MPI−187

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 749 (487 + / 262 −)

genes with fdr < 0.1 = 512 (338 + / 174 −)

genes with fdr < 0.05 = 433 (287 + / 146 −)

genes with fdr < 0.01 = 293 (201 + / 92 −)

genes in genesets = 13152

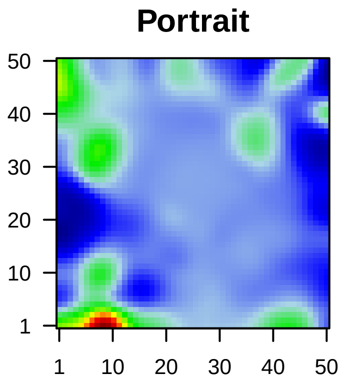
<FC> = 0

<t−score> = 0.07

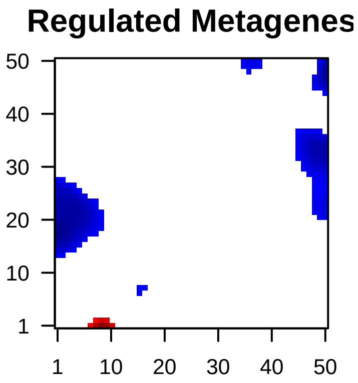
<p−value> = 0.24

<fdr> = 0.95

Portrait



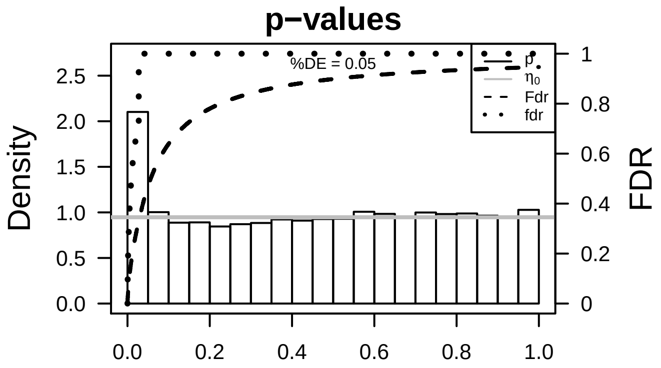
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1255_g_at	2.5	2e−16	2e−13	7 x 33	guanylate cyclase activator 1A [Source:HGNC Symbol;Acc:H
2	266_s_at	−2.12	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
3	201909_at	−1.43	2e−16	2e−13	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
4	202768_at	2.03	2e−16	2e−13	35 x 3	FosB proto−oncogene, AP−1 transcription factor subunit [Sou
5	203215_s_at	2.09	2e−16	2e−13	26 x 18	myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]
6	204540_at	2.25	2e−16	2e−13	18 x 3	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
7	205902_at	2.03	2e−16	2e−13	49 x 40	potassium calcium−activated channel subfamily N member 3
8	206018_at	2.88	2e−16	2e−13	6 x 32	forkhead box G1 [Source:HGNC Symbol;Acc:HGNC:3811]
9	206062_at	2.66	2e−16	2e−13	7 x 33	guanylate cyclase activator 1A [Source:HGNC Symbol;Acc:H
10	208650_s_at	−2.44	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
11	208651_x_at	−1.69	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
12	209771_x_at	−2.14	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	209772_s_at	−1.64	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
14	211644_x_at	2.39	2e−16	2e−13	0 x 1	immunoglobulin kappa variable 3−20 [Source:HGNC Symbol;
15	214669_x_at	1.04	2e−16	2e−13	0 x 3	
16	215176_x_at	−1.73	2e−16	2e−13	10 x 5	immunoglobulin kappa variable 1−39 (gene/pseudogene) [So
17	216379_x_at	−2.27	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
18	216542_x_at	1.96	2e−16	2e−13	10 x 5	immunoglobulin heavy variable 3−20 [Source:HGNC Symbol;
19	216557_x_at	1.86	2e−16	2e−13	10 x 5	immunoglobulin heavy variable 3−21 [Source:HGNC Symbol;
20	217281_x_at	2.11	2e−16	2e−13	10 x 5	immunoglobulin heavy variable 3−7 [Source:HGNC Symbol;A

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.93	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
2	14.27	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	13.24	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	12.42	NULL	78	Melanoma	Tirosh_CAF−cell specific genes
5	11.33	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
6	10.81	NULL	247	GSEA C2	BOQUEST_STEM_CELL_UP
7	10.61	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
8	10.51	NULL	214	Lymphoma	LENZ_Stromal signature 1
9	10.46	NULL	54	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
10	10.32	NULL	197	GSEA C2	NABA_CORE_MATRISOME
11	10.29	NULL	60	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
12	10.13	NULL	67	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
13	9.99	NULL	138	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
14	9.88	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
15	9.87	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
16	9.64	NULL	58	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
17	9.58	NULL	212	CC	extracellular matrix
18	9.51	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
19	9.15	NULL	138	GSEA C2	IGLESIAS_E2F_TARGETS_UP
20	9.1	NULL	48	GSEA C2	BURTON_ADIPOGENESIS_PEAK_AT_2HR
Underexpressed					
1	−10.21	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
2	−9.82	NULL	4528	Chromatin states	T CD8+ naive cells peripheral blood_4_Tx
3	−9.54	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
4	−9.51	NULL	5527	Chromatin states	T regulatory cells peripheral blood_4_Tx
5	−9.17	NULL	6099	Chromatin states	HSC_4_Tx
6	−8.67	NULL	5753	Chromatin states	T cells peripheral blood_4_Tx
7	−8.54	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
8	−8.31	NULL	2325	Chromatin states	HSC_8_ZNF_Rpts
9	−8.31	NULL	5766	Chromatin states	natural killer cells peripheral blood_4_Tx
10	−8.24	NULL	6244	Chromatin states	15_Quies_Fibroblasts
11	−8.09	NULL	5529	Lymphoma	HOPP_Txn_elongation
12	−7.83	NULL	3554	Chromatin states	8_ZNF_Rpts_ESC_Endoderm
13	−7.77	NULL	6637	Chromatin states	T cells peripheral blood_5_TxWk
14	−7.69	NULL	4683	Chromatin states	Overlap_fetal_midbrain_HetRpts
15	−7.56	NULL	34	Lymphoma	TARTE_B−cell signature
16	−7.55	NULL	5456	Chromatin states	5_Tx_Neuronal_Progenitor
17	−7.53	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
18	−7.46	NULL	35	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
19	−7.44	NULL	6068	Chromatin states	4_Tx_ESC_Endoderm
20	−7.42	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA