GW_036

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1627 (905 + / 722 −)

genes with fdr < 0.1 = 1136 (649 + / 487 −)

genes with fdr < 0.05 = 794 (462 + / 332 −)

genes with fdr < 0.01 = 550 (328 + / 222 −)

genes in genesets = 16332

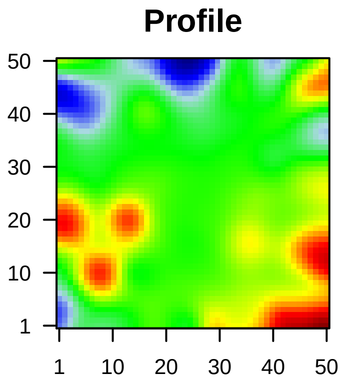
<FC> = 0

<shrinkage−t> = 0

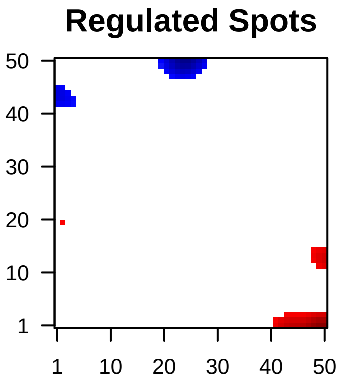
<p−value> = 0.14

<fdr> = 0.87

Profile



Regulated Spots



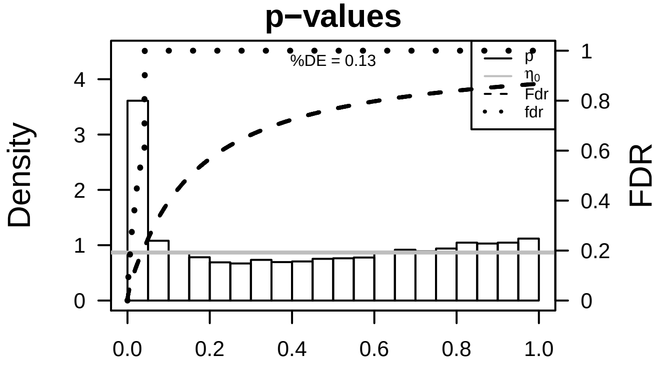
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	1.78	2e−16	8e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	1.55	2e−16	8e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	216	1.55	2e−16	8e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	401138	3.16	2e−16	8e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
5	80162	1.63	2e−16	8e−14	43 x 1	ATH1, acid trehalase−like 1 (yeast) [Source:HGNC Symbol;A
6	260436	2.25	2e−16	8e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
7	760	−1.68	2e−16	8e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	92291	1.61	2e−16	8e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
9	6363	2.09	2e−16	8e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
10	6366	1.61	2e−16	8e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
11	930	1.75	2e−16	8e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
12	1056	2.43	2e−16	8e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
13	169044	2.02	2e−16	8e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
14	49860	2.04	2e−16	8e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	1448	1.59	2e−16	8e−14	33 x 22	casein kappa [Source:HGNC Symbol;Acc:2446]
16	2327	2.03	2e−16	8e−14	50 x 11	flavin containing monooxygenase 2 (non−functional) [Source:
17	2328	1.61	2e−16	8e−14	48 x 8	flavin containing monooxygenase 3 [Source:HGNC Symbol;A
18	3169	1.71	2e−16	8e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
19	2568	2.22	2e−16	8e−14	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
20	2697	−1.59	2e−16	8e−14	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.65	NULL	15	CC	MHC class II protein complex
2	9.35	NULL	1135	Chr	Chr 19
3	7.32	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
4	6.72	NULL	10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
5	6.12	NULL	119	BP	xenobiotic metabolic process
6	5.79	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
7	5.69	NULL	83	BP	respiratory electron transport chain
8	5.56	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	5.34	NULL	52	Chr	Chr HSCHR6_MHC_QBL
10	5.33	NULL	9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
11	5.14	NULL	10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
12	5.06	NULL	1318	CC	mitochondrion
13	5.06	NULL	21	BP	drug metabolic process
14	4.97	NULL	21	CC	clathrin−coated endocytic vesicle membrane
15	4.95	NULL	8	GSEA C2	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
16	4.93	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
17	4.93	NULL	12	BP	dendritic cell chemotaxis
18	4.88	NULL	34	MF	NADH dehydrogenase (ubiquinone) activity
19	4.86	NULL	152	BP	cellular metabolic process
20	4.85	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
Underexpressed					
1	−10.3	NULL	436	miRNA target starBase	hsa−miR−548n
2	−9.9	NULL	603	miRNA target starBase	hsa−miR−20a
3	−9.66	NULL	262	miRNA target starBase	hsa−miR−548l
4	−9.08	NULL	538	miRNA target starBase	hsa−miR−17
5	−9.03	NULL	511	miRNA target starBase	hsa−miR−106b
6	−9.02	NULL	565	miRNA target starBase	hsa−miR−20b
7	−8.97	NULL	512	miRNA target starBase	hsa−miR−15a
8	−8.92	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
9	−8.76	NULL	488	miRNA target starBase	hsa−miR−16
10	−8.72	NULL	7	MMML CGS	MACIEJ_MMML 5
11	−8.7	NULL	315	miRNA target starBase	hsa−miR−30e
12	−8.7	NULL	517	miRNA target starBase	hsa−miR−106a
13	−8.51	NULL	852	Lymphoma	SPANG_BCR DN
14	−8.5	NULL	313	miRNA target starBase	hsa−miR−559
15	−8.43	NULL	494	miRNA target starBase	hsa−miR−107
16	−8.43	NULL	300	miRNA target starBase	hsa−miR−561
17	−8.42	NULL	479	miRNA target starBase	hsa−miR−15b
18	−8.4	NULL	318	miRNA target starBase	hsa−miR−590−3p
19	−8.36	NULL	319	miRNA target starBase	hsa−miR−367
20	−8.36	NULL	421	miRNA target starBase	hsa−let−7b

p−values



GW_036

Local Summary

%DE = 0.74

metagenes = 28

genes = 395

genes in genesets = 390

genes with fdr < 0.1 = 209 (206 + / 3 −)

genes with fdr < 0.05 = 173 (171 + / 2 −)

genes with fdr < 0.01 = 127 (126 + / 1 −)

<r> metagenes = 0.92

<r> genes = 0.49

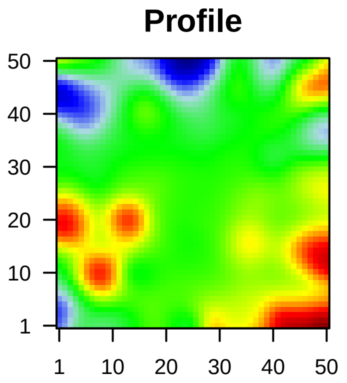
<FC> = 0.41

<shrinkage−t> = 14.41

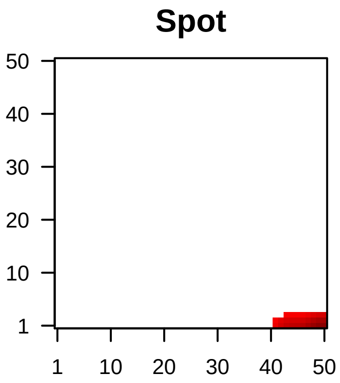
<p−value> = 0

<fdr> = 0.56

Profile

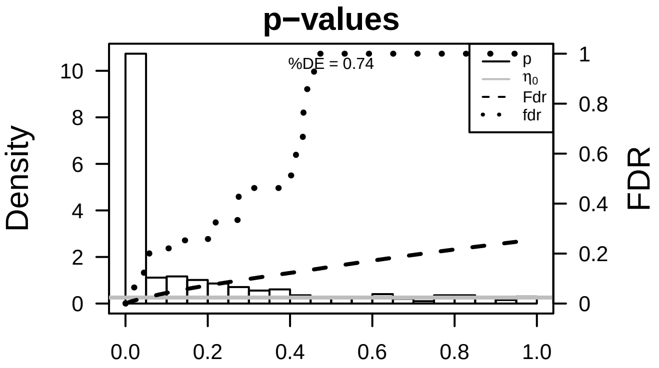


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	80162	1.63	2e−16	3e−15	43 x 1	ATH1, acid trehalase−like 1 (yeast) [Source:HGNC Symbol;A
2	260436	2.25	2e−16	3e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
3	6363	2.09	2e−16	3e−15	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
4	6366	1.61	2e−16	3e−15	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
5	930	1.75	2e−16	3e−15	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
6	169044	2.02	2e−16	3e−15	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
7	3127	2.59	2e−16	3e−15	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
8	10537	1.47	2e−16	3e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	57484	1.36	1e−14	3e−12	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
10	341	1.34	4e−14	3e−12	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
11	29802	1.33	7e−14	2e−10	47 x 2	pre−B lymphocyte 3 [Source:HGNC Symbol;Acc:12710]
12	3123	1.23	3e−12	2e−10	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
13	3128	1.22	5e−12	3e−10	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
14	23495	1.21	7e−12	1e−09	48 x 1	tumor necrosis factor receptor superfamily, member 13B [Sou
15	84824	1.19	2e−11	2e−09	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]
16	26580	1.17	4e−11	4e−09	43 x 1	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
17	348	1.13	2e−10	4e−09	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
18	1043	1.13	2e−10	4e−09	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
19	714	1.13	2e−10	4e−09	50 x 1	complement component 1, q subcomponent, C chain [Source
20	713	1.12	2e−10	5e−08	50 x 1	complement component 1, q subcomponent, B chain [Source



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.75	NULL	14 / 15	CC	MHC class II protein complex
2	19.97	NULL	16 / 47	BP	antigen processing and presentation
3	17.92	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
4	17.85	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
5	17.27	NULL	20 / 60	BP	T cell costimulation
6	16.97	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
7	16.76	NULL	109 / 417	H.Tiss	WIRTH_Immune system
8	16.46	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
9	15.74	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
10	15.72	NULL	5 / 12	BP	dendritic cell chemotaxis
11	15.51	NULL	60 / 312	BP	immune response
12	15.22	NULL	9 / 28	CC	transport vesicle membrane
13	14.8	NULL	5 / 12	BP	immunoglobulin mediated immune response
14	14.71	NULL	100 / 553	Cancer	Lembcke_Colonic Inflammation
15	14.51	NULL	16 / 87	BP	antigen processing and presentation of exogenous peptide antigen
16	14.12	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
17	13.97	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
18	13.88	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
19	13.74	NULL	2 / 10	BP	positive regulation of chemotaxis
20	13.63	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
21	13.43	NULL	9 / 35	CC	trans−Golgi network membrane
22	12.45	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
23	12.41	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
24	12.28	NULL	20 / 84	BP	T cell receptor signaling pathway
25	12.16	NULL	5 / 11	BP	positive regulation of B cell differentiation
26	11.88	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
27	11.48	NULL	9 / 46	CC	endocytic vesicle membrane
28	11.18	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
29	10.93	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
30	10.87	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
31	10.71	NULL	3 / 11	BP	negative regulation of lipid catabolic process
32	10.67	NULL	18 / 74	BP	regulation of immune response
33	10.66	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
34	10.55	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
35	10.48	NULL	4 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
36	10.39	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
37	10.36	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
38	10.17	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
39	10.09	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
40	10.08	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY

GW_036

Local Summary

%DE = 0.65

metagenes = 11

genes = 114

genes in genesets = 114

genes with fdr < 0.1 = 59 (55 + / 4 −)

genes with fdr < 0.05 = 46 (43 + / 3 −)

genes with fdr < 0.01 = 43 (41 + / 2 −)

<r> metagenes = 0.97

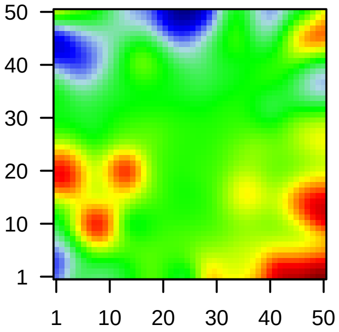
<r> genes = 0.33

<FC> = 0.4

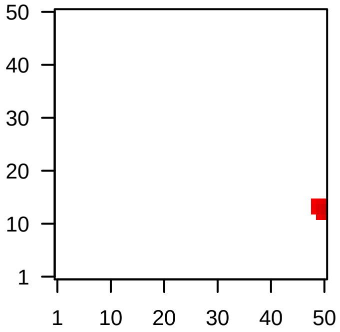
<shrinkage−t> = 13.96

<p−value> = 0

<fdr> = 0.53



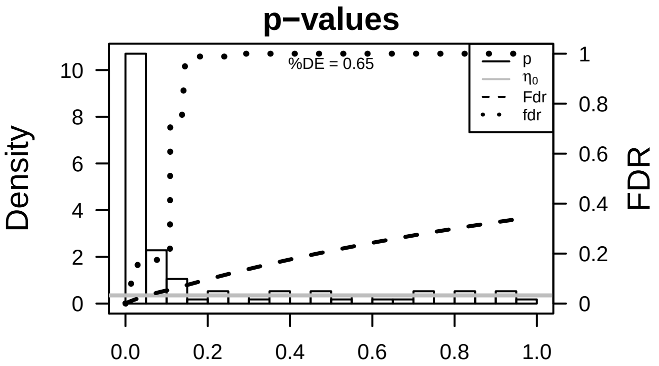
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	126	1.55	2e−16	2e−15	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
2	3169	1.71	2e−16	2e−15	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
3	2568	2.22	2e−16	2e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
4	7356	2.49	2e−16	2e−15	50 x 12	secretoglobin, family 1A, member 1 (uteroglobin) [Source:HG
5	399948	1.33	5e−14	1e−12	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
6	260293	1.33	7e−14	2e−11	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
7	9249	1.28	5e−13	4e−10	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
8	200931	1.2	1e−11	4e−07	50 x 14	solute carrier family 51, alpha subunit [Source:HGNC Symbol
9	6228	−0.99	2e−08	4e−07	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
10	8495	0.99	2e−08	2e−06	50 x 14	PTPRF interacting protein, binding protein 2 (liprin beta 2) [S
11	55930	0.96	6e−08	4e−06	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
12	158584	0.92	2e−07	1e−05	50 x 14	fatty acid amide hydrolase 2 [Source:HGNC Symbol;Acc:264
13	27134	0.89	4e−07	2e−05	50 x 12	tight junction protein 3 [Source:HGNC Symbol;Acc:11829]
14	155066	0.86	1e−06	6e−05	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
15	1365	0.82	3e−06	6e−05	50 x 15	claudin 3 [Source:HGNC Symbol;Acc:2045]
16	2644	0.81	5e−06	6e−05	48 x 14	GTP cyclohydrolase I feedback regulator [Source:HGNC Sym
17	23171	0.81	5e−06	7e−05	50 x 12	glycerol−3−phosphate dehydrogenase 1−like [Source:HGNC
18	9071	0.8	7e−06	1e−04	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
19	9423	0.77	1e−05	1e−04	50 x 13	netrin 1 [Source:HGNC Symbol;Acc:8029]
20	79877	0.77	1e−05	1e−04	50 x 15	dephospho−CoA kinase domain containing [Source:HGNC S



