Quantitative model for inferring dynamic regulation of the tumour suppressor gene p53
Supplementary Information
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Supplementary Table 2. Detailed information for the top 317 putative p53 target genes.
Here we list the putative p53 target gene information (i.e. AffyProbe ID, gene symbol and gene title), quantitative model estimation error, target gene regulation state inferred by quantitative model (regulation: 1 represents positive regulation by p53 but -1 represents negative regulation by p53), time delay effect (delay: hours), target gene regulation state inferred by event method (event score >0 represents positive regulation, event score <0 represents negative regulation), target gene regulation state inferred by correlation method (correlation coefficient >0 represents positive regulation, correlation coefficient <0 represents negative regulation), and the number of motif count of perfect match of 10-mer p53 binding motif on 10kb upstream region (motif counts).

| Order | Probe Set ID | Gene Symbol | Gene Title | model estimation error | regulation delay | event score | correlation coefficient | p-value | motif counts |
|-------|--------------|-------------|------------|------------------------|-----------------|-------------|------------------------|--------|--------------|
| 1     | 1 217732_S_AT | ITM2B       | integral membrane protein 2B | 0.0382 | 1 | 0 | 1 | 0.207 | 0.656 | 4 |
| 2     | 2 205347_S_AT | TMSL8       | thymosin-like 8 | 0.0828 | 1 | 1.823 | 3 | -0.1556 | 0.739 | 6 |
| 3     | 3 211630_S_AT | GSS         | glutathione synthetase | 0.11 | 1 | 0 | -6 | 0.4575 | 0.302 | 10 |
| 4     | 4 201202_AT   | PCNA        | proliferating cell nuclear antigen | 0.1148 | 1 | 1.07 | 2 | 0.6102 | 0.146 | 10 |
| 5     | 5 208812_X_AT | HLA-C       | major histocompatibility complex, class I, C | 0.1216 | 1 | 0 | 2 | 0.6533 | 0.112 NA |
| 6     | 6 202649_X_AT | RPS19       | ribosomal protein S19 | 0.1396 | 1 | 1.42 | 2 | 0.1243 | 0.791 | 12 |
| 7     | 7 211714_X_AT | TUBB        | tubulin, beta | 0.1495 | 1 | 1.403 | 0 | 0.5364 | 0.215 NA |
| 8     | 9 201761_AT   | MTHFD2      | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 | 0.1848 | -1 | 0.39 | 1 | -0.2435 | 0.599 | 4 |
| 9     | 10 202605_AT  | GUSB        | glucuronidase, beta | 0.1933 | 1 | 0.638 | 5 | 0.146 | 0.755 | 2 |
| 10    | 11 209140_X_AT | HLA-B       | major histocompatibility complex, class I, B | 0.1956 | 1 | 0.193 | 3 | 0.7715 | 0.042 | 3 |
| 11    | 12 210968_S_AT | RTN4        | reticulin 4 | 0.1996 | -1 | 0 | -3 | -0.72 | 0.068 | 10 |
| 12    | 13 201476_S_AT | RRM1        | ribonucleotide reductase M1 polypeptide | 0.2046 | 1 | 0.76 | 0 | 0.3134 | 0.494 | 10 |
| 13    | 14 204026_S_AT | ZWINT       | ZW10 interactor | 0.2087 | 1 | 1.564 | 3 | -0.0447 | 0.924 | 8 |
| 14    | 18 216705_S_AT | ADA         | adenosine deaminase | 0.2235 | 1 | 1.683 | 4 | -0.2144 | 0.644 | 4 |
| 15    | 20 202503_S_AT | KIAA0101    | KIAA0101 | 0.2318 | 1 | 1.191 | -4 | 0.0023 | 0.996 | 6 |
| 16    | 21 218740_S_AT | CDK5RAP3    | CDK5 regulatory subunit associated protein 3 | 0.2382 | 1 | 0.248 | 0 | 0.0714 | 0.879 | 4 |
| 17    | 23 213060_S_AT | CHICL2      | chitinase 3-like 2 | 0.2785 | 1 | 0.705 | 3 | 0.0297 | 0.95 | 12 |
| 18    | 24 221943_X_AT | RPL38       | Ribosomal protein L38 | 0.2858 | 1 | 1.44 | -2 | 0.5116 | 0.241 | 6 |
| 19    | 25 218883_S_AT | MLF1IP       | MLF1 interacting protein | 0.2891 | 1 | 0.974 | 0 | 0.252 | 0.586 | 4 |
20 30 201721_S_AT LAPT M5 lysosomal associated multispanning membrane protein 5 0.3121 1 1.545 2 -0.0289 0.951 4
21 31 208149_X_AT DDX11 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 0.3408 1 0.146 3 0.6388 0.123 4
22 32 209773_S_AT RRM2 ribonucleotide reductase M2 polypeptide 0.3454 1 0 0 -0.0744 0.874 4
23 33 218403_AT TRIAP1 TPS3 regulated inhibitor of apoptosis 1 0.35 1 0 2 0.7745 0.041 8
24 36 201577_AT NME1 non-metastatic cells 1, protein (NM23A) 0.3645 1 1.685 2 0.253 0.584 4
25 38 210774_S_AT NCOA4 nuclear receptor coactivator 4 0.3703 1 0 0 -0.0418 0.929 12
26 40 221083_AT DENND2D DENN/MADD domain containing 2D 0.3848 1 2E-04 -1 0.3352 0.462 10
27 41 208998_AT UCP2 uncoupling protein 2 (mitochondrial, proton carrier) 0.4023 1 0 4 0.4023 0.371 6
28 43 204386_S_AT MRP63 mitochondrial ribosomal protein 63 0.4127 1 1.876 0 -0.2646 0.566 6
29 47 218140_X_AT SRPRB signal recognition particle receptor, B subunit 0.447 -1 1.639 2 0.0962 0.838 8
30 48 218007_S_AT RPS27L ribosomal protein S27-like 0.4474 1 4E-04 -1 0.3573 0.431 6
31 50 218870_AT ARHGAP15 Rho GTPase activating protein 15 0.4526 -1 1.135 2 -0.6821 0.091 4
32 52 205932_S_AT MSX1 msh homeobox 1 0.4731 1 0 0 -0.064 0.892 2
33 55 221702_S_AT TM2D3 TM2 domain containing 3 0.485 -1 0.653 6 -0.4115 0.359 8
34 56 201416_AT SOX4 SRY (sex determining region Y)-box 4 0.4904 1 0 3 -0.1002 0.831 6
35 57 214041_X_AT RPL37A Ribosomal protein L37a 0.4914 1 0.296 4 0.7843 0.037 11
36 58 208796_S_AT CCNG1 cyclin G1 0.5079 1 8E-04 6 0.4262 0.34 4
37 59 201710_AT MYBL2 v-myb myeloblastosis viral oncogene homolog-2 0.5129 1 0 0 0.809 0.028 6
38 60 203995_S_AT DFN5 deafness, autosomal dominant 5 0.5244 1 0.497 0 -0.0838 0.858 6
39 62 214022_AT IFITM1 interferon induced transmembrane protein 1 (9-27) 0.5422 -1 0.194 0 -0.6534 0.112 NA
40 63 212414_S_AT N-PAC III SEPT6 septin 6 // cytokine-like nuclear factor n-pac 0.5563 -1 0 1 -0.3801 0.4 NA
41 65 218167_AT AXZ2 arcaemetincins-2 0.5655 1 0 0 0.4658 0.292 4
42 67 212971_AT CARS cysteinyl-riRNA synthetase 0.579 -1 1.378 -3 -0.0587 0.901 8
43 68 201626_AT INSIG1 insulin induced gene 1 0.5827 -1 0 0 0.1929 0.679 NA
44 69 203554_X_AT PTTG1 pituitary tumor-transforming 1 0.5878 -1 0 0 -0.8967 0.006 4
45 76 208634_S_AT MACF1 microtubule-actin crosslinking factor 1 0.6219 1 1.209 -1 0.2987 0.515 4
46 77 202120_AT DDX3X DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked 0.6354 -1 1.755 -2 -0.1888 0.685 4
47 78 203409_AT DDB2 damage-specific DNA binding protein 2, 48kDa 0.6436 1 0 6 0.5886 0.165 7
48 79 216320_X_AT MST1 macrophage stimulating 1 0.6562 1 0.916 -1 0.0215 0.964 7.33
49 81 202693_S_AT STK17A serine/threonine kinase 17a 0.6612 -1 1.914 0 0.6706 0.099 8
50 82 201478_S_AT DKC1 dyskeratosis congenita 1, dyskerin 0.6612 -1 1.325 -3 0.0145 0.976 4
51 83 200608_S_AT RAD21 RAD21 homolog (S. pombe) 0.6737 -1 0 0 -0.9242 0.003 4
52 84 203214_X_AT CDC2 cell division cycle 2, G1 to S and G2 to M 0.6748 1 1.774 0 -0.5441 0.207 0
53 85 212175_S_AT AK2 adenylate kinase 2 0.685 -1 0 1 -0.0708 0.88 12
54 87 202431_S_AT MYC v-myc myelocytomatosis viral oncogene homolog 0.6894 -1 0 -3 -0.3609 0.426 6
55 88 205961_S_AT PSIP1 PC4 and SFRS1 interacting protein 1 0.709 -1 0.001 -4 -0.9341 0.002 3
56 89 201222_S_AT RAD23B RAD23 homolog B (S. cerevisiae) 0.7108 -1 1.333 4 -0.6191 0.138 2
| SORL1 | sortilin-related receptor, L(DLR class) A repeats-containing | 0.745 | 1 | 1.695 | 0 | 0.2524 | 0.585 | 8 |
| ZNF277P | zinc finger protein 277 pseudogene | 0.7541 | 1 | 0 | 1 | 0.0729 | 0.877 | 6 |
| SLC38A1 | solute carrier family 38, member 1 | 0.7724 | -1 | 1.043 | -2 | -0.2515 | 0.586 | 6 |
| PNN | pinin, desmosome associated protein | 0.784 | -1 | 1.545 | 0 | -0.1922 | 0.68 | 14 |
| FDX1 | farnesyl-diphosphate farnesyltransferase 1 | 0.7841 | -1 | 0 | 2 | 0.531 | 0.22 | 4 |
| FXRD2 | FXRD domain containing ion transport regulator 2 | 0.7918 | 1 | 0 | 0 | -0.1412 | 0.763 | 5 |
| EIF1 | eukaryotic translation initiation factor 1 | 0.826 | -1 | 0 | 0 | 0.3385 | 0.458 | 4 |
| HIST1H3J | Histone cluster 1, H3j | 0.8272 | 1 | 0.255 | 0 | -0.1378 | 0.768 | 6.73 |
| RP6-213H19.1 | serine/threonine protein kinase MST4 | 0.8586 | -1 | 1.33 | 2 | -0.5911 | 0.162 | 8 |
| TXNIP | thioredoxin interacting protein | 0.8786 | 1 | 2E-04 | 1 | 0.0699 | 0.882 | 8 |
| OPHN1 | oligophrenin 1 | 0.8791 | 1 | 1.841 | 2 | 0.3604 | 0.427 | 4 |
| CD47 | CD47 molecule | 0.9055 | 1 | 1.462 | 0 | -0.6639 | 0.104 | 4 |
| FOXM1 | forkhead box M1 | 0.9156 | 1 | 0.725 | 0 | -0.1935 | 0.678 | 6 |
| ENO1 | enolase 1, (alpha) | 0.9282 | -1 | 1.639 | 0 | -0.0816 | 0.862 | 0.5 |
| PLEKHB2 | pleckstrin homology domain containing, family B (evectins) member 2 | 0.9509 | -1 | 1.218 | -1 | -0.3998 | 0.374 | 6 |
| MAN2B1 | mannosidase, alpha, class 2B, member 1 | 0.978 | 1 | 4E-04 | 0 | 0.703 | 0.078 | 8 |
| TPDS2 | tumor protein DS2 | 0.9861 | -1 | 0 | -2 | -0.0458 | 0.922 | 2 |
| PTRH2 | peptidyl-tRNA hydrolase 2 | 1.0112 | -1 | 1.494 | 1 | 0.1904 | 0.683 | 6 |
| HERC5 | hect domain and RLD 5 | 1.0149 | 1 | 0 | 0 | 0.3032 | 0.509 | 8 |
| ASP1B | ASF1 anti-silencing function 1 homolog B | 1.0202 | 1 | 0 | -2 | 0.2747 | 0.551 | 4 |
| CHD4 | chromodomain helicase DNA binding protein 4 | 1.028 | -1 | 1.303 | 0 | -0.0729 | 0.877 | 4 |
| CUL1 | cullin 1 | 1.037 | 1 | 2E-04 | -2 | 0.2006 | 0.666 | 10 |
| ANXA1 | annexin A1 | 1.047 | 1 | 6E-04 | -1 | 0.9383 | 0.002 | 6 |
| CD38 | CD38 molecule | 1.0689 | 1 | 6E-04 | 2 | 0.382 | 0.398 | 6 |
| MT2A | metallothionein 2A | 1.0698 | 1 | 0 | 0 | -0.3508 | 0.44 | 8 |
| UBC | ubiquitin C | 1.1005 | 1 | 0 | 2 | 0.8126 | 0.026 | 6 |
| APOBEC3C | apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C | 1.1158 | -1 | 0 | 0 | 0.089 | 0.849 | 4 |
| PARC | p53-associated parkin-like cytoplasmic protein | 1.1296 | 1 | 0 | 1 | 0.1756 | 0.706 | NA |
| ARHGEF10 | Rho guanine nucleotide exchange factor (GEF) 10 | 1.1367 | -1 | 1.567 | -1 | 0.3526 | 0.438 | 4 |
| GATA2A | GATA zinc finger domain containing 2A | 1.141 | -1 | 1.153 | -3 | -0.0535 | 0.909 | 4 |
| XPC | xeroderma pigmentosum, complementation group C | 1.1468 | 1 | 0.006 | 4 | 0.6337 | 0.127 | 0 |
| COL5A1 | collagen, type V, alpha 1 | 1.1566 | 1 | 0.801 | 0 | -0.1657 | 0.723 | 4 |
| PRKAB1 | protein kinase, AMP-activated, beta 1 non-catalytic subunit | 1.1574 | 1 | 0 | -2 | 0.8187 | 0.024 | 12 |
| CTS1L2 | cathepsin L2 | 1.1832 | 1 | 1.521 | 0 | -0.3079 | 0.502 | 8 |
| DDR1 | discoidin domain receptor family, member 1 | 1.1946 | -1 | 1.345 | 0 | 0.4795 | 0.276 | NA |
| RAD51C | RAD51 homolog C (S. cerevisiae) | 1.2028 | 1 | 6E-04 | 0 | 0.3346 | 0.463 | 0 |
| GPI | glucose phosphate isomerase | 1.2242 | -1 | 0 | 0 | 0.3118 | 0.496 | 8 |
| Gene ID          | Gene Name                                                                 | Description                                                                 | Log2 Fold Change | p Value  | FDR  |
|------------------|---------------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------|----------|------|
| 157 201251_AT    | PKM2                                                                      | pyruvate kinase, muscle                                                      | 1.2523          | -1       | 0    | 1   | 0.2504 | 0.588 | 14   |
| 159 219361_S_AT  | IGS2OL1                                                                   | interferon stimulated exonuclease gene 20kDa-like 1                          | 1.2623          | 1        | 0    | -2  | 0.8321 | 0.02  | 8    |
| 160 201663_S_AT  | SMC4                                                                     | structural maintenance of chromosomes 4                                     | 1.2648          | 1        | 0    | 5   | -0.4098 | 0.361 | 12   |
| 161 221434_S_AT  | C14orf156                                                                 | chromosome 14 open reading frame 156                                        | 1.2672          | -1       | 0    | 1   | 0.3701 | 0.414 | 6    |
| 162 206337_AT    | CCR7                                                                      | chemokine (C-C motif) receptor 7                                            | 1.2735          | 1        | 0    | 9E-04 | 0.2385 | 0.607 | 6    |
| 164 205548_S_AT  | BTG3                                                                      | BTG family, member 3                                                         | 1.3042          | 1        | 0.538| 0    | 0.7656 | 0.045 | 12   |
| 166 396_F_AT     | EPOR                                                                     | erythropoietin receptor                                                      | 1.3068          | 1        | 1.721| 3   | 0.3703 | 0.414 | 4    |
| 170 209685_S_AT  | PRKCB1                                                                    | protein kinase C, beta 1                                                     | 1.3258          | -1       | 0.718| 0   | -0.687 | 0.088 | 4    |
| 174 205255_X_AT  | TCF7                                                                      | transcription factor 7 (T-cell specific, HMG-box)                           | 1.3697          | 1        | 0    | -2  | -0.4909 | 0.253 | 4    |
| 178 204958_AT    | PLK3                                                                      | polo-like kinase 3 (Drosophila)                                             | 1.4262          | -1       | 1.517| 4   | 0.7745 | 0.041 | 4    |
| 180 207727_S_AT  | MUTYH                                                                    | mutY homolog (E. coli)                                                      | 1.4345          | 1        | 0    | 0   | -0.2684 | 0.561 | 12   |
| 183 209698_AT    | CCHCR1                                                                    | coiled-coil alpha-helical rod protein 1                                     | 1.4872          | 1        | 1.017| 0   | 0.2605 | 0.573 | 20   |
| 185 205266_AT    | LIF                                                                       | leukemia inhibitory factor                                                  | 1.5033          | 1        | 0    | 0.666| 0.5593 | 0.192 | 2    |
| 186 202718_AT    | IGFBP2                                                                    | insulin-like growth factor binding protein 2, 36kDa                        | 1.5237          | -1       | 0    | -3  | 0.0233 | 0.96  | 2    |
| 187 204825_AT    | MELK                                                                      | maternal embryonic leucine zipper kinase                                   | 1.5416          | 1        | 0    | 0   | -0.4584 | 0.301 | 6    |
| 188 204750_AT    | RCBTB2                                                                    | regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 | 1.5467          | -1       | 0    | 0   | -0.9148 | 0.004 | 4    |
| 189 216237_S_AT  | MCM5                                                                      | minichromosome maintenance complex component 5                             | 1.5526          | 1        | 0    | 1   | 0.7149 | 0.071 | 0    |
| 190 208152_S_AT  | DDX21                                                                     | DEAD (Asp-Glu-Ala-Asp) box polypeptide 21                                  | 1.5638          | -1       | 0    | 0   | 0.383  | 0.397 | 6    |
| 191 218690_AT    | PDLIM4                                                                    | PDZ and LIM domain 4                                                        | 1.5699          | 1        | 0.707| -3  | 0.0219 | 0.963 | 4    |
| 192 209974_S_AT  | BUB3                                                                      | BUB3 budding uninhibited by benzimidazoles 3                               | 1.5724          | -1       | 2E-04| 3   | -0.8857 | 0.008 | 4    |
| 193 207121_S_AT  | MAPK6                                                                     | mitogen-activated protein kinase 6                                          | 1.6002          | -1       | 1.617| -2  | 0.1758 | 0.706 | 3.33 |
| 196 212021_S_AT  | MKI67                                                                     | antigen identified by monoclonal antibody Ki-67                            | 1.6036          | 1        | 1.704| -2  | -0.6542 | 0.111 | 2    |
| 197 211615_S_AT  | LRPPRC                                                                   | leucine-rich PPR-motif containing                                          | 1.6042          | -1       | 0    | -1  | 0.0943 | 0.841 | 6    |
| 198 220729_S_AT  | LTBP1                                                                     | latent transforming growth factor beta binding protein 1                   | 1.6431          | 1        | 0.609| 1   | -0.0343 | 0.942 | 4    |
| 202 212393_S_AT  | TRIM22                                                                    | tripartite motif-containing 22                                              | 1.6431          | 1        | 0    | 0   | 0.5683 | 0.183 | 6    |
| 205 204321_AT    | NEO1                                                                      | neogenin homolog 1 (chicken)                                               | 1.6711          | 1        | 0    | 2   | 0.3467 | 0.446 | 6    |
| 207 220454_S_AT  | FAM35A                                                                    | family with sequence similarity 35, member A                               | 1.7078          | -1       | 0    | 4   | 0.0181 | 0.969 | 6.67 |
| 210 213039_AT    | ARHGEF18                                                                  | rho/raf guanine nucleotide exchange factor (GEF) 18                        | 1.7194          | -1       | 0    | -4  | -0.9647 | 4E-04 | 6    |
| 211 212048_S_AT  | YARS                                                                      | tyrosyl-tRNA synthetase                                                      | 1.7223          | -1       | 0    | -3  | 0.2746 | 0.551 | 6    |
| 212 206792_X_AT  | PDE4C                                                                     | phosphodiesterase 4C, CAMP-specific                                        | 1.7234          | 1        | 0    | 3   | -0.4213 | 0.347 | 4    |
| 213 204905_S_AT  | EEF1E1                                                                    | eukaryotic translation elongation factor 1 epsilon 1                      | 1.7318          | -1       | 0    | 0   | -0.143 | 0.76  | 8    |
| 214 206445_S_AT  | PRMT1                                                                     | protein arginine methyltransferase 1                                       | 1.7375          | -1       | 0    | 0   | 0.4594 | 0.3   | 2    |
| 215 205043_AT    | CFTR                                                                      | cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) | 1.7426          | 1        | 1.66 | -4  | -0.01  | 0.983 | 8    |
| 216 62987_R_AT   | CACNG4                                                                    | calcium channel, voltage-dependent, gamma subunit 4                       | 1.7512          | 1        | 1.958| 0   | 0.2812 | 0.541 | 4    |
| 218 208690_S_AT  | PDLIM1                                                                    | PDZ and LIM domain 1 (elfin)                                               | 1.7723          | 1        | 1.726| 0   | 0.0842 | 0.858 | 10   |
| 219 217716_S_AT  | SEC61A                                                                    | Sec61 alpha 1 subunit (S. cerevisiae)                                      | 1.7857          | 1        | 0    | 4   | 0.9787 | 1E-04 | 10   |
| 220 200751_S_AT  | HNRNPC                                                                    | heterogeneous nuclear ribonucleoprotein C (C1/C2)                          | 1.7902          | -1       | 0    | -1  | -0.0208 | 0.965 | 2.67 |
| Gene Symbol | Description | log2 Fold Change | p-value | q-value |
|-------------|-------------|-----------------|---------|---------|
| CKS2        | CDC28 protein kinase regulatory subunit 2 | 2.3519 | -0.216 | -0.9305 |
| MID1P1      | MID1 interacting protein 1 | 2.3678 | 1.303 | 0.1475 |
| HMGN4       | high mobility group nucleosomal binding domain 4 | 2.3802 | 1.055 | -0.7378 |
| MARS        | methionyl-RNA synthetase | 2.389  | 1 | 0.7356 |
| EIF6        | eukaryotic translation initiation factor 6 | 2.3989 | 0 | 0.3691 |
| LAMP3       | lysosomal-associated membrane protein 3 | 2.4068 | 1 | 0.5024 |
| JUND        | jun D proto-oncogene | 2.4195 | 1 | 0.6247 |
| LAT         | linker for activation of T cells | 2.4326 | 1 | -0.8319 |
| SS18        | synovial sarcoma translocation, chromosome 18 | 2.4477 | 0.247 | -1.555 |
| DLEC1       | deleted in lung and esophageal cancer 1 | 2.482  | 0.724 | 0.3512 |
| IL1F6       | interleukin 1 family, member 6 (epsilon) | 2.4864 | 3E-04 | 0.4739 |
| FANCA       | Fanconi anemia, complementation group A | 2.5067 | 1 | -0.6271 |
| CAMKK2      | calcium/calmodulin-dependent protein kinase kinase 2, beta | 2.5227 | 1.687 | 0.2658 |
| LIG3        | ligase III, DNA, ATP-dependent | 2.5334 | 1.729 | 0.8643 |
| MDM2        | Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) | 2.5517 | 1 | 0.7957 |
| BID         | BH3 interacting domain death agonist | 2.5805 | 1 | 0.863 |
| GLRX        | glutaredoxin (thioltransferase) | 2.5968 | 1 | 0.8004 |
| GADD45A     | growth arrest and DNA-damage-inducible, alpha | 2.6107 | 1 | 0.761 |
| TOX         | thymocyte selection-associated high mobility group box | 2.6176 | 1 | -0.7998 |
| MBOAT2      | membrane bound O-acetyltransferase domain containing 2 | 2.6226 | 1.089 | -0.1771 |
| RASAL1      | RAS protein activator like 1 (GAP1 like) | 2.6483 | 0.431 | 0.2934 |
| SLC7A6      | solute carrier family 7, member 6 | 2.658  | 1 | 0.6904 |
| MMP14       | matrix metallopeptidase 14 (membrane-inserted) | 2.6722 | 1 | 0.4555 |
| PIGR        | polymeric immunoglobulin receptor | 2.6813 | 1 | 0.2851 |
| SOX13       | SRY (sex determining region Y)-box 13 | 2.6878 | 1 | 0.4174 |
| STRA6       | stimulated by retinoic acid gene 6 homolog (mouse) | 2.6974 | 1 | -0.6688 |
| IGHMBP2     | immunoglobulin mu binding protein 2 | 2.7142 | 1 | 0.267 |
| AMHR2       | anti-Mullerian hormone receptor, type II | 2.738  | 1 | 0.3873 |
| TBCB        | tubulin folding cofactor B | 2.7736 | 0 | 0.0442 |
| NTRK3       | neurotrophic tyrosine kinase, receptor, type 3 | 2.7737 | 6E-04 | 1.3274 |
| MAT1A       | methionine adenosyltransferase I, alpha | 2.7742 | 1 | 0.3883 |
| UGT2B28     | UDP glucuronosyltransferase 2 family, polypeptide B28 | 2.7984 | 1 | 0.2354 |
| RhD         | Rh blood group, D antigen | 2.8076 | 1 | 0.0155 |
| POLS        | polymerase (DNA directed) sigma | 2.8305 | 1 | -0.6615 |
| EDA         | ectodysplasin A | 2.8346 | 0.446 | -0.2185 |
| BCAP31      | B-cell receptor-associated protein 31 | 2.8463 | 1.619 | 0.262 |
| ST7         | suppression of tumorigenicity 7 | 2.8716 | 1 | 0.2873 |
| Gene ID | Symbol | Description | log2 fold change | p-value | q-value |
|--------|--------|-------------|-----------------|---------|---------|
| 204 352 209083_AT | CORO1A | coronin, actin binding protein, 1A | 2.8759 | -1 | 0.1073 |
| 205 353 215416_S_AT | STOML2 | stomatin (EPB72)-like 2 | 2.8871 | -1 | 0.5201 |
| 206 358 211040_X_AT | GTSE1 | G-2 and S-phase expressed 1 | 2.9365 | 1 | 0.1484 |
| 207 360 206681_X_AT | GP2 | glycoprotein 2 (zymogen granule membrane) | 2.9659 | 1 | 0.2718 |
| 208 364 201853_S_AT | CDC25B | cell division cycle 25 homolog B (S. pombe) | 2.9981 | -1 | -0.6074 |
| 209 366 210577_AT | CASR | calcium-sensing receptor | 3.0246 | 1 | 0.3618 |
| 210 368 204178_S_AT | RBM14 | RNA binding motif protein 14 | 3.0801 | 1 | 0.8619 |
| 211 369 202963_AT | RXF5 | regulatory factor X, 5 | 3.0867 | 1 | 0.5331 |
| 212 370 214448_X_AT | NFKB1B | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta | 3.0975 | -1 | 0.6892 |
| 213 372 215543_S_AT | LARGE | like-glycosyltransferase | 3.1037 | 1 | 0.2355 |
| 214 373 209814_AT | ZNF330 | zinc finger protein 330 | 3.1067 | -1 | -0.1931 |
| 215 380 210405_X_AT | TNFRSF10B | tumor necrosis factor receptor superfamily, member 10b | 3.1484 | -1 | 0.7397 |
| 216 381 204401_AT | KCNN4 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 | 3.1529 | 1 | 0.3392 |
| 217 383 204197_S_AT | RUNX3 | runt-related transcription factor 3 | 3.1638 | -1 | 0.8256 |
| 218 385 201516_AT | SRM | spermidine synthase | 3.1711 | 1 | 0.5826 |
| 219 386 207644_AT | FOXH1 | forkhead box H1 | 3.1754 | 1 | 0.1014 |
| 220 387 38149_AT | ARHGAP25 | Rho GTPase activating protein 25 | 3.1883 | 1 | -0.2422 |
| 221 388 216356_X_AT | BAIAP3 | BAI1-associated protein 3 | 3.1903 | 1 | 0.5166 |
| 222 390 209626_S_AT | OSBPL3 | oxysterol binding protein-like 3 | 3.2098 | 1 | 0.3433 |
| 223 391 221407_AT | GJA9 | gap junction protein, alpha 9, 36kDa | 3.2126 | 1 | 0.4763 |
| 224 392 203476_AT | TPBG | trophoblast glycoprotein | 3.2153 | 1 | -0.5657 |
| 225 394 201292_AT | TOP2A | topoisomerase (DNA) II alpha 170kDa | 3.2295 | -1 | 0.7684 |
| 226 398 207669_AT | KRT83 | keratin 83 | 3.2388 | 1 | 0.4425 |
| 227 399 202504_AT | TRIM29 | tripartite motif-containing 29 | 3.2617 | 1 | 0.4337 |
| 228 401 206508_AT | CD70 | CD70 molecule | 3.2774 | 1 | 0.6811 |
| 229 404 202652_AT | APBB1 | amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65) | 3.2901 | 1 | 0.1727 |
| 230 405 213520_AT | RECQL4 | RecQ protein-like 4 | 3.2939 | 1 | 0.1501 |
| 231 410 201508_AT | IGFBP4 | insulin-like growth factor binding protein 4 | 3.3229 | 1 | 0.1975 |
| 232 413 212218_S_AT | FASN | fatty acid synthase | 3.3316 | 1 | 0.4701 |
| 233 414 65517_AT | AP1M2 | adaptor-related protein complex 1, mu 2 subunit | 3.3355 | 1 | 0.3989 |
| 234 417 208189_S_AT | MYO7A | myosin VI/IA | 3.3521 | 1 | 0.2458 |
| 235 418 218708_AT | NXXT1 | NTF2-like export factor 1 | 3.3559 | 1 | 0.3664 |
| 236 422 220379_AT | FCSCN3 | fascin homolog 3, actin-bundling protein, testicular | 3.3855 | 1 | 0.2638 |
| 237 424 202887_S_AT | DDIT4 | DNA-damage-inducible transcript 4 | 3.3989 | 1 | -0.2085 |
| 238 426 214805_AT | EIF4A1 | Eukaryotic translation initiation factor 4A, isoform 1 | 3.4231 | 1 | -0.3179 |
| 239 427 204620_S_AT | VCAN | versican | 3.4235 | 1 | 0.3856 |
| Gene Symbol       | Description                                                                 | Log2 Fold Change | p-value | Log2 Fold Change | p-value |
|-------------------|------------------------------------------------------------------------------|------------------|---------|------------------|---------|
| CDK3              | cyclin-dependent kinase inhibitor 3                                         | 3.4984           | -1      | 0.1783           | 0.035   |
| CGN               | regulator of G-protein signaling 16                                         | 3.5064           | -1      | 0.2645           | 0.035   |
| NF1X              | nuclear transcription factor, X-box binding 1                               | 3.5509           | -1      | 0.6015           | 0.035   |
| BCL2              | BCL2/adeno virus E1B 19kDa interacting protein 3-like                       | 3.5548           | -1      | 0.5936           | 0.035   |
| IL2R2             | interleukin 2 receptor, beta                                                | 3.5702           | -1      | 0.2766           | 0.035   |
| MPPE1             | metallophosphoesterase 1                                                   | 3.5961           | -1      | 0.2183           | 0.035   |
| KIAA0020          | KIAA0020                                                                    | 3.5976           | -1      | 0.4384           | 0.035   |
| LANCL2            | LanC lanthiont synthetase component C-like 2                               | 3.6428           | -1      | 0.8853           | 0.035   |
| TPX2              | TPX2, microtubule-associated, homolog                                      | 3.6494           | -1      | 0.7313           | 0.035   |
| LRDD              | leucine-rich repeats and death domain containing                            | 3.6573           | -1      | 0.4923           | 0.035   |
| CIB1              | calcium and integrin binding 1 (calmyrin)                                  | 3.6638           | -1      | 0.1189           | 0.035   |
| DCP1A             | DCP1 decapping enzyme homolog A                                            | 3.6753           | -1      | 0.7213           | 0.035   |
| NINJ1             | ninjurin 1                                                                  | 3.6756           | -1      | 0.7117           | 0.035   |
| RECK              | reversion-inducing-cysteine-rich protein with kazal motifs                  | 3.6788           | -1      | 0.3037           | 0.035   |
| SRC-1             | Src-like-adaptor                                                           | 3.6823           | -1      | 0.157            | 0.035   |
| RAB7A             | RAB7A, member RAS oncogene family                                          | 3.6833           | -1      | 0.3706           | 0.035   |
| BAZ1A             | bromodomain adjacent to zinc finger domain, 1A                             | 3.6862           | -1      | 0.3025           | 0.035   |
| NFKB1             | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | 3.6882           | -1      | 0.7783           | 0.035   |
| NKX3-1            | NK3 homeobox 1                                                              | 3.7467           | -1      | 0.4343           | 0.035   |
| BUB1              | BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)           | 3.7625           | -1      | 0.6966           | 0.035   |
| PFKFB1            | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1                       | 3.8235           | -1      | 0.4992           | 0.035   |
| CCNA2             | cyclin A2                                                                   | 3.8462           | -1      | 0.7477           | 0.035   |
| HLA-DOA           | major histocompatibility complex, class II, DO alpha                        | 3.8545           | -1      | 0.4543           | 0.035   |
| PRC1              | protein regulator of cytokinesis 1                                          | 3.8731           | -1      | 0.7422           | 0.035   |
| ID2 / ID2B        | inhibitor of DNA binding 2, dominant negative helix-loop-helix protein      | 3.9418           | -1      | 0.1243           | 0.035   |
| JUN               | jun oncogene                                                                | 3.9493           | -1      | 0.2114           | 0.035   |
| SESN1             | sestrin 1                                                                   | 4.0085           | -1      | 0.7022           | 0.035   |
| TFE3              | transcription factor binding to IGHM enhancer 3                            | 4.0232           | -1      | 0.6712           | 0.035   |
| WSRCR22           | Williams Beuren syndrome chromosome region 22                               | 4.0363           | -1      | 0.1793           | 0.035   |
| CHRNA3            | cholinergic receptor, nicotinic, alpha 3                                   | 4.0572           | -1      | 0.4362           | 0.035   |
| BAG1              | BCL2-associated athanogene                                                  | 4.0795           | -1      | 0.7451           | 0.035   |
| ENSA              | endosulfine alpha                                                           | 4.0835           | -1      | 0.5567           | 0.035   |
| GNRH2             | gonadotropin-releasing hormone 2                                            | 4.1084           | -1      | 0.4441           | 0.035   |
| HSPC111           | hypothetical protein HSPC11                                                 | 4.1151           | -1      | 0.0245           | 0.035   |
| PRDX4             | peroxiredoxin 4                                                             | 4.1214           | -1      | 0.1185           | 0.035   |
| Gene ID   | Symbol     | Description                                                                 | Log2FoldChange | FDR    |
|-----------|------------|------------------------------------------------------------------------------|----------------|--------|
| 525 209568_S_AT | RGL1      | Ral guanine nucleotide dissociation stimulator-like 1                        | 4.1663         | 0.5761 |
| 528 208985_S_AT | EIF3J     | Eukaryotic translation initiation factor 3, subunit J                       | 4.1754         | 0.1093 |
| 532 217850_AT | GNIT3     | Guanine nucleotide binding protein-like 3, (nucleolar)                      | 4.2014         | 0.2553 |
| 533 203007_X_AT | LYPLE1    | Lyophosphatidylase I                                                         | 4.2022         | 0.0271 |
| 537 209917_S_AT | TP53AP1   | TP53 activated protein 1                                                     | 4.2446         | 0.116  |
| 538 210308_AT | PRKCQ     | Protein kinase C, theta                                                      | 4.2448         | 0.804  |
| 544 201924_AT | AFF1      | AF4/FRM2 family, member 1                                                   | 4.287          | -0.9628|
| 545 200749_AT | RAN       | RAN, member RAS oncogene family                                             | 4.2938         | -0.1911|
| 546 201802_AT | SLC29A1   | Solute carrier family 29, member 1                                         | 4.3085         | 0.8428 |
| 551 207035_AT | SLC30A3   | Solute carrier family 30 (zinc transporter), member 3                       | 4.3869         | 0.0426 |
| 552 205902_AT | KCN3      | Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 |
| 556 207813_S_AT | FDXR      | Ferreredoxin reductase                                                      | 4.4911         | 0.6129 |
| 561 221073_S_AT | NOD1     | Nucleotide-binding oligomerization domain containing 1                      | 4.4941         | 0.3983 |
| 562 202934_AT | HK2       | Hexokinase 2                                                                | 4.496          | -0.1997|
| 563 208066_S_AT | GTF2B    | General transcription factor II                                             | 4.5054         | 0.7836 |
| 569 208490_X_AT | HIST1H2BF | Histone cluster 1, H2bf                                                      | 4.5726         | -0.4786|
| 571 218168_S_AT | CABC1     | Chaperone, ABC1 activity of bc1 complex homolog                            | 4.5767         | 0.8632 |
| 572 209649_X_AT | ALDH1B1   | Aldehyde dehydrogenase 1 family, member B1                                 | 4.5778         | 0.4176 |
| 574 212530_AT | NEK7      | NIMA-related kinase 7                                                       | 4.6148         | 0.7275 |
| 576 216263_S_AT | WWP1      | WW domain containing E3 ubiquitin protein ligase                            | 4.6344         | 0.1319 |
| 578 202704_AT | TOB1      | Transducer of ERBB2, 1                                                      | 4.6541         | 0.4192 |
| 582 212871_AT | MAPKAPK5  | Mitogen-activated protein kinase-activated protein kinase 5                 | 4.6664         | 0.4797 |
| 585 204947_AT | E2F1      | E2F transcription factor 1                                                  | 4.7037         | 0.8586 |
| 586 211410_X_AT | KIR2DL5A  | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A |
| 587 202705_AT | CCNB2     | Cyclin B2                                                                   | 4.7316         | -0.9412|
| 589 216396_S_AT | E124     | Etoposide induced 2.4 mRNA                                                  | 4.765          | 0.8026 |
| 594 203340_AT | BCL6      | B-cell CL/Lymphoma 6                                                        | 4.8581         | 0.0588 |
| 596 222062_AT | IL27RA    | Interleukin 27 receptor, alpha                                              | 4.8653         | 0.488  |
| 598 211146_AT | NFE2L2    | Nuclear factor (erythroid-derived 2)-like 2                               | 4.8836         | -0.5983|
| 602 204794_AT | DUSP2     | Dual specificity phosphatase 2                                              | 4.9511         | -0.2932|
| 606 210439_AT | ICOS      | Inducible T-cell co-stimulator                                              | 4.9664         | 0.6042 |
| 610 210746_AT | TP53      | Tumor protein p53 (Li-Fraumeni syndrome)                                   | 5.0265         | 0.5769 |
| 615 218751_S_AT | FBXW7    | F-box and WD repeat domain containing 7                                   | 5.0622         | 0.8541 |
| 624 201329_S_AT | ETS2     | v-ets erythroblastosis virus E26 oncogene homolog 2                       | 5.0995         | 0.3903 |
| 626 201379_S_AT | TP5D2L2   | Tumor protein D52-like 2                                                     | 5.134          | 0.1342 |
| 634 218239_S_AT | GTPBP4   | GTP binding protein 4                                                        | 5.2079         | -0.2943|
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 312 | 638 205780_AT | BIK | BCL2-interacting killer (apoptosis-inducing) | 5.2295 | 1 | 0 | -4 | 0.7607 | 0.047 | 6 |
| 313 | 643 207826_S_AT | ID3 | inhibitor of DNA binding 3 | 5.2733 | 1 | 0 | 4 | -0.6606 | 0.106 | 8 |
| 314 | 644 208070_S_AT | REV3L | REV3-like, catalytic subunit of DNA polymerase zeta | 5.2862 | 1 | 0 | 0 | 0.5224 | 0.229 | 2 |
| 315 | 645 208877_AT | PAK2 | p21 (CDKN1A)-activated kinase 2 | 5.2996 | -1 | 1.73 | 0 | -0.316 | 0.49 | 6 |
| 316 | 653 211135_X_AT | LILRB3 | leukocyte immunoglobulin-like receptor, subfamily B, member 3 | 5.4181 | 1 | 0 | 2 | 0.3641 | 0.422 | 3 |
| 317 | 654 218501_AT | ARHGEF3 | Rho guanine nucleotide exchange factor 3 | 5.4288 | 1 | 3E-04 | -3 | 0.2315 | 0.617 | 12 |