MPI−039

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 647 (324 + / 323 −)

genes with fdr < 0.1 = 445 (228 + / 217 −)

genes with fdr < 0.05 = 397 (207 + / 190 −)

genes with fdr < 0.01 = 209 (111 + / 98 −)

genes in genesets = 13152

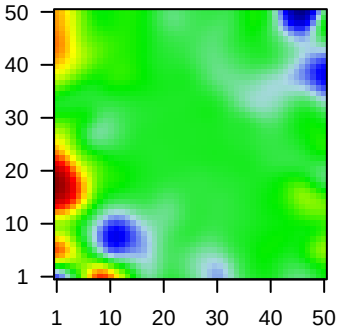
<FC> = 0

<t−score> = 0.07

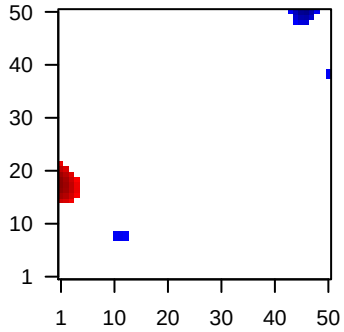
<p−value> = 0.25

<fdr> = 0.94

Portrait



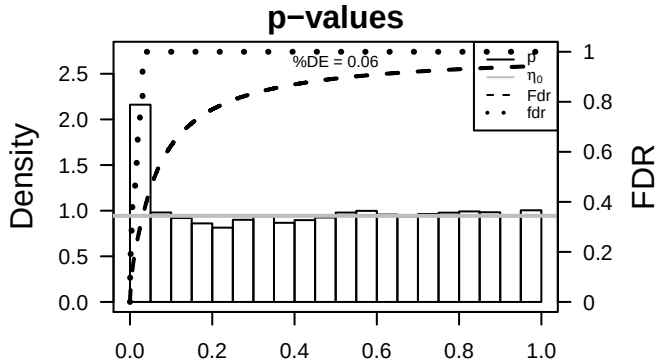
Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AFFX−r2−Hs1	2.18	2e−16	2e−13	49 x 47	
2	204018_x_at	1.53	2e−16	2e−13	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
3	206150_at	−1.42	2e−16	2e−13	49 x 38	CD27 molecule [Source:HGNC Symbol;Acc:HGNC:11922]
4	207534_at	2.16	2e−16	2e−13	1 x 16	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
5	209116_x_at	1.59	2e−16	2e−13	6 x 29	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
6	209201_x_at	−1.15	2e−16	2e−13	7 x 48	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
7	209374_s_at	−2.21	2e−16	2e−13	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
8	209458_x_at	1.53	2e−16	2e−13	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
9	209723_at	−1.44	2e−16	2e−13	12 x 10	serpin family B member 9 [Source:HGNC Symbol;Acc:HGNC
10	211596_s_at	−1.74	2e−16	2e−13	44 x 49	leucine rich repeats and immunoglobulin like domains 1 [Sou
11	211696_x_at	1.34	2e−16	2e−13	6 x 29	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
12	211699_x_at	1.7	2e−16	2e−13	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
13	211745_x_at	1.5	2e−16	2e−13	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
14	211796_s_at	−1.27	2e−16	2e−13	10 x 9	T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:H
15	212592_at	−2.37	2e−16	2e−13	45 x 49	joining chain of multimeric IgA and IgM [Source:HGNC Symb
16	212827_at	−2.34	2e−16	2e−13	41 x 44	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
17	214414_x_at	1.45	2e−16	2e−13	6 x 29	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
18	215121_x_at	−0.88	2e−16	2e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
19	215379_x_at	−1.39	2e−16	2e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
20	217022_s_at	−2.49	2e−16	2e−13	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.63	NULL	756	Chr	Chr 11
2	10.07	NULL	382	Chr	Chr 15
3	8.11	NULL	53	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
4	7.99	NULL	693	Chromatin states	Bcells peripheral blood_3_TxFlnk
5	7.81	NULL	59	GSEA C2	PID_BCR_5PATHWAY
6	7.67	NULL	85	Lymphoma	Rosha_DLBCL UP
7	7.61	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
8	7.6	NULL	173	Lymphoma	Victora_Light zone signature
9	7.32	NULL	3767	Chromatin states	Bcells peripheral blood_6_EnhG
10	6.83	NULL	32	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
11	6.64	NULL	269	Glioma	ScoV_0.5_Sturm_C3_Mesenchymal_DN
12	6.61	NULL	432	Chromatin states	monocytes peripheral blood_3_TxFlnk
13	6.52	NULL	54	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
14	6.46	NULL	67	GSEA C2	PID_AP1_PATHWAY
15	6.36	NULL	317	Cancer	SPANG_BCL6−index2
16	6.31	NULL	3223	Chromatin states	monocytes peripheral blood_6_EnhG
17	6.09	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
18	6.07	NULL	68	GSEA C2	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY
19	6.07	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
20	6.06	NULL	4	Lymphoma	WRIGHT_custom GCB−DLBCL UP
Underexpressed					
1	−15.28	NULL	16	MF	immunoglobulin receptor binding
2	−15.2	NULL	44	MF	antigen binding
3	−12.99	NULL	11	MF	peptidoglycan binding
4	−11.56	NULL	32	Reference Signatures	Novershtern_1,1_Plasma Cells
5	−10.92	NULL	19	BP	positive regulation of B cell activation
6	−10.68	NULL	52	BP	complement activation, classical pathway
7	−10.59	NULL	25	BP	antibacterial humoral response
8	−10.57	NULL	102	Reference Signatures	VERHAEN_EBV B−cells
9	−10.39	NULL	40	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−10.06	NULL	15	Lymphoma	Zare_Polarized immune response
11	−9.88	NULL	21	BP	phagocytosis, recognition
12	−8.82	NULL	33	Melanoma	Tirosh_T−cell specific genes−melanoma
13	−8.2	NULL	21	MF	phosphatidylcholine binding
14	−7.57	NULL	42	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_UP
15	−7.44	NULL	161	BP	adaptive immune response
16	−6.89	NULL	68	Reference Signatures	Novershtern_2,1_Cytotoxic cells
17	−6.71	NULL	10	GSEA C2	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL
18	−6.57	NULL	36	BP	phagocytosis, engulfment
19	−6.56	NULL	56	Pneumonia	Burnham_sep_vs_con_DN
20	−6.51	NULL	263	Lymphoma	SPANG_CD40 6hrs UP