MPI−188

Global Summary

%DE = 0.04

genes with fdr < 0.2 = 508 (248 + / 260 −)

genes with fdr < 0.1 = 372 (184 + / 188 −)

genes with fdr < 0.05 = 243 (116 + / 127 −)

genes with fdr < 0.01 = 184 (79 + / 105 −)

genes in genesets = 13152

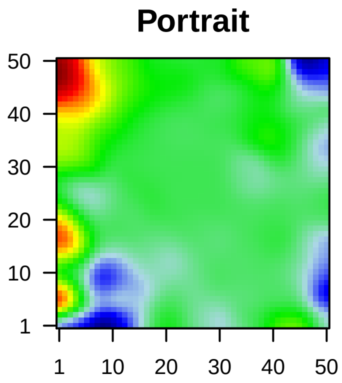
<FC> = 0

<t−score> = 0.16

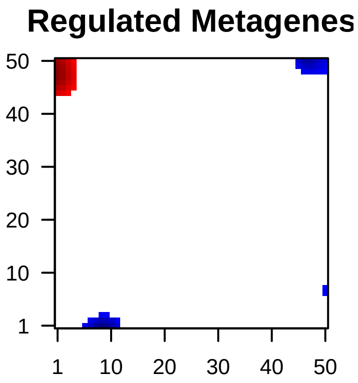
<p−value> = 0.27

<fdr> = 0.96

Portrait



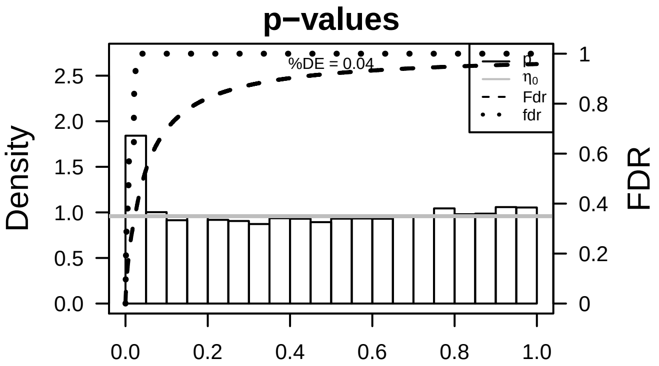
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39318_at	−2.1	2e−16	8e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	205671_s_at	−1.5	2e−16	8e−13	49 x 19	major histocompatibility complex, class II, DO beta [Source:H
3	209480_at	−1.74	2e−16	8e−13	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
4	209875_s_at	−1.85	2e−16	8e−13	8 x 0	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
5	209995_s_at	−2.69	2e−16	8e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
6	213831_at	−1.24	2e−16	8e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
7	220377_at	1.9	8e−15	7e−10	5 x 28	family with sequence similarity 30 member A [Source:HGNC
8	201909_at	−1.19	4e−14	7e−10	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
9	208791_at	1.24	1e−13	7e−10	0 x 3	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
10	213553_x_at	−1.08	1e−13	7e−10	5 x 2	apolipoprotein C1 [Source:HGNC Symbol;Acc:HGNC:607]
11	211813_x_at	−1.48	1e−13	1e−08	8 x 0	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
12	201462_at	−1.37	1e−12	1e−08	1 x 23	secernin 1 [Source:HGNC Symbol;Acc:HGNC:22192]
13	220027_s_at	1.72	2e−12	1e−08	40 x 16	Ras interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:
14	212094_at	−1.55	2e−12	8e−08	45 x 49	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:1
15	210982_s_at	−0.65	6e−12	9e−08	2 x 10	major histocompatibility complex, class II, DR alpha [Source:
16	215051_x_at	−1.05	1e−11	1e−07	9 x 9	allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:H
17	207339_s_at	−0.78	2e−11	1e−07	49 x 19	lymphotoxin beta [Source:HGNC Symbol;Acc:HGNC:6711]
18	206218_at	1.64	2e−11	1e−07	0 x 15	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
19	207314_x_at	1.63	2e−11	1e−07	12 x 28	killer cell immunoglobulin like receptor, three Ig domains and
20	209138_x_at	0.63	3e−11	1e−07	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.54	NULL	3767	Chromatin states	B cells peripheral blood_6_EnhG
2	11.11	NULL	4208	Chromatin states	T cells peripheral blood_6_EnhG
3	10.66	NULL	3524	Chromatin states	T regulatory cells peripheral blood_6_EnhG
4	10.24	NULL	355	Reference Signatures	WSRTH_Immune system
5	9.97	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
6	9.95	NULL	3682	Chromatin states	natural killer cells peripheral blood_6_EnhG
7	9.9	NULL	3938	Chromatin states	T helper cells peripheral blood_6_EnhG
8	9.8	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
9	9.75	NULL	4261	Lymphoma	HOPP_Txn_transition
10	9.67	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
11	9.3	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
12	9.13	NULL	8431	Chromatin states	T CD8+ naive cells peripheral blood_2_TssAFlnk
13	8.91	NULL	932	Chromatin states	T cells peripheral blood_3_TxFlnk
14	8.67	NULL	85	Lymphoma	Sha_DLBCL UP
15	8.66	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
16	8.5	NULL	2144	Chromatin states	T CD8+ naive cells peripheral blood_6_EnhG
17	8.5	NULL	8322	Chromatin states	T CD8+ naive cells peripheral blood_1_TssA
18	8.43	NULL	7930	Chromatin states	T regulatory cells peripheral blood_1_TssA
19	8.41	NULL	693	Chromatin states	B cells peripheral blood_3_TxFlnk
20	8.36	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
Underexpressed					
1	−15.12	NULL	18	CC	MHC class II protein complex
2	−14.55	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
3	−11	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	−10.03	NULL	12	MF	MHC class II receptor activity
5	−9.77	NULL	40	BP	antigen processing and presentation
6	−9.67	NULL	138	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
7	−9.37	NULL	67	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
8	−9.06	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
9	−8.88	NULL	747	GSEA C2	NABA_MATRISOME
10	−8.81	NULL	1611	CC	extracellular region
11	−8.81	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
12	−8.71	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
13	−8.56	NULL	12	Cancer	HLA2_signature
14	−8.37	NULL	22	MF	peptide antigen binding
15	−8.18	NULL	253	CC	proteinaceous extracellular matrix
16	−8.04	NULL	23	CC	integral component of lumenal side of endoplasmic reticulum meml
17	−7.96	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
18	−7.69	NULL	354	GSEA C2	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
19	−7.63	NULL	197	GSEA C2	NABA_CORE_MATRISOME
20	−7.62	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP