GW_262

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1614 (1052 + / 562 −)

genes with fdr < 0.1 = 1250 (861 + / 389 −)

genes with fdr < 0.05 = 1108 (779 + / 329 −)

genes with fdr < 0.01 = 801 (595 + / 206 −)

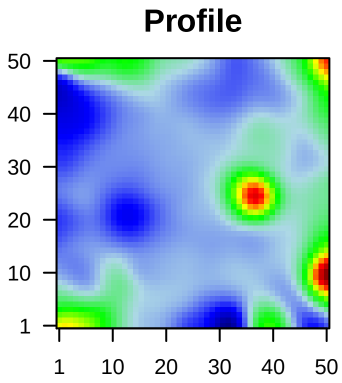
genes in genesets = 16332

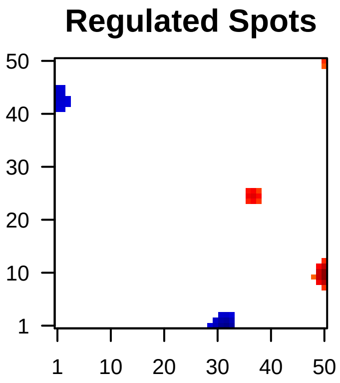
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.76	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	1.3	2e−16	2e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	10551	2.21	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	155465	1.4	2e−16	2e−14	50 x 10	anterior gradient 3 [Source:HGNC Symbol;Acc:24167]
5	57016	1.24	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	8644	1.92	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	1.67	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	216	1.57	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
9	220	1.14	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
10	218	2	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	9823	1.28	2e−16	2e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
12	25805	1.11	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
13	684	−1.21	2e−16	2e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
14	79949	1.61	2e−16	2e−14	50 x 10	pleckstrin homology domain containing, family S member 1 [
15	387695	−1.14	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
16	85016	1.11	2e−16	2e−14	50 x 25	chromosome 11 open reading frame 70 [Source:HGNC Sym
17	399949	1.38	2e−16	2e−14	37 x 25	chromosome 11 open reading frame 88 [Source:HGNC Sym
18	144809	1.44	2e−16	2e−14	45 x 8	family with sequence similarity 216, member B [Source:HGN
19	127003	1.35	2e−16	2e−14	37 x 25	chromosome 1 open reading frame 194 [Source:HGNC Sym
20	713	−1.16	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source

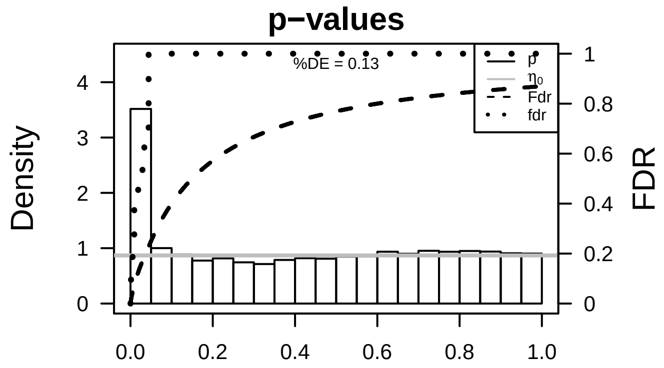
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	17.63	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	13.21	NULL	51	Glio	willscher_GBM_Verhaak−PNmut_expression_G_down
3	11.17	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
4	9.64	NULL	14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
5	9.51	NULL	1146	TF	HEBENSTREIT_low expression TF
6	9.36	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
7	9.3	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
8	8.74	NULL	9	GSEA C2	GOUYER_TATI_TARGETS_UP
9	8.64	NULL	683	CC	extracellular space
10	8.03	NULL	1182	CC	extracellular region
11	7.82	NULL	201	CC	apical plasma membrane
12	7.49	NULL	190	CC	extracellular matrix
13	7.23	NULL	64	BP	collagen catabolic process
14	7.22	NULL	85	Glio	GIEZELT_GBM_STS_down_VS_LTS
15	7.22	NULL	553	Cancer	Lembcke_Colonic Inflammation
16	7.09	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
17	7.07	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
18	6.95	NULL	242	BP	extracellular matrix organization
19	6.91	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
20	6.9	NULL	69	BP	extracellular matrix disassembly