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	26.06	NULL	2 / 7	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_DN
2	22.32	NULL	1 / 5	GSEA C2 SMID_BREAST_CANCER_ERBB2_DN
3	20.91	NULL	2 / 7	GSEA C2 NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
4	20.44	NULL	1 / 7	GSEA C2 WALLACE_PROSTATE_CANCER_RACE_UP
5	19.3	NULL	2 / 8	GSEA C2 NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
6	17.59	NULL	1 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
7	16.74	NULL	1 / 8	GSEA C2 HEIDENBLAD_AMPLICON_12P11_12_UP
8	16.53	NULL	1 / 15	Cancer LIU_PROSTATE_CANCER_DN
9	14.86	NULL	1 / 12	BP regulation of mRNA stability
10	14.67	NULL	1 / 10	MF GABA−A receptor activity
11	13.94	NULL	1 / 7	GSEA C2 NEBEN_AML_WITH_FLT3_OR_NRAS_UP
12	13.87	NULL	1 / 11	GSEA C2 JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
13	13.47	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
14	12.7	NULL	2 / 16	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
15	12.59	NULL	1 / 16	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	12.05	NULL	1 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
17	12.05	NULL	1 / 14	GSEA C2 TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
18	12.05	NULL	1 / 14	GSEA C2 RIZKI_TUMOR_INVASIVENESS_2D_DN
19	11.81	NULL	2 / 9	GSEA C2 REACTOME_ETHANOL_OXIDATION
20	11.58	NULL	1 / 15	GSEA C2 SABATES_COLORECTAL_ADENOMA_UP
21	11.58	NULL	1 / 15	GSEA C2 LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	11.28	NULL	1 / 3	miRNA 3UTR ACGGC−210
23	11.26	NULL	1 / 10	BP prostate gland epithelium morphogenesis
24	11.16	NULL	1 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
25	11.16	NULL	1 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
26	11.16	NULL	1 / 16	GSEA C2 DOANE_BREAST_CANCER_ESR1_DN
27	11.16	NULL	1 / 16	GSEA C2 ROY_WOUND_BLOOD_VESSEL_DN
28	11.16	NULL	1 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_DN
29	11.16	NULL	1 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
30	10.66	NULL	3 / 11	BP DNA integration
31	10.49	NULL	1 / 22	BP negative regulation of interferon−gamma production
32	10.11	NULL	1 / 12	BP neuron fate specification
33	9.98	NULL	1 / 24	BP negative regulation of T cell proliferation
34	9.65	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
35	9.65	NULL	1 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
36	9.57	NULL	2 / 14	GSEA C2 KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
37	9.5	NULL	2 / 18	MF aromatase activity
38	9.24	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition
39	9.07	NULL	2 / 10	BP epoxygenase P450 pathway
40	9.06	NULL	1 / 23	MF extracellular ligand−gated ion channel activity

GW_036

Local Summary

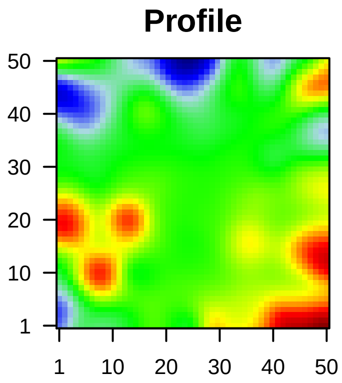
%DE = 0.78
metagenes = 1
genes = 7
genes in genesets = 7

genes with fdr < 0.1 = 5 (5 + / 0 −)
genes with fdr < 0.05 = 5 (5 + / 0 −)
genes with fdr < 0.01 = 2 (2 + / 0 −)

