MPI−166

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 630 (192 + / 438 −)

genes with fdr < 0.1 = 466 (123 + / 343 −)

genes with fdr < 0.05 = 338 (74 + / 264 −)

genes with fdr < 0.01 = 240 (47 + / 193 −)

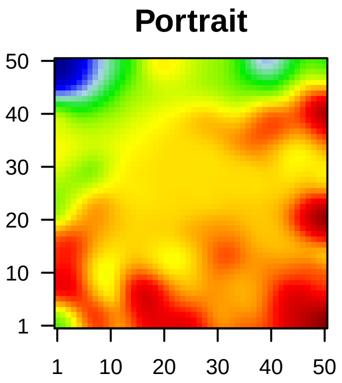
genes in genesets = 13152

<FC> = 0

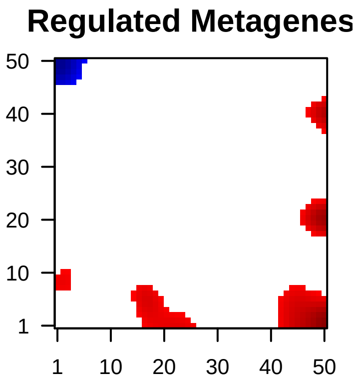
<t−score> = −0.3

<p−value> = 0.25

<fdr> = 0.95



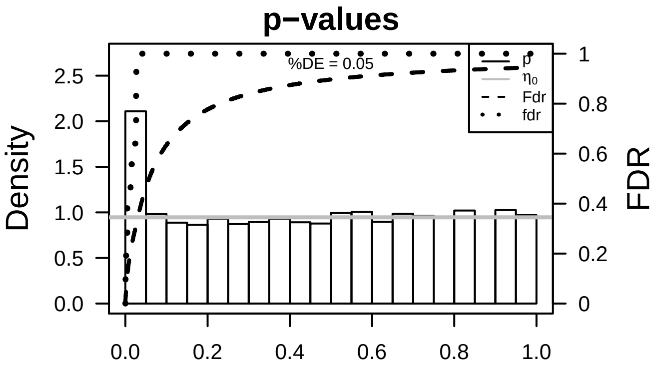
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39318_at	−1.51	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	44790_s_at	−1.94	2e−16	2e−13	42 x 49	RUN and cysteine rich domain containing beclin 1 interacting
3	200628_s_at	−1.59	2e−16	2e−13	0 x 0	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
4	200769_s_at	−1.93	2e−16	2e−13	2 x 47	methionine adenosyltransferase 2A [Source:HGNC Symbol;A
5	201008_s_at	−1.77	2e−16	2e−13	0 x 49	thioredoxin interacting protein [Source:HGNC Symbol;Acc:HG
6	201101_s_at	−2.3	2e−16	2e−13	1 x 49	BCL2 associated transcription factor 1 pseudogene 2 [Source
7	201123_s_at	−2.19	2e−16	2e−13	1 x 43	eukaryotic translation initiation factor 5A [Source:HGNC Syml
8	201635_s_at	−1.8	2e−16	2e−13	6 x 44	FMR1 autosomal homolog 1 [Source:HGNC Symbol;Acc:HGI
9	204152_s_at	−2.18	2e−16	2e−13	1 x 46	MFNG O−fucosylpeptide 3−beta−N−acetylglucosaminyltransf
10	205321_at	−2.48	2e−16	2e−13	1 x 45	eukaryotic translation initiation factor 2 subunit gamma B [Sou
11	206255_at	−1.84	2e−16	2e−13	48 x 45	BLK proto−oncogene, Src family tyrosine kinase [Source:HGI
12	208621_s_at	−2.79	2e−16	2e−13	0 x 48	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
13	208650_s_at	−2.09	2e−16	2e−13	44 x 49	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
14	209754_s_at	−1.82	2e−16	2e−13	2 x 46	thymopoietin [Source:HGNC Symbol;Acc:HGNC:11875]
15	209995_s_at	−2.33	2e−16	2e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
16	210935_s_at	−1.59	2e−16	2e−13	0 x 48	WD repeat domain 1 [Source:HGNC Symbol;Acc:HGNC:127
17	211090_s_at	−2.14	2e−16	2e−13	4 x 49	pre−mRNA processing factor 4B [Source:HGNC Symbol;Acc:
18	214305_s_at	−1.76	2e−16	2e−13	4 x 43	splicing factor 3b subunit 1 [Source:HGNC Symbol;Acc:HGN
19	215379_x_at	−1.29	2e−16	2e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
20	216212_s_at	−1.66	2e−16	2e−13	38 x 45	dyskerin pseudouridine synthase 1 [Source:HGNC Symbol;A



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.1	NULL	18	CC	MHC class II protein complex
2	8.96	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
3	7.71	NULL	14	Lymphoma	WRIGHT_GCB UP
4	7.13	NULL	3150	Chromatin states	monocytes peripheral blood_13_ReprPC
5	6.9	NULL	3724	Chromatin states	T cells peripheral blood_12_EnhBiv
6	6.82	NULL	3184	Chromatin states	monocytes peripheral blood_12_EnhBiv
7	6.82	NULL	2194	Chromatin states	T helper cells peripheral blood_12_EnhBiv
8	6.58	NULL	3272	Chromatin states	monocytes peripheral blood_14_ReprPCWk
9	6.53	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
10	6.46	NULL	2747	Chromatin states	B cells peripheral blood_12_EnhBiv
11	6.43	NULL	1841	Chromatin states	HSC_12_EnhBiv
12	6.39	NULL	2602	Chromatin states	natural killer cells peripheral blood_12_EnhBiv
13	6.29	NULL	512	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_DN
14	6.28	NULL	2015	Chromatin states	ReprPC_Colon
15	6.28	NULL	3168	Lymphoma	HOPP_Repressed
16	6.27	NULL	2300	Chromatin states	T helper cells peripheral blood_13_ReprPC
17	6.27	NULL	2134	Chromatin states	T regulatory cells peripheral blood_12_EnhBiv
18	6.25	NULL	4	Lymphoma	WRIGHT_custom GCB−DLBCL UP
19	6.23	NULL	585	Chr	Chr 7
20	6.15	NULL	1744	Chromatin states	ReprPCWk_Colon
Underexpressed					
1	−19.46	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	−17.71	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−17.47	NULL	439	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
4	−17.23	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
5	−16.62	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
6	−16.1	NULL	1052	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	−16.03	NULL	509	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
8	−15.86	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	−15.84	NULL	575	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
10	−15.58	NULL	1527	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
11	−15.02	NULL	226	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
12	−14.92	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
13	−14.76	NULL	174	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
14	−14.26	NULL	84	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−14.24	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
16	−14.21	NULL	305	Lymphoma	TARTE_Plasmablast signature
17	−14.12	NULL	14	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	−14.07	NULL	564	GSEA C2	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
19	−14.07	NULL	280	GSEA C2	MANALO_HYPOXIA_DN
20	−14	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanoma