

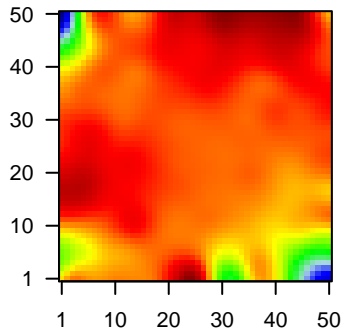
# GW\_078

## Global Summary

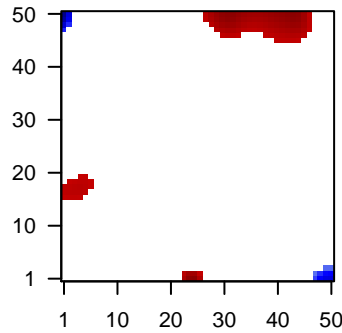
%DE = 0.14  
 # genes with fdr < 0.2 = 1721 ( 828 + / 893 - )  
 # genes with fdr < 0.1 = 1377 ( 665 + / 712 - )  
 # genes with fdr < 0.05 = 1178 ( 567 + / 611 - )  
 # genes with fdr < 0.01 = 817 ( 364 + / 453 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.11  
 <fdr> = 0.86

Profile



Regulated Spots



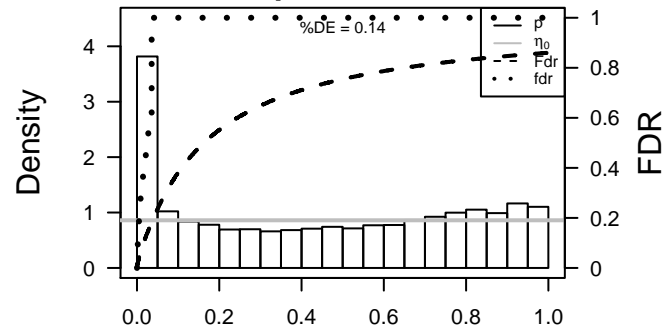
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	144568	-1.83	2e-16 4e-14 1 x 50	alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	58	2.5	2e-16 4e-14 25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	72	1.76	2e-16 4e-14 4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
4	131	-2.41	2e-16 4e-14 1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	57016	-2.78	2e-16 4e-14 1 x 50	aldo-keto reductase family 1, member B10 (aldose reductase
6	441282	-1.89	2e-16 4e-14 1 x 49	aldo-keto reductase family 1, member B15 [Source:HGNC S
7	1646	-1.84	2e-16 4e-14 13 x 50	aldo-keto reductase family 1, member C2 [Source:HGNC Syr
8	8644	-2.48	2e-16 4e-14 1 x 50	aldo-keto reductase family 1, member C3 [Source:HGNC Syr
9	1109	-2.39	2e-16 4e-14 13 x 50	aldo-keto reductase family 1, member C4 [Source:HGNC Syr
10	218	-2.48	2e-16 4e-14 1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
11	387695	-2.36	2e-16 4e-14 1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Synt
12	375791	-2.15	2e-16 4e-14 1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Synt
13	858	1.82	2e-16 4e-14 1 x 42	caveolin 2 [Source:HGNC Symbol;Acc:1528]
14	894	1.72	2e-16 4e-14 50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
15	9635	-2.39	2e-16 4e-14 1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
16	22802	-1.84	2e-16 4e-14 1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	1365	1.94	2e-16 4e-14 50 x 15	claudin 3 [Source:HGNC Symbol;Acc:2045]
18	9073	2.11	2e-16 4e-14 8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
19	9022	-1.88	2e-16 4e-14 1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
20	84518	-3.39	2e-16 4e-14 1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.4	NULL	743	Chr Chr 7
2	9.32	NULL	127	H.Tiss WIRTH_Muscle
3	7.95	NULL	36	BP muscle filament sliding
4	7.94	NULL	4640	CC nucleus
5	7.54	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
6	7.54	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
7	6.94	NULL	16	H.Tiss WIRTH_Hippocampus
8	6.93	NULL	24	TF Tissue/AQUERIZAS_Trachea
9	6.87	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
10	6.76	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
11	6.74	NULL	44	MF structural constituent of muscle
12	6.24	NULL	37	BP collagen fibril organization
13	6.17	NULL	949	CC nucleoplasm
14	6.15	NULL	14	GSEA C2JIANG_SILENCED_BY_METHYLATION_UP
15	6.13	NULL	1233	TF KIM_MYC targets
16	5.82	NULL	1318	CC mitochondrion
17	5.66	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
18	5.55	NULL	11	GSEA C2MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
19	5.49	NULL	232	BP mitosis
20	5.37	NULL	16	MMML C6SCIEJ_MMML 1
<i>Underexpressed</i>				
1	-18.49	NULL	572	Disease GUDJ_poriasis up
2	-15.61	NULL	553	Cancer Lembecke_Colonic Inflammation
3	-15.59	NULL	135	H.Tiss WIRTH_Mucosa
4	-14.47	NULL	42	BP keratinization
5	-13.8	NULL	21	CC cornified envelope
6	-13.28	NULL	312	BP immune response
7	-13.09	NULL	1182	CC extracellular region
8	-10.66	NULL	53	BP keratinocyte differentiation
9	-10.65	NULL	19	BP peptide cross-linking
10	-9.55	NULL	417	H.Tiss WIRTH_Immune system
11	-9.51	NULL	8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
12	-9.02	NULL	683	CC extracellular space
13	-8.84	NULL	47	BP antigen processing and presentation
14	-8.64	NULL	13	BP negative regulation of peptidase activity
15	-8.63	NULL	2659	CC plasma membrane
16	-8.56	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	-8.35	NULL	9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
18	-8.03	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
19	-8.03	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
20	-8.03	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down

p-values



# GW\_078

## Local Summary

%DE = 0.65  
 # metagenes = 8  
 # genes = 103  
 # genes in genesets = 103

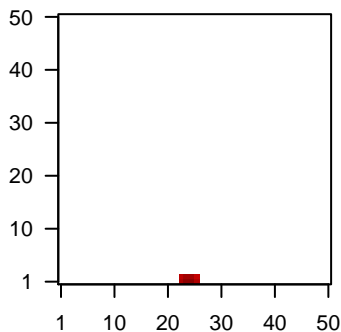
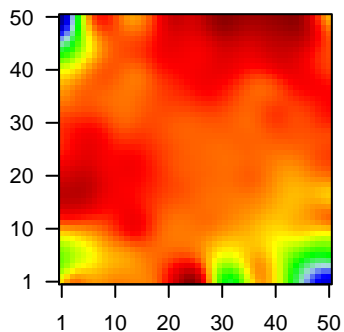
# genes with  $fdr < 0.1 = 49$  ( 48 + / 1 - )  
 # genes with  $fdr < 0.05 = 49$  ( 48 + / 1 - )  
 # genes with  $fdr < 0.01 = 32$  ( 31 + / 1 - )

<r> metagenes = 0.99  
 <r> genes = 0.65

<FC> = 0.53  
 <shrinkage-t> = 18.39  
 <p-value> = 0  
 <fdr> = 0.52

Profile

Spot



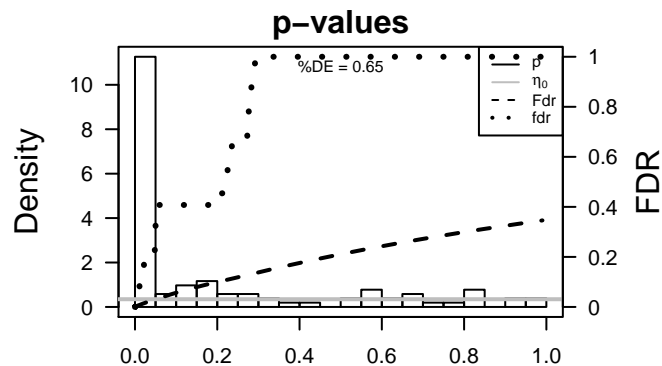
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	58	2.5	2e-16	2e-15	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	1410	1.77	2e-16	2e-15	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
3	283120	3.24	2e-16	2e-15	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
4	6588	1.78	2e-16	2e-15	25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]
5	7060	1.59	4e-15	1e-12	25 x 1 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
6	70	1.53	3e-14	2e-12	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
7	4620	1.51	8e-14	4e-11	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
8	1158	1.44	1e-12	5e-09	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
9	4633	1.29	1e-10	4e-08	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
10	10324	1.22	1e-09	7e-08	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
11	4619	1.19	4e-09	7e-08	25 x 1 myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC
12	2318	1.18	5e-09	1e-06	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
13	7134	1.11	4e-08	1e-06	25 x 1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
14	4608	1.09	6e-08	3e-06	25 x 1 myosin binding protein H [Source:HGNC Symbol;Acc:7552]
15	8557	1.04	2e-07	3e-06	25 x 1 titin-cap [Source:HGNC Symbol;Acc:11610]
16	4625	1.04	2e-07	7e-06	25 x 1 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
17	4703	1.02	4e-07	2e-05	25 x 1 nebulin [Source:HGNC Symbol;Acc:7720]
18	388115	-0.99	9e-07	7e-05	26 x 2 chromosome 15 open reading frame 52 [Source:HGNC Synt
19	202333	0.92	6e-06	7e-05	25 x 1 cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
20	27295	0.91	7e-06	7e-05	25 x 1 PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:20767]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	52.13	NULL	23 / 36	BP muscle filament sliding
2	49.38	NULL	57 / 127	H.Tiss WIRTH_Muscle
3	47.2	NULL	11 / 16	H.Tiss WIRTH_Hippocampus
