MPI−088

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 664 (407 + / 257 −)

genes with fdr < 0.1 = 513 (322 + / 191 −)

genes with fdr < 0.05 = 393 (251 + / 142 −)

genes with fdr < 0.01 = 248 (167 + / 81 −)

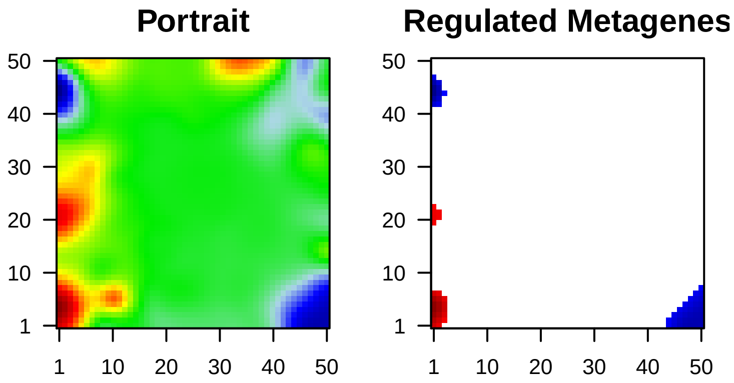
genes in genesets = 13152

<FC> = 0

<t−score> = 0.16

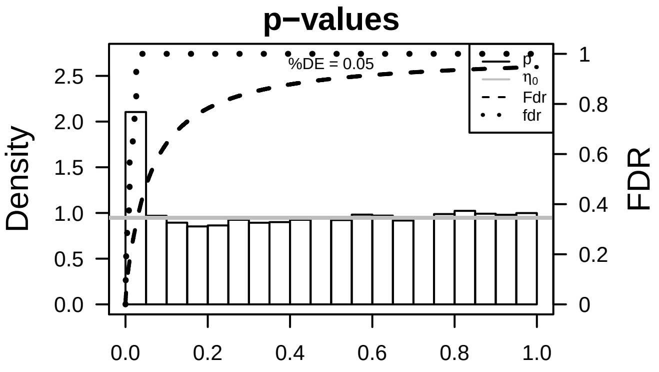
<p−value> = 0.25

<fdr> = 0.95



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	203290_at	1.71	2e−16	3e−13	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
2	206779_s_at	1.86	2e−16	3e−13	1 x 17	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
3	207521_s_at	−1.38	2e−16	3e−13	0 x 44	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
4	209038_s_at	−1.16	2e−16	3e−13	0 x 42	EH domain containing 1 [Source:HGNC Symbol;Acc:HGNC:3
5	209374_s_at	0.84	2e−16	3e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
6	210551_s_at	2.13	2e−16	3e−13	1 x 17	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
7	213606_s_at	−2.07	2e−16	3e−13	0 x 45	Rho GDP dissociation inhibitor alpha [Source:HGNC Symbol;
8	213831_at	1.18	2e−16	3e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
9	213986_s_at	−1.86	2e−16	3e−13	0 x 44	transmembrane protein 259 [Source:HGNC Symbol;Acc:HGN
10	214100_x_at	−1.17	2e−16	3e−13	41 x 41	NOP2/Sun RNA methyltransferase family member 5 pseudog
11	214464_at	1.95	2e−16	3e−13	19 x 19	CDC42 binding protein kinase alpha [Source:HGNC Symbol;
12	215379_x_at	0.9	2e−16	3e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
13	217022_s_at	1.31	2e−16	3e−13	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
14	221651_x_at	0.99	2e−16	3e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
15	221671_x_at	0.91	2e−16	3e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
16	214470_at	1.83	7e−16	6e−12	9 x 8	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
17	203892_at	1.82	1e−15	6e−11	23 x 7	WAP four−disulfide core domain 2 [Source:HGNC Symbol;Ac
18	213460_x_at	−1.09	1e−15	6e−11	48 x 7	NOP2/Sun RNA methyltransferase family member 5 pseudog
19	201367_s_at	−1.4	4e−15	7e−11	0 x 43	ZFP36 ring finger protein like 2 [Source:HGNC Symbol;Acc:H
20	210457_x_at	−1.11	9e−15	7e−11	0 x 44	high mobility group AT−hook 1 [Source:HGNC Symbol;Acc:H



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.43	NULL	32	Reference Signatures	Chaussabel_1,1_Plasma Cells
2	12.26	NULL	317	Cancer	SPANG_BCL6−index2
3	11.76	NULL	44	MF	antigen binding
4	11.2	NULL	102	Reference Signatures	Wright_EBV B−cells
5	11.11	NULL	18	CC	MHC class II protein complex
6	10.97	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
7	10.89	NULL	52	BP	complement activation, classical pathway
8	10.63	NULL	186	Cancer	SPANG_LPS−index2
9	9.95	NULL	40	BP	antigen processing and presentation
10	9.92	NULL	85	Lymphoma	Sha_DLBCL UP
11	9.84	NULL	16	MF	immunoglobulin receptor binding
12	9.55	NULL	23	CC	integral component of lumenal side of endoplasmic reticulum meml
13	9.33	NULL	161	BP	adaptive immune response
14	9.26	NULL	12	MF	MHC class II receptor activity
15	9.05	NULL	48	Pneumonia	Burnham_cap_fp_vs_con_DN
16	8.87	NULL	336	BP	immune response
17	8.65	NULL	480	Cancer	Lembcke_Colonic Inflammation
18	8.48	NULL	85	Lymphoma	Aukema_BCL2 DN_BCL6 UP
19	8.36	NULL	431	BP	immune system process
20	7.98	NULL	19	BP	positive regulation of B cell activation
Underexpressed					
1	−10.25	NULL	6368	Colon Cancer	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse c
2	−7.57	NULL	1600	Chromatin states	4_TxTrans_Melanocytes
3	−7.19	NULL	2380	Chromatin states	TxEnhG1_Colon
4	−7.17	NULL	2704	Chromatin states	4_TxTrans_Fibroblasts
5	−6.58	NULL	2563	Chromatin states	Mid_Frontal_Lobe_ZNF
6	−6.38	NULL	3803	Chromatin states	6_EnhG_Fibroblasts
7	−5.97	NULL	42	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_UP
8	−5.9	NULL	1911	Chromatin states	Mid_Frontal_Lobe_HetRpts
9	−5.64	NULL	239	GSEA C2	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
10	−5.25	NULL	287	GSEA C2	DAIRKEE_TERT_TARGETS_UP
11	−5.18	NULL	38	Glioma	WILLSCHER_GBM_Verhaak−PNwt_up
12	−5.15	NULL	127	GSEA C2	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
13	−5.14	NULL	188	Reference Signatures	Chaussabel_3,8_Enzymes
14	−4.98	NULL	4595	Chromatin states	6_EnhG_Melanocytes
15	−4.86	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
16	−4.69	NULL	33	GSEA C2	KAAB_FAILED_HEART_ATRIUM_UP
17	−4.66	NULL	657	GSEA C2	SMID_BREAST_CANCER_BASAL_DN
18	−4.47	NULL	1107	TF	ICGC_Myc_targets
19	−4.4	NULL	21	GSEA C2	JIANG_TIP30_TARGETS_DN
20	−4.38	NULL	42	BP	cellular response to amino acid stimulus