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−11.05	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	−10.02	NULL	51	BP	type I interferon signaling pathway
3	−9.64	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	−8.79	NULL	123	BP	defense response to virus
5	−8.78	NULL	519	Chr	Chr 14
6	−8.63	NULL	60	BP	interferon−gamma−mediated signaling pathway
7	−8.56	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
8	−8.07	NULL	1720	Chr	Chr 1
9	−7.87	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	−7.82	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	−7.71	NULL	204	BP	cytokine−mediated signaling pathway
12	−7.54	NULL	15	CC	MHC class II protein complex
13	−7.47	NULL	47	BP	antigen processing and presentation
14	−7.4	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
15	−6.96	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
16	−6.76	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
17	−6.75	NULL	4	MMML CGS	MACIEJ_MMML 47
18	−6.68	NULL	31	BP	negative regulation of viral genome replication
19	−6.6	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
20	−6.49	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1


p−values

GW_262

Local Summary

%DE = 0.76

metagenes = 11

genes = 154

genes in genesets = 153

genes with fdr < 0.1 = 107 (104 + / 3 −)

genes with fdr < 0.05 = 107 (104 + / 3 −)

genes with fdr < 0.01 = 97 (95 + / 2 −)

<r> metagenes = 0.95

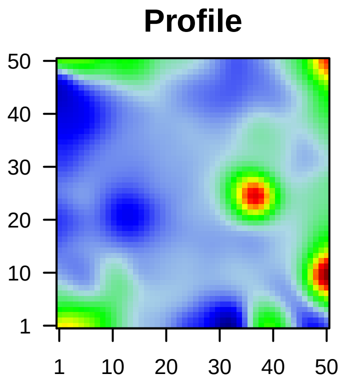
<r> genes = 0.3

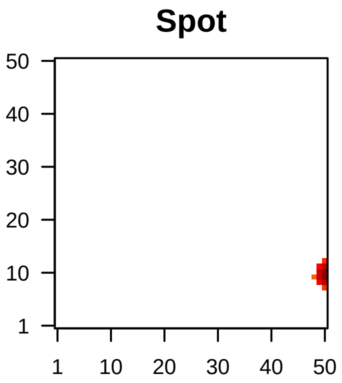
<FC> = 0.75

<shrinkage−t> = 26.29

<p−value> = 0

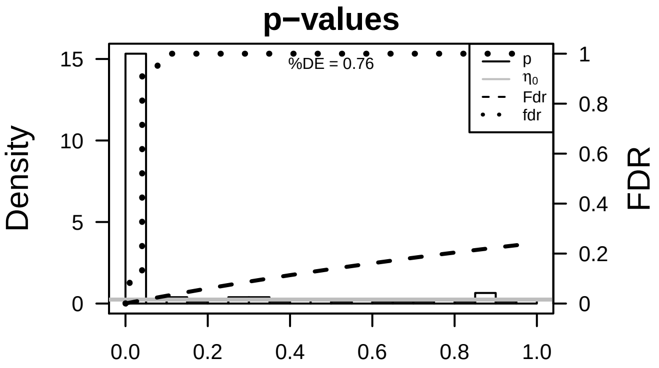
<fdr> = 0.29





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	2.21	2e−16	3e−16	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	155465	1.4	2e−16	3e−16	50 x 10	anterior gradient 3 [Source:HGNC Symbol;Acc:24167]
3	79949	1.61	2e−16	3e−16	50 x 10	pleckstrin homology domain containing, family S member 1 [S
4	92747	4.75	2e−16	3e−16	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
5	401546	1.47	2e−16	3e−16	50 x 11	chromosome 9 open reading frame 152 [Source:HGNC Symb
6	92291	1.91	2e−16	3e−16	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
7	83539	1.15	2e−16	3e−16	50 x 11	carbohydrate (N−acetylgalactosamine 4−0) sulfotransferase 9
8	54102	1.83	2e−16	3e−16	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
9	1755	1.93	2e−16	3e−16	50 x 10	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
10	8857	1.52	2e−16	3e−16	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
11	2327	1.4	2e−16	3e−16	50 x 11	flavin containing monooxygenase 2 (non−functional) [Source:
12	3169	1.78	2e−16	3e−16	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
13	2568	2.51	2e−16	3e−16	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
14	124220	1.62	2e−16	3e−16	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
15	10232	2.5	2e−16	3e−16	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
16	4477	2.96	2e−16	3e−16	50 x 11	microseminoprotein, beta− [Source:HGNC Symbol;Acc:7372]
17	94025	1.99	2e−16	3e−16	50 x 11	mucin 16, cell surface associated [Source:HGNC Symbol;Acc
18	4629	1.62	2e−16	3e−16	50 x 9	myosin, heavy chain 11, smooth muscle [Source:HGNC Syml
19	25891	1.15	2e−16	3e−16	50 x 8	peptidase domain containing associated with muscle regener
20	5284	2.31	2e−16	3e−16	50 x 10	polymeric immunoglobulin receptor [Source:HGNC Symbol;A



