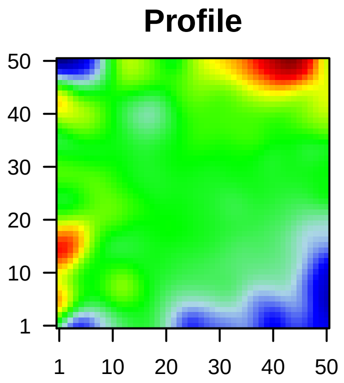
GW_233

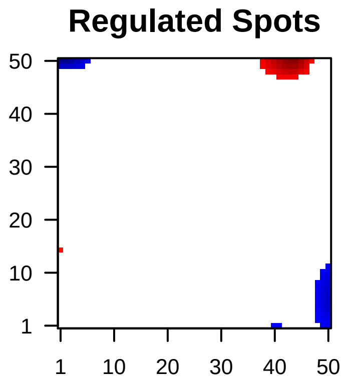
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1744 (973 + / 771 −)
genes with fdr < 0.1 = 1276 (728 + / 548 −)
genes with fdr < 0.05 = 1092 (621 + / 471 −)
genes with fdr < 0.01 = 692 (411 + / 281 −)

genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.13
<fdr> = 0.86



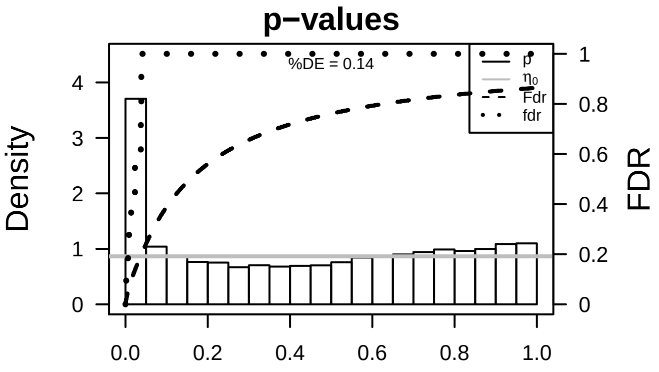


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.61	2e−16	8e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
2	55107	2.43	2e−16	8e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
3	260436	1.92	2e−16	8e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
4	79783	1.76	2e−16	8e−14	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
5	768	2.08	2e−16	8e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
6	51200	1.47	2e−16	8e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
7	1475	−1.71	2e−16	8e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
8	441520	2.17	2e−16	8e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
9	131566	1.52	2e−16	8e−14	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGNC
10	1673	2.04	2e−16	8e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	2167	1.54	2e−16	8e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
12	8772	1.74	2e−16	8e−14	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
13	10804	1.59	2e−16	8e−14	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
14	283120	−1.7	2e−16	8e−14	25 x 1	H19, imprinted maternally expressed transcript (non−protein
15	3006	1.56	2e−16	8e−14	5 x 20	histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
16	3127	1.63	2e−16	8e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
17	374918	1.67	2e−16	8e−14	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093]
18	3553	1.48	2e−16	8e−14	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
19	56300	1.67	2e−16	8e−14	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
20	3576	1.49	2e−16	8e−14	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.63	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	14.63	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	11.25	NULL	743	Chr	Chr 7
4	10.94	NULL	370	BP	mitotic cell cycle
5	8.48	NULL	530	Cancer	Lembcke_Normal vs Adenoma
6	7.82	NULL	7	MMML CGS	MACIEJ_MMML 9
7	7.77	NULL	1233	TF	KIM_MYC targets
8	7.75	NULL	918	Chr	Chr 17
9	7.7	NULL	1033	Chr	Chr 2
10	7.57	NULL	86	BP	nucleosome assembly
11	7.36	NULL	1318	CC	mitochondrion
12	7.25	NULL	232	BP	mitosis
13	6.97	NULL	47	CC	nucleosome
14	6.89	NULL	630	Chr	Chr X
15	6.77	NULL	15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
16	6.6	NULL	15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
17	6.55	NULL	13	GSEA C2	REACTOME_PACKAGING_OF_TELOMERE_ENDS
18	6.5	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
19	6.48	NULL	15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
20	6.37	NULL	16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
Underexpressed					
1	−13.34	NULL	135	H.Tiss	WIRTH_Mucosa
2	−11.01	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−10.33	NULL	1720	Chr	Chr 1
4	−9.34	NULL	190	CC	extracellular matrix
5	−8.52	NULL	19	BP	peptide cross−linking
6	−7.66	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	−7.22	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	−6.89	NULL	633	Chr	Chr 9
9	−6.82	NULL	16	MMML CGS	MACIEJ_MMML 1
10	−6.78	NULL	602	Chr	Chr 10
11	−6.72	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
12	−6.64	NULL	375	Disease	GUDJ_psoriasis down
13	−6.39	NULL	62	TF Tissue	VAQUERIZAS_Lung
14	−6.34	NULL	553	Cancer	Lembcke_Colonic Inflammation
15	−6.28	NULL	1146	TF	HEBENSTREIT_low expression TF
16	−6.16	NULL	504	Chr	Chr 15
17	−5.84	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
18	−5.84	NULL	1182	CC	extracellular region
19	−5.82	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
20	−5.82	NULL	683	CC	extracellular space



