MPI−150

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 741 (407 + / 334 −)

genes with fdr < 0.1 = 497 (281 + / 216 −)

genes with fdr < 0.05 = 426 (245 + / 181 −)

genes with fdr < 0.01 = 222 (128 + / 94 −)

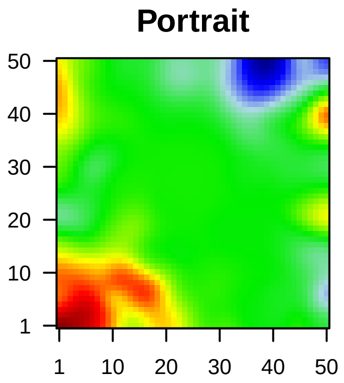
genes in genesets = 13152

<FC> = 0

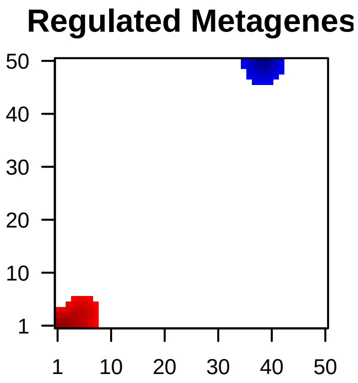
<t−score> = −0.04

<p−value> = 0.25

<fdr> = 0.94



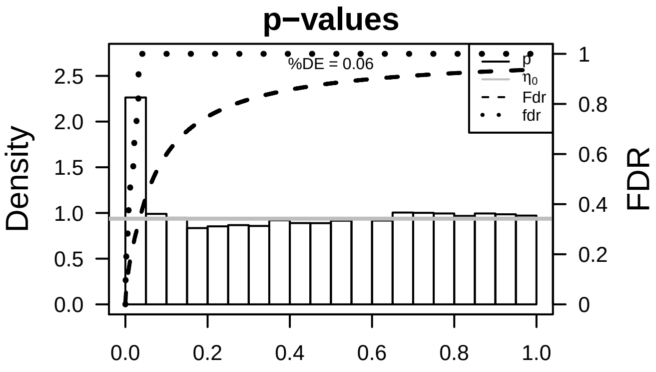
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	204749_at	2.27	2e−16	9e−13	13 x 28	nucleosome assembly protein 1 like 3 [Source:HGNC Symbo
2	207655_s_at	−1.84	2e−16	9e−13	0 x 22	B cell linker [Source:HGNC Symbol;Acc:HGNC:14211]
3	209942_x_at	2.39	2e−16	9e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
4	213831_at	−1.66	2e−16	9e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
5	214612_x_at	2.28	2e−16	9e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
6	209728_at	2.14	2e−15	2e−10	0 x 10	major histocompatibility complex, class II, DR beta 4 [Source:
7	208168_s_at	2.08	1e−14	2e−10	4 x 1	chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936]
8	207940_x_at	2.04	4e−14	2e−10	44 x 21	cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21
9	217232_x_at	−1.4	5e−14	2e−10	6 x 29	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
10	208243_s_at	2.03	5e−14	2e−10	44 x 21	cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21
11	207534_at	2.03	5e−14	5e−10	1 x 16	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
12	206218_at	2.02	7e−14	6e−09	0 x 15	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
13	208791_at	1.33	7e−13	6e−09	0 x 3	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
14	203915_at	0.95	9e−13	6e−09	0 x 0	C−X−C motif chemokine ligand 9 [Source:HGNC Symbol;Acc
15	218510_x_at	1.92	1e−12	2e−08	16 x 6	reticulophagy regulator 1 [Source:HGNC Symbol;Acc:HGNC:
16	204221_x_at	1.9	2e−12	7e−08	16 x 7	GLI pathogenesis related 1 [Source:HGNC Symbol;Acc:HGN
17	220448_at	1.86	6e−12	1e−07	49 x 40	potassium two pore domain channel subfamily K member 12
18	218055_s_at	−1.15	2e−11	1e−07	42 x 28	WD repeat domain 41 [Source:HGNC Symbol;Acc:HGNC:25
19	211748_x_at	0.83	2e−11	1e−07	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
20	203290_at	−1.58	2e−11	1e−07	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.2	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	15.62	NULL	102	Reference Signatures	WIRTH_EBV B−cells
3	14.55	NULL	214	Lymphoma	LENZ_Stromal signature 1
4	14.35	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
5	14.23	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	13.86	NULL	288	Colon Cancer	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
7	13.31	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
8	12.6	NULL	83	Melanoma	TCGA_melanoma_immune_high
9	12.39	NULL	62	Lymphoma	Monti_Host_response_cluster
10	12.18	NULL	6791	Chromatin states	7_Enh_ESC_Endoderm
11	11.94	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
12	11.75	NULL	480	Cancer	Lembcke_Colonic Inflammation
13	11.33	NULL	7078	Chromatin states	7_Enh_ESC_Mesoderm
14	11.32	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
15	11.2	NULL	317	Cancer	SPANG_BCL6−index2
16	11.2	NULL	355	Reference Signatures	WIRTH_Immune system
17	11.12	NULL	33	Melanoma	Tirosh_T−cell specific genes−melanoma
18	11.03	NULL	626	Chromatin states	natural killer cells peripheral blood_3_TxFlnk
19	10.99	NULL	166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	10.81	NULL	52	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
Underexpressed					
1	−21.82	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−21.37	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
3	−20.73	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−19.41	NULL	14	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	−18.94	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	−18.85	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
7	−18.33	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
8	−18.17	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
9	−17.98	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
10	−17.94	NULL	526	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	−17.44	NULL	174	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
12	−16.68	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
13	−16.17	NULL	84	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	−15.93	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
15	−15.63	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	−15.31	NULL	254	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
17	−15.3	NULL	703	GSEA C2	LEE_BMP2_TARGETS_DN
18	−15.26	NULL	102	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	−15.23	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanom
20	−15	NULL	294	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE