

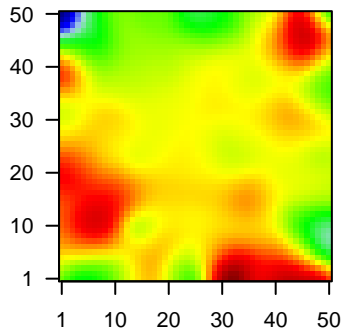
# GW\_238

## Global Summary

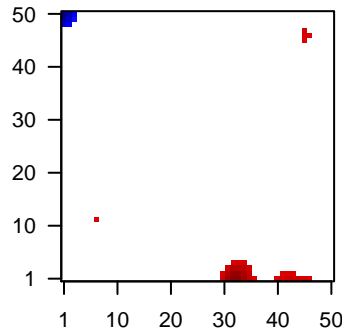
%DE = 0.15  
 # genes with  $fdr < 0.2$  = 1805 ( 997 + / 808 - )  
 # genes with  $fdr < 0.1$  = 1515 ( 819 + / 696 - )  
 # genes with  $fdr < 0.05$  = 1243 ( 664 + / 579 - )  
 # genes with  $fdr < 0.01$  = 774 ( 408 + / 366 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.1  
 <fdr> = 0.85

Profile



Regulated Spots



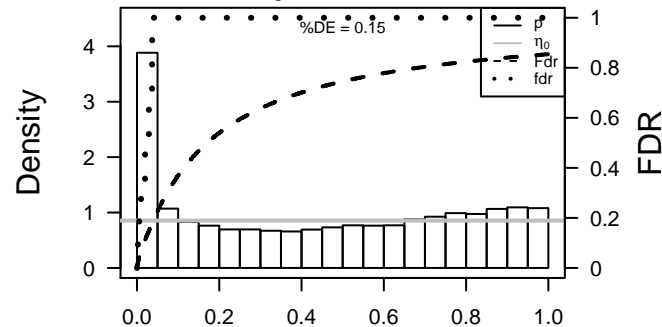
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	131	-2.09	2e-16 3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-1.55	2e-16 3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.74	2e-16 3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	-2.74	2e-16 3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
5	1109	-2.01	2e-16 3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
6	216	-2.08	2e-16 3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
7	220	-1.63	2e-16 3e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
8	260436	-1.57	2e-16 3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
9	768	1.75	2e-16 3e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
10	55450	1.91	2e-16 3e-14	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [S
11	595	-1.99	2e-16 3e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
12	4680	-1.77	2e-16 3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
13	1056	1.8	2e-16 3e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
14	22802	-2.24	2e-16 3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	84518	-1.95	2e-16 3e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
16	49860	-2.09	2e-16 3e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1410	-1.8	2e-16 3e-14	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
18	1469	1.59	2e-16 3e-14	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
19	1508	1.61	2e-16 3e-14	6 x 5 cathepsin B [Source:HGNC Symbol;Acc:2527]
20	3627	2.1	2e-16 3e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;A

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.7	NULL	633	Chr Chr 9
2	11.55	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
3	11.55	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
4	10.06	NULL	370	BP mitotic cell cycle
5	9.13	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIDOM
6	8.81	NULL	1135	Chr Chr 19
7	8.68	NULL	417	H,Tiss WIRTH_Immune system
8	8.34	NULL	51	BP type I interferon signaling pathway
9	7.79	NULL	4640	CC nucleus
10	7.42	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
11	7.41	NULL	123	BP defense response to virus
12	7.33	NULL	14	GSEA C2RADAeva_RESPONSE_TO_IFNA1_UP
13	7.29	NULL	949	CC nucleoplasm
14	7.19	NULL	11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
15	7.17	NULL	12	GSEA C2ZHU_CMV_8_HR_UP
16	7.08	NULL	232	BP mitosis
17	6.84	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
18	6.73	NULL	204	BP cytokine-mediated signaling pathway
19	6.71	NULL	530	Cancer Lembecke_Normal vs Adenoma
20	6.68	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
<i>Underexpressed</i>				
1	-16.99	NULL	135	H,Tiss WIRTH_Mucosa
2	-14.7	NULL	21	CC cornified envelope
3	-13.83	NULL	53	BP keratinocyte differentiation
4	-13.49	NULL	42	BP keratinization
5	-11.51	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
6	-10.87	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
7	-9.64	NULL	76	BP epidermis development
8	-8.59	NULL	16	GSEA C2JAeger_METASTASIS_DN
9	-8.41	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
10	-8.28	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
11	-8.14	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	-7.95	NULL	1033	Chr Chr 2
13	-7.92	NULL	1182	CC extracellular region
14	-7.54	NULL	19	BP peptide cross-linking
15	-7.46	NULL	1146	TF HEBENSTREIT_low expression TF
16	-7.42	NULL	914	Chr Chr 3
17	-7.4	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
18	-7.17	NULL	7	MMML C2CIEJ_MMML 5
19	-7.16	NULL	8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
20	-6.93	NULL	10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING

p-values



# GW\_238

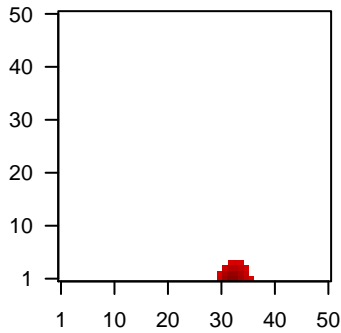
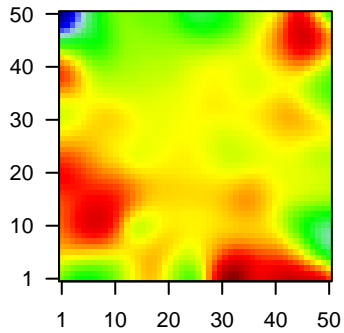
## Local Summary

%DE = 0.7  
 # metagenes = 21  
 # genes = 198  
 # genes in genesets = 195  
 # genes with  $fdr < 0.1 = 110$  ( 107 + / 3 - )  
 # genes with  $fdr < 0.05 = 96$  ( 95 + / 1 - )  
 # genes with  $fdr < 0.01 = 86$  ( 85 + / 1 - )

<r> metagenes = 0.93  
 <r> genes = 0.33  
 <FC> = 0.52  
 <shrinkage-t> = 18.37  
 <p-value> = 0  
 <fdr> = 0.48

Profile

Spot



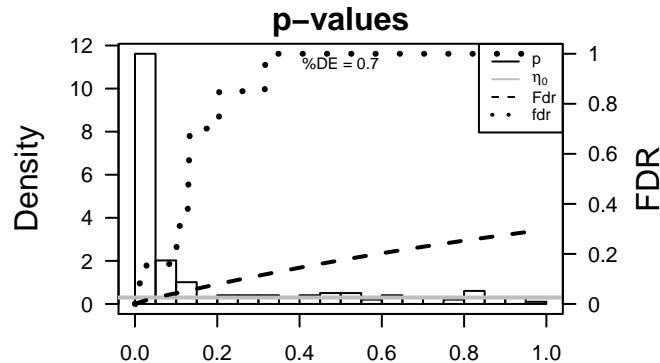
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3627	2.1	2e-16	1e-15	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:1989]
2	6373	2.3	2e-16	1e-15	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:1989]
3	2633	1.68	2e-16	1e-15	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:1989]
4	115362	1.71	2e-16	1e-15	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989]
5	9636	1.72	2e-16	1e-15	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:406]
6	3804	1.49	2e-16	1e-15	32 x 1 killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail [Source:HGNC Symbol;Acc:1989]
7	8743	1.54	2e-16	1e-15	32 x 1 tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:1989]
8	7453	1.75	2e-16	1e-15	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1989]
9	7503	2.48	2e-16	1e-15	34 x 4 X inactive specific transcript (non-protein coding) [Source:HGNC Symbol;Acc:1989]
10	6890	1.41	8e-15	3e-13	32 x 1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Source:HGNC Symbol;Acc:1989]
11	101	1.4	1e-14	2e-12	32 x 3 ADAM metalloproteinase domain 8 [Source:HGNC Symbol;Acc:1989]
12	3136	1.36	6e-14	2e-12	32 x 1
13	2537	1.36	7e-14	6e-12	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:1989]
14	23780	1.34	2e-13	2e-11	32 x 1 apolipoprotein L 2 [Source:HGNC Symbol;Acc:619]
15	6772	1.32	5e-13	2e-10	32 x 1 signal transducer and activator of transcription 1, 91kDa [Source:HGNC Symbol;Acc:1989]
16	94240	1.27	3e-12	1e-09	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbol;Acc:1989]
17	3628	1.22	2e-11	2e-09	33 x 1 inositol polyphosphate-1-phosphatase [Source:HGNC Symbol;Acc:1989]
18	55748	1.13	7e-11	2e-09	34 x 1 CNDP dipeptidase 2 (metalloproteinase M20 family) [Source:HGNC Symbol;Acc:1989]
19	684	1.18	7e-11	7e-09	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1989]
20	400759	1.14	3e-10	7e-09	32 x 1 guanylate binding protein 1, interferon-inducible pseudogene [Source:HGNC Symbol;Acc:1989]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	32.97	NULL	30 / 51	BP type I interferon signaling pathway
2	30.46	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
3	30.3	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
4	29.56	NULL	6 / 6	Lymphocyte activation-induced chemokine receptor 1
5	29.52	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
6	29.17	NULL	11 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
7	28.87	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
8	28.83	NULL	12 / 16	GSEA C2ENAV_INTERFERON_SIGNATURE_IN_CANCER
9	25.14	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
10	24.63	NULL	7 / 10	CC MHC class I protein complex
11	23.63	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	23.08	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
13	23.08	NULL	35 / 123	BP defense response to virus
14	22.4	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
15	22.4	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
16	22.21	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
17	21.7	NULL	8 / 18	MF peptide antigen binding
18	21.23	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
19	20.64	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
20	20.03	NULL	13 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
21	19.78	NULL	36 / 204	BP cytokine-mediated signaling pathway
22	19.29	NULL	2 / 10	BP positive regulation of cAMP-mediated signaling
23	18	NULL	2 / 2	MMML C2SCIEJ_MMML_27
24	17.69	NULL	17 / 60	BP interferon-gamma-mediated signaling pathway
25	17.4	NULL	2 / 12	BP positive regulation of leukocyte chemotaxis
26	16.66	NULL	15 / 31	BP negative regulation of viral genome replication
27	15.7	NULL	14 / 70	BP antigen processing and presentation of exogenous peptide antigen
28	15.5	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
29	15.22	NULL	14 / 74	BP antigen processing and presentation of exogenous peptide antigen
30	15.1	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
31	15.07	NULL	4 / 14	GSEA C2WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_DN
32	14.84	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP
33	14.67	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
34	14.59	NULL	15 / 91	BP antigen processing and presentation of peptide antigen via MHC class II
35	14.53	NULL	49 / 572	Disease GUDJ_poriasis_up
36	14.5	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
37	14.45	NULL	10 / 47	BP antigen processing and presentation
38	14.43	NULL	32 / 312	BP immune response
39	14.39	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
40	14.31	NULL	2 / 17	BP positive regulation of release of sequestered calcium ion into cytosol



# GW\_238

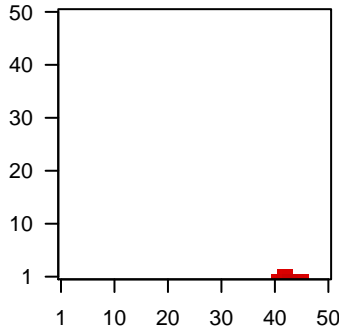
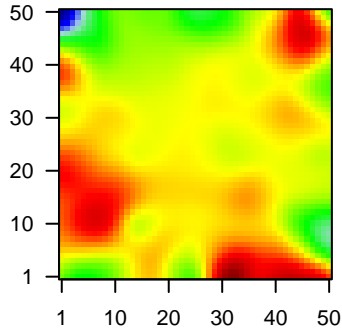
## Local Summary

%DE = 0.75  
 # metagenes = 10  
 # genes = 168  
 # genes in genesets = 159  
 # genes with  $fdr < 0.1$  = 106 ( 99 + / 7 - )  
 # genes with  $fdr < 0.05$  = 86 ( 82 + / 4 - )  
 # genes with  $fdr < 0.01$  = 51 ( 48 + / 3 - )

$\langle r \rangle$  metagenes = 0.92  
 $\langle r \rangle$  genes = 0.42  
 $\langle FC \rangle$  = 0.36  
 $\langle \text{shrinkage-t} \rangle$  = 12.77  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.53

Profile

Spot



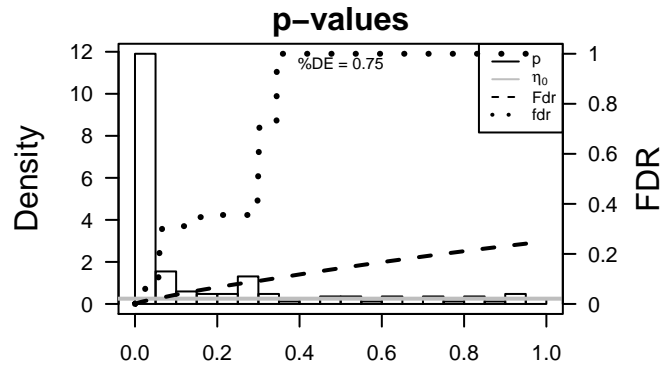
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1762	1.17	1e-10	2e-08	dystrophia myotonica, WD repeat containing [Source:HGNC Symbol;Acc:16830]
2	3123	-1.11	1e-09	2e-08	major histocompatibility complex, class II, DR beta 1 [Source:HGNC Symbol;Acc:16830]
3	6376	1.11	1e-09	3e-08	chemokine (C-X3-C motif) ligand 1 [Source:HGNC Symbol;Acc:16830]
4	79090	1.09	2e-09	2e-07	trafficking protein particle complex 6A [Source:HGNC Symbol;Acc:16830]
5	4034	1.05	8e-09	2e-07	leucine-rich repeats and calponin homology (CH) domain containing 1 [Source:HGNC Symbol;Acc:16830]
6	23646	1.02	2e-08	2e-07	phospholipase D family, member 3 [Source:HGNC Symbol;Acc:16830]
7	115703	1.02	2e-08	7e-07	Rho GTPase activating protein 33 [Source:HGNC Symbol;Acc:16830]
8	55876	1	3e-08	2e-06	gasdermin B [Source:HGNC Symbol;Acc:23690]
9	9235	0.96	1e-07	2e-06	interleukin 32 [Source:HGNC Symbol;Acc:16830]
10	26580	0.95	2e-07	2e-06	Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:HGNC Symbol;Acc:16830]
11	80162	0.95	2e-07	2e-06	ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;Acc:16830]
12	6364	0.93	3e-07	2e-06	chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:16830]
13	29944	0.93	3e-07	2e-06	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:16830]
14	348094	0.92	4e-07	1e-05	ankyrin repeat and death domain containing 1A [Source:HGNC Symbol;Acc:16830]
15	4851	0.9	6e-07	2e-05	notch 1 [Source:HGNC Symbol;Acc:7881]
16	23225	0.87	2e-06	2e-05	nucleoporin 210kDa [Source:HGNC Symbol;Acc:30052]
17	3902	0.87	2e-06	2e-05	lymphocyte-activation gene 3 [Source:HGNC Symbol;Acc:64]
18	23468	0.86	2e-06	3e-05	chromobox homolog 5 [Source:HGNC Symbol;Acc:1555]
19	3127	-0.85	3e-06	5e-05	major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:16830]
20	10299	0.84	4e-06	5e-05	membrane-associated ring finger (C3HC4) 6, E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:16830]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	11.37	NULL	3 / 16	BP negative regulation of neurogenesis
2	9.71	NULL	1 / 2	miRNA target-193a
3	8.91	NULL	2 / 14	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_DN
4	8.65	NULL	1 / 6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
5	8.37	NULL	2 / 12	BP negative regulation of T cell activation
6	8.12	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
7	8.12	NULL	1 / 8	GSEA C2BOQUEST_STEM_CELL_DN
8	8.08	NULL	2 / 13	GSEA C2ST_GAQ_PATHWAY
9	8.08	NULL	2 / 13	GSEA C2ST_GA13_PATHWAY
10	7.11	NULL	1 / 7	GSEA C2BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
11	7.07	NULL	2 / 10	GSEA C2CAMPS_COLON_CANCER_COPY_NUMBER_UP
12	7.03	NULL	1 / 8	GSEA C2ZEMBUTSU_SENSITIVITY_TO_MITOMYCIN
13	6.8	NULL	3 / 38	MF methylated histone residue binding
14	6.72	NULL	5 / 66	BP lipid catabolic process
15	6.59	NULL	1 / 8	GSEA C2KEGG_PRION_DISEASES
16	6.52	NULL	1 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
17	6.44	NULL	1 / 12	BP macrophage chemotaxis
18	6.38	NULL	1 / 11	GSEA C2SCIBETTA_KDMSB_TARGETS_DN
19	6.28	NULL	1 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
20	6.15	NULL	1 / 9	GSEA C2REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES
21	6.15	NULL	1 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
22	6.06	NULL	1 / 10	MF hydrolase activity, acting on glycosyl bonds
23	6.02	NULL	2 / 16	GSEA C2KEGG_DORSO_VENTRAL_AXIS_FORMATION
24	5.92	NULL	1 / 12	MF Rac GTPase activator activity
25	5.92	NULL	1 / 12	GSEA C2MCCABE_HOXC6_TARGETS_CANCER_UP
26	5.89	NULL	2 / 19	CC histone methyltransferase complex
27	5.85	NULL	2 / 26	BP negative regulation of catalytic activity
28	5.83	NULL	2 / 43	MF chemokine activity
29	5.79	NULL	1 / 13	GSEA C2SENGUPTA_EBNA1_ANTICORRELATED
30	5.79	NULL	1 / 10	BP anagen
31	5.79	NULL	1 / 10	BP cardiac epithelial to mesenchymal transition
32	5.79	NULL	1 / 10	BP inflammatory response to antigenic stimulus
33	5.79	NULL	1 / 10	BP negative regulation of cell-substrate adhesion
34	5.79	NULL	1 / 10	BP positive regulation of keratinocyte differentiation
35	5.79	NULL	1 / 10	BP prostate gland epithelium morphogenesis
36	5.79	NULL	1 / 10	BP somatic stem cell division
37	5.76	NULL	1 / 11	BP negative regulation of lipid catabolic process
38	5.76	NULL	1 / 11	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
39	5.72	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
40	5.66	NULL	1 / 15	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_DN



