

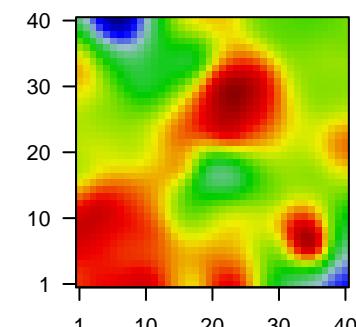
9076M

Global Summary

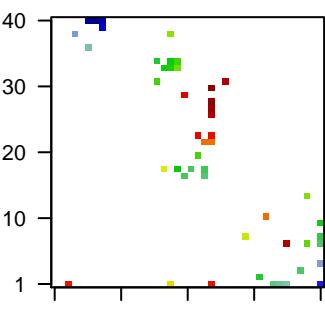
%DE = 0.07
 # genes with fdr < 0.2 = 1978 (886 + / 1092 -)
 # genes with fdr < 0.1 = 1483 (632 + / 851 -)
 # genes with fdr < 0.05 = 1075 (453 + / 622 -)
 # genes with fdr < 0.01 = 639 (257 + / 382 -)
 # genes in genesets = 16360

$\langle FC \rangle = 0$
 $\langle t\text{-score} \rangle = 0.14$
 $\langle p\text{-value} \rangle = 0.24$
 $\langle fdr \rangle = 0.93$

Portrait



Top 100 DE genes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description | Metagene |
|----------------------|--------------|---------|-------|---------|-------------|--|
| Overexpressed | | | | | | |
| 1 | 1554663_a_a' | 2.45 | 2e-16 | 4e-13 | 32 x 11 | nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC] |
| 2 | 1555804_a_a' | 1.81 | 2e-16 | 4e-13 | 22 x 23 | mitogen-activated protein kinase kinase kinase 19 [Source:HGNC Symbol;Acc:HGNC] |
| 3 | 1558678_s_at | -0.94 | 2e-16 | 4e-13 | 7 x 40 | metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC] |
| 4 | 201340_s_at | -1.16 | 2e-16 | 4e-13 | 40 x 1 | ectodermal-neural cortex 1 [Source:HGNC Symbol;Acc:HGNC] |
| 5 | 201909_at | -1.59 | 2e-16 | 4e-13 | 18 x 1 | ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC] |
| 6 | 202376_at | -1.08 | 2e-16 | 4e-13 | 19 x 34 | serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC] |
| 7 | 203348_s_at | -1 | 2e-16 | 4e-13 | 23 x 17 | ETS variant 5 [Source:HGNC Symbol;Acc:HGNC:3494] |
| 8 | 203849_s_at | -1.3 | 2e-16 | 4e-13 | 7 x 40 | kinesin family member 1A [Source:HGNC Symbol;Acc:HGNC] |
| 9 | 204533_at | 2.22 | 2e-16 | 4e-13 | 18 x 33 | C-X-C motif chemokine ligand 10 [Source:HGNC Symbol;Acc:HGNC] |
| 10 | 205000_at | -1.8 | 2e-16 | 4e-13 | 18 x 1 | DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:HGNC] |
| 11 | 207323_s_at | 0.89 | 2e-16 | 4e-13 | 35 x 7 | myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925] |
| 12 | 209072_at | 0.79 | 2e-16 | 4e-13 | 35 x 7 | myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925] |
| 13 | 210163_at | 1.84 | 2e-16 | 4e-13 | 16 x 31 | |
| 14 | 211122_s_at | 2.1 | 2e-16 | 4e-13 | 19 x 18 | C-X-C motif chemokine ligand 11 [Source:HGNC Symbol;Acc:HGNC] |
| 15 | 214218_s_at | 2.52 | 2e-16 | 4e-13 | 17 x 18 | X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC] |
| 16 | 214464_at | -1.57 | 2e-16 | 4e-13 | 7 x 40 | CDC42 binding protein kinase alpha [Source:HGNC Symbol;Acc:HGNC] |
| 17 | 221728_x_at | 2.21 | 2e-16 | 4e-13 | 17 x 18 | X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC] |
| 18 | 223940_x_at | -1.13 | 2e-16 | 4e-13 | 6 x 40 | metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC] |
| 19 | 224567_x_at | -0.86 | 2e-16 | 4e-13 | 6 x 40 | metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC] |
| 20 | 224568_x_at | -1.3 | 2e-16 | 4e-13 | 6 x 40 | metastasis associated lung adenocarcinoma transcript 1 [Source:HGNC Symbol;Acc:HGNC] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| Overexpressed | | | | |
| 1 | 7.34 | NULL | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 2 | 7.09 | NULL | 1145 | BP regulation of transcription by RNA polymerase II |
| 3 | 6.94 | NULL | 1387 | BP regulation of transcription, DNA-templated |
| 4 | 6.7 | NULL | 11 | BP T cell chemotaxis |
| 5 | 6.09 | NULL | 24 | BP leukocyte chemotaxis |
| 6 | 5.5 | NULL | 151 | BP cellular response to lipopolysaccharide |
| 7 | 5.13 | NULL | 6202 | BP cytoplasm |
| 8 | 4.94 | NULL | 26 | BP positive regulation of interleukin-8 production |
| 9 | 4.8 | NULL | 13 | BP central nervous system myelination |
| 10 | 4.75 | NULL | 31 | BP cellular response to cadmium ion |
| 11 | 4.72 | NULL | 843 | BP DNA-binding transcription factor activity |
| 12 | 4.47 | NULL | 12 | BP negative regulation by host of viral transcription |
| 13 | 4.32 | NULL | 175 | BP regulation of cell population proliferation |
| 14 | 4.28 | NULL | 40 | BP regulation of neurogenesis |
| 15 | 4.24 | NULL | 10 | BP negative regulation of inclusion body assembly |
| 16 | 4.17 | NULL | 1086 | BP positive regulation of transcription by RNA polymerase II |
| 17 | 4.13 | NULL | 43 | BP chemokine activity |
| 18 | 4.12 | NULL | 15 | BP lipoxygenase pathway |
| 19 | 4.07 | NULL | 38 | BP positive regulation of protein import into nucleus |
| 20 | 4.05 | NULL | 630 | BP cell cycle |
| Underexpressed | | | | |
| 1 | -7.31 | NULL | 236 | BP chemical synaptic transmission |
| 2 | -7.19 | NULL | 574 | BP synapse |
| 3 | -6.02 | NULL | 51 | BP neurotransmitter secretion |
| 4 | -5.93 | NULL | 43 | BP mitochondrial electron transport, NADH to ubiquinone |
| 5 | -5.72 | NULL | 627 | BP ion transport |
| 6 | -5.53 | NULL | 83 | BP mitochondrial translational elongation |
| 7 | -5.51 | NULL | 59 | BP mitochondrial respiratory chain complex I assembly |
| 8 | -5.49 | NULL | 276 | BP translation |
| 9 | -5.32 | NULL | 85 | BP mitochondrial translational termination |
| 10 | -5.32 | NULL | 17 | BP antigen processing and presentation of peptide or polysaccharide antigen to T cell receptor |
| 11 | -5.24 | NULL | 51 | BP regulation of synaptic vesicle exocytosis |
| 12 | -5.16 | NULL | 28 | BP synaptic vesicle exocytosis |
| 13 | -5.15 | NULL | 7387 | BP membrane |
| 14 | -5.14 | NULL | 13 | BP synaptic transmission, GABAergic |
| 15 | -5.08 | NULL | 240 | BP postsynaptic membrane |
| 16 | -4.6 | NULL | 4278 | BP plasma membrane |
| 17 | -4.57 | NULL | 657 | BP calcium ion binding |
| 18 | -4.42 | NULL | 25 | BP cytochrome-c oxidase activity |
| 19 | -4.35 | NULL | 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 20 | -4.29 | NULL | 57 | BP negative regulation of catalytic activity |

