| **Genes with significant differential expression for at least one time point.** | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | **Day 1** | **Day 3** | | **Day 6** | | **Day 10** | | **Day 13** | | **Day 27** | | **Day 42** | | **Day 70** | |
| **Gene Symbol** | **Probe Set ID** | **Gene Title** | **mean signal** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** |
| *ABCA1* | 203505_at | ATP-binding cassette, sub-family A (ABC1), member 1 | 359 | 1.75 | 0.00006 | 1.18 | 0.16047 | 1.37 | 0.00645 | 1.13 | 0.18533 | 1.15 | 0.17553 | 1.12 | 0.29663 | 1.29 | 0.03224 |
| *ABCC3* | 208161_s_at | ATP-binding cassette, sub-family C (CFTR/MRP), member 3 | 432 | 1.66* | 0.00006 | ND | | ND | | ND | | ND | | ND | | ND | |
| *ABHD2* | 63825_at | abhydrolase domain containing 2 | 997 | -1.29 | 0.00497 | -1.19 | 0.03054 | -1.47 | 0.00001 | -1.51 | 0.00030 | -1.64 | 0.00016 | -1.61 | 0.00001 | -1.75 | 0.00001 |
| *ADAR* | 201786_s_at | adenosine deaminase, RNA-specific | 7548 | 1.68 | 0.00000 | 1.5 | 0.00000 | 1.64 | 0.00000 | 1.47 | 0.00000 | 1.43 | 0.00000 | 1.38 | 0.00019 | 1.42 | 0.00000 |
| *ADK* | 204120_s_at | adenosine kinase | 162 | -1.54 | 0.00007 | -1.33 | 0.01659 | -1.27 | 0.01893 | -1.39 | 0.01355 | -1.14 | 0.21761 | -1.14 | 0.28551 | -1.42 | 0.00116 |
| *ADM* | 202912_at | adrenomedullin | 770 | 1.84 | 0.00097 | 1.27 | 0.12805 | 1.47 | 0.02847 | 1 | 0.98585 | 1.28 | 0.07742 | 1.13 | 0.31173 | 1.55 | 0.00139 |
| *AGRN* | 212285_s_at | agrin | 432 | 2.11 | 0.00000 | 1.69 | 0.00016 | 2.07 | 0.00000 | 1.86 | 0.00000 | 1.59 | 0.00003 | 1.73 | 0.00004 | 2.14 | 0.00000 |
| *AHR* | 202820_at | aryl hydrocarbon receptor | 609 | -1.26 | 0.02184 | -1.27 | 0.02097 | -1.34 | 0.01917 | -1.48 | 0.00341 | -1.56 | 0.00052 | -1.29 | 0.01896 | -1.63 | 0.00021 |
| *AIM2* | 206513_at | absent in melanoma 2 | 1078 | 1.64 | 0.00000 | -1.04 | 0.57488 | 1.18 | 0.01329 | -1.06 | 0.43730 | -1.06 | 0.45846 | -1.02 | 0.71671 | -1.07 | 0.45239 |
| *AKAP2 /// PALM2-AKAP2* | 202760_s_at | A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 protein | 711 | 1.53 | 0.00010 | 1.42 | 0.00023 | 1.74 | 0.00003 | 1.33 | 0.00679 | 1.45 | 0.00081 | 1.17 | 0.17255 | 1.53 | 0.00002 |
| *ALDH1A1* | 212224_at | aldehyde dehydrogenase 1 family, member A1 | 729 | -1.45 | 0.00001 | -1.72 | 0.00000 | -1.74 | 0.00000 | -2.03 | 0.00000 | -2.48 | 0.00000 | -2.47 | 0.00000 | -2.57 | 0.00000 |
| *ALDH2* | 201425_at | aldehyde dehydrogenase 2 family (mitochondrial) | 6406 | -1.45 | 0.00000 | -1.46 | 0.00000 | -1.55 | 0.00000 | -1.48 | 0.00000 | -1.52 | 0.00001 | -1.52 | 0.00004 | -1.45 | 0.00001 |
| *AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B /// LOC730924* | 208498_s_at | amylase, alpha 1A (salivary) /// alpha 1B (salivary) /// alpha 1C (salivary) /// alpha 2A (pancreatic) /// alpha 2B (pancreatic) /// similar to Pancreatic alpha-amylase precursor (PA) (1,4-alpha-D-glucan glucanohydrolase) | 407 | 1.05 | 0.35348 | 1.52 | 0.00082 | 1.22 | 0.05446 | 1.17 | 0.18637 | 1.26 | 0.00578 | 1.27 | 0.06444 | 1.21 | 0.12182 |
| *ANP32A* | 201043_s_at | acidic (leucine-rich) nuclear phosphoprotein 32 family, member A | 575 | -1.08 | 0.41214 | -1.07 | 0.52163 | -1.3 | 0.03065 | -1.21 | 0.14439 | -1.44 | 0.00388 | -1.34 | 0.02000 | -1.73 | 0.00004 |
| *APOBEC3A* | 210873_x_at | apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A | 2075 | 2.94 | 0.00000 | 2.01 | 0.00001 | 2.72 | 0.00000 | 1.88 | 0.00103 | 1.87 | 0.00011 | 1.81 | 0.00009 | 2 | 0.00000 |
| *ARRB1* | 218832_x_at | arrestin, beta 1 | 350 | 1.68* | 0.00008 | ND | | ND | | ND | | ND | | ND | | ND | |
| *ASGR1* | 206743_s_at | asialoglycoprotein receptor 1 | 478 | -1.08 | 0.23139 | -1.19# | 0.02344 | -1.18# | 0.04365 | -1.31# | 0.00360 | -1.56# | 0.00003 | -1.37# | 0.01383 | -1.41# | 0.00072 |
| *ATG12* | 204833_at | ATG12 autophagy related 12 homolog (S. cerevisiae) | 205 | 1.93* | 0.00002 | 1.58* | 0.00012 | ND | | ND | | ND | | ND | | ND | |
| *ATOX1* | 203454_s_at | ATX1 antioxidant protein 1 homolog (yeast) | 909 | 1.58* | 0.00000 | 1.12* | 0.12292 | 1.47* | 0.00190 | 1.13* | 0.17205 | ND | | 1.24* | 0.02927 | 1.18* | 0.03486 |
| *ATP10A* | 214255_at | ATPase, Class V, type 10A | 447 | 1.43 | 0.00189 | 1.39 | 0.00500 | 1.47 | 0.00030 | 1.48 | 0.00005 | 1.5 | 0.00014 | 1.66 | 0.00042 | 1.4 | 0.00304 |
| *ATP6V1B2* | 201089_at | ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2 | 6801 | -1.23 | 0.01018 | -1.43 | 0.00054 | -1.37 | 0.00105 | -1.27 | 0.00003 | -1.65 | 0.00000 | -1.42 | 0.00008 | -1.82 | 0.00000 |
| *ATXN1* | 203231_s_at | ataxin 1 | 656 | -1.58 | 0.00004 | -1.08 | 0.20372 | -1.31 | 0.00049 | -1.2 | 0.04337 | -1.26 | 0.07173 | -1.15 | 0.20957 | -1.2 | 0.08740 |
| *AXL* | 202686_s_at | AXL receptor tyrosine kinase | 192 | ND | | ND | | 2.36* | 0.00000 | ND | | ND | | ND | | ND | |
| *BCAT2* | 203576_at | branched chain aminotransferase 2, mitochondrial | 535 | -1.31# | 0.00241 | -1.27# | 0.00908 | -1.65# | 0.00005 | -1.18 | 0.06991 | -1.29# | 0.00872 | -1.22# | 0.10360 | -1.56# | 0.00025 |
| *BICD2* | 212702_s_at | bicaudal D homolog 2 (Drosophila) | 1493 | -1.25 | 0.00026 | -1.2 | 0.03693 | -1.28 | 0.00086 | -1.28 | 0.02563 | -1.51 | 0.00001 | -1.47 | 0.00046 | -1.48 | 0.00097 |
| *BID* | 204493_at | BH3 interacting domain death agonist | 1429 | 1.09 | 0.16140 | -1.14 | 0.07514 | -1.19 | 0.01781 | -1.29 | 0.00477 | -1.38 | 0.00007 | -1.38 | 0.00005 | -1.54 | 0.00000 |
| *BLVRA* | 203771_s_at | biliverdin reductase A | 591 | 1.63 | 0.00000 | 1.35 | 0.00077 | 1.74 | 0.00000 | 1.33 | 0.04107 | 1.33 | 0.00430 | 1.37 | 0.00428 | 1.43 | 0.00015 |
| *BLVRA* | 211729_x_at | biliverdin reductase A | 4388 | 1.61 | 0.00000 | 1.2 | 0.04307 | 1.63 | 0.00003 | 1.34 | 0.01107 | 1.34 | 0.00366 | 1.39 | 0.00650 | 1.37 | 0.00038 |
| *BLVRA* | 203773_x_at | biliverdin reductase A | 4704 | 1.55 | 0.00003 | 1.15 | 0.20750 | 1.52 | 0.00050 | 1.28 | 0.09852 | 1.19 | 0.11865 | 1.3 | 0.04536 | 1.19 | 0.13127 |
| *BST2* | 201641_at | bone marrow stromal cell antigen 2 | 2224 | 2.06 | 0.00000 | 1.59 | 0.00000 | 1.96 | 0.00000 | 1.6 | 0.00007 | 1.41 | 0.00138 | 1.55 | 0.00128 | 1.5 | 0.00015 |
| *C11orf2* | 217969_at | chromosome 11 open reading frame2 | 5350 | -1.63 | 0.00000 | -1.43 | 0.00000 | -1.68 | 0.00000 | -1.42 | 0.00001 | -1.32 | 0.00005 | -1.3 | 0.00022 | -1.44 | 0.00001 |
| *C14orf147* | 213508_at | chromosome 14 open reading frame 147 | 1049 | -1.34 | 0.00122 | -1.41 | 0.00038 | -1.54# | 0.00007 | -1.34 | 0.00225 | -1.58# | 0.00000 | -1.45# | 0.00029 | -1.75# | 0.00001 |
| *C1GALT1* | 219439_at | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 | 425 | 1.55 | 0.00000 | 1.35 | 0.00002 | 1.48 | 0.00001 | 1.34 | 0.00003 | 1.31 | 0.00000 | 1.31 | 0.00006 | 1.31 | 0.00008 |
| *C1QA* | 218232_at | complement component 1, q subcomponent, A chain | 381 | 1.63* | 0.00048 | ND | | 1.35* | 0.02319 | ND | | ND | | ND | | 1.10* | 0.25983 |
| *C1QB* | 202953_at | complement component 1, q subcomponent, B chain | 269 | 1.97* | 0.00000 | ND | | ND | | ND | | ND | | ND | | ND | |
| *C2* | 203052_at | complement component 2 | 389 | 1.66* | 0.00000 | 1.14* | 0.21241 | 1.46* | 0.00022 | 1.14* | 0.14268 | 1.08* | 0.40375 | 1.20* | 0.09251 | 1.18* | 0.01252 |
| *C2orf47* | 219176_at | chromosome 2 open reading frame 47 | 851 | 1.71 | 0.00000 | 1.41 | 0.00014 | 1.72 | 0.00000 | 1.54 | 0.00000 | 1.32 | 0.00025 | 1.27 | 0.00202 | 1.34 | 0.00234 |
| *C3AR1* | 209906_at | complement component 3a receptor 1 | 2635 | 2.27 | 0.00001 | 1.3 | 0.09530 | 1.92 | 0.00240 | 1.39 | 0.03361 | 1.11 | 0.41143 | 1.31 | 0.07757 | 1.16 | 0.31333 |
| *C4orf18* | 219872_at | chromosome 4 open reading frame 18 | 419 | -1.32 | 0.00813 | -1.31 | 0.05437 | -1.39 | 0.01428 | -1.59 | 0.00315 | -1.72 | 0.00049 | -1.53 | 0.01376 | -1.95 | 0.00044 |
| *C9orf40* | 218904_s_at | chromosome 9 open reading frame 40 | 155 | 1.15* | 0.16058 | 1.11* | 0.28196 | 1.27* | 0.02975 | 1.80* | 0.00039 | 1.47* | 0.00856 | 1.56* | 0.00990 | 1.42* | 0.07017 |
| *CA1* | 205950_s_at | carbonic anhydrase I | 679 | -1.41 | 0.08929 | 1.11 | 0.62325 | 3.83 | 0.00466 | 8.88 | 0.04929 | 13.87 | 0.00135 | 15.16 | 0.00727 | 21.24 | 0.00074 |
| *CALML4* | 221879_at | calmodulin-like 4 | 1012 | 1.72* | 0.00000 | ND | | 1.34* | 0.00241 | ND | | ND | | ND | | ND | |
| *CALML4* | 64408_s_at | calmodulin-like 4 | 223 | 1.83 | 0.00001 | 1.03 | 0.60859 | 1.4 | 0.00131 | 1.01 | 0.86013 | 1.04 | 0.67167 | 1.02 | 0.89067 | 1.12 | 0.25042 |
| *CAPN3* | 214475_x_at | calpain 3, (p94) | 301 | 1.49* | 0.00024 | 1.54* | 0.00025 | 1.37* | 0.01667 | ND | | ND | | ND | | ND | |
| *CBR1* | 209213_at | carbonyl reductase 1 | 410 | 1.73 | 0.00009 | 1.21 | 0.15141 | 1.58 | 0.00015 | 1.48 | 0.00354 | 1.07 | 0.60176 | 1.19 | 0.23581 | 1.12 | 0.42149 |
| *CCNG2* | 202770_s_at | cyclin G2 | 793 | -1.18 | 0.03832 | -1.21 | 0.03053 | -1.26 | 0.02758 | -1.21 | 0.02549 | -1.32 | 0.00386 | -1.26 | 0.03819 | -1.59 | 0.00028 |
| *CCR1* | 205099_s_at | chemokine (C-C motif) receptor 1 | 940 | 2.06 | 0.00000 | 1.42 | 0.00804 | 2.04 | 0.00000 | 1.74 | 0.00006 | 1.43 | 0.00456 | 1.5 | 0.00162 | 1.45 | 0.00233 |
| *CCR1* | 205098_at | chemokine (C-C motif) receptor 1 | 2924 | 1.89 | 0.00001 | 1.26 | 0.15310 | 1.83 | 0.00094 | 1.75 | 0.00014 | 1.21 | 0.02645 | 1.54 | 0.00115 | 1.16 | 0.33288 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| *CCR2 /// LOC729230* | 206978_at | chemokine (C-C motif) receptor 2 /// similar to C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2) (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CD192 antigen) | 4664 | -1.36 | 0.07241 | -1.37 | 0.09056 | -1.36 | 0.09553 | -1.14 | 0.33118 | -1.76 | 0.00017 | -1.25 | 0.13419 | -1.91 | 0.00714 |
| *CD1C* | 205987_at | CD1c molecule | 1300 | -2.51# | 0.00000 | -1.82# | 0.00000 | -1.89# | 0.00000 | -1.57# | 0.00028 | -1.28# | 0.00217 | -1.48# | 0.00006 | -1.57# | 0.00000 |
| *CD2AP* | 203593_at | CD2-associated protein | 549 | 1.63 | 0.00000 | 1.42 | 0.00005 | 1.67 | 0.00001 | 1.45 | 0.00089 | 1.45 | 0.00000 | 1.49 | 0.00000 | 1.48 | 0.00000 |
| *CD302* | 203799_at | CD302 molecule | 5393 | -1.46 | 0.00007 | -1.56 | 0.00008 | -1.57 | 0.00001 | -1.43 | 0.00019 | -1.51 | 0.00002 | -1.37 | 0.00033 | -1.41 | 0.00005 |
| *CD33* | 206120_at | CD33 molecule | 1564 | -1.02 | 0.83604 | -1.43 | 0.00218 | -1.36 | 0.00760 | -1.44 | 0.00234 | -1.63 | 0.00009 | -1.35 | 0.03709 | -1.57 | 0.00080 |
| *CD38* | 205692_s_at | CD38 molecule | 994 | 1.95 | 0.00000 | 1.34 | 0.00082 | 1.67 | 0.00005 | 1.3 | 0.01166 | 1.19 | 0.12365 | 1.16 | 0.22909 | 1.25 | 0.00448 |
| *CD44* | 212014_x_at | CD44 molecule (Indian blood group) | 6681 | -1.5 | 0.00001 | -1.37 | 0.00053 | -1.57 | 0.00000 | -1.6 | 0.00001 | -1.42 | 0.00005 | -1.49 | 0.00003 | -1.34 | 0.00088 |
| *CD44* | 209835_x_at | CD44 molecule (Indian blood group) | 8053 | -1.56 | 0.00000 | -1.35 | 0.00068 | -1.49 | 0.00002 | -1.52 | 0.00013 | -1.33 | 0.00012 | -1.4 | 0.00036 | -1.39 | 0.00009 |
| *CD93* | 202878_s_at | CD93 molecule | 5776 | -1.29 | 0.00124 | -1.41 | 0.00041 | -1.43 | 0.00043 | -1.32 | 0.00128 | -1.52 | 0.00000 | -1.33 | 0.00846 | -1.44 | 0.00065 |
| *CDKN1C* | 213182_x_at | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | 846 | 1.81 | 0.00016 | -1.97# | 0.00015 | -1.12 | 0.34801 | -2.07# | 0.00035 | -1.85 | 0.00105 | -1.90# | 0.00419 | -2.18# | 0.00030 |
| *CDKN1C* | 213348_at | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | 2473 | 1.88 | 0.00000 | -2.11 | 0.00000 | -1.1 | 0.29000 | -1.73 | 0.00000 | -1.69 | 0.00001 | -1.69 | 0.00006 | -1.66 | 0.00001 |
| *CDKN1C* | 216894_x_at | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | 813 | 2.21 | 0.00002 | -2.44 | 0.00001 | -1.16 | 0.37159 | -1.99 | 0.00298 | -2.08 | 0.00049 | -2.02 | 0.00294 | -2.05 | 0.00223 |
| *CDKN1C* | 219534_x_at | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | 1148 | 2.2 | 0.00003 | -2.47 | 0.00001 | -1.18 | 0.24011 | -2.03 | 0.00080 | -2.17 | 0.00034 | -1.98 | 0.00129 | -2.19 | 0.00073 |
| *CES1* | 209616_s_at | carboxylesterase 1 (monocyte/macrophage serine esterase 1) | 941 | 2.06 | 0.00000 | 1.27 | 0.00162 | 1.91 | 0.00002 | 1.47 | 0.00078 | 1.33 | 0.01051 | 1.5 | 0.04238 | 1.54 | 0.00845 |
| *CHKB /// CPT1B* | 210069_at | choline kinase beta /// carnitine palmitoyltransferase 1B (muscle) | 739 | 1.29 | 0.00004 | 1.47 | 0.00001 | 1.42 | 0.00007 | 1.41 | 0.00000 | 1.53 | 0.00000 | 1.72 | 0.01064 | 1.77 | 0.00000 |
| *CHMP5* | 219356_s_at | chromatin modifying protein 5 | 1478 | 2.78 | 0.00000 | 1.93 | 0.00000 | 2.63 | 0.00000 | 2.03 | 0.00002 | 1.88 | 0.00003 | 1.8 | 0.00005 | 1.92 | 0.00000 |
| *CHMP5* | 218085_at | chromatin modifying protein 5 | 692 | 2.56 | 0.00000 | 1.69 | 0.00003 | 2.43 | 0.00000 | 1.83 | 0.00004 | 1.52 | 0.00005 | 1.76 | 0.00001 | 1.62 | 0.00003 |
| *CHST12* | 218927_s_at | carbohydrate (chondroitin 4) sulfotransferase 12 | 1538 | 1.58 | 0.00000 | 1.2 | 0.00114 | 1.52 | 0.00022 | 1.39 | 0.00006 | 1.24 | 0.01121 | 1.29 | 0.00243 | 1.23 | 0.01747 |
| *CIITA* | 205101_at | class II, major histocompatibility complex, transactivator | 707 | -1.74# | 0.00000 | -1.38# | 0.00266 | -1.63# | 0.00000 | -1.43# | 0.00141 | -1.28# | 0.00337 | -1.36# | 0.00059 | -1.45# | 0.00001 |
| *CLIC5* | 213317_at | chloride intracellular channel 5 | 208 | -1.79# | 0.00038 | -1.17 | 0.33599 | -1.3 | 0.02574 | -1.42 | 0.00828 | -1.36 | 0.00822 | -1.44# | 0.00865 | -1.71# | 0.00037 |
| *CLU* | 208792_s_at | clusterin | 1057 | 1.62 | 0.00005 | -1.1 | 0.41693 | 1.51 | 0.00684 | -1.12 | 0.43963 | -1.1 | 0.33045 | 1 | 0.97406 | 1.35 | 0.02369 |
| *CMKLR1* | 207652_s_at | chemokine-like receptor 1 | 341 | 2.03* | 0.00000 | ND | | ND | | ND | | ND | | ND | | ND | |
| *CMKLR1* | 210659_at | chemokine-like receptor 1 | 349 | 1.69* | 0.00000 | ND | | 1.44* | 0.00004 | ND | | ND | | ND | | 1.40* | 0.00007 |
| *CNP* | 208912_s_at | 2',3'-cyclic nucleotide 3' phosphodiesterase | 1503 | 1.37* | 0.00001 | 1.10* | 0.12872 | 1.50* | 0.00000 | 1.39* | 0.00008 | 1.24* | 0.00068 | 1.32* | 0.00192 | 1.36* | 0.00004 |
| *COL6A2* | 209156_s_at | collagen, type VI, alpha 2 | 565 | -1.08 | 0.28423 | 1.05 | 0.47226 | -1.37 | 0.00189 | -1.14 | 0.17298 | -1.54 | 0.00005 | -1.39# | 0.02494 | -1.27 | 0.04430 |
| *COX15* | 221550_at | COX15 homolog, cytochrome c oxidase assembly protein (yeast) | 239 | -1.13 | 0.25508 | -1.56 | 0.01527 | -1.4 | 0.01383 | -1.32 | 0.04235 | -1.53# | 0.00084 | -1.50# | 0.00088 | -1.47# | 0.00288 |
| *CPD* | 201942_s_at | carboxypeptidase D | 475 | -1.1 | 0.10638 | -1.24 | 0.00090 | -1.35 | 0.00091 | -1.33 | 0.02211 | -1.53 | 0.00078 | -1.57 | 0.00058 | -1.84 | 0.00012 |
| *CPVL* | 208146_s_at | carboxypeptidase, vitellogenic-like | 4561 | -1.37 | 0.00061 | -1.54 | 0.00004 | -1.48 | 0.00020 | -1.43 | 0.00033 | -1.65 | 0.00000 | -1.6 | 0.00005 | -1.53 | 0.00006 |
| *CRIM1* | 202551_s_at | cysteine rich transmembrane BMP regulator 1 (chordin-like) | 154 | -1.60# | 0.00100 | -1.21# | 0.02097 | -1.30# | 0.01241 | -1.65# | 0.00000 | -1.20# | 0.06283 | -1.23# | 0.04054 | -1.27# | 0.05431 |
| *CRTAP* | 201380_at | cartilage associated protein | 1014 | -1.52 | 0.00000 | -1.43 | 0.00000 | -1.53 | 0.00000 | -1.39 | 0.00003 | -1.34 | 0.00003 | -1.37 | 0.00001 | -1.49 | 0.00000 |
| *CSF1R* | 203104_at | colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog | 6075 | 1.11 | 0.09692 | -1.36 | 0.00005 | -1.16 | 0.01038 | -1.31 | 0.00193 | -1.5 | 0.00000 | -1.39 | 0.00014 | -1.41 | 0.00003 |
| *CSF3R* | 203591_s_at | colony stimulating factor 3 receptor (granulocyte) | 2554 | -1.25 | 0.01115 | -1.3 | 0.01244 | -1.36 | 0.00009 | -1.44 | 0.00157 | -1.72 | 0.00000 | -1.65 | 0.00006 | -1.47 | 0.00277 |
| *CTBP1* | 213980_s_at | C-terminal binding protein 1 | 3019 | -1.18 | 0.00609 | -1.11 | 0.17033 | -1.24 | 0.04028 | -1.19 | 0.11318 | -1.42 | 0.00083 | -1.17 | 0.08941 | -1.67 | 0.00000 |
| *CTSL1* | 202087_s_at | cathepsin L1 | 771 | 2.4 | 0.00000 | 1.31 | 0.00084 | 1.82 | 0.00000 | 1.25 | 0.01816 | 1.32 | 0.00181 | 1.4 | 0.01327 | 1.45 | 0.00009 |
| *CTSZ* | 210042_s_at | cathepsin Z | 1329 | -1.35 | 0.06234 | -1.43 | 0.04157 | -1.6 | 0.00571 | -1.83 | 0.00096 | -1.5 | 0.01524 | -2.31 | 0.00023 | -1.76 | 0.00098 |
| *CUTL1* | 202367_at | cut-like 1, CCAAT displacement protein (Drosophila) | 1156 | 1.53 | 0.00001 | -1.24 | 0.01218 | 1.05 | 0.58619 | -1.23 | 0.01092 | -1.25 | 0.00061 | -1.16 | 0.09641 | -1.21 | 0.00453 |
| *CXCL10* | 204533_at | chemokine (C-X-C motif) ligand 10 | 703 | 3.95 | 0.00001 | -1.13 | 0.24698 | 2.39 | 0.00005 | -1.16 | 0.24142 | -1.21 | 0.11369 | -1.03 | 0.78536 | -1.09 | 0.50500 |
| *CXCL5* | 214974_x_at | chemokine (C-X-C motif) ligand 5 | 527 | -1.02 | 0.83780 | -1.59 | 0.00008 | -1.07 | 0.32346 | -1.68 | 0.00175 | -1.86 | 0.00019 | -1.85 | 0.00025 | -1.4 | 0.00082 |
| *CYP1B1* | 202435_s_at | cytochrome P450, family 1, subfamily B, polypeptide 1 | 887 | -1.46 | 0.00004 | -1.29 | 0.00984 | -1.53 | 0.00040 | -1.44 | 0.00108 | -1.49 | 0.00024 | -1.41 | 0.00954 | -1.46 | 0.01437 |
| *CYP1B1* | 202437_s_at | cytochrome P450, family 1, subfamily B, polypeptide 1 | 1524 | -1.38 | 0.00329 | -1.23 | 0.02353 | -1.6 | 0.00067 | -1.31 | 0.02331 | -1.56 | 0.00019 | -1.26 | 0.06591 | -1.51 | 0.00577 |
| *DDB2* | 203409_at | damage-specific DNA binding protein 2, 48kDa | 848 | 1.82 | 0.00000 | 1.35 | 0.00000 | 1.54 | 0.00001 | 1.31 | 0.00000 | 1.3 | 0.00001 | 1.5 | 0.00011 | 1.44 | 0.00000 |
| *DDX24* | 200702_s_at | DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 | 593 | 1.3 | 0.02330 | 1.53 | 0.00087 | 1.45 | 0.00004 | 1.27 | 0.02055 | 1.52 | 0.00519 | 1.36 | 0.06102 | 1.55 | 0.00436 |
| *DDX58* | 218943_s_at | DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 | 809 | 2.83 | 0.00000 | 1.77 | 0.00000 | 2.62 | 0.00000 | 1.65 | 0.00001 | 1.79 | 0.00003 | 1.63 | 0.00002 | 1.71 | 0.00000 |
| *DGAT1* | 203669_s_at | diacylglycerol O-acyltransferase homolog 1 (mouse) | 529 | -1.11 | 0.17625 | -1.37 | 0.00108 | -1.53 | 0.00020 | -1.34 | 0.00394 | -1.36# | 0.00121 | -1.3 | 0.05321 | -1.53 | 0.00073 |
| *DHX58* | 219364_at | DEXH (Asp-Glu-X-His) box polypeptide 58 | 255 | 2.97* | 0.00000 | 2.17* | 0.00000 | 2.75* | 0.00000 | 2.35* | 0.00001 | ND | | 2.45* | 0.00000 | ND | |
| *DPEP2* | 219452_at | dipeptidase 2 | 2087 | -1.13 | 0.03831 | -1.27 | 0.00006 | -1.57 | 0.00000 | -1.53 | 0.00000 | -1.5 | 0.00000 | -1.43 | 0.00003 | -1.39 | 0.00002 |
| *DSC2* | 204751_x_at | desmocollin 2 | 198 | -1.29 | 0.01506 | -1.38 | 0.00079 | -1.3 | 0.00752 | -1.46 | 0.00006 | -1.4 | 0.00182 | -1.37# | 0.00158 | -1.51 | 0.00002 |
| *ECGF1* | 217497_at | endothelial cell growth factor 1 (platelet-derived) | 1083 | 2.03 | 0.00000 | 1.67 | 0.00006 | 1.72 | 0.00002 | 1.54 | 0.00167 | 1.43 | 0.00232 | 1.41 | 0.00025 | 1.52 | 0.00058 |
| *ECGF1* | 204858_s_at | endothelial cell growth factor 1 (platelet-derived) | 2627 | 1.71 | 0.00000 | 1.24 | 0.00379 | 1.67 | 0.00002 | 1.32 | 0.01047 | 1.15 | 0.19014 | 1.29 | 0.04971 | 1.46 | 0.00076 |
| *EEF1B2 /// hCG_19809 /// hCG_1983058* | 200705_s_at | eukaryotic translation elongation factor 1 beta 2 /// hCG1983058 /// eukaryotic translation elongation factor 1 beta 2-like | 27667 | -1.67 | 0.00000 | -1.29 | 0.00000 | -1.51 | 0.00000 | -1.39 | 0.00000 | -1.24 | 0.00012 | -1.32 | 0.00000 | -1.39 | 0.00000 |
| *EEF1D* | 203113_s_at | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) | 12411 | -1.5 | 0.00001 | -1.07 | 0.36102 | -1.58 | 0.00001 | -1.55 | 0.00170 | -1.9 | 0.00000 | -1.73 | 0.00005 | -2.16 | 0.00000 |

| Gene Symbol | Probe Set ID | Gene Title | Day 1 mean signal | Day 3 Fold Chg | Day 3 p-value | Day 6 Fold Chg | Day 6 p-value | Day 10 Fold Chg | Day 10 p-value | Day 13 Fold Chg | Day 13 p-value | Day 27 Fold Chg | Day 27 p-value | Day 42 Fold Chg | Day 42 p-value | Day 70 Fold Chg | Day 70 p-value |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *EEF2* | 204102_s_at | eukaryotic translation elongation factor 2 | 19263 | -1.58 | 0.00000 | -1.31 | 0.00003 | -1.51 | 0.00000 | -1.36 | 0.00000 | -1.19 | 0.00145 | -1.31 | 0.00001 | -1.33 | 0.00001 |
| *EEF2* | 200094_s_at | eukaryotic translation elongation factor 2 | 19261 | -1.88 | 0.00000 | -1.52 | 0.00000 | -1.79 | 0.00000 | -1.41 | 0.00052 | -1.4 | 0.00001 | -1.57 | 0.00000 | -1.58 | 0.00000 |
| *EHBP1L1 /// MGC15523* | 91703_at | hypothetical protein MGC15523 /// EH domain binding protein 1-like 1 | 1364 | -1.1 | 0.17847 | -1.07 | 0.33105 | -1.23 | 0.02427 | -1.41 | 0.00029 | -1.64 | 0.00000 | -1.51 | 0.00026 | -1.55 | 0.00000 |
| *EIF2AK2* | 204211_x_at | eukaryotic translation initiation factor 2-alpha kinase 2 | 901 | 2.59 | 0.00000 | 1.89 | 0.00000 | 2.55 | 0.00000 | 2.2 | 0.00002 | 2.03 | 0.00002 | 1.99 | 0.00001 | 2.44 | 0.00000 |
| *EIF3EIP* | 217719_at | eukaryotic translation initiation factor 3, subunit E interacting protein | 16353 | -2.02 | 0.00000 | -1.59 | 0.00000 | -2.02 | 0.00000 | -1.76 | 0.00000 | -1.6 | 0.00000 | -1.63 | 0.00000 | -1.74 | 0.00000 |
| *EIF4B* | 211938_at | eukaryotic translation initiation factor 4B | 8307 | -1.88 | 0.00000 | -1.37 | 0.00026 | -1.77 | 0.00000 | -1.43 | 0.00001 | -1.43 | 0.00001 | -1.53 | 0.00000 | -1.55 | 0.00000 |
| *EIF4B* | 219599_at | eukaryotic translation initiation factor 4B | 1955 | -1.58 | 0.00008 | -1.3 | 0.00293 | -1.42 | 0.00018 | -1.46 | 0.00074 | -1.25 | 0.02002 | -1.4 | 0.00245 | -1.7 | 0.00000 |
| *EIF4B* | 211937_at | eukaryotic translation initiation factor 4B | 7116 | -1.97 | 0.00000 | -1.48 | 0.00000 | -1.96 | 0.00000 | -1.6 | 0.00009 | -1.54 | 0.00000 | -1.85 | 0.00000 | -1.82 | 0.00000 |
| *EIF4EBP1* | 221539_at | eukaryotic translation initiation factor 4E binding protein 1 | 997 | -1.21 | 0.02424 | -1.51 | 0.00022 | -1.33 | 0.00191 | -1.26 | 0.00361 | -1.29 | 0.00105 | -1.23 | 0.00859 | -1.22 | 0.01284 |
| *EIF4H* | 206621_s_at | eukaryotic translation initiation factor 4H | 7326 | -1.15 | 0.04048 | -1.11 | 0.01691 | -1.16 | 0.01007 | -1.31 | 0.00199 | -1.37 | 0.00012 | -1.31 | 0.00075 | -1.54 | 0.00001 |
| *EMR2* | 207610_s_at | egf-like module containing, mucin-like, hormone receptor-like 2 | 1134 | 1.1 | 0.10056 | -1.5 | 0.00002 | -1.14 | 0.01079 | -1.38 | 0.00179 | -1.24 | 0.02291 | -1.18 | 0.08326 | -1.23 | 0.01023 |
| *EMR3* | 210724_at | egf-like module containing, mucin-like, hormone receptor-like 3 | 369 | -1.17 | 0.09383 | -1.65# | 0.00303 | -1.95# | 0.00001 | -2.42# | 0.00009 | -1.98# | 0.00002 | -2.51# | 0.00000 | -1.90# | 0.00031 |
| *EPB41L3* | 206710_s_at | erythrocyte membrane protein band 4.1-like 3 | 753 | 1.63 | 0.00014 | 1.05 | 0.43380 | 1.38 | 0.00065 | 1.15 | 0.27164 | 1.01 | 0.89993 | 1.1 | 0.42522 | 1.28 | 0.03095 |
| *EPHB2* | 209589_s_at | EPH receptor B2 | 119 | 3.25* | 0.00000 | ND | | 3.46* | 0.00000 | ND | | ND | | ND | | ND | |
| *ERGIC3* | 216032_s_at | ERGIC and golgi 3 | 4084 | -1.46 | 0.00000 | -1.36 | 0.00000 | -1.5 | 0.00000 | -1.34 | 0.00000 | -1.38 | 0.00000 | -1.36 | 0.00000 | -1.53 | 0.00000 |
| *ETV7* | 221680_s_at | ets variant gene 7 (TEL2 oncogene) | 422 | 1.55 | 0.00000 | 1.33 | 0.00026 | 1.55 | 0.00000 | 1.29 | 0.00300 | 1.27 | 0.00746 | 1.42 | 0.00024 | 1.28 | 0.00001 |
| *EVI5* | 209717_at | ecotropic viral integration site 5 | 303 | -1.29# | 0.00646 | -1.43# | 0.00300 | -1.35# | 0.00096 | -1.44# | 0.00065 | -1.47# | 0.00020 | -1.28# | 0.00423 | -1.75# | 0.00003 |
| *FAM46A* | 221766_s_at | family with sequence similarity 46, member A | 3034 | 1.6 | 0.00000 | 1.21 | 0.00621 | 1.3 | 0.00335 | 1.09 | 0.17658 | 1.1 | 0.32120 | 1.12 | 0.10782 | 1.16 | 0.08447 |
| *FAM70A* | 219895_at | family with sequence similarity 70, member A | 78 | 3.57* | 0.00000 | 1.74* | 0.00000 | 2.64* | 0.00000 | 1.56* | 0.01254 | ND | | 1.78* | 0.00126 | 1.67* | 0.01016 |
| *FANCL* | 218397_at | Fanconi anemia, complementation group L | 264 | 1.63 | 0.00001 | 1.39 | 0.00056 | 1.45 | 0.00108 | 1.25 | 0.02494 | 1.19 | 0.03011 | 1.32 | 0.00191 | 1.23 | 0.01400 |
| *FBL* | 211623_s_at | fibrillarin | 8706 | -1.74 | 0.00000 | -1.37 | 0.00000 | -1.6 | 0.00000 | -1.37 | 0.00000 | -1.34 | 0.00000 | -1.34 | 0.00000 | -1.44 | 0.00000 |
| *FCER1A* | 211734_s_at | Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide | 2024 | -1.46 | 0.00277 | -1.69 | 0.00016 | -2.13 | 0.00000 | -2.19 | 0.00001 | -2.4 | 0.00000 | -3.01 | 0.00000 | -2.78 | 0.00000 |
| *FCGR1A* | 216950_s_at | Fc fragment of IgG, high affinity Ia, receptor (CD64) | 1770 | 1.54 | 0.00001 | 1.14 | 0.30537 | 1.5 | 0.00096 | 1.1 | 0.46389 | -1.09 | 0.23476 | 1.06 | 0.53759 | 1.07 | 0.35360 |
| *FCGR1B* | 214511_x_at | Fc fragment of IgG, high affinity Ib, receptor (CD64) | 1704 | 1.69 | 0.00000 | 1.11 | 0.48728 | 1.53 | 0.00190 | 1.2 | 0.21883 | 1.08 | 0.43579 | 1.24 | 0.10048 | 1.21 | 0.02724 |
| *FCGR3A /// FCGR3B* | 204006_s_at | Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b) | 7216 | 1.44 | 0.00013 | -1.32 | 0.00078 | 1.04 | 0.61541 | -1.34 | 0.00598 | -1.45 | 0.00096 | -1.46 | 0.00675 | -1.51 | 0.00056 |
| *FCGRT* | 218831_s_at | Fc fragment of IgG, receptor, transporter, alpha | 3650 | -1.2 | 0.01467 | -1.32 | 0.00115 | -1.38 | 0.00005 | -1.33 | 0.00013 | -1.63 | 0.00000 | -1.44 | 0.00028 | -1.45 | 0.00021 |
| *FFAR2* | 221345_at | free fatty acid receptor 2 | 546 | 2.68 | 0.00004 | 1.29 | 0.23929 | 2.11 | 0.00106 | 1.24 | 0.49632 | 1.13 | 0.56929 | 1.06 | 0.80657 | 1.24 | 0.33917 |
| *FGL1* | 205305_at | fibrinogen-like 1 | 285 | -1.12 | 0.18950 | -1.04 | 0.62991 | -1.08 | 0.33694 | 1.16 | 0.19839 | 1.1 | 0.28414 | 1.5 | 0.00007 | 1.25 | 0.03465 |