# GW\_238

## Local Summary

%DE = 0.44  
 # metagenes = 1  
 # genes = 5  
 # genes in genesets = 5  
 # genes with  $fdr < 0.1 = 1$  ( 1 + / 0 - )  
 # genes with  $fdr < 0.05 = 0$  ( 0 + / 0 - )  
 # genes with  $fdr < 0.01 = 0$  ( 0 + / 0 - )

<r> metagenes = NA

<r> genes = 0.48

<FC> = 0.27

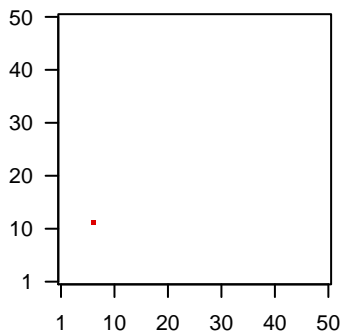
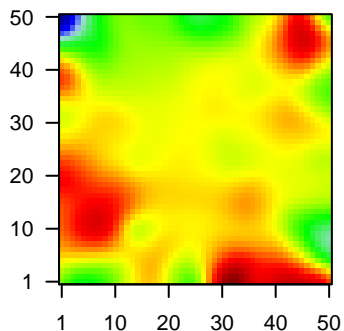
<shrinkage-t> = 9.28

<p-value> = 0.09

<fdr> = 0.73

Profile

Spot



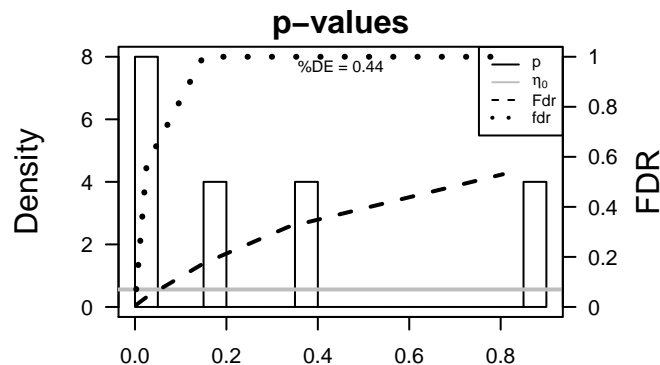
## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	23	0.54	0.003	0.07	7 x 12 ATP-binding cassette, sub-family F (GCN20), member 1 [So
2	57693	0.4	0.028	0.57	7 x 12 zinc finger protein 317 [Source:HGNC Symbol;Acc:13507]
3	85026	0.25	0.166	1.00	7 x 12 chromosome 9 open reading frame 37 [Source:HGNC Symbc
4	84619	0.16	0.372	1.00	7 x 12 zinc finger, CCCH-type with G patch domain [Source:HGNC
5	7874	-0.02	0.894	1.00	7 x 12 ubiquitin specific peptidase 7 (herpes virus-associated) [Sou

