

MPI-152

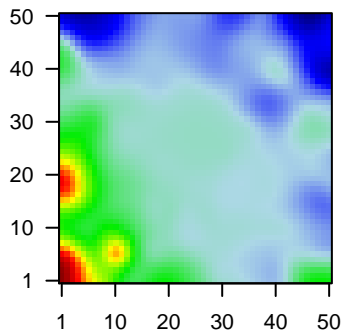
Global Summary

%DE = 0.05
 # genes with fdr < 0.2 = 627 (419 + / 208 -)
 # genes with fdr < 0.1 = 414 (295 + / 119 -)
 # genes with fdr < 0.05 = 341 (253 + / 88 -)
 # genes with fdr < 0.01 = 195 (159 + / 36 -)

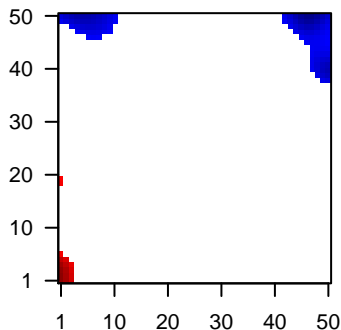
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.15
 <p-value> = 0.26
 <fdr> = 0.95

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr p-value | Description Metagene |
|------|-------------|---------|-------------|--|
| 1 | 206023_at | 2.03 | 2e-16 5e-13 | 33 x 46 neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859] |
| 2 | 207534_at | 1.94 | 2e-16 5e-13 | 1 x 16 MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 3 | 210551_s_at | 2.2 | 2e-16 5e-13 | 1 x 17 acetylserotonin O-methyltransferase [Source:HGNC Symbol;Acc:HGNC:7859] |
| 4 | 211430_s_at | 1.2 | 2e-16 5e-13 | 0 x 4 immunoglobulin heavy constant gamma 2 (G2m marker) [Source:HGNC Symbol;Acc:HGNC:7859] |
| 5 | 211644_x_at | 1.95 | 2e-16 5e-13 | 0 x 1 immunoglobulin kappa variable 3-20 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 6 | 214669_x_at | 0.96 | 2e-16 5e-13 | 0 x 3 |
| 7 | 216984_x_at | 1.92 | 2e-16 5e-13 | 10 x 5 |
| 8 | 221651_x_at | 0.9 | 2e-16 5e-13 | 0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:7859] |
| 9 | 221671_x_at | 0.87 | 2e-16 5e-13 | 0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:7859] |
| 10 | 209374_s_at | 0.83 | 4e-16 5e-12 | 0 x 22 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:7859] |
| 11 | 216401_x_at | 1.87 | 4e-16 5e-12 | 10 x 5 immunoglobulin kappa variable 1-37 (non-functional) [Source:HGNC Symbol;Acc:HGNC:7859] |
| 12 | 219360_s_at | 1.87 | 4e-16 5e-12 | 0 x 20 transient receptor potential cation channel subfamily M member 1 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 13 | 215176_x_at | 1.31 | 7e-16 9e-12 | 10 x 5 immunoglobulin kappa variable 1-39 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:7859] |
| 14 | 217022_s_at | 1.23 | 1e-15 9e-12 | 0 x 2 immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:HGNC:7859] |
| 15 | 202274_at | 1.6 | 2e-15 2e-11 | 0 x 4 actin, gamma 2, smooth muscle, enteric [Source:HGNC Symbol;Acc:HGNC:7859] |
| 16 | 217281_x_at | 1.82 | 3e-15 1e-10 | 10 x 5 immunoglobulin heavy variable 3-7 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 17 | 201909_at | -1.15 | 7e-15 2e-10 | 43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 18 | 211634_x_at | 1.76 | 2e-14 4e-09 | 10 x 5 immunoglobulin heavy variable 1-69 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 19 | 203980_at | 1.69 | 2e-13 7e-09 | 43 x 47 fatty acid binding protein 4 [Source:HGNC Symbol;Acc:HGNC:7859] |
| 20 | 212827_at | 0.76 | 5e-13 1e-08 | 41 x 44 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:7859] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 19.61 | NULL | 52 | BP complement activation, classical pathway |
| 2 | 19.3 | NULL | 44 | MF antigen binding |
| 3 | 18.32 | NULL | 589 | Colon Cancer, TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN |
| 4 | 17.11 | NULL | 447 | Glioma, ScoV_0.999_Sturm_E4_Mesenchymal_RTK1_PDGFR_A_DN |
| 5 | 17.05 | NULL | 39 | BP complement activation |
| 6 | 15.64 | NULL | 431 | BP immune system process |
| 7 | 15.43 | NULL | 85 | Lymphoma, Gha_DLBCL_UP |
| 8 | 15.36 | NULL | 53 | BP regulation of complement activation |
| 9 | 14.87 | NULL | 223 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 10 | 14.85 | NULL | 102 | Reference, B-cell |
| 11 | 14.53 | NULL | 336 | BP immune response |
| 12 | 14.35 | NULL | 161 | BP adaptive immune response |
| 13 | 14.06 | NULL | 32 | Reference, C5orf50es_1_1_Plasma Cells |
| 14 | 13.97 | NULL | 480 | Cancer, Lemcke_Colonc_Inflammation |
| 15 | 13.69 | NULL | 219 | GSEA C2MCLACHLAN_DENTAL_CARIES_DN |
| 16 | 13.31 | NULL | 317 | Cancer, SPANG_BCL6-index2 |
| 17 | 13.25 | NULL | 429 | GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP |
| 18 | 12.94 | NULL | 16 | MF immunoglobulin receptor binding |
| 19 | 12.93 | NULL | 67 | GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP |
| 20 | 12.72 | NULL | 116 | CC blood microparticle |
| <i>Underexpressed</i> | | | | |
| 1 | -11.03 | NULL | 7225 | Chromatin, state, fetal_midbrain_ReprPC |
| 2 | -10.04 | NULL | 5456 | Chromatin, state, Neuronal_Progenitor |
| 3 | -9.08 | NULL | 6997 | Chromatin, state, fetal_midbrain_K9K27me3 |
| 4 | -8.95 | NULL | 575 | GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP |
| 5 | -8.91 | NULL | 4683 | Chromatin, state, fetal_midbrain_HetRpts |
| 6 | -8.61 | NULL | 5529 | Lymphoma, Gha_Txn_elongation |
| 7 | -8.45 | NULL | 6068 | Chromatin, state, ESC_Endoderm |
| 8 | -8.1 | NULL | 9160 | Chromatin, state, Neuronal_Progenitor |
| 9 | -8.07 | NULL | 8641 | Chromatin, state, ESC_Endoderm |
| 10 | -7.98 | NULL | 3007 | Chromatin, state, Neuronal_Progenitor |
| 11 | -7.79 | NULL | 1578 | TF, ICGC_GabpPcr2_targets |
| 12 | -7.68 | NULL | 4528 | Chromatin, state, naive_cells_peripheral_blood_4_Tx |
| 13 | -7.55 | NULL | 6244 | Chromatin, state, Fibroblasts |
| 14 | -7.51 | NULL | 6034 | Chromatin, state, Fibroblasts |
| 15 | -7.49 | NULL | 3554 | Chromatin, state, Rpts_ESC_Endoderm |
| 16 | -7.47 | NULL | 7489 | Chromatin, state, T cells_peripheral_blood_5_TxWk |
| 17 | -7.47 | NULL | 1527 | GSEA C2JUJANA_BRCA1_PCC_NETWORK |
| 18 | -7.4 | NULL | 9 | GSEA C2RUNNE_GENDER_EFFECT_UP |
| 19 | -7.39 | NULL | 6099 | Chromatin, state, T cells_Tx |
| 20 | -7.23 | NULL | 6679 | Chromatin, state, Melanocytes |

p-values

