubule associated monoxygenase, calponin and LIM domain containing 3   | 0.437            |
| Cytoskeletal components/regulation                                    | or GgaAffx.2572.1.S1_at                        | dynein, cytoplasmic 1, light intermediate chain 1   | 0.420            |
| Cytoskeletal components/regulation                                    | or GgaAffx.10140.2.S1_s_at                     | kinesin family member 18A   | 0.393            |
| Cytoskeletal components/regulation                                    |  | Actin, gamma 1  | 0.363            |
| Cytoskeletal components/regulation                                    |  | centromere protein E, 312kDa  | 0.363            |
| DNA replication/repair DNA replication/repair                         | Gga.18956.1.S1_s_at<br>Gga.18300.1.S1_at       | polymerase (DNA directed), lambda excision repair cross-complementing rodent repair deficiency, complementation group 5 | 3.015<br>0.498   |
| DNA replication/repair  | Gga.7505.1.S1 at                               | REX2, RNA exonuclease 2 homolog (S. cerevisiae)   | 0.491            |
| DNA replication/repair  | Gga.2148.4.S1 a at                             | exonuclease NEF-sp  | 0.484            |
| DNA replication/repair  | Gga.10998.1.S1_s_at                            | RAD18 homolog (S. cerevisiae)   | 0.476            |
| DNA replication/repair  | GgaAffx.24832.2.S1_s_at                        | breast cancer 1, early onset  | 0.475            |
| DNA replication/repair  | GgaAffx.26038.1.S1_at                          | polymerase (DNA-directed), delta 3, accessory subunit   | 0.465            |
| DNA replication/repair  | Gga.4315.2.S1 a at                             | replication protein A2, 32kDa   | 0.455            |

| DNIA replication/repair  | Can 710 6 C1 a at  | nali marraca (DNA directed), garage   | 0.450            |
|--|--|---|------------------|
| DNA replication/repair DNA replication/repair                                    | Gga.710.6.S1_a_at<br>GgaAffx.4442.3.S1 s at                  | polymerase (DNA directed), gamma<br>replication factor C (activator 1) 3, 38kDa       | 0.450            |
| DNA replication/repair   | Gga.11871.1.S1_at  | minichromosome maintenance complex component 2  | 0.435            |
| DNA replication/repair   | Gga.12043.2.S1_a_at  | polymerase (DNA-directed), delta interacting protein 3                                | 0.428            |
| DNA replication/repair   | GgaAffx.7758.2.S1_s_at                                       | DNA2 DNA replication helicase 2-like (yeast)  | 0.408            |
| DNA replication/repair   | GgaAffx.21825.1.S1 s at                                      | RAD51-like 1 (S. cerevisiae)  | 0.398            |
| DNA replication/repair   | GgaAffx.25679.1.S1_s_at                                      | poly (ADP-ribose) polymerase family, member 11  | 0.380            |
| Extracellular matrix   | Gga.12800.1.S1_at  | matrix metallopeptidase 3 (stromelysin 1, progelatinase)                              | 67.335           |
| Extracellular matrix   | Gga.3994.3.S1_x_at   | Fibronectin 1   | 23.201           |
| Extracellular matrix   | Gga.9293.1.S1_at   | Fibronectin 1   | 21.558           |
| Extracellular matrix   | Gga.4078.1.S1_at   | lumican   | 21.079           |
| Extracellular matrix   | Gga.701.1.S1_s_at  | leukocyte ribonuclease A-1 /// leukocyte ribonuclease A-2                             | 20.283           |
| Extracellular matrix   | Gga.4851.1.S1_at   | collagen, type III, alpha 1   | 19.577           |
| Extracellular matrix   | GgaAffx.21771.1.S1_at  | collagen, type VI, alpha 1  | 16.921           |
| Extracellular matrix   | Gga.2073.1.S1_at   | Alpha-1 collagen (I)  | 16.450           |
| Extracellular matrix Extracellular matrix  | Gga.4941.1.S1_at<br>Gga.4128.1.S2 at                         | cadherin 11, type 2, OB-cadherin (osteoblast)   | 15.052           |
| Extracellular matrix   | Gga.3199.1.S1_at   | tensin 1 matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase,                   | 14.084<br>13.372 |
| Extracellular matrix   | Gga.3199.1.31_at   | 72kDa type IV collagenase)  | 13.372           |
| Extracellular matrix   | Gga.20018.1.S1 at  | thrombomucin  | 12.438           |
| Extracellular matrix   | Gga.4851.1.A1 at   | collagen, type III, alpha 1   | 11.954           |
| Extracellular matrix   | Gga.5255.1.S1 at   | EGF-containing fibulin-like extracellular matrix protein 1                            | 11.838           |
| Extracellular matrix   | Gga.12928.1.S1_at  | vascular cell adhesion molecule 1   | 11.757           |
| Extracellular matrix   | Gga.540.1.S1_at  | matrix Gla protein  | 11.638           |
| Extracellular matrix   | GgaAffx.11018.1.S1_s_at                                      | matrix metallopeptidase 1 (interstitial collagenase)                                  | 11.544           |
| Extracellular matrix   | Gga.5171.1.S1_at   | cadherin 5, type 2, VE-cadherin (vascular epithelium)                                 | 10.552           |
| Extracellular matrix   | Gga.1099.1.S1_at   | annexin A6  | 10.396           |
| Extracellular matrix   | Gga.4999.2.S1_at   | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4                            | 10.191           |
|  |  | receptor)   |                  |
| Extracellular matrix   | Gga.4884.1.S1_at   | annexin A1  | 9.299            |
| Extracellular matrix   | Gga.3104.1.S1_at   | collagen, type IV, alpha 2  | 9.177            |
| Extracellular matrix   | GgaAffx.6053.1.S1_at   | collagen, type I, alpha 2   | 7.860            |
| Extracellular matrix   | Gga.4507.1.S1_at   | integrin, beta 2 (complement component 3 receptor 3 and 4                             | 7.479            |
| E (100 - 10 10 - 10 - 12   | 0  | subunit)  | 7.004            |
| Extracellular matrix   | GgaAffx.5654.1.S1_at   | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4                            | 7.224            |
| Extracellular matrix   | Can 12020 1 C1 o ot  | receptor)   | 6.054            |
| Extracellular matrix Extracellular matrix  | Gga.12039.1.S1_a_at<br>GgaAffx.25534.1.S1 s at               | Matrix-remodelling associated 5 collagen, type III, alpha 1                           | 6.951            |
| Extracellular matrix   | GgaAffx.25192.2.S1 s at                                      | matrix metallopeptidase 1 (interstitial collagenase)                                  | 6.917<br>6.677   |
| Extracellular matrix   | Gga.9346.3.S1_a_at   | vimentin  | 6.418            |
| Extracellular matrix   | Gga.19452.1.S1_at  | CD44 molecule (Indian blood group)  | 6.208            |
| Extracellular matrix   | Gga.1168.1.S1 at   | annexin A5  | 6.099            |
| Extracellular matrix   | Gga.2679.1.S1 at   | fibulin 1   | 6.062            |
| Extracellular matrix   | Gga.5776.1.S1_at   | CD34 molecule   | 5.897            |
| Extracellular matrix   | GgaAffx.21790.1.S1 s at                                      | gap junction protein, alpha 1, 43kDa  | 5.744            |
| Extracellular matrix   | Gga.4051.1.S1 at   | connective tissue growth factor   | 5.690            |
| Extracellular matrix   | GgaAffx.11429.1.S1 s at                                      | matrix metallopeptidase 7 (matrilysin, uterine)                                       | 5.654            |
| Extracellular matrix   | Gga.6223.1.S1_at   | ADAM metallopeptidase domain 33   | 5.243            |
| Extracellular matrix   | Gga.4257.1.S1_at   | collagen, type VI, alpha 2  | 5.106            |
| Extracellular matrix   | Gga.566.1.S1_at  | integrin, alpha 1   | 4.793            |
| Extracellular matrix   | Gga.13442.1.S2_s_at  | radixin   | 4.708            |
| Extracellular matrix   | Gga.3572.1.S1_at   | CD44 molecule (Indian blood group)  | 4.619            |
| Extracellular matrix   | Gga.2965.1.S1_at   | TIMP metallopeptidase inhibitor 2   | 4.032            |
| Extracellular matrix   | GgaAffx.22999.1.S1_s_at                                      | collagen, type I, alpha 2   | 3.892            |
| Extracellular matrix   | Gga.13442.1.S1_at  | radixin   | 3.637            |
| Extracellular matrix   | Gga.1776.1.S1_at   | nidogen 1   | 3.562            |
| Extracellular matrix   | Gga.3572.1.S2_s_at   | CD44 molecule (Indian blood group)  | 3.164            |
| Extracellular matrix Extracellular matrix  | Gga.888.1.S1_at<br>Gga.198.1.S1_at                           | collagen, type VI, alpha 3 matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, | 3.103<br>3.028   |
| Extracellular matrix   | Gga. 196. 1.5 1_at   | 92kDa type IV collagenase)  | 3.020            |
| Extracellular matrix   | GgaAffx.26220.2.S1 s at                                      | integrin beta 1 binding protein 3   | 0.480            |
| Extracellular matrix   | GgaAffx.6391.2.S1 s at                                       | integrator complex subunit 2  | 0.475            |
| Extracellular matrix   | GgaAffx.22425.1.S1_s_at                                      | collagen, type XX, alpha 1  | 0.473            |
| Extracellular matrix   | GgaAffx.5541.1.S1 at   | Discoidin, CUB and LCCL domain containing 1   | 0.356            |
| Gene expression/regulation   | Gga.3548.1.S1_at   | zinc finger E-box binding homeobox 1  | 13.018           |
| Gene expression/regulation   | Gga.2551.2.S1 s at   | lactotransferrin  | 11.137           |
| Gene expression/regulation   | Gga.1313.1.S1_s_at   | spleen focus forming virus (SFFV) proviral integration oncogene                       | 10.008           |
|  |  | spi1  |                  |
| Gene expression/regulation   | GgaAffx.20792.1.S1_s_at                                      | zinc finger E-box binding homeobox 1  | 8.993            |
| Gene expression/regulation   | GgaAffx.12062.1.S1_s_at                                      | Friend leukemia virus integration 1   | 8.875            |
| Gene expression/regulation   | GgaAffx.3506.1.S1_at   | ecotropic viral integration site 2B   | 7.990            |
| Gene expression/regulation   | Gga.4285.1.S1_at   | CCAAT/enhancer binding protein (C/EBP), beta  | 7.344            |
|  |  |   | 7 000            |
| Gene expression/regulation   | Gga.6066.1.S1_at   | transcription factor 7 (T-cell specific, HMG-box)                                     | 7.083            |
| Gene expression/regulation Gene expression/regulation Gene expression/regulation | Gga.6066.1.S1_at<br>Gga.1378.1.S1_s_at<br>Gga.3731.2.S1_a_at | transcription factor 7 (1-cell specific, HMG-box) histone deacetylase 9 gammaFBP-A    | 5.821<br>5.230   |

| -   |   |  |  |
|---|---|--|--|
| Gene expression/regulation  | Gga.6375.1.S1_at  | basic helix-loop-helix domain containing, class B, 8   | 5.205  |
| Gene expression/regulation  | Gga.4919.1.S2_at  | CUG triplet repeat, RNA binding protein 2 /// hypothetical protein LOC769811   | 5.086  |
| Gene expression/regulation  | Gga.1108.1.S1 s at  | limb bud and heart development homolog (mouse)   | 4.534  |
| Gene expression/regulation  | Gga.4954.2.S1 a at  | TNFAIP3 interacting protein 1  | 4.510  |
| Gene expression/regulation  | Gga.4371.1.S1 s at  | putative homeodomain transcription factor 2  | 4.202  |
| Gene expression/regulation  | Gga.578.1.S1_at   | IKAROS family zinc finger 1 (Ikaros)   | 4.108  |
| Gene expression/regulation  | GgaAffx.21436.1.S1_s_at   | basic leucine zipper transcription factor, ATF-like  | 3.617  |
| Gene expression/regulation  | Gga.49.1.S1_at  | chromobox homolog 4 (Pc class homolog, Drosophila)   | 3.394  |
| Gene expression/regulation  Gene expression/regulation  | GgaAffx.24709.1.S1_s_at   | microphthalmia-associated transcription factor   | 0.498  |
| Gene expression/regulation  | Gga.16862.1.S1_at<br>GgaAffx.2752.1.S1_s_at   | TATA element modulatory factor 1  MAX interactor 1   | 0.492<br>0.491   |
| Gene expression/regulation  | GgaAffx.4023.1.S1_s_at  | REV3-like, catalytic subunit of DNA polymerase zeta (yeast)  | 0.491  |
| Gene expression/regulation  | GgaAffx.8903.3.S1 at  | nuclear receptor subfamily 6, group A, member 1  | 0.487  |
| Gene expression/regulation  | GgaAffx.21044.1.S1 s at   | pseudouridylate synthase 7 homolog (S. cerevisiae)   | 0.482  |
| Gene expression/regulation  | GgaAffx.2077.1.S1_s_at  | v-myc myelocytomatosis viral oncogene homolog (avian)  | 0.480  |
| Gene expression/regulation  | GgaAffx.25677.1.S1_s_at   | Sin3A-associated protein, 130kDa   | 0.475  |
| Gene expression/regulation  | GgaAffx.23089.1.S1_at   | general transcription factor IIA, 2, 12kDa   | 0.468  |
| Gene expression/regulation  | GgaAffx.25648.2.S1_s_at   | WD repeat domain 36  | 0.463  |
| Gene expression/regulation  | GgaAffx.26668.2.S1_s_at   | nuclear transcription factor Y, gamma  | 0.462  |
| Gene expression/regulation  | Gga.2475.1.S1_at<br>Gga.10895.1.S1 s at   | chromatin modifying protein 6  | 0.458<br>0.451   |
| Gene expression/regulation Gene expression/regulation   | GgaAffx.4249.1.S1_x_at  | threonyl-tRNA synthetase CTD (carboxy-terminal domain, RNA polymerase II, polypeptide  | 0.431  |
| Gene expression/regulation  | GyaA11X.4249.1.51_X_at  | A) phosphatase, subunit 1  | 0.446  |
| Gene expression/regulation  | Gga.4830.1.S2 at  | protein inhibitor of activated STAT, 2   | 0.446  |
| Gene expression/regulation  | Gga.5522.2.S1 a at  | activating signal cointegrator 1 complex subunit 3-like 1  | 0.440  |
| Gene expression/regulation  | GgaAffx.2639.1.S1 at  | adenosine deaminase, tRNA-specific 1   | 0.437  |
| Gene expression/regulation  | GgaAffx.4639.1.S1_at  | splicing factor 3b, subunit 4, 49kDa   | 0.435  |
| Gene expression/regulation  | Gga.6487.1.S1_at  | similar to nuclear cap binding protein subunit 2   | 0.434  |
| Gene expression/regulation  | GgaAffx.9629.1.S1_at  | chromatin licensing and DNA replication factor 1   | 0.427  |
| Gene expression/regulation  | GgaAffx.20192.1.S1_s_at   | ribosomal protein S11  | 0.417  |
| Gene expression/regulation  | Gga.2087.1.S1_s_at  | RNA polymerase 1-3   | 0.415  |
| Gene expression/regulation Gene expression/regulation   | GgaAffx.8122.1.S1_at<br>Gga.4010.1.S1 s at  | nucleolar protein 5A (56kDa with KKE/D repeat) integrator complex subunit 2  | 0.415<br>0.415   |
| Gene expression/regulation  | Gga.11672.1.S1 at   | PRP4 pre-mRNA processing factor 4 homolog (yeast)  | 0.413  |
| Gene expression/regulation  | GgaAffx.193.2.S1 s at   | integrator complex subunit 10  | 0.412  |
| Gene expression/regulation  | Gga.17691.1.S1 at   | activating transcription factor 4 (tax-responsive enhancer   | 0.408  |
|   |   |  |  |
|   |   | element B67)   |  |
| Gene expression/regulation  | GgaAffx.1279.2.S1_s_at  |  | 0.383  |
| Gene expression/regulation Gene expression/regulation   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at   | element B67) caudal type homeobox 2 ribosomal protein L36  | 0.342  |
| Gene expression/regulation  | GgaAffx.1279.2.S1_s_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha  |  |
| Gene expression/regulation Gene expression/regulation Gene expression/regulation  | GgaAffx.1279.2.S1 s at<br>GgaAffx.3047.2.S1 s at<br>GgaAffx.1433.3.S1_s_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  | 0.342  |
| Gene expression/regulation Gene expression/regulation Gene expression/regulation Gene expression/regulation   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1 s at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38  | 0.342<br>0.339<br>0.333  |
| Gene expression/regulation Gene expression/regulation Gene expression/regulation Gene expression/regulation Gene expression/regulation Gene expression/regulation   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1  | 0.342<br>0.339<br>0.333<br>0.319   |
| Gene expression/regulation  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like   | 0.342<br>0.339<br>0.333<br>0.319<br>0.316  |
| Gene expression/regulation   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3   | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315   |
| Gene expression/regulation  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316  |
| Gene expression/regulation   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  Biliverdin reductase A  quiescence-specific protein   | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576   |
| Gene expression/regulation General metabolism General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1_at Gga.739.1.S1_at GgaAffx.7420.1.S1_at   | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  guiescence-specific protein phospholipase D family, member 4  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185   |
| Gene expression/regulation General metabolism General metabolism General metabolism General metabolism General metabolism General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  Biliverdin reductase A  quiescence-specific protein phospholipase D family, member 4  GTPase, IMAP family member 8  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820  |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1_s_at Gga.19462.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  guiescence-specific protein  phospholipase D family, member 4  GTPase, IMAP family member 8  deoxyribonuclease I-like 3   | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752   |
| Gene expression/regulation General metabolism General metabolism General metabolism General metabolism General metabolism General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820  |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A quiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like)  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159  |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6017.1.S1_s at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A   | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159  |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 at Gga.12360.1.S1 at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1 at GgaAffx.7420.1.S1 at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.6017.1.S1_s_at Gga.6017.1.S1_s_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159   |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6017.1.S1_s at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A   | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159  |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.17674.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.6017.1.S1_at Gga.6236.1.S1_at Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.7765.1.S1_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  Biliverdin reductase A  guiescence-specific protein  phospholipase D family, member 4  GTPase, IMAP family member 8  deoxyribonuclease I-like 3  ELOVL family member 5, elongation of long chain fatty acids  (FEN1/Elo2, SUR4/Elo3-like)  Biliverdin reductase A  switch-associated protein 70  carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2  cholesterol 25-hydroxylase  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813                                     |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.17674.1.S1_at Gga.17674.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at  Gga.6017.1.S1_at  Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.10928.1.S1_at GgaAffx.10393.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease)  | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857                   |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.17674.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.6017.1.S1_at Gga.6236.1.S1_at Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.7765.1.S1_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous   | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922                            |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.11830.1.S1 at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.11830.1.S1_at Gga.1177.1.S1_at Gga.11830.1.S1_at Gga.11830.1.S1_at Gga.119331.S1_at Gga.119331.S1_at Gga.113365.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857          |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.17674.1.S1_at Gga.17674.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at  Gga.6017.1.S1_at  Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.10928.1.S1_at GgaAffx.10393.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A Biliverdin reductase A GTPase, IMAP family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-   | 0.342<br>0.339<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857                   |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.1177.1.S1_at  Gga.1177.1.S1_at  Gga.6017.1.S1_s at Gga.6236.1.S1_at Gga.10928.1.S1_at Gga.10928.1.S1_at GgaAffx.10393.1.S1_at Gga.13365.1.S1_at Gga.13365.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A Biliverdin reductase A quiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857<br>5.713 |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1 at Gga.17674.1.S1 at Gga.739.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1_s at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6017.1.S1 s at Gga.6236.1.S1 at Gga.7765.1.S1 at Gga.10928.1.S1 at Gga.13365.1.S1_at Gga.13365.1.S1_at Gga.14925.1.S1_at Gga.3807.1.S2_s_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857<br>5.713 |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.7420.1.S1_at GgaAffx.7420.1.S1_at GgaAffx.26353.1.S1_s at Gga.1177.1.S1_at  Gga.1177.1.S1_at  Gga.6017.1.S1_s at Gga.6236.1.S1_at Gga.10928.1.S1_at Gga.10928.1.S1_at GgaAffx.10393.1.S1_at Gga.13365.1.S1_at Gga.13365.1.S1_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857<br>5.713 |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.12360.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at  Gga.6017.1.S1_s_at Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.10928.1.S1_at Gga.10928.1.S1_at Gga.13365.1.S1_at Gga.14925.1.S1_at Gga.3807.1.S2_s_at Gga.3807.1.S2_s_at Gga.34401.1.S1_a_at  | element B67)  caudal type homeobox 2  ribosomal protein L36  similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa  ribosomal protein L38  exonuclease domain containing 1  transcriptional adaptor 2 (ADA2 homolog, yeast)-like  Splicing factor, arginine/serine-rich 3  Biliverdin reductase A  Biliverdin reductase A  guiescence-specific protein phospholipase D family, member 4  GTPase, IMAP family member 8  deoxyribonuclease I-like 3  ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like)  Biliverdin reductase A  switch-associated protein 70  carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2  cholesterol 25-hydroxylase  cytochrome b-245, beta polypeptide (chronic granulomatous disease)  1-acylglycerol-3-phosphate O-acyltransferase 4  (lysophosphatidic acid acyltransferase, delta)  mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminytransferase, isozyme A  aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)  | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 5.432 5.150                                     |
| Gene expression/regulation General metabolism   | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1 at Gga.17674.1.S1 at Gga.739.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1_s at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6017.1.S1 s at Gga.6236.1.S1 at Gga.7765.1.S1 at Gga.10928.1.S1 at Gga.13365.1.S1_at Gga.13365.1.S1_at Gga.14925.1.S1_at Gga.3807.1.S2_s_at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H  | 0.342<br>0.339<br>0.333<br>0.319<br>0.316<br>0.315<br>29.576<br>14.424<br>11.988<br>8.185<br>7.820<br>7.752<br>7.159<br>7.089<br>7.025<br>6.813<br>5.922<br>5.857<br>5.713 |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1_s_at GgaAffx.3310.1.S1_s_at GgaAffx.3310.1.S1_s_at Gga.19462.1.S1_s_at Gga.12360.1.S1_at Gga.12360.1.S1_at GgaAffx.23872.1.S1_at GgaAffx.26353.1.S1_s_at GgaAffx.26353.1.S1_s_at Gga.11830.1.S1_at Gga.1177.1.S1_at  Gga.6017.1.S1_s_at Gga.6236.1.S1_at Gga.7765.1.S1_at Gga.10928.1.S1_at Gga.10928.1.S1_at Gga.13365.1.S1_at Gga.14925.1.S1_at Gga.3807.1.S2_s_at Gga.3807.1.S2_s_at Gga.34401.1.S1_a_at  | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A Biliverdin reductase A GTPase, IMAP family member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 5.432 5.150                                     |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.10949.1.S1 s at GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.19462.1.S1 s at Gga.17674.1.S1 at Gga.739.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1 s at Gga.11830.1.S1 at Gga.11830.1.S1 at Gga.1177.1.S1 s at Gga.6017.1.S1 s at Gga.10928.1.S1 at Gga.10928.1.S1 at Gga.10928.1.S1 at Gga.13365.1.S1 at Gga.13365.1.S1 at Gga.14925.1.S1 at Gga.14925.1.S1 at Gga.3807.1.S2 s at Gga.4401.1.S1 a at   | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  phospholipase C, gamma 2 (phosphatidylinositol-specific) NK-lysin   | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 4.885   |
| Gene expression/regulation General metabolism  | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at Gga.739.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6236.1.S1 at Gga.10928.1.S1_at Gga.10928.1.S1_at Gga.13365.1.S1_at Gga.13365.1.S1_at Gga.14426.1.S1_at  Gga.14426.1.S1_at  Gga.7748.2.A1 at Gga.623612.2.A1 at Gga.64401.1.S1_a at Gga.7748.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  phospholipase C, gamma 2 (phosphatidylinositol-specific) NK-lysin thioredoxin domain containing 5 (endoplasmic reticulum)  | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 5.432 5.150 4.885 4.612 4.252 4.149             |
| Gene expression/regulation General metabolism | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.19462.1.S1 s at Gga.17674.1.S1 at Gga.17674.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6017.1.S1 s at Gga.1177.1.S1_at  Gga.10928.1.S1 at Gga.10928.1.S1 at Gga.13365.1.S1_at Gga.14925.1.S1_at  Gga.14925.1.S1_at  Gga.14426.1.S1_at  Gga.7148.2.A1 at Gga.7148.2.A1 at Gga.7148.2.A1 at Gga.612.2.A1_at Gga.12233.1.S1_at Gga.12233.1.S1_at                                   | element B67)  caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  phospholipase C, gamma 2 (phosphatidylinositol-specific) NK-lysin thioredoxin domain containing 5 (endoplasmic reticulum) N-acylsphingosine amidohydrolase (acid ceramidase)-like | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 5.432 5.150 4.885 4.612 4.252 4.149 4.123       |
| Gene expression/regulation General metabolism                                       | GgaAffx.1279.2.S1 s at GgaAffx.3047.2.S1 s at GgaAffx.1433.3.S1_s_at  GgaAffx.10949.1.S1 s at GgaAffx.3310.1.S1 s at GgaAffx.3310.1.S1 s at Gga.19462.1.S1 s at Gga.19462.1.S1 s at Gga.12360.1.S1_at Gga.17674.1.S1 at Gga.739.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.23872.1.S1 at GgaAffx.26353.1.S1_s at Gga.11830.1.S1 at Gga.1177.1.S1_at  Gga.6236.1.S1 at Gga.10928.1.S1_at Gga.10928.1.S1_at Gga.13365.1.S1_at Gga.13365.1.S1_at Gga.14426.1.S1_at  Gga.14426.1.S1_at  Gga.7748.2.A1 at Gga.623612.2.A1 at Gga.64401.1.S1_a at Gga.7748.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at Gga.6612.2.A1 at | element B67) caudal type homeobox 2 ribosomal protein L36 similar to general transcription factor IIIC, polypeptide 1, alpha 220kDa ribosomal protein L38 exonuclease domain containing 1 transcriptional adaptor 2 (ADA2 homolog, yeast)-like Splicing factor, arginine/serine-rich 3 Biliverdin reductase A Biliverdin reductase A guiescence-specific protein phospholipase D family, member 4 GTPase, IMAP family member 8 deoxyribonuclease I-like 3 ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like) Biliverdin reductase A switch-associated protein 70 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 cholesterol 25-hydroxylase cytochrome b-245, beta polypeptide (chronic granulomatous disease) 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme A aldehyde dehydrogenase 1 family, member A3 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  phospholipase C, gamma 2 (phosphatidylinositol-specific) NK-lysin thioredoxin domain containing 5 (endoplasmic reticulum)  | 0.342 0.339 0.333 0.319 0.316 0.315 29.576 14.424 11.988 8.185 7.820 7.752 7.159 7.089 7.025 6.813 5.922 5.857 5.713 5.460 5.432 5.150 4.885 4.612 4.252 4.149             |

| General metabolism                    | Gga.9879.1.S1_s_at                         | lipase A, lysosomal acid, cholesterol esterase (Wolman disease)                                     | 3.893            |
|---------------------------------------|--|---|------------------|
| General metabolism                    | Gga.3323.1.S1_s_at                         | fatty acid binding protein 5  | 3.892            |
| General metabolism                    | GgaAffx.1032.1.S1_s_at                     | inositol polyphosphate-5-phosphatase, 145kDa  | 3.863            |
| General metabolism                    | GgaAffx.12708.1.S1_s_at                    | similar to ornithine aminotransferase (gyrate atrophy) /// ornithine aminotransferase               | 3.692            |
| General metabolism                    | Gga.1161.1.S1_at                           | succinate dehydrogenase complex, subunit D, integral membrane protein                               | 3.504            |
| General metabolism                    | GgaAffx.22378.1.S1 s at                    | phospholipase C, gamma 2 (phosphatidylinositol-specific)  | 3.219            |
| General metabolism                    | Gga.7148.1.S1_at                           | phospholipase C, gamma 2 (phosphatidylinositol-specific)  | 3.218            |
| General metabolism                    | Gga.1758.1.S1_at                           | Arachidonate 5-lipoxygenase-activating protein  | 3.208            |
| General metabolism                    | Gga.7640.1.S1_a_at                         | Acyl-CoA synthetase long-chain family member 4  | 3.201            |
| General metabolism                    | Gga.593.1.S1_s_at                          | ADP-ribosyltransferase /// ADP-ribosyltransferase   | 3.188            |
| General metabolism                    | GgaAffx.4938.1.S1_at                       | phosphatidylinositol-5-phosphate 4-kinase, type II, alpha   | 3.020            |
| General metabolism General metabolism | Gga.10824.1.S1_s_at<br>Gga.7294.1.S1 at    | N-acetylglucosaminyltransferase VI choline phosphotransferase 1                                     | 0.490<br>0.490   |
| General metabolism                    | Gga.9508.1.S1_at                           | glutamine-fructose-6-phosphate transaminase 1   | 0.488            |
| General metabolism                    | GgaAffx.3796.1.S1 s at                     | phosphorylase kinase, beta  | 0.486            |
| General metabolism                    | GgaAffx.22454.1.S1_s_at                    | arachidonate 5-lipoxygenase   | 0.484            |
| General metabolism                    | GgaAffx.12570.1.S1 s at                    | Oxysterol binding protein-like 11   | 0.483            |
| General metabolism                    | GgaAffx.21140.1.S1_s_at                    | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa   | 0.476            |
| General metabolism                    | GgaAffx.23988.2.S1_s_at                    | gallinacin 1  | 0.475            |
| General metabolism                    | Gga.2908.1.S1_at                           | asparagine-linked glycosylation 11 homolog (S. cerevisiae,  | 0.472            |
| General metabolism                    | GgaAffx.24513.9.S1_s_at                    | alpha-1,2-mannosyltransferase) asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-     | 0.470            |
| General metabolism                    | GgaAffx.26615.2.S1 s at                    | 1,3-glucosyltransferase) Similar to dermatan 4-sulfotransferase-1                                   | 0.466            |
| General metabolism                    | Gga.11674.1.S1 at                          | methyltransferase like 8  | 0.442            |
| General metabolism                    | GgaAffx.24884.1.S1 s at                    | dUTP pyrophosphatase  | 0.438            |
| General metabolism                    | Gga.5263.3.S1_s_at                         | phospholipase C-like 2  | 0.438            |
| General metabolism                    | GgaAffx.882.2.S1_s_at                      | acyl-CoA synthetase long-chain family member 5  | 0.432            |
| General metabolism                    | Gga.8991.1.S1_at                           | glutathione S-transferase theta 1   | 0.424            |
| General metabolism                    | Gga.17281.1.S1_at                          | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1                                   | 0.417            |
| General metabolism                    | Gga.11447.1.S1_a_at                        | K(lysine) acetyltransferase 2A  | 0.408            |
| General metabolism                    | GgaAffx.23111.1.S1_s_at                    | uridine phosphorylase 2   | 0.397            |
| General metabolism                    | GgaAffx.25247.1.S1_at                      | UDP-glucuronate decarboxylase 1   | 0.395            |
| General metabolism                    | Gga.17284.1.S1_at                          | serine racemase   | 0.375            |
| General metabolism                    | GgaAffx.24100.1.S1_s_at                    | steroid 5 alpha-reductase 3   | 0.365            |
| General metabolism                    | GgaAffx.26520.1.S1_s_at                    | UDP-glucose pyrophosphorylase 2   | 0.364            |
| General metabolism General metabolism | Gga.12113.1.A1_at<br>GgaAffx.10350.1.S1 at | methyltransferase like 14 5'-nucleotidase, cytosolic III-like                                       | 0.359<br>0.356   |
| General metabolism                    | Gga.9596.1.S1_at                           | cytochrome P450, family 39, subfamily A, polypeptide 1  | 0.351            |
| General metabolism                    | GgaAffx.21089.1.S1_s_at                    | STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)                   | 0.349            |
| General metabolism                    | GgaAffx.5994.1.S1 at                       | methyltransferase like 10   | 0.304            |
| Immunity/defense                      | Gga.12186.1.S1 at                          | lymphatic vessel endothelial hyaluronan receptor 1  | 32.611           |
| Immunity/defense                      | Gga.1020.1.S1_at                           | chemokine (C-C motif) ligand 17   | 29.428           |
| Immunity/defense                      | Gga.701.1.S1_at                            | leukocyte ribonuclease A-2  | 18.493           |
| Immunity/defense                      | Gga.9873.1.S1_at                           | complement component 1, q subcomponent, C chain   | 16.683           |
| Immunity/defense                      | Gga.5396.1.S1_at                           | complement component 1, q subcomponent, B chain   | 14.962           |
| Immunity/defense                      | Gga.7298.1.S1_at                           | complement component 1, q subcomponent, A chain   | 14.601           |
| Immunity/defense Immunity/defense     | Gga.11955.1.S1_at<br>Gga.9513.1.S2_at      | Immunoglobulin superfamily, member 6 Chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor | 14.396<br>13.883 |
| Immunity/defense                      | Gga.9133.1.S1 at                           | 1) Chemokine ah221  | 12.744           |
| Immunity/defense                      | Gga.4374.1.S1_a_at                         | interferon regulatory factor 4  | 12.149           |
| Immunity/defense                      | Gga.3676.1.S1_at                           | B cell RAG associated protein   | 12.106           |
| Immunity/defense                      | Gga.4681.2.S1_s_at                         | dedicator of cytokinesis 10   | 11.854           |
| Immunity/defense                      | GgaAffx.2960.1.S1_s_at                     | complement component 1, q subcomponent, B chain   | 11.824           |
| Immunity/defense                      | Gga.703.1.S1_at                            | leukocyte ribonuclease A-1  | 11.803           |
| Immunity/defense                      | Gga.916.1.S2_at                            | interferon, gamma   | 11.653           |
| Immunity/defense                      | Gga.1307.1.S1_s_at                         | interleukin 16 (lymphocyte chemoattractant factor)  | 11.579<br>11.272 |
| Immunity/defense                      | Gga.2467.1.S1_at                           | immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides           |                  |
| Immunity/defense                      | Gga.17679.1.S1_s_at                        | immunoglobulin-like receptor CHIR-B5 /// immunoglobulin-like receptor CHIR-B6                       | 11.200           |
| Immunity/defense                      | Gga.4110.4.S1_x_at                         | immunoglobulin lambda-like polypeptide 1  | 11.067           |
| Immunity/defense                      | Gga.4110.10.S1_x_at                        | immunoglobulin lambda-like polypeptide 1  | 10.715           |
| Immunity/defense                      | Gga.5743.1.S1_at                           | lymphocyte antigen 96   | 10.485           |
| Immunity/defense                      | GgaAffx.151.1.S1_s_at                      | CD79b molecule, immunoglobulin-associated beta  | 9.962            |
| Immunity/defense                      | Gga.4110.11.S1_x_at                        | immunoglobulin lambda-like polypeptide 1 toll-like receptor 6                                       | 9.867            |
| Immunity/defense                      | GgaAffx.11201.1.S1_s_at                    | toil-like receptor o  | 9.819            |

|  | Gga.3145.1.S1_x_at  | similar to Moesin (Membrane-organizing extension spike protein)   | 9.804   |
|--|---|---|---|
| Immunity/defense   | Gga.1311.5.S1_s_at  | Similar to T-cell receptor V beta chain   | 9.765   |
| Immunity/defense   | GgaAffx.10617.2.S1_s_at   | toll-like receptor 7  | 9.749   |
| Immunity/defense   | GgaAffx.5458.1.S1_at  | cytotoxic T-lymphocyte-associated protein 4   | 9.664   |
| Immunity/defense   | Gga.6032.1.S1_at  | dedicator of cytokinesis 8  | 9.560   |
| Immunity/defense   | GgaAffx.25386.1.S1_at   | dedicator of cytokinesis 2  | 9.265   |
| Immunity/defense   | GgaAffx.21915.1.S1 at   | interferon-induced protein with tetratricopeptide repeats 5   | 9.081   |
| Immunity/defense   | GgaAffx.2421.1.S1_s_at  | T-cell immunoglobulin and mucin domain containing 4   | 9.060   |
| Immunity/defense   | Gga.723.1.S1 a at   | CD28 molecule   | 9.052   |
| Immunity/defense   | Gga.4491.1.S1_at  | Lymphocyte-specific protein 1   | 9.021   |
| Immunity/defense   | Gga.21.1.S1_a_at  | interleukin 2 receptor, gamma (severe combined immunodeficiency)  | 8.796   |
| Immunity/defense   | Gga.17647.1.S1_at   | neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)   | 8.778   |
| Immunity/defense   | Gga.690.1.S1_at   | lymphocyte antigen 86   | 8.760   |
| Immunity/defense   | GgaAffx.12658.1.S1_at   | neutrophil cytosolic factor 4, 40kDa  | 8.655   |
| Immunity/defense   | GgaAffx.26062.1.S1_s_at   | immunoglobulin-like receptor CHIR-B3 /// similar to immunoglobulin-like receptor CHIR-B3  | 8.641   |
| Immunity/defense   | GgaAffx.12842.1.S1_s_at   | immunoresponsive 1 homolog (mouse)  | 8.616   |
| Immunity/defense   | Gga.445.1.S1_at   | similar to T cell receptor alpha  | 8.522   |
| Immunity/defense   | Gga.445.2.S1 a at   | similar to T cell receptor alpha  | 8.396   |
| Immunity/defense   | Gga.9675.1.S1_at  | platelet derived growth factor D  | 8.338   |
| Immunity/defense   | Gga.3145.3.S1_a_at  | similar to Moesin (Membrane-organizing extension spike protein)   | 8.166   |
| Immunity/defense   | Gga.236.1.S1_at   | lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)   | 7.935   |
| Immunity/defense   | Gga.19049.1.S1_at   | interleukin 18 (interferon-gamma-inducing factor)   | 7.852   |
| Immunity/defense   | GgaAffx.25386.2.S1_s_at   | dedicator of cytokinesis 2  | 7.785   |
| Immunity/defense   | Gga.3366.1.S1 at  | interleukin 20 receptor, alpha  | 7.766   |
| Immunity/defense   | Gga.11522.1.S1 x at   | similar to immunoglobulin-like receptor CHIR-AB1  | 7.748   |
| Immunity/defense   | Gga.4110.4.S1_a_at  | immunoglobulin lambda-like polypeptide 1  | 7.729   |
| Immunity/defense   | GgaAffx.9789.1.S1 at  | T cell receptor associated transmembrane adaptor 1  | 7.620   |
| Immunity/defense   | Gga.217.1.S1 x at   | MHC class II antigen B-F minor heavy chain  | 7.599   |
| Immunity/defense   | Gga.4110.12.S1 a at   | immunoglobulin lambda-like polypeptide 1  | 7.546   |
| Immunity/defense   | Gga.14571.1.S1_s_at   | Hermansky-Pudlak syndrome 5   | 7.475   |
| Immunity/defense   |   | similar to Moesin (Membrane-organizing extension spike  | 7.466   |
|  | Gga.3145.2.S1_a_at  Gga.11522.1.S1 at   | protein) similar to immunoglobulin-like receptor CHIR-AB1   | 7.400   |
| Immunity/defense   |   |   |   |
| Immunity/defense   | GgaAffx.10876.2.S1_s_at   | lymphocyte cytosolic protein 1 (L-plastin)  | 7.125   |
| Immunity/defense   | GgaAffx.24185.1.S1_at   | interleukin 7 receptor  | 7.054   |
| Immunity/defense   | Gga.1220.1.A1_at  | pre-B lymphocyte gene 3   | 6.815   |
| Immunity/defense   | Gga.6332.1.S1_at  | similar to complement regulatory soluble protein  | 6.733   |
| Immunity/defense   | Gga.1311.3.S1_at  | similar to T-cell receptor beta   | 6.695   |
| Immunity/defense   | GgaAffx.11727.1.S1_at   | lymphocyte cytosolic protein 1 (L-plastin)  | 6.591   |
| Immunity/defense   | Gga.3380.1.S1_at  | T cell receptor alpha locus   | 6.418   |
| Immunity/defense   | Gga.13336.2.S1_x_at   | MHC class II antigen B-F minor heavy chain  | 6.280   |
| Immunity/defense   | GgaAffx.12851.1.S1_s_at   | complement component 3a receptor 1  |   |
|  |   | complement component sa receptor i  | 6.058   |
| Immunity/defense   | Gga.542.1.S1_at   | lymphotactin  | 6.058<br>6.045  |
| Immunity/defense Immunity/defense  |   |   |   |
|  | Gga.542.1.S1_at   | lymphotactin  | 6.045<br>5.998  |
| Immunity/defense Immunity/defense  | Gga.542.1.S1_at<br>GgaAffx.21398.1.S1_at<br>Gga.4491.1.S1_s_at  | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1  | 6.045<br>5.998<br>5.811   |
| Immunity/defense   | Gga.542.1.S1_at<br>GgaAffx.21398.1.S1_at  | lymphotactin dedicator of cytokinesis 10  | 6.045<br>5.998  |
| Immunity/defense<br>Immunity/defense<br>Immunity/defense<br>Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at  | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor   | 6.045<br>5.998<br>5.811<br>5.807  |
| Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at Gga.7064.1.S1_at  | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646   |
| Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at  | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor   | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554   |
| Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s at GgaAffx.24298.1.S1_s at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at  | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493  |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at  | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554   |
| Immunity/defense Immunity/defense Immunity/defense Immunity/defense Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3   | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489   |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s at GgaAffx.24298.1.S1_s at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x at Gga.4964.3.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489<br>5.488  |
| Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at  Gga.4964.2.S1_a_at   | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.489<br>5.488<br>5.468  |
| Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.1.S1_a_at  Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s_at GgaAffx.23145.3.S1_s_at   | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489<br>5.488<br>5.468   |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4491.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at Gga.4964.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s_at Gga.16655.1.S1_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489<br>5.468<br>5.468   |
| Immunity/defense   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s at GgaAffx.24298.1.S1_s at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s at Gga.16655.1.S1_at Gga.4964.54.A1_x_at  | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489<br>5.468<br>5.468<br>5.299<br>5.279   |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4491.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s_at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.4964.54.A1_x_at Gga.296.1.S1_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1   | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.488<br>5.468<br>5.454<br>5.299<br>5.279<br>5.271<br>5.250                                     |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s_at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.296.1.S1_at Gga.296.1.S1_at Gga.296.1.S1_at   | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1  interleukin 20 receptor, alpha  similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3  immunoglobulin superfamily, member 1  interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3  similar to T-cell receptor gamma Vg3-Jg3  similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3  similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3  chemokine (C-C motif) ligand 19  dedicator of cytokinesis 8 histocompatibility (minor) HA-1  Similar to T-cell receptor gamma chain Vg3-Jg3  chemokine (C-C motif) ligand 1  guanylate binding protein  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.489<br>5.488<br>5.468<br>5.454<br>5.279<br>5.271<br>5.250<br>5.180                            |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4491.1.S1_s_at GgaAffx.24298.1.S1_s_at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1_s_at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.296.1.S1_at Gga.296.1.S1_at Gga.178.1.S1_s_at Gga.178.1.S1_s_at Gga.4964.22.S1_x_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2   | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.488<br>5.468<br>5.454<br>5.299<br>5.279<br>5.271<br>5.250<br>5.180                            |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1 s at Gga.4491.1.S1 s at GgaAffx.24298.1.S1 s at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at  Gga.11252.1.S1_at GgaAffx.23145.3.S1 s at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.296.1.S1_at Gga.296.1.S1_at Gga.4964.52.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at GgaAffx.12157.1.S1_at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2 similar to immunoglobulin-like receptor CHIR-B2 precursor  | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.488<br>5.468<br>5.454<br>5.299<br>5.279<br>5.271<br>5.250<br>5.180<br>5.162                   |
| Immunity/defense                                   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1 s at Gga.4491.1.S1 s at Gga.4964.5.S1_a_at  Gga.7064.1.S1 at GgaAffx.8515.1.S1_at Gga.4964.17.S1_x_at Gga.4964.17.S1_x_at Gga.4964.11.S1_a_at  Gga.4964.2.S1_a_at  Gga.11252.1.S1_at Gga.4964.54.A1_x_at Gga.4964.54.A1_x_at Gga.178.1.S1_s_at Gga.178.1.S1_s_at Gga.178.1.S1_s_at Gga.178.1.S1_s_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4965.1.S1_a_at   | lymphotactin  dedicator of cytokinesis 10  Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2 similar to immunoglobulin-like receptor CHIR-B2 precursor similar to T-cell receptor gamma Vg3-Jg3                             | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.488<br>5.468<br>5.454<br>5.299<br>5.279<br>5.271<br>5.250<br>5.180<br>5.162<br>5.131          |
| Immunity/defense | Gga.542.1.S1_at GgaAffx.21398.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4964.5.S1_a_at Gga.7064.1.S1_at Gga.7064.1.S1_at Gga.4964.17.S1_x_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at Gga.4964.2.S1_a_at  Gga.16555.1.S1_at Gga.1781.S1_s_at Gga.1781.S1_s_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2 similar to immunoglobulin-like receptor CHIR-B2 precursor similar to T-cell receptor gamma Vg3-Jg3 Lymphocyte-specific protein 1 | 6.045 5.998 5.811 5.807 5.646 5.593 5.554 5.493 5.488 5.468 5.454 5.299 5.279 5.271 5.250 5.180 5.162 5.131 5.120 5.102   |
| Immunity/defense                                   | Gga.542.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s at GgaAffx.24298.1.S1_s at Gga.4964.5.S1_a_at  Gga.7064.1.S1_at Gga.4964.5.S1_a_at  Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.16655.1.S1_at Gga.4964.54.A1_x_at Gga.178.1.S1_s_at Gga.4964.22.S1_x_at Gga.4964.23.S1_x_at | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2 similar to T-cell receptor gamma Vg3-Jg3 Lymphocyte-specific protein 1 B-cell CLL/lymphoma 6 (zinc finger protein 51)            | 6.045 5.998 5.811 5.807 5.646 5.593 5.554 5.493 5.489 5.468 5.454 5.299 5.279 5.271 5.250 5.180 5.162 5.131 5.120 5.102 5.042   |
| Immunity/defense  | Gga.542.1.S1_at GgaAffx.21398.1.S1_at GgaAffx.21398.1.S1_at Gga.4491.1.S1_s_at Gga.4964.5.S1_a_at Gga.7064.1.S1_at Gga.7064.1.S1_at Gga.4964.17.S1_x_at Gga.4964.17.S1_x_at Gga.4964.3.S1_x_at Gga.4964.2.S1_a_at  Gga.11252.1.S1_at Gga.4964.2.S1_a_at  Gga.16555.1.S1_at Gga.1781.S1_s_at Gga.1781.S1_s_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.4964.22.S1_x_at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at Gga.6551.S1_a at   | lymphotactin dedicator of cytokinesis 10 Lymphocyte-specific protein 1 interleukin 20 receptor, alpha similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 immunoglobulin superfamily, member 1 interleukin 7 receptor similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma V2.6a /// similar to T-cell receptor gamma Vg3-Jg3 similar to T cell receptor gamma /// similar to T-cell receptor gamma Vg3-Jg3 chemokine (C-C motif) ligand 19 dedicator of cytokinesis 8 histocompatibility (minor) HA-1 Similar to T-cell receptor gamma chain Vg3-Jg3 chemokine (C-C motif) ligand 1 guanylate binding protein Similar to T-cell receptor gamma chain Vg1-Jg2 similar to immunoglobulin-like receptor CHIR-B2 precursor similar to T-cell receptor gamma Vg3-Jg3 Lymphocyte-specific protein 1 | 6.045<br>5.998<br>5.811<br>5.807<br>5.646<br>5.593<br>5.554<br>5.493<br>5.488<br>5.468<br>5.454<br>5.299<br>5.279<br>5.271<br>5.250<br>5.162<br>5.131<br>5.120<br>5.102 |

| Immunity/defense       | Gga.19.1.S1_at          | interleukin 1, beta  | 5.023 |
|------------------------|-------------------------|--|-------|
| Immunity/defense       | GgaAffx.1625.1.S1_s_at  | complement factor H  | 4.910 |
| Immunity/defense       | Gga.4964.1.S1 x at      | similar to T-cell receptor gamma Vg3-Jg3                         | 4.909 |
| Immunity/defense       | GgaAffx.7251.1.S1_at    | chemokine (C-C motif) receptor 6                                 | 4.853 |
| Immunity/defense       | GgaAffx.5454.1.S1_at    | inducible T-cell co-stimulator                                   | 4.850 |
|                        |                         |  |       |
| Immunity/defense       | Gga.6529.1.S1_at        | Fc fragment of IgE, high affinity I, receptor for; gamma         | 4.849 |
|                        |                         | polypeptide  |       |
| Immunity/defense       | GgaAffx.20498.1.S1_s_at | monocyte to macrophage differentiation-associated                | 4.758 |
| Immunity/defense       | Gga.4964.4.S1_x_at      | similar to T cell receptor gamma /// similar to T-cell receptor  | 4.613 |
| , ,, ,, ,,             | 3                       | gamma chain Vg1-Jg2  |       |
| Immunity/defense       | Cap 4414 1 S1 a at      | CD74 molecule, major histocompatibility complex, class II        | 4.574 |
| iriiriuriity/delerise  | Gga.4414.1.S1_s_at      | CD74 molecule, major histocompatibility complex, class if        | 4.574 |
|                        |                         | invariant chain  |       |
| Immunity/defense       | GgaAffx.26385.1.S1_s_at | dedicator of cytokinesis 10                                      | 4.569 |
| Immunity/defense       | Gga.18469.1.S1 s at     | dedicator of cytokinesis 8                                       | 4.459 |
| Immunity/defense       | Gga.276.1.S1_at         | early B-cell factor 1  | 4.410 |
| Immunity/defense       | Gga.65.1.S1 x at        | similar to T-cell receptor gamma Vg3-Jg3                         | 4.396 |
|                        | Gga.6492.1.S1 at        | similar to chemokine CXCL13/BCA-1                                |       |
| Immunity/defense       |                         |  | 4.390 |
| Immunity/defense       | Gga.3027.1.S1_at        | CD40 ligand (TNF superfamily, member 5, hyper-lgM syndrome)      | 4.359 |
|                        |                         |  |       |
| Immunity/defense       | Gga.4964.11.S1_x_at     | similar to T-cell receptor gamma V2.6a /// similar to T-cell     | 4.265 |
| •                      |                         | receptor gamma Vg3-Jg3   |       |
| Immunity/defense       | Gga.2734.1.S2 at        | activated leukocyte cell adhesion molecule                       | 4.249 |
| Immunity/defense       | Gga.15811.2.S1_at       | cytokine-like nuclear factor n-pac                               | 4.236 |
|                        |                         |  |       |
| Immunity/defense       | Gga.4964.53.S1_x_at     | similar to T-cell receptor gamma Vg3-Jg3                         | 4.206 |
| Immunity/defense       | Gga.4964.54.S1_x_at     | similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to T- | 4.099 |
|                        |                         | cell receptor gamma Vg3-Jg3                                      |       |
| Immunity/defense       | GgaAffx.7943.1.S1_s_at  | neutrophil cytosolic factor 4, 40kDa                             | 4.086 |
| Immunity/defense       | Gga.4964.20.S1_x_at     | similar to T-cell receptor gamma Vg3-Jg3 /// similar to T-cell   | 4.051 |
| IIIIII dility/deletise | Oga.+304.20.01_x_at     |  | 4.001 |
|                        | 0 0500 1 01 1           | receptor gamma chain Vg3-Jg1                                     | 4.00= |
| Immunity/defense       | Gga.9563.1.S1_at        | chemokine (C-C motif) ligand 4 /// chemokine (C-C motif) ligand  | 4.025 |
|                        |                         | 5  |       |
| Immunity/defense       | GgaAffx.7589.1.S1 at    | chemokine (C-X3-C motif) receptor 1                              | 4.018 |
| Immunity/defense       | Gga.12516.1.S1 s at     | interleukin 20 receptor, alpha                                   | 3.896 |
| Immunity/defense       | Gga.4964.25.S1_x_at     | similar to T-cell receptor gamma chain Vg3-Jg3 /// similar to T- | 3.794 |
| IIIIIIdility/deletise  | Oga.+304.25.01_x_at     | cell receptor gamma Vg3-Jg3                                      | 3.734 |
|                        | 0 40000 0 04            |  |       |
| Immunity/defense       | Gga.13336.3.S1_a_at     | MHC class II antigen B-F minor heavy chain /// MHC class II      | 3.775 |
|                        |                         | beta chain   |       |
| Immunity/defense       | Gga.575.1.S1 at         | CD8a molecule  | 3.768 |
| Immunity/defense       | Gga.4185.1.S2 at        | Interferon (alpha, beta and omega) receptor 1                    | 3.730 |
| Immunity/defense       | Gga.2510.1.S1 at        | complement component 3   | 3.701 |
| Immunity/defense       | Gga.13336.5.S1_x_at     | MHC class II antigen B-F minor heavy chain /// MHC class II      | 3.682 |
| inimunity/delense      | Gya. 15550.5.5 1_x_at   |  | 3.002 |
|                        |                         | beta chain   |       |
| Immunity/defense       | Gga.10606.1.S1_at       | suppressor of cytokine signaling 1                               | 3.610 |
| Immunity/defense       | Gga.13336.3.S1_x_at     | MHC class II antigen B-F minor heavy chain /// MHC class II      | 3.600 |
|                        |                         | beta chain   |       |
| Immunity/defense       | GgaAffx.8901.1.S1_at    | lymphoid-restricted membrane protein                             | 3.578 |
| Immunity/defense       | Gga.16267.1.S1_s_at     | similar to MHC Rfp-Y class I alpha chain /// similar to MHC Rfp- | 3.476 |
| inimunity/delense      | Gya. 10207. 1.51_5_at   |  | 3.470 |
|                        |                         | Y class I alpha chain  |       |
| Immunity/defense       | Gga.4491.1.A1_at        | Lymphocyte-specific protein 1                                    | 3.454 |
| Immunity/defense       | Gga.1328.2.A1_at        | Beta-2-microglobulin   | 3.439 |
| Immunity/defense       | Gga.4995.1.A1_at        | Similar to T-cell receptor gamma chain Vg2-Jg3                   | 3.401 |
| Immunity/defense       | GgaAffx.11658.1.S1 s at | neutrophil cytosolic factor 1                                    | 3.382 |
| Immunity/defense       | Gga.4964.6.S1 x at      | similar to T cell receptor gamma /// similar to T-cell receptor  | 3.380 |
| manufity/deletise      | Oga.+304.0.01_x_at      |  | 3.300 |
|                        | 0 0                     | gamma Vg3-Jg3  |       |
| Immunity/defense       | Gga.2529.1.S1_a_at      | interleukin 1 receptor-like 1                                    | 3.313 |
| Immunity/defense       | Gga.7100.1.S1_at        | similar to macrophage inflammatory protein-2                     | 3.199 |
| Immunity/defense       | Gga.15027.1.S1 at       | Signaling lymphocytic activation molecule family member 1        | 3.187 |
| Immunity/defense       | Gga.916.1.S1 at         | interferon, gamma  | 3.104 |
| Immunity/defense       | Gga.4973.3.S1_x_at      | MHC class I antigen B-F minor heavy chain                        | 3.085 |
|                        |                         |  |       |
| Immunity/defense       | GgaAffx.21845.2.S1_s_at | CD74 molecule, major histocompatibility complex, class II        | 3.070 |
|                        |                         | invariant chain  |       |
| Immunity/defense       | GgaAffx.12703.1.S1_at   | similar to Toll-like receptor 21                                 | 3.063 |
| Immunity/defense       | GgaAffx.12160.1.S1_s_at | cytokine receptor-like factor 3                                  | 3.041 |
| Immunity/defense       | Gga.7057.1.S1 at        | caspase recruitment domain family, member 11                     | 3.036 |
| Immunity/defense       | GgaAffx.26702.1.S1_s_at | similar to dedicator of cytokinesis 11                           | 3.026 |
| Immunity/defense       | Gga.9732.1.S1 at        | inter-alpha (globulin) inhibitor H5                              | 3.020 |
|                        |                         |  |       |
| Immunity/defense       | Gga.1045.1.S1_at        | similar to dedicator of cytokinesis 11                           | 3.002 |
| Immunity/defense       | Gga.8178.1.S1_at        | interferon stimulated exonuclease gene 20kDa-like 2              | 0.477 |
| Immunity/defense       | Gga.5922.2.S1_a_at      | platelet-activating factor acetylhydrolase 2, 40kDa              | 0.449 |
| Immunity/defense       | GgaAffx.26288.1.S1_s_at | complement component 1, r subcomponent                           | 0.447 |
| Immunity/defense       | Gga.11984.1.S1_at       | dedicator of cytokinesis 5                                       | 0.399 |
|                        |                         |  | 0.347 |
| Immunity/defense       | GgaAffx.20791.1.S1_at   | interleukin 28B (interferon, lambda 3)                           |       |
| Mitochondrial protein  | Gga.5224.1.S1_at        | Carbonic anhydrase VB, mitochondrial                             | 3.017 |
| Mitochondrial protein  | GgaAffx.12907.1.S1_at   | mitochondrial ribosomal protein L18                              | 0.495 |
| Mitochondrial protein  | GgaAffx.10169.1.S1_at   | leucyl-tRNA synthetase 2, mitochondrial                          | 0.493 |
|                        |                         | •  |       |

| Mitochondrial protein                      | GgaAffx.23789.1.S1_at                | peptidase (mitochondrial processing) alpha                                   | 0.489  |
|--|--------------------------------------|--|--------|
| Mitochondrial protein                      | Gga.6085.3.S1_a_at                   | mitochondrial ribosomal protein S6   | 0.444  |
| Mitochondrial protein                      | GgaAffx.1241.1.S1_at                 | mitochondrial ribosomal protein S31  | 0.444  |
| Mitochondrial protein                      | GgaAffx.2318.1.S1_at                 | similar to Translocase of outer mitochondrial membrane 20                    | 0.443  |
|  |                                      | homolog (yeast)  |        |
| Mitochondrial protein                      | GgaAffx.194.1.S1_at                  | mitochondrial ribosomal protein L3   | 0.411  |
| Mitochondrial protein                      | GgaAffx.9649.1.S1_at                 | solute carrier family 25 (mitochondrial carrier, brain), member 14           | 0.405  |
|  |                                      |  |        |
| Mitochondrial protein                      | GgaAffx.9403.1.S1_s_at               | mitochondrial translational initiation factor 3                              | 0.391  |
| Mitochondrial protein                      | Gga.4006.2.S1_a_at                   | mitochondrial ribosomal protein L39  | 0.380  |
| Mitochondrial protein                      | GgaAffx.23494.1.S1_s_at              | ATP synthase, H+ transporting, mitochondrial F0 complex,                     | 0.319  |
|  |                                      | subunit F2   |        |
| Protein degradation                        | Gga.1111.1.S1_a_at                   | ubiquitin specific peptidase 18  | 3.656  |
| Protein degradation                        | GgaAffx.26411.1.S1 s at              | proteasome (prosome, macropain) 26S subunit, non-ATPase, 6                   | 0.487  |
| Protein degradation                        | GgaAffx.25545.1.S1_at                | proteasome (prosome, macropain) subunit, beta type, 2                        | 0.467  |
| Protein degradation                        | GgaAffx.5008.1.S1 at                 | ubiquitin specific peptidase 34  | 0.413  |
| Protein degradation                        | GgaAffx.7526.1.S1_at                 | similar to cullin 4A   | 0.411  |
| Protein degradation                        | GgaAffx.26602.1.S1 at                | proteasome (prosome, macropain) 26S subunit, ATPase, 6                       | 0.400  |
| Protein degradation                        | Gga.4152.1.S1_s_at                   | proteasome (prosome, macropain) subunit, alpha type, 1                       | 0.382  |
| Protein degradation                        | GgaAffx.9792.1.S1 at                 | cullin-associated and neddylation-dissociated 2 (putative)                   | 0.373  |
| Protein degradation                        | GgaAffx.4984.2.S1 s at               | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1                   | 0.274  |
| Protein modification                       | Gga.6553.1.S1 at                     | cathepsin G  | 12.681 |
| Protein modification                       | Gga.5393.1.S1_at                     | similar to serine protease   | 12.146 |
| Protein modification                       | Gga.3867.1.S1 at                     | prion protein (p27-30) (Creutzfeldt-Jakob disease)                           | 10.834 |
| Protein modification                       | Gga.18980.1.S1 at                    | NUAK family, SNF1-like kinase, 1   | 10.073 |
| Protein modification                       | Gga.7788.1.S1 at                     | similar to phospholipase A2 inhibitor gamma subunit B                        | 9.230  |
| Protein modification                       | GgaAffx.5597.1.S1_at                 | mitogen-activated protein kinase kinase kinase kinase 4                      | 9.224  |
| Protein modification                       | Gga.11824.1.S1 at                    | Cystatin F (leukocystatin)   | 8.876  |
| Protein modification                       | Gga.606.1.S1_at                      | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene                        | 8.172  |
| Fioteni modification                       | Gga.000.1.31_at                      | homolog  | 0.172  |
| Protein modification                       | GgaAffx.20295.1.S1 at                | NUAK family, SNF1-like kinase, 1   | 8.084  |
| Protein modification                       | Gga.415.1.S1 at                      | serpin peptidase inhibitor, clade B (ovalbumin), member 10                   | 8.026  |
| Protein modification                       | Gga.415.1.51_at<br>Gga.1193.1.S2 at  |  | 7.156  |
|  | Gga.1193.1.S2_at<br>Gga.1193.1.S1 at | protein tyrosine phosphatase, receptor type, C                               | 6.665  |
| Protein modification  Protein modification | Gga.1148.1.S1_at                     | protein tyrosine phosphatase, receptor type, C                               | 6.428  |
|  | Gga.11016.1.S1_at                    | ST6 beta-galactosamide alpha-2,6-sialyltranferase 1  B locus M alpha chain 1 | 6.345  |
| Protein modification                       |                                      |  |        |
| Protein modification                       | Gga.16596.1.S1_at                    | phosphotyrosine interaction domain containing 1                              | 6.342  |
| Protein modification                       | GgaAffx.11885.1.S1_s_at              | Bruton agammaglobulinemia tyrosine kinase                                    | 6.278  |
| Protein modification                       | Gga.5273.1.S1_at                     | Adrenergic, beta, receptor kinase 2  | 6.103  |
| Protein modification                       | Gga.1148.1.S2_at                     | ST6 beta-galactosamide alpha-2,6-sialyltranferase 1                          | 5.965  |
| Protein modification                       | Gga.11456.1.S1_at                    | cystatin A (stefin A)  | 5.810  |
| Protein modification                       | Gga.3379.2.S1_at                     | SH3-domain kinase binding protein 1  | 5.403  |
| Protein modification                       | Gga.4105.2.S1_a_at                   | serpin peptidase inhibitor, clade E (nexin, plasminogen activator            | 5.271  |
|  |                                      | inhibitor type 1), member 2  |        |
| Protein modification                       | GgaAffx.7823.1.S1_s_at               | serine/threonine kinase 17a  | 5.240  |
| Protein modification                       | Gga.12533.1.S1_at                    | protein tyrosine phosphatase-like A domain containing 2                      | 5.231  |
| Protein modification                       | Gga.6964.1.S1_at                     | protein kinase C, beta   | 5.112  |
| Protein modification                       | GgaAffx.8960.1.S1_at                 | TXK tyrosine kinase  | 5.110  |
| Protein modification                       | GgaAffx.26700.1.S1_s_at              | protein kinase C, beta   | 4.995  |
| Protein modification                       | GgaAffx.8628.1.S1_at                 | granzyme K (granzyme 3; tryptase II)   | 4.983  |
| Protein modification                       | GgaAffx.12547.1.S1_at                | ST3 beta-galactoside alpha-2,3-sialyltransferase 2                           | 4.680  |
| Protein modification                       | Gga.1035.1.S1_at                     | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-                  | 4.648  |
|  |                                      | glutamyltransferase)   |        |
| Protein modification                       | GgaAffx.968.3.S1_s_at                | zeta-chain (TCR) associated protein kinase 70kDa                             | 4.625  |
| Protein modification                       | Gga.7157.1.S1_at                     | protein kinase C, beta   | 4.554  |
| Protein modification                       | GgaAffx.12557.1.S1_s_at              | tyrosylprotein sulfotransferase 2  | 4.469  |
| Protein modification                       | Gga.9012.1.S1_at                     | serine/threonine kinase 17b  | 4.276  |
| Protein modification                       | Gga.11865.1.S1_at                    | similar to Cathepsin L, a  | 4.073  |
| Protein modification                       | GgaAffx.6712.2.S1_s_at               | protein kinase D3  | 3.941  |
| Protein modification                       | Gga.6713.1.S1_at                     | granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated                    | 3.829  |
|  |                                      | serine esterase 3)   |        |
| Protein modification                       | Gga.7011.1.S1_a_at                   | similar to cAMP-dependent protein kinase inhibitor gamma                     | 3.823  |
| Protein modification                       | Gga.8329.1.S1_at                     | protein kinase C, eta  | 3.815  |
| Protein modification                       | GgaAffx.11653.1.S1_s_at              | serine/threonine kinase 17b  | 3.802  |
| Protein modification                       | Gga.2435.1.S2_at                     | Janus kinase 1 (a protein tyrosine kinase)                                   | 3.532  |
| Protein modification                       | Gga.12120.1.S1 at                    | protein kinase C and casein kinase substrate in neurons 3                    | 3.491  |
| Protein modification                       | Gga.11468.1.S1 a at                  | peptidylprolyl isomerase C (cyclophilin C)                                   | 3.474  |
| Protein modification                       | Gga.19289.1.S1_at                    | Prolylcarboxypeptidase (angiotensinase C)                                    | 3.378  |
| Protein modification                       | GgaAffx.6712.1.S1 at                 | protein kinase D3  | 3.231  |
| Protein modification                       | GgaAffx.378.1.S1_at                  | protein tyrosine phosphatase, non-receptor type 7                            | 3.158  |
| Protein modification                       | GgaAffx.12579.1.S1_at                | dual specificity phosphatase 10  | 3.107  |
| Protein modification                       | GgaAffx.22748.1.S1 at                | mitogen-activated protein kinase kinase kinase kinase 4                      | 3.033  |
| Protein modification                       | GgaAffx.9707.1.S1_s_at               | protein-L-isoaspartate (D-aspartate) O-methyltransferase                     | 3.012  |
|  |                                      | domain containing 1  | 0.012  |
| Protein modification                       | Gga.536.1.S1_a_at                    | 2'-5'-oligoadenylate synthetase-like   | 3.000  |
| 1 Totali modification                      | Oga.000.1.01_a_at                    | 2 0 digoaderiyiate syritictase-like  | 3.000  |

| Protein modification                    | GgaAffx.22730.1.S1_at                         | phosphatase and tensin homolog (mutated in multiple advanced                                 | 0.499            |
|---|---|--|------------------|
| Protein modification                    | GgaAlix.22730.1.51_at                         | cancers 1), pseudogene 1   | 0.499            |
| Protein modification                    | Gga.19366.1.S1 s at                           | CDC-like kinase 4  | 0.499            |
| Protein modification                    | GgaAffx.1012.1.S1_at                          | Tousled-like kinase 1  | 0.476            |
| Protein modification                    | GgaAffx.25489.1.S1_at                         | TBC domain-containing protein kinase-like  | 0.469            |
| Protein modification                    | GgaAffx.10968.1.S1_at                         | peptidylprolyl isomerase domain and WD repeat containing 1                                   | 0.465            |
| Protein modification                    | Gga.16991.2.S1_a_at                           | Phosphatase and tensin homolog   | 0.462            |
| Protein modification                    | GgaAffx.6526.1.S1_s_at                        | peptidylprolyl isomerase E (cyclophilin E)   | 0.455            |
| Protein modification                    | Gga.9011.2.S1_at                              | protein phosphatase 1, regulatory (inhibitor) subunit 12A                                    | 0.440            |
| Protein modification                    | Gga.7118.2.S1_s_at                            | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform                         | 0.439            |
| Protein modification                    | GgaAffx.9058.2.S1_s_at                        | protein phosphatase 1, regulatory (inhibitor) subunit 8                                      | 0.436            |
| Protein modification                    | GgaAffx.1184.1.S1_at                          | mitogen-activated protein kinase kinase kinase 4   | 0.433            |
| Protein modification                    | Gga.5698.1.S1_at                              | methyl-CpG binding domain protein 5  | 0.418            |
| Protein modification                    | Gga.267.1.S1_at                               | protein-L-isoaspartate (D-aspartate) O-methyltransferase                                     | 0.416            |
| Protein modification                    | GgaAffx.24899.1.S1_at                         | integrin-linked kinase-associated serine/threonine phosphatase 2C                            | 0.407            |
| Protein modification                    | GgaAffx.23800.1.S1_at                         | pitrilysin metallopeptidase 1  | 0.406            |
| Protein modification                    | Gga.19278.1.S1_s_at                           | protein arginine methyltransferase 7   | 0.401            |
| Protein modification                    | Gga.6118.1.S1_at                              | serine/threonine kinase receptor associated protein  | 0.399            |
| Protein modification                    | GgaAffx.2219.3.S1_s_at                        | cathepsin Z  | 0.395            |
| Protein modification                    | GgaAffx.8894.1.S1_at                          | calcium/calmodulin-dependent serine protein kinase (MAGUK family)                            | 0.392            |
| Protein modification                    | Gga.18973.1.S1 at                             | Megakaryocyte-associated tyrosine kinase   | 0.387            |
| Protein modification                    | GgaAffx.25618.1.S1 at                         | protein phosphatase 1, regulatory (inhibitor) subunit 1B                                     | 0.359            |
| Protein modification                    | Gga.16586.1.S1_at                             | protein phosphatase 1, regulatory (inhibitor) subunit 13B                                    | 0.357            |
| Protein modification                    | Gga.9700.4.S1_a_at                            | serine/threonine kinase 38 like  | 0.314            |
| Protein modification                    | Gga.51.1.S1_at                                | ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)             | 0.294            |
| Protein modification                    | GgaAffx.25266.1.S1 at                         | protein kinase C, alpha  | 0.282            |
| Signal transduction                     | Gga.8030.1.S1 at                              | tissue factor pathway inhibitor 2  | 19.735           |
| Signal transduction                     | Gga.3259.1.S1 at                              | angiopoietin 2   | 15.883           |
| Signal transduction                     | GgaAffx.13210.1.S1_at                         | Src-like-adaptor   | 15.548           |
| Signal transduction                     | GgaAffx.12646.1.S1_at                         | spleen tyrosine kinase   | 15.136           |
| Signal transduction                     | Gga.4070.1.S1_at                              | Colony stimulating factor 1 receptor   | 13.456           |
| Signal transduction                     | Gga.10829.1.S1_s_at                           | endothelin receptor type B   | 13.023           |
| Signal transduction                     | Gga.15362.1.S1_at                             | regulator of G-protein signalling 18   | 12.172           |
| Signal transduction                     | Gga.5008.1.S1_at                              | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)                          | 12.162           |
| Signal transduction                     | Gga.7838.1.S1_at                              | colony stimulating factor 2 receptor, alpha, low-affinity                                    | 11.274           |
|   |   | (granulocyte-macrophage)   |                  |
| Signal transduction                     | Gga.1287.1.S1_at                              | RAS guanyl releasing protein 3 (calcium and DAG-regulated)                                   | 11.087           |
| Signal transduction                     | GgaAffx.11475.1.S1_s_at                       | Ras association (RalGDS/AF-6) domain family member 2   | 10.759           |
| Signal transduction                     | GgaAffx.13138.1.S1_at<br>Gga.1348.1.S1 at     | tumor necrosis factor (ligand) superfamily, member 13b                                       | 10.559           |
| Signal transduction Signal transduction | Gga.1346.1.S1_at                              | Rho GTPase activating protein 24 colony stimulating factor 2 receptor, alpha, low-affinity   | 10.525<br>10.007 |
| Signal transduction                     | Gga.9002.1.31_at                              | (granulocyte-macrophage)   | 10.007           |
| Signal transduction                     | Gga.8508.1.S2_s_at                            | Src-like-adaptor   | 9.750            |
| Signal transduction                     | Gga.3306.1.S1_s_at                            | endothelin receptor type B   | 9.680            |
| Signal transduction                     | Gga.10418.1.S1_at                             | Guanine nucleotide binding protein (G protein), gamma 10                                     | 9.372            |
| Signal transduction                     | Gga.18933.1.S1_s_at                           | Ras association (RalGDS/AF-6) domain family 5  | 9.355            |
| Signal transduction                     | GgaAffx.13005.1.S1_at                         | purinergic receptor P2Y, G-protein coupled, 8  | 9.317            |
| Signal transduction                     | GgaAffx.7881.1.S1_s_at                        | Rho GTPase activating protein 15   | 9.272            |
| Signal transduction                     | Gga.1585.1.S2_at                              | stathmin-like 2  | 9.250            |
| Signal transduction Signal transduction | Gga.8164.1.S1_a_at<br>GgaAffx.11864.1.S1 at   | similar to Ras-related protein Rab-10 G protein-coupled receptor 174                         | 8.807<br>8.430   |
| Signal transduction                     | Gga.8789.1.S1_at                              | phosphoinositide-3-kinase, catalytic, delta polypeptide                                      | 8.124            |
| Signal transduction                     | Gga.18945.1.S1 at                             | phosphatidylinositol-3,4,5-trisphosphate-dependent Rac                                       | 8.070            |
| Oignai transduction                     | Gga. 10045. 1.01_at                           | exchange factor 1  | 0.070            |
| Signal transduction                     | Gga.9880.1.S1_at                              | Purinergic receptor P2Y, G-protein coupled, 13   | 8.046            |
| Signal transduction                     | Gga.7334.1.S1_at                              | amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein          | 7.585            |
| Signal transduction                     | GgaAffx.21779.1.S1_s_at                       | stathmin-like 2  | 7.539            |
| Signal transduction                     | Gga.10018.1.S1 at                             | Ras and Rab interactor 3   | 7.497            |
| Signal transduction                     | GgaAffx.12475.1.S1_at                         | TNF receptor-associated factor 5   | 7.471            |
| Signal transduction                     | GgaAffx.12029.1.S1_at                         | tumor necrosis factor receptor superfamily, member 1B  | 7.459            |
| Signal transduction                     | GgaAffx.12969.1.S1_at                         | phosphoinositide-3-kinase, regulatory subunit 5, p101  | 7.271            |
| Signal transduction                     | GgaAffx.11713.1.S1_s_at                       | Rho guanine nucleotide exchange factor (GEF) 3   | 7.242            |
| Signal transduction                     | Gga.2696.1.S1_at                              | similar to selectin ligand interactor cytoplasmic-1  | 7.207            |
| Signal transduction                     | GgaAffx.12948.1.S1_s_at                       | RAS guanyl releasing protein 3 (calcium and DAG-regulated)                                   | 7.062            |
| Signal transduction                     | GgaAffx.13096.1.S1_at                         | Ras association (RalGDS/AF-6) domain family 5  | 7.014            |
| Signal transduction Signal transduction | Gga.4359.1.S1_s_at<br>GgaAffx.26579.1.S1_s_at | tumor necrosis factor (ligand) superfamily, member 13b  Colony stimulating factor 1 receptor | 6.985<br>6.896   |
| Signal transduction                     | Gga.539.1.S1_at                               | CD247 molecule   | 6.880            |
| Signal transduction                     | Gga.8094.1.S1 a at                            | Rho GDP dissociation inhibitor (GDI) beta  | 6.646            |
| - grantaniodadion                       | 0.500 1.1.01_u_ut                             | 15. a.ooo.a.a  | 0.040            |

| Signal transduction                     | Gga.6239.1.S1_at        | regulator of G-protein signalling 1                             | 6.607  |
|---|-------------------------|---|--------|
| Signal transduction                     | Gga.11560.2.S1_a_at     | phosphoinositide-3-kinase adaptor protein 1                     | 6.604  |
| Signal transduction                     | Gga.6387.1.S1_at        | ras-related C3 botulinum toxin substrate 2 (rho family, small   | 6.596  |
|   |                         | GTP binding protein Rac2)                                       |        |
| Signal transduction                     | GgaAffx.6562.1.S1_at    | G protein-coupled receptor 171                                  | 6.591  |
| Signal transduction                     | GgaAffx.10679.1.S1_at   | colony stimulating factor 2 receptor, alpha, low-affinity       | 6.521  |
|   |                         | (granulocyte-macrophage)  |        |
| Signal transduction                     | Gga.3154.1.S1 at        | ras homolog gene family, member Q                               | 6.330  |
| Signal transduction                     | Gga.5148.1.S2 s at      | tumor necrosis factor receptor superfamily, member 1B           | 6.305  |
| Signal transduction                     | GgaAffx.6562.1.A1_at    | G protein-coupled receptor 171                                  | 6.256  |
| Signal transduction                     | GgaAffx.11426.1.S1_at   | tumor necrosis factor receptor superfamily, member 18           | 6.131  |
| Signal transduction                     | Gga.5148.1.S1 at        | tumor necrosis factor receptor superfamily, member 1B           | 5.991  |
| Signal transduction                     | Gga.8823.1.S1_s_at      | CKLF-like MARVEL transmembrane domain containing 7              | 5.990  |
| Signal transduction                     | GgaAffx.3477.1.S1 at    | G protein-coupled receptor 35                                   | 5.986  |
|   |                         |   |        |
| Signal transduction                     | GgaAffx.12575.1.S1_s_at | ankyrin repeat and SOCS box-containing 9                        | 5.942  |
| Signal transduction                     | Gga.1027.1.S1_at        | similar to Rho-GTPase-activating protein 6 (Rho-type GTPase-    | 5.775  |
|   |                         | activating protein RhoGAPX-1)                                   |        |
| Signal transduction                     | Gga.998.2.S1_a_at       | CD3d molecule, delta (CD3-TCR complex)                          | 5.712  |
| Signal transduction                     | Gga.11395.1.S1_at       | G protein-coupled receptor 34                                   | 5.576  |
| Signal transduction                     | GgaAffx.24611.2.S1_s_at | similar to histamine H3 receptor H3S                            | 5.551  |
| Signal transduction                     | GgaAffx.4780.1.S1_at    | signal transducer and activator of transcription 1, 91kDa       | 5.283  |
| Signal transduction                     | GgaAffx.12684.1.S1_s_at | Rho GTPase activating protein 25                                | 5.257  |
| Signal transduction                     | Gga.11516.1.S1_at       | Pyrimidinergic receptor P2Y, G-protein coupled, 6               | 5.235  |
| Signal transduction                     | Gga.4359.1.S2 s at      | tumor necrosis factor (ligand) superfamily, member 13b          | 5.162  |
| Signal transduction                     | GgaAffx.12918.1.S1 s at | cytohesin 4   | 5.126  |
| Signal transduction                     | Gga.4970.1.S1 at        | CD3e molecule, epsilon (CD3-TCR complex)                        | 4.995  |
| Signal transduction                     | Gga.4970.1.S1_at        | Similar to contactin associated protein                         | 4.995  |
| Signal transduction Signal transduction | GgaAffx.11771.1.S1 at   | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6            | 4.976  |
|   |                         |   |        |
| Signal transduction                     | Gga.352.1.S1_at         | regulator of G-protein signaling 20                             | 4.700  |
| Signal transduction                     | Gga.10030.1.S1_s_at     | phosphoinositide-3-kinase, regulatory subunit 5, p101           | 4.610  |
| Signal transduction                     | Gga.986.1.S1_s_at       | tumor necrosis factor receptor superfamily, member 18           | 4.476  |
| Signal transduction                     | GgaAffx.8756.1.S1_at    | similar to FKSG15   | 4.405  |
| Signal transduction                     | GgaAffx.10807.1.S1_at   | Epstein-Barr virus induced gene 2 (lymphocyte-specific G        | 4.287  |
|   |                         | protein-coupled receptor)                                       |        |
| Signal transduction                     | Gga.1092.1.S1_s_at      | G protein-coupled receptor 174                                  | 4.282  |
| Signal transduction                     | Gga.3624.1.S1 at        | phosphodiesterase 3B, cGMP-inhibited                            | 3.977  |
| Signal transduction                     | GgaAffx.12014.1.S1_s_at | amyloid beta (A4) precursor protein-binding, family B, member 1 | 3.879  |
| o.g.rar transcauction                   |                         | interacting protein   | 0.0.0  |
| Signal transduction                     | Gga.4113.1.S1 at        | ras homolog gene family, member F (in filopodia)                | 3.743  |
| Signal transduction                     | GgaAffx.11590.1.S1 s at | cytohesin 1   | 3.702  |
|   | Gga.5148.1.S1 s at      | ,   |        |
| Signal transduction                     |                         | tumor necrosis factor receptor superfamily, member 1B           | 3.601  |
| Signal transduction                     | Gga.8752.1.S1_s_at      | sorting nexin 10  | 3.594  |
| Signal transduction                     | GgaAffx.3442.2.S1_s_at  | Rho guanine nucleotide exchange factor (GEF) 3                  | 3.579  |
| Signal transduction                     | GgaAffx.9008.1.S1_s_at  | parvin, gamma   | 3.410  |
| Signal transduction                     | Gga.17410.1.S1_at       | Glucocorticoid induced transcript 1                             | 3.362  |
| Signal transduction                     | Gga.9999.1.S1_at        | RAS p21 protein activator 3                                     | 3.341  |
| Signal transduction                     | GgaAffx.11861.1.S1_at   | RasGEF domain family, member 1A                                 | 3.313  |
| Signal transduction                     | Gga.19099.2.S1_a_at     | secreted protein, acidic, cysteine-rich (osteonectin)           | 3.312  |
| Signal transduction                     | GgaAffx.9971.2.S1_s_at  | G protein-coupled receptor kinase 4                             | 3.309  |
| Signal transduction                     | Gga.10465.1.S1 s at     | G protein-coupled receptor 65                                   | 3.259  |
| Signal transduction                     | Gga.12335.2.S1 s at     | cytohesin 4   | 3.246  |
| Signal transduction                     | Gga.12662.1.S1_at       | signal transducer and activator of transcription 1, 91kDa       | 3.235  |
| Signal transduction                     | Gga.3175.1.S1_at        | Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)     | 3.223  |
| Signal transduction                     | GgaAffx.11756.1.S1_at   | G protein-coupled receptor 137B                                 | 3.153  |
| Signal transduction                     | GgaAffx.1027.1.S1_at    | TNF receptor-associated factor 1                                | 3.135  |
| Signal transduction Signal transduction |                         | signal transducing adaptor family member 1                      | 3.053  |
|   | GgaAffx.7443.1.S1_at    |   |        |
| Signal transduction                     | GgaAffx.1691.1.A1_at    | regulator of G-protein signalling 5                             | 3.029  |
| Signal transduction                     | GgaAffx.5618.1.S1_at    | amyloid beta (A4) precursor protein-binding, family B, member 1 | 0.499  |
|   |                         | interacting protein   |        |
| Signal transduction                     | Gga.7708.1.S1_at        | agrin   | 0.497  |
| Signal transduction                     | Gga.4589.1.S3_at        | thyroid hormone receptor interactor 12                          | 0.496  |
| Signal transduction                     | GgaAffx.22041.1.S1_s_at | src kinase associated phosphoprotein 2                          | 0.476  |
| Signal transduction                     | GgaAffx.25488.1.S1_at   | TNF receptor-associated factor 6                                | 0.467  |
| Signal transduction                     | Gga.4101.1.S1_s_at      | diacylglycerol kinase, delta 130kDa                             | 0.463  |
| Signal transduction                     | Gga.10747.1.S1_s_at     | ankyrin 3   | 0.461  |
| Signal transduction                     | Gga.2166.3.S1_a_at      | hepatocyte growth factor (hepapoietin A; scatter factor)        | 0.458  |
| Signal transduction                     | GgaAffx.21433.1.S1_s_at | RAS, dexamethasone-induced 1                                    | 0.457  |
| Signal transduction                     | Gga.7797.1.S1_s_at      | Rac GTPase activating protein 1                                 | 0.427  |
| Signal transduction                     | GgaAffx.23134.1.S1_at   | insulin receptor substrate 1                                    | 0.427  |
| Signal transduction                     | Gga.8230.1.S1_at        | discs, large homolog 7 (Drosophila)                             | 0.384  |
|   |                         |   |        |
| Signal transduction                     | GgaAffx.25114.2.S1_s_at | lipopolysaccharide-induced TNF factor                           | 0.320  |
| Transporter/membrane trafficking        | Gga.2680.1.S1_at        | aquaporin 1 (Colton blood group)                                | 19.758 |
| Transporter/membrane trafficking        | Gga.918.1.S1_at         | potassium large conductance calcium-activated channel,          | 11.604 |
|   |                         | subfamily M, beta member 1                                      |        |
| Transporter/membrane trafficking        | Gga.9077.1.S1_at        | hydrogen voltage-gated channel 1                                | 9.945  |
|   |                         |   |        |

| Transporter/membrane trafficking | Gga.11184.1.S1 at       | potassium channel tetramerisation domain containing 12            | 9.018  |
|----------------------------------|-------------------------|---|--------|
| Transporter/membrane trafficking | Gga.12076.1.S1 at       | purinergic receptor P2X, ligand-gated ion channel, 5              | 5.915  |
| Transporter/membrane trafficking | Gga.871.1.S1_at         | solute carrier family 2 (facilitated glucose transporter), member | 5.714  |
| Transporter/membrane transcring  | Oga.071.1.51_at         | 3   | 3.7 14 |
| Transporter/membrane trafficking | Gga.14445.1.S1_s_at     | solute carrier family 1 (high affinity aspartate/glutamate        | 5.374  |
|                                  |                         | transporter), member 6  |        |
| Transporter/membrane trafficking | Gga.16544.1.S1_s_at     | chloride intracellular channel 2                                  | 5.361  |
| Transporter/membrane trafficking | Gga.1235.2.S1_at        | potassium voltage-gated channel, shaker-related subfamily,        | 5.274  |
| ·                                |                         | beta member 2   |        |
| Transporter/membrane trafficking | Gga.7278.1.S1_at        | Solute carrier family 25, member 29                               | 4.881  |
| Transporter/membrane trafficking | GgaAffx.10727.2.S1_at   | ATPase, class V, type 10A   | 4.785  |
| Transporter/membrane trafficking | Gga.6246.1.S1_at        | Rab interacting lysosomal protein-like 2                          | 4.724  |
| Transporter/membrane trafficking | Gga.7430.1.S1_at        | synaptotagmin XI  | 4.698  |
| Transporter/membrane trafficking | GgaAffx.8046.1.S1_s_at  | solute carrier family 41, member 2                                | 4.674  |
| Transporter/membrane trafficking | GgaAffx.5539.1.S1_s_at  | solute carrier family 1 (glutamate/neutral amino acid             | 4.495  |
|                                  |                         | transporter), member 4  |        |
| Transporter/membrane trafficking | Gga.17590.1.S1_s_at     | chloride intracellular channel 2                                  | 4.422  |
| Transporter/membrane trafficking | Gga.4594.1.S2_at        | ATPase, Na+/K+ transporting, beta 3 polypeptide                   | 4.070  |
| Transporter/membrane trafficking | Gga.4451.1.S1_at        | gelsolin  | 3.981  |
| Transporter/membrane trafficking | GgaAffx.1584.1.S1_at    | solute carrier family 9 (sodium/hydrogen exchanger), member 9     | 3.831  |
| Transporter/membrane trafficking | GgaAffx.1584.2.S1_s_at  | solute carrier family 9 (sodium/hydrogen exchanger), member 9     | 3.608  |
| Transporter/membrane trafficking | Gga.9127.1.S1_at        | ATPase, class V, type 10D   | 3.476  |
| Transporter/membrane trafficking | Gga.9816.1.S1_s_at      | chloride intracellular channel 2                                  | 3.436  |
| Transporter/membrane trafficking | Gga.1235.1.S1_at        | potassium voltage-gated channel, shaker-related subfamily,        | 3.434  |
|                                  |                         | beta member 2   |        |
| Transporter/membrane trafficking | Gga.4594.1.S1_at        | ATPase, Na+/K+ transporting, beta 3 polypeptide                   | 3.420  |
| Transporter/membrane trafficking | Gga.6941.1.S1_at        | Similar to guanine nucleotide exchange factor Lbc                 | 3.374  |
| Transporter/membrane trafficking | Gga.2564.1.S1_s_at      | adaptor-related protein complex 1, sigma 2 subunit                | 3.276  |
| Transporter/membrane trafficking | GgaAffx.22282.1.S1_at   | solute carrier family 29 (nucleoside transporters), member 1      | 0.497  |
| Transporter/membrane trafficking | Gga.458.1.S1_s_at       | ATPase, Ca++ transporting, plasma membrane 4                      | 0.488  |
| Transporter/membrane trafficking | Gga.18339.1.S1_s_at     | nucleoporin 54kDa   | 0.488  |
| Transporter/membrane trafficking | Gga.5104.1.S1_at        | nucleoporin 35kDa   | 0.480  |
| Transporter/membrane trafficking | Gga.7586.1.S1_at        | solute carrier family 23 (nucleobase transporters), member 2      | 0.474  |
| Transporter/membrane trafficking | GgaAffx.1444.1.S1_at    | karyopherin alpha 5 (importin alpha 6)                            | 0.468  |
| Transporter/membrane trafficking | GgaAffx.22855.1.S1_at   | RAB14, member RAS oncogene family                                 | 0.467  |
| Transporter/membrane trafficking | Gga.6181.1.S1_at        | potassium channel tetramerisation domain containing 10            | 0.461  |
| Transporter/membrane trafficking | GgaAffx.26684.1.S1_at   | solute carrier family 16, member 13 (monocarboxylic acid          | 0.451  |
|                                  |                         | transporter 13)   |        |
| Transporter/membrane trafficking | GgaAffx.24196.1.S1_s_at | potassium channel tetramerisation domain containing 20            | 0.448  |
| Transporter/membrane trafficking | GgaAffx.10181.1.S1_at   | syntaxin binding protein 3  | 0.430  |
| Transporter/membrane trafficking | GgaAffx.4428.2.S1_s_at  | vacuolar protein sorting 53 homolog (S. cerevisiae)               | 0.424  |
| Transporter/membrane trafficking | GgaAffx.6526.7.S1_s_at  | importin 7  | 0.421  |
| Transporter/membrane trafficking | Gga.12255.1.S1_s_at     | ATPase, H+ transporting, lysosomal V0 subunit a1                  | 0.413  |
| Transporter/membrane trafficking | Gga.16527.1.S1_at       | solute carrier family 43, member 2                                | 0.412  |
| Transporter/membrane trafficking | Gga.13215.1.S1_at       | RAB, member RAS oncogene family-like 5                            | 0.396  |
| Transporter/membrane trafficking | Gga.7931.1.S1_at        | nucleoporin 133kDa  | 0.271  |
|                                  |                         | <del>-</del>  |        |