

MPI-038

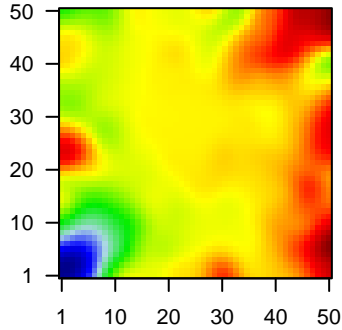
Global Summary

%DE = 0.05
 # genes with fdr < 0.2 = 670 (226 + / 444 -)
 # genes with fdr < 0.1 = 491 (163 + / 328 -)
 # genes with fdr < 0.05 = 417 (132 + / 285 -)
 # genes with fdr < 0.01 = 250 (83 + / 167 -)

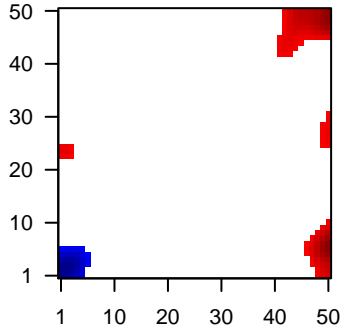
 # genes in genesets = 13152

<FC> = 0
 <t-score> = -0.09
 <p-value> = 0.24
 <fdr> = 0.95

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description | Metagene |
|------|-------------|---------|-------|---------|-------------|--|
| 1 | AFFX-r2-Hs1 | 2.63 | 2e-16 | 1e-13 | 49 x 47 | |
| 2 | 203915_at | -2.09 | 2e-16 | 1e-13 | 0 x 0 | C-X-C motif chemokine ligand 9 [Source:HGNC Symbol;Acc:HGNC:607] |
| 3 | 204416_x_at | -1.76 | 2e-16 | 1e-13 | 5 x 3 | apolipoprotein C1 [Source:HGNC Symbol;Acc:HGNC:607] |
| 4 | 204529_s_at | -1.93 | 2e-16 | 1e-13 | 3 x 6 | thymocyte selection associated high mobility group box [Source:HGNC Symbol;Acc:HGNC:607] |
| 5 | 204533_at | -1.71 | 2e-16 | 1e-13 | 0 x 0 | C-X-C motif chemokine ligand 10 [Source:HGNC Symbol;Acc:HGNC:607] |
| 6 | 204639_at | -1.95 | 2e-16 | 1e-13 | 4 x 15 | adenosine deaminase [Source:HGNC Symbol;Acc:HGNC:607] |
| 7 | 204780_s_at | -1.71 | 2e-16 | 1e-13 | 1 x 4 | Fas cell surface death receptor [Source:HGNC Symbol;Acc:HGNC:607] |
| 8 | 204890_s_at | -1.8 | 2e-16 | 1e-13 | 49 x 39 | LCK proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:607] |
| 9 | 205242_at | -2.23 | 2e-16 | 1e-13 | 0 x 3 | C-X-C motif chemokine ligand 13 [Source:HGNC Symbol;Acc:HGNC:607] |
| 10 | 205780_at | -1.47 | 2e-16 | 1e-13 | 40 x 49 | BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:607] |
| 11 | 205890_s_at | -2.04 | 2e-16 | 1e-13 | 2 x 2 | ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795] |
| 12 | 206413_s_at | 2.5 | 2e-16 | 1e-13 | 43 x 49 | T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HGNC:607] |
| 13 | 206666_at | -2.03 | 2e-16 | 1e-13 | 0 x 0 | granzyme K [Source:HGNC Symbol;Acc:HGNC:4711] |
| 14 | 209823_x_at | -1.22 | 2e-16 | 1e-13 | 2 x 8 | major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:607] |
| 15 | 210258_at | -2.65 | 2e-16 | 1e-13 | 49 x 40 | regulator of G protein signaling 13 [Source:HGNC Symbol;Acc:HGNC:607] |
| 16 | 211430_s_at | -1.33 | 2e-16 | 1e-13 | 0 x 4 | immunoglobulin heavy constant gamma 2 (G2m marker) [Source:HGNC Symbol;Acc:HGNC:607] |
| 17 | 211656_x_at | -1.76 | 2e-16 | 1e-13 | 2 x 9 | major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:607] |
| 18 | 211663_x_at | -1.67 | 2e-16 | 1e-13 | 2 x 3 | |
| 19 | 211748_x_at | -1.97 | 2e-16 | 1e-13 | 3 x 3 | prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGNC:607] |
| 20 | 212187_x_at | -1.63 | 2e-16 | 1e-13 | 3 x 3 | prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGNC:607] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 13.2 | NULL | 556 | Chr Chr X |
| 2 | 8.84 | NULL | 70 | CC nucleosome |
| 3 | 8.32 | NULL | 42 | GSEA C2REACTOME_RNA_POL_I_PROMOTER_OPENING |
| 4 | 8.28 | NULL | 324 | CC chromosome |
| 5 | 7.93 | NULL | 319 | Melanoma_Tier1_wt/wt_melanoma-cells-SpotA |
| 6 | 7.75 | NULL | 57 | GSEA C2REACTOME_MEIOTIC_SYNAPSIS |
| 7 | 7.68 | NULL | 98 | GSEA C2REACTOME_CHROMOSOME_MAINTENANCE |
| 8 | 7.68 | NULL | 88 | GSEA C2REACTOME_MEIOSIS |
| 9 | 7.6 | NULL | 61 | GSEA C2REACTOME_TELOMERE_MAINTENANCE |
| 10 | 7.52 | NULL | 36 | GSEA C2REACTOME_PACKAGING_OF_TELOMERE_ENDS |
| 11 | 7.51 | NULL | 62 | GSEA C2REACTOME_MEIOTIC_RECOMBINATION |
| 12 | 7.47 | NULL | 1541 | MF DNA binding |
| 13 | 7.47 | NULL | 852 | MF nucleic acid binding |
| 14 | 7.46 | NULL | 4579 | CC nucleus |
| 15 | 7.34 | NULL | 46 | GSEA C2REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NU |
| 16 | 7.22 | NULL | 526 | GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 17 | 7.21 | NULL | 187 | HM HALLMARK_E2F_TARGETS |
| 18 | 7.03 | NULL | 62 | GSEA C2REACTOME_RNA_POL_I_TRANSCRIPTION |
| 19 | 6.91 | NULL | 78 | BP nucleosome assembly |
| 20 | 6.85 | NULL | 5456 | Chromatin_State_Neural_Progenitor |
| <i>Underexpressed</i> | | | | |
| 1 | -18.53 | NULL | 102 | Reference_Scatterplot_B-cells |
| 2 | -17.9 | NULL | 85 | Lymphoma_Tha_DLCL UP |
| 3 | -17.86 | NULL | 589 | Colon_Cancer_Lembcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN |
| 4 | -16.97 | NULL | 447 | Glioma_ScoV_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN |
| 5 | -13.97 | NULL | 176 | GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP |
| 6 | -13.87 | NULL | 194 | GSEA C2JAATINEN_HEMATOPOIETIC_STEM_CELL_DN |
| 7 | -13.59 | NULL | 186 | Cancer_SPANG_LPS-index2 |
| 8 | -13.58 | NULL | 336 | BP immune response |
| 9 | -13.37 | NULL | 404 | GSEA C2RUTELLA_RESPONSE_TO_HGF_UP |
| 10 | -13.23 | NULL | 83 | Melanoma_TCGA_melanoma_immune_high |
| 11 | -12.74 | NULL | 78 | Melanoma_Tirosh_expression_higher_in_CAFs_than_in_T-cells |
| 12 | -12.58 | NULL | 265 | GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP |
| 13 | -12.49 | NULL | 223 | GSEA C2MCLACHLAN_DENTAL_CARIES_UP |
| 14 | -12.24 | NULL | 480 | Cancer_Lembcke_Colonc_Inflammation |
| 15 | -11.91 | NULL | 288 | Colon_Cancer_Track_CRC_TCGA_corr_J_msi-h_UP_mss_DN |
| 16 | -11.89 | NULL | 269 | Glioma_ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 17 | -11.82 | NULL | 261 | GSEA C2POOLA_INVASIVE_BREAST_CANCER_UP |
| 18 | -11.74 | NULL | 386 | GSEA C2RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP |
| 19 | -11.46 | NULL | 317 | Cancer_SPANG_BCL6-index2 |
| 20 | -11.32 | NULL | 214 | Lymphoma_TENZ_Stromal_signature_1 |

