MPI−002

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 843 (568 + / 275 −)

genes with fdr < 0.1 = 689 (475 + / 214 −)

genes with fdr < 0.05 = 575 (412 + / 163 −)

genes with fdr < 0.01 = 389 (310 + / 79 −)

genes in genesets = 13152

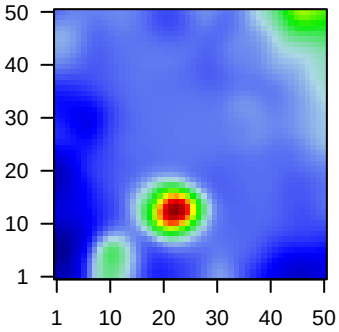
<FC> = 0

<t−score> = −0.05

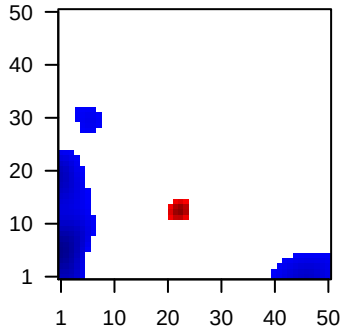
<p−value> = 0.2

<fdr> = 0.94

Portrait



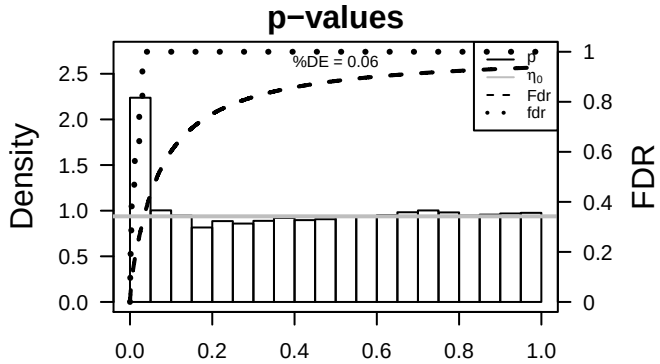
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AFFX−HUMR	2.72	2e−16	6e−14	49 x 47	microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835
2	AFFX−HUMR	2.23	2e−16	6e−14	49 x 47	
3	AFFX−HUMR	2.41	2e−16	6e−14	49 x 47	
4	AFFX−r2−Hs1	2.58	2e−16	6e−14	49 x 47	
5	AFFX−r2−Hs1	2.42	2e−16	6e−14	49 x 47	
6	AFFX−r2−Hs1	3.08	2e−16	6e−14	49 x 47	
7	AFFX−r2−Hs2	2.17	2e−16	6e−14	49 x 46	
8	41469_at	2.41	2e−16	6e−14	22 x 12	peptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:8947
9	200606_at	2.63	2e−16	6e−14	21 x 12	desmoplakin [Source:HGNC Symbol;Acc:HGNC:3052]
10	201820_at	2.7	2e−16	6e−14	22 x 12	keratin 5 [Source:HGNC Symbol;Acc:HGNC:6442]
11	202286_s_at	2.75	2e−16	6e−14	22 x 12	tumor associated calcium signal transducer 2 [Source:HGNC
12	202489_s_at	2.05	2e−16	6e−14	20 x 12	FXYD domain containing ion transport regulator 3 [Source:HC
13	202504_at	2.8	2e−16	6e−14	22 x 12	tripartite motif containing 29 [Source:HGNC Symbol;Acc:HGN
14	202917_s_at	1.96	2e−16	6e−14	0 x 0	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:
15	203021_at	2.15	2e−16	6e−14	22 x 12	secretory leukocyte peptidase inhibitor [Source:HGNC Symbo
16	203407_at	2.58	2e−16	6e−14	22 x 12	periplakin [Source:HGNC Symbol;Acc:HGNC:9273]
17	203535_at	2.34	2e−16	6e−14	0 x 0	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
18	203691_at	2.25	2e−16	6e−14	22 x 12	peptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:8947
19	203757_s_at	2.45	2e−16	6e−14	20 x 12	carcinoembryonic antigen related cell adhesion molecule 6 [S
20	204018_x_at	−1.7	2e−16	6e−14	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	44.54	NULL	105	Reference	VARTIKI_MUCOSA
2	35.39	NULL	248	GSEA C2	JAEGER_METASTASIS_DN
3	28.21	NULL	46	GSEA C2	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
4	26.2	NULL	78	BP	cornification
5	25.7	NULL	453	GSEA C2	ONDER_CDH1_TARGETS_2_DN
6	24.05	NULL	72	BP	keratinization
7	22.79	NULL	51	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	21.97	NULL	35	CC	cornified envelope
9	18.71	NULL	93	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
10	16.97	NULL	82	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
11	16.69	NULL	46	BP	keratinocyte differentiation
12	16.27	NULL	35	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	15.28	NULL	57	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	15.21	NULL	28	BP	peptide cross−linking
15	15.01	NULL	59	Melanoma	TCGA_melanoma_keratin_high
16	14.97	NULL	47	GSEA C2	CROMER_TUMORIGENESIS_DN
17	14.52	NULL	74	BP	epidermis development
18	14.51	NULL	58	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
19	14.38	NULL	608	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
20	14.31	NULL	23	CC	desmosome
Underexpressed					
1	−14.1	NULL	317	Cancer	SPANG_BCL6−index2
2	−11.93	NULL	85	Lymphoma	Rosha_DLBCL UP
3	−10.92	NULL	589	Colon Cancer	Leinbocke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	−10.69	NULL	90	GSEA C2	BASSO_CD40_SIGNALING_UP
5	−10.55	NULL	186	Cancer	SPANG_LPS−index2
6	−9.51	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
7	−9.08	NULL	78	Melanoma	Tirosh_expression higher in CAFs than in T−cells
8	−9.05	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
9	−8.99	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
10	−8.9	NULL	18	CC	MHC class II protein complex
11	−8.6	NULL	173	Lymphoma	Victora_Light zone signature
12	−8.52	NULL	22	Lymphoma	DAVE_NFkB BL DN
13	−8.51	NULL	14	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_DN
14	−8.13	NULL	4	Lymphoma	MASCQUE_mBL DOWN
15	−8.07	NULL	40	BP	antigen processing and presentation
16	−8	NULL	66	BP	interferon−gamma−mediated signaling pathway
17	−7.93	NULL	353	Lymphoma	SPANG_CD40 6hrs DN
18	−7.46	NULL	88	GSEA C2	WIELAND_UP_BY_HBV_INFECTION
19	−7.4	NULL	166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	−7.28	NULL	23	CC	integral component of lumenal side of endoplasmic reticulum meml