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	43.52	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	20.04	NULL	3 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
3	20	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
4	18.9	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
5	17.6	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
6	15.55	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
7	13.92	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
8	12.73	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
9	12.57	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
10	12.56	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
11	12.32	NULL	2 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
12	11.91	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	11.62	NULL	3 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
14	11.32	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
15	11.19	NULL	1 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
16	11.16	NULL	2 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
17	10.62	NULL	2 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
18	10.62	NULL	1 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
19	10.06	NULL	2 / 16	GSEA C2	VALK_AML_CLUSTER_9
20	9.75	NULL	2 / 11	CC	photoreceptor outer segment membrane
21	9.54	NULL	2 / 7	GSEA C2	NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
22	9.52	NULL	3 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
23	9.19	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
24	9.09	NULL	1 / 15	Cancer	LIU_PROSTATE_CANCER_DN
25	9.01	NULL	2 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
26	9	NULL	4 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
27	8.83	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
28	8.78	NULL	2 / 8	GSEA C2	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
29	8.67	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
30	8.48	NULL	3 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
31	8.22	NULL	2 / 12	MF	calcium−dependent cysteine−type endopeptidase activity
32	8.16	NULL	1 / 12	BP	retina layer formation
33	8.12	NULL	2 / 4	miRNA target	miR−204
34	8.02	NULL	1 / 10	MF	GABA−A receptor activity
35	8	NULL	5 / 61	CC	secretory granule
36	7.87	NULL	1 / 5	GSEA C2	VALK_AML_WITH_T_8_21_TRANSLOCATION
37	7.85	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
38	7.64	NULL	23 / 683	CC	extracellular space
39	7.56	NULL	1 / 11	GSEA C2	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
40	7.55	NULL	2 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT

GW_262

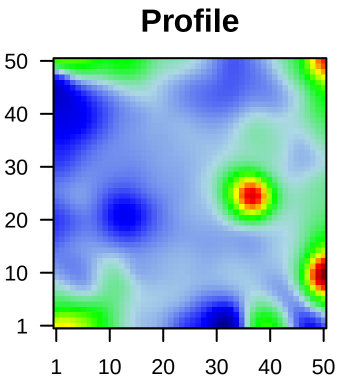
Local Summary

%DE = 0.98
metagenes = 9
genes = 103
genes in genesets = 102

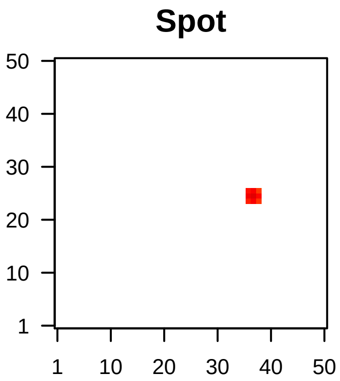
genes with fdr < 0.1 = 100 (100 + / 0 −)
genes with fdr < 0.05 = 99 (99 + / 0 −)
genes with fdr < 0.01 = 99 (99 + / 0 −)

