

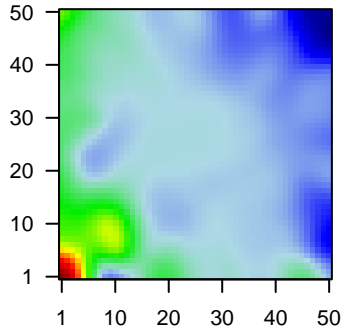
# MPI-234

## Global Summary

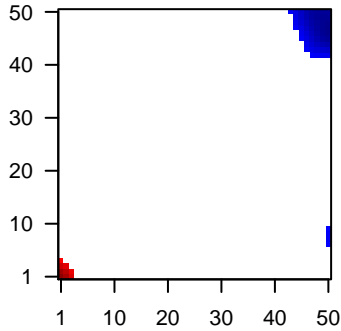
%DE = 0.06  
 # genes with  $fdr < 0.2 = 777$  ( 538 + / 239 -)  
 # genes with  $fdr < 0.1 = 581$  ( 418 + / 163 -)  
 # genes with  $fdr < 0.05 = 422$  ( 317 + / 105 -)  
 # genes with  $fdr < 0.01 = 242$  ( 182 + / 60 -)  
  
 # genes in genesets = 13152

<FC> = 0  
 <t-score> = 0.14  
 <p-value> = 0.24  
 <fdr> = 0.94

Portrait



Regulated Metagenes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	39318_at	-1.46	2e-16	4e-13	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:39318]
2	201123_s_at	-1.44	2e-16	4e-13	1 x 43 eukaryotic translation initiation factor 5A [Source:HGNC Syml
3	202953_at	1.09	2e-16	4e-13	0 x 0 complement C1q B chain [Source:HGNC Symbol;Acc:HGNC:202953]
4	203290_at	1.71	2e-16	4e-13	7 x 0 major histocompatibility complex, class II, DQ alpha 2 [Source:HGNC Symbol;Acc:HGNC:203290]
5	205819_at	1.92	2e-16	4e-13	1 x 0 macrophage receptor with collagenous structure [Source:HGNC Symbol;Acc:HGNC:205819]
6	206680_at	1.97	2e-16	4e-13	35 x 26 CD5 molecule like [Source:HGNC Symbol;Acc:HGNC:1690]
7	208791_at	1.3	2e-16	4e-13	0 x 3 clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
8	209480_at	-1.99	2e-16	4e-13	49 x 16 major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:209480]
9	209995_s_at	-1.84	2e-16	4e-13	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:209995]
10	212464_s_at	-1.11	2e-16	4e-13	8 x 0 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	213831_at	-1.65	2e-16	4e-13	49 x 16 major histocompatibility complex, class II, DQ alpha 1 [Source:HGNC Symbol;Acc:HGNC:213831]
12	215379_x_at	0.9	2e-16	4e-13	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:215379]
13	216442_x_at	-0.98	2e-16	4e-13	8 x 0 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
14	218232_at	0.89	1e-15	8e-11	0 x 0 complement C1q A chain [Source:HGNC Symbol;Acc:HGNC:218232]
15	201909_at	-1.11	7e-15	8e-11	43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909]
16	208792_s_at	1.02	2e-14	8e-11	0 x 3 clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
17	215121_x_at	0.66	2e-14	8e-11	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:215121]
18	210495_x_at	-0.85	2e-14	2e-10	8 x 0 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
19	212094_at	-1.53	2e-14	4e-10	45 x 49 paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:212094]
20	205242_at	1.04	6e-14	4e-10	0 x 3 C-X-C motif chemokine ligand 13 [Source:HGNC Symbol;Acc:HGNC:205242]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.33	NULL	589	Colon Cancer_Lembecke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	23.27	NULL	102	Reference:GSE14564_B-cells
3	21.3	NULL	447	Glioma_ScoV_0.999_Sturm_E4_Mesenchymal_RTK1_PDGFR_A_DN
4	19.44	NULL	431	BP immune system process
5	18.15	NULL	265	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
6	17.43	NULL	78	Melanoma_Tirosh_expression_higher_in_CAFs_than_in_T-cells
7	17.03	NULL	480	Cancer_Lembecke_Colonc_Inflammation
8	16.79	NULL	62	Lymphoma_Monti_Host_response_cluster
9	16.74	NULL	429	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	16.03	NULL	88	GSEA C2WIELAND_UP_BY_HBV_INFECTION
11	15.9	NULL	194	GSEA C2JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
12	15.83	NULL	223	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
13	15.78	NULL	355	Reference:GSE14564_immune system
14	15.65	NULL	52	BP complement activation, classical pathway
15	15.62	NULL	336	BP immune response
16	15.18	NULL	432	Chromatin_state:melanocytes_peripheral_blood_3_TxFnk
17	15.17	NULL	39	BP complement activation
18	15.12	NULL	71	Melanoma_Tirosh_Macrophage_specific_genes-melanoma
19	15.12	NULL	166	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
20	15.11	NULL	626	Chromatin_state:killer_cells_peripheral_blood_3_TxFnk
<i>Underexpressed</i>				
1	-14.79	NULL	7225	Chromatin_state:fetal_midbrain_ReprPC
2	-12.53	NULL	8641	Chromatin_state:ESC_Endoderm
3	-11.9	NULL	6068	Chromatin_state:ESC_Endoderm
4	-11.62	NULL	5456	Chromatin_state:Neuronal_Progenitor
5	-11.49	NULL	9160	Chromatin_state:Neuronal_Progenitor
6	-10.61	NULL	8918	Chromatin_state:ESC_Mesoderm
7	-9.84	NULL	8275	Chromatin_state:Fibroblasts
8	-9.71	NULL	6997	Chromatin_state:fetal_midbrain_K9K27me3
9	-9.55	NULL	8766	Chromatin_state:Melanocytes
10	-9.48	NULL	602	Colon_Cancertrack_CRC_TCGA_corr_R_normal_DN
11	-9.17	NULL	4683	Chromatin_state:fetal_midbrain_HetRpts
12	-8.94	NULL	6389	Chromatin_state:ESC_Mesoderm
13	-8.65	NULL	9576	Chromatin_state:MSC_Adipocyte
14	-8.51	NULL	1161	MF RNA binding
15	-8.39	NULL	1527	GSEA C2PUJANA_BRCA1_PCC_NETWORK
16	-8.36	NULL	561	Colon_Cancertrack_CRC_TCGA_group.over_C_normal_DN
17	-8.18	NULL	6034	Chromatin_state:Fibroblasts
18	-8.05	NULL	7833	Chromatin_state:peripheral_blood_1_TssA
19	-8.04	NULL	6679	Chromatin_state:Melanocytes
20	-8	NULL	9	GSEA C2RUNNE_GENDER_EFFECT_UP

p-values