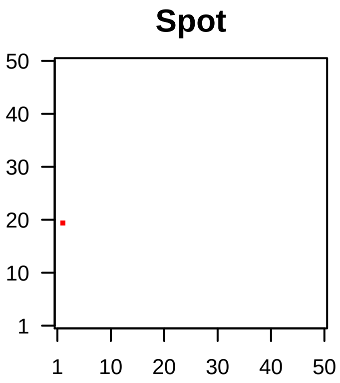
<r> metagenes = NA
<r> genes = 0.4

<FC> = 0.5
<shrinkage−t> = 17.38
<p−value> = 0
<fdr> = 0.37

Profile



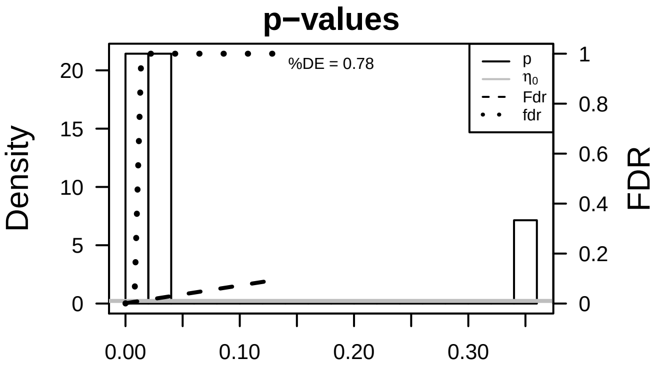
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	430	0.95	7e−08	2e−04	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
2	85359	0.68	1e−04	7e−03	2 x 20	DiGeorge syndrome critical region gene 6−like [Source:HGN
3	30968	0.5	5e−03	1e−02	2 x 20	stomatin (EPB72)−like 2 [Source:HGNC Symbol;Acc:14559]
4	55168	0.41	2e−02	1e−02	2 x 20	mitochondrial ribosomal protein S18A [Source:HGNC Symbo
5	27237	0.4	2e−02	5e−02	2 x 20	Rho guanine nucleotide exchange factor (GEF) 16 [Source:H
6	113000	0.37	4e−02	1e+00	2 x 20	RNA pseudouridylate synthase domain containing 1 [Source:
7	51016	0.16	4e−01	1e+00	2 x 20	ER membrane protein complex subunit 9 [Source:HGNC Sym

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.8	NULL	1 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
2	23.71	NULL	1 / 26	MF	E−box binding
3	23.38	NULL	1 / 12	CC	T cell receptor complex
4	21.81	NULL	1 / 29	BP	peripheral nervous system development
5	21.63	NULL	1 / 14	BP	mitochondrial ATP synthesis coupled proton transport
6	19.41	NULL	1 / 34	BP	somatic stem cell maintenance
7	19	NULL	1 / 16	CC	extrinsic to plasma membrane
8	18.81	NULL	1 / 12	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
9	17.94	NULL	1 / 38	BP	placenta development
10	17.4	NULL	1 / 14	GSEA C2	BIOCARTA_MYOSIN_PATHWAY
11	17.4	NULL	1 / 14	GSEA C2	BIOCARTA_PAR1_PATHWAY
12	16.33	NULL	1 / 15	GSEA C2	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK
13	15.76	NULL	1 / 14	MF	pseudouridine synthase activity
14	15.27	NULL	1 / 16	GSEA C2	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_A
15	15.27	NULL	1 / 16	GSEA C2	REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS
16	15.27	NULL	1 / 16	GSEA C2	REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING
17	15.27	NULL	1 / 16	GSEA C2	REACTOME_RHO_GTPASE_CYCLE
18	13.22	NULL	1 / 24	CC	immunological synapse
19	13.17	NULL	1 / 19	CC	mitochondrial small ribosomal subunit
20	13.03	NULL	1 / 17	BP	RNA modification
21	12.96	NULL	1 / 19	BP	positive regulation of establishment of protein localization to plasma
22	12.34	NULL	1 / 18	BP	pseudouridine synthesis
23	11.41	NULL	1 / 22	BP	cell chemotaxis
24	10.59	NULL	1 / 32	CC	COP9 signalosome
25	9.96	NULL	1 / 26	MF	receptor tyrosine kinase binding
26	9.85	NULL	1 / 96	BP	central nervous system development
27	9.19	NULL	1 / 39	BP	mitochondrion organization
28	8.32	NULL	1 / 45	BP	protein oligomerization
29	8.31	NULL	1 / 33	MF	Rho GTPase binding
30	8.24	NULL	1 / 10	CC	ER membrane protein complex
31	7.85	NULL	1 / 49	CC	mitochondrial intermembrane space
32	7.49	NULL	1 / 151	BP	response to hypoxia
33	7.34	NULL	1 / 156	MF	protein dimerization activity
34	5.85	NULL	1 / 228	BP	in utero embryonic development
35	5.79	NULL	1 / 78	BP	cellular calcium ion homeostasis
36	5.52	NULL	1 / 84	BP	T cell receptor signaling pathway
37	5.26	NULL	1 / 64	BP	regulation of Rho protein signal transduction
38	5.16	NULL	1 / 66	MF	Rho guanyl−nucleotide exchange factor activity
39	4.9	NULL	1 / 306	BP	regulation of transcription from RNA polymerase II promoter
40	4.75	NULL	1 / 75	MF	PDZ domain binding

GW_036

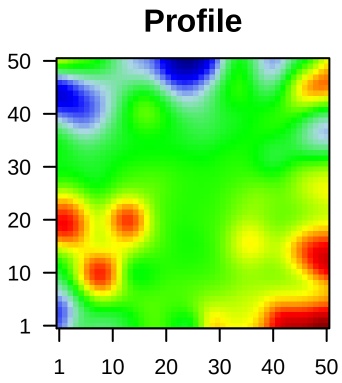
Local Summary

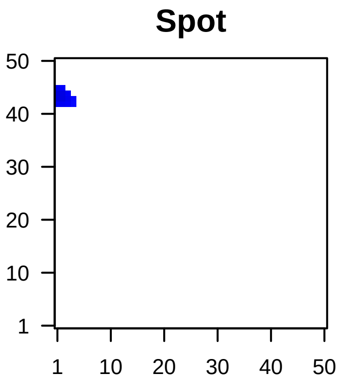
%DE = 0.73
metagenes = 13
genes = 163
genes in genesets = 162

genes with fdr < 0.1 = 96 (2 + / 94 −)
genes with fdr < 0.05 = 88 (2 + / 86 −)
genes with fdr < 0.01 = 59 (1 + / 58 −)

<r> metagenes = 0.98
<r> genes = 0.39

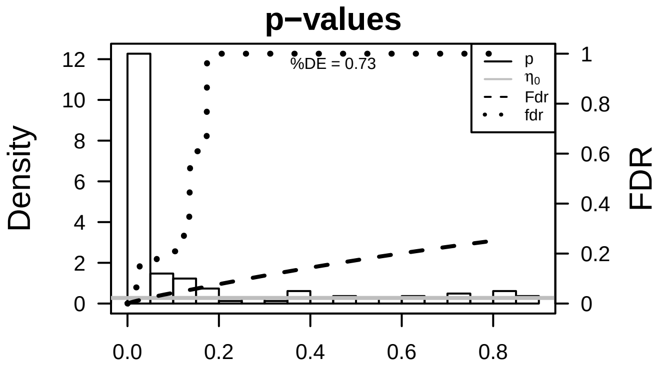
<FC> = −0.44
<shrinkage−t> = −15.25
<p−value> = 0
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	760	−1.68	2e−16	5e−15	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	2697	−1.59	2e−16	5e−15	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
3	3306	−1.31	1e−13	6e−12	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
4	1825	−1.29	3e−13	5e−11	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
5	664	−1.25	1e−12	1e−08	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H
6	3489	−1.12	3e−10	5e−08	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
7	56901	−1.05	3e−09	5e−08	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
8	5358	−1.04	4e−09	5e−08	1 x 43	plastin 3 [Source:HGNC Symbol;Acc:9091]
9	7280	−1.04	4e−09	5e−08	1 x 45	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
10	4753	−1.03	5e−09	3e−07	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
11	122786	−1.01	1e−08	3e−07	3 x 43	FERM domain containing 6 [Source:HGNC Symbol;Acc:1983
12	3861	−0.91	2e−08	5e−07	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
13	29966	−0.97	4e−08	5e−07	4 x 42	striatin, calmodulin binding protein 3 [Source:HGNC Symbol;
14	3099	−0.96	5e−08	5e−07	1 x 44	hexokinase 2 [Source:HGNC Symbol;Acc:4923]
15	5836	−0.96	5e−08	5e−07	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:9
16	5597	−0.95	7e−08	5e−07	1 x 44	mitogen−activated protein kinase 6 [Source:HGNC Symbol;A
17	64127	−0.95	8e−08	4e−06	1 x 45	nucleotide−binding oligomerization domain containing 2 [Sou
18	222584	−0.92	2e−07	4e−06	1 x 44	family with sequence similarity 83, member B [Source:HGNC
19	2167	−0.9	4e−07	4e−06	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
20	8111	−0.9	4e−07	7e−06	1 x 42	G protein−coupled receptor 68 [Source:HGNC Symbol;Acc:4



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−17.94	NULL	2 / 6	GSEA C2 WALLACE_PROSTATE_CANCER_DN
2	−16.05	NULL	4 / 12	BP hemidesmosome assembly
3	−13.61	NULL	4 / 16	GSEA C2 ELVIDGE_HIF1A_TARGETS_DN
4	−13.41	NULL	4 / 16	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	−13.19	NULL	1 / 2	miRNA target miR−346
6	−12.46	NULL	1 / 6	GSEA C2 SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
7	−11.71	NULL	3 / 16	GSEA C2 ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
8	−11.48	NULL	3 / 16	GSEA C2 HARRIS_HYPOXIA
9	−11.43	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
10	−11.16	NULL	2 / 15	GSEA C2 STOSSI_RESPONSE_TO_ESTRADIOL
11	−11.02	NULL	2 / 10	BP skeletal muscle tissue regeneration
12	−10.41	NULL	1 / 9	GSEA C2 HEDVAT_ELF4_TARGETS_UP
13	−10.27	NULL	2 / 16	GSEA C2 GALLUZZI_PERMEABILIZE_MITOCHONDRIA
14	−10.11	NULL	2 / 12	CC fascia adherens
15	−10.07	NULL	2 / 10	BP negative regulation of interleukin−2 production
16	−9.82	NULL	3 / 25	BP brown fat cell differentiation
17	−9.79	NULL	2 / 16	GSEA C2 WILLERT_WNT_SIGNALING
18	−9.72	NULL	1 / 5	GSEA C2 BUSA_SAM68_TARGETS_UP
19	−9.63	NULL	3 / 16	GSEA C2 LEONARD_HYPOXIA
20	−9.61	NULL	2 / 16	GSEA C2 BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
21	−9.47	NULL	11 / 82	CC intermediate filament
22	−9.33	NULL	2 / 25	BP response to zinc ion
23	−9.32	NULL	2 / 22	BP bicarbonate transport
24	−9.26	NULL	1 / 11	BP positive regulation of bone resorption
25	−9.23	NULL	1 / 10	BP chronic inflammatory response
26	−9.23	NULL	1 / 10	MF gap junction channel activity
27	−9.23	NULL	1 / 10	CC Golgi−associated vesicle membrane
28	−9.23	NULL	1 / 10	BP regulation of ventricular cardiac muscle cell membrane repolarizati
29	−9.23	NULL	1 / 10	GSEA C2 CONRAD_STEM_CELL
30	−9.23	NULL	1 / 10	GSEA C2 REACTOME_GAP_JUNCTION_DEGRADATION
31	−9.16	NULL	2 / 16	GSEA C2 SANA_RESPONSE_TO_IFNG_DN
32	−9.11	NULL	2 / 15	GSEA C2 KANG_CISPLATIN_RESISTANCE_UP
33	−8.95	NULL	2 / 16	GSEA C2 JAEGER_METASTASIS_DN
34	−8.8	NULL	1 / 12	GSEA C2 HO_LIVER_CANCER_VASCULAR_INVASION
35	−8.79	NULL	9 / 76	BP epidermis development
36	−8.75	NULL	2 / 17	BP morphogenesis of an epithelium
37	−8.69	NULL	2 / 8	GSEA C2 LIU_CDX2_TARGETS_DN
38	−8.66	NULL	2 / 25	BP one−carbon metabolic process
39	−8.6	NULL	2 / 20	MF scaffold protein binding
40	−8.38	NULL	2 / 16	GSEA C2 SESTO_RESPONSE_TO_UV_C1

GW_036

Local Summary

%DE = 0.89

metagenes = 30

genes = 371

genes in genesets = 366

genes with fdr < 0.1 = 282 (2 + / 280 −)

genes with fdr < 0.05 = 257 (2 + / 255 −)

genes with fdr < 0.01 = 196 (2 + / 194 −)

<r> metagenes = 0.93

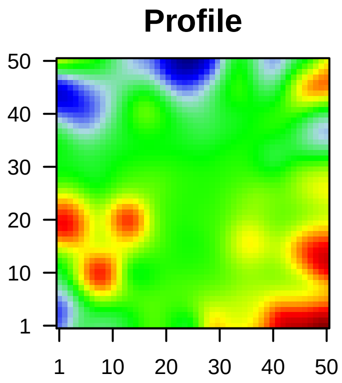
<r> genes = 0.26

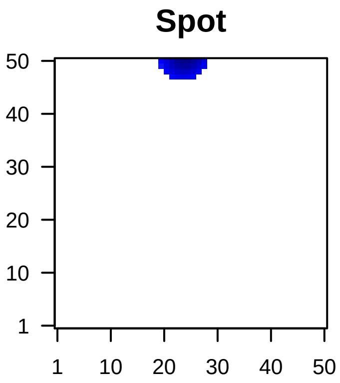
<FC> = −0.43

<shrinkage−t> = −15.2

<p−value> = 0.01

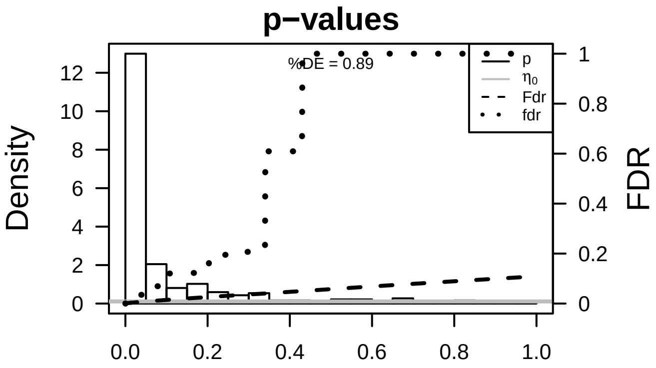
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4609	−1.31	1e−13	2e−11	22 x 50	v−myc avian myelocytomatosis viral oncogene homolog [Sou
2	1958	−1.27	7e−13	3e−11	22 x 50	early growth response 1 [Source:HGNC Symbol;Acc:3238]
3	10787	−1.25	1e−12	1e−10	25 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]
4	100008589	−1.23	4e−12	7e−10	23 x 50	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
5	71	−1.09	2e−11	7e−10	24 x 50	actin, gamma 1 [Source:HGNC Symbol;Acc:144]
6	25800	−1.17	4e−11	1e−07	25 x 50	solute carrier family 39 (zinc transporter), member 6 [Source:
7	960	−1.05	3e−09	2e−07	24 x 50	CD44 molecule (Indian blood group) [Source:HGNC Symbol;
8	3716	−1.02	9e−09	4e−07	25 x 49	Janus kinase 1 [Source:HGNC Symbol;Acc:6190]
9	114908	−0.99	2e−08	4e−07	26 x 50	transmembrane protein 123 [Source:HGNC Symbol;Acc:301
10	9643	−0.98	3e−08	4e−07	26 x 50	mortality factor 4 like 2 [Source:HGNC Symbol;Acc:16849]
11	8349	−0.97	4e−08	4e−07	21 x 50	histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760]
12	1176	−0.97	5e−08	5e−07	26 x 50	adaptor−related protein complex 3, sigma 1 subunit [Source:
13	51014	−0.96	6e−08	1e−06	26 x 50	transmembrane emp24 protein transport domain containing 7
14	57162	−0.94	1e−07	1e−06	23 x 50	pellino E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;A
15	51030	−0.93	1e−07	3e−06	26 x 50	trans−golgi network vesicle protein 23 homolog B (S. cerevisi
16	678	−0.91	3e−07	3e−06	23 x 50	ZFP36 ring finger protein−like 2 [Source:HGNC Symbol;Acc:
17	2970	−0.9	3e−07	3e−06	23 x 50	
18	6386	−0.9	4e−07	1e−05	25 x 50	syndecan binding protein (syntenin) [Source:HGNC Symbol;
19	8676	−0.88	7e−07	1e−05	23 x 50	syntaxin 11 [Source:HGNC Symbol;Acc:11429]
20	2632	−0.86	1e−06	2e−05	25 x 50	glucan (1,4−alpha−), branching enzyme 1 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.67	NULL	4 / 8	MMML CGS	MACIEJ_MMML 50
2	−14.18	NULL	1 / 2	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
3	−12.93	NULL	2 / 3	miRNA target	miR−373
4	−12.76	NULL	55 / 436	miRNA target starBase	hsa−miR−548n
5	−11.26	NULL	1 / 2	miRNA target	miR−328
6	−11	NULL	39 / 269	miRNA target starBase	hsa−miR−1244
7	−10.84	NULL	29 / 189	miRNA target starBase	hsa−miR−513a−3p
8	−10.18	NULL	12 / 67	miRNA target starBase	hsa−miR−1246
9	−10.1	NULL	8 / 16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
10	−10.07	NULL	18 / 134	miRNA target starBase	hsa−miR−656
11	−9.88	NULL	47 / 517	miRNA target starBase	hsa−miR−106a
12	−9.79	NULL	2 / 7	GSEA C2	TURJANSKI_MAPK7_TARGETS
13	−9.78	NULL	21 / 155	miRNA target starBase	hsa−miR−802
14	−9.74	NULL	37 / 313	miRNA target starBase	hsa−miR−559
15	−9.74	NULL	14 / 61	miRNA target starBase	hsa−miR−1278
16	−9.7	NULL	18 / 99	miRNA target starBase	hsa−miR−21
17	−9.59	NULL	33 / 324	miRNA target starBase	hsa−miR−18a
18	−9.59	NULL	33 / 318	miRNA target starBase	hsa−miR−590−3p
19	−9.52	NULL	34 / 302	miRNA target starBase	hsa−miR−548i
20	−9.46	NULL	1 / 4	GSEA C2	TESAR_ALK_TARGETS_HUMAN_ES_4D_DN
21	−9.46	NULL	1 / 4	miRNA target	miR−34b
22	−9.46	NULL	1 / 4	miRNA target	miR−34c
23	−9.33	NULL	27 / 235	miRNA target starBase	hsa−miR−1252
24	−9.31	NULL	46 / 511	miRNA target starBase	hsa−miR−106b
25	−9.29	NULL	37 / 336	miRNA target starBase	hsa−miR−548d−5p
26	−9.29	NULL	23 / 151	miRNA target starBase	hsa−miR−429
27	−9.26	NULL	3 / 10	MF	lamin binding
28	−9.26	NULL	32 / 271	miRNA target starBase	hsa−miR−548h
29	−9.24	NULL	18 / 114	miRNA target starBase	hsa−miR−498
30	−9.23	NULL	30 / 217	miRNA target starBase	hsa−miR−548m
31	−9.2	NULL	26 / 167	miRNA target starBase	hsa−miR−548g
32	−9.15	NULL	32 / 313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
33	−9.15	NULL	32 / 313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
34	−9.15	NULL	32 / 313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up
35	−9.15	NULL	1 / 4	GSEA C2	IGARASHI_ATF4_TARGETS_UP
36	−9.15	NULL	40 / 310	miRNA target starBase	hsa−miR−340
37	−9.14	NULL	2 / 9	GSEA C2	FUNG_IL2_SIGNALING_2
38	−9.13	NULL	35 / 307	miRNA target starBase	hsa−miR−548c−5p
39	−9.1	NULL	42 / 463	miRNA target starBase	hsa−miR−301a
40	−9.05	NULL	7 / 16	GSEA C2	AMIT_DELAYED_EARLY_GENES