<r> metagenes = 0.99
<r> genes = 0.36

<FC> = 0.67
<shrinkage−t> = 23.54
<p−value> = 0
<fdr> = 0.07



Profile



Spot

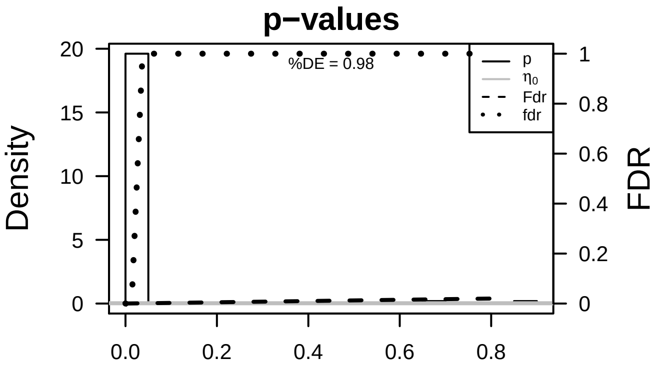
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	399949	1.38	2e−16	6e−17	37 x 25	chromosome 11 open reading frame 88 [Source:HGNC Symb
2	127003	1.35	2e−16	6e−17	37 x 25	chromosome 1 open reading frame 194 [Source:HGNC Symb
3	84688	1.44	2e−16	6e−17	37 x 25	chromosome 9 open reading frame 24 [Source:HGNC Symbo
4	83657	1.31	2e−16	6e−17	37 x 25	dynein, light chain, roadblock−type 2 [Source:HGNC Symbol;
5	222256	1.28	2e−16	6e−17	37 x 25	cadherin−related family member 3 [Source:HGNC Symbol;Ac
6	83853	1.14	2e−16	6e−17	37 x 25	rhophilin associated tail protein 1−like [Source:HGNC Symbo
7	345895	1.13	2e−16	6e−17	37 x 25	radial spoke head 4 homolog A (Chlamydomonas) [Source:H
8	89765	1.24	2e−16	6e−17	37 x 25	radial spoke head 1 homolog (Chlamydomonas) [Source:HG
9	83538	1.11	2e−16	6e−17	37 x 25	tetratricopeptide repeat domain 25 [Source:HGNC Symbol;Ac
10	2302	1.09	7e−16	8e−16	37 x 25	forkhead box J1 [Source:HGNC Symbol;Acc:3816]
11	83659	1.09	9e−16	1e−15	37 x 25	tektin 1 [Source:HGNC Symbol;Acc:15534]
12	128602	1.08	1e−15	1e−14	37 x 25	chromosome 20 open reading frame 85 [Source:HGNC Symb
13	9518	1.05	6e−15	1e−14	37 x 26	growth differentiation factor 15 [Source:HGNC Symbol;Acc:30
14	284434	1.05	1e−14	6e−14	36 x 24	NACHT and WD repeat domain containing 1 [Source:HGNC
15	80217	1.02	4e−14	6e−14	37 x 25	WD repeat domain 96 [Source:HGNC Symbol;Acc:26684]
16	83661	1.01	7e−14	4e−13	37 x 25	membrane−spanning 4−domains, subfamily A, member 8 [So
17	138255	0.98	4e−13	4e−13	37 x 25	chromosome 9 open reading frame 135 [Source:HGNC Symb
18	27019	0.98	4e−13	2e−12	37 x 25	dynein, axonemal, intermediate chain 1 [Source:HGNC Symb
19	8382	0.96	1e−12	2e−12	36 x 24	NME/NM23 family member 5 [Source:HGNC Symbol;Acc:785
20	55259	0.95	2e−12	4e−12	37 x 25	cancer susceptibility candidate 1 [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	46.53	NULL	25 / 51	Glio	willscher_GBM_Verhaak−PNmut_expression_G_down
2	12.84	NULL	3 / 7	GSEA C2	NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
3	11.25	NULL	7 / 76	Glio	GIEZELT_GBM_STSwt_up_VS_LTSwt
4	10.55	NULL	4 / 30	CC	axoneme
5	9.71	NULL	2 / 9	GSEA C2	KORKOLA_CHORIOCARCINOMA_DN
6	9.27	NULL	8 / 102	CC	cilium
7	9.09	NULL	2 / 10	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_DN
8	9.09	NULL	2 / 10	GSEA C2	KORKOLA_SEMINOMA_DN
9	8.57	NULL	2 / 11	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_DN
10	8.11	NULL	1 / 7	GSEA C2	GENTILE_UV_LOW_DOSE_DN
11	8.11	NULL	1 / 7	GSEA C2	GENTILE_UV_LOW_DOSE_UP
12	7.96	NULL	1 / 6	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_CISPLATIN
13	7.86	NULL	6 / 85	Glio	GIEZELT_GBM_STS_down_VS_LTS
14	7.74	NULL	3 / 20	CC	dynein complex
15	7.69	NULL	1 / 2	miRNA target	miR−433
16	7.59	NULL	1 / 6	GSEA C2	WEBER_METHYLATED_HCP_IN_FIBROBLAST_UP
17	7.58	NULL	1 / 13	BP	cellular protein complex assembly
18	7.44	NULL	1 / 8	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
19	7.26	NULL	3 / 32	BP	cell projection organization
20	7.07	NULL	2 / 32	CC	motile cilium
21	6.9	NULL	2 / 8	GSEA C2	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
22	6.9	NULL	1 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP
23	6.89	NULL	1 / 13	CC	cytoplasmic dynein complex
24	6.84	NULL	2 / 16	BP	ciliary or bacterial−type flagellar motility
25	6.46	NULL	1 / 10	GSEA C2	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
26	6.46	NULL	1 / 10	GSEA C2	CHUANG_OXIDATIVE_STRESS_RESPONSE_UP
27	6.29	NULL	1 / 11	BP	activation of Rho GTPase activity
28	6.2	NULL	1 / 9	GSEA C2	KORKOLA_TERATOMA_DN
29	6.08	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_UP
30	5.85	NULL	1 / 10	BP	GTP biosynthetic process
31	5.85	NULL	1 / 10	BP	negative regulation of intrinsic apoptotic signaling pathway in respo
32	5.74	NULL	4 / 75	BP	cilium assembly
33	5.72	NULL	1 / 10	GSEA C2	PATTERSON_DOCETAXEL_RESISTANCE
34	5.62	NULL	1 / 14	GSEA C2	NOUZOVA_METHYLATED_IN_APL
35	5.61	NULL	3 / 49	BP	spermatid development
36	5.51	NULL	1 / 11	BP	CTP biosynthetic process
37	5.51	NULL	1 / 11	BP	UTP biosynthetic process
38	5.51	NULL	1 / 11	BP	ventricular system development
39	5.37	NULL	3 / 48	BP	cilium morphogenesis
40	5.33	NULL	1 / 23	MF	alpha−tubulin binding



p−values

GW_262

Local Summary

%DE = 0.72

metagenes = 2

genes = 94

genes in genesets = 93

genes with fdr < 0.1 = 61 (60 + / 1 −)

genes with fdr < 0.05 = 57 (57 + / 0 −)

genes with fdr < 0.01 = 50 (50 + / 0 −)

