MPI−250

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 610 (334 + / 276 −)

genes with fdr < 0.1 = 508 (277 + / 231 −)

genes with fdr < 0.05 = 343 (181 + / 162 −)

genes with fdr < 0.01 = 224 (118 + / 106 −)

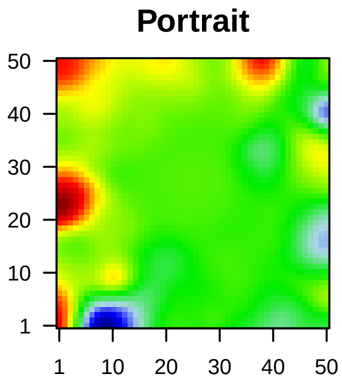
genes in genesets = 13152

<FC> = 0

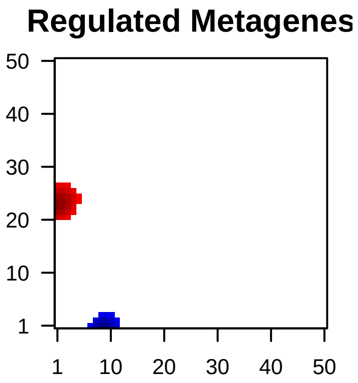
<t−score> = 0.17

<p−value> = 0.24

<fdr> = 0.94



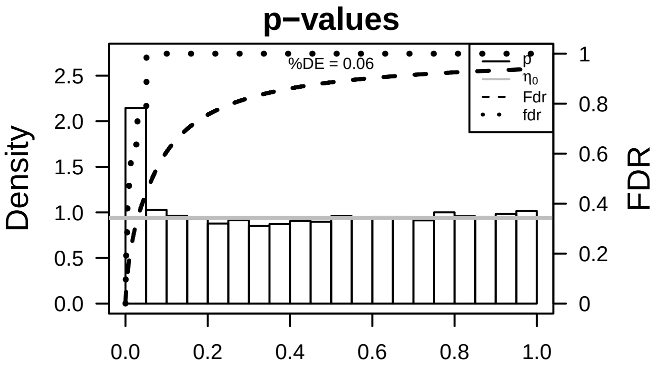
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	201893_x_at	−1.3	2e−16	2e−13	8 x 0	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
2	202310_s_at	−0.93	2e−16	2e−13	9 x 0	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HG
3	204257_at	−1.16	2e−16	2e−13	49 x 39	fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35
4	204581_at	−1.51	2e−16	2e−13	49 x 41	CD22 molecule [Source:HGNC Symbol;Acc:HGNC:1643]
5	205124_at	−1.26	2e−16	2e−13	49 x 41	myocyte enhancer factor 2B [Source:HGNC Symbol;Acc:HGN
6	207861_at	1.97	2e−16	2e−13	0 x 20	C−C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:
7	209374_s_at	0.81	2e−16	2e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
8	209480_at	−1.77	2e−16	2e−13	49 x 16	major histocompatibility complex, class II, DQ beta 1 [Source:
9	210495_x_at	−1.27	2e−16	2e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
10	211719_x_at	−1.31	2e−16	2e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	212464_s_at	−1.24	2e−16	2e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
12	213094_at	2.22	2e−16	2e−13	33 x 26	adhesion G protein−coupled receptor G6 [Source:HGNC Sym
13	213110_s_at	1.95	2e−16	2e−13	2 x 25	collagen type IV alpha 5 chain [Source:HGNC Symbol;Acc:H
14	213831_at	−1.71	2e−16	2e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Source
15	214669_x_at	1.01	2e−16	2e−13	0 x 3	
16	215176_x_at	1.51	2e−16	2e−13	10 x 5	immunoglobulin kappa variable 1−39 (gene/pseudogene) [So
17	216080_s_at	−1.31	2e−16	2e−13	49 x 39	fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35
18	216442_x_at	−1.43	2e−16	2e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
19	218717_s_at	1.83	2e−16	2e−13	1 x 23	prolyl 3−hydroxylase 2 [Source:HGNC Symbol;Acc:HGNC:19
20	219518_s_at	−1.22	2e−16	2e−13	49 x 41	



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.59	NULL	5529	Lymphoma	HOPP_Txn_elongation
2	14.5	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
3	14.31	NULL	7635	Chromatin states	monocytes peripheral blood_1_TssA
4	14.14	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
5	13.56	NULL	7930	Chromatin states	T regulatory cells peripheral blood_1_TssA
6	13.53	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
7	13.19	NULL	8322	Chromatin states	T CD8+ naive cells peripheral blood_1_TssA
8	12.97	NULL	8068	Chromatin states	T helper cells peripheral blood_1_TssA
9	12.82	NULL	4261	Lymphoma	HOPP_Txn_transition
10	12.78	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
11	12.77	NULL	6099	Chromatin states	HSC_4_Tx
12	12.54	NULL	8200	Chromatin states	monocytes peripheral blood_2_TssAFlnk
13	12.52	NULL	8431	Chromatin states	T CD8+ naive cells peripheral blood_2_TssAFlnk
14	12.45	NULL	5908	Lymphoma	HOPP_Active_promoter
15	12.36	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
16	12.19	NULL	8816	Chromatin states	T helper cells peripheral blood_2_TssAFlnk
17	12.06	NULL	8370	Chromatin states	natural killer cells peripheral blood_2_TssAFlnk
18	11.67	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
19	11.66	NULL	4528	Chromatin states	T CD8+ naive cells peripheral blood_4_Tx
20	10.91	NULL	5766	Chromatin states	natural killer cells peripheral blood_4_Tx
Underexpressed					
1	−14.24	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
2	−13.01	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
3	−12.48	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	−11.78	NULL	3724	Chromatin states	T cells peripheral blood_12_EnhBiv
5	−11.75	NULL	197	GSEA C2	NABA_CORE_MATRISOME
6	−11.62	NULL	78	Melanoma	Tirosh_CAF−cell specific genes
7	−11.09	NULL	3918	Chromatin states	T cells peripheral blood_14_ReprPCWk
8	−11.08	NULL	212	CC	extracellular matrix
9	−11.03	NULL	3168	Lymphoma	HOPP_Repressed
10	−10.98	NULL	214	Lymphoma	LENZ_Stromal signature 1
11	−10.97	NULL	747	GSEA C2	NABA_MATRISOME
12	−10.88	NULL	3150	Chromatin states	monocytes peripheral blood_13_ReprPC
13	−10.64	NULL	253	CC	proteinaceous extracellular matrix
14	−10.41	NULL	3272	Chromatin states	monocytes peripheral blood_14_ReprPCWk
15	−10.34	NULL	247	GSEA C2	BOQUEST_STEM_CELL_UP
16	−10.27	NULL	2765	Chromatin states	T regulatory cells peripheral blood_13_ReprPC
17	−10.05	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
18	−9.96	NULL	2405	Chromatin states	B cells peripheral blood_13_ReprPC
19	−9.86	NULL	2300	Chromatin states	T helper cells peripheral blood_13_ReprPC
20	−9.8	NULL	2602	Chromatin states	natural killer cells peripheral blood_12_EnhBiv