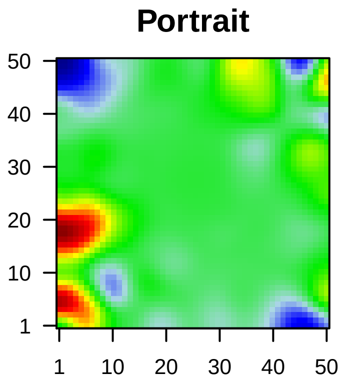
MPI−063

Global Summary

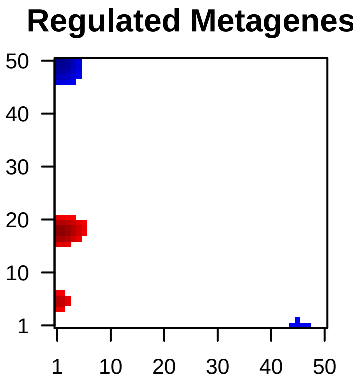
%DE = 0.04
genes with fdr < 0.2 = 535 (322 + / 213 −)
genes with fdr < 0.1 = 373 (235 + / 138 −)
genes with fdr < 0.05 = 290 (189 + / 101 −)
genes with fdr < 0.01 = 221 (145 + / 76 −)

genes in genesets = 13152

<FC> = 0
<t−score> = 0.14
<p−value> = 0.26
<fdr> = 0.96



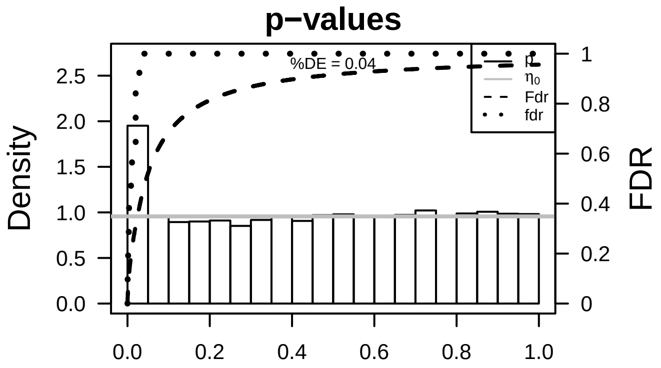
Portrait



Regulated Metagenes

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39318_at	−2.09	2e−16	4e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	201037_at	−1.11	2e−16	4e−13	6 x 40	phosphofructokinase, platelet [Source:HGNC Symbol;Acc:HG
3	202296_s_at	−1.26	2e−16	4e−13	3 x 31	retention in endoplasmic reticulum sorting receptor 1 [Source
4	204753_s_at	2.46	2e−16	4e−13	2 x 18	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
5	204755_x_at	2.62	2e−16	4e−13	4 x 18	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
6	209995_s_at	−2.26	2e−16	4e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
7	210551_s_at	2.1	2e−16	4e−13	1 x 17	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
8	212827_at	−1.28	2e−16	4e−13	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
9	213674_x_at	2.16	2e−16	4e−13	44 x 49	immunoglobulin heavy constant delta [Source:HGNC Symbol
10	215379_x_at	−1.18	2e−16	4e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
11	216733_s_at	−1.39	2e−16	4e−13	0 x 19	glycine amidinotransferase [Source:HGNC Symbol;Acc:HGN
12	202274_at	1.67	7e−16	2e−10	0 x 4	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
13	211300_s_at	−1.47	2e−14	2e−10	1 x 46	tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]
14	AFFX−M2783	1.78	2e−14	3e−10	49 x 47	
15	217022_s_at	−1.2	3e−14	3e−10	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
16	214106_s_at	1.07	5e−14	5e−10	0 x 6	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc
17	206084_at	1.78	7e−14	6e−10	8 x 19	protein tyrosine phosphatase, receptor type R [Source:HGNC
18	203510_at	1.76	1e−13	6e−10	1 x 16	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
19	204754_at	1.76	1e−13	9e−10	5 x 18	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
20	207768_at	1.75	2e−13	2e−09	15 x 21	early growth response 4 [Source:HGNC Symbol;Acc:HGNC:3



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.28	NULL	85	Lymphoma	Sha_DLBCL UP
2	9.83	NULL	85	Lymphoma	Aukema_BCL2 DN_BCL6 UP
3	9.41	NULL	317	Cancer	SPANG_BCL6−index2
4	9.22	NULL	90	GSEA C2	BASSO_CD40_SIGNALING_UP
5	8.59	NULL	173	Lymphoma	Victora_Light zone signature
6	8.47	NULL	22	Lymphoma	DAVE_NFkB BL DN
7	8.05	NULL	12	Lymphoma	BENTINK_mBL DOWN
8	7.93	NULL	14	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_DN
9	7.57	NULL	9544	Chromatin states	HSC_2_TssAFlnk
10	7.48	NULL	4	Lymphoma	MASCQUE_mBL DOWN
11	7.44	NULL	8200	Chromatin states	monocytes peripheral blood_2_TssAFlnk
12	7.2	NULL	9114	Chromatin states	natural killer cells peripheral blood_7_Enh
13	7.14	NULL	353	Lymphoma	SPANG_CD40 6hrs DN
14	6.9	NULL	9440	Chromatin states	HSC_7_Enh
15	6.9	NULL	9299	Chromatin states	monocytes peripheral blood_7_Enh
16	6.75	NULL	186	Cancer	SPANG_LPS−index2
17	6.73	NULL	8899	Chromatin states	7_Enh_MSC_Adipocyte
18	6.68	NULL	9298	Chromatin states	Bcells peripheral blood_7_Enh
19	6.67	NULL	7887	Chromatin states	5_TxWk_ESC_Mesoderm
20	6.59	NULL	8829	Chromatin states	7_Enh_Melanocytes
Underexpressed					
1	−10.44	NULL	44	MF	antigen binding
2	−8.84	NULL	52	BP	complement activation, classical pathway
3	−7.92	NULL	32	Reference Signatures	Chaussabel_1,1_Plasma Cells
4	−7.91	NULL	36	GSEA C2	REACTOME_PACKAGING_OF_TELOMERE_ENDS
5	−7.85	NULL	70	CC	nucleosome
6	−7.79	NULL	25	BP	antibacterial humoral response
7	−7.76	NULL	42	GSEA C2	REACTOME_RNA_POL_I_PROMOTER_OPENING
8	−7.73	NULL	16	MF	immunoglobulin receptor binding
9	−7.07	NULL	57	GSEA C2	REACTOME_MEIOTIC_SYNAPSIS
10	−6.98	NULL	263	Lymphoma	SPANG_CD40 6hrs UP
11	−6.96	NULL	62	GSEA C2	REACTOME_MEIOTIC_RECOMBINATION
12	−6.95	NULL	161	BP	adaptive immune response
13	−6.92	NULL	9	GSEA C2	RUNNE_GENDER_EFFECT_UP
14	−6.86	NULL	40	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
15	−6.67	NULL	88	GSEA C2	REACTOME_MEIOSIS
16	−6.65	NULL	60	GSEA C2	REACTOME_AMYLOIDS
17	−6.3	NULL	21	BP	phagocytosis, recognition
18	−6.27	NULL	16	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
19	−6.24	NULL	113	BP	regulation of immune response
20	−6.04	NULL	61	GSEA C2	REACTOME_TELOMERE_MAINTENANCE