

3960M

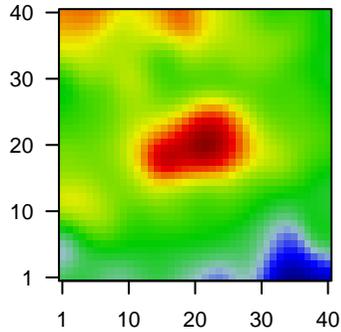
Global Summary

%DE = 0.09
 # genes with fdr < 0.2 = 3233 (1328 + / 1905 -)
 # genes with fdr < 0.1 = 2540 (978 + / 1562 -)
 # genes with fdr < 0.05 = 2040 (736 + / 1304 -)
 # genes with fdr < 0.01 = 1395 (432 + / 963 -)

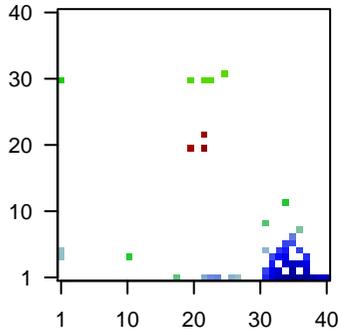
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.24
 <p-value> = 0.17
 <fdr> = 0.91

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|--|
| 1 | 1552439_s_at | -2 | 2e-16 | 5e-14 | 1 x 5 multiple EGF like domains 11 [Source:HGNC Symbol;Acc:HGNC:1552439] |
| 2 | 1553797_a_at | -1.61 | 2e-16 | 5e-14 | 33 x 4 sciatic injury induced lincRNA upregulator of SOX11 [Source:HGNC Symbol;Acc:HGNC:1553797] |
| 3 | 1555958_at | -2.04 | 2e-16 | 5e-14 | 33 x 1 cartilage acidic protein 1 [Source:HGNC Symbol;Acc:HGNC:1555958] |
| 4 | 1557122_s_at | -2.04 | 2e-16 | 5e-14 | 40 x 1 gamma-aminobutyric acid type A receptor beta2 subunit [Source:HGNC Symbol;Acc:HGNC:1557122] |
| 5 | 1559072_s_at | -2.4 | 2e-16 | 5e-14 | 32 x 1 extracellular leucine rich repeat and fibronectin type III domain 1 [Source:HGNC Symbol;Acc:HGNC:1559072] |
| 6 | 1568603_at | -2.23 | 2e-16 | 5e-14 | 24 x 1 calcium dependent secretion activator [Source:HGNC Symbol;Acc:HGNC:1568603] |
| 7 | 1568604_a_at | -1.92 | 2e-16 | 5e-14 | 24 x 1 calcium dependent secretion activator [Source:HGNC Symbol;Acc:HGNC:1568604] |
| 8 | 1568612_at | -2.42 | 2e-16 | 5e-14 | 38 x 1 gamma-aminobutyric acid type A receptor gamma2 subunit [Source:HGNC Symbol;Acc:HGNC:1568612] |
| 9 | 201041_s_at | -1.51 | 2e-16 | 5e-14 | 31 x 9 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:201041] |
| 10 | 201348_at | -1.51 | 2e-16 | 5e-14 | 25 x 31 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:201348] |
| 11 | 201525_at | -1.24 | 2e-16 | 5e-14 | 34 x 12 apolipoprotein D [Source:HGNC Symbol;Acc:HGNC:201525] |
| 12 | 201761_at | -1.18 | 2e-16 | 5e-14 | 22 x 1 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) [Source:HGNC Symbol;Acc:HGNC:201761] |
| 13 | 201909_at | -1.79 | 2e-16 | 5e-14 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909] |
| 14 | 201951_at | -1.17 | 2e-16 | 5e-14 | 1 x 5 activated leukocyte cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:201951] |
| 15 | 202178_at | -2.07 | 2e-16 | 5e-14 | 36 x 3 protein kinase C zeta [Source:HGNC Symbol;Acc:HGNC:202178] |
| 16 | 202363_at | -1.13 | 2e-16 | 5e-14 | 31 x 5 SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1 [Source:HGNC Symbol;Acc:HGNC:202363] |
| 17 | 202507_s_at | -2.18 | 2e-16 | 5e-14 | 38 x 1 synaptosome associated protein 25 [Source:HGNC Symbol;Acc:HGNC:202507] |
| 18 | 202508_s_at | -2.06 | 2e-16 | 5e-14 | 37 x 1 synaptosome associated protein 25 [Source:HGNC Symbol;Acc:HGNC:202508] |
| 19 | 203000_at | -2.07 | 2e-16 | 5e-14 | 37 x 1 stathmin 2 [Source:HGNC Symbol;Acc:HGNC:203000] |
| 20 | 203001_s_at | -1.81 | 2e-16 | 5e-14 | 38 x 1 stathmin 2 [Source:HGNC Symbol;Acc:HGNC:203001] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 7.76 | NULL | 394 | BP cell division |
| 2 | 7.73 | NULL | 158 | BP DNA replication |
| 3 | 7.16 | NULL | 630 | BP cell cycle |
| 4 | 6.67 | NULL | 366 | BP DNA repair |
| 5 | 6.43 | NULL | 32 | BP cilium movement |
| 6 | 5.92 | NULL | 180 | BP cell projection organization |
| 7 | 5.82 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 8 | 5.55 | NULL | 31 | BP mitotic sister chromatid segregation |
| 9 | 5.4 | NULL | 164 | BP mitotic cell cycle |
| 10 | 5.36 | NULL | 173 | BP cilium assembly |
| 11 | 5.25 | NULL | 39 | BP CENP-A containing nucleosome assembly |
| 12 | 4.98 | NULL | 79 | BP microtubule-based movement |
| 13 | 4.9 | NULL | 85 | BP chromosome segregation |
| 14 | 4.76 | NULL | 14 | BP inner dynein arm assembly |
| 15 | 4.53 | NULL | 22 | BP mitotic spindle assembly checkpoint |
| 16 | 4.52 | NULL | 78 | BP anaphase-promoting complex-dependent catabolic process |
| 17 | 4.48 | NULL | 21 | BP motile cilium assembly |
| 18 | 4.47 | NULL | 17 | BP epithelial cilium movement |
| 19 | 4.34 | NULL | 112 | BP motor activity |
| 20 | 4.31 | NULL | 13 | BP kinetochore assembly |
| <i>Underexpressed</i> | | | | |
| 1 | -20.28 | NULL | 574 | BP synapse |
| 2 | -15.61 | NULL | 4278 | BP plasma membrane |
| 3 | -14.87 | NULL | 236 | BP chemical synaptic transmission |
| 4 | -13.93 | NULL | 7387 | BP membrane |
| 5 | -13.07 | NULL | 505 | BP nervous system development |
| 6 | -13.04 | NULL | 240 | BP postsynaptic membrane |
| 7 | -10.65 | NULL | 119 | BP postsynapse |
| 8 | -9.91 | NULL | 65 | BP learning |
| 9 | -9.74 | NULL | 36 | BP synaptic vesicle endocytosis |
| 10 | -9.6 | NULL | 131 | BP presynapse |
| 11 | -9.41 | NULL | 79 | BP memory |
| 12 | -8.89 | NULL | 28 | BP synaptic vesicle exocytosis |
| 13 | -8.69 | NULL | 31 | BP regulation of NMDA receptor activity |
| 14 | -8.66 | NULL | 627 | BP ion transport |
| 15 | -8.52 | NULL | 27 | BP glutamate secretion |
| 16 | -8.41 | NULL | 133 | BP neuron projection development |
| 17 | -8.26 | NULL | 33 | BP regulation of exocytosis |
| 18 | -8.13 | NULL | 27 | BP gamma-aminobutyric acid signaling pathway |
| 19 | -8.05 | NULL | 48 | BP synapse organization |
| 20 | -8.01 | NULL | 1500 | BP signal transduction |

p-values

