

4826P

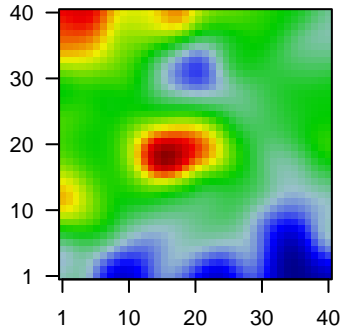
Global Summary

%DE = 0.1
 # genes with fdr < 0.2 = 3322 (1274 + / 2048 -)
 # genes with fdr < 0.1 = 2339 (821 + / 1518 -)
 # genes with fdr < 0.05 = 1752 (581 + / 1171 -)
 # genes with fdr < 0.01 = 1123 (345 + / 778 -)

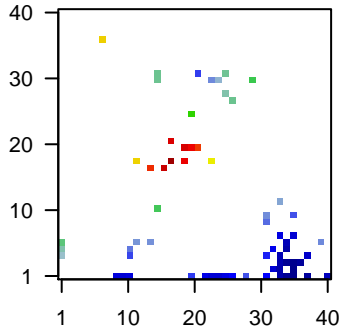
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.3
 <p-value> = 0.19
 <fdr> = 0.9

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|--|
| 1 | 1555907_at | 3.31 | 2e-16 | 1e-13 | 19 x 20 AGAP2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:1555907] |
| 2 | 1558009_at | -1.91 | 2e-16 | 1e-13 | 9 x 1 solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:HGNC:1558009] |
| 3 | 1558010_s_at | -2.13 | 2e-16 | 1e-13 | 10 x 1 solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:HGNC:1558010] |
| 4 | 200831_s_at | -1.49 | 2e-16 | 1e-13 | 25 x 1 stearyl-CoA desaturase [Source:HGNC Symbol;Acc:HGNC:200831] |
| 5 | 201348_at | -2.49 | 2e-16 | 1e-13 | 25 x 31 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:201348] |
| 6 | 202246_s_at | 1.34 | 2e-16 | 1e-13 | 14 x 17 cyclin dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC:202246] |
| 7 | 203498_at | -1.29 | 2e-16 | 1e-13 | 37 x 4 regulator of calcineurin 2 [Source:HGNC Symbol;Acc:HGNC:203498] |
| 8 | 203661_s_at | -1.55 | 2e-16 | 1e-13 | 15 x 30 tropomodulin 1 [Source:HGNC Symbol;Acc:HGNC:11871] |
| 9 | 203662_s_at | -1.5 | 2e-16 | 1e-13 | 15 x 31 tropomodulin 1 [Source:HGNC Symbol;Acc:HGNC:11871] |
| 10 | 204563_at | -1.74 | 2e-16 | 1e-13 | 26 x 27 selectin L [Source:HGNC Symbol;Acc:HGNC:10720] |
| 11 | 204688_at | -1.96 | 2e-16 | 1e-13 | 12 x 6 sarcoglycan epsilon [Source:HGNC Symbol;Acc:HGNC:1080] |
| 12 | 204953_at | -1.38 | 2e-16 | 1e-13 | 34 x 1 synaptosome associated protein 91 [Source:HGNC Symbol;Acc:HGNC:204953] |
| 13 | 205110_s_at | -1.74 | 2e-16 | 1e-13 | 35 x 2 fibroblast growth factor 13 [Source:HGNC Symbol;Acc:HGNC:205110] |
| 14 | 205751_at | -1.23 | 2e-16 | 1e-13 | 24 x 1 SH3 domain containing GRB2 like 2, endophilin A1 [Source:HGNC Symbol;Acc:HGNC:205751] |
| 15 | 206154_at | 3.04 | 2e-16 | 1e-13 | 23 x 18 retinaldehyde binding protein 1 [Source:HGNC Symbol;Acc:HGNC:206154] |
| 16 | 206243_at | -1.46 | 2e-16 | 1e-13 | 15 x 11 TIMP metalloproteinase inhibitor 4 [Source:HGNC Symbol;Acc:HGNC:206243] |
| 17 | 206710_s_at | -1.46 | 2e-16 | 1e-13 | 34 x 5 erythrocyte membrane protein band 4.1 like 3 [Source:HGNC Symbol;Acc:HGNC:206710] |
| 18 | 206785_s_at | -1.7 | 2e-16 | 1e-13 | 1 x 5 killer cell lectin like receptor C2 [Source:HGNC Symbol;Acc:HGNC:206785] |
| 19 | 207414_s_at | -1.89 | 2e-16 | 1e-13 | 34 x 6 proprotein convertase subtilisin/kexin type 6 [Source:HGNC Symbol;Acc:HGNC:207414] |
| 20 | 208650_s_at | 2.09 | 2e-16 | 1e-13 | 1 x 5 CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:208650] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 12.98 | NULL | 630 | BP cell cycle |
| 2 | 12.89 | NULL | 394 | BP cell division |
| 3 | 12.25 | NULL | 158 | BP DNA replication |
| 4 | 10.97 | NULL | 366 | BP DNA repair |
| 5 | 9.7 | NULL | 1387 | BP regulation of transcription, DNA-templated |
| 6 | 9.54 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 7 | 8.88 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 8 | 8.74 | NULL | 1145 | BP regulation of transcription by RNA polymerase II |
| 9 | 8.4 | NULL | 164 | BP mitotic cell cycle |
| 10 | 8.21 | NULL | 39 | BP CENP-A containing nucleosome assembly |
| 11 | 7.89 | NULL | 98 | BP G1/S transition of mitotic cell cycle |
| 12 | 7.87 | NULL | 85 | BP chromosome segregation |
| 13 | 7.53 | NULL | 400 | BP chromatin binding |
| 14 | 7.17 | NULL | 33 | BP DNA replication initiation |
| 15 | 6.97 | NULL | 31 | BP mitotic sister chromatid segregation |
| 16 | 6.71 | NULL | 97 | BP DNA recombination |
| 17 | 6.25 | NULL | 22 | BP mitotic spindle assembly checkpoint |
| 18 | 6.06 | NULL | 130 | BP regulation of signal transduction by p53 class mediator |
| 19 | 6 | NULL | 13 | BP kinetochore assembly |
| 20 | 5.99 | NULL | 229 | BP mRNA splicing, via spliceosome |
| <i>Underexpressed</i> | | | | |
| 1 | -21.94 | NULL | 7387 | BP membrane |
| 2 | -20.43 | NULL | 4278 | BP plasma membrane |
| 3 | -14.88 | NULL | 574 | BP synapse |
| 4 | -11.46 | NULL | 1500 | BP signal transduction |
| 5 | -10.77 | NULL | 240 | BP postsynaptic membrane |
| 6 | -9.62 | NULL | 236 | BP chemical synaptic transmission |
| 7 | -9.58 | NULL | 627 | BP ion transport |
| 8 | -9.03 | NULL | 1242 | BP Golgi apparatus |
| 9 | -8.47 | NULL | 777 | BP G protein-coupled receptor signaling pathway |
| 10 | -8.45 | NULL | 119 | BP postsynapse |
| 11 | -8.06 | NULL | 131 | BP presynapse |
| 12 | -7.96 | NULL | 388 | BP immune response |
| 13 | -7.74 | NULL | 149 | BP regulation of ion transmembrane transport |
| 14 | -7.6 | NULL | 460 | BP neutrophil degranulation |
| 15 | -7.38 | NULL | 132 | BP membrane organization |
| 16 | -7.08 | NULL | 79 | BP memory |
| 17 | -7.01 | NULL | 275 | BP ion transmembrane transport |
| 18 | -6.9 | NULL | 521 | BP lipid metabolic process |
| 19 | -6.88 | NULL | 65 | BP learning |
| 20 | -6.86 | NULL | 505 | BP nervous system development |

p-values

