

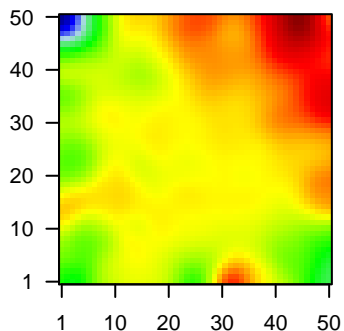
GW_073

Global Summary

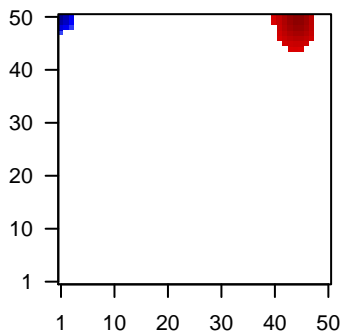
%DE = 0.14
 # genes with fdr < 0.2 = 1827 (914 + / 913 -)
 # genes with fdr < 0.1 = 1256 (639 + / 617 -)
 # genes with fdr < 0.05 = 1001 (504 + / 497 -)
 # genes with fdr < 0.01 = 663 (315 + / 348 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.86

Profile



Regulated Spots



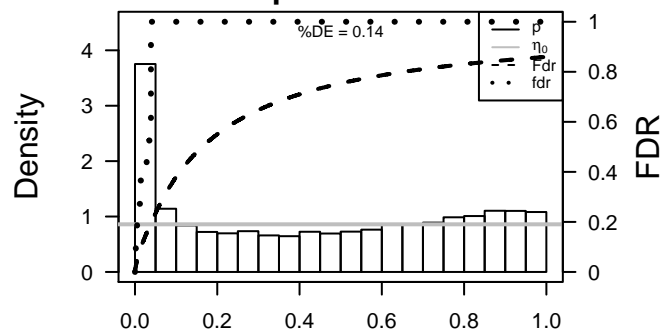
Global Genelist

Rank	ID	log(FC)	fdr	Description
		p-value	Metagene	
1	144568	-1.75	2e-16	6e-14 1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	-1.97	2e-16	6e-14 1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	445328	-2.31	2e-16	6e-14 4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
4	483	1.68	2e-16	6e-14 13 x 50 ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
5	375791	-2.01	2e-16	6e-14 1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
6	51806	-1.79	2e-16	6e-14 4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
7	8900	1.68	2e-16	6e-14 1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
8	100133941	-1.8	2e-16	6e-14 3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
9	4680	-2.45	2e-16	6e-14 1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	9022	-1.94	2e-16	6e-14 1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
11	84518	-2.68	2e-16	6e-14 1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
12	54544	-1.81	2e-16	6e-14 1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987:
13	1396	-1.76	2e-16	6e-14 50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
14	55894	-1.75	2e-16	6e-14 1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	414325	-2.63	2e-16	6e-14 1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1828	-1.72	2e-16	6e-14 1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
17	2125	-1.65	2e-16	6e-14 1 x 50 envoplakin [Source:HGNC Symbol;Acc:3503]
18	128876	-1.83	2e-16	6e-14 1 x 48 family with sequence similarity 83, member C [Source:HGNC
19	3123	-1.68	2e-16	6e-14 45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
20	9955	1.65	2e-16	6e-14 5 x 43 heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 [So

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.11	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	14.11	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	11.36	NULL	370	BP mitotic cell cycle
4	11.03	NULL	280	Chr Chr 13
5	10.35	NULL	4640	CC nucleus
6	8.89	NULL	949	CC nucleoplasm
7	7.79	NULL	15	GSEA C2AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
8	7.44	NULL	386	Chr Chr 22
9	7.38	NULL	1233	TF KIM_MYC targets
10	7.29	NULL	51	BP type I interferon signaling pathway
11	7.15	NULL	595	MF RNA binding
12	6.84	NULL	1749	MF DNA binding
13	6.64	NULL	14	MMML C6CIEJ_MMML 4
14	6.62	NULL	16	GSEA C2TCGA_GLIOMASTOMA_COPY_NUMBER_UP
15	6.6	NULL	20	LymphomaBOSOLOWSKI_red UP
16	6.58	NULL	232	BP mitosis
17	6.53	NULL	16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
18	6.5	NULL	1318	CC mitochondrion
19	6.44	NULL	220	CC mitochondrial matrix
20	6.41	NULL	940	MF nucleic acid binding
<i>Underexpressed</i>				
1	-20.28	NULL	21	CC cornified envelope
2	-19.28	NULL	135	H.Tiss WIRTH_Mucosa
3	-17.13	NULL	42	BP keratinization
4	-13.44	NULL	19	BP peptide cross-linking
5	-13.25	NULL	53	BP keratinocyte differentiation
6	-12.35	NULL	1182	CC extracellular region
7	-12.27	NULL	76	BP epidermis development
8	-9.62	NULL	683	CC extracellular space
9	-9.6	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	-9.39	NULL	553	Cancer Lembcke_Colonc Inflammation
11	-9.2	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
12	-7.79	NULL	186	MF structural molecule activity
13	-7.59	NULL	250	LymphomaENZ_Stromal signature 1
14	-7.53	NULL	957	Chr Chr 11
15	-7.45	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
16	-7.34	NULL	190	CC extracellular matrix
17	-7.23	NULL	122	MF serine-type endopeptidase activity
18	-7.05	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
19	-6.71	NULL	572	Disease GUDJ_psooriasis up
20	-6.48	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN

p-values



GW_073

Local Summary

%DE = 0.71
 # metagenes = 45
 # genes = 553
 # genes in genesets = 548
 # genes with $fdr < 0.1$ = 276 (262 + / 14 -)
 # genes with $fdr < 0.05$ = 218 (206 + / 12 -)
 # genes with $fdr < 0.01$ = 145 (140 + / 5 -)

$\langle r \rangle$ metagenes = 0.91

$\langle r \rangle$ genes = 0.32

$\langle FC \rangle$ = 0.36

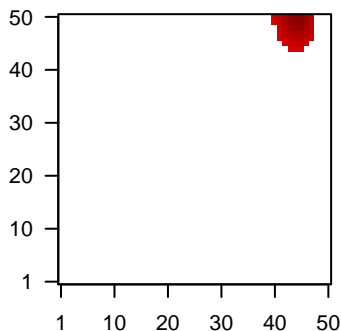
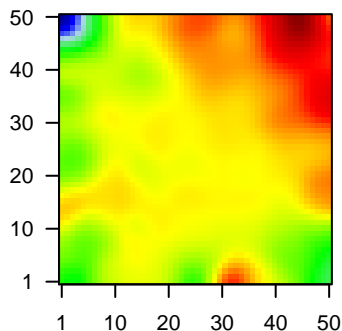
$\langle \text{shrinkage-t} \rangle$ = 12.73

$\langle p\text{-value} \rangle$ = 0.01

$\langle fdr \rangle$ = 0.58

Profile

Spot



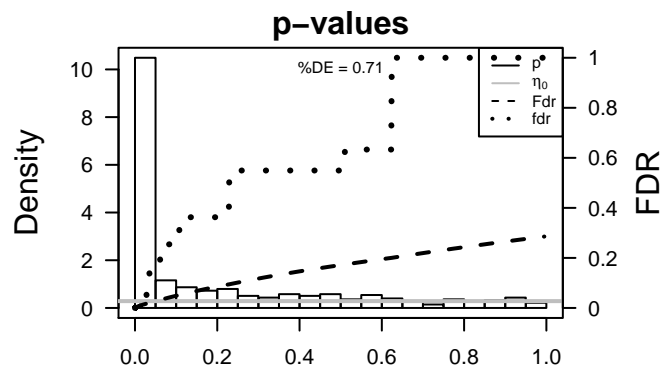
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84223	1.71	2e-16	4e-14	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
2	26872	1.38	4e-12	7e-08	40 x 50 six transmembrane epithelial antigen of the prostate 1 [Source:HGNC Symbol;Acc:25251]
3	100008588	1.24	5e-10	2e-07	41 x 46 RNA, 18S ribosomal 5 [Source:HGNC Symbol;Acc:37657]
4	8318	1.19	2e-09	2e-07	45 x 49 cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
5	55872	1.17	3e-09	4e-07	45 x 49 PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
6	10165	1.15	6e-09	1e-06	40 x 50 solute carrier family 25 (aspartate/glutamate carrier), member 1 [Source:HGNC Symbol;Acc:11616]
7	26255	1.12	2e-08	1e-06	44 x 48 pituitary tumor-transforming 3, pseudogene [Source:HGNC Symbol;Acc:11616]
8	1786	1.11	2e-08	1e-06	45 x 47 DNA (cytosine-5-)-methyltransferase 1 [Source:HGNC Symbol;Acc:11616]
9	142	1.1	3e-08	1e-06	47 x 46 poly (ADP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:11616]
10	51203	1.09	4e-08	1e-06	45 x 48 nucleolar and spindle associated protein 1 [Source:HGNC Symbol;Acc:11616]
11	55165	1.08	5e-08	1e-06	44 x 50 centrosomal protein 55kDa [Source:HGNC Symbol;Acc:11616]
12	57570	1.08	6e-08	1e-06	46 x 45 tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141]
13	54478	1.07	7e-08	1e-06	45 x 49 family with sequence similarity 64, member A [Source:HGNC Symbol;Acc:11616]
14	9212	1.07	8e-08	1e-06	45 x 48 aurora kinase B [Source:HGNC Symbol;Acc:11390]
15	5984	1.06	8e-08	1e-06	46 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Symbol;Acc:11616]
16	128061	1.06	9e-08	6e-06	41 x 50 chromosome 1 open reading frame 131 [Source:HGNC Symbol;Acc:11616]
17	51659	1.05	1e-07	1e-05	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Symbol;Acc:11616]
18	8317	1.03	2e-07	1e-05	45 x 47 cell division cycle 7 [Source:HGNC Symbol;Acc:1745]
19	5902	1.02	3e-07	2e-05	43 x 50 RAN binding protein 1 [Source:HGNC Symbol;Acc:9847]
20	9918	0.99	6e-07	2e-05	45 x 49 non-SMC condensin I complex, subunit D2 [Source:HGNC Symbol;Acc:11616]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	46.49	NULL	101 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	46.49	NULL	101 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	26.93	NULL	128 / 370	BP mitotic cell cycle
4	24.64	NULL	13 / 14	MMML C6S3CIEJ_MMML_4
5	23.94	NULL	15 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
6	22.75	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
7	22.69	NULL	119 / 530	Cancer Lembecke_Normal vs Adenoma
8	22.2	NULL	14 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
9	21.04	NULL	9 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
10	20.15	NULL	16 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
11	19.21	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	18.41	NULL	66 / 232	BP mitosis
13	17.95	NULL	25 / 57	Glio developing astrocytes
14	17.33	NULL	12 / 15	GSEA C2CHANG_CYCLING_GENES
15	16.88	NULL	56 / 149	BP DNA replication
16	16.79	NULL	13 / 18	BP spindle organization
17	16.48	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
18	16.17	NULL	11 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
19	15.79	NULL	11 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
20	15.26	NULL	12 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
21	15.2	NULL	146 / 949	CC nucleoplasm
22	15.11	NULL	10 / 16	GSEA C2KEGG_MISMATCH_REPAIR
23	15.05	NULL	9 / 15	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_UP
24	14.64	NULL	12 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
25	14.17	NULL	9 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
26	14.07	NULL	12 / 33	CC spindle microtubule
27	13.93	NULL	11 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
28	13.8	NULL	21 / 30	BP DNA strand elongation involved in DNA replication
29	13.58	NULL	5 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
30	13.55	NULL	23 / 83	CC spindle pole
31	13.5	NULL	26 / 66	CC condensed chromosome kinetochore
32	13.34	NULL	68 / 572	Disease GUDJ_poriasis up
33	13.03	NULL	7 / 13	GSEA C2NADERI_BREAST_CANCER_PROGNOSIS_UP
34	12.97	NULL	25 / 67	BP chromosome segregation
35	12.89	NULL	9 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
36	12.88	NULL	12 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
37	12.39	NULL	7 / 12	BP mitotic chromosome condensation
38	12.23	NULL	12 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
39	12.23	NULL	9 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
40	12.12	NULL	12 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN



GW_073

Local Summary

%DE = 0.9
 # metagenes = 10
 # genes = 162
 # genes in genesets = 157

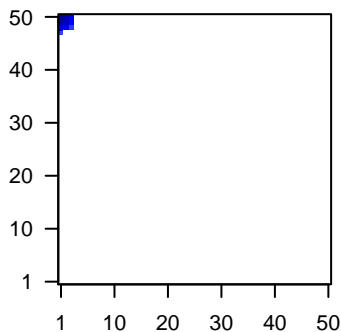
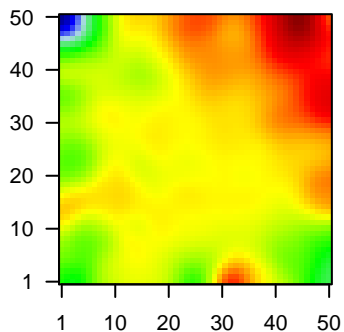
genes with $fdr < 0.1 = 136$ (6 + / 130 -)
 # genes with $fdr < 0.05 = 136$ (6 + / 130 -)
 # genes with $fdr < 0.01 = 120$ (4 + / 116 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.49

$\langle FC \rangle = -1.02$
 $\langle \text{shrinkage-t} \rangle = -36.01$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.19$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-1.75	2e-16	1e-16	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	-1.97	2e-16	1e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	375791	-2.01	2e-16	1e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
4	100133941	-1.8	2e-16	1e-16	3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
5	4680	-2.45	2e-16	1e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (I
6	9022	-1.94	2e-16	1e-16	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
7	84518	-2.68	2e-16	1e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	-1.81	2e-16	1e-16	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987:
9	55894	-1.75	2e-16	1e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	414325	-2.63	2e-16	1e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1828	-1.72	2e-16	1e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
12	2125	-1.65	2e-16	1e-16	1 x 50 envoplakin [Source:HGNC Symbol;Acc:3503]
13	128876	-1.83	2e-16	1e-16	1 x 48 family with sequence similarity 83, member C [Source:HGNC
14	26525	-1.9	2e-16	1e-16	1 x 49 interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
15	5653	-2.8	2e-16	1e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63f
16	5650	-1.97	2e-16	1e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63f
17	3848	-1.88	2e-16	1e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
18	144501	-1.75	2e-16	1e-16	1 x 49 keratin 80 [Source:HGNC Symbol;Acc:27056]
19	388533	-3.24	2e-16	1e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
20	84648	-2.09	2e-16	1e-16	1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-53.91	NULL	15 / 21	CC cornified envelope
2	-49.49	NULL	68 / 135	H.Tiss WIRTH_Mucosa
3	-44.61	NULL	18 / 42	BP keratinization
4	-35.53	NULL	20 / 53	BP keratinocyte differentiation
5	-32.51	NULL	8 / 19	BP peptide cross-linking
6	-26.36	NULL	18 / 76	BP epidermis development
7	-23.41	NULL	74 / 572	Disease GUDJ_psooriasis up
8	-20.96	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	-19.35	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	-18.97	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	-16.94	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
12	-16.44	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
13	-13.09	NULL	17 / 186	MF structural molecule activity
14	-12.85	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
15	-12.49	NULL	6 / 13	BP negative regulation of peptidase activity
16	-11.19	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	-10.75	NULL	5 / 51	MF protein binding, bridging
18	-10.31	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
19	-10.28	NULL	11 / 122	MF serine-type endopeptidase activity
20	-9.96	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
21	-9.82	NULL	5 / 21	CC desmosome
22	-9.72	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
23	-9.71	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
24	-9.62	NULL	2 / 17	Disease BCHETNIA_EBM up
25	-9.5	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
26	-8.65	NULL	45 / 1182	CC extracellular region
27	-8.54	NULL	3 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
28	-8.53	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_U
29	-8.36	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
30	-8.04	NULL	2 / 12	H.Tiss WIRTH_Prim_lymphoid organs
31	-7.99	NULL	4 / 23	MF peptidase inhibitor activity
32	-7.95	NULL	4 / 15	MF retinol dehydrogenase activity
33	-7.74	NULL	8 / 52	BP negative regulation of endopeptidase activity
34	-7.69	NULL	8 / 44	CC keratin filament
35	-7.63	NULL	4 / 27	BP response to bacterium
36	-7.4	NULL	5 / 29	BP regulation of proteolysis
37	-7.36	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
38	-7.35	NULL	3 / 18	BP retinol metabolic process
39	-7.22	NULL	3 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
40	-7.19	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL

