MPI−054

Global Summary

%DE = 0.04

genes with fdr < 0.2 = 283 (107 + / 176 −)

genes with fdr < 0.1 = 191 (76 + / 115 −)

genes with fdr < 0.05 = 127 (48 + / 79 −)

genes with fdr < 0.01 = 82 (33 + / 49 −)

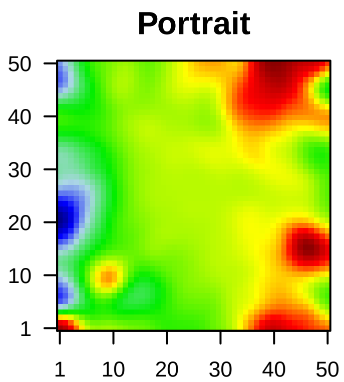
genes in genesets = 13152

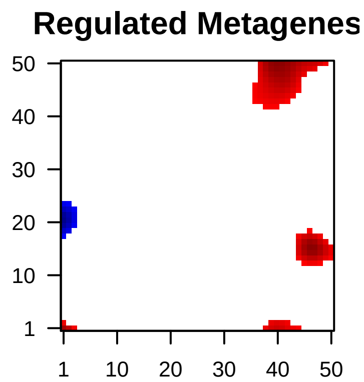
<FC> = 0

<t−score> = 0.17

<p−value> = 0.3

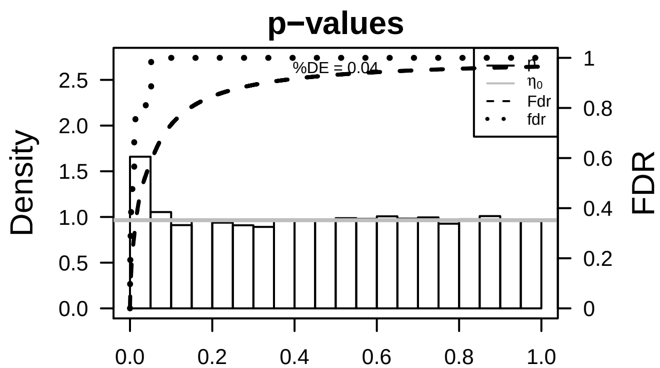
<fdr> = 0.96





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	209374_s_at	−1.08	2e−16	2e−12	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
2	212827_at	−1.25	2e−16	2e−12	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
3	202716_at	−1.47	1e−14	2e−10	0 x 4	protein tyrosine phosphatase, non−receptor type 1 [Source:H
4	212574_x_at	−1.84	1e−14	2e−10	0 x 44	transmembrane protein 259 [Source:HGNC Symbol;Acc:HGN
5	202369_s_at	−1.72	2e−14	6e−10	6 x 29	translocation associated membrane protein 2 [Source:HGNC
6	215379_x_at	−0.94	7e−14	6e−10	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
7	218332_at	2.08	8e−14	1e−07	35 x 3	brain expressed X−linked 1 [Source:HGNC Symbol;Acc:HGN
8	218340_s_at	−1.77	7e−12	6e−07	4 x 49	ubiquitin like modifier activating enzyme 6 [Source:HGNC Syr
9	215118_s_at	1.67	4e−11	5e−06	28 x 1	
10	218935_at	−1.41	4e−10	5e−06	0 x 5	EH domain containing 3 [Source:HGNC Symbol;Acc:HGNC:3
11	211430_s_at	−0.79	6e−10	5e−06	0 x 4	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
12	213986_s_at	−1.41	9e−10	5e−06	0 x 44	transmembrane protein 259 [Source:HGNC Symbol;Acc:HGN
13	211791_s_at	−1.7	1e−09	5e−06	0 x 46	potassium voltage−gated channel subfamily A regulatory beta
14	201909_at	1.09	1e−09	9e−06	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
15	32128_at	0.84	2e−09	9e−06	20 x 49	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:H
16	203649_s_at	1.66	3e−09	9e−06	12 x 0	phospholipase A2 group IIA [Source:HGNC Symbol;Acc:HGN
17	209995_s_at	0.97	3e−09	9e−06	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
18	39318_at	0.87	3e−09	9e−06	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
19	209806_at	−0.85	3e−09	2e−05	0 x 20	
20	203915_at	0.81	4e−09	2e−05	0 x 0	C−X−C motif chemokine ligand 9 [Source:HGNC Symbol;Acc



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all		Geneset
1	13.52	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
2	13.42	NULL	102	Reference Signatures	WIRTH_EBV B−cells
3	13.01	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	12.63	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
5	12.2	NULL	187	HM	HALLMARK_E2F_TARGETS
6	11.91	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	11.54	NULL	192	Lymphoma	Victora_Dark zone signature
8	11.25	NULL	400	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
9	11.21	NULL	226	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
10	11.13	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	10.86	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
12	10.68	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
13	10.61	NULL	93	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
14	10.05	NULL	14	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	9.89	NULL	1052	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
16	9.88	NULL	254	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
17	9.82	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	9.77	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
19	9.69	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
20	9.58	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanoma

Underexpressed

Rank	GSZ	p−value	#all		Geneset
1	−11.12	NULL	317	Cancer	SPANG_BCL6−index2
2	−9.34	NULL	8406	Chromatin states	Bcells peripheral blood_2_TssAFlnk
3	−9.14	NULL	7331	Chromatin states	TssA_Colon
4	−8.83	NULL	7833	Chromatin states	Bcells peripheral blood_1_TssA
5	−8.74	NULL	9544	Chromatin states	HSC_2_TssAFlnk
6	−8.49	NULL	9146	Chromatin states	3_TssA_Skeletal_Muscle
7	−8.47	NULL	70	CC	nucleosome
8	−8.32	NULL	5682	Lymphoma	HOPP_Weak_promoter
9	−8.22	NULL	18	Lymphoma	WRIGHT_ABC UP
10	−8.09	NULL	7635	Chromatin states	monocytes peripheral blood_1_TssA
11	−8.07	NULL	9576	Chromatin states	2_TssA_MSC_Adipocyte
12	−8.06	NULL	7165	Chromatin states	Tx_Colon
13	−8.06	NULL	6590	Chromatin states	Tregulatory cells peripheral blood_5_TxWk
14	−8.05	NULL	5716	Chromatin states	Bcells peripheral blood_4_Tx
15	−8.05	NULL	6839	Chromatin states	T CD8+ naive cells peripheral blood_5_TxWk
16	−7.93	NULL	8766	Chromatin states	2_TssA_Melanocytes
17	−7.91	NULL	8068	Chromatin states	Thelper cells peripheral blood_1_TssA
18	−7.89	NULL	6466	Chromatin states	5_Tx_MSC_Adipocyte
19	−7.85	NULL	42	GSEA C2	REACTOME_RNA_POL_I_PROMOTER_OPENING
20	−7.82	NULL	8816	Chromatin states	Thelper cells peripheral blood_2_TssAFlnk