MPI−161

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 620 (239 + / 381 −)

genes with fdr < 0.1 = 417 (159 + / 258 −)

genes with fdr < 0.05 = 299 (106 + / 193 −)

genes with fdr < 0.01 = 149 (41 + / 108 −)

genes in genesets = 13152

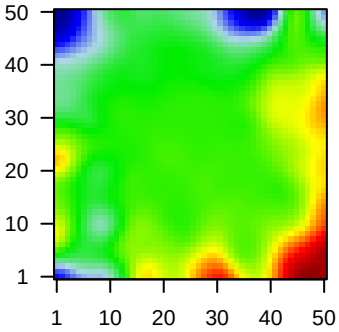
<FC> = 0

<t−score> = −0.06

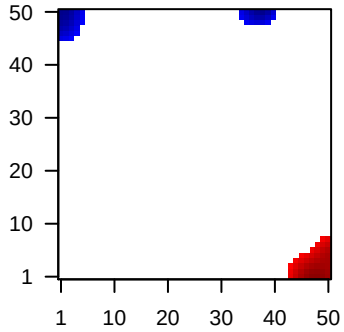
<p−value> = 0.26

<fdr> = 0.94

Portrait



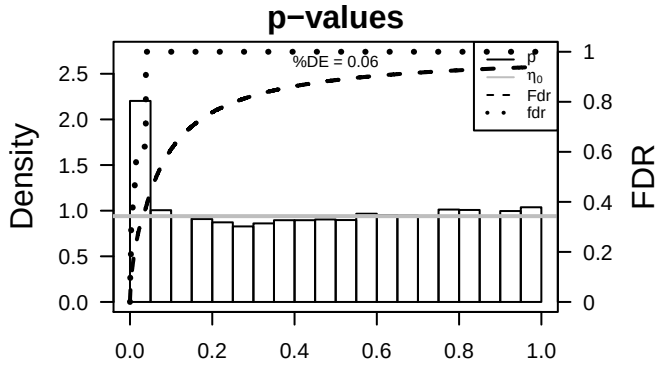
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	203645_s_at	−1.92	2e−16	6e−13	8 x 10	CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]
2	203819_s_at	−2.42	2e−16	6e−13	49 x 45	insulin like growth factor 2 mRNA binding protein 3 [Source:H
3	203820_s_at	−1.85	2e−16	6e−13	43 x 40	insulin like growth factor 2 mRNA binding protein 3 [Source:H
4	209199_s_at	−1.69	2e−16	6e−13	16 x 6	myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HGN
5	210258_at	−2.47	2e−16	6e−13	49 x 40	regulator of G protein signaling 13 [Source:HGNC Symbol;Ac
6	215049_x_at	−2.65	2e−16	6e−13	8 x 10	CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]
7	218236_s_at	−1.63	2e−16	6e−13	8 x 20	protein kinase D3 [Source:HGNC Symbol;Acc:HGNC:9408]
8	220377_at	2.72	2e−16	6e−13	5 x 28	family with sequence similarity 30 member A [Source:HGNC
9	200648_s_at	−1.49	4e−16	1e−11	2 x 0	glutamate−ammonia ligase [Source:HGNC Symbol;Acc:HGN
10	216576_x_at	2.32	1e−15	1e−11	10 x 5	
11	202953_at	−1.39	2e−15	1e−11	0 x 0	complement C1q B chain [Source:HGNC Symbol;Acc:HGNC:
12	202917_s_at	−1.65	3e−15	1e−10	0 x 0	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:
13	209200_at	−1.6	3e−15	1e−10	16 x 6	myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HGN
14	201272_at	−1.09	8e−15	7e−09	24 x 49	aldo−keto reductase family 1 member B [Source:HGNC Symb
15	211699_x_at	−1.41	7e−13	7e−09	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
16	204073_s_at	2.13	7e−13	1e−08	44 x 7	myelin regulatory factor [Source:HGNC Symbol;Acc:HGNC:1
17	215051_x_at	−1.33	1e−12	1e−08	9 x 9	allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:HG
18	204900_x_at	−1.47	2e−12	8e−08	33 x 46	Sin3A associated protein 30 [Source:HGNC Symbol;Acc:HGN
19	200987_x_at	−1.26	6e−12	9e−08	2 x 46	proteasome activator subunit 3 [Source:HGNC Symbol;Acc:H
20	218677_at	2.02	1e−11	2e−07	21 x 12	S100 calcium binding protein A14 [Source:HGNC Symbol;Acc

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	7.16	NULL	2374	Chromatin_States_9_ReprPCWk_Fibroblasts
2	7.05	NULL	2993	Chromatin_States_monocytes peripheral blood_9_Het
3	6.95	NULL	2825	Chromatin_States_9_Het_ESC_Mesoderm
4	6.8	NULL	4214	Chromatin_States_monocytes peripheral blood_15_Quies
5	6.34	NULL	669	Chr Chr 6
6	6.33	NULL	1535	Chromatin_States_Bcells peripheral blood_8_ZNF_Rpts
7	6.25	NULL	2548	Chromatin_States_HSC_9_Het
8	6.21	NULL	2240	Chromatin_States_1_Tss3_Fibroblasts
9	6.21	NULL	275	GSEA C2 HADDAD_B_LYMPHOCYTE_PROGENITOR
10	6.1	NULL	1259	Chromatin_States_14_ZNF_Melanocytes
11	6.08	NULL	1946	Chromatin_States_13_HetRpts_Neuronal_Progenitor
12	6.03	NULL	1581	Chromatin_States_12_Het_Neuronal_Progenitor
13	6.01	NULL	1233	Chromatin_States_13_HetRpts_Melanocytes
14	6.01	NULL	54	GSEA C2 GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
15	5.9	NULL	2974	Chromatin_States_9_Het_ESC_Endoderm
16	5.88	NULL	3272	Chromatin_States_monocytes peripheral blood_14_ReprPCWk
17	5.86	NULL	713	Chromatin_States_7_NA_Colon
18	5.85	NULL	3734	Chromatin_States_Tcells peripheral blood_13_ReprPC
19	5.8	NULL	2173	Chromatin_States_HSC_13_ReprPC
20	5.79	NULL	4079	Chromatin_States_15_Quies_ESC_Endoderm
Underexpressed				
1	−19.68	NULL	319	Melanoma Gerber_wt/wt_melanoma−cells−SpotA
2	−17.63	NULL	244	GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−17.35	NULL	219	Reference MSigDB C3 B−cells
4	−17.24	NULL	137	GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	−16.61	NULL	431	GSEA C2 GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	−16.58	NULL	439	GSEA C2 SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
7	−16.36	NULL	776	Chr Chr 17
8	−16.34	NULL	254	GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	−15.94	NULL	115	Glioma WILLSCHER_GBM_Verhaak−CL_up (C)
10	−15.79	NULL	187	HM HALLMARK_E2F_TARGETS
11	−15.42	NULL	966	GSEA C2 KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	−15.25	NULL	79	Melanoma Tirosh_core cycling genes in low− and high−proliferation melanoma
13	−14.99	NULL	174	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
14	−14.87	NULL	14	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	−14.5	NULL	93	GSEA C2 CROONQUIST_IL6_DEPRIVATION_DN
16	−14.15	NULL	102	GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	−14	NULL	84	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−13.48	NULL	321	GSEA C2 BLUM_RESPONSE_TO_SALIRASIB_DN
19	−13.27	NULL	226	GSEA C2 ZHANG_TLX_TARGETS_60HR_DN
20	−13.04	NULL	297	GSEA C2 GOLDRATH_ANTIGEN_RESPONSE