GW_127

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1500 (919 + / 581 −)

genes with fdr < 0.1 = 1232 (792 + / 440 −)

genes with fdr < 0.05 = 997 (671 + / 326 −)

genes with fdr < 0.01 = 720 (513 + / 207 −)

genes in genesets = 16332

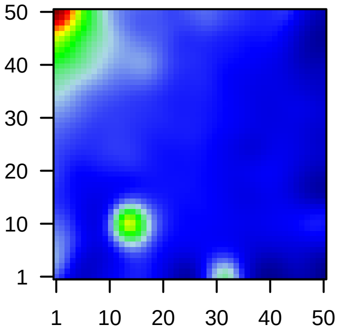
<FC> = 0

<shrinkage−t> = 0

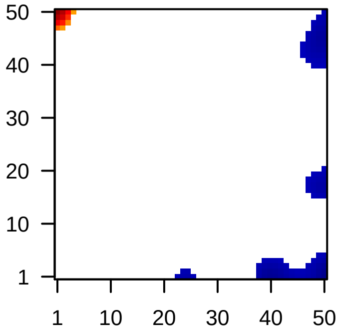
<p−value> = 0.11

<fdr> = 0.88

Profile



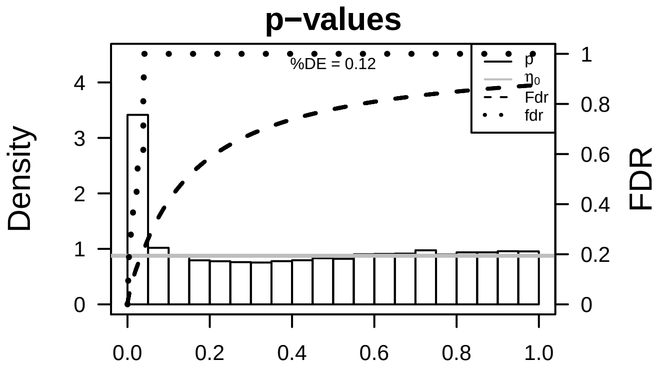
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.16	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	58	−1.15	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	57016	1.32	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	55107	−1.24	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
5	80117	1.02	2e−16	2e−14	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:2
6	10409	1.28	2e−16	2e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
7	618	1.29	2e−16	2e−14	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
8	387695	1.28	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	84419	1.02	2e−16	2e−14	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
10	260436	−1.1	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
11	375791	1.71	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
12	810	0.92	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
13	55450	1.05	2e−16	2e−14	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
14	92291	1.02	2e−16	2e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
15	84290	1.03	2e−16	2e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	414062	−1.42	2e−16	2e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
17	9560	−1.32	2e−16	2e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
18	8900	1.93	2e−16	2e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
19	978	1.02	2e−16	2e−14	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
20	1048	1.15	2e−16	2e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	29.45	NULL	135	H.Tiss	WIRTH_Mucosa
2	20.75	NULL	572	Disease	GUDJ_psoriasis up
3	13.17	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	12.07	NULL	21	CC	cornified envelope
5	11.4	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	11.33	NULL	76	BP	epidermis development
7	10.96	NULL	519	Chr	Chr 14
8	10.8	NULL	19	BP	peptide cross−linking
9	10.79	NULL	51	BP	type I interferon signaling pathway
10	10.24	NULL	53	BP	keratinocyte differentiation
11	9.89	NULL	31	BP	negative regulation of viral genome replication
12	9.25	NULL	699	Chr	Chr 5
13	9.1	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	9.06	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
15	9	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
16	8.95	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
17	8.91	NULL	42	BP	keratinization
18	8.7	NULL	12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
19	8.6	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
20	8.04	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
Underexpressed					
1	−7.31	NULL	534	Chr	Chr 8
2	−7.07	NULL	15	CC	MHC class II protein complex
3	−6.38	NULL	36	BP	muscle filament sliding
4	−6.22	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
5	−5.28	NULL	127	H.Tiss	WIRTH_Muscle
6	−5.02	NULL	232	Chr	Chr 18
7	−4.82	NULL	7	MMML CGS	MACIEJ_MMML 13
8	−4.62	NULL	16	H.Tiss	WIRTH_Hippocampus
9	−4.57	NULL	187	Chr	Chr 21
10	−4.43	NULL	12	CC	myosin filament
11	−4.4	NULL	10	BP	cellular response to zinc ion
12	−4.39	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
13	−4.29	NULL	15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
14	−4.26	NULL	43	MF	chemokine activity
15	−4.02	NULL	1574	BP	transcription, DNA−templated
16	−3.98	NULL	1720	Chr	Chr 1
17	−3.86	NULL	1749	MF	DNA binding
18	−3.77	NULL	6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
19	−3.69	NULL	36	BP	neutrophil chemotaxis
20	−3.68	NULL	426	Lymphoma	SPANG_CD40 6hrs DN

GW_127

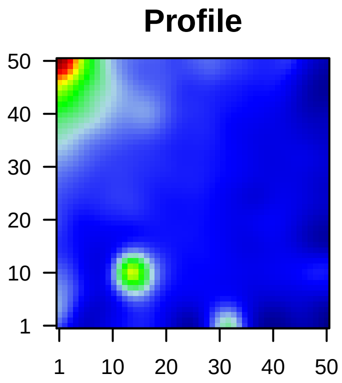
Local Summary

%DE = 0.93
metagenes = 12
genes = 187
genes in genesets = 182

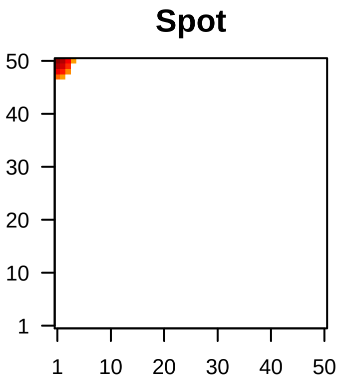
genes with fdr < 0.1 = 164 (156 + / 8 −)
genes with fdr < 0.05 = 160 (154 + / 6 −)
genes with fdr < 0.01 = 145 (141 + / 4 −)

<r> metagenes = 0.98
<r> genes = 0.48

<FC> = 0.72
<shrinkage−t> = 25.6
<p−value> = 0
<fdr> = 0.18



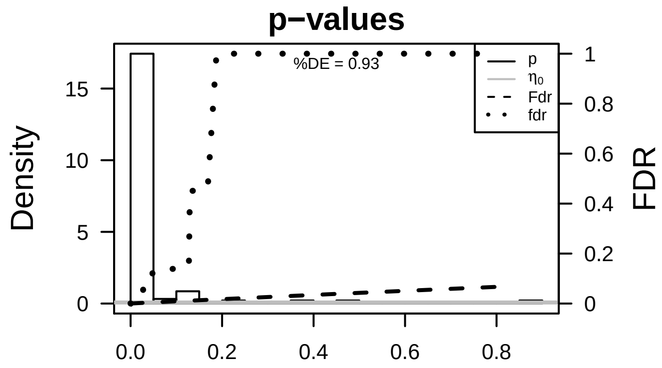
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.16	2e−16	6e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:2
2	57016	1.32	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
3	387695	1.28	2e−16	6e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
4	375791	1.71	2e−16	6e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
5	810	0.92	2e−16	6e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
6	84290	1.03	2e−16	6e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	1048	1.15	2e−16	6e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
8	4680	1.17	2e−16	6e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
9	1087	1.09	2e−16	6e−17	4 x 50	carcinoembryonic antigen−related cell adhesion molecule 7 [
10	22802	1.31	2e−16	6e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	9022	1.07	2e−16	6e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
12	84518	1.73	2e−16	6e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
13	54544	1.43	2e−16	6e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
14	49860	3.16	2e−16	6e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	1475	1.18	2e−16	6e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
16	1562	1.07	2e−16	6e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
17	1828	1	2e−16	6e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	2012	0.98	2e−16	6e−17	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
19	163351	1.09	2e−16	6e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
20	2877	1.1	2e−16	6e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	59.52	NULL	74 / 135	H.Tiss	WIRTH_Mucosa
2	29.58	NULL	16 / 21	CC	cornified envelope
3	24.43	NULL	9 / 19	BP	peptide cross−linking
4	22.86	NULL	19 / 42	BP	keratinization
5	22.8	NULL	21 / 53	BP	keratinocyte differentiation
6	21.87	NULL	81 / 572	Disease	GUDJ_psoriasis up
7	19.81	NULL	20 / 76	BP	epidermis development
8	19.57	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	17.71	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
10	16.04	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	15.81	NULL	6 / 13	BP	negative regulation of peptidase activity
12	14.93	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	14.3	NULL	8 / 44	CC	keratin filament
14	13.99	NULL	7 / 38	BP	epithelial cell differentiation
15	12.27	NULL	12 / 122	MF	serine−type endopeptidase activity
16	11.95	NULL	18 / 186	MF	structural molecule activity
17	11.71	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
18	11.51	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
19	11.1	NULL	5 / 10	MF	RAGE receptor binding
20	11.07	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
21	10.85	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
22	10.41	NULL	10 / 82	CC	intermediate filament
23	10.37	NULL	49 / 1182	CC	extracellular region
24	9.66	NULL	1 / 11	Glio	VERHAAK_Brain
25	9.17	NULL	1 / 12	MF	channel activity
26	8.74	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
27	8.64	NULL	5 / 21	CC	desmosome
28	8.59	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
29	8.58	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
30	8.55	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
31	8.45	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
32	8.41	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
33	8.31	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
34	8.03	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via dea
35	8.03	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
36	7.99	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
37	7.96	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
38	7.89	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
39	7.76	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
40	7.73	NULL	1 / 16	Cancer	GENTLES_modul11

