

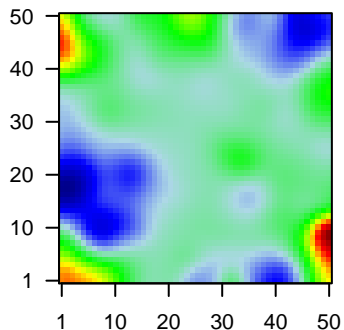
# GW\_117

## Global Summary

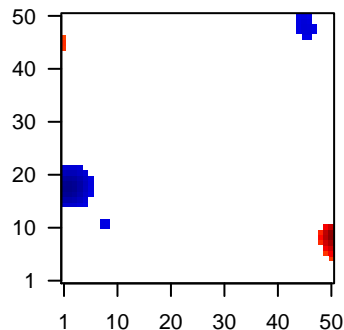
%DE = 0.16  
 # genes with fdr < 0.2 = 2047 ( 1206 + / 841 - )  
 # genes with fdr < 0.1 = 1632 ( 1028 + / 604 - )  
 # genes with fdr < 0.05 = 1397 ( 914 + / 483 - )  
 # genes with fdr < 0.01 = 970 ( 709 + / 261 - )  
  
 # genes in genesets = 16332

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

Profile



Regulated Spots



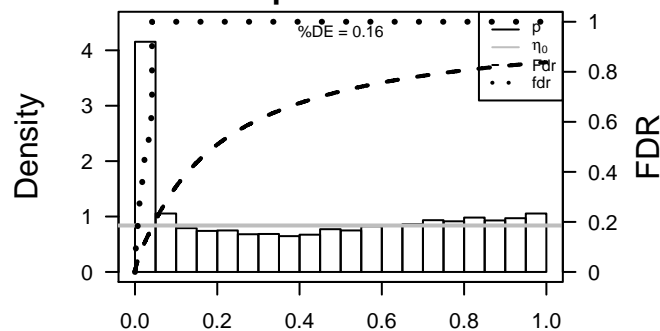
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	9510	1.31	2e-16	2e-14	6 x 1 ADAM metallopeptidase with thrombospondin type 1 motif, 1
2	10551	2.23	2e-16	2e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	401138	3.08	2e-16	2e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
4	147463	1.59	2e-16	2e-14	25 x 50 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
5	147495	1.87	2e-16	2e-14	2 x 44 adenomatosis polyposis coli down-regulated 1 [Source:HGNC Symbol;Acc:10551]
6	347	1.91	2e-16	2e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
7	563	1.31	2e-16	2e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol;Acc:10551]
8	25805	1.62	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC Symbol;Acc:10551]
9	80341	2.25	2e-16	2e-14	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symbol;Acc:10551]
10	440712	1.3	2e-16	2e-14	1 x 39 chromosome 1 open reading frame 186 [Source:HGNC Symbol;Acc:10551]
11	92747	4.33	2e-16	2e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:10551]
12	352999	3.07	2e-16	2e-14	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbol;Acc:10551]
13	760	1.82	2e-16	2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
14	26256	1.47	2e-16	2e-14	50 x 50 calcium binding tyrosine-(Y)-phosphorylation regulated [Source:HGNC Symbol;Acc:10551]
15	51806	1.85	2e-16	2e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
16	83643	1.34	2e-16	2e-14	7 x 1 coiled-coil domain containing 3 [Source:HGNC Symbol;Acc:10551]
17	6347	1.44	2e-16	2e-14	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:10551]
18	6364	-1.83	2e-16	2e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:10551]
19	3075	1.31	2e-16	2e-14	50 x 7 complement factor H [Source:HGNC Symbol;Acc:4883]
20	56994	1.65	2e-16	2e-14	50 x 16 choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	19.96	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	19.3	NULL	1182	CC extracellular region
3	16.63	NULL	683	CC extracellular space
4	15.74	NULL	250	LymphocyteENZ_Stromal signature 1
5	12.7	NULL	190	CC extracellular matrix
6	11.24	NULL	553	Cancer Lembecke_Colonc Inflammation
7	11.18	NULL	183	CC proteinaceous extracellular matrix
8	11.18	NULL	242	BP extracellular matrix organization
9	9.72	NULL	403	BP cell adhesion
10	9.65	NULL	5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
11	8.73	NULL	2659	CC plasma membrane
12	8.7	NULL	5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
13	8.62	NULL	1146	TF HEBENSTREIT_low expression TF
14	8.57	NULL	83	CC basement membrane
15	8.54	NULL	375	Disease GUDJ_poriasis down
16	8.18	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	8.11	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
18	8.11	NULL	3274	CC integral to membrane
19	8.1	NULL	112	MF heparin binding
20	8	NULL	15	GSEA C2FRIDMAN_IMMORTALIZATION_DN
<i>Underexpressed</i>				
1	-11.66	NULL	142	Glo willscher_GBM_Verhaak-CL_expression_C_up
2	-11.66	NULL	142	Glo willscher_GBM_Verhaak-PNmut_expression_C_down
3	-11.23	NULL	4640	CC nucleus
4	-10.07	NULL	949	CC nucleoplasm
5	-8.75	NULL	649	BP gene expression
6	-8.48	NULL	370	BP mitotic cell cycle
7	-8.14	NULL	595	MF RNA binding
8	-7.75	NULL	253	BP translation
9	-7.47	NULL	153	MF structural constituent of ribosome
10	-7.37	NULL	298	BP DNA repair
11	-7.24	NULL	940	MF nucleic acid binding
12	-7.15	NULL	1749	MF DNA binding
13	-7.15	NULL	1233	TF KIM_MYC targets
14	-6.97	NULL	242	BP RNA metabolic process
15	-6.89	NULL	167	CC ribosome
16	-6.6	NULL	1318	CC mitochondrion
17	-6.5	NULL	96	BP rRNA processing
18	-6.5	NULL	128	BP translational initiation
19	-6.32	NULL	219	BP mRNA metabolic process
20	-6.26	NULL	287	BP viral process

p-values



# GW\_117

## Local Summary

%DE = 0.81  
 # metagenes = 16  
 # genes = 221  
 # genes in genesets = 220

# genes with  $fdr < 0.1$  = 145 ( 143 + / 2 - )  
 # genes with  $fdr < 0.05$  = 130 ( 129 + / 1 - )  
 # genes with  $fdr < 0.01$  = 121 ( 120 + / 1 - )

<r> metagenes = 0.91  
 <r> genes = 0.3

<FC> = 0.72  
 <shrinkage-t> = 25.16  
 <p-value> = 0  
 <fdr> = 0.37

## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	10551	2.23	2e-16	3e-16	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	347	1.91	2e-16	3e-16	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
3	563	1.31	2e-16	3e-16	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol]
4	80341	2.25	2e-16	3e-16	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symb]
5	92747	4.33	2e-16	3e-16	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb]
6	352999	3.07	2e-16	3e-16	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbc]
7	3075	1.31	2e-16	3e-16	50 x 7 complement factor H [Source:HGNC Symbol;Acc:4883]
8	1359	1.3	2e-16	3e-16	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:612]
9	1396	1.28	2e-16	3e-16	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:612]
10	1755	1.71	2e-16	3e-16	50 x 10 deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:612]
11	2487	1.54	2e-16	3e-16	50 x 5 frizzled-related protein [Source:HGNC Symbol;Acc:3959]
12	3158	1.45	2e-16	3e-16	50 x 10 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
13	57535	1.57	2e-16	3e-16	50 x 10 KIAA1324 [Source:HGNC Symbol;Acc:29618]
14	124220	2.75	2e-16	3e-16	50 x 10 zymogen granule protein 16B [Source:HGNC Symbol;Acc:30720]
15	389816	2.45	2e-16	3e-16	50 x 10 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc:612]
16	4057	2.05	2e-16	3e-16	50 x 10 lactotransferrin [Source:HGNC Symbol;Acc:6720]
17	4239	1.68	2e-16	3e-16	50 x 6 microfibrillar-associated protein 4 [Source:HGNC Symbol;Acc:612]
18	4256	1.89	2e-16	3e-16	50 x 6 matrix Gla protein [Source:HGNC Symbol;Acc:7060]
19	4477	3.4	2e-16	3e-16	50 x 11 microseminoprotein, beta- [Source:HGNC Symbol;Acc:7372]
20	4824	1.8	2e-16	3e-16	50 x 10 NK3 homeobox 1 [Source:HGNC Symbol;Acc:7838]

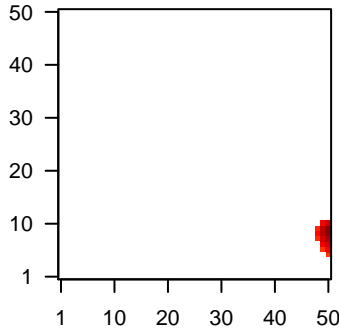
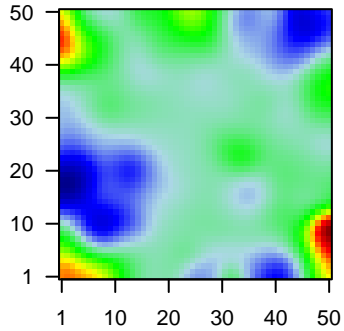
## Local Geneset Analysis

Overexpression

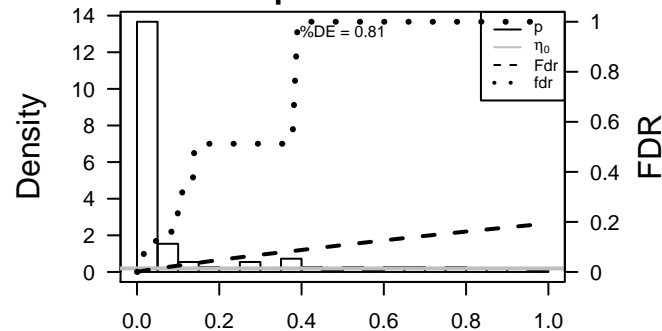
Rank	GSZ	p-value	#in/all	Geneset
1	46.72	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	16.8	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	14.89	NULL	2 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
4	14.28	NULL	2 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
5	13.29	NULL	57 / 1182	CC extracellular region
6	12.99	NULL	3 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
7	11.87	NULL	2 / 15	GSEA C2OPES_METHYLATED_IN_COLON_CANCER_UP
8	11.85	NULL	43 / 683	CC extracellular space
9	11.59	NULL	2 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
10	11.46	NULL	1 / 9	GSEA C2GOUYER_TATI_TARGETS_UP
11	10.66	NULL	36 / 375	Disease GUDJ_psooriasis down
12	9.78	NULL	4 / 7	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
13	9.32	NULL	5 / 61	CC secretory granule
14	9.28	NULL	3 / 14	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_UP
15	9.25	NULL	1 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
16	9.23	NULL	2 / 7	TF Tissu/AQUERIZAS_Appendix
17	8.79	NULL	1 / 15	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
18	8.68	NULL	3 / 17	BP iron ion transport
19	8.44	NULL	2 / 15	GSEA C2KORKOLA_TERATOMA
20	8.37	NULL	4 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
21	8.3	NULL	2 / 15	GSEA C2ABE_INNER_EAR
22	8.1	NULL	2 / 8	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP
23	7.85	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_CARCINOMA_UP
24	7.84	NULL	2 / 4	GSEA C2LU_TUMOR_ENDOTHELIAL_MARKERS_DN
25	7.69	NULL	2 / 10	Glio wilscher_GBM_LTSwt_proteomics-G_UP
26	7.47	NULL	2 / 16	GSEA C2AIYAR_COBRA1_TARGETS_UP
27	7.46	NULL	6 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
28	7.45	NULL	2 / 12	GSEA C2LEE_LIVER_CANCER_MYC_DN
29	7.26	NULL	2 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
30	7.2	NULL	2 / 15	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
31	7.12	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
32	7.12	NULL	2 / 14	GSEA C2PENG_RAPAMYCIN_RESPONSE_UP
33	6.92	NULL	5 / 20	BP complement activation
34	6.85	NULL	3 / 37	BP digestion
35	6.73	NULL	5 / 85	Glio laffaire_hypermeth_LGG_vs_control
36	6.63	NULL	1 / 15	GSEA C2HORIUCHI_WTAP_TARGETS_UP
37	6.63	NULL	1 / 15	GSEA C2SENESE_HDAC1_TARGETS_UP
38	6.63	NULL	1 / 15	GSEA C2DOUGLAS_BMI1_TARGETS_DN
39	6.59	NULL	4 / 53	Glio Christensen_hypermethylated_in_primary_glioblastoma
40	6.52	NULL	2 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP

Profile

Spot



p-values



# GW\_117

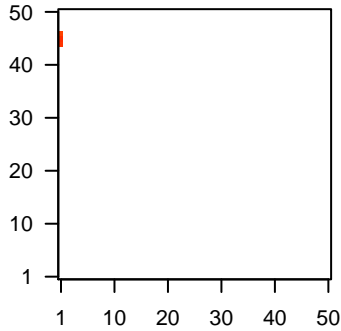
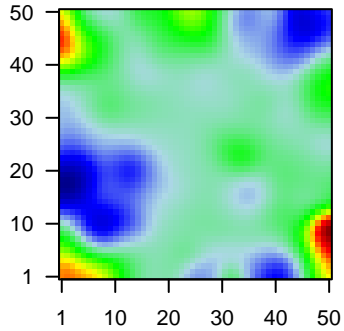
## Local Summary

%DE = 0.83  
 # metagenes = 3  
 # genes = 71  
 # genes in genesets = 71  
 # genes with  $fdr < 0.1$  = 53 ( 47 + / 6 - )  
 # genes with  $fdr < 0.05$  = 47 ( 43 + / 4 - )  
 # genes with  $fdr < 0.01$  = 46 ( 42 + / 4 - )

<r> metagenes = 0.98  
 <r> genes = 0.45  
 <FC> = 0.56  
 <shrinkage-t> = 19.62  
 <p-value> = 0  
 <fdr> = 0.31

Profile

Spot



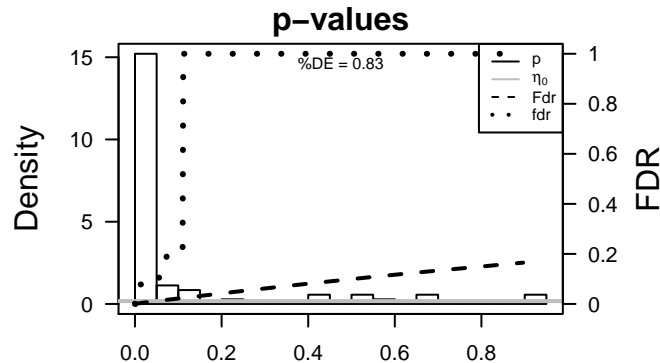
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	760	1.82	2e-16	3e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	9635	1.86	2e-16	3e-16	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
3	9547	2.4	2e-16	3e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
4	2167	-1.51	2e-16	3e-16	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
5	56169	1.79	2e-16	3e-16	1 x 46 gasdermin C [Source:HGNC Symbol;Acc:7151]
6	3489	1.66	2e-16	3e-16	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
7	3861	1.41	2e-16	3e-16	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
8	3868	1.54	2e-16	3e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
9	9119	2.12	2e-16	3e-16	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]
10	56901	1.24	4e-16	4e-14	1 x 44 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-li
11	5317	1.24	4e-16	4e-14	1 x 46 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [ε
12	5803	1.18	8e-15	4e-14	1 x 45 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
13	143686	1.18	9e-15	4e-14	1 x 44 sestrin 3 [Source:HGNC Symbol;Acc:23060]
14	113146	1.18	1e-14	3e-13	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
15	3613	1.15	5e-14	3e-13	1 x 46 inositol(myo)-1(or 4)-monophosphatase 2 [Source:HGNC Sy
16	2697	1.15	5e-14	2e-12	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;v
17	978	1.12	2e-13	1e-10	1 x 46 cytidine deaminase [Source:HGNC Symbol;Acc:1712]
18	771	1.04	8e-12	5e-10	1 x 44 carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
19	27065	1	5e-11	2e-09	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1)
20	4753	0.97	2e-10	4e-08	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	32.09	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
2	31.55	NULL	5 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	20.14	NULL	2 / 7	GSEA C2YE_METASTATIC_LIVER_CANCER
4	18.67	NULL	3 / 25	BP response to zinc ion
5	17.68	NULL	9 / 82	CC intermediate filament
6	17.51	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
7	17.02	NULL	3 / 13	BP intermediate filament cytoskeleton organization
8	16.97	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
9	15.82	NULL	4 / 44	CC keratin filament
10	14.59	NULL	1 / 11	GSEA C2TO_PTTG1_TARGETS_UP
11	14.58	NULL	2 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
12	14.26	NULL	2 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP
13	12.58	NULL	1 / 14	GSEA C2MAHADEVAN_IMATINIB_RESISTANCE_UP
14	12.58	NULL	1 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
15	12.51	NULL	1 / 9	GSEA C2HEDVAT_ELF4_TARGETS_UP
16	12.47	NULL	12 / 135	H.Tiss WIRTH_Mucosa
17	12.3	NULL	2 / 17	BP morphogenesis of an epithelium
18	12.06	NULL	1 / 15	GSEA C2FRIDMAN_IMMORTALIZATION_DN
19	12.06	NULL	1 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
20	11.85	NULL	2 / 12	BP hemidesmosome assembly
21	11.6	NULL	1 / 16	GSEA C2BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
22	11.46	NULL	2 / 22	BP bicarbonate transport
23	11.36	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
24	11.36	NULL	2 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_UP
25	11.21	NULL	6 / 21	CC desmosome
26	11.01	NULL	1 / 11	BP positive regulation of bone resorption
27	10.97	NULL	2 / 15	GSEA C2STOSI_RESPONSE_TO ESTRADIOL
28	10.63	NULL	2 / 25	BP one-carbon metabolic process
29	10.43	NULL	1 / 12	GSEA C2HO_LIVER_CANCER_VASCULAR_INVASION
30	10.28	NULL	1 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
31	9.67	NULL	2 / 35	CC cell periphery
32	9.48	NULL	1 / 12	GSEA C2SANCHEZ_MDM2_TARGETS
33	9.48	NULL	1 / 14	BP positive regulation of osteoclast differentiation
34	9.48	NULL	1 / 14	GSEA C2NIELSEN_GIST
35	9.38	NULL	8 / 186	MF structural molecule activity
36	9.34	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
37	9.31	NULL	1 / 15	GSEA C2DOANE_BREAST_CANCER_CLASSES_UP
38	9.24	NULL	6 / 82	MF structural constituent of cytoskeleton
39	9.22	NULL	2 / 38	BP epithelial cell differentiation
40	9.02	NULL	1 / 13	GSEA C2REACTOME_REGULATION_OF_INSULIN LIKE_GROWTH_FACT



# GW\_117

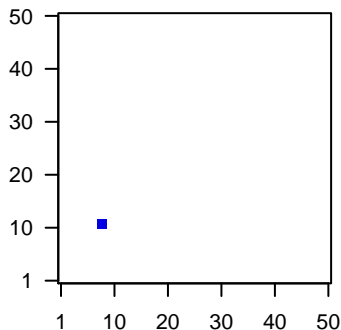
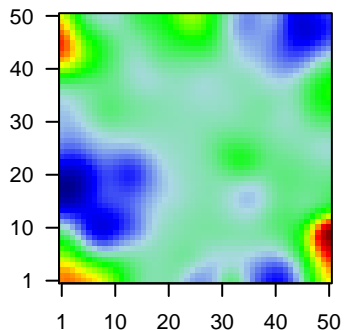
## Local Summary

%DE = 0.93  
 # metagenes = 4  
 # genes = 62  
 # genes in genesets = 62  
 # genes with  $fdr < 0.1 = 49$  ( 2 + / 47 - )  
 # genes with  $fdr < 0.05 = 39$  ( 0 + / 39 - )  
 # genes with  $fdr < 0.01 = 31$  ( 0 + / 31 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.38  
 $\langle FC \rangle = -0.32$   
 $\langle \text{shrinkage-t} \rangle = -11.2$   
 $\langle p\text{-value} \rangle = 0.01$   
 $\langle fdr \rangle = 0.54$

Profile

Spot



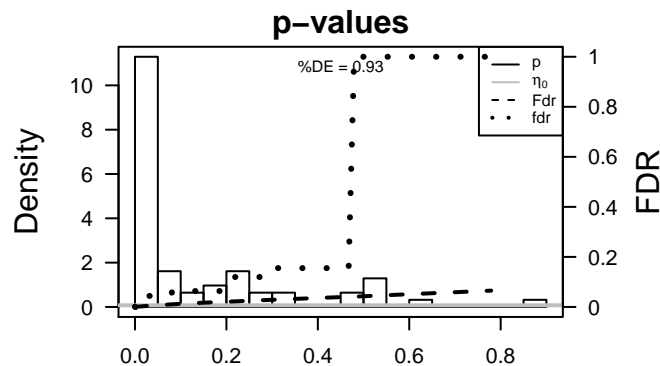
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	55643	-0.9	3e-09	3e-06	9 x 12 BTB (POZ) domain containing 2 [Source:HGNC Symbol;Acc:...
2	57176	-0.76	7e-07	5e-05	9 x 11 Valine--tRNA ligase, mitochondrial [Source:UniProtKB/TrEM...
3	56893	-0.67	1e-05	7e-05	9 x 12 ubiquitin 4 [Source:HGNC Symbol;Acc:1237]
4	116138	-0.64	3e-05	3e-04	9 x 11 kelch domain containing 3 [Source:HGNC Symbol;Acc:20704
5	147841	-0.6	9e-05	8e-04	8 x 11 SPC24, NDC80 kinetochore complex component [Source:HG...
6	51490	-0.53	5e-04	8e-04	8 x 12 chromosome 9 open reading frame 114 [Source:HGNC Synt...
7	7064	-0.52	7e-04	8e-04	8 x 12 thimet oligopeptidase 1 [Source:HGNC Symbol;Acc:11793]
8	51021	-0.51	8e-04	8e-04	8 x 11 mitochondrial ribosomal protein S16 [Source:HGNC Symbol;...
9	10432	-0.51	8e-04	8e-04	8 x 12 RNA binding motif protein 14 [Source:HGNC Symbol;Acc:142
10	54965	-0.5	1e-03	8e-04	9 x 12 phosphatidylinositol glycan anchor biosynthesis, class X [Sou...
11	10629	-0.5	1e-03	2e-03	9 x 11 TAF6--like RNA polymerase II, p300/CBP--associated factor (I...
12	93643	-0.48	2e-03	2e-03	9 x 11 tight junction associated protein 1 (peripheral) [Source:HGNC
13	6621	-0.47	2e-03	2e-03	8 x 11 small nuclear RNA activating complex, polypeptide 4, 190kDa
14	221927	-0.46	3e-03	2e-03	9 x 11 BRCA1--associated ATM activator 1 [Source:HGNC Symbol;...
15	5442	-0.46	3e-03	2e-03	8 x 11 polymerase (RNA) mitochondrial (DNA directed) [Source:HGI...
16	11165	-0.45	3e-03	2e-03	9 x 11 nudix (nucleoside diphosphate linked moiety X)--type motif 3  ...
17	692227	-0.45	3e-03	2e-03	8 x 11 small nucleolar RNA, C/D box 104 [Source:HGNC Symbol;Ac...
18	653121	-0.44	4e-03	3e-03	8 x 11 zinc finger and BTB domain containing 8A [Source:HGNC Sy...
19	64710	-0.43	5e-03	3e-03	9 x 11 nuclear casein kinase and cyclin--dependent kinase substrate
20	8189	-0.43	5e-03	3e-03	8 x 11 symplekin [Source:HGNC Symbol;Acc:22935]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-12.88	NULL	2 / 12	GSEA C2BROWNE_HCMV_INFECTION_14HR_UP
2	-11.54	NULL	1 / 12	GSEA C2BARRIER_COLON_CANCER_RECURRENCE_DN
3	-11.54	NULL	1 / 12	GSEA C2KAAB_FAILED_HEART_ATRIUM_UP
4	-10.6	NULL	1 / 14	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
5	-10.48	NULL	2 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
6	-10.22	NULL	1 / 5	GSEA C2NAGY_PCAF_COMPONENTS_HUMAN
7	-9.45	NULL	1 / 14	Cancer LIU_COMMON_CANCER_GENES
8	-9.23	NULL	2 / 13	GSEA C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
9	-8.86	NULL	2 / 14	GSEA C2KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
10	-8.86	NULL	2 / 14	GSEA C2REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
11	-8.84	NULL	1 / 4	miRNA target-122
12	-8.75	NULL	2 / 22	MF polyubiquitin binding
13	-8.54	NULL	1 / 12	GSEA C2BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_DN
14	-8.53	NULL	2 / 15	GSEA C2REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
15	-8.51	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
16	-8.51	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
17	-8.51	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
18	-8.23	NULL	2 / 16	BP preassembly of GPI anchor in ER membrane
19	-8.11	NULL	1 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
20	-7.85	NULL	1 / 8	GSEA C2NAGY_STAGA_COMPONENTS_HUMAN
21	-7.55	NULL	1 / 15	GSEA C2VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP
22	-7.53	NULL	2 / 51	CC cytoplasmic mRNA processing body
23	-7.23	NULL	2 / 12	GSEA C2TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
24	-7.19	NULL	2 / 16	GSEA C2COLLIS_PRKDC_SUBSTRATES
25	-6.96	NULL	1 / 9	GSEA C2REACTOME_RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL
26	-6.93	NULL	1 / 10	GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
27	-6.78	NULL	1 / 11	Cancer GENTLES_modul5
28	-6.75	NULL	1 / 23	Chr Chr HSCHR6_MHC_DBB
29	-6.57	NULL	1 / 11	GSEA C2KEGG_BASAL_TRANSCRIPTION_FACTORS
30	-6.56	NULL	1 / 10	GSEA C2REACTOME_TRANSCRIPTION
31	-6.51	NULL	1 / 12	GSEA C2SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
32	-6.51	NULL	1 / 12	GSEA C2DANG_REGULATED_BY_MYC_UP
33	-6.42	NULL	2 / 25	BP C-terminal protein lipidation
34	-6.31	NULL	2 / 45	miRNA target-34835
35	-6.28	NULL	2 / 26	BP GPI anchor biosynthetic process
36	-6.25	NULL	1 / 12	GSEA C2DOANE_RESPONSE_TO_ANDROGEN_UP
37	-6.25	NULL	1 / 12	GSEA C2KIM_WT1_TARGETS_12HR_UP
38	-6.25	NULL	1 / 12	GSEA C2TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
39	-6.22	NULL	1 / 13	GSEA C2KEGG_RENIN_ANGIOTENSIN_SYSTEM
40	-6.01	NULL	1 / 8	miRNA target-423





# GW\_117

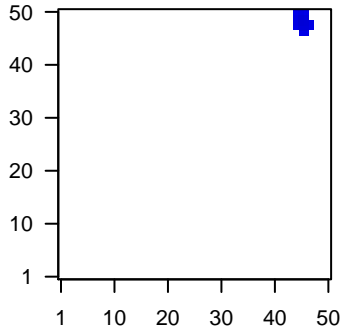
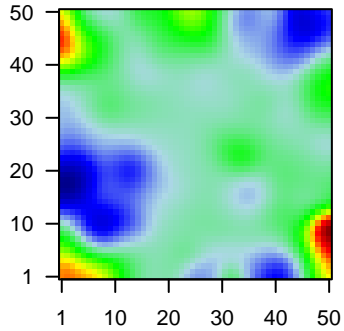
## Local Summary

%DE = 0.71  
 # metagenes = 16  
 # genes = 193  
 # genes in genesets = 191  
 # genes with  $fdr < 0.1 = 106$  ( 4 + / 102 - )  
 # genes with  $fdr < 0.05 = 94$  ( 2 + / 92 - )  
 # genes with  $fdr < 0.01 = 50$  ( 1 + / 49 - )

<r> metagenes = 0.96  
 <r> genes = 0.45  
 <FC> = -0.33  
 <shrinkage-t> = -11.68  
 <p-value> = 0.01  
 <fdr> = 0.55

