GW_084

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2159 (1210 + / 949 −)

genes with fdr < 0.1 = 1700 (965 + / 735 −)

genes with fdr < 0.05 = 1385 (791 + / 594 −)

genes with fdr < 0.01 = 952 (530 + / 422 −)

genes in genesets = 16332

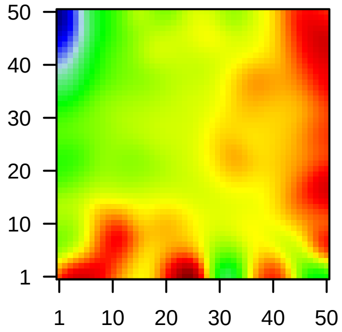
<FC> = 0

<shrinkage−t> = 0

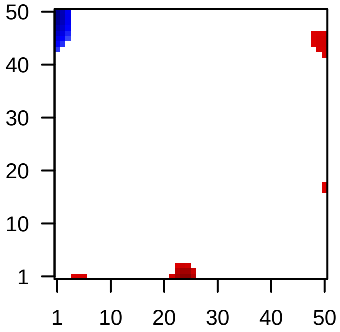
<p−value> = 0.08

<fdr> = 0.84

Profile



Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.95	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.13	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	57016	−2.36	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.84	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	249	1.78	2e−16	2e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
6	244	−1.78	2e−16	2e−14	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
7	347	1.83	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	9823	1.78	2e−16	2e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
9	64073	−2.3	2e−16	2e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
10	29113	2.84	2e−16	2e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
11	375791	−2	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
12	771	−1.84	2e−16	2e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
13	23705	2.03	2e−16	2e−14	50 x 7	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
14	810	−2.87	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
15	875	2.01	2e−16	2e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
16	1000	1.92	2e−16	2e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
17	4680	−2.14	2e−16	2e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
18	1158	2.79	2e−16	2e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
19	9635	−2.09	2e−16	2e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
20	9076	−2.03	2e−16	2e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]

Global Geneset Analysis

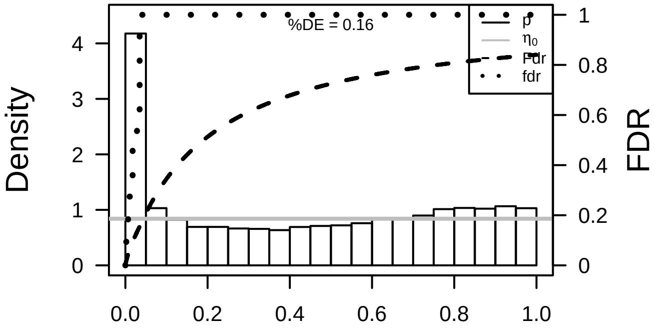
Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	18.07	NULL	127	H.Tiss	WIRTH_Muscle
2	15.7	NULL	36	BP	muscle filament sliding
3	14.85	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	12.91	NULL	44	MF	structural constituent of muscle
5	12.37	NULL	16	H.Tiss	WIRTH_Hippocampus
6	10.2	NULL	37	CC	sarcomere
7	10.11	NULL	84	BP	muscle contraction
8	9.06	NULL	12	CC	myosin filament
9	8.94	NULL	15	Cancer	BEN−PORATH_UP
10	8.47	NULL	375	Disease	GUDJ_psoriasis down
11	8.13	NULL	914	Chr	Chr 3
12	7.87	NULL	11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
13	7.66	NULL	13	CC	muscle myosin complex
14	7.62	NULL	57	MF	extracellular matrix structural constituent
15	7.62	NULL	1033	Chr	Chr 2
16	7.52	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
17	7.41	NULL	400	H.Tiss	WIRTH_Nervous System
18	7.2	NULL	190	CC	extracellular matrix
19	7.19	NULL	7	MMML CGS	MACIEJ_MMML 5
20	7.18	NULL	280	Chr	Chr 13

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−32.78	NULL	135	H.Tiss	WIRTH_Mucosa
2	−25.77	NULL	572	Disease	GUDJ_psoriasis up
3	−16.69	NULL	21	CC	cornified envelope
4	−16.09	NULL	76	BP	epidermis development
5	−14.31	NULL	53	BP	keratinocyte differentiation
6	−14	NULL	42	BP	keratinization
7	−11.09	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	−10.11	NULL	21	CC	desmosome
9	−9.66	NULL	417	H.Tiss	WIRTH_Immune system
10	−9.35	NULL	82	CC	intermediate filament
11	−9.11	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	−8.98	NULL	44	CC	keratin filament
13	−8.94	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	−8.9	NULL	51	BP	type I interferon signaling pathway
15	−8.86	NULL	312	BP	immune response
16	−8.71	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
17	−8.69	NULL	553	Cancer	Lembcke_Colonic Inflammation
18	−8.03	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
19	−8.03	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
20	−7.92	NULL	12	BP	hemidesmosome assembly

p−values



GW_084

Local Summary

%DE = 0.67

metagenes = 3

genes = 101

genes in genesets = 100

genes with fdr < 0.1 = 51 (50 + / 1 −)

genes with fdr < 0.05 = 50 (49 + / 1 −)

genes with fdr < 0.01 = 34 (34 + / 0 −)

