MPI−241

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 655 (451 + / 204 −)

genes with fdr < 0.1 = 514 (360 + / 154 −)

genes with fdr < 0.05 = 400 (284 + / 116 −)

genes with fdr < 0.01 = 270 (200 + / 70 −)

genes in genesets = 13152

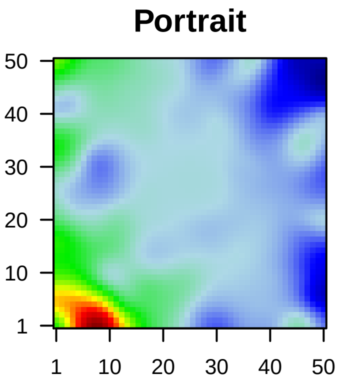
<FC> = 0

<t−score> = 0.1

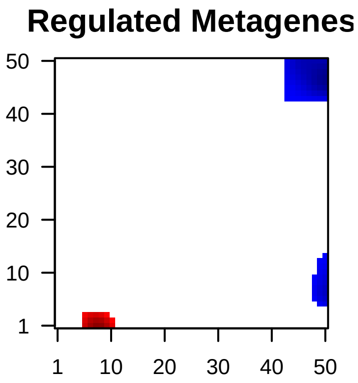
<p−value> = 0.24

<fdr> = 0.95

Portrait



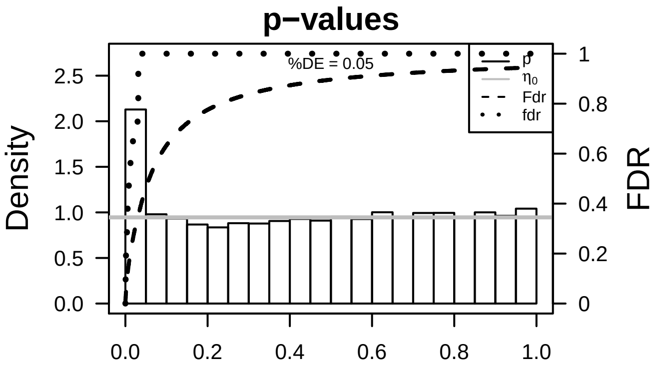
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39318_at	−1.84	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	201427_s_at	−1.07	2e−16	2e−13	47 x 37	selenoprotein P [Source:HGNC Symbol;Acc:HGNC:10751]
3	201852_x_at	0.93	2e−16	2e−13	8 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HG
4	201909_at	−1.62	2e−16	2e−13	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
5	203290_at	1.7	2e−16	2e−13	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
6	204475_at	2.46	2e−16	2e−13	7 x 0	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
7	205040_at	2.11	2e−16	2e−13	5 x 0	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
8	205041_s_at	2.14	2e−16	2e−13	5 x 0	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
9	205671_s_at	−2	2e−16	2e−13	49 x 19	major histocompatibility complex, class II, DO beta [Source:H
10	205828_at	2.19	2e−16	2e−13	13 x 0	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC
11	206779_s_at	1.93	2e−16	2e−13	1 x 17	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
12	208650_s_at	−1.48	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	208651_x_at	−1.28	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
14	209480_at	−1.87	2e−16	2e−13	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
15	209771_x_at	−0.95	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
16	209995_s_at	−2.3	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
17	210551_s_at	2.15	2e−16	2e−13	1 x 17	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
18	212464_s_at	1.07	2e−16	2e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
19	213831_at	−1.48	2e−16	2e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
20	216379_x_at	−1.19	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.32	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	19.66	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	17.86	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
4	16.53	NULL	397	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
5	16.48	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
6	16.34	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	16.1	NULL	480	Cancer	Lembcke_Colonic Inflammation
8	14.9	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
9	14.15	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
10	13.9	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
11	13.54	NULL	297	Colon Cancer	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	13.36	NULL	138	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
13	13.11	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
14	12.99	NULL	212	CC	extracellular matrix
15	12.78	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
16	12.67	NULL	902	GSEA C2	CHEN_METABOLIC_SYNDROM_NETWORK
17	12.52	NULL	58	BP	collagen catabolic process
18	12.15	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
19	11.99	NULL	202	GSEA C2	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
20	11.94	NULL	60	GSEA C2	CROMER_TUMORIGENESIS_UP
Underexpressed					
1	−9.11	NULL	4208	Chromatin states	T cells peripheral blood_6_EnhG
2	−8.61	NULL	9	GSEA C2	RUNNE_GENDER_EFFECT_UP
3	−8.55	NULL	3938	Chromatin states	T helper cells peripheral blood_6_EnhG
4	−8.53	NULL	4528	Chromatin states	T CD8+ naive cells peripheral blood_4_Tx
5	−7.75	NULL	5456	Chromatin states	5_Tx_Neuronal_Progenitor
6	−7.35	NULL	3524	Chromatin states	T regulatory cells peripheral blood_6_EnhG
7	−7.3	NULL	5753	Chromatin states	T cells peripheral blood_4_Tx
8	−7.14	NULL	5527	Chromatin states	T regulatory cells peripheral blood_4_Tx
9	−7.1	NULL	6997	Chromatin states	Overlap_fetal_midbrain_K9K27me3
10	−7.04	NULL	852	MF	nucleic acid binding
11	−7.02	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
12	−6.59	NULL	1161	MF	RNA binding
13	−6.51	NULL	25	Lymphoma	ROSOLOWSKI_red UP
14	−6.36	NULL	1174	Colon Cancer	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_trans
15	−6.3	NULL	99	Lymphoma	Sha_BL UP
16	−6.17	NULL	4683	Chromatin states	Overlap_fetal_midbrain_HetRpts
17	−6.17	NULL	2144	Chromatin states	T CD8+ naive cells peripheral blood_6_EnhG
18	−6.08	NULL	110	BP	translational initiation
19	−5.9	NULL	6839	Chromatin states	T CD8+ naive cells peripheral blood_5_TxWk
20	−5.87	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk