MPI−155

Global Summary

%DE = 0.04

genes with fdr < 0.2 = 395 (211 + / 184 −)

genes with fdr < 0.1 = 214 (125 + / 89 −)

genes with fdr < 0.05 = 162 (103 + / 59 −)

genes with fdr < 0.01 = 90 (63 + / 27 −)

genes in genesets = 13152

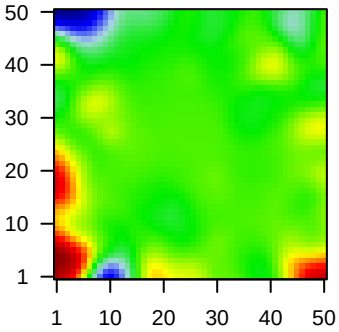
<FC> = 0

<t−score> = 0.2

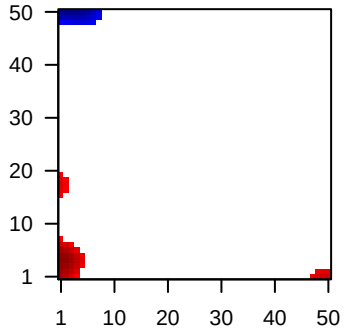
<p−value> = 0.28

<fdr> = 0.96

Portrait



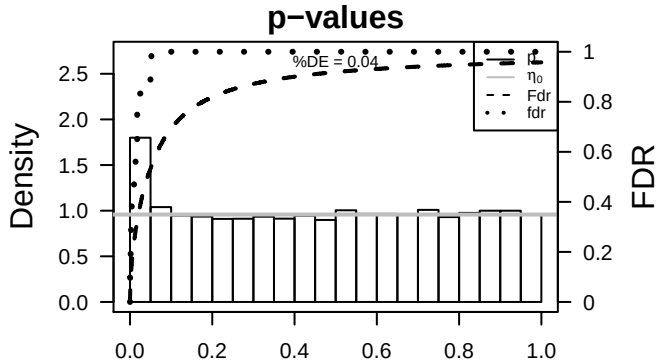
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	205529_s_at	2.09	2e−16	5e−13	41 x 16	RUNX1 translocation partner 1 [Source:HGNC Symbol;Acc:H
2	207534_at	2.37	2e−16	5e−13	1 x 16	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
3	209138_x_at	0.8	2e−16	5e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
4	209942_x_at	2.54	2e−16	5e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
5	213831_at	−1.55	2e−16	5e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Sourc
6	214254_at	2.34	2e−16	5e−13	11 x 27	MAGE family member A4 [Source:HGNC Symbol;Acc:HGNC
7	214612_x_at	2.43	2e−16	5e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
8	215121_x_at	0.95	2e−16	5e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
9	215946_x_at	1.25	2e−16	5e−13	41 x 42	immunoglobulin lambda like polypeptide 3, pseudogene [Sou
10	217022_s_at	−1.46	2e−16	5e−13	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
11	214677_x_at	0.77	7e−16	3e−11	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
12	202018_s_at	1.95	2e−15	1e−10	11 x 4	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
13	206413_s_at	1.91	7e−15	4e−09	43 x 49	T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG
14	219360_s_at	1.79	4e−13	4e−09	0 x 20	transient receptor potential cation channel subfamily M memb
15	219759_at	−1.52	5e−13	4e−09	49 x 24	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Sym
16	215379_x_at	0.8	6e−13	8e−08	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
17	201909_at	−1.09	5e−12	8e−08	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
18	206218_at	1.68	8e−12	1e−07	0 x 15	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
19	213502_x_at	0.81	1e−11	2e−07	41 x 42	
20	213385_at	1.64	3e−11	2e−07	0 x 17	chimerin 2 [Source:HGNC Symbol;Acc:HGNC:1944]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.58	NULL	4	Immunome	Angelova_CRC_MSS−neoantigens
2	8.78	NULL	85	Lymphoma	Rosenwald_DLBCL UP
3	8.67	NULL	13	Immunome	Angelova_CRC_MSS^−neoantigens
4	8.47	NULL	7	Immunome	Angelova_CRC_MSI−neoantigens
5	8.3	NULL	589	Colon Cancer	Leinbacke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	8.13	NULL	83	Melanoma	TCGA_melanoma_immune_high
7	7.98	NULL	585	Chr	Chr 7
8	7.51	NULL	255	GSEA C2	HELLER_SILENCED_BY_METHYLATION_UP
9	7.07	NULL	22	Lymphoma	DAVE_NFkB BL DN
10	6.88	NULL	102	Reference Signatures	Virgin_IgD+ B−cells
11	6.62	NULL	432	Chromatin States	monocytes peripheral blood_3_TxFlnk
12	6.5	NULL	693	Chromatin States	B−cells peripheral blood_3_TxFlnk
13	6.43	NULL	429	GSEA C2	SMID_BREAST_CANCER_NORMAL_LIKE_UP
14	6.21	NULL	317	Cancer	SPANG_BCL6−index2
15	6.14	NULL	833	Chr	Chr 19
16	5.99	NULL	626	Chromatin States	natural killer cells peripheral blood_3_TxFlnk
17	5.9	NULL	7	Glioma	Donson−cytotoxic effectors−associated with LTS in HGA
18	5.82	NULL	186	GSEA C2	PENG_RAPAMYCIN_RESPONSE_UP
19	5.75	NULL	176	HM	HALLMARK_ALLOGRAFT_REJECTION
20	5.62	NULL	700	Chr	Chr 12
Underexpressed					
1	−7.77	NULL	6244	Chromatin States	15_Quies_Fibroblasts
2	−7.45	NULL	7225	Chromatin States	Overlap_fetal_midbrain_ReprPC
3	−7.32	NULL	7581	Chromatin States	15_Quies_Melanocytes
4	−7.27	NULL	2626	Chromatin States	6_ZNFs_Rpts_ESC_Mesoderm
5	−7.14	NULL	6034	Chromatin States	15_Quies_Fibroblasts
6	−7.11	NULL	6389	Chromatin States	4_TssE_ESC_Mesoderm
7	−6.9	NULL	9	GSEA C2	RUNNE_GENDER_EFFECT_UP
8	−6.74	NULL	18	CC	MHC class II protein complex
9	−6.64	NULL	17	BP	antigen processing and presentation of peptide or polysaccharide a
10	−6.38	NULL	7066	Chromatin States	Overlap_fetal_midbrain_ReprPCWk
11	−6.36	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
12	−6.3	NULL	7887	Chromatin States	5_TxWk_ESC_Mesoderm
13	−6.28	NULL	6068	Chromatin States	4_TssE_ESC_Endoderm
14	−6.23	NULL	3906	Chromatin States	6_EnhG_MSC_Adipocyte
15	−6.22	NULL	3554	Chromatin States	6_ZNFs_Rpts_ESC_Endoderm
16	−6.01	NULL	689	Chr	Chr 3
17	−5.86	NULL	4683	Chromatin States	Overlap_fetal_midbrain_HetRpts
18	−5.75	NULL	6637	Chromatin States	T cells peripheral blood_5_TxWk
19	−5.75	NULL	6466	Chromatin States	5_TxWk_MSC_Adipocyte
20	−5.71	NULL	9160	Chromatin States	2_TssA_Neuronal_Progenitor