MPI−227

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 693 (347 + / 346 −)

genes with fdr < 0.1 = 461 (227 + / 234 −)

genes with fdr < 0.05 = 344 (168 + / 176 −)

genes with fdr < 0.01 = 210 (87 + / 123 −)

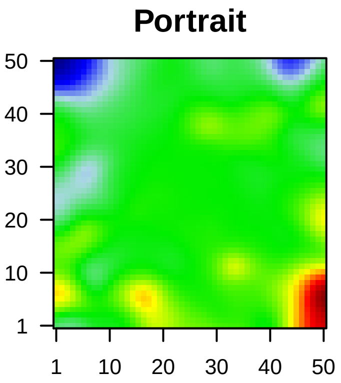
genes in genesets = 13152

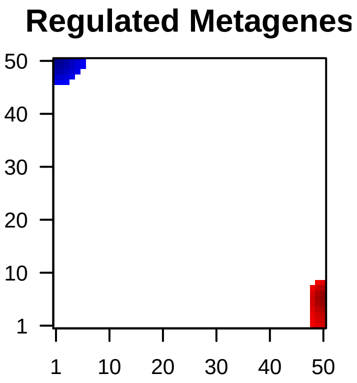
<FC> = 0

<t−score> = −0.11

<p−value> = 0.25

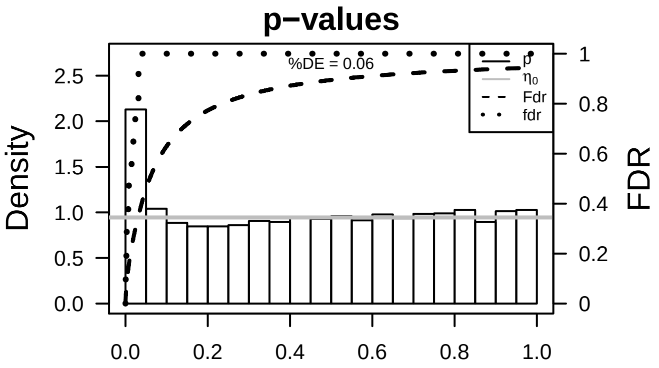
<fdr> = 0.94





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	200628_s_at	−1.58	2e−16	9e−13	0 x 0	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
2	201008_s_at	−1.55	2e−16	9e−13	0 x 49	thioredoxin interacting protein [Source:HGNC Symbol;Acc:HG
3	205780_at	−1.53	2e−16	9e−13	40 x 49	BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:10
4	205980_s_at	2.56	2e−16	9e−13	33 x 11	PRR5−ARHGAP8 readthrough [Source:HGNC Symbol;Acc:H
5	219471_at	−1.56	2e−16	9e−13	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
6	209825_s_at	−1.67	4e−16	5e−10	39 x 47	uridine−cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
7	44790_s_at	−1.27	2e−14	5e−10	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
8	208621_s_at	−1.28	6e−14	5e−10	0 x 48	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
9	219841_at	−1.88	7e−14	6e−10	1 x 17	activation induced cytidine deaminase [Source:HGNC Symbo
10	211656_x_at	−1.11	1e−13	8e−10	2 x 9	major histocompatibility complex, class II, DQ beta 1 [Source:
11	201161_s_at	−1.45	1e−13	2e−08	42 x 48	Y−box binding protein 3 [Source:HGNC Symbol;Acc:HGNC:2
12	217232_x_at	−1.52	1e−12	2e−08	6 x 29	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
13	202274_at	1.9	2e−12	2e−08	0 x 4	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
14	211496_s_at	2.17	3e−12	2e−08	33 x 11	phosducin [Source:HGNC Symbol;Acc:HGNC:8759]
15	37117_at	2.16	4e−12	4e−08	33 x 11	PRR5−ARHGAP8 readthrough [Source:HGNC Symbol;Acc:H
16	208097_s_at	−1.28	6e−12	7e−08	5 x 48	thioredoxin related transmembrane protein 1 [Source:HGNC
17	207534_at	2.12	1e−11	7e−08	1 x 16	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
18	204152_s_at	−1.49	1e−11	2e−07	1 x 46	MFNG O−fucosylpeptide 3−beta−N−acetylglucosaminyltransf
19	206218_at	2.08	2e−11	2e−07	0 x 15	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
20	217770_at	−1.31	3e−11	2e−07	19 x 0	phosphatidylinositol glycan anchor biosynthesis class T [Sour



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.1	NULL	832	Chr	Chr 2
2	8.22	NULL	833	Chr	Chr 19
3	7.31	NULL	14	Lymphoma	WRIGHT_GCB UP
4	7.17	NULL	556	Chr	Chr X
5	6.58	NULL	2867	Chromatin states	9_ReprPCWk_MSC_Adipocyte
6	6.53	NULL	42	GSEA C2	VILIMAS_NOTCH1_TARGETS_UP
7	6.08	NULL	12	Lymphoma	DAVE_BL_DN
8	5.85	NULL	20	Reference Signatures	Cluster 2,7_Unknown function
9	5.49	NULL	55	GSEA C2	DIRMEIER_LMP1_RESPONSE_EARLY
10	5.3	NULL	238	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
11	5.22	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
12	5.04	NULL	173	Lymphoma	Victora_Light zone signature
13	4.99	NULL	1639	Chromatin states	Fetal_TssF
14	4.89	NULL	16	GSEA C2	BIOCARTA_CTLA4_PATHWAY
15	4.89	NULL	12	Lymphoma	BENTINK_mBL DOWN
16	4.85	NULL	967	Chromatin states	11_K9K27me3_MSC_Adipocyte
17	4.81	NULL	50	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_B
18	4.78	NULL	1813	Chromatin states	8_EnhP_Fibroblasts
19	4.77	NULL	2254	Chromatin states	10_ReprPC_MSC_Adipocyte
20	4.7	NULL	1602	GSEA C2	BLALOCK_ALZHEIMERS_DISEASE_UP
Underexpressed					
1	−10.01	NULL	282	Glioma	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	−8.64	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
3	−8.63	NULL	136	Reference Signatures	Cluster 2,9_Cytosceleton
4	−7.74	NULL	509	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
5	−7.69	NULL	61	GSEA C2	BASSO_CD40_SIGNALING_DN
6	−7.68	NULL	344	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_UP
7	−7.39	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	−7.32	NULL	683	CC	endoplasmic reticulum membrane
9	−7.24	NULL	75	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
10	−7.12	NULL	1052	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	−6.96	NULL	1035	CC	endoplasmic reticulum
12	−6.95	NULL	1550	GSEA C2	PILON_KLF1_TARGETS_DN
13	−6.95	NULL	564	GSEA C2	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
14	−6.95	NULL	77	Lymphoma	TARTE_Plasma cell signature
15	−6.63	NULL	5908	Lymphoma	HOPP_Active_promoter
16	−6.61	NULL	9	GSEA C2	RUNNE_GENDER_EFFECT_UP
17	−6.6	NULL	5529	Lymphoma	HOPP_Txn_elongation
18	−6.54	NULL	616	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
19	−6.54	NULL	673	GSEA C2	SCHLOSSER_SERUM_RESPONSE_DN
20	−6.41	NULL	372	GSEA C2	SENESE_HDAC1_TARGETS_UP