

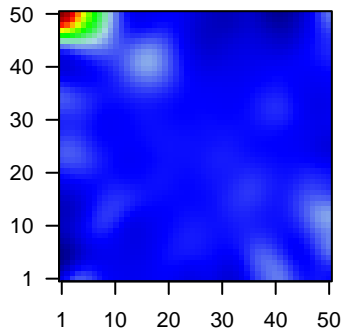
# GW\_007

## Global Summary

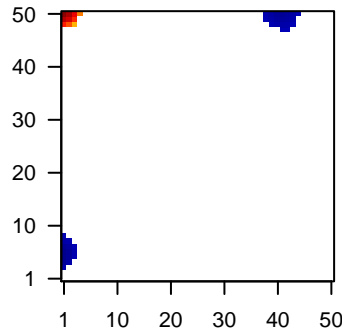
%DE = 0.13  
 # genes with  $fdr < 0.2$  = 1694 ( 997 + / 697 - )  
 # genes with  $fdr < 0.1$  = 1363 ( 830 + / 533 - )  
 # genes with  $fdr < 0.05$  = 1060 ( 684 + / 376 - )  
 # genes with  $fdr < 0.01$  = 744 ( 521 + / 223 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.1  
 <fdr> = 0.87

Profile



Regulated Spots



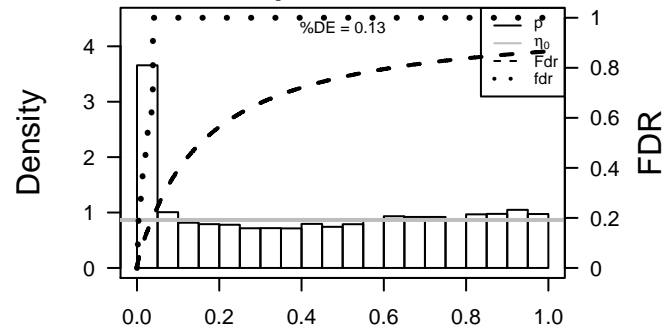
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.81	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	220	1.7	2e-16	2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
3	239	1.42	2e-16	2e-14	5 x 49 arachidonate 12-lipoxygenase [Source:HGNC Symbol;Acc:4:
4	249	1.21	2e-16	2e-14	6 x 1 alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
5	25805	-1.18	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC 3
6	391267	1.52	2e-16	2e-14	50 x 13 ankyrin repeat domain 20 family, member A11, pseudogene [
7	260436	-1.46	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symb
8	394263	2.07	2e-16	2e-14	3 x 50
9	375791	2.11	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symb
10	810	1.09	2e-16	2e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
11	57172	1.38	2e-16	2e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
12	84290	1.27	2e-16	2e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	6366	1.14	2e-16	2e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
14	1048	1.14	2e-16	2e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
15	4680	1.52	2e-16	2e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
16	1087	1.14	2e-16	2e-14	4 x 50 carcinoembryonic antigen-related cell adhesion molecule 7 [
17	1056	1.26	2e-16	2e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
18	22802	1.97	2e-16	2e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
19	9076	1.46	2e-16	2e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
20	9022	1.62	2e-16	2e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	34.86	NULL	135	H.Tiss WIRTH_Mucosa
2	16.02	NULL	21	CC cornified envelope
3	14.52	NULL	53	BP keratinocyte differentiation
4	14.18	NULL	42	BP keratinization
5	11.53	NULL	19	BP peptide cross-linking
6	11.44	NULL	76	BP epidermis development
7	10.96	NULL	572	Disease GUDJ_psooriasis up
8	10.66	NULL	16	GSEA C2ROMER_TUMORIGENESIS_DN
9	9.39	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	8.96	NULL	186	MF structural molecule activity
11	8.89	NULL	38	BP epithelial cell differentiation
12	8.87	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	8.79	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
14	8.78	NULL	1720	Chr Chr 1
15	8.45	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	8.31	NULL	82	CC intermediate filament
17	8.17	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
18	8.17	NULL	44	CC keratin filament
19	7.91	NULL	504	Chr Chr 15
20	6.85	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
<i>Underexpressed</i>				
1	-8.48	NULL	699	Chr Chr 5
2	-7.38	NULL	534	Chr Chr 8
3	-6.99	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
4	-6.8	NULL	7	MMML C2CICIEJ_MMML 5
5	-5.96	NULL	7	MMML C2CICIEJ_MMML 13
6	-5.88	NULL	1095	TF HEBENSTREIT_high expression TF
7	-5.87	NULL	10	BP cellular response to zinc ion
8	-5.42	NULL	1233	TF KIM_MYC targets
9	-5.22	NULL	253	BP translation
10	-5.03	NULL	153	MF structural constituent of ribosome
11	-4.92	NULL	34	Chr Chr Y
12	-4.86	NULL	957	Chr Chr 11
13	-4.81	NULL	128	BP translational initiation
14	-4.68	NULL	167	CC ribosome
15	-4.66	NULL	9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
16	-4.57	NULL	15	BP negative regulation of growth
17	-4.47	NULL	9	GSEA C2KEGG_RIBOSOME
18	-4.45	NULL	127	H.Tiss WIRTH_Muscle
19	-4.45	NULL	92	BP translational elongation
20	-4.45	NULL	9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND

p-values



# GW\_007

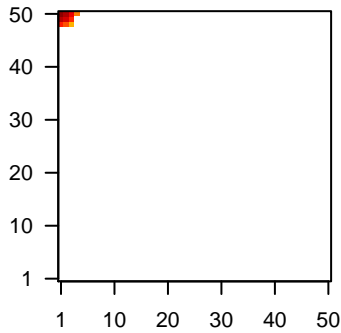
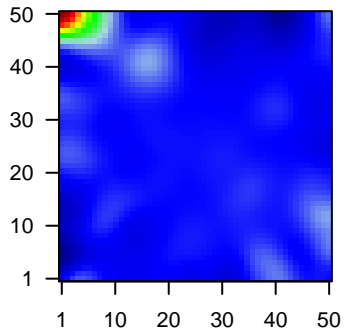
## Local Summary

%DE = 0.98  
 # metagenes = 10  
 # genes = 163  
 # genes in genesets = 160  
 # genes with  $fdr < 0.1$  = 151 ( 145 + / 6 - )  
 # genes with  $fdr < 0.05$  = 151 ( 145 + / 6 - )  
 # genes with  $fdr < 0.01$  = 143 ( 139 + / 4 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.49  
 $\langle FC \rangle$  = 1.14  
 $\langle \text{shrinkage-t} \rangle$  = 40.08  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.1

Profile

Spot



## Local Genelist

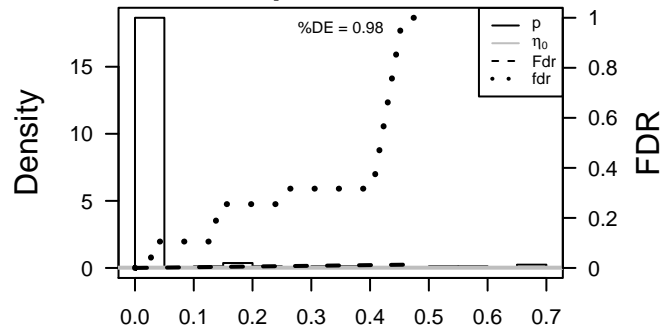
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.81	2e-16	1e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	394263	2.07	2e-16	1e-17	3 x 50
3	375791	2.11	2e-16	1e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
4	810	1.09	2e-16	1e-17	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
5	84290	1.27	2e-16	1e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	1048	1.14	2e-16	1e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
7	4680	1.52	2e-16	1e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
8	1087	1.14	2e-16	1e-17	4 x 50 carcinoembryonic antigen-related cell adhesion molecule 7 [
9	22802	1.97	2e-16	1e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	9022	1.62	2e-16	1e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
11	84518	1.94	2e-16	1e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
12	54544	2.23	2e-16	1e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
13	49860	4.08	2e-16	1e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
14	1562	1.34	2e-16	1e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
15	414325	2.81	2e-16	1e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1673	2.41	2e-16	1e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1828	1.16	2e-16	1e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	1893	1.46	2e-16	1e-17	3 x 50 extracellular matrix protein 1 [Source:HGNC Symbol;Acc:315
19	2012	1.46	2e-16	1e-17	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
20	54869	1.29	2e-16	1e-17	3 x 50 EPS8-like 1 [Source:HGNC Symbol;Acc:21295]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	54.05	NULL	68 / 135	H.Tiss WIRTH_Mucosa
2	31.59	NULL	14 / 21	CC cornified envelope
3	27.46	NULL	16 / 42	BP keratinization
4	26.54	NULL	19 / 53	BP keratinocyte differentiation
5	20.83	NULL	6 / 16	GSEA C2CRROMER_TUMORIGENESIS_DN
6	20.54	NULL	18 / 76	BP epidermis development
7	20.19	NULL	71 / 572	Disease GUDD_pсорiasis up
8	18.68	NULL	8 / 19	BP peptide cross-linking
9	17.57	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	15.3	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
11	14.78	NULL	6 / 38	BP epithelial cell differentiation
12	12.91	NULL	6 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	11.8	NULL	6 / 13	BP negative regulation of peptidase activity
14	11.37	NULL	3 / 16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
15	10.83	NULL	13 / 186	MF structural molecule activity
16	10.81	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
17	10.66	NULL	4 / 44	CC keratin filament
18	10.51	NULL	6 / 82	CC intermediate filament
19	9.68	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
20	9.46	NULL	10 / 122	MF serine-type endopeptidase activity
21	9.31	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
22	9.21	NULL	5 / 21	CC desmosome
23	9.2	NULL	5 / 10	MF RAGE receptor binding
24	9.07	NULL	45 / 1182	CC extracellular region
25	9	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
26	8.86	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
27	8.78	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
28	8.71	NULL	4 / 23	MF peptidase inhibitor activity
29	8.69	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	8.52	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
31	8.27	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HP31_DN
32	8.03	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
33	7.92	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
34	7.81	NULL	2 / 17	Disease BCHETNIA_EBM up
35	7.73	NULL	1 / 11	Glio VERHAAK_Brain
36	7.34	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
37	7.33	NULL	1 / 12	MF channel activity
38	7.29	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
39	7.07	NULL	1 / 7	GSEA C2DASU_IL6_SIGNALING_DN
40	7	NULL	3 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP

p-values



# GW\_007

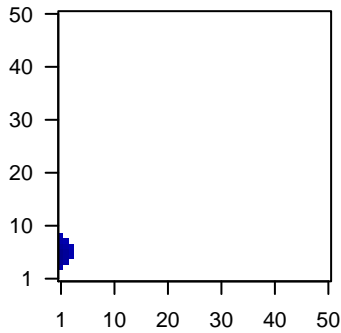
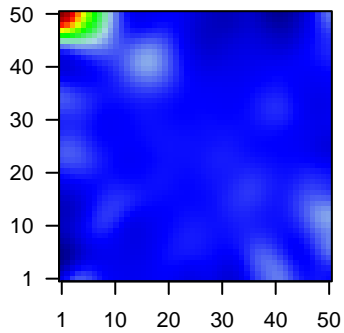
## Local Summary

%DE = 0.64  
 # metagenes = 15  
 # genes = 258  
 # genes in genesets = 255  
 # genes with  $fdr < 0.1$  = 114 ( 8 + / 106 - )  
 # genes with  $fdr < 0.05$  = 104 ( 8 + / 96 - )  
 # genes with  $fdr < 0.01$  = 57 ( 4 + / 53 - )

<r> metagenes = 0.97  
 <r> genes = 0.33  
 <FC> = -0.26  
 <shrinkage-t> = -9.18  
 <p-value> = 0  
 <fdr> = 0.59