GW_233

Local Summary

%DE = 0.86

metagenes = 1

genes = 22

genes in genesets = 22

genes with fdr < 0.1 = 13 (12 + / 1 −)

genes with fdr < 0.05 = 9 (9 + / 0 −)

genes with fdr < 0.01 = 8 (8 + / 0 −)

<r> metagenes = NA

<r> genes = 0.36

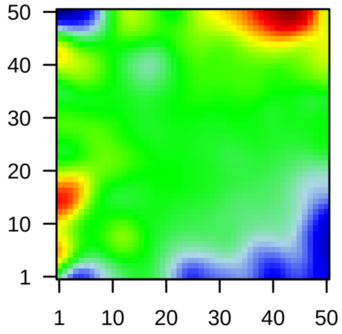
<FC> = 0.41

<shrinkage−t> = 14.4

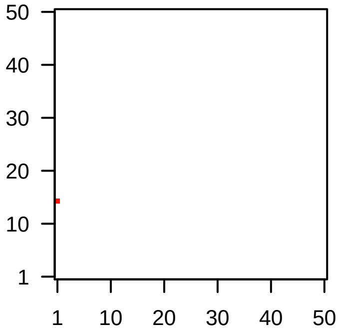
<p−value> = 0

<fdr> = 0.57

Profile



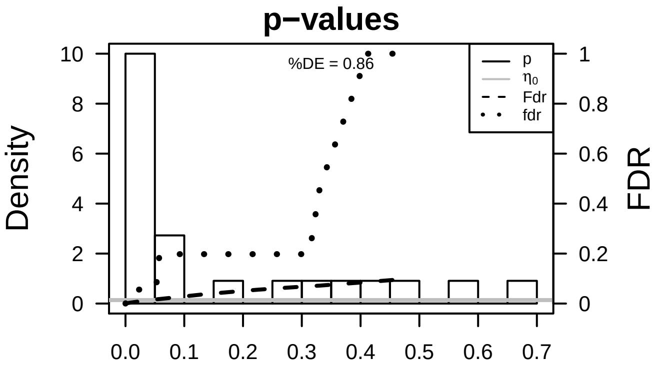
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	219927	1.04	7e−09	4e−08	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;A
2	2050	1.01	2e−08	6e−08	1 x 15	EPH receptor B4 [Source:HGNC Symbol;Acc:3395]
3	10428	0.99	4e−08	2e−06	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
4	10552	0.89	7e−07	2e−06	1 x 15	actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
5	9688	0.88	1e−06	5e−04	1 x 15	nucleoporin 93kDa [Source:HGNC Symbol;Acc:28958]
6	116447	0.68	2e−04	1e−03	1 x 15	topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbo
7	55257	0.63	5e−04	3e−03	1 x 15	MRG/MORF4L binding protein [Source:HGNC Symbol;Acc:1
8	8345	0.57	2e−03	6e−03	1 x 15	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:4755]
9	10471	0.52	4e−03	2e−02	1 x 15	prefoldin subunit 6 [Source:HGNC Symbol;Acc:4926]
10	51083	0.47	9e−03	6e−02	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
11	5690	−0.36	5e−02	6e−02	1 x 15	proteasome (prosome, macropain) subunit, beta type, 2 [Sou
12	79711	0.34	6e−02	6e−02	1 x 15	importin 4 [Source:HGNC Symbol;Acc:19426]
13	3217	0.32	7e−02	6e−02	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
14	8662	0.31	8e−02	2e−01	1 x 15	eukaryotic translation initiation factor 3, subunit B [Source:HG
15	10202	0.23	2e−01	2e−01	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
16	79581	0.19	3e−01	2e−01	1 x 15	solute carrier family 52 (riboflavin transporter), member 2 [So
17	7965	0.18	3e−01	2e−01	1 x 15	aminoacyl tRNA synthetase complex−interacting multifunctio
18	26233	0.15	4e−01	2e−01	1 x 15	F−box and leucine−rich repeat protein 6 [Source:HGNC Sym
19	23481	0.14	4e−01	2e−01	1 x 15	pescadillo ribosomal biogenesis factor 1 [Source:HGNC Sym
20	10195	−0.13	5e−01	5e−01	1 x 15	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Sym

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	37.65	NULL	1 / 5	GSEA C2 VERRECCHIA_RESPONSE_TO_TGFB1_C6
2	24.59	NULL	1 / 7	GSEA C2 PARK_HSC_MARKERS
3	19.74	NULL	1 / 11	GSEA C2 MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
4	19.74	NULL	1 / 11	GSEA C2 VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
5	18.57	NULL	1 / 12	MF ephrin receptor activity
6	18.57	NULL	1 / 12	GSEA C2 AMIT_EGF_RESPONSE_120_HELA
7	17.57	NULL	1 / 13	BP cell migration involved in sprouting angiogenesis
8	17.44	NULL	1 / 11	GSEA C2 HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
9	17.44	NULL	1 / 11	GSEA C2 KEGG_REGULATION_OF_ACTIN_CYTOSKELETON
10	17.08	NULL	1 / 11	CC nuclear periphery
11	16.72	NULL	1 / 14	MMML CGS MACIEJ_MMML 26
12	16.72	NULL	1 / 14	GSEA C2 VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN
13	15.96	NULL	1 / 15	GSEA C2 WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
14	15.96	NULL	1 / 15	GSEA C2 FIRESTEIN_PROLIFERATION
15	15.96	NULL	1 / 15	GSEA C2 KEGG_AXON_GUIDANCE
16	15.6	NULL	1 / 7	MMML CGS MACIEJ_MMML 9
17	15.53	NULL	1 / 13	GSEA C2 HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP
18	15.53	NULL	1 / 13	GSEA C2 WELCSH_BRCA1_TARGETS_1_UP
19	15.53	NULL	1 / 13	GSEA C2 CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
20	15.53	NULL	1 / 13	GSEA C2 KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
21	15.53	NULL	1 / 13	GSEA C2 BIOCARTA_SALMONELLA_PATHWAY
22	15.3	NULL	1 / 16	GSEA C2 DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN
23	15.3	NULL	1 / 16	GSEA C2 TIEN_INTESTINE_PROBIOTICS_2HR_UP
24	15.3	NULL	1 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
25	15.3	NULL	1 / 16	GSEA C2 MAHAJAN_RESPONSE_TO_IL1A_DN
26	14.77	NULL	1 / 14	BP regulation of actin filament polymerization
27	14.77	NULL	1 / 14	GSEA C2 PROVENZANI_METASTASIS_DN
28	14.69	NULL	1 / 6	GSEA C2 REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
29	14.69	NULL	1 / 6	GSEA C2 REACTOME_GPCR_LIGAND_BINDING
30	14.1	NULL	1 / 15	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
31	14.1	NULL	1 / 15	GSEA C2 SASSON_RESPONSE_TO_GONADOTROPHINS_UP
32	14.1	NULL	1 / 15	GSEA C2 SASSON_RESPONSE_TO_FORSKOLIN_UP
33	14.1	NULL	1 / 15	GSEA C2 KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS
34	14.1	NULL	1 / 15	GSEA C2 BIOCARTA_ACTINY_PATHWAY
35	13.51	NULL	1 / 16	GSEA C2 IGARASHI_ATF4_TARGETS_DN
36	13.51	NULL	1 / 16	GSEA C2 ZHAN_LATE_DIFFERENTIATION_GENES_UP
37	13.51	NULL	1 / 16	GSEA C2 HAHTOLA_CTCL_CUTANEOUS
38	13.51	NULL	1 / 16	GSEA C2 BIOCARTA_MPR_PATHWAY
39	13.51	NULL	1 / 16	GSEA C2 BIOCARTA_RHO_PATHWAY
40	13.51	NULL	1 / 16	GSEA C2 BIOCARTA_CDC42RAC_PATHWAY

GW_233

Local Summary

%DE = 0.64

metagenes = 31

genes = 456

genes in genesets = 452

genes with fdr < 0.1 = 186 (184 + / 2 −)

genes with fdr < 0.05 = 184 (182 + / 2 −)

genes with fdr < 0.01 = 128 (128 + / 0 −)

