

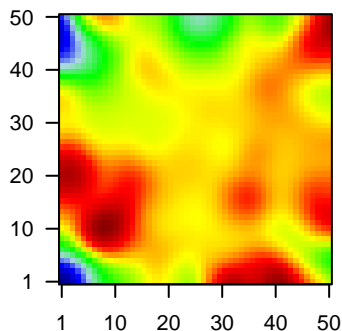
# GW\_305

## Global Summary

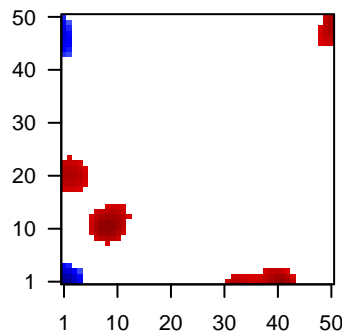
%DE = 0.15  
 # genes with fdr < 0.2 = 1949 ( 1019 + / 930 - )  
 # genes with fdr < 0.1 = 1522 ( 787 + / 735 - )  
 # genes with fdr < 0.05 = 1220 ( 616 + / 604 - )  
 # genes with fdr < 0.01 = 859 ( 413 + / 446 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.1  
 <fdr> = 0.85

Profile



Regulated Spots



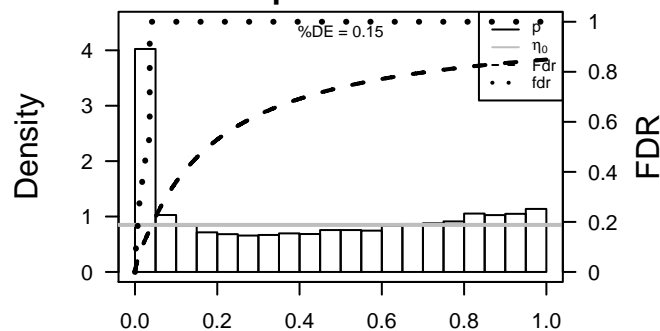
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	131	1.88	2e-16 4e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	10551	1.8	2e-16 4e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	57016	-2.35	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	-1.7	2e-16 4e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
5	216	1.75	2e-16 4e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
6	200810	1.81	2e-16 4e-14	49 x 50 ALG1, chitobiosylidiphosphodolichol beta-mannosyltransferas
7	249	1.72	2e-16 4e-14	6 x 1 alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
8	655	1.7	2e-16 4e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
9	664	-1.65	2e-16 4e-14	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK
10	339512	2.59	2e-16 4e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
11	375791	-1.72	2e-16 4e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
12	760	-2.12	2e-16 4e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	857	-1.65	2e-16 4e-14	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
14	6364	1.7	2e-16 4e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
15	1048	1.67	2e-16 4e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
16	4680	1.85	2e-16 4e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
17	9076	-1.76	2e-16 4e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
18	54102	1.71	2e-16 4e-14	50 x 10 chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2t
19	84518	-2.02	2e-16 4e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
20	22837	-1.79	2e-16 4e-14	6 x 50 cordon-bleu WH2 repeat protein-like 1 [Source:HGNC Symb

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.12	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
2	7.97	NULL	51	BP type I interferon signaling pathway
3	7.95	NULL	1135	Chr Chr 19
4	7.71	NULL	1749	MF DNA binding
5	7.13	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
6	7.04	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	6.75	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	6.5	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
9	6.05	NULL	52	Chr Chr H5CHR6_MHC_QBL
10	6.04	NULL	918	Chr Chr 17
11	5.81	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	5.62	NULL	11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	5.37	NULL	1581	BP regulation of transcription, DNA-dependent
14	5.34	NULL	519	Chr Chr 14
15	5.29	NULL	940	MF nucleic acid binding
16	5.15	NULL	1318	CC mitochondrion
17	5.14	NULL	1574	BP transcription, DNA-templated
18	5.09	NULL	4640	CC nucleus
19	5.03	NULL	6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
20	5.02	NULL	866	Chr Chr 12
<i>Underexpressed</i>				
1	-17.03	NULL	250	Lymphoma ENZ_Stromal signature 1
2	-15	NULL	135	H.Tiss WIRTH_Mucosa
3	-13.83	NULL	1182	CC extracellular region
4	-13.78	NULL	683	CC extracellular space
5	-13.62	NULL	76	BP epidermis development
6	-13.56	NULL	190	CC extracellular matrix
7	-12.75	NULL	242	BP extracellular matrix organization
8	-12.55	NULL	21	CC cornified envelope
9	-12.45	NULL	572	Disease GUDJ_psooriasis up
10	-12.29	NULL	553	Cancer Lembecke_Colonc Inflammation
11	-12.16	NULL	53	BP keratinocyte differentiation
12	-11.78	NULL	42	BP keratinization
13	-11.23	NULL	16	MMML C6CIEJ_MMML 1
14	-10.21	NULL	19	BP peptide cross-linking
15	-9.68	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	-9.68	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	-9.68	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	-9.68	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
19	-9.59	NULL	35	Glio Colman_survival_associated
20	-9.57	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP

p-values



# GW\_305

## Local Summary

%DE = 0.67  
 # metagenes = 30  
 # genes = 430  
 # genes in genesets = 401

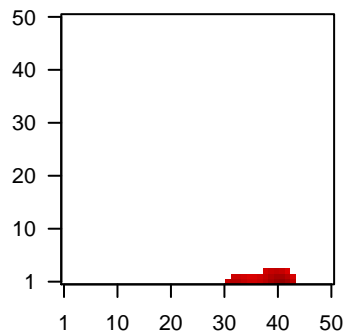
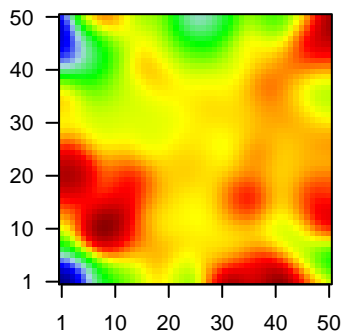
# genes with  $fdr < 0.1$  = 197 ( 185 + / 12 - )  
 # genes with  $fdr < 0.05$  = 172 ( 162 + / 10 - )  
 # genes with  $fdr < 0.01$  = 117 ( 111 + / 6 - )

<r> metagenes = 0.79  
 <r> genes = 0.28

<FC> = 0.38  
 <shrinkage-t> = 13.28  
 <p-value> = 0.01  
 <fdr> = 0.59

Profile

Spot



## Local Genelist

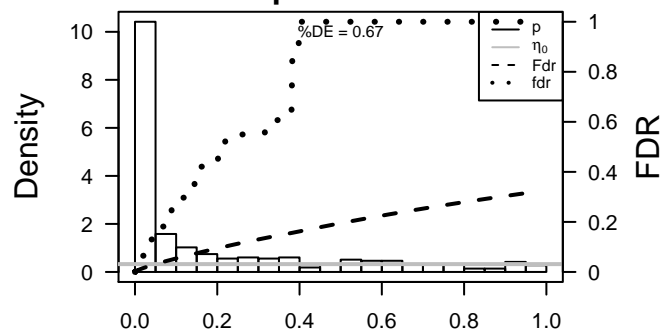
Rank	ID	log(FC)	fdr	p-value	Description
1	7453	2.35	2e-16	3e-14	tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1:
2	9636	1.58	1e-15	5e-13	ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:406
3	29944	1.58	1e-15	5e-13	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187
4	684	1.55	4e-15	6e-12	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
5	6773	1.49	5e-14	2e-11	signal transducer and activator of transcription 2, 113kDa [So
6	6772	1.44	3e-13	2e-11	signal transducer and activator of transcription 1, 91kDa [Sou
7	629	1.43	4e-13	3e-11	complement factor B [Source:HGNC Symbol;Acc:1037]
8	55008	1.42	7e-13	3e-11	HECT and RLD domain containing E3 ubiquitin protein ligase
9	84875	1.41	7e-13	7e-10	poly (ADP-ribose) polymerase family, member 10 [Source:HC
10	10964	1.35	7e-12	7e-10	interferon-induced protein 44-like [Source:HGNC Symbol;Ac
11	64108	1.34	1e-11	2e-09	receptor (chemosensory) transporter protein 4 [Source:HGNC
12	4599	1.2	3e-11	2e-09	myxovirus (influenza virus) resistance 1, interferon-inducible
13	3959	1.29	5e-11	2e-09	lectin, galactoside-binding, soluble, 3 binding protein [Source
14	80233	1.29	6e-11	6e-09	chromosome 17 open reading frame 70 [Source:HGNC Synt
15	115362	1.27	1e-10	4e-08	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
16	404093	1.23	4e-10	4e-08	CUE domain containing 1 [Source:HGNC Symbol;Acc:31350]
17	727956	1.21	7e-10	8e-08	succinate dehydrogenase complex, subunit A, flavoprotein ps
18	6890	1.19	2e-09	8e-08	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP
19	79058	1.18	2e-09	8e-08	alveolar soft part sarcoma chromosome region, candidate 1 [
20	3430	1.18	2e-09	6e-07	interferon-induced protein 35 [Source:HGNC Symbol;Acc:53:

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	30.69	NULL	12 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
2	30.2	NULL	12 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	30.14	NULL	30 / 51	BP type I interferon signaling pathway
4	26.75	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	24.98	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
6	24.75	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	21.5	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
8	20.31	NULL	35 / 123	BP defense response to virus
9	20.15	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
10	18	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
11	17.25	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
12	16.66	NULL	14 / 31	BP negative regulation of viral genome replication
13	16.49	NULL	7 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
14	15.88	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
15	15.71	NULL	36 / 204	BP cytokine-mediated signaling pathway
16	15.64	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
17	15.38	NULL	2 / 2	MMML C2SCIEJ_MMML_27
18	15.2	NULL	4 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
19	15.05	NULL	12 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
20	14.66	NULL	6 / 12	GSEA C2TSAL_DNAJB4_TARGETS_UP
21	14.56	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
22	14.24	NULL	7 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
23	13.77	NULL	3 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
24	13.65	NULL	10 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
25	13	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
26	12.42	NULL	4 / 14	GSEA C2SANA_TNF_SIGNALING_UP
27	12.4	NULL	18 / 60	BP interferon-gamma-mediated signaling pathway
28	12.38	NULL	29 / 109	BP response to virus
29	12.3	NULL	2 / 12	H.Tiss WIRTH_Lymphocytes
30	11.79	NULL	2 / 8	GSEA C2S_TYPE_I_INTERFERON_PATHWAY
31	11.74	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
32	11.66	NULL	6 / 6	LymphomaAVE_MHCCII BL DN
33	11.52	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
34	11.4	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
35	11.34	NULL	7 / 18	MF peptide antigen binding
36	11.29	NULL	6 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
37	10.95	NULL	5 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_LB_DN
38	10.94	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
39	10.88	NULL	2 / 16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
40	10.75	NULL	33 / 274	LymphomaPANG_IL21 DN

p-values



# GW\_305

## Local Summary

%DE = 0.72  
 # metagenes = 45  
 # genes = 387  
 # genes in genesets = 382

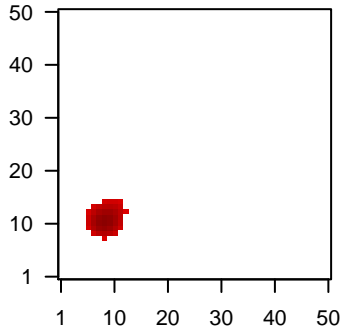
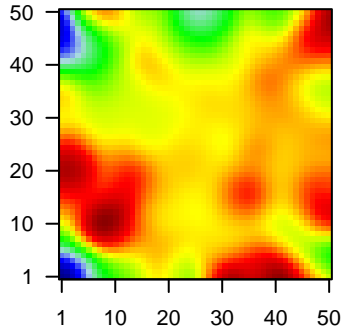
# genes with  $fdr < 0.1$  = 199 ( 197 + / 2 - )  
 # genes with  $fdr < 0.05$  = 166 ( 165 + / 1 - )  
 # genes with  $fdr < 0.01$  = 96 ( 95 + / 1 - )

<r> metagenes = 0.9  
 <r> genes = 0.25

<FC> = 0.4  
 <shrinkage-t> = 13.86  
 <p-value> = 0.02  
 <fdr> = 0.59

Profile

Spot



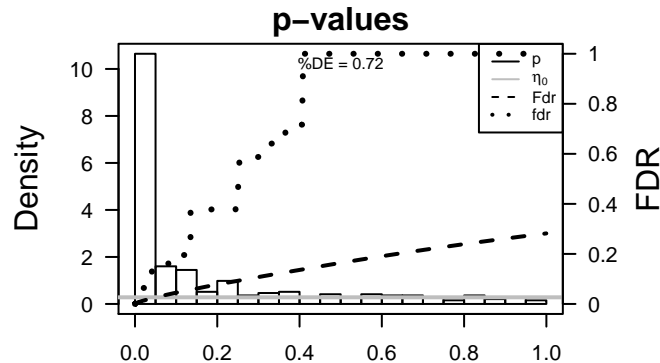
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	93109	1.37	3e-12	6e-10	10 x 12 transmembrane protein 44 [Source:HGNC Symbol;Acc:25120]
2	80728	1.35	8e-12	5e-09	10 x 11 Rho GTPase activating protein 39 [Source:HGNC Symbol;Acc:25120]
3	55653	1.29	6e-11	6e-09	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Symbol;Acc:25120]
4	2642	1.27	1e-10	4e-08	12 x 12 glucagon receptor [Source:HGNC Symbol;Acc:4192]
5	3636	1.23	4e-10	4e-06	8 x 9 inositol polyphosphate phosphatase-like 1 [Source:HGNC Symbol;Acc:25120]
6	65980	1.08	4e-08	4e-06	9 x 10 bromodomain containing 9 [Source:HGNC Symbol;Acc:25120]
7	80235	1.06	7e-08	6e-06	11 x 14 phosphatidylinositol glycan anchor biosynthesis, class Z [Source:HGNC Symbol;Acc:25120]
8	154197	1.04	1e-07	3e-05	12 x 13 poly(A)-specific ribonuclease (PARN)-like domain containing
9	254528	0.98	7e-07	3e-05	12 x 14 meiosis specific with OB domains [Source:HGNC Symbol;Acc:25120]
10	4485	0.97	8e-07	3e-05	12 x 12 macrophage stimulating 1 (hepatocyte growth factor-like) [Source:HGNC Symbol;Acc:25120]
11	9772	0.96	1e-06	3e-05	10 x 13 KIAA0195 [Source:HGNC Symbol;Acc:28983]
12	57176	0.96	1e-06	3e-05	9 x 11 Valine--tRNA ligase, mitochondrial [Source:UniProtKB/TrEMBL]
13	100128927	0.95	1e-06	1e-04	11 x 11 zinc finger and BTB domain containing 42 [Source:HGNC Symbol;Acc:25120]
14	64710	0.9	5e-06	1e-04	9 x 11 nuclear casein kinase and cyclin-dependent kinase substrate
15	140467	0.89	6e-06	1e-04	9 x 8 zinc finger protein 358 [Source:HGNC Symbol;Acc:16838]
16	8893	0.89	7e-06	1e-04	10 x 12 eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82 kDa [Source:HGNC Symbol;Acc:25120]
17	9130	0.88	7e-06	1e-04	8 x 9 family with sequence similarity 50, member A [Source:HGNC Symbol;Acc:25120]
18	54764	0.87	9e-06	1e-04	8 x 9 zinc finger, RAN-binding domain containing 1 [Source:HGNC Symbol;Acc:25120]
19	90678	0.87	9e-06	2e-04	6 x 10 leucine rich repeat and sterile alpha motif containing 1 [Source:HGNC Symbol;Acc:25120]
20	9146	0.87	1e-05	7e-04	6 x 10 hepatocyte growth factor-regulated tyrosine kinase substrate

