

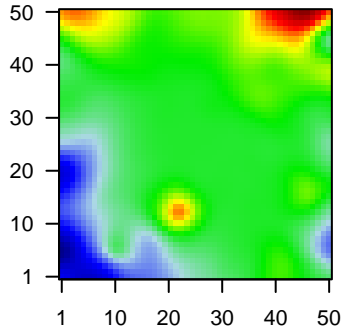
MPI-034

Global Summary

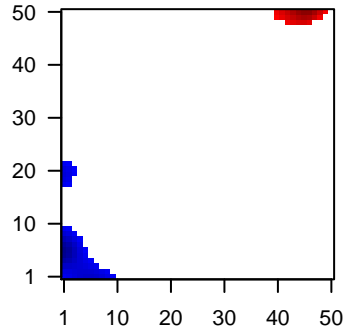
%DE = 0.03
 # genes with fdr < 0.2 = 352 (146 + / 206 -)
 # genes with fdr < 0.1 = 270 (121 + / 149 -)
 # genes with fdr < 0.05 = 212 (98 + / 114 -)
 # genes with fdr < 0.01 = 100 (51 + / 49 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.14
 <p-value> = 0.29
 <fdr> = 0.97

Portrait



Regulated Metagenes



Global Genelist

| Rank | ID | log(FC) | fdr | p-value | Description |
|------|-------------|---------|-------|---------|---|
| 1 | 206413_s_at | 2.55 | 2e-16 | 1e-12 | 43 x 49 T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HGNC:6415] |
| 2 | 207935_s_at | 2.75 | 2e-16 | 1e-12 | 22 x 12 keratin 13 [Source:HGNC Symbol;Acc:HGNC:6415] |
| 3 | 213240_s_at | 2.92 | 2e-16 | 1e-12 | 22 x 12 keratin 4 [Source:HGNC Symbol;Acc:HGNC:6441] |
| 4 | 214777_at | 2.57 | 2e-16 | 1e-12 | 10 x 5 immunoglobulin kappa variable 4-1 [Source:HGNC Symbol;Acc:HGNC:6441] |
| 5 | 218990_s_at | 2.32 | 2e-16 | 1e-12 | 22 x 12 small proline rich protein 3 [Source:HGNC Symbol;Acc:HGNC:6441] |
| 6 | 219140_s_at | 2.08 | 7e-14 | 9e-10 | 34 x 28 retinol binding protein 4 [Source:HGNC Symbol;Acc:HGNC:6441] |
| 7 | 221671_x_at | 0.83 | 8e-14 | 3e-09 | 0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:6441] |
| 8 | 211981_at | -1.43 | 2e-13 | 2e-08 | 9 x 0 collagen type IV alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:6441] |
| 9 | 221651_x_at | 0.78 | 1e-12 | 6e-08 | 0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:6441] |
| 10 | 205064_at | 1.92 | 4e-12 | 6e-08 | 22 x 12 small proline rich protein 1B [Source:HGNC Symbol;Acc:HGNC:6441] |
| 11 | 213796_at | 1.9 | 6e-12 | 9e-07 | 22 x 12 small proline rich protein 1A [Source:HGNC Symbol;Acc:HGNC:6441] |
| 12 | 220090_at | 1.81 | 6e-11 | 9e-07 | 22 x 12 cornulin [Source:HGNC Symbol;Acc:HGNC:1230] |
| 13 | 205185_at | 1.8 | 9e-11 | 9e-07 | 22 x 12 serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symbol;Acc:HGNC:1230] |
| 14 | 201909_at | 1.14 | 1e-10 | 1e-06 | 43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:1230] |
| 15 | 211639_x_at | 1.76 | 2e-10 | 1e-06 | 20 x 13 immunoglobulin heavy variable 4-34 [Source:HGNC Symbol;Acc:HGNC:1230] |
| 16 | 214055_x_at | -1.04 | 2e-10 | 3e-06 | 49 x 8 proline rich coiled-coil 2C [Source:HGNC Symbol;Acc:HGNC:1230] |
| 17 | 202286_s_at | 1.74 | 4e-10 | 6e-06 | 22 x 12 tumor associated calcium signal transducer 2 [Source:HGNC Symbol;Acc:HGNC:1230] |
| 18 | 204998_s_at | -0.93 | 8e-10 | 6e-06 | 0 x 18 activating transcription factor 5 [Source:HGNC Symbol;Acc:HGNC:1230] |
| 19 | 209125_at | 1.7 | 9e-10 | 7e-06 | 22 x 12 keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443] |
| 20 | 218677_at | 1.67 | 2e-09 | 7e-06 | 21 x 12 S100 calcium binding protein A14 [Source:HGNC Symbol;Acc:HGNC:6443] |

Global Geneset Analysis

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|--------|---------|------|---|
| <i>Overexpressed</i> | | | | |
| 1 | 15.52 | NULL | 105 | Reference:SPANG_LPS-index2 |
| 2 | 15.24 | NULL | 726 | GSEA C2P_UJANA_CHEK2_PCC_NETWORK |
| 3 | 14.48 | NULL | 966 | GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 4 | 14.32 | NULL | 1527 | GSEA C2P_UJANA_BRCA1_PCC_NETWORK |
| 5 | 13.93 | NULL | 319 | Melanoma:Berber_wt/wt_melanoma-cells-SpotA |
| 6 | 13.63 | NULL | 99 | Lymphoma:Sha_BL_UP |
| 7 | 12.85 | NULL | 46 | GSEA C2BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE |
| 8 | 12.46 | NULL | 280 | GSEA C2MANALO_HYPOXIA_DN |
| 9 | 12.31 | NULL | 575 | GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP |
| 10 | 12.24 | NULL | 400 | GSEA C2P_UJANA_BRCA2_PCC_NETWORK |
| 11 | 11.8 | NULL | 187 | HM HALLMARK_E2F_TARGETS |
| 12 | 11.7 | NULL | 78 | BP cornification |
| 13 | 11.51 | NULL | 115 | Glioma WILLSCHER_GBM_Verhaak-CL_up (C) |
| 14 | 11.09 | NULL | 192 | Lymphoma:Micro_Dark zone signature |
| 15 | 10.98 | NULL | 42 | GSEA C2HUMMEL_BURKITTIS_LYMPHOMA_UP |
| 16 | 10.85 | NULL | 137 | GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER |
| 17 | 10.84 | NULL | 14 | Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 18 | 10.83 | NULL | 439 | GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 19 | 10.69 | NULL | 72 | BP keratinization |
| 20 | 10.67 | NULL | 431 | GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| <i>Underexpressed</i> | | | | |
| 1 | -15.34 | NULL | 317 | Cancer SPANG_BCL6-index2 |
| 2 | -12.79 | NULL | 85 | Lymphoma:Sha_DLCL UP |
| 3 | -12.38 | NULL | 335 | GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP |
| 4 | -11.49 | NULL | 231 | Glioma WILLSCHER_GBM_Verhaak-CL & MES_up |
| 5 | -11.49 | NULL | 447 | Glioma ScoV_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN |
| 6 | -11.09 | NULL | 269 | Glioma ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 7 | -11.03 | NULL | 190 | HM HALLMARK_TNFA_SIGNALING_VIA_NFKB |
| 8 | -10.4 | NULL | 432 | Chromatin:Macrophages_peripheral_blood_3_TxFnk |
| 9 | -9.89 | NULL | 186 | Cancer SPANG_LPS-index2 |
| 10 | -9.72 | NULL | 288 | Colon Ca:ReTrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN |
| 11 | -9.72 | NULL | 902 | GSEA C2CHEN_METABOLIC_SYNDROM_NETWORK |
| 12 | -9.68 | NULL | 202 | GSEA C2VERHAAK_GLIOMASTOMA_MESENCHYMAL |
| 13 | -9.67 | NULL | 297 | Colon Ca:ReTrack_CRC_TCGA_group.over_B_msi-h_UP |
| 14 | -9.6 | NULL | 213 | Lymphoma:SPANG_IL21 DN |
| 15 | -9.37 | NULL | 90 | GSEA C2BASSO_CD40_SIGNALING_UP |
| 16 | -9.08 | NULL | 589 | GSEA C2WONG_ADULT_TISSUE_STEM_MODULE |
| 17 | -9.05 | NULL | 104 | GSEA C2ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENT |
| 18 | -8.9 | NULL | 404 | GSEA C2RUTELLA_RESPONSE_TO_HGF_UP |
| 19 | -8.88 | NULL | 71 | Melanoma:Micro_Macrophage_specific_genes-melanoma |
| 20 | -8.76 | NULL | 397 | GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN |

p-values

