# MPI−123

## Global Summary

%DE = 0.05

# genes with fdr < 0.2 = 626 ( 340 + / 286 −)

# genes with fdr < 0.1 = 470 ( 259 + / 211 −)

# genes with fdr < 0.05 = 378 ( 211 + / 167 −)

# genes with fdr < 0.01 = 238 ( 143 + / 95 −)

# genes in genesets = 13152

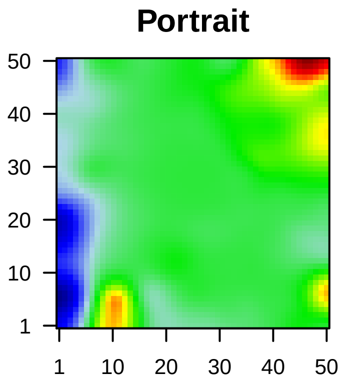
<FC> = 0

<t−score> = 0.13

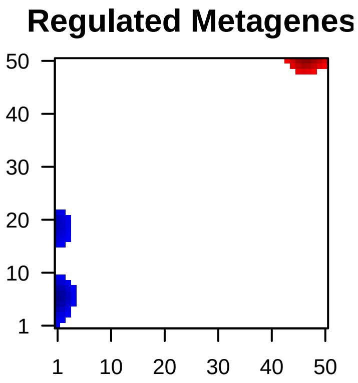
<p−value> = 0.25

<fdr> = 0.95

**Portrait**



**Regulated Metagenes**



## Global Genelist

| Rank | ID | log(FC) | p−value | fdr | Metagene | Description |
|---|---|---|---|---|---|---|
| 1 | 203760_s_at | −1.22 | 2e−16 | 3e−13 | 0 x 20 | Src like adaptor [Source:HGNC Symbol;Acc:HGNC:10902] |
| 2 | 205681_at | −1.09 | 2e−16 | 3e−13 | 0 x 4 | BCL2 related protein A1 [Source:HGNC Symbol;Acc:HGNC: |
| 3 | 206424_at | 2.12 | 2e−16 | 3e−13 | 33 x 35 | cytochrome P450 family 26 subfamily A member 1 [Source:H |
| 4 | 208456_s_at | −1.63 | 2e−16 | 3e−13 | 0 x 7 | RAS related 2 [Source:HGNC Symbol;Acc:HGNC:17271] |
| 5 | 209480_at | −1.7 | 2e−16 | 3e−13 | 49 x 16 | major histocompatibility complex, class II, DQ beta 1 [Source: |
| 6 | 211430_s_at | 0.98 | 2e−16 | 3e−13 | 0 x 4 | immunoglobulin heavy constant gamma 2 (G2m marker) [Sou |
| 7 | 212589_at | −1.62 | 2e−16 | 3e−13 | 0 x 7 | RAS related 2 [Source:HGNC Symbol;Acc:HGNC:17271] |
| 8 | 212590_at | −1.59 | 2e−16 | 3e−13 | 0 x 7 | RAS related 2 [Source:HGNC Symbol;Acc:HGNC:17271] |
| 9 | 213831_at | −1.65 | 2e−16 | 3e−13 | 49 x 16 | major histocompatibility complex, class II, DQ alpha 1 [Source |
| 10 | 215214_at | 2.41 | 2e−16 | 3e−13 | 10 x 5 | immunoglobulin lambda variable 3−25 [Source:HGNC Symbo |
| 11 | 215379_x_at | 0.92 | 2e−16 | 3e−13 | 41 x 42 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 12 | 215946_x_at | 1.03 | 2e−16 | 3e−13 | 41 x 42 | immunoglobulin lambda like polypeptide 3, pseudogene [Sou |
| 13 | 216560_x_at | 2.3 | 2e−16 | 3e−13 | 11 x 5 | immunoglobulin lambda variable 3−10 [Source:HGNC Symbo |
| 14 | 219655_at | 2.11 | 2e−16 | 3e−13 | 47 x 40 | succinyl−CoA:glutarate−CoA transferase [Source:HGNC Sym |
| 15 | 220377_at | 2.09 | 2e−16 | 3e−13 | 5 x 28 | family with sequence similarity 30 member A [Source:HGNC |
| 16 | 215121_x_at | 0.74 | 7e−16 | 7e−12 | 41 x 42 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 17 | 38149_at | −1.07 | 9e−16 | 4e−11 | 0 x 6 | Rho GTPase activating protein 25 [Source:HGNC Symbol;Ac |
| 18 | 209138_x_at | 0.72 | 4e−15 | 4e−11 | 41 x 42 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 19 | 203685_at | −1.5 | 6e−15 | 4e−11 | 0 x 21 | BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC |
| 20 | 211644_x_at | 1.58 | 6e−15 | 4e−11 | 0 x 1 | immunoglobulin kappa variable 3−20 [Source:HGNC Symbol; |

## Global Geneset Analysis

| Rank | GSZ | p−value | #all | Geneset | |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | 16.06 | NULL | 32 | Reference Signatures | Chaussabel_1,1_Plasma Cells |
| 2 | 15.67 | NULL | 42 | GSEA C2 | HUMMEL_BURKITTS_LYMPHOMA_UP |
| 3 | 15.02 | NULL | 44 | MF | antigen binding |
| 4 | 13.97 | NULL | 99 | Lymphoma | Sha_BL UP |
| 5 | 12.19 | NULL | 726 | GSEA C2 | PUJANA_CHEK2_PCC_NETWORK |
| 6 | 11.84 | NULL | 1052 | GSEA C2 | DODD_NASOPHARYNGEAL_CARCINOMA_DN |
| 7 | 11.5 | NULL | 319 | Melanoma | Gerber_wt/wt_melanoma−cells−SpotA |
| 8 | 11.2 | NULL | 1527 | GSEA C2 | PUJANA_BRCA1_PCC_NETWORK |
| 9 | 10.97 | NULL | 575 | GSEA C2 | CAIRO_HEPATOBLASTOMA_CLASSES_UP |
| 10 | 10.82 | NULL | 192 | Lymphoma | Victora_Dark zone signature |
| 11 | 10.43 | NULL | 321 | GSEA C2 | BLUM_RESPONSE_TO_SALIRASIB_DN |
| 12 | 10.38 | NULL | 966 | GSEA C2 | KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 13 | 9.82 | NULL | 16 | MF | immunoglobulin receptor binding |
| 14 | 9.8 | NULL | 52 | BP | complement activation, classical pathway |
| 15 | 9.78 | NULL | 244 | GSEA C2 | KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 16 | 9.77 | NULL | 294 | GSEA C2 | WONG_EMBRYONIC_STEM_CELL_CORE |
| 17 | 9.72 | NULL | 280 | GSEA C2 | MANALO_HYPOXIA_DN |
| 18 | 9.59 | NULL | 15 | Lymphoma | BENTINK_mBL UP |
| 19 | 9.59 | NULL | 431 | GSEA C2 | GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 20 | 9.5 | NULL | 400 | GSEA C2 | PUJANA_BRCA2_PCC_NETWORK |
| *Underexpressed* | | | | | |
| 1 | −19.34 | NULL | 317 | Cancer | SPANG_BCL6−index2 |
| 2 | −17.66 | NULL | 85 | Lymphoma | Sha_DLBCL UP |
| 3 | −13.18 | NULL | 90 | GSEA C2 | BASSO_CD40_SIGNALING_UP |
| 4 | −10.96 | NULL | 14 | GSEA C2 | HUMMEL_BURKITTS_LYMPHOMA_DN |
| 5 | −10.55 | NULL | 186 | Cancer | SPANG_LPS−index2 |
| 6 | −10.37 | NULL | 353 | Lymphoma | SPANG_CD40 6hrs DN |
| 7 | −10.32 | NULL | 12 | Lymphoma | BENTINK_mBL DOWN |
| 8 | −10.25 | NULL | 22 | Lymphoma | DAVE_NFkB BL DN |
| 9 | −10.07 | NULL | 3223 | Chromatin states | monocytes peripheral blood_6_EnhG |
| 10 | −9.88 | NULL | 173 | Lymphoma | Victora_Light zone signature |
| 11 | −9.48 | NULL | 229 | GSEA C2 | QI_PLASMACYTOMA_UP |
| 12 | −8.8 | NULL | 213 | Lymphoma | SPANG_IL21 DN |
| 13 | −8.68 | NULL | 355 | Reference Signatures | WIRTH_Immune system |
| 14 | −8.45 | NULL | 4 | Lymphoma | MASCQUE_mBL DOWN |
| 15 | −8.19 | NULL | 447 | Glioma | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 16 | −8.18 | NULL | 906 | Lymphoma | SPANG_BCR DN |
| 17 | −8.15 | NULL | 589 | Colon Cancer | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 18 | −8.01 | NULL | 432 | Chromatin states | monocytes peripheral blood_3_TxFlnk |
| 19 | −7.97 | NULL | 12 | Cancer | HLA2_signature |
| 20 | −7.79 | NULL | 3682 | Chromatin states | natural killer cells peripheral blood_6_EnhG |

**p−values**