MPI−154

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 567 (324 + / 243 −)

genes with fdr < 0.1 = 371 (229 + / 142 −)

genes with fdr < 0.05 = 303 (189 + / 114 −)

genes with fdr < 0.01 = 171 (121 + / 50 −)

genes in genesets = 13152

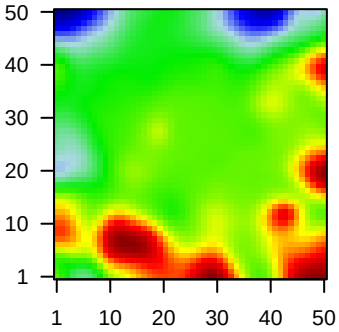
<FC> = 0

<t−score> = 0.03

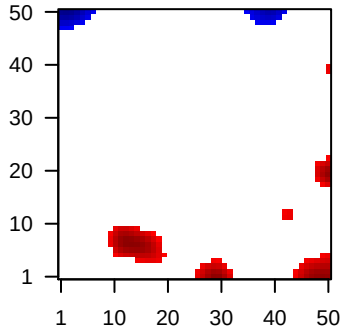
<p−value> = 0.26

<fdr> = 0.95

Portrait



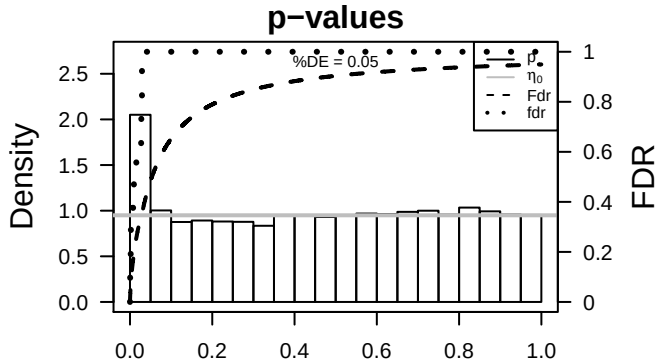
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	203872_at	2.52	2e−16	3e−13	42 x 12	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:H(
2	204631_at	2.49	2e−16	3e−13	42 x 12	myosin heavy chain 2 [Source:HGNC Symbol;Acc:HGNC:757
3	204810_s_at	2.44	2e−16	3e−13	42 x 11	creatine kinase, M−type [Source:HGNC Symbol;Acc:HGNC:1
4	205054_at	2.41	2e−16	3e−13	42 x 12	nebulin [Source:HGNC Symbol;Acc:HGNC:7720]
5	205374_at	2.56	2e−16	3e−13	42 x 12	sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]
6	205553_s_at	2.65	2e−16	3e−13	42 x 11	cysteine and glycine rich protein 3 [Source:HGNC Symbol;Ac
7	206310_at	2.3	2e−16	3e−13	17 x 6	serine peptidase inhibitor, Kazal type 2 [Source:HGNC Symb
8	209888_s_at	2.52	2e−16	3e−13	42 x 13	myosin light chain 1 [Source:HGNC Symbol;Acc:HGNC:7582
9	209987_s_at	2.71	2e−16	3e−13	28 x 0	achaete−scute family bHLH transcription factor 1 [Source:HG
10	209988_s_at	3.22	2e−16	3e−13	28 x 0	achaete−scute family bHLH transcription factor 1 [Source:HG
11	211583_x_at	2.41	2e−16	3e−13	20 x 3	natural cytotoxicity triggering receptor 3 [Source:HGNC Symt
12	213768_s_at	2.71	2e−16	3e−13	27 x 2	achaete−scute family bHLH transcription factor 1 [Source:HG
13	219106_s_at	2.49	2e−16	3e−13	42 x 12	kelch like family member 41 [Source:HGNC Symbol;Acc:HGN
14	219471_at	−1.19	2e−16	3e−13	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
15	217469_at	2.27	4e−16	1e−11	49 x 20	immunoglobulin heavy constant epsilon [Source:HGNC Symt
16	209806_at	−1.15	1e−15	1e−11	0 x 20	
17	209904_at	2.23	2e−15	2e−11	42 x 11	troponin C1, slow skeletal and cardiac type [Source:HGNC Sy
18	213201_s_at	2.21	3e−15	2e−11	19 x 27	troponin T1, slow skeletal type [Source:HGNC Symbol;Acc:H
19	214087_s_at	2.2	3e−15	1e−10	42 x 12	myosin binding protein C, slow type [Source:HGNC Symbol;A
20	203861_s_at	2.17	8e−15	2e−10	42 x 11	actinin alpha 2 [Source:HGNC Symbol;Acc:HGNC:164]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.57	NULL	83	Reference	VERHAAK_Muscle
2	21.97	NULL	47	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	16.6	NULL	16	Reference	VERHAAK_Hippocampus
4	16.2	NULL	38	BP	muscle filament sliding
5	14.61	NULL	31	GSEA C2	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP
6	14.14	NULL	194	HM	HALLMARK_MYOGENESIS
7	13.93	NULL	27	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
8	13.04	NULL	61	GSEA C2	KUNINGER_IGF1_VS_PDGFB_TARGETS_UP
9	12.75	NULL	41	MF	structural constituent of muscle
10	12.01	NULL	429	GSEA C2	SMID_BREAST_CANCER_NORMAL_LIKE_UP
11	10.98	NULL	49	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
12	10.24	NULL	45	GSEA C2	REACTOME_MUSCLE_CONTRACTION
13	10.21	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
14	9.85	NULL	17	CC	I band
15	9.73	NULL	41	BP	cardiac muscle contraction
16	9.46	NULL	16	GSEA C2	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
17	9.28	NULL	14	Lymphoma	WRIGHT_GCB UP
18	9.06	NULL	33	CC	myofibril
19	9.04	NULL	95	BP	muscle contraction
20	9.03	NULL	21	CC	muscle myosin complex
Underexpressed					
1	−11.78	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
2	−11.75	NULL	1052	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	−11.67	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	−11.3	NULL	6068	Chromatin_State_5	ESC_Endoderm
5	−10.86	NULL	5456	Chromatin_State_5	Neuronal_Progenitor
6	−10.78	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
7	−10.58	NULL	509	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
8	−10.51	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
9	−10.49	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
10	−10.33	NULL	6034	Chromatin_State_5	Fibroblasts
11	−10.19	NULL	526	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	−10.15	NULL	6679	Chromatin_State_5	Melanocytes
13	−10.11	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
14	−10.06	NULL	8275	Chromatin_State_2	Fibroblasts
15	−10.01	NULL	7225	Chromatin_State_2	Overlap_fetal_midbrain_ReprPC
16	−9.82	NULL	254	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
17	−9.79	NULL	8766	Chromatin_State_2	Melanocytes
18	−9.76	NULL	8641	Chromatin_State_1	ESC_Endoderm
19	−9.59	NULL	9160	Chromatin_State_2	Neuronal_Progenitor
20	−9.39	NULL	6389	Chromatin_State_4	ESC_Mesoderm