<r> metagenes = 0.92

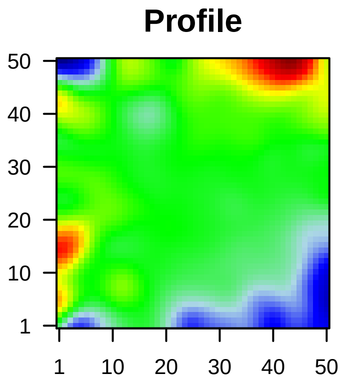
<r> genes = 0.34

<FC> = 0.36

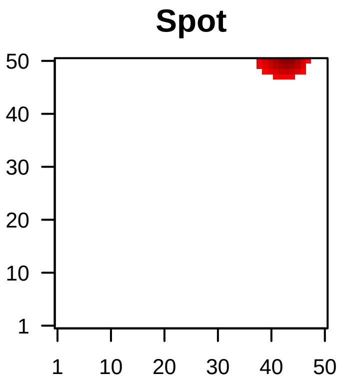
<shrinkage−t> = 12.74

<p−value> = 0.01

<fdr> = 0.58



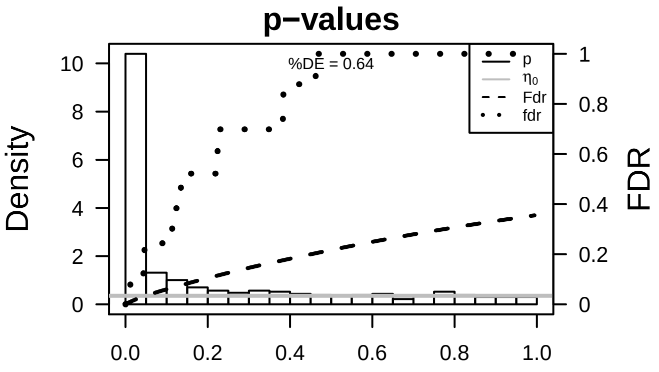
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55839	1.45	9e−16	1e−13	44 x 50	centromere protein N [Source:HGNC Symbol;Acc:30873]
2	51659	1.44	1e−15	4e−13	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
3	7037	1.3	4e−15	2e−11	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
4	9918	1.34	1e−13	1e−10	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
5	8500	1.29	8e−13	2e−10	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
6	7153	1.27	2e−12	1e−09	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
7	10635	1.23	1e−11	8e−09	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
8	7167	1.18	6e−11	2e−08	41 x 50	triosephosphate isomerase 1 [Source:HGNC Symbol;Acc:12
9	1894	1.15	2e−10	2e−08	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
10	3945	1.14	2e−10	1e−07	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
11	3161	1.1	1e−09	1e−07	43 x 50	hyaluronan−mediated motility receptor (RHAMM) [Source:HG
12	494514	1.09	2e−09	1e−07	46 x 48	chromosome 18 open reading frame 56 [Source:HGNC Symb
13	11062	1.07	3e−09	3e−07	39 x 50	dihydrouridine synthase 4−like (S. cerevisiae) [Source:HGNC
14	10606	1.06	5e−09	3e−07	43 x 50	phosphoribosylaminoimidazole carboxylase, phosphoribosyla
15	3251	1.04	8e−09	3e−07	42 x 50	hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
16	83461	1.04	9e−09	3e−07	44 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:1
17	1033	1.03	1e−08	2e−06	43 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
18	699	1	3e−08	2e−06	44 x 50	BUB1 mitotic checkpoint serine/threonine kinase [Source:HG
19	150468	0.99	5e−08	2e−06	43 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symbo
20	60488	0.98	5e−08	2e−06	40 x 50	mitochondrial ribosomal protein S35 [Source:HGNC Symbol;



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	43.96	NULL	78 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	43.96	NULL	78 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	23.51	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	23.45	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
5	22.58	NULL	88 / 370	BP	mitotic cell cycle
6	21.86	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
7	21.71	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
8	20.69	NULL	22 / 57	Glio	developing astrocytes
9	19.78	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
10	19.49	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
11	18.15	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	17.87	NULL	81 / 530	Cancer	Lembcke_Normal vs Adenoma
13	17.69	NULL	9 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
14	17.46	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
15	17.34	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	17.29	NULL	9 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
17	16.92	NULL	7 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
18	16.67	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	16.14	NULL	46 / 232	BP	mitosis
20	15.81	NULL	21 / 56	CC	chromosome, centromeric region
21	15.49	NULL	70 / 572	Disease	GUDJ_psoriasis up
22	15.21	NULL	12 / 18	BP	spindle organization
23	14.94	NULL	8 / 15	GSEA C2	LY_AGING_MIDDLE_DN
24	14.82	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
25	14.75	NULL	8 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
26	14.72	NULL	9 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	14.67	NULL	10 / 16	Cancer	WOLFER_overlap genes
28	14.5	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
29	14.47	NULL	11 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
30	14.41	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
31	14.41	NULL	5 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
32	13.1	NULL	6 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
33	12.99	NULL	17 / 67	BP	chromosome segregation
34	12.93	NULL	5 / 15	GSEA C2	FERRANDO_HOX11_NEIGHBORS
35	12.81	NULL	4 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
36	12.42	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
37	12.37	NULL	8 / 11	BP	mitotic metaphase plate congression
38	12.27	NULL	7 / 16	GSEA C2	BENPORATH_PROLIFERATION
39	12.26	NULL	5 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY
40	12.17	NULL	5 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN

GW_233

Local Summary

%DE = 0.86

metagenes = 2

genes = 61

genes in genesets = 53

genes with fdr < 0.1 = 45 (2 + / 43 −)

genes with fdr < 0.05 = 35 (1 + / 34 −)

genes with fdr < 0.01 = 23 (1 + / 22 −)

<r> metagenes = 1

<r> genes = 0.63

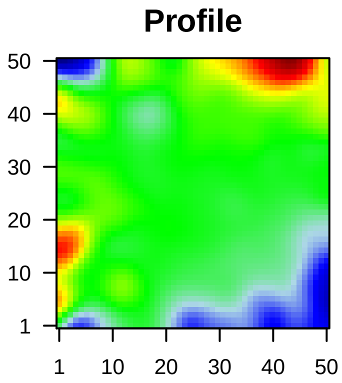
<FC> = −0.33

<shrinkage−t> = −11.62

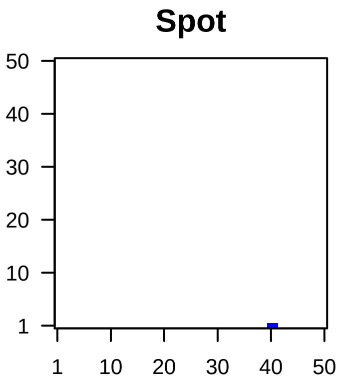
<p−value> = 0.01

<fdr> = 0.58

Profile



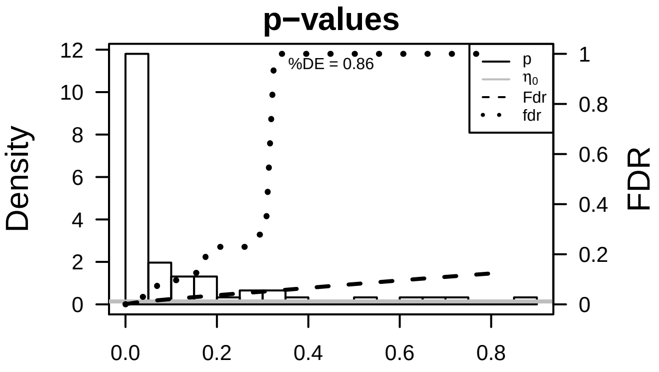
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	125050	1.35	8e−14	9e−05	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
2	27148	−0.79	1e−05	2e−04	41 x 1	serine/threonine kinase 36 [Source:HGNC Symbol;Acc:1720
3	23524	−0.75	4e−05	2e−04	40 x 1	serine/arginine repetitive matrix 2 [Source:HGNC Symbol;Ac
4	255031	−0.73	5e−05	3e−04	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
5	440353	−0.71	9e−05	9e−04	40 x 1	
6	25862	−0.66	3e−04	9e−04	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
7	1186	−0.64	4e−04	9e−04	41 x 1	chloride channel, voltage−sensitive 7 [Source:HGNC Symbol
8	250	−0.64	4e−04	3e−03	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
9	641737	−0.55	1e−03	3e−03	40 x 1	
10	7766	−0.57	1e−03	3e−03	40 x 1	Zinc finger protein 223 [Source:UniProtKB/TrEMBL;Acc:K7E
11	81576	−0.57	2e−03	3e−03	41 x 1	coiled−coil domain containing 130 [Source:HGNC Symbol;Ac
12	136051	−0.55	2e−03	3e−03	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
13	440275	−0.53	3e−03	3e−03	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
14	90639	−0.53	4e−03	3e−03	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
15	26279	−0.52	4e−03	3e−03	40 x 1	phospholipase A2, group IID [Source:HGNC Symbol;Acc:903
16	100134868	−0.52	4e−03	3e−03	40 x 1	
17	728294	−0.51	5e−03	3e−03	40 x 1	D−2−hydroxyglutarate dehydrogenase [Source:HGNC Symb
18	375775	−0.5	5e−03	3e−03	41 x 1	patatin−like phospholipase domain containing 7 [Source:HG
19	84839	−0.5	5e−03	3e−03	40 x 1	retina and anterior neural fold homeobox 2 [Source:HGNC Sy
20	57835	−0.5	5e−03	3e−03	40 x 1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.54	NULL	1 / 7	GSEA C2	LIU_CMYB_TARGETS_DN
2	−9.59	NULL	1 / 11	MF	C2H2 zinc finger domain binding
3	−9.11	NULL	1 / 12	Glio	Phillips PN up vs MES & Prolif
4	−9.11	NULL	1 / 12	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
5	−8.99	NULL	1 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
6	−8.51	NULL	1 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
7	−8.45	NULL	2 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
8	−8.21	NULL	1 / 11	MF	antiporter activity
9	−8.17	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS
10	−8.01	NULL	1 / 15	GSEA C2	JIANG_TIP30_TARGETS_DN
11	−7.44	NULL	1 / 19	BP	positive regulation of smoothened signaling pathway
12	−7.37	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
13	−7.22	NULL	1 / 20	miRNA target starBase	hsa−miR−330*
14	−7.13	NULL	1 / 14	MF	voltage−gated chloride channel activity
15	−7.13	NULL	1 / 14	GSEA C2	JAZAG_TGFB1_SIGNALING_DN
16	−6.78	NULL	1 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
17	−6.6	NULL	1 / 16	GSEA C2	DORSAM_HOXA9_TARGETS_DN
18	−6.57	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
19	−6.57	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
20	−6.48	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
21	−6.27	NULL	1 / 12	BP	phosphatidylinositol acyl−chain remodeling
22	−6.16	NULL	1 / 18	MF	adenyl nucleotide binding
23	−5.98	NULL	1 / 13	BP	phosphatidylserine acyl−chain remodeling
24	−5.8	NULL	2 / 14	BP	cellular response to estradiol stimulus
25	−5.8	NULL	1 / 13	MF	dynein binding
26	−5.72	NULL	1 / 14	BP	phosphatidylglycerol acyl−chain remodeling
27	−5.7	NULL	1 / 27	miRNA target starBase	hsa−miR−483−3p
28	−5.58	NULL	2 / 24	BP	negative regulation of T cell proliferation
29	−5.5	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
30	−5.5	NULL	1 / 15	MF	phospholipase A2 activity
31	−5.49	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
32	−5.48	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
33	−5.48	NULL	1 / 12	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_DN
34	−5.42	NULL	1 / 15	BP	2−oxoglutarate metabolic process
35	−5.41	NULL	1 / 33	BP	regulation of sequence−specific DNA binding transcription factor a
36	−5.3	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
37	−5.3	NULL	1 / 14	MMML CGS	MACIEJ_MMML 8
38	−5.24	NULL	2 / 69	miRNA target starBase	hsa−miR−578
39	−5.23	NULL	1 / 13	GSEA C2	WANG_RESPONSE_TO_ANDROGEN_UP
40	−5.07	NULL	1 / 11	GSEA C2	KEGG_NON_HOMOLOGOUS_END_JOINING

GW_233

Local Summary

%DE = 0.74

metagenes = 31

genes = 468

genes in genesets = 466

genes with fdr < 0.1 = 194 (17 + / 177 −)

genes with fdr < 0.05 = 142 (13 + / 129 −)

genes with fdr < 0.01 = 79 (9 + / 70 −)

<r> metagenes = 0.83

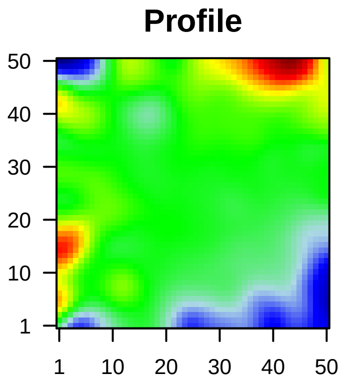
<r> genes = 0.32

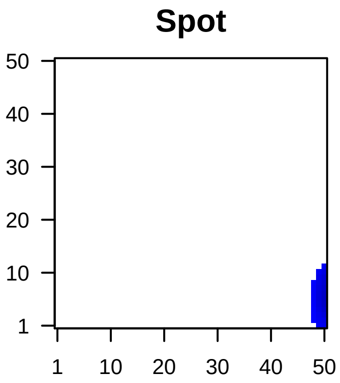
<FC> = −0.28

<shrinkage−t> = −9.89

<p−value> = 0.02

<fdr> = 0.69





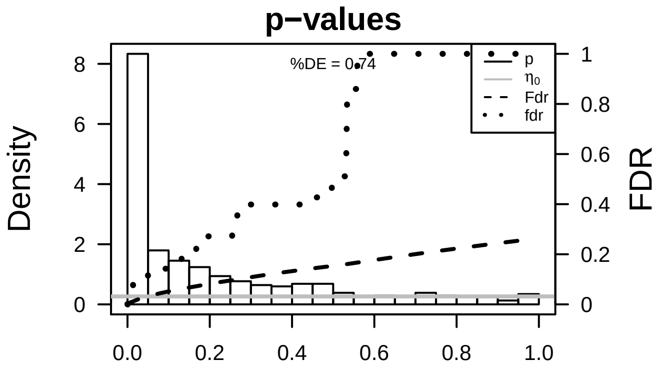
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	1.92	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	1675	−1.22	1e−11	1e−09	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
3	10232	−1.21	2e−11	3e−08	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
4	10365	−1.14	3e−10	4e−08	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
5	894	−1.1	1e−09	4e−08	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
6	9071	1.1	1e−09	1e−07	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
7	3169	−1.08	2e−09	7e−07	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
8	1545	−1.03	1e−08	7e−07	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
9	1116	−1.03	1e−08	3e−06	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
10	5341	0.98	5e−08	3e−06	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
11	7033	−0.98	6e−08	7e−06	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
12	4256	−0.94	2e−07	7e−06	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
13	2878	−0.94	2e−07	7e−06	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
14	83699	−0.93	2e−07	7e−06	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
15	1831	−0.92	3e−07	7e−06	49 x 5	TSC22 domain family, member 3 [Source:HGNC Symbol;Acc
16	57484	−0.92	3e−07	7e−05	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
17	92747	−0.88	1e−06	7e−05	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
18	1363	−0.87	1e−06	7e−05	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
19	55638	−0.86	2e−06	1e−04	50 x 11	syntabulin (syntaxin−interacting) [Source:HGNC Symbol;Acc:
20	1573	−0.83	5e−06	1e−04	50 x 11	cytochrome P450, family 2, subfamily J, polypeptide 2 [Sourc

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.02	NULL	10 / 15	CC	MHC class II protein complex
2	−13.27	NULL	5 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
3	−12.87	NULL	3 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
4	−12.63	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
5	−11.36	NULL	4 / 16	GSEA C2	VALK_AML_CLUSTER_9
6	−11.15	NULL	5 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
7	−10.63	NULL	4 / 16	GSEA C2	KORKOLA_TERATOMA_UP
8	−10.57	NULL	4 / 13	Cancer	GENTLES_modul17
9	−10.35	NULL	4 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
10	−10.07	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
11	−9.91	NULL	8 / 28	CC	transport vesicle membrane
12	−9.89	NULL	4 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
13	−9.65	NULL	7 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
14	−9.36	NULL	4 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP
15	−9.11	NULL	3 / 15	GSEA C2	VALK_AML_CLUSTER_4
16	−9	NULL	3 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
17	−8.86	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
18	−8.69	NULL	69 / 683	CC	extracellular space
19	−8.61	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
20	−8.57	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT
21	−8.57	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
22	−8.57	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
23	−8.46	NULL	12 / 47	BP	antigen processing and presentation
24	−8.44	NULL	6 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
25	−8.41	NULL	3 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
26	−8.25	NULL	3 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
27	−8.23	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
28	−8.09	NULL	2 / 10	BP	epoxygenase P450 pathway
29	−8.09	NULL	4 / 10	BP	germ cell migration
30	−7.98	NULL	3 / 8	Lymphoma	MASCQUE_ABC UP
31	−7.98	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
32	−7.94	NULL	3 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
33	−7.89	NULL	2 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
34	−7.87	NULL	5 / 16	Lymphoma	WRIGHT_ABC UP
35	−7.84	NULL	3 / 15	GSEA C2	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
36	−7.82	NULL	4 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
37	−7.81	NULL	6 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
38	−7.79	NULL	2 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
39	−7.79	NULL	3 / 14	GSEA C2	FRASOR_RESPONSE_TO_ESTRADIOL_UP
40	−7.72	NULL	91 / 553	Cancer	Lembcke_Colonic Inflammation



GW_233

Local Summary

%DE = 0.85

metagenes = 11

genes = 206

genes in genesets = 202

genes with fdr < 0.1 = 143 (14 + / 129 −)

genes with fdr < 0.05 = 135 (14 + / 121 −)

genes with fdr < 0.01 = 99 (10 + / 89 −)

<r> metagenes = 0.98

<r> genes = 0.46

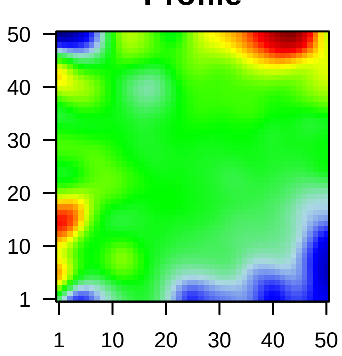
<FC> = −0.46

<shrinkage−t> = −16.12

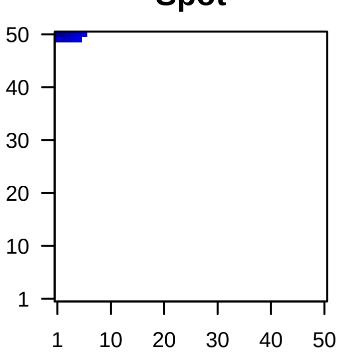
<p−value> = 0

<fdr> = 0.39

Profile



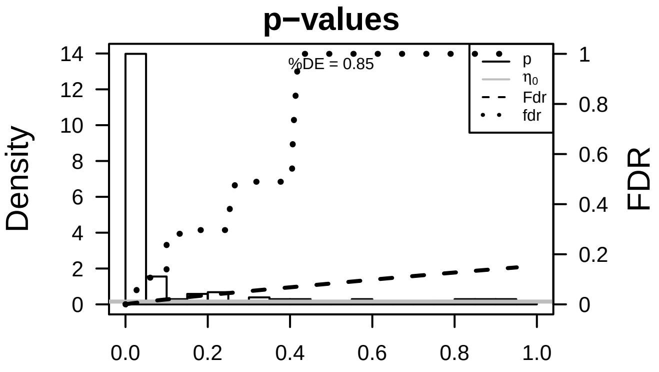
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.61	2e−16	7e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	1475	−1.71	2e−16	7e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
3	1673	2.04	2e−16	7e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
4	26085	−1.68	2e−16	7e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
5	192666	−1.57	2e−16	7e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
6	3851	−1.94	2e−16	7e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
7	51458	−1.6	2e−16	7e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
8	6286	−1.48	2e−16	7e−16	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
9	5275	−1.95	2e−16	7e−16	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 13 [
10	7053	−1.74	2e−16	7e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
11	43849	−1.46	7e−16	5e−13	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
12	6337	−1.38	2e−14	4e−11	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source
13	51806	−1.28	1e−12	9e−11	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
14	9245	−1.25	4e−12	6e−10	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
15	79852	−1.2	3e−11	6e−10	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
16	200958	−1.19	4e−11	6e−10	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Acc
17	3934	−1.17	8e−11	6e−10	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
18	375791	−1.17	8e−11	3e−09	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
19	2125	−1.15	2e−10	3e−09	1 x 50	envoplakin [Source:HGNC Symbol;Acc:3503]
20	2877	1.14	3e−10	3e−09	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−42.45	NULL	65 / 135	H.Tiss	WIRTH_Mucosa
2	−23.75	NULL	7 / 19	BP	peptide cross−linking
3	−19.35	NULL	5 / 13	BP	negative regulation of peptidase activity
4	−18.9	NULL	12 / 21	CC	cornified envelope
5	−17.95	NULL	16 / 53	BP	keratinocyte differentiation
6	−17.29	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	−16.02	NULL	5 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
8	−15.11	NULL	13 / 42	BP	keratinization
9	−14.59	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
10	−13.41	NULL	63 / 572	Disease	GUDJ_psoriasis up
11	−13.33	NULL	3 / 12	BP	cellular aldehyde metabolic process
12	−13.2	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
13	−12.6	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
14	−12.07	NULL	3 / 16	CC	microvillus membrane
15	−11.63	NULL	7 / 38	BP	epithelial cell differentiation
16	−11.52	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−11.06	NULL	17 / 76	BP	epidermis development
18	−11.05	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
19	−10.98	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
20	−10.77	NULL	9 / 52	BP	negative regulation of endopeptidase activity
21	−10.66	NULL	5 / 29	BP	regulation of proteolysis
22	−10.62	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
23	−9.86	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
24	−9.82	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
25	−9.6	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
26	−9.59	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
27	−9.08	NULL	13 / 186	MF	structural molecule activity
28	−8.6	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
29	−8.42	NULL	3 / 22	MF	cysteine−type endopeptidase inhibitor activity
30	−8.07	NULL	1 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
31	−8.02	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
32	−7.98	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
33	−7.57	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
34	−7.54	NULL	12 / 122	MF	serine−type endopeptidase activity
35	−7.32	NULL	4 / 51	MF	protein binding, bridging
36	−7.29	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
37	−7.26	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
38	−7.24	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
39	−7.22	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
40	−7.09	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP