MPI−202

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 522 (247 + / 275 −)

genes with fdr < 0.1 = 368 (159 + / 209 −)

genes with fdr < 0.05 = 198 (89 + / 109 −)

genes with fdr < 0.01 = 124 (58 + / 66 −)

genes in genesets = 13152

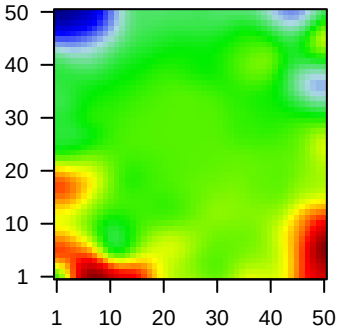
<FC> = 0

<t−score> = −0.16

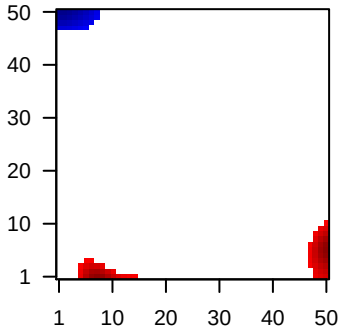
<p−value> = 0.27

<fdr> = 0.95

Portrait



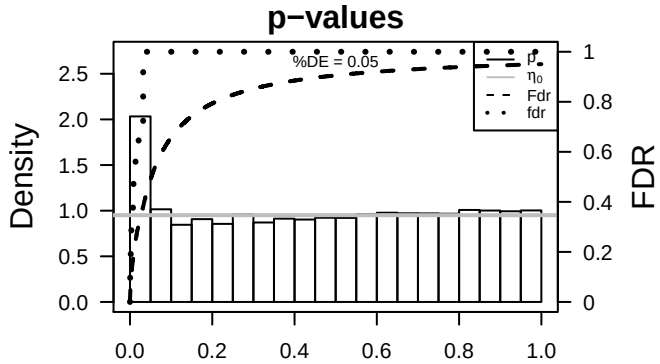
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	208621_s_at	−2.52	2e−16	7e−13	0 x 48	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
2	208650_s_at	−1.92	2e−16	7e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
3	208651_x_at	−2.14	2e−16	7e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
4	209201_x_at	−1.67	2e−16	7e−13	7 x 48	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
5	209771_x_at	−1.88	2e−16	7e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
6	212592_at	−1.99	2e−16	7e−13	45 x 49	joining chain of multimeric IgA and IgM [Source:HGNC Symb
7	216379_x_at	−1.93	2e−16	7e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
8	201427_s_at	−1.36	1e−15	5e−11	47 x 37	selenoprotein P [Source:HGNC Symbol;Acc:HGNC:10751]
9	205040_at	2.58	6e−15	5e−11	5 x 0	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
10	202003_s_at	−1.41	6e−15	3e−10	34 x 49	acetyl−CoA acyltransferase 2 [Source:HGNC Symbol;Acc:HG
11	266_s_at	−1.77	2e−14	7e−10	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
12	204475_at	2.48	6e−14	7e−10	7 x 0	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
13	210317_s_at	−1.45	8e−14	1e−09	2 x 45	tyrosine 3−monooxygenase/tryptophan 5−monooxygenase ac
14	201746_at	−1.46	1e−13	1e−09	45 x 37	tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]
15	205041_s_at	2.42	2e−13	8e−09	5 x 0	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
16	203608_at	−1.48	6e−13	3e−08	45 x 49	aldehyde dehydrogenase 5 family member A1 [Source:HGNC
17	217211_at	−1.63	2e−12	1e−07	0 x 49	actin, beta pseudogene 9 [Source:HGNC Symbol;Acc:HGNC
18	203936_s_at	1.04	9e−12	3e−07	5 x 3	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
19	205692_s_at	−1.51	4e−11	3e−07	49 x 38	CD38 molecule [Source:HGNC Symbol;Acc:HGNC:1667]
20	205828_at	2.18	4e−11	3e−07	13 x 0	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.47	NULL	214	Lymphoma	LENZ_Stromal signature 1
2	12.48	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
3	12.36	NULL	58	BP	collagen catabolic process
4	12.23	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	12.23	NULL	3724	Chromatin states	T cells peripheral blood_12_EnhBiv
6	11.91	NULL	212	CC	extracellular matrix
7	11.68	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
8	11.59	NULL	3918	Chromatin states	T cells peripheral blood_14_ReprPCWk
9	11.18	NULL	253	CC	proteinaceous extracellular matrix
10	11.15	NULL	747	GSEA C2	NABA_MATRISOME
11	11.01	NULL	75	GSEA C2	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION
12	10.97	NULL	2507	Chromatin states	Mid_Frontal_Lobe_ReprPC
13	10.76	NULL	2704	Chromatin states	4−TaTs_Fibroblasts
14	10.65	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
15	10.6	NULL	2602	Chromatin states	natural killer cells peripheral blood_12_EnhBiv
16	10.48	NULL	404	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
17	10.43	NULL	3150	Chromatin states	monocytes peripheral blood_13_ReprPC
18	10.33	NULL	2765	Chromatin states	T regulatory cells peripheral blood_13_ReprPC
19	10.25	NULL	1930	Chromatin states	Fetal_TssA
20	10.2	NULL	2747	Chromatin states	B cells peripheral blood_12_EnhBiv
Underexpressed					
1	−13.18	NULL	7225	Chromatin states	Ovaries_fetal_midbrain_ReprPC
2	−12.75	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
3	−11.97	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
4	−11.61	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
5	−11.57	NULL	8322	Chromatin states	T cells naive cells peripheral blood_1_TssA
6	−11.56	NULL	282	Glioma	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	−11.47	NULL	5529	Lymphoma	HOPP_Txn_elongation
8	−11.42	NULL	4528	Chromatin states	T cells naive cells peripheral blood_4_Tx
9	−11.41	NULL	5908	Lymphoma	HOPP_Active_promoter
10	−11.28	NULL	8068	Chromatin states	T helper cells peripheral blood_1_TssA
11	−10.64	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	−10.63	NULL	7635	Chromatin states	monocytes peripheral blood_1_TssA
13	−10.6	NULL	7930	Chromatin states	T regulatory cells peripheral blood_1_TssA
14	−10.58	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
15	−10.5	NULL	1338	GSEA C2	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
16	−10.38	NULL	136	Reference Signatures	Cytoskeleton_2,9_Cytosceleton
17	−10.34	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
18	−10.3	NULL	8431	Chromatin states	T cells naive cells peripheral blood_2_TssAFlnk
19	−10.23	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
20	−10.02	NULL	6099	Chromatin states	HSC_4_Tx