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	39.69	NULL	1 / 5	GSEA C2GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
2	18.52	NULL	1 / 23	Chr Chr HSCHR6_MHC_DBB
3	18.15	NULL	1 / 24	MF translation factor activity, nucleic acid binding
4	16.85	NULL	1 / 28	MF ribosome binding
5	14.54	NULL	1 / 38	BP positive regulation of translation
6	8.23	NULL	1 / 120	CC nuclear envelope
7	8.06	NULL	1 / 125	miRNA target site 337
8	7.97	NULL	1 / 128	BP translational initiation
9	7.88	NULL	1 / 131	MF nucleoside-triphosphatase activity
10	7.59	NULL	1 / 141	MF ATPase activity
11	6.96	NULL	1 / 167	CC ribosome
12	5.61	NULL	1 / 253	BP translation
13	5.43	NULL	1 / 269	BP inflammatory response
14	5.05	NULL	1 / 171	miRNA target site 452
15	3.86	NULL	1 / 504	MF nucleotide binding
16	3.85	NULL	1 / 48	miRNA target site 432
17	3.65	NULL	1 / 313	Glio willscher_GBM_Verhaak-CL_expression_D_up
18	3.65	NULL	1 / 313	Glio willscher_GBM_Verhaak-MES_expression_D_down
19	3.65	NULL	1 / 313	Glio willscher_GBM_Verhaak-PNwt_expression_D_up
20	2.8	NULL	2 / 940	MF nucleic acid binding
21	2.65	NULL	1 / 949	CC nucleoplasm
22	2.1	NULL	1 / 1344	MF ATP binding
23	1.99	NULL	1 / 852	Lymphon SPANG_BCR DN
24	1.98	NULL	2 / 1574	BP transcription, DNA-templated
25	1.77	NULL	2 / 1820	MF metal ion binding
26	1.62	NULL	1 / 1135	Chr Chr 19
27	1.61	NULL	1 / 1142	CC intracellular
28	1.4	NULL	1 / 633	Chr Chr 9
29	1.23	NULL	1 / 1581	BP regulation of transcription, DNA-dependent
30	1.12	NULL	1 / 1749	MF DNA binding
31	1.08	NULL	1 / 423	BP negative regulation of transcription, DNA-dependent
32	1.03	NULL	1 / 449	Chr Chr 20
33	0.95	NULL	1 / 500	MF sequence-specific DNA binding
34	0.59	NULL	1 / 823	MF sequence-specific DNA binding transcription factor activity
35	0.5	NULL	2 / 4310	CC cytoplasm
36	0.48	NULL	3 / 4640	CC nucleus
37	0.4	NULL	1 / 1095	TF HEBENSTREIT_high expression TF
38	0.32	NULL	1 / 1233	TF KIM_MYC targets
39	0.07	NULL	3 / 8023	MF protein binding
40	-0.02	NULL	0 / 2	Cancer GENTLES_modul8



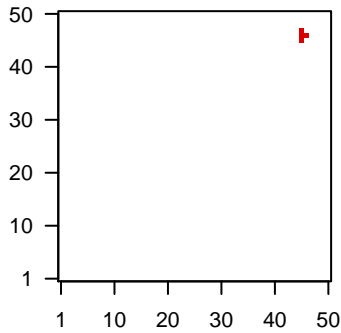
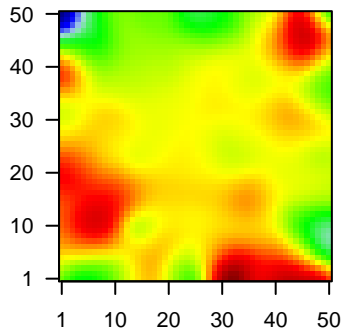
# GW\_238

## Local Summary

%DE = 0.7  
 # metagenes = 4  
 # genes = 41  
 # genes in genesets = 41  
  
 # genes with  $fdr < 0.1 = 24$  ( 24 + / 0 - )  
 # genes with  $fdr < 0.05 = 20$  ( 20 + / 0 - )  
 # genes with  $fdr < 0.01 = 17$  ( 17 + / 0 - )  
  
 $\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.45  
  
 $\langle FC \rangle = 0.44$   
 $\langle \text{shrinkage-t} \rangle = 15.5$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.46$

Profile

Spot



## Local Genelist

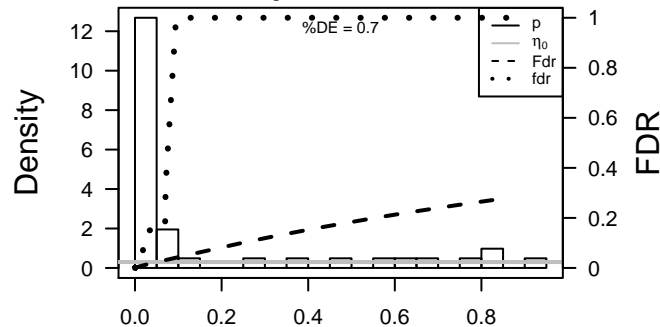
Rank	ID	log(FC)	fdr	p-value	Description
1	1029	1.14	3e-10	5e-07	45 x 45 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol;Acc:1745]
2	2189	0.99	4e-08	4e-05	45 x 45 Fanconi anemia, complementation group G [Source:HGNC S
3	8317	0.82	7e-06	4e-05	45 x 47 cell division cycle 7 [Source:HGNC Symbol;Acc:1745]
4	6472	0.8	1e-05	4e-05	45 x 45 serine hydroxymethyltransferase 2 (mitochondrial) [Source:HG
5	10024	0.8	1e-05	4e-05	45 x 47 trophinin associated protein [Source:HGNC Symbol;Acc:1232
6	9735	0.79	1e-05	4e-05	46 x 46 kinetochore associated 1 [Source:HGNC Symbol;Acc:17255]
7	8819	0.78	2e-05	2e-04	46 x 46 Sin3A-associated protein, 30kDa [Source:HGNC Symbol;Acc
8	899	0.75	3e-05	2e-04	45 x 46 cyclin F [Source:HGNC Symbol;Acc:1591]
9	6839	0.74	5e-05	9e-04	45 x 45 suppressor of variegation 3-9 homolog 1 (Drosophila) [Sourc
10	10535	0.69	1e-04	9e-04	45 x 47 ribonuclease H2, subunit A [Source:HGNC Symbol;Acc:1851]
11	4174	0.68	2e-04	3e-03	46 x 46 minichromosome maintenance complex component 5 [Source:HGNC
12	3148	0.63	5e-04	3e-03	46 x 46 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
13	1786	0.62	7e-04	3e-03	45 x 47 DNA (cytosine-5-)-methyltransferase 1 [Source:HGNC Sym
14	8438	0.6	9e-04	3e-03	45 x 47 RAD54-like (S. cerevisiae) [Source:HGNC Symbol;Acc:9826]
15	78995	0.59	1e-03	7e-03	46 x 46 chromosome 17 open reading frame 53 [Source:HGNC Synt
16	8208	0.55	3e-03	7e-03	45 x 47 chromatin assembly factor 1, subunit B (p60) [Source:HGNC
17	1854	0.55	3e-03	7e-03	45 x 45 deoxyuridine triphosphatase [Source:HGNC Symbol;Acc:307
18	23234	0.54	3e-03	2e-02	45 x 47 DnaJ (Hsp40) homolog, subfamily C, member 9 [Source:HG
19	1017	0.52	4e-03	2e-02	45 x 47 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:1771]
20	81620	0.49	7e-03	2e-02	45 x 47 chromatin licensing and DNA replication factor 1 [Source:HG

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.02	NULL	1 / 2	miRNA target-152
2	22.24	NULL	2 / 16	BP cell cycle checkpoint
3	21.65	NULL	1 / 6	GSEA C2OHM_EMBRYONIC_CARCINOMA_DN
4	19.54	NULL	2 / 13	GSEA C2SA_REG_CASCADE_OF_CYCLIN_EXPR
5	19.07	NULL	1 / 3	miRNA target-148a
6	18.7	NULL	2 / 14	GSEA C2TENEDINI_MEGAKARYOCYTE_MARKERS
7	18.7	NULL	2 / 14	GSEA C2BIOCARTA_G1_PATHWAY
8	18.68	NULL	4 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
9	18.56	NULL	4 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
10	18.05	NULL	2 / 14	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
11	17.95	NULL	2 / 15	GSEA C2BIOCARTA_CELLCYCLE_PATHWAY
12	17.95	NULL	2 / 15	GSEA C2SA_G1_AND_S_PHASES
13	15.66	NULL	1 / 10	BP negative regulation of cell-matrix adhesion
14	15.66	NULL	1 / 10	BP positive regulation of protein sumoylation
15	15.66	NULL	1 / 10	BP somatic stem cell division
16	15.66	NULL	1 / 10	GSEA C2LOPES_METHYLATED_IN_COLON_CANCER_DN
17	15.66	NULL	1 / 10	GSEA C2SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES
18	15.6	NULL	13 / 149	BP DNA replication
19	15.47	NULL	3 / 15	GSEA C2REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
20	14.78	NULL	1 / 11	BP positive regulation of DNA damage response, signal transduction b
21	14.61	NULL	3 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
22	14.38	NULL	2 / 16	GSEA C2Y_AGING_PREMATURE_DN
23	14.26	NULL	2 / 15	GSEA C2WILLIAMS_ESR1_TARGETS_UP
24	14.23	NULL	3 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
25	14.02	NULL	1 / 12	MF cyclin-dependent protein serine/threonine kinase inhibitor activity
26	14.02	NULL	1 / 12	GSEA C2BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
27	14.02	NULL	1 / 12	GSEA C2YAMASHITA_LIVER_CANCER_STEM_CELL_UP
28	13.92	NULL	19 / 530	Cancer Lembecke_Normal vs Adenoma
29	13.84	NULL	4 / 15	GSEA C2KEGG_DNA_REPLICATION
30	13.6	NULL	1 / 10	CC Fanconi anaemia nuclear complex
31	13.6	NULL	1 / 10	BP phosphorelay signal transduction system
32	13.6	NULL	1 / 10	GSEA C2MATHEW_FANCONI_ANEMIA_GENES
33	13.36	NULL	1 / 13	BP negative regulation of B cell proliferation
34	13.36	NULL	1 / 13	GSEA C2OHM_METHYLATED_IN_ADULT_CANCERS
35	13.36	NULL	1 / 13	GSEA C2HOQUE_METHYLATED_IN_CANCER
36	13.36	NULL	1 / 13	miRNA target-517A--517C
37	13.08	NULL	8 / 148	BP G1/S transition of mitotic cell cycle
38	12.78	NULL	1 / 14	GSEA C2TAKADA_GASTRIC_CANCER_COPY_NUMBER_DN
39	12.78	NULL	1 / 14	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B
40	12.78	NULL	1 / 14	GSEA C2DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY

p-values



# GW\_238

## Local Summary

%DE = 0.9  
 # metagenes = 8  
 # genes = 137  
 # genes in genesets = 134

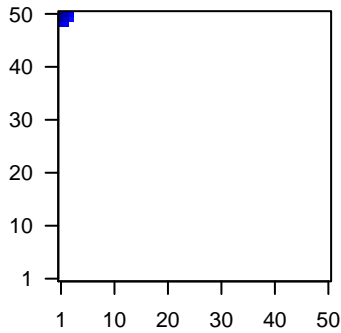
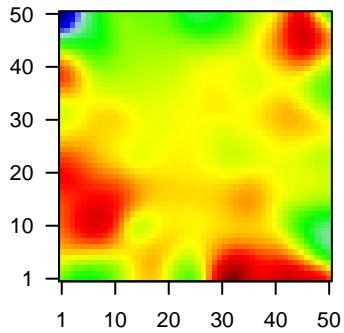
# genes with  $fdr < 0.1$  = 115 ( 6 + / 109 - )  
 # genes with  $fdr < 0.05$  = 106 ( 4 + / 102 - )  
 # genes with  $fdr < 0.01$  = 102 ( 3 + / 99 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.52

$\langle FC \rangle = -1.08$   
 $\langle \text{shrinkage-t} \rangle = -38.23$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.21$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.09	2e-16	7e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-1.55	2e-16	7e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.74	2e-16	7e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
4	8644	-2.74	2e-16	7e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
5	4680	-1.77	2e-16	7e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
6	22802	-2.24	2e-16	7e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	-1.95	2e-16	7e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	49860	-2.09	2e-16	7e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
9	92196	-1.8	2e-16	7e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
10	1672	-2.16	2e-16	7e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	414325	-1.88	2e-16	7e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	-2.66	2e-16	7e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1828	-1.54	2e-16	7e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	2877	-2.17	2e-16	7e-17	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy]
15	26085	-1.82	2e-16	7e-17	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6]
16	5653	-2.59	2e-16	7e-17	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63]
17	5650	-2.17	2e-16	7e-17	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63]
18	192666	-1.6	2e-16	7e-17	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
19	3851	-2.34	2e-16	7e-17	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
20	388533	-1.98	2e-16	7e-17	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-43.17	NULL	63 / 135	H.Tiss WIRTH_Mucosa
2	-42.3	NULL	14 / 21	CC cornified envelope
3	-38.04	NULL	19 / 53	BP keratinocyte differentiation
4	-36.36	NULL	16 / 42	BP keratinization
5	-27.5	NULL	16 / 76	BP epidermis development
6	-23.55	NULL	5 / 16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
7	-23.14	NULL	65 / 572	Disease GUDJ_psooriasis up
8	-21.78	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	-21.27	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	-19.85	NULL	8 / 19	BP peptide cross-linking
11	-18.19	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
12	-17.28	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
13	-16.73	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	-16.06	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
15	-14.95	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
16	-14.95	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
17	-14.86	NULL	2 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
18	-14.02	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
19	-13.97	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
20	-13.76	NULL	4 / 15	MF retinol dehydrogenase activity
21	-13.24	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
22	-13.23	NULL	3 / 16	GSEA C2JAEGER_METASTASIS_DN
23	-12.93	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
24	-12.88	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
25	-12.84	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
26	-12.72	NULL	4 / 10	MF RAGE receptor binding
27	-12.28	NULL	4 / 23	MF peptidase inhibitor activity
28	-11.98	NULL	2 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
29	-11.97	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	-11.62	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
31	-11.38	NULL	10 / 122	MF serine-type endopeptidase activity
32	-11	NULL	2 / 15	GSEA C2ZONDER_CDH1_TARGETS_2_DN
33	-11	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
34	-10.94	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
35	-10.2	NULL	5 / 21	CC desmosome
36	-10.19	NULL	41 / 1182	CC extracellular region
37	-10.14	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
38	-9.98	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
39	-9.77	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
40	-9.48	NULL	1 / 16	BP response to reactive oxygen species

