

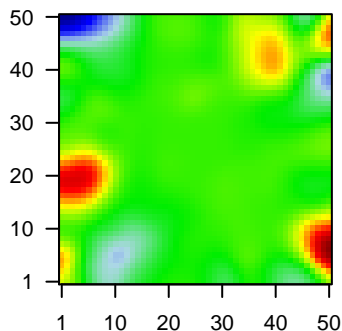
# MPI-146

## Global Summary

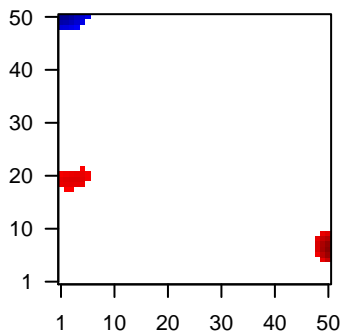
%DE = 0.07  
 # genes with fdr < 0.2 = 720 ( 386 + / 334 - )  
 # genes with fdr < 0.1 = 510 ( 279 + / 231 - )  
 # genes with fdr < 0.05 = 440 ( 239 + / 201 - )  
 # genes with fdr < 0.01 = 208 ( 116 + / 92 - )  
 # genes in genesets = 13152

<FC> = 0  
 <t-score> = -0.06  
 <p-value> = 0.24  
 <fdr> = 0.93

### Portrait



### Regulated Metagenes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	212311_at	-1.4	2e-16	2e-12	49 x 39 SEL1L family member 3 [Source:HGNC Symbol;Acc:HGNC:2
2	212592_at	-1.63	2e-16	2e-12	45 x 49 joining chain of multimeric IgA and IgM [Source:HGNC Symb
3	214106_s_at	-1.49	2e-16	2e-12	0 x 6 GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc
4	203797_at	2.31	5e-15	4e-10	5 x 20 visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
5	201008_s_at	-1.34	2e-14	4e-10	0 x 49 thioredoxin interacting protein [Source:HGNC Symbol;Acc:HC
6	212314_at	-1.11	7e-14	4e-10	49 x 39 SEL1L family member 3 [Source:HGNC Symbol;Acc:HGNC:2
7	220635_at	2.21	7e-14	4e-10	4 x 19 psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;
8	208621_s_at	-1.21	8e-14	4e-09	0 x 48 ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
9	202720_at	-1.33	3e-13	4e-09	14 x 6 testin LIM domain protein [Source:HGNC Symbol;Acc:HGNC
10	210162_s_at	-1.5	5e-13	4e-09	0 x 24 nuclear factor of activated T cells 1 [Source:HGNC Symbol;A
11	206228_at	2.12	6e-13	4e-09	24 x 34 paired box 2 [Source:HGNC Symbol;Acc:HGNC:8616]
12	217767_at	-1.26	8e-13	4e-09	5 x 3 complement C3 [Source:HGNC Symbol;Acc:HGNC:1318]
13	204805_s_at	-1.45	1e-12	1e-08	49 x 39 H1 histone family member X [Source:HGNC Symbol;Acc:HGI
14	204998_s_at	1.14	2e-12	1e-08	0 x 18 activating transcription factor 5 [Source:HGNC Symbol;Acc:H
15	206059_at	-1.46	2e-12	1e-08	49 x 22 zinc finger protein 91 [Source:HGNC Symbol;Acc:HGNC:131
16	206023_at	2.07	2e-12	1e-08	33 x 46 neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
17	219812_at	-1.21	3e-12	4e-08	49 x 38 stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356]
18	206114_at	2.03	6e-12	4e-08	5 x 18 EPH receptor A4 [Source:HGNC Symbol;Acc:HGNC:3388]
19	207826_s_at	-1.09	7e-12	4e-08	43 x 49 inhibitor of DNA binding 3, HLH protein [Source:HGNC Symb
20	214961_at	2.01	9e-12	4e-08	28 x 37 microtubule associated scaffold protein 2 [Source:HGNC Syrr

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.25	NULL	2704	Chromatin states_Fibroblasts
2	9.26	NULL	3803	Chromatin states_Fibroblasts
3	8.35	NULL	3150	TF_ICGC_Creb1_targets
4	8.25	NULL	548	Chr Chr 16
5	8.2	NULL	4261	Lymphoma_Txn_transition
6	7.95	NULL	85	Lymphoma_kema_BCL2_DN_BCL6_UP
7	7.77	NULL	85	Lymphoma_kema_DLBCL_UP
8	7.75	NULL	4595	Chromatin states_Melanocytes
9	7.65	NULL	9	GSEA C2RUNNE_GENDER_EFFECT_UP
10	7.42	NULL	173	Lymphoma_tora_Light zone signature
11	7.32	NULL	18	Lymphoma_WRIGHT_ABC_UP
12	7.03	NULL	1600	Chromatin states_Melanocytes
13	6.97	NULL	4319	TF_ICGC_Pou2_targets
14	6.82	NULL	3564	TF_ICGC_Taf1_targets
15	6.66	NULL	353	Lymphoma_SPANG_CD40_6hrs_DN
16	6.59	NULL	8406	Chromatin states_peripheral blood_2_TssAFInk
17	6.54	NULL	3796	TF_ICGC_Nficsc81335_targets
18	6.4	NULL	8200	Chromatin states_peripheral blood_2_TssAFInk
19	6.39	NULL	71	Melanoma_tirosh_Macrophage specific genes-melanoma
20	6.33	NULL	7635	Chromatin states_peripheral blood_1_TssA
<i>Underexpressed</i>				
1	-10.26	NULL	136	Reference_Signature_2.9_Cytoskeleton
2	-10.07	NULL	282	Glioma_WILLSCHER_GBM_Verhaak-PNwt & CL_UP
3	-9.13	NULL	669	Chr Chr 6
4	-9.08	NULL	61	GSEA C2BASSO_CD40_SIGNALING_DN
5	-7.95	NULL	214	Lymphoma_ENZ_Stromal signature 1
6	-7.67	NULL	417	GSEA C2SHEN_SMARCA2_TARGETS_UP
7	-7.2	NULL	42	GSEA C2HUMMEL_BURKITTs_LYMPHOMA_UP
8	-7.09	NULL	3168	Lymphoma_HOPP_Repressed
9	-7.08	NULL	18	CC MHC class II protein complex
10	-6.97	NULL	642	GSEA C2CUI_TCF21_TARGETS_2_DN
11	-6.93	NULL	17	BP antigen processing and presentation of peptide or polysaccharide
12	-6.8	NULL	39	BP complement activation
13	-6.71	NULL	12	MF MHC class II receptor activity
14	-6.7	NULL	40	BP antigen processing and presentation
15	-6.5	NULL	500	GSEA C2ONKEN_UVEAL_MELANOMA_DN
16	-6.45	NULL	17	Lymphoma_kema_BCL2_UP_BCL6_DN
17	-6.2	NULL	23	CC integral component of luminal side of endoplasmic reticulum mem
18	-6.2	NULL	310	Reference_Signature_3.4_Protein phosphatases
19	-6.18	NULL	176	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
20	-6.15	NULL	52	BP complement activation, classical pathway

### p-values

