

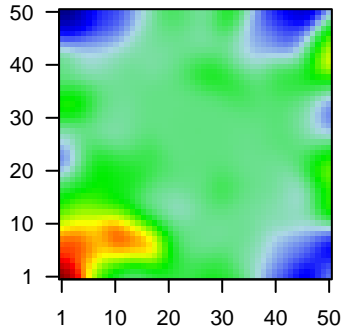
MPI-127

Global Summary

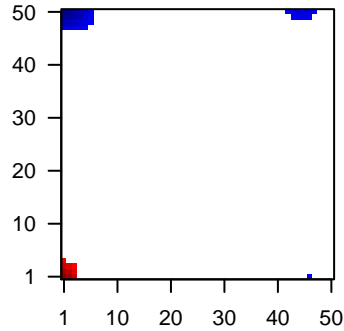
%DE = 0.05
 # genes with fdr < 0.2 = 453 (258 + / 195 -)
 # genes with fdr < 0.1 = 316 (176 + / 140 -)
 # genes with fdr < 0.05 = 290 (159 + / 131 -)
 # genes with fdr < 0.01 = 163 (85 + / 78 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.04
 <p-value> = 0.27
 <fdr> = 0.95

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr | Description | |
|------|-------------|---------|-------|-------------|--|
| | | p-value | | Metagene | |
| 1 | 39318_at | -2.16 | 2e-16 | 5e-13 | 46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:10000] |
| 2 | 44790_s_at | -1.44 | 2e-16 | 5e-13 | 42 x 49 RUN and cysteine rich domain containing beclin 1 interacting |
| 3 | 202005_at | -1.46 | 2e-16 | 5e-13 | 43 x 47 suppression of tumorigenicity 14 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 4 | 207391_s_at | -1.97 | 2e-16 | 5e-13 | 7 x 46 phosphatidylinositol-4-phosphate 5-kinase type 1 alpha [Source:HGNC Symbol;Acc:HGNC:10000] |
| 5 | 207599_at | 2.47 | 2e-16 | 5e-13 | 16 x 7 matrix metalloproteinase 20 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 6 | 209374_s_at | -1.17 | 2e-16 | 5e-13 | 0 x 22 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:10000] |
| 7 | 209995_s_at | -2.13 | 2e-16 | 5e-13 | 46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:10000] |
| 8 | 212827_at | -1.67 | 2e-16 | 5e-13 | 41 x 44 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:10000] |
| 9 | 213831_at | -1.78 | 2e-16 | 5e-13 | 49 x 16 major histocompatibility complex, class II, DQ alpha 1 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 10 | 203290_at | 1.97 | 4e-16 | 3e-11 | 7 x 0 major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 11 | 396_f_at | -1.56 | 2e-15 | 3e-11 | 44 x 0 erythropoietin receptor [Source:HGNC Symbol;Acc:HGNC:10000] |
| 12 | 219471_at | -1.12 | 3e-15 | 1e-10 | 42 x 49 RUN and cysteine rich domain containing beclin 1 interacting |
| 13 | 212387_at | -1.14 | 8e-15 | 2e-09 | 0 x 21 transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:11662] |
| 14 | 205485_at | 2.05 | 1e-13 | 4e-09 | 5 x 10 ryanodine receptor 1 [Source:HGNC Symbol;Acc:HGNC:10410] |
| 15 | 212009_s_at | -1.19 | 7e-13 | 4e-09 | 1 x 49 stress induced phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 16 | 204429_s_at | -1.5 | 7e-13 | 4e-09 | 0 x 49 solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:HGNC:10000] |
| 17 | 213920_at | 1.99 | 7e-13 | 4e-08 | 45 x 49 cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934] |
| 18 | 201222_s_at | -0.96 | 3e-12 | 4e-08 | 10 x 49 RAD23 homolog B, nucleotide excision repair protein [Source:HGNC Symbol;Acc:HGNC:10000] |
| 19 | 219753_at | 1.31 | 4e-12 | 5e-08 | 49 x 39 stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356] |
| 20 | 208164_s_at | 1.9 | 7e-12 | 5e-08 | 17 x 23 interleukin 9 receptor [Source:HGNC Symbol;Acc:HGNC:603] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 15.77 | NULL | 102 | Reference:Sharma/B-cells |
| 2 | 14.62 | NULL | 589 | Colon Cancer:TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN |
| 3 | 14.43 | NULL | 447 | Glioma:SCOVID_0.999_Sturm_E4_Mesenchymal_RTK1_PDGFR4_DN |
| 4 | 12.43 | NULL | 265 | GSEA:WALLACE_PROSTATE_CANCER_RACE_UP |
| 5 | 11.68 | NULL | 78 | Melanoma:mirosh_expression_higher_in_CAFs_than_in_T-cells |
| 6 | 11.07 | NULL | 62 | Lymphoma:anti_Host_response_cluster |
| 7 | 11.05 | NULL | 166 | HM: HALLMARK_INTERFERON_GAMMA_RESPONSE |
| 8 | 10.82 | NULL | 429 | GSEA:SMID_BREAST_CANCER_NORMAL_LIKE_UP |
| 9 | 10.21 | NULL | 512 | GSEA:WEST_ADRENOCORTICAL_TUMOR_DN |
| 10 | 10.13 | NULL | 33 | Melanoma:mirosh_T-cell_specific_genes-melanoma |
| 11 | 9.94 | NULL | 336 | BP: immune response |
| 12 | 9.87 | NULL | 71 | Melanoma:mirosh_Macrophage_specific_genes-melanoma |
| 13 | 9.7 | NULL | 67 | GSEA:NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP |
| 14 | 9.63 | NULL | 223 | GSEA:MCLACHLAN_DENTAL_CARIES_UP |
| 15 | 9.56 | NULL | 431 | BP: immune system process |
| 16 | 9.55 | NULL | 88 | GSEA:WIELAND_UP_BY_HBV_INFECTION |
| 17 | 9.53 | NULL | 62 | GSEA:BROWNE_INTERFERON_RESPONSIVE_GENES |
| 18 | 9.51 | NULL | 72 | Reference:Stylianou_3.1_Interferon-inducible |
| 19 | 9.49 | NULL | 317 | Cancer:SPANG_BCL6-index2 |
| 20 | 9.47 | NULL | 331 | GSEA:INDGREN_BLADDER_CANCER_CLUSTER_2B |
| <i>Underexpressed</i> | | | | |
| 1 | -8.84 | NULL | 99 | Lymphoma:Sharma_BL_UP |
| 2 | -8.47 | NULL | 319 | Melanoma:Berber_wt/wt_melanoma-cells-SpotA |
| 3 | -8.15 | NULL | 192 | Lymphoma:Victoria_Dark_zone_signature |
| 4 | -7.79 | NULL | 966 | GSEA:KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 5 | -7.78 | NULL | 6368 | Colon Cancer:TCGA-mucosa-position_kmeans_F_cecum_colon_transverse_c |
| 6 | -7.7 | NULL | 726 | GSEA:PUJANA_CHEK2_PCC_NETWORK |
| 7 | -7.63 | NULL | 4559 | Lymphoma:HOPE_Weak_enhancer |
| 8 | -7.46 | NULL | 226 | GSEA:ZHANG_TLX_TARGETS_60HR_DN |
| 9 | -7.32 | NULL | 18 | Lymphoma:RIGHT_ABC_UP |
| 10 | -6.91 | NULL | 244 | GSEA:KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 11 | -6.9 | NULL | 5456 | Chromatin:StachNeuronal_Progenitor |
| 12 | -6.81 | NULL | 195 | HM: HALLMARK_G2M_CHECKPOINT |
| 13 | -6.77 | NULL | 561 | Colon Cancer:TCGA_CRC_TCGA_group.over_C_normal_DN |
| 14 | -6.74 | NULL | 400 | GSEA:PUJANA_BRCA2_PCC_NETWORK |
| 15 | -6.7 | NULL | 102 | GSEA:WHITEFORD_PEDIATRIC_CANCER_MARKERS |
| 16 | -6.67 | NULL | 321 | GSEA:TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C |
| 17 | -6.6 | NULL | 11 | MF: peptidoglycan binding |
| 18 | -6.57 | NULL | 1527 | GSEA:PUJANA_BRCA1_PCC_NETWORK |
| 19 | -6.48 | NULL | 290 | GSEA:WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN |
| 20 | -6.47 | NULL | 594 | GSEA:PATIL_LIVER_CANCER |

p-values

