

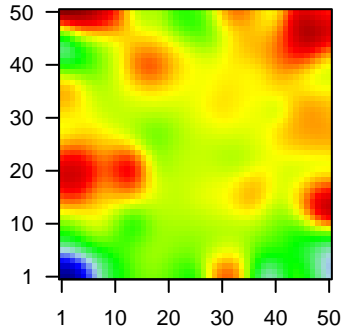
# GW\_027

## Global Summary

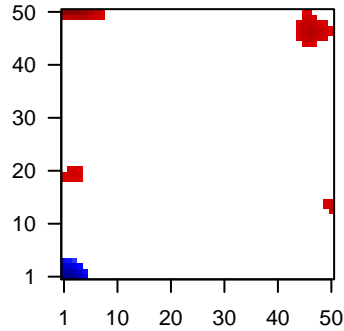
%DE = 0.14  
 # genes with  $fdr < 0.2$  = 1787 ( 935 + / 852 - )  
 # genes with  $fdr < 0.1$  = 1346 ( 703 + / 643 - )  
 # genes with  $fdr < 0.05$  = 1132 ( 586 + / 546 - )  
 # genes with  $fdr < 0.01$  = 720 ( 376 + / 344 - )  
 # genes in genesets = 16332

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

Profile



Regulated Spots



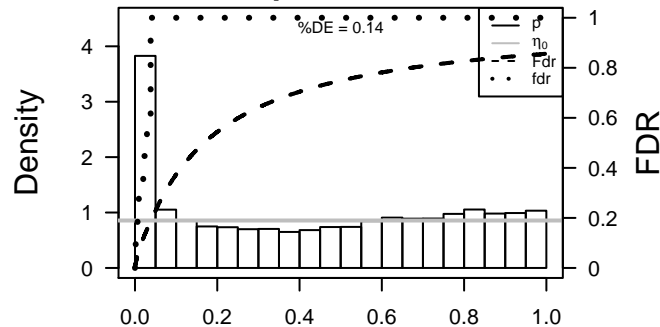
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	2.35	2e-16	7e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:328]
2	131	1.53	2e-16	7e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	10551	1.55	2e-16	7e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	8644	-1.83	2e-16	7e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:328]
5	1109	-1.62	2e-16	7e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:328]
6	260436	3.43	2e-16	7e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:328]
7	760	-1.52	2e-16	7e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	6364	1.87	2e-16	7e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:1373]
9	9071	1.58	2e-16	7e-14	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
10	1294	-1.62	2e-16	7e-14	1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
11	49860	1.76	2e-16	7e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
12	1490	-1.49	2e-16	7e-14	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2214]
13	9547	-1.62	2e-16	7e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:1373]
14	1571	1.49	2e-16	7e-14	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Source:HGNC Symbol;Acc:1373]
15	414325	-1.6	2e-16	7e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	131177	1.62	2e-16	7e-14	3 x 50 family with sequence similarity 3, member D [Source:HGNC Symbol;Acc:1373]
17	2353	-2.32	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog A [Source:HGNC Symbol;Acc:1373]
18	2354	-2.38	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:1373]
19	2568	1.65	2e-16	7e-14	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:1373]
20	283120	-1.75	2e-16	7e-14	25 x 1 H19, imprinted maternally expressed transcript (non-protein coding) [Source:HGNC Symbol;Acc:1373]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.42	NULL	135	H.Tiss WIRTH_Mucosa
2	11.25	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
3	11.25	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
4	10.63	NULL	1318	CC mitochondrion
5	9.33	NULL	370	BP mitotic cell cycle
6	8.64	NULL	83	BP respiratory electron transport chain
7	7.91	NULL	304	CC mitochondrial inner membrane
8	7.77	NULL	572	Disease GUDJ_poriasis up
9	7.4	NULL	16	GSEA C25ENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	7.29	NULL	152	BP cellular metabolic process
11	6.53	NULL	36	CC mitochondrial respiratory chain complex I
12	6.48	NULL	30	BP DNA strand elongation involved in DNA replication
13	6.33	NULL	15	GSEA C2WOO_LIVER_CANCER_RECURRENCE_DN
14	6.27	NULL	10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
15	6.14	NULL	949	CC nucleoplasm
16	6.1	NULL	4640	CC nucleus
17	6.07	NULL	220	CC mitochondrial matrix
18	6.03	NULL	15	GSEA C2DELYS_THYROID_CANCER_UP
19	6.02	NULL	298	BP DNA repair
20	6.01	NULL	34	MF NADH dehydrogenase (ubiquinone) activity
<i>Underexpressed</i>				
1	-14.61	NULL	504	Chr Chr 15
2	-13.93	NULL	250	Lymphoma ENZ_Stromal signature 1
3	-13.15	NULL	553	Cancer Lembecke_Colonc Inflammation
4	-12.95	NULL	190	CC extracellular matrix
5	-12.94	NULL	242	BP extracellular matrix organization
6	-11.45	NULL	683	CC extracellular space
7	-10.9	NULL	1182	CC extracellular region
8	-9.9	NULL	69	BP extracellular matrix disassembly
9	-9.77	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
10	-9.62	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
11	-9.44	NULL	16	MMML C63CIEJ_MMML 1
12	-9.41	NULL	64	BP collagen catabolic process
13	-9.34	NULL	4	MMML C63CIEJ_MMML 23
14	-9.19	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
15	-8.96	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	-8.96	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	-8.96	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	-8.96	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
19	-8.8	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
20	-8.61	NULL	56	BP response to mechanical stimulus

p-values



# GW\_027

## Local Summary

%DE = 0.71  
 # metagenes = 5  
 # genes = 60  
 # genes in genesets = 60  
 # genes with  $fdr < 0.1$  = 33 ( 32 + / 1 - )  
 # genes with  $fdr < 0.05$  = 32 ( 31 + / 1 - )  
 # genes with  $fdr < 0.01$  = 27 ( 26 + / 1 - )

<r> metagenes = 0.98

<r> genes = 0.36

<FC> = 0.44

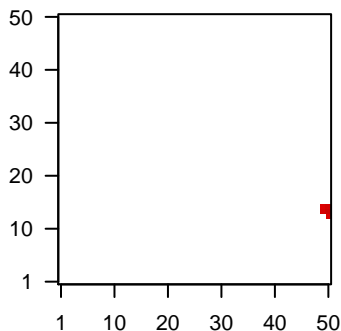
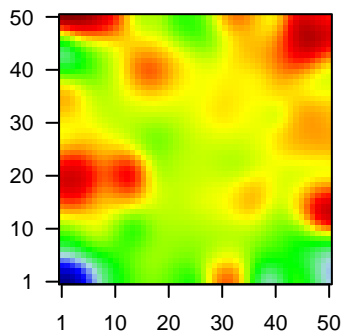
<shrinkage-t> = 15.53

<p-value> = 0

<fdr> = 0.46

Profile

Spot



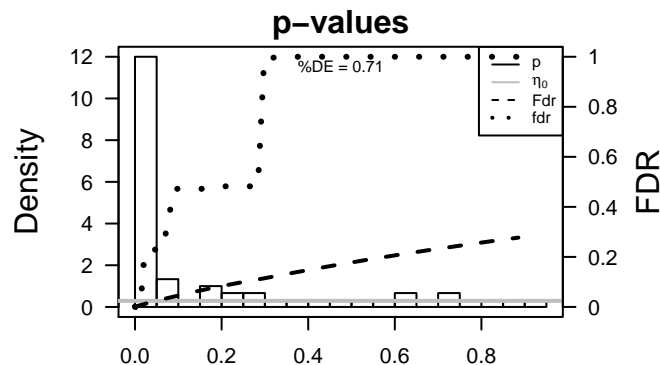
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	2568	1.65	2e-16	2e-15	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HG
2	51316	1.84	2e-16	2e-15	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
3	6920	1.37	4e-14	5e-13	50 x 13 transcription elongation factor A (SII), 3 [Source:HGNC Symb
4	26471	1.36	6e-14	9e-08	49 x 14 nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
5	79085	1.06	5e-09	9e-08	50 x 13 solute carrier family 25 (mitochondrial carrier; phosphate carr
6	260293	1.03	1e-08	9e-08	50 x 14 cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
7	9423	1.02	2e-08	9e-08	50 x 13 netrin 1 [Source:HGNC Symbol;Acc:8029]
8	85315	1.02	2e-08	4e-07	50 x 15 progesterin and adiponectin receptor family member VIII [Source:H
9	217	0.99	4e-08	2e-05	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HC
10	2139	0.87	2e-06	2e-05	50 x 13 eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;
11	391267	0.86	2e-06	2e-05	50 x 13 ankyrin repeat domain 20 family, member A11, pseudogene [
12	5764	0.84	3e-06	1e-04	49 x 14 pleiotrophin [Source:HGNC Symbol;Acc:9630]
13	8543	0.8	1e-05	1e-04	50 x 15 LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
14	9649	0.78	1e-05	2e-04	50 x 15 Ral GEF with PH domain and SH3 binding motif 1 [Source:H
15	8857	0.75	4e-05	2e-04	50 x 13 Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
16	399948	0.73	5e-05	2e-04	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
17	285195	0.73	6e-05	2e-04	49 x 14 solute carrier family 9, subfamily A (NHE9, cation proton anti
18	66002	0.73	6e-05	2e-04	50 x 13 cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
19	6493	0.72	7e-05	8e-04	49 x 14 single-minded family bHLH transcription factor 2 [Source:HG
20	7155	-0.68	2e-04	8e-04	50 x 15 topoisomerase (DNA) II beta 180kDa [Source:HGNC Symbol

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	24.2	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
2	20.62	NULL	2 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	17.66	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
4	17.58	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
5	17.58	NULL	1 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
6	17.49	NULL	2 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_U
7	16.12	NULL	1 / 11	BP negative regulation of multicellular organism growth
8	15.33	NULL	1 / 10	MF GABA-A receptor activity
9	14.48	NULL	1 / 4	GSEA C2CALVET_IRINOTECAN_SENSITIVE_VS_RESISTANT_UP
10	14.45	NULL	1 / 11	GSEA C2AZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
11	12.62	NULL	1 / 10	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_3_DN
12	12.47	NULL	1 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
13	12.47	NULL	1 / 14	GSEA C2TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
14	12.47	NULL	1 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
15	11.96	NULL	1 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
16	11.96	NULL	1 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
17	11.75	NULL	2 / 12	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
18	11.56	NULL	1 / 7	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
19	11.51	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_U
20	11.51	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_U
21	11.51	NULL	1 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
22	11.51	NULL	1 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
23	11.51	NULL	1 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
24	11.51	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
25	11.47	NULL	2 / 18	MF aromatase activity
26	11.36	NULL	1 / 12	BP regulation of DNA-dependent transcription, elongation
27	11.27	NULL	1 / 12	BP acute inflammatory response
28	10.84	NULL	1 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
29	10.45	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
30	9.97	NULL	1 / 5	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_DN
31	9.88	NULL	1 / 25	BP brown fat cell differentiation
32	9.82	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
33	9.61	NULL	2 / 12	GSEA C2PEPPER_CHRONIC_LYMPHOCTIC_LEUKEMIA_UP
34	9.28	NULL	1 / 23	MF extracellular ligand-gated ion channel activity
35	8.84	NULL	2 / 10	BP epoxygenase P450 pathway
36	8.4	NULL	1 / 12	BP negative regulation of axon extension
37	7.94	NULL	2 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
38	7.94	NULL	2 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
39	7.88	NULL	2 / 30	BP response to cold
40	7.76	NULL	1 / 10	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP



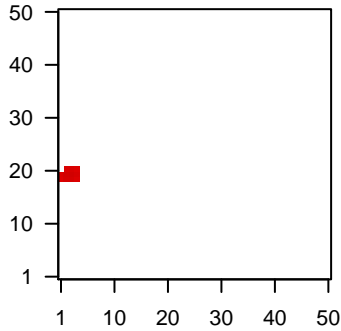
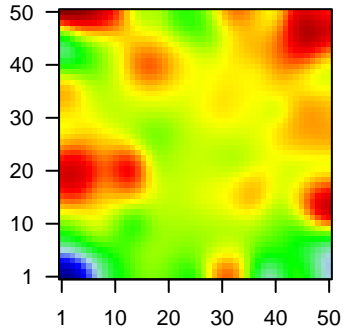
# GW\_027

## Local Summary

%DE = 0.61  
 # metagenes = 11  
 # genes = 111  
 # genes in genesets = 110  
  
 # genes with  $fdr < 0.1$  = 40 ( 38 + / 2 - )  
 # genes with  $fdr < 0.05$  = 33 ( 32 + / 1 - )  
 # genes with  $fdr < 0.01$  = 21 ( 21 + / 0 - )  
  
 $\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.32  
  
 $\langle FC \rangle = 0.28$   
 $\langle \text{shrinkage-t} \rangle = 9.95$   
 $\langle p\text{-value} \rangle = 0.03$   
 $\langle fdr \rangle = 0.66$

Profile

Spot



## Local Genelist

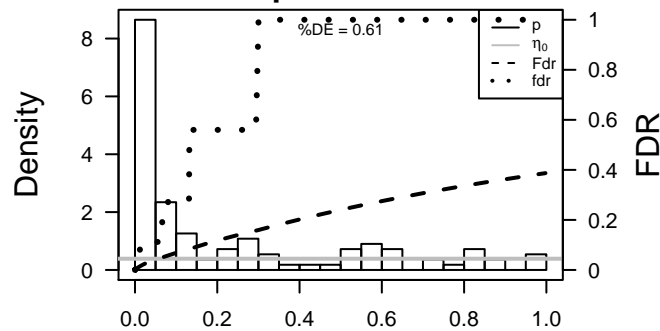
Rank	ID	log(FC)	fdr	p-value	Description
1	6510	1.02	2e-08	6e-05	2 x 19 solute carrier family 1 (neutral amino acid transporter), memb
2	51337	0.87	1e-06	1e-04	3 x 21 thioesterase superfamily member 6 [Source:HGNC Symbol;A
3	10682	0.83	5e-06	5e-04	3 x 20 empamil binding protein (sterol isomerase) [Source:HGNC S
4	374291	0.77	2e-05	5e-04	3 x 21 NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (†
5	51079	0.75	4e-05	5e-04	2 x 21 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13]
6	4704	0.75	4e-05	2e-03	3 x 19 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 3
7	55168	0.71	8e-05	2e-03	2 x 20 mitochondrial ribosomal protein S18A [Source:HGNC Symbo
8	201254	0.69	1e-04	2e-03	4 x 20 stimulated by retinoic acid 13 [Source:HGNC Symbol;Acc:114
9	2224	0.68	2e-04	4e-03	4 x 20 farnesyl diphosphate synthase [Source:HGNC Symbol;Acc:3f
10	7936	0.64	4e-04	4e-03	1 x 19 negative elongation factor complex member E [Source:HGNC
11	83444	0.63	5e-04	4e-03	4 x 21 INO80 complex subunit B [Source:HGNC Symbol;Acc:13324]
12	3028	0.62	6e-04	4e-03	3 x 21 hydroxysteroid (17-beta) dehydrogenase 10 [Source:HGNC S
13	79763	0.62	7e-04	4e-03	3 x 19 isochorismatase domain containing 2 [Source:HGNC Symbol
14	84232	0.61	7e-04	4e-03	1 x 19 MAF1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:24
15	51016	0.61	8e-04	6e-03	2 x 20 ER membrane protein complex subunit 9 [Source:HGNC Syrr
16	26519	0.6	9e-04	7e-03	1 x 19 translocase of inner mitochondrial membrane 10 homolog (ye
17	197370	0.59	1e-03	1e-02	1 x 20 non-SMC element 1 homolog (S. cerevisiae) [Source:HGNC
18	28992	0.58	1e-03	1e-02	4 x 20 MACRO domain containing 1 [Source:HGNC Symbol;Acc:29f
19	51181	0.56	2e-03	1e-02	2 x 21 dicarbonyl/L-xylulose reductase [Source:HGNC Symbol;Acc:
20	8570	0.56	2e-03	1e-02	2 x 19 KH-type splicing regulatory protein [Source:HGNC Symbol;A

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	22.56	NULL	3 / 10	MF NADH dehydrogenase activity
2	14.44	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
3	10.72	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
4	10.55	NULL	4 / 34	MF NADH dehydrogenase (ubiquinone) activity
5	10.22	NULL	4 / 36	CC mitochondrial respiratory chain complex I
6	10.01	NULL	1 / 10	MF neutral amino acid transmembrane transporter activity
7	9.85	NULL	37 / 1318	CC mitochondrion
8	9.72	NULL	3 / 12	BP apoptotic nuclear changes
9	9.33	NULL	2 / 10	GSEA C2REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_VI
10	9.2	NULL	1 / 8	GSEA C2EMELYANOV_GR_TARGETS_DN
11	9.05	NULL	1 / 12	BP neutral amino acid transport
12	8.93	NULL	3 / 15	GSEA C2NAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
13	8.88	NULL	3 / 40	miRNA target sites 156a-3p
14	8.78	NULL	1 / 2	miRNA 3035CG-371
15	8.66	NULL	1 / 13	GSEA C2REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLAS
16	8.43	NULL	2 / 12	GSEA C2REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE
17	8.13	NULL	1 / 10	BP drug transmembrane transport
18	8.13	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
19	8	NULL	1 / 15	GSEA C2AIRKEE_CANCER_PRONE_RESPONSE_E2
20	7.95	NULL	2 / 13	GSEA C2ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
21	7.78	NULL	8 / 153	MF structural constituent of ribosome
22	7.75	NULL	2 / 33	BP cholesterol biosynthetic process
23	7.75	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
24	7.75	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF
25	7.75	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
26	7.75	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
27	7.71	NULL	1 / 11	BP sterol biosynthetic process
28	7.56	NULL	1 / 10	MF quinone binding
29	7.48	NULL	1 / 8	GSEA C2CHANG_CORE_SERUM_RESPONSE_DN
30	7.46	NULL	1 / 17	MF amino acid transmembrane transporter activity
31	7.45	NULL	2 / 15	GSEA C2REACTOME_REMOVAL_OF_DNA_PATCH_CONTAINING_ABASI
32	7.41	NULL	12 / 304	CC mitochondrial inner membrane
33	7.39	NULL	2 / 11	MF glutathione binding
34	7.35	NULL	1 / 12	BP sterol metabolic process
35	7.3	NULL	1 / 10	MF 3-beta-hydroxy-delta5-steroid dehydrogenase activity
36	7.18	NULL	1 / 3	TF MYC_Tumor supressor genes UP
37	7.17	NULL	1 / 6	GSEA C2REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1
38	7.12	NULL	1 / 5	GSEA C2GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
39	7.07	NULL	1 / 8	GSEA C2REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
40	7.01	NULL	1 / 19	BP amino acid transmembrane transport

p-values



# GW\_027

## Local Summary

%DE = 0.62  
 # metagenes = 34  
 # genes = 316  
 # genes in genesets = 315  
 # genes with  $fdr < 0.1$  = 124 ( 121 + / 3 - )  
 # genes with  $fdr < 0.05$  = 84 ( 83 + / 1 - )  
 # genes with  $fdr < 0.01$  = 59 ( 58 + / 1 - )

$\langle r \rangle$  metagenes = 0.92

$\langle r \rangle$  genes = 0.32

$\langle FC \rangle = 0.32$

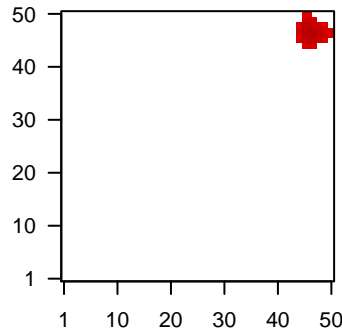
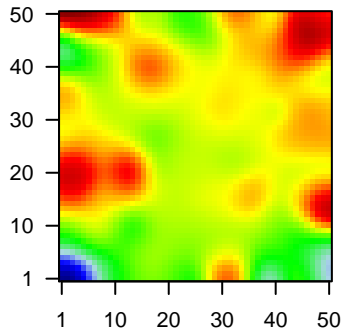
$\langle \text{shrinkage-t} \rangle = 11.2$

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

$\langle fdr \rangle = 0.64$

Profile

Spot



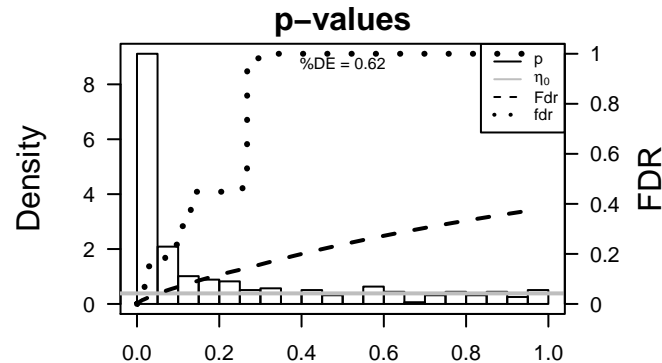
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3787	1.83	2e-16	3e-14	46 x 45 potassium voltage-gated channel, delayed-rectifier, subfamil
2	4744	1.4	9e-15	3e-11	45 x 44 neurofilament, heavy polypeptide [Source:HGNC Symbol;Acc
3	79190	1.33	2e-13	1e-09	50 x 47 iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
4	1029	1.22	2e-11	1e-09	45 x 45 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol;
5	7083	1.22	2e-11	7e-09	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
6	59342	1.18	9e-11	7e-09	50 x 47 serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
7	400916	1.16	1e-10	1e-08	50 x 47 coiled-coil-helix-coiled-coil-helix domain containing 10 [So
8	51087	1.15	2e-10	7e-07	47 x 46 Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
9	10388	1.06	6e-09	8e-07	47 x 46 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
10	7345	1.03	1e-08	1e-06	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
11	9232	1.01	3e-08	1e-06	44 x 48 pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:9e
12	79682	1	4e-08	4e-06	46 x 47 centromere protein U [Source:HGNC Symbol;Acc:21348]
13	387103	0.98	7e-08	3e-05	45 x 49 centromere protein W [Source:HGNC Symbol;Acc:21488]
14	26255	0.92	3e-07	5e-05	44 x 48 pituitary tumor-transforming 3, pseudogene [Source:HGNC S
15	128178	0.89	8e-07	1e-04	47 x 45 EDAR-associated death domain [Source:HGNC Symbol;Acc
16	9212	0.86	2e-06	1e-04	45 x 48 aurora kinase B [Source:HGNC Symbol;Acc:11390]
17	91057	0.85	3e-06	1e-04	46 x 47 coiled-coil domain containing 34 [Source:HGNC Symbol;Acc
18	57570	0.82	6e-06	1e-04	46 x 45 tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141]
19	3148	0.81	7e-06	1e-04	46 x 46 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
20	168002	0.81	7e-06	1e-04	50 x 46 dishevelled-binding antagonist of beta-catenin 2 [Source:HG

