GW_198

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1749 (913 + / 836 −)

genes with fdr < 0.1 = 1427 (772 + / 655 −)

genes with fdr < 0.05 = 1261 (695 + / 566 −)

genes with fdr < 0.01 = 867 (519 + / 348 −)

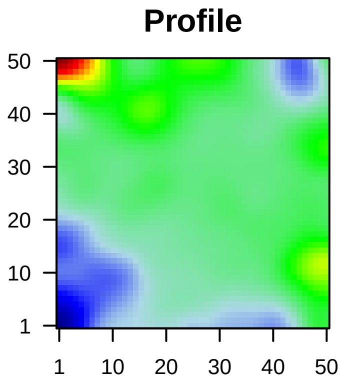
genes in genesets = 16332

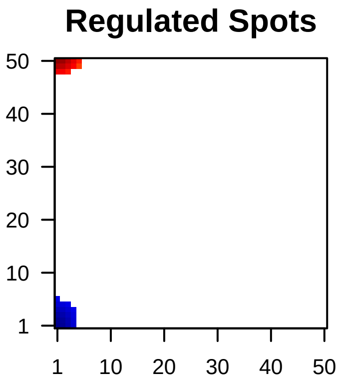
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

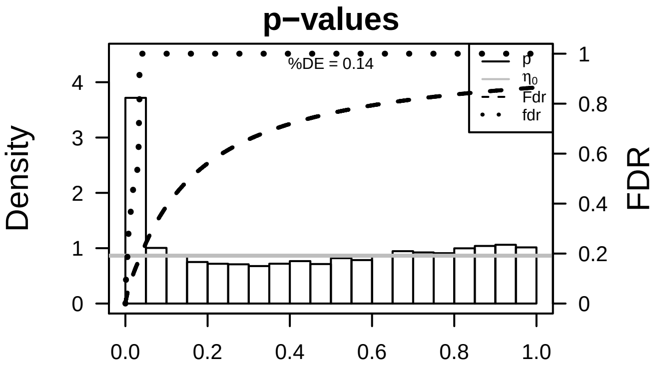
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.57	2e−16	3e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	72	−1.37	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	131	1.51	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.65	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.61	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	8644	1.59	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	1.55	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	218	1.58	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
9	360	1.34	2e−16	3e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
10	23120	1.45	2e−16	3e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
11	8424	1.52	2e−16	3e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
12	633	−1.44	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
13	329	1.49	2e−16	3e−14	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
14	260436	2.97	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
15	394263	1.64	2e−16	3e−14	3 x 50	
16	768	−1.33	2e−16	3e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
17	57172	1.53	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
18	84290	1.34	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
19	414062	−1.5	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
20	91612	1.37	2e−16	3e−14	24 x 48	churchill domain containing 1 [Source:HGNC Symbol;Acc:20



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	31.59	NULL	135	H.Tiss	WIRTH_Mucosa
2	13.87	NULL	53	BP	keratinocyte differentiation
3	11.95	NULL	21	CC	cornified envelope
4	9.92	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
5	9.07	NULL	572	Disease	GUDJ_psoriasis up
6	8.96	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	8.9	NULL	119	BP	xenobiotic metabolic process
8	8.37	NULL	42	BP	keratinization
9	7.83	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
10	7.29	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
11	7.26	NULL	19	BP	peptide cross−linking
12	6.84	NULL	76	BP	epidermis development
13	6.7	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
14	6.46	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
15	6.44	NULL	18	MF	aromatase activity
16	6.38	NULL	44	CC	keratin filament
17	6.38	NULL	296	MF	oxidoreductase activity
18	6.36	NULL	614	CC	endoplasmic reticulum membrane
19	6.22	NULL	20	MF	glutathione transferase activity
20	6.21	NULL	122	MF	serine−type endopeptidase activity
Underexpressed					
1	−13.54	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−13.54	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−13.41	NULL	242	BP	extracellular matrix organization
4	−12.27	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−11.43	NULL	190	CC	extracellular matrix
6	−10.74	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
7	−10.54	NULL	530	Cancer	Lembcke_Normal vs Adenoma
8	−10.45	NULL	403	BP	cell adhesion
9	−10.29	NULL	69	BP	extracellular matrix disassembly
10	−9.91	NULL	64	BP	collagen catabolic process
11	−9.3	NULL	83	CC	basement membrane
12	−8.96	NULL	57	Glio	developing astrocytes
13	−8.69	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
14	−8.6	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
15	−8.6	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
16	−8.6	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
17	−8.6	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
18	−8.57	NULL	57	MF	extracellular matrix structural constituent
19	−8.53	NULL	11	MF	platelet−derived growth factor binding
20	−8.51	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes

GW_198

Local Summary

%DE = 0.98

metagenes = 13

genes = 199

genes in genesets = 195

genes with fdr < 0.1 = 189 (187 + / 2 −)

genes with fdr < 0.05 = 185 (183 + / 2 −)

genes with fdr < 0.01 = 177 (175 + / 2 −)

<r> metagenes = 0.98

<r> genes = 0.47

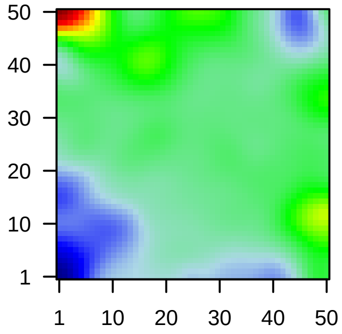
<FC> = 1.06

<shrinkage−t> = 37.29

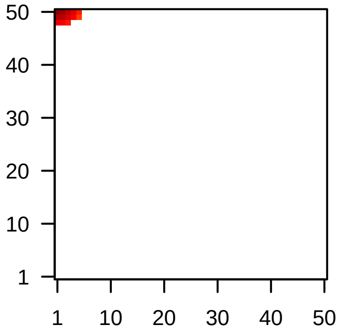
<p−value> = 0

<fdr> = 0.09

Profile



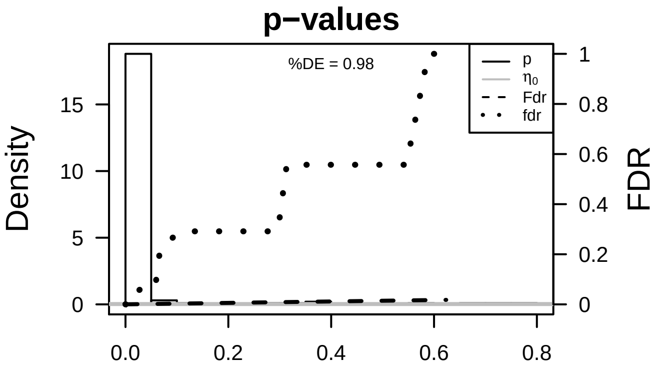
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.57	2e−16	2e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	1.51	2e−16	2e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.65	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.61	2e−16	2e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	1.59	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	1.58	2e−16	2e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	360	1.34	2e−16	2e−17	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
8	23120	1.45	2e−16	2e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
9	8424	1.52	2e−16	2e−17	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
10	394263	1.64	2e−16	2e−17	3 x 50	
11	84290	1.34	2e−16	2e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
12	22802	2.29	2e−16	2e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	84518	1.34	2e−16	2e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	49860	3.52	2e−16	2e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	1475	1.41	2e−16	2e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
16	1562	1.44	2e−16	2e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
17	1577	1.69	2e−16	2e−17	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
18	92196	1.79	2e−16	2e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	1828	1.75	2e−16	2e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
20	26298	1.69	2e−16	2e−17	4 x 50	ets homologous factor [Source:HGNC Symbol;Acc:3246]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	60.38	NULL	74 / 135	H.Tiss	WIRTH_Mucosa
2	27.8	NULL	14 / 21	CC	cornified envelope
3	26.04	NULL	19 / 53	BP	keratinocyte differentiation
4	23.06	NULL	16 / 42	BP	keratinization
5	22.1	NULL	77 / 572	Disease	GUDJ_psoriasis up
6	19.39	NULL	8 / 19	BP	peptide cross−linking
7	18.27	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	16.65	NULL	19 / 76	BP	epidermis development
9	14.63	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
10	14.04	NULL	6 / 13	BP	negative regulation of peptidase activity
11	13.4	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
12	13.2	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	13.02	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	12.83	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	12.29	NULL	12 / 122	MF	serine−type endopeptidase activity
16	11.67	NULL	7 / 38	BP	epithelial cell differentiation
17	11.3	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	11.26	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
19	10.74	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
20	10.71	NULL	5 / 10	MF	RAGE receptor binding
21	10.64	NULL	4 / 15	MF	retinol dehydrogenase activity
22	9.95	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
23	9.86	NULL	5 / 21	CC	desmosome
24	9.45	NULL	50 / 1182	CC	extracellular region
25	9.23	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
26	9.15	NULL	13 / 186	MF	structural molecule activity
27	9.1	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
28	8.98	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
29	8.98	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
30	8.89	NULL	3 / 12	BP	cellular aldehyde metabolic process
31	8.67	NULL	4 / 23	MF	peptidase inhibitor activity
32	8.66	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
33	8.41	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
34	8.01	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
35	8.01	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
36	7.97	NULL	4 / 44	CC	keratin filament
37	7.56	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
38	7.54	NULL	6 / 82	CC	intermediate filament
39	7.37	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
40	7.33	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN

GW_198

Local Summary

%DE = 0.89

metagenes = 20

genes = 305

genes in genesets = 303

genes with fdr < 0.1 = 250 (7 + / 243 −)

genes with fdr < 0.05 = 222 (5 + / 217 −)

genes with fdr < 0.01 = 213 (5 + / 208 −)

<r> metagenes = 0.95

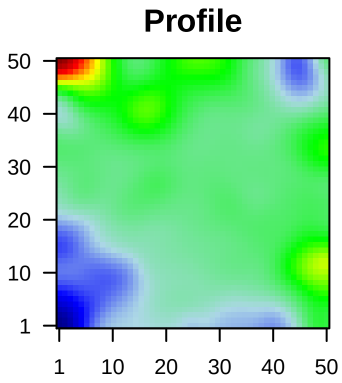
<r> genes = 0.36

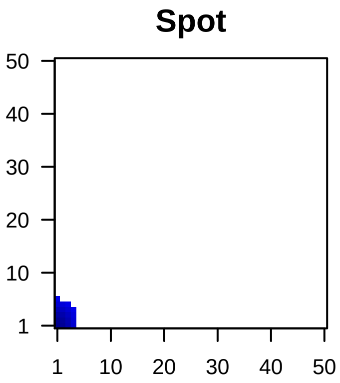
<FC> = −0.64

<shrinkage−t> = −22.53

<p−value> = 0

<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	−1.37	2e−16	2e−16	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	633	−1.44	2e−16	2e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	768	−1.33	2e−16	2e−16	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
4	414062	−1.5	2e−16	2e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
5	1277	−2	2e−16	2e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
6	1282	−1.34	2e−16	2e−16	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
7	1289	−1.41	2e−16	2e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
8	1290	−1.37	2e−16	2e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	1293	−1.33	2e−16	2e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	54541	−1.48	2e−16	2e−16	1 x 4	DNA−damage−inducible transcript 4 [Source:HGNC Symbol;
11	1687	−1.68	2e−16	2e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
12	3553	−1.44	2e−16	2e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
13	3569	−1.5	2e−16	2e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
14	3678	−1.71	2e−16	2e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
15	3918	−1.66	2e−16	2e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
16	3956	−1.36	2e−16	2e−16	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
17	4312	−1.5	2e−16	2e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
18	4320	−1.64	2e−16	2e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
19	4314	−1.68	2e−16	2e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
20	4318	−1.4	2e−16	2e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.24	NULL	70 / 242	BP	extracellular matrix organization
2	−32.91	NULL	59 / 190	CC	extracellular matrix
3	−30.02	NULL	69 / 250	Lymphoma	LENZ_Stromal signature 1
4	−29.68	NULL	33 / 69	BP	extracellular matrix disassembly
5	−28.95	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
6	−28.53	NULL	29 / 64	BP	collagen catabolic process
7	−28.46	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
8	−27.46	NULL	7 / 11	MF	platelet−derived growth factor binding
9	−25.31	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
10	−23.17	NULL	8 / 12	miRNA target	miR−29c
11	−22.93	NULL	12 / 19	MF	extracellular matrix binding
12	−22.92	NULL	13 / 35	Glio	Colman_survival_associated
13	−22.78	NULL	16 / 37	BP	collagen fibril organization
14	−22.15	NULL	21 / 57	MF	extracellular matrix structural constituent
15	−21.47	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
16	−20.89	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
17	−20.69	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	−20.69	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	−20.69	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	−20.69	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	−20.67	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
22	−19.99	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
23	−19.29	NULL	38 / 183	CC	proteinaceous extracellular matrix
24	−18.72	NULL	23 / 83	CC	basement membrane
25	−18.65	NULL	108 / 1182	CC	extracellular region
26	−18.29	NULL	11 / 40	BP	cellular response to amino acid stimulus
27	−18.23	NULL	79 / 683	CC	extracellular space
28	−18.23	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
29	−18.15	NULL	66 / 553	Cancer	Lembcke_Colonic Inflammation
30	−17.76	NULL	16 / 68	Glio	cultured astroglia vs. in vivo astrocytes
31	−16.9	NULL	56 / 403	BP	cell adhesion
32	−16.69	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
33	−16.64	NULL	9 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
34	−16.36	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
35	−16.04	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
36	−15.72	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
37	−15.69	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
38	−15.67	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
39	−15.64	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
40	−15.4	NULL	6 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN