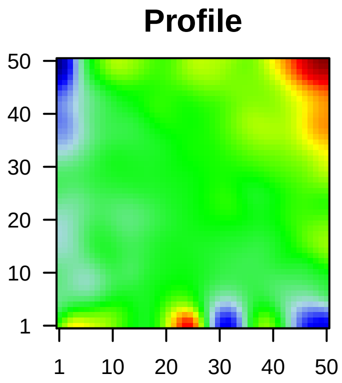
GW_259

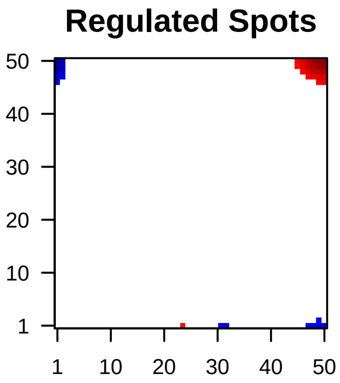
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1863 (1007 + / 856 −)
genes with fdr < 0.1 = 1423 (771 + / 652 −)
genes with fdr < 0.05 = 1194 (646 + / 548 −)
genes with fdr < 0.01 = 773 (420 + / 353 −)

genes in genesets = 16332

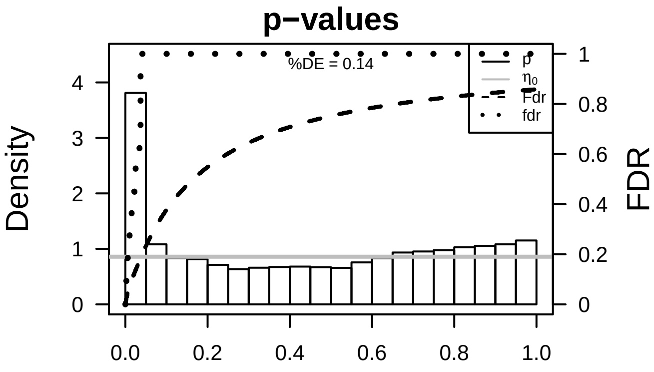
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.81	2e−16	4e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.6	2e−16	4e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	216	2.52	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
4	445328	−1.79	2e−16	4e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
5	760	−1.98	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
6	6364	−2.45	2e−16	4e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
7	595	−1.95	2e−16	4e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
8	1000	2	2e−16	4e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
9	4680	−2.58	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
10	1114	2.19	2e−16	4e−14	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Ac
11	1158	2.57	2e−16	4e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
12	22802	−1.71	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	84518	−1.77	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	49860	−1.92	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	54541	−1.73	2e−16	4e−14	1 x 4	DNA−damage−inducible transcript 4 [Source:HGNC Symbol;
16	115265	1.99	2e−16	4e−14	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
17	1672	−2.35	2e−16	4e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	414325	−2.15	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	1673	−2.71	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	2201	1.79	2e−16	4e−14	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	15.16	NULL	127	H.Tiss	WIRTH_Muscle
2	13.9	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	12.25	NULL	633	Chr	Chr 9
4	12.17	NULL	36	BP	muscle filament sliding
5	11.05	NULL	44	MF	structural constituent of muscle
6	10.76	NULL	914	Chr	Chr 3
7	10.38	NULL	16	H.Tiss	WIRTH_Hippocampus
8	7.91	NULL	313	miRNA target−starBase	hsa−miR−559
9	7.74	NULL	84	BP	muscle contraction
10	7.71	NULL	391	miRNA 3UTR	TGAA−181A−−181B−−181C−−181D
11	7.68	NULL	463	miRNA target−starBase	hsa−miR−301a
12	7.59	NULL	16	MMML CGS	MACIEJ_MMML 1
13	7.53	NULL	232	Chr	Chr 18
14	7.53	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
15	7.5	NULL	14	CC	contractile fiber
16	7.47	NULL	184	miRNA target−starBase	hsa−miR−586
17	7.38	NULL	421	miRNA target−starBase	hsa−let−7b
18	7.37	NULL	362	miRNA 3UTR	CAGT−200B−−200C−−429
19	7.29	NULL	396	miRNA target−starBase	hsa−miR−301b
20	7.24	NULL	603	miRNA target−starBase	hsa−miR−20a
Underexpressed					
1	−19.38	NULL	572	Disease	GUDJ_psoriasis up
2	−16	NULL	717	Chr	Chr 16
3	−13.22	NULL	21	CC	cornified envelope
4	−12.95	NULL	135	H.Tiss	WIRTH_Mucosa
5	−12.19	NULL	553	Cancer	Lembcke_Colonic Inflammation
6	−12.15	NULL	312	BP	immune response
7	−11.96	NULL	42	BP	keratinization
8	−11.4	NULL	918	Chr	Chr 17
9	−11.39	NULL	76	BP	epidermis development
10	−11.16	NULL	51	BP	type I interferon signaling pathway
11	−9.98	NULL	53	BP	keratinocyte differentiation
12	−8.7	NULL	10	MF	RAGE receptor binding
13	−8.69	NULL	204	BP	cytokine−mediated signaling pathway
14	−8.56	NULL	417	H.Tiss	WIRTH_Immune system
15	−8.51	NULL	269	BP	inflammatory response
16	−8.41	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
17	−8.38	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	−8.24	NULL	60	BP	interferon−gamma−mediated signaling pathway
19	−8.23	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
20	−8.16	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up

GW_259

Local Summary

%DE = 0.67

metagenes = 1

genes = 15

genes in genesets = 15

genes with fdr < 0.1 = 9 (9 + / 0 −)

genes with fdr < 0.05 = 8 (8 + / 0 −)

genes with fdr < 0.01 = 3 (3 + / 0 −)

<r> metagenes = NA

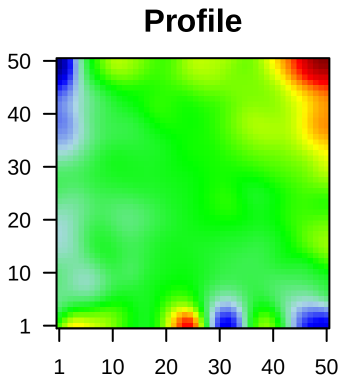
<r> genes = 0.64

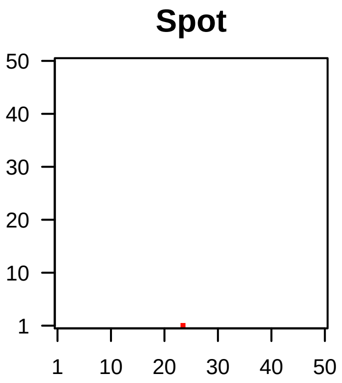
<FC> = 0.5

<shrinkage−t> = 17.59

<p−value> = 0.01

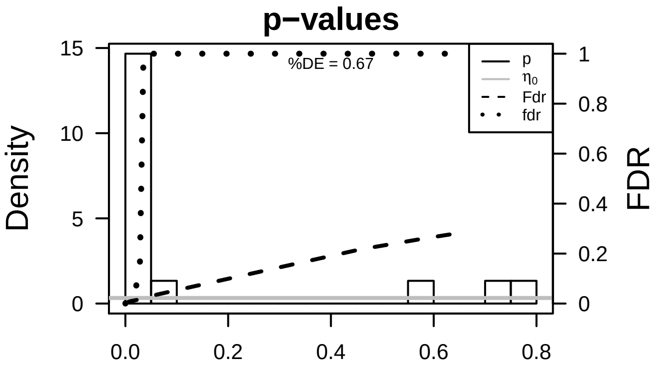
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	22998	1.18	1e−08	3e−05	24 x 1	LIM and calponin homology domains 1 [Source:HGNC Symb
2	222166	0.94	5e−06	7e−04	24 x 1	maturin, neural progenitor differentiation regulator homolog (X
3	148738	0.78	1e−04	9e−03	24 x 1	hemochromatosis type 2 (juvenile) [Source:HGNC Symbol;Ac
4	10486	0.64	2e−03	2e−02	24 x 1	CAP, adenylate cyclase−associated protein, 2 (yeast) [Source
5	786	0.58	5e−03	2e−02	24 x 1	calcium channel, voltage−dependent, gamma subunit 1 [Sour
6	4618	0.51	1e−02	2e−02	24 x 1	myogenic factor 6 (herculin) [Source:HGNC Symbol;Acc:7566
7	477	0.5	2e−02	2e−02	24 x 1	ATPase, Na+/K+ transporting, alpha 2 polypeptide [Source:H
8	9172	0.48	2e−02	2e−02	24 x 1	myomesin 2 [Source:HGNC Symbol;Acc:7614]
9	84665	0.47	2e−02	5e−02	24 x 1	myopalladin [Source:HGNC Symbol;Acc:23246]
10	150572	0.43	4e−02	1e−01	24 x 1	SET and MYND domain containing 1 [Source:HGNC Symbol;
11	200539	0.42	4e−02	1e+00	24 x 1	ankyrin repeat domain 23 [Source:HGNC Symbol;Acc:24470]
12	7111	0.37	8e−02	1e+00	24 x 1	tropomodulin 1 [Source:HGNC Symbol;Acc:11871]
13	131377	0.12	6e−01	1e+00	24 x 1	kelch−like family member 40 [Source:HGNC Symbol;Acc:303
14	4634	0.07	7e−01	1e+00	24 x 1	myosin, light chain 3, alkali; ventricular, skeletal, slow [Source
15	844	0.05	8e−01	1e+00	24 x 1	calsequestrin 1 (fast−twitch, skeletal muscle) [Source:HGNC



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.92	NULL	1 / 14	BP	actomyosin structure organization
2	20.97	NULL	1 / 16	GSEA C2	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_UP
3	15.49	NULL	4 / 20	CC	I band
4	15.14	NULL	8 / 127	H.Tiss	WIRTH_Muscle
5	12.6	NULL	1 / 10	BP	skeletal muscle tissue regeneration
6	12.6	NULL	1 / 10	TF Tissue	VAQUERIZAS_Skeletal.muscle.psoas
7	12.37	NULL	1 / 14	GSEA C2	NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON
8	12.27	NULL	1 / 10	BP	regulation of respiratory gaseous exchange by neurological system
9	11.67	NULL	1 / 21	BP	iron ion homeostasis
10	11.33	NULL	1 / 22	MF	coreceptor activity
11	11.31	NULL	1 / 16	GSEA C2	REACTOME_SIGNALING_BY_ROBO_RECEPTOR
12	10.76	NULL	1 / 12	BP	regulation of smooth muscle contraction
13	10.43	NULL	1 / 34	miRNA target−starBase	hsa−miR−615−5p
14	10.39	NULL	1 / 12	CC	myosin filament
15	10.18	NULL	1 / 13	GSEA C2	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
16	9.92	NULL	1 / 11	BP	positive regulation of myoblast differentiation
17	9.67	NULL	1 / 14	MF	hydrolase activity, acting on acid anhydrides, catalyzing transmemb
18	9.48	NULL	1 / 15	GSEA C2	REACTOME_MYOGENESSIS
19	9.38	NULL	3 / 84	BP	muscle contraction
20	9.37	NULL	2 / 18	BP	regulation of the force of heart contraction
21	9.23	NULL	1 / 15	Cancer	BEN−PORATH_UP
22	9.23	NULL	1 / 15	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP
23	9.23	NULL	3 / 34	CC	myofibril
24	9.21	NULL	1 / 22	BP	activation of adenylate cyclase activity
25	9.08	NULL	1 / 16	GSEA C2	HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY
26	8.9	NULL	1 / 12	MF	titin binding
27	8.84	NULL	1 / 16	GSEA C2	BROWNE_HCMV_INFECTION_2HR_UP
28	8.71	NULL	4 / 297	MF	actin binding
29	8.68	NULL	2 / 47	BP	skeletal muscle cell differentiation
30	8.53	NULL	1 / 16	CC	M band
31	8.5	NULL	1 / 25	BP	establishment or maintenance of cell polarity
32	8.22	NULL	2 / 44	BP	adult locomotory behavior
33	8.18	NULL	1 / 18	BP	regulation of muscle contraction
34	7.9	NULL	1 / 19	BP	ATP biosynthetic process
35	7.9	NULL	1 / 19	BP	regulation of vasoconstriction
36	7.9	NULL	1 / 19	BP	response to nicotine
37	7.84	NULL	1 / 24	CC	voltage−gated calcium channel complex
38	7.82	NULL	1 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
39	7.12	NULL	1 / 28	MF	voltage−gated calcium channel activity
40	7.02	NULL	1 / 14	MF	tropomyosin binding

GW_259

Local Summary

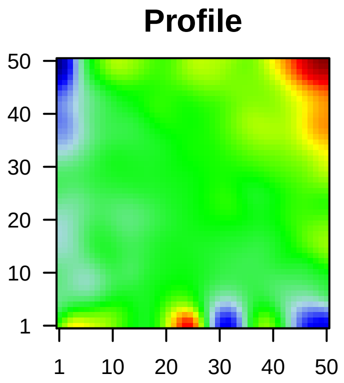
%DE = 0.75
metagenes = 23
genes = 300
genes in genesets = 298

genes with fdr < 0.1 = 179 (171 + / 8 −)
genes with fdr < 0.05 = 160 (153 + / 7 −)
genes with fdr < 0.01 = 134 (128 + / 6 −)

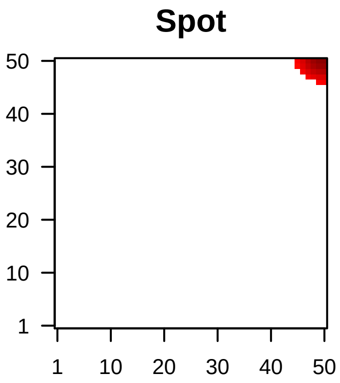
<r> metagenes = 0.92
<r> genes = 0.27

<FC> = 0.58
<shrinkage−t> = 20.37
<p−value> = 0
<fdr> = 0.44

Profile



Spot



Local Genelist

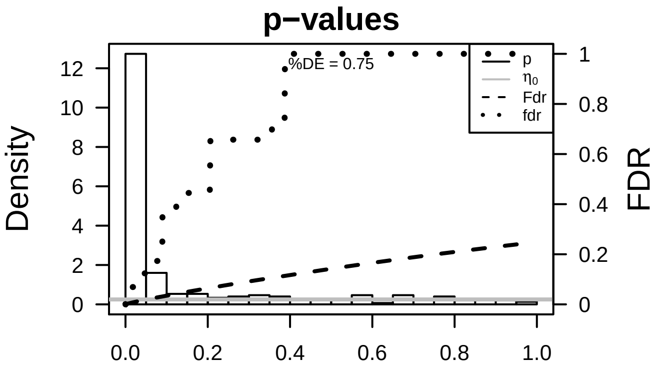
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	2.52	2e−16	2e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	2719	2.08	2e−16	2e−15	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
3	57110	1.71	2e−16	2e−15	50 x 50	HRAS−like suppressor [Source:HGNC Symbol;Acc:14922]
4	10643	1.77	2e−16	2e−15	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
5	3880	2.02	2e−16	2e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
6	4922	4.25	2e−16	2e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
7	139728	1.9	2e−16	2e−15	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
8	5984	1.72	2e−16	2e−15	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sy
9	6657	1.85	2e−16	2e−15	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
10	7037	1.59	2e−16	2e−15	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
11	1894	1.64	2e−15	6e−13	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
12	56922	1.6	1e−14	6e−13	50 x 50	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
13	116832	1.58	2e−14	6e−13	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
14	10655	1.57	2e−14	2e−12	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:
15	8702	1.55	6e−14	4e−12	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
16	1780	1.51	2e−13	4e−12	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
17	11166	1.51	2e−13	4e−12	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
18	57526	1.51	2e−13	8e−12	50 x 50	protocadherin 19 [Source:HGNC Symbol;Acc:14270]
19	86	1.5	3e−13	1e−10	46 x 50	actin−like 6A [Source:HGNC Symbol;Acc:24124]
20	7546	1.45	2e−12	3e−10	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.51	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	14.84	NULL	73 / 914	Chr	Chr 3
3	14.05	NULL	6 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
4	13.41	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
5	12.66	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
6	12.19	NULL	4 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
7	12.16	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
8	12.11	NULL	4 / 13	BP	regulation of blood vessel size
9	12.06	NULL	1 / 11	Glio	neurons_glio
10	10.43	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
11	10.28	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
12	10.11	NULL	1 / 15	MF	neuropeptide hormone activity
13	10	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
14	9.69	NULL	4 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
15	9.48	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
16	9.47	NULL	3 / 16	GSEA C2	CAFFAREL_RESPONSE_TO_THC_UP
17	9.42	NULL	3 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
18	9.03	NULL	3 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
19	8.88	NULL	3 / 13	GSEA C2	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
20	8.86	NULL	2 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
21	8.49	NULL	4 / 14	GSEA C2	KORKOLA_YOLK_SAC_TUMOR
22	8.45	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
23	8.31	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
24	7.93	NULL	3 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
25	7.89	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
26	7.89	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
27	7.88	NULL	4 / 11	GSEA C2	KALMA_E2F1_TARGETS
28	7.83	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
29	7.76	NULL	4 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
30	7.6	NULL	3 / 16	GSEA C2	SANA_RESPONSE_TO_IFNG_DN
31	7.6	NULL	1 / 5	miRNA target	miR−320
32	7.48	NULL	4 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
33	7.44	NULL	2 / 21	BP	osteoclast differentiation
34	7.42	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
35	7.42	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
36	7.36	NULL	2 / 16	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN
37	7.24	NULL	2 / 11	GSEA C2	DANG_MYC_TARGETS_UP
38	7.1	NULL	3 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
39	7.07	NULL	2 / 11	GSEA C2	CUI_GLUCOSE_DEPRIVATION
40	6.79	NULL	2 / 12	BP	cellular aldehyde metabolic process

p−values



GW_259

Local Summary

%DE = 0.91

metagenes = 2

genes = 100

genes in genesets = 98

genes with fdr < 0.1 = 86 (3 + / 83 −)

genes with fdr < 0.05 = 77 (1 + / 76 −)

genes with fdr < 0.01 = 65 (1 + / 64 −)

<r> metagenes = 1

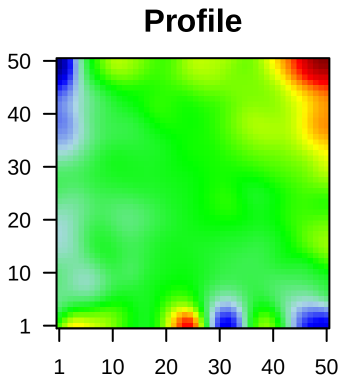
<r> genes = 0.51

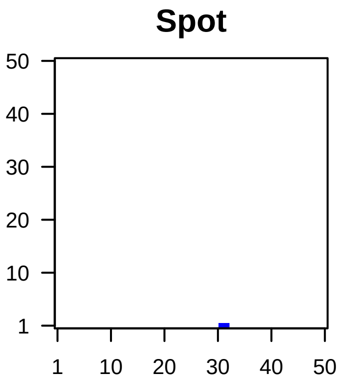
<FC> = −0.7

<shrinkage−t> = −24.53

<p−value> = 0

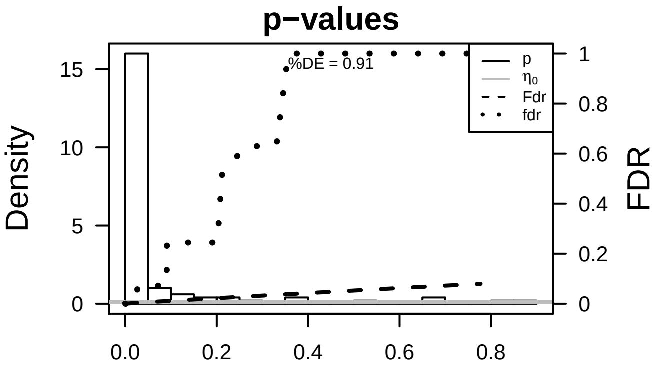
<fdr> = 0.29





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3136	−1.7	2e−16	1e−15	32 x 1	
2	4061	−1.72	2e−16	1e−15	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
3	4599	−1.54	4e−16	2e−13	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
4	629	−1.58	2e−14	2e−13	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
5	684	−1.56	5e−14	1e−10	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
6	10866	−1.4	1e−11	2e−09	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
7	9997	−1.31	2e−10	2e−09	32 x 1	SCO2 cytochrome c oxidase assembly protein [Source:HGNC
8	3106	−1.18	5e−10	2e−09	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
9	3134	−1.28	6e−10	2e−09	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
10	85441	−1.26	9e−10	2e−09	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
11	8519	−1.26	1e−09	1e−08	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
12	3135	−1.21	5e−09	1e−08	32 x 1	major histocompatibility complex, class I, G [Source:HGNC Sy
13	5699	−1.21	5e−09	1e−08	32 x 1	proteasome (prosome, macropain) subunit, beta type, 10 [Sou
14	10410	−1.1	6e−09	4e−08	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC S
15	10581	−1.09	1e−08	4e−07	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC S
16	64135	−1.12	6e−08	4e−07	32 x 1	interferon induced with helicase C domain 1 [Source:HGNC S
17	3133	−1.09	1e−07	4e−07	32 x 1	major histocompatibility complex, class I, E [Source:HGNC Sy
18	7453	−1.08	2e−07	8e−07	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
19	9636	−1.06	3e−07	8e−07	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
20	6772	−1.05	3e−07	3e−06	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−55.9	NULL	28 / 51	BP	type I interferon signaling pathway
2	−48.36	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
3	−44.6	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	−43.25	NULL	5 / 6	Lymphoma	DAVE_MHCCII BL DN
5	−42.89	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
6	−38.76	NULL	7 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	−36.87	NULL	10 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
8	−36.19	NULL	13 / 31	BP	negative regulation of viral genome replication
9	−34.39	NULL	6 / 10	CC	MHC class I protein complex
10	−33.54	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	−32.31	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
12	−32.31	NULL	30 / 123	BP	defense response to virus
13	−29.26	NULL	33 / 204	BP	cytokine−mediated signaling pathway
14	−29.08	NULL	26 / 109	BP	response to virus
15	−28.95	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
16	−28.54	NULL	7 / 18	BP	positive regulation of T cell mediated cytotoxicity
17	−26.9	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
18	−26.64	NULL	6 / 18	MF	peptide antigen binding
19	−26.15	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
20	−25.84	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
21	−25.65	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
22	−25.41	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
23	−24.78	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
24	−24.39	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
25	−24.37	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
26	−23.38	NULL	5 / 18	BP	response to interferon−gamma
27	−23.09	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
28	−21.82	NULL	30 / 274	Lymphoma	SPANG_IL21 DN
29	−21.59	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
30	−20.41	NULL	1 / 2	miRNA target	miR−152
31	−20.09	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
32	−20.01	NULL	5 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_LB_DN
33	−19.64	NULL	5 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
34	−19.37	NULL	46 / 572	Disease	GUDJ_psoriasis up
35	−19.04	NULL	11 / 70	BP	antigen processing and presentation of exogenous peptide antigen
36	−18.46	NULL	11 / 74	BP	antigen processing and presentation of exogenous peptide antigen
37	−17.89	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
38	−17.68	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
39	−17.44	NULL	11 / 74	BP	regulation of immune response
40	−16.83	NULL	3 / 9	GSEA C2	FURUKAWA_DUSP6_TARGETS_PCI35_UP

GW_259

Local Summary

%DE = 0.94

metagenes = 5

genes = 158

genes in genesets = 156

genes with fdr < 0.1 = 134 (1 + / 133 −)

genes with fdr < 0.05 = 120 (1 + / 119 −)

genes with fdr < 0.01 = 97 (1 + / 96 −)

<r> metagenes = 1

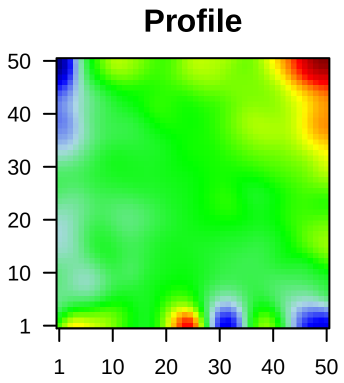
<r> genes = 0.66

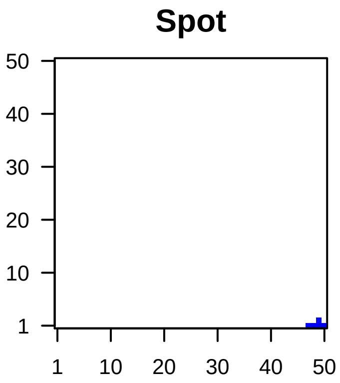
<FC> = −0.53

<shrinkage−t> = −18.68

<p−value> = 0

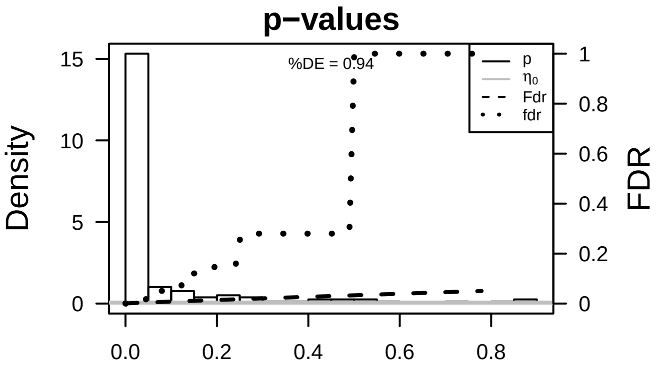
<fdr> = 0.44





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	5880	−1.72	2e−16	2e−15	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small (
2	3128	−1.45	2e−12	4e−08	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
3	260436	−1.21	5e−09	5e−08	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
4	3936	−1.18	1e−08	3e−07	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
5	3512	−1.11	7e−08	3e−07	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
6	3108	−1.11	8e−08	1e−06	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
7	3059	−1.08	2e−07	2e−06	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
8	972	−1.03	5e−07	2e−06	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
9	10537	−1.03	6e−07	2e−06	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
10	5552	−1.02	8e−07	9e−06	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
11	5341	−0.97	3e−06	9e−06	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
12	397	−0.96	3e−06	2e−05	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Syı
13	1535	−0.94	5e−06	3e−05	47 x 1	cytochrome b−245, alpha polypeptide [Source:HGNC Symbo
14	57172	−0.91	1e−05	3e−05	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
15	924	−0.89	1e−05	3e−05	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
16	3385	−0.89	2e−05	5e−05	50 x 1	intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc
17	5996	−0.87	3e−05	5e−05	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
18	7454	−0.86	3e−05	5e−05	50 x 1	Wiskott−Aldrich syndrome [Source:HGNC Symbol;Acc:12731
19	3620	−0.86	3e−05	5e−05	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:(
20	241	−0.84	4e−05	5e−05	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−32.74	NULL	12 / 15	CC	MHC class II protein complex
2	−30.38	NULL	69 / 417	H.Tiss	WIRTH_Immune system
3	−21.5	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
4	−20.71	NULL	14 / 47	BP	antigen processing and presentation
5	−20.09	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
6	−19.81	NULL	38 / 312	BP	immune response
7	−18.95	NULL	5 / 12	BP	immunoglobulin mediated immune response
8	−18.77	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	−18.75	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
10	−18.47	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
11	−18.07	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
12	−17.43	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	−16.57	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
14	−16.31	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
15	−16.22	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT
16	−16.22	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
17	−16.22	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
18	−16.21	NULL	27 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
19	−16.21	NULL	27 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
20	−16.21	NULL	27 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
21	−16.21	NULL	27 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
22	−16.12	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
23	−16.11	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
24	−15.53	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
25	−15.45	NULL	3 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
26	−14.87	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
27	−14.87	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
28	−14.8	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
29	−14.28	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
30	−14.07	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
31	−13.46	NULL	14 / 74	BP	regulation of immune response
32	−13.19	NULL	4 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
33	−13.08	NULL	12 / 60	BP	T cell costimulation
34	−12.97	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
35	−12.97	NULL	5 / 13	Cancer	GENTLES_modul18
36	−12.82	NULL	3 / 10	BP	negative thymic T cell selection
37	−12.68	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
38	−12.65	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
39	−12.6	NULL	7 / 28	CC	transport vesicle membrane
40	−12.58	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION

GW_259

Local Summary

%DE = 0.83

metagenes = 9

genes = 165

genes in genesets = 161

genes with fdr < 0.1 = 121 (8 + / 113 −)

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

genes with fdr < 0.01 = 108 (6 + / 102 −)

<r> metagenes = 0.97

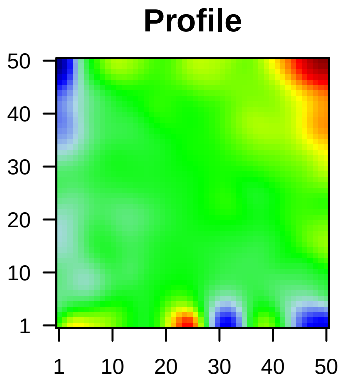
<r> genes = 0.49

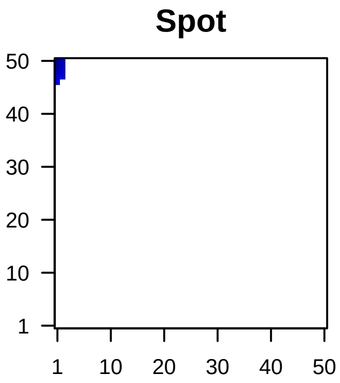
<FC> = −0.88

<shrinkage−t> = −30.99

<p−value> = 0

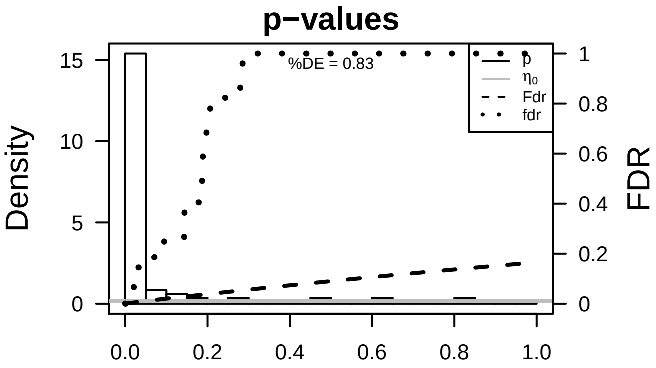
<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4680	−2.58	2e−16	2e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
2	22802	−1.71	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
3	84518	−1.77	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
4	49860	−1.92	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
5	1672	−2.35	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
6	414325	−2.15	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
7	1673	−2.71	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	56300	−1.84	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
9	5653	−2.02	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
10	5650	−2.03	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
11	3868	−1.77	2e−16	2e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
12	3851	−1.79	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
13	388533	−2.71	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
14	84648	−1.82	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
15	8581	−2	2e−16	2e−16	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
16	342897	−1.97	2e−16	2e−16	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebraf
17	51458	−1.68	2e−16	2e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
18	6283	−1.8	2e−16	2e−16	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac
19	6278	−2.9	2e−16	2e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
20	338324	−2.06	2e−16	2e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−45.14	NULL	18 / 21	CC	cornified envelope
2	−36.36	NULL	70 / 135	H.Tiss	WIRTH_Mucosa
3	−34.33	NULL	19 / 42	BP	keratinization
4	−32.66	NULL	23 / 53	BP	keratinocyte differentiation
5	−27.25	NULL	21 / 76	BP	epidermis development
6	−25.96	NULL	78 / 572	Disease	GUDJ_psoriasis up
7	−25.81	NULL	4 / 10	MF	RAGE receptor binding
8	−20.13	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−19.91	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
10	−18.87	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	−15.71	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−14.68	NULL	10 / 19	BP	peptide cross−linking
13	−14.22	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
14	−13.57	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
15	−12.59	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
16	−11.26	NULL	6 / 73	BP	defense response to bacterium
17	−10.62	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
18	−10.41	NULL	5 / 13	BP	negative regulation of peptidase activity
19	−10.08	NULL	45 / 1182	CC	extracellular region
20	−9.59	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
21	−9.46	NULL	5 / 38	BP	epithelial cell differentiation
22	−9.03	NULL	2 / 16	GSEA C2	MURATA_VIRULENCE_OF_H_PILORI
23	−8.92	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	−8.89	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
25	−8.82	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
26	−8.78	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	−8.78	NULL	3 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
28	−8.67	NULL	9 / 44	CC	keratin filament
29	−8.64	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
30	−8.56	NULL	20 / 186	MF	structural molecule activity
31	−8.43	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
32	−8.41	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
33	−7.85	NULL	2 / 14	BP	defense response to fungus
34	−7.81	NULL	6 / 53	MF	serine−type peptidase activity
35	−7.81	NULL	12 / 122	MF	serine−type endopeptidase activity
36	−7.77	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
37	−7.72	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
38	−7.67	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
39	−7.64	NULL	10 / 52	BP	negative regulation of endopeptidase activity
40	−7.62	NULL	3 / 12	BP	cellular aldehyde metabolic process