GW_204

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1918 (994 + / 924 −)

genes with fdr < 0.1 = 1526 (807 + / 719 −)

genes with fdr < 0.05 = 1262 (685 + / 577 −)

genes with fdr < 0.01 = 934 (542 + / 392 −)

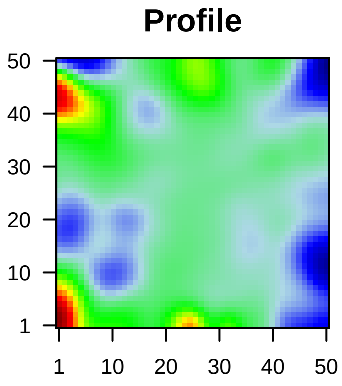
genes in genesets = 16332

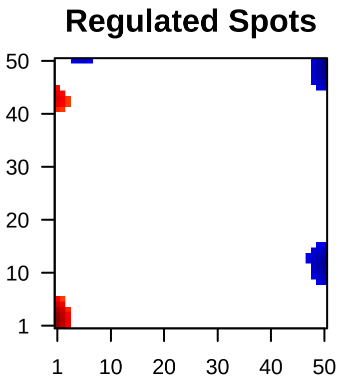
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

<fdr> = 0.86



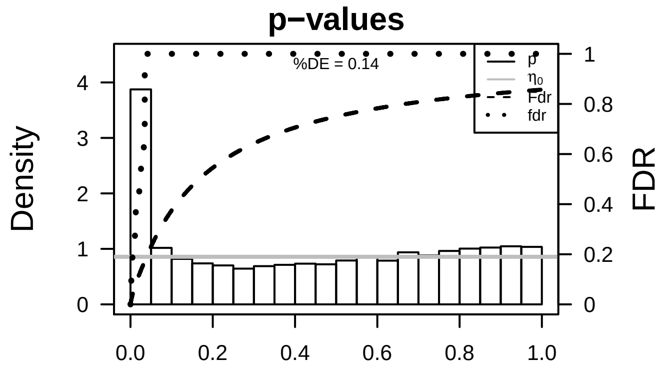


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.35	2e−16	2e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	58	3.07	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	3.12	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	131	−1.97	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	8644	−1.48	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	216	−1.82	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
7	218	−2.27	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
8	401138	1.56	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
9	27063	1.52	2e−16	2e−14	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Sy
10	118429	1.48	2e−16	2e−14	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
11	306	1.44	2e−16	2e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
12	147495	1.55	2e−16	2e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
13	140458	1.37	2e−16	2e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
14	445	−1.87	2e−16	2e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
15	655	−1.69	2e−16	2e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
16	387695	1.57	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
17	140851	1.45	2e−16	2e−14	1 x 5	
18	260436	−1.35	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
19	135398	2.16	2e−16	2e−14	1 x 40	chromosome 6 open reading frame 141 [Source:HGNC Sym
20	845	1.52	2e−16	2e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.81	NULL	36	BP	muscle filament sliding
2	13.23	NULL	127	H.Tiss	WIRTH_Muscle
3	12.74	NULL	242	BP	extracellular matrix organization
4	12.1	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	11.75	NULL	190	CC	extracellular matrix
6	11.7	NULL	250	Lymphoma	LENZ_Stromal signature 1
7	11.29	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
8	11.16	NULL	12	BP	hemidesmosome assembly
9	10.44	NULL	69	BP	extracellular matrix disassembly
10	10.16	NULL	16	H.Tiss	WIRTH_Hippocampus
11	10.06	NULL	64	BP	collagen catabolic process
12	9.36	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
13	9.32	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	9.06	NULL	37	CC	sarcomere
15	8.78	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	8.57	NULL	12	CC	myosin filament
17	8.54	NULL	14	CC	contractile fiber
18	8.35	NULL	572	Disease	GUDJ_psoriasis up
19	8.35	NULL	16	MMML CGS	MACIEJ_MMML 1
20	8.31	NULL	13	GSEA C2	FRIDMAN_SENESCENCE_UP
Underexpressed					
1	−9.3	NULL	504	Chr	Chr 15
2	−7.98	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
3	−7.47	NULL	918	Chr	Chr 17
4	−7.46	NULL	24	TF Tissue	VAQUERIZAS_Trachea
5	−7.34	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
6	−6.24	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
7	−5.71	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
8	−5.59	NULL	1318	CC	mitochondrion
9	−5.52	NULL	52	Chr	Chr HSCHR6_MHC_QBL
10	−5.49	NULL	4	MMML CGS	MACIEJ_MMML 23
11	−5.23	NULL	11	MF	glutathione binding
12	−5.14	NULL	390	BP	metabolic process
13	−5.07	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
14	−5.02	NULL	220	CC	mitochondrial matrix
15	−4.89	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
16	−4.76	NULL	15	CC	MHC class II protein complex
17	−4.76	NULL	304	CC	mitochondrial inner membrane
18	−4.74	NULL	6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
19	−4.73	NULL	8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
20	−4.66	NULL	14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM



GW_204

Local Summary

%DE = 0.88

metagenes = 16

genes = 249

genes in genesets = 247

genes with fdr < 0.1 = 201 (192 + / 9 −)

genes with fdr < 0.05 = 185 (180 + / 5 −)

genes with fdr < 0.01 = 156 (153 + / 3 −)

<r> metagenes = 0.95

<r> genes = 0.37

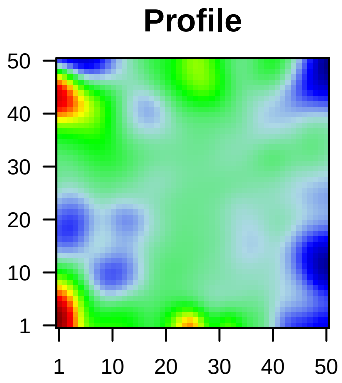
<FC> = 0.69

<shrinkage−t> = 24.04

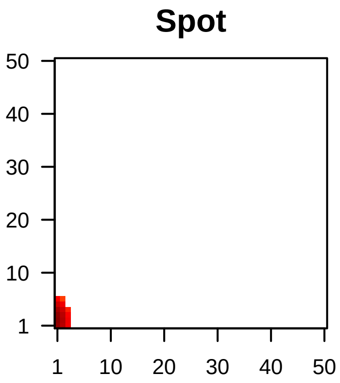
<p−value> = 0

<fdr> = 0.28

Profile



Spot



Local Genelist

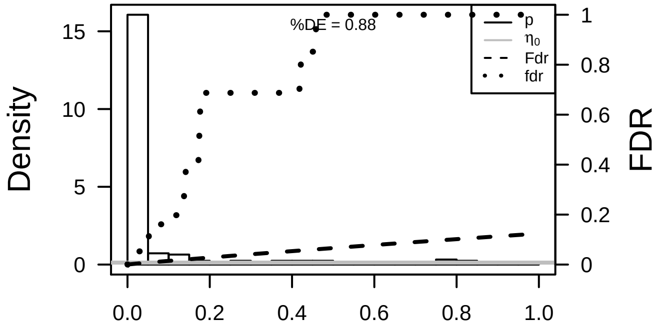
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	401138	1.56	2e−16	2e−16	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
2	118429	1.48	2e−16	2e−16	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
3	140851	1.45	2e−16	2e−16	1 x 5	
4	1278	1.33	2e−16	2e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1293	1.49	2e−16	2e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
6	1437	1.65	2e−16	2e−16	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
7	56603	1.71	2e−16	2e−16	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
8	1909	1.42	2e−16	2e−16	3 x 1	endothelin receptor type A [Source:HGNC Symbol;Acc:3179]
9	2191	1.35	2e−16	2e−16	1 x 1	fibroblast activation protein, alpha [Source:HGNC Symbol;Ac
10	2195	1.47	2e−16	2e−16	1 x 5	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
11	3909	1.59	2e−16	2e−16	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
12	3918	1.66	2e−16	2e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
13	4312	1.78	2e−16	2e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
14	4319	2.38	2e−16	2e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
15	4320	1.6	2e−16	2e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
16	4314	2.03	2e−16	2e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
17	4493	1.45	2e−16	2e−16	1 x 5	metallothionein 1E [Source:HGNC Symbol;Acc:7397]
18	4502	1.47	2e−16	2e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
19	644314	1.56	2e−16	2e−16	1 x 5	
20	4907	1.87	2e−16	2e−16	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.76	NULL	46 / 190	CC	extracellular matrix
2	28.21	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
3	27.66	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	27.64	NULL	57 / 242	BP	extracellular matrix organization
5	26.78	NULL	58 / 250	Lymphoma	LENZ_Stromal signature 1
6	26.69	NULL	24 / 64	BP	collagen catabolic process
7	26.38	NULL	25 / 69	BP	extracellular matrix disassembly
8	24.57	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	23.14	NULL	7 / 11	MF	platelet−derived growth factor binding
10	21.99	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
11	20.48	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
12	20.16	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
13	19.37	NULL	31 / 183	CC	proteinaceous extracellular matrix
14	19.37	NULL	51 / 403	BP	cell adhesion
15	18.74	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
16	18.51	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
17	18.24	NULL	13 / 37	BP	collagen fibril organization
18	18	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
19	18	NULL	7 / 12	miRNA target	miR−29c
20	17.25	NULL	18 / 83	CC	basement membrane
21	17.03	NULL	12 / 35	Glio	Colman_survival_associated
22	16.95	NULL	16 / 57	MF	extracellular matrix structural constituent
23	16.6	NULL	68 / 683	CC	extracellular space
24	16.3	NULL	10 / 40	BP	cellular response to amino acid stimulus
25	15.75	NULL	90 / 1182	CC	extracellular region
26	15.63	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
27	15.59	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
28	14.97	NULL	5 / 11	Glio	Phillips MES up vs Prolif & PN
29	14.96	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
30	14.78	NULL	36 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
31	14.78	NULL	36 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
32	14.78	NULL	36 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
33	14.78	NULL	36 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
34	14.76	NULL	7 / 16	MF	fibronectin binding
35	14.75	NULL	5 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
36	14.72	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP
37	14.68	NULL	5 / 16	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C1
38	14.53	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
39	14.39	NULL	54 / 553	Cancer	Lembcke_Colonic Inflammation
40	14.35	NULL	5 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR

p−values



GW_204

Local Summary

%DE = 0.84

metagenes = 11

genes = 154

genes in genesets = 153

genes with fdr < 0.1 = 123 (112 + / 11 −)

genes with fdr < 0.05 = 112 (103 + / 9 −)

genes with fdr < 0.01 = 98 (92 + / 6 −)

<r> metagenes = 0.98

<r> genes = 0.39

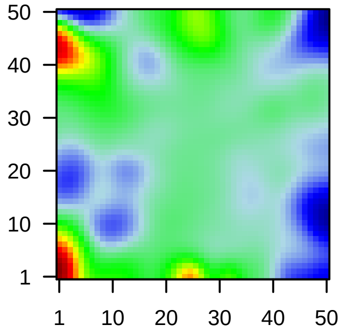
<FC> = 0.58

<shrinkage−t> = 20.27

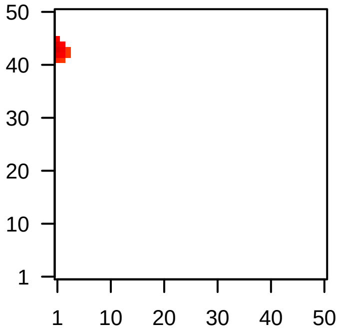
<p−value> = 0

<fdr> = 0.3

Profile



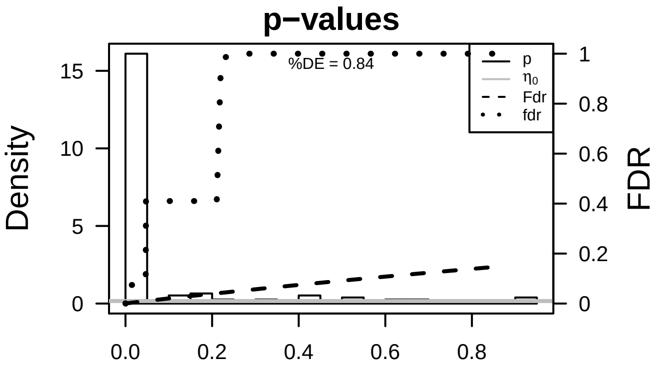
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	147495	1.55	2e−16	5e−16	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
2	1308	1.91	2e−16	5e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
3	51200	1.84	2e−16	5e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
4	1515	1.46	2e−16	5e−16	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
5	2152	1.94	2e−16	5e−16	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
6	2352	1.68	2e−16	5e−16	1 x 42	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
7	8111	1.53	2e−16	5e−16	1 x 42	G protein−coupled receptor 68 [Source:HGNC Symbol;Acc:4
8	3552	1.34	2e−16	5e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
9	9119	2.29	2e−16	5e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
10	56901	−1.7	2e−16	5e−16	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
11	8601	1.5	2e−16	5e−16	1 x 44	regulator of G−protein signaling 20 [Source:HGNC Symbol;A
12	144406	1.3	2e−15	3e−14	1 x 42	WD repeat domain 66 [Source:HGNC Symbol;Acc:28506]
13	3861	1.19	2e−15	3e−14	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
14	7039	1.29	3e−15	1e−13	1 x 44	transforming growth factor, alpha [Source:HGNC Symbol;Acc
15	222584	1.27	8e−15	1e−13	1 x 44	family with sequence similarity 83, member B [Source:HGNC
16	2697	1.26	1e−14	8e−13	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
17	244	1.23	5e−14	8e−13	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
18	5947	1.22	8e−14	8e−12	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
19	5744	1.17	7e−13	8e−12	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
20	6273	1.17	8e−13	8e−12	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.95	NULL	4 / 12	BP	hemidesmosome assembly
2	13.21	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
3	11.51	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
4	10.94	NULL	3 / 15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
5	10.82	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA
6	10.75	NULL	2 / 11	BP	positive regulation of positive chemotaxis
7	10.46	NULL	2 / 14	GSEA C2	MAINA_VHL_TARGETS_DN
8	10.33	NULL	34 / 572	Disease	GUDJ_psoriasis up
9	10.2	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
10	10.05	NULL	2 / 2	miRNA target	miR−199a*
11	9.84	NULL	10 / 82	CC	intermediate filament
12	9.39	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	9.33	NULL	7 / 76	BP	epidermis development
14	9.02	NULL	2 / 13	GSEA C2	HASINA_NOL7_TARGETS_UP
15	8.61	NULL	4 / 44	CC	keratin filament
16	8.6	NULL	2 / 13	BP	response to copper ion
17	8.52	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
18	8.51	NULL	3 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
19	8.46	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
20	8.46	NULL	1 / 10	GSEA C2	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CAS
21	8.37	NULL	6 / 70	BP	cell junction assembly
22	8.28	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
23	8.27	NULL	3 / 16	GSEA C2	LEONARD_HYPOXIA
24	8.26	NULL	2 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
25	8.19	NULL	3 / 12	BP	keratinocyte proliferation
26	8.16	NULL	1 / 4	MMML CGS	MACIEJ_MMML 47
27	7.99	NULL	1 / 11	GSEA C2	BIOCARTA_EXTRINSIC_PATHWAY
28	7.99	NULL	2 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
29	7.89	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
30	7.78	NULL	8 / 112	Glio	Christensen_hypermethylated_in_grade2_oligoastrocytoma
31	7.76	NULL	7 / 85	Glio	laffaire_hypermeth_LGG_vs_control
32	7.6	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C2
33	7.58	NULL	1 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
34	7.47	NULL	9 / 132	Glio	Christensen_hypermethylated_in_grade3_oligoastrocytoma
35	7.4	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
36	7.24	NULL	1 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
37	7.24	NULL	1 / 13	GSEA C2	BAELDE_DIABETIC_NEPHROPATHY_DN
38	7.19	NULL	1 / 12	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP
39	7.18	NULL	1 / 6	GSEA C2	OHM_EMBRYONIC_CARCINOMA_DN
40	7.16	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP

GW_204

Local Summary

%DE = 0.84

metagenes = 24

genes = 273

genes in genesets = 269

genes with fdr < 0.1 = 181 (10 + / 171 −)

genes with fdr < 0.05 = 151 (7 + / 144 −)

genes with fdr < 0.01 = 117 (6 + / 111 −)

<r> metagenes = 0.91

<r> genes = 0.26

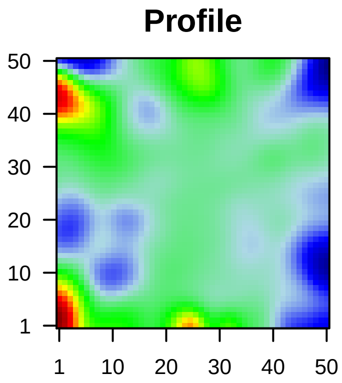
<FC> = −0.39

<shrinkage−t> = −13.73

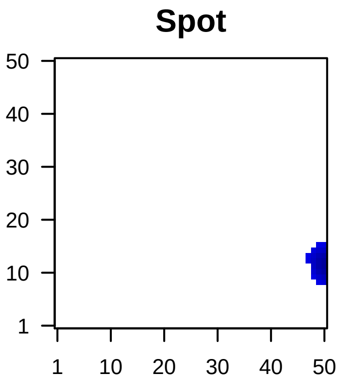
<p−value> = 0

<fdr> = 0.5

Profile



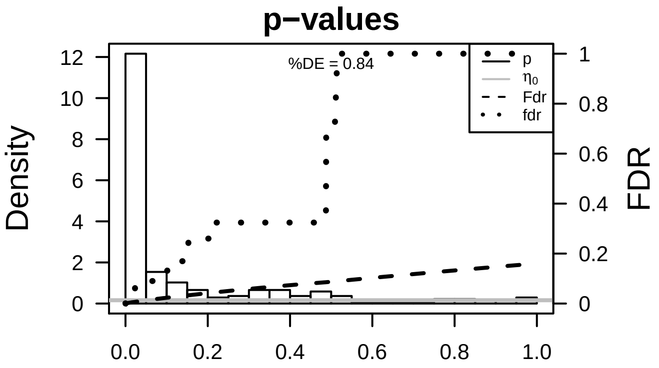
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3169	−1.5	2e−16	2e−15	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	2568	−1.34	2e−16	2e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
3	10232	−1.52	2e−16	2e−15	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
4	6920	−1.53	2e−16	2e−15	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
5	4255	−1.24	3e−14	1e−10	48 x 15	O−6−methylguanine−DNA methyltransferase [Source:HGNC
6	9249	−1.12	6e−12	1e−10	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
7	2878	−1.12	7e−12	5e−10	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
8	92747	−1.08	3e−11	5e−10	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
9	84952	−1.08	3e−11	7e−10	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
10	29116	−1.07	6e−11	7e−10	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
11	79085	−1.07	7e−11	7e−10	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr
12	6192	−1.06	8e−11	7e−10	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
13	260293	−1.06	1e−10	4e−09	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
14	2762	−1.03	2e−10	4e−09	50 x 12	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc
15	55268	−1.03	3e−10	2e−08	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy
16	135112	−1.01	6e−10	9e−08	50 x 13	nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21
17	8857	0.97	3e−09	1e−07	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
18	28958	−0.95	6e−09	1e−07	49 x 13	cytochrome c oxidase assembly factor 3 [Source:HGNC Sym
19	51316	−0.94	7e−09	2e−07	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
20	2139	−0.93	1e−08	2e−07	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.55	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−13.86	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−13.5	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
4	−12.11	NULL	3 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
5	−11.72	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
6	−11.29	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
7	−10.96	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
8	−10.84	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
9	−10.59	NULL	3 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
10	−9.95	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
11	−9.45	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
12	−8.89	NULL	2 / 11	CC	photoreceptor outer segment membrane
13	−8.59	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
14	−8.46	NULL	4 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
15	−8.36	NULL	2 / 14	BP	negative regulation of epithelial to mesenchymal transition
16	−8.09	NULL	2 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
17	−8.06	NULL	1 / 4	GSEA C2	NICK_RESPONSE_TO_PROC_TREATMENT_UP
18	−8.04	NULL	1 / 3	miRNA 3UTR	ACGC−210
19	−7.99	NULL	2 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
20	−7.93	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
21	−7.85	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
22	−7.76	NULL	2 / 14	GSEA C2	PEREZ_TP53_AND_TP63_TARGETS
23	−7.76	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
24	−7.73	NULL	4 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
25	−7.7	NULL	3 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN
26	−7.38	NULL	3 / 14	MF	selenium binding
27	−7.37	NULL	3 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
28	−7.25	NULL	4 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
29	−7.21	NULL	2 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
30	−7.17	NULL	3 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
31	−7.12	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_DN
32	−7.09	NULL	3 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
33	−7.05	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
34	−7	NULL	1 / 10	BP	prostate gland epithelium morphogenesis
35	−6.94	NULL	4 / 21	BP	drug metabolic process
36	−6.94	NULL	2 / 12	CC	apical junction complex
37	−6.93	NULL	2 / 13	GSEA C2	CERVERA_SDHB_TARGETS_2
38	−6.87	NULL	3 / 11	BP	DNA integration
39	−6.78	NULL	2 / 12	BP	nitric oxide biosynthetic process
40	−6.69	NULL	2 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN

GW_204

Local Summary

%DE = 0.8

metagenes = 17

genes = 224

genes in genesets = 223

genes with fdr < 0.1 = 140 (14 + / 126 −)

genes with fdr < 0.05 = 115 (9 + / 106 −)

genes with fdr < 0.01 = 80 (5 + / 75 −)

<r> metagenes = 0.96

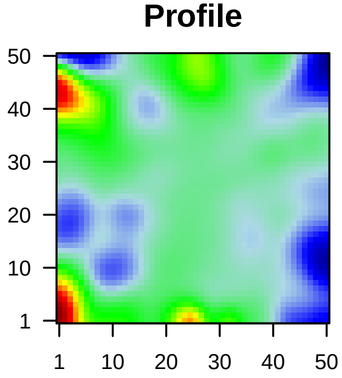
<r> genes = 0.26

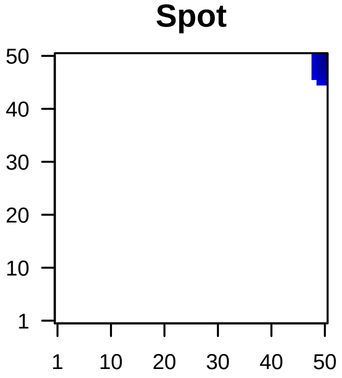
<FC> = −0.42

<shrinkage−t> = −14.68

<p−value> = 0

<fdr> = 0.5





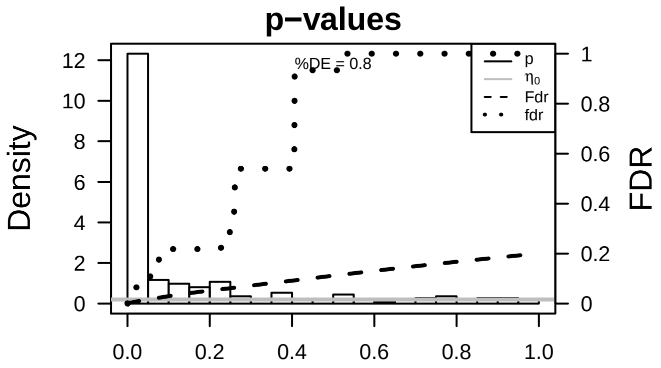
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.82	2e−16	9e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	445	−1.87	2e−16	9e−16	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
3	655	−1.69	2e−16	9e−16	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
4	875	−1.45	2e−16	9e−16	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
5	4072	−1.62	2e−16	9e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
6	3304	−1.35	2e−16	9e−16	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
7	3866	−2.56	2e−16	9e−16	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
8	3880	−3.66	2e−16	9e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
9	3856	−1.93	2e−16	9e−16	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
10	26227	−2.09	2e−16	9e−16	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
11	256764	−2.64	2e−16	9e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
12	139728	−1.31	9e−16	1e−13	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
13	200634	−1.29	3e−15	3e−12	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
14	84707	−1.22	7e−14	9e−12	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
15	2944	−1.19	4e−13	9e−12	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
16	4922	−1.18	5e−13	2e−11	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
17	400916	−1.17	1e−12	2e−11	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [So
18	28978	1.15	2e−12	2e−11	49 x 50	transmembrane protein 14A [Source:HGNC Symbol;Acc:210
19	26047	−1.15	2e−12	4e−10	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
20	4953	1.11	1e−11	2e−09	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.14	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−15.15	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
3	−14.58	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
4	−14	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
5	−13.27	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
6	−12.81	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
7	−12.73	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
8	−12.57	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
9	−12.3	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
10	−12.24	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
11	−12.24	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
12	−11.81	NULL	3 / 11	MF	glutathione binding
13	−11.81	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
14	−11.81	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
15	−11.81	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
16	−11.78	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
17	−11.59	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
18	−11.38	NULL	4 / 19	BP	cellular amino acid biosynthetic process
19	−11.05	NULL	1 / 18	CC	costamere
20	−10.73	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
21	−10.61	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
22	−10.28	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
23	−10.25	NULL	5 / 20	MF	glutathione transferase activity
24	−10.15	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
25	−10.13	NULL	1 / 21	BP	sarcomere organization
26	−10.07	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
27	−9.96	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
28	−9.54	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
29	−9.26	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
30	−9.24	NULL	2 / 15	BP	spinal cord development
31	−8.83	NULL	4 / 82	MF	structural constituent of cytoskeleton
32	−8.74	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
33	−8.66	NULL	2 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
34	−8.59	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
35	−8.46	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
36	−8.43	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
37	−8.38	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
38	−8.38	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
39	−8.15	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
40	−8.15	NULL	2 / 8	GSEA C2	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE



GW_204

Local Summary

%DE = 0.93

metagenes = 4

genes = 117

genes in genesets = 116

genes with fdr < 0.1 = 93 (4 + / 89 −)

genes with fdr < 0.05 = 87 (3 + / 84 −)

genes with fdr < 0.01 = 71 (2 + / 69 −)

<r> metagenes = 0.99

<r> genes = 0.4

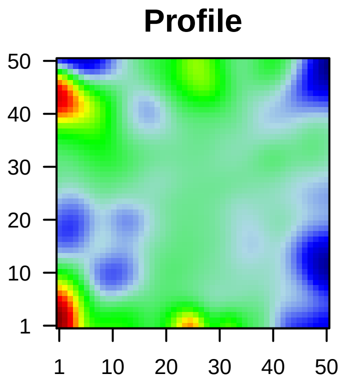
<FC> = −0.51

<shrinkage−t> = −17.8

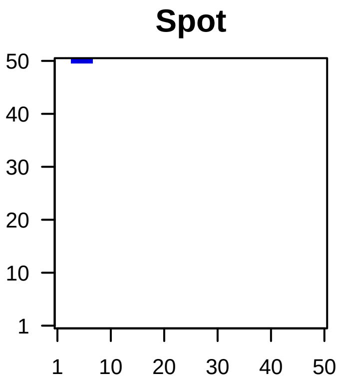
<p−value> = 0

<fdr> = 0.38

Profile



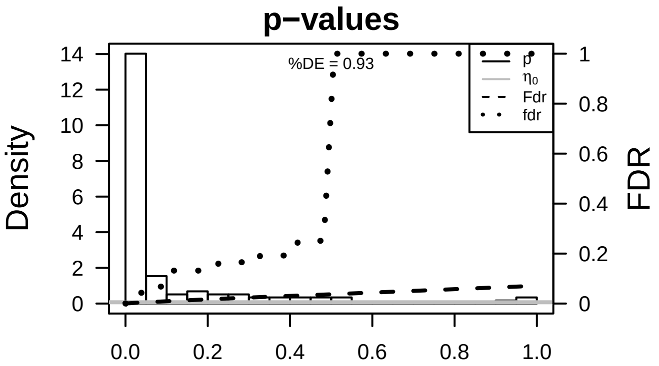
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1366	−1.79	2e−16	4e−16	6 x 50	claudin 7 [Source:HGNC Symbol;Acc:2049]
2	9245	−1.61	2e−16	4e−16	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
3	5603	−1.35	2e−16	4e−16	7 x 50	mitogen−activated protein kinase 13 [Source:HGNC Symbol;
4	4582	−1.39	2e−16	4e−16	7 x 50	mucin 1, cell surface associated [Source:HGNC Symbol;Acc:
5	5226	−1.39	2e−16	4e−16	6 x 50	phosphogluconate dehydrogenase [Source:HGNC Symbol;A
6	548596	−1.27	6e−15	2e−13	4 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc
7	1999	−1.24	3e−14	1e−12	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
8	154043	−1.2	2e−13	2e−12	6 x 50	CNKSR family member 3 [Source:HGNC Symbol;Acc:23034]
9	10874	−1.18	5e−13	7e−10	4 x 50	neuromedin U [Source:HGNC Symbol;Acc:7859]
10	1159	−1.06	9e−11	1e−09	5 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc
11	58489	−1.04	2e−10	6e−09	7 x 50	abhydrolase domain containing 17C [Source:HGNC Symbol;
12	200958	−1	9e−10	7e−09	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Acc
13	58528	−0.97	2e−09	7e−09	6 x 50	Ras−related GTP binding D [Source:HGNC Symbol;Acc:199
14	79007	−0.97	3e−09	1e−08	6 x 50	dysbindin (dystrobrevin binding protein 1) domain containing
15	284340	−0.96	4e−09	3e−08	6 x 50	chemokine (C−X−C motif) ligand 17 [Source:HGNC Symbol;
16	7263	−0.94	7e−09	4e−08	5 x 50	thiosulfate sulfurtransferase (rhodanese) [Source:HGNC Sym
17	23593	−0.93	1e−08	4e−08	6 x 50	heme binding protein 2 [Source:HGNC Symbol;Acc:15716]
18	8681	−0.92	2e−08	4e−08	5 x 50	phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym
19	80223	−0.91	2e−08	1e−07	6 x 50	RAB11 family interacting protein 1 (class I) [Source:HGNC S
20	51195	−0.89	5e−08	1e−07	5 x 50	Rap guanine nucleotide exchange factor (GEF)−like 1 [Sourc

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−20.34	NULL	3 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
2	−18.17	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
3	−14.16	NULL	1 / 6	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_FLUOROURACIL
4	−14.08	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
5	−13.25	NULL	1 / 8	GSEA C2	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
6	−12.18	NULL	1 / 6	GSEA C2	GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION
7	−11.61	NULL	1 / 10	GSEA C2	LUI_TARGETS_OF_PAX8_PPARG_FUSION
8	−11.57	NULL	2 / 13	GSEA C2	KEGG_O_GLYCAN_BIOSYNTHESIS
9	−11.2	NULL	3 / 45	BP	O−glycan processing
10	−10.97	NULL	2 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
11	−10.59	NULL	2 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
12	−10.38	NULL	2 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP
13	−10.33	NULL	4 / 38	BP	epithelial cell differentiation
14	−10.23	NULL	1 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24
15	−9.51	NULL	4 / 28	BP	negative regulation of ERK1 and ERK2 cascade
16	−9.49	NULL	2 / 12	GSEA C2	RUTELLA_RESPONSE_TO_HGF_DN
17	−9.16	NULL	1 / 15	GSEA C2	LUI_THYROID_CANCER_PAX8_PPARG_DN
18	−9.16	NULL	1 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_3
19	−9.16	NULL	1 / 15	GSEA C2	FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN
20	−9.16	NULL	1 / 15	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP
21	−9.16	NULL	1 / 15	GSEA C2	REACTOME_TIGHT_JUNCTION_INTERACTIONS
22	−9.16	NULL	1 / 15	GSEA C2	REACTOME_CELL_JUNCTION_ORGANIZATION
23	−9.11	NULL	1 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
24	−9.02	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
25	−8.95	NULL	1 / 10	BP	negative regulation of transcription by competitive promoter binding
26	−8.82	NULL	1 / 16	GSEA C2	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
27	−8.82	NULL	1 / 16	GSEA C2	REACTOME_CELL_CELL_ADHESION_SYSTEMS
28	−8.53	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
29	−8.53	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
30	−8.49	NULL	1 / 9	GSEA C2	DORN_ADENOVIRUS_INFECTION_32HR_UP
31	−8.3	NULL	2 / 12	MF	lysophospholipase activity
32	−8.27	NULL	3 / 24	TF Tissue	VAQUERIZAS_Trachea
33	−8.21	NULL	1 / 15	MF	acetylglucosaminyltransferase activity
34	−8.14	NULL	2 / 12	Pathw Act	BENTINK_e2f3.1
35	−8.07	NULL	3 / 16	miRNA target−starBase	hsa−miR−1298
36	−8.05	NULL	1 / 12	GSEA C2	XU_RESPONSE_TO_TRETINOIN_UP
37	−8.04	NULL	1 / 12	BP	negative regulation of intrinsic apoptotic signaling pathway in respo
38	−8.04	NULL	1 / 12	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17
39	−7.98	NULL	1 / 19	BP	calcium−independent cell−cell adhesion
40	−7.97	NULL	1 / 10	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_DN