

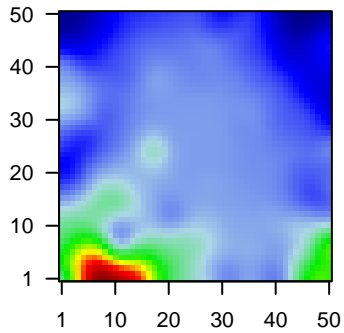
# MPI-221

## Global Summary

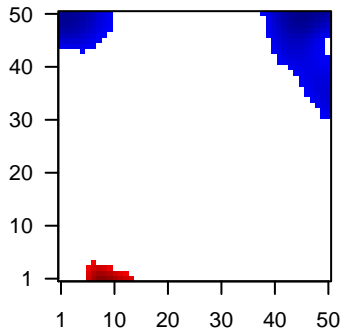
%DE = 0.06  
 # genes with  $fdr < 0.2$  = 810 ( 520 + / 290 -)  
 # genes with  $fdr < 0.1$  = 604 ( 400 + / 204 -)  
 # genes with  $fdr < 0.05$  = 476 ( 311 + / 165 -)  
 # genes with  $fdr < 0.01$  = 287 ( 188 + / 99 -)  
  
 # genes in genesets = 13152

<FC> = 0  
 <t-score> = -0.06  
 <p-value> = 0.23  
 <fdr> = 0.94

Portrait



Regulated Metagenes



## Global Genelist

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	201427_s_at	-2.06	2e-16	2e-13 47 x 37 selenoprotein P [Source:HGNC Symbol;Acc:HGNC:10751]
2	202859_x_at	2.59	2e-16	2e-13 13 x 0 C-X-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:HGNC:10751]
3	202953_at	-2.11	2e-16	2e-13 0 x 0 complement C1q B chain [Source:HGNC Symbol;Acc:HGNC:10751]
4	203795_s_at	-1.69	2e-16	2e-13 42 x 49 BCL tumor suppressor 7A [Source:HGNC Symbol;Acc:HGNC:10751]
5	203915_at	-1.84	2e-16	2e-13 0 x 0 C-X-C motif chemokine ligand 9 [Source:HGNC Symbol;Acc:HGNC:10751]
6	204470_at	2.29	2e-16	2e-13 13 x 0 C-X-C motif chemokine ligand 1 [Source:HGNC Symbol;Acc:HGNC:10751]
7	204475_at	2.81	2e-16	2e-13 7 x 0 matrix metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:10751]
8	204637_at	2.29	2e-16	2e-13 17 x 24 glycoprotein hormones, alpha polypeptide [Source:HGNC Symbol;Acc:HGNC:10751]
9	204891_s_at	-1.49	2e-16	2e-13 49 x 39 LCK proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:10751]
10	205484_at	-1.71	2e-16	2e-13 43 x 44 signaling threshold regulating transmembrane adaptor 1 [Source:HGNC Symbol;Acc:HGNC:10751]
11	205828_at	2.85	2e-16	2e-13 13 x 0 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC:10751]
12	207802_at	2.38	2e-16	2e-13 17 x 24 cysteine rich secretory protein 3 [Source:HGNC Symbol;Acc:HGNC:10751]
13	209374_s_at	-2.37	2e-16	2e-13 0 x 22 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:10751]
14	212827_at	-1.65	2e-16	2e-13 41 x 44 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:10751]
15	214974_x_at	2.66	2e-16	2e-13 13 x 0 C-X-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:10751]
16	215101_s_at	2.45	2e-16	2e-13 14 x 0 C-X-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:10751]
17	215121_x_at	-1.09	2e-16	2e-13 41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:10751]
18	215379_x_at	-1.47	2e-16	2e-13 41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:10751]
19	216733_s_at	-1.9	2e-16	2e-13 0 x 19 glycine amidinotransferase [Source:HGNC Symbol;Acc:HGNC:10751]
20	218232_at	-1.47	2e-16	2e-13 0 x 0 complement C1q A chain [Source:HGNC Symbol;Acc:HGNC:10751]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.74	NULL	214	Lymphoma T1ENZ_Stromal signature 1
2	18.88	NULL	196	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	18.14	NULL	335	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	16.45	NULL	397	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
5	16.07	NULL	60	GSEA C2CROMER_TUMORIGENESIS_UP
6	15.73	NULL	190	HM HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	14.93	NULL	212	CC extracellular matrix
8	14.89	NULL	63	GSEA C2ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
9	14.7	NULL	288	Colon Cancer track_CRC_TCGA_corr_J_msi-h_UP_mss_DN
10	14.4	NULL	231	Glioma WILLSCHER_GBM_Verhaak-CL & MES_up
11	14	NULL	269	Glioma ScoV_0.5_Sturm_C3_Mesenchymal_DN
12	13.89	NULL	85	Glioma ScoV_0.999_Sturm_E2_IDH_DN
13	13.77	NULL	747	GSEA C2NABA_MATRISOME
14	13.5	NULL	72	GSEA C2GHANDHI_BYSTANDER_IRRADIATION_UP
15	13.31	NULL	480	Cancer Lembecke_Colonc Inflammation
16	12.78	NULL	404	GSEA C2RUTELLA_RESPONSE_TO_HGF_UP
17	12.77	NULL	58	BP collagen catabolic process
18	12.75	NULL	202	GSEA C2VERHAAK_GLIOMASTOMA_MESENCHYMAL
19	12.66	NULL	589	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
20	12.59	NULL	253	CC proteinaceous extracellular matrix
<i>Underexpressed</i>				
1	-11.97	NULL	4528	Chromatin states naive cells peripheral blood_4_Tx
2	-11.37	NULL	6099	Chromatin states T1
3	-11.32	NULL	5716	Chromatin states peripheral blood_4_Tx
4	-11.22	NULL	5601	Chromatin states naive cells peripheral blood_4_Tx
5	-11.2	NULL	5753	Chromatin states peripheral blood_4_Tx
6	-10.84	NULL	5527	Chromatin states regulatory cells peripheral blood_4_Tx
7	-10.78	NULL	7420	Chromatin states peripheral blood_1_TssA
8	-10.62	NULL	52	BP complement activation, classical pathway
9	-10.49	NULL	32	Reference dataset_1_1_Plasma Cells
10	-10.38	NULL	44	MF antigen binding
11	-10.35	NULL	5766	Chromatin states killer cells peripheral blood_4_Tx
12	-10.21	NULL	5529	Lymphoma T1OPP_Txn_elongation
13	-10.07	NULL	7833	Chromatin states peripheral blood_1_TssA
14	-10.02	NULL	4261	Lymphoma T1OPP_Txn_transition
15	-9.46	NULL	1527	GSEA C2PUJANA_BRCA1_PCC_NETWORK
16	-9.45	NULL	7407	Chromatin states killer cells peripheral blood_5_TxWk
17	-9.44	NULL	7751	Chromatin states killer cells peripheral blood_1_TssA
18	-9.36	NULL	4683	Chromatin states fetal_midbrain_HetRpts
19	-9.36	NULL	7957	Chromatin states peripheral blood_2_TssAFlnk
20	-9.26	NULL	6590	Chromatin states regulatory cells peripheral blood_5_TxWk

p-values

