GW_042

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1684 (988 + / 696 −)

genes with fdr < 0.1 = 1308 (787 + / 521 −)

genes with fdr < 0.05 = 1080 (660 + / 420 −)

genes with fdr < 0.01 = 754 (486 + / 268 −)

genes in genesets = 16332

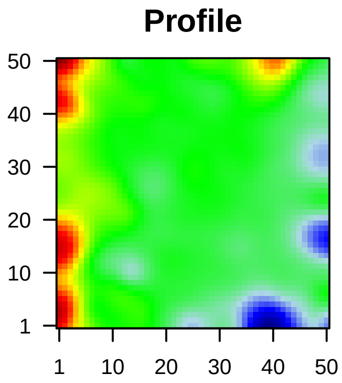
<FC> = 0

<shrinkage−t> = 0

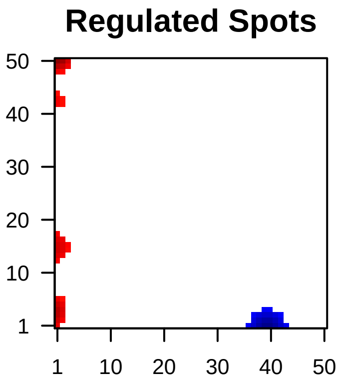
<p−value> = 0.12

<fdr> = 0.87

Profile



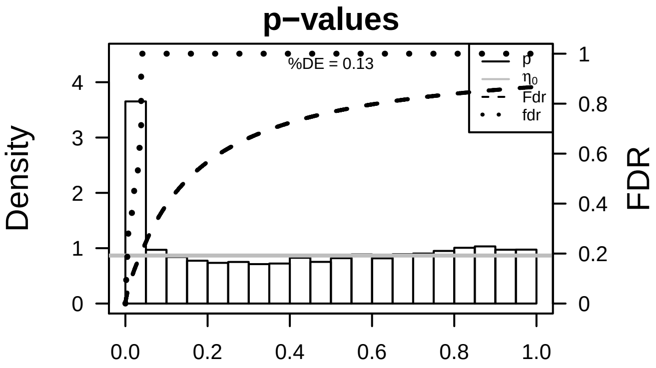
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	−1.31	2e−16	4e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	131	−1.6	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	218	1.21	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	8412	1.17	2e−16	4e−14	1 x 5	breast cancer anti−estrogen resistance 3 [Source:HGNC Sym
5	768	1.21	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
6	57172	1.53	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
7	857	1.65	2e−16	4e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
8	6364	−1.4	2e−16	4e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
9	595	1.18	2e−16	4e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
10	970	1.45	2e−16	4e−14	33 x 2	CD70 molecule [Source:HGNC Symbol;Acc:11937]
11	1048	1.28	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
12	1056	1.43	2e−16	4e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
13	1152	1.35	2e−16	4e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
14	22802	1.54	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	26047	−1.25	2e−16	4e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
16	1288	1.36	2e−16	4e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
17	51200	1.57	2e−16	4e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
18	51755	1.3	2e−16	4e−14	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
19	49860	1.55	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
20	2919	1.17	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.74	NULL	135	H.Tiss	WIRTH_Mucosa
2	10.62	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
3	9.8	NULL	482	BP	cellular protein metabolic process
4	9.68	NULL	683	CC	extracellular space
5	9.6	NULL	242	BP	extracellular matrix organization
6	8.78	NULL	12	BP	hemidesmosome assembly
7	8.49	NULL	83	CC	basement membrane
8	8.47	NULL	530	Cancer	Lembcke_Normal vs Adenoma
9	8.03	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
10	7.72	NULL	253	BP	translation
11	7.65	NULL	76	BP	epidermis development
12	7.57	NULL	572	Disease	GUDJ_psoriasis up
13	7.27	NULL	11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
14	7.25	NULL	519	Chr	Chr 14
15	6.9	NULL	190	CC	extracellular matrix
16	6.86	NULL	1182	CC	extracellular region
17	6.69	NULL	19	BP	peptide cross−linking
18	6.62	NULL	9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
19	6.57	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
20	6.39	NULL	22	MF	insulin−like growth factor binding
Underexpressed					
1	−5.94	NULL	417	H.Tiss	WIRTH_Immune system
2	−5.51	NULL	1574	BP	transcription, DNA−templated
3	−5.38	NULL	618	Chr	Chr 4
4	−5.14	NULL	4640	CC	nucleus
5	−5	NULL	15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
6	−4.9	NULL	1749	MF	DNA binding
7	−4.87	NULL	1581	BP	regulation of transcription, DNA−dependent
8	−4.81	NULL	127	H.Tiss	WIRTH_Muscle
9	−4.81	NULL	1820	MF	metal ion binding
10	−4.65	NULL	274	Lymphoma	SPANG_IL21 DN
11	−4.44	NULL	10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
12	−4.43	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
13	−4.35	NULL	3	MMML CGS	MACIEJ_MMML 7
14	−4.33	NULL	158	miRNA 3UTR	MIR−448
15	−4.32	NULL	1033	Chr	Chr 2
16	−4.27	NULL	5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
17	−4.16	NULL	12	CC	myosin filament
18	−4.12	NULL	44	MF	structural constituent of muscle
19	−4.09	NULL	940	MF	nucleic acid binding
20	−3.97	NULL	41	TF Tissue	VAQUERIZAS_Thymus

GW_042

Local Summary

%DE = 0.68

metagenes = 11

genes = 176

genes in genesets = 174

genes with fdr < 0.1 = 99 (87 + / 12 −)

genes with fdr < 0.05 = 88 (78 + / 10 −)

genes with fdr < 0.01 = 70 (63 + / 7 −)

<r> metagenes = 0.97

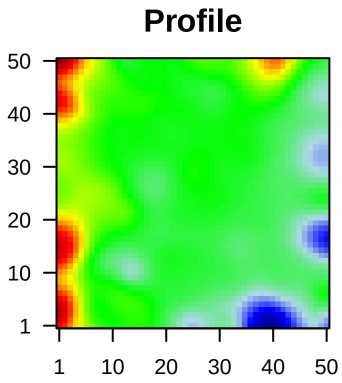
<r> genes = 0.37

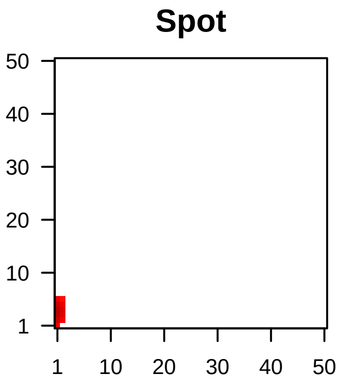
<FC> = 0.35

<shrinkage−t> = 12.24

<p−value> = 0

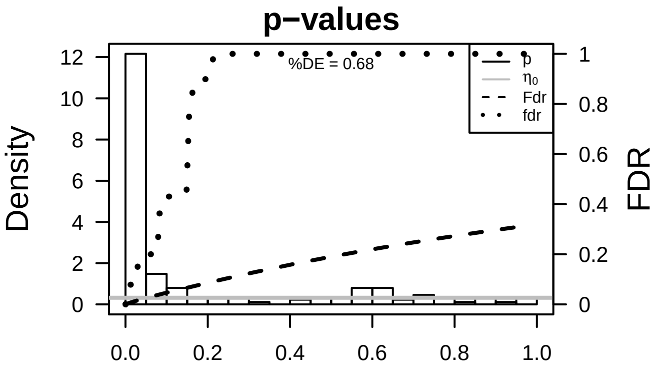
<fdr> = 0.46





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8412	1.17	2e−16	7e−16	1 x 5	breast cancer anti−estrogen resistance 3 [Source:HGNC Sym
2	768	1.21	2e−16	7e−16	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	857	1.65	2e−16	7e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
4	595	1.18	2e−16	7e−16	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
5	2919	1.17	2e−16	7e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
6	84141	1.2	2e−16	7e−16	1 x 2	eva−1 homolog A (C. elegans) [Source:HGNC Symbol;Acc:25
7	10644	1.24	2e−16	7e−16	1 x 6	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
8	11009	1.42	2e−16	7e−16	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
9	3678	1.63	2e−16	7e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
10	3909	1.26	2e−16	7e−16	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
11	3918	1.38	2e−16	7e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
12	4319	1.66	2e−16	7e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
13	4322	1.68	2e−16	7e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
14	6695	1.18	2e−16	7e−16	1 x 2	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
15	6781	1.61	2e−16	7e−16	1 x 3	stanniocalcin 1 [Source:HGNC Symbol;Acc:11373]
16	7045	1.07	2e−16	7e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
17	7057	1.29	2e−16	7e−16	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
18	3371	1.32	2e−16	7e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
19	4314	1.12	5e−15	2e−13	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
20	56603	1.11	7e−15	3e−11	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	23.54	NULL	1 / 2	miRNA target miR−101b
2	21.69	NULL	2 / 7	GSEA C2 FREDERICK_PRKCI_TARGETS
3	18.99	NULL	4 / 13	GSEA C2 CHIN_BREAST_CANCER_COPY_NUMBER_UP
4	18.86	NULL	4 / 14	GSEA C2 SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
5	18.4	NULL	1 / 2	miRNA target miR−16−1
6	18.26	NULL	8 / 15	GSEA C2 CROMER_TUMORIGENESIS_UP
7	18.21	NULL	4 / 16	GSEA C2 LI_PROSTATE_CANCER_EPIGENETIC
8	17.86	NULL	4 / 15	BP negative regulation of anoikis
9	16.54	NULL	2 / 4	miRNA target miR−195
10	16.48	NULL	30 / 242	BP extracellular matrix organization
11	16.46	NULL	6 / 15	GSEA C2 LEE_LIVER_CANCER_HEPATOBLAST
12	16.23	NULL	2 / 5	GSEA C2 VERNELL_RETINOBLASTOMA_PATHWAY_DN
13	16.16	NULL	3 / 12	BP hemidesmosome assembly
14	15.97	NULL	9 / 35	Glio Colman_survival_associated
15	14.87	NULL	2 / 6	GSEA C2 FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN
16	14.84	NULL	3 / 15	GSEA C2 SAGIV_CD24_TARGETS_DN
17	14.75	NULL	10 / 68	Glio cultured astroglia vs. in vivo astrocytes
18	14.21	NULL	43 / 683	CC extracellular space
19	13.98	NULL	1 / 3	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
20	13.96	NULL	3 / 10	GSEA C2 JEON_SMAD6_TARGETS_UP
21	13.77	NULL	4 / 16	GSEA C2 KEGG_BLADDER_CANCER
22	13.58	NULL	2 / 13	GSEA C2 WANG_METHYLATED_IN_BREAST_CANCER
23	13.22	NULL	2 / 15	GSEA C2 MUELLER_METHYLATED_IN_GLIOBLASTOMA
24	13.08	NULL	5 / 16	MF fibronectin binding
25	13.04	NULL	3 / 15	GSEA C2 SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
26	12.96	NULL	2 / 11	BP response to magnesium ion
27	12.95	NULL	2 / 6	GSEA C2 AGARWAL_AKT_PATHWAY_TARGETS
28	12.91	NULL	2 / 6	miRNA target let−7b
29	12.87	NULL	2 / 14	GSEA C2 DORSEY_GAB2_TARGETS
30	12.58	NULL	3 / 16	GSEA C2 DORN_ADENOVIRUS_INFECTION_32HR_DN
31	12.58	NULL	3 / 16	GSEA C2 DORN_ADENOVIRUS_INFECTION_48HR_DN
32	12.5	NULL	14 / 190	CC extracellular matrix
33	12.4	NULL	2 / 8	GSEA C2 NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
34	12.26	NULL	4 / 13	BP response to vitamin D
35	12.01	NULL	13 / 183	CC proteinaceous extracellular matrix
36	11.77	NULL	2 / 13	GSEA C2 OHM_METHYLATED_IN_ADULT_CANCERS
37	11.76	NULL	4 / 16	GSEA C2 KERLEY_RESPONSE_TO_CISPLATIN_UP
38	11.68	NULL	2 / 9	GSEA C2 ITO_PTTG1_TARGETS_DN
39	11.65	NULL	5 / 51	BP regulation of cell migration
40	11.63	NULL	3 / 19	MF extracellular matrix binding

GW_042

Local Summary

%DE = 0.68

metagenes = 12

genes = 165

genes in genesets = 165

genes with fdr < 0.1 = 72 (69 + / 3 −)

genes with fdr < 0.05 = 56 (54 + / 2 −)

genes with fdr < 0.01 = 42 (40 + / 2 −)

<r> metagenes = 0.97

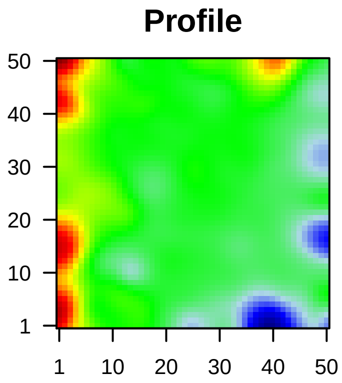
<r> genes = 0.3

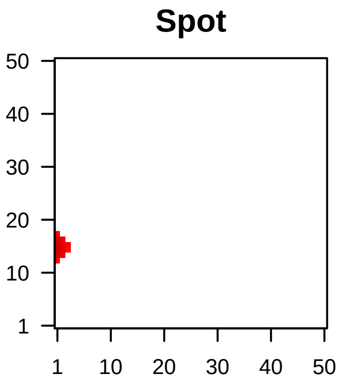
<FC> = 0.27

<shrinkage−t> = 9.62

<p−value> = 0.01

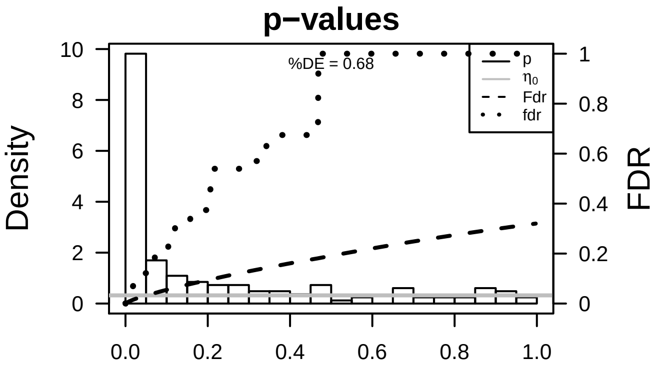
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1152	1.35	2e−16	3e−15	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
2	8772	1.74	2e−16	3e−15	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
3	51083	1.85	2e−16	3e−15	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
4	283869	2.46	2e−16	3e−15	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
5	2017	1.16	4e−16	3e−10	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]
6	2194	0.98	6e−12	9e−09	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
7	2030	0.91	2e−10	1e−06	1 x 14	solute carrier family 29 (equilibrative nucleoside transporter),
8	219927	0.78	4e−08	1e−06	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
9	286053	0.78	5e−08	5e−06	1 x 17	non−SMC element 2, MMS21 homolog (S. cerevisiae) [Sourc
10	51373	0.74	2e−07	5e−06	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
11	9688	0.74	2e−07	5e−06	1 x 15	nucleoporin 93kDa [Source:HGNC Symbol;Acc:28958]
12	25902	0.73	3e−07	3e−05	1 x 13	methylenetetrahydrofolate dehydrogenase (NADP+ depender
13	219931	0.7	9e−07	2e−04	1 x 14	two pore segment channel 2 [Source:HGNC Symbol;Acc:208
14	10598	0.66	4e−06	2e−04	1 x 14	AHA1, activator of heat shock 90kDa protein ATPase homolo
15	79929	0.64	8e−06	4e−04	1 x 16	MAP6 domain containing 1 [Source:HGNC Symbol;Acc:2575
16	23028	0.6	2e−05	4e−04	1 x 14	lysine (K)−specific demethylase 1A [Source:HGNC Symbol;A
17	5881	0.6	3e−05	4e−04	3 x 16	ras−related C3 botulinum toxin substrate 3 (rho family, small
18	55240	0.6	3e−05	4e−04	3 x 16	STEAP family member 3, metalloreductase [Source:HGNC S
19	4839	0.59	4e−05	4e−04	2 x 15	NOP2 nucleolar protein [Source:HGNC Symbol;Acc:7867]
20	92856	0.58	5e−05	4e−04	1 x 18	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	21.1	NULL	2 / 21	BP	feeding behavior
2	18.87	NULL	2 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
3	18.08	NULL	1 / 6	GSEA C2	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
4	18.08	NULL	1 / 6	GSEA C2	REACTOME_GPCR_LIGAND_BINDING
5	16.98	NULL	1 / 6	GSEA C2	GALI_TP53_TARGETS_APOPTOTIC_DN
6	16.54	NULL	1 / 7	GSEA C2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
7	15.32	NULL	1 / 8	GSEA C2	SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
8	15.32	NULL	1 / 8	GSEA C2	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
9	14.6	NULL	2 / 11	GSEA C2	SCIBETTA_KDM5B_TARGETS_DN
10	14.17	NULL	2 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
11	13.9	NULL	2 / 12	GSEA C2	BHATTACHARYA_EMBRYONIC_STEM_CELL
12	13.52	NULL	2 / 10	BP	creatine metabolic process
13	13.49	NULL	1 / 10	GSEA C2	WELCSH_BRCA1_TARGETS_1_DN
14	13.49	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
15	13.47	NULL	2 / 18	BP	smooth muscle contraction
16	13.45	NULL	1 / 9	GSEA C2	BIOCARTA_RELA_PATHWAY
17	13.45	NULL	1 / 9	GSEA C2	BIOCARTA_NFKB_PATHWAY
18	13.45	NULL	1 / 9	GSEA C2	BIOCARTA_SODD_PATHWAY
19	13.45	NULL	1 / 9	GSEA C2	REACTOME_DEATH_RECEPTOR_SIGNALLING
20	13.06	NULL	2 / 13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
21	12.79	NULL	1 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
22	12.79	NULL	1 / 11	GSEA C2	PARK_APL_PATHOGENESIS_DN
23	12.67	NULL	1 / 10	MF	death receptor binding
24	12.67	NULL	1 / 10	BP	positive regulation of macrophage differentiation
25	12.59	NULL	2 / 14	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_DN
26	12.48	NULL	2 / 10	GSEA C2	ZHU_CMV_24_HR_UP
27	12.48	NULL	2 / 10	GSEA C2	ZHU_CMV_ALL_UP
28	12	NULL	1 / 11	BP	regulation of extrinsic apoptotic signaling pathway in absence of lig
29	12	NULL	1 / 11	GSEA C2	HOFMANN_CELL_LYMPHOMA_DN
30	12	NULL	1 / 11	GSEA C2	ST_TUMOR_NECROSIS_FACTOR_PATHWAY
31	11.64	NULL	1 / 13	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
32	11.42	NULL	1 / 12	GSEA C2	BIOCARTA_FAS_PATHWAY
33	11.34	NULL	2 / 65	BP	neuropeptide signaling pathway
34	11.16	NULL	1 / 14	GSEA C2	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL
35	11.16	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP
36	10.92	NULL	1 / 13	BP	lymph node development
37	10.92	NULL	1 / 13	GSEA C2	BIOCARTA_TNFR1_PATHWAY
38	10.73	NULL	1 / 15	MF	neuropeptide hormone activity
39	10.73	NULL	1 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
40	10.73	NULL	1 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC

GW_042

Local Summary

%DE = 0.75

metagenes = 5

genes = 96

genes in genesets = 95

genes with fdr < 0.1 = 58 (51 + / 7 −)

genes with fdr < 0.05 = 52 (45 + / 7 −)

genes with fdr < 0.01 = 37 (34 + / 3 −)

<r> metagenes = 0.99

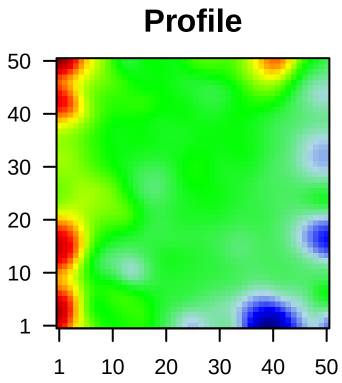
<r> genes = 0.41

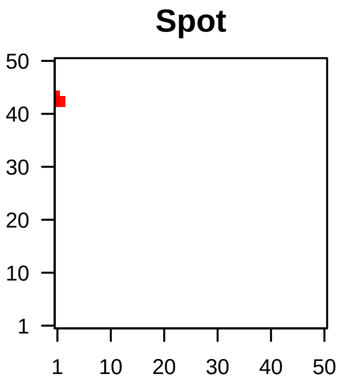
<FC> = 0.35

<shrinkage−t> = 12.14

<p−value> = 0

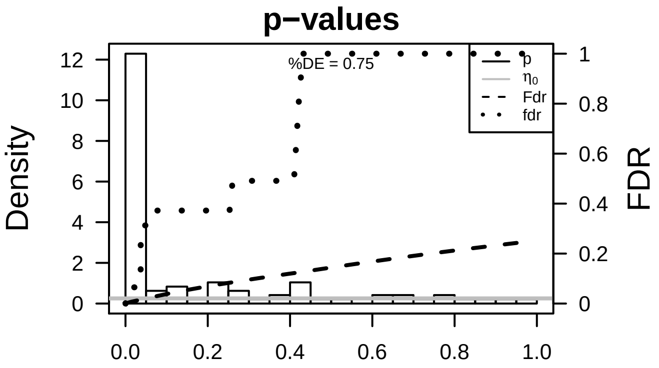
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1288	1.36	2e−16	7e−16	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
2	51200	1.57	2e−16	7e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
3	2152	1.55	2e−16	7e−16	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
4	3489	1.22	2e−16	7e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
5	50805	1.42	2e−16	7e−16	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
6	55214	2.02	2e−16	7e−16	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
7	4753	−1.47	2e−16	7e−16	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
8	5744	1.35	2e−16	7e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
9	8140	1.16	4e−16	1e−14	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
10	5836	1.15	9e−16	1e−14	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:97
11	1001	1.14	1e−15	1e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
12	2167	−1.13	2e−15	1e−12	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
13	80115	1.07	6e−14	2e−11	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
14	6713	1.02	8e−13	4e−11	2 x 43	squalene epoxidase [Source:HGNC Symbol;Acc:11279]
15	858	1	2e−12	2e−09	1 x 42	caveolin 2 [Source:HGNC Symbol;Acc:1528]
16	3306	0.92	1e−10	6e−09	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
17	4747	0.9	3e−10	5e−08	1 x 43	
18	3655	0.85	3e−09	1e−07	1 x 42	integrin, alpha 6 [Source:HGNC Symbol;Acc:6142]
19	205	0.81	1e−08	1e−07	2 x 42	adenylate kinase 4 [Source:HGNC Symbol;Acc:363]
20	3852	0.74	1e−08	1e−06	1 x 44	keratin 5 [Source:HGNC Symbol;Acc:6442]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.96	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
2	15.55	NULL	2 / 11	BP	positive regulation of positive chemotaxis
3	14.08	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
4	13.43	NULL	3 / 12	BP	hemidesmosome assembly
5	13.34	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
6	12.77	NULL	3 / 16	GSEA C2	LEONARD_HYPOXIA
7	12.54	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
8	12.17	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
9	11.87	NULL	1 / 6	miRNA target-starBase	hsa−miR−126
10	11.63	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
11	11.61	NULL	1 / 10	GSEA C2	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASC
12	11.32	NULL	1 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
13	11.15	NULL	2 / 15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
14	10.96	NULL	1 / 11	GSEA C2	BIOCARTA_EXTRINSIC_PATHWAY
15	10.66	NULL	2 / 13	GSEA C2	HASINA_NOL7_TARGETS_UP
16	10.65	NULL	1 / 7	GSEA C2	BIOCARTA_FEEDER_PATHWAY
17	10.64	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
18	10.54	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
19	10.5	NULL	1 / 12	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP
20	10.48	NULL	1 / 6	GSEA C2	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_
21	10.41	NULL	4 / 83	CC	basement membrane
22	10.39	NULL	1 / 19	MF	L−ascorbic acid binding
23	10.38	NULL	6 / 112	Glio	Christensen_hypermethylated_in_grade2_oligoastrocytoma
24	10.18	NULL	1 / 10	GSEA C2	BIOCARTA_ACE2_PATHWAY
25	10.12	NULL	5 / 85	Glio	laffaire_hypermeth_LGG_vs_control
26	10.06	NULL	1 / 10	BP	surfactant homeostasis
27	9.92	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
28	9.92	NULL	1 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
29	9.92	NULL	1 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
30	9.92	NULL	1 / 13	GSEA C2	BAELDE_DIABETIC_NEPHROPATHY_DN
31	9.79	NULL	1 / 5	GSEA C2	ZHAN_EARLY_DIFFERENTIATION_GENES_UP
32	9.75	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
33	9.67	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA
34	9.64	NULL	2 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
35	9.61	NULL	1 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
36	9.58	NULL	1 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
37	9.53	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
38	9.49	NULL	1 / 14	GSEA C2	CHANG_CORE_SERUM_RESPONSE_UP
39	9.46	NULL	6 / 132	Glio	Christensen_hypermethylated_in_grade3_oligoastrocytoma
40	9.34	NULL	1 / 5	miRNA target	miR−196a

GW_042

Local Summary

%DE = 0.8

metagenes = 8

genes = 137

genes in genesets = 134

genes with fdr < 0.1 = 92 (78 + / 14 −)

genes with fdr < 0.05 = 92 (78 + / 14 −)

genes with fdr < 0.01 = 77 (65 + / 12 −)

