

8269M

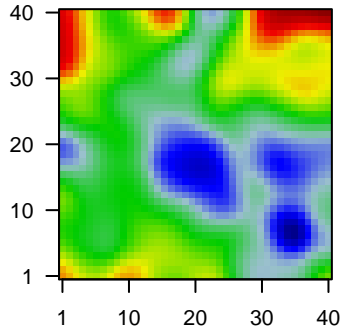
Global Summary

%DE = 0.04
 # genes with $fdr < 0.2$ = 837 (342 + / 495 -)
 # genes with $fdr < 0.1$ = 448 (192 + / 256 -)
 # genes with $fdr < 0.05$ = 347 (146 + / 201 -)
 # genes with $fdr < 0.01$ = 171 (70 + / 101 -)

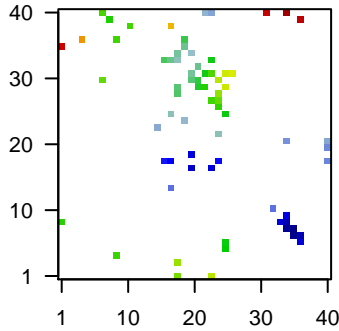
 # genes in genesets = 16360

 $\langle FC \rangle = 0$
 $\langle t\text{-score} \rangle = 0.05$
 $\langle p\text{-value} \rangle = 0.3$
 $\langle fdr \rangle = 0.96$

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|--|
| 1 | 1554663_a_a | 2.56 | 2e-16 | 2e-12 | 32 x 11 nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC:339] |
| 2 | 213592_at | -1.44 | 2e-16 | 2e-12 | 19 x 36 apelin receptor [Source:HGNC Symbol;Acc:HGNC:339] |
| 3 | 223699_at | -2.21 | 2e-16 | 2e-12 | 35 x 7 carnosine dipeptidase 1 [Source:HGNC Symbol;Acc:HGNC:2] |
| 4 | 224588_at | 2.54 | 2e-16 | 2e-12 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:339] |
| 5 | 226769_at | -1.3 | 2e-16 | 2e-12 | 23 x 27 fin bud initiation factor homolog [Source:HGNC Symbol;Acc:HGNC:339] |
| 6 | 243489_at | 2.73 | 2e-16 | 2e-12 | 17 x 38 |
| 7 | 227671_at | 2.36 | 5e-15 | 2e-10 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:339] |
| 8 | 204036_at | -1.23 | 9e-15 | 5e-10 | 34 x 8 lysophosphatidic acid receptor 1 [Source:HGNC Symbol;Acc:HGNC:339] |
| 9 | 224576_at | -1.37 | 9e-15 | 5e-10 | 23 x 40 endoplasmic reticulum-golgi intermediate compartment 1 [Source:HGNC Symbol;Acc:HGNC:339] |
| 10 | 231597_x_at | 2.31 | 2e-14 | 5e-09 | 36 x 39 |
| 11 | 214218_s_at | 2.21 | 2e-13 | 5e-09 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:339] |
| 12 | 212556_at | -1.1 | 2e-13 | 5e-09 | 15 x 23 scribbled planar cell polarity protein [Source:HGNC Symbol;Acc:HGNC:339] |
| 13 | 209189_at | 1.2 | 3e-13 | 2e-08 | 20 x 30 Fos proto-oncogene, AP-1 transcription factor subunit [Source:HGNC Symbol;Acc:HGNC:339] |
| 14 | 231001_at | -1.62 | 8e-13 | 2e-08 | 24 x 26 |
| 15 | 211506_s_at | 2.15 | 1e-12 | 5e-08 | 25 x 6 C-X-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:HGNC:339] |
| 16 | 202589_at | -1.49 | 2e-12 | 5e-08 | 16 x 18 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12] |
| 17 | 201909_at | -1.44 | 3e-12 | 7e-08 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:12] |
| 18 | 221728_x_at | 2.05 | 4e-12 | 3e-07 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:339] |
| 19 | 204073_s_at | -1.8 | 2e-11 | 3e-07 | 35 x 7 myelin regulatory factor [Source:HGNC Symbol;Acc:HGNC:12] |
| 20 | 230087_at | -1.59 | 2e-11 | 3e-07 | 34 x 10 proline rich membrane anchor 1 [Source:HGNC Symbol;Acc:HGNC:12] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 5.76 | NULL | 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 2 | 5.73 | NULL | 43 | BP chemokine activity |
| 3 | 5.51 | NULL | 159 | BP response to lipopolysaccharide |
| 4 | 5.23 | NULL | 65 | BP chemokine-mediated signaling pathway |
| 5 | 5.15 | NULL | 90 | BP viral transcription |
| 6 | 5.12 | NULL | 59 | BP antimicrobial humoral immune response mediated by antimicrobial |
| 7 | 5.04 | NULL | 10 | BP response to molecule of bacterial origin |
| 8 | 5.02 | NULL | 31 | BP cellular response to fibroblast growth factor stimulus |
| 9 | 4.89 | NULL | 207 | BP cytokine activity |
| 10 | 4.88 | NULL | 151 | BP cellular response to lipopolysaccharide |
| 11 | 4.67 | NULL | 24 | BP leukocyte chemotaxis |
| 12 | 4.55 | NULL | 148 | BP chemotaxis |
| 13 | 4.49 | NULL | 18 | BP cellular response to extracellular stimulus |
| 14 | 4.4 | NULL | 120 | BP translational initiation |
| 15 | 4.34 | NULL | 84 | BP nucleosome assembly |
| 16 | 4.33 | NULL | 1086 | BP positive regulation of transcription by RNA polymerase II |
| 17 | 4.32 | NULL | 289 | BP cytokine-mediated signaling pathway |
| 18 | 4.3 | NULL | 19 | BP innate immune response in mucosa |
| 19 | 4.26 | NULL | 18 | BP eosinophil chemotaxis |
| 20 | 4.25 | NULL | 783 | BP negative regulation of transcription by RNA polymerase II |
| <i>Underexpressed</i> | | | | |
| 1 | -10.3 | NULL | 7387 | BP membrane |
| 2 | -6.57 | NULL | 6202 | BP cytoplasm |
| 3 | -5.9 | NULL | 1242 | BP Golgi apparatus |
| 4 | -5.31 | NULL | 4278 | BP plasma membrane |
| 5 | -5.07 | NULL | 231 | BP extracellular matrix organization |
| 6 | -5.02 | NULL | 52 | BP myelination |
| 7 | -4.91 | NULL | 521 | BP lipid metabolic process |
| 8 | -4.82 | NULL | 577 | BP proteolysis |
| 9 | -4.63 | NULL | 484 | BP peptidase activity |
| 10 | -4.63 | NULL | 27 | BP coronary vasculature development |
| 11 | -4.48 | NULL | 170 | BP protein glycosylation |
| 12 | -4.42 | NULL | 553 | BP oxidoreductase activity |
| 13 | -4.21 | NULL | 190 | BP actin filament binding |
| 14 | -4.2 | NULL | 41 | BP negative regulation of viral genome replication |
| 15 | -4.2 | NULL | 564 | BP immune system process |
| 16 | -4.19 | NULL | 815 | BP protein homodimerization activity |
| 17 | -4.13 | NULL | 11 | BP oligosaccharide metabolic process |
| 18 | -4.07 | NULL | 44 | BP collagen fibril organization |
| 19 | -3.96 | NULL | 671 | BP oxidation-reduction process |
| 20 | -3.93 | NULL | 14 | BP L-alpha-amino acid transmembrane transport |

p-values

