MPI−142

Global Summary

%DE = 0.03

genes with fdr < 0.2 = 240 (53 + / 187 −)

genes with fdr < 0.1 = 157 (33 + / 124 −)

genes with fdr < 0.05 = 118 (23 + / 95 −)

genes with fdr < 0.01 = 76 (12 + / 64 −)

genes in genesets = 13152

<FC> = 0

<t−score> = −0.52

<p−value> = 0.31

<fdr> = 0.97

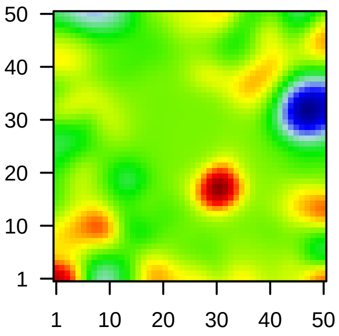
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	44790_s_at	−2.07	2e−16	1e−12	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
2	209374_s_at	−2.18	2e−16	1e−12	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
3	210258_at	−2.41	2e−16	1e−12	49 x 40	regulator of G protein signaling 13 [Source:HGNC Symbol;Ac
4	212827_at	−2.35	2e−16	1e−12	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
5	219471_at	−2.12	2e−16	1e−12	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
6	39318_at	−1.79	1e−13	8e−09	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
7	209995_s_at	−1.94	5e−13	1e−07	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
8	201811_x_at	−1.65	5e−12	4e−06	0 x 21	SH3 domain binding protein 5 [Source:HGNC Symbol;Acc:HG
9	212592_at	−1.72	2e−10	7e−06	45 x 49	joining chain of multimeric IgA and IgM [Source:HGNC Symb
10	202901_x_at	−1.84	7e−10	7e−06	11 x 12	cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
11	201909_at	−1.81	8e−10	2e−05	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
12	212476_at	−1.64	2e−09	2e−05	46 x 30	ArfGAP with coiled−coil, ankyrin repeat and PH domains 2 [S
13	212454_x_at	−1.45	3e−09	2e−05	47 x 5	heterogeneous nuclear ribonucleoprotein D like [Source:HGN
14	203881_s_at	−2.22	3e−09	9e−05	0 x 16	dystrophin [Source:HGNC Symbol;Acc:HGNC:2928]
15	201222_s_at	−1.3	1e−08	9e−05	10 x 49	RAD23 homolog B, nucleotide excision repair protein [Source
16	217802_s_at	−1.24	2e−08	9e−05	49 x 27	nuclear casein kinase and cyclin dependent kinase substrate
17	202404_s_at	−1.64	2e−08	9e−05	9 x 0	collagen type I alpha 2 chain [Source:HGNC Symbol;Acc:HG
18	217144_at	−1.6	2e−08	9e−05	44 x 30	ubiquitin B pseudogene 1 [Source:HGNC Symbol;Acc:HGNC
19	203203_s_at	−1.61	3e−08	9e−05	46 x 31	KRR1, small subunit processome component homolog [Sourc
20	202950_at	−1.51	3e−08	9e−05	20 x 47	crystallin zeta [Source:HGNC Symbol;Acc:HGNC:2419]

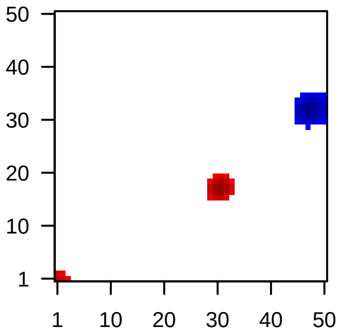
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.57	NULL	102	Reference Signatures	WIRTH_EBV B−cells
2	9.13	NULL	2507	Chromatin_states	Mid_Frontal_Lobe_ReprPC
3	8.88	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	8.43	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
5	8.34	NULL	2704	Chromatin_states	4_TxTrans_Fibroblasts
6	8.18	NULL	2203	Chromatin_states	EnhA_Colon
7	7.88	NULL	833	Chr	Chr 19
8	7.77	NULL	548	Chr	Chr 16
9	7.74	NULL	1600	Chromatin_states	4_TxTrans_Melanocytes
10	7.52	NULL	2380	Chromatin_states	TxEnhG1_Colon
11	7.35	NULL	62	Lymphoma	Monti_Host_response_cluster
12	7.05	NULL	333	Chr	Chr 22
13	6.99	NULL	88	GSEA C2	WIELAND_UP_BY_HBV_INFECTION
14	6.75	NULL	92	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
15	6.67	NULL	78	Melanoma	Tirosh_expression higher in CAFs than in T−cells
16	6.52	NULL	33	Melanoma	Tirosh_T−cell specific genes−melanoma
17	6.32	NULL	2375	Chromatin_states	10_ReprPC_Fibroblasts
18	6.3	NULL	431	BP	immune system process
19	6.13	NULL	2563	Chromatin_states	Mid_Frontal_Lobe_ZNF
20	6.08	NULL	2867	Chromatin_states	9_ReprPCWk_MSC_Adipocyte
Underexpressed					
1	−16.85	NULL	310	Reference Signatures	C[illegible]_3,4_Protein phosphatases
2	−16.02	NULL	5529	Lymphoma	HOPP_Txn_elongation
3	−15.81	NULL	5908	Lymphoma	HOPP_Active_promoter
4	−15.73	NULL	6244	Chromatin_states	15_Quies_Fibroblasts
5	−14.6	NULL	4559	Lymphoma	HOPP_Weak_enhancer
6	−14.45	NULL	7581	Chromatin_states	15_Quies_Melanocytes
7	−13.88	NULL	5682	Lymphoma	HOPP_Weak_promoter
8	−13.57	NULL	4683	Chromatin_states	Overlap_fetal_midbrain_HetRpts
9	−13.49	NULL	669	GSEA C2	JOHNSTONE_PARVB_TARGETS_3_DN
10	−13.42	NULL	6068	Chromatin_states	4_Tx_ESC_Endoderm
11	−13.22	NULL	7583	Chromatin_states	15_Quies_Skeletal_Muscle
12	−13.21	NULL	7225	Chromatin_states	Overlap_fetal_midbrain_ReprPC
13	−13.13	NULL	3554	Chromatin_states	8_ZNF_Rpts_ESC_Endoderm
14	−13.1	NULL	830	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	−13.07	NULL	6099	Chromatin_states	HSC_4_Tx
16	−13.01	NULL	528	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_
17	−12.97	NULL	6389	Chromatin_states	4_Tx_ESC_Mesoderm
18	−12.95	NULL	673	GSEA C2	SCHLOSSER_SERUM_RESPONSE_DN
19	−12.73	NULL	7066	Chromatin_states	Overlap_fetal_midbrain_ReprPCWk
20	−12.67	NULL	516	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP

Portrait



Regulated Metagenes



p−values