MPI−200

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 661 (396 + / 265 −)

genes with fdr < 0.1 = 442 (273 + / 169 −)

genes with fdr < 0.05 = 342 (205 + / 137 −)

genes with fdr < 0.01 = 187 (110 + / 77 −)

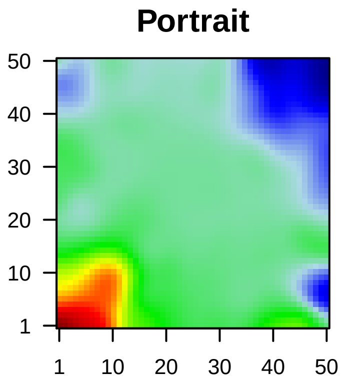
genes in genesets = 13152

<FC> = 0

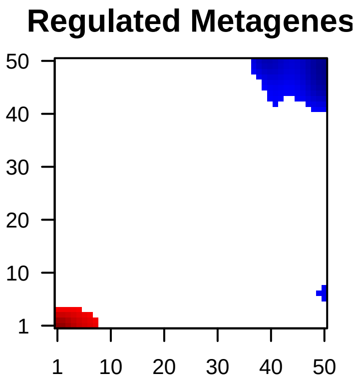
<t−score> = −0.12

<p−value> = 0.25

<fdr> = 0.94



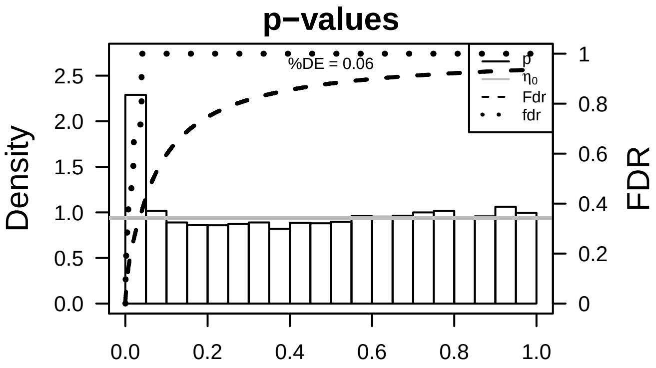
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201123_s_at	−1.49	2e−16	7e−13	1 x 43	eukaryotic translation initiation factor 5A [Source:HGNC Syml
2	204259_at	3.09	2e−16	7e−13	6 x 3	matrix metallopeptidase 7 [Source:HGNC Symbol;Acc:HGNC
3	208650_s_at	−1.99	2e−16	7e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
4	210258_at	−1.52	2e−16	7e−13	49 x 40	regulator of G protein signaling 13 [Source:HGNC Symbol;Ac
5	214870_x_at	−2.06	2e−16	7e−13	49 x 5	nuclear pore complex−interacting protein family member A5 is
6	215714_s_at	−1.84	2e−16	7e−13	46 x 49	SWI/SNF related, matrix associated, actin dependent regulato
7	221501_x_at	−1.68	2e−16	7e−13	49 x 6	nuclear pore complex−interacting protein family member A5 is
8	202726_at	−2.07	4e−16	4e−09	49 x 49	DNA ligase 1 [Source:HGNC Symbol;Acc:HGNC:6598]
9	203290_at	1.91	2e−13	2e−08	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
10	211430_s_at	0.97	1e−12	6e−08	0 x 4	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
11	201122_x_at	−1.21	4e−12	9e−08	49 x 43	eukaryotic translation initiation factor 5A [Source:HGNC Syml
12	209771_x_at	−1.01	8e−12	1e−07	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	212094_at	−1.82	1e−11	3e−07	45 x 49	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:1
14	203795_s_at	−1.39	3e−11	3e−07	42 x 49	BCL tumor suppressor 7A [Source:HGNC Symbol;Acc:HGNC
15	211748_x_at	0.9	4e−11	3e−07	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
16	203915_at	0.96	7e−11	3e−07	0 x 0	C−X−C motif chemokine ligand 9 [Source:HGNC Symbol;Acc
17	212187_x_at	0.89	7e−11	3e−07	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
18	207730_x_at	−1.22	9e−11	3e−07	49 x 6	
19	204237_at	1.92	9e−11	3e−07	23 x 8	GULP, engulfment adaptor PTB domain containing 1 [Source:
20	214100_x_at	−1.18	1e−10	3e−07	41 x 41	NOP2/Sun RNA methyltransferase family member 5 pseudog



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	26.55	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	24.8	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
3	24.38	NULL	102	Reference Signatures	WSRT_EBV B−cells
4	21.62	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	19.74	NULL	1611	CC	extracellular region
6	19.21	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	19.12	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
8	19.06	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
9	19.01	NULL	214	Lymphoma	LENZ_Stromal signature 1
10	18.47	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
11	18.3	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
12	18.2	NULL	480	Cancer	Lembcke_Colonic Inflammation
13	17.62	NULL	194	GSEA C2	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
14	17.42	NULL	1090	CC	extracellular space
15	17.08	NULL	336	BP	immune response
16	16.81	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
17	16.64	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
18	16.39	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
19	16.36	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
20	16.24	NULL	331	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
Underexpressed					
1	−23.89	NULL	5456	Chromatin states	5_Tx_Neuronal_Progenitor
2	−21.86	NULL	6068	Chromatin states	4_Tx_ESC_Endoderm
3	−20.86	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
4	−20.4	NULL	5529	Lymphoma	HOPP_Txn_elongation
5	−20.1	NULL	7833	Chromatin states	Bcells peripheral blood_1_TssA
6	−20.01	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
7	−19.74	NULL	4261	Lymphoma	HOPP_Txn_transition
8	−19.68	NULL	4579	CC	nucleus
9	−19.51	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
10	−19.2	NULL	7225	Chromatin states	Overlap_fetal_midbrain_ReprPC
11	−19.19	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
12	−19.04	NULL	6099	Chromatin states	HSC_4_Tx
13	−18.58	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	−18.38	NULL	4683	Chromatin states	Overlap_fetal_midbrain_HetRpts
15	−18.13	NULL	2541	CC	nucleoplasm
16	−18.06	NULL	6997	Chromatin states	Overlap_fetal_midbrain_K9K27me3
17	−18.01	NULL	6389	Chromatin states	4_Tx_ESC_Mesoderm
18	−17.98	NULL	5716	Chromatin states	Bcells peripheral blood_4_Tx
19	−17.97	NULL	9160	Chromatin states	2_TssA_Neuronal_Progenitor
20	−17.94	NULL	8641	Chromatin states	1_TssA_ESC_Endoderm