

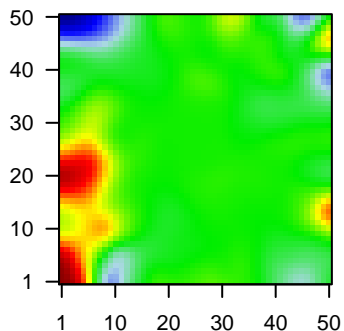
MPI-130

Global Summary

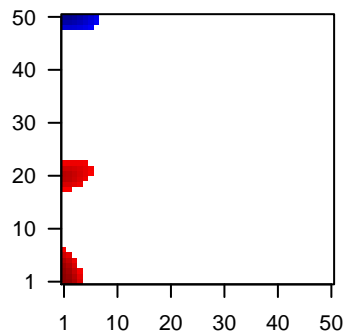
%DE = 0.04
 # genes with fdr < 0.2 = 486 (275 + / 211 -)
 # genes with fdr < 0.1 = 344 (200 + / 144 -)
 # genes with fdr < 0.05 = 276 (161 + / 115 -)
 # genes with fdr < 0.01 = 161 (105 + / 56 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0
 <p-value> = 0.27
 <fdr> = 0.96

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|---|
| 1 | 204489_s_at | 1.42 | 1e-15 | 3e-11 | 0 x 4 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1080] |
| 2 | 220068_at | -1.46 | 3e-15 | 6e-10 | 49 x 39 V-set pre-B cell surrogate light chain 3 [Source:HGNC Synt |
| 3 | 207391_s_at | -1.52 | 6e-14 | 6e-10 | 7 x 46 phosphatidylinositol-4-phosphate 5-kinase type 1 alpha (So |
| 4 | 212009_s_at | -1.31 | 7e-14 | 6e-10 | 1 x 49 stress induced phosphoprotein 1 [Source:HGNC Symbol;Acc |
| 5 | 214412_at | 2.18 | 9e-14 | 1e-09 | 4 x 17 H2A histone family member B2 [Source:HGNC Symbol;Acc:HGNC:1080] |
| 6 | 204490_s_at | 1.1 | 2e-13 | 7e-09 | 0 x 4 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1080] |
| 7 | 213400_s_at | -1.93 | 5e-13 | 1e-08 | 0 x 15 transducin beta like 1 X-linked [Source:HGNC Symbol;Acc:HGNC:1080] |
| 8 | 207534_at | 2.07 | 2e-12 | 1e-08 | 1 x 16 MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC:1080] |
| 9 | 200951_s_at | 2.05 | 2e-12 | 1e-08 | 0 x 20 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 10 | 209810_at | 2.05 | 3e-12 | 1e-08 | 0 x 22 surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080] |
| 11 | 209835_x_at | 1.06 | 3e-12 | 1e-08 | 0 x 4 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1080] |
| 12 | 217997_at | 2.03 | 4e-12 | 8e-08 | 5 x 22 pleckstrin homology like domain family A member 1 [Source:HGNC:1080] |
| 13 | 202953_at | 1.18 | 8e-12 | 1e-07 | 0 x 0 complement C1q B chain [Source:HGNC Symbol;Acc:HGNC:1080] |
| 14 | 201909_at | -1.26 | 2e-11 | 1e-07 | 43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:1080] |
| 15 | 212014_x_at | 1.05 | 2e-11 | 1e-07 | 0 x 4 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1080] |
| 16 | 202310_s_at | -1 | 3e-11 | 3e-07 | 9 x 0 collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:1080] |
| 17 | 214370_at | 1.93 | 4e-11 | 3e-07 | 24 x 14 |
| 18 | 201852_x_at | -0.92 | 5e-11 | 3e-07 | 8 x 0 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:1080] |
| 19 | 218000_s_at | 1.91 | 6e-11 | 4e-07 | 8 x 23 pleckstrin homology like domain family A member 1 [Source:HGNC:1080] |
| 20 | 202917_s_at | 1.34 | 8e-11 | 1e-06 | 0 x 0 S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:HGNC:1080] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 17.62 | NULL | 589 | Colon Cancer,TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN |
| 2 | 17.23 | NULL | 447 | Glioma ScoV_0.999_Sturm_E4_Mesenchymal_RTK1_PDGFR4_DN |
| 3 | 15.56 | NULL | 71 | Melanoma_Microsh_Macrophage specific genes-melanoma |
| 4 | 13.94 | NULL | 223 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 5 | 13.61 | NULL | 85 | Lymphoma_Ma_DLBCL UP |
| 6 | 13.6 | NULL | 317 | Cancer SPANG_BCL6-index2 |
| 7 | 13.07 | NULL | 219 | GSEA C2MCLACHLAN_DENTAL_CARIES_DN |
| 8 | 12.57 | NULL | 166 | GSEA C2VERHAAK_AML_WITH_NPM1_MUTATED_UP |
| 9 | 12.33 | NULL | 269 | Glioma ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 10 | 12.15 | NULL | 102 | Reference_Signature_B-cells |
| 11 | 11.58 | NULL | 78 | Melanoma_Microsh_expression higher in CAFs than in T-cells |
| 12 | 11.4 | NULL | 323 | BP inflammatory response |
| 13 | 10.99 | NULL | 187 | HM HALLMARK_INFLAMMATORY_RESPONSE |
| 14 | 10.89 | NULL | 173 | Lymphoma_Microsh_Light zone signature |
| 15 | 10.73 | NULL | 99 | Reference_Signature_1.5_Myeloid lineage |
| 16 | 10.68 | NULL | 85 | Lymphoma_MuKema_BCL2_DN_BCL6 UP |
| 17 | 10.53 | NULL | 22 | Lymphoma_MAVE_NFkB BL DN |
| 18 | 10.49 | NULL | 90 | GSEA C2BASSO_CD40_SIGNALING_UP |
| 19 | 10.3 | NULL | 186 | Cancer SPANG_LPS-index2 |
| 20 | 10.12 | NULL | 432 | Chromatin states peripheral blood_3_TxFln |
| <i>Underexpressed</i> | | | | |
| 1 | -9.63 | NULL | 282 | Glioma WILLSCHER_GBM_Verhaak-PNwt & CL_up |
| 2 | -9.1 | NULL | 136 | Reference_Signature_2.9_Cytoskeleton |
| 3 | -7.98 | NULL | 966 | GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 4 | -7.57 | NULL | 254 | GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP |
| 5 | -7.3 | NULL | 42 | GSEA C2HUMMEL_BURKITT'S_LYMPHOMA_UP |
| 6 | -7.19 | NULL | 400 | GSEA C2PUJANA_BRCA2_PCC_NETWORK |
| 7 | -7.16 | NULL | 1527 | GSEA C2PUJANA_BRCA1_PCC_NETWORK |
| 8 | -7.1 | NULL | 726 | GSEA C2PUJANA_CHEK2_PCC_NETWORK |
| 9 | -7.04 | NULL | 319 | Melanoma_Serber_wt/wt_melanoma-cells-SpotA |
| 10 | -6.94 | NULL | 99 | Lymphoma_Ma_BL UP |
| 11 | -6.67 | NULL | 58 | GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL |
| 12 | -6.62 | NULL | 192 | Lymphoma_Microsh_Dark zone signature |
| 13 | -6.51 | NULL | 955 | Lymphoma_SPANG_BCR UP |
| 14 | -6.48 | NULL | 1338 | GSEA C2DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP |
| 15 | -6.4 | NULL | 160 | GSEA C2PUJANA_XPRSS_INT_NETWORK |
| 16 | -6.36 | NULL | 63 | GSEA C2ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN |
| 17 | -6.33 | NULL | 169 | GSEA C2FUJII_YBX1_TARGETS_DN |
| 18 | -6.29 | NULL | 32 | Reference_Signature_1.1_Plasma Cells |
| 19 | -6.25 | NULL | 250 | GSEA C2HORIUCHI_WTAP_TARGETS_DN |
| 20 | -6.21 | NULL | 321 | GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN |

p-values