4	45.23	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
5	35.6	NULL	21 / 44	MF structural constituent of muscle
6	34.62	NULL	10 / 12	CC myosin filament
7	30.67	NULL	8 / 14	CC contractile fiber
8	30.46	NULL	12 / 37	CC sarcomere
9	30.22	NULL	23 / 84	BP muscle contraction
10	25.6	NULL	8 / 13	CC muscle myosin complex
11	24.11	NULL	9 / 20	CC I band
12	23.42	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
13	23.14	NULL	20 / 88	CC Z disc
14	22.63	NULL	14 / 34	CC myofibril
15	20.36	NULL	8 / 16	CC M band
16	20.31	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
17	18.96	NULL	6 / 12	BP skeletal muscle contraction
18	18.46	NULL	3 / 15	Cancer BEN-PORATH_UP
19	18.41	NULL	9 / 37	BP cardiac muscle contraction
20	18.09	NULL	6 / 12	MF titin binding
21	17.97	NULL	4 / 11	CC A band
22	16.3	NULL	2 / 10	BP heart contraction
23	15.66	NULL	2 / 20	MF myosin binding
24	15.3	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_UP
25	15.3	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_DN
26	14.98	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
27	14.98	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
28	14.38	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
29	14.34	NULL	8 / 42	CC myosin complex
30	14.22	NULL	7 / 15	BP striated muscle contraction
31	13.85	NULL	1 / 6	GSEA C2Y_AGING_OLD_UP
32	13.79	NULL	2 / 14	GSEA C2BIOCARTA_UCALPAIN_PATHWAY
33	13.76	NULL	4 / 14	BP adult heart development
34	13.5	NULL	7 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
35	13.4	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
36	13.25	NULL	2 / 15	GSEA C2BIOCARTA_INTEGRIN_PATHWAY
37	13.1	NULL	4 / 16	MF microfilament motor activity
38	12.92	NULL	25 / 297	MF actin binding
39	12.92	NULL	1 / 12	GSEA C2BIOCARTA_NO1_PATHWAY
40	12.92	NULL	1 / 12	GSEA C2BIOCARTA_RAB_PATHWAY



# GW\_078

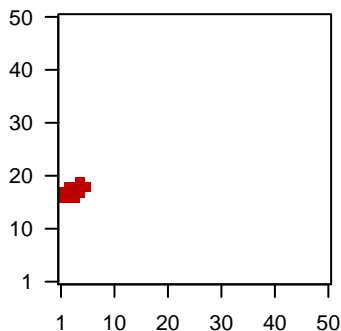
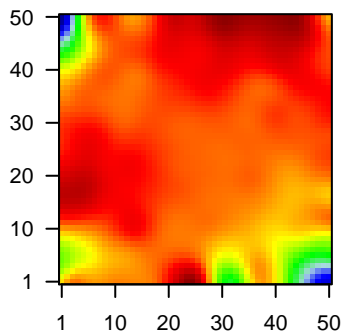
## Local Summary

%DE = 0.36  
 # metagenes = 22  
 # genes = 208  
 # genes in genesets = 207  
 # genes with  $fdr < 0.1$  = 25 ( 23 + / 2 - )  
 # genes with  $fdr < 0.05$  = 24 ( 22 + / 2 - )  
 # genes with  $fdr < 0.01$  = 15 ( 13 + / 2 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.31  
 $\langle FC \rangle = 0.2$   
 $\langle \text{shrinkage-t} \rangle = 7.07$   
 $\langle p\text{-value} \rangle = 0.07$   
 $\langle fdr \rangle = 0.82$

Profile

Spot



## Local Genelist

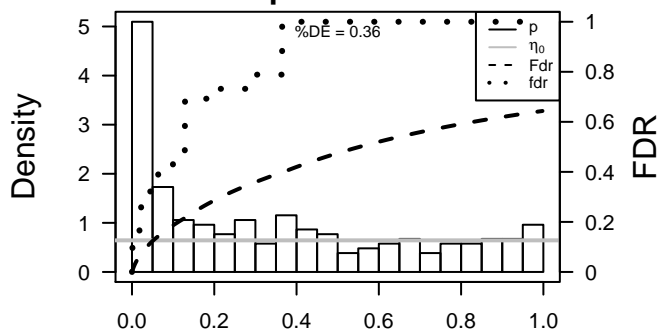
Rank	ID	log(FC)	fdr	p-value	Description
1	1152	-1.34	3e-11	5e-07	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
2	10467	1.19	4e-09	1e-05	2 x 18 zinc finger, HIT-type containing 1 [Source:HGNC Symbol;Acc:211]
3	7205	1.08	9e-08	2e-05	2 x 16 thyroid hormone receptor interactor 6 [Source:HGNC Symbol;Acc:211]
4	221908	1.04	3e-07	5e-05	5 x 17 protein phosphatase 1, regulatory subunit 35 [Source:HGNC Symbol;Acc:211]
5	10980	1	7e-07	1e-04	4 x 18 COP9 signalosome subunit 6 [Source:HGNC Symbol;Acc:211]
6	10248	0.97	2e-06	2e-04	1 x 16 processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae)
7	8896	0.94	3e-06	3e-04	3 x 18 BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:211]
8	284085	0.91	7e-06	3e-04	3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]
9	7784	0.9	8e-06	1e-03	5 x 20 zona pellucida glycoprotein 3 (sperm receptor) [Source:HGNC Symbol;Acc:211]
10	3068	0.86	2e-05	1e-03	4 x 17 hepatoma-derived growth factor [Source:HGNC Symbol;Acc:211]
11	5439	0.85	2e-05	2e-03	1 x 16 polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa [Source:HGNC Symbol;Acc:211]
12	131076	-0.83	4e-05	2e-03	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:211]
13	9551	0.82	5e-05	2e-03	3 x 18 ATP synthase, H+ transporting, mitochondrial Fo complex, subunit c [Source:HGNC Symbol;Acc:211]
14	9328	0.8	7e-05	2e-03	4 x 20 general transcription factor IIC, polypeptide 5, 63kDa [Source:HGNC Symbol;Acc:211]
15	56993	0.79	8e-05	2e-03	3 x 19 translocase of outer mitochondrial membrane 22 homolog (yeast) [Source:HGNC Symbol;Acc:211]
16	10360	0.79	9e-05	1e-02	1 x 17 nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:211]
17	113655	0.74	2e-04	1e-02	1 x 18 major facilitator superfamily domain containing 3 [Source:HGNC Symbol;Acc:211]
18	79590	0.73	3e-04	1e-02	6 x 19 mitochondrial ribosomal protein L24 [Source:HGNC Symbol;Acc:211]
19	389541	0.72	4e-04	1e-02	3 x 19 late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [Source:HGNC Symbol;Acc:211]
20	84300	0.71	4e-04	1e-02	2 x 18 ubiquinol-cytochrome c reductase complex assembly factor 2 [Source:HGNC Symbol;Acc:211]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	12.33	NULL	2 / 15	GSEA C2HOOI_ST7_TARGETS_UP
2	12.27	NULL	3 / 14	GSEA C2LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
3	9.28	NULL	2 / 14	GSEA C2ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR
4	9.27	NULL	1 / 6	GSEA C2HSIAO_HOUSEKEEPING_GENES
5	9.1	NULL	2 / 8	GSEA C2MUELLER_PLURINET
6	9.01	NULL	2 / 10	GSEA C2REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
7	9.01	NULL	2 / 10	GSEA C2REACTOME_MRNA_PROCESSING
8	9.01	NULL	2 / 10	GSEA C2REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INT
9	8.77	NULL	2 / 15	GSEA C2WANTVEER_BREAST_CANCER_BRCA1_UP
10	8.49	NULL	2 / 12	GSEA C2WANG_SMARCE1_TARGETS_DN
11	8.43	NULL	2 / 13	GSEA C2CHIBA_RESPONSE_TO_TSA_UP
12	8.11	NULL	5 / 40	BP transcription from RNA polymerase III promoter
13	7.99	NULL	2 / 13	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
14	7.96	NULL	3 / 16	GSEA C2REACTOME_MICRORNA_BIOGENESIS
15	7.94	NULL	2 / 9	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
16	7.74	NULL	18 / 743	Chr Chr 7
17	7.74	NULL	6 / 37	CC mitochondrial nucleoid
18	7.7	NULL	2 / 16	CC multivesicular body
19	7.52	NULL	2 / 9	GSEA C2KEGG_RNA_POLYMERASE
20	7.49	NULL	1 / 5	GSEA C2NIELSEN_LIPOSARCOMA_DN
21	7.08	NULL	1 / 14	GSEA C2KIM_WT1_TARGETS_DN
22	6.96	NULL	2 / 14	GSEA C2REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS
23	6.82	NULL	1 / 15	GSEA C2AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
24	6.81	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
25	6.78	NULL	2 / 14	GSEA C2CHANG_CORE_SERUM_RESPONSE_UP
26	6.77	NULL	1 / 8	GSEA C2SIBULAN_UV_RESPONSE_NORMAL_UP
27	6.77	NULL	1 / 8	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
28	6.77	NULL	1 / 8	GSEA C2REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
29	6.7	NULL	2 / 15	CC DNA-directed RNA polymerase II, core complex
30	6.68	NULL	2 / 11	GSEA C2REACTOME_TRANSCRIPTION_COUPLED_NER
31	6.66	NULL	2 / 14	GSEA C2RUIZ_TNC_TARGETS_DN
32	6.66	NULL	1 / 13	Glio Christensen_hypomethylated_in_grade2_astrocytoma
33	6.66	NULL	1 / 13	Glio Christensen_hypomethylated_in_grade2_oligodendrogloma
34	6.52	NULL	1 / 11	GSEA C2JAZAG_TGFB1_SIGNALING_VIA_SMAD4_UP
35	6.46	NULL	2 / 12	GSEA C2KEGG_PURINE_METABOLISM
36	6.4	NULL	1 / 14	Glio Christensen_hypomethylated_in_grade2_oligoastrocytoma
37	6.4	NULL	1 / 14	Glio Christensen_hypomethylated_in_grade3_oligoastrocytoma
38	6.4	NULL	1 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
39	6.4	NULL	1 / 14	GSEA C2TOMIDA_METASTASIS_DN
40	6.39	NULL	2 / 24	MF protein phosphatase inhibitor activity

p-values



# GW\_078

## Local Summary

%DE = 0.51  
 # metagenes = 94  
 # genes = 1166  
 # genes in genesets = 1144

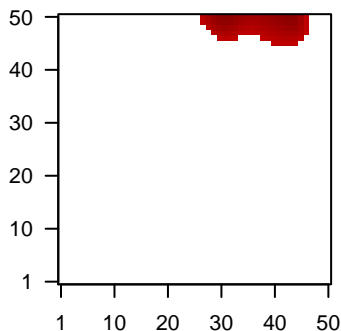
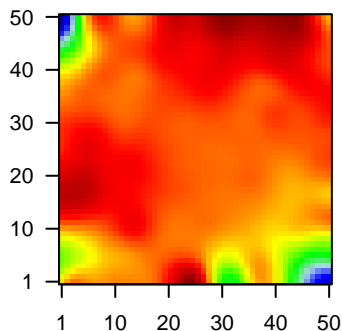
# genes with  $fdr < 0.1$  = 283 ( 252 + / 31 - )  
 # genes with  $fdr < 0.05$  = 150 ( 139 + / 11 - )  
 # genes with  $fdr < 0.01$  = 57 ( 54 + / 3 - )

<r> metagenes = 0.73  
 <r> genes = 0.22

<FC> = 0.21  
 <shrinkage-t> = 7.49  
 <p-value> = 0.07  
 <fdr> = 0.78

Profile

Spot



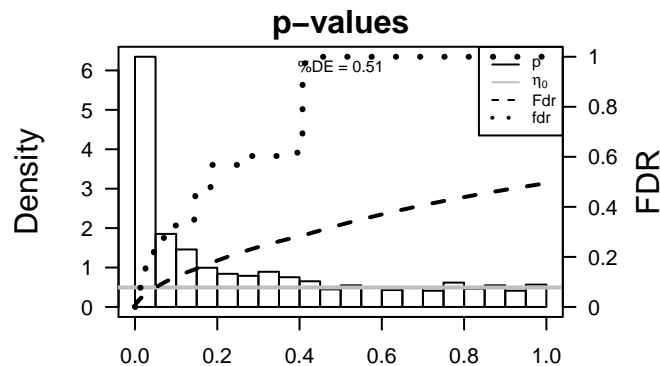
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	9582	1.33	5e-11	1e-07	46 x 49 apolipoprotein B mRNA editing enzyme, catalytic polypeptide
2	154807	1.28	3e-10	6e-07	40 x 50 vitamin K epoxide reductase complex, subunit 1-like 1 [Source:HGNC Symbol;Acc:21488]
3	51119	1.22	2e-09	6e-07	27 x 50 Shwachman-Bodian-Diamond syndrome [Source:HGNC Symbol;Acc:21488]
4	548644	1.2	2e-09	6e-07	36 x 50 polymerase (RNA) II (DNA directed) polypeptide J3 [Source:HGNC Symbol;Acc:21488]
5	54517	1.19	3e-09	1e-06	41 x 50 pseudouridylylase 7 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:21488]
6	1738	1.18	5e-09	4e-06	28 x 50 dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc:21488]
7	11062	1.15	1e-08	4e-05	39 x 50 dihydrouridine synthase 4-like (S. cerevisiae) [Source:HGNC Symbol;Acc:21488]
8	5701	1.08	9e-08	4e-05	41 x 50 proteasome (prosome, macropain) 26S subunit, ATPase, 2 [Source:HGNC Symbol;Acc:21488]
9	387103	1.06	2e-07	9e-05	45 x 49 centromere protein W [Source:HGNC Symbol;Acc:21488]
10	84946	1.02	5e-07	9e-05	37 x 50 LTV1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:21488]
11	246721	0.99	9e-07	9e-05	37 x 50 polymerase (RNA) II (DNA directed) polypeptide J3 [Source:HGNC Symbol;Acc:21488]
12	3945	-0.99	1e-06	9e-05	40 x 50 lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
13	84128	0.99	1e-06	9e-05	39 x 50 WD repeat domain 75 [Source:HGNC Symbol;Acc:25725]
14	1163	0.98	1e-06	9e-05	44 x 50 CDC28 protein kinase regulatory subunit 1B [Source:HGNC Symbol;Acc:21488]
15	3992	-0.98	1e-06	9e-05	45 x 50 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
16	55069	0.97	1e-06	9e-05	39 x 50 transmembrane protein 248 [Source:HGNC Symbol;Acc:2547]
17	139886	0.97	1e-06	3e-04	31 x 50 spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
18	83787	0.94	3e-06	3e-04	39 x 50 armadillo repeat containing 10 [Source:HGNC Symbol;Acc:21488]
19	389524	0.93	4e-06	3e-04	35 x 50 GTF2I repeat domain containing 2B [Source:HGNC Symbol;Acc:21488]
20	51256	0.93	4e-06	3e-04	35 x 50 TBC1 domain family, member 7 [Source:HGNC Symbol;Acc:21488]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	22.01	NULL	102 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	22.01	NULL	102 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	14.19	NULL	133 / 370	BP mitotic cell cycle
4	13.24	NULL	75 / 232	BP mitosis
5	12.44	NULL	13 / 14	MMML C22ORONQUIST_MMML_4
6	12.26	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
7	10.39	NULL	15 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
8	10.21	NULL	9 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
9	9.99	NULL	30 / 66	CC condensed chromosome kinetochore
10	9.81	NULL	14 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
11	9.73	NULL	14 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
12	9.46	NULL	11 / 16	Cancer WOLFER_overlap genes
13	9.42	NULL	12 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	9.26	NULL	11 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
15	9.1	NULL	25 / 56	CC chromosome, centromeric region
16	8.88	NULL	20 / 61	CC kinetochore
17	8.75	NULL	125 / 530	Cancer Lemcke_Normal vs Adenoma
18	8.7	NULL	13 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
19	8.69	NULL	12 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
20	8.43	NULL	7 / 12	BP mitotic chromosome condensation
21	8.41	NULL	13 / 18	BP spindle organization
22	8.41	NULL	16 / 35	BP mitotic nuclear envelope disassembly
23	8.37	NULL	13 / 22	BP CENP-A containing nucleosome assembly at centromere
24	8.06	NULL	7 / 9	GSEA C2REACTOME_CELL_CYCLE_CHECKPOINTS
25	8.01	NULL	11 / 15	GSEA C2CHANG_CYCLING_GENES
26	7.82	NULL	10 / 15	GSEA C2Y_AGING_MIDDLE_DN
27	7.82	NULL	25 / 83	CC spindle pole
28	7.7	NULL	8 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
29	7.6	NULL	11 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
30	7.6	NULL	23 / 57	Glio developing astrocytes
31	7.55	NULL	14 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
32	7.47	NULL	11 / 15	Cancer GENTLES_modul6
33	7.32	NULL	180 / 949	CC nucleoplasm
34	7.2	NULL	7 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
35	7.17	NULL	23 / 67	BP chromosome segregation
36	7.05	NULL	9 / 16	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
37	7.02	NULL	16 / 64	BP tRNA processing
38	6.99	NULL	14 / 23	CC mitochondrial ribosome
39	6.98	NULL	11 / 16	GSEA C2HORIUCHI_WTAP_TARGETS_DN
40	6.97	NULL	9 / 18	BP mitotic sister chromatid segregation



# GW\_078

## Local Summary

%DE = 0.92  
 # metagenes = 10  
 # genes = 220  
 # genes in genesets = 218

# genes with  $fdr < 0.1 = 185$  ( 2 + / 183 - )  
 # genes with  $fdr < 0.05 = 185$  ( 2 + / 183 - )  
 # genes with  $fdr < 0.01 = 145$  ( 1 + / 144 - )

<r> metagenes = 1

<r> genes = 0.63

<FC> = -0.67

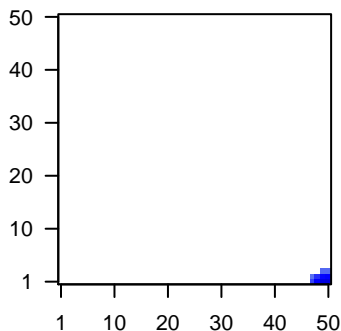
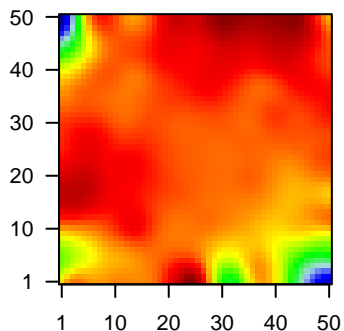
<shrinkage-t> = -23.52

<p-value> = 0

<fdr> = 0.31

Profile

Spot



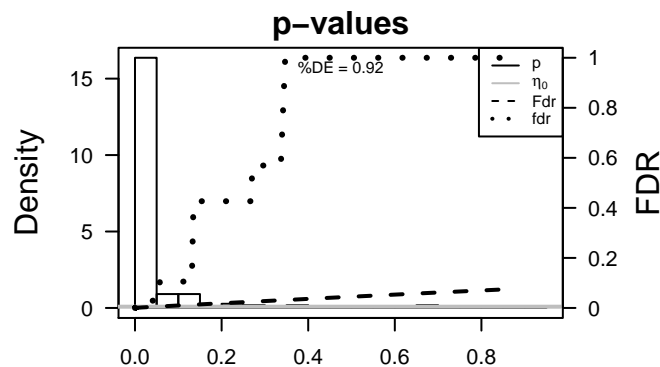
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3122	-1.54	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:18795]
2	3512	-1.77	2e-16	1e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
3	3543	-3.17	2e-16	1e-15	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:18795]
4	5880	-1.82	2e-16	1e-15	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP-binding protein)
5	10537	-1.6	2e-15	7e-13	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
6	3936	-1.53	4e-14	5e-12	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:18795]
7	5341	-1.47	3e-13	3e-11	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
8	9806	-1.4	4e-12	3e-11	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycan 1
9	972	-1.4	4e-12	5e-11	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain
10	5920	-1.39	7e-12	1e-10	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC Symbol;Acc:18795]
11	5996	-1.35	2e-11	1e-10	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:18795]
12	3113	-1.35	2e-11	4e-10	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:18795]
13	260436	-1.33	5e-11	2e-09	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:18795]
14	3689	-1.28	2e-10	2e-09	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit beta 2)
15	57172	-1.28	2e-10	2e-09	49 x 1 calcium/calmodulin-dependent protein kinase I gamma [Source:HGNC Symbol;Acc:18795]
16	3108	-1.27	3e-10	4e-09	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:18795]
17	1436	-1.25	6e-10	4e-09	50 x 1 colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:18795]
18	3059	-1.24	9e-10	4e-09	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:18795]
19	3128	-1.23	1e-09	4e-09	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene)
20	5552	-1.23	1e-09	9e-09	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-35.02	NULL	12 / 15	CC MHC class II protein complex
2	-29.51	NULL	83 / 417	H.Tiss WIRTH_Immune system
3	-22.96	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
4	-22.4	NULL	78 / 553	Cancer Lembcke_Colonc Inflammation
5	-22.01	NULL	45 / 312	BP immune response
6	-19.94	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
7	-19.74	NULL	14 / 47	BP antigen processing and presentation
8	-19.52	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
9	-19.13	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
10	-18.84	NULL	2 / 4	MMML C6SCIEJ_MMML_2
11	-18.3	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDDP_SIGNATURE
12	-18.01	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
13	-17.47	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	-17.44	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
15	-17.19	NULL	1 / 6	H.Tiss WIRTH_Bone marrow
16	-17.18	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
17	-16.58	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
18	-16.57	NULL	35 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
19	-16.57	NULL	35 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
20	-16.57	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
21	-16.57	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
22	-16.33	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
23	-16.05	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
24	-15.79	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
25	-14.86	NULL	5 / 12	BP immunoglobulin mediated immune response
26	-14.62	NULL	7 / 28	CC transport vesicle membrane
27	-14.6	NULL	13 / 60	BP T cell costimulation
28	-14.41	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
29	-14.36	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
30	-14.33	NULL	3 / 8	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_D
31	-13.75	NULL	16 / 74	BP regulation of immune response
32	-13.61	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
33	-13.56	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
34	-13.53	NULL	2 / 12	GSEA C2MCCABE_HOXC6_TARGETS_CANCER_UP
35	-13.42	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
36	-12.89	NULL	7 / 35	CC trans-Golgi network membrane
37	-12.86	NULL	12 / 87	BP antigen processing and presentation of exogenous peptide antigen
38	-12.74	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
39	-12.69	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENT
40	-12.68	NULL	2 / 5	GSEA C2WEST_ADRENOCORCORTICAL_CARCINOMA_VS_ADENOMA_DN



# GW\_078

## Local Summary

%DE = 0.91  
 # metagenes = 7  
 # genes = 140  
 # genes in genesets = 136

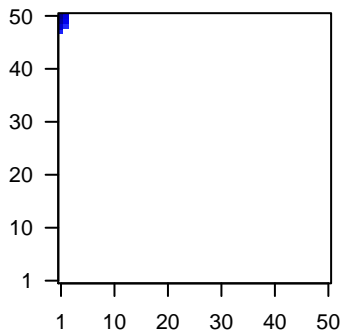
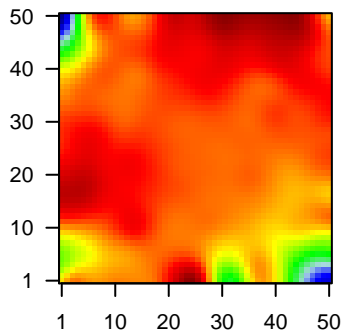
# genes with  $fdr < 0.1$  = 121 ( 15 + / 106 - )  
 # genes with  $fdr < 0.05$  = 121 ( 15 + / 106 - )  
 # genes with  $fdr < 0.01$  = 106 ( 8 + / 98 - )

<r> metagenes = 0.98  
 <r> genes = 0.51

<FC> = -1.12  
 <shrinkage-t> = -39.64  
 <p-value> = 0  
 <fdr> = 0.17

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	-1.83	2e-16	7e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	-2.41	2e-16	7e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-2.78	2e-16	7e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	-1.89	2e-16	7e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	8644	-2.48	2e-16	7e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	218	-2.48	2e-16	7e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
7	387695	-2.36	2e-16	7e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
8	375791	-2.15	2e-16	7e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
9	22802	-1.84	2e-16	7e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	9022	-1.88	2e-16	7e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
11	84518	-3.39	2e-16	7e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
12	49860	-2.79	2e-16	7e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	414325	-2.1	2e-16	7e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1673	-2.86	2e-16	7e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
15	10804	-2.68	2e-16	7e-17	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
16	26085	-1.89	2e-16	7e-17	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6
17	5653	-2.25	2e-16	7e-17	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
18	5650	-1.79	2e-16	7e-17	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63
19	192666	-1.71	2e-16	7e-17	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
20	388533	-3.17	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	-42.84	NULL	61 / 135	H.Tiss WIRTH_Mucosa
2	-36.62	NULL	15 / 21	CC cornified envelope
3	-35.66	NULL	18 / 42	BP keratinization
4	-30.01	NULL	8 / 19	BP peptide cross-linking
5	-28.89	NULL	20 / 53	BP keratinocyte differentiation
6	-24.71	NULL	67 / 572	Disease GUDJ_psooriasis up
7	-19.54	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
8	-18.7	NULL	17 / 76	BP epidermis development
9	-18.21	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
10	-16.89	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
11	-15.89	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
12	-15.72	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
13	-15.39	NULL	5 / 13	BP negative regulation of peptidase activity
14	-14.81	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
15	-14.76	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPICON
16	-14.73	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
17	-14.27	NULL	4 / 23	MF peptidase inhibitor activity
18	-13.94	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
19	-13.81	NULL	3 / 12	BP cellular aldehyde metabolic process
20	-13.75	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
21	-13.43	NULL	3 / 15	GSEA C2LIU_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	-13.11	NULL	3 / 16	GSEA C2JAEGER_METASTASIS_DN
23	-12.86	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
24	-12.77	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
25	-12.62	NULL	2 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
26	-12.22	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
27	-11.78	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
28	-11.59	NULL	2 / 15	GSEA C2ZONDER_CDH1_TARGETS_2_DN
29	-11.59	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
30	-11.43	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
31	-10.97	NULL	2 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
32	-10.96	NULL	8 / 52	BP negative regulation of endopeptidase activity
33	-10.77	NULL	4 / 34	MF endopeptidase inhibitor activity
34	-10.76	NULL	3 / 15	MF retinol dehydrogenase activity
35	-10.71	NULL	40 / 1182	CC extracellular region
36	-10.34	NULL	4 / 27	BP response to bacterium
37	-10.23	NULL	1 / 10	GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
38	-10.07	NULL	2 / 15	GSEA C2FERNANDEZ_BOUND_BY_MYC
39	-10	NULL	5 / 16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
40	-9.96	NULL	2 / 15	GSEA C2BILD_HRAS_ONCOGENIC_SIGNATURE