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	28.17	NULL	48 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	28.17	NULL	48 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	24.11	NULL	6 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
4	20.47	NULL	11 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
5	19.48	NULL	9 / 11	GSEA C2KALMA_E2F1_TARGETS
6	19.45	NULL	40 / 149	BP DNA replication
7	17.86	NULL	14 / 30	BP DNA strand elongation involved in DNA replication
8	17.56	NULL	9 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
9	17.41	NULL	9 / 15	GSEA C2KEGG_DNA_REPLICATION
10	16.68	NULL	9 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
11	16.4	NULL	63 / 370	BP mitotic cell cycle
12	15.77	NULL	8 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
13	14.37	NULL	6 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
14	14.24	NULL	6 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
15	13.68	NULL	9 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
16	13.62	NULL	64 / 530	Cancer Lembcke_Normal vs Adenoma
17	13.54	NULL	5 / 16	Cancer WOLFER_overlap genes
18	13.2	NULL	4 / 13	GSEA C2REN_BOUND_BY_E2F
19	12.95	NULL	4 / 13	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
20	12.95	NULL	5 / 15	GSEA C2BASAKI_YB1_TARGETS_UP
21	12.93	NULL	8 / 26	BP chromosome organization
22	12.73	NULL	8 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
23	12.67	NULL	7 / 16	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
24	12.66	NULL	6 / 15	GSEA C2KAUFFMANN_DNA_REPLICATION_GENES
25	12.52	NULL	6 / 15	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_UP
26	12.45	NULL	5 / 8	GSEA C2REACTOME_DNA_REPLICATION_PRE_INITIATION
27	12.37	NULL	9 / 22	BP DNA replication initiation
28	12.31	NULL	41 / 298	BP DNA repair
29	12.22	NULL	9 / 21	BP telomere maintenance via semi-conservative replication
30	11.91	NULL	7 / 15	GSEA C2REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
31	11.78	NULL	4 / 9	miRNA target-24
32	11.73	NULL	4 / 10	CC lateral element
33	11.66	NULL	7 / 16	GSEA C2REACTOME_LAGGING_STRAND_SYNTHESIS
34	11.65	NULL	5 / 13	GSEA C2SA_REG_CASCADE_OF_CYCLIN_EXPR
35	11.59	NULL	6 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
36	11.5	NULL	5 / 12	GSEA C2REACTOME_CELL_CYCLE_MITOTIC
37	11.35	NULL	9 / 24	BP telomere maintenance via recombination
38	11.28	NULL	14 / 57	Glio developing astrocytes
39	11.24	NULL	6 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
40	11.14	NULL	5 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53



# GW\_027

## Local Summary

%DE = 0.74  
 # metagenes = 16  
 # genes = 279  
 # genes in genesets = 275

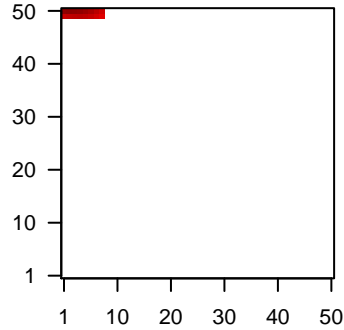
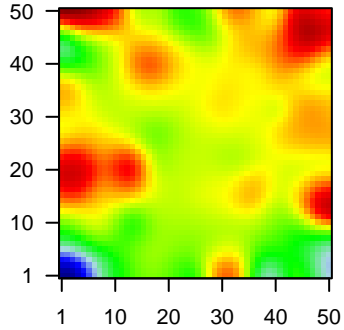
# genes with  $fdr < 0.1 = 166$  ( 149 + / 17 - )  
 # genes with  $fdr < 0.05 = 155$  ( 139 + / 16 - )  
 # genes with  $fdr < 0.01 = 121$  ( 112 + / 9 - )

<r> metagenes = 0.97  
 <r> genes = 0.41

<FC> = 0.47  
 <shrinkage-t> = 16.6  
 <p-value> = 0  
 <fdr> = 0.45

Profile

Spot



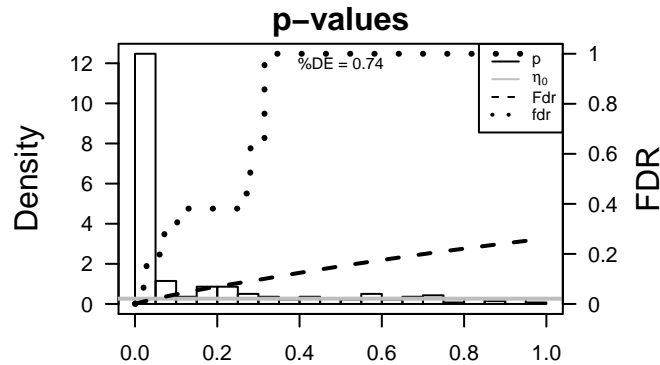
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	1.53	2e-16	1e-15	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	-1.83	2e-16	1e-15	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
3	49860	1.76	2e-16	1e-15	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
4	1571	1.49	2e-16	1e-15	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
5	131177	1.62	2e-16	1e-15	3 x 50 family with sequence similarity 3, member D [Source:HGNC S
6	192666	2.75	2e-16	1e-15	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
7	3851	1.94	2e-16	1e-15	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
8	3934	1.79	2e-16	1e-15	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]
9	137797	1.9	2e-16	1e-15	1 x 50 LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
10	5266	1.54	2e-16	1e-15	1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Ac
11	6590	2.2	2e-16	1e-15	1 x 49 secretory leukocyte peptidase inhibitor [Source:HGNC Symb
12	7113	1.6	2e-16	1e-15	5 x 50 transmembrane protease, serine 2 [Source:HGNC Symbol;Ac
13	3860	1.33	1e-15	5e-14	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
14	7053	1.44	2e-15	1e-13	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	1048	1.42	5e-15	1e-12	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
16	120224	1.42	5e-15	1e-12	2 x 49 transmembrane protein 45B [Source:HGNC Symbol;Acc:251
17	284340	1.39	2e-14	3e-12	6 x 50 chemokine (C-X-C motif) ligand 17 [Source:HGNC Symbol;A
18	1475	1.35	9e-14	3e-12	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	6707	1.23	1e-13	3e-12	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126
20	222	1.34	1e-13	6e-12	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	42.58	NULL	68 / 135	H.Tiss WIRTH_Mucosa
2	21.57	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
3	19.95	NULL	12 / 21	CC cornified envelope
4	18.69	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
5	16.31	NULL	4 / 16	GSEA C2JAEGER_METASTASIS_DN
6	16.06	NULL	13 / 42	BP keratinization
7	15.97	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
8	15.92	NULL	67 / 572	Disease GUDJ_psooriasis up
9	15.73	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
10	15.3	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
11	15.17	NULL	7 / 19	BP peptide cross-linking
12	14.85	NULL	6 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
13	14.31	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
14	14.3	NULL	7 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
15	14.04	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	13.48	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
17	13.13	NULL	7 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
18	12.77	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
19	12.67	NULL	3 / 15	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
20	12.63	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
21	12.56	NULL	17 / 76	BP epidermis development
22	12.5	NULL	3 / 11	GSEA C2REACTOME_XENOBIOTICS
23	12.32	NULL	16 / 53	BP keratinocyte differentiation
24	11.7	NULL	3 / 15	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
25	11.68	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
26	11.66	NULL	4 / 23	MF peptidase inhibitor activity
27	11.61	NULL	2 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
28	11.49	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
29	11.49	NULL	3 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME
30	11.2	NULL	5 / 13	H.Tiss WIRTH_Tonsil
31	11.19	NULL	3 / 15	GSEA C2FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP
32	10.84	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
33	10.71	NULL	2 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
34	10.71	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
35	10.23	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
36	10.2	NULL	4 / 10	MF RAGE receptor binding
37	10	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
38	9.71	NULL	14 / 186	MF structural molecule activity
39	9.37	NULL	2 / 8	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
40	9.15	NULL	2 / 14	GSEA C2CAIRO_HEPATOBLASTOMA_DN



# GW\_027

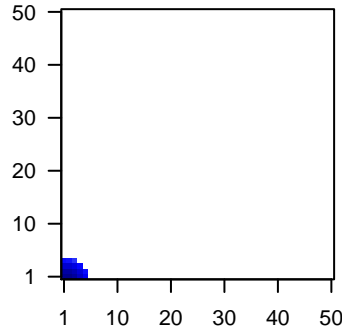
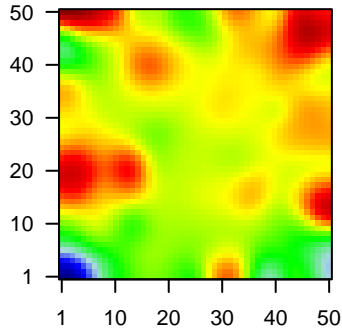
## Local Summary

%DE = 0.91  
 # metagenes = 17  
 # genes = 263  
 # genes in genesets = 262  
 # genes with  $fdr < 0.1$  = 223 ( 10 + / 213 - )  
 # genes with  $fdr < 0.05$  = 193 ( 8 + / 185 - )  
 # genes with  $fdr < 0.01$  = 170 ( 8 + / 162 - )

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.4  
 $\langle FC \rangle = -0.62$   
 $\langle \text{shrinkage-t} \rangle = -21.83$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.3$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1490	-1.49	2e-16	4e-16	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2
2	3039	-1.66	2e-16	4e-16	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
3	3040	-2.76	2e-16	4e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3043	-3.29	2e-16	4e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
5	8870	-1.49	2e-16	4e-16	1 x 3 immediate early response 3 [Source:HGNC Symbol;Acc:5392]
6	4312	-1.87	2e-16	4e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:H
7	4314	-1.68	2e-16	4e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
8	388	-1.48	2e-16	4e-16	2 x 3 ras homolog family member B [Source:HGNC Symbol;Acc:66
9	7058	-1.51	2e-16	4e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
10	7076	-1.49	2e-16	4e-16	4 x 1 TIMP metalloproteinase inhibitor 1 [Source:HGNC Symbol;Acc
11	25907	-1.87	2e-16	4e-16	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC
12	3371	-1.81	2e-16	4e-16	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
13	6515	-1.47	4e-16	3e-15	3 x 1 solute carrier family 2 (facilitated glucose transporter), memb
14	87	-1.46	7e-16	5e-15	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
15	1462	-1.47	7e-16	5e-15	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
16	3491	-1.46	9e-16	6e-14	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
17	1290	-1.42	4e-15	6e-14	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
18	1277	-1.41	6e-15	4e-13	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
19	4319	-1.38	2e-14	3e-12	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
20	10962	-1.34	1e-13	1e-11	5 x 1 myeloid/lymphoid or mixed-lineage leukemia (thorax homol

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-32.78	NULL	63 / 190	CC extracellular matrix
2	-32.74	NULL	15 / 16	MMML C6ACIEJ_MMML 1
3	-32.4	NULL	72 / 250	LymphoidENZ_Stromal signature 1
4	-31.62	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
5	-31.61	NULL	2 / 4	MMML C6ACIEJ_MMML 23
6	-30.25	NULL	67 / 242	BP extracellular matrix organization
7	-30.1	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
8	-28.19	NULL	31 / 69	BP extracellular matrix disassembly
9	-26.18	NULL	28 / 64	BP collagen catabolic process
10	-24.43	NULL	8 / 11	MF platelet-derived growth factor binding
11	-22.88	NULL	8 / 12	miRNA target-29c
12	-22.36	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
13	-22.1	NULL	11 / 19	MF extracellular matrix binding
14	-21.86	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
15	-20.92	NULL	12 / 35	Glio Colman_survival_associated
16	-20.86	NULL	15 / 37	BP collagen fibril organization
17	-20.44	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
18	-20.28	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
19	-20.19	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
20	-19.78	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
21	-19.72	NULL	103 / 1182	CC extracellular region
22	-19.22	NULL	20 / 57	MF extracellular matrix structural constituent
23	-18.99	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
24	-18.8	NULL	3 / 11	MF oxygen transporter activity
25	-18.77	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HEL4
26	-18.71	NULL	37 / 183	CC proteinaceous extracellular matrix
27	-18.66	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
28	-18.63	NULL	2 / 10	CC hemoglobin complex
29	-18.63	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
30	-18.34	NULL	76 / 683	CC extracellular space
31	-18.33	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
32	-18.06	NULL	3 / 14	CC endocytic vesicle lumen
33	-17.93	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
34	-17.65	NULL	2 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
35	-17.4	NULL	2 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
36	-16.79	NULL	5 / 19	MF peroxidase activity
37	-16.28	NULL	3 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
38	-16.13	NULL	22 / 83	CC basement membrane
39	-16.08	NULL	4 / 7	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_UP
40	-16.05	NULL	39 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up

p-values

