

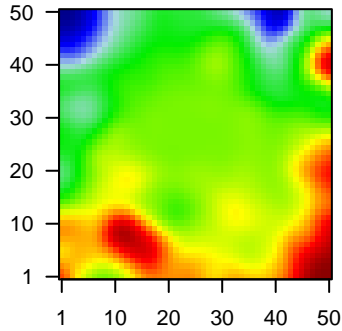
MPI-203

Global Summary

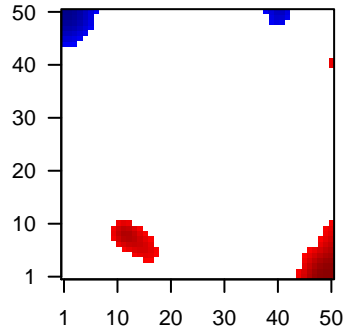
%DE = 0.03
 # genes with fdr < 0.2 = 334 (128 + / 206 -)
 # genes with fdr < 0.1 = 280 (110 + / 170 -)
 # genes with fdr < 0.05 = 181 (70 + / 111 -)
 # genes with fdr < 0.01 = 100 (41 + / 59 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = -0.11
 <p-value> = 0.29
 <fdr> = 0.97

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	205321_at	-2.04	2e-16	2e-12	1 x 45 eukaryotic translation initiation factor 2 subunit gamma B [So
2	209825_s_at	-1.98	2e-16	2e-12	39 x 47 uridine-cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
3	216977_x_at	-1.59	4e-15	2e-09	37 x 49 small nuclear ribonucleoprotein polypeptide A' [Source:HGNC
4	212563_at	-1.72	2e-13	2e-09	39 x 46 block of proliferation 1 [Source:HGNC Symbol;Acc:HGNC:15:
5	209942_x_at	2.51	3e-13	2e-09	10 x 27 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
6	209173_at	2.5	3e-13	6e-09	17 x 13 anterior gradient 2, protein disulphide isomerase family memt
7	200648_s_at	-1.52	8e-13	6e-09	2 x 0 glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGN
8	214612_x_at	2.45	9e-13	4e-08	10 x 27 MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
9	201801_s_at	-1.77	3e-12	4e-08	0 x 44 solute carrier family 29 member 1 (Augustine blood group) [S
10	206023_at	2.37	5e-12	7e-08	33 x 46 neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
11	202003_s_at	-1.29	8e-12	1e-07	34 x 49 acetyl-CoA acyltransferase 2 [Source:HGNC Symbol;Acc:HC
12	217211_at	-1.63	2e-11	1e-07	0 x 49 actin, beta pseudogene 9 [Source:HGNC Symbol;Acc:HGNC
13	201514_s_at	-1.38	2e-11	6e-07	5 x 45 G3BP stress granule assembly factor 1 [Source:HGNC Symb
14	202188_at	-1.41	4e-11	6e-06	33 x 49 nucleoporin 93 [Source:HGNC Symbol;Acc:HGNC:28958]
15	218051_s_at	-1.64	3e-10	7e-06	39 x 47 5'-nucleotidase domain containing 2 [Source:HGNC Symbol;
16	200730_s_at	-1.64	8e-10	7e-06	5 x 49 protein tyrosine phosphatase type IVA, member 1 [Source:HC
17	44790_s_at	-1.12	1e-09	7e-06	42 x 49 RUN and cysteine rich domain containing beclin 1 interacting
18	204249_s_at	1.19	1e-09	7e-06	2 x 4 LIM domain only 2 [Source:HGNC Symbol;Acc:HGNC:6642]
19	210467_x_at	2.06	2e-09	7e-06	10 x 27 MAGE family member A12 [Source:HGNC Symbol;Acc:HGNC
20	218532_s_at	2.06	2e-09	1e-05	15 x 5 reticulophagy regulator 1 [Source:HGNC Symbol;Acc:HGNC:

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.82	NULL	429	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	10.46	NULL	589	Colon Cancerbcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
3	9.54	NULL	3838	ChromatinStates_ESC_Mesoderm
4	9.21	NULL	265	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
5	9.21	NULL	102	ReferenceGenes/B-cells
6	8.82	NULL	83	MelanomaCGA_melanoma_immune_high
7	8.76	NULL	33	MelanomaTirosh_T-cell specific genes-melanoma
8	8.66	NULL	4079	ChromatinStates_ESC_Endoderm
9	8.39	NULL	56	PneumoniaBurham_sep_vs_con_DN
10	8.23	NULL	3110	ChromatinStatesPCWk_ESC_Endoderm
11	8.19	NULL	2972	ChromatinStatesPC_ESC_Endoderm
12	7.9	NULL	516	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
13	7.75	NULL	2825	ChromatinStatesESC_Mesoderm
14	7.72	NULL	42	GSEA C2SHIPP_DLCL_VS_FOLLICULAR_LYMPHOMA_DN
15	7.71	NULL	143	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
16	7.7	NULL	15	LymphomaGare_Polarized immune response
17	7.68	NULL	62	LymphomaMonti_Host_response_cluster
18	7.48	NULL	40	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
19	7.47	NULL	299	GSEA C2DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
20	7.39	NULL	42	GSEA C2WILMS_NOTCH1_TARGETS_UP
<i>Underexpressed</i>				
1	-14.38	NULL	575	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
2	-12.99	NULL	728	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	-12.49	NULL	280	GSEA C2MANALO_HYPOXIA_DN
4	-11.51	NULL	703	GSEA C2LEE_BMP2_TARGETS_DN
5	-11.29	NULL	966	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
6	-11.28	NULL	651	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	-11.08	NULL	1161	MF RNA binding
8	-10.91	NULL	1527	GSEA C2PUJANA_BRCA1_PCC_NETWORK
9	-10.79	NULL	1052	GSEA C2DODD_NASOPHARYNGEAL_CARCIOMA_DN
10	-10.32	NULL	726	GSEA C2PUJANA_CHEK2_PCC_NETWORK
11	-10.12	NULL	406	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
12	-10.08	NULL	190	HM HALLMARK_MYC_TARGETS_V1
13	-10.01	NULL	4261	LymphomaHOPP_Txn_transition
14	-9.92	NULL	233	GSEA C2PENG_RAPAMYCIN_RESPONSE_DN
15	-9.9	NULL	55	HM HALLMARK_MYC_TARGETS_V2
16	-9.88	NULL	2204	ChromatinStatesESC_Mesoderm
17	-9.82	NULL	314	GSEA C2PENG_GlutAMINE_DEPRIVATION_DN
18	-9.74	NULL	677	ReferenceGenes/INFLAS_esophagus
19	-9.64	NULL	1221	CC mitochondrion
20	-9.62	NULL	268	GSEA C2MUELLER_PLURINET

p-values

