MPI−119

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 645 (452 + / 193 −)

genes with fdr < 0.1 = 479 (358 + / 121 −)

genes with fdr < 0.05 = 387 (293 + / 94 −)

genes with fdr < 0.01 = 216 (174 + / 42 −)

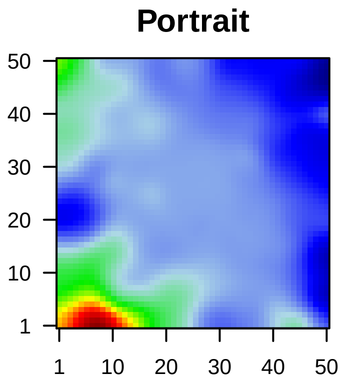
genes in genesets = 13152

<FC> = 0

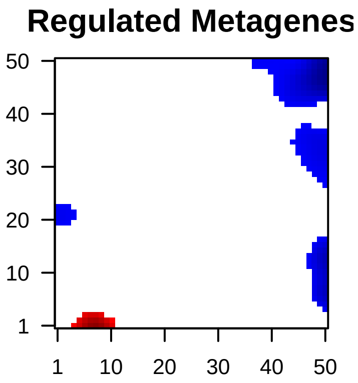
<t−score> = 0

<p−value> = 0.25

<fdr> = 0.94



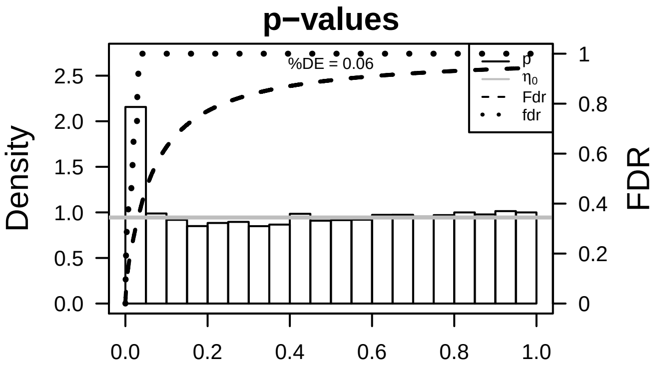
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201688_s_at	−1.53	2e−16	4e−13	49 x 37	tumor protein D52 [Source:HGNC Symbol;Acc:HGNC:12005]
2	201689_s_at	−1.6	2e−16	4e−13	49 x 37	tumor protein D52 [Source:HGNC Symbol;Acc:HGNC:12005]
3	201690_s_at	−1.45	2e−16	4e−13	49 x 37	tumor protein D52 [Source:HGNC Symbol;Acc:HGNC:12005]
4	204286_s_at	−1.76	2e−16	4e−13	3 x 24	phorbol−12−myristate−13−acetate−induced protein 1 [Source
5	204637_at	3.04	2e−16	4e−13	17 x 24	glycoprotein hormones, alpha polypeptide [Source:HGNC Sy
6	209374_s_at	−1	2e−16	4e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
7	210546_x_at	2.24	2e−16	4e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:
8	211674_x_at	2.35	2e−16	4e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:
9	213831_at	−1.48	2e−16	4e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
10	215733_x_at	2.27	2e−16	4e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:
11	217339_x_at	2.22	2e−16	4e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:
12	206413_s_at	2.16	7e−16	6e−12	43 x 49	T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG
13	206023_at	2.14	1e−15	9e−12	33 x 46	neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
14	209480_at	−1.83	1e−15	9e−12	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
15	201852_x_at	1.02	2e−15	1e−10	8 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
16	215076_s_at	0.95	1e−14	1e−10	8 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
17	212185_x_at	0.96	1e−14	1e−10	3 x 0	metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
18	215101_s_at	2.05	2e−14	5e−10	14 x 0	C−X−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc
19	213757_at	−0.93	4e−14	1e−09	30 x 49	G protein pathway suppressor 2 [Source:HGNC Symbol;Acc:
20	214974_x_at	1.97	1e−13	1e−09	13 x 0	C−X−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	21.95	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	19.81	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	18.58	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	18.58	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
5	18.16	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
6	18.06	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
7	17.91	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
8	17.16	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
9	16.95	NULL	219	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
10	16.94	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
11	16.78	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
12	16.44	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
13	16.28	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
14	16.11	NULL	397	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
15	15.82	NULL	1611	CC	extracellular region
16	15.7	NULL	331	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
17	15.47	NULL	480	Cancer	Lembcke_Colonic Inflammation
18	14.4	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
19	14.36	NULL	190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	14.11	NULL	1090	CC	extracellular space
Underexpressed					
1	−11.69	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
2	−11.52	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
3	−11.42	NULL	4261	Lymphoma	HOPP_Txn_transition
4	−11.18	NULL	5529	Lymphoma	HOPP_Txn_elongation
5	−10.85	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
6	−10.78	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
7	−10.67	NULL	7930	Chromatin states	T regulatory cells peripheral blood_1_TssA
8	−10.61	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
9	−10.41	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
10	−10.3	NULL	602	Colon Cancer	Pentrack_CRC_TCGA_corr_R_normal_DN
11	−10.28	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
12	−10.14	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
13	−9.85	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
14	−9.71	NULL	6099	Chromatin states	HSC_4_Tx
15	−9.6	NULL	8068	Chromatin states	T helper cells peripheral blood_1_TssA
16	−9.47	NULL	5527	Chromatin states	T regulatory cells peripheral blood_4_Tx
17	−9.47	NULL	8322	Chromatin states	T CD8+ naive cells peripheral blood_1_TssA
18	−9.45	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
19	−9.4	NULL	4528	Chromatin states	T CD8+ naive cells peripheral blood_4_Tx
20	−9.39	NULL	6839	Chromatin states	T CD8+ naive cells peripheral blood_5_TxWk