

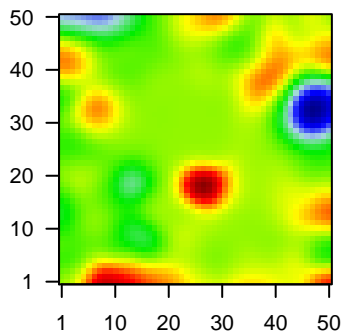
MPI-143

Global Summary

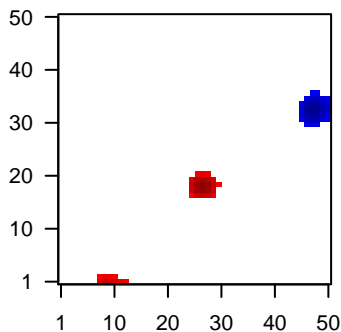
%DE = 0.03
 # genes with fdr < 0.2 = 167 (30 + / 137 -)
 # genes with fdr < 0.1 = 117 (19 + / 98 -)
 # genes with fdr < 0.05 = 71 (11 + / 60 -)
 # genes with fdr < 0.01 = 50 (6 + / 44 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = -0.41
 <p-value> = 0.32
 <fdr> = 0.97

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	206513_at	-1.78	2e-13	2e-08	1 x 8 absent in melanoma 2 [Source:HGNC Symbol;Acc:HGNC:35]
2	202131_s_at	-2.26	1e-12	9e-08	45 x 31 RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]
3	215379_x_at	1.41	5e-12	9e-07	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:11451]
4	203132_at	-1.75	5e-11	4e-06	46 x 30 RB transcriptional corepressor 1 [Source:HGNC Symbol;Acc:HGNC:11451]
5	216899_s_at	-1.81	2e-10	2e-05	0 x 13 src kinase associated phosphoprotein 2 [Source:HGNC Symbol;Acc:HGNC:11451]
6	210538_s_at	-1.5	1e-09	5e-05	3 x 6 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:HGNC:11451]
7	217466_x_at	-1.1	5e-09	5e-05	15 x 8 ribosomal protein S2 pseudogene 46 [Source:HGNC Symbol;Acc:HGNC:11451]
8	210396_s_at	-1.54	7e-09	5e-05	44 x 30 SMG1 pseudogene 5 [Source:HGNC Symbol;Acc:HGNC:498]
9	203302_at	-1.4	8e-09	5e-05	47 x 35 deoxycytidine kinase [Source:HGNC Symbol;Acc:HGNC:270]
10	209023_s_at	-1.48	1e-08	1e-04	46 x 30 stromal antigen 2 [Source:HGNC Symbol;Acc:HGNC:11355]
11	207783_x_at	-0.98	2e-08	1e-04	45 x 28 tumor protein, translationally-controlled 1 [Source:HGNC Symbol;Acc:HGNC:11355]
12	202906_s_at	-1.59	2e-08	1e-04	13 x 18 nibrin [Source:HGNC Symbol;Acc:HGNC:7652]
13	217985_s_at	-1.65	3e-08	2e-04	46 x 29 bromodomain adjacent to zinc finger domain 1A [Source:HGNC Symbol;Acc:HGNC:11355]
14	218871_x_at	-2.17	3e-08	3e-04	46 x 31 chondroitin sulfate N-acetylgalactosaminyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:11355]
15	218172_s_at	-1.55	5e-08	3e-04	45 x 31 derlin 1 [Source:HGNC Symbol;Acc:HGNC:28454]
16	218700_s_at	-1.87	7e-08	3e-04	0 x 5 RAB29, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:11355]
17	214836_x_at	-1.23	9e-08	3e-04	0 x 3
18	217745_s_at	-1.14	1e-07	6e-04	45 x 30 N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:HGNC Symbol;Acc:HGNC:11355]
19	206062_at	2.38	1e-07	1e-03	7 x 33 guanylate cyclase activator 1A [Source:HGNC Symbol;Acc:HGNC:11355]
20	205091_x_at	-1.53	2e-07	1e-03	46 x 32 RecQ like helicase [Source:HGNC Symbol;Acc:HGNC:9948]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.92	NULL	2704	Chromatin state 6
2	13.27	NULL	3724	Chromatin state 6 peripheral blood_12_EnhBiv
3	12.11	NULL	3734	Chromatin state 6 peripheral blood_13_ReprPC
4	11.32	NULL	2747	Chromatin state 6 peripheral blood_12_EnhBiv
5	11.18	NULL	3150	Chromatin state 6 myeloid cells peripheral blood_13_ReprPC
6	10.82	NULL	2380	Chromatin state 6
7	10.64	NULL	3184	Chromatin state 6 myeloid cells peripheral blood_12_EnhBiv
8	10.54	NULL	2507	Chromatin state 6 frontal_Lobe_ReprPC
9	10.41	NULL	2154	Chromatin state 6 regulatory cells peripheral blood_11_BivFink
10	10.27	NULL	2602	Chromatin state 6 killer cells peripheral blood_12_EnhBiv
11	10.08	NULL	2765	Chromatin state 6 regulatory cells peripheral blood_13_ReprPC
12	10.04	NULL	2134	Chromatin state 6 regulatory cells peripheral blood_12_EnhBiv
13	10.01	NULL	833	Chr Chr 19
14	9.84	NULL	3803	Chromatin state 6 Fibroblasts
15	9.77	NULL	196	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	9.43	NULL	747	GSEA C2NABA_MATRISOME
17	9.42	NULL	2724	Chromatin state 6 peripheral blood_11_BivFink
18	9.35	NULL	2203	Chromatin state 6 Colon
19	9.15	NULL	1239	Chromatin state 6 Colon
20	9.03	NULL	1943	Chromatin state 6 Colon
<i>Underexpressed</i>				
1	-18.13	NULL	4528	Chromatin state 6 naive cells peripheral blood_4_Tx
2	-17.98	NULL	310	Reference Signal 3,4_Protein phosphatases
3	-17.3	NULL	5529	Lymphoid tissue development
4	-17.1	NULL	6244	Chromatin state 6 Fibroblasts
5	-17.06	NULL	5908	Lymphoid tissue development
6	-17.06	NULL	5766	Chromatin state 6 killer cells peripheral blood_4_Tx
7	-16.97	NULL	2325	Chromatin state 6 ZNF_Rpts
8	-16.96	NULL	5716	Chromatin state 6 peripheral blood_4_Tx
9	-16.85	NULL	5753	Chromatin state 6 peripheral blood_4_Tx
10	-16.63	NULL	6099	Chromatin state 6 Tx
11	-16.26	NULL	5527	Chromatin state 6 regulatory cells peripheral blood_4_Tx
12	-15.96	NULL	5601	Chromatin state 6 naive cells peripheral blood_4_Tx
13	-15.8	NULL	5682	Lymphoid tissue development
14	-15.79	NULL	5738	Chromatin state 6 myeloid cells peripheral blood_4_Tx
15	-15.18	NULL	6637	Chromatin state 6 peripheral blood_5_TxWk
16	-15.17	NULL	417	GSEA C2SHEN_SMARCA2_TARGETS_UP
17	-14.76	NULL	4683	Chromatin state 6 chr19_fetal_midbrain_HetRpts
18	-14.75	NULL	3554	Chromatin state 6 chr19_Rpts_ESC_Endoderm
19	-14.74	NULL	7420	Chromatin state 6 peripheral blood_1_TssA
20	-14.01	NULL	4357	Lymphoid tissue development

p-values

