

31091P

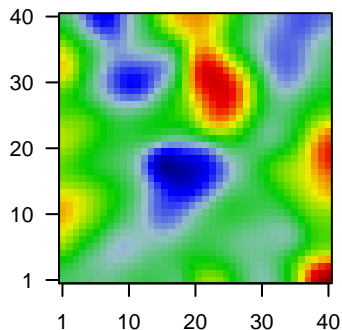
Global Summary

%DE = 0.05
 # genes with fdr < 0.2 = 1438 (834 + / 604 -)
 # genes with fdr < 0.1 = 915 (543 + / 372 -)
 # genes with fdr < 0.05 = 649 (399 + / 250 -)
 # genes with fdr < 0.01 = 337 (200 + / 137 -)

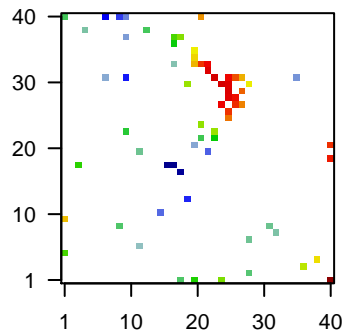
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.16
 <p-value> = 0.27
 <fdr> = 0.95

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|--|
| 1 | 201348_at | 0.99 | 2e-16 | 2e-12 | 25 x 31 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:201348] |
| 2 | 201909_at | -1.81 | 2e-16 | 2e-12 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909] |
| 3 | 202589_at | -1.24 | 2e-16 | 2e-12 | 16 x 18 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:202589] |
| 4 | 214091_s_at | 0.99 | 2e-16 | 2e-12 | 24 x 30 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:214091] |
| 5 | 219890_at | 1.69 | 2e-16 | 2e-12 | 20 x 35 C-type lectin domain containing 5A [Source:HGNC Symbol;Acc:HGNC:219890] |
| 6 | 224588_at | 1.78 | 2e-16 | 2e-12 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588] |
| 7 | 237898_at | 1.76 | 2e-16 | 2e-12 | 25 x 30 |
| 8 | 227671_at | 1.68 | 4e-16 | 5e-11 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:227671] |
| 9 | 214680_at | 0.78 | 1e-15 | 6e-11 | 26 x 28 neurotrophic receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:214680] |
| 10 | 243952_at | 1.64 | 2e-15 | 5e-10 | 24 x 30 TPTE pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:243952] |
| 11 | 237622_at | 1.58 | 2e-14 | 5e-10 | 20 x 1 aconitase 1 [Source:HGNC Symbol;Acc:HGNC:117] |
| 12 | 204409_s_at | -1.55 | 2e-14 | 8e-10 | 18 x 1 eukaryotic translation initiation factor 1A Y-linked [Source:HGNC Symbol;Acc:HGNC:204409] |
| 13 | 203083_at | -0.8 | 4e-14 | 1e-09 | 19 x 13 thrombospondin 2 [Source:HGNC Symbol;Acc:HGNC:11786] |
| 14 | 232122_s_at | -1.53 | 8e-14 | 1e-09 | 26 x 27 ventricular zone expressed PH domain containing 1 [Source:HGNC Symbol;Acc:HGNC:232122] |
| 15 | 205000_at | -1.46 | 9e-14 | 3e-09 | 18 x 1 DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:HGNC:205000] |
| 16 | 236158_at | 1.53 | 2e-13 | 8e-09 | 10 x 40 novel zinc finger protein pseudogene |
| 17 | 221623_at | 0.77 | 3e-13 | 2e-08 | 27 x 29 brevican [Source:HGNC Symbol;Acc:HGNC:23059] |
| 18 | 228492_at | -1.47 | 9e-13 | 2e-08 | 18 x 1 ubiquitin specific peptidase 9 Y-linked [Source:HGNC Symbol;Acc:HGNC:228492] |
| 19 | 1556552_a_at | 1.47 | 1e-12 | 1e-07 | 10 x 23 acyl-CoA synthetase family member 3 [Source:HGNC Symbol;Acc:HGNC:1556552] |
| 20 | 209293_x_at | 0.67 | 6e-12 | 1e-07 | 25 x 30 inhibitor of DNA binding 4, HLH protein [Source:HGNC Symbol;Acc:HGNC:209293] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 10.64 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide antigen fragments |
| 2 | 8.35 | NULL | 43 | BP antigen processing and presentation |
| 3 | 7.04 | NULL | 574 | BP synapse |
| 4 | 6.06 | NULL | 4278 | BP plasma membrane |
| 5 | 6.05 | NULL | 6202 | BP cytoplasm |
| 6 | 5.74 | NULL | 684 | BP phosphorylation |
| 7 | 5.68 | NULL | 1086 | BP positive regulation of transcription by RNA polymerase II |
| 8 | 5.37 | NULL | 783 | BP negative regulation of transcription by RNA polymerase II |
| 9 | 5.26 | NULL | 28 | BP synaptic vesicle exocytosis |
| 10 | 5.26 | NULL | 175 | BP regulation of cell population proliferation |
| 11 | 5.22 | NULL | 400 | BP protein serine/threonine kinase activity |
| 12 | 5.06 | NULL | 1242 | BP Golgi apparatus |
| 13 | 5.03 | NULL | 79 | BP cellular response to calcium ion |
| 14 | 5.02 | NULL | 541 | BP negative regulation of transcription, DNA-templated |
| 15 | 4.96 | NULL | 7387 | BP membrane |
| 16 | 4.85 | NULL | 33 | BP long-term memory |
| 17 | 4.79 | NULL | 21 | BP positive regulation of long-term synaptic potentiation |
| 18 | 4.7 | NULL | 613 | BP positive regulation of transcription, DNA-templated |
| 19 | 4.61 | NULL | 18 | BP cellular response to extracellular stimulus |
| 20 | 4.55 | NULL | 1387 | BP regulation of transcription, DNA-templated |
| <i>Underexpressed</i> | | | | |
| 1 | -6.99 | NULL | 394 | BP cell division |
| 2 | -6.53 | NULL | 78 | BP anaphase-promoting complex-dependent catabolic process |
| 3 | -5.59 | NULL | 59 | BP mitochondrial respiratory chain complex I assembly |
| 4 | -5.46 | NULL | 43 | BP mitochondrial electron transport, NADH to ubiquinone |
| 5 | -5.25 | NULL | 630 | BP cell cycle |
| 6 | -4.7 | NULL | 31 | BP mitotic sister chromatid segregation |
| 7 | -4.64 | NULL | 78 | BP regulation of mitotic cell cycle phase transition |
| 8 | -4.63 | NULL | 85 | BP chromosome segregation |
| 9 | -4.37 | NULL | 11 | BP engulfment of apoptotic cell |
| 10 | -4.29 | NULL | 35 | BP mitotic metaphase plate congression |
| 11 | -4.29 | NULL | 158 | BP DNA replication |
| 12 | -4.21 | NULL | 164 | BP mitotic cell cycle |
| 13 | -3.86 | NULL | 83 | BP mitochondrial translational elongation |
| 14 | -3.85 | NULL | 85 | BP mitochondrial translational termination |
| 15 | -3.79 | NULL | 12 | BP mitotic nuclear envelope disassembly |
| 16 | -3.51 | NULL | 25 | BP cytochrome-c oxidase activity |
| 17 | -3.5 | NULL | 18 | BP eosinophil chemotaxis |
| 18 | -3.43 | NULL | 18 | BP mitochondrial respiratory chain complex IV assembly |
| 19 | -3.41 | NULL | 22 | BP mitotic spindle assembly checkpoint |
| 20 | -3.38 | NULL | 35 | BP translesion synthesis |

p-values

