

GW_180

Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1695 (1031 + / 664 -)
 # genes with fdr < 0.1 = 1221 (793 + / 428 -)
 # genes with fdr < 0.05 = 1007 (681 + / 326 -)
 # genes with fdr < 0.01 = 687 (490 + / 197 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.86

Global Genelist

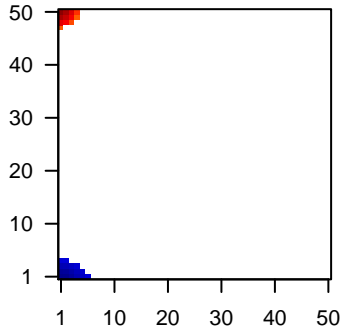
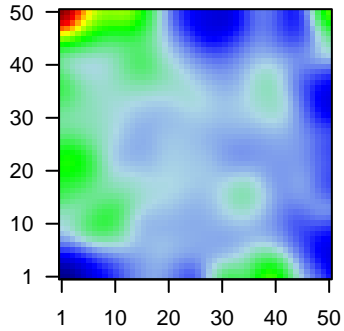
Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.8	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
2	441282	1.84	2e-16	5e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	8644	1.56	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
4	1109	1.56	2e-16	5e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
5	218	1.73	2e-16	5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	242	1.71	2e-16	5e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
7	586	1.6	2e-16	5e-14	6 x 1 branched chain amino-acid transaminase 1, cytosolic [Sourc
8	655	1.38	2e-16	5e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
9	684	1.71	2e-16	5e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	387695	1.48	2e-16	5e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
11	339512	1.76	2e-16	5e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
12	260436	1.95	2e-16	5e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
13	29113	2.52	2e-16	5e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
14	375791	1.57	2e-16	5e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
15	51806	1.83	2e-16	5e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
16	84518	1.54	2e-16	5e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
17	49860	2.98	2e-16	5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1410	1.82	2e-16	5e-14	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
19	1571	1.73	2e-16	5e-14	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
20	57834	2.65	2e-16	5e-14	13 x 50 cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour

Global Geneset Analysis

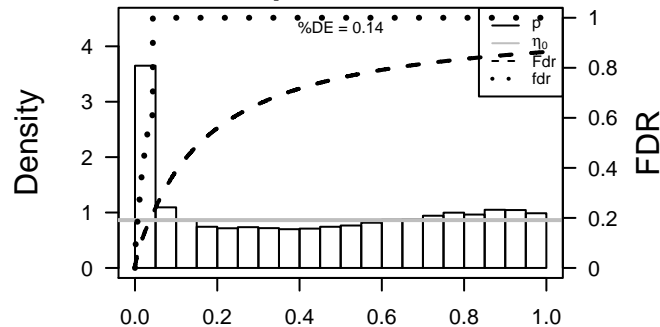
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.91	NULL	135	H.Tiss WIRTH_Mucosa
2	12.94	NULL	572	Disease GUDJ_psooriasis up
3	11.77	NULL	21	CC cornified envelope
4	11.57	NULL	42	BP keratinization
5	10.43	NULL	53	BP keratinocyte differentiation
6	8.71	NULL	76	BP epidermis development
7	8.39	NULL	19	BP peptide cross-linking
8	8.32	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
9	7.91	NULL	15	GSEA C2CRICKMAN_HEAD_AND_NECK_CANCER_E
10	7.67	NULL	13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_E
11	7.58	NULL	717	Chr Chr 16
12	7.4	NULL	1135	Chr Chr 19
13	7.38	NULL	44	CC keratin filament
14	7.16	NULL	743	Chr Chr 7
15	6.82	NULL	7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
16	6.75	NULL	38	BP epithelial cell differentiation
17	6.61	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
18	6.57	NULL	11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	6.18	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
20	6.16	NULL	10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
<i>Underexpressed</i>				
1	-9.46	NULL	250	LymphomaEENZ_Stromal signature 1
2	-8.87	NULL	190	CC extracellular matrix
3	-8.12	NULL	280	Chr Chr 13
4	-7.74	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
5	-7.74	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
6	-7.74	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
7	-7.74	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
8	-7.6	NULL	81	BP viral transcription
9	-7.56	NULL	87	BP translational termination
10	-7.52	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
11	-7.4	NULL	242	BP extracellular matrix organization
12	-7.37	NULL	92	BP translational elongation
13	-7.31	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
14	-7.31	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
15	-7.12	NULL	43	MF chemokine activity
16	-7.02	NULL	92	BP viral life cycle
17	-6.9	NULL	69	BP extracellular matrix disassembly
18	-6.8	NULL	553	Cancer Lembecke_Colonc Inflammation
19	-6.61	NULL	128	BP translational initiation
20	-6.49	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated

Profile

Regulated Spots



p-values



GW_180

Local Summary

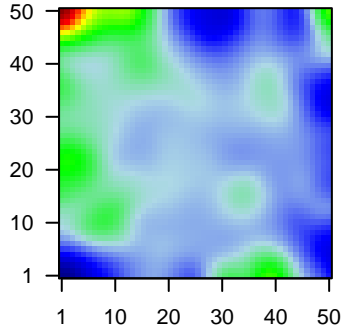
%DE = 0.9
 # metagenes = 12
 # genes = 189
 # genes in genesets = 184

genes with $fdr < 0.1 = 163$ (160 + / 3 -)
 # genes with $fdr < 0.05 = 153$ (152 + / 1 -)
 # genes with $fdr < 0.01 = 141$ (140 + / 1 -)

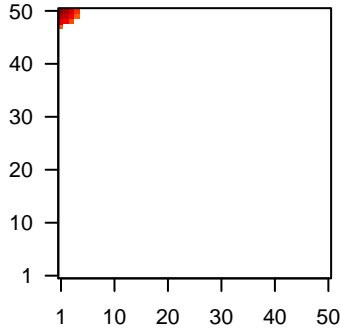
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.48

$\langle FC \rangle = 0.87$
 $\langle \text{shrinkage-t} \rangle = 30.69$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.21$

Profile



Spot



Local Genelist

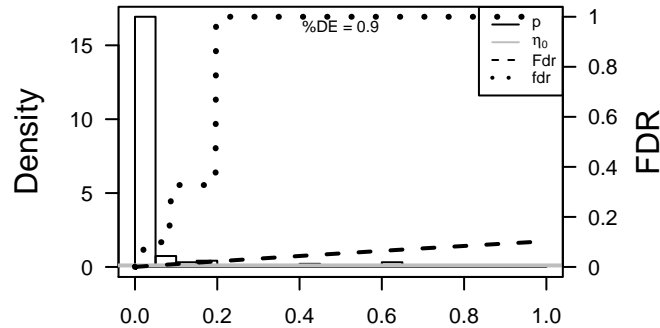
Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.8	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
2	441282	1.84	2e-16	1e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	1.56	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
4	218	1.73	2e-16	1e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	242	1.71	2e-16	1e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
6	387695	1.48	2e-16	1e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
7	375791	1.57	2e-16	1e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
8	51806	1.83	2e-16	1e-16	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
9	84518	1.54	2e-16	1e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
10	49860	2.98	2e-16	1e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
11	126410	1.83	2e-16	1e-16	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
12	92196	1.8	2e-16	1e-16	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
13	1673	1.58	2e-16	1e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	2877	2.43	2e-16	1e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syr
15	5653	1.61	2e-16	1e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63i
16	5650	1.41	2e-16	1e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63i
17	3860	1.52	2e-16	1e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
18	3851	2.27	2e-16	1e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
19	196374	1.63	2e-16	1e-16	1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926]
20	388533	2.18	2e-16	1e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	57.49	NULL	75 / 135	H.Tiss WIRTH_Mucosa
2	29.04	NULL	15 / 21	CC cornified envelope
3	26.35	NULL	18 / 42	BP keratinization
4	25.65	NULL	20 / 53	BP keratinocyte differentiation
5	23.95	NULL	80 / 572	Disease GUDJ_psooriasis up
6	23.27	NULL	8 / 19	BP peptide cross-linking
7	19.51	NULL	20 / 76	BP epidermis development
8	16.85	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	15.86	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	15.16	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	13.97	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	12.9	NULL	3 / 12	BP cellular aldehyde metabolic process
13	12.85	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	12.29	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
15	12.04	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
16	11.77	NULL	8 / 44	CC keratin filament
17	11.44	NULL	5 / 10	MF RAGE receptor binding
18	11.18	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
19	11.03	NULL	17 / 186	MF structural molecule activity
20	10.95	NULL	3 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
21	10.23	NULL	4 / 15	GSEA C2IN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	9.61	NULL	4 / 15	MF retinol dehydrogenase activity
23	9.56	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
24	9.3	NULL	10 / 82	CC intermediate filament
25	9.08	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
26	9.05	NULL	6 / 13	BP negative regulation of peptidase activity
27	8.84	NULL	4 / 16	GSEA C2OLDREN_GEFITINIB_RESISTANCE_DN
28	8.71	NULL	49 / 1182	CC extracellular region
29	8.71	NULL	7 / 38	BP epithelial cell differentiation
30	8.67	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
31	8.48	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
32	8.37	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
33	8.12	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
34	8.09	NULL	4 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
35	7.86	NULL	4 / 23	MF peptidase inhibitor activity
36	7.8	NULL	11 / 122	MF serine-type endopeptidase activity
37	7.77	NULL	1 / 11	Glio VERHAAK_Brain
38	7.6	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
39	7.55	NULL	1 / 12	GSEA C2ODONNELL_METASTASIS_DN
40	7.55	NULL	1 / 12	GSEA C2SYED ESTRADIOL_RESPONSE

p-values



GW_180

Local Summary

%DE = 0.81
 # metagenes = 17
 # genes = 292
 # genes in genesets = 291
 # genes with $fdr < 0.1$ = 172 (7 + / 165 -)
 # genes with $fdr < 0.05$ = 145 (6 + / 139 -)
 # genes with $fdr < 0.01$ = 106 (4 + / 102 -)

$\langle r \rangle$ metagenes = 0.95

$\langle r \rangle$ genes = 0.39

$\langle FC \rangle = -0.4$

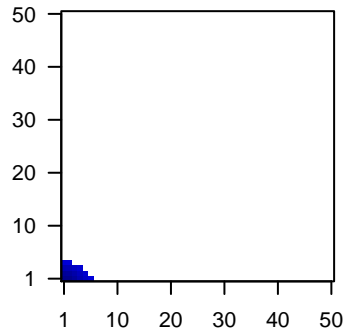
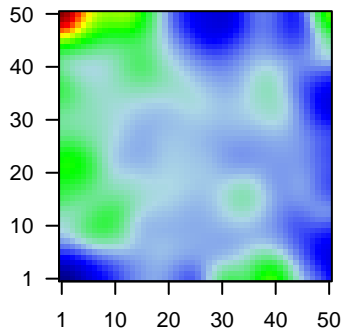
$\langle \text{shrinkage-t} \rangle = -14.09$

$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.52$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	586	1.6	2e-16	2e-15	6 x 1 branched chain amino-acid transaminase 1, cytosolic [Source:HGNC Symbol;Acc:2114]
2	29940	-1.42	2e-16	2e-15	1 x 4 dermatan sulfate epimerase [Source:HGNC Symbol;Acc:2114]
3	3040	-1.39	2e-16	2e-15	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3576	-2.3	2e-16	2e-15	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
5	4319	-1.57	2e-16	2e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:2114]
6	4316	-1.57	2e-16	2e-15	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC Symbol;Acc:2114]
7	6423	-1.49	2e-16	2e-15	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:2114]
8	131566	-1.22	2e-13	4e-11	1 x 4 discoidin, CUB and LCLC domain containing 2 [Source:HGNC Symbol;Acc:2114]
9	6372	-1.17	2e-12	4e-11	1 x 1 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Acc:2114]
10	2919	-1.17	2e-12	4e-11	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimulatory protein 1) [Source:HGNC Symbol;Acc:2114]
11	3491	-1.17	2e-12	7e-11	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol;Acc:2114]
12	5270	-1.15	4e-12	7e-11	1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) member 1 [Source:HGNC Symbol;Acc:2114]
13	7057	-1.15	5e-12	1e-09	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
14	3490	-1.1	4e-11	1e-09	3 x 1 insulin-like growth factor binding protein 7 [Source:HGNC Symbol;Acc:2114]
15	10409	-1.09	5e-11	2e-09	1 x 2 brain abundant, membrane attached signal protein 1 [Source:HGNC Symbol;Acc:2114]
16	12	-1.08	9e-11	7e-09	1 x 1
17	7058	-1.05	2e-10	7e-09	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
18	10631	-1.04	3e-10	2e-08	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Acc:2114]
19	7128	-1.03	6e-10	2e-08	1 x 1 tumor necrosis factor, alpha-induced protein 3 [Source:HGNC Symbol;Acc:2114]
20	414062	-1.01	1e-09	2e-08	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:2114]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-29.88	NULL	67 / 190	CC extracellular matrix
2	-26.56	NULL	80 / 250	Lymphocyte ENZ_Stromal signature 1
3	-24.58	NULL	66 / 242	BP extracellular matrix organization
4	-24	NULL	6 / 12	GSEA C2Y_AGING_MIDDLE_UP
5	-23.65	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
6	-22.99	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
7	-22.88	NULL	31 / 69	BP extracellular matrix disassembly
8	-21.85	NULL	27 / 64	BP collagen catabolic process
9	-20.68	NULL	15 / 16	MMML C6CIEJ_MMML 1
10	-20.45	NULL	1 / 3	GSEA C2REN_MIF_TARGETS_DN
11	-19.97	NULL	84 / 683	CC extracellular space
12	-19.91	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
13	-19.83	NULL	2 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
14	-19.72	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
15	-19.27	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
16	-19.06	NULL	109 / 1182	CC extracellular region
17	-18.97	NULL	4 / 7	GSEA C2SUNODA_CISPLATIN_RESISTANCE_UP
18	-18.78	NULL	7 / 16	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC
19	-17.71	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
20	-17.02	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
21	-16.72	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
22	-16.52	NULL	2 / 4	MMML C6CIEJ_MMML 23
23	-16.49	NULL	11 / 19	MF extracellular matrix binding
24	-16.24	NULL	6 / 13	GSEA C2TAI_RESPONSE_TO_RADIATION_THERAPY
25	-15.91	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
26	-15.89	NULL	5 / 16	BP fibronectin binding
27	-15.53	NULL	5 / 11	MF dermatan sulfate biosynthetic process
28	-15.53	NULL	8 / 11	MF platelet-derived growth factor binding
29	-15.33	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
30	-15.32	NULL	70 / 553	Cancer Lembecke_Colonc Inflammation
31	-15.27	NULL	2 / 6	Glio Martinez_Glio_hypometh
32	-15.23	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
33	-15.21	NULL	1 / 5	GSEA C2DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCCOC
34	-15.19	NULL	2 / 9	GSEA C2HEDVAT_ELF4_TARGETS_UP
35	-15.15	NULL	3 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
36	-14.78	NULL	4 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
37	-14.71	NULL	8 / 12	miRNA target-29c
38	-14.09	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
39	-14.04	NULL	3 / 10	BP negative regulation of G-protein coupled receptor protein signaling
40	-13.97	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR