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3148	-1.13	1e-13	4e-11	46 x 46 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
2	51659	-1.09	8e-13	6e-11	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
3	9918	-1.07	2e-12	4e-10	45 x 49 non-SMC condensin I complex, subunit D2 [Source:HGNC S
4	116028	-1.04	8e-12	2e-08	46 x 47 RecQ mediated genome instability 2 [Source:HGNC Symbol;
5	55839	-0.96	3e-10	4e-08	44 x 50 centromere protein N [Source:HGNC Symbol;Acc:30873]
6	79682	-0.92	2e-09	4e-08	46 x 47 centromere protein U [Source:HGNC Symbol;Acc:21348]
7	899	-0.92	2e-09	4e-08	45 x 46 cyclin F [Source:HGNC Symbol;Acc:1591]
8	4171	-0.91	2e-09	2e-07	46 x 48 minichromosome maintenance complex component 2 [Source
9	51203	-0.88	7e-09	1e-06	45 x 48 nucleolar and spindle associated protein 1 [Source:HGNC Sy
10	113130	-0.85	3e-08	1e-06	44 x 49 cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
11	81620	-0.83	6e-08	1e-06	45 x 47 chromatin licensing and DNA replication factor 1 [Source:HGI
12	10635	-0.82	7e-08	1e-06	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
13	2178	-0.82	8e-08	1e-05	46 x 49 Fanconi anemia, complementation group E [Source:HGNC S
14	78995	-0.77	4e-07	1e-05	46 x 46 chromosome 17 open reading frame 53 [Source:HGNC Synt
15	10721	-0.75	8e-07	1e-05	46 x 48 polymerase (DNA directed), theta [Source:HGNC Symbol;Acc
16	3833	-0.75	9e-07	1e-05	45 x 48 kinesin family member C1 [Source:HGNC Symbol;Acc:6389]
17	54830	-0.73	1e-06	1e-05	45 x 49 nucleoporin 62kDa C-terminal like [Source:HGNC Symbol;Ac
18	387103	-0.73	2e-06	1e-05	45 x 49 centromere protein W [Source:HGNC Symbol;Acc:21488]
19	55215	-0.73	2e-06	3e-05	45 x 48 Fanconi anemia, complementation group I [Source:HGNC Sy
20	83461	-0.71	3e-06	3e-05	44 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:1

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-53.43	NULL	73 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-53.43	NULL	73 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-28.31	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
4	-27.84	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	-27.68	NULL	8 / 16	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
6	-27.59	NULL	23 / 57	Glio developing astrocytes
7	-27.38	NULL	10 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
8	-26.94	NULL	6 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
9	-26.8	NULL	65 / 370	BP mitotic cell cycle
10	-26.8	NULL	14 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
11	-25.92	NULL	9 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
12	-25.73	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
13	-24.42	NULL	9 / 15	GSEA C2Y_AGING_MIDDLE_DN
14	-24.35	NULL	11 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
15	-24.31	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
16	-24.21	NULL	8 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
17	-24.14	NULL	8 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
18	-24.03	NULL	7 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
19	-23.89	NULL	6 / 9	GSEA C2REACTOME_CELL_CYCLE_CHECKPOINTS
20	-23.61	NULL	6 / 16	GSEA C2Y_AGING_PREMATURE_DN
21	-23.44	NULL	6 / 12	BP mitotic chromosome condensation
22	-23.33	NULL	6 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
23	-23.09	NULL	7 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
24	-22.75	NULL	7 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
25	-22.5	NULL	9 / 16	GSEA C2SIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
26	-22.18	NULL	67 / 530	Cancer Lembcke_Normal vs Adenoma
27	-21.44	NULL	32 / 149	BP DNA replication
28	-21.14	NULL	13 / 30	BP DNA strand elongation involved in DNA replication
29	-21.14	NULL	8 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
30	-20.86	NULL	9 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
31	-20.77	NULL	8 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
32	-20.72	NULL	7 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
33	-20.7	NULL	8 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
34	-19.77	NULL	6 / 15	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
35	-19.58	NULL	8 / 22	BP CENP-A containing nucleosome assembly at centromere
36	-19.34	NULL	34 / 232	BP mitosis
37	-19.08	NULL	8 / 15	GSEA C2CHANG_CYCLING_GENES
38	-18.99	NULL	6 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
39	-18.67	NULL	9 / 18	BP spindle organization
40	-18.45	NULL	7 / 11	GSEA C2KALMA_E2F1_TARGETS

