

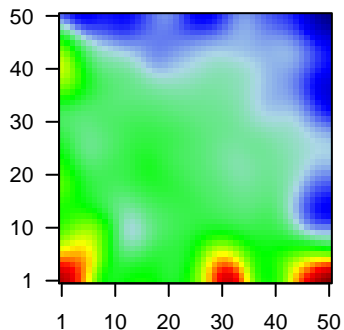
# GW\_173

## Global Summary

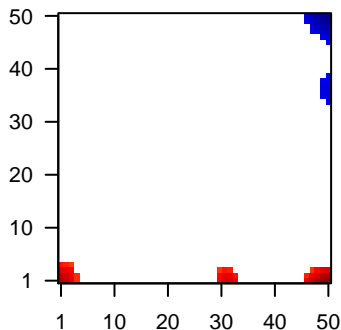
%DE = 0.13  
 # genes with fdr < 0.2 = 1570 ( 954 + / 616 - )  
 # genes with fdr < 0.1 = 1258 ( 812 + / 446 - )  
 # genes with fdr < 0.05 = 989 ( 681 + / 308 - )  
 # genes with fdr < 0.01 = 681 ( 503 + / 178 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.12  
 <fdr> = 0.87

Profile



Regulated Spots



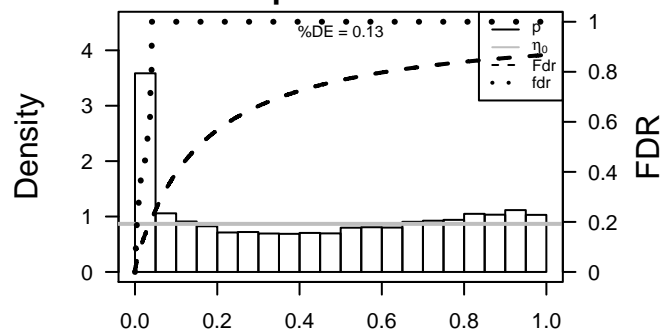
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	9510	1.72	2e-16 5e-14	6 x 1 ADAM metallopeptidase with thrombospondin type 1 motif, 1
2	131	-1.88	2e-16 5e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	-1.61	2e-16 5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
4	218	-1.7	2e-16 5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	341	1.87	2e-16 5e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
6	366	1.94	2e-16 5e-14	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
7	713	1.89	2e-16 5e-14	50 x 1 complement component 1, q subcomponent, B chain [Source
8	55450	1.7	2e-16 5e-14	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
9	6357	1.72	2e-16 5e-14	6 x 2 chemokine (C-C motif) ligand 13 [Source:HGNC Symbol;Acc
10	414062	2.41	2e-16 5e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
11	9560	2.29	2e-16 5e-14	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
12	388372	1.84	2e-16 5e-14	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
13	6355	1.74	2e-16 5e-14	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:
14	1116	1.66	2e-16 5e-14	50 x 4 chitinase 3-like 1 (cartilage glycoprotein-39) [Source:HGNC
15	1437	1.71	2e-16 5e-14	1 x 4 colony stimulating factor 2 (granulocyte-macrophage) [Source
16	3627	2.36	2e-16 5e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;#
17	6373	1.62	2e-16 5e-14	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;#
18	92196	-2.37	2e-16 5e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
19	2152	1.89	2e-16 5e-14	1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:H
20	2203	1.85	2e-16 5e-14	47 x 6 fructose-1,6-bisphosphatase 1 [Source:HGNC Symbol;Acc:1

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.79	NULL	553	Cancer Lembecke_Colonin Inflammation
2	20.26	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
3	20.26	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
4	20.26	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
5	20.26	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
6	19.79	NULL	312	BP immune response
7	16.11	NULL	1182	CC extracellular region
8	15.26	NULL	269	BP inflammatory response
9	14.75	NULL	683	CC extracellular space
10	13.98	NULL	4	MMML C63CIEJ_MMML 23
11	13.45	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	12.18	NULL	417	H.Tiss WIRTH_Immune system
13	12.13	NULL	43	MF chemokine activity
14	11.8	NULL	274	Lymphon SPANG_IL21 DN
15	11.77	NULL	51	BP type I interferon signaling pathway
16	11.7	NULL	60	BP interferon-gamma-mediated signaling pathway
17	11.15	NULL	572	Disease GUDJ_poriasis up
18	10.77	NULL	111	BP chemotaxis
19	10.63	NULL	123	BP defense response to virus
20	10.63	NULL	204	BP cytokine-mediated signaling pathway
<i>Underexpressed</i>				
1	-7.13	NULL	135	H.Tiss WIRTH_Mucosa
2	-7.06	NULL	914	Chr Chr 3
3	-6.78	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
4	-6.66	NULL	1033	Chr Chr 2
5	-6.59	NULL	296	MF oxidoreductase activity
6	-6.57	NULL	717	Chr Chr 16
7	-6.43	NULL	25	BP glutathione derivative biosynthetic process
8	-6.41	NULL	434	BP oxidation-reduction process
9	-6.32	NULL	220	CC mitochondrial matrix
10	-6.02	NULL	368	miRNA target star3144
11	-5.85	NULL	1318	CC mitochondrion
12	-5.76	NULL	20	MF glutathione transferase activity
13	-5.62	NULL	311	miRNA target star3302c
14	-5.57	NULL	325	miRNA target star3302d
15	-5.53	NULL	4640	CC nucleus
16	-5.52	NULL	390	BP metabolic process
17	-5.42	NULL	153	miRNA target star3450b-5p
18	-5.42	NULL	316	miRNA target star3302a
19	-5.36	NULL	1253	BP small molecule metabolic process
20	-5.28	NULL	318	miRNA target star3500-3p

p-values



# GW\_173

## Local Summary

%DE = 0.79  
 # metagenes = 14  
 # genes = 217  
 # genes in genesets = 217

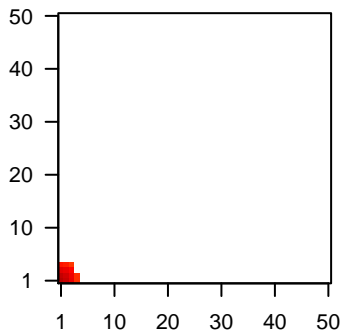
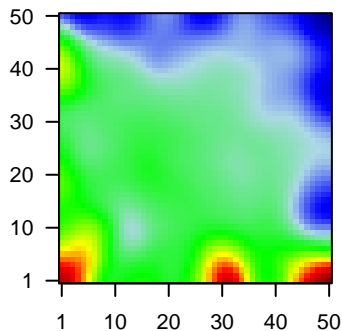
# genes with  $fdr < 0.1$  = 139 ( 135 + / 4 - )  
 # genes with  $fdr < 0.05$  = 117 ( 113 + / 4 - )  
 # genes with  $fdr < 0.01$  = 106 ( 103 + / 3 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.41

$\langle FC \rangle$  = 0.61  
 $\langle \text{shrinkage-t} \rangle$  = 21.56  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.43

Profile

Spot



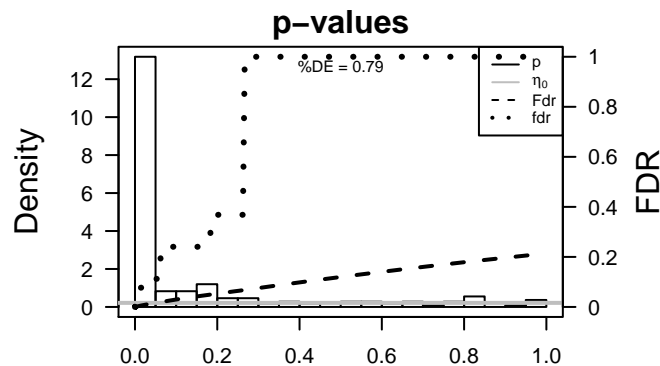
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	366	1.94	2e-16	7e-16	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
2	55450	1.7	2e-16	7e-16	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [S]
3	414062	2.41	2e-16	7e-16	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
4	1437	1.71	2e-16	7e-16	1 x 4 colony stimulating factor 2 (granulocyte-macrophage) [Sourc
5	3040	3.2	2e-16	7e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
6	3569	1.69	2e-16	7e-16	1 x 1 interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:f
7	4312	1.97	2e-16	7e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:H
8	4314	2.52	2e-16	7e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
9	4316	1.84	2e-16	7e-16	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC
10	4318	1.78	2e-16	7e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9:
11	4973	2.15	2e-16	7e-16	1 x 1 oxidized low density lipoprotein (lectin-like) receptor 1 [Sourc
12	6515	2.17	2e-16	7e-16	3 x 1 solute carrier family 2 (facilitated glucose transporter), membe
13	6696	3.24	2e-16	7e-16	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125f
14	7045	1.49	2e-16	7e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG
15	7130	1.59	2e-16	7e-16	1 x 1 tumor necrosis factor, alpha-induced protein 6 [Source:HGNC
16	3576	1.55	7e-16	6e-14	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
17	3678	1.55	7e-16	6e-14	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
18	871	1.52	3e-15	6e-14	1 x 1 serpin peptidase inhibitor, clade H (heat shock protein 47), m
19	1464	1.52	3e-15	7e-13	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
20	7128	1.47	2e-14	6e-12	1 x 1 tumor necrosis factor, alpha-induced protein 3 [Source:HGNC

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	29.52	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
2	29.02	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
3	24.36	NULL	61 / 242	BP extracellular matrix organization
4	23.37	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
5	22.6	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
6	21.78	NULL	31 / 69	BP extracellular matrix disassembly
7	21.26	NULL	56 / 190	CC extracellular matrix
8	20.61	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
9	20.46	NULL	28 / 64	BP collagen catabolic process
10	20.12	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
11	19.51	NULL	12 / 35	Glio Colman_survival_associated
12	19.38	NULL	11 / 19	MF extracellular matrix binding
13	19.05	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
14	18.92	NULL	3 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER
15	18.26	NULL	63 / 250	Lymphocyte_chemokine_response_1
16	17.88	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
17	17.76	NULL	1 / 4	MMML C2SCIEJ_MMMML_23
18	17.4	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
19	17.3	NULL	4 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
20	17.07	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
21	17	NULL	90 / 1182	CC extracellular region
22	16.98	NULL	6 / 16	GSEA C2U_TUMOR_VASCULATURE_UP
23	16.6	NULL	6 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
24	16.6	NULL	70 / 683	CC extracellular space
25	16.58	NULL	6 / 13	GSEA C2SAI_RESPONSE_TO_RADIATION_THERAPY
26	16.38	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
27	16.22	NULL	4 / 11	GSEA C2TO_PTTG1_TARGETS_UP
28	16.2	NULL	4 / 14	GSEA C2WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
29	16.06	NULL	3 / 11	GSEA C2BIOCARTA_STEM_PATHWAY
30	16.03	NULL	6 / 16	GSEA C2AMIT_SERUM_RESPONSE_60_MCF10A
31	15.91	NULL	4 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
32	15.27	NULL	3 / 16	GSEA C2U_TUMOR_ANGIOGENESIS_UP
33	15.27	NULL	2 / 6	Glio Martinez_Glio_hypometh
34	15.1	NULL	8 / 36	BP embryo implantation
35	14.99	NULL	34 / 183	CC proteinaceous extracellular matrix
36	14.98	NULL	36 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
37	14.98	NULL	36 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
38	14.98	NULL	36 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
39	14.98	NULL	36 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
40	14.85	NULL	57 / 553	Cancer Lembecke_Colonc Inflammation



# GW\_173

## Local Summary

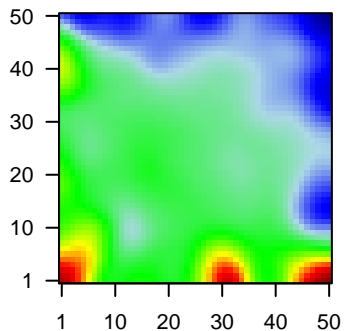
%DE = 0.96  
 # metagenes = 11  
 # genes = 137  
 # genes in genesets = 134

# genes with  $fdr < 0.1$  = 117 ( 116 + / 1 - )  
 # genes with  $fdr < 0.05$  = 114 ( 113 + / 1 - )  
 # genes with  $fdr < 0.01$  = 97 ( 96 + / 1 - )

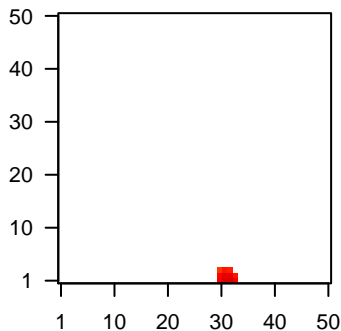
<r> metagenes = 0.98  
 <r> genes = 0.41

