

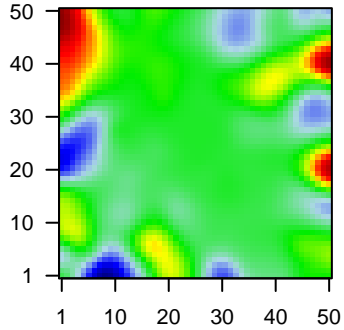
MPI-121

Global Summary

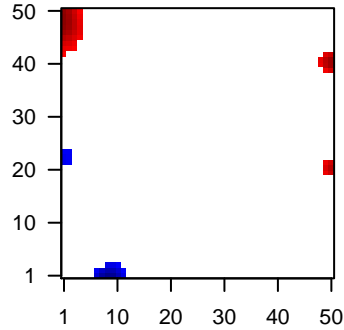
%DE = 0.06
 # genes with fdr < 0.2 = 795 (464 + / 331 -)
 # genes with fdr < 0.1 = 503 (298 + / 205 -)
 # genes with fdr < 0.05 = 428 (252 + / 176 -)
 # genes with fdr < 0.01 = 225 (123 + / 102 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.05
 <p-value> = 0.24
 <fdr> = 0.94

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	39318_at	-1.72	2e-16	4e-13	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:3778]
2	204053_x_at	-1.26	2e-16	4e-13	18 x 23 phosphatase and tensin homolog pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:3778]
3	204794_at	-1.41	2e-16	4e-13	0 x 7 dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:HGNC:3778]
4	207325_x_at	2.58	2e-16	4e-13	10 x 27 MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC:3778]
5	209193_at	-1.35	2e-16	4e-13	0 x 20 Pim-1 proto-oncogene, serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:3778]
6	209942_x_at	2.73	2e-16	4e-13	10 x 27 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:3778]
7	209995_s_at	-1.55	2e-16	4e-13	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:3778]
8	210495_x_at	-1.09	2e-16	4e-13	8 x 0 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
9	210809_s_at	-1.92	2e-16	4e-13	9 x 0 periostin [Source:HGNC Symbol;Acc:HGNC:16953]
10	212464_s_at	-1.17	2e-16	4e-13	8 x 0 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	214612_x_at	2.56	2e-16	4e-13	10 x 27 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:3778]
12	218051_s_at	-1.58	2e-16	4e-13	39 x 47 5'-nucleotidase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:3778]
13	219093_at	2.07	2e-16	4e-13	15 x 17 phosphotyrosine interaction domain containing 1 [Source:HGNC Symbol;Acc:HGNC:3778]
14	219841_at	-1.64	4e-16	1e-11	1 x 17 activation induced cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:3778]
15	205780_at	-1.2	1e-15	1e-11	40 x 49 BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:10710]
16	217734_s_at	-1.51	2e-15	5e-11	41 x 42 WD repeat domain 6 [Source:HGNC Symbol;Acc:HGNC:12717]
17	202986_at	1.95	6e-15	5e-11	0 x 18 aryl hydrocarbon receptor nuclear translocator 2 [Source:HGNC Symbol;Acc:HGNC:3778]
18	206218_at	1.95	7e-15	8e-11	0 x 15 MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC:3778]
19	209374_s_at	-0.86	1e-14	8e-11	0 x 22 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:3778]
20	204562_at	-1.13	2e-14	8e-11	0 x 20 interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGNC:3778]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.6	NULL	585	Chr Chr 7
2	10.95	NULL	556	Chr Chr X
3	9.99	NULL	4	ImmunoChromosome 10q25.31
4	9.66	NULL	492	Chr Chr 9
5	9.02	NULL	5716	Chromatin state peripheral blood_4_Tx
6	8.61	NULL	7420	Chromatin state peripheral blood_1_TssA
7	8.36	NULL	4357	Lymphoid tissue development
8	8.09	NULL	7833	Chromatin state peripheral blood_1_TssA
9	8.06	NULL	7635	Chromatin state T cells peripheral blood_1_TssA
10	8.02	NULL	5766	Chromatin state killer cells peripheral blood_4_Tx
11	7.88	NULL	14	Lymphoid tissue development
12	7.73	NULL	7	ImmunoChromosome 10q25.31
13	7.69	NULL	7751	Chromatin state killer cells peripheral blood_1_TssA
14	7.6	NULL	5738	Chromatin state T cells peripheral blood_4_Tx
15	7.35	NULL	8406	Chromatin state peripheral blood_2_TssAFlnk
16	7.32	NULL	7078	Chromatin state peripheral blood_5_TxWk
17	7.32	NULL	5753	Chromatin state peripheral blood_4_Tx
18	7.24	NULL	95	GSEA C2:INDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q
19	6.99	NULL	7957	Chromatin state peripheral blood_2_TssAFlnk
20	6.99	NULL	5601	Chromatin state killer cells peripheral blood_4_Tx
<i>Underexpressed</i>				
1	-11.73	NULL	85	Lymphoid tissue development
2	-9.29	NULL	18	Lymphoid tissue development
3	-7.6	NULL	63	GSEA C2:ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
4	-7.49	NULL	689	Chr Chr 3
5	-7.39	NULL	669	Chr Chr 6
6	-7.15	NULL	196	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	-7.15	NULL	2747	Chromatin state peripheral blood_12_EnhBiv
8	-7.08	NULL	2405	Chromatin state peripheral blood_13_ReprPC
9	-6.68	NULL	3724	Chromatin state peripheral blood_12_EnhBiv
10	-6.66	NULL	2765	Chromatin state regulatory cells peripheral blood_13_ReprPC
11	-6.64	NULL	2154	Chromatin state regulatory cells peripheral blood_11_BivFlnk
12	-6.41	NULL	3734	Chromatin state peripheral blood_13_ReprPC
13	-6.4	NULL	3150	Chromatin state T cells peripheral blood_13_ReprPC
14	-6.25	NULL	1799	Chromatin state naive cells peripheral blood_13_ReprPC
15	-6.22	NULL	747	GSEA C2:NABA_MATRISOME
16	-6.21	NULL	2602	Chromatin state killer cells peripheral blood_12_EnhBiv
17	-6.14	NULL	2194	Chromatin state T cells peripheral blood_12_EnhBiv
18	-6.12	NULL	10	Lymphoid tissue development
19	-6.07	NULL	132	Colon Cancer
20	-5.93	NULL	1660	Chromatin state naive cells peripheral blood_12_EnhBiv

p-values

