GW_010

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1784 (1010 + / 774 −)

genes with fdr < 0.1 = 1197 (703 + / 494 −)

genes with fdr < 0.05 = 1007 (607 + / 400 −)

genes with fdr < 0.01 = 699 (450 + / 249 −)

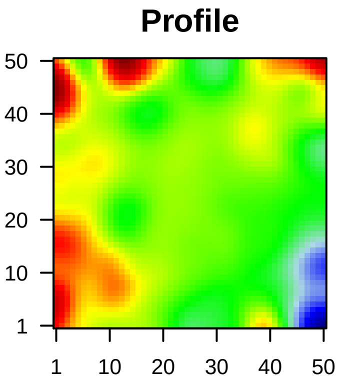
genes in genesets = 16332

<FC> = 0

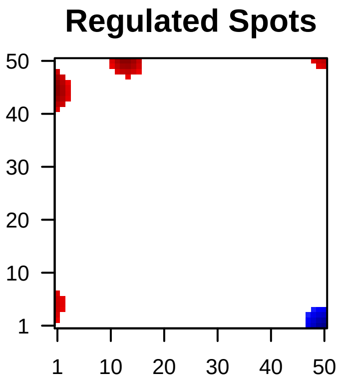
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



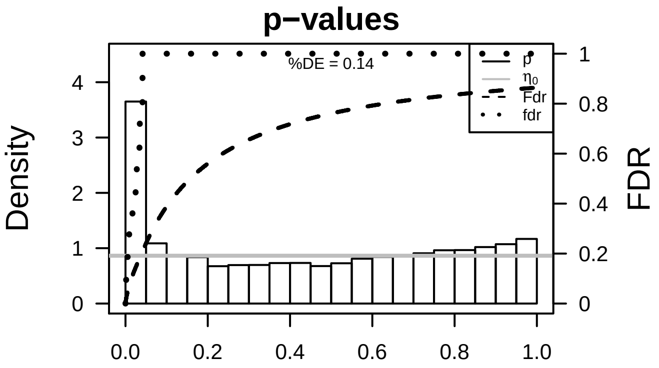
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.49	2e−16	6e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	57016	2.2	2e−16	6e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	1.95	2e−16	6e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	1109	1.9	2e−16	6e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	218	2.24	2e−16	6e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	222	1.48	2e−16	6e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
7	242	1.81	2e−16	6e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
8	260436	−1.73	2e−16	6e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
9	29113	1.97	2e−16	6e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
10	26256	1.53	2e−16	6e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
11	8900	1.39	2e−16	6e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
12	894	1.78	2e−16	6e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
13	10576	1.4	2e−16	6e−14	41 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
14	972	−1.44	2e−16	6e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
15	63928	1.42	2e−16	6e−14	13 x 50	calcineurin−like EF−hand protein 2 [Source:HGNC Symbol;A
16	22802	−2.36	2e−16	6e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	49860	−2.4	2e−16	6e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1466	−1.56	2e−16	6e−14	5 x 43	cysteine and glycine−rich protein 2 [Source:HGNC Symbol;A
19	1515	1.67	2e−16	6e−14	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
20	9547	1.67	2e−16	6e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.65	NULL	42	BP	keratinization
2	10.91	NULL	866	Chr	Chr 12
3	10.06	NULL	717	Chr	Chr 16
4	9.94	NULL	21	CC	cornified envelope
5	9.33	NULL	53	BP	keratinocyte differentiation
6	8.77	NULL	918	Chr	Chr 17
7	8.6	NULL	76	BP	epidermis development
8	8.5	NULL	15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
9	8.35	NULL	19	BP	peptide cross−linking
10	7.72	NULL	21	CC	desmosome
11	6.36	NULL	16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
12	6.15	NULL	14	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON
13	6.1	NULL	11	GSEA C2	ITO_PTTG1_TARGETS_UP
14	6.08	NULL	449	Chr	Chr 20
15	5.99	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
16	5.85	NULL	11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
17	5.75	NULL	572	Disease	GUDJ_psoriasis up
18	5.63	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
19	5.61	NULL	242	BP	extracellular matrix organization
20	5.55	NULL	11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
Underexpressed					
1	−12	NULL	15	CC	MHC class II protein complex
2	−11.01	NULL	618	Chr	Chr 4
3	−10.62	NULL	417	H.Tiss	WIRTH_Immune system
4	−8.88	NULL	47	BP	antigen processing and presentation
5	−8.84	NULL	1720	Chr	Chr 1
6	−7.41	NULL	312	BP	immune response
7	−7.15	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
8	−7.04	NULL	21	CC	clathrin−coated endocytic vesicle membrane
9	−6.73	NULL	32	CC	ER to Golgi transport vesicle membrane
10	−6.64	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
11	−6.58	NULL	60	BP	T cell costimulation
12	−6.57	NULL	28	CC	transport vesicle membrane
13	−6.37	NULL	6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
14	−6.24	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
15	−6.19	NULL	1135	Chr	Chr 19
16	−6.02	NULL	7	MMML CGS	MACIEJ_MMML 5
17	−5.87	NULL	84	BP	T cell receptor signaling pathway
18	−5.84	NULL	35	CC	trans−Golgi network membrane
19	−5.76	NULL	87	BP	antigen processing and presentation of exogenous peptide antigen
20	−5.72	NULL	60	BP	interferon−gamma−mediated signaling pathway

