

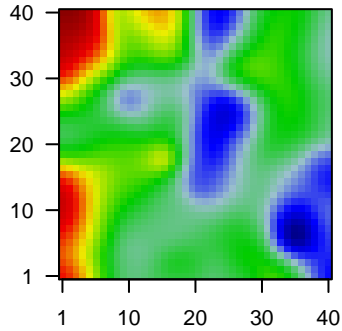
3078F

Global Summary

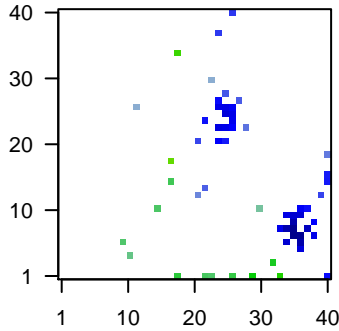
%DE = 0.1
 # genes with fdr < 0.2 = 3426 (1494 + / 1932 -)
 # genes with fdr < 0.1 = 2028 (777 + / 1251 -)
 # genes with fdr < 0.05 = 1579 (536 + / 1043 -)
 # genes with fdr < 0.01 = 859 (231 + / 628 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.36
 <p-value> = 0.2
 <fdr> = 0.9

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|--|
| 1 | 200621_at | -1.31 | 2e-16 | 3e-13 | 37 x 8 cysteine and glycine rich protein 1 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 2 | 201397_at | -1.7 | 2e-16 | 3e-13 | 26 x 26 phosphoglycerate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:10000] |
| 3 | 202017_at | -1.4 | 2e-16 | 3e-13 | 40 x 15 epoxide hydrolase 1 [Source:HGNC Symbol;Acc:HGNC:3401] |
| 4 | 202439_s_at | -1.87 | 2e-16 | 3e-13 | 38 x 7 iduronate 2-sulfatase [Source:HGNC Symbol;Acc:HGNC:536] |
| 5 | 204081_at | -1.38 | 2e-16 | 3e-13 | 40 x 1 neurogranin [Source:HGNC Symbol;Acc:HGNC:8000] |
| 6 | 204378_at | -1.94 | 2e-16 | 3e-13 | 34 x 8 breast carcinoma amplified sequence 1 [Source:HGNC Symb] |
| 7 | 204805_s_at | -1.47 | 2e-16 | 3e-13 | 40 x 19 H1 histone family member X [Source:HGNC Symbol;Acc:HGNC:10000] |
| 8 | 204955_at | -1.98 | 2e-16 | 3e-13 | 26 x 25 sushi repeat containing protein X-linked [Source:HGNC Symb] |
| 9 | 205523_at | -2.16 | 2e-16 | 3e-13 | 29 x 1 hyaluronan and proteoglycan link protein 1 [Source:HGNC Sy] |
| 10 | 205856_at | -2.47 | 2e-16 | 3e-13 | 24 x 27 solute carrier family 14 member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:HGNC:10000] |
| 11 | 205970_at | -1.96 | 2e-16 | 3e-13 | 24 x 21 |
| 12 | 206243_at | -1.79 | 2e-16 | 3e-13 | 15 x 11 TIMP metalloproteinase inhibitor 4 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 13 | 206373_at | -1.72 | 2e-16 | 3e-13 | 17 x 15 Zic family member 1 [Source:HGNC Symbol;Acc:HGNC:1287] |
| 14 | 206899_at | -2.25 | 2e-16 | 3e-13 | 36 x 7 neurotensin receptor 2 [Source:HGNC Symbol;Acc:HGNC:80] |
| 15 | 207323_s_at | -1.42 | 2e-16 | 3e-13 | 35 x 7 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925] |
| 16 | 207659_s_at | -2.2 | 2e-16 | 3e-13 | 35 x 7 myelin-associated oligodendrocyte basic protein [Source:HGNC Symbol;Acc:HGNC:10000] |
| 17 | 208758_at | -1.63 | 2e-16 | 3e-13 | 12 x 26 5-aminoimidazole-4-carboxamide ribonucleotide formyltrans |
| 18 | 209072_at | -1.43 | 2e-16 | 3e-13 | 35 x 7 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925] |
| 19 | 209301_at | -1.84 | 2e-16 | 3e-13 | 33 x 8 carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137] |
| 20 | 209590_at | -1.66 | 2e-16 | 3e-13 | 28 x 23 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:HGNC:10000] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 10.85 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-speci |
| 2 | 10.64 | NULL | 1145 | BP regulation of transcription by RNA polymerase II |
| 3 | 10.44 | NULL | 1387 | BP regulation of transcription, DNA-templated |
| 4 | 7.84 | NULL | 90 | BP viral transcription |
| 5 | 7.29 | NULL | 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 6 | 6.96 | NULL | 98 | BP nuclear-transcribed mRNA catabolic process, nonsense-mediated |
| 7 | 6.06 | NULL | 120 | BP translational initiation |
| 8 | 5.9 | NULL | 358 | BP mRNA processing |
| 9 | 5.8 | NULL | 279 | BP RNA splicing |
| 10 | 5.69 | NULL | 342 | BP chromatin organization |
| 11 | 5.66 | NULL | 366 | BP DNA repair |
| 12 | 5.2 | NULL | 158 | BP DNA replication |
| 13 | 5.02 | NULL | 400 | BP chromatin binding |
| 14 | 4.94 | NULL | 64 | BP complement activation, classical pathway |
| 15 | 4.76 | NULL | 229 | BP mRNA splicing, via spliceosome |
| 16 | 4.53 | NULL | 19 | BP mRNA splice site selection |
| 17 | 4.52 | NULL | 39 | BP CENP-A containing nucleosome assembly |
| 18 | 4.32 | NULL | 99 | BP mRNA export from nucleus |
| 19 | 4.31 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 20 | 4.3 | NULL | 29 | BP positive regulation of B cell activation |
| <i>Underexpressed</i> | | | | |
| 1 | -20.47 | NULL | 7387 | BP membrane |
| 2 | -15.45 | NULL | 4278 | BP plasma membrane |
| 3 | -13.33 | NULL | 6202 | BP cytoplasm |
| 4 | -11.38 | NULL | 4740 | BP cytosol |
| 5 | -10.6 | NULL | 460 | BP neutrophil degranulation |
| 6 | -10.48 | NULL | 1435 | BP mitochondrion |
| 7 | -9.92 | NULL | 671 | BP oxidation-reduction process |
| 8 | -9.53 | NULL | 553 | BP oxidoreductase activity |
| 9 | -9.41 | NULL | 500 | BP catalytic activity |
| 10 | -9.18 | NULL | 521 | BP lipid metabolic process |
| 11 | -7.77 | NULL | 1242 | BP Golgi apparatus |
| 12 | -7.16 | NULL | 815 | BP protein homodimerization activity |
| 13 | -7.1 | NULL | 21 | BP cellular response to copper ion |
| 14 | -6.75 | NULL | 41 | BP receptor internalization |
| 15 | -6.67 | NULL | 17 | BP cellular response to zinc ion |
| 16 | -6.6 | NULL | 350 | BP GTP binding |
| 17 | -6.6 | NULL | 52 | BP myelination |
| 18 | -6.41 | NULL | 574 | BP synapse |
| 19 | -6.34 | NULL | 156 | BP fatty acid metabolic process |
| 20 | -6.1 | NULL | 254 | BP angiogenesis |

p-values