GW_127

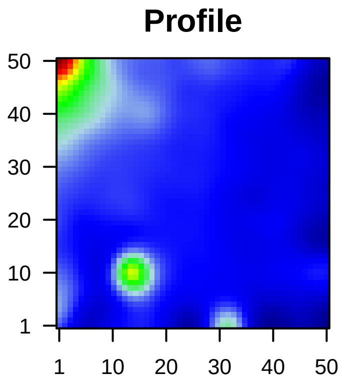
Local Summary

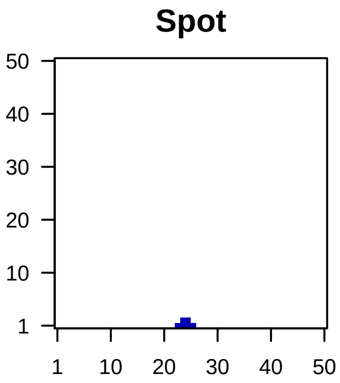
%DE = 0.65
metagenes = 6
genes = 99
genes in genesets = 99

genes with fdr < 0.1 = 34 (4 + / 30 −)
genes with fdr < 0.05 = 30 (4 + / 26 −)
genes with fdr < 0.01 = 26 (3 + / 23 −)

<r> metagenes = 1
<r> genes = 0.66

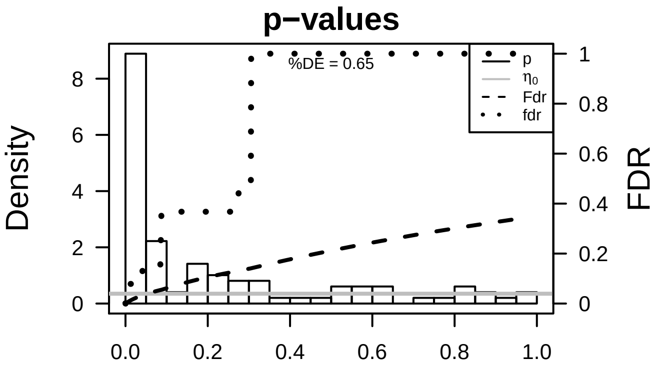
<FC> = −0.21
<shrinkage−t> = −7.31
<p−value> = 0.01
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	−1.15	2e−16	8e−15	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	1410	0.93	3e−14	5e−10	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
3	70	−0.83	1e−11	7e−09	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	2318	−0.78	2e−10	5e−07	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
5	4608	−0.69	1e−08	1e−06	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
6	222166	−0.67	5e−08	4e−06	24 x 1	maturin, neural progenitor differentiation regulator homolog (
7	4151	−0.64	2e−07	4e−06	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
8	1158	−0.63	3e−07	1e−05	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
9	6588	−0.61	6e−07	6e−04	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
10	1013	0.51	3e−05	6e−04	26 x 1	cadherin 15, type 1, M−cadherin (myotubule) [Source:HGNC
11	283120	−0.51	3e−05	6e−04	25 x 1	H19, imprinted maternally expressed transcript (non−protein
12	4621	−0.5	5e−05	7e−04	25 x 1	myosin, heavy chain 3, skeletal muscle, embryonic [Source:H
13	7134	−0.49	7e−05	3e−03	25 x 1	troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
14	4703	−0.46	2e−04	3e−03	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
15	2027	−0.45	2e−04	3e−03	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
16	7140	−0.43	4e−04	3e−03	25 x 1	troponin T type 3 (skeletal, fast) [Source:HGNC Symbol;Acc:1
17	4625	−0.43	5e−04	3e−03	25 x 1	myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
18	2273	−0.42	5e−04	5e−03	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
19	202333	−0.41	8e−04	5e−03	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:143
20	10324	−0.41	9e−04	5e−03	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−53.16	NULL	23 / 36	BP	muscle filament sliding
2	−51.66	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	−43.52	NULL	55 / 127	H.Tiss	WIRTH_Muscle
4	−39.75	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	−38.85	NULL	10 / 12	CC	myosin filament
6	−35.1	NULL	21 / 44	MF	structural constituent of muscle
7	−27.93	NULL	12 / 37	CC	sarcomere
8	−23.1	NULL	3 / 15	Cancer	BEN−PORATH_UP
9	−22.85	NULL	6 / 12	BP	skeletal muscle contraction
10	−22.81	NULL	8 / 13	CC	muscle myosin complex
11	−21.16	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
12	−19.92	NULL	6 / 18	BP	regulation of muscle contraction
13	−19.25	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
14	−19.21	NULL	14 / 34	CC	myofibril
15	−18.41	NULL	8 / 16	CC	M band
16	−17.89	NULL	9 / 37	BP	cardiac muscle contraction
17	−17.76	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
18	−17.5	NULL	2 / 20	MF	myosin binding
19	−16.99	NULL	23 / 84	BP	muscle contraction
20	−15.76	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
21	−15.72	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
22	−15.72	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
23	−15.54	NULL	2 / 10	BP	heart contraction
24	−15.02	NULL	3 / 15	BP	actin filament−based movement
25	−14.82	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
26	−14.69	NULL	2 / 15	BP	skeletal muscle fiber development
27	−14.42	NULL	3 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
28	−13.99	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
29	−13.99	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
30	−13.45	NULL	2 / 12	BP	muscle fiber development
31	−13.38	NULL	1 / 12	GSEA C2	BIOCARTA_NO1_PATHWAY
32	−13.38	NULL	1 / 12	GSEA C2	BIOCARTA_RAB_PATHWAY
33	−13.37	NULL	8 / 42	CC	myosin complex
34	−13.27	NULL	4 / 16	MF	microfilament motor activity
35	−12.8	NULL	1 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP
36	−12.8	NULL	1 / 13	GSEA C2	BIOCARTA_SALMONELLA_PATHWAY
37	−12.8	NULL	1 / 13	GSEA C2	BIOCARTA_NFAT_PATHWAY
38	−12.78	NULL	8 / 14	CC	contractile fiber
39	−12.76	NULL	3 / 37	CC	actin filament
40	−12.69	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY

GW_127

Local Summary

%DE = 0.56

metagenes = 45

genes = 647

genes in genesets = 618

genes with fdr < 0.1 = 190 (34 + / 156 −)

genes with fdr < 0.05 = 142 (27 + / 115 −)

genes with fdr < 0.01 = 73 (16 + / 57 −)

<r> metagenes = 0.83

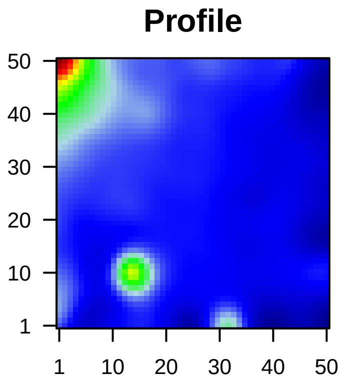
<r> genes = 0.37

<FC> = −0.14

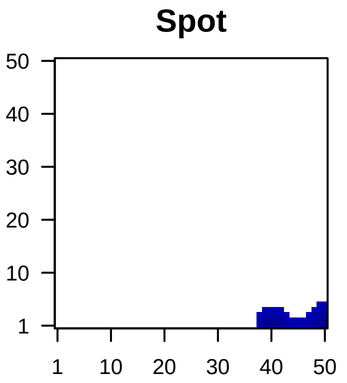
<shrinkage−t> = −5.04

<p−value> = 0.02

<fdr> = 0.73



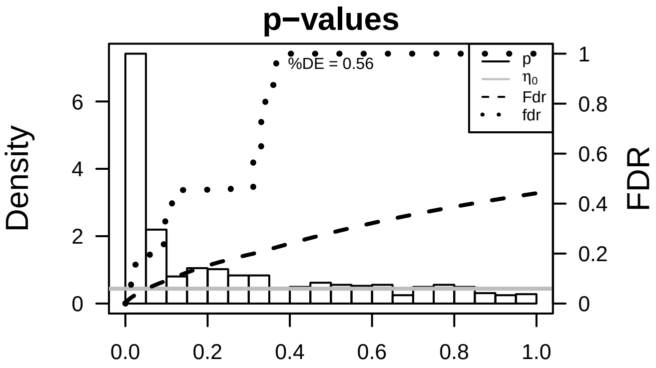
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	618	1.29	2e−16	3e−14	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
2	260436	−1.1	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
3	5552	−0.99	4e−16	3e−12	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
4	4034	0.95	1e−14	1e−11	43 x 1	leucine−rich repeats and calponin homology (CH) domain co
5	3127	−0.92	5e−14	4e−11	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
6	64005	0.89	2e−13	4e−11	49 x 4	myosin IG [Source:HGNC Symbol;Acc:13880]
7	3128	−0.89	4e−13	4e−11	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
8	23231	−0.88	4e−13	7e−11	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
9	341	−0.88	7e−13	1e−10	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
10	6364	−0.87	1e−12	4e−09	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
11	5996	−0.83	1e−11	2e−08	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
12	5730	0.79	9e−11	5e−08	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
13	51326	0.77	3e−10	6e−08	42 x 1	ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc
14	3113	−0.76	5e−10	1e−07	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
15	3122	−0.7	8e−10	2e−07	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
16	9056	−0.73	2e−09	2e−07	50 x 1	solute carrier family 7 (amino acid transporter light chain, y+L
17	3620	−0.73	2e−09	7e−07	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
18	3512	−0.71	6e−09	7e−07	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
19	347733	−0.7	1e−08	7e−07	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
20	5341	−0.7	1e−08	7e−07	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−29.6	NULL	14 / 15	CC	MHC class II protein complex
2	−17.59	NULL	17 / 47	BP	antigen processing and presentation
3	−15.17	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
4	−14.44	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
5	−14.15	NULL	3 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
6	−13.29	NULL	10 / 28	CC	transport vesicle membrane
7	−12.58	NULL	17 / 87	BP	antigen processing and presentation of exogenous peptide antigen
8	−12.07	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
9	−11.94	NULL	11 / 35	CC	trans−Golgi network membrane
10	−11.49	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	−11.49	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	−11.49	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	−11.49	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	−11.36	NULL	11 / 46	CC	endocytic vesicle membrane
15	−10.99	NULL	5 / 12	BP	immunoglobulin mediated immune response
16	−10.89	NULL	5 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
17	−10.79	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
18	−10.06	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
19	−9.98	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
20	−9.75	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
21	−9.73	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
22	−9.55	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
23	−9.24	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
24	−8.62	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
25	−8.39	NULL	67 / 312	BP	immune response
26	−8.12	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
27	−8.09	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
28	−8.04	NULL	5 / 13	MMML CGS	MACIEJ_MMML 6
29	−8.03	NULL	3 / 14	Lymphoma	WRIGHT_GCB UP
30	−7.86	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
31	−7.75	NULL	23 / 215	CC	lysosomal membrane
32	−7.66	NULL	4 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
33	−7.63	NULL	3 / 16	GSEA C2	KAAB_FAILED_HEART_VENTRICLE_DN
34	−7.47	NULL	3 / 13	GSEA C2	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN
35	−7.44	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
36	−7.39	NULL	3 / 16	GSEA C2	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN
37	−7.37	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
38	−7.26	NULL	3 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
39	−6.92	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
40	−6.92	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE

GW_127

Local Summary

%DE = 0.5

metagenes = 19

genes = 220

genes in genesets = 216

genes with fdr < 0.1 = 38 (4 + / 34 −)

genes with fdr < 0.05 = 33 (4 + / 29 −)

genes with fdr < 0.01 = 18 (4 + / 14 −)

<r> metagenes = 0.98

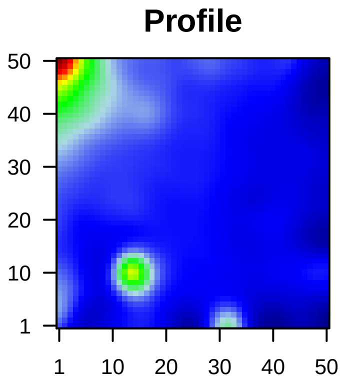
<r> genes = 0.33

<FC> = −0.15

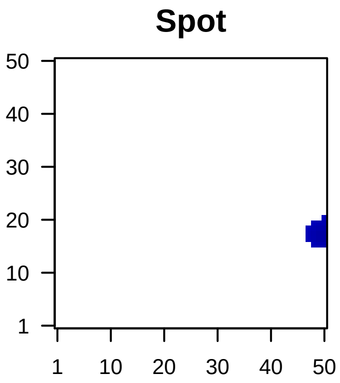
<shrinkage−t> = −5.2

<p−value> = 0.05

<fdr> = 0.77



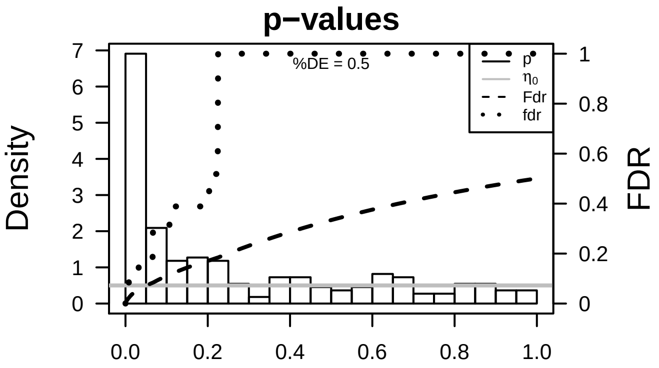
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9662	1.02	2e−16	2e−14	50 x 19	centrosomal protein 135kDa [Source:HGNC Symbol;Acc:290
2	10439	0.91	1e−13	7e−05	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
3	3670	0.6	1e−06	7e−05	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
4	728715	−0.59	1e−06	1e−04	50 x 18	
5	1298	−0.57	2e−06	2e−04	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
6	1875	−0.56	4e−06	1e−03	50 x 17	E2F transcription factor 5, p130−binding [Source:HGNC Sym
7	57639	−0.53	2e−05	1e−03	50 x 16	coiled−coil domain containing 146 [Source:HGNC Symbol;Ac
8	130872	−0.51	3e−05	1e−03	50 x 19	AHA1, activator of heat shock 90kDa protein ATPase homolo
9	6542	−0.5	5e−05	1e−03	50 x 16	solute carrier family 7 (cationic amino acid transporter, y+ sys
10	641638	−0.49	5e−05	1e−03	50 x 18	small nucleolar RNA host gene 6 (non−protein coding) [Sour
11	54959	−0.49	7e−05	1e−03	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
12	727	−0.48	8e−05	3e−03	50 x 16	complement component 5 [Source:HGNC Symbol;Acc:1331]
13	55063	−0.47	1e−04	3e−03	50 x 16	zinc finger, CW type with PWWP domain 1 [Source:HGNC S
14	79161	−0.46	2e−04	3e−03	49 x 16	transmembrane protein 243, mitochondrial [Source:HGNC S
15	6091	0.46	2e−04	3e−03	50 x 17	roundabout, axon guidance receptor, homolog 1 (Drosophila)
16	9204	−0.46	2e−04	5e−03	50 x 19	
17	7267	−0.44	3e−04	5e−03	50 x 18	tetratricopeptide repeat domain 3 [Source:HGNC Symbol;Acc
18	4602	−0.44	3e−04	5e−03	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
19	22882	−0.44	3e−04	1e−02	50 x 18	zinc fingers and homeoboxes 2 [Source:HGNC Symbol;Acc:1
20	9603	−0.43	5e−04	1e−02	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−8.43	NULL	2 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
2	−8	NULL	3 / 13	Lymphoma	BENTINK_mBL UP
3	−7.65	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
4	−7.52	NULL	3 / 5	Lymphoma	MASCQUE_mBL UP
5	−6.78	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
6	−6.5	NULL	1 / 2	miRNA target	miR−153
7	−6.47	NULL	2 / 13	BP	natural killer cell differentiation
8	−6.28	NULL	2 / 15	GSEA C2	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN
9	−6.28	NULL	2 / 15	GSEA C2	MULLIGHAN_NPM1_SIGNATURE_3_DN
10	−6.27	NULL	2 / 11	MF	poly(A)−specific ribonuclease activity
11	−6.21	NULL	1 / 7	GSEA C2	BIOCARTA_LECTIN_PATHWAY
12	−5.95	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
13	−5.8	NULL	1 / 2	TF	MYC_Chromatin_modification UP
14	−5.67	NULL	2 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
15	−5.59	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
16	−5.59	NULL	2 / 15	BP	embryonic digestive tract development
17	−5.32	NULL	4 / 42	BP	B cell differentiation
18	−5.26	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
19	−5.25	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
20	−5.19	NULL	1 / 9	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
21	−5.15	NULL	4 / 29	TF Tissue	VAQUERIZAS_Lymph node
22	−5.12	NULL	1 / 10	BP	positive regulation of chemotaxis
23	−5.11	NULL	2 / 16	GSEA C2	REACTOME_DEADENYLATION_OF_MRNA
24	−5.1	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
25	−5.07	NULL	2 / 16	BP	cytolysis
26	−5.02	NULL	2 / 13	GSEA C2	BIDUS_METASTASIS_DN
27	−5	NULL	1 / 8	GSEA C2	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
28	−5	NULL	1 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL
29	−4.97	NULL	3 / 13	BP	histone H4−K16 acetylation
30	−4.94	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
31	−4.94	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
32	−4.91	NULL	3 / 21	TF Tissue	VAQUERIZAS_Tonsil
33	−4.86	NULL	9 / 81	miRNA target starBase	hsa−miR−188−5p
34	−4.81	NULL	1 / 15	Cancer	RHODES_CANCER_META_SIGNATURE
35	−4.81	NULL	1 / 15	GSEA C2	REACTOME_G1_PHASE
36	−4.81	NULL	2 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_UP
37	−4.79	NULL	1 / 12	BP	nitric oxide biosynthetic process
38	−4.77	NULL	3 / 34	BP	thymus development
39	−4.75	NULL	2 / 15	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_UP
40	−4.75	NULL	2 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP

GW_127

Local Summary

%DE = 0.59

metagenes = 39

genes = 429

genes in genesets = 424

genes with fdr < 0.1 = 116 (22 + / 94 −)

genes with fdr < 0.05 = 79 (17 + / 62 −)

genes with fdr < 0.01 = 40 (9 + / 31 −)

<r> metagenes = 0.91

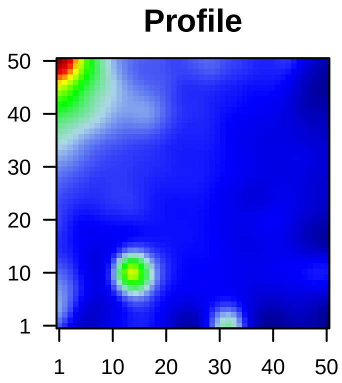
<r> genes = 0.2

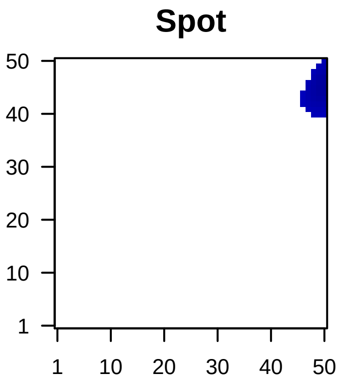
<FC> = −0.14

<shrinkage−t> = −4.8

<p−value> = 0.03

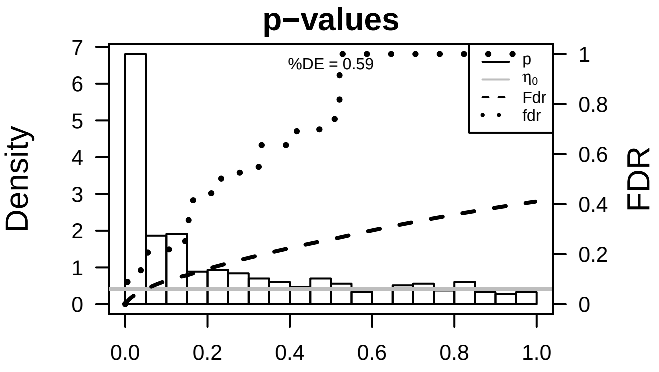
<fdr> = 0.76





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2944	1.04	2e−16	1e−14	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
2	84223	1.15	2e−16	1e−14	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
3	4922	−1.23	2e−16	1e−14	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
4	339512	−0.98	9e−16	8e−10	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
5	875	−0.85	4e−12	1e−09	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
6	139728	−0.83	1e−11	4e−08	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
7	10655	−0.77	2e−10	3e−07	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
8	8492	0.73	2e−09	1e−06	50 x 47	protease, serine, 12 (neurotrypsin, motopsin) [Source:HGNC
9	445	0.7	9e−09	4e−06	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
10	114926	−0.66	5e−08	4e−06	50 x 46	small integral membrane protein 19 [Source:HGNC Symbol;A
11	23514	−0.66	6e−08	4e−06	50 x 48	scaffolding protein involved in DNA repair [Source:HGNC Sy
12	51060	−0.66	7e−08	2e−05	50 x 42	thioredoxin domain containing 12 (endoplasmic reticulum) [S
13	4856	−0.63	3e−07	2e−05	50 x 40	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:
14	51804	−0.62	4e−07	2e−05	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
15	11166	0.61	6e−07	2e−05	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
16	3205	−0.61	6e−07	1e−04	49 x 45	homeobox A9 [Source:HGNC Symbol;Acc:5109]
17	84171	−0.58	2e−06	1e−04	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
18	64757	−0.58	2e−06	2e−04	48 x 47	mitochondrial amidoxime reducing component 1 [Source:HG
19	79679	−0.56	4e−06	2e−04	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:
20	7345	−0.56	4e−06	2e−04	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.9	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
2	−12.59	NULL	2 / 11	Glio	neurons_glio
3	−11.16	NULL	4 / 13	BP	regulation of blood vessel size
4	−9.72	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
5	−8.72	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
6	−8.6	NULL	5 / 15	GSEA C2	KIM_MYCN_AMPLIFICATION_TARGETS_DN
7	−8.27	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
8	−7.96	NULL	3 / 16	GSEA C2	IGARASHI_ATF4_TARGETS_DN
9	−7.87	NULL	2 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
10	−7.76	NULL	1 / 6	GSEA C2	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
11	−7.67	NULL	3 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
12	−7.53	NULL	2 / 13	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
13	−7.52	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
14	−7.35	NULL	2 / 16	GSEA C2	KEGG_SELENOAMINO_ACID_METABOLISM
15	−6.99	NULL	3 / 15	GSEA C2	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
16	−6.98	NULL	3 / 18	BP	superoxide metabolic process
17	−6.97	NULL	1 / 15	MF	neuropeptide hormone activity
18	−6.96	NULL	2 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
19	−6.96	NULL	4 / 16	GSEA C2	BILD_E2F3_ONCOGENIC_SIGNATURE
20	−6.78	NULL	2 / 10	BP	anatomical structure development
21	−6.72	NULL	2 / 16	GSEA C2	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
22	−6.71	NULL	1 / 2	miRNA target	miR−129
23	−6.68	NULL	4 / 37	BP	embryonic skeletal system development
24	−6.64	NULL	1 / 8	GSEA C2	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
25	−6.13	NULL	1 / 5	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
26	−6.13	NULL	1 / 5	miRNA target	miR−126
27	−6.05	NULL	1 / 8	GSEA C2	NIELSEN_LIPOSARCOMA_UP
28	−5.96	NULL	3 / 31	BP	response to nutrient levels
29	−5.92	NULL	2 / 14	MF	calmodulin−dependent protein kinase activity
30	−5.74	NULL	3 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
31	−5.7	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_DN
32	−5.66	NULL	2 / 15	Cancer	BEN−PORATH_UP
33	−5.57	NULL	1 / 11	GSEA C2	BENPORATH_MYC_TARGETS_WITH_EBOX
34	−5.57	NULL	1 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_PLASMABLAST_UP
35	−5.57	NULL	1 / 11	GSEA C2	HELLER_HDAC_TARGETS_DN
36	−5.57	NULL	1 / 11	GSEA C2	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
37	−5.56	NULL	2 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
38	−5.54	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
39	−5.42	NULL	2 / 10	MF	omega peptidase activity
40	−5.4	NULL	2 / 15	BP	spinal cord development