<r> metagenes = 0.99

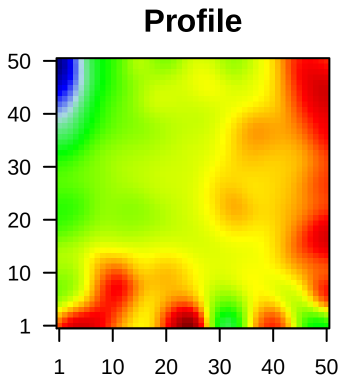
<r> genes = 0.46

<FC> = 0.56

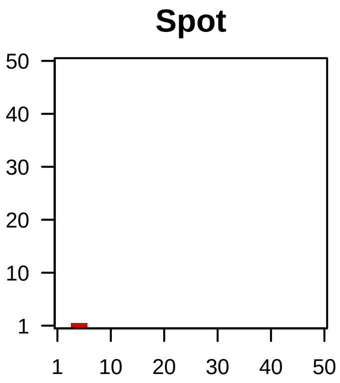
<shrinkage−t> = 19.53

<p−value> = 0

<fdr> = 0.52



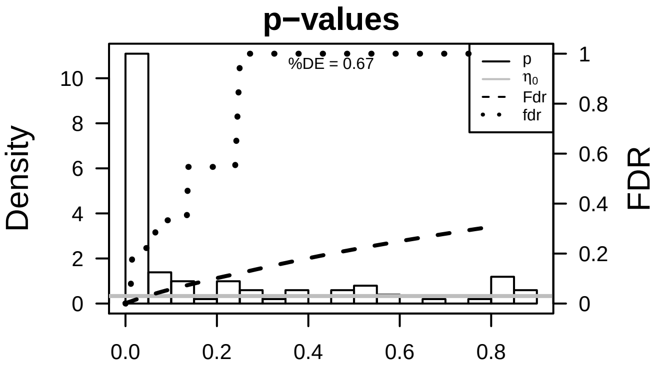
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	249	1.78	2e−16	2e−15	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
2	1000	1.92	2e−16	2e−15	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
3	7857	2.16	2e−16	2e−15	4 x 1	secretogranin II [Source:HGNC Symbol;Acc:10575]
4	8910	2.29	2e−16	2e−15	6 x 1	sarcoglycan, epsilon [Source:HGNC Symbol;Acc:10808]
5	10962	1.68	8e−15	6e−12	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
6	1809	1.59	2e−13	1e−09	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
7	387914	1.43	4e−11	2e−09	6 x 1	shisa family member 2 [Source:HGNC Symbol;Acc:20366]
8	55384	1.4	1e−10	3e−09	4 x 1	maternally expressed 3 (non−protein coding) [Source:HGNC
9	27253	1.36	4e−10	3e−09	4 x 1	protocadherin 17 [Source:HGNC Symbol;Acc:14267]
10	30008	1.36	4e−10	3e−09	5 x 1	EGF containing fibulin−like extracellular matrix protein 2 [Sou
11	2882	1.35	4e−10	3e−09	6 x 1	glutathione peroxidase 7 [Source:HGNC Symbol;Acc:4559]
12	5118	1.35	5e−10	4e−09	4 x 1	procollagen C−endopeptidase enhancer [Source:HGNC Sym
13	10979	1.34	6e−10	6e−08	4 x 1	fermitin family member 2 [Source:HGNC Symbol;Acc:15767]
14	54749	1.27	4e−09	6e−08	5 x 1	ependymin related 1 [Source:HGNC Symbol;Acc:17572]
15	51313	1.27	4e−09	2e−06	4 x 1	family with sequence similarity 198, member B [Source:HGN
16	7076	1.17	6e−08	4e−06	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
17	1306	1.13	2e−07	3e−05	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
18	51655	1.06	1e−06	1e−04	6 x 1	RAS, dexamethasone−induced 1 [Source:HGNC Symbol;Acc
19	56999	0.99	5e−06	1e−04	6 x 1	ADAM metallopeptidase with thrombospondin type 1 motif, 9
20	401237	0.97	7e−06	2e−04	6 x 1	cancer susceptibility candidate 15 (non−protein coding) [Sour



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.86	NULL	1 / 2	MMML CGS	MACIEJ_MMML 46
2	21.77	NULL	1 / 2	miRNA target	miR−346
3	16.26	NULL	1 / 7	GSEA C2	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_UP
4	15.02	NULL	1 / 8	GSEA C2	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
5	14.95	NULL	1 / 6	GSEA C2	TAKAYAMA_BOUND_BY_AR
6	14.7	NULL	3 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
7	14.25	NULL	21 / 190	CC	extracellular matrix
8	14.11	NULL	1 / 3	GSEA C2	KONDO_HYPOXIA
9	14.01	NULL	1 / 9	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_UP
10	13.17	NULL	1 / 15	Cancer	LIU_PROSTATE_CANCER_DN
11	12.46	NULL	1 / 11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
12	11.84	NULL	1 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
13	11.41	NULL	5 / 70	BP	cell−matrix adhesion
14	11.3	NULL	25 / 250	Lymphoma	LENZ_Stromal signature 1
15	10.83	NULL	1 / 14	GSEA C2	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP
16	10.77	NULL	2 / 22	CC	filamentous actin
17	10.66	NULL	1 / 13	BP	induction of positive chemotaxis
18	10.6	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
19	10.44	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
20	10.42	NULL	1 / 11	MF	gamma−catenin binding
21	10.41	NULL	1 / 15	GSEA C2	BILBAN_B_CLL_LPL_UP
22	10.41	NULL	1 / 15	GSEA C2	GOZGIT_ESR1_TARGETS_UP
23	10.41	NULL	1 / 15	GSEA C2	SCHLOSSER_SERUM_RESPONSE_DN
24	10.41	NULL	1 / 15	GSEA C2	YANG_BREAST_CANCER_ESR1_LASER_DN
25	10.41	NULL	1 / 15	GSEA C2	TOMLINS_PROSTATE_CANCER_DN
26	10.41	NULL	1 / 15	GSEA C2	POTTI_CYTOXAN_SENSITIVITY
27	10.41	NULL	1 / 15	GSEA C2	JIANG_HYPOXIA_NORMAL
28	10.22	NULL	1 / 10	GSEA C2	MARTINELLI_IMMATURE_NEUTROPHIL_DN
29	10.03	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
30	10.03	NULL	1 / 16	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
31	10.03	NULL	1 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
32	10.03	NULL	1 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP
33	10.03	NULL	1 / 16	GSEA C2	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
34	9.95	NULL	3 / 23	BP	negative regulation of endothelial cell proliferation
35	9.91	NULL	1 / 12	CC	fascia adherens
36	9.9	NULL	3 / 18	BP	focal adhesion assembly
37	9.81	NULL	1 / 15	BP	negative regulation of endothelial cell apoptotic process
38	9.66	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS
39	9.62	NULL	1 / 10	GSEA C2	ZHU_CMV_24_HR_UP
40	9.62	NULL	1 / 10	GSEA C2	ZHU_CMV_ALL_UP

GW_084

Local Summary

%DE = 0.85

metagenes = 12

genes = 118

genes in genesets = 117

genes with fdr < 0.1 = 92 (92 + / 0 −)

genes with fdr < 0.05 = 83 (83 + / 0 −)

genes with fdr < 0.01 = 78 (78 + / 0 −)

<r> metagenes = 0.99

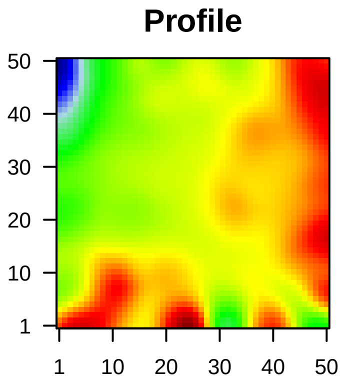
<r> genes = 0.62

<FC> = 1.09

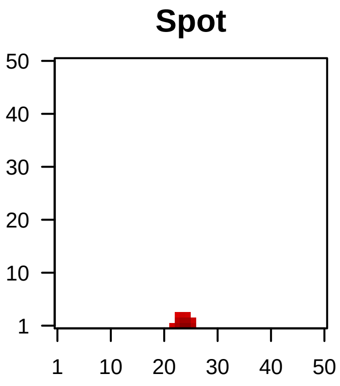
<shrinkage−t> = 38.31

<p−value> = 0

<fdr> = 0.27



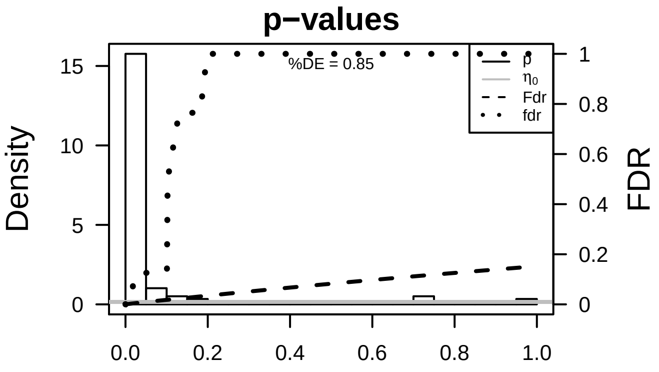
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.95	2e−16	2e−16	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.13	2e−16	2e−16	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1158	2.79	2e−16	2e−16	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	202333	2.11	2e−16	2e−16	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
5	115265	2.16	2e−16	2e−16	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Syn
6	8788	2.01	2e−16	2e−16	23 x 1	delta−like 1 homolog (Drosophila) [Source:HGNC Symbol;Ac
7	1917	2.91	2e−16	2e−16	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
8	2273	2.23	2e−16	2e−16	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
9	2318	1.96	2e−16	2e−16	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
10	10324	2.66	2e−16	2e−16	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
11	4151	2.37	2e−16	2e−16	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
12	4604	1.77	2e−16	2e−16	25 x 1	myosin binding protein C, slow type [Source:HGNC Symbol;A
13	4620	3.27	2e−16	2e−16	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
14	4625	2.37	2e−16	2e−16	25 x 1	myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
15	4632	1.84	2e−16	2e−16	25 x 1	myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
16	4633	2.56	2e−16	2e−16	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
17	8736	1.88	2e−16	2e−16	25 x 1	myomesin 1 [Source:HGNC Symbol;Acc:7613]
18	9499	2.44	2e−16	2e−16	25 x 1	myotilin [Source:HGNC Symbol;Acc:12399]
19	4703	2.83	2e−16	2e−16	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
20	6588	3.45	2e−16	2e−16	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	60	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	57.92	NULL	23 / 36	BP	muscle filament sliding
3	54.2	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	49.66	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	47.45	NULL	22 / 44	MF	structural constituent of muscle
6	38.24	NULL	10 / 12	CC	myosin filament
7	34.37	NULL	12 / 37	CC	sarcomere
8	30.44	NULL	23 / 84	BP	muscle contraction
9	30.43	NULL	8 / 13	CC	muscle myosin complex
10	27.47	NULL	8 / 14	CC	contractile fiber
11	27.07	NULL	9 / 16	CC	M band
12	26.44	NULL	14 / 34	CC	myofibril
13	25.46	NULL	21 / 88	CC	Z disc
14	24.48	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
15	24.28	NULL	9 / 37	BP	cardiac muscle contraction
16	22.19	NULL	10 / 20	CC	I band
17	20.66	NULL	6 / 12	BP	skeletal muscle contraction
18	19.98	NULL	6 / 12	MF	titin binding
19	19.86	NULL	7 / 15	BP	striated muscle contraction
20	19.68	NULL	5 / 11	CC	A band
21	18.85	NULL	3 / 15	Cancer	BEN−PORATH_UP
22	18.17	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
23	17.66	NULL	2 / 10	BP	heart contraction
24	16.25	NULL	6 / 18	BP	regulation of muscle contraction
25	16.24	NULL	4 / 14	BP	adult heart development
26	15.56	NULL	8 / 42	CC	myosin complex
27	15.23	NULL	25 / 297	MF	actin binding
28	15.11	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
29	14.91	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
30	14.8	NULL	4 / 16	MF	microfilament motor activity
31	14.67	NULL	2 / 20	MF	myosin binding
32	14.18	NULL	4 / 18	CC	costamere
33	13.82	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
34	13.61	NULL	3 / 13	CC	pseudopodium
35	13.22	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
36	13.16	NULL	2 / 13	GSEA C2	BIOCARTA_NFAT_PATHWAY
37	13.14	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
38	13.14	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
39	13.01	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
40	13.01	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN

GW_084

Local Summary

%DE = 0.66

metagenes = 2

genes = 68

genes in genesets = 68

genes with fdr < 0.1 = 40 (40 + / 0 −)

genes with fdr < 0.05 = 39 (39 + / 0 −)

genes with fdr < 0.01 = 31 (31 + / 0 −)

<r> metagenes = 1

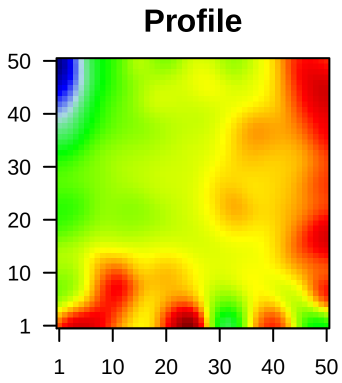
<r> genes = 0.4

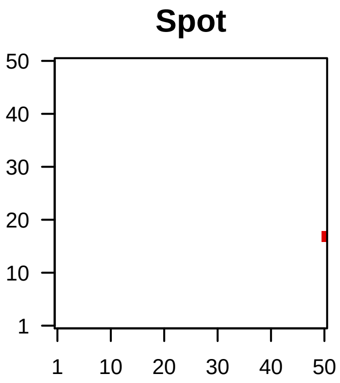
<FC> = 0.6

<shrinkage−t> = 20.9

<p−value> = 0

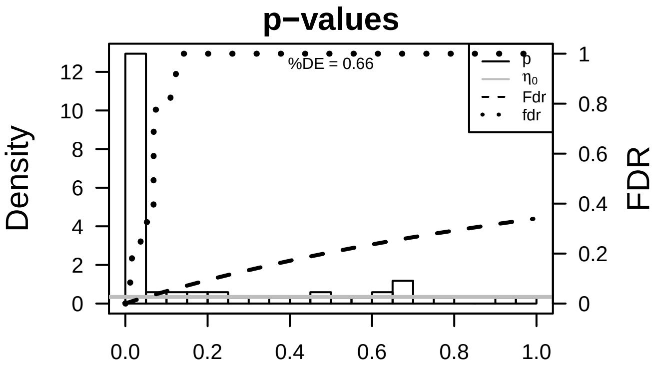
<fdr> = 0.42





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	728715	2.34	2e−16	3e−15	50 x 18	
2	54959	2.41	2e−16	3e−15	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
3	57556	1.72	2e−15	2e−12	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic
4	4613	1.61	9e−14	8e−11	50 x 17	v−myc avian myelocytomatosis viral oncogene neuroblastoma
5	3977	1.5	4e−12	8e−11	50 x 17	leukemia inhibitory factor receptor alpha [Source:HGNC Sym
6	29091	1.49	7e−12	7e−09	50 x 17	syntaxin binding protein 6 (amisyn) [Source:HGNC Symbol;A
7	1298	1.36	3e−10	8e−07	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
8	9915	1.18	5e−08	8e−07	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
9	28951	1.16	8e−08	8e−07	50 x 17	tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:30809]
10	6432	1.15	1e−07	2e−06	50 x 17	serine/arginine−rich splicing factor 7 [Source:HGNC Symbol;
11	7267	1.12	2e−07	2e−06	50 x 18	tetratricopeptide repeat domain 3 [Source:HGNC Symbol;Acc
12	57728	1.11	3e−07	3e−05	50 x 18	WD repeat domain 19 [Source:HGNC Symbol;Acc:18340]
13	21	1.02	3e−06	3e−05	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sou
14	53826	1.01	3e−06	3e−05	50 x 18	FXYD domain containing ion transport regulator 6 [Source:H
15	648	1	4e−06	1e−04	50 x 17	COMMD3−BMI1 readthrough [Source:HGNC Symbol;Acc:48
16	83988	0.96	1e−05	2e−04	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
17	10461	0.92	2e−05	2e−04	50 x 17	c−mer proto−oncogene tyrosine kinase [Source:HGNC Symb
18	84450	0.9	3e−05	2e−04	50 x 18	zinc finger protein 512 [Source:HGNC Symbol;Acc:29380]
19	9189	0.89	4e−05	3e−04	50 x 18	zinc finger, BED−type containing 1 [Source:HGNC Symbol;A
20	6431	0.82	5e−05	4e−04	50 x 18	serine/arginine−rich splicing factor 6 [Source:HGNC Symbol;



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.34	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
2	16.9	NULL	1 / 5	TF	MYC_TFs
3	16.9	NULL	1 / 5	miRNA target	miR−101
4	16.84	NULL	2 / 12	GSEA C2	KIM_WT1_TARGETS_12HR_UP
5	13.96	NULL	2 / 15	GSEA C2	DELYS_THYROID_CANCER_DN
6	13.92	NULL	1 / 13	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN
7	13.32	NULL	1 / 14	BP	biomineral tissue development
8	12.83	NULL	1 / 3	miRNA target	miR−148a
9	11.61	NULL	1 / 10	BP	centrosome localization
10	11.42	NULL	1 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
11	10.85	NULL	1 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
12	10.85	NULL	1 / 10	GSEA C2	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
13	10.75	NULL	2 / 15	BP	negative regulation of mRNA splicing, via spliceosome
14	10.39	NULL	1 / 12	GSEA C2	SHI_SPARC_TARGETS_UP
15	10.3	NULL	2 / 13	miRNA target	miR−34a
16	10.24	NULL	1 / 11	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
17	10.24	NULL	1 / 11	GSEA C2	HELLER_HDAC_TARGETS_DN
18	10.24	NULL	1 / 11	GSEA C2	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
19	10	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
20	9.71	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
21	9.71	NULL	1 / 12	GSEA C2	KIM_MYCN_AMPLIFICATION_TARGETS_UP
22	9.71	NULL	1 / 12	GSEA C2	BLALOCK_ALZHEIMERS_DISEASE_UP
23	9.51	NULL	2 / 16	GSEA C2	HOEBEKE_LYMPHOID_STEM_CELL_UP
24	9.25	NULL	1 / 13	GSEA C2	ENK_UV_RESPONSE_KERATINOCYTE_UP
25	9.25	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
26	9.09	NULL	1 / 15	BP	semaphorin−plexin signaling pathway
27	9.06	NULL	1 / 8	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
28	8.85	NULL	1 / 14	GSEA C2	GRABARCZYK_BCL11B_TARGETS_UP
29	8.85	NULL	1 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
30	8.85	NULL	1 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
31	8.85	NULL	1 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
32	8.85	NULL	1 / 14	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
33	8.85	NULL	1 / 14	GSEA C2	SWEET_KRAS_ONCOGENIC_SIGNATURE
34	8.75	NULL	1 / 16	GSEA C2	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
35	8.64	NULL	2 / 13	GSEA C2	CHENG_IMPRINTED_BY_ESTRADIOL
36	8.49	NULL	1 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
37	8.49	NULL	1 / 15	GSEA C2	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN
38	8.49	NULL	1 / 15	GSEA C2	KORKOLA_TERATOMA
39	8.49	NULL	1 / 15	GSEA C2	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS
40	8.49	NULL	1 / 15	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3

GW_084

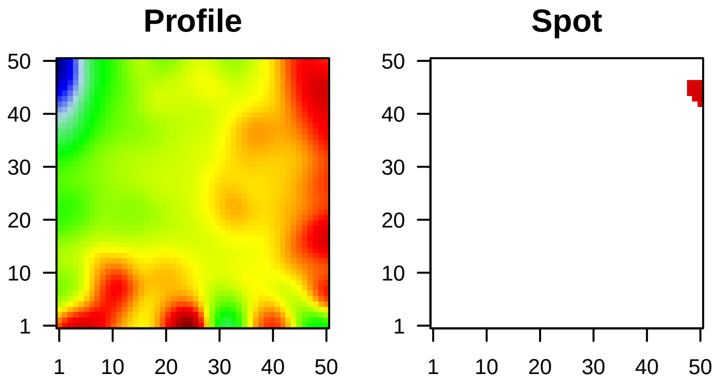
Local Summary

%DE = 0.74
metagenes = 12
genes = 124
genes in genesets = 122

genes with fdr < 0.1 = 60 (58 + / 2 −)
genes with fdr < 0.05 = 55 (53 + / 2 −)
genes with fdr < 0.01 = 43 (42 + / 1 −)

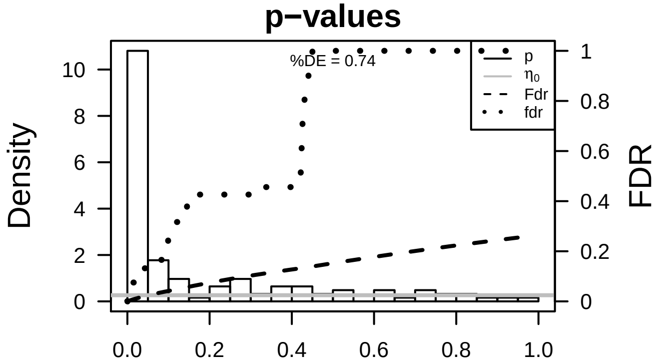
<r> metagenes = 0.98
<r> genes = 0.24

<FC> = 0.54
<shrinkage−t> = 19.07
<p−value> = 0
<fdr> = 0.53



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4897	1.86	2e−16	2e−15	50 x 45	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:
2	26227	1.93	2e−16	2e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
3	157869	2.04	2e−16	2e−15	50 x 42	somatomedin B and thrombospondin, type 1 domain containi
4	11013	2.04	2e−16	2e−15	49 x 45	thymosin beta 15a [Source:HGNC Symbol;Acc:30744]
5	23462	1.67	1e−14	6e−12	50 x 45	hes−related family bHLH transcription factor with YRPW moti
6	9965	1.59	2e−13	1e−11	50 x 42	fibroblast growth factor 19 [Source:HGNC Symbol;Acc:3675]
7	388228	1.56	5e−13	4e−10	50 x 45	SH3 domain binding kinase 1 [Source:HGNC Symbol;Acc:17
8	80164	1.46	2e−11	4e−10	50 x 43	Protein FLJ22184 [Source:UniProtKB/TrEMBL;Acc:F5H1R7]
9	23089	1.44	2e−11	8e−10	50 x 42	paternally expressed 10 [Source:HGNC Symbol;Acc:14005]
10	8975	1.42	5e−11	2e−08	50 x 44	ubiquitin specific peptidase 13 (isopeptidase T−3) [Source:H
11	440	1.33	8e−10	6e−08	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
12	55502	1.29	3e−09	9e−08	48 x 45	hes family bHLH transcription factor 6 [Source:HGNC Symbo
13	2119	1.25	7e−09	9e−08	50 x 43	ets variant 5 [Source:HGNC Symbol;Acc:3494]
14	55964	1.24	9e−09	9e−08	49 x 45	septin 3 [Source:HGNC Symbol;Acc:10750]
15	201161	1.24	1e−08	1e−06	50 x 45	centromere protein V [Source:HGNC Symbol;Acc:29920]
16	57161	1.18	5e−08	9e−06	50 x 42	pellino E3 ubiquitin protein ligase family member 2 [Source:H
17	6608	1.1	4e−07	9e−06	50 x 42	smoothened, frizzled family receptor [Source:HGNC Symbol;
18	80144	1.07	7e−07	9e−06	50 x 42	Fraser syndrome 1 [Source:HGNC Symbol;Acc:19185]
19	3205	1.06	1e−06	9e−06	49 x 45	homeobox A9 [Source:HGNC Symbol;Acc:5109]
20	51804	1.05	1e−06	1e−05	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.64	NULL	1 / 2	MMML CGS	MACIEJ_MMML 46
2	15.24	NULL	1 / 4	GSEA C2	LUCAS_HNF4A_TARGETS_DN
3	13.37	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
4	13.18	NULL	3 / 19	BP	cellular amino acid biosynthetic process
5	12.51	NULL	2 / 18	BP	glutamine metabolic process
6	11.84	NULL	3 / 15	GSEA C2	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
7	11.74	NULL	2 / 15	GSEA C2	HOOI_ST7_TARGETS_UP
8	11.7	NULL	3 / 16	GSEA C2	BILD_E2F3_ONCOGENIC_SIGNATURE
9	11.48	NULL	2 / 15	BP	spinal cord development
10	11.09	NULL	1 / 2	miRNA target	miR−129
11	10.31	NULL	3 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
12	10.22	NULL	1 / 11	MF	polysaccharide binding
13	9.55	NULL	2 / 29	MF	cofactor binding
14	9.4	NULL	2 / 13	GSEA C2	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
15	9.28	NULL	1 / 13	GSEA C2	LIU_TARGETS_OF_VMYB_VS_CMYB_UP
16	9.05	NULL	2 / 15	BP	positive regulation of branching involved in ureteric bud morphogen
17	8.97	NULL	2 / 10	GSEA C2	AMUNDSON_RESPONSE_TO_ARSENITE
18	8.82	NULL	1 / 10	BP	cardiac epithelial to mesenchymal transition
19	8.62	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
20	8.62	NULL	2 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
21	8.52	NULL	2 / 24	miRNA 3UTR	TTGC−191
22	8.43	NULL	1 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
23	8.36	NULL	1 / 5	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
24	8.36	NULL	1 / 5	miRNA target	miR−126
25	8.35	NULL	1 / 11	BP	negative regulation of transcription regulatory region DNA binding
26	8.24	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
27	8.17	NULL	2 / 15	GSEA C2	POTTI_CYTOXAN_SENSITIVITY
28	8.1	NULL	1 / 15	GSEA C2	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP
29	8.1	NULL	1 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
30	8.1	NULL	2 / 30	BP	neurogenesis
31	8.09	NULL	2 / 23	BP	ventricular septum morphogenesis
32	8.08	NULL	1 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
33	8.08	NULL	1 / 14	MF	ankyrin binding
34	8.08	NULL	1 / 14	BP	axonal fasciculation
35	8.02	NULL	2 / 11	GSEA C2	CUI_GLUCOSE_DEPRIVATION
36	7.82	NULL	2 / 15	GSEA C2	KIM_MYCN_AMPLIFICATION_TARGETS_DN
37	7.8	NULL	1 / 16	GSEA C2	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN
38	7.77	NULL	1 / 6	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_DN
39	7.77	NULL	2 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
40	7.76	NULL	1 / 15	BP	retinal ganglion cell axon guidance

GW_084

Local Summary

%DE = 0.97

metagenes = 21

genes = 300

genes in genesets = 292

genes with fdr < 0.1 = 283 (6 + / 277 −)

genes with fdr < 0.05 = 279 (6 + / 273 −)

genes with fdr < 0.01 = 266 (6 + / 260 −)

<r> metagenes = 0.91

<r> genes = 0.38

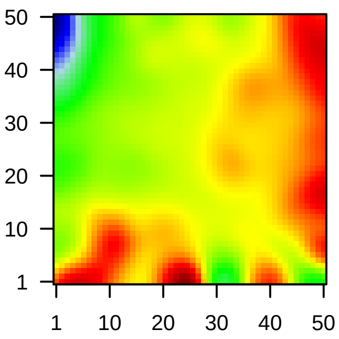
<FC> = −1.18

<shrinkage−t> = −41.82

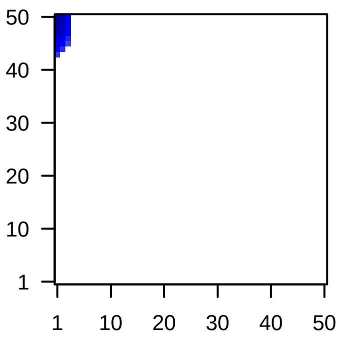
<p−value> = 0

<fdr> = 0.11

Profile



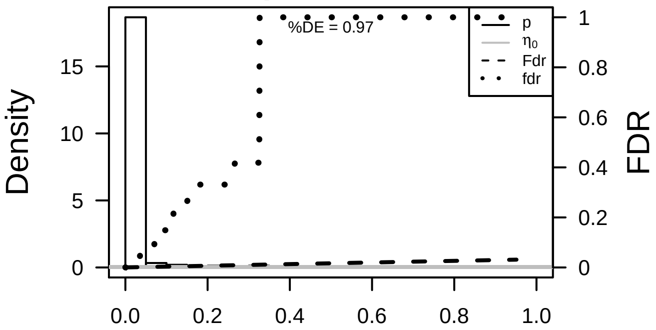
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−2.36	2e−16	3e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	−1.84	2e−16	3e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	244	−1.78	2e−16	3e−17	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
4	64073	−2.3	2e−16	3e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
5	29113	2.84	2e−16	3e−17	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
6	375791	−2	2e−16	3e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
7	771	−1.84	2e−16	3e−17	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
8	810	−2.87	2e−16	3e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
9	4680	−2.14	2e−16	3e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
10	9635	−2.09	2e−16	3e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
11	84518	−2.09	2e−16	3e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
12	1475	−1.87	2e−16	3e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
13	1672	−2.16	2e−16	3e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
14	414325	−1.99	2e−16	3e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1824	−1.8	2e−16	3e−17	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
16	1825	−1.8	2e−16	3e−17	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
17	1828	−1.97	2e−16	3e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	1830	−2.39	2e−16	3e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
19	128876	−1.86	2e−16	3e−17	1 x 48	family with sequence similarity 83, member C [Source:HGNC
20	9982	−2.52	2e−16	3e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−63.02	NULL	88 / 135	H.Tiss	WIRTH_Mucosa
2	−38.35	NULL	18 / 21	CC	cornified envelope
3	−32.83	NULL	111 / 572	Disease	GUDJ_psoriasis up
4	−29.29	NULL	20 / 42	BP	keratinization
5	−28.48	NULL	24 / 53	BP	keratinocyte differentiation
6	−28.42	NULL	27 / 76	BP	epidermis development
7	−24.41	NULL	12 / 21	CC	desmosome
8	−19.32	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	−18.46	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	−18.25	NULL	13 / 44	CC	keratin filament
11	−18.05	NULL	21 / 82	CC	intermediate filament
12	−17.87	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	−17.16	NULL	10 / 19	BP	peptide cross−linking
14	−16.36	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	−15.84	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
16	−14.73	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
17	−14.37	NULL	30 / 186	MF	structural molecule activity
18	−12.99	NULL	5 / 10	MF	RAGE receptor binding
19	−12.53	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
20	−12.1	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
21	−12	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
22	−11.67	NULL	3 / 12	BP	hemidesmosome assembly
23	−11.58	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
24	−11.41	NULL	10 / 52	BP	negative regulation of endopeptidase activity
25	−11.29	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
26	−11.18	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
27	−11.11	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
28	−11.08	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
29	−11.08	NULL	8 / 38	BP	epithelial cell differentiation
30	−10.91	NULL	7 / 29	BP	regulation of proteolysis
31	−10.89	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
32	−10.87	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
33	−10.77	NULL	6 / 13	BP	negative regulation of peptidase activity
34	−10.77	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
35	−10.76	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
36	−10.7	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
37	−10.59	NULL	11 / 82	MF	structural constituent of cytoskeleton
38	−10.29	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
39	−9.77	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
40	−9.55	NULL	2 / 5	miRNA target	miR−196a