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	8.84	NULL	12 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
2	8.72	NULL	3 / 14	GSEA_C2KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
3	8.17	NULL	2 / 9	miRNA target set miR-184
4	7.66	NULL	69 / 1135	Chr Chr 19
5	7.46	NULL	1 / 5	miRNA target set miR-205
6	6.79	NULL	2 / 16	GSEA_C2BIOCARTA_IGF1MTOR_PATHWAY
7	6.16	NULL	1 / 7	GSEA_C2ANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2
8	6.13	NULL	4 / 23	Chr Chr HSCR6_MHC_DBB
9	6.07	NULL	3 / 14	GSEA_C2RIZKI_TUMOR_INVASIVENESS_2D_DN
10	6.06	NULL	2 / 10	MF K63-linked polyubiquitin binding
11	6.05	NULL	3 / 26	BP GPI anchor biosynthetic process
12	5.89	NULL	3 / 16	BP intracellular steroid hormone receptor signaling pathway
13	5.44	NULL	4 / 24	miRNA target set miR-502
14	5.42	NULL	4 / 26	BP histone acetylation
15	5.31	NULL	2 / 12	GSEA_C2TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
16	5.16	NULL	5 / 29	miRNA target set miR-296
17	5.08	NULL	2 / 16	MF histone acetyl-lysine binding
18	5.05	NULL	2 / 15	GSEA_C2OLSSON_E2F3_TARGETS_DN
19	5.02	NULL	2 / 13	GSEA_C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
20	4.96	NULL	1 / 8	GSEA_C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
21	4.93	NULL	2 / 13	GSEA_C2WALLACE_JAK2_TARGETS_UP
22	4.91	NULL	2 / 13	CC STAGA complex
23	4.86	NULL	2 / 10	BP positive regulation of macroautophagy
24	4.81	NULL	2 / 11	GSEA_C2LAIHO_COLORECTAL_CANCER_SERRATED_DN
25	4.8	NULL	2 / 10	GSEA_C2BOYALTY_LIVER_CANCER_SUBCLASS_G6_DN
26	4.79	NULL	2 / 14	GSEA_C2REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
27	4.74	NULL	2 / 8	miRNA target set miR-423
28	4.69	NULL	4 / 19	MF hydrolase activity, acting on acid anhydrides, in phosphorus-contain
29	4.68	NULL	2 / 16	GSEA_C2KENNY_CTNNB1_TARGETS_UP
30	4.63	NULL	2 / 8	GSEA_C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
31	4.59	NULL	2 / 15	GSEA_C2REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
32	4.59	NULL	5 / 29	BP lysosome organization
33	4.55	NULL	2 / 27	BP response to starvation
34	4.46	NULL	39 / 717	Chr Chr 16
35	4.42	NULL	1 / 13	GSEA_C2REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS
36	4.42	NULL	1 / 13	GSEA_C2REACTOME_GS_ALPHA_MEDIATED_EVENTS_IN_GLUCAGON
37	4.41	NULL	2 / 16	BP preassembly of GPI anchor in ER membrane
38	4.37	NULL	4 / 16	GSEA_C2SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
39	4.32	NULL	2 / 15	GSEA_C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
40	4.31	NULL	3 / 24	BP tissue development



# GW\_305

## Local Summary

%DE = 0.57  
 # metagenes = 29  
 # genes = 288  
 # genes in genesets = 283

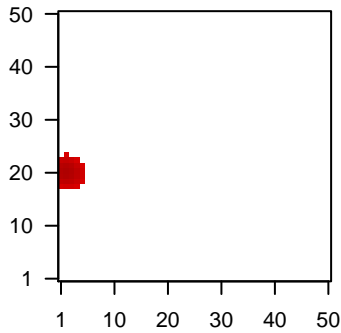
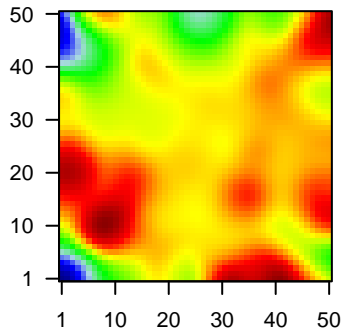
# genes with  $fdr < 0.1 = 99$  ( 97 + / 2 - )  
 # genes with  $fdr < 0.05 = 62$  ( 60 + / 2 - )  
 # genes with  $fdr < 0.01 = 24$  ( 23 + / 1 - )

<r> metagenes = 0.96  
 <r> genes = 0.28

<FC> = 0.32  
 <shrinkage-t> = 11.05  
 <p-value> = 0.05  
 <fdr> = 0.71

Profile

Spot



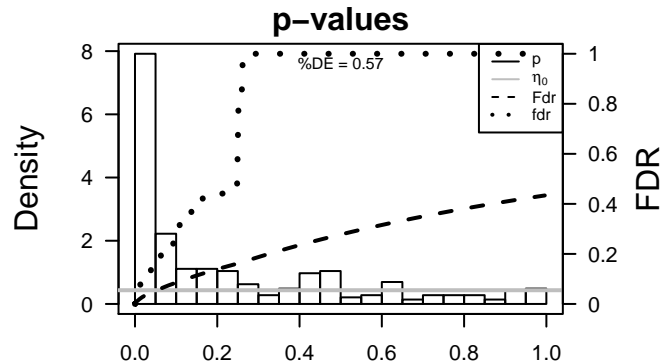
## Local Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	80154	1.03	2e-07 4e-05	1 x 23
2	728489	0.99	5e-07 1e-04	1 x 19 DNL-type zinc finger [Source:HGNC Symbol;Acc:33879]
3	26519	0.95	1e-06 5e-04	1 x 19 translocase of inner mitochondrial membrane 10 homolog (ye
4	284085	0.9	5e-06 6e-04	3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
5	51181	0.87	1e-05 6e-04	2 x 21 dicarbonyl/L-xylulose reductase [Source:HGNC Symbol;Acc:
6	112724	0.84	2e-05 6e-04	1 x 23 retinol dehydrogenase 13 (all-trans-9-cis) [Source:HGNC Sy
7	5652	0.83	3e-05 6e-04	1 x 22 protease, serine, 8 [Source:HGNC Symbol;Acc:9491]
8	64978	0.82	3e-05 6e-04	3 x 19 mitochondrial ribosomal protein L38 [Source:HGNC Symbol;/
9	128869	0.82	3e-05 7e-04	2 x 19 phosphatidylinositol glycan anchor biosynthesis, class U [Sou
10	51079	0.81	4e-05 4e-03	2 x 21 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
11	90990	0.78	7e-05 4e-03	1 x 23 kinesin family member C2 [Source:HGNC Symbol;Acc:29530
12	1173	0.76	1e-04 4e-03	1 x 20 adaptor-related protein complex 2, mu 1 subunit [Source:HGI
13	55168	0.76	1e-04 4e-03	2 x 20 mitochondrial ribosomal protein S18A [Source:HGNC Symbo
14	201254	0.74	2e-04 4e-03	4 x 20 stimulated by retinoic acid 13 [Source:HGNC Symbol;Acc:114
15	283991	0.73	2e-04 4e-03	4 x 22 UBA-like domain containing 2 [Source:HGNC Symbol;Acc:28
16	57407	0.72	3e-04 4e-03	1 x 20 NmrA-like family domain containing 1 [Source:HGNC Symbo
17	1468	0.71	3e-04 4e-03	2 x 22 Mitochondrial dicarboxylate carrier; Uncharacterized protein; i
18	51702	-0.71	3e-04 4e-03	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;A
19	30833	0.7	4e-04 4e-03	3 x 19 5', 3'-nucleotidase, cytosolic [Source:HGNC Symbol;Acc:171
20	60343	0.7	4e-04 4e-03	2 x 22 family with sequence similarity 3, member A [Source:HGNC S

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	11.78	NULL	76 / 1318	CC mitochondrion
2	10.9	NULL	3 / 10	MF NADH dehydrogenase activity
3	10.65	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
4	10.22	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
5	8.33	NULL	10 / 83	BP respiratory electron transport chain
6	7.99	NULL	4 / 16	GSEA C2NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
7	7.64	NULL	2 / 10	GSEA C2REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_V
8	7.61	NULL	19 / 153	MF structural constituent of ribosome
9	7.58	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
10	7.39	NULL	25 / 304	CC mitochondrial inner membrane
11	7.23	NULL	4 / 34	MF NADH dehydrogenase (ubiquinone) activity
12	7.2	NULL	14 / 152	BP cellular metabolic process
13	7.19	NULL	1 / 2	miRNA 30653-371
14	6.99	NULL	4 / 36	CC mitochondrial respiratory chain complex I
15	6.95	NULL	3 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
16	6.91	NULL	2 / 12	GSEA C2REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE
17	6.85	NULL	1 / 5	GSEA C2ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
18	6.83	NULL	2 / 7	GSEA C2PARK_HSC_MARKERS
19	6.81	NULL	4 / 15	CC mitochondrial large ribosomal subunit
20	6.72	NULL	3 / 15	GSEA C2KEGG_PROPANOATE_METABOLISM
21	6.26	NULL	3 / 12	BP apoptotic nuclear changes
22	6.21	NULL	2 / 13	GSEA C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
23	6.09	NULL	2 / 15	GSEA C2REACTOME_REMOVAL_OF_DNA_PATCH_CONTAINING_ABASI
24	6.01	NULL	2 / 10	GSEA C2REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS
25	5.99	NULL	20 / 253	BP translation
26	5.99	NULL	3 / 13	GSEA C2MOOHA_VOXPHOS
27	5.96	NULL	2 / 14	GSEA C2KEGG_GLYCOSYLPHOSPHATIDYLOSITOL_GPI_ANCHOR_BI
28	5.96	NULL	2 / 14	GSEA C2REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
29	5.91	NULL	15 / 167	CC ribosome
30	5.89	NULL	2 / 13	CC mitochondrial respiratory chain
31	5.81	NULL	25 / 918	Chr Chr 17
32	5.76	NULL	1 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
33	5.74	NULL	4 / 36	MF coenzyme binding
34	5.69	NULL	2 / 11	GSEA C2REACTOME_HIV_INFECTION
35	5.55	NULL	3 / 25	BP C-terminal protein lipidation
36	5.39	NULL	2 / 15	GSEA C2AIRKEE_CANCER_PRONE_RESPONSE_E2
37	5.37	NULL	5 / 47	BP protein targeting to mitochondrion
38	5.15	NULL	3 / 15	GSEA C2REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL
39	5.1	NULL	2 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
40	5.1	NULL	2 / 10	GSEA C2REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION



# GW\_305

## Local Summary

%DE = 0.64  
 # metagenes = 16  
 # genes = 203  
 # genes in genesets = 202

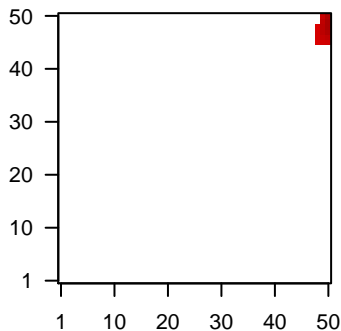
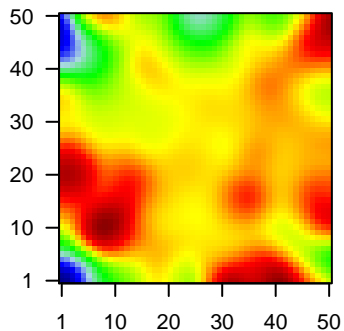
# genes with  $fdr < 0.1 = 104$  ( 90 + / 14 - )  
 # genes with  $fdr < 0.05 = 82$  ( 74 + / 8 - )  
 # genes with  $fdr < 0.01 = 65$  ( 60 + / 5 - )

<r> metagenes = 0.96  
 <r> genes = 0.26

<FC> = 0.39  
 <shrinkage-t> = 13.54  
 <p-value> = 0  
 <fdr> = 0.51

Profile

Spot



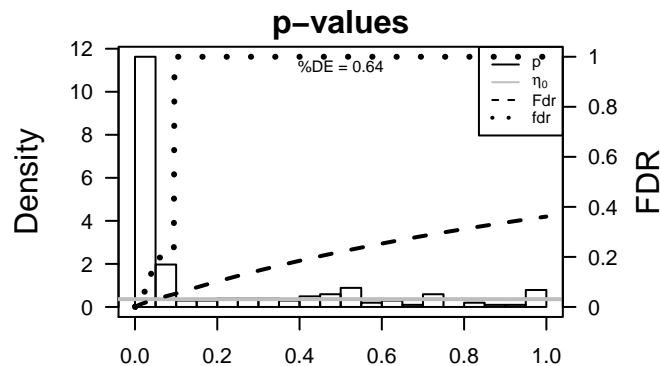
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	1.75	2e-16	2e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	200810	1.81	2e-16	2e-15	49 x 50 ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferas
3	655	1.7	2e-16	2e-15	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
4	339512	2.59	2e-16	2e-15	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
5	9076	-1.76	2e-16	2e-15	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
6	3880	2.21	2e-16	2e-15	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
7	3856	1.74	2e-16	2e-15	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
8	4922	2.3	2e-16	2e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
9	79679	1.98	2e-16	2e-15	50 x 50 V-set domain containing T cell activation inhibitor 1 [Source:†
10	256764	1.63	2e-16	2e-15	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
11	56963	1.52	1e-14	7e-13	50 x 50 repulsive guidance molecule family member a [Source:HGNC
12	286676	1.51	2e-14	3e-12	50 x 49 immunoglobulin-like domain containing receptor 1 [Source:H
13	23321	1.48	6e-14	8e-12	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:1597z
14	875	1.45	2e-13	5e-11	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15f
15	26047	-1.41	9e-13	5e-11	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
16	84707	1.39	2e-12	5e-11	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
17	56475	1.38	2e-12	8e-10	50 x 47 reprimo, TP53 dependent G2 arrest mediator candidate [Sou
18	3790	1.32	2e-11	8e-10	50 x 50 potassium voltage-gated channel, delayed-rectifier, subfamil
19	168002	1.32	2e-11	9e-09	50 x 46 dishevelled-binding antagonist of beta-catenin 2 [Source:HG
20	1690	1.26	1e-10	1e-08	50 x 47 cochlin [Source:HGNC Symbol;Acc:2180]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	16.67	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	13.57	NULL	4 / 13	BP regulation of blood vessel size
3	12.83	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
4	12.76	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
5	12.02	NULL	1 / 5	GSEA C2TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
6	11.75	NULL	3 / 14	GSEA C2KORKOLA_YOLK_SAC_TUMOR
7	11.59	NULL	3 / 16	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G1_DN
8	11.13	NULL	1 / 2	miRNA target-127
9	10.8	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
10	10.27	NULL	2 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
11	9.51	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
12	8.95	NULL	3 / 15	GSEA C2JDAYAKUMAR_MED1_TARGETS_UP
13	8.87	NULL	1 / 11	Glio neurons_glio
14	8.83	NULL	3 / 16	GSEA C2KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
15	8.72	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
16	8.69	NULL	1 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
17	8.51	NULL	1 / 11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN
18	8.28	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
19	8.21	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
20	7.88	NULL	1 / 6	GSEA C2SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
21	7.84	NULL	1 / 8	GSEA C2MCCABE_HOXC6_TARGETS_UP
22	7.83	NULL	2 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
23	7.75	NULL	2 / 19	BP anatomical structure formation involved in morphogenesis
24	7.73	NULL	1 / 13	GSEA C2CHEN_LUNG_CANCER_SURVIVAL
25	7.53	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
26	7.51	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
27	7.51	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
28	7.44	NULL	2 / 16	GSEA C2MENSE_HYPOXIA_UP
29	7.43	NULL	1 / 15	MF neuropeptide hormone activity
30	7.41	NULL	1 / 14	GSEA C2JIANG_SILENCED_BY_METHYLATION_UP
31	7.24	NULL	1 / 12	BP negative regulation of T cell activation
32	7.17	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
33	7.16	NULL	3 / 26	MF potassium channel regulator activity
34	7.13	NULL	2 / 22	BP eye development
35	7.13	NULL	1 / 15	GSEA C2LE_SKI_TARGETS_UP
36	7.13	NULL	1 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
37	7.09	NULL	1 / 5	GSEA C2NIELSEN_SCHWANNOMA_DN
38	7.07	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
39	7.07	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
40	7.03	NULL	2 / 14	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM



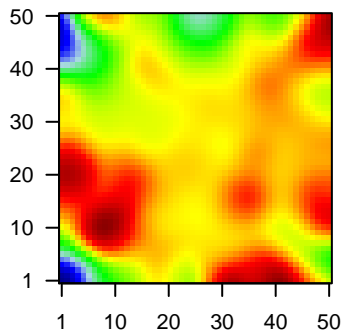
# GW\_305

## Local Summary

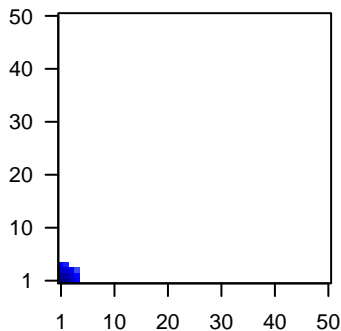
%DE = 0.92  
 # metagenes = 14  
 # genes = 218  
 # genes in genesets = 218  
 # genes with  $fdr < 0.1$  = 189 ( 4 + / 185 - )  
 # genes with  $fdr < 0.05$  = 182 ( 3 + / 179 - )  
 # genes with  $fdr < 0.01$  = 173 ( 3 + / 170 - )

<r> metagenes = 0.97  
 <r> genes = 0.41  
 <FC> = -0.82  
 <shrinkage-t> = -28.94  
 <p-value> = 0  
 <fdr> = 0.19

Profile



Spot



## Local Genelist

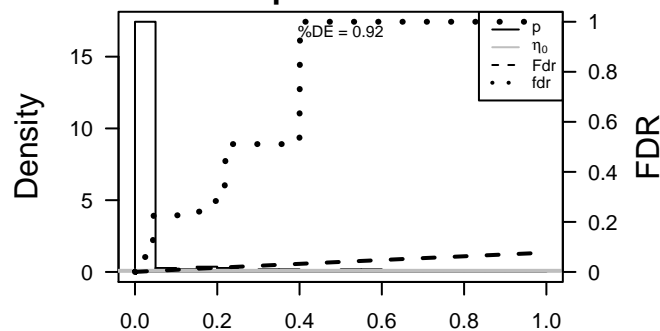
Rank	ID	log(FC)	fdr	p-value	Description
1	857	-1.65	2e-16	3e-16	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:2209]
2	1289	-1.96	2e-16	3e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
3	2274	-2	2e-16	3e-16	1 x 4 four and a half LIM domains 2 [Source:HGNC Symbol;Acc:37]
4	3040	-1.79	2e-16	3e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3553	-2.15	2e-16	3e-16	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
6	3576	-1.69	2e-16	3e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
7	3956	-1.94	2e-16	3e-16	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:11785]
8	4312	-2.11	2e-16	3e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:11785]
9	4314	-1.95	2e-16	3e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:11785]
10	55714	-1.69	2e-16	3e-16	1 x 1 teneurin transmembrane protein 3 [Source:HGNC Symbol;Acc:11785]
11	7045	-1.88	2e-16	3e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:11785]
12	7057	-1.94	2e-16	3e-16	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
13	25907	-1.9	2e-16	3e-16	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:11785]
14	3371	-1.98	2e-16	3e-16	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
15	3491	-1.55	3e-15	1e-14	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol;Acc:11785]
16	4489	-1.43	3e-15	1e-14	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
17	25878	-1.55	3e-15	1e-14	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:11785]
18	12	-1.55	4e-15	1e-14	1 x 1
19	29940	-1.54	5e-15	1e-14	1 x 4 dermatan sulfate epimerase [Source:HGNC Symbol;Acc:2114]
20	1490	-1.54	6e-15	4e-13	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2114]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-39.42	NULL	15 / 16	MMML C6S1CIEJ_MMML_1
2	-35.23	NULL	56 / 190	CC extracellular matrix
3	-31.53	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
4	-31.35	NULL	63 / 250	LymphomaL1ENZ_Stromal signature 1
5	-30.01	NULL	60 / 242	BP extracellular matrix organization
6	-28.39	NULL	30 / 69	BP extracellular matrix disassembly
7	-28.13	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
8	-27.74	NULL	27 / 64	BP collagen catabolic process
9	-26.82	NULL	7 / 11	MF platelet-derived growth factor binding
10	-25.73	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
11	-25.35	NULL	8 / 12	miRNA target-29c
12	-23.99	NULL	11 / 19	MF extracellular matrix binding
13	-22.56	NULL	12 / 35	Glio Colman_survival_associated
14	-21.7	NULL	18 / 57	MF extracellular matrix structural constituent
15	-21.55	NULL	70 / 683	CC extracellular space
16	-21.12	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
17	-20.97	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
18	-20.86	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
19	-20.62	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
20	-20.56	NULL	6 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
21	-19.89	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
22	-19.68	NULL	89 / 1182	CC extracellular region
23	-19.43	NULL	23 / 119	LymphomaBOSOLOWSKI_green total
24	-19.31	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
25	-18.81	NULL	14 / 37	BP collagen fibril organization
26	-18.46	NULL	33 / 183	CC proteinaceous extracellular matrix
27	-18.39	NULL	19 / 83	CC basement membrane
28	-18.32	NULL	6 / 16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
29	-18.05	NULL	58 / 553	Cancer Lembcke_Colonc Inflammation
30	-17.94	NULL	5 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
31	-17.53	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
32	-17.44	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
33	-17.31	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
34	-17.26	NULL	11 / 40	BP cellular response to amino acid stimulus
35	-17.02	NULL	38 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
36	-17.02	NULL	38 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
37	-17.02	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
38	-17.02	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
39	-17.01	NULL	5 / 16	GSEA C2JRS_ADIPOCYTE_DIFFERENTIATION_DN
40	-16.96	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET

p-values



# GW\_305

## Local Summary

%DE = 0.91  
 # metagenes = 15  
 # genes = 258  
 # genes in genesets = 252

# genes with  $fdr < 0.1 = 219$  ( 17 + / 202 - )  
 # genes with  $fdr < 0.05 = 217$  ( 17 + / 200 - )  
 # genes with  $fdr < 0.01 = 186$  ( 13 + / 173 - )

<r> metagenes = 0.9  
 <r> genes = 0.39

<FC> = -0.8  
 <shrinkage-t> = -28.31  
 <p-value> = 0  
 <fdr> = 0.21

## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	1.88	2e-16	1e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.35	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.7	2e-16	1e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	664	-1.65	2e-16	1e-16	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK
5	375791	-1.72	2e-16	1e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
6	760	-2.12	2e-16	1e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
7	4680	1.85	2e-16	1e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
8	84518	-2.02	2e-16	1e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
9	1382	-1.93	2e-16	1e-16	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
10	49860	-2.06	2e-16	1e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
11	1475	-1.7	2e-16	1e-16	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
12	1672	2.26	2e-16	1e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	1673	-1.88	2e-16	1e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	11072	-1.66	2e-16	1e-16	1 x 44 dual specificity phosphatase 14 [Source:HGNC Symbol;Acc:1
15	2697	-2.06	2e-16	1e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;A
16	3552	-2.26	2e-16	1e-16	1 x 43 interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
17	5653	-2.07	2e-16	1e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
18	3860	-3.54	2e-16	1e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
19	3861	-2.99	2e-16	1e-16	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
20	3868	-2.22	2e-16	1e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]

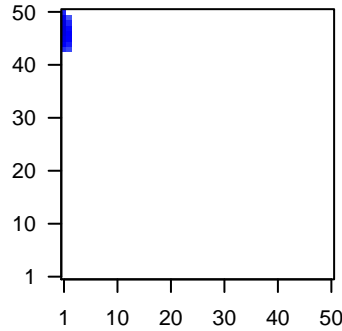
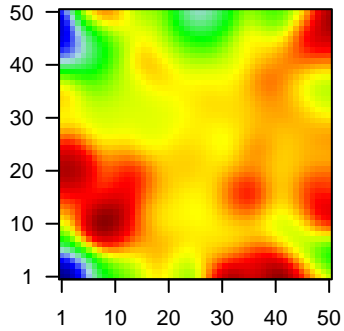
## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-41.39	NULL	77 / 135	H.Tiss WIRTH_Mucosa
2	-34.76	NULL	18 / 21	CC cornified envelope
3	-29.41	NULL	26 / 76	BP epidermis development
4	-29.03	NULL	20 / 42	BP keratinization
5	-28.32	NULL	24 / 53	BP keratinocyte differentiation
6	-23.79	NULL	100 / 572	Disease GUDJ_psoriasis up
7	-21.07	NULL	10 / 19	BP peptide cross-linking
8	-20.49	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	-18.63	NULL	3 / 8	GSEA C2LUCD_X2_TARGETS_DN
10	-17.76	NULL	21 / 82	CC intermediate filament
11	-17.07	NULL	13 / 44	CC keratin filament
12	-14.94	NULL	29 / 186	MF structural molecule activity
13	-14.37	NULL	5 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
14	-13.53	NULL	7 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
15	-13.47	NULL	7 / 38	BP epithelial cell differentiation
16	-13.33	NULL	10 / 52	BP negative regulation of endopeptidase activity
17	-13.31	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
18	-13.27	NULL	5 / 13	BP negative regulation of peptidase activity
19	-13.19	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
20	-13.02	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
21	-12.96	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
22	-12.83	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
23	-12.81	NULL	3 / 13	BP intermediate filament cytoskeleton organization
24	-12.31	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
25	-12.06	NULL	2 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
26	-11.87	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
27	-11.76	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
28	-11.63	NULL	3 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
29	-11.48	NULL	7 / 29	BP regulation of proteolysis
30	-11.45	NULL	4 / 25	BP response to zinc ion
31	-11.44	NULL	3 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
32	-11.25	NULL	4 / 15	GSEA C2LUCD_SILENCED_BY_TUMOR_MICROENVIRONMENT
33	-11.08	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
34	-11	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
35	-10.76	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HP31_DN
36	-10.61	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
37	-10.37	NULL	5 / 23	MF peptidase inhibitor activity
38	-9.98	NULL	4 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
39	-9.87	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
40	-9.84	NULL	3 / 12	BP hemidesmosome assembly

Profile

Spot



p-values

