MPI−210

Global Summary

%DE = 0.08

genes with fdr < 0.2 = 989 (402 + / 587 −)

genes with fdr < 0.1 = 660 (253 + / 407 −)

genes with fdr < 0.05 = 532 (200 + / 332 −)

genes with fdr < 0.01 = 329 (116 + / 213 −)

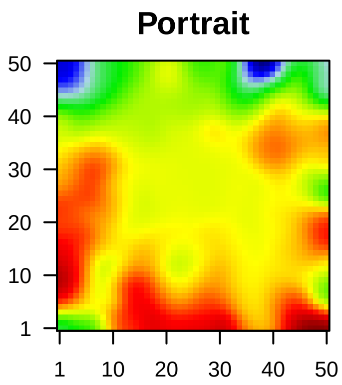
genes in genesets = 13152

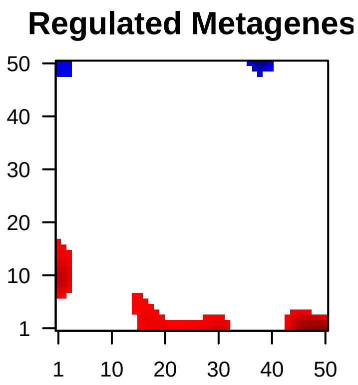
<FC> = 0

<t−score> = −0.15

<p−value> = 0.22

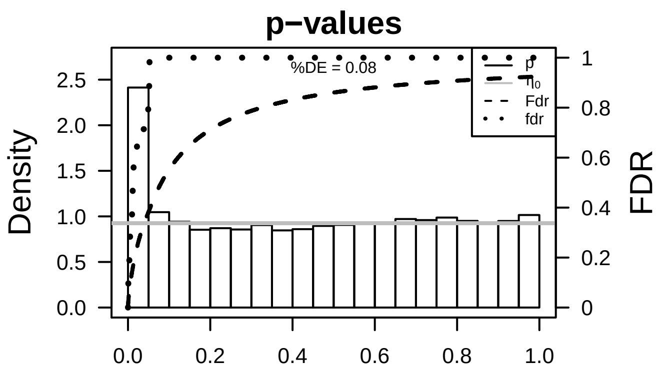
<fdr> = 0.93





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39729_at	−1.29	2e−16	2e−13	49 x 49	peroxiredoxin 2 [Source:HGNC Symbol;Acc:HGNC:9353]
2	201291_s_at	−1.62	2e−16	2e−13	37 x 49	DNA topoisomerase II alpha [Source:HGNC Symbol;Acc:HGI
3	201764_at	−1.65	2e−16	2e−13	36 x 49	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
4	202412_s_at	−1.65	2e−16	2e−13	48 x 45	ubiquitin specific peptidase 1 [Source:HGNC Symbol;Acc:HG
5	203276_at	−1.57	2e−16	2e−13	49 x 29	lamin B1 [Source:HGNC Symbol;Acc:HGNC:6637]
6	203418_at	−1.62	2e−16	2e−13	37 x 49	cyclin A2 [Source:HGNC Symbol;Acc:HGNC:1578]
7	203980_at	2.41	2e−16	2e−13	43 x 47	fatty acid binding protein 4 [Source:HGNC Symbol;Acc:HGNC
8	204446_s_at	−1.71	2e−16	2e−13	44 x 49	arachidonate 5−lipoxygenase [Source:HGNC Symbol;Acc:HG
9	204580_at	−2.08	2e−16	2e−13	3 x 31	matrix metallopeptidase 12 [Source:HGNC Symbol;Acc:HGN
10	205081_at	−1.39	2e−16	2e−13	2 x 6	
11	209374_s_at	−2.04	2e−16	2e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
12	210915_x_at	−1.51	2e−16	2e−13	10 x 8	T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:H
13	211796_s_at	−1.42	2e−16	2e−13	10 x 9	T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:H
14	212827_at	−1.76	2e−16	2e−13	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
15	214669_x_at	−1.81	2e−16	2e−13	0 x 3	
16	214836_x_at	−1.52	2e−16	2e−13	0 x 3	
17	219518_s_at	−1.86	2e−16	2e−13	49 x 41	
18	221651_x_at	−1.85	2e−16	2e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
19	221671_x_at	−2.27	2e−16	2e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
20	202870_s_at	−1.25	9e−16	5e−12	37 x 49	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	8.68	NULL	153	GSEA C2 SMIRNOV_RESPONSE_TO_IR_6HR_UP
2	7.9	NULL	3734	Chromatin states T cells peripheral blood_13_ReprPC
3	7.71	NULL	41	GSEA C2 KERLEY_RESPONSE_TO_CISPLATIN_UP
4	7.67	NULL	548	Chr Chr 16
5	7.29	NULL	2374	Chromatin states 9_ReprPCWk_Fibroblasts
6	7.21	NULL	57	Pneumonia Burnham_viral_UP
7	7.15	NULL	2375	Chromatin states 10_ReprPC_Fibroblasts
8	7.14	NULL	1813	Chromatin states 8_EnhP_Fibroblasts
9	7.04	NULL	47	GSEA C2 DAUER_STAT3_TARGETS_DN
10	7.02	NULL	85	Lymphoma Aukema_BCL2 DN_BCL6 UP
11	7.01	NULL	2327	Chromatin states 14_ReprPCWk_ESC_Mesoderm
12	6.96	NULL	75	Melanoma Tirosh_Endothelial−cell specific genes−melanoma
13	6.93	NULL	3272	Chromatin states monocytes peripheral blood_14_ReprPCWk
14	6.91	NULL	26	GSEA C2 MOSERLE_IFNA_RESPONSE
15	6.84	NULL	2867	Chromatin states 9_ReprPCWk_MSC_Adipocyte
16	6.75	NULL	756	Chr Chr 11
17	6.68	NULL	669	Chr Chr 6
18	6.66	NULL	3089	Chromatin states T regulatory cells peripheral blood_14_ReprPCWk
19	6.66	NULL	37	Pneumonia Sweeney_viral_up
20	6.66	NULL	3918	Chromatin states T cells peripheral blood_14_ReprPCWk
Underexpressed				
1	−29.73	NULL	319	Melanoma Gerber_wt/wt_melanoma−cells−SpotA
2	−28.94	NULL	115	Glioma WILLSCHER_GBM_Verhaak−CL_up (C)
3	−28.59	NULL	137	GSEA C2 ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−28.41	NULL	244	GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	−24.82	NULL	14	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	−24.14	NULL	254	GSEA C2 DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
7	−23.8	NULL	431	GSEA C2 GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	−23.57	NULL	219	Reference Signatures WSRTH_GC B−cells
9	−23.43	NULL	52	GSEA C2 KANG_DOXORUBICIN_RESISTANCE_UP
10	−23.38	NULL	439	GSEA C2 SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	−23.08	NULL	79	Melanoma Tirosh_core cycling genes in low− and high−proliferation melanoma
12	−22.97	NULL	93	GSEA C2 CROONQUIST_IL6_DEPRIVATION_DN
13	−22.36	NULL	966	GSEA C2 KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	−21.32	NULL	102	GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS
15	−21.11	NULL	174	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	−20.88	NULL	44	Melanoma Tirosh_top50 correlated genes PC2
17	−20.52	NULL	226	GSEA C2 ZHANG_TLX_TARGETS_60HR_DN
18	−20.51	NULL	187	HM HALLMARK_E2F_TARGETS
19	−20.48	NULL	84	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	−20.32	NULL	400	GSEA C2 PUJANA_BRCA2_PCC_NETWORK