MPI−245

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 587 (317 + / 270 −)

genes with fdr < 0.1 = 382 (223 + / 159 −)

genes with fdr < 0.05 = 268 (161 + / 107 −)

genes with fdr < 0.01 = 198 (123 + / 75 −)

genes in genesets = 13152

<FC> = 0

<t−score> = 0.07

<p−value> = 0.26

<fdr> = 0.95

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	204141_at	−1.67	2e−16	4e−13	46 x 49	tubulin beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:1
2	209728_at	2.38	2e−16	4e−13	0 x 10	major histocompatibility complex, class II, DR beta 4 [Source:
3	213787_s_at	−1.48	2e−16	4e−13	34 x 47	emopamil binding protein (sterol isomerase) [Source:HGNC
4	213831_at	−2.08	2e−16	4e−13	49 x 16	major histocompatibility complex, class II, DQ alpha 1 [Sourc
5	215121_x_at	0.85	2e−16	4e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215379_x_at	1.14	2e−16	4e−13	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
7	219517_at	−1.26	2e−16	4e−13	49 x 41	
8	219518_s_at	−1.53	2e−16	4e−13	49 x 41	
9	219521_at	2.71	2e−16	4e−13	31 x 13	beta−1,3−glucuronyltransferase 1 [Source:HGNC Symbol;Ac
10	219841_at	−1.82	2e−16	4e−13	1 x 17	activation induced cytidine deaminase [Source:HGNC Symb
11	220377_at	2.33	2e−16	4e−13	5 x 28	family with sequence similarity 30 member A [Source:HGNC
12	213005_s_at	−1.74	1e−15	3e−11	49 x 39	KN motif and ankyrin repeat domains 1 [Source:HGNC Symb
13	201909_at	1.29	4e−15	5e−11	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
14	213830_at	2	4e−15	5e−11	8 x 9	
15	203509_at	−1.06	6e−15	6e−10	49 x 40	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
16	209138_x_at	0.74	5e−14	6e−10	41 x 42	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
17	206843_at	1.9	8e−14	6e−10	11 x 33	crystallin beta A4 [Source:HGNC Symbol;Acc:HGNC:2396]
18	207005_s_at	1.88	1e−13	6e−10	0 x 26	BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC
19	216977_x_at	−1.11	2e−13	6e−10	37 x 49	small nuclear ribonucleoprotein polypeptide A' [Source:HGNC
20	206461_x_at	1.18	2e−13	6e−10	0 x 1	metallothionein 1H [Source:HGNC Symbol;Acc:HGNC:7400]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.11	NULL	223	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
2	11.49	NULL	589	Colon Cancer	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	10.6	NULL	14	BP	cellular response to zinc ion
4	10.05	NULL	219	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
5	10.03	NULL	102	Reference Signatures	Wright_EBV B−cells
6	9.83	NULL	14	BP	negative regulation of growth
7	9.18	NULL	585	Chr	Chr 7
8	8.82	NULL	88	GSEA C2	WIELAND_UP_BY_HBV_INFECTION
9	8.71	NULL	62	Lymphoma	Monti_Host_response_cluster
10	8.59	NULL	85	Lymphoma	Sha_DLBCL UP
11	8.56	NULL	386	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
12	8.45	NULL	17	GSEA C2	ZHENG_RESPONSE_TO_ARSENITE_UP
13	8.08	NULL	355	Reference Signatures	Wright_Immune system
14	8.06	NULL	166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	7.98	NULL	447	Glioma	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
16	7.91	NULL	317	Cancer	SPANG_BCL6−index2
17	7.83	NULL	297	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
18	7.81	NULL	105	GSEA C2	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
19	7.78	NULL	71	Melanoma	Tirosh_Macrophage specific genes−melanoma
20	7.61	NULL	265	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
Underexpressed					
1	−13.42	NULL	319	Melanoma	Gerber_wt/wt_melanoma−cells−SpotA
2	−11.55	NULL	244	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	−11.32	NULL	137	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	−11.16	NULL	431	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	−10.53	NULL	115	Glioma	WILLSCHER_GBM_Verhaak−CL_up (C)
6	−10.35	NULL	219	Reference Signatures	Wright_GC B−cells
7	−10.32	NULL	14	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	−10.16	NULL	7225	Chromatin states	Overlap_fetal_midbrain_ReprPC
9	−10.07	NULL	726	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
10	−9.9	NULL	400	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
11	−9.81	NULL	79	Melanoma	Tirosh_core cycling genes in low− and high−proliferation melanoma
12	−9.79	NULL	966	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	−9.47	NULL	192	Lymphoma	Victora_Dark zone signature
14	−9.35	NULL	52	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
15	−9.26	NULL	174	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	−9.23	NULL	8918	Chromatin states	1_TssA_ESC_Mesoderm
17	−9.11	NULL	93	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
18	−9.1	NULL	9576	Chromatin states	2_TssA_MSC_Adipocyte
19	−9.04	NULL	1325	Chr	Chr 1
20	−8.89	NULL	669	GSEA C2	JOHNSTONE_PARVB_TARGETS_3_DN