Profile

Spot



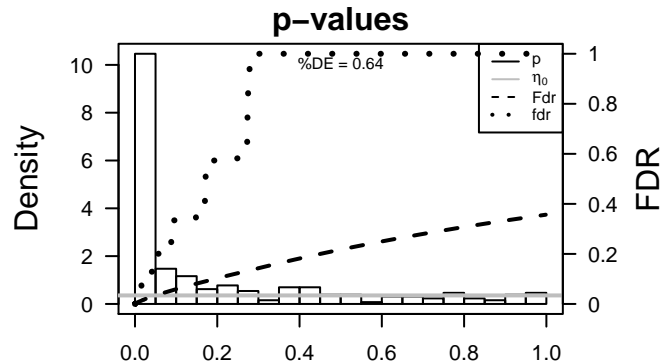
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	54541	-1.34	2e-16	5e-15	1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol;Acc:113733]
2	4502	-1.37	2e-16	5e-15	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
3	5270	-1.14	2e-16	5e-15	1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1)
4	6781	-1.11	2e-16	5e-15	1 x 3 stanniocalcin 1 [Source:HGNC Symbol;Acc:113733]
5	55107	-1.08	2e-15	6e-13	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:113733]
6	4319	-1.05	8e-15	8e-12	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:113733]
7	8727	-1.01	9e-14	3e-11	1 x 5 catenin (cadherin-associated protein), alpha-like 1 [Source:HGNC Symbol;Acc:113733]
8	3486	-0.98	7e-13	3e-11	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Symbol;Acc:113733]
9	4489	-0.89	7e-13	4e-10	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
10	401138	-0.94	5e-12	5e-08	1 x 5 melatonin [Source:HGNC Symbol;Acc:33188]
11	3909	-0.84	5e-10	7e-08	1 x 5 laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
12	10644	0.82	1e-09	7e-08	1 x 6 insulin-like growth factor 2 mRNA binding protein 2 [Source:HGNC Symbol;Acc:113733]
13	153572	-0.81	2e-09	9e-08	1 x 5 iroquois homeobox 2 [Source:HGNC Symbol;Acc:14359]
14	768	-0.8	4e-09	9e-08	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
15	3918	-0.8	5e-09	9e-08	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
16	140851	-0.79	5e-09	1e-07	1 x 5
17	1051	-0.72	6e-09	2e-06	1 x 4 CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:113733]
18	4493	-0.75	3e-08	2e-06	1 x 5 metallothionein 1E [Source:HGNC Symbol;Acc:7397]
19	8988	-0.74	6e-08	2e-06	1 x 4 heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248]
20	54972	-0.74	6e-08	2e-06	1 x 7 transmembrane protein 132A [Source:HGNC Symbol;Acc:31132]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20	NULL	3 / 10	BP cellular response to zinc ion
2	-17.53	NULL	1 / 2	miRNA target set 101b
3	-17.25	NULL	4 / 15	GSEA C2KANG_FLUOROURACIL_RESISTANCE_DN
4	-16.9	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
5	-16.88	NULL	4 / 9	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_DN
6	-16.6	NULL	2 / 7	MMML C6SCIEJ_MMML 13
7	-16.04	NULL	3 / 15	BP negative regulation of growth
8	-15.62	NULL	5 / 12	BP hemidesmosome assembly
9	-15.55	NULL	4 / 8	GSEA C2SASAKI_TARGETS_OF_TP73_AND_TP63
10	-14.85	NULL	4 / 17	BP negative regulation of signal transduction
11	-13.51	NULL	3 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_F
12	-13.14	NULL	5 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
13	-12.84	NULL	6 / 16	MF fibronectin binding
14	-11.79	NULL	3 / 13	BP response to vitamin D
15	-11.47	NULL	2 / 9	GSEA C2KOMMAGANI_TP63_GAMMA_TARGETS
16	-11.36	NULL	2 / 11	BP cellular copper ion homeostasis
17	-10.69	NULL	3 / 16	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_UP
18	-10.51	NULL	3 / 16	BP decidualization
19	-10.4	NULL	3 / 12	miRNA target set 101b
20	-10.26	NULL	3 / 16	BP negative regulation of peptidyl-serine phosphorylation
21	-10.19	NULL	7 / 51	BP regulation of cell migration
22	-9.69	NULL	11 / 70	BP cell junction assembly
23	-9.69	NULL	2 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
24	-9.53	NULL	2 / 13	BP cellular response to cadmium ion
25	-9.37	NULL	3 / 16	GSEA C2I_PROSTATE_CANCER_EPIGENETIC
26	-9.33	NULL	28 / 242	BP extracellular matrix organization
27	-9.17	NULL	3 / 11	GSEA C2YAMANAKA_GLIOMASTOMA_SURVIVAL_UP
28	-9.06	NULL	6 / 55	BP odontogenesis of dentin-containing tooth
29	-8.99	NULL	3 / 27	miRNA target set 101b
30	-8.99	NULL	2 / 14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G4
31	-8.8	NULL	1 / 7	GSEA C2RUGO_STRESS_RESPONSE_SUBSET_F
32	-8.8	NULL	1 / 7	GSEA C2KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION
33	-8.66	NULL	3 / 13	BP cellular response to glucocorticoid stimulus
34	-8.55	NULL	59 / 1182	CC extracellular region
35	-8.4	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
36	-8.39	NULL	3 / 13	GSEA C2LAMB_CCND1_TARGETS
37	-8.38	NULL	2 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
38	-8.33	NULL	2 / 9	GSEA C2WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
39	-8.3	NULL	2 / 14	GSEA C2ENGELMANN_CANCER_PROGENITORS_UP
40	-8.27	NULL	4 / 14	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN



# GW\_007

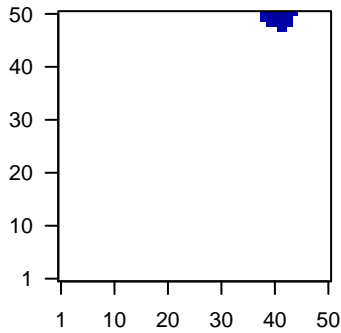
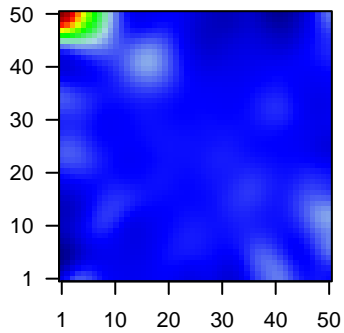
## Local Summary

%DE = 0.66  
 # metagenes = 20  
 # genes = 319  
 # genes in genesets = 317  
 # genes with  $fdr < 0.1 = 121$  ( 6 + / 115 - )  
 # genes with  $fdr < 0.05 = 82$  ( 4 + / 78 - )  
 # genes with  $fdr < 0.01 = 40$  ( 3 + / 37 - )

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.35  
 $\langle FC \rangle = -0.21$   
 $\langle \text{shrinkage-t} \rangle = -7.32$   
 $\langle p\text{-value} \rangle = 0.03$   
 $\langle fdr \rangle = 0.7$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1033	-0.94	3e-12	4e-09	43 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	10797	-0.9	4e-11	8e-08	43 x 50 methylenetetrahydrofolate dehydrogenase (NADP+ depend
3	6119	-0.83	1e-09	8e-08	43 x 48 replication protein A3, 14kDa [Source:HGNC Symbol;Acc:10
4	6788	-0.82	1e-09	1e-06	39 x 50 serine/threonine kinase 3 [Source:HGNC Symbol;Acc:11406]
5	3251	-0.77	1e-08	1e-06	42 x 50 hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
6	136	-0.76	2e-08	7e-06	41 x 50 adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
7	26872	-0.73	9e-08	8e-06	40 x 50 six transmembrane epithelial antigen of the prostate 1 [Sour
8	56943	-0.71	2e-07	8e-06	40 x 50 enhancer of yellow 2 homolog (Drosophila) [Source:HGNC S
9	29081	-0.7	3e-07	8e-06	39 x 50 methyltransferase like 5 [Source:HGNC Symbol;Acc:25006]
10	29028	-0.69	3e-07	8e-05	44 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Sym
11	55353	-0.66	1e-06	2e-04	42 x 50 lysosomal protein transmembrane 4 beta [Source:HGNC Syrr
12	10732	-0.62	5e-06	2e-04	40 x 50 transcription factor-like 5 (basic helix-loop-helix) [Source:HC
13	28998	-0.62	6e-06	2e-04	39 x 50 mitochondrial ribosomal protein L13 [Source:HGNC Symbol;f
14	9141	-0.61	7e-06	2e-04	41 x 50 programmed cell death 5 [Source:HGNC Symbol;Acc:8764]
15	9521	-0.61	7e-06	2e-04	42 x 50 eukaryotic translation elongation factor 1 epsilon 1 [Source:Hi
16	401233	0.61	8e-06	4e-04	39 x 49
17	7411	-0.59	1e-05	5e-04	42 x 50 von Hippel-Lindau binding protein 1 [Source:HGNC Symbol;v
18	54443	-0.58	2e-05	5e-04	43 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
19	51659	-0.57	3e-05	5e-04	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
20	55706	-0.56	3e-05	5e-04	40 x 50 NDC1 transmembrane nucleoporin [Source:HGNC Symbol;A

