GW_172

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1664 (941 + / 723 −)

genes with fdr < 0.1 = 1396 (815 + / 581 −)

genes with fdr < 0.05 = 1208 (729 + / 479 −)

genes with fdr < 0.01 = 927 (596 + / 331 −)

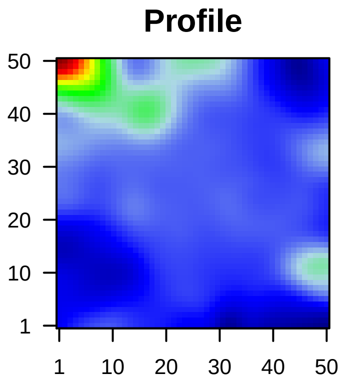
genes in genesets = 16332

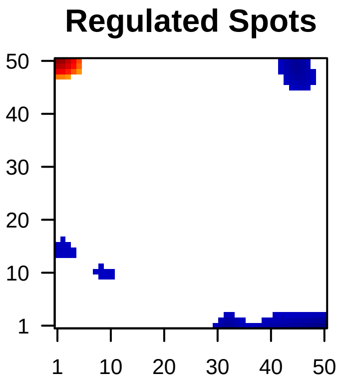
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.96	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	79852	1.5	2e−16	2e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	83543	1.49	2e−16	2e−14	5 x 50	allograft inflammatory factor 1−like [Source:HGNC Symbol;Ac
4	57016	1.46	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.33	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
6	220	1.59	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
7	353322	1.73	2e−16	2e−14	6 x 48	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:29593]
8	306	1.25	2e−16	2e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
9	360	1.46	2e−16	2e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
10	8424	1.62	2e−16	2e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
11	387695	2.11	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
12	84419	1.33	2e−16	2e−14	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
13	260436	3.92	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
14	394263	2.19	2e−16	2e−14	3 x 50	
15	29923	1.68	2e−16	2e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Syr
16	375791	1.95	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
17	810	1.5	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
18	875	−1.35	2e−16	2e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
19	6347	−1.31	2e−16	2e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
20	978	1.29	2e−16	2e−14	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]

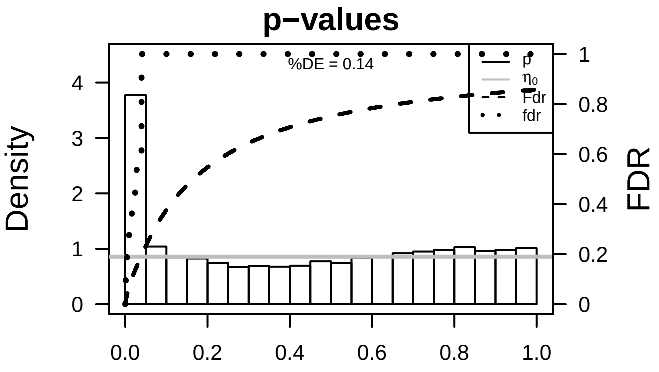
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	36.35	NULL	135	H.Tiss	WIRTH_Mucosa
2	12.55	NULL	21	CC	cornified envelope
3	10.64	NULL	53	BP	keratinocyte differentiation
4	10.62	NULL	19	BP	peptide cross−linking
5	9.97	NULL	76	BP	epidermis development
6	9.85	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	9.61	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
8	8.99	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
9	8.95	NULL	42	BP	keratinization
10	8.76	NULL	16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
11	8.26	NULL	44	CC	keratin filament
12	8.24	NULL	14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
13	8.05	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	8.04	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
15	7.85	NULL	572	Disease	GUDJ_psoriasis up
16	7.52	NULL	13	BP	negative regulation of peptidase activity
17	7.33	NULL	618	Chr	Chr 4
18	7.16	NULL	82	CC	intermediate filament
19	7.01	NULL	186	MF	structural molecule activity
20	6.91	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−11.94	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−11.94	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−10.62	NULL	51	BP	type I interferon signaling pathway
4	−10.24	NULL	312	BP	immune response
5	−9.61	NULL	204	BP	cytokine−mediated signaling pathway
6	−8.57	NULL	370	BP	mitotic cell cycle
7	−8.55	NULL	417	H.Tiss	WIRTH_Immune system
8	−8.51	NULL	60	BP	interferon−gamma−mediated signaling pathway
9	−8.44	NULL	57	Glio	developing astrocytes
10	−8.08	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	−8.05	NULL	123	BP	defense response to virus
12	−7.57	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
13	−7.55	NULL	149	BP	DNA replication
14	−7.42	NULL	74	BP	regulation of immune response
15	−7.36	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
16	−7.33	NULL	530	Cancer	Lembcke_Normal vs Adenoma
17	−7.29	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
18	−7.26	NULL	949	CC	nucleoplasm
19	−7.23	NULL	717	Chr	Chr 16
20	−6.96	NULL	47	BP	antigen processing and presentation



GW_172

Local Summary

%DE = 0.98

metagenes = 18

genes = 251

genes in genesets = 244

genes with fdr < 0.1 = 236 (225 + / 11 −)

genes with fdr < 0.05 = 236 (225 + / 11 −)

genes with fdr < 0.01 = 222 (214 + / 8 −)

<r> metagenes = 0.97

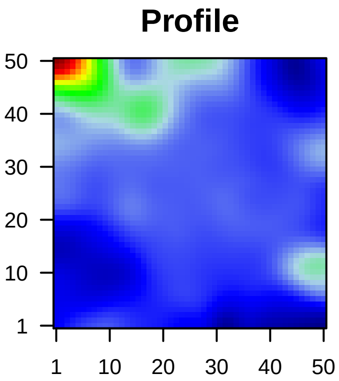
<r> genes = 0.46

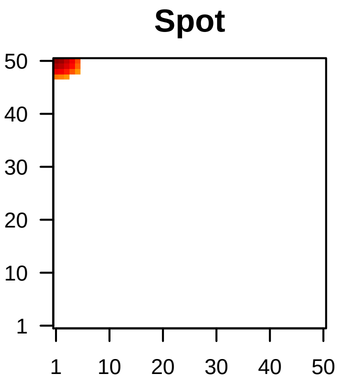
<FC> = 1.04

<shrinkage−t> = 36.49

<p−value> = 0

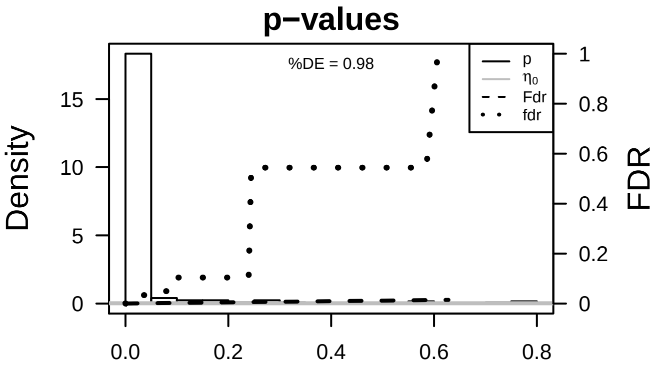
<fdr> = 0.11





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.96	2e−16	1e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	79852	1.5	2e−16	1e−17	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	83543	1.49	2e−16	1e−17	5 x 50	allograft inflammatory factor 1−like [Source:HGNC Symbol;Ac
4	57016	1.46	2e−16	1e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.33	2e−16	1e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	360	1.46	2e−16	1e−17	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	8424	1.62	2e−16	1e−17	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
8	387695	2.11	2e−16	1e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	84419	1.33	2e−16	1e−17	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
10	394263	2.19	2e−16	1e−17	3 x 50	
11	375791	1.95	2e−16	1e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
12	810	1.5	2e−16	1e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
13	1048	1.35	2e−16	1e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
14	4680	1.97	2e−16	1e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
15	1087	1.33	2e−16	1e−17	4 x 50	carcinoembryonic antigen−related cell adhesion molecule 7 [
16	22802	2.51	2e−16	1e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	9022	1.78	2e−16	1e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
18	84518	1.77	2e−16	1e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
19	54544	2.23	2e−16	1e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
20	49860	3.4	2e−16	1e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	62.48	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
2	24.98	NULL	17 / 21	CC	cornified envelope
3	23.81	NULL	95 / 572	Disease	GUDJ_psoriasis up
4	19.65	NULL	19 / 42	BP	keratinization
5	18.18	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
6	18.11	NULL	10 / 19	BP	peptide cross−linking
7	18.06	NULL	22 / 53	BP	keratinocyte differentiation
8	17.55	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	16.66	NULL	6 / 13	BP	negative regulation of peptidase activity
10	16.64	NULL	10 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
11	16.58	NULL	21 / 76	BP	epidermis development
12	13.31	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	12.8	NULL	8 / 44	CC	keratin filament
14	12.47	NULL	15 / 122	MF	serine−type endopeptidase activity
15	11.8	NULL	8 / 38	BP	epithelial cell differentiation
16	11.74	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
17	11.31	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
18	11.06	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
19	10.88	NULL	56 / 1182	CC	extracellular region
20	10.67	NULL	5 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
21	10.64	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
22	10.35	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
23	10.34	NULL	21 / 186	MF	structural molecule activity
24	9.96	NULL	7 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
25	9.81	NULL	6 / 29	BP	regulation of proteolysis
26	9.69	NULL	11 / 82	CC	intermediate filament
27	9.65	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
28	9.64	NULL	5 / 21	CC	desmosome
29	9.64	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
30	9.01	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
31	8.99	NULL	9 / 52	BP	negative regulation of endopeptidase activity
32	8.72	NULL	4 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
33	8.61	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
34	8.56	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
35	8.42	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
36	8.29	NULL	8 / 53	MF	serine−type peptidase activity
37	8.27	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
38	8.18	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
39	7.88	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
40	7.82	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP

GW_172

Local Summary

%DE = 0.79

metagenes = 50

genes = 723

genes in genesets = 691

genes with fdr < 0.1 = 411 (17 + / 394 −)

genes with fdr < 0.05 = 313 (11 + / 302 −)

genes with fdr < 0.01 = 212 (7 + / 205 −)

<r> metagenes = 0.75

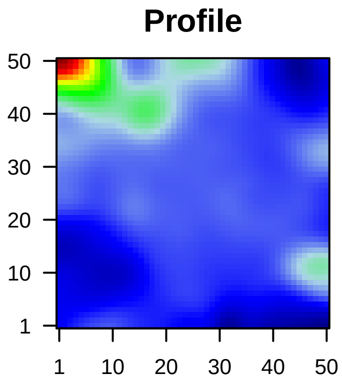
<r> genes = 0.32

<FC> = −0.33

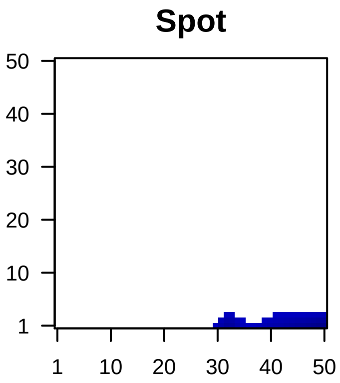
<shrinkage−t> = −11.47

<p−value> = 0

<fdr> = 0.58



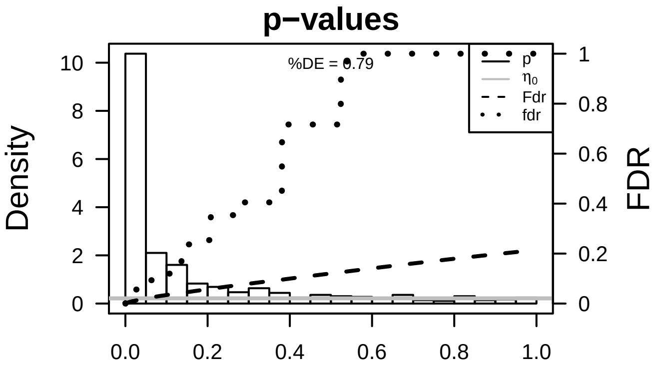
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	3.92	2e−16	4e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	629	−1.62	2e−16	4e−15	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
3	3627	−1.42	2e−16	4e−15	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
4	10866	−1.34	2e−16	4e−15	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
5	51191	−1.31	2e−16	4e−15	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
6	3106	−1.27	2e−16	4e−15	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
7	3123	−1.68	2e−16	4e−15	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
8	3433	−1.31	2e−16	4e−15	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
9	10537	−1.51	2e−16	4e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
10	7453	−1.24	4e−16	8e−12	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
11	3134	−1.14	1e−13	8e−12	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
12	3430	−1.13	1e−13	1e−11	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
13	4321	1.12	2e−13	4e−11	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
14	6890	−1.1	5e−13	3e−10	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
15	6355	−1.06	3e−12	3e−10	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
16	3127	−1.06	4e−12	3e−10	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
17	9636	−1.05	5e−12	4e−10	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
18	3122	−0.97	8e−12	9e−10	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
19	8519	−1.03	1e−11	5e−09	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
20	10581	−0.92	6e−11	5e−09	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC S



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−30.55	NULL	35 / 51	BP	type I interferon signaling pathway
2	−24.4	NULL	14 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
3	−24	NULL	93 / 312	BP	immune response
4	−23.61	NULL	58 / 204	BP	cytokine−mediated signaling pathway
5	−23.35	NULL	10 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
6	−22.11	NULL	30 / 60	BP	interferon−gamma−mediated signaling pathway
7	−21.77	NULL	14 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	−21.77	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
9	−21.7	NULL	14 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
10	−21.3	NULL	13 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
11	−21.25	NULL	25 / 47	BP	antigen processing and presentation
12	−21.05	NULL	14 / 15	CC	MHC class II protein complex
13	−20.66	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
14	−19.54	NULL	41 / 123	BP	defense response to virus
15	−19.49	NULL	15 / 32	CC	ER to Golgi transport vesicle membrane
16	−18.3	NULL	17 / 52	Chr	Chr HSCHR6_MHC_QBL
17	−18.16	NULL	7 / 10	CC	MHC class I protein complex
18	−18.06	NULL	126 / 417	H.Tiss	WIRTH_Immune system
19	−17.71	NULL	11 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
20	−17.69	NULL	30 / 74	BP	regulation of immune response
21	−17.6	NULL	33 / 109	BP	response to virus
22	−17.54	NULL	11 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
23	−17.03	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
24	−16.91	NULL	14 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
25	−16.87	NULL	17 / 31	BP	negative regulation of viral genome replication
26	−16.09	NULL	5 / 12	GSEA C2	ZHU_CMV_8_HR_UP
27	−15.49	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
28	−15.33	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
29	−14.99	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
30	−14.98	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
31	−14.97	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
32	−14.68	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
33	−13.7	NULL	5 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
34	−13.65	NULL	9 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
35	−13.51	NULL	23 / 60	BP	T cell costimulation
36	−13.48	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
37	−13.3	NULL	52 / 274	Lymphoma	SPANG_IL21 DN
38	−13.11	NULL	7 / 18	MF	peptide antigen binding
39	−12.81	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
40	−12.76	NULL	17 / 74	BP	antigen processing and presentation of exogenous peptide antigen

GW_172

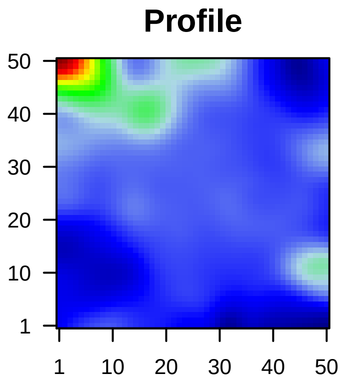
Local Summary

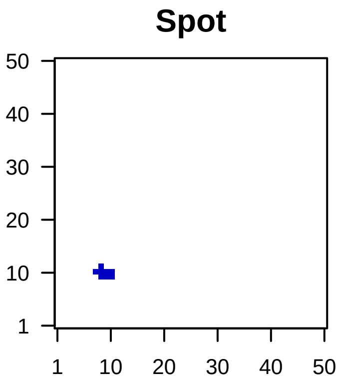
%DE = 0.55
metagenes = 8
genes = 83
genes in genesets = 83

genes with fdr < 0.1 = 21 (0 + / 21 −)
genes with fdr < 0.05 = 19 (0 + / 19 −)
genes with fdr < 0.01 = 1 (0 + / 1 −)

<r> metagenes = 0.97
<r> genes = 0.34

<FC> = −0.22
<shrinkage−t> = −7.55
<p−value> = 0.07
<fdr> = 0.77





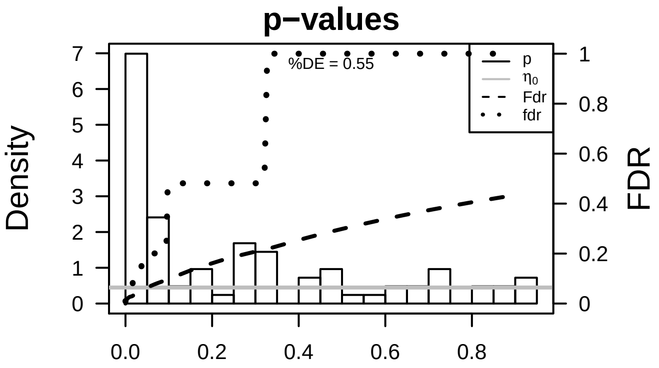
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2026	−1.03	2e−11	0.009	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
2	65980	−0.56	2e−04	0.018	9 x 10	bromodomain containing 9 [Source:HGNC Symbol;Acc:2581
3	692227	−0.51	9e−04	0.018	8 x 11	small nucleolar RNA, C/D box 104 [Source:HGNC Symbol;Ac
4	55653	−0.49	1e−03	0.018	9 x 10	breast carcinoma amplified sequence 4 [Source:HGNC Sym
5	10362	−0.47	2e−03	0.018	9 x 11	high mobility group 20B [Source:HGNC Symbol;Acc:5002]
6	51477	−0.47	2e−03	0.036	10 x 10	inositol−3−phosphate synthase 1 [Source:HGNC Symbol;Acc
7	100170841	−0.45	3e−03	0.036	10 x 10	chromosome 17 open reading frame 96 [Source:HGNC Sym
8	79412	−0.41	8e−03	0.036	9 x 10	kringle containing transmembrane protein 2 [Source:HGNC S
9	80755	−0.4	8e−03	0.036	8 x 11	alanyl−tRNA synthetase domain containing 1 [Source:HGNC
10	6621	−0.4	9e−03	0.036	8 x 11	small nuclear RNA activating complex, polypeptide 4, 190kD
11	5442	−0.4	9e−03	0.036	8 x 11	polymerase (RNA) mitochondrial (DNA directed) [Source:HG
12	93643	−0.39	1e−02	0.036	9 x 11	tight junction associated protein 1 (peripheral) [Source:HGNC
13	26121	−0.38	1e−02	0.036	8 x 11	pre−mRNA processing factor 31 [Source:HGNC Symbol;Acc:
14	11000	−0.38	1e−02	0.036	9 x 11	solute carrier family 27 (fatty acid transporter), member 3 [So
15	9170	−0.38	1e−02	0.036	8 x 11	lysophosphatidic acid receptor 2 [Source:HGNC Symbol;Acc:
16	54965	−0.38	1e−02	0.036	9 x 12	phosphatidylinositol glycan anchor biosynthesis, class X [Sou
17	8189	−0.37	1e−02	0.036	8 x 11	symplekin [Source:HGNC Symbol;Acc:22935]
18	22913	−0.37	1e−02	0.036	8 x 11	RALY heterogeneous nuclear ribonucleoprotein [Source:HGN
19	100101267	−0.37	2e−02	0.036	11 x 11	POM121 transmembrane nucleoporin C [Source:HGNC Sym
20	29927	−0.37	2e−02	0.064	9 x 10	Sec61 alpha 1 subunit (S. cerevisiae) [Source:HGNC Symbol

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.39	NULL	1 / 13	GSEA C2	REACTOME_GLYCOLYSIS
2	−12.9	NULL	1 / 14	GSEA C2	TOMIDA_METASTASIS_DN
3	−12.46	NULL	1 / 15	GSEA C2	MOOTHA_GLYCOLYSIS
4	−12.46	NULL	1 / 15	GSEA C2	REACTOME_GLUCONEOGENESIS
5	−12.05	NULL	1 / 16	CC	photoreceptor inner segment
6	−12.05	NULL	1 / 16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
7	−12.05	NULL	1 / 16	GSEA C2	MOOTHA_GLUCONEOGENESIS
8	−12.05	NULL	1 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
9	−9.26	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
10	−8.24	NULL	2 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
11	−8.24	NULL	2 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
12	−8.24	NULL	2 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
13	−8.01	NULL	1 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
14	−8.01	NULL	1 / 5	GSEA C2	CHEN_HOXA5_TARGETS_6HR_DN
15	−7.79	NULL	1 / 37	CC	perikaryon
16	−7.58	NULL	2 / 13	GSEA C2	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
17	−7.58	NULL	1 / 39	BP	gluconeogenesis
18	−7.58	NULL	1 / 39	BP	glycolysis
19	−7.29	NULL	2 / 14	GSEA C2	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
20	−7.29	NULL	2 / 14	GSEA C2	REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
21	−7.04	NULL	2 / 15	GSEA C2	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
22	−7	NULL	1 / 6	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
23	−6.8	NULL	2 / 16	BP	preassembly of GPI anchor in ER membrane
24	−6.71	NULL	2 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
25	−6.58	NULL	2 / 27	CC	MLL1 complex
26	−6.49	NULL	1 / 16	MF	histone acetyl−lysine binding
27	−6.34	NULL	2 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
28	−6.3	NULL	1 / 12	GSEA C2	HOSHIDA_LIVER_CANCER_SURVIVAL_UP
29	−6.24	NULL	1 / 8	GSEA C2	OSAWA_TNF_TARGETS
30	−6.15	NULL	1 / 9	GSEA C2	REACTOME_RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL_
31	−6	NULL	4 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
32	−5.83	NULL	2 / 12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
33	−5.82	NULL	1 / 10	GSEA C2	REACTOME_TRANSCRIPTION
34	−5.8	NULL	2 / 16	GSEA C2	COLLIS_PRKDC_SUBSTRATES
35	−5.77	NULL	2 / 13	CC	STAGA complex
36	−5.64	NULL	2 / 15	GSEA C2	OLSSON_E2F3_TARGETS_DN
37	−5.63	NULL	1 / 8	GSEA C2	BIOCARTA_STRESS_PATHWAY
38	−5.58	NULL	1 / 15	GSEA C2	KEGG_INOSITOL_PHOSPHATE_METABOLISM
39	−5.56	NULL	1 / 10	BP	positive regulation of Rho protein signal transduction
40	−5.56	NULL	1 / 10	GSEA C2	BIOCARTA_AKAP13_PATHWAY



GW_172

Local Summary

%DE = 0.75

metagenes = 12

genes = 117

genes in genesets = 117

genes with fdr < 0.1 = 65 (0 + / 65 −)

genes with fdr < 0.05 = 42 (0 + / 42 −)

genes with fdr < 0.01 = 17 (0 + / 17 −)

<r> metagenes = 0.98

<r> genes = 0.31

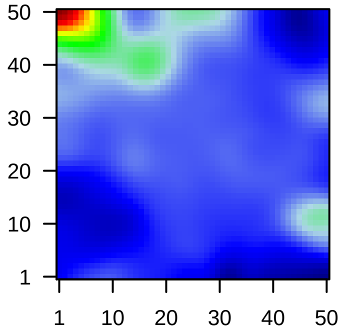
<FC> = −0.28

<shrinkage−t> = −9.97

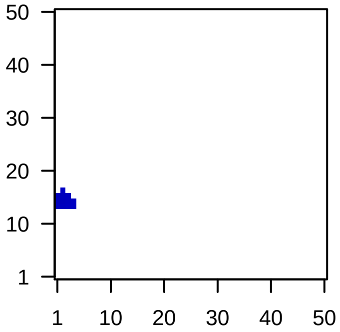
<p−value> = 0.03

<fdr> = 0.68

Profile



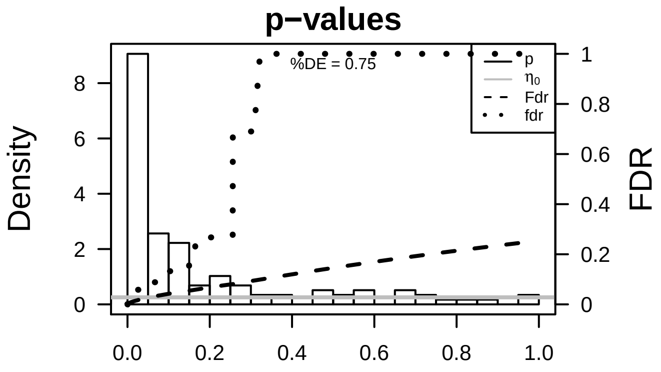
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	991	−0.79	2e−07	1e−05	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
2	4728	−0.76	6e−07	2e−05	2 x 17	NADH dehydrogenase (ubiquinone) Fe−S protein 8, 23kDa (
3	83596	−0.74	1e−06	2e−04	3 x 16	BCL2−like 12 (proline rich) [Source:HGNC Symbol;Acc:1378
4	3326	−0.68	6e−06	3e−04	1 x 14	heat shock protein 90kDa alpha (cytosolic), class B member
5	8772	−0.65	2e−05	3e−04	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
6	3217	−0.64	3e−05	1e−03	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
7	4141	−0.61	7e−05	2e−03	4 x 14	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:689
8	131076	−0.58	1e−04	2e−03	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
9	10963	−0.57	2e−04	2e−03	1 x 16	stress−induced−phosphoprotein 1 [Source:HGNC Symbol;Ac
10	220064	−0.55	3e−04	2e−03	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
11	2030	−0.54	4e−04	2e−03	1 x 14	solute carrier family 29 (equilibrative nucleoside transporter),
12	283643	−0.53	5e−04	2e−03	2 x 17	chromosome 14 open reading frame 80 [Source:HGNC Sym
13	11004	−0.53	5e−04	2e−03	2 x 16	kinesin family member 2C [Source:HGNC Symbol;Acc:6393]
14	10598	−0.52	6e−04	2e−03	1 x 14	AHA1, activator of heat shock 90kDa protein ATPase homolo
15	23246	−0.52	6e−04	2e−03	1 x 16	block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
16	203068	−0.52	7e−04	6e−03	3 x 15	tubulin, beta class I [Source:HGNC Symbol;Acc:20778]
17	6535	−0.51	9e−04	9e−03	1 x 16	solute carrier family 6 (neurotransmitter transporter), member
18	5690	−0.49	1e−03	2e−02	1 x 15	proteasome (prosome, macropain) subunit, beta type, 2 [Sou
19	5708	−0.46	3e−03	2e−02	1 x 14	proteasome (prosome, macropain) 26S subunit, non−ATPase
20	10528	−0.46	3e−03	2e−02	1 x 16	NOP56 ribonucleoprotein [Source:HGNC Symbol;Acc:15911]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.92	NULL	1 / 3	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
2	−15.92	NULL	1 / 3	GSEA C2	KEGG_PARKINSONS_DISEASE
3	−15.4	NULL	2 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
4	−15.24	NULL	3 / 15	GSEA C2	LY_AGING_MIDDLE_DN
5	−13.63	NULL	1 / 4	GSEA C2	REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETI
6	−13.63	NULL	1 / 4	GSEA C2	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
7	−13.63	NULL	1 / 4	GSEA C2	REACTOME_REGULATION_OF_INSULIN_SECRETION
8	−12.84	NULL	2 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
9	−12.4	NULL	3 / 10	GSEA C2	TOMIDA_METASTASIS_UP
10	−12.4	NULL	3 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
11	−12.24	NULL	2 / 10	GSEA C2	STEIN_ESRRA_TARGETS
12	−12.09	NULL	1 / 5	GSEA C2	REACTOME_ELECTRON_TRANSPORT_CHAIN
13	−11.4	NULL	1 / 6	GSEA C2	WAESCH_ANAPHASE_PROMOTING_COMPLEX
14	−11.22	NULL	2 / 10	GSEA C2	ZHU_CMV_24_HR_UP
15	−11.22	NULL	2 / 10	GSEA C2	ZHU_CMV_ALL_UP
16	−11.1	NULL	2 / 10	GSEA C2	KEGG_HUNTINGTONS_DISEASE
17	−10.61	NULL	2 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
18	−10.22	NULL	2 / 14	GSEA C2	STEIN_ESRRA_TARGETS_UP
19	−10.11	NULL	7 / 66	BP	positive regulation of ubiquitin−protein ligase activity involved in mi
20	−10.08	NULL	2 / 11	GSEA C2	SCIBETTA_KDM5B_TARGETS_DN
21	−9.78	NULL	7 / 70	BP	regulation of ubiquitin−protein ligase activity involved in mitotic cell
22	−9.61	NULL	2 / 12	GSEA C2	BHATTACHARYA_EMBRYONIC_STEM_CELL
23	−9.51	NULL	2 / 16	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
24	−9.51	NULL	2 / 16	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
25	−9.51	NULL	2 / 16	GSEA C2	MOOTHA_MITOCHONDRIA
26	−9.47	NULL	7 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−
27	−9.36	NULL	1 / 6	GSEA C2	GALI_TP53_TARGETS_APOPTOTIC_DN
28	−9.15	NULL	1 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
29	−8.8	NULL	1 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
30	−8.76	NULL	6 / 62	BP	negative regulation of ubiquitin−protein ligase activity involved in m
31	−8.74	NULL	2 / 10	GSEA C2	HONMA_DOCETAXEL_RESISTANCE
32	−8.65	NULL	1 / 10	BP	regulation of dendrite development
33	−8.31	NULL	1 / 10	MF	NADH dehydrogenase activity
34	−8.31	NULL	1 / 10	MF	oxidoreductase activity, acting on NAD(P)H
35	−8.31	NULL	1 / 10	GSEA C2	KEGG_ALZHEIMERS_DISEASE
36	−8.31	NULL	2 / 9	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
37	−8.21	NULL	1 / 11	BP	positive regulation of synapse maturation
38	−8.11	NULL	3 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
39	−8.01	NULL	2 / 9	GSEA C2	BIOCARTA_GLYCOLYSIS_PATHWAY
40	−7.97	NULL	4 / 43	MF	chaperone binding

GW_172

Local Summary

%DE = 0.67

metagenes = 35

genes = 391

genes in genesets = 389

genes with fdr < 0.1 = 179 (2 + / 177 −)

genes with fdr < 0.05 = 153 (2 + / 151 −)

genes with fdr < 0.01 = 92 (0 + / 92 −)

<r> metagenes = 0.92

<r> genes = 0.36

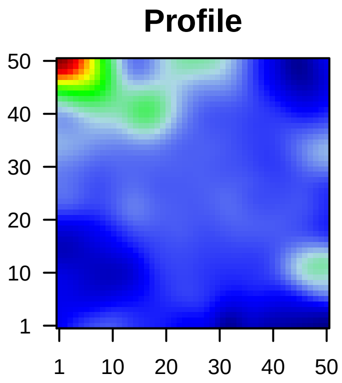
<FC> = −0.32

<shrinkage−t> = −11.05

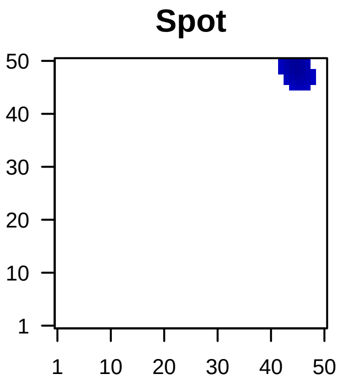
<p−value> = 0.01

<fdr> = 0.6

Profile



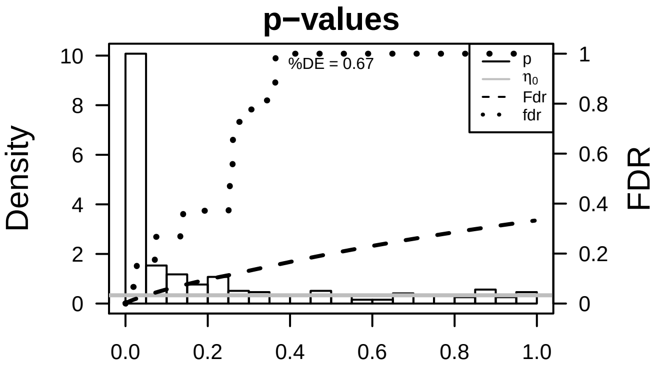
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	7083	−1.01	3e−11	2e−08	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
2	84223	−0.98	1e−10	3e−08	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
3	4171	−0.93	9e−10	3e−08	46 x 48	minichromosome maintenance complex component 2 [Source
4	113130	−0.93	9e−10	3e−08	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
5	7037	−0.86	9e−10	2e−06	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
6	10376	−0.77	5e−08	2e−06	44 x 46	tubulin, alpha 1b [Source:HGNC Symbol;Acc:18809]
7	23580	−0.83	6e−08	2e−06	47 x 45	CDC42 effector protein (Rho GTPase binding) 4 [Source:HGN
8	3992	−0.82	7e−08	2e−06	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
9	55723	−0.81	1e−07	2e−06	46 x 47	anti−silencing function 1B histone chaperone [Source:HGNC
10	5984	−0.81	1e−07	2e−06	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sym
11	8318	−0.81	1e−07	2e−06	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
12	1033	−0.8	1e−07	2e−06	43 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
13	55689	−0.8	1e−07	2e−06	46 x 50	YEATS domain containing 2 [Source:HGNC Symbol;Acc:254
14	9212	−0.8	2e−07	7e−06	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
15	1894	−0.79	2e−07	1e−05	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
16	5050	−0.78	3e−07	1e−05	47 x 45	platelet−activating factor acetylhydrolase 1b, catalytic subunit
17	10635	−0.77	4e−07	1e−05	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
18	116028	−0.77	5e−07	1e−05	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
19	29089	−0.76	6e−07	1e−05	45 x 49	ubiquitin−conjugating enzyme E2T (putative) [Source:HGNC
20	64770	−0.76	7e−07	1e−04	47 x 45	coiled−coil domain containing 14 [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−54.4	NULL	95 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−54.4	NULL	95 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−32.28	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	−29.87	NULL	26 / 57	Glio	developing astrocytes
5	−29.02	NULL	18 / 30	BP	DNA strand elongation involved in DNA replication
6	−27.56	NULL	101 / 370	BP	mitotic cell cycle
7	−27.23	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
8	−26.36	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
9	−26.32	NULL	107 / 530	Cancer	Lembcke_Normal vs Adenoma
10	−26.22	NULL	49 / 149	BP	DNA replication
11	−25.65	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	−25.15	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
13	−25.1	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
14	−24.54	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
15	−24.36	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	−24.11	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
17	−23.62	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
18	−23.57	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
19	−23.42	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	−23.16	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
21	−22.97	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
22	−22.87	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
23	−22.74	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
24	−22.48	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
25	−20.55	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
26	−20.35	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
27	−20.31	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
28	−20.3	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
29	−20.29	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
30	−19.87	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
31	−19.59	NULL	55 / 232	BP	mitosis
32	−19.42	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
33	−19.42	NULL	12 / 22	BP	DNA replication initiation
34	−19.16	NULL	10 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
35	−19	NULL	7 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
36	−18.99	NULL	8 / 16	GSEA C2	BENPORATH_PROLIFERATION
37	−18.85	NULL	13 / 18	BP	spindle organization
38	−18.82	NULL	8 / 16	GSEA C2	LY_AGING_PREMATURE_DN
39	−18.75	NULL	12 / 21	BP	telomere maintenance via semi−conservative replication
40	−18.29	NULL	11 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER