GW_016

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1893 (1048 + / 845 −)

genes with fdr < 0.1 = 1606 (899 + / 707 −)

genes with fdr < 0.05 = 1333 (754 + / 579 −)

genes with fdr < 0.01 = 942 (551 + / 391 −)

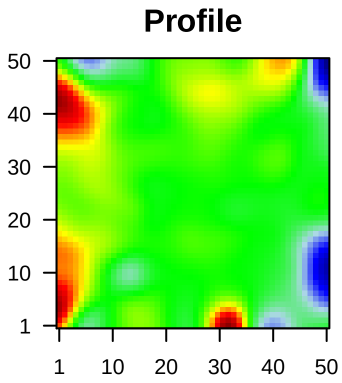
genes in genesets = 16332

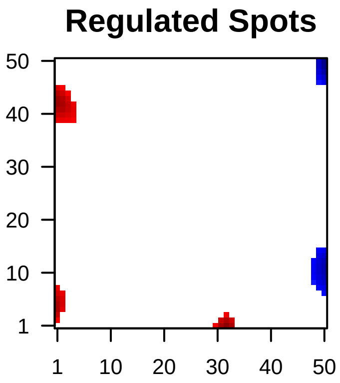
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

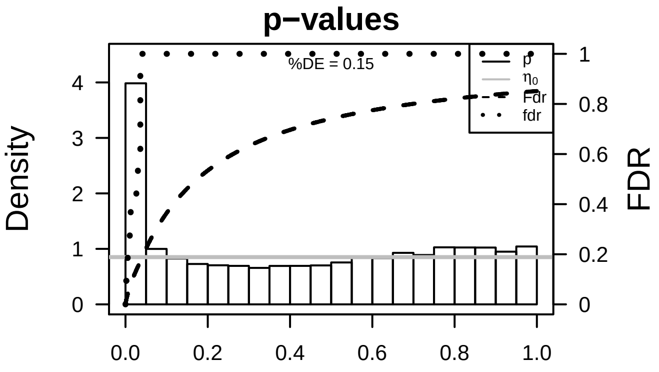
<fdr> = 0.85


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	87	1.39	2e−16	3e−14	1 x 3	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	1646	−1.31	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
3	8644	−2.16	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	−1.71	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	244	1.47	2e−16	3e−14	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
6	341	1.26	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
7	558	1.37	2e−16	3e−14	5 x 3	AXL receptor tyrosine kinase [Source:HGNC Symbol;Acc:90
8	25805	−1.28	2e−16	3e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
9	116071	1.29	2e−16	3e−14	32 x 1	basic leucine zipper transcription factor, ATF−like 2 [Source:H
10	8424	1.37	2e−16	3e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamm
11	8412	1.32	2e−16	3e−14	1 x 5	breast cancer anti−estrogen resistance 3 [Source:HGNC Sy
12	388115	1.51	2e−16	3e−14	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Sym
13	260436	−1.73	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
14	51806	−1.41	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
15	55450	1.67	2e−16	3e−14	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
16	857	1.39	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
17	894	1.32	2e−16	3e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
18	400916	−1.29	2e−16	3e−14	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [So
19	22802	−1.3	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
20	9076	−1.72	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.56	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	13.05	NULL	633	Chr	Chr 9
3	11.08	NULL	135	H.Tiss	WIRTH_Mucosa
4	10.98	NULL	51	BP	type I interferon signaling pathway
5	10.96	NULL	519	Chr	Chr 14
6	10.59	NULL	123	BP	defense response to virus
7	10.37	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	9.34	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	8.76	NULL	10	BP	positive regulation of cAMP−mediated signaling
10	8.52	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	8.35	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	8.34	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
13	8.28	NULL	8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
14	8.18	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
15	7.92	NULL	204	BP	cytokine−mediated signaling pathway
16	7.79	NULL	14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
17	7.36	NULL	17	BP	positive regulation of release of sequestered calcium ion into cytos
18	7.22	NULL	31	BP	negative regulation of viral genome replication
19	7.15	NULL	60	BP	interferon−gamma−mediated signaling pathway
20	7.13	NULL	572	Disease	GUDJ_psoriasis up
Underexpressed					
1	−7.86	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
2	−7.81	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
3	−6.71	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	−6.63	NULL	1720	Chr	Chr 1
5	−6.62	NULL	7	MMML CGS	MACIEJ_MMML 5
6	−6.45	NULL	630	Chr	Chr X
7	−6.36	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−6.14	NULL	3274	CC	integral to membrane
9	−6.12	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
10	−5.96	NULL	119	BP	xenobiotic metabolic process
11	−5.8	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
12	−5.71	NULL	34	BP	glutathione metabolic process
13	−5.65	NULL	20	MF	glutathione transferase activity
14	−5.61	NULL	1253	BP	small molecule metabolic process
15	−5.39	NULL	15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
16	−5.19	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
17	−5.09	NULL	296	MF	oxidoreductase activity
18	−5.07	NULL	553	Cancer	Lembcke_Colonic Inflammation
19	−4.95	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
20	−4.88	NULL	327	Lymphoma	SPANG_CD40 6hrs UP

GW_016

Local Summary

%DE = 0.87

metagenes = 8

genes = 127

genes in genesets = 124

genes with fdr < 0.1 = 99 (93 + / 6 −)

genes with fdr < 0.05 = 99 (93 + / 6 −)

genes with fdr < 0.01 = 78 (75 + / 3 −)

<r> metagenes = 0.99

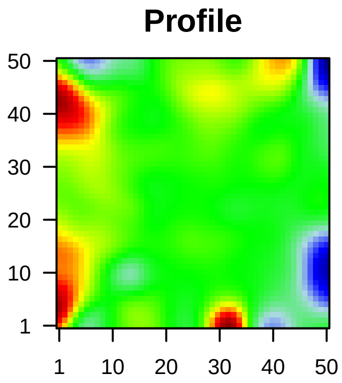
<r> genes = 0.43

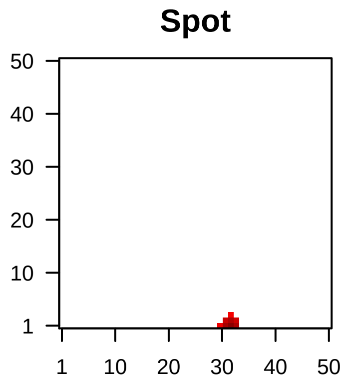
<FC> = 0.62

<shrinkage−t> = 21.85

<p−value> = 0

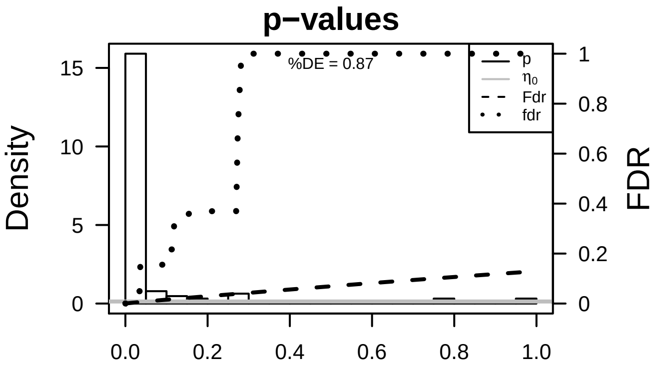
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	116071	1.29	2e−16	2e−16	32 x 1	basic leucine zipper transcription factor, ATF−like 2 [Source:H
2	3627	2.56	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
3	6373	2.89	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
4	94240	1.43	2e−16	2e−16	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
5	2633	1.78	2e−16	2e−16	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HG
6	115362	2.11	2e−16	2e−16	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
7	10964	1.66	2e−16	2e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
8	3433	1.44	2e−16	2e−16	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
9	8519	1.48	2e−16	2e−16	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
10	10581	1.32	2e−16	2e−16	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC
11	10410	1.38	2e−16	2e−16	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
12	400759	1.35	2e−16	2e−16	32 x 1	guanylate binding protein 1, interferon−inducible pseudogene
13	4321	1.34	2e−16	2e−16	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
14	10346	1.51	2e−16	2e−16	32 x 1	tripartite motif containing 22 [Source:HGNC Symbol;Acc:163
15	7453	1.9	2e−16	2e−16	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
16	9636	1.2	1e−15	2e−14	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
17	6737	1.19	3e−15	8e−13	32 x 1	tripartite motif containing 21 [Source:HGNC Symbol;Acc:113
18	55601	1.13	7e−14	8e−13	32 x 1	DEAD (Asp−Glu−Ala−Asp) box polypeptide 60 [Source:HGN
19	3431	1.12	1e−13	4e−12	32 x 1	SP110 nuclear body protein [Source:HGNC Symbol;Acc:540
20	3136	1.1	3e−13	6e−12	32 x 1	



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	56.04	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	42.93	NULL	29 / 51	BP	type I interferon signaling pathway
3	40.16	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
4	37.79	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	37.04	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
6	35.34	NULL	31 / 123	BP	defense response to virus
7	35.31	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
8	34.81	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
9	32.68	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
10	32.09	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
11	31.95	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	31.81	NULL	27 / 109	BP	response to virus
13	30.14	NULL	13 / 31	BP	negative regulation of viral genome replication
14	30.02	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
15	26.79	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
16	26.55	NULL	2 / 10	BP	positive regulation of cAMP−mediated signaling
17	25.9	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
18	25.81	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
19	24.74	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
20	24.6	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
21	23.86	NULL	2 / 12	BP	positive regulation of leukocyte chemotaxis
22	23.38	NULL	34 / 204	BP	cytokine−mediated signaling pathway
23	22.64	NULL	47 / 572	Disease	GUDJ_psoriasis up
24	22.59	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
25	22.47	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
26	21.96	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
27	21.89	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
28	21.35	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
29	21.1	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
30	21.02	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
31	20.96	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
32	20.96	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
33	19.78	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
34	19.51	NULL	2 / 17	BP	positive regulation of release of sequestered calcium ion into cytos
35	19.38	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
36	19.08	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
37	19.04	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
38	18.17	NULL	5 / 18	BP	response to interferon−gamma
39	18.13	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
40	17.9	NULL	4 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_UP

GW_016

Local Summary

%DE = 0.64

metagenes = 11

genes = 221

genes in genesets = 218

genes with fdr < 0.1 = 123 (111 + / 12 −)

genes with fdr < 0.05 = 117 (106 + / 11 −)

genes with fdr < 0.01 = 96 (91 + / 5 −)

<r> metagenes = 0.96

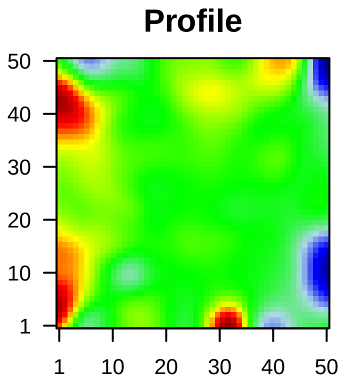
<r> genes = 0.34

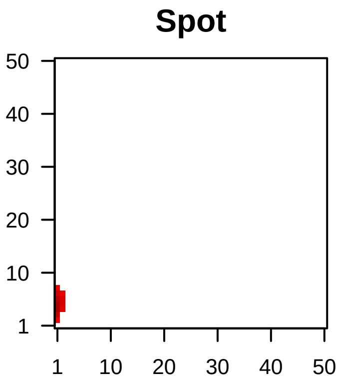
<FC> = 0.4

<shrinkage−t> = 14.14

<p−value> = 0

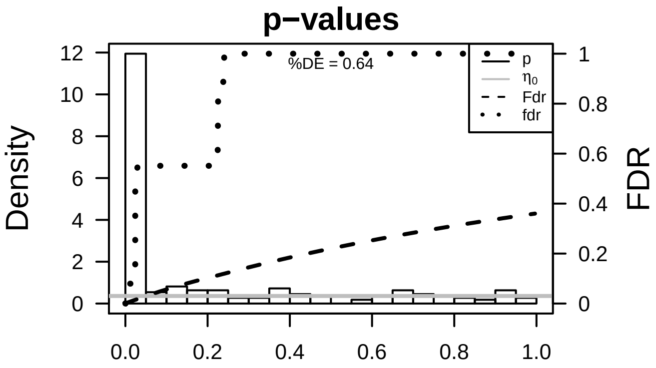
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	87	1.39	2e−16	8e−16	1 x 3	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	8412	1.32	2e−16	8e−16	1 x 5	breast cancer anti−estrogen resistance 3 [Source:HGNC Sym
3	55450	1.67	2e−16	8e−16	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
4	857	1.39	2e−16	8e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
5	8727	1.53	2e−16	8e−16	1 x 5	catenin (cadherin−associated protein), alpha−like 1 [Source:H
6	131566	1.87	2e−16	8e−16	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
7	1687	1.54	2e−16	8e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
8	27122	1.42	2e−16	8e−16	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
9	84141	1.37	2e−16	8e−16	1 x 2	eva−1 homolog A (C. elegans) [Source:HGNC Symbol;Acc:2
10	10644	1.23	2e−16	8e−16	1 x 6	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
11	3486	−1.75	2e−16	8e−16	1 x 6	insulin−like growth factor binding protein 3 [Source:HGNC Sy
12	4319	1.47	2e−16	8e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
13	4489	1.35	2e−16	8e−16	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
14	4502	1.76	2e−16	8e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
15	644314	1.28	2e−16	8e−16	1 x 5	
16	4907	1.37	2e−16	8e−16	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
17	5328	1.24	2e−16	8e−16	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
18	5054	1.88	2e−16	8e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
19	7045	1.55	2e−16	8e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
20	3371	1.27	2e−16	8e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.07	NULL	3 / 10	BP	cellular response to zinc ion
2	16.94	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNwt_expression_N_down
3	16.94	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNmut_expression_N_up
4	16.55	NULL	4 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
5	14.86	NULL	4 / 16	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
6	14.26	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
7	13.97	NULL	2 / 10	BP	regulation of receptor activity
8	13.97	NULL	2 / 10	GSEA C2	BIOCARTA_FIBRINOLYSIS_PATHWAY
9	13.8	NULL	2 / 14	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN
10	13.59	NULL	3 / 15	BP	negative regulation of growth
11	13.55	NULL	3 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
12	13.42	NULL	5 / 12	BP	hemidesmosome assembly
13	13.21	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
14	12.76	NULL	2 / 11	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
15	12.74	NULL	2 / 7	MMML CGS	MACIEJ_MMML 13
16	12.66	NULL	32 / 242	BP	extracellular matrix organization
17	11.98	NULL	3 / 14	GSEA C2	PROVENZANI_METASTASIS_DN
18	11.79	NULL	3 / 15	BP	fibrinolysis
19	11.6	NULL	2 / 13	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
20	11.55	NULL	2 / 10	BP	negative regulation of blood coagulation
21	11.53	NULL	3 / 15	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
22	11.3	NULL	3 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
23	11.21	NULL	3 / 16	GSEA C2	KIM_WT1_TARGETS_UP
24	11.2	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
25	11.12	NULL	2 / 14	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
26	11.12	NULL	2 / 14	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
27	11.12	NULL	2 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
28	11.12	NULL	2 / 14	GSEA C2	ACEVEDO_LIVER_CANCER_DN
29	11.01	NULL	36 / 403	BP	cell adhesion
30	10.92	NULL	2 / 15	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP
31	10.68	NULL	4 / 37	Glio	Christensen_hypomethylated_in_ependymoma
32	10.67	NULL	6 / 35	Glio	Colman_survival_associated
33	10.35	NULL	4 / 43	CC	platelet alpha granule lumen
34	10.31	NULL	2 / 16	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
35	10.23	NULL	1 / 7	GSEA C2	GAUTSCHI_SRC_SIGNALING
36	10.23	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
37	10.03	NULL	2 / 14	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
38	9.82	NULL	1 / 2	miRNA target	miR−124a
39	9.8	NULL	4 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C8
40	9.73	NULL	4 / 11	Glio	Phillips MES up vs Prolif & PN

GW_016

Local Summary

%DE = 0.73

metagenes = 24

genes = 268

genes in genesets = 265

genes with fdr < 0.1 = 152 (126 + / 26 −)

genes with fdr < 0.05 = 131 (108 + / 23 −)

genes with fdr < 0.01 = 113 (93 + / 20 −)

