

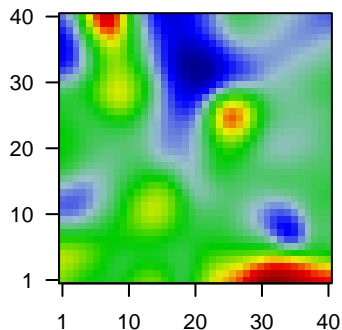
3741H

Global Summary

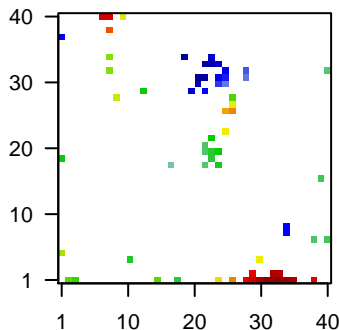
%DE = 0.07
 # genes with fdr < 0.2 = 2158 (1384 + / 774 -)
 # genes with fdr < 0.1 = 1587 (1040 + / 547 -)
 # genes with fdr < 0.05 = 1185 (786 + / 399 -)
 # genes with fdr < 0.01 = 714 (485 + / 229 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.15
 <p-value> = 0.23
 <fdr> = 0.93

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|--------------|---------|-------|---------|---------------------------------------------------------------------|
| 1 | 1552455_at | -1.45 | 2e-16 | 4e-13 | 1 x 37 prune homolog 2 with BCH domain [Source:HGNC Symbol;A |
| 2 | 1553415_at | 1.67 | 2e-16 | 4e-13 | 30 x 1 solute carrier family 17 member 8 [Source:HGNC Symbol;Acc |
| 3 | 1555230_a_a | 1.57 | 2e-16 | 4e-13 | 33 x 1 potassium voltage-gated channel interacting protein 2 [Sourc |
| 4 | 1556573_s_at | 1.71 | 2e-16 | 4e-13 | 30 x 1 novel transcript |
| 5 | 201289_at | -1.12 | 2e-16 | 4e-13 | 25 x 32 cellular communication network factor 1 [Source:HGNC Symt |
| 6 | 201909_at | -1.78 | 2e-16 | 4e-13 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:I |
| 7 | 203548_s_at | -0.87 | 2e-16 | 4e-13 | 26 x 28 lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677] |
| 8 | 203549_s_at | -0.87 | 2e-16 | 4e-13 | 26 x 28 lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677] |
| 9 | 204179_at | 1.69 | 2e-16 | 4e-13 | 9 x 28 myoglobin [Source:HGNC Symbol;Acc:HGNC:6915] |
| 10 | 204563_at | 1.2 | 2e-16 | 4e-13 | 26 x 27 selectin L [Source:HGNC Symbol;Acc:HGNC:10720] |
| 11 | 204713_s_at | 2.04 | 2e-16 | 4e-13 | 8 x 40 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542 |
| 12 | 204714_s_at | 1.72 | 2e-16 | 4e-13 | 30 x 1 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542 |
| 13 | 205000_at | -1.74 | 2e-16 | 4e-13 | 18 x 1 DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:t |
| 14 | 205100_at | -1.12 | 2e-16 | 4e-13 | 24 x 31 glutamine-fructose-6-phosphate transaminase 2 [Source:H |
| 15 | 205168_at | -1.22 | 2e-16 | 4e-13 | 23 x 33 discoidin domain receptor tyrosine kinase 2 [Source:HGNC S |
| 16 | 206700_s_at | -1.87 | 2e-16 | 4e-13 | 18 x 1 lysine demethylase 5D [Source:HGNC Symbol;Acc:HGNC:11 |
| 17 | 207455_at | 1.61 | 2e-16 | 4e-13 | 22 x 18 purinergic receptor P2Y1 [Source:HGNC Symbol;Acc:HGNC: |
| 18 | 209101_at | -0.98 | 2e-16 | 4e-13 | 11 x 4 cellular communication network factor 2 [Source:HGNC Symt |
| 19 | 214218_s_at | 1.99 | 2e-16 | 4e-13 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HG |
| 20 | 221319_at | 1.85 | 2e-16 | 4e-13 | 2 x 1 protocadherin beta 8 [Source:HGNC Symbol;Acc:HGNC:869: |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|-----------------------------------------------------------------------|
| <i>Overexpressed</i> | | | | |
| 1 | 8.23 | NULL | 240 | BP postsynaptic membrane |
| 2 | 8.1 | NULL | 574 | BP synapse |
| 3 | 7.31 | NULL | 1435 | BP mitochondrion |
| 4 | 7 | NULL | 505 | BP nervous system development |
| 5 | 6.5 | NULL | 236 | BP chemical synaptic transmission |
| 6 | 6.22 | NULL | 50 | BP nervous system process |
| 7 | 6.12 | NULL | 13 | BP synaptic transmission, GABAergic |
| 8 | 5.7 | NULL | 27 | BP gamma-aminobutyric acid signaling pathway |
| 9 | 5.38 | NULL | 12 | BP regulation of postsynaptic neurotransmitter receptor activity |
| 10 | 5.33 | NULL | 83 | BP mitochondrial translational elongation |
| 11 | 5.33 | NULL | 85 | BP mitochondrial translational termination |
| 12 | 4.82 | NULL | 29 | BP negative regulation of insulin secretion |
| 13 | 4.76 | NULL | 16 | BP L-glutamate transmembrane transport |
| 14 | 4.46 | NULL | 13 | BP negative regulation of transcription regulatory region DNA binding |
| 15 | 4.45 | NULL | 627 | BP ion transport |
| 16 | 4.44 | NULL | 22 | BP regulation of AMPA receptor activity |
| 17 | 4.17 | NULL | 249 | BP brain development |
| 18 | 4.17 | NULL | 31 | BP adult behavior |
| 19 | 4.09 | NULL | 12 | BP lysine catabolic process |
| 20 | 4.03 | NULL | 108 | BP neuron migration |
| <i>Underexpressed</i> | | | | |
| 1 | -6.96 | NULL | 364 | BP inflammatory response |
| 2 | -6.44 | NULL | 564 | BP immune system process |
| 3 | -6.21 | NULL | 388 | BP immune response |
| 4 | -5.7 | NULL | 289 | BP cytokine-mediated signaling pathway |
| 5 | -5.55 | NULL | 222 | BP adaptive immune response |
| 6 | -5.44 | NULL | 460 | BP neutrophil degranulation |
| 7 | -5.13 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide |
| 8 | -4.82 | NULL | 44 | BP collagen fibril organization |
| 9 | -4.78 | NULL | 231 | BP extracellular matrix organization |
| 10 | -4.73 | NULL | 155 | BP regulation of immune response |
| 11 | -4.56 | NULL | 93 | BP integrin-mediated signaling pathway |
| 12 | -4.33 | NULL | 417 | BP innate immune response |
| 13 | -4.31 | NULL | 49 | BP positive regulation of fibroblast proliferation |
| 14 | -4.27 | NULL | 66 | BP response to mechanical stimulus |
| 15 | -4.26 | NULL | 11 | BP chondrocyte proliferation |
| 16 | -4.19 | NULL | 151 | BP defense response to bacterium |
| 17 | -4.14 | NULL | 66 | BP phagocytosis |
| 18 | -4.13 | NULL | 72 | BP positive regulation of inflammatory response |
| 19 | -4.07 | NULL | 89 | BP Fc-gamma receptor signaling pathway involved in phagocytosis |
| 20 | -4.07 | NULL | 64 | BP regulation of complement activation |

p-values

