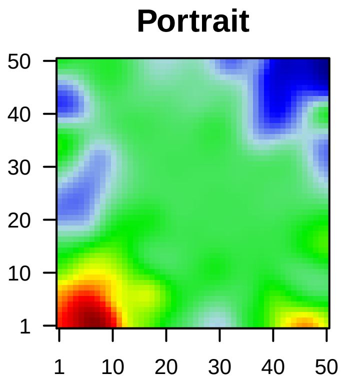
MPI−207

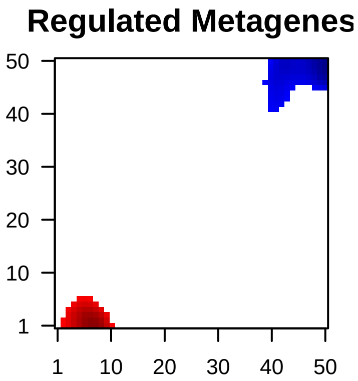
Global Summary

%DE = 0.05
genes with fdr < 0.2 = 471 (232 + / 239 −)
genes with fdr < 0.1 = 300 (148 + / 152 −)
genes with fdr < 0.05 = 247 (125 + / 122 −)
genes with fdr < 0.01 = 140 (75 + / 65 −)

genes in genesets = 13152

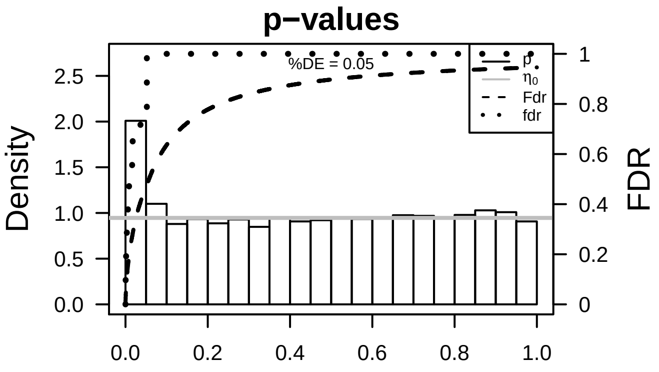
<FC> = 0
<t−score> = 0.02
<p−value> = 0.27
<fdr> = 0.95


Portrait


Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	207599_at	2.49	2e−16	8e−13	16 x 7	matrix metallopeptidase 20 [Source:HGNC Symbol;Acc:HGN
2	209138_x_at	−1.09	2e−16	8e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
3	209995_s_at	−1.57	2e−16	8e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
4	214677_x_at	−1.05	2e−16	8e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
5	215121_x_at	−1.03	2e−16	8e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215379_x_at	−1.58	2e−16	8e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
7	44790_s_at	−1.25	4e−16	4e−11	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
8	212496_s_at	−1.44	3e−15	4e−11	46 x 38	lysine demethylase 4B [Source:HGNC Symbol;Acc:HGNC:29
9	209374_s_at	−1	5e−15	1e−10	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
10	207900_at	2.22	1e−14	1e−10	3 x 6	C−C motif chemokine ligand 17 [Source:HGNC Symbol;Acc:H
11	219471_at	−1.13	2e−14	8e−10	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
12	214470_at	2.17	6e−14	1e−08	9 x 8	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
13	39318_at	−1.09	6e−13	3e−07	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
14	207328_at	1.93	2e−11	3e−07	17 x 20	arachidonate 15−lipoxygenase [Source:HGNC Symbol;Acc:H
15	217796_s_at	−1.35	3e−11	3e−07	0 x 39	NPL4 homolog, ubiquitin recognition factor [Source:HGNC Sy
16	203760_s_at	−1.2	4e−11	4e−07	0 x 20	Src like adaptor [Source:HGNC Symbol;Acc:HGNC:10902]
17	206255_at	−1.19	6e−11	6e−07	48 x 45	BLK proto−oncogene, Src family tyrosine kinase [Source:HG
18	206140_at	1.87	9e−11	8e−07	5 x 12	LIM homeobox 2 [Source:HGNC Symbol;Acc:HGNC:6594]
19	213036_x_at	−0.88	1e−10	8e−07	0 x 40	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
20	219255_x_at	1.83	2e−10	8e−07	0 x 19	interleukin 17 receptor B [Source:HGNC Symbol;Acc:HGNC:


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	17.2	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	14.53	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	14.39	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	12.68	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
5	12.63	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
6	12.52	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
7	11.71	NULL	288	Colon Cancer	Peetrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	11.63	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
9	11.58	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
10	11.27	NULL	327	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
11	11.17	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
12	11.16	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
13	10.46	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	10.43	NULL	255	GSEA C2	HELLER_SILENCED_BY_METHYLATION_UP
15	10.37	NULL	261	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_UP
16	10.36	NULL	331	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
17	10.36	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
18	10.34	NULL	589	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
19	10.29	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
20	10.22	NULL	166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
Underexpressed					
1	−13.28	NULL	6997	Chromatin states	Overlap_fetal_midbrain_K9K27me3
2	−12.76	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
3	−12.62	NULL	5620	Chromatin states	TssF_Colon
4	−11.93	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
5	−11.57	NULL	7331	Chromatin states	TssA_Colon
6	−11.55	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
7	−11.35	NULL	2704	Chromatin states	4_TxTrans_Fibroblasts
8	−11.34	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
9	−11.18	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
10	−11.01	NULL	7165	Chromatin states	Tx_Colon
11	−10.77	NULL	8068	Chromatin states	T helper cells peripheral blood_1_TssA
12	−10.7	NULL	4208	Chromatin states	T cells peripheral blood_6_EnhG
13	−10.68	NULL	8431	Chromatin states	T CD8+ naive cells peripheral blood_2_TssAFlnk
14	−10.56	NULL	8370	Chromatin states	natural killer cells peripheral blood_2_TssAFlnk
15	−10.47	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
16	−10.41	NULL	728	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	−10.4	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
18	−10.39	NULL	5527	Chromatin states	T regulatory cells peripheral blood_4_Tx
19	−10.15	NULL	4595	Chromatin states	6_EnhG_Melanocytes
20	−10.09	NULL	8322	Chromatin states	T CD8+ naive cells peripheral blood_1_TssA