

3016F

Global Summary

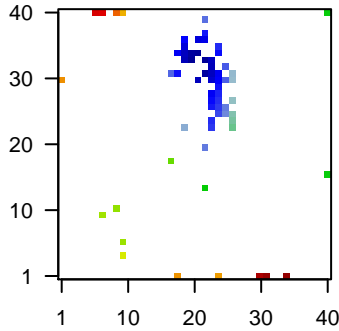
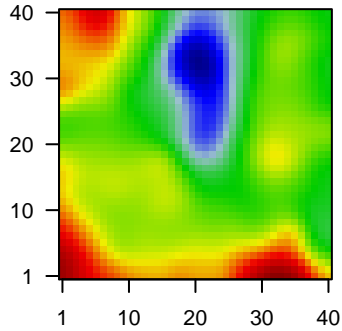
%DE = 0.07
 # genes with fdr < 0.2 = 2424 (1069 + / 1355 -)
 # genes with fdr < 0.1 = 1759 (762 + / 997 -)
 # genes with fdr < 0.05 = 1329 (565 + / 764 -)
 # genes with fdr < 0.01 = 844 (337 + / 507 -)

 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.08
 <p-value> = 0.22
 <fdr> = 0.93

Portrait

Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | Description | |
|------|--------------|---------|-------|-------------|---|
| | | p-value | | Metagene | |
| 1 | 1556573_s_at | 2.06 | 2e-16 | 2e-13 | 30 x 1 novel transcript |
| 2 | 1569110_x_at | -1.13 | 2e-16 | 2e-13 | 7 x 10 programmed cell death 6 (PDCD6) pseudogene |
| 3 | 200665_s_at | -0.8 | 2e-16 | 2e-13 | 9 x 11 secreted protein acidic and cysteine rich [Source:HGNC Sym |
| 4 | 200872_at | -1.2 | 2e-16 | 2e-13 | 21 x 36 S100 calcium binding protein A10 [Source:HGNC Symbol;Acc |
| 5 | 201028_s_at | -1.19 | 2e-16 | 2e-13 | 23 x 30 CD99 molecule (Xg blood group) [Source:HGNC Symbol;Acc |
| 6 | 201029_s_at | -0.91 | 2e-16 | 2e-13 | 24 x 34 CD99 molecule (Xg blood group) [Source:HGNC Symbol;Acc |
| 7 | 201289_at | -1.12 | 2e-16 | 2e-13 | 25 x 32 cellular communication network factor 1 [Source:HGNC Symt |
| 8 | 201324_at | -0.98 | 2e-16 | 2e-13 | 21 x 30 epithelial membrane protein 1 [Source:HGNC Symbol;Acc;HC |
| 9 | 201325_s_at | -1.21 | 2e-16 | 2e-13 | 21 x 30 epithelial membrane protein 1 [Source:HGNC Symbol;Acc;HC |
| 10 | 201426_s_at | -0.85 | 2e-16 | 2e-13 | 19 x 34 vimentin [Source:HGNC Symbol;Acc:HGNC:12692] |
| 11 | 201667_at | -0.88 | 2e-16 | 2e-13 | 23 x 26 gap junction protein alpha 1 [Source:HGNC Symbol;Acc:HGNC |
| 12 | 201792_at | -1.87 | 2e-16 | 2e-13 | 22 x 20 AE binding protein 1 [Source:HGNC Symbol;Acc:HGNC:303] |
| 13 | 202269_x_at | -1.4 | 2e-16 | 2e-13 | 20 x 34 guanylate binding protein 1 [Source:HGNC Symbol;Acc:HGNC |
| 14 | 202270_at | -1.46 | 2e-16 | 2e-13 | 20 x 33 guanylate binding protein 1 [Source:HGNC Symbol;Acc:HGNC |
| 15 | 202295_s_at | -0.94 | 2e-16 | 2e-13 | 23 x 32 cathepsin H [Source:HGNC Symbol;Acc:HGNC:2535] |
| 16 | 202376_at | -1.16 | 2e-16 | 2e-13 | 19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC |
| 17 | 202436_s_at | -1.61 | 2e-16 | 2e-13 | 22 x 14 cytochrome P450 family 1 subfamily B member 1 [Source:HG |
| 18 | 202554_s_at | -1.06 | 2e-16 | 2e-13 | 26 x 23 glutathione S-transferase mu 3 [Source:HGNC Symbol;Acc;t |
| 19 | 203705_s_at | -1.64 | 2e-16 | 2e-13 | 23 x 27 frizzled class receptor 7 [Source:HGNC Symbol;Acc:HGNC:4 |
| 20 | 203706_s_at | -1.64 | 2e-16 | 2e-13 | 23 x 27 frizzled class receptor 7 [Source:HGNC Symbol;Acc:HGNC:4 |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 6.81 | NULL | 505 | BP nervous system development |
| 2 | 6.72 | NULL | 240 | BP postsynaptic membrane |
| 3 | 5.83 | NULL | 1145 | BP regulation of transcription by RNA polymerase II |
| 4 | 5.82 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-speci |
| 5 | 5.65 | NULL | 342 | BP chromatin organization |
| 6 | 5.61 | NULL | 574 | BP synapse |
| 7 | 5.47 | NULL | 236 | BP chemical synaptic transmission |
| 8 | 5.31 | NULL | 48 | BP synapse organization |
| 9 | 4.95 | NULL | 15 | BP axon development |
| 10 | 4.88 | NULL | 1387 | BP regulation of transcription, DNA-templated |
| 11 | 4.88 | NULL | 400 | BP chromatin binding |
| 12 | 4.74 | NULL | 10 | BP presynaptic membrane assembly |
| 13 | 4.7 | NULL | 51 | BP neurotransmitter secretion |
| 14 | 4.45 | NULL | 15 | BP neuron cell-cell adhesion |
| 15 | 4.35 | NULL | 61 | BP positive regulation of synapse assembly |
| 16 | 4.35 | NULL | 358 | BP mRNA processing |
| 17 | 4.22 | NULL | 27 | BP gamma-aminobutyric acid signaling pathway |
| 18 | 4.14 | NULL | 64 | BP synapse assembly |
| 19 | 4.09 | NULL | 215 | BP ubiquitin protein ligase activity |
| 20 | 4.07 | NULL | 630 | BP cell cycle |
| <i>Underexpressed</i> | | | | |
| 1 | -13.86 | NULL | 564 | BP immune system process |
| 2 | -12.46 | NULL | 388 | BP immune response |
| 3 | -11.38 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide |
| 4 | -11.03 | NULL | 417 | BP innate immune response |
| 5 | -11 | NULL | 460 | BP neutrophil degranulation |
| 6 | -10.67 | NULL | 364 | BP inflammatory response |
| 7 | -10.66 | NULL | 43 | BP antigen processing and presentation |
| 8 | -8.56 | NULL | 159 | BP response to lipopolysaccharide |
| 9 | -8.4 | NULL | 231 | BP extracellular matrix organization |
| 10 | -8.3 | NULL | 155 | BP regulation of immune response |
| 11 | -8.22 | NULL | 88 | BP cellular response to interferon-gamma |
| 12 | -8.08 | NULL | 118 | BP platelet degranulation |
| 13 | -8.05 | NULL | 289 | BP cytokine-mediated signaling pathway |
| 14 | -7.9 | NULL | 47 | BP complement activation |
| 15 | -7.84 | NULL | 184 | BP defense response to virus |
| 16 | -7.63 | NULL | 151 | BP cellular response to lipopolysaccharide |
| 17 | -7.18 | NULL | 109 | BP response to virus |
| 18 | -7.1 | NULL | 64 | BP complement activation, classical pathway |
| 19 | -6.71 | NULL | 64 | BP regulation of complement activation |
| 20 | -6.68 | NULL | 172 | BP positive regulation of I-kappaB kinase/NF-kappaB signaling |

p-values