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.69	NULL	38 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	-14.69	NULL	38 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	-13.45	NULL	6 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
4	-12.31	NULL	6 / 15	GSEA C2REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
5	-12.24	NULL	5 / 10	CC zona pellucida receptor complex
6	-11.89	NULL	3 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
7	-11.16	NULL	36 / 534	Chr 8
8	-10.73	NULL	3 / 15	Cancer RHODES_CANCER_META_SIGNATURE
9	-10.7	NULL	9 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
10	-10.66	NULL	9 / 36	BP 'de novo' posttranslational protein folding
11	-10.56	NULL	49 / 370	BP mitotic cell cycle
12	-10.23	NULL	6 / 16	Cancer WOLFER_overlap genes
13	-9.58	NULL	8 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
14	-9.49	NULL	9 / 35	BP mitotic nuclear envelope disassembly
15	-8.8	NULL	5 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
16	-8.57	NULL	12 / 59	CC nuclear pore
17	-8.55	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
18	-8.51	NULL	4 / 14	GSEA C2MAYBURD_RESPONSE_TO_L663536_DN
19	-8.39	NULL	7 / 29	BP regulation of glucose transport
20	-8.35	NULL	51 / 530	Cancer Lembecke_Normal vs Adenoma
21	-8.31	NULL	3 / 19	miRNA target sites
22	-8.3	NULL	4 / 15	GSEA C2FERRANDO_HOX11_NEIGHBORS
23	-7.77	NULL	4 / 30	BP DNA strand elongation involved in DNA replication
24	-7.76	NULL	5 / 23	BP binding of sperm to zona pellucida
25	-7.73	NULL	8 / 18	BP spindle organization
26	-7.52	NULL	5 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	-7.48	NULL	6 / 15	Cancer GENTLES_modul6
28	-7.34	NULL	5 / 22	BP CENP-A containing nucleosome assembly at centromere
29	-7.29	NULL	7 / 37	BP hexose transport
30	-7.29	NULL	2 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_F
31	-7.28	NULL	6 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
32	-7.22	NULL	6 / 14	MMML C6SCIEJ_MMML_4
33	-7.21	NULL	2 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
34	-7.17	NULL	2 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
35	-7.11	NULL	39 / 572	Disease GUDJ_psooriasis up
36	-6.99	NULL	8 / 53	BP mRNA transport
37	-6.92	NULL	11 / 56	CC chromosome, centromeric region
38	-6.88	NULL	20 / 148	BP G1/S transition of mitotic cell cycle
39	-6.76	NULL	3 / 14	BP purine nucleotide biosynthetic process
40	-6.67	NULL	15 / 150	BP protein folding

p-values

