

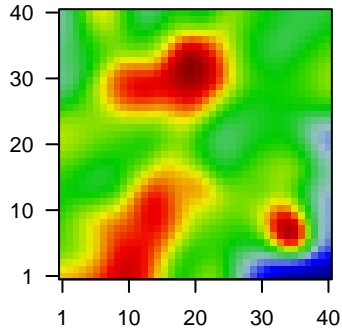
2580N

Global Summary

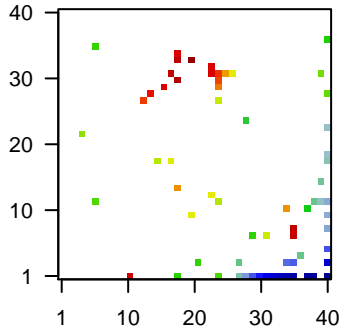
%DE = 0.08
 # genes with fdr < 0.2 = 2244 (1142 + / 1102 -)
 # genes with fdr < 0.1 = 1493 (717 + / 776 -)
 # genes with fdr < 0.05 = 1039 (473 + / 566 -)
 # genes with fdr < 0.01 = 553 (227 + / 326 -)
 # genes in genesets = 16360

<FC> = 0
 <t-score> = 0.04
 <p-value> = 0.23
 <fdr> = 0.92

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr p-value | Description Metagene |
|------|--------------|---------|-------------|---|
| 1 | 1553830_s_at | 1.94 | 2e-16 7e-13 | 4 x 22 MAGE family member A2B [Source:HGNC Symbol;Acc:HGNC:1553830] |
| 2 | 1557369_a_at | 1.94 | 2e-16 7e-13 | 24 x 31 long intergenic non-protein coding RNA 698 [Source:HGNC Symbol;Acc:HGNC:1557369] |
| 3 | 201909_at | -1.68 | 2e-16 7e-13 | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909] |
| 4 | 204465_s_at | -1.24 | 2e-16 7e-13 | 34 x 1 internexin neuronal intermediate filament protein alpha [Source:HGNC Symbol;Acc:HGNC:204465] |
| 5 | 209942_x_at | 3.15 | 2e-16 7e-13 | 20 x 10 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:209942] |
| 6 | 210467_x_at | 2.81 | 2e-16 7e-13 | 14 x 28 MAGE family member A12 [Source:HGNC Symbol;Acc:HGNC:210467] |
| 7 | 214603_at | 2.02 | 2e-16 7e-13 | 40 x 28 MAGE family member A2B [Source:HGNC Symbol;Acc:HGNC:214603] |
| 8 | 214612_x_at | 2.85 | 2e-16 7e-13 | 24 x 12 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:214612] |
| 9 | 216370_s_at | 2 | 2e-16 7e-13 | 23 x 31 transketolase like 1 [Source:HGNC Symbol;Acc:HGNC:216370] |
| 10 | 218720_x_at | -1.52 | 2e-16 7e-13 | 34 x 1 seizure related 6 homolog like 2 [Source:HGNC Symbol;Acc:HGNC:218720] |
| 11 | 220445_s_at | 2.14 | 2e-16 7e-13 | 13 x 27 CSAG family member 3 [Source:HGNC Symbol;Acc:HGNC:220445] |
| 12 | 223183_at | -1.11 | 2e-16 7e-13 | 38 x 12 1-acylglycerol-3-phosphate O-acyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:223183] |
| 13 | 224588_at | 2.1 | 2e-16 7e-13 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588] |
| 14 | 227671_at | 2 | 2e-16 7e-13 | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:227671] |
| 15 | 229651_at | -1.67 | 2e-16 7e-13 | 30 x 1 seizure related 6 homolog [Source:HGNC Symbol;Acc:HGNC:229651] |
| 16 | 230262_at | -1.56 | 2e-16 7e-13 | 35 x 1 ST8 alpha-N-acetylneuraminide alpha-2,8-sialyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:230262] |
| 17 | 233337_s_at | -1.63 | 2e-16 7e-13 | 34 x 1 seizure related 6 homolog like 2 [Source:HGNC Symbol;Acc:HGNC:233337] |
| 18 | 203839_s_at | -1.04 | 4e-16 3e-11 | 29 x 1 tyrosine kinase non receptor 2 [Source:HGNC Symbol;Acc:HGNC:203839] |
| 19 | 232028_at | -1.24 | 4e-16 3e-11 | 6 x 35 zinc finger protein 678 [Source:HGNC Symbol;Acc:HGNC:232028] |
| 20 | 229300_at | -1.69 | 1e-15 3e-11 | 38 x 1 RAB3C, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:229300] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 12.74 | NULL | 1435 | BP mitochondrion |
| 2 | 9.51 | NULL | 460 | BP neutrophil degranulation |
| 3 | 8.39 | NULL | 85 | BP mitochondrial translational termination |
| 4 | 8.38 | NULL | 83 | BP mitochondrial translational elongation |
| 5 | 7.13 | NULL | 671 | BP oxidation-reduction process |
| 6 | 6.49 | NULL | 88 | BP electron transport chain |
| 7 | 6.31 | NULL | 276 | BP translation |
| 8 | 6.22 | NULL | 75 | BP electron transfer activity |
| 9 | 6.21 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide antigen fragments |
| 10 | 5.88 | NULL | 67 | BP antigen processing and presentation of exogenous peptide antigen fragments |
| 11 | 5.63 | NULL | 75 | BP cellular oxidant detoxification |
| 12 | 5.45 | NULL | 59 | BP mitochondrial respiratory chain complex I assembly |
| 13 | 5.39 | NULL | 388 | BP immune response |
| 14 | 5.36 | NULL | 43 | BP antigen processing and presentation |
| 15 | 5.08 | NULL | 18 | BP glutathione peroxidase activity |
| 16 | 5.07 | NULL | 15 | BP positive regulation of interleukin-8 secretion |
| 17 | 4.96 | NULL | 31 | BP cellular response to cadmium ion |
| 18 | 4.9 | NULL | 36 | BP mitochondrial translation |
| 19 | 4.81 | NULL | 564 | BP immune system process |
| 20 | 4.79 | NULL | 659 | BP apoptotic process |
| <i>Underexpressed</i> | | | | |
| 1 | -13.57 | NULL | 574 | BP synapse |
| 2 | -10.33 | NULL | 240 | BP postsynaptic membrane |
| 3 | -10.18 | NULL | 505 | BP nervous system development |
| 4 | -9.24 | NULL | 4278 | BP plasma membrane |
| 5 | -8.57 | NULL | 236 | BP chemical synaptic transmission |
| 6 | -8.53 | NULL | 627 | BP ion transport |
| 7 | -7.74 | NULL | 149 | BP regulation of ion transmembrane transport |
| 8 | -7.7 | NULL | 22 | BP regulation of AMPA receptor activity |
| 9 | -7.45 | NULL | 12 | BP regulation of postsynaptic neurotransmitter receptor activity |
| 10 | -7.17 | NULL | 61 | BP positive regulation of synapse assembly |
| 11 | -7.07 | NULL | 64 | BP synapse assembly |
| 12 | -6.79 | NULL | 48 | BP synapse organization |
| 13 | -6.65 | NULL | 79 | BP memory |
| 14 | -6.52 | NULL | 73 | BP modulation of chemical synaptic transmission |
| 15 | -6.5 | NULL | 125 | BP calcium ion transmembrane transport |
| 16 | -6.49 | NULL | 51 | BP regulation of synaptic plasticity |
| 17 | -6.42 | NULL | 28 | BP positive regulation of synaptic transmission, glutamatergic |
| 18 | -6.25 | NULL | 131 | BP potassium ion transport |
| 19 | -6.24 | NULL | 51 | BP neurotransmitter secretion |
| 20 | -6.17 | NULL | 69 | BP sodium ion transmembrane transport |

p-values