GW_010

Local Summary

%DE = 0.77

metagenes = 9

genes = 178

genes in genesets = 176

genes with fdr < 0.1 = 83 (81 + / 2 −)

genes with fdr < 0.05 = 73 (71 + / 2 −)

genes with fdr < 0.01 = 62 (60 + / 2 −)

<r> metagenes = 0.97

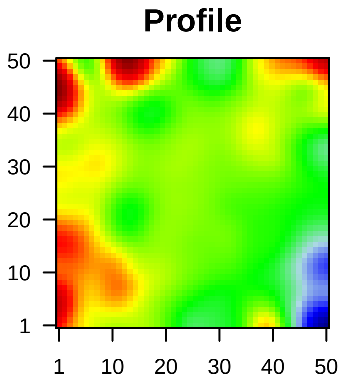
<r> genes = 0.36

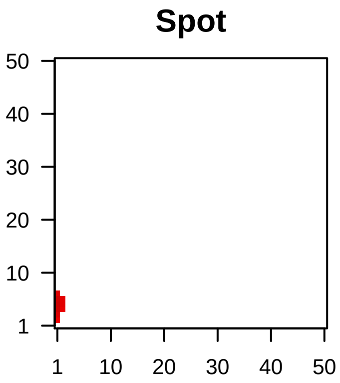
<FC> = 0.36

<shrinkage−t> = 12.83

<p−value> = 0

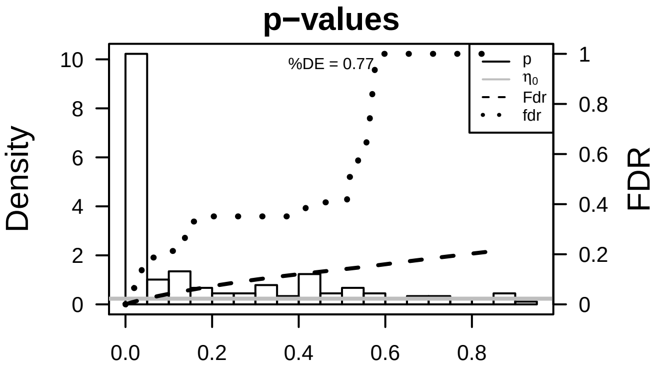
<fdr> = 0.55





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	22943	1.48	2e−16	2e−15	1 x 7	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Sy
2	10644	1.52	2e−16	2e−15	1 x 6	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
3	284111	1.52	2e−16	2e−15	1 x 7	solute carrier family 13 (sodium−dependent citrate transporte
4	3371	2.13	2e−16	2e−15	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
5	5054	1.34	2e−15	8e−14	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
6	10468	1.32	4e−15	4e−13	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
7	7045	1.19	1e−14	7e−11	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
8	650	1.19	2e−12	2e−10	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10
9	2201	1.15	9e−12	2e−10	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
10	51330	1.14	2e−11	2e−10	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
11	8870	1.13	2e−11	4e−09	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:5392
12	3918	1.09	1e−10	1e−08	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
13	5834	1.04	6e−10	1e−08	1 x 7	phosphorylase, glycogen; brain [Source:HGNC Symbol;Acc:9
14	1294	1.04	7e−10	3e−08	1 x 5	collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
15	54972	1.02	1e−09	1e−07	1 x 7	transmembrane protein 132A [Source:HGNC Symbol;Acc:31
16	3625	0.99	4e−09	2e−07	2 x 5	inhibin, beta B [Source:HGNC Symbol;Acc:6067]
17	857	0.97	9e−09	1e−06	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
18	1948	0.92	4e−08	2e−06	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]
19	54549	0.9	1e−07	2e−06	1 x 7	sidekick cell adhesion molecule 2 [Source:HGNC Symbol;Acc
20	84058	0.87	2e−07	2e−06	1 x 7	WD repeat domain 54 [Source:HGNC Symbol;Acc:25770]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.94	NULL	4 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
2	18.23	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
3	15.56	NULL	6 / 35	Glio	Colman_survival_associated
4	13.35	NULL	4 / 16	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
5	13.22	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
6	13.14	NULL	3 / 28	BP	negative regulation of cell adhesion
7	12.67	NULL	4 / 12	BP	hemidesmosome assembly
8	12.64	NULL	9 / 83	CC	basement membrane
9	12.5	NULL	3 / 16	BP	negative regulation of peptidyl−serine phosphorylation
10	12.44	NULL	3 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
11	12.4	NULL	1 / 10	BP	prostate gland epithelium morphogenesis
12	11.97	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
13	11.86	NULL	1 / 6	GSEA C2	REACTOME_GLUCOSE_AND_OTHER_SUGAR_SLC_TRANSPC
14	11.71	NULL	2 / 10	BP	regulation of receptor activity
15	11.71	NULL	2 / 10	GSEA C2	BIOCARTA_FIBRINOLYSIS_PATHWAY
16	11.54	NULL	1 / 2	miRNA target	miR−16−1
17	11.51	NULL	27 / 242	BP	extracellular matrix organization
18	11.48	NULL	32 / 403	BP	cell adhesion
19	11.42	NULL	3 / 14	GSEA C2	DITTMER_PTHLH_TARGETS_DN
20	11.4	NULL	2 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
21	11.39	NULL	2 / 4	miRNA target	miR−195
22	11.26	NULL	3 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
23	11.01	NULL	2 / 10	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_DN
24	10.93	NULL	4 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
25	10.79	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
26	10.77	NULL	2 / 10	BP	negative regulation of blood coagulation
27	10.71	NULL	4 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
28	10.68	NULL	1 / 13	Cancer	GENTLES_modul17
29	10.65	NULL	2 / 12	GSEA C2	KIM_WT1_TARGETS_8HR_UP
30	10.56	NULL	4 / 55	BP	odontogenesis of dentin−containing tooth
31	10.38	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
32	10.24	NULL	3 / 16	GSEA C2	KIM_WT1_TARGETS_UP
33	10.21	NULL	6 / 93	BP	anatomical structure morphogenesis
34	10.15	NULL	3 / 14	GSEA C2	CLIMENT_BREAST_CANCER_COPY_NUMBER_UP
35	9.95	NULL	3 / 11	Glio	Phillips MES up vs Prolif & PN
36	9.93	NULL	1 / 2	miRNA target	miR−101b
37	9.84	NULL	1 / 15	CC	interstitial matrix
38	9.84	NULL	1 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
39	9.81	NULL	4 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C8
40	9.75	NULL	2 / 12	BP	keratinocyte proliferation

GW_010

Local Summary

%DE = 0.86

metagenes = 18

genes = 241

genes in genesets = 236

genes with fdr < 0.1 = 169 (150 + / 19 −)

genes with fdr < 0.05 = 155 (141 + / 14 −)

genes with fdr < 0.01 = 110 (102 + / 8 −)

<r> metagenes = 0.93

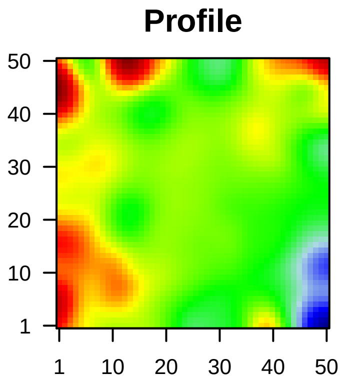
<r> genes = 0.39

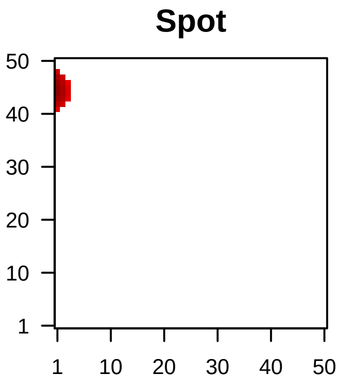
<FC> = 0.46

<shrinkage−t> = 16.31

<p−value> = 0

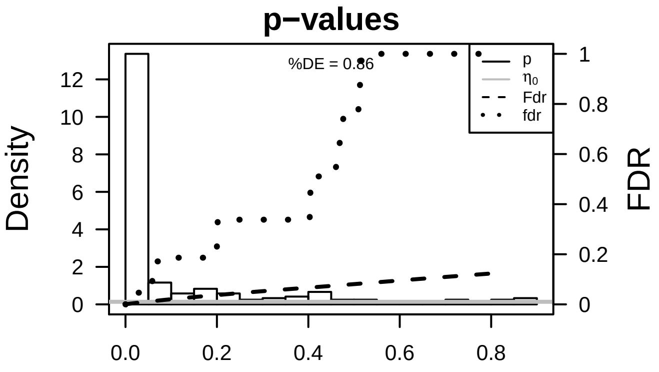
<fdr> = 0.42





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	242	1.81	2e−16	6e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
2	29113	1.97	2e−16	6e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
3	8900	1.39	2e−16	6e−16	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
4	1515	1.67	2e−16	6e−16	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
5	9547	1.67	2e−16	6e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
6	1823	2.17	2e−16	6e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
7	3848	1.68	2e−16	6e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
8	84648	1.62	2e−16	6e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
9	3963	1.66	2e−16	6e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
10	653499	1.49	2e−16	6e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
11	118430	1.84	2e−16	6e−16	2 x 44	mucin−like 1 [Source:HGNC Symbol;Acc:30588]
12	5744	1.99	2e−16	6e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
13	6706	2.82	2e−16	6e−16	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
14	29094	1.36	7e−16	2e−14	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
15	4753	1.34	2e−15	2e−14	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
16	286887	1.23	2e−15	2e−14	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
17	1241	1.33	3e−15	2e−14	1 x 46	leukotriene B4 receptor [Source:HGNC Symbol;Acc:6713]
18	55076	1.33	3e−15	3e−14	1 x 46	transmembrane protein 45A [Source:HGNC Symbol;Acc:254
19	3397	1.32	4e−15	8e−13	2 x 45	inhibitor of DNA binding 1, dominant negative helix−loop−heli
20	9119	1.28	3e−14	1e−12	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.27	NULL	10 / 21	CC	desmosome
2	14.72	NULL	16 / 82	CC	intermediate filament
3	14.59	NULL	9 / 44	CC	keratin filament
4	14.34	NULL	35 / 135	H.Tiss	WIRTH_Mucosa
5	13.97	NULL	2 / 2	miRNA target	miR−199a*
6	13.35	NULL	6 / 42	BP	keratinization
7	12.99	NULL	71 / 572	Disease	GUDJ_psoriasis up
8	12.64	NULL	4 / 21	CC	gap junction
9	11.82	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
10	11.07	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
11	10.59	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
12	10.34	NULL	14 / 76	BP	epidermis development
13	10.22	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	10.19	NULL	5 / 21	CC	cornified envelope
15	10.13	NULL	17 / 186	MF	structural molecule activity
16	10.04	NULL	2 / 10	BP	lipoxygenase pathway
17	9.8	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
18	9.67	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
19	9.47	NULL	4 / 38	BP	epithelial cell differentiation
20	9.25	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
21	9.04	NULL	2 / 12	BP	linoleic acid metabolic process
22	8.76	NULL	2 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
23	8.55	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
24	8.52	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
25	8.5	NULL	3 / 15	CC	connexon complex
26	8.15	NULL	7 / 53	BP	keratinocyte differentiation
27	7.95	NULL	2 / 11	MF	gamma−catenin binding
28	7.95	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
29	7.91	NULL	3 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
30	7.84	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
31	7.51	NULL	1 / 10	BP	surfactant homeostasis
32	7.36	NULL	2 / 15	GSEA C2	GHO_ATF5_TARGETS_DN
33	7.2	NULL	6 / 99	BP	homophilic cell adhesion
34	7.13	NULL	2 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
35	7.12	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
36	7.12	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
37	7.03	NULL	3 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
38	6.94	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
39	6.92	NULL	2 / 19	BP	ceramide biosynthetic process
40	6.76	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN

GW_010

Local Summary

%DE = 0.7

metagenes = 18

genes = 185

genes in genesets = 184

genes with fdr < 0.1 = 89 (87 + / 2 −)

genes with fdr < 0.05 = 88 (86 + / 2 −)

genes with fdr < 0.01 = 61 (60 + / 1 −)

<r> metagenes = 0.97

<r> genes = 0.25

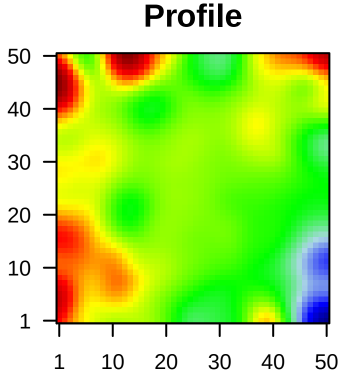
<FC> = 0.42

<shrinkage−t> = 14.67

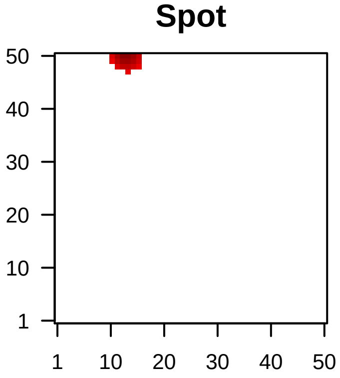
<p−value> = 0

<fdr> = 0.53

Profile



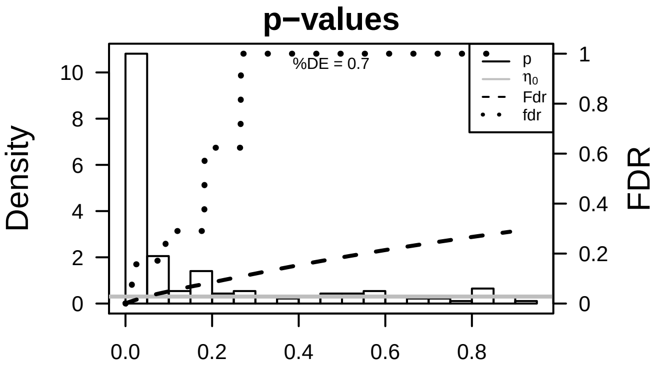
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1109	1.9	2e−16	2e−15	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
2	63928	1.42	2e−16	2e−15	13 x 50	calcineurin−like EF−hand protein 2 [Source:HGNC Symbol;A
3	57834	2.25	2e−16	2e−15	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
4	7062	1.76	2e−16	2e−15	13 x 50	trichohyalin [Source:HGNC Symbol;Acc:11791]
5	83857	1.47	2e−16	2e−15	16 x 50	transmembrane and tetratricopeptide repeat containing 1 [So
6	493861	1.31	9e−15	1e−11	14 x 50	EP300 interacting inhibitor of differentiation 3 [Source:HGNC
7	10457	1.23	3e−13	9e−11	13 x 50	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
8	51071	1.19	2e−12	1e−09	13 x 50	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
9	5217	1.12	3e−11	1e−09	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]
10	2539	1.11	5e−11	7e−09	13 x 50	glucose−6−phosphate dehydrogenase [Source:HGNC Symbo
11	344752	1.07	3e−10	7e−09	11 x 50	arylacetamide deacetylase−like 2 [Source:HGNC Symbol;Acc
12	2690	1.06	3e−10	3e−08	15 x 50	growth hormone receptor [Source:HGNC Symbol;Acc:4263]
13	4741	1.02	2e−09	3e−08	15 x 50	neurofilament, medium polypeptide [Source:HGNC Symbol;A
14	483	1.01	2e−09	3e−08	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
15	340307	1.01	2e−09	3e−08	13 x 50	CTAGE family, member 6 [Source:HGNC Symbol;Acc:28644]
16	121536	1	3e−09	1e−07	11 x 50	AE binding protein 2 [Source:HGNC Symbol;Acc:24051]
17	144193	0.99	5e−09	1e−07	15 x 50	amidohydrolase domain containing 1 [Source:HGNC Symbol;
18	406988	0.98	6e−09	3e−07	12 x 50	MIR205 host gene (non−protein coding) [Source:HGNC Syml
19	1749	0.96	1e−08	8e−07	13 x 50	distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918]
20	3005	0.94	3e−08	8e−07	14 x 50	H1 histone family, member 0 [Source:HGNC Symbol;Acc:471

