

MPI-069

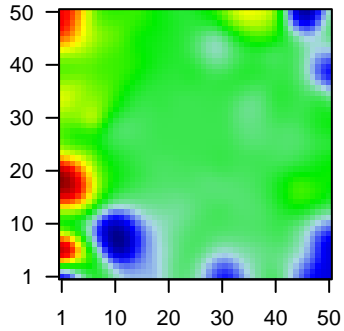
Global Summary

%DE = 0.05
 # genes with fdr < 0.2 = 654 (331 + / 323 -)
 # genes with fdr < 0.1 = 443 (218 + / 225 -)
 # genes with fdr < 0.05 = 383 (188 + / 195 -)
 # genes with fdr < 0.01 = 222 (111 + / 111 -)

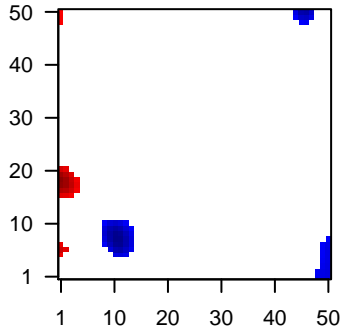
 # genes in genesets = 13152

<FC> = 0
 <t-score> = 0.12
 <p-value> = 0.25
 <fdr> = 0.95

Portrait



Regulated Metagenes



Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	201427_s_at	-1.54	2e-16	2e-13	47 x 37 selenoprotein P [Source:HGNC Symbol;Acc:HGNC:10751]
2	201597_at	-1.27	2e-16	2e-13	29 x 42 cytochrome c oxidase subunit 7A2 [Source:HGNC Symbol;Acc:HGNC:10752]
3	201909_at	-1.37	2e-16	2e-13	43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:10753]
4	204018_x_at	1.34	2e-16	2e-13	6 x 29 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:10754]
5	204891_s_at	-1.49	2e-16	2e-13	49 x 39 LCK proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:10755]
6	206150_at	-1.79	2e-16	2e-13	49 x 38 CD27 molecule [Source:HGNC Symbol;Acc:HGNC:11922]
7	209116_x_at	1.36	2e-16	2e-13	6 x 29 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:10756]
8	209458_x_at	1.31	2e-16	2e-13	6 x 29 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:10757]
9	209823_x_at	-1.22	2e-16	2e-13	2 x 8 major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:10758]
10	210162_s_at	-1.59	2e-16	2e-13	0 x 24 nuclear factor of activated T cells 1 [Source:HGNC Symbol;Acc:HGNC:10759]
11	211105_s_at	-1.53	2e-16	2e-13	46 x 40 nuclear factor of activated T cells 1 [Source:HGNC Symbol;Acc:HGNC:10760]
12	211696_x_at	1.2	2e-16	2e-13	6 x 29 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:10761]
13	211699_x_at	1.45	2e-16	2e-13	6 x 29 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:10762]
14	211745_x_at	1.26	2e-16	2e-13	6 x 29 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:10763]
15	213537_at	-1.5	2e-16	2e-13	9 x 10 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:HGNC:10764]
16	215176_x_at	-1.52	2e-16	2e-13	10 x 5 immunoglobulin kappa variable 1-39 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:10765]
17	217022_s_at	-2.09	2e-16	2e-13	0 x 2 immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:HGNC:10766]
18	217232_x_at	1.39	2e-16	2e-13	6 x 29 hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:10767]
19	217249_x_at	-1.25	2e-16	2e-13	29 x 43 cytochrome c oxidase subunit 7A2 pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:10768]
20	217414_x_at	1.81	2e-16	2e-13	6 x 29 hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:10769]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.24	NULL	585	Chr Chr 7
2	8.69	NULL	85	Lymphoma_Tha_DLBCL UP
3	7.49	NULL	85	Lymphoma_Leukemia_BCL2 DN_BCL6 UP
4	7.47	NULL	353	Lymphoma_PANG_CD40 6hrs DN
5	7.21	NULL	173	Lymphoma_Mactora_Light zone signature
6	6.64	NULL	18	Lymphoma_RIGHT_ABC UP
7	6.44	NULL	14	GSEA C2HUMMEL_BURKITTIS_LYMPHOMA_DN
8	6.34	NULL	10	Lymphoma_MASCQUE_ABC UP
9	6.13	NULL	213	Lymphoma_PANG_IL21 DN
10	6.04	NULL	7833	Chromatin_Protein_peripheral_blood_1_TssA
11	6.01	NULL	4261	Lymphoma_HOPP_Txn_transition
12	5.82	NULL	90	GSEA C2BASSO_CD40_SIGNALING_UP
13	5.79	NULL	8406	Chromatin_Protein_peripheral_blood_2_TssAFink
14	5.63	NULL	3564	TF_ICGC_Taf1_targets
15	5.61	NULL	3451	TF_ICGC_Atf2_targets
16	5.54	NULL	3804	TF_ICGC_Stat5_targets
17	5.52	NULL	3150	TF_ICGC_Creb1_targets
18	5.43	NULL	12	Lymphoma_BENTINK_mBL DOWN
19	5.15	NULL	3420	TF_ICGC_Bclaf101388_targets
20	5.12	NULL	3769	TF_ICGC_Pmlsc71910_targets
<i>Underexpressed</i>				
1	-11.44	NULL	102	Reference_Spleen_T_H17 B-cells
2	-10.02	NULL	12	MF_MHC class II receptor activity
3	-9.26	NULL	39	BP_complement activation
4	-8.67	NULL	17	BP_antigen processing and presentation of peptide or polysaccharide antigen fragments
5	-8.43	NULL	18	CC_MHC class II protein complex
6	-8.27	NULL	22	MF_peptide antigen binding
7	-8.26	NULL	40	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
8	-8.21	NULL	33	Melanoma_Microsh_T-cell specific genes-melanoma
9	-8.1	NULL	23	CC_integral component of luminal side of endoplasmic reticulum membrane
10	-8.05	NULL	431	BP_immune system process
11	-8.02	NULL	669	Chr Chr 6
12	-7.82	NULL	52	BP_complement activation, classical pathway
13	-7.23	NULL	67	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
14	-7.07	NULL	62	Lymphoma_Monti_Host_response_cluster
15	-6.78	NULL	8	GSEA C2BIOCARTA_TCRA_PATHWAY
16	-6.71	NULL	56	Pneumonia_Burnham_sep_vs_con_DN
17	-6.7	NULL	53	BP_regulation of complement activation
18	-6.62	NULL	9	GSEA C2RUNNE_GENDER_EFFECT_UP
19	-6.55	NULL	9	GSEA C2REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE
20	-6.45	NULL	113	BP_regulation of immune response

p-values

