MPI−212

Global Summary

%DE = 0.03

genes with fdr < 0.2 = 291 (170 + / 121 −)

genes with fdr < 0.1 = 188 (107 + / 81 −)

genes with fdr < 0.05 = 105 (53 + / 52 −)

genes with fdr < 0.01 = 70 (28 + / 42 −)

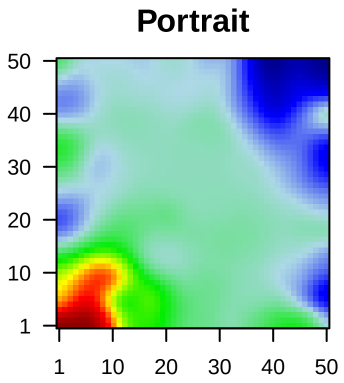
genes in genesets = 13152

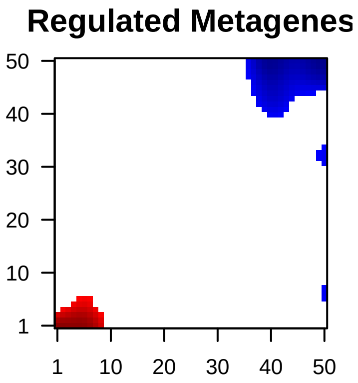
<FC> = 0

<t−score> = −0.13

<p−value> = 0.31

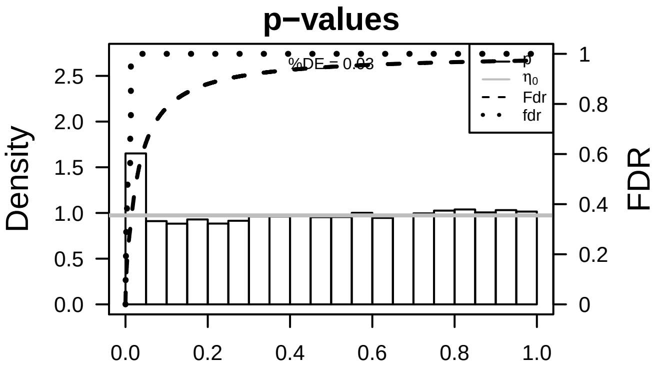
<fdr> = 0.97


Portrait


Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	219471_at	−1.46	4e−16	7e−12	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
2	39318_at	−1.48	7e−16	3e−10	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
3	209772_s_at	−2.11	2e−14	3e−10	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
4	204538_x_at	−1.88	2e−14	3e−10	49 x 6	nuclear pore complex−interacting protein family member A5 is
5	214870_x_at	−1.63	4e−14	1e−09	49 x 5	nuclear pore complex−interacting protein family member A5 is
6	221501_x_at	−1.77	1e−13	1e−09	49 x 6	nuclear pore complex−interacting protein family member A5 is
7	209995_s_at	−1.51	1e−13	1e−09	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
8	213831_at	−1.59	2e−13	3e−08	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
9	208651_x_at	−1.57	2e−12	3e−08	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
10	208650_s_at	−1.53	4e−12	3e−08	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
11	44790_s_at	−1.29	5e−12	3e−07	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
12	216379_x_at	−1.17	2e−11	6e−07	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	203290_at	2	7e−11	6e−07	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
14	212680_x_at	−1.21	7e−11	9e−07	39 x 45	protein phosphatase 1 regulatory inhibitor subunit 14B [Sourc
15	218051_s_at	−1.71	1e−10	9e−07	39 x 47	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
16	212187_x_at	1.03	2e−10	9e−07	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
17	202431_s_at	−1.09	2e−10	9e−07	42 x 47	MYC proto−oncogene, bHLH transcription factor [Source:HG
18	209771_x_at	−1.11	2e−10	5e−06	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
19	206310_at	2.18	5e−10	5e−06	17 x 6	serine peptidase inhibitor, Kazal type 2 [Source:HGNC Symb
20	211748_x_at	0.98	9e−10	5e−06	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.36	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	21.77	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	20.95	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	20.29	NULL	102	Reference Signatures	WIRTH_EBV B−cells
5	19.69	NULL	214	Lymphoma	LENZ_Stromal signature 1
6	17.74	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
7	17.43	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
8	17.43	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
9	17.16	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
10	17.13	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
11	16.7	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
12	16.18	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
13	16.02	NULL	202	GSEA C2	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
14	15.86	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
15	15.85	NULL	78	Melanoma	Tirosh_expression higher in CAFs than in T−cells
16	15.64	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
17	15.07	NULL	67	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
18	15.05	NULL	397	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
19	14.86	NULL	194	GSEA C2	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
20	14.82	NULL	1611	CC	extracellular region
Underexpressed					
1	−17.37	NULL	5456	Chromatin states	5_Tx_Neuronal_Progenitor
2	−16.69	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
3	−16.62	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
4	−16.52	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
5	−15.88	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
6	−15.46	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
7	−14.92	NULL	6068	Chromatin states	4_Tx_ESC_Endoderm
8	−14.71	NULL	5529	Lymphoma	HOPP_Txn_elongation
9	−14.32	NULL	4261	Lymphoma	HOPP_Txn_transition
10	−14.15	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
11	−13.89	NULL	7833	Chromatin states	Bcells peripheral blood_1_TssA
12	−13.66	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
13	−13.58	NULL	6997	Chromatin states	Overlap_fetal_midbrain_K9K27me3
14	−13.57	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
15	−13.19	NULL	703	GSEA C2	LEE_BMP2_TARGETS_DN
16	−13.07	NULL	6099	Chromatin states	HSC_4_Tx
17	−12.92	NULL	2541	CC	nucleoplasm
18	−12.88	NULL	5716	Chromatin states	Bcells peripheral blood_4_Tx
19	−12.84	NULL	187	HM	HALLMARK_E2F_TARGETS
20	−12.82	NULL	4579	CC	nucleus