MPI−007

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 604 (253 + / 351 −)

genes with fdr < 0.1 = 401 (153 + / 248 −)

genes with fdr < 0.05 = 326 (121 + / 205 −)

genes with fdr < 0.01 = 200 (71 + / 129 −)

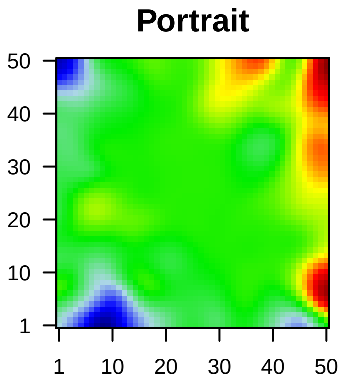
genes in genesets = 13152

<FC> = 0

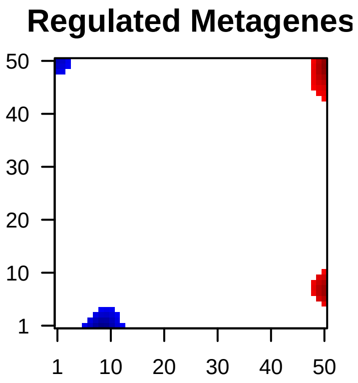
<t−score> = 0

<p−value> = 0.26

<fdr> = 0.95



Portrait



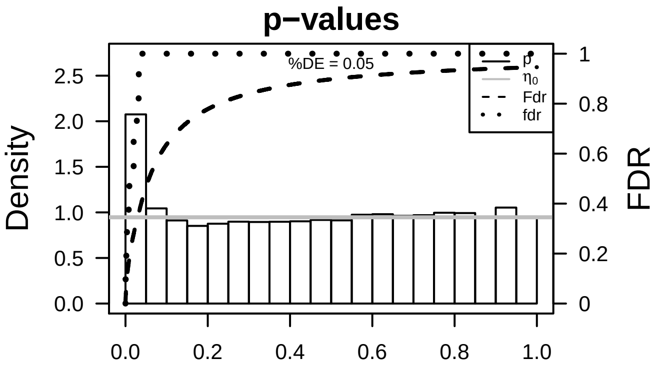
Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AFFX−HUMR	2.59	2e−16	5e−13	49 x 47	microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835
2	AFFX−r2−Hs1	2.98	2e−16	5e−13	49 x 47	
3	201008_s_at	−2	2e−16	5e−13	0 x 49	thioredoxin interacting protein [Source:HGNC Symbol;Acc:HG
4	201852_x_at	−1.24	2e−16	5e−13	8 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HG
5	202310_s_at	−1.48	2e−16	5e−13	9 x 0	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HG
6	211896_s_at	−1.6	2e−16	5e−13	8 x 0	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
7	211981_at	−1.85	2e−16	5e−13	9 x 0	collagen type IV alpha 1 chain [Source:HGNC Symbol;Acc:HG
8	212415_at	−1.25	2e−16	5e−13	0 x 14	septin 6 [Source:HGNC Symbol;Acc:HGNC:15848]
9	215076_s_at	−1.09	2e−16	5e−13	8 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HG
10	210809_s_at	−1.86	4e−16	3e−11	9 x 0	periostin [Source:HGNC Symbol;Acc:HGNC:16953]
11	201909_at	−1.45	2e−15	8e−11	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
12	202403_s_at	−1.05	6e−15	8e−11	9 x 0	collagen type I alpha 2 chain [Source:HGNC Symbol;Acc:HG
13	209875_s_at	−1.88	1e−14	8e−11	8 x 0	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
14	211161_s_at	−1.35	1e−14	1e−10	9 x 0	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HG
15	217022_s_at	−1.45	2e−14	1e−10	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
16	209458_x_at	−1.36	3e−14	2e−10	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
17	208997_s_at	−0.99	4e−14	6e−10	0 x 40	uncoupling protein 2 [Source:HGNC Symbol;Acc:HGNC:1251
18	205321_at	−1.17	7e−14	7e−10	1 x 45	eukaryotic translation initiation factor 2 subunit gamma B [Sou
19	AFFX−r2−Hs1	2.1	1e−13	7e−10	49 x 47	
20	208650_s_at	−1.32	2e−13	7e−10	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.68	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
2	15.87	NULL	7930	Chromatin states	T regulatory cells peripheral blood_1_TssA
3	15.49	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
4	15.3	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
5	15.3	NULL	8068	Chromatin states	T helper cells peripheral blood_1_TssA
6	15.08	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
7	14.95	NULL	8322	Chromatin states	T CD8+ naive cells peripheral blood_1_TssA
8	14.74	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
9	14.6	NULL	5529	Lymphoma	HOPP_Txn_elongation
10	13.92	NULL	8245	Chromatin states	T regulatory cells peripheral blood_2_TssAFlnk
11	13.46	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
12	13.38	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
13	13.33	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
14	13.21	NULL	3564	TF	ICGC_Taf1_targets
15	13.16	NULL	5766	Chromatin states	natural killer cells peripheral blood_4_Tx
16	13.05	NULL	8370	Chromatin states	natural killer cells peripheral blood_2_TssAFlnk
17	13.04	NULL	7225	Chromatin states	Overlap_fetal_midbrain_ReprPC
18	12.97	NULL	6099	Chromatin states	HSC_4_Tx
19	12.87	NULL	219	Reference Signatures	WSRH_GC B−cells
20	12.78	NULL	7835	Chromatin states	HSC_1_TssA
Underexpressed					
1	−17.85	NULL	335	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	−16.65	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	−15.69	NULL	176	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	−15.45	NULL	1611	CC	extracellular region
5	−14.82	NULL	1090	CC	extracellular space
6	−14.04	NULL	747	GSEA C2	NABA_MATRISOME
7	−13.67	NULL	214	Lymphoma	LENZ_Stromal signature 1
8	−13.58	NULL	78	Melanoma	Tirosh_CAF−cell specific genes
9	−13.49	NULL	2239	CC	extracellular exosome
10	−13.48	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
11	−13.37	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
12	−13.36	NULL	443	GSEA C2	CHICAS_RB1_TARGETS_CONFLUENT
13	−12.99	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
14	−12.96	NULL	197	GSEA C2	NABA_CORE_MATRISOME
15	−12.89	NULL	397	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
16	−12.79	NULL	212	CC	extracellular matrix
17	−12.58	NULL	70	GSEA C2	KIM_GLIS2_TARGETS_UP
18	−12.56	NULL	224	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
19	−12.39	NULL	231	Glioma	WILLSCHER_GBM_Verhaak−CL & MES_up
20	−12.31	NULL	331	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B



p−values