<r> metagenes = 1

<r> genes = 0.34

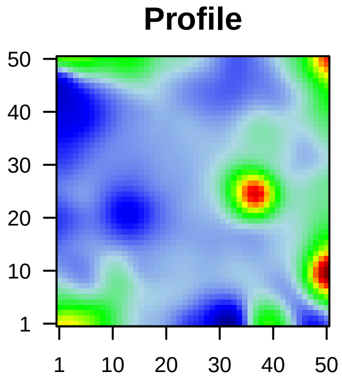
<FC> = 0.53

<shrinkage−t> = 18.56

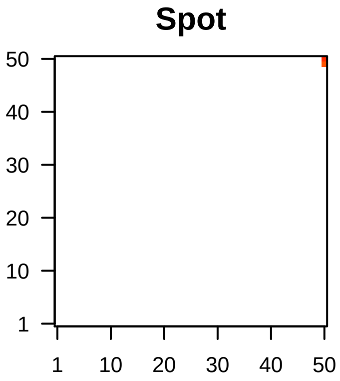
<p−value> = 0

<fdr> = 0.37

Profile



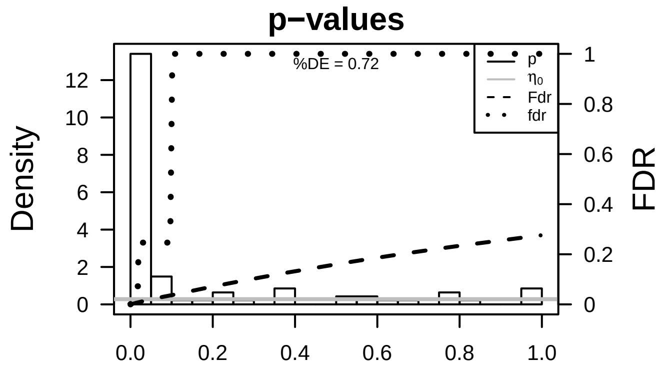
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.76	2e−16	6e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	1.3	2e−16	6e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	216	1.57	2e−16	6e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	26047	1.61	2e−16	6e−16	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
5	4072	1.11	2e−16	6e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
6	3880	1.88	2e−16	6e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
7	4922	2.32	2e−16	6e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
8	8544	1.11	2e−16	6e−16	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;A
9	11166	1.36	2e−16	6e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
10	7348	2.06	2e−16	6e−16	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
11	4915	1.08	1e−15	8e−13	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
12	56548	1.03	3e−14	2e−12	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7 [
13	256764	1	1e−13	5e−12	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
14	54578	0.98	3e−13	3e−11	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
15	89894	0.95	2e−12	3e−11	50 x 50	transmembrane protein 116 [Source:HGNC Symbol;Acc:250
16	214	0.95	3e−12	8e−11	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC S
17	2222	0.93	6e−12	9e−11	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
18	23321	0.92	1e−11	9e−11	50 x 50	tripartite motif containing 2 [Source:HGNC Symbol;Acc:1597
19	83959	0.91	1e−11	3e−10	50 x 50	solute carrier family 4, sodium borate transporter, member 11
20	1780	0.9	2e−11	1e−09	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.86	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	23.21	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	18.98	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
4	17.29	NULL	3 / 13	BP	regulation of blood vessel size
5	16.03	NULL	1 / 2	miRNA target	miR−127
6	15.16	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
7	14.39	NULL	1 / 11	Glio	neurons_glio
8	14.2	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
9	14.2	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
10	13.53	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
11	12.85	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
12	12.25	NULL	2 / 12	BP	cellular aldehyde metabolic process
13	12.11	NULL	1 / 12	GSEA C2	DAZARD_RESPONSE_TO_UV_SCC_UP
14	11.95	NULL	1 / 15	MF	neuropeptide hormone activity
15	11.58	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
16	11.04	NULL	1 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
17	11.04	NULL	1 / 14	GSEA C2	LOPEZ_EPITHELIOID_MESOTHELIOMA
18	10.96	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
19	10.96	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
20	10.47	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
21	10.26	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
22	10.26	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
23	10.01	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
24	9.94	NULL	1 / 11	CC	axolemma
25	9.61	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
26	9.6	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
27	9.6	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
28	9.42	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
29	9.41	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
30	9.3	NULL	3 / 48	BP	cerebral cortex development
31	9.24	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
32	9.24	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
33	9.18	NULL	1 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
34	9.15	NULL	11 / 119	BP	xenobiotic metabolic process
35	9.01	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
36	8.96	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
37	8.77	NULL	1 / 5	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_
38	8.71	NULL	2 / 23	BP	stem cell differentiation
39	8.61	NULL	1 / 18	CC	costamere
40	8.58	NULL	1 / 14	BP	transmission of nerve impulse

GW_262

Local Summary

%DE = 0.97

metagenes = 12

genes = 150

genes in genesets = 147

genes with fdr < 0.1 = 139 (13 + / 126 −)

genes with fdr < 0.05 = 121 (8 + / 113 −)

genes with fdr < 0.01 = 97 (6 + / 91 −)

<r> metagenes = 0.98

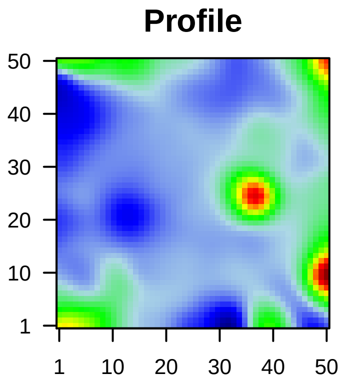
<r> genes = 0.39

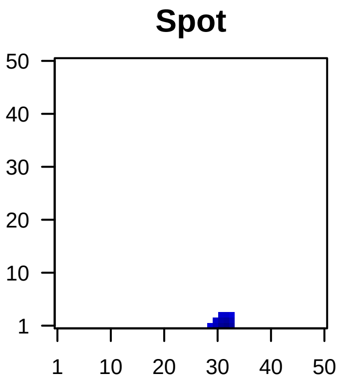
<FC> = −0.36

<shrinkage−t> = −12.79

<p−value> = 0

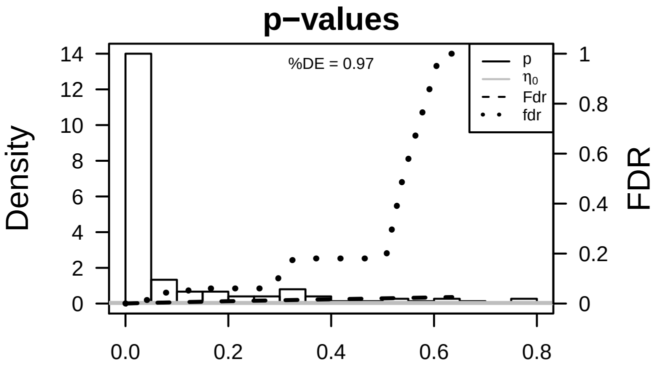
<fdr> = 0.41





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−1.21	2e−16	1e−16	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	629	1.19	2e−16	1e−16	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
3	3627	−1.59	2e−16	1e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
4	51191	−1.14	2e−16	1e−16	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
5	10561	−1.22	2e−16	1e−16	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
6	10964	−1.29	2e−16	1e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
7	2537	−1.27	2e−16	1e−16	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
8	9636	−1.46	2e−16	1e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
9	6289	1.67	2e−16	1e−16	29 x 1	serum amyloid A2 [Source:HGNC Symbol;Acc:10514]
10	2633	−1.09	9e−16	3e−13	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HG
11	3433	−1.02	5e−14	5e−12	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
12	6291	0.95	2e−12	5e−12	29 x 1	serum amyloid A4, constitutive [Source:HGNC Symbol;Acc:1
13	94240	−0.95	2e−12	7e−11	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
14	55008	−0.91	2e−11	2e−10	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
15	6890	−0.88	6e−11	5e−10	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
16	7453	−0.85	4e−10	5e−10	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
17	3665	−0.84	4e−10	5e−10	32 x 1	interferon regulatory factor 7 [Source:HGNC Symbol;Acc:612
18	91543	−0.84	4e−10	5e−10	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:
19	3134	−0.84	4e−10	2e−09	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
20	6772	−0.83	9e−10	4e−09	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−56.47	NULL	13 / 16	GSEA C2 MOSERLE_IFNA_RESPONSE
2	−47.72	NULL	29 / 51	BP type I interferon signaling pathway
3	−46.21	NULL	11 / 16	GSEA C2 EINAV_INTERFERON_SIGNATURE_IN_CANCER
4	−43.47	NULL	9 / 10	GSEA C2 BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	−41.34	NULL	6 / 8	GSEA C2 ROETH_TERT_TARGETS_UP
6	−40.32	NULL	10 / 13	GSEA C2 BOWIE_RESPONSE_TO_TAMOXIFEN
7	−38.19	NULL	11 / 16	GSEA C2 ZHANG_INTERFERON_RESPONSE
8	−36.31	NULL	11 / 16	GSEA C2 UROSEVIC_RESPONSE_TO_IMIQUIMOD
9	−35.89	NULL	31 / 123	BP defense response to virus
10	−35.45	NULL	3 / 4	GSEA C2 KRASNOSELSKAYA_ILF3_TARGETS_UP
11	−34.93	NULL	3 / 5	GSEA C2 KIM_LRRC3B_TARGETS
12	−33.23	NULL	8 / 10	GSEA C2 GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
13	−33.18	NULL	8 / 11	GSEA C2 BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	−32.54	NULL	27 / 109	BP response to virus
15	−31.22	NULL	7 / 16	GSEA C2 MAHADEVAN_RESPONSE_TO_MP470_UP
16	−30.28	NULL	13 / 31	BP negative regulation of viral genome replication
17	−29.53	NULL	4 / 12	GSEA C2 ZHU_CMV_8_HR_UP
18	−29.23	NULL	6 / 14	GSEA C2 RADAEVA_RESPONSE_TO_IFNA1_UP
19	−28.37	NULL	5 / 16	GSEA C2 FARMER_BREAST_CANCER_CLUSTER_1
20	−28.33	NULL	3 / 4	MMML CGS MACIEJ_MMML 47
21	−28.12	NULL	6 / 12	GSEA C2 TSAI_DNAJB4_TARGETS_UP
22	−27.33	NULL	34 / 204	BP cytokine−mediated signaling pathway
23	−25.46	NULL	4 / 16	GSEA C2 SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
24	−24.45	NULL	4 / 15	GSEA C2 BECKER_TAMOXIFEN_RESISTANCE_UP
25	−24.29	NULL	6 / 16	GSEA C2 XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
26	−23.88	NULL	33 / 274	Lymphoma SPANG_IL21 DN
27	−23.88	NULL	4 / 14	GSEA C2 TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
28	−23.82	NULL	3 / 9	GSEA C2 DER_IFN_ALPHA_RESPONSE_UP
29	−23.82	NULL	3 / 9	GSEA C2 DER_IFN_GAMMA_RESPONSE_UP
30	−23.08	NULL	6 / 6	Lymphoma DAVE_MHCCII BL DN
31	−22.48	NULL	6 / 14	GSEA C2 XU_AKT1_TARGETS_6HR
32	−22.34	NULL	4 / 10	GSEA C2 DAUER_STAT3_TARGETS_DN
33	−21.82	NULL	16 / 60	BP interferon−gamma−mediated signaling pathway
34	−21.63	NULL	6 / 14	Glio Donson−immune cell intra signaling−associated with LTS in HGA
35	−19.85	NULL	5 / 14	GSEA C2 TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
36	−19.7	NULL	49 / 572	Disease GUDJ_psoriasis up
37	−19.31	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
38	−19.26	NULL	4 / 14	GSEA C2 SANA_TNF_SIGNALING_UP
39	−18.87	NULL	7 / 10	CC MHC class I protein complex
40	−18.84	NULL	4 / 10	GSEA C2 GRANDVAUX_IRF3_TARGETS_UP

GW_262

Local Summary

%DE = 0.67

metagenes = 12

genes = 162

genes in genesets = 161

genes with fdr < 0.1 = 59 (10 + / 49 −)

genes with fdr < 0.05 = 59 (10 + / 49 −)

genes with fdr < 0.01 = 42 (9 + / 33 −)

<r> metagenes = 0.98

<r> genes = 0.39

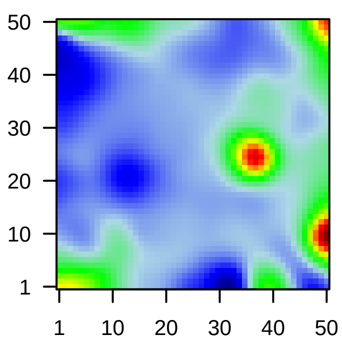
<FC> = −0.19

<shrinkage−t> = −6.52

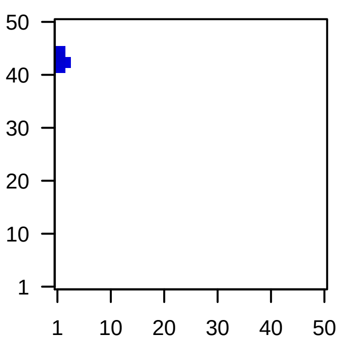
<p−value> = 0

<fdr> = 0.61

Profile



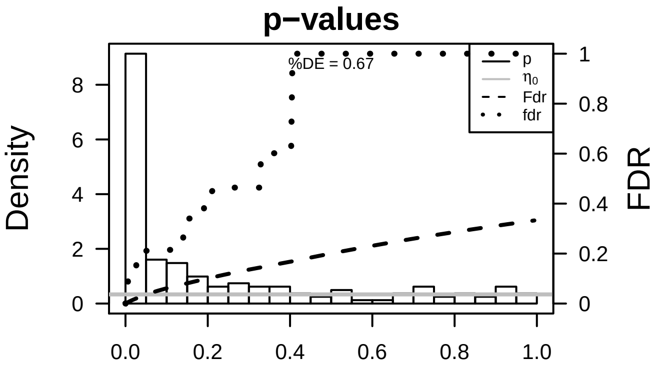
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2167	−1.4	2e−16	4e−15	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
2	3429	−1.08	2e−16	4e−15	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
3	50805	−1.1	2e−16	4e−15	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
4	3306	−1.08	1e−15	1e−12	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
5	80115	−1.03	2e−14	3e−12	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
6	116211	−1.01	8e−14	4e−10	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
7	2152	0.92	8e−12	8e−10	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
8	9935	−0.9	2e−11	8e−10	1 x 45	v−maf avian musculoaponeurotic fibrosarcoma oncogene hor
9	55214	−0.89	4e−11	9e−10	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
10	51200	−0.89	5e−11	9e−09	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
11	374918	−0.86	2e−10	1e−07	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093
12	83882	−0.79	5e−09	1e−07	1 x 43	tetraspanin 10 [Source:HGNC Symbol;Acc:29942]
13	6665	−0.79	5e−09	2e−07	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Sym
14	29984	−0.77	1e−08	2e−06	1 x 45	ras homolog family member D [Source:HGNC Symbol;Acc:67
15	3489	−0.74	5e−08	2e−06	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
16	143686	0.72	1e−07	2e−06	1 x 44	sestrin 3 [Source:HGNC Symbol;Acc:23060]
17	404203	−0.71	2e−07	2e−06	1 x 43	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
18	3949	0.7	2e−07	2e−06	1 x 41	low density lipoprotein receptor [Source:HGNC Symbol;Acc:6
19	8900	0.7	2e−07	6e−05	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
20	3038	0.64	2e−06	6e−05	1 x 43	hyaluronan synthase 3 [Source:HGNC Symbol;Acc:4820]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.81	NULL	1 / 4	MMML CGS	MACIEJ_MMML 47
2	−11.14	NULL	1 / 10	BP	white fat cell differentiation
3	−10.65	NULL	1 / 8	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_UP
4	−10.56	NULL	1 / 11	GSEA C2	REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_
5	−10.07	NULL	1 / 12	MF	fatty acid binding
6	−9.95	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
7	−9.63	NULL	1 / 13	BP	cellular response to lithium ion
8	−8.92	NULL	2 / 9	GSEA C2	KORKOLA_CORRELATED_WITH_POU5F1
9	−8.9	NULL	1 / 15	BP	triglyceride catabolic process
10	−8.71	NULL	3 / 25	BP	brown fat cell differentiation
11	−8.64	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
12	−8.62	NULL	1 / 10	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_5_DN
13	−8.5	NULL	2 / 15	MF	cytoskeletal adaptor activity
14	−8.39	NULL	2 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
15	−8.39	NULL	2 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
16	−8.3	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
17	−8.12	NULL	1 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
18	−8.08	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
19	−7.9	NULL	2 / 10	GSEA C2	RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
20	−7.9	NULL	2 / 10	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
21	−7.84	NULL	3 / 21	BP	filopodium assembly
22	−7.79	NULL	1 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
23	−7.15	NULL	1 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
24	−7.13	NULL	1 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
25	−6.87	NULL	1 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
26	−6.79	NULL	2 / 16	Glio	VERHAAK_MES subtype
27	−6.7	NULL	1 / 25	BP	cytokine production
28	−6.63	NULL	1 / 16	CC	male germ cell nucleus
29	−6.52	NULL	1 / 15	CC	vesicle membrane
30	−6.33	NULL	1 / 12	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP
31	−6.19	NULL	2 / 11	BP	response to metal ion
32	−6.06	NULL	1 / 6	miRNA target starBase	hsa−miR−126
33	−5.85	NULL	1 / 20	CC	synaptonemal complex
34	−5.82	NULL	1 / 7	MMML CGS	MACIEJ_MMML 13
35	−5.81	NULL	1 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
36	−5.71	NULL	2 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
37	−5.69	NULL	1 / 15	GSEA C2	WANG_RECURRENT_LIVER_CANCER_DN
38	−5.58	NULL	1 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
39	−5.58	NULL	1 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
40	−5.58	NULL	1 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3