

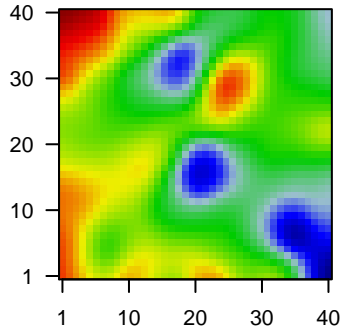
# 3853K

## Global Summary

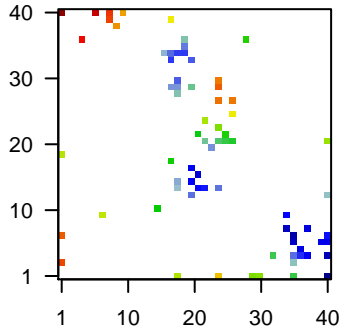
%DE = 0.07  
 # genes with fdr < 0.2 = 1851 ( 844 + / 1007 -)  
 # genes with fdr < 0.1 = 1336 ( 575 + / 761 -)  
 # genes with fdr < 0.05 = 911 ( 362 + / 549 -)  
 # genes with fdr < 0.01 = 500 ( 176 + / 324 -)  
 # genes in genesets = 16360

<FC> = 0  
 <t-score> = 0.09  
 <p-value> = 0.24  
 <fdr> = 0.93

Portrait



Top 100 DE genes



## Global Genelist

| Rank | ID           | log(FC) | fdr   | p-value | Description   |
|------|--------------|---------|-------|---------|---|
| 1    | 1568870_at   | -1.81   | 2e-16 | 4e-13   | 35 x 3 solute carrier family 24 member 4 [Source:HGNC Symbol;Acc:HGNC:156887]                     |
| 2    | 1569110_x_at | -1.05   | 2e-16 | 4e-13   | 7 x 10 programmed cell death 6 (PDCD6) pseudogene   |
| 3    | 201909_at    | -1.75   | 2e-16 | 4e-13   | 18 x 1 ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909]                       |
| 4    | 202284_s_at  | -1.31   | 2e-16 | 4e-13   | 21 x 14 cyclin dependent kinase inhibitor 1A [Source:HGNC Symbol;Acc:HGNC:202284]                 |
| 5    | 202376_at    | -1.22   | 2e-16 | 4e-13   | 19 x 34 serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC:202376]                             |
| 6    | 203903_s_at  | -1.51   | 2e-16 | 4e-13   | 37 x 8 hephaestin [Source:HGNC Symbol;Acc:HGNC:4866]  |
| 7    | 205000_at    | -1.88   | 2e-16 | 4e-13   | 18 x 1 DEAD-box helicase 3 Y-linked [Source:HGNC Symbol;Acc:HGNC:205000]                          |
| 8    | 205856_at    | -1.68   | 2e-16 | 4e-13   | 24 x 27 solute carrier family 14 member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:HGNC:205856] |
| 9    | 206395_at    | -1.66   | 2e-16 | 4e-13   | 29 x 1 diacylglycerol kinase gamma [Source:HGNC Symbol;Acc:HGNC:206395]                           |
| 10   | 207574_s_at  | -0.96   | 2e-16 | 4e-13   | 18 x 29 growth arrest and DNA damage inducible beta [Source:HGNC Symbol;Acc:HGNC:207574]          |
| 11   | 208951_at    | -1.07   | 2e-16 | 4e-13   | 25 x 22 aldehyde dehydrogenase 7 family member A1 [Source:HGNC Symbol;Acc:HGNC:208951]            |
| 12   | 210095_s_at  | -1.6    | 2e-16 | 4e-13   | 21 x 16 insulin like growth factor binding protein 3 [Source:HGNC Symbol;Acc:HGNC:210095]         |
| 13   | 210524_x_at  | -1.09   | 2e-16 | 4e-13   | 25 x 22 metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]                                     |
| 14   | 211597_s_at  | -1.3    | 2e-16 | 4e-13   | 40 x 7 HOP homeobox [Source:HGNC Symbol;Acc:HGNC:24961]   |
| 15   | 211964_at    | -1.07   | 2e-16 | 4e-13   | 20 x 17 collagen type IV alpha 2 chain [Source:HGNC Symbol;Acc:HGNC:211964]                       |
| 16   | 213592_at    | -1.23   | 2e-16 | 4e-13   | 19 x 36 apelin receptor [Source:HGNC Symbol;Acc:HGNC:339]   |
| 17   | 213629_x_at  | -1.04   | 2e-16 | 4e-13   | 25 x 22 metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]                                     |
| 18   | 214218_s_at  | 2.23    | 2e-16 | 4e-13   | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:214218]                       |
| 19   | 216336_x_at  | -0.9    | 2e-16 | 4e-13   | 25 x 21   |
| 20   | 221728_x_at  | 2.03    | 2e-16 | 4e-13   | 17 x 18 X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:221728]                       |

## Global Geneset Analysis

| Rank                  | GSZ    | p-value | #all | Geneset  |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i>  |        |         |      |  |
| 1                     | 9.13   | NULL    | 279  | BP RNA splicing  |
| 2                     | 9      | NULL    | 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 3                     | 8.74   | NULL    | 358  | BP mRNA processing   |
| 4                     | 8.6    | NULL    | 1387 | BP regulation of transcription, DNA-templated                            |
| 5                     | 8.12   | NULL    | 229  | BP mRNA splicing, via spliceosome  |
| 6                     | 8.09   | NULL    | 1145 | BP regulation of transcription by RNA polymerase II                      |
| 7                     | 6.61   | NULL    | 342  | BP chromatin organization  |
| 8                     | 5.14   | NULL    | 99   | BP mRNA export from nucleus  |
| 9                     | 5.05   | NULL    | 366  | BP DNA repair  |
| 10                    | 4.74   | NULL    | 61   | BP regulation of alternative mRNA splicing, via spliceosome              |
| 11                    | 4.66   | NULL    | 783  | BP negative regulation of transcription by RNA polymerase II             |
| 12                    | 4.65   | NULL    | 400  | BP chromatin binding   |
| 13                    | 4.5    | NULL    | 56   | BP mRNA 3'-end processing  |
| 14                    | 4.41   | NULL    | 12   | BP negative regulation of oligodendrocyte differentiation                |
| 15                    | 4.34   | NULL    | 541  | BP negative regulation of transcription, DNA-templated                   |
| 16                    | 4.19   | NULL    | 630  | BP cell cycle  |
| 17                    | 4.16   | NULL    | 11   | BP limb bud formation  |
| 18                    | 4.15   | NULL    | 41   | BP RNA export from nucleus   |
| 19                    | 4.15   | NULL    | 12   | BP planar cell polarity pathway involved in neural tube closure          |
| 20                    | 4.11   | NULL    | 394  | BP cell division   |
| <i>Underexpressed</i> |        |         |      |  |
| 1                     | -15.63 | NULL    | 7387 | BP membrane  |
| 2                     | -13.23 | NULL    | 4278 | BP plasma membrane   |
| 3                     | -10.37 | NULL    | 460  | BP neutrophil degranulation  |
| 4                     | -8.68  | NULL    | 21   | BP cellular response to copper ion                                       |
| 5                     | -8.37  | NULL    | 388  | BP immune response   |
| 6                     | -7.91  | NULL    | 254  | BP angiogenesis  |
| 7                     | -7.82  | NULL    | 1435 | BP mitochondrion   |
| 8                     | -7.8   | NULL    | 16   | BP negative regulation of growth   |
| 9                     | -7.78  | NULL    | 23   | BP cellular zinc ion homeostasis   |
| 10                    | -7.32  | NULL    | 17   | BP cellular response to zinc ion   |
| 11                    | -7.28  | NULL    | 657  | BP calcium ion binding   |
| 12                    | -6.97  | NULL    | 118  | BP platelet degranulation  |
| 13                    | -6.67  | NULL    | 152  | BP leukocyte migration   |
| 14                    | -6.5   | NULL    | 21   | BP tissue regeneration   |
| 15                    | -6.41  | NULL    | 671  | BP oxidation-reduction process   |
| 16                    | -6.27  | NULL    | 627  | BP ion transport   |
| 17                    | -6.18  | NULL    | 31   | BP cellular response to cadmium ion                                      |
| 18                    | -6.09  | NULL    | 20   | BP response to corticosterone  |
| 19                    | -6.02  | NULL    | 564  | BP immune system process   |
| 20                    | -5.99  | NULL    | 521  | BP lipid metabolic process   |

p-values

