

41159P

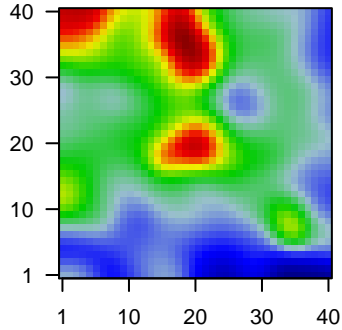
Global Summary

%DE = 0.08
 # genes with fdr < 0.2 = 2582 (1540 + / 1042 -)
 # genes with fdr < 0.1 = 1724 (1041 + / 683 -)
 # genes with fdr < 0.05 = 1316 (786 + / 530 -)
 # genes with fdr < 0.01 = 719 (411 + / 308 -)

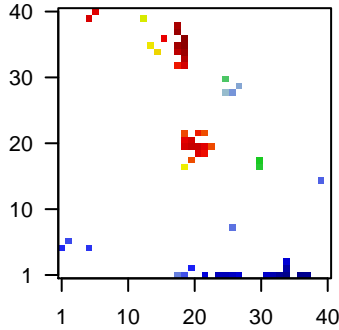
 # genes in genesets = 16360

<FC> = 0
 <t-score> = -0.15
 <p-value> = 0.22
 <fdr> = 0.92

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr p-value | Description Metagene |
|------|-------------|---------|-------------|--|
| 1 | 204041_at | 1.31 | 2e-16 4e-13 | 23 x 20 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68] |
| 2 | 204260_at | -1.64 | 2e-16 4e-13 | 33 x 1 chromogranin B [Source:HGNC Symbol;Acc:HGNC:1930] |
| 3 | 204465_s_at | -1.46 | 2e-16 4e-13 | 34 x 1 internexin neuronal intermediate filament protein alpha [Source:HGNC Symbol;Acc:HGNC:11089] |
| 4 | 205289_at | -1.4 | 2e-16 4e-13 | 1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:11089] |
| 5 | 205290_s_at | -1.6 | 2e-16 4e-13 | 1 x 5 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:11089] |
| 6 | 205374_at | 2.5 | 2e-16 4e-13 | 19 x 33 sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089] |
| 7 | 206858_s_at | 2.73 | 2e-16 4e-13 | 20 x 20 homeobox C6 [Source:HGNC Symbol;Acc:HGNC:5128] |
| 8 | 207542_s_at | 1.42 | 2e-16 4e-13 | 22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1932] |
| 9 | 209047_at | 1.33 | 2e-16 4e-13 | 22 x 22 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc:HGNC:1932] |
| 10 | 209395_at | 1.73 | 2e-16 4e-13 | 21 x 19 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932] |
| 11 | 209550_at | -1.43 | 2e-16 4e-13 | 24 x 1 neccdin, MAGE family member [Source:HGNC Symbol;Acc:HGNC:1932] |
| 12 | 213664_at | -1.25 | 2e-16 4e-13 | 26 x 1 solute carrier family 1 member 1 [Source:HGNC Symbol;Acc:HGNC:1932] |
| 13 | 214651_s_at | 2.46 | 2e-16 4e-13 | 16 x 36 homeobox A9 [Source:HGNC Symbol;Acc:HGNC:5109] |
| 14 | 219093_at | -1.43 | 2e-16 4e-13 | 26 x 1 phosphotyrosine interaction domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1932] |
| 15 | 219537_x_at | -1.56 | 2e-16 4e-13 | 1 x 5 delta like canonical Notch ligand 3 [Source:NCBI gene;Acc:HGNC:1932] |
| 16 | 221623_at | -1.27 | 2e-16 4e-13 | 27 x 29 brevican [Source:HGNC Symbol;Acc:HGNC:23059] |
| 17 | 223122_s_at | -2.22 | 2e-16 4e-13 | 24 x 1 secreted frizzled related protein 2 [Source:HGNC Symbol;Acc:HGNC:23059] |
| 18 | 223977_s_at | 2.49 | 2e-16 4e-13 | 30 x 17 long intergenic non-protein coding RNA 470 [Source:HGNC Symbol;Acc:HGNC:23059] |
| 19 | 227062_at | 1.39 | 2e-16 4e-13 | 18 x 38 nuclear paraspeckle assembly transcript 1 [Source:HGNC Symbol;Acc:HGNC:23059] |
| 20 | 227690_at | -1.43 | 2e-16 4e-13 | 34 x 1 gamma-aminobutyric acid type A receptor beta3 subunit [Source:HGNC Symbol;Acc:HGNC:23059] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 10.52 | NULL | 564 | BP immune system process |
| 2 | 9.68 | NULL | 417 | BP innate immune response |
| 3 | 9.64 | NULL | 460 | BP neutrophil degranulation |
| 4 | 8.83 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide antigen fragments |
| 5 | 7.76 | NULL | 388 | BP immune response |
| 6 | 7.45 | NULL | 43 | BP antigen processing and presentation |
| 7 | 7.38 | NULL | 364 | BP inflammatory response |
| 8 | 6.91 | NULL | 184 | BP defense response to virus |
| 9 | 6.42 | NULL | 394 | BP cell division |
| 10 | 6.03 | NULL | 23 | BP proximal/distal pattern formation |
| 11 | 5.96 | NULL | 41 | BP negative regulation of viral genome replication |
| 12 | 5.7 | NULL | 155 | BP regulation of immune response |
| 13 | 5.49 | NULL | 59 | BP positive regulation of T cell proliferation |
| 14 | 5.34 | NULL | 13 | BP immunoglobulin mediated immune response |
| 15 | 5.33 | NULL | 231 | BP extracellular matrix organization |
| 16 | 5.24 | NULL | 109 | BP response to virus |
| 17 | 5.03 | NULL | 95 | BP anterior/posterior pattern specification |
| 18 | 5.01 | NULL | 141 | BP regulation of cell shape |
| 19 | 4.96 | NULL | 118 | BP platelet degranulation |
| 20 | 4.94 | NULL | 630 | BP cell cycle |
| <i>Underexpressed</i> | | | | |
| 1 | -11 | NULL | 574 | BP synapse |
| 2 | -10.53 | NULL | 236 | BP chemical synaptic transmission |
| 3 | -9.13 | NULL | 240 | BP postsynaptic membrane |
| 4 | -6.53 | NULL | 27 | BP glutamate secretion |
| 5 | -6.22 | NULL | 51 | BP neurotransmitter secretion |
| 6 | -6.11 | NULL | 28 | BP synaptic vesicle exocytosis |
| 7 | -6.03 | NULL | 27 | BP gamma-aminobutyric acid signaling pathway |
| 8 | -5.76 | NULL | 505 | BP nervous system development |
| 9 | -5.66 | NULL | 13 | BP regulation of short-term neuronal synaptic plasticity |
| 10 | -5.42 | NULL | 30 | BP sterol biosynthetic process |
| 11 | -5.37 | NULL | 13 | BP synaptic transmission, GABAergic |
| 12 | -5.14 | NULL | 627 | BP ion transport |
| 13 | -5.01 | NULL | 23 | BP synaptic membrane adhesion |
| 14 | -4.95 | NULL | 50 | BP nervous system process |
| 15 | -4.86 | NULL | 48 | BP long-term synaptic potentiation |
| 16 | -4.75 | NULL | 61 | BP positive regulation of synapse assembly |
| 17 | -4.67 | NULL | 1435 | BP mitochondrion |
| 18 | -4.66 | NULL | 36 | BP cellular response to BMP stimulus |
| 19 | -4.65 | NULL | 131 | BP presynapse |
| 20 | -4.64 | NULL | 249 | BP brain development |

p-values

