GW_068

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1537 (783 + / 754 −)

genes with fdr < 0.1 = 1204 (630 + / 574 −)

genes with fdr < 0.05 = 959 (520 + / 439 −)

genes with fdr < 0.01 = 639 (377 + / 262 −)

genes in genesets = 16332

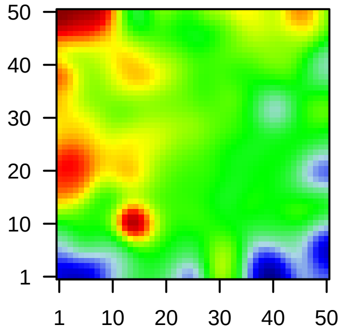
<FC> = 0

<shrinkage−t> = 0

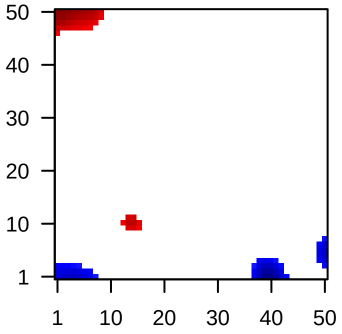
<p−value> = 0.13

<fdr> = 0.87

Profile



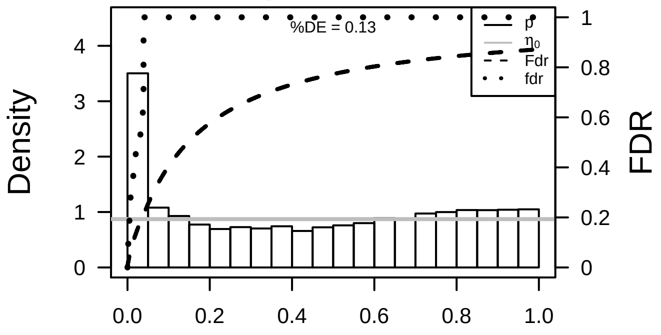
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	2.37	2e−16	5e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	220	1.68	2e−16	5e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
3	218	−2.07	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	51806	1.65	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
5	84290	1.68	2e−16	5e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	6364	3.03	2e−16	5e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
7	948	1.88	2e−16	5e−14	6 x 44	CD36 molecule (thrombospondin receptor) [Source:HGNC Sy
8	4680	1.75	2e−16	5e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
9	1308	−1.77	2e−16	5e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
10	49860	−1.83	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	2919	2.11	2e−16	5e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
12	1673	2.22	2e−16	5e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1717	2.47	2e−16	5e−14	13 x 50	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
14	1917	1.73	2e−16	5e−14	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
15	1999	1.71	2e−16	5e−14	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
16	2167	3.96	2e−16	5e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	729428	2.84	2e−16	5e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
18	729422	3.12	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	100008586	2.56	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
20	645073	2.73	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.62	NULL	572	Disease	GUDJ_psoriasis up
2	10.38	NULL	717	Chr	Chr 16
3	10.33	NULL	21	CC	cornified envelope
4	8.5	NULL	135	H.Tiss	WIRTH_Mucosa
5	8.24	NULL	1720	Chr	Chr 1
6	8.17	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
7	6.94	NULL	1135	Chr	Chr 19
8	6.93	NULL	42	BP	keratinization
9	6.85	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
10	6.8	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
11	6.76	NULL	53	BP	keratinocyte differentiation
12	6.63	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
13	6.01	NULL	83	BP	respiratory electron transport chain
14	6.01	NULL	10	MF	RAGE receptor binding
15	5.68	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
16	5.68	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
17	5.65	NULL	914	Chr	Chr 3
18	5.51	NULL	15	GSEA C2	LEE_LIVER_CANCER_CIPROFIBRATE_UP
19	5.46	NULL	1318	CC	mitochondrion
20	5.45	NULL	33	BP	cholesterol biosynthetic process
Underexpressed					
1	−9.29	NULL	242	BP	extracellular matrix organization
2	−8.73	NULL	83	CC	basement membrane
3	−8.69	NULL	190	CC	extracellular matrix
4	−8.37	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−7.13	NULL	630	Chr	Chr X
6	−7.11	NULL	918	Chr	Chr 17
7	−6.82	NULL	85	MF	integrin binding
8	−6.38	NULL	35	Glio	Colman_survival_associated
9	−6.33	NULL	12	BP	hemidesmosome assembly
10	−6.16	NULL	36	BP	muscle filament sliding
11	−6.12	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
12	−6.03	NULL	957	Chr	Chr 11
13	−5.92	NULL	69	BP	extracellular matrix disassembly
14	−5.88	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
15	−5.82	NULL	72	CC	extracellular vesicular exosome
16	−5.74	NULL	403	BP	cell adhesion
17	−5.61	NULL	10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
18	−5.6	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
19	−5.48	NULL	162	CC	external side of plasma membrane
20	−5.4	NULL	45	BP	negative regulation of angiogenesis

GW_068

Local Summary

%DE = 0.54

metagenes = 9

genes = 69

genes in genesets = 48

genes with fdr < 0.1 = 32 (30 + / 2 −)

genes with fdr < 0.05 = 30 (29 + / 1 −)

genes with fdr < 0.01 = 30 (29 + / 1 −)

<r> metagenes = 0.99

<r> genes = 0.37

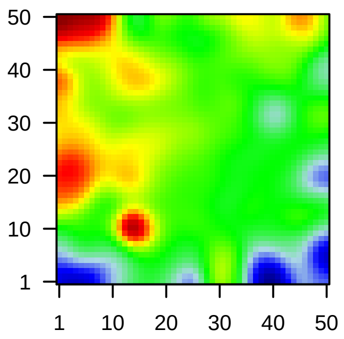
<FC> = 0.76

<shrinkage−t> = 26.58

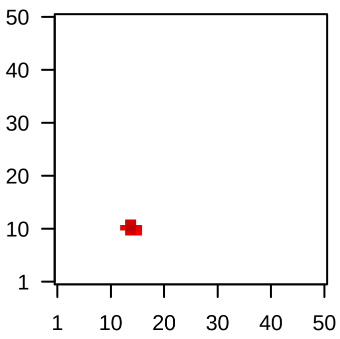
<p−value> = 0

<fdr> = 0.5

Profile



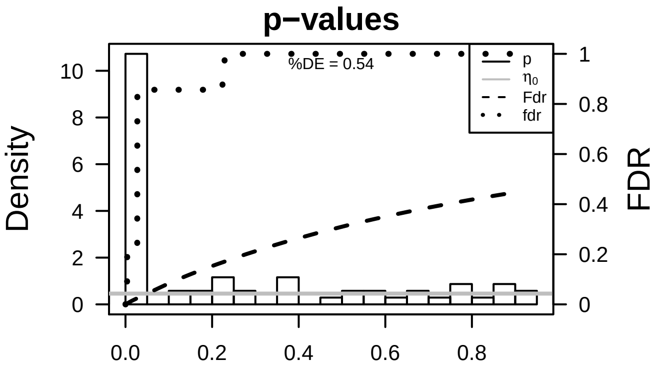
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	2.84	2e−16	5e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	3.12	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100008586	2.56	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	645073	2.73	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	729442	2.93	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	26748	2.72	2e−16	5e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
7	729396	2.12	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
8	729447	2.15	2e−16	5e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
9	645037	3.03	2e−16	5e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
10	26749	2.21	2e−16	5e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
11	2576	2.81	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
12	2577	2.8	2e−16	5e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2579	2.16	2e−16	5e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
14	100101629	1.65	2e−16	5e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
15	64591	2.12	2e−16	5e−16	15 x 11	testis specific protein, Y−linked 2 [Source:HGNC Symbol;Acc
16	2578	1.62	9e−16	1e−13	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
17	728403	1.58	4e−15	5e−10	16 x 11	testis specific protein, Y−linked 8 [Source:HGNC Symbol;Acc
18	56884	1.36	1e−11	2e−07	16 x 11	follistatin−like 5 [Source:HGNC Symbol;Acc:21386]
19	121355	1.17	7e−09	2e−07	14 x 11	gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
20	729431	1.15	1e−08	4e−07	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	16.24	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
2	15.9	NULL	1 / 10	GSEA C2	CONRAD_GERMLINE_STEM_CELL
3	14.09	NULL	1 / 12	GSEA C2	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
4	13.09	NULL	2 / 34	Chr	Chr Y
5	10.93	NULL	29 / 630	Chr	Chr X
6	7.69	NULL	2 / 86	BP	nucleosome assembly
7	6.6	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
8	5.44	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
9	5.2	NULL	1 / 17	BP	positive regulation of interleukin−1 beta secretion
10	4.57	NULL	8 / 120	H.Tiss	WIRTH_Testis
11	4.52	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
12	4.47	NULL	1 / 15	GSEA C2	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS
13	3.72	NULL	7 / 259	BP	spermatogenesis
14	3.53	NULL	6 / 419	CC	cellular_component
15	3.47	NULL	5 / 346	BP	cell differentiation
16	3.43	NULL	1 / 57	Glio	developing astrocytes
17	3.39	NULL	1 / 58	Glio	OPC
18	3.22	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
19	3.2	NULL	1 / 37	BP	positive regulation of cysteine−type endopeptidase activity involved
20	3.14	NULL	8 / 481	BP	biological_process
21	2.8	NULL	9 / 549	MF	molecular_function
22	2.76	NULL	1 / 32	BP	adherens junction organization
23	2.67	NULL	1 / 85	miRNA 3UTR	ACTG−17−3P
24	2.53	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
25	2.5	NULL	2 / 48	Cancer	KUIPER_MM poor survival
26	2.44	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
27	2.44	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
28	2.36	NULL	3 / 99	BP	homophilic cell adhesion
29	2.33	NULL	1 / 16	GSEA C2	JAEGER_METASTASIS_UP
30	2.27	NULL	2 / 23	BP	calcium−dependent cell−cell adhesion
31	2.16	NULL	1 / 68	MF	histone deacetylase binding
32	1.9	NULL	1 / 57	BP	cell−cell junction organization
33	1.66	NULL	2 / 37	BP	synapse assembly
34	1.66	NULL	1 / 70	BP	cell junction assembly
35	1.58	NULL	1 / 7	GSEA C2	REACTOME_AMINE_LIGAND_BINDING_RECEPTORS
36	1.49	NULL	4 / 579	MF	calcium ion binding
37	1.27	NULL	1 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
38	1.16	NULL	2 / 89	Glio	WIRTH_Normal Brain
39	0.99	NULL	1 / 314	miRNA 3UTR	TTGC−130A−−301−−130B
40	0.98	NULL	1 / 13	BP	positive regulation of smooth muscle contraction

GW_068

Local Summary

%DE = 0.68

metagenes = 34

genes = 471

genes in genesets = 462

genes with fdr < 0.1 = 233 (176 + / 57 −)

genes with fdr < 0.05 = 219 (167 + / 52 −)

genes with fdr < 0.01 = 176 (140 + / 36 −)

<r> metagenes = 0.94

<r> genes = 0.37

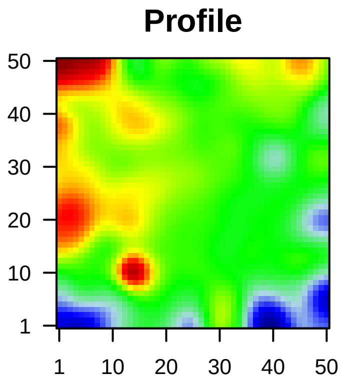
<FC> = 0.3

<shrinkage−t> = 10.66

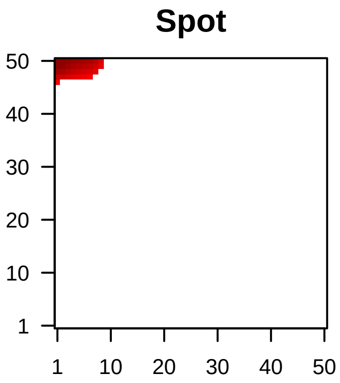
<p−value> = 0

<fdr> = 0.51

Profile



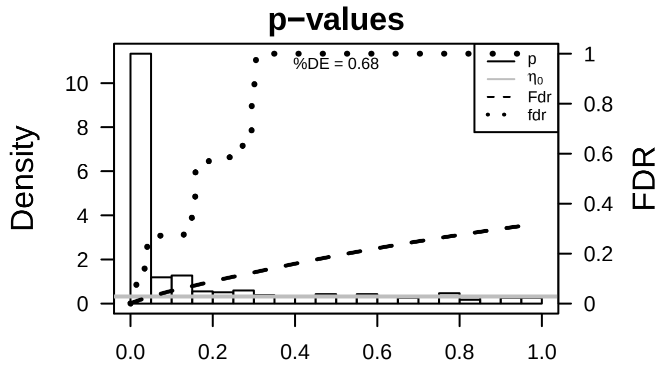
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	2.37	2e−16	1e−15	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	218	−2.07	2e−16	1e−15	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	51806	1.65	2e−16	1e−15	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
4	84290	1.68	2e−16	1e−15	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
5	4680	1.75	2e−16	1e−15	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	49860	−1.83	2e−16	1e−15	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
7	1673	2.22	2e−16	1e−15	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	1999	1.71	2e−16	1e−15	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
9	26085	2.66	2e−16	1e−15	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
10	5653	1.99	2e−16	1e−15	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
11	388533	2.18	2e−16	1e−15	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
12	3934	2.66	2e−16	1e−15	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
13	4118	−1.73	2e−16	1e−15	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
14	200958	2.02	2e−16	1e−15	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Acc
15	10158	1.87	2e−16	1e−15	1 x 47	PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:168
16	83886	1.77	2e−16	1e−15	1 x 50	protease, serine 27 [Source:HGNC Symbol;Acc:15475]
17	6283	2.43	2e−16	1e−15	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac
18	338324	2.31	2e−16	1e−15	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
19	6700	1.59	2e−16	1e−15	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
20	6701	2.46	2e−16	1e−15	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	27.32	NULL	19 / 21	CC	cornified envelope
2	19.14	NULL	101 / 135	H.Tiss	WIRTH_Mucosa
3	18.38	NULL	19 / 42	BP	keratinization
4	17.28	NULL	120 / 572	Disease	GUDJ_psoriasis up
5	17.18	NULL	28 / 76	BP	epidermis development
6	16.81	NULL	25 / 53	BP	keratinocyte differentiation
7	15.74	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	14.61	NULL	5 / 10	MF	RAGE receptor binding
9	13.77	NULL	4 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
10	13.1	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
11	11	NULL	10 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	9.63	NULL	1 / 2	Cancer	GENTLES_modul8
13	9.51	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
14	9.46	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
15	9.4	NULL	9 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
16	9.38	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
17	9.11	NULL	8 / 13	H.Tiss	WIRTH_Tonsil
18	8.55	NULL	5 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
19	8.53	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
20	8.26	NULL	3 / 17	Disease	BCHETNIA_EBM up
21	8.18	NULL	19 / 122	MF	serine−type endopeptidase activity
22	8.16	NULL	2 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
23	8.06	NULL	7 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	7.85	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
25	7.78	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
26	7.75	NULL	3 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
27	7.6	NULL	5 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
28	7.49	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
29	7.49	NULL	8 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
30	7.34	NULL	12 / 19	BP	peptide cross−linking
31	7.11	NULL	3 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
32	6.94	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
33	6.92	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
34	6.65	NULL	2 / 14	BP	protein homotrimerization
35	6.45	NULL	1 / 10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP
36	6.44	NULL	8 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
37	6.39	NULL	8 / 73	BP	defense response to bacterium
38	6.34	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
39	6.28	NULL	2 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
40	6.22	NULL	80 / 1182	CC	extracellular region

GW_068

Local Summary

%DE = 0.7

metagenes = 20

genes = 334

genes in genesets = 333

genes with fdr < 0.1 = 163 (27 + / 136 −)

genes with fdr < 0.05 = 146 (25 + / 121 −)

genes with fdr < 0.01 = 123 (21 + / 102 −)

<r> metagenes = 0.95

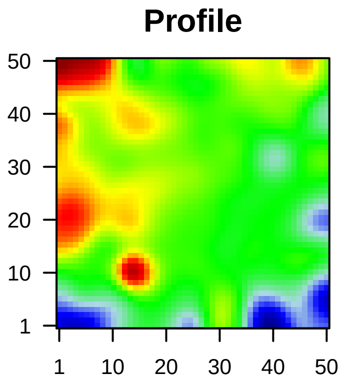
<r> genes = 0.39

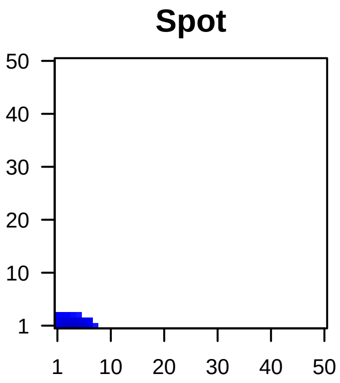
<FC> = −0.32

<shrinkage−t> = −11.03

<p−value> = 0

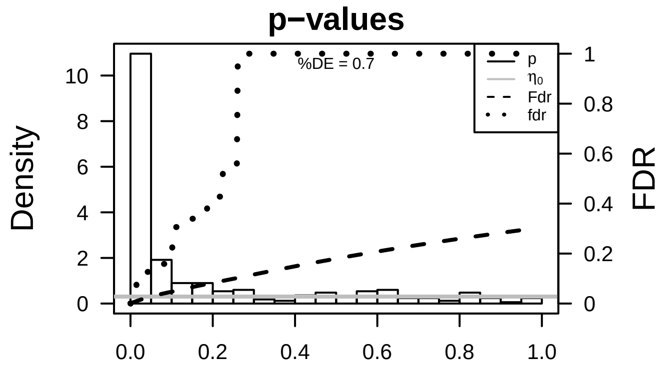
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2919	2.11	2e−16	4e−15	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimul
2	3576	2.09	2e−16	4e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
3	4060	2.14	2e−16	4e−15	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
4	4314	−2.13	2e−16	4e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
5	7057	−1.99	2e−16	4e−15	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
6	3371	−1.85	2e−16	4e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
7	5270	−1.59	3e−15	1e−12	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
8	12	1.55	2e−14	2e−11	1 x 1	
9	7431	−1.47	2e−13	2e−11	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
10	7076	−1.46	4e−13	3e−10	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
11	4692	1.39	5e−12	3e−10	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
12	3043	−1.39	5e−12	9e−09	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
13	5328	−1.29	1e−10	9e−09	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
14	6372	1.28	2e−10	1e−08	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
15	22920	−1.27	3e−10	2e−07	7 x 1	kinesin−associated protein 3 [Source:HGNC Symbol;Acc:170
16	366	1.2	3e−09	2e−07	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
17	4638	1.19	3e−09	2e−07	8 x 1	myosin light chain kinase [Source:HGNC Symbol;Acc:7590]
18	4312	−1.16	9e−09	2e−07	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
19	3553	1.16	9e−09	2e−07	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
20	5054	−1.15	1e−08	6e−07	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.07	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
2	−22.19	NULL	71 / 190	CC	extracellular matrix
3	−20.27	NULL	67 / 242	BP	extracellular matrix organization
4	−20.08	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
5	−18.77	NULL	89 / 250	Lymphoma	LENZ_Stromal signature 1
6	−18.12	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
7	−16.77	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
8	−16.38	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
9	−16.3	NULL	12 / 35	Glio	Colman_survival_associated
10	−16.13	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
11	−16.02	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN
12	−15.94	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
13	−15.92	NULL	5 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
14	−15.21	NULL	31 / 69	BP	extracellular matrix disassembly
15	−15.14	NULL	22 / 83	CC	basement membrane
16	−14.52	NULL	8 / 12	miRNA target	miR−29c
17	−14.38	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
18	−13.6	NULL	7 / 16	GSEA C2	ZHU_CMV_ALL_DN
19	−13.59	NULL	8 / 11	MF	platelet−derived growth factor binding
20	−13.36	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
21	−13.33	NULL	4 / 13	GSEA C2	REACTOME_FORMATION_OF_PLATELET_PLUG
22	−13.33	NULL	4 / 13	GSEA C2	REACTOME_PLATELET_ACTIVATION
23	−13.27	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
24	−13.26	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
25	−12.85	NULL	2 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
26	−12.8	NULL	4 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
27	−12.74	NULL	4 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
28	−12.49	NULL	5 / 10	BP	negative regulation of fibroblast growth factor receptor signaling pa
29	−12.36	NULL	6 / 16	GSEA C2	ZHU_CMV_24_HR_DN
30	−12.1	NULL	15 / 72	CC	extracellular vesicular exosome
31	−12	NULL	6 / 8	GSEA C2	YAGUE_PRETUMOR_DRUG_RESISTANCE_DN
32	−11.97	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
33	−11.84	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
34	−11.78	NULL	18 / 85	MF	integrin binding
35	−11.72	NULL	2 / 12	CC	platelet alpha granule
36	−11.44	NULL	3 / 11	BP	negative regulation of endothelial cell migration
37	−11.38	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
38	−11.19	NULL	8 / 43	CC	platelet alpha granule lumen
39	−11.08	NULL	27 / 64	BP	collagen catabolic process
40	−10.95	NULL	4 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP

GW_068

Local Summary

%DE = 0.73

metagenes = 23

genes = 337

genes in genesets = 309

genes with fdr < 0.1 = 152 (11 + / 141 −)

genes with fdr < 0.05 = 103 (1 + / 102 −)

genes with fdr < 0.01 = 65 (0 + / 65 −)

<r> metagenes = 0.97

<r> genes = 0.43

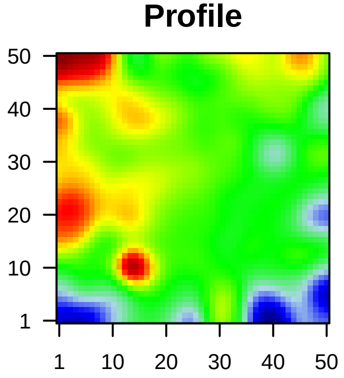
<FC> = −0.34

<shrinkage−t> = −11.83

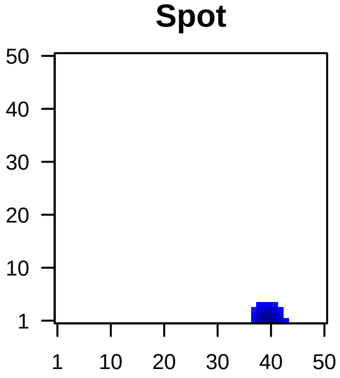
<p−value> = 0.02

<fdr> = 0.68

Profile



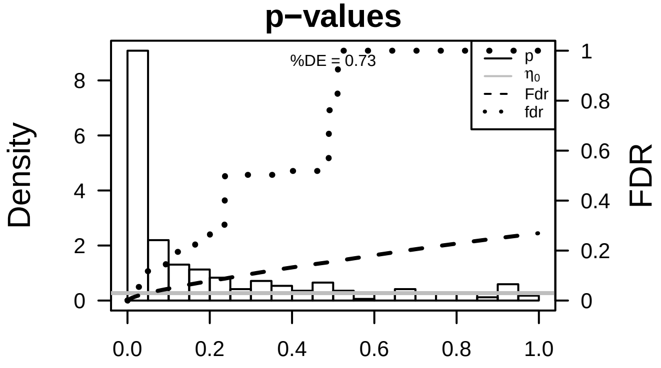
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	440353	−1.27	3e−10	7e−08	40 x 1	
2	641737	−1.15	1e−09	2e−07	40 x 1	
3	9905	−1.2	3e−09	1e−06	40 x 2	small G protein signaling modulator 2 [Source:HGNC Symbol
4	27148	−1.13	2e−08	4e−06	41 x 1	serine/threonine kinase 36 [Source:HGNC Symbol;Acc:1720
5	100132247	−1.09	6e−08	1e−05	39 x 3	nuclear pore complex interacting protein family, member B5 [
6	56203	−1.05	2e−07	2e−05	39 x 1	leiomodin 3 (fetal) [Source:HGNC Symbol;Acc:6649]
7	442578	−1.01	6e−07	2e−05	39 x 1	
8	728404	−0.99	8e−07	2e−05	39 x 2	ArfGAP with GTPase domain, ankyrin repeat and PH domain
9	25862	−0.98	1e−06	2e−05	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
10	319085	−0.96	1e−06	2e−05	39 x 1	ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
11	404093	−0.97	2e−06	2e−05	39 x 1	CUE domain containing 1 [Source:HGNC Symbol;Acc:31350]
12	613037	−0.96	2e−06	2e−05	40 x 2	nuclear pore complex interacting protein family, member B5 [
13	728294	−0.96	2e−06	1e−04	40 x 1	D−2−hydroxyglutarate dehydrogenase [Source:HGNC Symb
14	728903	−0.94	3e−06	1e−04	39 x 1	
15	23015	−0.92	5e−06	1e−04	39 x 1	golgin A8 family, member A [Source:HGNC Symbol;Acc:3197
16	100128288	−0.91	5e−06	1e−04	39 x 1	
17	3127	−0.9	7e−06	1e−04	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
18	84278	−0.9	7e−06	1e−04	39 x 1	
19	79716	−0.9	8e−06	3e−04	41 x 2	aminopeptidase−like 1 [Source:HGNC Symbol;Acc:16244]
20	727866	−0.87	2e−05	3e−04	38 x 3	family with sequence similarity 156, member B [Source:HGN

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−8.84	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−7.36	NULL	2 / 11	GSEA C2	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
3	−7.09	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
4	−6.5	NULL	4 / 14	MMML CGS	MACIEJ_MMML 8
5	−6.33	NULL	3 / 13	GSEA C2	ST_GAQ_PATHWAY
6	−5.71	NULL	1 / 11	GSEA C2	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
7	−4.93	NULL	11 / 163	BP	mRNA splicing, via spliceosome
8	−4.93	NULL	2 / 13	GSEA C2	ST_GA13_PATHWAY
9	−4.92	NULL	2 / 16	GSEA C2	LUI_THYROID_CANCER_CLUSTER_1
10	−4.87	NULL	2 / 14	BP	cellular response to estradiol stimulus
11	−4.81	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
12	−4.78	NULL	2 / 13	GSEA C2	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
13	−4.4	NULL	2 / 15	GSEA C2	REACTOME_DARPP32_EVENTS
14	−4.38	NULL	4 / 34	MF	hydrolase activity, hydrolyzing O−glycosyl compounds
15	−4.32	NULL	2 / 19	MF	3',5'−cyclic−nucleotide phosphodiesterase activity
16	−4.28	NULL	1 / 14	MF	tropomyosin binding
17	−4.19	NULL	1 / 3	GSEA C2	RUNNE_GENDER_EFFECT_DN
18	−4.15	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
19	−4.14	NULL	2 / 8	GSEA C2	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLEC
20	−4.09	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
21	−4.07	NULL	2 / 10	BP	cellular response to peptide hormone stimulus
22	−4.07	NULL	2 / 17	BP	glycogen catabolic process
23	−3.99	NULL	1 / 12	MF	metalloexopeptidase activity
24	−3.98	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
25	−3.92	NULL	2 / 15	GSEA C2	SAGIV_CD24_TARGETS_UP
26	−3.91	NULL	1 / 13	GSEA C2	LUI_THYROID_CANCER_PAX8_PPARG_UP
27	−3.91	NULL	3 / 19	BP	sprouting angiogenesis
28	−3.9	NULL	1 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
29	−3.88	NULL	1 / 19	BP	positive regulation of smoothened signaling pathway
30	−3.8	NULL	2 / 12	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
31	−3.75	NULL	1 / 20	miRNA target starBase	hsa−miR−380*
32	−3.75	NULL	1 / 15	BP	2−oxoglutarate metabolic process
33	−3.75	NULL	2 / 14	BP	mitochondrion morphogenesis
34	−3.73	NULL	1 / 14	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
35	−3.73	NULL	2 / 16	GSEA C2	YANAGIHARA_ESX1_TARGETS
36	−3.67	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
37	−3.67	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
38	−3.65	NULL	2 / 19	MF	mitogen−activated protein kinase kinase kinase binding
39	−3.59	NULL	2 / 15	GSEA C2	WONG_IFNA2_RESISTANCE_DN
40	−3.58	NULL	1 / 15	GSEA C2	WENDT_COHESIN_TARGETS_UP

GW_068

Local Summary

%DE = 0.73

metagenes = 10

genes = 167

genes in genesets = 167

genes with fdr < 0.1 = 77 (7 + / 70 −)

genes with fdr < 0.05 = 71 (6 + / 65 −)

genes with fdr < 0.01 = 48 (5 + / 43 −)

<r> metagenes = 0.94

<r> genes = 0.39

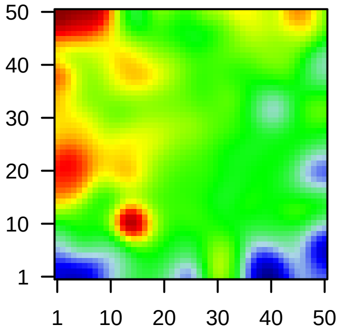
<FC> = −0.36

<shrinkage−t> = −12.62

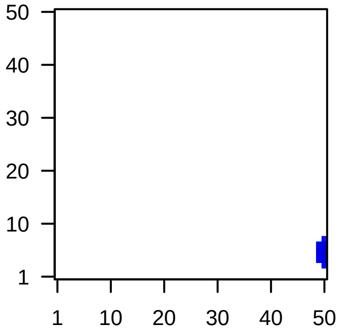
<p−value> = 0.01

<fdr> = 0.59

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3488	−1.71	2e−16	5e−15	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
2	6578	−1.67	2e−16	5e−15	50 x 4	solute carrier organic anion transporter family, member 2A1 [S
3	56892	1.45	5e−13	9e−08	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
4	8404	−1.21	2e−09	2e−07	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
5	6347	−1.17	6e−09	1e−06	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
6	929	1.11	4e−08	1e−05	50 x 3	CD14 molecule [Source:HGNC Symbol;Acc:1628]
7	1359	−1.03	3e−07	1e−05	50 x 7	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
8	1266	−0.99	9e−07	1e−05	50 x 6	calponin 3, acidic [Source:HGNC Symbol;Acc:2157]
9	347733	−0.99	9e−07	2e−05	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
10	7450	−0.96	2e−06	2e−05	50 x 6	von Willebrand factor [Source:HGNC Symbol;Acc:12726]
11	4781	−0.96	2e−06	4e−05	50 x 8	nuclear factor I/B [Source:HGNC Symbol;Acc:7785]
12	26249	−0.95	3e−06	4e−05	50 x 7	kelch−like family member 3 [Source:HGNC Symbol;Acc:6354
13	128553	−0.93	4e−06	4e−05	50 x 8	teashirt zinc finger homeobox 2 [Source:HGNC Symbol;Acc:1
14	25891	−0.92	5e−06	4e−05	50 x 8	peptidase domain containing associated with muscle regener
15	10791	0.91	6e−06	1e−04	50 x 4	vesicle−associated membrane protein 5 [Source:HGNC Sym
16	5175	−0.89	1e−05	1e−04	50 x 4	platelet/endothelial cell adhesion molecule 1 [Source:HGNC
17	1511	−0.88	1e−05	2e−04	50 x 7	cathepsin G [Source:HGNC Symbol;Acc:2532]
18	58480	0.86	2e−05	2e−04	50 x 8	ras homolog family member U [Source:HGNC Symbol;Acc:17
19	894	−0.85	3e−05	2e−04	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
20	347	−0.84	3e−05	2e−04	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.73	NULL	2 / 13	GSEA C2	ZIRN_TRETINOIN_RESPONSE_UP
2	−14.29	NULL	5 / 15	Cancer	GENTLES_modul13
3	−13.65	NULL	1 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
4	−12.65	NULL	5 / 43	BP	cellular response to organic cyclic compound
5	−12.45	NULL	2 / 14	MF	lipid transporter activity
6	−12.25	NULL	2 / 12	BP	regulation of glucose metabolic process
7	−11.67	NULL	2 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
8	−11.46	NULL	6 / 59	Lymphoma	LENZ_Stromal signature 2
9	−11.45	NULL	2 / 10	BP	angiotensin maturation
10	−11.33	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
11	−11.08	NULL	3 / 10	GSEA C2	FERRANDO_LYL1_NEIGHBORS
12	−10.99	NULL	2 / 16	GSEA C2	FURUKAWA_DUSP6_TARGETS_PCI35_DN
13	−10.89	NULL	4 / 26	BP	negative regulation of osteoblast differentiation
14	−10.77	NULL	4 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
15	−10.65	NULL	3 / 14	GSEA C2	TAVOR_CEBPA_TARGETS_UP
16	−10.61	NULL	3 / 16	GSEA C2	KORKOLA_TERATOMA_UP
17	−10.51	NULL	4 / 15	GSEA C2	NAKAJIMA_MAST_CELL
18	−10.37	NULL	3 / 16	GSEA C2	RODRIGUES_NTN1_TARGETS_UP
19	−10.2	NULL	2 / 11	BP	negative regulation of smooth muscle cell migration
20	−9.93	NULL	1 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
21	−9.88	NULL	2 / 13	GSEA C2	KEGG_RENIN_ANGIOTENSIN_SYSTEM
22	−9.85	NULL	4 / 19	BP	positive regulation of epithelial to mesenchymal transition
23	−9.42	NULL	2 / 10	GSEA C2	REACTOME_INTRINSIC_PATHWAY
24	−9.4	NULL	1 / 11	GSEA C2	ROZANOV_MMP14_CORRELATED
25	−9.29	NULL	2 / 12	GSEA C2	SHI_SPARC_TARGETS_DN
26	−9.26	NULL	1 / 6	GSEA C2	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP
27	−9.16	NULL	4 / 27	BP	negative regulation of smooth muscle cell proliferation
28	−9.16	NULL	3 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
29	−9.15	NULL	2 / 15	GSEA C2	ROY_WOUND_BLOOD_VESSEL_UP
30	−9.07	NULL	2 / 10	GSEA C2	EHRLICH_ICF_SYNDROM_UP
31	−9.01	NULL	3 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
32	−9	NULL	2 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
33	−8.95	NULL	1 / 12	BP	sodium−independent organic anion transport
34	−8.93	NULL	2 / 11	BP	blood coagulation, intrinsic pathway
35	−8.9	NULL	3 / 14	BP	regulation of Wnt signaling pathway
36	−8.83	NULL	1 / 4	GSEA C2	MARTINELLI_IMMATURE_NEUTROPHIL_UP
37	−8.8	NULL	1 / 13	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C3
38	−8.8	NULL	1 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
39	−8.75	NULL	3 / 10	BP	germ cell migration
40	−8.61	NULL	2 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC

p−values