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	14.83	NULL	1 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
2	12.56	NULL	3 / 10	BP	response to food
3	11.82	NULL	2 / 14	BP	bile acid and bile salt transport
4	11.02	NULL	2 / 9	Glio	Colman_survival_robust
5	10.5	NULL	4 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
6	9.48	NULL	3 / 31	BP	bile acid metabolic process
7	9.22	NULL	1 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
8	9.14	NULL	1 / 12	BP	androgen metabolic process
9	8.68	NULL	4 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_7
10	8.63	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
11	8.62	NULL	1 / 18	MF	aromatase activity
12	8.54	NULL	4 / 32	MF	NADP binding
13	8.29	NULL	4 / 51	BP	osteoblast differentiation
14	8.28	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_UP
15	8.13	NULL	2 / 12	BP	head development
16	7.79	NULL	3 / 22	BP	proximal/distal pattern formation
17	7.63	NULL	2 / 16	GSEA C2	REACTOME_BASIGIN_INTERACTIONS
18	7.62	NULL	2 / 15	BP	pentose−phosphate shunt
19	7.57	NULL	2 / 13	BP	regulation of smoothened signaling pathway
20	7.57	NULL	2 / 13	GSEA C2	BIOCARTA_SHH_PATHWAY
21	7.4	NULL	1 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_DN
22	7.27	NULL	3 / 17	MF	proline−rich region binding
23	7.22	NULL	1 / 18	BP	bile acid biosynthetic process
24	7.17	NULL	3 / 15	BP	digestive tract morphogenesis
25	7.11	NULL	2 / 35	MF	monooxygenase activity
26	7	NULL	2 / 12	BP	nitric oxide biosynthetic process
27	6.81	NULL	1 / 6	GSEA C2	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS
28	6.81	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
29	6.66	NULL	2 / 16	BP	hormone−mediated signaling pathway
30	6.65	NULL	4 / 63	MF	oxidoreductase activity, acting on paired donors, with incorporation
31	6.63	NULL	3 / 34	BP	glutathione metabolic process
32	6.6	NULL	4 / 39	BP	retinoid metabolic process
33	6.49	NULL	1 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
34	6.46	NULL	2 / 44	BP	steroid metabolic process
35	6.35	NULL	2 / 16	GSEA C2	BIOCARTA_EIF4_PATHWAY
36	6.35	NULL	3 / 15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
37	6.27	NULL	2 / 10	BP	oxaloacetate metabolic process
38	6.25	NULL	2 / 12	BP	positive regulation of protein import into nucleus
39	6.14	NULL	1 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
40	6.13	NULL	2 / 16	GSEA C2	BIOCARTA_TFF_PATHWAY

GW_010

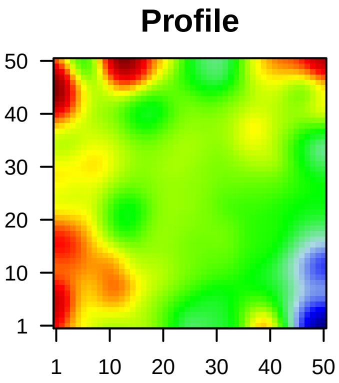
Local Summary

%DE = 0.7
metagenes = 5
genes = 130
genes in genesets = 129

genes with fdr < 0.1 = 64 (57 + / 7 −)
genes with fdr < 0.05 = 64 (57 + / 7 −)
genes with fdr < 0.01 = 45 (44 + / 1 −)

<r> metagenes = 0.99
<r> genes = 0.31

<FC> = 0.39
<shrinkage−t> = 13.51
<p−value> = 0
<fdr> = 0.51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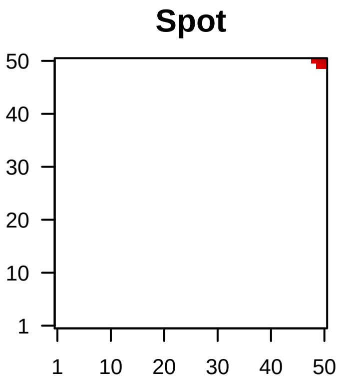
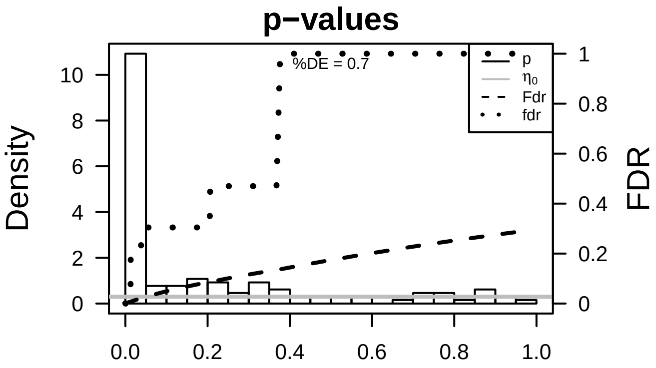

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	26256	1.53	2e−16	2e−15	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
2	2719	1.93	2e−16	2e−15	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
3	2947	1.46	2e−16	2e−15	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symbo
4	4922	1.65	2e−16	2e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
5	2304	1.31	8e−15	7e−13	50 x 50	forkhead box E1 (thyroid transcription factor 2) [Source:HGNC
6	139728	1.28	3e−14	3e−11	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:I
7	10655	1.21	8e−13	6e−11	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
8	4915	1.18	2e−12	7e−10	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
9	2729	1.13	2e−11	7e−10	50 x 50	glutamate−cysteine ligase, catalytic subunit [Source:HGNC S
10	4072	1.11	4e−11	5e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
11	344905	1.05	4e−10	5e−09	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
12	26047	1.05	5e−10	5e−09	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
13	205428	1.05	5e−10	5e−09	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
14	4953	1.04	6e−10	1e−08	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
15	55086	1.04	8e−10	1e−07	48 x 50	chromosome X open reading frame 57 [Source:HGNC Symbo
16	94234	0.99	4e−09	1e−07	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
17	84171	0.97	8e−09	5e−07	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
18	655	0.94	2e−08	5e−07	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
19	3866	−0.93	3e−08	6e−07	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
20	54578	0.92	5e−08	8e−06	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	21.4	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
2	17.11	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	16.63	NULL	3 / 13	BP	regulation of blood vessel size
4	14.39	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
5	13.12	NULL	6 / 25	BP	glutathione derivative biosynthetic process
6	12.49	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
7	11.34	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
8	11.08	NULL	1 / 12	MF	heparan sulfate proteoglycan binding
9	10.97	NULL	1 / 2	miRNA target	miR−127
10	10.82	NULL	2 / 12	GSEA C2	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN
11	10.58	NULL	1 / 13	BP	positive regulation of endocytosis
12	10.49	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
13	10.3	NULL	8 / 34	BP	glutathione metabolic process
14	10.02	NULL	11 / 119	BP	xenobiotic metabolic process
15	9.95	NULL	1 / 11	Glio	neurons_glio
16	9.91	NULL	5 / 20	MF	glutathione transferase activity
17	9.9	NULL	3 / 33	BP	regulation of sequence−specific DNA binding transcription factor ac
18	9.74	NULL	1 / 15	BP	anterior/posterior axis specification
19	9.74	NULL	1 / 15	BP	negative regulation of growth
20	9.74	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
21	9.71	NULL	1 / 10	GSEA C2	WEBER_METHYLATED_HCP_IN_SPERM_DN
22	9.52	NULL	3 / 32	BP	glycosaminoglycan biosynthetic process
23	9.38	NULL	2 / 24	BP	positive regulation of glucose import
24	9.34	NULL	3 / 11	MF	glutathione binding
25	9.34	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
26	9.33	NULL	2 / 20	TF	MYC_Metabolism UP
27	9.33	NULL	2 / 16	GSEA C2	GOUYER_TATI_TARGETS_DN
28	9.24	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
29	9.14	NULL	2 / 23	BP	hair follicle morphogenesis
30	8.81	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
31	8.81	NULL	2 / 14	CC	membrane−bounded vesicle
32	8.77	NULL	1 / 18	CC	anchored to plasma membrane
33	8.73	NULL	1 / 8	GSEA C2	NIELSEN_LIPOSARCOMA_UP
34	8.63	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
35	8.5	NULL	1 / 19	BP	negative regulation of smoothened signaling pathway
36	8.5	NULL	1 / 19	BP	positive regulation of smoothened signaling pathway
37	8.36	NULL	1 / 12	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN
38	8.3	NULL	1 / 15	MF	neuropeptide hormone activity
39	8.2	NULL	2 / 20	BP	long−term memory
40	8.16	NULL	1 / 7	GSEA C2	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE

GW_010

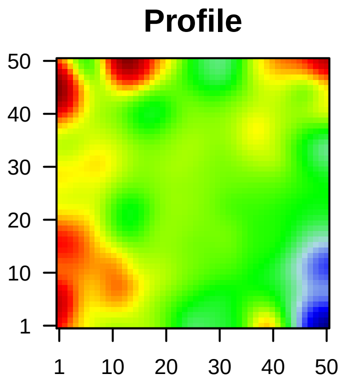
Local Summary

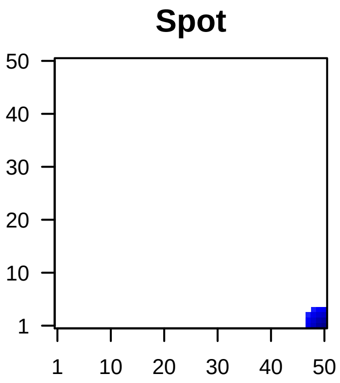
%DE = 0.9
metagenes = 15
genes = 260
genes in genesets = 258

genes with fdr < 0.1 = 217 (12 + / 205 −)
genes with fdr < 0.05 = 217 (12 + / 205 −)
genes with fdr < 0.01 = 149 (9 + / 140 −)

<r> metagenes = 0.99
<r> genes = 0.59

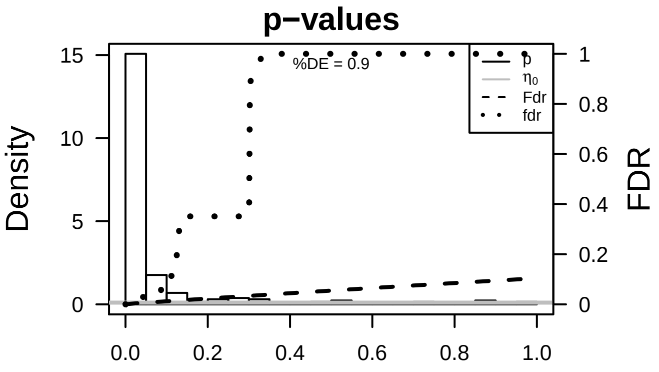
<FC> = −0.47
<shrinkage−t> = −16.45
<p−value> = 0
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.73	2e−16	1e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	894	1.78	2e−16	1e−15	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
3	972	−1.44	2e−16	1e−15	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
4	3109	−1.45	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
5	3113	−1.4	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
6	3122	−1.59	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
7	6363	−1.28	3e−14	4e−13	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
8	3108	−1.28	3e−14	1e−12	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
9	2634	−1.26	8e−14	1e−11	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HGN
10	713	−1.21	6e−13	1e−11	50 x 1	complement component 1, q subcomponent, B chain [Source
11	3512	−1.21	8e−13	4e−11	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	7351	−1.18	2e−12	6e−11	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
13	4283	−1.17	5e−12	5e−10	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
14	3936	−1.13	2e−11	8e−09	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
15	3689	−1.06	3e−10	2e−08	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
16	241	−1.03	1e−09	7e−08	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
17	9806	−0.98	7e−09	7e−08	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
18	3620	−0.98	7e−09	7e−08	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:6
19	3394	−0.97	9e−09	8e−08	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
20	51755	0.96	1e−08	9e−08	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:2422



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−40.48	NULL	12 / 15	CC	MHC class II protein complex
2	−24.75	NULL	15 / 47	BP	antigen processing and presentation
3	−23.09	NULL	89 / 417	H.Tiss	WIRTH_Immune system
4	−21.03	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
5	−20.18	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
6	−20	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
7	−20	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
8	−19.28	NULL	48 / 312	BP	immune response
9	−19.16	NULL	92 / 553	Cancer	Lembcke_Colonic Inflammation
10	−18.7	NULL	14 / 60	BP	T cell costimulation
11	−17.94	NULL	7 / 28	CC	transport vesicle membrane
12	−17.33	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	−17.33	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	−17.33	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	−17.33	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	−17.16	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
17	−17	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
18	−16.67	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
19	−16.66	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
20	−16.54	NULL	8 / 35	CC	trans−Golgi network membrane
21	−16.42	NULL	5 / 12	BP	immunoglobulin mediated immune response
22	−16.3	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
23	−15.67	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
24	−15.62	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
25	−15.43	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
26	−15.35	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
27	−15.26	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
28	−15.16	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
29	−14.8	NULL	8 / 46	CC	endocytic vesicle membrane
30	−14.41	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
31	−14.25	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
32	−14.19	NULL	5 / 12	BP	dendritic cell chemotaxis
33	−14.11	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
34	−14.11	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
35	−14.11	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
36	−14.06	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
37	−13.98	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
38	−13.74	NULL	10 / 60	BP	interferon−gamma−mediated signaling pathway
39	−13.52	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
40	−13.31	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL