

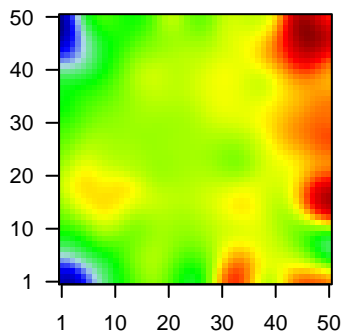
# GW\_041

## Global Summary

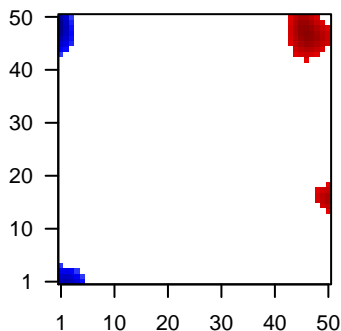
%DE = 0.16  
 # genes with  $fdr < 0.2$  = 2096 ( 1075 + / 1021 - )  
 # genes with  $fdr < 0.1$  = 1715 ( 902 + / 813 - )  
 # genes with  $fdr < 0.05$  = 1418 ( 742 + / 676 - )  
 # genes with  $fdr < 0.01$  = 996 ( 495 + / 501 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.08  
 <fdr> = 0.84

Profile



Regulated Spots



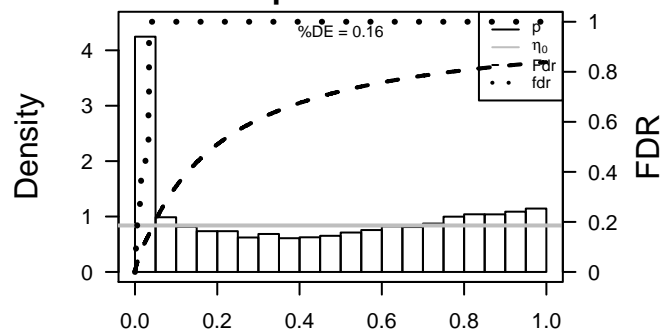
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	87	-1.83	2e-16	3e-14	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	113146	-1.79	2e-16	3e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	-3.46	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	-2.33	2e-16	3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
5	8644	-2.58	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr]
6	1109	-2.19	2e-16	3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr]
7	401138	2.47	2e-16	3e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
8	55107	-2.21	2e-16	3e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
9	84707	1.74	2e-16	3e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
10	633	-2.02	2e-16	3e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
11	330	1.72	2e-16	3e-14	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A]
12	387695	-1.91	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
13	399948	2.01	2e-16	3e-14	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3]
14	64073	-2	2e-16	3e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt]
15	260436	4.34	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc]
16	135398	2.11	2e-16	3e-14	1 x 40 chromosome 6 open reading frame 141 [Source:HGNC Synt]
17	760	-1.84	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	810	-1.92	2e-16	3e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
19	6364	2.92	2e-16	3e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc]
20	9635	-2.49	2e-16	3e-14	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.08	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	16.08	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	12.66	NULL	370	BP mitotic cell cycle
4	12.32	NULL	4640	CC nucleus
5	10.84	NULL	949	CC nucleoplasm
6	10.82	NULL	630	Chr Chr X
7	10	NULL	1749	MF DNA binding
8	9.39	NULL	149	BP DNA replication
9	8.76	NULL	274	LymphoBP SPANG_IL21 DN
10	8.48	NULL	298	BP DNA repair
11	7.84	NULL	232	BP mitosis
12	7.83	NULL	16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
13	7.55	NULL	30	BP DNA strand elongation involved in DNA replication
14	7.52	NULL	1574	BP transcription, DNA-templated
15	7.21	NULL	232	Chr Chr 18
16	6.92	NULL	1581	BP regulation of transcription, DNA-dependent
17	6.85	NULL	123	BP defense response to virus
18	6.71	NULL	56	CC chromosome, centromeric region
19	6.49	NULL	417	H.Tiss WIRTH_Immune system
20	6.38	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
<i>Underexpressed</i>				
1	-19.2	NULL	135	H.Tiss WIRTH_Mucosa
2	-17.63	NULL	190	CC extracellular matrix
3	-14.93	NULL	1182	CC extracellular region
4	-14.46	NULL	250	LymphoBP ENZ_Stromal signature 1
5	-14.41	NULL	683	CC extracellular space
6	-12.86	NULL	242	BP extracellular matrix organization
7	-12.55	NULL	16	MMML C2SCIEJ_MMML 1
8	-12.04	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
9	-11.53	NULL	183	CC proteinaceous extracellular matrix
10	-11.12	NULL	64	BP collagen catabolic process
11	-10.94	NULL	69	BP extracellular matrix disassembly
12	-10.31	NULL	717	Chr Chr 16
13	-10.24	NULL	19	BP peptide cross-linking
14	-9.91	NULL	57	MF extracellular matrix structural constituent
15	-9.73	NULL	11	MF platelet-derived growth factor binding
16	-9.52	NULL	76	BP epidermis development
17	-9.5	NULL	53	BP keratinocyte differentiation
18	-9.17	NULL	579	MF calcium ion binding
19	-9.11	NULL	21	CC cornified envelope
20	-9.1	NULL	12	miRNA target-29c

p-values





# GW\_041

## Local Summary

%DE = 0.73  
 # metagenes = 57  
 # genes = 556  
 # genes in genesets = 552

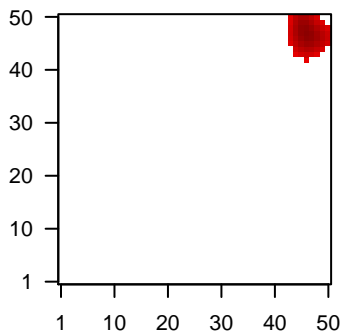
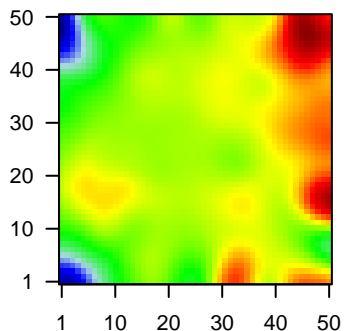
# genes with  $fdr < 0.1$  = 343 ( 341 + / 2 - )  
 # genes with  $fdr < 0.05$  = 295 ( 295 + / 0 - )  
 # genes with  $fdr < 0.01$  = 217 ( 217 + / 0 - )

$\langle r \rangle$  metagenes = 0.88  
 $\langle r \rangle$  genes = 0.29

$\langle FC \rangle = 0.52$   
 $\langle \text{shrinkage-t} \rangle = 18.33$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.49$

Profile

Spot



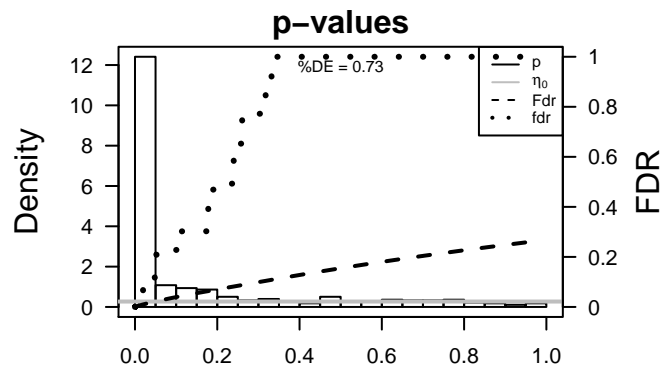
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84707	1.74	2e-16	5e-15	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
2	168002	1.82	2e-16	5e-15	50 x 46 dishevelled-binding antagonist of beta-catenin 2 [Source:HG
3	26227	1.74	2e-16	5e-15	50 x 46 phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
4	139728	1.86	2e-16	5e-15	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l
5	5625	1.8	2e-16	5e-15	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ar
6	7345	1.84	2e-16	5e-15	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
7	7546	2.29	2e-16	5e-15	48 x 50 Zic family member 2 [Source:HGNC Symbol;Acc:12873]
8	55190	1.67	4e-16	5e-14	47 x 50 nudix (nucleoside diphosphate linked moiety X)-type motif 11
9	875	1.64	1e-15	2e-12	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15:
10	84223	1.65	1e-15	2e-12	47 x 46 IQ motif containing G [Source:HGNC Symbol;Acc:25251]
11	7298	1.58	2e-14	2e-11	46 x 48 thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
12	3787	1.52	1e-13	2e-10	46 x 45 potassium voltage-gated channel, delayed-rectifier, subfamil
13	22974	1.44	3e-12	2e-10	44 x 50 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:1:
14	7153	1.43	3e-12	7e-10	45 x 49 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
15	10635	1.39	1e-11	7e-10	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169:
16	59342	1.39	1e-11	7e-10	50 x 47 serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
17	7083	1.38	2e-11	1e-08	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
18	191	1.32	1e-10	1e-08	47 x 48 adenosylhomocysteinase [Source:HGNC Symbol;Acc:343]
19	80258	1.31	2e-10	1e-08	50 x 45 EF-hand domain (C-terminal) containing 2 [Source:HGNC S
20	26255	1.29	3e-10	1e-08	44 x 48 pituitary tumor-transforming 3, pseudogene [Source:HGNC S

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	47.68	NULL	95 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	47.68	NULL	95 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	27.16	NULL	16 / 16	GSEA C27GUCHI_CELL_CYCLE_RB1_TARGETS
4	24.29	NULL	102 / 370	BP mitotic cell cycle
5	21.45	NULL	106 / 530	Cancer Lembecke_Normal vs Adenoma
6	21.14	NULL	26 / 57	Glio developing astrocytes
7	20.92	NULL	51 / 149	BP DNA replication
8	20.73	NULL	19 / 30	BP DNA strand elongation involved in DNA replication
9	20.04	NULL	9 / 11	GSEA C2KALMA_E2F1_TARGETS
10	19.92	NULL	12 / 16	GSEA C27ARMER_BREAST_CANCER_CLUSTER_2
11	19.26	NULL	9 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
12	17.61	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
13	17.47	NULL	10 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
14	17.4	NULL	12 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
15	17.09	NULL	11 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
16	16.95	NULL	11 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
17	16.49	NULL	13 / 22	BP DNA replication initiation
18	16.29	NULL	60 / 232	BP mitosis
19	16.01	NULL	11 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
20	15.76	NULL	13 / 21	BP telomere maintenance via semi-conservative replication
21	15.26	NULL	11 / 14	MMML C29CIEJ_MMML_4
22	15.2	NULL	7 / 12	BP mitotic chromosome condensation
23	15.15	NULL	24 / 56	CC chromosome, centromeric region
24	14.96	NULL	11 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
25	14.91	NULL	13 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
26	14.84	NULL	12 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
27	14.69	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
28	14.63	NULL	11 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
29	14.42	NULL	7 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
30	14.37	NULL	14 / 24	BP telomere maintenance via recombination
31	14.35	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
32	14.27	NULL	10 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
33	14.27	NULL	9 / 16	Cancer WOLFER_overlap genes
34	13.83	NULL	8 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
35	13.79	NULL	55 / 298	BP DNA repair
36	13.65	NULL	11 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
37	13.56	NULL	6 / 14	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
38	13.54	NULL	6 / 9	GSEA C2SEMBA_FHIT_TARGETS_DN
39	13.5	NULL	7 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
40	13.46	NULL	12 / 15	GSEA C2ZHANG_CYCLING_GENES



# GW\_041

## Local Summary

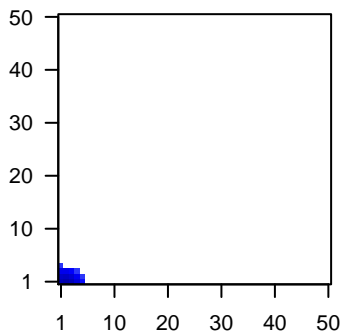
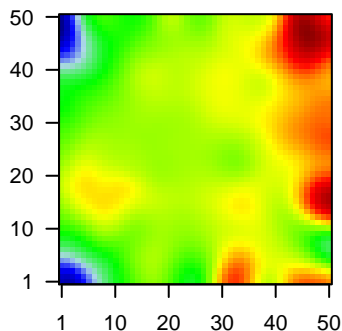
%DE = 0.91  
 # metagenes = 15  
 # genes = 251  
 # genes in genesets = 250

# genes with  $fdr < 0.1 = 214$  ( 13 + / 201 - )  
 # genes with  $fdr < 0.05 = 212$  ( 12 + / 200 - )  
 # genes with  $fdr < 0.01 = 185$  ( 11 + / 174 - )

<r> metagenes = 0.96  
 <r> genes = 0.4  
 <FC> = -0.84  
 <shrinkage-t> = -29.34  
 <p-value> = 0  
 <fdr> = 0.2

Profile

Spot



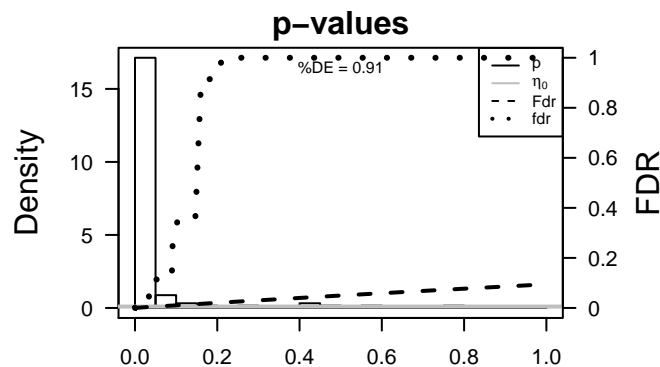
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	87	-1.83	2e-16	2e-16	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	633	-2.02	2e-16	2e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	1277	-2.52	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	-2.43	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	-2.58	2e-16	2e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1290	-2.19	2e-16	2e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1293	-2.34	2e-16	2e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	4060	-2.27	2e-16	2e-16	2 x 1 lumican [Source:HGNC Symbol;Acc:6724]
9	10962	-1.82	2e-16	2e-16	5 x 1 myeloid/lymphoid or mixed-lineage leukemia (trithorax homol
10	4312	-1.95	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:H
11	4319	-1.89	2e-16	2e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
12	4320	-1.78	2e-16	2e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
13	4314	-1.92	2e-16	2e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
14	4318	-1.75	2e-16	2e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9:
15	25878	-1.83	2e-16	2e-16	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:
16	4692	-1.89	2e-16	2e-16	5 x 1 necdin, melanoma antigen (MAGE) family member [Source:H
17	5159	-1.7	2e-16	2e-16	3 x 1 platelet-derived growth factor receptor, beta polypeptide [Sou
18	6678	-1.76	2e-16	2e-16	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:i
19	7045	-1.89	2e-16	2e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG
20	7058	-1.9	2e-16	2e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-41.89	NULL	62 / 190	CC extracellular matrix
2	-39.89	NULL	15 / 16	MMML C6ACIEJ_MMML 1
3	-39.01	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
4	-36.45	NULL	71 / 250	LymphomaL2ENZ_Stromal signature 1
5	-33.85	NULL	30 / 69	BP extracellular matrix disassembly
6	-33.13	NULL	65 / 242	BP extracellular matrix organization
7	-32.79	NULL	27 / 64	BP collagen catabolic process
8	-31.87	NULL	8 / 11	MF platelet-derived growth factor binding
9	-30.66	NULL	8 / 12	miRNA target-29c
10	-26.69	NULL	19 / 57	MF extracellular matrix structural constituent
11	-25.71	NULL	14 / 37	BP collagen fibril organization
12	-24.44	NULL	11 / 19	MF extracellular matrix binding
13	-23.21	NULL	35 / 183	CC proteinaceous extracellular matrix
14	-21.96	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
15	-21.52	NULL	12 / 35	Glio Colman_survival_associated
16	-21.46	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
17	-20.81	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
18	-19.55	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
19	-19.41	NULL	12 / 40	BP cellular response to amino acid stimulus
20	-19.15	NULL	75 / 683	CC extracellular space
21	-18.85	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
22	-18.67	NULL	100 / 1182	CC extracellular region
23	-18.53	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
24	-18.18	NULL	5 / 11	BP dermatan sulfate biosynthetic process
25	-18.14	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
26	-17.78	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
27	-17.63	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
28	-17.47	NULL	21 / 83	CC basement membrane
29	-16.94	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
30	-16.87	NULL	4 / 10	BP protein heterotrimerization
31	-16.71	NULL	23 / 119	LymphomaBOSOLOWSKI_green total
32	-16.31	NULL	39 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
33	-16.31	NULL	39 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
34	-16.31	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
35	-16.31	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
36	-15.98	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
37	-15.97	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
38	-15.91	NULL	17 / 85	MF integrin binding
39	-15.68	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
40	-15.26	NULL	17 / 68	CC collagen



# GW\_041

## Local Summary

%DE = 0.88  
 # metagenes = 21  
 # genes = 300  
 # genes in genesets = 292  
 # genes with  $fdr < 0.1$  = 234 ( 13 + / 221 - )  
 # genes with  $fdr < 0.05$  = 225 ( 12 + / 213 - )  
 # genes with  $fdr < 0.01$  = 197 ( 10 + / 187 - )

$\langle r \rangle$  metagenes = 0.91

$\langle r \rangle$  genes = 0.38

$\langle FC \rangle = -0.89$

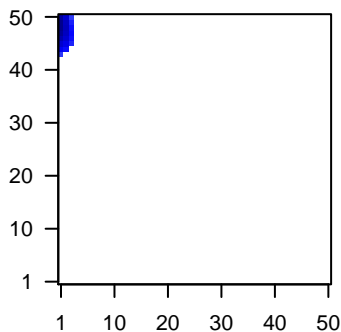
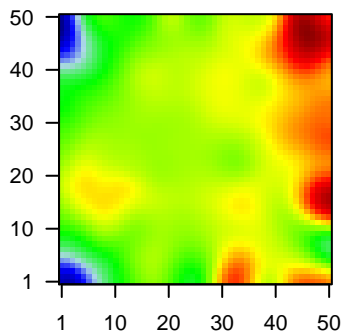
$\langle \text{shrinkage-t} \rangle = -31.36$

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

$\langle fdr \rangle = 0.26$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	113146	-1.79	2e-16	2e-16	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	57016	-3.46	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
3	441282	-2.33	2e-16	2e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
4	8644	-2.58	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym]
5	387695	-1.91	2e-16	2e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
6	64073	-2	2e-16	2e-16	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt]
7	760	-1.84	2e-16	2e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	810	-1.92	2e-16	2e-16	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
9	9635	-2.49	2e-16	2e-16	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20]
10	1382	-2.49	2e-16	2e-16	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol]
11	54544	-1.71	2e-16	2e-16	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
12	49860	-3.23	2e-16	2e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	9547	-2.02	2e-16	2e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
14	414325	-1.88	2e-16	2e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	-2.56	2e-16	2e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	93099	-1.76	2e-16	2e-16	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
17	2171	-2.46	2e-16	2e-16	1 x 46 fatty acid binding protein 5 (psoriasis-associated) [Source:HC
18	9982	-1.95	2e-16	2e-16	1 x 47 fibroblast growth factor binding protein 1 [Source:HGNC Sym]
19	2706	-2.7	2e-16	2e-16	1 x 47 gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
20	10804	-2.66	2e-16	2e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-49.03	NULL	88 / 135	H.Tiss WIRTH_Mucosa
2	-27.55	NULL	111 / 572	Disease GUDJ_psooriasis up
3	-22.74	NULL	18 / 21	CC cornified envelope
4	-22.65	NULL	27 / 76	BP epidermis development
5	-22.11	NULL	24 / 53	BP keratinocyte differentiation
6	-19.64	NULL	20 / 42	BP keratinization
7	-18.16	NULL	8 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
8	-17.82	NULL	10 / 19	BP peptide cross-linking
9	-16.01	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	-14.8	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	-13.84	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
12	-13.24	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
13	-13.01	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
14	-12.95	NULL	6 / 13	BP negative regulation of peptidase activity
15	-12.63	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
16	-12.61	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
17	-11.57	NULL	4 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
18	-11.45	NULL	3 / 15	CC connexon complex
19	-11.27	NULL	13 / 44	CC keratin filament
20	-11.25	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
21	-11.14	NULL	5 / 10	MF RAGE receptor binding
22	-11.12	NULL	8 / 38	BP epithelial cell differentiation
23	-10.5	NULL	4 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
24	-10.37	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
25	-10.33	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
26	-10.2	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
27	-10.08	NULL	4 / 21	CC gap junction
28	-9.98	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
29	-9.96	NULL	67 / 1182	CC extracellular region
30	-9.91	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
31	-9.56	NULL	7 / 29	BP regulation of proteolysis
32	-9.27	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
33	-9.18	NULL	3 / 13	BP intermediate filament cytoskeleton organization
34	-9.18	NULL	21 / 82	CC intermediate filament
35	-9.13	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
36	-9.03	NULL	5 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
37	-8.97	NULL	5 / 25	BP response to zinc ion
38	-8.96	NULL	2 / 10	MF gap junction channel activity
39	-8.86	NULL	10 / 52	BP negative regulation of endopeptidase activity
40	-8.82	NULL	4 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN

