

MPI-113

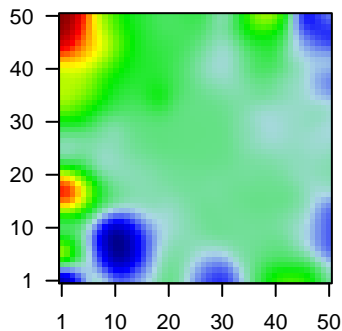
Global Summary

%DE = 0.06
 # genes with fdr < 0.2 = 786 (374 + / 412 -)
 # genes with fdr < 0.1 = 562 (261 + / 301 -)
 # genes with fdr < 0.05 = 379 (174 + / 205 -)
 # genes with fdr < 0.01 = 271 (126 + / 145 -)

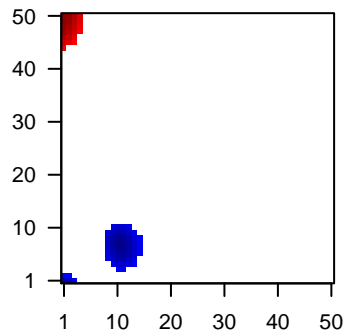
genes in genesets = 13152

<FC> = 0
 <t-score> = 0.08
 <p-value> = 0.24
 <fdr> = 0.94

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|---|
| 1 | 39729_at | -1.9 | 2e-16 | 3e-13 | 49 x 49 peroxiredoxin 2 [Source:HGNC Symbol;Acc:HGNC:9353] |
| 2 | 200953_s_at | -1.71 | 2e-16 | 3e-13 | 0 x 3 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 3 | 206413_s_at | 2.1 | 2e-16 | 3e-13 | 43 x 49 T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HGNC:1583] |
| 4 | 209670_at | -1.19 | 2e-16 | 3e-13 | 10 x 9 T cell receptor alpha constant [Source:HGNC Symbol;Acc:HGNC:1583] |
| 5 | 210072_at | -1.48 | 2e-16 | 3e-13 | 0 x 2 C-C motif chemokine ligand 19 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 6 | 210551_s_at | 2.21 | 2e-16 | 3e-13 | 1 x 17 acetylserotonin O-methyltransferase [Source:HGNC Symbol;Acc:HGNC:1583] |
| 7 | 210915_x_at | -1.8 | 2e-16 | 3e-13 | 10 x 8 T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 8 | 210972_x_at | -1.32 | 2e-16 | 3e-13 | 10 x 9 T cell receptor alpha constant [Source:HGNC Symbol;Acc:HGNC:1583] |
| 9 | 211658_at | -1.74 | 2e-16 | 3e-13 | 48 x 49 |
| 10 | 211796_s_at | -1.95 | 2e-16 | 3e-13 | 10 x 9 T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 11 | 212592_at | -1.96 | 2e-16 | 3e-13 | 45 x 49 joining chain of multimeric IgA and IgM [Source:HGNC Symbol;Acc:HGNC:1583] |
| 12 | 213193_x_at | -1.55 | 2e-16 | 3e-13 | 10 x 8 T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 13 | 213558_at | 2.09 | 2e-16 | 3e-13 | 18 x 34 piccolo presynaptic cytomatrix protein [Source:HGNC Symbol;Acc:HGNC:1583] |
| 14 | 213757_at | -1.07 | 2e-16 | 3e-13 | 30 x 49 G protein pathway suppressor 2 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 15 | 215051_x_at | -1.38 | 2e-16 | 3e-13 | 9 x 9 allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 16 | 217022_s_at | -1.52 | 2e-16 | 3e-13 | 0 x 2 immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:HGNC:1583] |
| 17 | 217092_x_at | -1.08 | 2e-16 | 3e-13 | 42 x 32 ribosomal protein L7 pseudogene 52 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 18 | 219109_at | -1.91 | 1e-15 | 2e-11 | 49 x 37 sperm associated antigen 16 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 19 | 206779_s_at | 2.01 | 2e-15 | 3e-11 | 1 x 17 acetylserotonin O-methyltransferase [Source:HGNC Symbol;Acc:HGNC:1583] |
| 20 | 213095_x_at | -1.4 | 4e-15 | 3e-11 | 9 x 9 allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:HGNC:1583] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 9.25 | NULL | 966 | GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 2 | 9.18 | NULL | 353 | LymphomaPANG_CD40 6hrs DN |
| 3 | 9.06 | NULL | 244 | GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 4 | 8.86 | NULL | 4261 | LymphomaOPP_Txn_transition |
| 5 | 8.41 | NULL | 319 | MelanomaBerber_wt/wt_melanoma-cells-SpotA |
| 6 | 7.92 | NULL | 439 | GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 7 | 7.6 | NULL | 6368 | Colon CancerPointe_mucosa-position_kmeans_F_cecum colon_transverse c |
| 8 | 7.11 | NULL | 187 | HM HALLMARK_E2F_TARGETS |
| 9 | 7.02 | NULL | 254 | GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP |
| 10 | 7.02 | NULL | 85 | Lymphomaoha_DLBCL UP |
| 11 | 6.97 | NULL | 409 | Cancer Lembecke_Normal vs Adenoma |
| 12 | 6.95 | NULL | 5529 | LymphomaOPP_Txn_elongation |
| 13 | 6.75 | NULL | 195 | HM HALLMARK_G2M_CHECKPOINT |
| 14 | 6.68 | NULL | 376 | GSEA C2GARY_CD5_TARGETS_UP |
| 15 | 6.61 | NULL | 270 | GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_2 |
| 16 | 6.46 | NULL | 9 | GSEA C2RUNNE_GENDER_EFFECT_UP |
| 17 | 6.46 | NULL | 226 | GSEA C2ZHANG_TLX_TARGETS_60HR_DN |
| 18 | 6.45 | NULL | 1527 | GSEA C2PUJANA_BRCA1_PCC_NETWORK |
| 19 | 6.42 | NULL | 115 | Glioma WILLSCHER_GBM_Verhaak-CL_up (C) |
| 20 | 6.42 | NULL | 79 | MelanomaTirosh_core cycling genes in low- and high-proliferation melanom |
| <i>Underexpressed</i> | | | | |
| 1 | -14.22 | NULL | 15 | LymphomaCare_Polarized immune response |
| 2 | -12.22 | NULL | 40 | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1 |
| 3 | -12.07 | NULL | 429 | GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP |
| 4 | -11.88 | NULL | 102 | ReferenceSrinivas/B-cells |
| 5 | -9.63 | NULL | 62 | LymphomaMonti_Host_response_cluster |
| 6 | -9.32 | NULL | 176 | GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP |
| 7 | -9.31 | NULL | 68 | ReferenceSrinivas_2,1_Cytotoxic cells |
| 8 | -9.08 | NULL | 39 | BP complement activation |
| 9 | -8.95 | NULL | 56 | PneumoniaBurnham_sep_vs_con_DN |
| 10 | -8.26 | NULL | 48 | PneumoniaBurnham_cap_fp_vs_con_DN |
| 11 | -8.26 | NULL | 516 | GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN |
| 12 | -8.13 | NULL | 44 | MF antigen binding |
| 13 | -8.12 | NULL | 33 | MelanomaTirosh_T-cell specific genes-melanoma |
| 14 | -8.01 | NULL | 265 | GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP |
| 15 | -7.85 | NULL | 9 | GSEA C2CHASSOT_SKIN_WOUND |
| 16 | -7.83 | NULL | 122 | GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP |
| 17 | -7.82 | NULL | 336 | BP immune response |
| 18 | -7.57 | NULL | 83 | MelanomaTCGA_melanoma_immune_high |
| 19 | -7.5 | NULL | 589 | Colon CancerLembecke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 20 | -7.23 | NULL | 57 | PneumoniaBurnham_viral_UP |

p-values