<r> metagenes = 0.97

<r> genes = 0.34

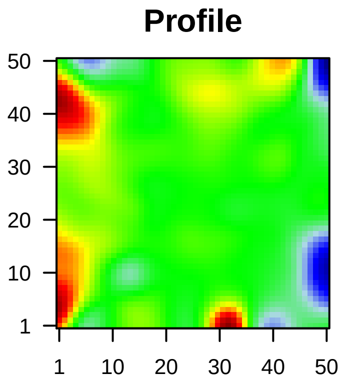
<FC> = 0.29

<shrinkage−t> = 10.15

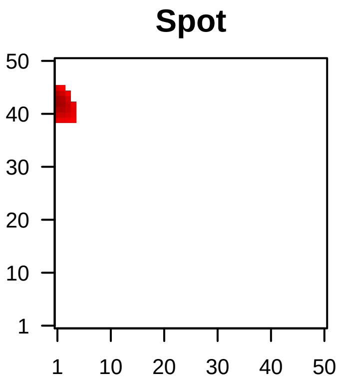
<p−value> = 0

<fdr> = 0.47

Profile



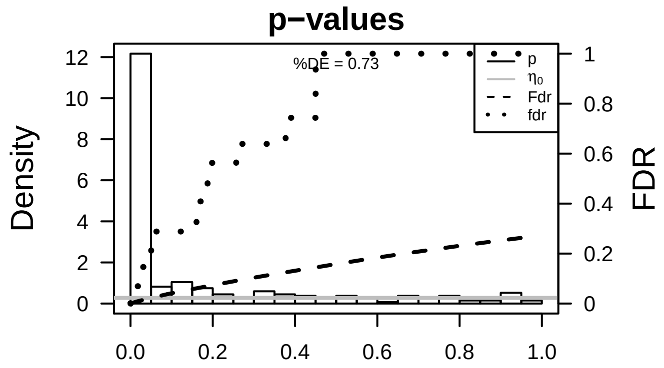
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	244	1.47	2e−16	2e−15	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
2	51200	2.05	2e−16	2e−15	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
3	1515	1.32	2e−16	2e−15	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
4	3306	1.27	2e−16	2e−15	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
5	3489	1.74	2e−16	2e−15	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
6	26499	1.58	2e−16	2e−15	1 x 42	pleckstrin 2 [Source:HGNC Symbol;Acc:19238]
7	8601	1.31	2e−16	2e−15	1 x 44	regulator of G−protein signaling 20 [Source:HGNC Symbol;A
8	6274	1.21	1e−15	8e−14	1 x 43	S100 calcium binding protein A3 [Source:HGNC Symbol;Acc:
9	3861	1.1	2e−15	1e−11	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
10	780851	1.11	2e−13	1e−11	2 x 39	small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
11	780854	1.1	3e−13	3e−11	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
12	1308	1.07	1e−12	3e−11	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
13	3775	−1.07	1e−12	5e−11	1 x 43	potassium channel, subfamily K, member 1 [Source:HGNC S
14	8821	1.06	2e−12	6e−11	3 x 41	inositol polyphosphate−4−phosphatase, type II, 105kDa [Sou
15	5744	1.05	3e−12	2e−10	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
16	7039	1.04	6e−12	3e−10	1 x 44	transforming growth factor, alpha [Source:HGNC Symbol;Acc
17	29984	1.02	1e−11	5e−10	1 x 45	ras homolog family member D [Source:HGNC Symbol;Acc:67
18	8140	1	3e−11	5e−10	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
19	10848	1	3e−11	5e−10	1 x 44	protein phosphatase 1, regulatory subunit 13 like [Source:HG
20	55214	−0.99	4e−11	5e−10	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	13.67	NULL	5 / 12	BP	hemidesmosome assembly
2	12.1	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
3	11.75	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
4	9.98	NULL	1 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
5	9.92	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
6	9.65	NULL	3 / 15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
7	9.05	NULL	2 / 2	miRNA target	miR−199a*
8	8.71	NULL	1 / 12	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP
9	8.54	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
10	8.52	NULL	2 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
11	8.09	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	7.99	NULL	1 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
13	7.94	NULL	3 / 16	GSEA C2	LEONARD_HYPOXIA
14	7.83	NULL	9 / 76	BP	epidermis development
15	7.81	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
16	7.79	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
17	7.77	NULL	3 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
18	7.68	NULL	1 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
19	7.68	NULL	1 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
20	7.61	NULL	53 / 572	Disease	GUDJ_psoriasis up
21	7.41	NULL	2 / 11	BP	positive regulation of positive chemotaxis
22	7.38	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA
23	7.37	NULL	2 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
24	7.37	NULL	2 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
25	7.35	NULL	1 / 12	GSEA C2	SANCHEZ_MDM2_TARGETS
26	7.24	NULL	7 / 70	BP	cell junction assembly
27	7.21	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
28	7.15	NULL	1 / 17	MF	carboxypeptidase activity
29	7.15	NULL	1 / 17	MF	metallocarboxypeptidase activity
30	7.06	NULL	3 / 10	GSEA C2	XU_RESPONSE_TO_TRETINOIN_DN
31	7.05	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
32	7.02	NULL	1 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
33	6.94	NULL	2 / 10	GSEA C2	RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
34	6.94	NULL	2 / 10	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
35	6.91	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
36	6.78	NULL	3 / 12	GSEA C2	MIZUKAMI_HYPOXIA_UP
37	6.76	NULL	3 / 15	Pathw Act	GUSTAFSON_PI3K_DN
38	6.72	NULL	8 / 82	MF	structural constituent of cytoskeleton
39	6.63	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
40	6.49	NULL	3 / 15	GSEA C2	NAKAMURA_METASTASIS_MODEL_DN

GW_016

Local Summary

%DE = 0.76

metagenes = 22

genes = 275

genes in genesets = 272

genes with fdr < 0.1 = 145 (8 + / 137 −)

genes with fdr < 0.05 = 131 (6 + / 125 −)

genes with fdr < 0.01 = 97 (4 + / 93 −)

<r> metagenes = 0.9

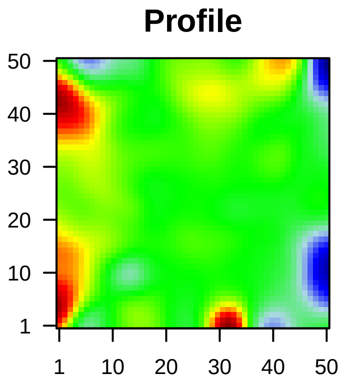
<r> genes = 0.25

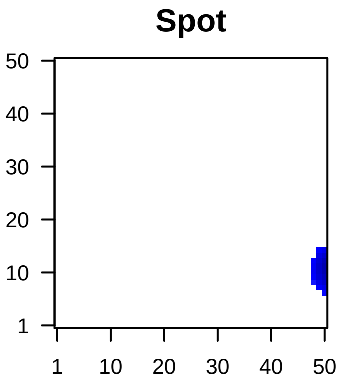
<FC> = −0.33

<shrinkage−t> = −11.48

<p−value> = 0

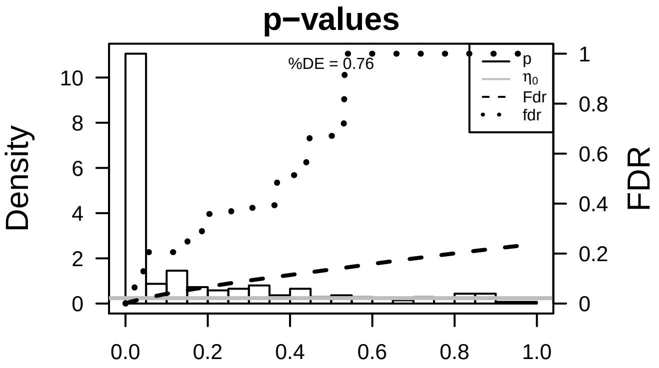
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2568	−1.59	2e−16	5e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
2	51316	−1.31	2e−16	5e−15	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
3	6192	−2.04	2e−16	5e−15	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
4	92747	−1.14	3e−14	1e−12	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
5	8857	−1.14	4e−14	1e−10	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
6	3169	−1.06	2e−12	1e−10	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
7	9071	−1.05	3e−12	2e−10	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
8	79085	−1.04	6e−12	4e−10	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr
9	140032	−1.02	1e−11	4e−10	49 x 10	ribosomal protein S4, Y−linked 2 [Source:HGNC Symbol;Acc
10	10232	−1.01	2e−11	2e−09	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
11	6920	−0.99	5e−11	2e−09	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
12	1359	−0.98	8e−11	7e−09	50 x 7	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc
13	1363	−0.95	2e−10	7e−09	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
14	9086	−0.95	3e−10	3e−08	48 x 9	eukaryotic translation initiation factor 1A, Y−linked [Source:H
15	10551	−0.92	1e−09	3e−08	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
16	260293	−0.91	1e−09	3e−08	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
17	148170	−0.91	1e−09	5e−08	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HG
18	8543	−0.9	2e−09	1e−07	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
19	92304	−0.88	5e−09	1e−07	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
20	7033	−0.87	6e−09	5e−06	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.6	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−19.92	NULL	2 / 7	MMML CGS	MACIEJ_MMML 5
3	−18.51	NULL	2 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	−15.15	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
5	−13.87	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
6	−13.84	NULL	4 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
7	−13.74	NULL	4 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
8	−13.52	NULL	1 / 7	GSEA C2	LEE_NAIVE_T_LYMPHOCYTE
9	−13.13	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
10	−13.08	NULL	2 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	−12.55	NULL	1 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
12	−11.75	NULL	1 / 9	GSEA C2	KEGG_RIBOSOME
13	−11.75	NULL	1 / 9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
14	−11.75	NULL	1 / 9	GSEA C2	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_
15	−11.75	NULL	1 / 9	GSEA C2	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_
16	−11.75	NULL	1 / 9	GSEA C2	REACTOME_PEPTIDE_CHAIN_ELONGATION
17	−11.75	NULL	1 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
18	−11.75	NULL	1 / 9	GSEA C2	REACTOME_VIRAL_MRNA_TRANSLATION
19	−11.23	NULL	3 / 34	Chr	Chr Y
20	−11.16	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
21	−11.15	NULL	2 / 20	Lymphoma	ROSOLOWSKI_red UP
22	−11.13	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
23	−11.08	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
24	−11.08	NULL	1 / 10	GSEA C2	REACTOME_TRANSLATION
25	−10.98	NULL	4 / 17	MF	metallocarboxypeptidase activity
26	−10.96	NULL	2 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
27	−10.5	NULL	1 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
28	−10	NULL	1 / 12	GSEA C2	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND
29	−10	NULL	1 / 12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
30	−10	NULL	1 / 12	GSEA C2	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATI
31	−9.93	NULL	5 / 19	BP	calcium−independent cell−cell adhesion
32	−9.76	NULL	3 / 17	MF	carboxypeptidase activity
33	−9.74	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
34	−9.72	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
35	−9.7	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
36	−9.68	NULL	2 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
37	−9.64	NULL	2 / 27	MF	rRNA binding
38	−9.56	NULL	1 / 13	GSEA C2	KANG_IMMORTALIZED_BY_TERT_UP
39	−9.56	NULL	1 / 13	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP
40	−9.31	NULL	3 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION

GW_016

Local Summary

%DE = 0.87

metagenes = 10

genes = 160

genes in genesets = 159

genes with fdr < 0.1 = 120 (2 + / 118 −)

genes with fdr < 0.05 = 112 (2 + / 110 −)

genes with fdr < 0.01 = 68 (1 + / 67 −)

<r> metagenes = 0.97

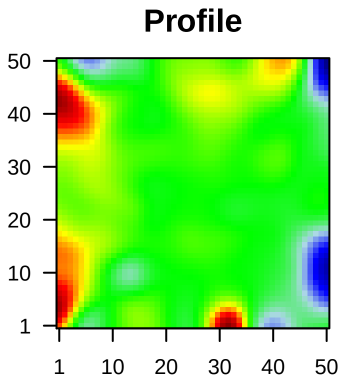
<r> genes = 0.28

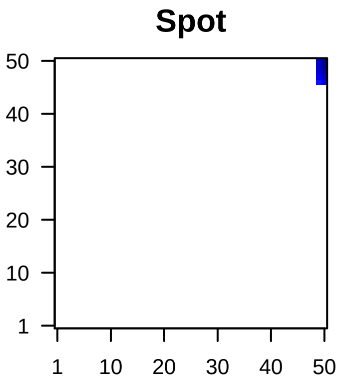
<FC> = −0.47

<shrinkage−t> = −16.48

<p−value> = 0

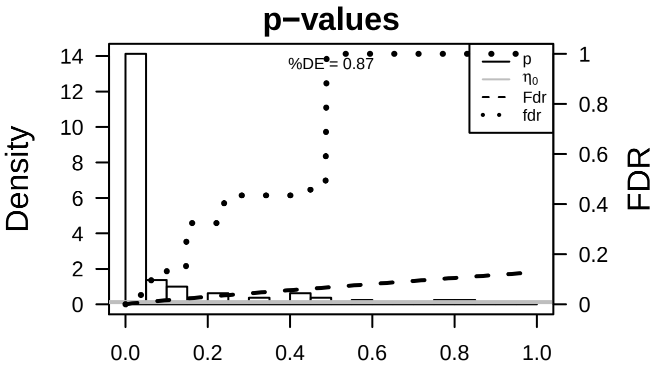
<fdr> = 0.44





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	400916	−1.29	2e−16	7e−16	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [Sou
2	9076	−1.72	2e−16	7e−16	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
3	4072	−1.82	2e−16	7e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
4	3880	−2.43	2e−16	7e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
5	59342	−1.28	2e−16	7e−16	50 x 47	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
6	11166	−1.34	2e−16	7e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
7	256764	−2.03	2e−16	7e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
8	2944	−1.14	3e−14	6e−13	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
9	4922	−1.13	5e−14	3e−12	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	26227	−1.11	2e−13	5e−12	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
11	655	−1.09	5e−13	5e−12	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
12	2946	−1.08	7e−13	1e−11	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
13	7345	−1.07	1e−12	3e−10	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
14	56977	−1.01	2e−11	3e−10	50 x 49	storkhead box 2 [Source:HGNC Symbol;Acc:25450]
15	84707	−0.99	4e−11	3e−10	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
16	3790	−0.99	5e−11	3e−10	50 x 50	potassium voltage−gated channel, delayed−rectifier, subfamil
17	200634	−0.99	6e−11	5e−09	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
18	216	−0.95	3e−10	5e−09	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
19	3866	0.93	6e−10	5e−09	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
20	154664	−0.93	7e−10	1e−08	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.69	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
2	−17.66	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
3	−15.73	NULL	3 / 11	MF	glutathione binding
4	−15.73	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
5	−14.12	NULL	5 / 20	MF	glutathione transferase activity
6	−13.48	NULL	6 / 25	BP	glutathione derivative biosynthetic process
7	−13.39	NULL	8 / 34	BP	glutathione metabolic process
8	−12.86	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
9	−12.21	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
10	−11.68	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
11	−11.62	NULL	1 / 2	miRNA target	miR−127
12	−11.19	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
13	−11.14	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
14	−10.75	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
15	−10.75	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
16	−10.71	NULL	4 / 13	BP	regulation of blood vessel size
17	−10.64	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
18	−10.6	NULL	3 / 37	CC	lateral plasma membrane
19	−10.36	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
20	−10.36	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
21	−9.81	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
22	−9.81	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
23	−9.72	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
24	−9.68	NULL	1 / 18	CC	costamere
25	−8.94	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
26	−8.92	NULL	11 / 119	BP	xenobiotic metabolic process
27	−8.85	NULL	1 / 21	BP	sarcomere organization
28	−8.61	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
29	−8.25	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
30	−7.99	NULL	1 / 15	H.Tiss	WIRTH_Telencephalon
31	−7.78	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
32	−7.59	NULL	2 / 16	GSEA C2	GOUYER_TATI_TARGETS_DN
33	−7.5	NULL	1 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
34	−7.5	NULL	1 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
35	−7.34	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
36	−7.22	NULL	1 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
37	−7.19	NULL	13 / 375	Disease	GUDJ_psoriasis down
38	−7.13	NULL	2 / 42	BP	ureteric bud development
39	−7.03	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
40	−6.99	NULL	2 / 13	BP	retinoic acid metabolic process