<r> metagenes = 0.99

<r> genes = 0.52

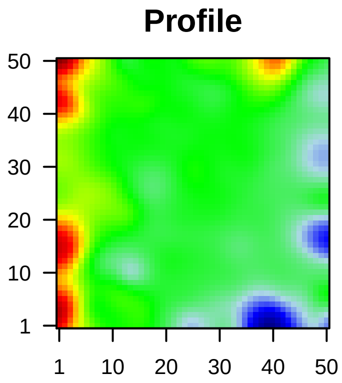
<FC> = 0.38

<shrinkage−t> = 13.49

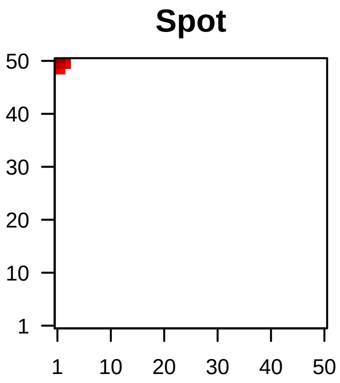
<p−value> = 0

<fdr> = 0.33

Profile



Spot



Local Genelist

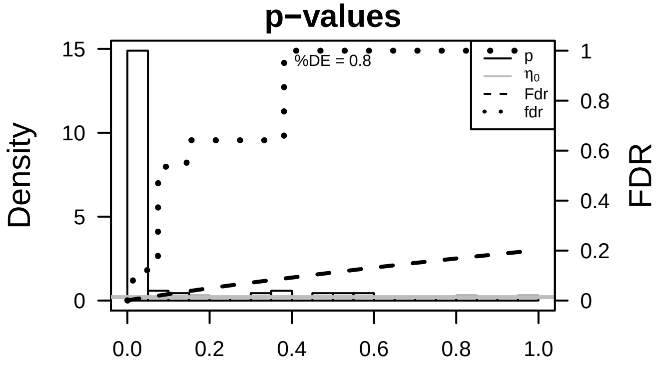
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.6	2e−16	4e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	1.21	2e−16	4e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	1048	1.28	2e−16	4e−16	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
4	22802	1.54	2e−16	4e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	49860	1.55	2e−16	4e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	26085	1.39	2e−16	4e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
7	3860	1.29	2e−16	4e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
8	3851	2.08	2e−16	4e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
9	84648	−1.79	2e−16	4e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
10	5507	1.18	2e−16	4e−16	3 x 50	protein phosphatase 1, regulatory subunit 3C [Source:HGNC
11	51458	1.31	2e−16	4e−16	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
12	84659	−1.53	2e−16	4e−16	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
13	6337	1.32	2e−16	4e−16	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
14	57152	1.21	2e−16	4e−16	1 x 50	secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
15	6707	1.28	2e−16	4e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
16	7053	1.58	2e−16	4e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
17	4118	1.16	4e−16	1e−13	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
18	6698	1.02	6e−15	1e−13	1 x 50	small proline−rich protein 1A [Source:HGNC Symbol;Acc:112
19	1992	1.11	9e−15	1e−12	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Sc
20	6702	1.07	7e−14	1e−12	1 x 50	

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	51.42	NULL	63 / 135	H.Tiss	WIRTH_Mucosa
2	22.25	NULL	14 / 21	CC	cornified envelope
3	21.22	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	20.9	NULL	8 / 19	BP	peptide cross−linking
5	18.43	NULL	6 / 13	BP	negative regulation of peptidase activity
6	18.08	NULL	19 / 53	BP	keratinocyte differentiation
7	17.55	NULL	16 / 42	BP	keratinization
8	15.76	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	14.42	NULL	16 / 76	BP	epidermis development
10	13.83	NULL	65 / 572	Disease	GUDJ_psoriasis up
11	11.45	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
12	11.34	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
13	11.33	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
14	11.07	NULL	4 / 38	BP	epithelial cell differentiation
15	10.87	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	10.48	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	10.17	NULL	3 / 12	BP	cellular aldehyde metabolic process
18	10.07	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
19	9.94	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
20	9.52	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
21	9.29	NULL	10 / 122	MF	serine−type endopeptidase activity
22	9.21	NULL	5 / 29	BP	regulation of proteolysis
23	9.12	NULL	8 / 52	BP	negative regulation of endopeptidase activity
24	8.94	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
25	8.56	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
26	8.36	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
27	8.34	NULL	4 / 44	CC	keratin filament
28	8.23	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
29	7.91	NULL	1 / 6	GSEA C2	CLAUS_PGR_POSITIVE_MENINGIOMA_UP
30	7.78	NULL	13 / 186	MF	structural molecule activity
31	7.71	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
32	7.52	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
33	7.49	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
34	7.49	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
35	7.44	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
36	7.41	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
37	7.31	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
38	7.21	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
39	7.19	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
40	7.19	NULL	1 / 7	Glio	KIM_epithelial−mesenchymal−transition related genes_decreased

p−values



GW_042

Local Summary

%DE = 0.69

metagenes = 22

genes = 324

genes in genesets = 296

genes with fdr < 0.1 = 136 (5 + / 131 −)

genes with fdr < 0.05 = 115 (5 + / 110 −)

genes with fdr < 0.01 = 59 (3 + / 56 −)

<r> metagenes = 0.97

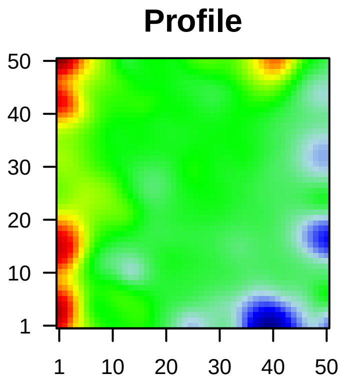
<r> genes = 0.43

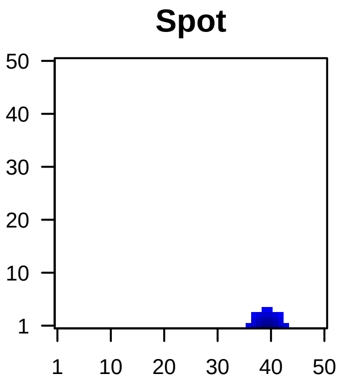
<FC> = −0.26

<shrinkage−t> = −9.02

<p−value> = 0.02

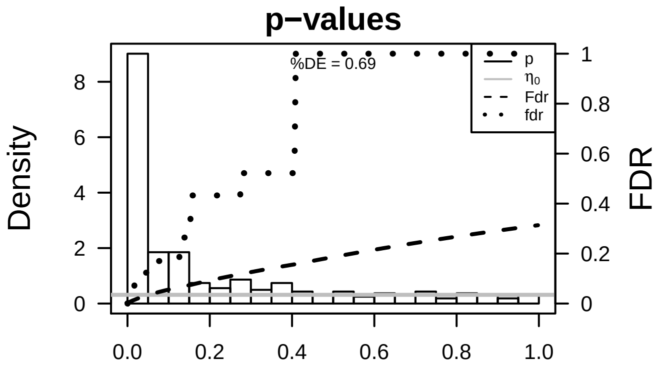
<fdr> = 0.66





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	−1.03	6e−13	1e−09	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	51326	0.97	1e−11	3e−06	42 x 1	ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc
3	55142	−0.79	3e−08	7e−06	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symbo
4	57464	−0.76	1e−07	1e−05	40 x 1	striatin interacting protein 2 [Source:HGNC Symbol;Acc:2220
5	250	−0.73	3e−07	1e−05	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
6	115703	−0.72	4e−07	1e−05	41 x 1	Rho GTPase activating protein 33 [Source:HGNC Symbol;Ac
7	401494	−0.72	4e−07	1e−05	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [Sou
8	3586	−0.66	6e−07	1e−05	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
9	152485	−0.71	8e−07	1e−05	41 x 1	zinc finger protein 827 [Source:HGNC Symbol;Acc:27193]
10	84061	−0.7	9e−07	1e−05	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
11	126205	−0.7	1e−06	1e−05	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
12	374860	−0.69	1e−06	2e−05	40 x 1	ankyrin repeat domain 30B [Source:HGNC Symbol;Acc:2416
13	90639	−0.69	1e−06	2e−05	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
14	641737	−0.64	1e−06	3e−05	40 x 1	
15	113277	−0.68	2e−06	3e−05	40 x 1	transmembrane protein 106A [Source:HGNC Symbol;Acc:28
16	22834	−0.68	2e−06	3e−05	40 x 1	zinc finger protein 652 [Source:HGNC Symbol;Acc:29147]
17	442578	−0.67	2e−06	1e−04	39 x 1	
18	414918	0.65	5e−06	1e−04	43 x 1	DENN/MADD domain containing 6B [Source:HGNC Symbol;
19	26279	−0.65	6e−06	1e−04	40 x 1	phospholipase A2, group IID [Source:HGNC Symbol;Acc:903
20	255031	−0.64	6e−06	2e−04	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.61	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−10.93	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−10.12	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
4	−9.59	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
5	−7.28	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
6	−7.13	NULL	3 / 24	BP	negative regulation of T cell proliferation
7	−7.02	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
8	−6.57	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
9	−6.57	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
10	−6.48	NULL	2 / 14	BP	mitochondrion morphogenesis
11	−6.41	NULL	2 / 14	BP	cellular response to estradiol stimulus
12	−6.4	NULL	3 / 15	GSEA C2	WANG_CLIM2_TARGETS_UP
13	−6.14	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
14	−5.73	NULL	1 / 15	CC	MHC class II protein complex
15	−5.58	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
16	−5.48	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
17	−5.26	NULL	2 / 23	BP	protein N−linked glycosylation
18	−5.19	NULL	2 / 15	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_DN
19	−5.15	NULL	2 / 13	GSEA C2	ST_GAQ_PATHWAY
20	−5.15	NULL	2 / 13	GSEA C2	ST_GA13_PATHWAY
21	−4.9	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
22	−4.9	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
23	−4.83	NULL	2 / 16	TF Tissue	VAQUERIZAS_Fetal thyroid
24	−4.83	NULL	1 / 10	CC	oligosaccharyltransferase complex
25	−4.79	NULL	2 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
26	−4.78	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS
27	−4.73	NULL	2 / 22	BP	negative regulation of interferon−gamma production
28	−4.69	NULL	1 / 21	CC	clathrin−coated endocytic vesicle membrane
29	−4.68	NULL	1 / 3	GSEA C2	RUNNE_GENDER_EFFECT_DN
30	−4.64	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
31	−4.63	NULL	1 / 11	BP	negative regulation of interleukin−12 production
32	−4.63	NULL	1 / 11	GSEA C2	SU_PANCREAS
33	−4.6	NULL	2 / 28	CC	transport vesicle membrane
34	−4.58	NULL	4 / 60	BP	T cell costimulation
35	−4.49	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
36	−4.49	NULL	1 / 12	MF	Rac GTPase activator activity
37	−4.49	NULL	1 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
38	−4.45	NULL	1 / 4	GSEA C2	KORKOLA_CHORIOCARCINOMA
39	−4.43	NULL	1 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
40	−4.4	NULL	1 / 12	BP	negative regulation of growth of symbiont in host