

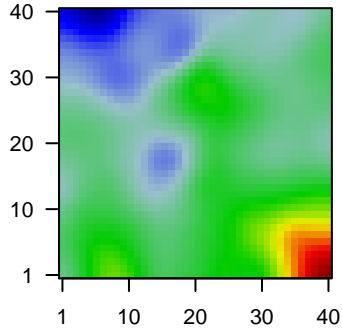
42639E

Global Summary

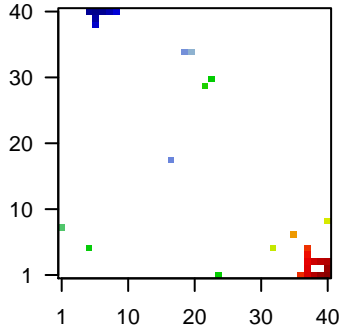
%DE = 0.09
 # genes with fdr < 0.2 = 3319 (1945 + / 1374 -)
 # genes with fdr < 0.1 = 2407 (1465 + / 942 -)
 # genes with fdr < 0.05 = 1918 (1205 + / 713 -)
 # genes with fdr < 0.01 = 1260 (815 + / 445 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.06
 <p-value> = 0.19
 <fdr> = 0.91

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|---|
| 1 | 1552715_a_a | 1.81 | 2e-16 | 2e-13 | 38 x 1 relaxin family peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:10577] |
| 2 | 1554299_at | 1.83 | 2e-16 | 2e-13 | 40 x 9 neuronal PAS domain protein 4 [Source:HGNC Symbol;Acc:HGNC:11509] |
| 3 | 1555800_at | 1.93 | 2e-16 | 2e-13 | 40 x 1 zinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:2157] |
| 4 | 1558678_s_al | -0.99 | 2e-16 | 2e-13 | 7 x 40 metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC:12722] |
| 5 | 1558747_at | -1.51 | 2e-16 | 2e-13 | 7 x 40 structural maintenance of chromosomes flexible hinge domain 1 [Source:HGNC Symbol;Acc:HGNC:8000] |
| 6 | 1569607_s_al | -1.46 | 2e-16 | 2e-13 | 6 x 39 ankyrin repeat domain 20 family member A3 [Source:HGNC Symbol;Acc:HGNC:8000] |
| 7 | 1569608_x_al | -1.52 | 2e-16 | 2e-13 | 7 x 40 ankyrin repeat domain 20 family, member A3 (ANKRD20A3) [Source:HGNC Symbol;Acc:HGNC:8000] |
| 8 | 1569969_a_a | 1.68 | 2e-16 | 2e-13 | 40 x 1 unc-13 homolog C [Source:HGNC Symbol;Acc:HGNC:23148] |
| 9 | 201341_at | 0.88 | 2e-16 | 2e-13 | 40 x 3 ectodermal-neural cortex 1 [Source:HGNC Symbol;Acc:HGNC:11509] |
| 10 | 201445_at | -0.87 | 2e-16 | 2e-13 | 22 x 29 calponin 3 [Source:HGNC Symbol;Acc:HGNC:2157] |
| 11 | 203001_s_at | 0.94 | 2e-16 | 2e-13 | 38 x 1 stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577] |
| 12 | 203413_at | 0.86 | 2e-16 | 2e-13 | 40 x 3 neural EGFL like 2 [Source:HGNC Symbol;Acc:HGNC:7751] |
| 13 | 203797_at | 1.08 | 2e-16 | 2e-13 | 40 x 1 visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722] |
| 14 | 203999_at | 1.17 | 2e-16 | 2e-13 | 40 x 1 synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:11509] |
| 15 | 204081_at | 1.1 | 2e-16 | 2e-13 | 40 x 1 neurogranin [Source:HGNC Symbol;Acc:HGNC:8000] |
| 16 | 204229_at | 1.2 | 2e-16 | 2e-13 | 40 x 1 solute carrier family 17 member 7 [Source:HGNC Symbol;Acc:HGNC:8000] |
| 17 | 204324_s_at | -0.9 | 2e-16 | 2e-13 | 8 x 40 golgi integral membrane protein 4 [Source:HGNC Symbol;Acc:HGNC:8000] |
| 18 | 205967_at | -1.09 | 2e-16 | 2e-13 | 6 x 40 histone cluster 1 H4 family member c [Source:HGNC Symbol;Acc:HGNC:8000] |
| 19 | 206084_at | 1.77 | 2e-16 | 2e-13 | 40 x 1 protein tyrosine phosphatase, receptor type R [Source:HGNC Symbol;Acc:HGNC:8000] |
| 20 | 206115_at | 1.04 | 2e-16 | 2e-13 | 37 x 5 early growth response 3 [Source:HGNC Symbol;Acc:HGNC:8000] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 19.66 | NULL | 4278 | BP plasma membrane |
| 2 | 18.92 | NULL | 574 | BP synapse |
| 3 | 18.13 | NULL | 7387 | BP membrane |
| 4 | 15.68 | NULL | 236 | BP chemical synaptic transmission |
| 5 | 12.7 | NULL | 240 | BP postsynaptic membrane |
| 6 | 11.2 | NULL | 505 | BP nervous system development |
| 7 | 11.04 | NULL | 27 | BP glutamate secretion |
| 8 | 10.42 | NULL | 28 | BP synaptic vesicle exocytosis |
| 9 | 10.32 | NULL | 627 | BP ion transport |
| 10 | 10.14 | NULL | 1500 | BP signal transduction |
| 11 | 10.04 | NULL | 33 | BP regulation of exocytosis |
| 12 | 9.68 | NULL | 65 | BP learning |
| 13 | 9.32 | NULL | 51 | BP neurotransmitter secretion |
| 14 | 9.12 | NULL | 119 | BP postsynapse |
| 15 | 8.81 | NULL | 79 | BP memory |
| 16 | 8.44 | NULL | 149 | BP regulation of ion transmembrane transport |
| 17 | 8.19 | NULL | 131 | BP presynapse |
| 18 | 8.11 | NULL | 36 | BP synaptic vesicle endocytosis |
| 19 | 8.08 | NULL | 118 | BP exocytosis |
| 20 | 8.04 | NULL | 777 | BP G protein-coupled receptor signaling pathway |
| <i>Underexpressed</i> | | | | |
| 1 | -7.8 | NULL | 276 | BP translation |
| 2 | -6.99 | NULL | 152 | BP rRNA processing |
| 3 | -6.9 | NULL | 83 | BP mitochondrial translational elongation |
| 4 | -6.75 | NULL | 366 | BP DNA repair |
| 5 | -6.72 | NULL | 85 | BP mitochondrial translational termination |
| 6 | -6.45 | NULL | 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 7 | -6.24 | NULL | 90 | BP viral transcription |
| 8 | -6.18 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 9 | -5.78 | NULL | 229 | BP mRNA splicing, via spliceosome |
| 10 | -5.7 | NULL | 93 | BP ribosome biogenesis |
| 11 | -5.7 | NULL | 158 | BP DNA replication |
| 12 | -5.46 | NULL | 630 | BP cell cycle |
| 13 | -5.46 | NULL | 98 | BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay |
| 14 | -5.32 | NULL | 564 | BP immune system process |
| 15 | -5.24 | NULL | 43 | BP mitochondrial electron transport, NADH to ubiquinone |
| 16 | -5.11 | NULL | 120 | BP translational initiation |
| 17 | -5.11 | NULL | 279 | BP RNA splicing |
| 18 | -5.03 | NULL | 39 | BP CENP-A containing nucleosome assembly |
| 19 | -5.01 | NULL | 394 | BP cell division |
| 20 | -4.98 | NULL | 59 | BP mitochondrial respiratory chain complex I assembly |

p-values

