MPI−074

Global Summary

%DE = 0.04

genes with fdr < 0.2 = 559 (325 + / 234 −)

genes with fdr < 0.1 = 417 (247 + / 170 −)

genes with fdr < 0.05 = 328 (198 + / 130 −)

genes with fdr < 0.01 = 218 (132 + / 86 −)

genes in genesets = 13152

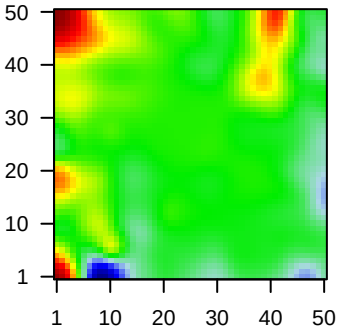
<FC> = 0

<t−score> = 0.08

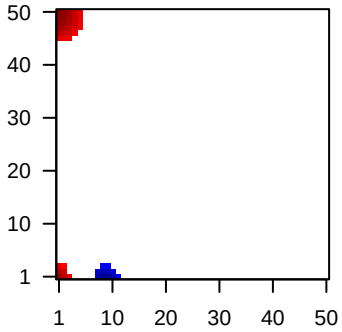
<p−value> = 0.26

<fdr> = 0.96

Portrait



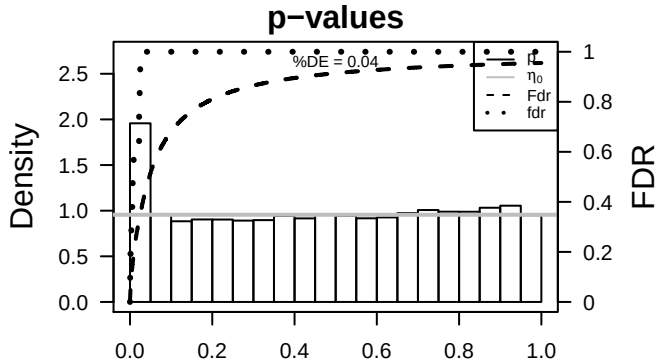
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	205047_s_at	−1.49	2e−16	6e−13	37 x 44	
2	205541_s_at	−1.78	2e−16	6e−13	0 x 33	G1 to S phase transition 2 [Source:HGNC Symbol;Acc:HGNC
3	206018_at	2.43	2e−16	6e−13	6 x 32	forkhead box G1 [Source:HGNC Symbol;Acc:HGNC:3811]
4	210546_x_at	2.67	2e−16	6e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2
5	211674_x_at	2.71	2e−16	6e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2
6	215733_x_at	2.51	2e−16	6e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2
7	217339_x_at	2.64	2e−16	6e−13	10 x 27	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2
8	220635_at	2.51	2e−16	6e−13	4 x 19	psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;
9	215273_s_at	−1.21	4e−16	1e−11	21 x 4	transcriptional adaptor 3 [Source:HGNC Symbol;Acc:HGNC:1
10	214290_s_at	1.11	1e−15	1e−11	0 x 21	histone cluster 2 H2A family member a3 [Source:HGNC Syml
11	211430_s_at	0.94	2e−15	9e−11	0 x 4	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
12	213322_at	−1.43	6e−15	1e−09	44 x 39	O−acyl−ADP−ribose deacylase 1 [Source:HGNC Symbol;Acc
13	209398_at	1.55	5e−14	4e−09	0 x 20	histone cluster 1 H1 family member c [Source:HGNC Symbol
14	210809_s_at	−1.54	2e−13	4e−09	9 x 0	periostin [Source:HGNC Symbol;Acc:HGNC:16953]
15	212587_s_at	0.89	4e−13	4e−09	49 x 23	protein tyrosine phosphatase, receptor type C [Source:HGNC
16	207238_s_at	0.91	8e−13	4e−09	0 x 35	protein tyrosine phosphatase, receptor type C [Source:HGNC
17	203881_s_at	−1.53	8e−13	4e−08	0 x 16	dystrophin [Source:HGNC Symbol;Acc:HGNC:2928]
18	218280_x_at	1.14	3e−12	4e−08	1 x 21	histone cluster 2 H2A family member a3 [Source:HGNC Syml
19	201909_at	1.16	5e−12	1e−07	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
20	209260_at	1.77	1e−11	1e−07	21 x 12	stratifin [Source:HGNC Symbol;Acc:HGNC:10773]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.96	NULL	44	MF	antigen binding
2	10.49	NULL	52	BP	complement activation, classical pathway
3	9.6	NULL	9	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	9.37	NULL	39	BP	complement activation
5	9.25	NULL	85	Lymphoma	ukema_BCL2 DN_BCL6 UP
6	9.01	NULL	53	BP	regulation of complement activation
7	8.24	NULL	353	Lymphoma	SPANG_CD40 6hrs DN
8	8.18	NULL	32	Reference Signatures	1,1_Plasma Cells
9	7.85	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
10	7.84	NULL	314	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_DN
11	7.84	NULL	113	BP	regulation of immune response
12	7.6	NULL	102	Reference Signatures	B−cells
13	7.41	NULL	233	GSEA C2	PENG_RAPAMYCIN_RESPONSE_DN
14	7.38	NULL	178	GSEA C2	PENG_LEUCINE_DEPRIVATION_DN
15	7.28	NULL	675	GSEA C2	GRADE_COLON_CANCER_UP
16	7.1	NULL	76	BP	Fc−gamma receptor signaling pathway involved in phagocytosis
17	6.78	NULL	728	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
18	6.69	NULL	496	Reference Signatures	BIOTEMAS_spleen
19	6.61	NULL	651	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
20	6.6	NULL	4261	Lymphoma	HOPP_Txn_transition
Underexpressed					
1	−11.62	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	−9.61	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
3	−8.46	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	−8.42	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	−8.35	NULL	4214	Chromatin states	myocytes peripheral blood_15_Quies
6	−7.97	NULL	3272	Chromatin states	myocytes peripheral blood_14_ReprPCWk
7	−7.97	NULL	2993	Chromatin states	myocytes peripheral blood_9_Het
8	−7.73	NULL	1001	Colon Cancer	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending c
9	−7.39	NULL	3150	Chromatin states	myocytes peripheral blood_13_ReprPC
10	−7.31	NULL	249	GSEA C2	ONDER_CDH1_TARGETS_2_UP
11	−7.28	NULL	58	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
12	−7.16	NULL	78	Melanoma	Tirosh_CAF−cell specific genes
13	−7.03	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
14	−6.87	NULL	197	GSEA C2	NABA_CORE_MATRISOME
15	−6.77	NULL	6791	Chromatin states	Embs ESC_Endoderm
16	−6.75	NULL	7583	Chromatin states	15_Quies_Skeletal_Muscle
17	−6.72	NULL	8088	Chromatin states	15_Quies_MSC_Adipocyte
18	−6.7	NULL	247	GSEA C2	BOQUEST_STEM_CELL_UP
19	−6.67	NULL	2974	Chromatin states	9_Het_ESC_Endoderm
20	−6.65	NULL	18	CC	MHC class II protein complex