MPI−100

Global Summary

%DE = 0.05

genes with fdr < 0.2 = 539 (297 + / 242 −)

genes with fdr < 0.1 = 310 (183 + / 127 −)

genes with fdr < 0.05 = 277 (166 + / 111 −)

genes with fdr < 0.01 = 162 (102 + / 60 −)

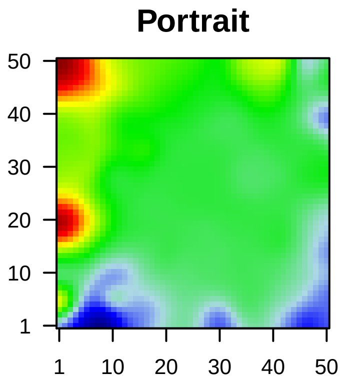
genes in genesets = 13152

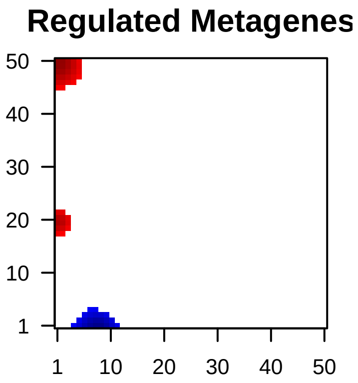
<FC> = 0

<t−score> = 0.07

<p−value> = 0.27

<fdr> = 0.95





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	200872_at	−1.1	2e−16	4e−13	4 x 13	S100 calcium binding protein A10 [Source:HGNC Symbol;Ac
2	201909_at	1.45	2e−16	4e−13	43 x 49	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
3	210495_x_at	−1.38	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
4	211719_x_at	−1.26	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
5	212464_s_at	−1.2	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
6	213400_s_at	−2.12	2e−16	4e−13	0 x 15	transducin beta like 1 X−linked [Source:HGNC Symbol;Acc:H
7	214768_x_at	2.67	2e−16	4e−13	10 x 5	immunoglobulin kappa variable 2−28 [Source:HGNC Symbol;
8	214836_x_at	1.29	2e−16	4e−13	0 x 3	
9	216442_x_at	−1.32	2e−16	4e−13	8 x 0	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
10	221651_x_at	0.99	2e−16	4e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
11	221671_x_at	0.95	2e−16	4e−13	0 x 3	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
12	206023_at	2.11	4e−15	5e−11	33 x 46	neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
13	217466_x_at	−0.88	5e−15	6e−10	15 x 8	ribosomal protein S2 pseudogene 46 [Source:HGNC Symbol
14	209374_s_at	0.91	3e−14	2e−09	0 x 22	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
15	217022_s_at	1.33	1e−13	2e−09	0 x 2	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
16	215783_s_at	1.96	3e−13	2e−09	27 x 49	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
17	207861_at	1.96	3e−13	2e−08	0 x 20	C−C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:
18	220377_at	1.91	1e−12	4e−08	5 x 28	family with sequence similarity 30 member A [Source:HGNC
19	200952_s_at	1.88	3e−12	5e−08	0 x 21	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
20	214333_x_at	−1.16	7e−12	5e−08	45 x 0	isocitrate dehydrogenase 3 (NAD(+)) gamma [Source:HGNC

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	14.3	NULL	5716	Chromatin states B cells peripheral blood_4_Tx
2	13.14	NULL	5527	Chromatin states T regulatory cells peripheral blood_4_Tx
3	13.12	NULL	4261	Lymphoma HOPP_Txn_transition
4	13	NULL	7833	Chromatin states B cells peripheral blood_1_TssA
5	12.4	NULL	5753	Chromatin states T cells peripheral blood_4_Tx
6	12.36	NULL	6099	Chromatin states HSC_4_Tx
7	12.31	NULL	4528	Chromatin states T CD8+ naive cells peripheral blood_4_Tx
8	12.24	NULL	8406	Chromatin states B cells peripheral blood_2_TssAFlnk
9	12.12	NULL	5601	Chromatin states T helper cells peripheral blood_4_Tx
10	12.08	NULL	5529	Lymphoma HOPP_Txn_elongation
11	12.02	NULL	6068	Chromatin states 4_Tx_ESC_Endoderm
12	11.86	NULL	9	GSEA C2 RUNNE_GENDER_EFFECT_UP
13	11.66	NULL	8068	Chromatin states T helper cells peripheral blood_1_TssA
14	11.47	NULL	7930	Chromatin states T regulatory cells peripheral blood_1_TssA
15	11.4	NULL	5766	Chromatin states natural killer cells peripheral blood_4_Tx
16	11.14	NULL	7751	Chromatin states natural killer cells peripheral blood_1_TssA
17	11.12	NULL	6590	Chromatin states T regulatory cells peripheral blood_5_TxWk
18	10.89	NULL	8245	Chromatin states T regulatory cells peripheral blood_2_TssAFlnk
19	10.87	NULL	4683	Chromatin states Overlap_fetal_midbrain_HetRpts
20	10.85	NULL	7957	Chromatin states T cells peripheral blood_2_TssAFlnk
Underexpressed				
1	−12.82	NULL	214	Lymphoma LENZ_Stromal signature 1
2	−11.76	NULL	335	GSEA C2 SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	−11.54	NULL	63	GSEA C2 ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
4	−9.92	NULL	747	GSEA C2 NABA_MATRISOME
5	−9.88	NULL	132	Colon Cancer Marisa_CRC−cluster−a
6	−9.66	NULL	548	Chr Chr 16
7	−9.66	NULL	196	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	−9.15	NULL	197	GSEA C2 NABA_CORE_MATRISOME
9	−8.95	NULL	3734	Chromatin states T cells peripheral blood_13_ReprPC
10	−8.87	NULL	247	GSEA C2 BOQUEST_STEM_CELL_UP
11	−8.79	NULL	78	Melanoma Tirosh_CAF−cell specific genes
12	−8.47	NULL	3001	Chromatin states B cells peripheral blood_14_ReprPCWk
13	−8.04	NULL	176	GSEA C2 PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	−7.97	NULL	212	CC extracellular matrix
15	−7.93	NULL	102	Reference Signatures WIRTH_EBV B−cells
16	−7.92	NULL	2747	Chromatin states B cells peripheral blood_12_EnhBiv
17	−7.84	NULL	3168	Lymphoma HOPP_Repressed
18	−7.84	NULL	138	GSEA C2 VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
19	−7.83	NULL	18	GSEA C2 FARMER_BREAST_CANCER_CLUSTER_5
20	−7.83	NULL	58	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_