

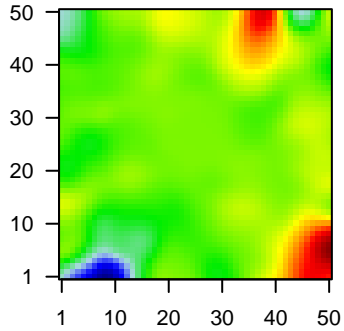
MPI-201

Global Summary

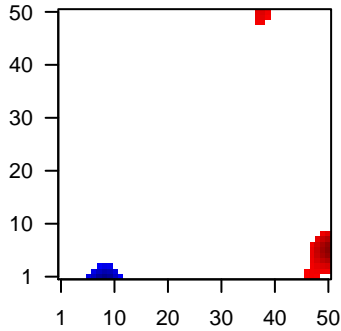
%DE = 0.04
 # genes with $fdr < 0.2$ = 373 (86 + / 287 -)
 # genes with $fdr < 0.1$ = 253 (59 + / 194 -)
 # genes with $fdr < 0.05$ = 222 (53 + / 169 -)
 # genes with $fdr < 0.01$ = 129 (26 + / 103 -)
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.16
 <p-value> = 0.29
 <fdr> = 0.96

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	201122_x_at	-1.7	2e-16	6e-13	49 x 43 eukaryotic translation initiation factor 5A [Source:HGNC Sym]
2	201123_s_at	-1.99	2e-16	6e-13	1 x 43 eukaryotic translation initiation factor 5A [Source:HGNC Sym]
3	201909_at	-1.46	2e-16	6e-13	43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:
4	205859_at	-1.65	2e-16	6e-13	49 x 39 lymphocyte antigen 86 [Source:HGNC Symbol;Acc:HGNC:16
5	209199_s_at	-2.02	2e-16	6e-13	16 x 6 myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HGNC:16
6	209200_at	-1.71	2e-16	6e-13	16 x 6 myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HGNC:16
7	211656_x_at	-1.15	2e-16	6e-13	2 x 9 major histocompatibility complex, class II, DQ beta 1 [Source:
8	215379_x_at	-1.08	2e-16	6e-13	41 x 42 immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:
9	204446_s_at	-1.43	7e-16	7e-12	44 x 49 arachidonate 5-lipoxygenase [Source:HGNC Symbol;Acc:HGNC:16
10	216733_s_at	-1.46	9e-16	2e-11	0 x 19 glycine amidinotransferase [Source:HGNC Symbol;Acc:HGNC:16
11	207861_at	2.09	2e-15	2e-11	0 x 20 C-C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:HGNC:16
12	201893_x_at	-1.43	3e-15	5e-10	8 x 0 decorin [Source:HGNC Symbol;Acc:HGNC:2705]
13	39318_at	1.06	3e-14	2e-09	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:16
14	212094_at	-1.76	1e-13	2e-09	45 x 49 paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:16
15	201161_s_at	-1.22	2e-13	6e-09	42 x 48 Y-box binding protein 3 [Source:HGNC Symbol;Acc:HGNC:2
16	201403_s_at	-1.13	7e-13	6e-09	6 x 4 microsomal glutathione S-transferase 3 [Source:HGNC Sym]
17	202371_at	-1.53	7e-13	1e-08	0 x 7 transcription elongation factor A like 4 [Source:HGNC Symbo
18	209995_s_at	1.1	1e-12	8e-08	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:16
19	211813_x_at	-1.49	6e-12	8e-08	8 x 0 decorin [Source:HGNC Symbol;Acc:HGNC:2705]
20	216598_s_at	-1.43	8e-12	5e-07	3 x 0 C-C motif chemokine ligand 2 [Source:HGNC Symbol;Acc:HGNC:16

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.12	NULL	319	Melanoma_Gerber_wt/wt_melanoma-cells-SpotA
2	13.23	NULL	115	Glioma_WILLSCHER_GBM_Verhaak-CL_up (C)
3	13.18	NULL	137	GSEA_C2R0STY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	13.18	NULL	244	GSEA_C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	12.47	NULL	254	GSEA_C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
6	12.28	NULL	14	Cancer_SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	11.98	NULL	726	GSEA_C2PUJANA_CHEK2_PCC_NETWORK
8	11.71	NULL	84	GSEA_C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
9	11.58	NULL	187	HM_HALLMARK_E2F_TARGETS
10	11.55	NULL	431	GSEA_C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	11.45	NULL	1527	GSEA_C2PUJANA_BRCA1_PCC_NETWORK
12	11.06	NULL	400	GSEA_C2PUJANA_BRCA2_PCC_NETWORK
13	10.92	NULL	79	Melanoma_Irosh_core cycling genes in low- and high-proliferation melanoma
14	10.69	NULL	93	GSEA_C2CROONQUIST_IL6_DEPRIVATION_DN
15	10.3	NULL	439	GSEA_C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	10.26	NULL	966	GSEA_C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
17	9.96	NULL	526	GSEA_C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
18	9.95	NULL	7930	Chromatin_Regulatory cells peripheral blood_1_TssA
19	9.95	NULL	117	GSEA_C2ZHANG_CYCLING_GENES
20	9.94	NULL	52	GSEA_C2KANG_DOXORUBICIN_RESISTANCE_UP
<i>Underexpressed</i>				
1	-13.08	NULL	335	GSEA_C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	-12.85	NULL	2154	Chromatin_Regulatory cells peripheral blood_11_BivFink
3	-12.61	NULL	2765	Chromatin_Regulatory cells peripheral blood_13_ReprPC
4	-12.05	NULL	3089	Chromatin_Regulatory cells peripheral blood_14_ReprPCWk
5	-12.05	NULL	247	GSEA_C2BOQUEST_STEM_CELL_UP
6	-11.93	NULL	3724	Chromatin_Regulatory cells peripheral blood_12_EnhBiv
7	-11.91	NULL	1611	Chromatin_Regulatory cells killer cells peripheral blood_11_BivFink
8	-11.78	NULL	1700	Chromatin_Regulatory cells peripheral blood_11_BivFink
9	-11.71	NULL	2747	Chromatin_Regulatory cells peripheral blood_12_EnhBiv
10	-11.68	NULL	2724	Chromatin_Regulatory cells peripheral blood_11_BivFink
11	-11.42	NULL	196	HM_HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	-11.32	NULL	1372	Chromatin_Regulatory cells peripheral blood_10_TssBiv
13	-11.02	NULL	2602	Chromatin_Regulatory cells killer cells peripheral blood_12_EnhBiv
14	-10.77	NULL	3001	Chromatin_Regulatory cells peripheral blood_14_ReprPCWk
15	-10.76	NULL	2194	Chromatin_Regulatory cells peripheral blood_12_EnhBiv
16	-10.6	NULL	1694	Chromatin_Regulatory cells peripheral blood_11_BivFink
17	-10.59	NULL	2134	Chromatin_Regulatory cells peripheral blood_12_EnhBiv
18	-10.57	NULL	63	GSEA_C2ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
19	-10.36	NULL	3918	Chromatin_Regulatory cells peripheral blood_14_ReprPCWk
20	-10.34	NULL	3734	Chromatin_Regulatory cells peripheral blood_13_ReprPC

p-values