| *FKBP8* | 40850_at | FK506 binding protein 8, 38kDa | 444 | ND | | ND | | ND | | ND | | ND | | ND | | 3.47* | 0.00053 |
| *FLJ11151* | 218610_s_at | hypothetical protein FLJ11151 | 733 | -1.18 | 0.02682 | -1.32 | 0.03634 | -1.43 | 0.00050 | -1.44 | 0.00004 | -1.45 | 0.00031 | -1.55 | 0.00003 | -1.43 | 0.00006 |
| *FLJ11286* | 218429_s_at | hypothetical protein FLJ11286 | 3098 | 1.78 | 0.00000 | 1.53 | 0.00000 | 1.77 | 0.00000 | 1.61 | 0.00001 | 1.51 | 0.00000 | 1.58 | 0.00000 | 1.6 | 0.00000 |
| *FLJ11286* | 53720_at | hypothetical protein FLJ11286 | 1603 | 1.71 | 0.00000 | 1.49 | 0.00000 | 1.69 | 0.00000 | 1.44 | 0.00001 | 1.49 | 0.00000 | 1.49 | 0.00000 | 1.49 | 0.00000 |
| *FLJ20035* | 218986_s_at | hypothetical protein FLJ20035 | 1446 | 3.75 | 0.00000 | 2.96 | 0.00000 | 3.55 | 0.00000 | 2.67 | 0.00002 | 2.46 | 0.00000 | 2.61 | 0.00000 | 2.66 | 0.00000 |
| *FOS* | 209189_at | v-fos FBJ murine osteosarcoma viral oncogene homolog | 18955 | -1.4 | 0.00094 | -1.02 | 0.91257 | -1.49 | 0.00285 | -1.67 | 0.00837 | -1.53 | 0.00282 | -1.62 | 0.00085 | -1.52 | 0.00331 |
| *FPRL1* | 210773_s_at | formyl peptide receptor-like 1 | 736 | 1.57 | 0.00034 | 1.11 | 0.28332 | 1.54 | 0.00032 | 1.11 | 0.19963 | 1.09 | 0.14171 | 1.05 | 0.65384 | -1.07 | 0.45145 |
| *FZD2* | 210220_at | frizzled homolog 2 (Drosophila) | 332 | 1.02 | 0.79654 | -1.22# | 0.14621 | -1.05 | 0.72692 | -1.12 | 0.31604 | -1.52# | 0.00037 | -1.12# | 0.24087 | -1.64# | 0.00288 |
| *GAB2* | 203853_s_at | GRB2-associated binding protein 2 | 1285 | -1.08 | 0.35801 | -1.46# | 0.00027 | -1.42# | 0.00026 | -1.63# | 0.00048 | -1.77# | 0.00001 | -1.71# | 0.00017 | -1.80# | 0.00001 |
| *GAS7* | 202192_s_at | growth arrest-specific 7 | 2980 | -1.55 | 0.00000 | -1.47 | 0.00000 | -1.62 | 0.00000 | -1.45 | 0.00000 | -1.43 | 0.00000 | -1.34 | 0.00002 | -1.4 | 0.00000 |
| *GAS7* | 202191_s_at | growth arrest-specific 7 | 1784 | -1.48 | 0.00004 | -1.33 | 0.00030 | -1.51 | 0.00004 | -1.66 | 0.00002 | -1.47 | 0.00000 | -1.64 | 0.00004 | -1.43 | 0.00068 |
| *GATA2* | 209710_at | GATA binding protein 2 | 563 | -1.12 | 0.13536 | -1.27 | 0.02946 | -1.19 | 0.17124 | -1.3 | 0.08284 | -1.89 | 0.00018 | -1.76 | 0.00296 | -1.74 | 0.00773 |
| *GATM* | 203178_at | glycine amidinotransferase (L-arginine:glycine amidinotransferase) | 129 | -1.61 | 0.00086 | -1.37 | 0.04764 | -1.44 | 0.00339 | -1.12 | 0.35500 | -1.26 | 0.04576 | -1.26 | 0.03167 | -1.65 | 0.00023 |
| *GBP1* | 202270_at | guanylate binding protein 1, interferon-inducible, 67kDa | 929 | 2.32 | 0.00000 | 1.33 | 0.00787 | 2.13 | 0.00000 | 1.37 | 0.00975 | 1.19 | 0.18167 | 1.34 | 0.01591 | 1.26 | 0.05329 |
| *GBP1* | 202269_x_at | guanylate binding protein 1, interferon-inducible, 67kDa | 2762 | 1.8 | 0.00000 | 1.17 | 0.00425 | 1.73 | 0.00000 | 1.26 | 0.00026 | 1.21 | 0.03786 | 1.11 | 0.23141 | 1.23 | 0.01037 |
| *GCA* | 203765_at | grancalcin, EF-hand calcium binding protein | 2367 | -1.12 | 0.18707 | -1.27 | 0.02101 | -1.3 | 0.00766 | -1.34 | 0.00095 | -1.56 | 0.00000 | -1.32 | 0.00263 | -1.59 | 0.00002 |
| *GIMAP4* | 219243_at | GTPase, IMAP family member 4 | 6893 | 1.53 | 0.00040 | 1.04 | 0.79506 | 1.29 | 0.06113 | 1.43 | 0.00331 | 1.03 | 0.73730 | 1.12 | 0.34266 | -1.04 | 0.80989 |
| *GIT1* | 218030_at | G protein-coupled receptor kinase interactor 1 | 940 | 1.04 | 0.70275 | 1.11 | 0.32720 | 1.3 | 0.00428 | 1.53 | 0.07368 | 1.64 | 0.00063 | 1.67 | 0.00498 | 1.96 | 0.00042 |
| *GLS* | 203159_at | glutaminase | 2115 | -1.51 | 0.00000 | -1.19 | 0.03761 | -1.41 | 0.00022 | 1.02 | 0.83490 | -1.09 | 0.15077 | -1.11 | 0.15643 | -1.28 | 0.00901 |
| *GLUL* | 200648_s_at | glutamate-ammonia ligase (glutamine synthetase) | 1147 | 1.56 | 0.00005 | -1.02 | 0.91021 | 1.35 | 0.05554 | 1.19 | 0.35193 | 1.25 | 0.16702 | 1.2 | 0.23483 | 1.8 | 0.05642 |
| *GMPR* | 204187_at | guanosine monophosphate reductase | 480 | 1.86* | 0.00000 | 1.27* | 0.04478 | 2.14* | 0.00000 | 2.36* | 0.05103 | 2.43* | 0.00161 | 2.76* | 0.03489 | 4.48* | 0.00448 |
| *GNG11* | 204115_at | guanine nucleotide binding protein (G protein), gamma 11 | 1677 | 1.37 | 0.03951 | -1.31 | 0.01728 | 1.35 | 0.06739 | -1.56 | 0.00081 | -1.32 | 0.01298 | -1.2 | 0.15963 | 1.06 | 0.63679 |
| *GPR109B* | 205220_at | G protein-coupled receptor 109B | 1859 | 1.27 | 0.31025 | 1.23 | 0.49550 | -1.03 | 0.90008 | -1 | 0.99470 | -1.37 | 0.13537 | -2.73 | 0.00030 | -1.79 | 0.02396 |
| *GPR18* | 210279_at | G protein-coupled receptor 18 | 1618 | 1.33 | 0.00333 | 1.45 | 0.00541 | 1.36 | 0.01453 | 1.5 | 0.00082 | 1.43 | 0.00285 | 1.15 | 0.10211 | 1.05 | 0.59431 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene Symbol** | **Probe Set ID** | **Gene Title** | **mean signal** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** |
| *GRN* | 216041_x_at | granulin | 10638 | 1.5 | 0.00000 | 1.06 | 0.23158 | 1.3 | 0.00094 | 1.2 | 0.05348 | 1 | 0.99417 | 1.13 | 0.28612 | 1.15 | 0.13857 |
| *GSPT1* | 215438_x_at | G1 to S phase transition 1 | 1400 | -1.13 | 0.12739 | -1.05 | 0.37751 | 1.18 | 0.08714 | 1.65 | 0.09908 | 1.92 | 0.00063 | 2.18 | 0.01772 | 2.63 | 0.01075 |
| *GYPA* | 211820_x_at | glycophorin A (MNS blood group) | 93 | ND | | ND | | ND | | ND | | ND | | ND | | 6.86* | 0.00046 |
| *GYPA* | 211821_x_at | glycophorin A (MNS blood group) | 54 | ND | | ND | | ND | | ND | | 14.69* | 0.00141 | ND | | 17.33* | 0.00020 |
| *GYPB* | 214407_x_at | glycophorin B (MNS blood group) | 244 | ND | | ND | | ND | | ND | | 6.04* | 0.00355 | 6.47* | 0.00856 | 7.52* | 0.00022 |
| *GYPB* | 207459_x_at | glycophorin B (MNS blood group) | 299 | ND | | ND | | ND | | ND | | ND | | ND | | 5.02* | 0.00003 |
| *GYPB /// GYPE* | 216833_x_at | glycophorin B (MNS blood group) /// glycophorin E | 235 | ND | | ND | | ND | | ND | | 3.15* | 0.01193 | 3.29* | 0.00824 | 3.67* | 0.00013 |
| *GZMB* | 210164_at | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) | 6882 | 1.61 | 0.00000 | 1.28 | 0.00004 | 1.48 | 0.00110 | 1.53 | 0.00056 | 1.33 | 0.00117 | 1.37 | 0.00220 | 1.51 | 0.00010 |
| *H1F0* | 208886_at | H1 histone family, member 0 | 651 | 3.13 | 0.00001 | 1.62 | 0.00000 | 2.14 | 0.00000 | 1.78 | 0.00010 | 1.89 | 0.00001 | 2.11 | 0.00003 | 2.54 | 0.00001 |
| *H2BFS* | 208579_x_at | H2B histone family, member S | 1578 | 1.94 | 0.00003 | 1.4 | 0.00813 | 1.93 | 0.00018 | 1.19 | 0.21376 | 1.26 | 0.09250 | 1.13 | 0.33230 | 1.73 | 0.00106 |
| *H3F3B* | 211998_at | H3 histone, family 3B (H3.3B) | 5179 | 1.1 | 0.29117 | 1.01 | 0.90243 | 1.07 | 0.56375 | -1.17 | 0.15029 | 1.28 | 0.00093 | 1.24 | 0.01746 | 1.66 | 0.00005 |
| *HADHA* | 208631_s_at | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit | 3917 | -1.51 | 0.00000 | -1.49 | 0.00001 | -1.62 | 0.00000 | -1.43 | 0.00002 | -1.55 | 0.00000 | -1.54 | 0.00000 | -1.69 | 0.00000 |
| *HBA1 /// HBA2* | 211699_x_at | hemoglobin, alpha 1 /// hemoglobin, alpha 2 | 57541 | 1.09 | 0.38622 | -1.09 | 0.39088 | 1.19 | 0.10586 | 1.26 | 0.06477 | 1.49 | 0.00009 | 1.33 | 0.00472 | 1.52 | 0.00001 |
| *HBD* | 206834_at | hemoglobin, delta | 2510 | -1.12 | 0.65336 | -1 | 0.98347 | 2.78 | 0.00888 | 4.78 | 0.02411 | 7.61 | 0.00015 | 6.98 | 0.00251 | 9.39 | 0.00001 |
| *HBG1 /// HBG2* | 213515_x_at | hemoglobin, gamma A /// hemoglobin, gamma G | 6275 | -1.19 | 0.44359 | -1.19 | 0.37492 | 1.62 | 0.02309 | 2.45 | 0.08160 | 4.67 | 0.00014 | 4.72 | 0.00088 | 6.53 | 0.00000 |
| *HBG1 /// HBG2* | 204848_x_at | hemoglobin, gamma A /// hemoglobin, gamma G | 6641 | -1.2 | 0.51621 | -1.28 | 0.41289 | 1.76 | 0.02209 | 2.47 | 0.09180 | 4.9 | 0.00001 | 4.64 | 0.00093 | 6.45 | 0.00000 |
| *HBG2* | 204419_x_at | hemoglobin, gamma G | 7115 | -1.21 | 0.48469 | -1.26 | 0.44314 | 1.79 | 0.01860 | 2.49 | 0.08914 | 5.04 | 0.00002 | 5.02 | 0.00079 | 6.75 | 0.00000 |
| *hCG_1776259* | 206548_at | hypothetical protein FLJ23556 | 166 | 1.91* | 0.00050 | ND | | ND | | ND | | ND | | ND | | ND | |
| *HEMK1* | 218621_at | HemK methyltransferase family member 1 | 382 | 1.10* | 0.30026 | 1.23* | 0.02160 | 1.27* | 0.01584 | 1.22* | 0.10372 | 1.53* | 0.00006 | 1.54* | 0.00184 | 1.51* | 0.00019 |
| *HERC5* | 219863_at | hect domain and RLD 5 | 1046 | 4.54 | 0.00000 | 2.14 | 0.00000 | 4.07 | 0.00000 | 2.46 | 0.00000 | 2.55 | 0.00000 | 2.52 | 0.00000 | 2.72 | 0.00000 |
| *HERC6* | 219352_at | hect domain and RLD 6 | 651 | 5.88 | 0.00000 | 4.09 | 0.00000 | 5.74 | 0.00000 | 4.07 | 0.00000 | 4.07 | 0.00000 | 4.22 | 0.00000 | 4.23 | 0.00000 |
| *HESX1* | 211267_at | HESX homeobox 1 | 34 | 11.52* | 0.00000 | ND | | 10.31* | 0.00000 | ND | | ND | | ND | | ND | |
| *HIST1H1C* | 209398_at | histone cluster 1, H1c | 712 | 2.56 | 0.00000 | 1.63 | 0.00014 | 2.4 | 0.00000 | 1.73 | 0.00000 | 2.63 | 0.00047 | 2.39 | 0.00035 | 3.18 | 0.00000 |
| *HIST1H2AC* | 215071_s_at | histone cluster 1, H2ac | 3816 | 1.51 | 0.00142 | 1.08 | 0.28337 | 1.6 | 0.00091 | 1.01 | 0.92044 | 1.13 | 0.20578 | 1.19 | 0.14911 | 1.71 | 0.00081 |
| *HIST1H2AE* | 214469_at | histone cluster 1, H2ae | 153 | 2.40* | 0.00002 | 1.95* | 0.00002 | 3.30* | 0.00001 | 2.12* | 0.00023 | 2.53* | 0.00006 | 2.60* | 0.00003 | 3.84* | 0.00000 |
| *HIST1H2AG* | 207156_at | histone cluster 1, H2ag | 203 | ND | | ND | | 1.84* | 0.00161 | ND | | ND | | 1.26* | 0.10246 | 1.84* | 0.00003 |
| *HIST1H2AJ* | 208583_x_at | histone cluster 1, H2aj | 577 | 1.77* | 0.00004 | ND | | ND | | ND | | ND | | ND | | ND | |
| *HIST1H2BC /// HIST1H2BG* | 214455_at | histone cluster 1, H2bg /// histone cluster 1, H2bc | 132 | 2.52* | 0.00011 | 1.96* | 0.00091 | 2.73* | 0.00000 | 1.91* | 0.00013 | 2.03* | 0.00003 | 2.16* | 0.00229 | 2.82* | 0.00000 |
| *HIST1H2BD* | 222067_x_at | histone cluster 1, H2bd | 1191 | 3.37 | 0.00000 | 2.51 | 0.00001 | 3.42 | 0.00000 | 2.04 | 0.00108 | 2.42 | 0.00003 | 2.02 | 0.00349 | 3.28 | 0.00000 |
| *HIST1H2BD* | 209911_x_at | histone cluster 1, H2bd | 1283 | 2.14 | 0.00000 | 1.72 | 0.00001 | 2.26 | 0.00001 | 1.58 | 0.00007 | 1.69 | 0.00000 | 1.61 | 0.00041 | 2.2 | 0.00000 |
| *HIST1H2BE* | 208527_x_at | histone cluster 1, H2be | 711 | 1.9 | 0.00002 | 1.54 | 0.00020 | 2.04 | 0.00002 | 1.41 | 0.00674 | 1.56 | 0.00104 | 1.4 | 0.00624 | 2 | 0.00000 |
| *HIST1H2BF* | 208490_x_at | histone cluster 1, H2bf | 731 | 2.4 | 0.00001 | 1.92 | 0.00001 | 2.54 | 0.00001 | 1.75 | 0.00025 | 1.91 | 0.00003 | 1.5 | 0.01006 | 2.19 | 0.00000 |
| *HIST1H2BG* | 210387_at | histone cluster 1, H2bg | 165 | 4.25* | 0.00002 | 2.76* | 0.00012 | 3.62* | 0.00010 | 3.47* | 0.00002 | 3.29* | 0.00000 | 2.43* | 0.00534 | 3.37* | 0.00000 |
| *HIST1H2BG* | 215779_s_at | histone cluster 1, H2bg | 231 | 3.13* | 0.00000 | 2.23* | 0.00001 | 2.65* | 0.00002 | 1.96* | 0.00000 | 2.18* | 0.00000 | ND | | 2.19* | 0.00001 |
| *HIST1H2BH* | 208546_x_at | histone cluster 1, H2bh | 361 | 2.10* | 0.00016 | 1.58* | 0.00266 | 2.50* | 0.00001 | 1.43* | 0.07162 | 1.70* | 0.00590 | 1.38* | 0.09242 | 2.45* | 0.00026 |
| *HIST1H2BI* | 208523_x_at | histone cluster 1, H2bi | 345 | 2.35 | 0.00001 | 1.93 | 0.00003 | 2.52 | 0.00004 | 1.86 | 0.00050 | 1.95 | 0.00002 | 1.47 | 0.02142 | 2.19 | 0.00002 |
| *HIST1H3D* | 214472_at | histone cluster 1, H3d | 116 | 3.11* | 0.00000 | 2.76* | 0.00000 | 3.53* | 0.00000 | ND | | ND | | ND | | ND | |
| *HIST1H3H* | 206110_at | histone cluster 1, H3h | 1317 | 1.54 | 0.00224 | 1.47 | 0.00406 | 1.95 | 0.00021 | 1.39 | 0.02999 | 1.79 | 0.00009 | 1.93 | 0.00045 | 2.82 | 0.00000 |
| *HIST1H4H* | 208180_s_at | histone cluster 1, H4h | 190 | 1.63 | 0.00126 | 1.85 | 0.00255 | 3.12 | 0.00004 | 2.18 | 0.00084 | 3.04 | 0.00111 | 2.42 | 0.00001 | 4.65 | 0.00013 |
| *HIST2H2AA3 /// HIST2H2AA4* | 214290_s_at | histone cluster 2, H2aa3 /// histone cluster 2, H2aa4 | 7248 | 3.14 | 0.00000 | 1.76 | 0.00004 | 2.83 | 0.00000 | 1.79 | 0.00059 | 2.09 | 0.00000 | 2.08 | 0.00006 | 2.76 | 0.00000 |
| *HIST2H2AA3 /// HIST2H2AA4* | 218280_x_at | histone cluster 2, H2aa3 /// histone cluster 2, H2aa4 | 2660 | 2.89 | 0.00000 | 1.56 | 0.00089 | 2.55 | 0.00001 | 1.5 | 0.01173 | 1.86 | 0.00002 | 1.87 | 0.00013 | 2.45 | 0.00000 |
| *HIST2H2BE* | 202708_s_at | histone cluster 2, H2be | 1609 | 2.62 | 0.00000 | 1.63 | 0.00008 | 2.47 | 0.00000 | 1.47 | 0.00770 | 1.75 | 0.00019 | 1.68 | 0.00141 | 2.28 | 0.00000 |
| *HIST3H2A* | 221582_at | histone cluster 3, H2a | 953 | 1.11 | 0.22967 | 1.12 | 0.24862 | 1.21 | 0.05131 | 1.33 | 0.00969 | 1.44 | 0.00050 | 1.53 | 0.00000 | 1.29 | 0.00226 |
| *HK3* | 205936_s_at | hexokinase 3 (white cell) | 2708 | -1.08 | 0.19525 | -1.45 | 0.00039 | -1.28 | 0.03063 | -1.37 | 0.00345 | -1.64 | 0.00007 | -1.32 | 0.02022 | -1.45 | 0.00026 |
| *HLA-DMB* | 203932_at | major histocompatibility complex, class II, DM beta | 9491 | -1.23 | 0.04403 | -1.34 | 0.02458 | -1.49 | 0.00797 | -1.4 | 0.01691 | -1.88 | 0.00006 | -1.87 | 0.00001 | -2.01 | 0.00000 |
| *HLA-DQB1* | 209823_x_at | major histocompatibility complex, class II, DQ beta 1 | 5133 | -1.45 | 0.00005 | -1.4 | 0.00142 | -1.59 | 0.00005 | -1.26 | 0.03170 | -1.42 | 0.00018 | -1.41 | 0.00372 | -1.48 | 0.00756 |
| *HMBS* | 203040_s_at | hydroxymethylbilane synthase | 939 | -1.05 | 0.26165 | -1.05 | 0.30238 | -1.01 | 0.79700 | 1.26 | 0.06478 | 1.4 | 0.00116 | 1.47 | 0.00136 | 1.5 | 0.00020 |
| *HNRNPA1 /// LOC728844* | 222040_at | heterogeneous nuclear ribonucleoprotein A1 /// hypothetical protein LOC728844 | 1693 | -1.07 | 0.51167 | 1.2 | 0.17571 | 1.09 | 0.52122 | -1.04 | 0.80102 | 1.3 | 0.03336 | 1.19 | 0.06884 | 1.62 | 0.00099 |
| *HPSE* | 219403_s_at | heparanase | 1257 | 1.7 | 0.00000 | 1.2 | 0.00428 | 1.57 | 0.00000 | 1.29 | 0.01857 | 1.21 | 0.03036 | 1.32 | 0.02143 | 1.55 | 0.00005 |
| *HRASLS* | 219983_at | HRAS-like suppressor | 172 | -1.33# | 0.00621 | -1.48# | 0.00168 | -1.28# | 0.00793 | -1.52# | 0.00053 | -1.22# | 0.02570 | -1.20# | 0.04041 | -1.23# | 0.07581 |
| *ICAM3* | 204949_at | intercellular adhesion molecule 3 | 5713 | -1.28 | 0.00000 | -1.32 | 0.00031 | -1.43 | 0.00000 | -1.41 | 0.00007 | -1.56 | 0.00002 | -1.37 | 0.00026 | -1.56 | 0.00024 |
| *IFI16* | 206332_s_at | interferon, gamma-inducible protein 16 | 4915 | 1.78 | 0.00000 | 1.51 | 0.00006 | 1.74 | 0.00000 | 1.47 | 0.00007 | 1.44 | 0.00006 | 1.52 | 0.00000 | 1.48 | 0.00001 |
| *IFI16* | 208966_x_at | interferon, gamma-inducible protein 16 | 7072 | 1.76 | 0.00000 | 1.45 | 0.00001 | 1.68 | 0.00000 | 1.51 | 0.00008 | 1.45 | 0.00044 | 1.57 | 0.00001 | 1.4 | 0.00008 |
| *IFI16* | 208965_s_at | interferon, gamma-inducible protein 16 | 2462 | 1.74 | 0.00000 | 1.45 | 0.00001 | 1.76 | 0.00000 | 1.37 | 0.00758 | 1.34 | 0.01364 | 1.22 | 0.01812 | 1.28 | 0.00340 |
| *IFI27* | 202411_at | interferon, alpha-inducible protein 27 | 322 | 73.30* | 0.00000 | 70.29* | 0.00000 | 98.01* | 0.00000 | 93.53* | 0.00000 | 94.83* | 0.00000 | 97.44* | 0.00000 | 107.70* | 0.00000 |
| *IFI35* | 209417_s_at | interferon-induced protein 35 | 1906 | 3.19 | 0.00000 | 2.03 | 0.00000 | 2.86 | 0.00000 | 2.02 | 0.00000 | 1.76 | 0.00011 | 1.88 | 0.00013 | 1.88 | 0.00000 |
| *IFI44* | 214453_s_at | interferon-induced protein 44 | 2711 | 5.97 | 0.00000 | 4.61 | 0.00000 | 6 | 0.00000 | 4.65 | 0.00000 | 4.91 | 0.00000 | 5.2 | 0.00000 | 5.45 | 0.00000 |
| *IFI44* | 214059_at | Interferon-induced protein 44 | 523 | 7.09 | 0.00000 | 4.75 | 0.00000 | 6.45 | 0.00000 | 4.78 | 0.00000 | 4.53 | 0.00000 | 5.15 | 0.00000 | 4.98 | 0.00000 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| *IFI44L* | 204439_at | interferon-induced protein 44-like | 1836 | 10.07 | 0.00000 | 8.17 | 0.00000 | 9.68 | 0.00000 | 7.58 | 0.00000 | 7.5 | 0.00000 | 7.99 | 0.00000 | 8.38 | 0.00000 |
| *IFIH1* | 219209_at | interferon induced with helicase C domain 1 | 616 | 3.31 | 0.00000 | 2.01 | 0.00000 | 3.26 | 0.00000 | 2.37 | 0.00000 | 2.12 | 0.00000 | 2.29 | 0.00000 | 2.15 | 0.00000 |
| *IFIT1* | 203153_at | interferon-induced protein with tetratricopeptide repeats 1 | 828 | 12.23* | 0.00000 | 4.06* | 0.00000 | 9.91* | 0.00000 | 6.00* | 0.00000 | 4.76* | 0.00004 | 5.59* | 0.00000 | 4.81* | 0.00006 |
| *IFIT2* | 217502_at | interferon-induced protein with tetratricopeptide repeats 2 | 929 | 4.16* | 0.00001 | ND | | 3.73* | 0.00018 | 1.71* | 0.00064 | ND | | ND | | 1.40* | 0.02177 |
| *IFIT3* | 204747_at | interferon-induced protein with tetratricopeptide repeats 3 | 1316 | 7.11 | 0.00000 | 3.3 | 0.00000 | 6.76 | 0.00000 | 3.79 | 0.00000 | 3.43 | 0.00001 | 3.54 | 0.00001 | 3.85 | 0.00000 |
| *IFIT5* | 203596_s_at | interferon-induced protein with tetratricopeptide repeats 5 | 677 | 2.74* | 0.00000 | 1.86* | 0.00015 | 2.72* | 0.00000 | 2.36* | 0.00000 | 2.03* | 0.00001 | 2.24* | 0.00000 | 1.80* | 0.00028 |
| *IFIT5* | 203595_s_at | interferon-induced protein with tetratricopeptide repeats 5 | 965 | 2.25 | 0.00000 | 1.41 | 0.00015 | 1.99 | 0.00001 | 1.56 | 0.00002 | 1.45 | 0.00054 | 1.52 | 0.00001 | 1.3 | 0.02059 |
| *IFITM1* | 201601_x_at | interferon induced transmembrane protein 1 (9-27) | 18622 | 2.01 | 0.00000 | 1.63 | 0.00000 | 1.89 | 0.00000 | 1.67 | 0.00000 | 1.67 | 0.00000 | 1.74 | 0.00000 | 1.74 | 0.00000 |
| *IFITM1* | 214022_s_at | interferon induced transmembrane protein 1 (9-27) | 22532 | 1.71 | 0.00000 | 1.47 | 0.00000 | 1.68 | 0.00000 | 1.54 | 0.00000 | 1.54 | 0.00000 | 1.55 | 0.00000 | 1.58 | 0.00000 |
| *IFITM2* | 201315_x_at | interferon induced transmembrane protein 2 (1-8D) | 22495 | 1.7 | 0.00000 | 1.47 | 0.00000 | 1.64 | 0.00000 | 1.55 | 0.00000 | 1.36 | 0.00001 | 1.43 | 0.00000 | 1.5 | 0.00000 |
| *IFITM3* | 212203_x_at | interferon induced transmembrane protein 3 (1-8U) | 15734 | 2.15 | 0.00000 | 1.77 | 0.00000 | 2.07 | 0.00000 | 1.75 | 0.00000 | 1.67 | 0.00000 | 1.78 | 0.00000 | 1.97 | 0.00000 |
| *IFT81* | 219372_at | intraflagellar transport 81 homolog (Chlamydomonas) | 86 | -1.51# | 0.00063 | -1.11# | 0.28166 | -1.18# | 0.26463 | -1.28# | 0.03452 | 1.08# | 0.62846 | -1.09# | 0.46919 | -1.32# | 0.02870 |
| *IGF2BP3* | 203820_s_at | insulin-like growth factor 2 mRNA binding protein 3 | 176 | 1.67 | 0.00002 | 1.17 | 0.02011 | 1.66 | 0.00009 | 1.12 | 0.16337 | -1.05 | 0.61512 | 1.03 | 0.82312 | 1.14 | 0.19708 |
| *IGHA1* | 215118_s_at | Immunoglobulin heavy constant alpha 1 | 1117 | -1.84 | 0.00000 | -1.47 | 0.00016 | -1.97 | 0.00000 | -1.34 | 0.02670 | -1.5 | 0.00002 | -1.47 | 0.06343 | -2.01 | 0.00270 |
| *IGHD* | 214973_x_at | immunoglobulin heavy constant delta | 886 | -1.3 | 0.00482 | -1.08 | 0.40400 | -1.5 | 0.00014 | -1.14 | 0.22305 | -1.29 | 0.01542 | -1.35 | 0.00568 | -1.56# | 0.00112 |
| *IGHG1 /// IGHG2 /// IGHG3 /// IGHM /// IGHV4-31* | 211430_s_at | immunoglobulin heavy constant gamma 1 (G1m marker) /// gamma 2 (G2m marker) /// gamma 3 (G3m marker) /// mu /// immunoglobulin heavy variable 4-31 | 6712 | -1.39 | 0.00672 | -1.09 | 0.55640 | -2.17 | 0.00047 | -1.64 | 0.02145 | -2.3 | 0.00077 | -1.83 | 0.02203 | -3.17 | 0.00027 |
| *IGHV1-69* | 211635_x_at | Immunoglobulin heavy variable 1-69 | 944 | -1.44 | 0.00149 | -1.11 | 0.31515 | -1.47 | 0.00335 | -1.34 | 0.05517 | -1.24 | 0.07239 | -1.62 | 0.00035 | -1.59 | 0.00875 |
| *IL13RA1* | 201887_at | interleukin 13 receptor, alpha 1 | 1657 | -1.53 | 0.00005 | -1.4 | 0.00009 | -1.57 | 0.00002 | -1.44 | 0.00019 | -1.46 | 0.00001 | -1.4 | 0.00009 | -1.47 | 0.00004 |
| *IL1RN* | 212659_s_at | interleukin 1 receptor antagonist | 700 | 1.51 | 0.00000 | 1.12 | 0.01432 | 1.39 | 0.00002 | 1.12 | 0.16678 | ND | | ND | | ND | |
| *IL1RN* | 216243_s_at | interleukin 1 receptor antagonist | 982 | 1.56 | 0.00000 | 1.11 | 0.17858 | 1.51 | 0.00005 | 1.27 | 0.00595 | 1.12# | 0.21890 | 1.13 | 0.34278 | 1.3 | 0.02978 |
| *IL1RN* | 212657_s_at | interleukin 1 receptor antagonist | 1454 | 2.12 | 0.00001 | 1.14 | 0.11428 | 1.56 | 0.00018 | 1.36 | 0.11997 | 1.19 | 0.20644 | 1.18 | 0.10854 | 1.26 | 0.01422 |
| *IL8* | 217281_x_at | Interleukin 8 | 412 | -1.48# | 0.00728 | -1.17# | 0.22690 | -1.95# | 0.00068 | -1.36# | 0.16970 | -1.30# | 0.09618 | -1.92# | 0.00302 | -1.79# | 0.01762 |
| *INSR* | 213792_s_at | insulin receptor | 364 | -1.48 | 0.00320 | -1.56# | 0.00091 | -1.61# | 0.00016 | -1.94 | 0.00002 | -1.96# | 0.00002 | -1.97# | 0.00000 | -1.60# | 0.00049 |
| *IRF1* | 202531_at | interferon regulatory factor 1 | 4893 | -1.13 | 0.11828 | -1.36 | 0.00079 | -1.24 | 0.00128 | -1.33 | 0.00200 | -1.62 | 0.00001 | -1.6 | 0.00003 | -1.59 | 0.00000 |
| *IRF7* | 208436_s_at | interferon regulatory factor 7 | 3052 | 3.65 | 0.00000 | 2.44 | 0.00000 | 3.34 | 0.00000 | 2.48 | 0.00000 | 2.22 | 0.00000 | 2.49 | 0.00000 | 2.38 | 0.00000 |
| *IRS2* | 209185_s_at | insulin receptor substrate 2 | 7235 | -1.69 | 0.00319 | -1.36 | 0.04881 | -1.57 | 0.00380 | -1.74 | 0.00001 | -1.4 | 0.00297 | -1.53 | 0.00113 | -1.32 | 0.05489 |
| *IRS2* | 209184_s_at | insulin receptor substrate 2 | 3142 | -1.54 | 0.00254 | -1.22 | 0.12321 | -1.38 | 0.01327 | -1.5 | 0.00000 | -1.21 | 0.02529 | -1.41 | 0.00154 | -1.35 | 0.02744 |
| *ISG15* | 205483_s_at | ISG15 ubiquitin-like modifier | 4167 | 6.76 | 0.00000 | 3.76 | 0.00000 | 6.59 | 0.00000 | 4 | 0.00000 | 3.9 | 0.00000 | 4.36 | 0.00000 | 4.23 | 0.00000 |
| *ISG20* | 204698_at | interferon stimulated exonuclease gene 20kDa | 2731 | 2.54 | 0.00000 | 1.82 | 0.00000 | 2.64 | 0.00000 | 1.77 | 0.00000 | 1.71 | 0.00002 | 1.64 | 0.00002 | 1.68 | 0.00000 |
| *ISG20* | 33304_at | interferon stimulated exonuclease gene 20kDa | 5053 | 1.79 | 0.00000 | 1.49 | 0.00000 | 1.86 | 0.00000 | 1.51 | 0.00000 | 1.47 | 0.00000 | 1.44 | 0.00000 | 1.44 | 0.00000 |
| *ITGA2B* | 206493_at | integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41) | 1644 | 1.44 | 0.00581 | -1.58 | 0.01623 | 1.17 | 0.24084 | -1.79 | 0.00486 | -1.67 | 0.00097 | -1.45 | 0.01784 | -1.19 | 0.14249 |
| *ITGAE* | 205055_at | integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) | 3873 | -1.57 | 0.00000 | -1.47 | 0.00001 | -1.59 | 0.00000 | -1.43 | 0.00000 | -1.54 | 0.00000 | -1.47 | 0.00000 | -1.71 | 0.00000 |
| *JAK2* | 205842_s_at | Janus kinase 2 (a protein tyrosine kinase) | 1457 | 1.64 | 0.00000 | 1.16 | 0.00618 | 1.42 | 0.00000 | 1.15 | 0.13422 | 1.08 | 0.42341 | 1.03 | 0.74974 | 1.12 | 0.22717 |
| *JAK2* | 205841_at | Janus kinase 2 (a protein tyrosine kinase) | 326 | 1.65 | 0.00004 | 1.16 | 0.14528 | 1.25 | 0.01794 | -1.29 | 0.05805 | -1.07 | 0.42345 | -1.01 | 0.96680 | -1.16 | 0.14795 |
| *JUP* | 201015_s_at | junction plakoglobin | 549 | 3.39* | 0.00000 | 1.86* | 0.00046 | 2.93* | 0.00000 | 2.51* | 0.00019 | 1.78* | 0.00188 | 1.87* | 0.00646 | 2.03* | 0.00139 |
| *KCTD14* | 58916_at | potassium channel tetramerisation domain containing 14 | 151 | 1.82* | 0.00002 | 1.63* | 0.00002 | 2.24* | 0.00001 | 1.50* | 0.00208 | ND | | 1.34* | 0.02279 | 1.31* | 0.00084 |
| *KIAA0125* | 206478_at | KIAA0125 | 947 | -1.57 | 0.00000 | -1.14 | 0.17871 | -1.37 | 0.00081 | -1.18 | 0.20607 | -1.02 | 0.87180 | -1.05 | 0.65459 | -1.13 | 0.24014 |
| *KIAA0430* | 202386_s_at | KIAA0430 | 2757 | 1.07 | 0.12730 | 1.16 | 0.00395 | 1.19 | 0.00030 | 1.39 | 0.00039 | 1.42 | 0.00001 | 1.5 | 0.00235 | 1.6 | 0.00076 |
| *KIAA1466* | 222139_at | KIAA1466 gene | 430 | 1.64 | 0.00002 | 1.46 | 0.01651 | 1.56 | 0.00192 | 1.05 | 0.62352 | 1.33 | 0.01236 | 1.29 | 0.01021 | 1.45 | 0.00221 |
| *KIR2DL4* | 208426_x_at | killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 | 606 | 1.19 | 0.02849 | 1.12 | 0.17349 | 1.18 | 0.04725 | 1.14 | 0.10311 | 1.27 | 0.00654 | 1.16 | 0.04997 | 1.52 | 0.00003 |
| *KLF4* | 221841_s_at | Kruppel-like factor 4 (gut) | 7570 | -1.04 | 0.67717 | -1.43 | 0.00123 | -1.23 | 0.03220 | -1.58 | 0.00100 | -1.48 | 0.00016 | -1.55 | 0.00028 | -1.23 | 0.01153 |
| *KLF4* | 220266_s_at | Kruppel-like factor 4 (gut) | 1812 | -1.1 | 0.30637 | -1.26 | 0.02746 | -1.21 | 0.06797 | -1.49 | 0.00716 | -1.64 | 0.00001 | -1.69 | 0.00083 | -1.33 | 0.01373 |
| *KLF9* | 203542_s_at | Kruppel-like factor 9 | 1371 | -1.39 | 0.03089 | -1.05 | 0.79164 | -1.1 | 0.53720 | -1.57 | 0.00026 | -1.11 | 0.40340 | -1.49 | 0.00491 | -1.13 | 0.39022 |
| *KLHL21* | 203068_at | kelch-like 21 (Drosophila) | 746 | -1.30# | 0.01225 | -1.14 | 0.28866 | -1.56# | 0.00040 | -1.22# | 0.06043 | -1.47# | 0.00373 | -1.43# | 0.00510 | -1.62# | 0.00025 |
| *KLRB1* | 214470_at | killer cell lectin-like receptor subfamily B, member 1 | 9732 | -1.41 | 0.00004 | -1.21 | 0.00155 | -1.32 | 0.00004 | -1.25 | 0.00411 | -1.32 | 0.00001 | -1.37 | 0.00002 | -1.5 | 0.00001 |
| *KLRD1* | 207795_s_at | killer cell lectin-like receptor subfamily D, member 1 | 2957 | 1.51 | 0.00000 | 1.34 | 0.00043 | 1.32 | 0.00075 | 1.43 | 0.00004 | 1.11 | 0.23922 | 1.01 | 0.90546 | 1.05 | 0.35928 |
| *KMO* | 211138_s_at | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | 791 | 1.77 | 0.00000 | 1.24 | 0.00395 | 1.64 | 0.00000 | 1.29 | 0.00005 | 1.24 | 0.00379 | 1.3 | 0.00605 | 1.23 | 0.00291 |
| *KMO* | 205306_x_at | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | 699 | 1.73 | 0.00000 | 1.23 | 0.00273 | 1.57 | 0.00000 | 1.33 | 0.00005 | 1.27 | 0.00030 | 1.26 | 0.00193 | 1.22 | 0.00231 |
| *KRT10* | 207023_x_at | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) | 3120 | -1.54 | 0.00000 | -1.3 | 0.00033 | -1.47 | 0.00000 | -1.46 | 0.00002 | -1.31 | 0.00232 | -1.37 | 0.00004 | -1.43 | 0.00011 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene Symbol** | **Probe Set ID** | **Gene Title** | **mean signal** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** |
| *KRT10* | 210633_x_at | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) | 4516 | -1.63 | 0.00000 | -1.37 | 0.00042 | -1.6 | 0.00000 | -1.53 | 0.00003 | -1.37 | 0.00073 | -1.41 | 0.00086 | -1.45 | 0.00036 |
