

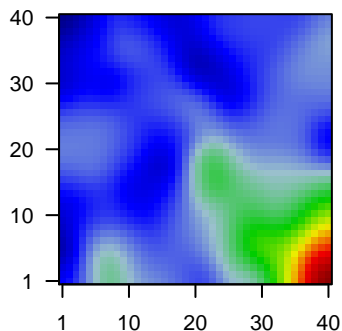
# group 3

## Global Summary

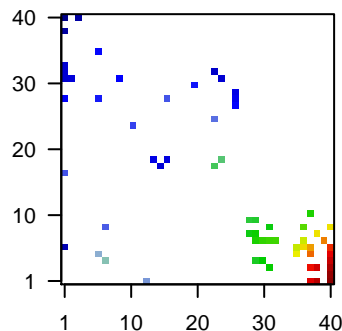
%DE = 0.56  
 # genes with fdr < 0.2 = 19699 ( 9225 + / 10474 -)  
 # genes with fdr < 0.1 = 12760 ( 6595 + / 6165 -)  
 # genes with fdr < 0.05 = 7576 ( 4402 + / 3174 -)  
 # genes with fdr < 0.01 = 1394 ( 1021 + / 373 -)  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0.01  
 <p-value> = 0.09  
 <fdr> = 0.44

Portrait



Top 100 DE genes



## Global Genelist

| Rank | ID           | log(FC) | fdr p-value | Description | Metagene  |
|------|--------------|---------|-------------|-------------|---|
| 1    | 227417_at    | 0.67    | 5e-07       | 0.004       | 40 x 5 mitochondrial amidoxime reducing component 2 [Source:HGNC]   |
| 2    | 228365_at    | 1.17    | 6e-07       | 0.004       | 40 x 5 copine 8 [Source:HGNC Symbol;Acc:HGNC:23498]                 |
| 3    | 226863_at    | 1.13    | 1e-06       | 0.004       | 40 x 5 family with sequence similarity 110 member C [Source:HGNC]   |
| 4    | 208600_s_at  | -0.23   | 1e-06       | 0.004       | 11 x 24 G protein-coupled receptor 39 [Source:HGNC Symbol;Acc:H]    |
| 5    | 200862_at    | 0.57    | 2e-06       | 0.004       | 36 x 6 24-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:     |
| 6    | 244868_at    | -0.95   | 2e-06       | 0.004       | 1 x 40  |
| 7    | 215943_at    | -0.9    | 2e-06       | 0.004       | 1 x 40  |
| 8    | 238878_at    | 1.1     | 2e-06       | 0.004       | 40 x 1 aristaless related homeobox [Source:HGNC Symbol;Acc:HGNC]    |
| 9    | 223823_at    | 0.57    | 3e-06       | 0.004       | 31 x 3 potassium calcium-activated channel subfamily M regulatory   |
| 10   | 226568_at    | 0.57    | 3e-06       | 0.004       | 30 x 7 family with sequence similarity 102 member B [Source:HGNC]   |
| 11   | 242524_at    | 1.43    | 3e-06       | 0.004       | 40 x 1 cerebellin 4 precursor [Source:HGNC Symbol;Acc:HGNC:162]     |
| 12   | 219354_at    | 0.76    | 3e-06       | 0.004       | 39 x 7 kelch like family member 26 [Source:HGNC Symbol;Acc:HGNC]    |
| 13   | 231807_at    | 0.85    | 3e-06       | 0.004       | 40 x 4 KIAA1217 [Source:HGNC Symbol;Acc:HGNC:25428]                 |
| 14   | 219949_at    | 1.06    | 3e-06       | 0.004       | 40 x 4 leucine rich repeat containing 2 [Source:HGNC Symbol;Acc:H]  |
| 15   | 234982_at    | 0.24    | 3e-06       | 0.004       | 6 x 5 ubiquitin protein ligase E3 component n-recognin 3 [Source:H] |
| 16   | 1560091_a_at | -0.56   | 3e-06       | 0.004       | 1 x 6 PHD finger protein 21B [Source:HGNC Symbol;Acc:HGNC:21]       |
| 17   | 206529_x_at  | 1.16    | 3e-06       | 0.004       | 40 x 6 solute carrier family 26 member 4 [Source:HGNC Symbol;Acc:   |
| 18   | 204888_s_at  | 0.75    | 4e-06       | 0.004       | 40 x 9 neuralized E3 ubiquitin protein ligase 1 [Source:HGNC Symb]  |
| 19   | 212992_at    | 1.16    | 4e-06       | 0.004       | 40 x 3 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:HGNC:2]        |
| 20   | 237157_at    | -0.52   | 4e-06       | 0.004       | 1 x 31  |

## Global Geneset Analysis

| Rank                  | GSZ   | p-value | #all | Geneset   |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i>  |       |         |      |   |
| 1                     | 18.8  | NULL    | 574  | BP synapse  |
| 2                     | 18.77 | NULL    | 7387 | BP membrane   |
| 3                     | 17.94 | NULL    | 4278 | BP plasma membrane  |
| 4                     | 15.1  | NULL    | 236  | BP chemical synaptic transmission                                     |
| 5                     | 13.44 | NULL    | 240  | BP postsynaptic membrane  |
| 6                     | 11.44 | NULL    | 627  | BP ion transport  |
| 7                     | 9.72  | NULL    | 505  | BP nervous system development   |
| 8                     | 9.31  | NULL    | 51   | BP neurotransmitter secretion   |
| 9                     | 9.27  | NULL    | 28   | BP synaptic vesicle exocytosis  |
| 10                    | 8.56  | NULL    | 119  | BP postsynapse  |
| 11                    | 8.53  | NULL    | 131  | BP presynapse   |
| 12                    | 8.44  | NULL    | 1500 | BP signal transduction  |
| 13                    | 8.41  | NULL    | 615  | BP transmembrane transport  |
| 14                    | 8.38  | NULL    | 33   | BP regulation of exocytosis   |
| 15                    | 8.31  | NULL    | 118  | BP exocytosis   |
| 16                    | 8.24  | NULL    | 27   | BP glutamate secretion  |
| 17                    | 8.06  | NULL    | 149  | BP regulation of ion transmembrane transport                          |
| 18                    | 7.98  | NULL    | 131  | BP potassium ion transport  |
| 19                    | 7.81  | NULL    | 48   | BP long-term synaptic potentiation                                    |
| 20                    | 7.8   | NULL    | 133  | BP protein localization to plasma membrane                            |
| <i>Underexpressed</i> |       |         |      |   |
| 1                     | -8.69 | NULL    | 90   | BP viral transcription  |
| 2                     | -8.5  | NULL    | 120  | BP translational initiation   |
| 3                     | -8.36 | NULL    | 276  | BP translation  |
| 4                     | -8.34 | NULL    | 229  | BP mRNA splicing, via spliceosome                                     |
| 5                     | -8.16 | NULL    | 69   | BP SRP-dependent cotranslational protein targeting to membrane        |
| 6                     | -7.89 | NULL    | 98   | BP nuclear-transcribed mRNA catabolic process, nonsense-mediated      |
| 7                     | -7.84 | NULL    | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-speci |
| 8                     | -7.63 | NULL    | 1387 | BP regulation of transcription, DNA-templated                         |
| 9                     | -7.44 | NULL    | 1145 | BP regulation of transcription by RNA polymerase II                   |
| 10                    | -7.12 | NULL    | 366  | BP DNA repair   |
| 11                    | -7.09 | NULL    | 152  | BP rRNA processing  |
| 12                    | -6.73 | NULL    | 158  | BP DNA replication  |
| 13                    | -6.45 | NULL    | 279  | BP RNA splicing   |
| 14                    | -6.35 | NULL    | 358  | BP mRNA processing  |
| 15                    | -6.18 | NULL    | 484  | BP cellular response to DNA damage stimulus                           |
| 16                    | -5.89 | NULL    | 342  | BP chromatin organization   |
| 17                    | -5.86 | NULL    | 630  | BP cell cycle   |
| 18                    | -5.85 | NULL    | 1086 | BP positive regulation of transcription by RNA polymerase II          |
| 19                    | -5.42 | NULL    | 93   | BP ribosome biogenesis  |
| 20                    | -5.39 | NULL    | 564  | BP immune system process  |

p-values

