

3662M

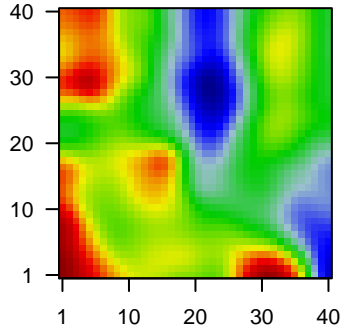
Global Summary

%DE = 0.08
 # genes with fdr < 0.2 = 2664 (1308 + / 1356 -)
 # genes with fdr < 0.1 = 2142 (1061 + / 1081 -)
 # genes with fdr < 0.05 = 1742 (862 + / 880 -)
 # genes with fdr < 0.01 = 1035 (543 + / 492 -)

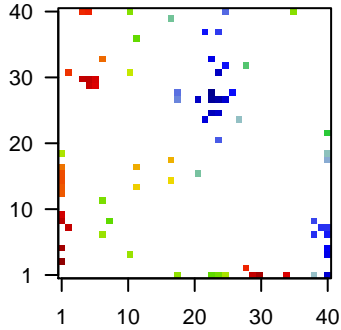
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.08
 <p-value> = 0.2
 <fdr> = 0.92

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr p-value | Description Metagene |
|------|-------------|---------|-------------|---|
| 1 | 1561604_at | 2.34 | 2e-16 3e-13 | 2 x 31 |
| 2 | 1570101_at | 2.33 | 2e-16 3e-13 | 1 x 16 |
| 3 | 201289_at | -1.68 | 2e-16 3e-13 | 25 x 32 cellular communication network factor 1 [Source:HGNC Synt |
| 4 | 201909_at | -1.85 | 2e-16 3e-13 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:1 |
| 5 | 202861_at | -1.89 | 2e-16 3e-13 | 40 x 19 period circadian regulator 1 [Source:NCBI gene;Acc:5187] |
| 6 | 203973_s_at | -1.15 | 2e-16 3e-13 | 22 x 37 CCAAT enhancer binding protein delta [Source:HGNC Symb |
| 7 | 205113_at | -1.87 | 2e-16 3e-13 | 40 x 1 neurofilament medium [Source:HGNC Symbol;Acc:HGNC:77 |
| 8 | 205856_at | -1.87 | 2e-16 3e-13 | 24 x 27 solute carrier family 14 member 1 (Kidd blood group) [Source |
| 9 | 205970_at | -1.45 | 2e-16 3e-13 | 24 x 21 |
| 10 | 206481_s_at | -1.5 | 2e-16 3e-13 | 40 x 8 LIM domain binding 2 [Source:HGNC Symbol;Acc:HGNC:65 |
| 11 | 208168_s_at | 2.53 | 2e-16 3e-13 | 11 x 31 chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936] |
| 12 | 209101_at | -1.66 | 2e-16 3e-13 | 11 x 4 cellular communication network factor 2 [Source:HGNC Synt |
| 13 | 210095_s_at | -1.69 | 2e-16 3e-13 | 21 x 16 insulin like growth factor binding protein 3 [Source:HGNC Syr |
| 14 | 212473_s_at | -1.52 | 2e-16 3e-13 | 40 x 1 microtubule associated monooxygenase, calponin and LIM do |
| 15 | 213245_at | -1.67 | 2e-16 3e-13 | 40 x 4 adenylate cyclase 1 [Source:HGNC Symbol;Acc:HGNC:232] |
| 16 | 214053_at | -1.8 | 2e-16 3e-13 | 24 x 27 erb-b2 receptor tyrosine kinase 4 [Source:HGNC Symbol;Acc |
| 17 | 214218_s_at | 2.4 | 2e-16 3e-13 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGN |
| 18 | 215017_s_at | -1.32 | 2e-16 3e-13 | 23 x 28 formin binding protein 1 like [Source:HGNC Symbol;Acc:HGN |
| 19 | 216027_at | 2.73 | 2e-16 3e-13 | 5 x 29 thioredoxin related transmembrane protein 4 [Source:HGNC ! |
| 20 | 224588_at | 2.38 | 2e-16 3e-13 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGN |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 4.98 | NULL | 84 | BP nucleosome assembly |
| 2 | 4.89 | NULL | 358 | BP mRNA processing |
| 3 | 4.8 | NULL | 158 | BP DNA replication |
| 4 | 4.53 | NULL | 279 | BP RNA splicing |
| 5 | 4.25 | NULL | 366 | BP DNA repair |
| 6 | 4.09 | NULL | 229 | BP mRNA splicing, via spliceosome |
| 7 | 3.93 | NULL | 29 | BP cytoplasmic translation |
| 8 | 3.71 | NULL | 90 | BP viral transcription |
| 9 | 3.66 | NULL | 276 | BP translation |
| 10 | 3.32 | NULL | 59 | BP mitochondrial respiratory chain complex I assembly |
| 11 | 3.26 | NULL | 85 | BP chromosome segregation |
| 12 | 3.24 | NULL | 54 | BP DNA duplex unwinding |
| 13 | 3.22 | NULL | 120 | BP translational initiation |
| 14 | 3.2 | NULL | 39 | BP CENP-A containing nucleosome assembly |
| 15 | 3.19 | NULL | 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 16 | 3.17 | NULL | 130 | BP regulation of signal transduction by p53 class mediator |
| 17 | 3.15 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 18 | 3.15 | NULL | 56 | BP mRNA 3'-end processing |
| 19 | 3.11 | NULL | 98 | BP nuclear-transcribed mRNA catabolic process, nonsense-mediated |
| 20 | 3.1 | NULL | 47 | BP protein heterotetramerization |
| <i>Underexpressed</i> | | | | |
| 1 | -15.31 | NULL | 4278 | BP plasma membrane |
| 2 | -13.54 | NULL | 7387 | BP membrane |
| 3 | -12.72 | NULL | 6202 | BP cytoplasm |
| 4 | -9.72 | NULL | 1500 | BP signal transduction |
| 5 | -8.82 | NULL | 4740 | BP cytosol |
| 6 | -7.57 | NULL | 777 | BP G protein-coupled receptor signaling pathway |
| 7 | -6.77 | NULL | 231 | BP extracellular matrix organization |
| 8 | -6.61 | NULL | 1242 | BP Golgi apparatus |
| 9 | -6.52 | NULL | 594 | BP cell adhesion |
| 10 | -6.51 | NULL | 50 | BP positive regulation of fat cell differentiation |
| 11 | -6.51 | NULL | 412 | BP negative regulation of cell population proliferation |
| 12 | -6.47 | NULL | 219 | BP positive regulation of cell migration |
| 13 | -6.36 | NULL | 159 | BP response to lipopolysaccharide |
| 14 | -6.35 | NULL | 168 | BP response to hypoxia |
| 15 | -6.29 | NULL | 657 | BP calcium ion binding |
| 16 | -6.26 | NULL | 289 | BP cytokine-mediated signaling pathway |
| 17 | -5.98 | NULL | 513 | BP positive regulation of cell population proliferation |
| 18 | -5.92 | NULL | 261 | BP cell surface receptor signaling pathway |
| 19 | -5.88 | NULL | 364 | BP inflammatory response |
| 20 | -5.88 | NULL | 59 | BP positive regulation of osteoblast differentiation |

p-values

