

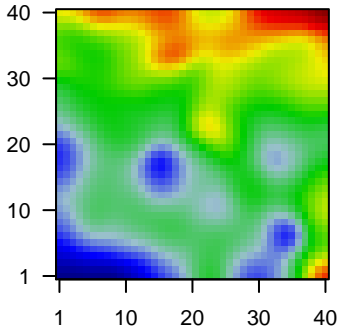
8270F

Global Summary

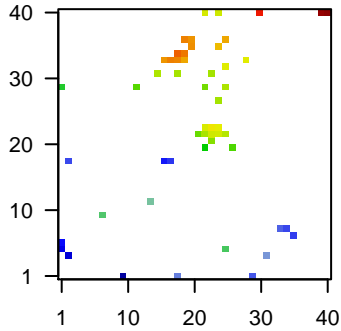
%DE = 0.04
 # genes with fdr < 0.2 = 877 (464 + / 413 -)
 # genes with fdr < 0.1 = 630 (338 + / 292 -)
 # genes with fdr < 0.05 = 460 (254 + / 206 -)
 # genes with fdr < 0.01 = 238 (141 + / 97 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.03
 <p-value> = 0.29
 <fdr> = 0.96

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|---|
| 1 | 1569110_x_at | -1.88 | 2e-16 | 1e-12 | 7 x 10 programmed cell death 6 (PDCD6) pseudogene |
| 2 | 202589_at | -1.9 | 2e-16 | 1e-12 | 16 x 18 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12 |
| 3 | 204850_s_at | -1.33 | 2e-16 | 1e-12 | 1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714] |
| 4 | 204851_s_at | -1.46 | 2e-16 | 1e-12 | 1 x 5 doublecortin [Source:HGNC Symbol;Acc:HGNC:2714] |
| 5 | 209116_x_at | 1.19 | 2e-16 | 1e-12 | 40 x 40 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:2 |
| 6 | 209138_x_at | 2.62 | 2e-16 | 1e-12 | 18 x 33 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac |
| 7 | 214677_x_at | 2.66 | 2e-16 | 1e-12 | 18 x 33 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac |
| 8 | 215121_x_at | 2.52 | 2e-16 | 1e-12 | 18 x 33 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac |
| 9 | 217022_s_at | 3.24 | 2e-16 | 1e-12 | 18 x 33 immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc |
| 10 | 211430_s_at | 2.42 | 1e-15 | 8e-11 | 18 x 34 immunoglobulin heavy constant gamma 2 (G2m marker) [Sou |
| 11 | 217232_x_at | 1.14 | 1e-15 | 8e-11 | 40 x 40 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:2 |
| 12 | 206799_at | 2.38 | 5e-15 | 8e-11 | 23 x 22 secretoglobulin family 1D member 2 [Source:HGNC Symbol;Ac |
| 13 | 231044_at | 2.37 | 6e-15 | 8e-11 | 24 x 35 chromosome 1 open reading frame 194 [Source:HGNC Symt |
| 14 | 224588_at | 2.33 | 6e-15 | 8e-10 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGN |
| 15 | 215379_x_at | 2.32 | 2e-14 | 2e-09 | 18 x 33 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Ac |
| 16 | 201289_at | 1.36 | 9e-14 | 2e-09 | 25 x 32 cellular communication network factor 1 [Source:HGNC Symt |
| 17 | 219890_at | 2.25 | 1e-13 | 3e-09 | 20 x 35 C-type lectin domain containing 5A [Source:HGNC Symbol;A |
| 18 | 205374_at | 2.24 | 2e-13 | 7e-09 | 19 x 33 sarcophilin [Source:HGNC Symbol;Acc:HGNC:11089] |
| 19 | 231077_at | 2.21 | 4e-13 | 7e-09 | 23 x 23 cilia and flagella associated protein 126 [Source:HGNC Symt |
| 20 | 204719_at | -1.37 | 4e-13 | 1e-08 | 33 x 8 ATP binding cassette subfamily A member 8 [Source:HGNC S |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 9.18 | NULL | 64 | BP complement activation, classical pathway |
| 2 | 8.88 | NULL | 47 | BP complement activation |
| 3 | 8.82 | NULL | 29 | BP positive regulation of B cell activation |
| 4 | 8.81 | NULL | 32 | BP cilium movement |
| 5 | 8.17 | NULL | 30 | BP immunoglobulin production |
| 6 | 7.77 | NULL | 152 | BP leukocyte migration |
| 7 | 7.31 | NULL | 388 | BP immune response |
| 8 | 7.17 | NULL | 64 | BP regulation of complement activation |
| 9 | 6.82 | NULL | 30 | BP phagocytosis, recognition |
| 10 | 6.81 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide |
| 11 | 6.76 | NULL | 56 | BP B cell receptor signaling pathway |
| 12 | 6.64 | NULL | 14 | BP inner dynein arm assembly |
| 13 | 6.54 | NULL | 47 | BP phagocytosis, engulfment |
| 14 | 6.49 | NULL | 16 | BP negative regulation of growth |
| 15 | 6.34 | NULL | 222 | BP adaptive immune response |
| 16 | 6.11 | NULL | 89 | BP Fc-gamma receptor signaling pathway involved in phagocytosis |
| 17 | 6.11 | NULL | 173 | BP cilium assembly |
| 18 | 6.1 | NULL | 148 | BP chemotaxis |
| 19 | 5.91 | NULL | 180 | BP cell projection organization |
| 20 | 5.87 | NULL | 418 | BP regulation of signaling receptor activity |
| <i>Underexpressed</i> | | | | |
| 1 | -7.16 | NULL | 630 | BP cell cycle |
| 2 | -7.06 | NULL | 394 | BP cell division |
| 3 | -6.68 | NULL | 366 | BP DNA repair |
| 4 | -6.09 | NULL | 4740 | BP cytosol |
| 5 | -6.02 | NULL | 158 | BP DNA replication |
| 6 | -5.71 | NULL | 484 | BP cellular response to DNA damage stimulus |
| 7 | -5.34 | NULL | 33 | BP DNA replication initiation |
| 8 | -5.28 | NULL | 7387 | BP membrane |
| 9 | -5.14 | NULL | 630 | BP protein transport |
| 10 | -4.96 | NULL | 1145 | BP regulation of transcription by RNA polymerase II |
| 11 | -4.91 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-speci |
| 12 | -4.65 | NULL | 545 | BP protein ubiquitination |
| 13 | -4.63 | NULL | 31 | BP mitotic sister chromatid segregation |
| 14 | -4.28 | NULL | 10 | BP presynaptic membrane assembly |
| 15 | -4.25 | NULL | 66 | BP double-strand break repair |
| 16 | -4.16 | NULL | 97 | BP DNA recombination |
| 17 | -4.16 | NULL | 14 | BP unsaturated fatty acid biosynthetic process |
| 18 | -3.99 | NULL | 521 | BP lipid metabolic process |
| 19 | -3.99 | NULL | 85 | BP chromosome segregation |
| 20 | -3.95 | NULL | 20 | BP DNA helicase activity |

p-values