<FC> = 0.77  
 <shrinkage-t> = 27.13  
 <p-value> = 0  
 <fdr> = 0.29

Profile



Spot



## Local Genelist

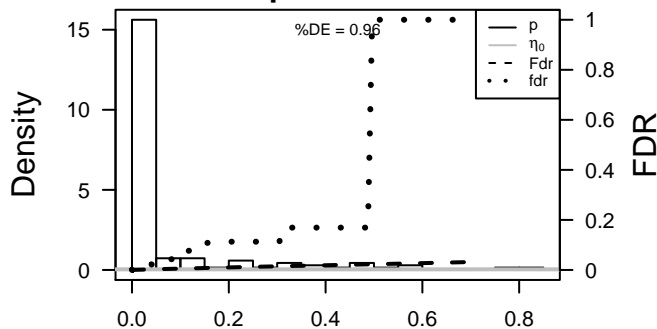
Rank	ID	log(FC)	fdr	p-value	Description
1	9560	2.29	2e-16	1e-16	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
2	388372	1.84	2e-16	1e-16	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
3	6355	1.74	2e-16	1e-16	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:1
4	3627	2.36	2e-16	1e-16	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
5	6373	1.62	2e-16	1e-16	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;f
6	115362	2.16	2e-16	1e-16	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
7	9636	2.09	2e-16	1e-16	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405
8	4321	2.01	2e-16	1e-16	32 x 1 matrix metalloproteinase 12 (macrophage elastase) [Source:H
9	7453	1.76	2e-16	1e-16	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1
10	6288	1.52	2e-15	3e-14	31 x 1 serum amyloid A1 [Source:HGNC Symbol;Acc:10513]
11	51296	1.49	8e-15	1e-12	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3
12	4277	1.41	2e-13	1e-12	32 x 1 MHC class I polypeptide-related sequence B [Source:HGNC
13	3659	1.39	5e-13	4e-12	32 x 1 interferon regulatory factor 1 [Source:HGNC Symbol;Acc:611
14	91543	1.37	1e-12	1e-10	32 x 1 radical S-adenosyl methionine domain containing 2 [Source:l
15	1591	1.29	2e-11	1e-10	33 x 2 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
16	8519	1.27	4e-11	3e-10	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC S
17	629	1.23	1e-10	3e-10	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
18	85441	1.23	2e-10	3e-10	32 x 1 helicase with zinc finger 2, transcriptional coactivator [Source
19	684	1.21	3e-10	3e-10	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
20	23780	1.21	3e-10	3e-10	32 x 1 apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	43.2	NULL	29 / 51	BP type I interferon signaling pathway
2	41.29	NULL	11 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
3	40.35	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	37.4	NULL	13 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
5	36.22	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
6	35.69	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
7	33.74	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
8	32.07	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
9	31.86	NULL	11 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
10	29.96	NULL	14 / 31	BP negative regulation of viral genome replication
11	29.74	NULL	31 / 123	BP defense response to virus
12	28.96	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
13	28.52	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
14	27.03	NULL	27 / 109	BP response to virus
15	26.73	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
16	26.31	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
17	25.72	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
18	24.56	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
19	23.96	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
20	23.82	NULL	34 / 204	BP cytokine-mediated signaling pathway
21	22.48	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
22	21.43	NULL	6 / 6	Lymphocyte_AVE_MHCII BL DN
23	20.69	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
24	20.28	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
25	20.16	NULL	2 / 2	MMML C2SCIEJ_MMML 27
26	20.03	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
27	19.79	NULL	33 / 274	Lymphocyte_SPANG_IL21 DN
28	19.75	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
29	19.75	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
30	19.26	NULL	49 / 572	Disease GUDJ_psooriasis up
31	19.23	NULL	5 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
32	18.32	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
33	18.28	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
34	18.12	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
35	17.91	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
36	17.86	NULL	7 / 10	CC MHC class I protein complex
37	17.8	NULL	3 / 4	MMML C2SCIEJ_MMML 47
38	17.46	NULL	3 / 14	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_A
39	17.23	NULL	2 / 10	BP positive regulation of cAMP-mediated signaling
40	17.23	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP

p-values



# GW\_173

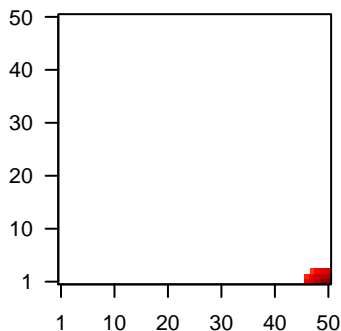
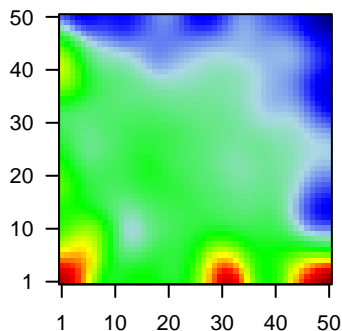
## Local Summary

%DE = 0.9  
 # metagenes = 14  
 # genes = 247  
 # genes in genesets = 245  
 # genes with  $fdr < 0.1$  = 201 ( 193 + / 8 - )  
 # genes with  $fdr < 0.05$  = 160 ( 154 + / 6 - )  
 # genes with  $fdr < 0.01$  = 129 ( 127 + / 2 - )

<r> metagenes = 0.99  
 <r> genes = 0.62  
 <FC> = 0.63  
 <shrinkage-t> = 22.2  
 <p-value> = 0  
 <fdr> = 0.39

Profile

Spot



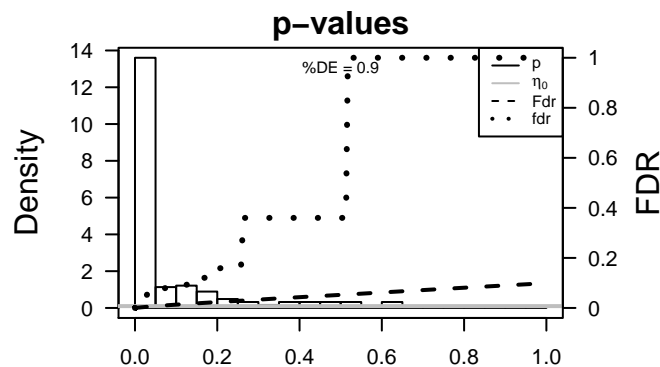
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	341	1.87	2e-16	6e-16	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
2	713	1.89	2e-16	6e-16	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:607]
3	2207	1.76	2e-16	6e-16	50 x 1 Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide chain [Source:HGNC Symbol;Acc:607]
4	84868	1.83	2e-16	6e-16	50 x 1 hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Acc:607]
5	3128	1.78	2e-16	6e-16	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene) [Source:HGNC Symbol;Acc:607]
6	3620	1.84	2e-16	6e-16	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:607]
7	3575	1.63	2e-16	6e-16	50 x 2 interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
8	7133	1.61	2e-16	6e-16	50 x 1 tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:6024]
9	7305	1.66	2e-16	6e-16	50 x 1 TYRO protein tyrosine kinase binding protein [Source:HGNC Symbol;Acc:6024]
10	10537	1.54	9e-16	1e-14	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
11	6352	1.53	1e-15	2e-14	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:9361]
12	5552	1.52	2e-15	2e-13	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
13	3689	1.48	1e-14	2e-13	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit beta 2) [Source:HGNC Symbol;Acc:9361]
14	4283	1.47	2e-14	5e-13	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:9361]
15	5341	1.45	4e-14	1e-12	50 x 1 plectstrin [Source:HGNC Symbol;Acc:9070]
16	3002	1.43	8e-14	1e-12	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated protein 10) [Source:HGNC Symbol;Acc:9361]
17	2359	1.42	1e-13	1e-12	50 x 3 formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]
18	3543	1.29	3e-13	1e-12	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:9361]
19	3108	1.4	3e-13	1e-12	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:9361]
20	348	1.4	3e-13	1e-12	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	28.55	NULL	89 / 417	H.Tiss WIRTH_Immune system
2	22.62	NULL	12 / 15	CC MHC class II protein complex
3	21.5	NULL	39 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
4	21.5	NULL	39 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
5	21.5	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
6	21.5	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
7	21.43	NULL	89 / 553	Cancer Lembcke_Colonic Inflammation
8	20.63	NULL	50 / 312	BP immune response
9	20.18	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
10	18.64	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
11	18.41	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
12	18.37	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
13	18.09	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENTATION
14	17.57	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
15	17.43	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
16	16.94	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
17	16.53	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
18	16.52	NULL	7 / 28	Lymphoma GSEA_C2HAHTOLA_CTCL_PATHOGENESIS
19	16.32	NULL	17 / 74	BP regulation of immune response
20	16.3	NULL	2 / 4	MMML C6SCIEJ_MMML 2
21	16.25	NULL	5 / 12	BP immunoglobulin mediated immune response
22	15.84	NULL	6 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
23	15.51	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
24	15.44	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
25	15.23	NULL	4 / 13	MMML C6SCIEJ_MMML 6
26	15.09	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
27	14.9	NULL	16 / 60	BP T cell costimulation
28	14.62	NULL	3 / 11	GSEA C2KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
29	14.41	NULL	25 / 162	CC external side of plasma membrane
30	14.27	NULL	3 / 8	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_D
31	13.82	NULL	5 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
32	13.56	NULL	14 / 47	BP antigen processing and presentation
33	13.43	NULL	3 / 16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
34	13.25	NULL	2 / 3	MMML C6SCIEJ_MMML 7
35	13.03	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
36	13	NULL	2 / 7	GSEA C2BIOCARTA_COMP_PATHWAY
37	12.96	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_SURVIVAL
38	12.89	NULL	4 / 16	BP cytolysis
39	12.6	NULL	1 / 2	GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION
40	12.6	NULL	1 / 2	GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE



# GW\_173

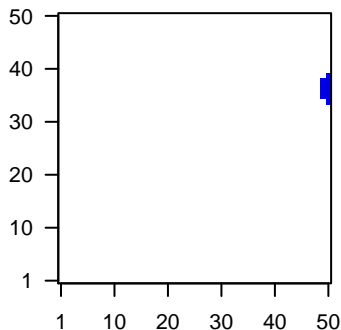
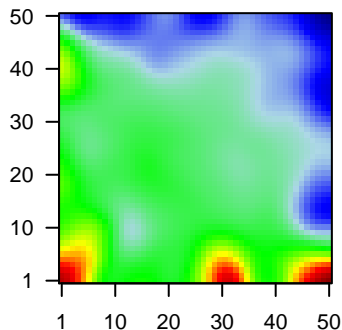
## Local Summary

%DE = 0.88  
 # metagenes = 10  
 # genes = 211  
 # genes in genesets = 211  
 # genes with  $fdr < 0.1$  = 146 ( 0 + / 146 - )  
 # genes with  $fdr < 0.05$  = 143 ( 0 + / 143 - )  
 # genes with  $fdr < 0.01$  = 72 ( 0 + / 72 - )

<r> metagenes = 0.97  
 <r> genes = 0.3  
 <FC> = -0.38  
 <shrinkage-t> = -13.48  
 <p-value> = 0.03  
 <fdr> = 0.64

Profile

Spot



## Local Genelist

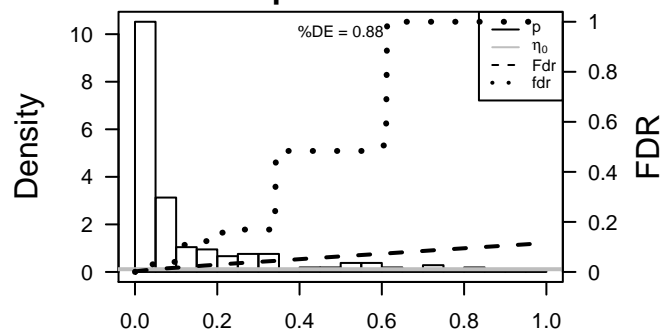
Rank	ID	log(FC)	fdr	p-value	Description
1	1429	-1.23	2e-10	9e-05	50 x 34 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
2	55170	-0.89	4e-06	3e-04	50 x 37 protein arginine methyltransferase 6 [Source:HGNC Symbol;A
3	5934	-0.83	1e-05	8e-04	50 x 36 retinoblastoma-like 2 (p130) [Source:HGNC Symbol;Acc:989
4	4942	-0.78	5e-05	9e-04	50 x 35 ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
5	9849	-0.74	1e-04	9e-04	50 x 35 zinc finger protein 518A [Source:HGNC Symbol;Acc:29009]
6	27075	-0.74	1e-04	9e-04	50 x 38 tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
7	57223	-0.71	2e-04	9e-04	50 x 36 SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Sourc
8	56916	-0.7	3e-04	9e-04	50 x 37 SWI/SNF-related, matrix-associated actin-dependent regula
9	9202	-0.69	3e-04	9e-04	50 x 36 zinc finger, MYM-type 4 [Source:HGNC Symbol;Acc:13055]
10	10314	-0.69	3e-04	9e-04	50 x 35 LanC lantibiotic synthetase component C-like 1 (bacterial) [S
11	80208	-0.68	4e-04	9e-04	50 x 35 spastic paraplegia 11 (autosomal recessive) [Source:HGNC S
12	23151	-0.68	4e-04	9e-04	50 x 38 GRAM domain containing 4 [Source:HGNC Symbol;Acc:2911
13	9685	-0.68	4e-04	9e-04	50 x 34 clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
14	55556	-0.68	4e-04	1e-03	50 x 37 enolase superfamily member 1 [Source:HGNC Symbol;Acc:3
15	10015	-0.67	5e-04	1e-03	50 x 34 programmed cell death 6 interacting protein [Source:HGNC S
16	8443	-0.67	5e-04	2e-03	49 x 38 glyceronephosphate O-acyltransferase [Source:HGNC Symb
17	7520	-0.66	6e-04	3e-03	50 x 35 X-ray repair complementing defective repair in Chinese ham
18	9581	-0.65	8e-04	3e-03	50 x 36 prolyl endopeptidase-like [Source:HGNC Symbol;Acc:30228]
19	23190	-0.63	1e-03	3e-03	50 x 35 UBX domain protein 4 [Source:HGNC Symbol;Acc:14860]
20	54431	-0.63	1e-03	3e-03	50 x 37 DnaJ (Hsp40) homolog, subfamily C, member 10 [Source:HG

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-12.37	NULL	1 / 2	miRNA target-miR-98
2	-11.58	NULL	2 / 10	MF NADPH binding
3	-9.56	NULL	7 / 51	miRNA target-miR-556-3p
4	-8.9	NULL	3 / 11	MF AU-rich element binding
5	-8.85	NULL	10 / 93	miRNA target-miR-348
6	-8.37	NULL	1 / 4	miRNA target-miR-348
7	-8.37	NULL	1 / 4	miRNA target-miR-348
8	-7.99	NULL	20 / 271	miRNA target-miR-348
9	-7.56	NULL	9 / 90	miRNA target-miR-348
10	-7.18	NULL	9 / 108	miRNA target-miR-348
11	-7.15	NULL	11 / 122	miRNA target-miR-348
12	-7.13	NULL	1 / 2	MMML C63CIEJ_MMML 38
13	-6.73	NULL	11 / 100	miRNA target-miR-348
14	-6.65	NULL	1 / 6	miRNA target-miR-348
15	-6.65	NULL	1 / 6	miRNA target-miR-348
16	-6.65	NULL	1 / 6	miRNA target-miR-26a
17	-6.63	NULL	2 / 15	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
18	-6.58	NULL	1 / 14	GSEA C2CHECK_RESPONSE_TO_HD_MTX_DN
19	-6.39	NULL	2 / 12	BP glycerol ether metabolic process
20	-6.39	NULL	7 / 95	miRNA target-miR-348
21	-6.35	NULL	18 / 215	miRNA target-miR-348
22	-6.33	NULL	12 / 171	miRNA target-miR-348-3p
23	-6.18	NULL	4 / 39	miRNA target-miR-562-3p
24	-6.17	NULL	2 / 11	GSEA C2ROZANOV_MMP14_CORRELATED
25	-6.1	NULL	9 / 127	miRNA target-miR-348
26	-6.07	NULL	9 / 101	miRNA target-miR-348
27	-6.03	NULL	8 / 95	miRNA target-miR-365
28	-6.02	NULL	20 / 381	miRNA target-miR-205
29	-6.01	NULL	6 / 49	miRNA target-miR-154-487
30	-5.94	NULL	1 / 4	GSEA C2LUCAS_HNF4A_TARGETS_DN
31	-5.92	NULL	12 / 121	miRNA target-miR-348
32	-5.91	NULL	2 / 10	BP positive regulation of SMAD protein import into nucleus
33	-5.89	NULL	22 / 421	miRNA target-miR-205
34	-5.88	NULL	2 / 14	GSEA C2PUJANA_BRCA2_PCC_NETWORK
35	-5.88	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C5
36	-5.82	NULL	12 / 172	miRNA target-miR-348
37	-5.7	NULL	10 / 134	miRNA target-miR-348
38	-5.7	NULL	21 / 303	miRNA target-miR-348
39	-5.67	NULL	8 / 123	miRNA target-miR-348
40	-5.54	NULL	6 / 41	BP mRNA 3'-end processing

p-values



# GW\_173

## Local Summary

%DE = 0.89  
 # metagenes = 21  
 # genes = 277  
 # genes in genesets = 275

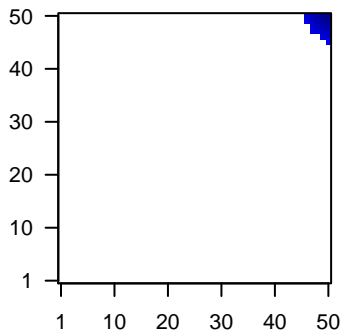
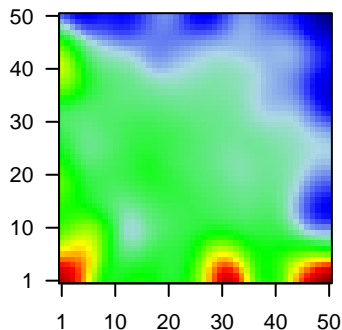
# genes with  $fdr < 0.1$  = 203 ( 7 + / 196 - )  
 # genes with  $fdr < 0.05$  = 170 ( 6 + / 164 - )  
 # genes with  $fdr < 0.01$  = 106 ( 4 + / 102 - )

<r> metagenes = 0.94  
 <r> genes = 0.26

<FC> = -0.43  
 <shrinkage-t> = -15.1  
 <p-value> = 0  
 <fdr> = 0.54

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	11166	-1.61	2e-16	7e-15	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symt
2	4922	-1.46	3e-14	5e-12	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
3	6657	-1.42	2e-13	9e-10	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbx
4	928	-1.27	4e-11	9e-10	50 x 50 CD9 molecule [Source:HGNC Symbol;Acc:1709]
5	339512	-1.26	6e-11	3e-09	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
6	3866	-1.23	2e-10	4e-09	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
7	28978	-1.21	3e-10	1e-08	49 x 50 transmembrane protein 14A [Source:HGNC Symbol;Acc:2101
8	4780	-1.19	6e-10	1e-07	50 x 50 nuclear factor, erythroid 2-like 2 [Source:HGNC Symbol;Acc:
9	8544	-1.12	5e-09	6e-07	50 x 50 piron (iron-binding nuclear protein) [Source:HGNC Symbol;Ac
10	3856	1.07	3e-08	6e-07	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
11	2946	-1.05	5e-08	6e-07	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr
12	5625	-1.04	6e-08	9e-07	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ac
13	154664	-1.03	9e-08	1e-06	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Soi
14	57216	-1.01	2e-07	1e-06	50 x 48 VANGL planar cell polarity protein 2 [Source:HGNC Symbol;A
15	200634	-1	2e-07	1e-06	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
16	2944	-0.99	3e-07	1e-06	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
17	7345	-0.99	3e-07	2e-06	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
18	56977	-0.98	3e-07	7e-06	50 x 49 storkhead box 2 [Source:HGNC Symbol;Acc:25450]
19	216	-0.94	1e-06	7e-06	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
20	56963	-0.94	1e-06	7e-06	50 x 50 repulsive guidance molecule family member a [Source:HGNC

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.11	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	-16.04	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
3	-12.72	NULL	4 / 13	BP regulation of blood vessel size
4	-12.3	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
5	-11.82	NULL	8 / 34	BP glutathione metabolic process
6	-10.99	NULL	6 / 25	BP glutathione derivative biosynthetic process
7	-10.6	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
8	-10.52	NULL	3 / 11	MF glutathione binding
9	-10.52	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
10	-10.46	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
11	-10.17	NULL	67 / 914	Chr Chr 3
12	-10.02	NULL	5 / 20	MF glutathione transferase activity
13	-9.3	NULL	3 / 16	GSEA C2KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
14	-9.09	NULL	5 / 14	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
15	-8.75	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME
16	-8.67	NULL	2 / 23	BP stem cell differentiation
17	-8.13	NULL	4 / 15	GSEA C2JDAYAKUMAR_MED1_TARGETS_UP
18	-8.06	NULL	3 / 13	GSEA C2JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
19	-8.04	NULL	4 / 15	GSEA C2REACTOME_GLUTATHIONE_CONJUGATION
20	-8.03	NULL	2 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
21	-7.82	NULL	4 / 14	GSEA C2VANTVEER_BREAST_CANCER_METASTASIS_DN
22	-7.78	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
23	-7.78	NULL	1 / 7	miRNA target-mir-145
24	-7.68	NULL	4 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
25	-7.65	NULL	2 / 11	BP planar cell polarity pathway involved in neural tube closure
26	-7.6	NULL	1 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP
27	-7.43	NULL	4 / 15	GSEA C2MMS_MOUSE_LYMPH_HIGH_4HRS_UP
28	-7.31	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
29	-7.31	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_E2F1_UP
30	-7.28	NULL	2 / 12	BP Wnt signaling pathway, planar cell polarity pathway
31	-7.2	NULL	1 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
32	-7.2	NULL	1 / 8	miRNA target-mir-450
33	-7.03	NULL	2 / 6	miRNA target-mir-3126
34	-7.02	NULL	3 / 16	GSEA C2GARASHI_ATF4_TARGETS_DN
35	-6.92	NULL	3 / 16	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G1_DN
36	-6.76	NULL	3 / 11	Pathw AcBENTINK_e2f3.2
37	-6.75	NULL	4 / 30	BP negative regulation of cell death
38	-6.69	NULL	4 / 19	BP cellular amino acid biosynthetic process
39	-6.64	NULL	4 / 16	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
40	-6.6	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS

