

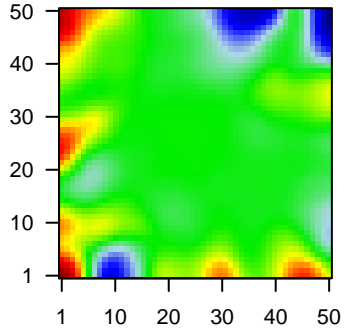
# MPI-245

## Global Summary

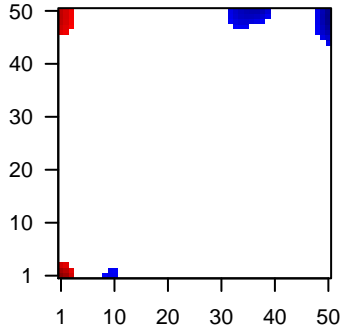
%DE = 0.05  
 # genes with fdr < 0.2 = 587 ( 317 + / 270 -)  
 # genes with fdr < 0.1 = 382 ( 223 + / 159 -)  
 # genes with fdr < 0.05 = 268 ( 161 + / 107 -)  
 # genes with fdr < 0.01 = 198 ( 123 + / 75 -)  
  
 # genes in genesets = 13152

<FC> = 0  
 <t-score> = 0.07  
 <p-value> = 0.26  
 <fdr> = 0.95

Portrait



Regulated Metagenes



## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	204141_at	-1.67	2e-16 4e-13	46 x 49 tubulin beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:1
2	209728_at	2.38	2e-16 4e-13	0 x 10 major histocompatibility complex, class II, DR beta 4 [Source:
3	213787_s_at	-1.48	2e-16 4e-13	34 x 47 empamil binding protein (sterol isomerase) [Source:HGNC S
4	213831_at	-2.08	2e-16 4e-13	49 x 16 major histocompatibility complex, class II, DQ alpha 1 [Source
5	215121_x_at	0.85	2e-16 4e-13	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215379_x_at	1.14	2e-16 4e-13	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
7	219517_at	-1.26	2e-16 4e-13	49 x 41
8	219518_s_at	-1.53	2e-16 4e-13	49 x 41
9	219521_at	2.71	2e-16 4e-13	31 x 13 beta-1,3-glucuronyltransferase 1 [Source:HGNC Symbol;Acc
10	219841_at	-1.82	2e-16 4e-13	1 x 17 activation induced cytidine deaminase [Source:HGNC Symbc
11	220377_at	2.33	2e-16 4e-13	5 x 28 family with sequence similarity 30 member A [Source:HGNC :
12	213005_s_at	-1.74	1e-15 3e-11	49 x 39 KN motif and ankyrin repeat domains 1 [Source:HGNC Symb
13	201909_at	1.29	4e-15 5e-11	43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:
14	213830_at	2	4e-15 5e-11	8 x 9
15	203509_at	-1.06	6e-15 6e-10	49 x 40 sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
16	209138_x_at	0.74	5e-14 6e-10	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
17	206843_at	1.9	8e-14 6e-10	11 x 33 crystallin beta A4 [Source:HGNC Symbol;Acc:HGNC:2396]
18	207005_s_at	1.88	1e-13 6e-10	0 x 26 BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC
19	216977_x_at	-1.11	2e-13 6e-10	37 x 49 small nuclear ribonucleoprotein polypeptide A' [Source:HGNC
20	206461_x_at	1.18	2e-13 6e-10	0 x 1 metallothionein 1H [Source:HGNC Symbol;Acc:HGNC:7400]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.11	NULL	223	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
2	11.49	NULL	589	Colon Cancerbckc_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	10.6	NULL	14	BP cellular response to zinc ion
4	10.05	NULL	219	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
5	10.03	NULL	102	ReferenceGSEA C2MCLACHLAN_DENTAL_CARIES_DN
6	9.83	NULL	14	BP negative regulation of growth
7	9.18	NULL	585	Chr Chr 7
8	8.82	NULL	88	GSEA C2MELAND_UP_BY_HBV_INFECTION
9	8.71	NULL	62	LymphomaMonti_Host_response_cluster
10	8.59	NULL	85	LymphomaChia_DLBCL_UP
11	8.56	NULL	386	GSEA C2RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
12	8.45	NULL	17	GSEA C2ZHENG_RESPONSE_TO_ARSENITE_UP
13	8.08	NULL	355	ReferenceGSEA C2ZHENG_RESPONSE_TO_ARSENITE_UP
14	8.06	NULL	166	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
15	7.98	NULL	447	Glioma ScoV_0.999_Sturm_E4_Mesenchymal_RTKI_PDGFRFA_DN
16	7.91	NULL	317	Cancer SPANG_BCL6-index2
17	7.83	NULL	297	GSEA C2RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
18	7.81	NULL	105	GSEA C2CHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
19	7.78	NULL	71	MelanomaTirosh_Macrophage specific genes-melanoma
20	7.61	NULL	265	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
<i>Underexpressed</i>				
1	-13.42	NULL	319	MelanomaSerber_wt/wt_melanoma-cells-SpotA
2	-11.55	NULL	244	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	-11.32	NULL	137	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	-11.16	NULL	431	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	-10.53	NULL	115	Glioma WILLSCHER_GBM_Verhaak-CL_up (C)
6	-10.35	NULL	219	ReferenceGSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	-10.32	NULL	14	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	-10.16	NULL	7225	ChromatinOstrep_fetal_midbrain_ReprPC
9	-10.07	NULL	726	GSEA C2PUJANA_CHEK2_PCC_NETWORK
10	-9.9	NULL	400	GSEA C2PUJANA_BRCA2_PCC_NETWORK
11	-9.81	NULL	79	MelanomaTirosh_core cycling genes in low- and high-proliferation melanoma
12	-9.79	NULL	966	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	-9.47	NULL	192	LymphomaTictora_Dark zone signature
14	-9.35	NULL	52	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
15	-9.26	NULL	174	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
16	-9.23	NULL	8918	ChromatinTirosh_ESC_Mesoderm
17	-9.11	NULL	93	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
18	-9.1	NULL	9576	ChromatinTirosh_MSC_Adipocyte
19	-9.04	NULL	1325	Chr Chr 1
20	-8.89	NULL	669	GSEA C2JOHNSTONE_PARVB_TARGETS_3_DN

p-values

