MPI−251

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 706 (463 + / 243 −)

genes with fdr < 0.1 = 541 (360 + / 181 −)

genes with fdr < 0.05 = 432 (289 + / 143 −)

genes with fdr < 0.01 = 298 (198 + / 100 −)

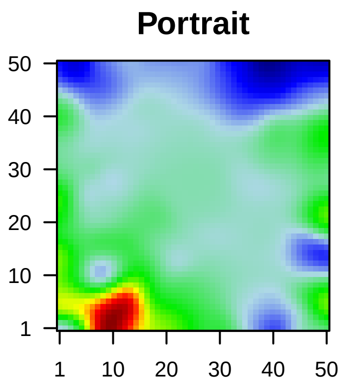
genes in genesets = 13152

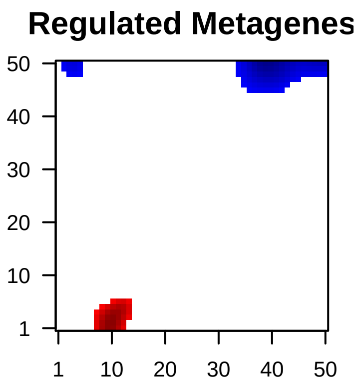
<FC> = 0

<t−score> = 0.11

<p−value> = 0.24

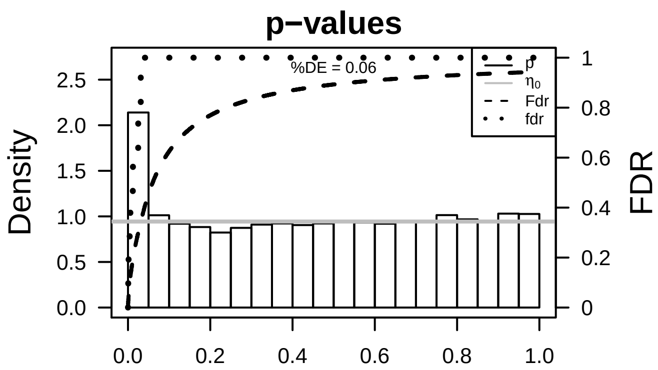
<fdr> = 0.94





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201909_at	−1.36	2e−16	3e−13	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
2	202953_at	−1.83	2e−16	3e−13	0 x 0	complement C1q B chain [Source:HGNC Symbol;Acc:HGNC:
3	203645_s_at	−1.55	2e−16	3e−13	8 x 10	CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]
4	205242_at	1.28	2e−16	3e−13	0 x 3	C−X−C motif chemokine ligand 13 [Source:HGNC Symbol;Ac
5	205476_at	2.12	2e−16	3e−13	17 x 12	C−C motif chemokine ligand 20 [Source:HGNC Symbol;Acc:H
6	207861_at	2.26	2e−16	3e−13	0 x 20	C−C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:H
7	208791_at	1.47	2e−16	3e−13	0 x 3	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
8	208792_s_at	1.2	2e−16	3e−13	0 x 3	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
9	209374_s_at	0.95	2e−16	3e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
10	209480_at	−1.95	2e−16	3e−13	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
11	213831_at	−1.93	2e−16	3e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
12	214974_x_at	1.95	2e−16	3e−13	13 x 0	C−X−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc
13	215049_x_at	−1.47	2e−16	3e−13	8 x 10	CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]
14	216705_s_at	−1.15	2e−16	3e−13	4 x 15	adenosine deaminase [Source:HGNC Symbol;Acc:HGNC:18
15	218232_at	−1.23	2e−16	3e−13	0 x 0	complement C1q A chain [Source:HGNC Symbol;Acc:HGNC:
16	221651_x_at	0.84	2e−16	3e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:H
17	32128_at	−0.95	4e−16	2e−12	20 x 49	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:H
18	221671_x_at	0.76	4e−16	2e−12	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:H
19	209924_at	−0.95	7e−16	2e−12	20 x 49	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:H
20	220448_at	1.9	7e−16	2e−12	49 x 40	potassium two pore domain channel subfamily K member 12



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	17.64	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	17.02	NULL	429	GSEA C2	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	14.19	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	13.64	NULL	247	GSEA C2	BOQUEST_STEM_CELL_UP
5	13.43	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	13.1	NULL	480	Cancer	Lembcke_Colonic Inflammation
7	12.59	NULL	516	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
8	12.37	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
9	11.89	NULL	78	Melanoma	Tirosh_CAF−cell specific genes
10	11.83	NULL	693	Chromatin states	Bcells peripheral blood_3_TxFlnk
11	11.37	NULL	197	GSEA C2	NABA_CORE_MATRISOME
12	11.08	NULL	366	GSEA C2	LIM_MAMMARY_STEM_CELL_UP
13	11.02	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
14	10.98	NULL	589	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
15	10.91	NULL	1001	Colon Cancer	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending c
16	10.66	NULL	75	Melanoma	Tirosh_Endothelial−cell specific genes−melanoma
17	10.66	NULL	249	GSEA C2	ONDER_CDH1_TARGETS_2_UP
18	10.62	NULL	397	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
19	10.58	NULL	183	BP	extracellular matrix organization
20	10.52	NULL	14	Cancer	LIU_PROSTATE_CANCER_DN
Underexpressed					
1	−14.21	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
2	−12.89	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
3	−12.75	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−12.48	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	−12.43	NULL	14	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	−12.17	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
7	−11.49	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
8	−11.45	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	−11.28	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
10	−11.11	NULL	254	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
11	−11	NULL	1052	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
12	−10.65	NULL	187	HM	HALLMARK_E2F_TARGETS
13	−10.64	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
14	−10.31	NULL	219	Reference Signatures	WSPH_GC B−cells
15	−10	NULL	93	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
16	−9.78	NULL	526	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
17	−9.73	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
18	−9.69	NULL	226	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
19	−9.68	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanoma
20	−9.31	NULL	52	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP