MPI−051

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 776 (347 + / 429 −)

genes with fdr < 0.1 = 603 (263 + / 340 −)

genes with fdr < 0.05 = 399 (176 + / 223 −)

genes with fdr < 0.01 = 243 (109 + / 134 −)

genes in genesets = 13152

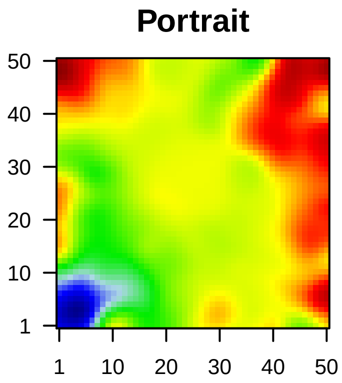
<FC> = 0

<t−score> = 0.08

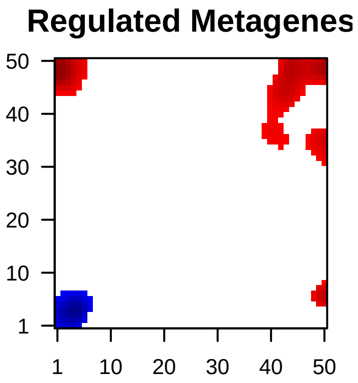
<p−value> = 0.24

<fdr> = 0.94

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AFFX−HUMR	2.15	2e−16	2e−13	49 x 47	
2	AFFX−r2−Hs1	2.32	2e−16	2e−13	49 x 47	
3	203509_at	−1.62	2e−16	2e−13	49 x 40	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
4	203534_at	−1.27	2e−16	2e−13	30 x 46	LSM1 homolog, mRNA degradation associated [Source:HGN
5	204086_at	2	2e−16	2e−13	0 x 17	preferentially expressed antigen in melanoma [Source:HGNC
6	204416_x_at	−1.87	2e−16	2e−13	5 x 3	apolipoprotein C1 [Source:HGNC Symbol;Acc:HGNC:607]
7	207534_at	2.12	2e−16	2e−13	1 x 16	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
8	210258_at	−2.4	2e−16	2e−13	49 x 40	regulator of G protein signaling 13 [Source:HGNC Symbol;Ac
9	211663_x_at	−1.77	2e−16	2e−13	2 x 3	
10	211748_x_at	−1.86	2e−16	2e−13	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
11	212187_x_at	−1.68	2e−16	2e−13	3 x 3	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
12	212560_at	−2.06	2e−16	2e−13	49 x 40	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
13	212592_at	−1.48	2e−16	2e−13	45 x 49	joining chain of multimeric IgA and IgM [Source:HGNC Symb
14	213553_x_at	−1.44	2e−16	2e−13	5 x 2	apolipoprotein C1 [Source:HGNC Symbol;Acc:HGNC:607]
15	213757_at	−0.96	2e−16	2e−13	30 x 49	G protein pathway suppressor 2 [Source:HGNC Symbol;Acc:
16	214777_at	2.5	2e−16	2e−13	10 x 5	immunoglobulin kappa variable 4−1 [Source:HGNC Symbol;A
17	216834_at	−1.24	2e−16	2e−13	5 x 3	regulator of G protein signaling 1 [Source:HGNC Symbol;Acc
18	217022_s_at	−2.12	2e−16	2e−13	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
19	219259_at	−1.52	2e−16	2e−13	6 x 3	semaphorin 4A [Source:HGNC Symbol;Acc:HGNC:10729]
20	219360_s_at	1.98	2e−16	2e−13	0 x 20	transient receptor potential cation channel subfamily M memb

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.33	NULL	585	Chr	Chr 7
2	9.05	NULL	3767	Chromatin states	B cells peripheral blood_6_EnhG
3	8.44	NULL	693	Chromatin states	B cells peripheral blood_3_TxFlnk
4	8.14	NULL	42	Reference Signatures	Chaussabel_1,3_B−cells
5	8.06	NULL	4528	Chromatin states	T CD8+ naive cells peripheral blood_4_Tx
6	7.83	NULL	1161	MF	RNA binding
7	6.82	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
8	6.48	NULL	275	GSEA C2	HADDAD_B_LYMPHOCYTE_PROGENITOR
9	6.39	NULL	24	Melanoma	Tirosh_B−cell specific genes−melanoma
10	6.18	NULL	17	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN
11	5.66	NULL	4138	Chromatin states	6_EnhG_Skeletal_Muscle
12	5.32	NULL	174	BP	rRNA processing
13	5.3	NULL	3938	Chromatin states	T helper cells peripheral blood_6_EnhG
14	5.24	NULL	190	HM	HALLMARK_MYC_TARGETS_V1
15	5.24	NULL	5529	Lymphoma	HOPP_Txn_elongation
16	5.23	NULL	1535	Chromatin states	B cells peripheral blood_8_ZNF_Rpts
17	5.19	NULL	127	GSEA C2	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
18	5.19	NULL	1312	GSEA C2	PUJANA_ATM_PCC_NETWORK
19	5.15	NULL	105	Reference Signatures	Chaussabel_2,4_Ribosomal proteins
20	5.13	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
Underexpressed					
1	−11.66	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
2	−11.36	NULL	219	Reference Signatures	WRIGHT_GC B−cells
3	−10.04	NULL	327	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
4	−9.13	NULL	102	Reference Signatures	WRIGHT_EBV B−cells
5	−8.67	NULL	194	GSEA C2	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
6	−8.34	NULL	317	Cancer	SPANG_BCL6−index2
7	−8.28	NULL	85	Lymphoma	Sha_DLBCL UP
8	−8.15	NULL	214	Lymphoma	LENZ_Stromal signature 1
9	−8.12	NULL	453	GSEA C2	ONDER_CDH1_TARGETS_2_DN
10	−8.11	NULL	261	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_UP
11	−7.9	NULL	195	GSEA C2	HOLLMANN_APOPTOSIS_VIA_CD40_UP
12	−7.84	NULL	186	Cancer	SPANG_LPS−index2
13	−7.77	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
14	−7.72	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
15	−7.62	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
16	−7.47	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
17	−7.18	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
18	−7.17	NULL	1611	CC	extracellular region
19	−7.15	NULL	2747	Chromatin states	B cells peripheral blood_12_EnhBiv
20	−7.14	NULL	44	MF	antigen binding

p−values