MPI−022

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 841 (521 + / 320 −)

genes with fdr < 0.1 = 596 (372 + / 224 −)

genes with fdr < 0.05 = 442 (287 + / 155 −)

genes with fdr < 0.01 = 278 (178 + / 100 −)

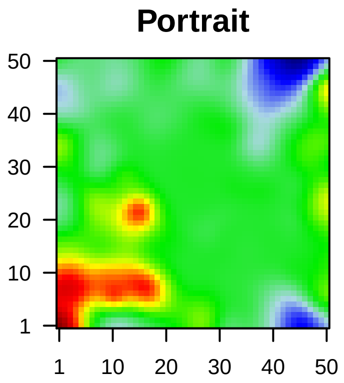
genes in genesets = 13152

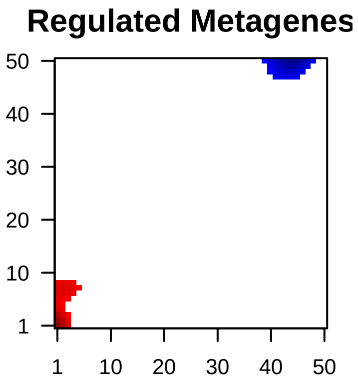
<FC> = 0

<t−score> = −0.09

<p−value> = 0.23

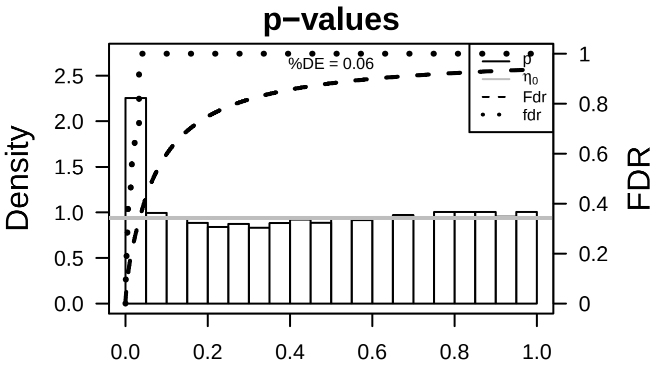
<fdr> = 0.94





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	266_s_at	−1.69	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
2	39318_at	−2.06	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
3	203290_at	2.16	2e−16	2e−13	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
4	204698_at	−1.4	2e−16	2e−13	4 x 15	interferon stimulated exonuclease gene 20 [Source:HGNC Sy
5	205445_at	2.65	2e−16	2e−13	14 x 21	prolactin [Source:HGNC Symbol;Acc:HGNC:9445]
6	205719_s_at	2.47	2e−16	2e−13	34 x 28	phenylalanine hydroxylase [Source:HGNC Symbol;Acc:HGNC
7	206255_at	−2.11	2e−16	2e−13	48 x 45	BLK proto−oncogene, Src family tyrosine kinase [Source:HGN
8	206633_at	2.34	2e−16	2e−13	15 x 21	cholinergic receptor nicotinic alpha 1 subunit [Source:HGNC
9	207339_s_at	−1.15	2e−16	2e−13	49 x 19	lymphotoxin beta [Source:HGNC Symbol;Acc:HGNC:6711]
10	207599_at	2.6	2e−16	2e−13	16 x 7	matrix metallopeptidase 20 [Source:HGNC Symbol;Acc:HGN
11	208650_s_at	−1.65	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
12	208651_x_at	−1.82	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	209201_x_at	−1.82	2e−16	2e−13	7 x 48	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
14	209374_s_at	−1.54	2e−16	2e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
15	209771_x_at	−1.75	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
16	209995_s_at	−1.7	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
17	210356_x_at	−1.22	2e−16	2e−13	0 x 14	membrane spanning 4−domains A1 [Source:HGNC Symbol;A
18	210448_s_at	−1.14	2e−16	2e−13	0 x 18	purinergic receptor P2X 5 [Source:HGNC Symbol;Acc:HGNC
19	212827_at	−1.48	2e−16	2e−13	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
20	216379_x_at	−1.71	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.2	NULL	18	CC	MHC class II protein complex
2	13.05	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
3	11.28	NULL	336	BP	immune response
4	11.03	NULL	12	MF	MHC class II receptor activity
5	10.82	NULL	832	Chr	Chr 2
6	10.73	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
7	10.6	NULL	102	Reference Signatures	WRIGHT_EBV B−cells
8	10.6	NULL	556	Chr	Chr X
9	10.56	NULL	40	BP	antigen processing and presentation
10	10.39	NULL	23	CC	integral component of lumenal side of endoplasmic reticulum meml
11	10.25	NULL	906	Lymphoma	SPANG_BCR DN
12	10.17	NULL	317	Cancer	SPANG_BCL6−index2
13	10.07	NULL	173	Lymphoma	Victora_Light zone signature
14	9.46	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
15	9.41	NULL	113	BP	regulation of immune response
16	9.37	NULL	53	BP	regulation of complement activation
17	9.32	NULL	39	BP	complement activation
18	9.29	NULL	431	BP	immune system process
19	9.1	NULL	299	GSEA C2	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
20	8.53	NULL	67	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
Underexpressed					
1	−11.44	NULL	192	Lymphoma	Victora_Dark zone signature
2	−9.68	NULL	99	Lymphoma	Sha_BL UP
3	−8.05	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
4	−7.83	NULL	18	Lymphoma	WRIGHT_ABC UP
5	−7.31	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	−7.22	NULL	400	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
7	−6.89	NULL	5620	Chromatin states	TssF_Colon
8	−6.78	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
9	−6.72	NULL	42	Reference Signatures	Chaussabel_1,3_B−cells
10	−6.54	NULL	42	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_UP
11	−6.41	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
12	−6.37	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
13	−6.28	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
14	−6.22	NULL	294	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
15	−6.13	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
16	−6.06	NULL	113	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
17	−6.05	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	−6.04	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
19	−5.9	NULL	25	Lymphoma	ROSOLOWSKI_red UP
20	−5.9	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanoma