MPI−099

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 534 (273 + / 261 −)

genes with fdr < 0.1 = 371 (190 + / 181 −)

genes with fdr < 0.05 = 306 (149 + / 157 −)

genes with fdr < 0.01 = 190 (90 + / 100 −)

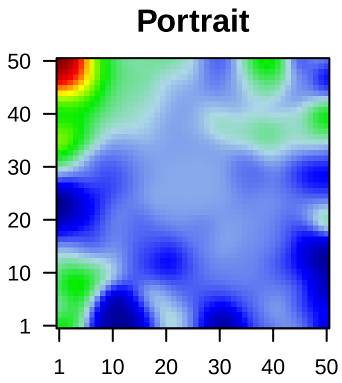
genes in genesets = 13152

<FC> = 0

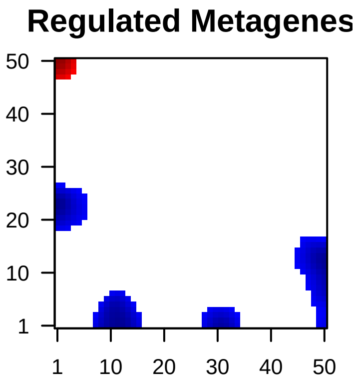
<t−score> = 0.17

<p−value> = 0.26

<fdr> = 0.95



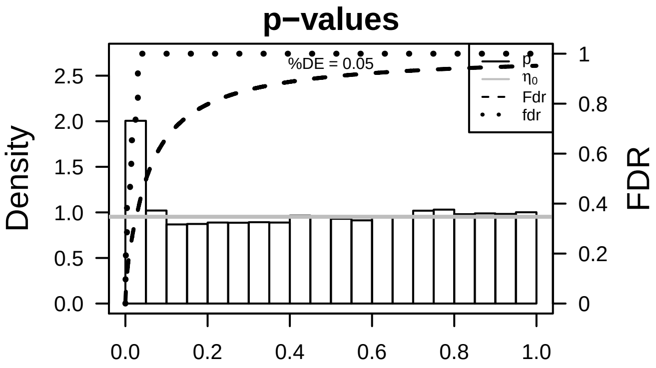
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201563_at	−1.36	2e−16	3e−13	41 x 47	sorbitol dehydrogenase 2, pseudogene [Source:HGNC Symb
2	203290_at	−1.7	2e−16	3e−13	7 x 0	major histocompatibility complex, class II, DQ alpha 2 [Source
3	204562_at	−1.26	2e−16	3e−13	0 x 20	interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGI
4	205229_s_at	−1.9	2e−16	3e−13	39 x 49	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
5	206310_at	2.14	2e−16	3e−13	17 x 6	serine peptidase inhibitor, Kazal type 2 [Source:HGNC Symb
6	207783_x_at	−2.29	2e−16	3e−13	45 x 28	tumor protein, translationally−controlled 1 [Source:HGNC Syr
7	209374_s_at	−1.61	2e−16	3e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
8	209728_at	1.96	2e−16	3e−13	0 x 10	major histocompatibility complex, class II, DR beta 4 [Source:
9	209806_at	0.96	2e−16	3e−13	0 x 20	
10	209823_x_at	0.99	2e−16	3e−13	2 x 8	major histocompatibility complex, class II, DQ beta 1 [Source:
11	212827_at	−1.7	2e−16	3e−13	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
12	213831_at	−1.85	2e−16	3e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
13	217002_s_at	2.06	2e−16	3e−13	3 x 5	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
14	219753_at	1.54	2e−16	3e−13	49 x 39	stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356]
15	39318_at	0.96	7e−16	8e−12	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
16	214290_s_at	0.96	2e−15	8e−12	0 x 21	histone cluster 2 H2A family member a3 [Source:HGNC Syml
17	209480_at	−1.54	2e−15	8e−12	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
18	216615_s_at	1.8	2e−15	8e−12	2 x 5	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
19	204083_s_at	−1.27	2e−15	4e−11	0 x 22	tropomyosin 2 [Source:HGNC Symbol;Acc:HGNC:12011]
20	209995_s_at	1.04	6e−15	4e−11	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	11.85	NULL	355	Reference Signatures	WSRTH_Immune system
2	10.53	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	10.23	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
4	9.75	NULL	5908	Lymphoma	HOPP_Active_promoter
5	9.66	NULL	88	GSEA C2	WIELAND_UP_BY_HBV_INFECTION
6	9.3	NULL	219	Reference Signatures	WSRTH_GC B−cells
7	9.15	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
8	8.84	NULL	4261	Lymphoma	HOPP_Txn_transition
9	8.58	NULL	8200	Chromatin states	monocytes peripheral blood_2_TssAFlnk
10	8.39	NULL	7635	Chromatin states	monocytes peripheral blood_1_TssA
11	8.36	NULL	92	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	8.31	NULL	5529	Lymphoma	HOPP_Txn_elongation
13	8.26	NULL	678	Reference Signatures	PROTEINATLAS_lymph node
14	8.25	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
15	8.22	NULL	3223	Chromatin states	monocytes peripheral blood_6_EnhG
16	7.97	NULL	5682	Lymphoma	HOPP_Weak_promoter
17	7.93	NULL	83	Melanoma	TCGA_melanoma_immune_high
18	7.93	NULL	1312	GSEA C2	PUJANA_ATM_PCC_NETWORK
19	7.91	NULL	192	Lymphoma	Victora_Dark zone signature
20	7.91	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
Underexpressed					
1	−13.42	NULL	3184	Chromatin states	monocytes peripheral blood_12_EnhBiv
2	−12.45	NULL	3150	Chromatin states	monocytes peripheral blood_13_ReprPC
3	−11.43	NULL	2197	Chromatin states	monocytes peripheral blood_11_BivFlnk
4	−11.38	NULL	3272	Chromatin states	monocytes peripheral blood_14_ReprPCWk
5	−11.22	NULL	2724	Chromatin states	T cells peripheral blood_11_BivFlnk
6	−10.91	NULL	2154	Chromatin states	Tregulatory cells peripheral blood_11_BivFlnk
7	−10.73	NULL	3724	Chromatin states	T cells peripheral blood_12_EnhBiv
8	−10.44	NULL	2515	Chromatin states	natural killer cells peripheral blood_13_ReprPC
9	−10.44	NULL	2747	Chromatin states	B cells peripheral blood_12_EnhBiv
10	−10.42	NULL	2765	Chromatin states	Tregulatory cells peripheral blood_13_ReprPC
11	−10.18	NULL	2300	Chromatin states	T helper cells peripheral blood_13_ReprPC
12	−10	NULL	1700	Chromatin states	B cells peripheral blood_11_BivFlnk
13	−9.88	NULL	2602	Chromatin states	natural killer cells peripheral blood_12_EnhBiv
14	−9.64	NULL	2134	Chromatin states	Tregulatory cells peripheral blood_12_EnhBiv
15	−9.59	NULL	2405	Chromatin states	B cells peripheral blood_13_ReprPC
16	−9.58	NULL	2984	Chromatin states	natural killer cells peripheral blood_14_ReprPCWk
17	−9.35	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
18	−9.31	NULL	1694	Chromatin states	T helper cells peripheral blood_11_BivFlnk
19	−9.24	NULL	3918	Chromatin states	T cells peripheral blood_14_ReprPCWk
20	−9.23	NULL	2600	Chromatin states	HSC_14_ReprPCWk