| *LAG3* | 206486_at | lymphocyte-activation gene 3 | 434 | 1.75* | 0.00000 | 1.47* | 0.00022 | 1.81* | 0.00000 | ND | | ND | | ND | | ND | |
| *LAMP3* | 205569_at | lysosomal-associated membrane protein 3 | 185 | 6.02* | 0.00000 | 3.11* | 0.00000 | 6.68* | 0.00000 | 3.29* | 0.00000 | 3.80* | 0.00000 | 3.93* | 0.00000 | 4.41* | 0.00000 |
| *LAP3* | 217933_s_at | leucine aminopeptidase 3 | 3873 | 2.04 | 0.00000 | 1.49 | 0.00001 | 1.96 | 0.00000 | 1.53 | 0.00017 | 1.44 | 0.00035 | 1.48 | 0.00258 | 1.59 | 0.00000 |
| *LBA1* | 213261_at | lupus brain antigen 1 | 1508 | 1.52 | 0.00000 | 1.29 | 0.00006 | 1.49 | 0.00000 | 1.38 | 0.00003 | 1.26 | 0.00349 | 1.32 | 0.00000 | 1.24 | 0.00008 |
| *LCN2* | 212531_at | lipocalin 2 (oncogene 24p3) | 559 | 1.75* | 0.01044 | 1.32* | 0.07925 | 2.62* | 0.00001 | 1.92* | 0.00147 | 1.83* | 0.00028 | 1.76* | 0.00162 | 2.84* | 0.00012 |
| *LDLR* | 202068_s_at | low density lipoprotein receptor (familial hypercholesterolemia) | 994 | 1.7 | 0.00001 | 1.39 | 0.00003 | 1.5 | 0.00002 | 1.33 | 0.00168 | 1.35 | 0.00023 | 1.35 | 0.00041 | 1.37 | 0.00001 |
| *LEPR* | 209894_at | leptin receptor | 154 | -1.16 | 0.09118 | -1.38 | 0.00131 | -1.09 | 0.18777 | -1.48 | 0.00890 | -1.57 | 0.00010 | -1.22 | 0.05404 | -1.19 | 0.15730 |
| *LGALS3BP* | 200923_at | lectin, galactoside-binding, soluble, 3 binding protein | 970 | 3.99* | 0.00000 | 2.23* | 0.00000 | 4.02* | 0.00000 | 2.84* | 0.00000 | 2.61* | 0.00005 | 2.95* | 0.00000 | 3.14* | 0.00000 |
| *LGALS9* | 203236_s_at | lectin, galactoside-binding, soluble, 9 (galectin 9) | 1832 | 1.88 | 0.00000 | 1.34 | 0.00037 | 1.75 | 0.00000 | 1.48 | 0.00001 | 1.31 | 0.00145 | 1.54 | 0.00006 | 1.67 | 0.00001 |
| *LILRA1* | 210660_at | leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 | 2204 | 1.18 | 0.03025 | -1.32 | 0.00001 | -1.06 | 0.40321 | -1.32 | 0.00301 | -1.5 | 0.00003 | -1.28 | 0.02738 | -1.19 | 0.03794 |
| *LILRA2* | 211102_s_at | leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 | 981 | 1.15 | 0.03835 | -1.1 | 0.13326 | -1.01 | 0.87071 | -1.18 | 0.03044 | -1.54 | 0.00000 | -1.34 | 0.00681 | -1.33 | 0.00169 |
| *LILRA3* | 206881_s_at | leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3 | 1824 | 1.57 | 0.00001 | -1.04 | 0.72135 | 1.29 | 0.01684 | 1.08 | 0.44151 | -1.08 | 0.46215 | 1.18 | 0.26344 | 1.27 | 0.05120 |
| *LILRB2* | 210146_x_at | leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 | 2758 | 1.54 | 0.00000 | 1.07 | 0.43348 | 1.32 | 0.00268 | -1.04 | 0.66149 | -1.08 | 0.36402 | 1.04 | 0.67447 | 1.08 | 0.30925 |
| *LOC150759* | 213703_at | hypothetical protein LOC150759 | 356 | -1.04 | 0.55740 | 1.53 | 0.00006 | 1.26 | 0.07798 | 1.16 | 0.11009 | 1.31 | 0.03802 | 1.43 | 0.00255 | 1.39 | 0.02541 |
| *LOC26010* | 222154_s_at | viral DNA polymerase-transactivated protein 6 | 857 | 4.32 | 0.00000 | 2.45 | 0.00000 | 4.17 | 0.00000 | 3.03 | 0.00000 | 2.97 | 0.00000 | 3.06 | 0.00000 | 3.28 | 0.00000 |
| *LOC391020* | 216565_x_at | interferon induced transmembrane protein pseudogene | 2444 | 2.68 | 0.00000 | 1.96 | 0.00000 | 2.65 | 0.00000 | 2.17 | 0.00000 | 2.13 | 0.00000 | 2.18 | 0.00000 | 2.48 | 0.00000 |
| *LOC442171* | 217379_at | similar to ribosomal protein L10 | 9003 | -1.65 | 0.00000 | -1.25 | 0.01718 | -1.55 | 0.00000 | -1.44 | 0.00003 | -1.42 | 0.00036 | -1.37 | 0.00039 | -1.52 | 0.00000 |
| *LOC442215* | 217142_at | similar to Elongation FacTor family member (eft-4) | 873 | -1.63 | 0.00017 | -1.23 | 0.12208 | -1.59 | 0.00054 | -1.49 | 0.00588 | -1.23 | 0.01830 | -1.47 | 0.00246 | -1.4 | 0.00225 |
| *LST1* | 214181_x_at | leukocyte specific transcript 1 | 6884 | 1.03 | 0.67475 | -1.45 | 0.00024 | -1.27 | 0.01046 | -1.42 | 0.00112 | -1.6 | 0.00006 | -1.39 | 0.00616 | -1.38 | 0.00072 |
| *LST1* | 215633_x_at | leukocyte specific transcript 1 | 6680 | 1.05 | 0.45336 | -1.46 | 0.00005 | -1.25 | 0.00769 | -1.4 | 0.00203 | -1.6 | 0.00009 | -1.39 | 0.00855 | -1.42 | 0.00083 |
| *LTA4H* | 208771_s_at | leukotriene A4 hydrolase | 15548 | -1.73 | 0.00000 | -1.74 | 0.00000 | -1.95 | 0.00000 | -1.71 | 0.00001 | -1.55 | 0.00007 | -1.61 | 0.00000 | -1.62 | 0.00001 |
| *LY6E* | 202145_at | lymphocyte antigen 6 complex, locus E | 2143 | 4.11 | 0.00000 | 2.68 | 0.00000 | 3.98 | 0.00000 | 3.07 | 0.00000 | 2.78 | 0.00000 | 3.04 | 0.00000 | 3.39 | 0.00000 |
| *MAFB* | 218559_s_at | v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) | 4224 | 1.65 | 0.00000 | 1.24 | 0.04572 | 1.52 | 0.00011 | 1.23 | 0.24339 | 1.16 | 0.06186 | 1.22 | 0.09459 | 1.12 | 0.21386 |
| *MAP3K12* | 205448_s_at | mitogen-activated protein kinase kinase kinase 12 | 560 | -1.14 | 0.07723 | -1.12 | 0.05936 | -1.08 | 0.30760 | -1.43 | 0.00011 | -1.1 | 0.40330 | -1.28# | 0.00146 | -1.5 | 0.00047 |
| *MARCKS* | 201670_s_at | myristoylated alanine-rich protein kinase C substrate | 896 | 2.43 | 0.00000 | 1.14 | 0.20741 | 1.82 | 0.00002 | 1.13 | 0.42762 | 1.12 | 0.39994 | -1.05 | 0.72064 | 1.26 | 0.12299 |
| *MARCKS* | 201669_s_at | myristoylated alanine-rich protein kinase C substrate | 3083 | 2.07 | 0.00000 | 1.2 | 0.02656 | 1.69 | 0.00000 | 1.25 | 0.05666 | 1.13 | 0.17988 | 1.17 | 0.13138 | 1.22 | 0.02941 |
| *MARCKS* | 201668_x_at | myristoylated alanine-rich protein kinase C substrate | 412 | 1.93 | 0.00069 | 1.19 | 0.06105 | 1.4 | 0.00035 | 1.01 | 0.88069 | 1.13# | 0.21574 | 1.05# | 0.73004 | 1.13 | 0.34104 |
| *MARCKS* | 213002_at | myristoylated alanine-rich protein kinase C substrate | 836 | 1.74 | 0.00000 | 1.15 | 0.07049 | 1.44 | 0.00073 | 1.11 | 0.39621 | 1.15 | 0.04558 | 1.04 | 0.62333 | 1.1 | 0.22370 |
| *MARCO* | 205819_at | macrophage receptor with collagenous structure | 140 | 2.58* | 0.00009 | ND | | ND | | ND | | ND | | ND | | ND | |
| *MARK2* | 203942_s_at | MAP/microtubule affinity-regulating kinase 2 | 639 | -1.09 | 0.26664 | -1.14 | 0.21105 | -1.2 | 0.03976 | -1.1 | 0.26517 | -1.41# | 0.00012 | -1.50# | 0.00050 | -1.25 | 0.01759 |
| *MEGF9* | 212831_at | multiple EGF-like-domains 9 | 510 | -1.37 | 0.00607 | -1.75# | 0.00014 | -1.45# | 0.00879 | -1.62# | 0.01539 | -1.54# | 0.00246 | -1.72# | 0.00006 | -1.18# | 0.13295 |
| *MGC5618* | 221477_s_at | hypothetical protein MGC5618 | 2232 | -1.27 | 0.08924 | -1.57 | 0.00735 | -1.59 | 0.00122 | -1.67 | 0.00007 | -1.48 | 0.00960 | -1.6 | 0.00137 | -1.69 | 0.00040 |
| *MICAL2* | 212473_s_at | microtubule associated monoxygenase, calponin and LIM domain containing 2 | 2623 | -1.63 | 0.00000 | -1.44 | 0.00002 | -1.49 | 0.00000 | 1 | 0.98122 | -1.01 | 0.92530 | 1.01 | 0.92674 | 1.15 | 0.24246 |
| *MICAL2* | 212472_at | microtubule associated monoxygenase, calponin and LIM domain containing 2 | 1906 | -1.68 | 0.00000 | -1.46 | 0.00049 | -1.56 | 0.00004 | -1.07 | 0.73078 | -1.11 | 0.41955 | -1 | 0.99629 | 1.13 | 0.37395 |
| *MLC1* | 213395_at | megalencephalic leukoencephalopathy with subcortical cysts 1 | 297 | ND | | ND | | ND | | 1.51* | 0.02751 | ND | | ND | | 1.74* | 0.00022 |
| *MMRN1* | 205612_at | multimerin 1 | 100 | 1.22 | 0.28054 | -1.32 | 0.01295 | -1.05 | 0.74988 | -1.32# | 0.03212 | -1.45# | 0.00734 | -1.67# | 0.00081 | -1.50# | 0.00877 |
| *MRPL42* | 217919_s_at | mitochondrial ribosomal protein L42 | 1409 | 1.53 | 0.00003 | 1.27 | 0.00690 | 1.34 | 0.01092 | 1.3 | 0.03812 | 1.16 | 0.10065 | 1.12 | 0.21335 | 1.14 | 0.11808 |
| *MRPS12* | 204330_s_at | mitochondrial ribosomal protein S12 | 148 | 1.19 | 0.10127 | 1.28 | 0.02929 | 1.35 | 0.00857 | 1.26 | 0.09073 | 1.58 | 0.00060 | 1.32 | 0.03246 | 1.5 | 0.00630 |
| *MS4A4A* | 219607_s_at | membrane-spanning 4-domains, subfamily A, member 4 | 588 | 3.86 | 0.00000 | 1.36 | 0.02743 | 2.59 | 0.00000 | 1.64 | 0.00163 | 1.54 | 0.00429 | 1.97 | 0.00178 | 1.67 | 0.00009 |
| *MT1E* | 212859_x_at | metallothionein 1E | 1847 | 1.74 | 0.00000 | 1.33 | 0.00042 | 1.63 | 0.00001 | 1.34 | 0.00846 | 1.17 | 0.16731 | 1.39 | 0.00576 | 1.44 | 0.00001 |
| *MT1F* | 217165_x_at | metallothionein 1F | 1263 | 1.8 | 0.00000 | 1.28 | 0.00067 | 1.77 | 0.00000 | 1.28 | 0.01099 | 1.25 | 0.01476 | 1.23 | 0.01319 | 1.38 | 0.00037 |
| *MT1G* | 204745_x_at | metallothionein 1G | 2358 | 1.63 | 0.00000 | 1.19 | 0.01953 | 1.54 | 0.00001 | 1.17 | 0.01654 | 1.18 | 0.00071 | 1.27 | 0.00210 | 1.38 | 0.00000 |
| *MT1P2* | 211456_x_at | metallothionein 1 pseudogene 2 | 2938 | 2.38 | 0.00000 | 1.32 | 0.01842 | 2.01 | 0.00012 | 1.38 | 0.00862 | 1.22 | 0.02554 | 1.35 | 0.02432 | 1.71 | 0.00000 |
| *MT1P2 /// MT1A /// MT1M* | 216336_x_at | metallothionein 1A /// metallothionein 1M /// metallothionein 1 pseudogene 2 | 1363 | 1.72 | 0.00000 | 1.24 | 0.00222 | 1.72 | 0.00000 | 1.34 | 0.00746 | 1.21 | 0.02322 | 1.34 | 0.00141 | 1.56 | 0.00000 |
| *MT1P2 /// MT1H* | 206461_x_at | metallothionein 1H /// metallothionein 1 pseudogene 2 | 2264 | 2.28 | 0.00000 | 1.45 | 0.00064 | 2.12 | 0.00000 | 1.46 | 0.00079 | 1.34 | 0.00160 | 1.49 | 0.00007 | 1.66 | 0.00017 |
| *MT1X* | 208581_x_at | metallothionein 1X | 3045 | 2.49 | 0.00000 | 1.53 | 0.00015 | 2.24 | 0.00000 | 1.4 | 0.00192 | 1.25 | 0.02202 | 1.36 | 0.00081 | 1.67 | 0.00021 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| *MT1X* | 204326_x_at | metallothionein 1X | 1682 | 1.56 | 0.00000 | 1.29 | 0.00005 | 1.57 | 0.00000 | 1.24 | 0.00607 | 1.26 | 0.00311 | 1.28 | 0.00026 | 1.39 | 0.00008 |
| *MT2A* | 212185_x_at | metallothionein 2A | 8207 | 2.03 | 0.00000 | 1.37 | 0.00063 | 1.91 | 0.00000 | 1.26 | 0.00606 | 1.29 | 0.00091 | 1.37 | 0.00030 | 1.49 | 0.00001 |
| *MTMR11* | 205076_s_at | myotubularin related protein 11 | 1645 | -1.06 | 0.23040 | -1.43 | 0.00010 | -1.21 | 0.03474 | -1.43 | 0.00013 | -1.5 | 0.00001 | -1.35 | 0.00241 | -1.42 | 0.00013 |
| *MX1* | 202086_at | myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) | 4087 | 5.02 | 0.00000 | 3.52 | 0.00000 | 4.88 | 0.00000 | 3.81 | 0.00000 | 3.74 | 0.00000 | 3.93 | 0.00000 | 4.13 | 0.00000 |
| *MX2* | 204994_at | myxovirus (influenza virus) resistance 2 (mouse) | 3661 | 3.13 | 0.00000 | 2.1 | 0.00000 | 2.92 | 0.00000 | 2.21 | 0.00000 | 2.23 | 0.00000 | 2.34 | 0.00000 | 2.43 | 0.00000 |
| *MYCL1* | 214058_at | v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) | 1261 | 1.06 | 0.47987 | -1.23 | 0.00602 | -1.07 | 0.37074 | -1.22 | 0.05582 | -1.39 | 0.00048 | -1.29 | 0.00699 | -1.57 | 0.00001 |
| *MYL4* | 210088_x_at | myosin, light chain 4, alkali; atrial, embryonic | 698 | -1.01 | 0.89481 | -1.06 | 0.62400 | 1.41 | 0.00428 | 2.23 | 0.06526 | 2.93 | 0.00301 | 3.23 | 0.01850 | 3.71 | 0.00070 |
| *MYL4* | 217274_x_at | myosin, light chain 4, alkali; atrial, embryonic | 406 | 1.04 | 0.63769 | 1.08# | 0.56747 | 1.37 | 0.00918 | 1.86 | 0.01837 | 2.52 | 0.00075 | 2.48 | 0.00466 | 3.18 | 0.00010 |
| *N4BP1* | 204601_at | Nedd4 binding protein 1 | 752 | 1.92* | 0.00000 | 1.46* | 0.00044 | 1.70* | 0.00000 | 1.45* | 0.00001 | 1.27* | 0.02422 | 1.38* | 0.00143 | 1.18* | 0.01345 |
| *N4BP1* | 221867_at | Nedd4 binding protein 1 | 677 | 1.54 | 0.00000 | 1.54 | 0.00000 | 1.71 | 0.00000 | 1.56 | 0.00000 | 1.57 | 0.00002 | 1.71 | 0.00003 | 1.59 | 0.00000 |
| *N4BP1* | 32069_at | Nedd4 binding protein 1 | 889 | 1.83 | 0.00000 | 1.54 | 0.00000 | 1.85 | 0.00000 | 1.56 | 0.00001 | 1.54 | 0.00001 | 1.43 | 0.00007 | 1.54 | 0.00000 |
| *NDC80* | 204162_at | NDC80 homolog, kinetochore complex component (S. cerevisiae) | 165 | 1.51 | 0.00001 | 1.15 | 0.15726 | 1.37 | 0.00222 | 1.23# | 0.11073 | 1.22# | 0.09451 | 1.32# | 0.02042 | 1.33# | 0.01371 |
| *NELL2* | 203413_at | NEL-like 2 (chicken) | 4486 | -1.51 | 0.00002 | -1.06 | 0.17764 | -1.41 | 0.00000 | -1.28 | 0.00440 | -1.01 | 0.92974 | -1.14 | 0.04230 | -1.1 | 0.09855 |
| *NGFRAP1* | 217963_s_at | nerve growth factor receptor (TNFRSF16) associated protein 1 | 3633 | 1.67 | 0.00025 | 1.14 | 0.15893 | 1.71 | 0.00038 | 1.31 | 0.05180 | 1.64 | 0.00000 | 1.61 | 0.00105 | 2.26 | 0.00000 |
| *NMI* | 203964_at | N-myc (and STAT) interactor | 3919 | 1.86 | 0.00000 | 1.27 | 0.00106 | 1.63 | 0.00000 | 1.37 | 0.00000 | 1.23 | 0.01096 | 1.24 | 0.00757 | 1.32 | 0.00005 |
| *NRG1* | 206343_s_at | neuregulin 1 | 863 | -2.73# | 0.00009 | -1.70# | 0.00761 | -2.55# | 0.00032 | -1.78# | 0.00875 | -1.82# | 0.00082 | -1.50# | 0.02875 | -1.55# | 0.04408 |
| *NRGN* | 204081_at | neurogranin (protein kinase C substrate, RC3) | 8064 | 1.3 | 0.06488 | -1.43 | 0.01201 | 1.17 | 0.15988 | -1.56 | 0.00188 | -1.62 | 0.00002 | -1.37 | 0.03281 | 1 | 0.96273 |
| *OAS1* | 205552_s_at | 2',5'-oligoadenylate synthetase 1, 40/46kDa | 1310 | 4.29 | 0.00000 | 2.4 | 0.00000 | 3.76 | 0.00000 | 2.51 | 0.00000 | 2.08 | 0.00008 | 2.33 | 0.00007 | 2.33 | 0.00000 |
| *OAS1* | 202869_at | 2',5'-oligoadenylate synthetase 1, 40/46kDa | 2334 | 3.91 | 0.00000 | 2.04 | 0.00000 | 3.51 | 0.00000 | 2.37 | 0.00001 | 1.98 | 0.00002 | 2.65 | 0.00003 | 2.3 | 0.00002 |
| *OAS2* | 204972_at | 2'-5'-oligoadenylate synthetase 2, 69/71kDa | 2791 | 3.5 | 0.00000 | 2.37 | 0.00000 | 3.4 | 0.00000 | 2.9 | 0.00000 | 2.4 | 0.00000 | 2.49 | 0.00000 | 2.49 | 0.00000 |
| *OAS2* | 206553_at | 2'-5'-oligoadenylate synthetase 2, 69/71kDa | 833 | 1.93 | 0.00000 | 1.49 | 0.00000 | 1.99 | 0.00000 | 1.57 | 0.00000 | 1.6 | 0.00007 | 1.51 | 0.00008 | 1.57 | 0.00001 |
| *OAS3* | 218400_at | 2'-5'-oligoadenylate synthetase 3, 100kDa | 2136 | 4.48 | 0.00000 | 2.64 | 0.00000 | 3.76 | 0.00000 | 2.74 | 0.00000 | 2.34 | 0.00001 | 2.45 | 0.00001 | 2.83 | 0.00000 |
| *OASL* | 205660_at | 2'-5'-oligoadenylate synthetase-like | 954 | 4.56 | 0.00000 | 2.13 | 0.00000 | 4.07 | 0.00000 | 2.65 | 0.00000 | 2.23 | 0.00000 | 2.45 | 0.00000 | 2.58 | 0.00000 |
| *OASL* | 210797_s_at | 2'-5'-oligoadenylate synthetase-like | 1144 | 4.02 | 0.00000 | 2.39 | 0.00000 | 3.69 | 0.00000 | 2.55 | 0.00000 | 2.32 | 0.00000 | 2.55 | 0.00000 | 2.51 | 0.00000 |
| *OLFM1* | 213131_at | olfactomedin 1 | 371 | -2.34# | 0.00000 | -1.44 | 0.00432 | -1.79# | 0.00023 | -1.18# | 0.04273 | -1.38# | 0.01579 | -1.31# | 0.00466 | -1.23# | 0.16443 |
| *P2RX7* | 207091_at | purinergic receptor P2X, ligand-gated ion channel, 7 | 404 | 1.05 | 0.51215 | -1.07 | 0.35499 | -1.14 | 0.07667 | -1.22# | 0.08093 | -1.55# | 0.00033 | -1.32# | 0.01196 | -1.38# | 0.00094 |
| *P2RY13* | 220005_at | purinergic receptor P2Y, G-protein coupled, 13 | 1470 | 1.41 | 0.03370 | -1.25 | 0.09869 | 1.08 | 0.61443 | -1.09 | 0.34985 | -1.62 | 0.00005 | -1.31 | 0.11287 | -1.58 | 0.01795 |
| *PABPC4* | 201064_s_at | poly(A) binding protein, cytoplasmic 4 (inducible form) | 3291 | -1.53 | 0.00000 | -1.31 | 0.00008 | -1.49 | 0.00000 | -1.41 | 0.00001 | -1.27 | 0.00024 | -1.4 | 0.00000 | -1.28 | 0.00003 |
| *PALLD* | 200897_s_at | palladin, cytoskeletal associated protein | 531 | -1.06 | 0.55671 | -1.3 | 0.00072 | -1.34 | 0.00352 | -1.4 | 0.00134 | -1.62 | 0.00007 | -1.47 | 0.00125 | -1.55 | 0.00007 |
| *PAPSS2* | 203060_s_at | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | 319 | -1.73# | 0.00005 | -1.74# | 0.00001 | -1.76# | 0.00001 | -1.58# | 0.00008 | -1.55# | 0.00005 | -1.32# | 0.00424 | -1.57# | 0.00000 |
| *PARP11* | 220315_at | poly (ADP-ribose) polymerase family, member 11 | 172 | 1.60* | 0.00004 | 1.24* | 0.07717 | 1.51* | 0.00044 | 1.52* | 0.00015 | ND | | ND | | 1.49* | 0.00002 |
| *PARP12* | 218543_s_at | poly (ADP-ribose) polymerase family, member 12 | 3445 | 2.44 | 0.00000 | 1.79 | 0.00000 | 2.31 | 0.00000 | 1.77 | 0.00003 | 1.77 | 0.00000 | 1.91 | 0.00000 | 1.94 | 0.00000 |
| *PARVB* | 216253_s_at | parvin, beta | 349 | -1.1 | 0.28329 | -1.36 | 0.00957 | -1.1 | 0.29959 | -1.18 | 0.08023 | -1.52 | 0.00008 | -1.21 | 0.07586 | -1.28 | 0.01914 |
| *PCTP* | 218676_s_at | phosphatidylcholine transfer protein | 518 | -1.29 | 0.01758 | -1.64 | 0.00058 | -1.31 | 0.05446 | -1.07 | 0.56230 | 1.04 | 0.85209 | 1.17 | 0.62394 | 1.76 | 0.16714 |
| *PDGFC* | 218718_at | platelet derived growth factor C | 1240 | -1.21 | 0.01160 | -1.51 | 0.00010 | -1.31 | 0.00241 | -1.57 | 0.00004 | -1.4 | 0.00025 | -1.33 | 0.00103 | -1.27 | 0.00560 |
| *PDHB* | 211023_at | pyruvate dehydrogenase (lipoamide) beta | 3815 | 1 | 0.95283 | -1.13 | 0.25000 | -1.26 | 0.03026 | -1.14 | 0.16995 | -1.28 | 0.01524 | -1.13 | 0.25622 | -1.57 | 0.00047 |
| *PF4* | 206390_x_at | platelet factor 4 (chemokine (C-X-C motif) ligand 4) | 10386 | 1.7 | 0.00028 | 1.04 | 0.62465 | 1.62 | 0.00042 | -1.13 | 0.14207 | -1.12 | 0.13682 | -1.13 | 0.33129 | 1.24 | 0.04945 |
| *PGAP1* | 213469_at | GPI deacylase | 67 | 2.00* | 0.00002 | 1.80* | 0.00021 | 2.27* | 0.00000 | ND | | 1.98* | 0.00000 | ND | | 2.04* | 0.00000 |
| *PGAP1* | 220576_at | GPI deacylase | 239 | 1.91 | 0.00000 | 1.7 | 0.00245 | 2.19 | 0.00068 | 1.23 | 0.00341 | 1.83 | 0.00001 | 1.82 | 0.00002 | 2.01 | 0.00014 |
| *PHF11* | 221816_s_at | PHD finger protein 11 | 5834 | 1.8 | 0.00000 | 1.59 | 0.00000 | 1.77 | 0.00000 | 1.6 | 0.00000 | 1.66 | 0.00000 | 1.7 | 0.00000 | 1.7 | 0.00000 |
| *PHLDA2* | 209803_s_at | pleckstrin homology-like domain, family A, member 2 | 215 | 1.64 | 0.12643 | 1.34 | 0.09865 | 1.51 | 0.04184 | 1.18 | 0.37317 | 1.43 | 0.02906 | 1.28 | 0.05610 | 1.87 | 0.00059 |
| *PID1* | 219093_at | phosphotyrosine interaction domain containing 1 | 1358 | -1.96 | 0.00005 | -1.75 | 0.00019 | -2.29 | 0.00002 | -1.76 | 0.00103 | -1.82 | 0.00007 | -1.87 | 0.00011 | -1.9 | 0.00038 |
| *PILRA* | 219788_at | paired immunoglobin-like type 2 receptor alpha | 1272 | 1.33 | 0.00144 | -1.11 | 0.18600 | -1.07 | 0.38478 | -1.27 | 0.00560 | -1.56 | 0.00000 | -1.44 | 0.00163 | -1.48 | 0.00003 |
| *PIP4K2A* | 212829_at | phosphatidylinositol-5-phosphate 4-kinase, type II, alpha | 7793 | -1.03 | 0.39496 | 1.01 | 0.84386 | 1.03 | 0.53862 | 1.22 | 0.09077 | 1.24 | 0.00546 | 1.29 | 0.01886 | 1.58 | 0.00017 |
| *PLAC8* | 219014_at | placenta-specific 8 | 14056 | 1.85 | 0.00000 | 1.3 | 0.00007 | 1.71 | 0.00000 | 1.36 | 0.00001 | 1.35 | 0.00020 | 1.32 | 0.00037 | 1.4 | 0.00000 |
| *PLSCR1* | 202446_s_at | phospholipid scramblase 1 | 3924 | 3.06 | 0.00000 | 1.93 | 0.00000 | 2.8 | 0.00000 | 2.08 | 0.00000 | 2.06 | 0.00000 | 2.06 | 0.00000 | 2.36 | 0.00000 |
| *PLSCR1* | 202430_s_at | phospholipid scramblase 1 | 934 | 2.6 | 0.00000 | 1.73 | 0.00000 | 2.39 | 0.00000 | 2.02 | 0.00000 | 1.81 | 0.00000 | 1.83 | 0.00001 | 1.88 | 0.00000 |
| *PML /// LOC161527* | 211012_s_at | promyelocytic leukemia /// hypothetical protein LOC161527 | 745 | 2.34* | 0.00000 | 1.61* | 0.00003 | 2.11* | 0.00000 | ND | | ND | | ND | | 1.55* | 0.00260 |
| *POU2AF1* | 205267_at | POU class 2 associating factor 1 | 2449 | -1.51 | 0.00002 | -1.14 | 0.01881 | -1.44 | 0.00008 | -1.12 | 0.19448 | 1.04 | 0.58193 | -1.07 | 0.61991 | -1.15 | 0.24413 |
| *PPBP* | 214146_s_at | pro-platelet basic protein (chemokine (C-X-C motif) ligand 7) | 17295 | 1.19 | 0.00770 | -1.4 | 0.00008 | 1.03 | 0.69427 | -1.71 | 0.00001 | -1.61 | 0.00001 | -1.57 | 0.00057 | -1.15 | 0.15638 |
| *PPM1F* | 37384_at | protein phosphatase 1F (PP2C domain containing) | 2234 | -1.43 | 0.00008 | -1.48 | 0.00018 | -1.66 | 0.00000 | -1.42 | 0.00308 | -1.46 | 0.00042 | -1.29 | 0.00440 | -1.45 | 0.00007 |
| *PPM1F* | 203063_at | protein phosphatase 1F (PP2C domain containing) | 2364 | -1.55 | 0.00153 | -1.61 | 0.00150 | -1.84 | 0.00040 | -1.58 | 0.00478 | -1.81 | 0.00051 | -1.37 | 0.02372 | -1.62 | 0.00057 |
| *PPM2C* | 218273_s_at | protein phosphatase 2C, magnesium-dependent, catalytic subunit | 1016 | -1.24 | 0.00162 | -1.17 | 0.04965 | -1.22 | 0.01531 | -1.49 | 0.00046 | -1.31 | 0.01081 | -1.51 | 0.00029 | -1.34 | 0.00479 |
| *PRDX6* | 200844_s_at | peroxiredoxin 6 | 3289 | 1.01 | 0.90005 | -1.08 | 0.07951 | 1.13 | 0.01382 | 1.22 | 0.09326 | 1.38 | 0.00503 | 1.37 | 0.02077 | 1.75 | 0.00054 |
| *PRKAR2B* | 203680_at | protein kinase, cAMP-dependent, regulatory, type II, beta | 2192 | 1.18 | 0.13891 | -1.46 | 0.00241 | 1.12 | 0.37012 | -1.69 | 0.00075 | -1.6 | 0.00073 | -1.5 | 0.00834 | -1.11 | 0.40896 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| *PRKCD* | 202545_at | protein kinase C, delta | 2771 | 1.1 | 0.06279 | -1.16 | 0.11778 | -1.08 | 0.24598 | -1.21 | 0.05144 | -1.62 | 0.00000 | -1.38 | 0.00360 | -1.47 | 0.00037 |
| *PTAFR* | 206278_at | platelet-activating factor receptor | 419 | -1.21 | 0.04324 | -1.37 | 0.01114 | -1.53 | 0.00058 | -1.60# | 0.00084 | -1.86# | 0.00000 | -1.63# | 0.00028 | -1.81# | 0.00032 |
| *PTCH1* | 209815_at | patched homolog 1 (Drosophila) | 666 | 1.22 | 0.00128 | 1.43 | 0.00025 | 1.26 | 0.00705 | 1.61 | 0.00056 | 1.22 | 0.02253 | 1.17 | 0.10535 | 1.06 | 0.61365 |
| *PTOV1* | 212032_s_at | prostate tumor overexpressed gene 1 | 704 | -1.47# | 0.00359 | -1.12 | 0.30765 | -1.54# | 0.00410 | -1.42# | 0.00230 | -1.59# | 0.00097 | -1.54# | 0.01858 | -1.62# | 0.00048 |
| *PTPRO* | 208121_s_at | protein tyrosine phosphatase, receptor type, O | 460 | 1.72 | 0.00001 | 1.22 | 0.03919 | 1.45 | 0.01164 | 1.2 | 0.10154 | 1.1 | 0.24103 | 1.12 | 0.15811 | -1.05 | 0.40871 |
| *QARS* | 217846_at | glutaminyl-tRNA synthetase | 6877 | -1.56 | 0.00000 | -1.38 | 0.00000 | -1.51 | 0.00000 | -1.33 | 0.00000 | -1.33 | 0.00000 | -1.3 | 0.00001 | -1.4 | 0.00000 |
| *RAB31* | 217763_s_at | RAB31, member RAS oncogene family | 3665 | -1.22 | 0.00393 | -1.53 | 0.00001 | -1.35 | 0.00002 | -1.44 | 0.00001 | -1.48 | 0.00001 | -1.35 | 0.00239 | -1.21 | 0.03929 |
| *RABGAP1L* | 213982_s_at | RAB GTPase activating protein 1-like | 2002 | 1.61 | 0.00000 | 1.17 | 0.00454 | 1.41 | 0.00000 | 1.22 | 0.00528 | 1.14 | 0.02797 | 1.22 | 0.00395 | 1.14 | 0.06268 |
| *RBX1* | 218117_at | ring-box 1 | 3462 | 1.46 | 0.00000 | 1.2 | 0.01619 | 1.5 | 0.00000 | 1.41 | 0.00019 | 1.4 | 0.00004 | 1.4 | 0.00011 | 1.64 | 0.00000 |
| *RGL1* | 209568_s_at | ral guanine nucleotide dissociation stimulator-like 1 | 659 | 1.54 | 0.00000 | 1.28 | 0.00334 | 1.56 | 0.00002 | 1.22 | 0.00839 | 1.3 | 0.00002 | 1.42 | 0.00013 | 1.27 | 0.00003 |
| *RGS1* | 216834_at | regulator of G-protein signaling 1 | 4361 | -1.43 | 0.06423 | -1.23 | 0.40107 | -1.43 | 0.13300 | -1.71 | 0.01831 | -1.33 | 0.10865 | -1.78 | 0.02656 | -2.36 | 0.00094 |
| *RGS2* | 202388_at | regulator of G-protein signaling 2, 24kDa | 19526 | -1.34 | 0.00201 | -1.42 | 0.00011 | -1.79 | 0.00000 | -1.57 | 0.00009 | -1.5 | 0.00004 | -1.56 | 0.00002 | -1.73 | 0.00000 |
| *RHOB* | 212099_at | ras homolog gene family, member B | 4049 | 1.65 | 0.00059 | 1.37 | 0.09397 | 1.18 | 0.32632 | 1.17 | 0.40469 | 1.19 | 0.34697 | -1.08 | 0.70536 | 1.07 | 0.60849 |
| *RHOBTB1* | 212651_at | Rho-related BTB domain containing 1 | 102 | 2.50* | 0.00009 | ND | | 2.41* | 0.00065 | ND | | ND | | ND | | ND | |
| *RIN2* | 209684_at | Ras and Rab interactor 2 | 947 | 1.53 | 0.00010 | 1.01 | 0.93518 | 1.35 | 0.00395 | 1.11 | 0.15205 | -1.02 | 0.68325 | 1.08 | 0.44990 | 1.07 | 0.36964 |
| *RNASE1* | 201785_at | ribonuclease, RNase A family, 1 (pancreatic) | 495 | 1.32* | 0.01349 | 1.28* | 0.05466 | 1.66* | 0.00061 | ND | | 1.50* | 0.01894 | 1.59* | 0.00871 | 2.12* | 0.00267 |
| *RNASE2* | 206111_at | ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) | 3620 | 2.86 | 0.00000 | 1.85 | 0.00001 | 2.32 | 0.00000 | 1.76 | 0.00132 | 1.65 | 0.00002 | 1.73 | 0.00045 | 1.94 | 0.00000 |
| *ROGDI* | 218394_at | rogdi homolog (Drosophila) | 1530 | -1.28 | 0.00001 | -1.52 | 0.00000 | -1.4 | 0.00002 | -1.26 | 0.00062 | -1.38 | 0.00002 | -1.23 | 0.00269 | -1.27 | 0.00627 |
| *RP2* | 205191_at | retinitis pigmentosa 2 (X-linked recessive) | 346 | 1.05 | 0.60752 | -1.29 | 0.02624 | -1.1 | 0.36854 | -1.16 | 0.07932 | -1.41 | 0.00011 | -1.16 | 0.09760 | -1.52 | 0.00001 |
| *RPH3A* | 205230_at | rabphilin 3A homolog (mouse) | 523 | -1.79 | 0.00188 | -1.71 | 0.00099 | -1.86 | 0.00054 | -1.68 | 0.00721 | -1.52 | 0.00212 | -1.68 | 0.00095 | -1.64 | 0.00524 |
| *RPIA* | 212973_at | ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) | 2172 | -1.08 | 0.18904 | 1.02 | 0.62404 | 1.06 | 0.17144 | 1.37 | 0.05336 | 1.42 | 0.00048 | 1.43 | 0.01382 | 1.63 | 0.00085 |
| *RPL10L* | 217559_at | ribosomal protein L10-like | 297 | -1.76# | 0.00058 | -1.55 | 0.00041 | -1.11 | 0.23911 | -1.25# | 0.11655 | 1.07 | 0.52035 | -1.21# | 0.10899 | -1 | 0.96511 |
| *RPL18A /// hCG_2040224 /// LOC285053 /// LOC390354 /// LOC729955* | 216383_at | 60S ribosomal protein L18a /// similar to ribosomal protein L18a; | 988 | -1.48 | 0.00179 | -1.08 | 0.39132 | -1.4 | 0.01108 | -1.33 | 0.05189 | -1.24 | 0.06867 | -1.57 | 0.00229 | -1.67 | 0.00013 |
| *RPL22* | 214042_s_at | ribosomal protein L22 | 9528 | -1.52 | 0.00000 | -1.2 | 0.00051 | -1.4 | 0.00000 | -1.19 | 0.00400 | -1.13 | 0.07384 | -1.22 | 0.00069 | -1.22 | 0.00041 |
| *RPL3* | 211666_x_at | ribosomal protein L3 | 41213 | -1.51 | 0.00000 | -1.18 | 0.00000 | -1.35 | 0.00000 | -1.23 | 0.00017 | -1.12 | 0.00371 | -1.23 | 0.00000 | -1.22 | 0.00000 |
| *RPL4* | 211710_x_at | ribosomal protein L4 | 40945 | -1.58 | 0.00000 | -1.27 | 0.00000 | -1.5 | 0.00000 | -1.34 | 0.00002 | -1.22 | 0.00010 | -1.26 | 0.00006 | -1.36 | 0.00000 |
| *RPL4* | 201154_x_at | ribosomal protein L4 | 41802 | -1.63 | 0.00000 | -1.27 | 0.00000 | -1.55 | 0.00000 | -1.36 | 0.00004 | -1.27 | 0.00003 | -1.3 | 0.00016 | -1.42 | 0.00000 |
| *RPL4* | 200089_s_at | ribosomal protein L4 | 19883 | -1.56 | 0.00000 | -1.23 | 0.00000 | -1.45 | 0.00000 | -1.35 | 0.00001 | -1.25 | 0.00009 | -1.32 | 0.00005 | -1.43 | 0.00000 |
| *RPS5 /// LOC392424* | 200024_at | ribosomal protein S5 /// similar to ribosomal protein S5 | 27131 | -1.56 | 0.00000 | -1.26 | 0.00033 | -1.46 | 0.00000 | -1.28 | 0.00046 | -1.12 | 0.01883 | -1.18 | 0.00523 | -1.23 | 0.00295 |
| *RRAS* | 212647_at | related RAS viral (r-ras) oncogene homolog | 610 | 1.92 | 0.00000 | -1.02 | 0.87555 | 1.46 | 0.00231 | 1.16 | 0.19707 | -1.01 | 0.92829 | 1.12 | 0.38602 | 1.11 | 0.46655 |
| *RSAD2* | 213797_at | radical S-adenosyl methionine domain containing 2 | 616 | 12.78 | 0.00000 | 5.26 | 0.00000 | 11.56 | 0.00000 | 6.79 | 0.00000 | 6.43 | 0.00005 | 6.42 | 0.00000 | 6.59 | 0.00000 |
| *RSL1D1* | 212019_at | ribosomal L1 domain containing 1 | 399 | -1.38# | 0.00029 | -1.13# | 0.09480 | -1.50# | 0.00004 | -1.12 | 0.11135 | -1.14 | 0.10320 | -1.13# | 0.14310 | -1.19 | 0.03466 |
| *RTN1* | 210222_s_at | reticulon 1 | 1330 | -2.05 | 0.00000 | -1.97 | 0.00000 | -2.15 | 0.00000 | -1.93 | 0.00000 | -2.15 | 0.00000 | -1.93 | 0.00000 | -2.05 | 0.00000 |
| *RTN1* | 203485_at | reticulon 1 | 985 | -2.17 | 0.00000 | -1.94 | 0.00004 | -2.29 | 0.00000 | -1.96 | 0.00001 | -1.99 | 0.00000 | -1.98 | 0.00000 | -2.25 | 0.00000 |
| *RTN2* | 34408_at | reticulon 2 | 492 | -1.11 | 0.16442 | -1.53 | 0.00019 | -1.07 | 0.33146 | -1.18 | 0.08834 | -1.14 | 0.09135 | -1.06 | 0.46576 | 1.01 | 0.89214 |
| *RTP4* | 219684_at | receptor (chemosensory) transporter protein 4 | 638 | 3.13* | 0.00000 | 1.71* | 0.00307 | 2.59* | 0.00005 | 2.04* | 0.00002 | ND | | 1.72* | 0.00193 | ND | |
| *SAMD4A* | 215495_s_at | sterile alpha motif domain containing 4A | 167 | 2.56* | 0.00000 | ND | | 2.03* | 0.00000 | ND | | ND | | ND | | ND | |
| *SAMD4A* | 212845_at | sterile alpha motif domain containing 4A | 541 | 2.77 | 0.00000 | 1.35 | 0.00423 | 2.18 | 0.00000 | 1.56 | 0.00038 | 1.32 | 0.02468 | 1.56 | 0.00346 | 1.48 | 0.00027 |
| *SAMD9* | 219691_at | sterile alpha motif domain containing 9 | 514 | 3.82 | 0.00000 | 2.1 | 0.00001 | 3.26 | 0.00000 | 2.62 | 0.00000 | 2.05 | 0.00015 | 2.12 | 0.00004 | 2.01 | 0.00001 |
| *SCO2* | 205241_at | SCO cytochrome oxidase deficient homolog 2 (yeast) | 3018 | 2.28 | 0.00000 | 1.7 | 0.00020 | 2.03 | 0.00001 | 1.61 | 0.00580 | 1.58 | 0.00223 | 1.71 | 0.00017 | 1.94 | 0.00000 |
| *SEMA3C* | 203789_s_at | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C | 194 | -1.66 | 0.00002 | -1.4 | 0.00700 | -1.5 | 0.00005 | -1.39 | 0.00296 | -1.48 | 0.00037 | -1.36 | 0.00215 | -1.5 | 0.00005 |
| *SERPING1* | 200986_at | serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary) | 415 | 4.93 | 0.00000 | 1.87 | 0.00015 | 4.07 | 0.00000 | 2.25 | 0.00008 | 1.9 | 0.00062 | 1.99 | 0.00029 | 2.12 | 0.00000 |
| *SIGLEC1* | 219519_s_at | sialic acid binding Ig-like lectin 1, sialoadhesin | 183 | 27.14* | 0.00000 | 16.48* | 0.00000 | 23.13* | 0.00000 | 17.00* | 0.00000 | 13.68* | 0.00000 | 18.17* | 0.00000 | 20.93* | 0.00000 |
| *SIGLEC1* | 44673_at | sialic acid binding Ig-like lectin 1, sialoadhesin | 679 | 6.41 | 0.00000 | 4.28 | 0.00000 | 5.54 | 0.00000 | 4.33 | 0.00000 | 3.55 | 0.00000 | 4.57 | 0.00000 | 4.88 | 0.00000 |
| *SKAP2* | 204361_s_at | src kinase associated phosphoprotein 2 | 775 | -1.07 | 0.22501 | -1.26 | 0.00617 | -1.16 | 0.00805 | -1.31 | 0.00232 | -1.38 | 0.00004 | -1.52 | 0.00004 | -1.34 | 0.00010 |
| *SLC14A1* | 205856_at | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | 124 | -1.24 | 0.02589 | 1.07 | 0.47745 | 1.21 | 0.11107 | 1.85 | 0.14698 | 1.91 | 0.04938 | 2.05 | 0.01073 | 2.19 | 0.00066 |
| *SLC25A6* | 212826_s_at | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | 18507 | -1.4 | 0.00001 | -1.36 | 0.00061 | -1.58 | 0.00000 | -1.64 | 0.00000 | -1.43 | 0.00003 | -1.42 | 0.00001 | -1.46 | 0.00000 |
| *SLC25A6* | 212085_at | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | 16829 | -1.57 | 0.00000 | -1.44 | 0.00000 | -1.59 | 0.00000 | -1.52 | 0.00000 | -1.42 | 0.00000 | -1.5 | 0.00000 | -1.55 | 0.00000 |
| *SLC31A2* | 204204_at | solute carrier family 31 (copper transporters), member 2 | 2025 | 1.74 | 0.00000 | -1.17 | 0.08792 | 1.41 | 0.00051 | 1.08 | 0.35602 | -1.09 | 0.08252 | 1.08 | 0.48747 | -1.05 | 0.54131 |
| *SLC7A7* | 204588_s_at | solute carrier family 7 (cationic amino acid transporter, y+ system), member 7 | 8576 | -1.07 | 0.19910 | -1.51 | 0.00000 | -1.29 | 0.00011 | -1.49 | 0.00001 | -1.64 | 0.00000 | -1.41 | 0.00041 | -1.57 | 0.00000 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene Symbol** | **Probe Set ID** | **Gene Title** | **mean signal** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** | **Fold Chg** | **p-value** |
| *SMCHD1* | 212569_at | structural maintenance of chromosomes flexible hinge domain containing 1 | 1402 | 1.66 | 0.00000 | 1.49 | 0.00003 | 1.63 | 0.00002 | 1.3 | 0.01137 | 1.4 | 0.00018 | 1.33 | 0.00097 | 1.42 | 0.00099 |
| *SMCHD1* | 212579_at | structural maintenance of chromosomes flexible hinge domain containing 1 | 1697 | 1.53 | 0.00000 | 1.37 | 0.00001 | 1.54 | 0.00002 | 1.33 | 0.00032 | 1.31 | 0.00000 | 1.26 | 0.00126 | 1.41 | 0.00013 |
| *SMCHD1* | 212577_at | structural maintenance of chromosomes flexible hinge domain containing 1 | 3613 | 1.58 | 0.00000 | 1.48 | 0.00000 | 1.57 | 0.00000 | 1.34 | 0.00055 | 1.36 | 0.00000 | 1.22 | 0.02942 | 1.27 | 0.00553 |
| *SMOX* | 210357_s_at | spermine oxidase | 569 | 1.84* | 0.00035 | 1.29* | 0.02582 | 1.92* | 0.00011 | 1.30* | 0.18036 | 1.39* | 0.04419 | 1.63* | 0.01551 | 2.03* | 0.00110 |
| *SMPDL3A* | 213624_at | sphingomyelin phosphodiesterase, acid-like 3A | 762 | 1.23 | 0.02865 | -1.45 | 0.00346 | -1.29 | 0.00986 | -1.47 | 0.00142 | -1.66 | 0.00001 | -1.41 | 0.00096 | -1.43 | 0.00088 |
| *SNAP23* | 209131_s_at | synaptosomal-associated protein, 23kDa | 626 | 1.01 | 0.92998 | -1.16 | 0.07157 | -1.07 | 0.25177 | -1.41 | 0.01308 | -1.31 | 0.03291 | -1.63 | 0.00053 | -1.49 | 0.00350 |
| *SOBP* | 218974_at | sine oculis binding protein homolog (Drosophila) | 233 | 1.41 | 0.00021 | 1.35 | 0.01005 | 1.56 | 0.00001 | 1.44 | 0.00063 | 1.41 | 0.00016 | 1.41 | 0.00117 | 1.33 | 0.00545 |
| *SOD2* | 215223_s_at | superoxide dismutase 2, mitochondrial | 2499 | -1.11 | 0.41139 | -1.57 | 0.01628 | -1.38 | 0.03394 | -1.7 | 0.00276 | -1.41 | 0.00707 | -1.52 | 0.00055 | -1.1 | 0.52876 |
| *SOX15* | 217040_x_at | SRY (sex determining region Y)-box 15 | 820 | ND | | ND | | 1.17* | 0.05558 | ND | | 1.49* | 0.00386 | 1.39* | 0.06922 | 1.71* | 0.00048 |
| *SOX4* | 201417_at | SRY (sex determining region Y)-box 4 | 721 | -1.37 | 0.00016 | -1.23 | 0.03696 | -1.46 | 0.00003 | -1.48 | 0.00016 | -1.47 | 0.00011 | -1.69 | 0.00007 | -1.38 | 0.00050 |
| *SP100* | 210218_s_at | SP100 nuclear antigen | 348 | 1.85 | 0.00000 | 1.66 | 0.00006 | 1.89 | 0.00000 | 1.64 | 0.00006 | 1.64 | 0.00001 | 1.5 | 0.00001 | 1.75 | 0.00000 |
| *SP100* | 202864_s_at | SP100 nuclear antigen | 2387 | 1.93 | 0.00000 | 1.77 | 0.00002 | 1.83 | 0.00000 | 1.44 | 0.00028 | 1.62 | 0.00003 | 1.54 | 0.00005 | 1.6 | 0.00006 |
| *SP100* | 202863_at | SP100 nuclear antigen | 2231 | 1.77 | 0.00000 | 1.52 | 0.00001 | 1.73 | 0.00000 | 1.37 | 0.00012 | 1.44 | 0.00000 | 1.45 | 0.00000 | 1.55 | 0.00000 |
| *SP100* | 210985_s_at | SP100 nuclear antigen | 175 | 1.66 | 0.00002 | 1.56 | 0.00056 | 1.82 | 0.00002 | 1.43 | 0.00881 | 1.46 | 0.00130 | 1.33 | 0.00559 | 1.37 | 0.00104 |
| *SP110* | 208012_x_at | SP110 nuclear body protein | 5268 | 1.94 | 0.00000 | 1.46 | 0.00000 | 1.85 | 0.00000 | 1.52 | 0.00001 | 1.54 | 0.00000 | 1.5 | 0.00000 | 1.59 | 0.00000 |
| *SP110* | 209762_x_at | SP110 nuclear body protein | 4433 | 1.87 | 0.00000 | 1.4 | 0.00011 | 1.81 | 0.00000 | 1.57 | 0.00000 | 1.53 | 0.00000 | 1.58 | 0.00000 | 1.56 | 0.00000 |
| *SP110* | 208392_x_at | SP110 nuclear body protein | 1737 | 1.72 | 0.00000 | 1.46 | 0.00004 | 1.77 | 0.00000 | 1.44 | 0.00000 | 1.57 | 0.00001 | 1.39 | 0.00030 | 1.5 | 0.00000 |
| *SP110* | 209761_s_at | SP110 nuclear body protein | 5876 | 1.7 | 0.00000 | 1.44 | 0.00000 | 1.63 | 0.00000 | 1.3 | 0.00042 | 1.37 | 0.00001 | 1.29 | 0.00075 | 1.41 | 0.00000 |
| *SPTLC2* | 203127_s_at | serine palmitoyltransferase, long chain base subunit 2 | 2699 | 1.56 | 0.00000 | 1.13 | 0.04549 | 1.5 | 0.00005 | 1.21 | 0.03547 | 1.18 | 0.00356 | 1.31 | 0.00200 | 1.35 | 0.00036 |
| *SPTLC2* | 216202_s_at | serine palmitoyltransferase, long chain base subunit 2 | 1091 | 1.92 | 0.00000 | 1.16 | 0.15527 | 1.73 | 0.00072 | 1.26 | 0.04730 | 1.07 | 0.56961 | 1.27 | 0.08534 | 1.29 | 0.05098 |
| *SSPN* | 204963_at | sarcospan (Kras oncogene-associated gene) | 134 | -1.52# | 0.00304 | -1.08# | 0.42101 | -1.80# | 0.00065 | -1.00# | 0.99059 | -1.62# | 0.00191 | -1.17# | 0.20517 | -1.65# | 0.00549 |
| *STAP1* | 220059_at | signal transducing adaptor family member 1 | 629 | 1.32 | 0.00503 | 1.4 | 0.00822 | 1.46 | 0.00786 | 1.41 | 0.01629 | 1.58 | 0.00006 | 1.32 | 0.01030 | 1.84 | 0.00013 |
| *STAT1* | AFFX-HUMISGF | signal transducer and activator of transcription 1, 91kDa | 1305 | 2.46 | 0.00000 | 1.54 | 0.00007 | 2.42 | 0.00000 | 1.65 | 0.00033 | 1.49 | 0.00174 | 1.37 | 0.01116 | 1.47 | 0.00171 |
| *STAT1* | 209969_s_at | signal transducer and activator of transcription 1, 91kDa | 2479 | 2.37 | 0.00000 | 1.45 | 0.00077 | 2.26 | 0.00000 | 1.4 | 0.00143 | 1.46 | 0.00107 | 1.52 | 0.00658 | 1.44 | 0.00194 |
| *STAT1* | AFFX-HUMISGF3A /M97935_3_at | signal transducer and activator of transcription 1, 91kDa | 4980 | 1.78 | 0.00000 | 1.35 | 0.00001 | 1.76 | 0.00000 | 1.43 | 0.00014 | 1.41 | 0.00001 | 1.41 | 0.00001 | 1.39 | 0.00000 |
| *STAT1* | AFFX-HUMISGF | signal transducer and activator of transcription 1, 91kDa | 569 | 2.56 | 0.00000 | 1.7 | 0.00068 | 2.71 | 0.00001 | 1.72 | 0.00261 | 1.58 | 0.01509 | 1.33 | 0.04333 | 1.39 | 0.04431 |
| *STAT1* | AFFX-HUMISGF | signal transducer and activator of transcription 1, 91kDa | 2027 | 2.57 | 0.00000 | 1.66 | 0.00002 | 2.48 | 0.00000 | 1.73 | 0.00030 | 1.46 | 0.00327 | 1.36 | 0.02601 | 1.38 | 0.00945 |
| *STAT1* | 200887_s_at | signal transducer and activator of transcription 1, 91kDa | 9193 | 1.69 | 0.00000 | 1.3 | 0.00006 | 1.7 | 0.00000 | 1.41 | 0.00014 | 1.38 | 0.00008 | 1.45 | 0.00000 | 1.36 | 0.00009 |
| *STAT2* | 205170_at | signal transducer and activator of transcription 2, 113kDa | 637 | 1.69 | 0.00102 | 1.22 | 0.06832 | 1.7 | 0.00015 | 1.13 | 0.14572 | 1.19 | 0.11073 | -1.04 | 0.73713 | 1.2 | 0.06244 |
| *TAL1* | 216925_s_at | T-cell acute lymphocytic leukemia 1 | 274 | ND | | ND | | 1.43* | 0.04380 | 1.63* | 0.07204 | 2.09* | 0.00160 | 1.87* | 0.05818 | 2.71* | 0.00055 |
| *TAP1* | 202307_s_at | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) | 3093 | 2.09 | 0.00000 | 1.37 | 0.00006 | 1.93 | 0.00000 | 1.47 | 0.00159 | 1.22 | 0.08957 | 1.39 | 0.00689 | 1.29 | 0.01117 |
| *TBC1D22A* | 210144_at | TBC1 domain family, member 22A | 703 | -1.3 | 0.00039 | -1.24 | 0.02330 | -1.32 | 0.00173 | -1.27 | 0.00397 | -1.48 | 0.00026 | -1.48 | 0.00005 | -1.89 | 0.00000 |
| *TBC1D9* | 212956_at | TBC1 domain family, member 9 (with GRAM domain) | 2064 | -1.51 | 0.00006 | -1.55 | 0.00001 | -1.69 | 0.00000 | -1.38 | 0.00056 | -1.45 | 0.00000 | -1.49 | 0.00002 | -1.76 | 0.00000 |
| *TBCD* | 201759_at | tubulin folding cofactor D | 340 | -1.31# | 0.01483 | -1.23 | 0.05912 | 1.03 | 0.83393 | 1.19 | 0.37024 | 1.64 | 0.00046 | 1.47 | 0.01017 | 1.52 | 0.00091 |
| *TBXAS1* | 208130_s_at | thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) | 1567 | -1.08 | 0.36451 | -1.3 | 0.00532 | -1.27 | 0.00561 | -1.28 | 0.01657 | -1.57 | 0.00004 | -1.3 | 0.04686 | -1.29 | 0.02243 |
| *TCN2* | 204043_at | transcobalamin II; macrocytic anemia | 552 | 2.16 | 0.00000 | 1.24 | 0.00537 | 1.68 | 0.00000 | 1.31 | 0.00875 | 1.3 | 0.00920 | 1.45 | 0.00096 | 1.42 | 0.00005 |
| *TDRD7* | 213361_at | tudor domain containing 7 | 1338 | 1.64 | 0.00000 | 1.28 | 0.00000 | 1.6 | 0.00000 | 1.49 | 0.00000 | 1.39 | 0.00004 | 1.46 | 0.00000 | 1.46 | 0.00000 |
| *TFDP2* | 203588_s_at | transcription factor Dp-2 (E2F dimerization partner 2) | 490 | 1.14 | 0.04720 | 1.14 | 0.15297 | 1.22 | 0.03339 | 1.27 | 0.01546 | 1.51 | 0.00001 | 1.37 | 0.01297 | 1.54 | 0.00117 |
| *TK2* | 204276_at | thymidine kinase 2, mitochondrial | 503 | 1.03 | 0.67289 | -1.09 | 0.39985 | -1.21 | 0.03306 | -1.05 | 0.61286 | -1.19 | 0.04185 | -1.16 | 0.04035 | -1.51 | 0.00032 |
| *TKT* | 208699_x_at | transketolase (Wernicke-Korsakoff syndrome) | 9769 | -1.3 | 0.00004 | -1.53 | 0.00000 | -1.51 | 0.00000 | -1.45 | 0.00001 | -1.61 | 0.00000 | -1.54 | 0.00001 | -1.48 | 0.00000 |
| *TKT* | 208700_s_at | transketolase (Wernicke-Korsakoff syndrome) | 10936 | -1.18 | 0.02885 | -1.33 | 0.00620 | -1.35 | 0.00179 | -1.43 | 0.00007 | -1.51 | 0.00043 | -1.5 | 0.00009 | -1.58 | 0.00000 |
| *TLR1* | 210176_at | toll-like receptor 1 | 846 | 1.59 | 0.00032 | -1.06 | 0.52935 | 1.23 | 0.03395 | 1.02 | 0.79288 | -1.01 | 0.91169 | 1.09 | 0.38678 | -1.07 | 0.43712 |
| *TLR3* | 206271_at | toll-like receptor 3 | 147 | 1.50* | 0.00319 | 1.34* | 0.03399 | 1.49* | 0.00695 | 1.54* | 0.00070 | ND | | ND | | 1.13* | 0.31138 |
| *TLR7* | 220146_at | toll-like receptor 7 | 399 | 2.24 | 0.00001 | 1.17 | 0.22160 | 1.96 | 0.00025 | 1.39 | 0.06554 | 1 | 0.99649 | 1.33 | 0.02171 | 1.01 | 0.91565 |
| *TMED2* | 204426_at | transmembrane emp24 domain trafficking protein 2 | 667 | -1.17 | 0.08846 | -1.11 | 0.22827 | -1.11 | 0.27462 | -1.34 | 0.02184 | -1.18 | 0.13850 | -1.76 | 0.00032 | -1.34 | 0.03497 |
| *TMEM140* | 218999_at | transmembrane protein 140 | 1049 | 2.41 | 0.00000 | 1.31 | 0.00094 | 2.22 | 0.00000 | 1.31 | 0.00420 | 1.2 | 0.05455 | 1.35 | 0.00928 | 1.54 | 0.00073 |
| *TMOD3* | 220800_s_at | tropomodulin 3 (ubiquitous) | 169 | 1.63 | 0.00055 | 1.39 | 0.04117 | 1.48 | 0.00071 | 1.39 | 0.02636 | 1.31 | 0.09044 | 1.01 | 0.90932 | 1.16 | 0.37191 |
| *TNFAIP6* | 206025_s_at | tumor necrosis factor, alpha-induced protein 6 | 233 | 1.87* | 0.00322 | ND | | 1.51* | 0.00051 | ND | | ND | | ND | | ND | |
| *TNFAIP6* | 206026_s_at | tumor necrosis factor, alpha-induced protein 6 | 231 | 2.07 | 0.00099 | -1 | 0.99210 | 1.59 | 0.00253 | 1.2 | 0.29455 | 1.1 | 0.54454 | 1.09 | 0.56358 | 1.08 | 0.63088 |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| *TNFRSF25* | 211841_s_at | tumor necrosis factor receptor superfamily, member 25 | 683 | 1.15 | 0.07056 | 1.51 | 0.00002 | 1.35 | 0.00044 | 1.59 | 0.00034 | 1.44 | 0.00003 | 1.55 | 0.01370 | 1.46 | 0.00076 |
| *TNFRSF8* | 206729_at | tumor necrosis factor receptor superfamily, member 8 | 658 | 1 | 0.96923 | -1.49 | 0.00039 | -1.34 | 0.00732 | -1.64 | 0.00003 | -1.61 | 0.00000 | -1.6 | 0.00005 | -1.7 | 0.00000 |
| *TNFSF10* | 202687_s_at | tumor necrosis factor (ligand) superfamily, member 10 | 2896 | 2.34 | 0.00000 | 1.16 | 0.06597 | 1.95 | 0.00000 | 1.4 | 0.00149 | 1.1 | 0.27355 | 1.11 | 0.40561 | 1.11 | 0.43599 |
| *TNFSF10* | 202688_at | tumor necrosis factor (ligand) superfamily, member 10 | 7233 | 2.04 | 0.00000 | 1.06 | 0.46959 | 1.59 | 0.00002 | 1.17 | 0.03032 | -1.01 | 0.87814 | 1.09 | 0.39137 | 1.08 | 0.48364 |
| *TNFSF10* | 214329_x_at | tumor necrosis factor (ligand) superfamily, member 10 | 1467 | 2.01 | 0.00000 | -1 | 0.99181 | 1.72 | 0.00182 | 1.29 | 0.07697 | -1.16 | 0.22638 | 1.16 | 0.30896 | -1.19 | 0.25887 |
| *TNS1* | 221748_s_at | tensin 1 | 562 | 1.4 | 0.00545 | 1.08 | 0.53973 | 1.7 | 0.00001 | 2.37 | 0.07299 | 2.29 | 0.00167 | 2.6 | 0.02500 | 3.26 | 0.00243 |
| *TOB2* | 222243_s_at | transducer of ERBB2, 2 | 702 | -1.1 | 0.20294 | -1.05 | 0.55289 | -1.15 | 0.05550 | -1.02 | 0.81786 | -1.39 | 0.00027 | -1.2 | 0.01561 | -1.71 | 0.00000 |
| *TOR1B* | 209593_s_at | torsin family 1, member B (torsin B) | 1585 | 1.89 | 0.00000 | 1.29 | 0.00026 | 1.65 | 0.00000 | 1.53 | 0.00000 | 1.3 | 0.00191 | 1.39 | 0.00448 | 1.35 | 0.00043 |
| *TRAFD1* | 202837_at | TRAF-type zinc finger domain containing 1 | 387 | 1.99* | 0.00001 | ND | | 1.37* | 0.04119 | ND | | ND | | ND | | ND | |
| *TRAK2* | 202125_s_at | trafficking protein, kinesin binding 2 | 1770 | 1.04 | 0.24888 | 1.08 | 0.07092 | 1.16 | 0.00112 | 1.41 | 0.00617 | 1.5 | 0.00010 | 1.62 | 0.00022 | 1.67 | 0.00064 |
| *TREX1* | 205875_s_at | three prime repair exonuclease 1 | 1871 | 1.97* | 0.00000 | 1.13* | 0.08996 | 1.79* | 0.00000 | 1.32* | 0.00683 | ND | | 1.36* | 0.00350 | 1.35* | 0.00137 |
| *TRIM14* | 203148_s_at | tripartite motif-containing 14 | 2531 | 1.51 | 0.00001 | 1.29 | 0.00952 | 1.4 | 0.00053 | 1.33 | 0.00121 | 1.13 | 0.14676 | 1.22 | 0.01181 | 1.06 | 0.34513 |
| *TRIM21* | 204804_at | tripartite motif-containing 21 | 1531 | 1.64 | 0.00002 | 1.2 | 0.05582 | 1.69 | 0.00012 | 1.4 | 0.00472 | 1.19 | 0.06869 | 1.27 | 0.03776 | 1.23 | 0.04461 |
| *TRIM22* | 213293_s_at | tripartite motif-containing 22 | 10465 | 1.72 | 0.00000 | 1.45 | 0.00000 | 1.65 | 0.00000 | 1.47 | 0.00000 | 1.46 | 0.00000 | 1.41 | 0.00000 | 1.5 | 0.00000 |
| *TRIM38* | 203567_s_at | tripartite motif-containing 38 | 3072 | 1.63 | 0.00000 | 1.32 | 0.00002 | 1.5 | 0.00000 | 1.34 | 0.00001 | 1.29 | 0.00004 | 1.21 | 0.00418 | 1.23 | 0.00274 |
| *TRIM38* | 203610_s_at | tripartite motif-containing 38 | 1396 | 1.82 | 0.00000 | 1.35 | 0.00003 | 1.55 | 0.00000 | 1.34 | 0.00016 | 1.19 | 0.00987 | 1.1 | 0.17158 | 1.13 | 0.06292 |
| *TRIM5* | 210705_s_at | tripartite motif-containing 5 | 459 | 1.81 | 0.00003 | 1.22 | 0.08498 | 1.55 | 0.00183 | 1.46 | 0.00592 | 1.34 | 0.00791 | 1.34 | 0.01796 | 1.24 | 0.08066 |
| *TRIM58* | 215047_at | tripartite motif-containing 58 | 726 | 1.73 | 0.05524 | -1.12 | 0.72417 | 2.53 | 0.00073 | 2.6 | 0.04365 | 4 | 0.00094 | 3.28 | 0.00928 | 4.16 | 0.00018 |
| *TRIM6-TRIM34* | 221044_s_at | tripartite motif-containing 6 and tripartite motif-containing 34 | 1196 | 1.69 | 0.00000 | 1.29 | 0.00342 | 1.51 | 0.00006 | 1.35 | 0.00013 | 1.23 | 0.00110 | 1.23 | 0.02391 | 1.17 | 0.06064 |
| *TRIP6* | 209129_at | thyroid hormone receptor interactor 6 | 245 | 1.57 | 0.00001 | 1.37 | 0.00086 | 1.41 | 0.00034 | 1.28 | 0.00661 | 1.35 | 0.00225 | 1.42 | 0.00115 | 1.28 | 0.00085 |
| *TSC22D1* | 215111_s_at | TSC22 domain family, member 1 | 2072 | 1.33 | 0.00448 | 1.24 | 0.01004 | 1.57 | 0.00029 | 1.07 | 0.37527 | 1.21 | 0.00656 | 1.23 | 0.00487 | 1.69 | 0.00016 |
| *TSC22D3* | 207001_x_at | TSC22 domain family, member 3 | 2220 | -1.53 | 0.00869 | 1.09 | 0.66441 | -1.13 | 0.51701 | -2.03 | 0.00053 | -1.65 | 0.00519 | -1.83 | 0.00665 | -1.57 | 0.01786 |
| *TUBA1A* | 209118_s_at | tubulin, alpha 1a | 7743 | -1.2 | 0.00212 | -1.36 | 0.00081 | -1.4 | 0.00015 | -1.7 | 0.00022 | -1.42 | 0.00022 | -1.43 | 0.00002 | -1.4 | 0.00002 |
| *TUBB1* | 208601_s_at | tubulin, beta 1 | 1467 | 1.57 | 0.02238 | -1.18 | 0.30296 | 1.05 | 0.71619 | -1.38 | 0.04566 | -1.68# | 0.00089 | -1.27 | 0.22907 | -1.01 | 0.94267 |
| *TXNDC5* | 221253_s_at | thioredoxin domain containing 5 | 3419 | -1.43 | 0.00657 | -1.22 | 0.14290 | -1.78 | 0.00053 | -1.41 | 0.04817 | -1.48 | 0.02379 | -1.4 | 0.16100 | -1.85 | 0.00559 |
| *TYMS* | 202589_at | thymidylate synthetase | 744 | 1.25 | 0.03261 | 1.22 | 0.10831 | 1.37 | 0.01644 | 1.19 | 0.12184 | 1.3 | 0.01334 | 1.48 | 0.00068 | 1.5 | 0.00039 |
| *UBAP2L* | 201377_at | ubiquitin associated protein 2-like | 1133 | 1.07 | 0.22277 | 1.26 | 0.00480 | 1.23 | 0.00520 | 1.19 | 0.05869 | 1.36 | 0.01194 | 1.24 | 0.01020 | 1.51 | 0.00008 |
| *UBE2L6* | 201649_at | ubiquitin-conjugating enzyme E2L 6 | 6323 | 1.91 | 0.00000 | 1.32 | 0.00001 | 1.81 | 0.00000 | 1.31 | 0.00093 | 1.25 | 0.00218 | 1.26 | 0.00085 | 1.27 | 0.00008 |
| *UBL3* | 201534_s_at | ubiquitin-like 3 | 2189 | -1.29 | 0.00801 | -1.16 | 0.26636 | -1.33 | 0.01555 | -1.35 | 0.01097 | -1.66 | 0.00062 | -1.61 | 0.00162 | -1.85 | 0.00002 |
| *UNC119B* | 202365_at | unc-119 homolog B (C. elegans) | 995 | -1.58 | 0.00000 | -1.28 | 0.00204 | -1.61 | 0.00000 | -1.24 | 0.00233 | -1.22 | 0.00282 | -1.25 | 0.00078 | -1.33 | 0.00013 |
| *UQCRB* | 209066_x_at | ubiquinol-cytochrome c reductase binding protein | 10284 | -1.27 | 0.01217 | -1.07 | 0.52318 | -1.36 | 0.00081 | -1.41 | 0.01819 | -1.54 | 0.00069 | -1.53 | 0.00013 | -1.58 | 0.00003 |
| *USP18 /// LOC727996 /// LOC728216 /// LOC728438* | 219211_at | ubiquitin specific peptidase 18 /// similar to ubiquitin specific peptidase 18 | 287 | 7.43* | 0.00000 | 4.93* | 0.00000 | 7.47* | 0.00000 | 5.07* | 0.00000 | 4.50* | 0.00000 | 5.28* | 0.00000 | 5.50* | 0.00000 |
| *UTRN* | 213023_at | utrophin | 691 | 1.51 | 0.00008 | 1.24 | 0.00304 | 1.32 | 0.00111 | 1.17 | 0.04872 | 1.16 | 0.13223 | -1.04 | 0.65005 | -1.03 | 0.73095 |
| *VDR* | 204255_s_at | vitamin D (1,25- dihydroxyvitamin D3) receptor | 539 | 1.6 | 0.00001 | 1.02 | 0.80767 | 1.17 | 0.04634 | 1.08 | 0.33407 | 1.03 | 0.66745 | 1.16 | 0.25408 | 1.22 | 0.06791 |
| *VPREB3* | 220068_at | pre-B lymphocyte gene 3 | 600 | ND | | 1.44 | 0.01914 | ND | | 1.46 | 0.00615 | 1.5 | 0.00093 | 1.48 | 0.05441 | 1.28 | 0.05493 |
| *WARS* | 200629_at | tryptophanyl-tRNA synthetase | 6088 | 1.09 | 0.26161 | -1.44 | 0.00177 | -1.16 | 0.12151 | -1.61 | 0.00040 | -1.52 | 0.00059 | -1.45 | 0.00407 | -1.4 | 0.01123 |
| *WBP5* | 217975_at | WW domain binding protein 5 | 158 | 1.31 | 0.00146 | 1.47 | 0.00005 | 1.63 | 0.00021 | 1.43 | 0.00250 | 1.65 | 0.00006 | 1.77 | 0.00002 | 1.91 | 0.00000 |
| *WDR1* | 210935_s_at | WD repeat domain 1 | 992 | -1.12 | 0.11360 | -1.26 | 0.03185 | -1.2 | 0.07726 | -1.12 | 0.22391 | -1.35 | 0.00407 | -1.51 | 0.00066 | -1.57 | 0.00098 |
| *WRB* | 202749_at | tryptophan rich basic protein | 1069 | -1 | 0.99843 | -1.04 | 0.63399 | -1.11 | 0.26350 | -1.09 | 0.54838 | -1.52 | 0.00012 | -1.26 | 0.05054 | -1.67 | 0.00012 |
| *WSB1* | 210561_s_at | WD repeat and SOCS box-containing 1 | 3340 | 1.52 | 0.00000 | 1.19 | 0.03237 | 1.37 | 0.00063 | 1.2 | 0.07249 | 1.12 | 0.10727 | -1.03 | 0.74941 | 1.15 | 0.11347 |
| *XAF1* | 206133_at | XIAP associated factor-1 | 1551 | 4.25 | 0.00000 | 3.29 | 0.00000 | 3.76 | 0.00000 | 2.93 | 0.00000 | 2.93 | 0.00001 | 2.47 | 0.00000 | 3.08 | 0.00000 |
| *XK* | 206698_at | X-linked Kx blood group (McLeod syndrome) | 293 | 1.61 | 0.00353 | 1.17 | 0.15331 | 2.06 | 0.00002 | 2.6 | 0.03571 | 3.84 | 0.00433 | 4.42 | 0.01340 | 5.68 | 0.00211 |
| *ZBP1* | 208087_s_at | Z-DNA binding protein 1 | 176 | 3.03* | 0.00000 | 2.19* | 0.00001 | 3.03* | 0.00000 | 2.22* | 0.00001 | 2.05* | 0.00003 | 2.16* | 0.00029 | 2.21* | 0.00001 |
| *ZCCHC2* | 219062_s_at | zinc finger, CCHC domain containing 2 | 1318 | 2.26 | 0.00000 | 1.89 | 0.00001 | 2.24 | 0.00000 | 1.68 | 0.00032 | 1.79 | 0.00000 | 1.84 | 0.00000 | 1.76 | 0.00000 |
| *ZEB2* | 203603_s_at | zinc finger E-box binding homeobox 2 | 924 | 1.12 | 0.20456 | -1.26 | 0.00240 | -1.23 | 0.05835 | -1.39 | 0.00849 | -1.47 | 0.00138 | -1.41 | 0.00221 | -1.53 | 0.00034 |
| *ZFX* | 214678_x_at | zinc finger protein, X-linked | 215 | -1.15 | 0.16097 | -1.1 | 0.41807 | -1.22 | 0.06382 | -1.45 | 0.00488 | -1.32 | 0.01256 | -1.37 | 0.00833 | -1.54 | 0.00034 |
| *ZNF652* | 205594_at | zinc finger protein 652 | 805 | -1.48 | 0.00141 | -1.26 | 0.04962 | -1.7 | 0.00008 | -1.28 | 0.05005 | -1.28 | 0.05052 | -1.5 | 0.00015 | -1.48 | 0.00255 |
| --- | 212605_s_at | AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig | 1616 | -1.6 | 0.00000 | -1.16 | 0.01702 | -1.48 | 0.00000 | -1.36 | 0.00010 | -1.34 | 0.00002 | -1.29 | 0.00020 | -1.35 | 0.00000 |
| --- | 221973_at | CDNA clone IMAGE:5217021, with apparent retained intron | 701 | 1.05 | 0.60288 | 1.39 | 0.00090 | 1.28 | 0.02683 | 1.16 | 0.04008 | 1.31 | 0.00514 | 1.5 | 0.00032 | 1.43 | 0.01323 |
| --- | 215617_at | CDNA FLJ11754 fis, clone HEMBA1005588 | 90 | 3.12* | 0.00000 | 2.38* | 0.00003 | 3.12* | 0.00000 | 2.32* | 0.00001 | 2.57* | 0.00000 | 2.55* | 0.00000 | 2.61* | 0.00000 |
| --- | 213817_at | CDNA FLJ13601 fis, clone PLACE1010069 | 591 | -1.14 | 0.14782 | -1.23 | 0.05893 | -1.24 | 0.09077 | -1.28 | 0.03051 | -1.55 | 0.00001 | -1.18 | 0.14125 | -1.42 | 0.00004 |
| --- | 213294_at | Full-length cDNA clone CS0DK002YF13 of HeLa cells Cot 25-normalized of Homo sapiens (human) | 2142 | 3.34 | 0.00000 | 2.64 | 0.00000 | 3.39 | 0.00000 | 2.55 | 0.00000 | 2.5 | 0.00000 | 2.67 | 0.00000 | 2.8 | 0.00000 |
| --- | 213710_s_at | Transcribed locus | 1343 | -1.31 | 0.00082 | -1.21 | 0.03008 | -1.19 | 0.02478 | -1.11 | 0.34402 | -1.13 | 0.16092 | -1.22 | 0.02284 | -1.54 | 0.00029 |
| --- | 202015_x_at | --- | 46 | 1.38* | 0.18350 | 1.31* | 0.13573 | 1.58* | 0.00093 | 1.18* | 0.39859 | ND | | ND | | ND | |

| | | | Day 1 | Day 3 | | Day 6 | | Day 10 | | Day 13 | | Day 27 | | Day 42 | | Day 70 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene Symbol | Probe Set ID | Gene Title | mean signal | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value | Fold Chg | p-value |
| --- | 211781_x_at | --- | 295 | 1.18* | 0.20604 | 1.33* | 0.09583 | 2.57* | 0.00094 | 4.81* | 0.00781 | 7.37* | 0.00100 | 7.68* | 0.01292 | 11.19* | 0.00083 |
| --- | 217019_at | --- | 196 | -1.63 | 0.00107 | -1.32 | 0.02501 | -1.61# | 0.00083 | -1.33 | 0.08376 | -1.59# | 0.00288 | -1.48 | 0.02907 | -1.98# | 0.00003 |
| --- | 211600_at | --- | 15352 | -1.37 | 0.00534 | -1.32 | 0.02561 | -1.53 | 0.00078 | -1.63 | 0.00107 | -1.52 | 0.00161 | -1.77 | 0.00008 | -1.48 | 0.00174 |
| --- | 210596_at | --- | 671 | -1.15 | 0.06996 | -1.27 | 0.01484 | -1.18 | 0.07926 | -1.38 | 0.02024 | -1.08 | 0.40754 | -1.29 | 0.01053 | -1.55 | 0.00056 |
| --- | 220494_s_at | --- | 1723 | -1.08 | 0.37671 | -1.09 | 0.38333 | -1.13 | 0.17846 | -1.23 | 0.04707 | -1.32 | 0.01359 | -1.31 | 0.00385 | -1.72 | 0.00026 |

* Gene turned on: not detected on day 1, but expressed at this time point; fold change may be inaccurate.
# Gene turned off: detected on day 1 but not detected at this time point; fold change may be inaccurate.
ND: gene not detected either at day 1 or this time point.