

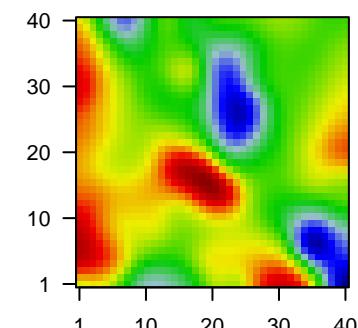
6428M

Global Summary

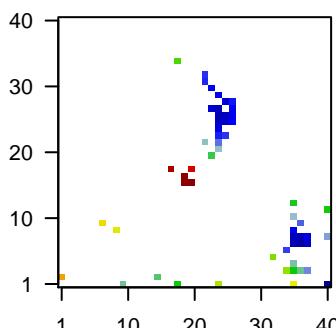
$\%DE = 0.08$
genes with fdr < 0.2 = 3062 (1166 + / 1896 -)
genes with fdr < 0.1 = 2397 (867 + / 1530 -)
genes with fdr < 0.05 = 1958 (681 + / 1277 -)
genes with fdr < 0.01 = 1370 (451 + / 919 -)
genes in genesets = 16360

$\langle FC \rangle = 0$
 $\langle t\text{-score} \rangle = -0.12$
 $\langle p\text{-value} \rangle = 0.17$
 $\langle fdr \rangle = 0.92$

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description | Metagene |
|-----------------------|---------------|---------|-------|---------|-------------|---|
| <i>Overexpressed</i> | | | | | | |
| 1 | 1552721_a_a' | -1.98 | 2e-16 | 6e-14 | 24 x 24 | fibroblast growth factor 1 [Source:HGNC Symbol;Acc:HGNC:2171] |
| 2 | 1552848_a_a' | -2.37 | 2e-16 | 6e-14 | 24 x 25 | patched domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2172] |
| 3 | 1554784_at | -1.5 | 2e-16 | 6e-14 | 24 x 1 | contactin 1 [Source:HGNC Symbol;Acc:HGNC:2171] |
| 4 | 1555807_a_a' | -2.13 | 2e-16 | 6e-14 | 35 x 7 | myelin oligodendrocyte glycoprotein [Source:HGNC Symbol;Acc:HGNC:2173] |
| 5 | 1556499_s_atl | 1.73 | 2e-16 | 6e-14 | 18 x 34 | collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:2174] |
| 6 | 1556904_at | -2.48 | 2e-16 | 6e-14 | 36 x 3 | novel transcript, overlapping GABRB1 |
| 7 | 1557256_a_a' | -2.45 | 2e-16 | 6e-14 | 35 x 4 | |
| 8 | 1565162_s_atl | -1.8 | 2e-16 | 6e-14 | 23 x 27 | microsomal glutathione S-transferase 1 [Source:HGNC Symbol;Acc:HGNC:2175] |
| 9 | 1565809_x_atl | -1.79 | 2e-16 | 6e-14 | 35 x 7 | |
| 10 | 1569110_x_atl | -1.95 | 2e-16 | 6e-14 | 7 x 10 | programmed cell death 6 (PDCD6) pseudogene |
| <i>Underexpressed</i> | | | | | | |
| 11 | 201028_s_at | -1.05 | 2e-16 | 6e-14 | 23 x 30 | CD99 molecule (Xg blood group) [Source:HGNC Symbol;Acc:HGNC:2176] |
| 12 | 201438_at | 2.43 | 2e-16 | 6e-14 | 20 x 16 | collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:HGNC:2177] |
| 13 | 201852_x_at | 2.51 | 2e-16 | 6e-14 | 19 x 16 | collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:2178] |
| 14 | 201909_at | -1.79 | 2e-16 | 6e-14 | 18 x 1 | ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:2179] |
| 15 | 202071_at | -1.42 | 2e-16 | 6e-14 | 24 x 22 | syndecan 4 [Source:HGNC Symbol;Acc:HGNC:10661] |
| 16 | 202191_s_at | -1.27 | 2e-16 | 6e-14 | 37 x 8 | growth arrest specific 7 [Source:HGNC Symbol;Acc:HGNC:411] |
| 17 | 202310_s_at | 2.27 | 2e-16 | 6e-14 | 19 x 17 | collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:2180] |
| 18 | 202404_s_at | 2.2 | 2e-16 | 6e-14 | 19 x 17 | collagen type I alpha 2 chain [Source:HGNC Symbol;Acc:HGNC:2181] |
| 19 | 202834_at | -1.38 | 2e-16 | 6e-14 | 25 x 25 | angiotensinogen [Source:HGNC Symbol;Acc:HGNC:333] |
| 20 | 203381_s_at | -1.17 | 2e-16 | 6e-14 | 25 x 28 | apolipoprotein E [Source:HGNC Symbol;Acc:HGNC:613] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 8.31 | NULL | 231 | BP extracellular matrix organization |
| 2 | 6.93 | NULL | 44 | BP collagen fibril organization |
| 3 | 6.09 | NULL | 12 | BP keratan sulfate catabolic process |
| 4 | 5.06 | NULL | 158 | BP DNA replication |
| 5 | 4.95 | NULL | 29 | BP endodermal cell differentiation |
| 6 | 4.47 | NULL | 630 | BP cell cycle |
| 7 | 4.43 | NULL | 254 | BP angiogenesis |
| 8 | 4.28 | NULL | 101 | BP ossification |
| 9 | 4.25 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide antigen by professional antigen-presenting cell |
| 10 | 4.18 | NULL | 15 | BP proteoglycan binding |
| 11 | 4.14 | NULL | 12 | BP basement membrane organization |
| 12 | 4.01 | NULL | 394 | BP cell division |
| 13 | 3.99 | NULL | 85 | BP chromosome segregation |
| 14 | 3.97 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 15 | 3.84 | NULL | 31 | BP mitotic sister chromatid segregation |
| 16 | 3.77 | NULL | 400 | BP chromatin binding |
| 17 | 3.76 | NULL | 66 | BP response to mechanical stimulus |
| 18 | 3.7 | NULL | 24 | BP non-canonical Wnt signaling pathway |
| 19 | 3.54 | NULL | 13 | BP type B pancreatic cell development |
| 20 | 3.45 | NULL | 13 | BP supramolecular fiber organization |
| <i>Underexpressed</i> | | | | |
| 1 | -9.13 | NULL | 4278 | BP plasma membrane |
| 2 | -8.64 | NULL | 7387 | BP membrane |
| 3 | -6.51 | NULL | 12 | BP negative regulation of long-term synaptic potentiation |
| 4 | -6.4 | NULL | 15 | BP water transport |
| 5 | -6.35 | NULL | 13 | BP central nervous system myelination |
| 6 | -6.14 | NULL | 55 | BP phospholipase C-activating G protein-coupled receptor signaling pathway |
| 7 | -6.04 | NULL | 574 | BP synapse |
| 8 | -6.04 | NULL | 17 | BP cellular response to zinc ion |
| 9 | -5.85 | NULL | 21 | BP cellular response to copper ion |
| 10 | -5.82 | NULL | 52 | BP myelination |
| 11 | -5.75 | NULL | 43 | BP substantia nigra development |
| 12 | -5.66 | NULL | 521 | BP lipid metabolic process |
| 13 | -5.45 | NULL | 12 | BP negative regulation of amyloid-beta formation |
| 14 | -5.34 | NULL | 156 | BP fatty acid metabolic process |
| 15 | -5.3 | NULL | 89 | BP neuropeptide signaling pathway |
| 16 | -5.26 | NULL | 236 | BP chemical synaptic transmission |
| 17 | -5.25 | NULL | 16 | BP negative regulation of growth |
| 18 | -5.19 | NULL | 777 | BP G protein-coupled receptor signaling pathway |
| 19 | -5.18 | NULL | 30 | BP associative learning |
| 20 | -5.12 | NULL | 23 | BP cellular zinc ion homeostasis |

