MPI−121

Global Summary

%DE = 0.06

genes with fdr < 0.2 = 795 (464 + / 331 −)

genes with fdr < 0.1 = 503 (298 + / 205 −)

genes with fdr < 0.05 = 428 (252 + / 176 −)

genes with fdr < 0.01 = 225 (123 + / 102 −)

genes in genesets = 13152

<FC> = 0

<t−score> = 0.05

<p−value> = 0.24

<fdr> = 0.94

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	39318_at	−1.72	2e−16	4e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	204053_x_at	−1.26	2e−16	4e−13	18 x 23	phosphatase and tensin homolog pseudogene 1 [Source:HGI
3	204794_at	−1.41	2e−16	4e−13	0 x 7	dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:H
4	207325_x_at	2.58	2e−16	4e−13	10 x 27	MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC
5	209193_at	−1.35	2e−16	4e−13	0 x 20	Pim−1 proto−oncogene, serine/threonine kinase [Source:HGI
6	209942_x_at	2.73	2e−16	4e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
7	209995_s_at	−1.55	2e−16	4e−13	46 x 49	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
8	210495_x_at	−1.09	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
9	210809_s_at	−1.92	2e−16	4e−13	9 x 0	periostin [Source:HGNC Symbol;Acc:HGNC:16953]
10	212464_s_at	−1.17	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
11	214612_x_at	2.56	2e−16	4e−13	10 x 27	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
12	218051_s_at	−1.58	2e−16	4e−13	39 x 47	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
13	219093_at	2.07	2e−16	4e−13	15 x 17	phosphotyrosine interaction domain containing 1 [Source:HG
14	219841_at	−1.64	4e−16	1e−11	1 x 17	activation induced cytidine deaminase [Source:HGNC Symbo
15	205780_at	−1.2	1e−15	1e−11	40 x 49	BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:10
16	217734_s_at	−1.51	2e−15	5e−11	41 x 42	WD repeat domain 6 [Source:HGNC Symbol;Acc:HGNC:127
17	202986_at	1.95	6e−15	5e−11	0 x 18	aryl hydrocarbon receptor nuclear translocator 2 [Source:HGI
18	206218_at	1.95	7e−15	8e−11	0 x 15	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
19	209374_s_at	−0.86	1e−14	8e−11	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
20	204562_at	−1.13	2e−14	8e−11	0 x 20	interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGI

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.6	NULL	585	Chr	Chr 7
2	10.95	NULL	556	Chr	Chr X
3	9.99	NULL	4	Immunome	Angelova_CRC_MSS−neoantigens
4	9.66	NULL	492	Chr	Chr 9
5	9.02	NULL	5716	Chromatin states	B cells peripheral blood_4_Tx
6	8.61	NULL	7420	Chromatin states	T cells peripheral blood_1_TssA
7	8.36	NULL	4357	Lymphoma	HOPP_Weak_txn
8	8.09	NULL	7833	Chromatin states	B cells peripheral blood_1_TssA
9	8.06	NULL	7635	Chromatin states	monocytes peripheral blood_1_TssA
10	8.02	NULL	5766	Chromatin states	natural killer cells peripheral blood_4_Tx
11	7.88	NULL	14	Lymphoma	WRIGHT_GCB UP
12	7.73	NULL	7	Immunome	Angelova_CRC_MSI−neoantigens
13	7.69	NULL	7751	Chromatin states	natural killer cells peripheral blood_1_TssA
14	7.6	NULL	5738	Chromatin states	monocytes peripheral blood_4_Tx
15	7.35	NULL	8406	Chromatin states	B cells peripheral blood_2_TssAFlnk
16	7.32	NULL	7078	Chromatin states	B cells peripheral blood_5_TxWk
17	7.32	NULL	5753	Chromatin states	T cells peripheral blood_4_Tx
18	7.24	NULL	95	GSEA C2	LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q
19	6.99	NULL	7957	Chromatin states	T cells peripheral blood_2_TssAFlnk
20	6.99	NULL	5601	Chromatin states	T helper cells peripheral blood_4_Tx
Underexpressed					
1	−11.73	NULL	85	Lymphoma	Aukema_BCL2 DN_BCL6 UP
2	−9.29	NULL	18	Lymphoma	WRIGHT_ABC UP
3	−7.6	NULL	63	GSEA C2	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
4	−7.49	NULL	689	Chr	Chr 3
5	−7.39	NULL	669	Chr	Chr 6
6	−7.15	NULL	196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	−7.15	NULL	2747	Chromatin states	B cells peripheral blood_12_EnhBiv
8	−7.08	NULL	2405	Chromatin states	B cells peripheral blood_13_ReprPC
9	−6.68	NULL	3724	Chromatin states	T cells peripheral blood_12_EnhBiv
10	−6.66	NULL	2765	Chromatin states	T regulatory cells peripheral blood_13_ReprPC
11	−6.64	NULL	2154	Chromatin states	T regulatory cells peripheral blood_11_BivFlnk
12	−6.41	NULL	3734	Chromatin states	T cells peripheral blood_13_ReprPC
13	−6.4	NULL	3150	Chromatin states	monocytes peripheral blood_13_ReprPC
14	−6.25	NULL	1799	Chromatin states	T CD8+ naive cells peripheral blood_13_ReprPC
15	−6.22	NULL	747	GSEA C2	NABA_MATRISOME
16	−6.21	NULL	2602	Chromatin states	natural killer cells peripheral blood_12_EnhBiv
17	−6.14	NULL	2194	Chromatin states	T helper cells peripheral blood_12_EnhBiv
18	−6.12	NULL	10	Lymphoma	MASCQUE_ABC UP
19	−6.07	NULL	132	Colon Cancer	Marisa_CRC−cluster−a
20	−5.93	NULL	1660	Chromatin states	T CD8+ naive cells peripheral blood_12_EnhBiv