

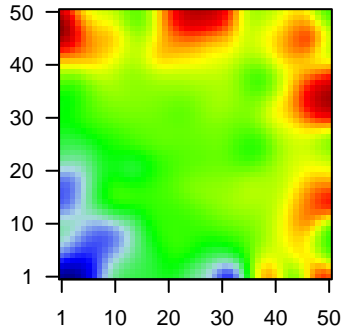
# GW\_285

## Global Summary

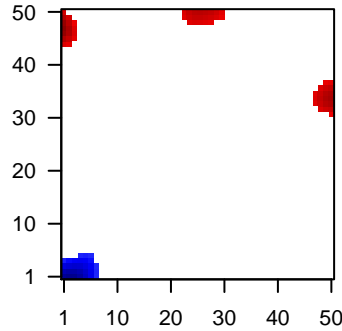
%DE = 0.14  
 # genes with  $fdr < 0.2$  = 1651 ( 882 + / 769 - )  
 # genes with  $fdr < 0.1$  = 1318 ( 721 + / 597 - )  
 # genes with  $fdr < 0.05$  = 1053 ( 587 + / 466 - )  
 # genes with  $fdr < 0.01$  = 664 ( 368 + / 296 - )  
 # genes in genesets = 16332

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

Profile



Regulated Spots



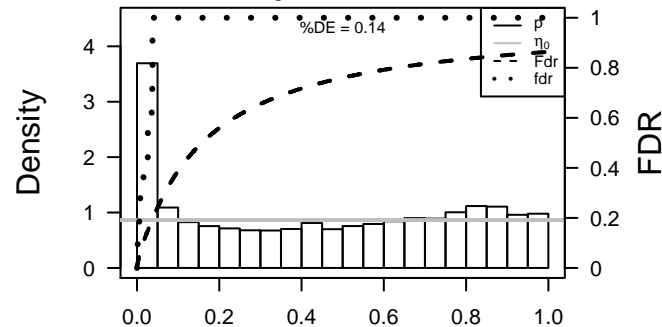
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	57016	1.77	2e-16 5e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
2	441282	1.5	2e-16 5e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	445328	-1.97	2e-16 5e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:H]
4	387695	1.39	2e-16 5e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
5	113802	1.6	2e-16 5e-14	46 x 46 HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:HC
6	260436	2.15	2e-16 5e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
7	760	1.78	2e-16 5e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	595	-1.38	2e-16 5e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
9	9076	-1.53	2e-16 5e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
10	9547	2.27	2e-16 5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
11	27065	1.64	2e-16 5e-14	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1)
12	92196	1.46	2e-16 5e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
13	55894	1.46	2e-16 5e-14	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	1.67	2e-16 5e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	2.46	2e-16 5e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	8560	1.34	2e-16 5e-14	27 x 50 delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;A
17	1776	1.37	2e-16 5e-14	48 x 12 deoxyribonuclease I-like 3 [Source:HGNC Symbol;Acc:2959]
18	1824	1.4	2e-16 5e-14	1 x 48 desmocollin 2 [Source:HGNC Symbol;Acc:3036]
19	1825	1.52	2e-16 5e-14	1 x 45 desmocollin 3 [Source:HGNC Symbol;Acc:3037]
20	94240	-1.42	2e-16 5e-14	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.32	NULL	1720	Chr Chr 1
2	13.69	NULL	135	H.Tiss WIRTH_Mucosa
3	9.86	NULL	232	Chr Chr 18
4	8.67	NULL	417	H.Tiss WIRTH_Immune system
5	8.03	NULL	15	GSEA C2P5EON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
6	7.65	NULL	53	BP keratinocyte differentiation
7	7.59	NULL	8	GSEA C2JU_CD_X2_TARGETS_DN
8	7.21	NULL	76	BP epidermis development
9	6.93	NULL	42	BP keratinization
10	6.92	NULL	511	miRNA target-starB106b
11	6.9	NULL	4640	CC nucleus
12	6.84	NULL	603	miRNA target-starB30a
13	6.59	NULL	21	CC cornified envelope
14	6.57	NULL	426	miRNA target-starB30d
15	6.57	NULL	545	miRNA target-starB30e
16	6.52	NULL	153	miRNA target-starB45b-5p
17	6.5	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
18	6.42	NULL	293	miRNA target-starB106
19	6.23	NULL	335	miRNA target-starB102-5p
20	6.22	NULL	261	miRNA target-starB30a
<i>Underexpressed</i>				
1	-9.98	NULL	190	CC extracellular matrix
2	-9.96	NULL	683	CC extracellular space
3	-9.6	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
4	-9.58	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
5	-9.49	NULL	1182	CC extracellular region
6	-8.64	NULL	16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
7	-8.24	NULL	51	BP type I interferon signaling pathway
8	-8.2	NULL	13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
9	-7.96	NULL	123	BP defense response to virus
10	-7.86	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
11	-7.86	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
12	-7.86	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
13	-7.86	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
14	-7.69	NULL	16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
15	-7.67	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
16	-7.63	NULL	242	BP extracellular matrix organization
17	-7.48	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
18	-7.41	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
19	-7.27	NULL	31	BP negative regulation of viral genome replication
20	-7.12	NULL	1135	Chr Chr 19

p-values



# GW\_285

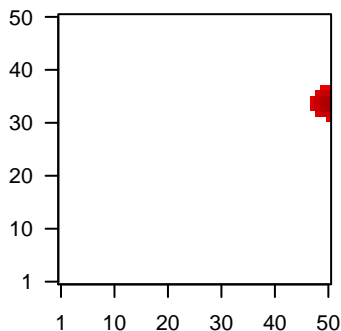
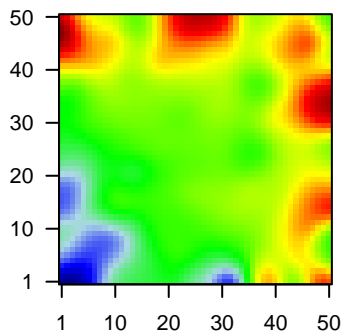
## Local Summary

%DE = 0.57  
 # metagenes = 21  
 # genes = 301  
 # genes in genesets = 301  
 # genes with  $fdr < 0.1 = 107$  ( 106 + / 1 - )  
 # genes with  $fdr < 0.05 = 71$  ( 70 + / 1 - )  
 # genes with  $fdr < 0.01 = 46$  ( 45 + / 1 - )

<r> metagenes = 0.97  
 <r> genes = 0.29  
 <FC> = 0.27  
 <shrinkage-t> = 9.63  
 <p-value> = 0.03  
 <fdr> = 0.7

Profile

Spot



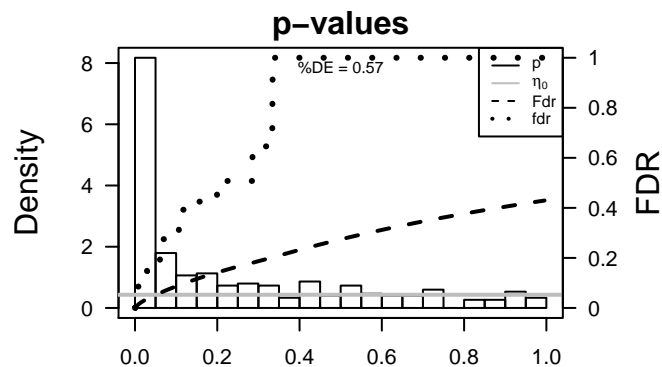
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	34	0.98	1e-09	8e-06	50 x 34 acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Source:HGNC Symbol;Acc:10040]
2	25874	0.87	6e-08	2e-05	50 x 34 mitochondrial pyruvate carrier 2 [Source:HGNC Symbol;Acc:10040]
3	9497	0.83	3e-07	2e-05	50 x 34 solute carrier family 4, sodium bicarbonate cotransporter, member 1 [Source:HGNC Symbol;Acc:10040]
4	5636	0.82	3e-07	3e-05	50 x 37 phosphoribosyl pyrophosphate synthetase-associated protein 1 [Source:HGNC Symbol;Acc:10040]
5	26135	0.81	6e-07	3e-05	50 x 32 SERPINE1 mRNA binding protein 1 [Source:HGNC Symbol;Acc:10040]
6	26009	0.8	8e-07	7e-05	49 x 36 zinc finger, ZZ-type containing 3 [Source:HGNC Symbol;Acc:10040]
7	284611	0.76	2e-06	7e-05	50 x 33 family with sequence similarity 102, member B [Source:HGNC Symbol;Acc:10040]
8	58155	0.76	2e-06	7e-05	50 x 36 polypyrimidine tract binding protein 2 [Source:HGNC Symbol;Acc:10040]
9	3187	0.76	2e-06	8e-05	50 x 35 heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGNC Symbol;Acc:10040]
10	55197	0.75	3e-06	2e-04	50 x 32 regulation of nuclear pre-mRNA domain containing 1A [Source:HGNC Symbol;Acc:10040]
11	79366	0.73	7e-06	2e-04	50 x 32 high mobility group nucleosome binding domain 5 [Source:HGNC Symbol;Acc:10040]
12	153830	0.72	7e-06	2e-04	47 x 33 ring finger protein 145 [Source:HGNC Symbol;Acc:20853]
13	29929	0.72	8e-06	3e-04	50 x 33 ALG6, alpha-1,3-glucosyltransferase [Source:HGNC Symbol;Acc:10040]
14	9295	0.71	1e-05	3e-04	48 x 36 serine/arginine-rich splicing factor 11 [Source:HGNC Symbol;Acc:10040]
15	4089	0.7	1e-05	3e-04	50 x 35 SMAD family member 4 [Source:HGNC Symbol;Acc:6770]
16	23318	0.69	2e-05	3e-04	50 x 37 zinc finger, CCHC domain containing 11 [Source:HGNC Symbol;Acc:10040]
17	57088	0.69	2e-05	3e-04	50 x 36 phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649]
18	51015	0.69	2e-05	3e-04	50 x 33 isochorismatase domain containing 1 [Source:HGNC Symbol;Acc:10040]
19	84146	0.69	2e-05	3e-04	49 x 34 zinc finger protein 644 [Source:HGNC Symbol;Acc:29222]
20	55170	0.68	2e-05	3e-04	50 x 37 protein arginine methyltransferase 6 [Source:HGNC Symbol;Acc:10040]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	9.82	NULL	4 / 14	GSEA C2:REACTOME_MRNA_3_END_PROCESSING
2	8.93	NULL	18 / 232	Chr Chr 18
3	8.89	NULL	4 / 30	miRNA target-miR-5566
4	8.68	NULL	2 / 15	BP glycogen biosynthetic process
5	8.14	NULL	15 / 121	miRNA target-miR-3983
6	7.97	NULL	16 / 153	miRNA target-miR-146b-5p
7	7.77	NULL	7 / 45	miRNA target-miR-3491
8	7.73	NULL	2 / 8	GSEA C2:RUNNE_GENDER_EFFECT_UP
9	7.46	NULL	19 / 264	miRNA target-miR-3490a
10	7.29	NULL	3 / 16	GSEA C2:HOI_ATL_CHRONIC_VS_ACUTE_DN
11	7.27	NULL	3 / 21	BP regulation of RNA splicing
12	7.22	NULL	8 / 51	miRNA target-miR-5566-3p
13	7.12	NULL	18 / 150	miRNA target-miR-3933
14	7.08	NULL	32 / 463	miRNA target-miR-3901a
15	7.08	NULL	18 / 181	miRNA target-miR-3991
16	7.07	NULL	3 / 15	BP mRNA splice site selection
17	6.96	NULL	25 / 318	miRNA target-miR-5569-3p
18	6.9	NULL	5 / 51	miRNA target-miR-5569-5p
19	6.9	NULL	16 / 229	miRNA target-miR-5569g
20	6.75	NULL	3 / 26	miRNA target-miR-397-5p
21	6.74	NULL	12 / 142	miRNA target-miR-5522
22	6.71	NULL	6 / 33	miRNA target-miR-392b
23	6.69	NULL	20 / 267	miRNA target-miR-397
24	6.69	NULL	3 / 15	GSEA C2:DE_Y1_TARGETS_DN
25	6.62	NULL	4 / 27	MF nucleotidyltransferase activity
26	6.62	NULL	28 / 440	miRNA target-miR-399a
27	6.55	NULL	43 / 1720	Chr Chr 1
28	6.5	NULL	6 / 41	BP mRNA 3'-end processing
29	6.48	NULL	11 / 151	miRNA target-miR-556a-5p
30	6.47	NULL	9 / 99	miRNA target-miR-3497
31	6.44	NULL	2 / 13	BP regulation of transforming growth factor beta receptor signaling pathway
32	6.4	NULL	8 / 49	miRNA target-miR-154-487
33	6.36	NULL	11 / 155	miRNA target-miR-397
34	6.34	NULL	2 / 10	MF co-SMAD binding
35	6.34	NULL	3 / 15	GSEA C2:BIOCARTA_CTCF_PATHWAY
36	6.28	NULL	1 / 10	GSEA C2:LUI_THYROID_CANCER_CLUSTER_5
37	6.28	NULL	1 / 10	GSEA C2:REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
38	6.26	NULL	27 / 396	miRNA target-miR-3901b
39	6.24	NULL	8 / 96	miRNA target-miR-3903
40	6.22	NULL	6 / 44	BP termination of RNA polymerase II transcription



# GW\_285

## Local Summary

%DE = 0.71  
 # metagenes = 17  
 # genes = 246  
 # genes in genesets = 240

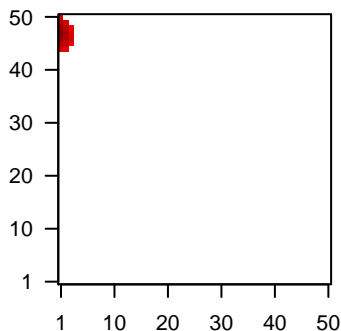
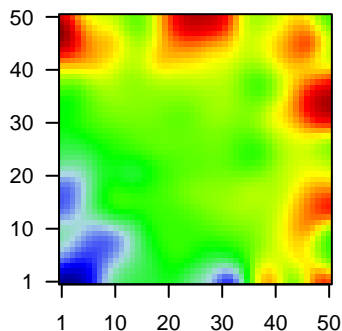
# genes with  $fdr < 0.1$  = 153 ( 118 + / 35 - )  
 # genes with  $fdr < 0.05$  = 138 ( 108 + / 30 - )  
 # genes with  $fdr < 0.01$  = 122 ( 98 + / 24 - )

$\langle r \rangle$  metagenes = 0.93  
 $\langle r \rangle$  genes = 0.42

$\langle FC \rangle = 0.35$   
 $\langle \text{shrinkage-t} \rangle = 12.53$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.41$

Profile

Spot



## Local Genelist

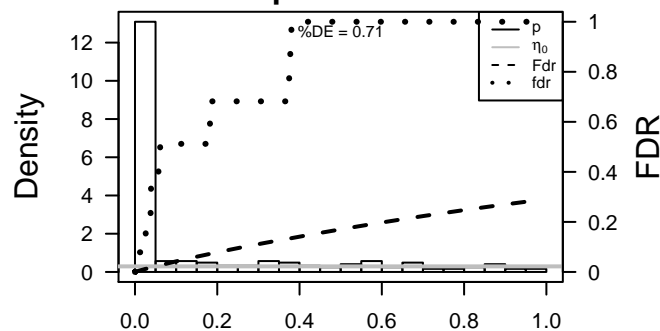
Rank	ID	log(FC)	fdr	p-value	Description	
1	57016	1.77	2e-16	6e-16	1 x 50	aldo-keto reductase family 1, member B10 (aldose reductase)
2	441282	1.5	2e-16	6e-16	1 x 49	aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	387695	1.39	2e-16	6e-16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Synt
4	760	1.78	2e-16	6e-16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	9547	2.27	2e-16	6e-16	1 x 46	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
6	27065	1.64	2e-16	6e-16	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1)
7	55894	1.46	2e-16	6e-16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	414325	1.67	2e-16	6e-16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	1673	2.46	2e-16	6e-16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	1824	1.4	2e-16	6e-16	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
11	1825	1.52	2e-16	6e-16	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
12	2697	1.43	2e-16	6e-16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;A
13	2706	1.27	2e-16	6e-16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
14	3489	-1.83	2e-16	6e-16	1 x 44	insulin-like growth factor binding protein 6 [Source:HGNC Sy
15	3848	1.89	2e-16	6e-16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
16	3858	1.37	2e-16	6e-16	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]
17	3868	1.34	2e-16	6e-16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
18	192666	1.58	2e-16	6e-16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
19	84648	2.19	2e-16	6e-16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615]
20	3963	1.46	2e-16	6e-16	1 x 47	lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	33.5	NULL	79 / 135	H.Tiss WIRTH_Mucosa
2	21.79	NULL	19 / 42	BP keratinization
3	21.23	NULL	24 / 53	BP keratinocyte differentiation
4	20.5	NULL	18 / 21	CC cornified envelope
5	16.67	NULL	97 / 572	Disease GUDJ_psooriasis up
6	16.59	NULL	23 / 76	BP epidermis development
7	15.29	NULL	3 / 8	GSEA C2LJU_CDX2_TARGETS_DN
8	15.27	NULL	12 / 21	CC desmosome
9	14.93	NULL	19 / 82	CC intermediate filament
10	14.35	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
11	14.23	NULL	12 / 44	CC keratin filament
12	13.83	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	13.26	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
14	13.11	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
15	12.91	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
16	12.55	NULL	10 / 19	BP peptide cross-linking
17	12.38	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
18	12.15	NULL	5 / 25	BP response to zinc ion
19	11.56	NULL	3 / 15	CC connexon complex
20	11.17	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
21	10.88	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
22	10.49	NULL	27 / 186	MF structural molecule activity
23	10.37	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
24	10.14	NULL	5 / 13	BP negative regulation of peptidase activity
25	10.08	NULL	2 / 10	MF gap junction channel activity
26	9.89	NULL	2 / 5	miRNA target-196a
27	9.71	NULL	3 / 10	BP chronic inflammatory response
28	9.57	NULL	3 / 13	BP intermediate filament cytoskeleton organization
29	9.49	NULL	5 / 10	MF RAGE receptor binding
30	9.24	NULL	2 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
31	9.16	NULL	4 / 21	CC gap junction
32	9	NULL	7 / 29	BP regulation of proteolysis
33	8.73	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
34	8.41	NULL	2 / 10	BP skeletal muscle tissue regeneration
35	8.37	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
36	8.18	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
37	8.09	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
38	7.91	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
39	7.65	NULL	1 / 11	GSEA C2TO_PTTG1_TARGETS_UP
40	7.49	NULL	3 / 20	MF scaffold protein binding

p-values



# GW\_285

## Local Summary

%DE = 0.58  
 # metagenes = 21  
 # genes = 330  
 # genes in genesets = 324

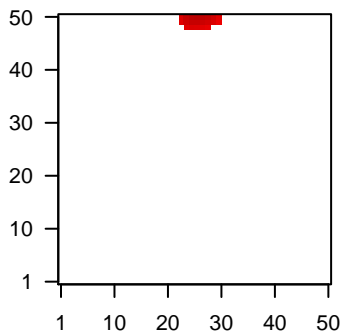
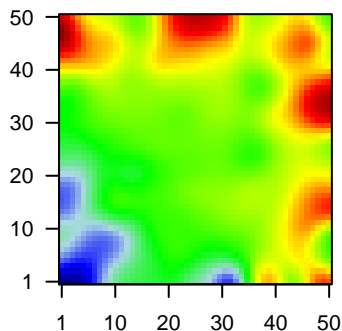
# genes with  $fdr < 0.1 = 125$  ( 113 + / 12 - )  
 # genes with  $fdr < 0.05 = 74$  ( 71 + / 3 - )  
 # genes with  $fdr < 0.01 = 40$  ( 40 + / 0 - )

<r> metagenes = 0.93  
 <r> genes = 0.3

<FC> = 0.25  
 <shrinkage-t> = 8.66  
 <p-value> = 0.03  
 <fdr> = 0.71

Profile

Spot



## Local Genelist

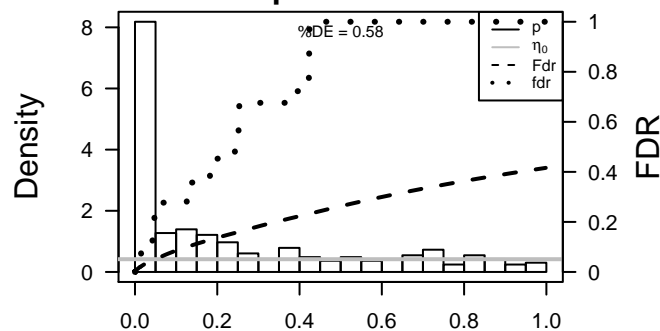
Rank	ID	log(FC)	fdr	p-value	Description
1	8560	1.34	2e-16	2e-14	delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;A
2	25800	1.48	2e-16	2e-14	solute carrier family 39 (zinc transporter), member 6 [Source:
3	965	1.23	2e-14	4e-08	CD58 molecule [Source:HGNC Symbol;Acc:1688]
4	91612	1.02	3e-10	2e-07	churchill domain containing 1 [Source:HGNC Symbol;Acc:20k
5	6814	0.97	2e-09	2e-07	syntaxin binding protein 3 [Source:HGNC Symbol;Acc:11446]
6	84693	0.96	3e-09	5e-06	methylmalonyl CoA epimerase [Source:HGNC Symbol;Acc:1f
7	10929	0.89	4e-08	6e-06	Homo sapiens serine/arginine-rich splicing factor 8 (SRSF8),
8	100008589	0.87	8e-08	5e-05	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
9	2632	0.8	8e-07	5e-05	glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Syr
10	1665	0.79	9e-07	5e-05	DEAH (Asp-Glu-Ala-His) box helicase 15 [Source:HGNC Sy
11	1810	0.78	1e-06	5e-05	down-regulator of transcription 1, TBP-binding (negative cof
12	55858	0.78	1e-06	4e-04	transmembrane protein 165 [Source:HGNC Symbol;Acc:307f
13	829	0.74	5e-06	4e-04	capping protein (actin filament) muscle Z-line, alpha 1 [Sourc
14	51377	0.73	7e-06	6e-04	ubiquitin carboxyl-terminal hydrolase L5 [Source:HGNC Sym
15	8624	0.71	1e-05	6e-04	proteasome (prosome, macropain) assembly chaperone 1 [Si
16	5868	0.69	2e-05	6e-04	RAB5A, member RAS oncogene family [Source:HGNC Symb
17	9652	0.69	2e-05	6e-04	tetratricopeptide repeat domain 37 [Source:HGNC Symbol;Ac
18	23515	0.68	2e-05	8e-04	MORC family CW-type zinc finger 3 [Source:HGNC Symbol;v
19	81573	0.67	4e-05	8e-04	ankyrin repeat domain 13C [Source:HGNC Symbol;Acc:2537
20	134510	0.67	4e-05	8e-04	ubiquitin-like domain containing CTD phosphatase 1 [Source

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.76	NULL	2 / 13	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G2
2	12.03	NULL	22 / 155	miRNA target set miR-392
3	11.38	NULL	30 / 307	miRNA target set miR-554c-5p
4	11.3	NULL	26 / 271	miRNA target set miR-391h
5	10.05	NULL	33 / 313	miRNA target set miR-399
6	9.91	NULL	2 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_DN
7	9.88	NULL	1 / 7	GSEA C2KEGG_SPHINGOLIPID_METABOLISM
8	9.51	NULL	1 / 9	GSEA C2REACTOME_ZINC_INFLUX_INTO_CELLS_BY_THE_SLC39_GE
9	9.5	NULL	27 / 321	miRNA target set miR-554a-5p
10	9.37	NULL	27 / 336	miRNA target set miR-554b-5p
11	9.01	NULL	4 / 15	GSEA C2SEIDEN_ONCOGENESIS_BY_MET
12	9	NULL	42 / 436	miRNA target set miR-391n
13	8.92	NULL	29 / 336	miRNA target set miR-554c-5p
14	8.86	NULL	25 / 288	miRNA target set miR-554j
15	8.69	NULL	30 / 324	miRNA target set miR-391a
16	8.68	NULL	2 / 4	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN
17	8.65	NULL	14 / 130	miRNA target set miR-391f
18	8.57	NULL	5 / 8	MMML C63CIEJ_MMML 50
19	8.53	NULL	1 / 5	MMML C63CIEJ_MMML 28
20	8.44	NULL	26 / 302	miRNA target set miR-391i
21	8.42	NULL	29 / 310	miRNA target set miR-391e
22	8.18	NULL	2 / 16	CC lamellipodium membrane
23	8.13	NULL	14 / 122	miRNA target set miR-554e-3p
24	8.11	NULL	1 / 12	BP zinc ion transmembrane transporter
25	8.11	NULL	1 / 12	MF zinc ion transmembrane transporter activity
26	8.09	NULL	1 / 6	miRNA target set miR-125a
27	7.81	NULL	26 / 301	miRNA target set miR-391b
28	7.78	NULL	36 / 517	miRNA target set miR-391c
29	7.69	NULL	1 / 11	GSEA C2GALE_APL_WITH_FLT3_MUTATED_DN
30	7.56	NULL	1 / 2	TF MYC_Signal transduction UP
31	7.56	NULL	5 / 16	GSEA C2CAFFAREL_RESPONSE_TO_THC_UP
32	7.55	NULL	3 / 15	GSEA C2AVTVEER_BREAST_CANCER_BRCA1_UP
33	7.53	NULL	2 / 15	GSEA C2GENTILE_UV_RESPONSE_CLUSTER_D1
34	7.47	NULL	34 / 269	miRNA target set miR-391d
35	7.43	NULL	1 / 14	MF metal ion transmembrane transporter activity
36	7.41	NULL	23 / 198	miRNA target set miR-391g
37	7.36	NULL	35 / 511	miRNA target set miR-391b
38	7.29	NULL	17 / 197	miRNA target set miR-391e
39	7.27	NULL	35 / 538	miRNA target set miR-391e
40	7.25	NULL	20 / 241	miRNA target set miR-391z

p-values



# GW\_285

## Local Summary

%DE = 0.79  
 # metagenes = 30  
 # genes = 421  
 # genes in genesets = 416

# genes with  $fdr < 0.1 = 256$  ( 25 + / 231 - )  
 # genes with  $fdr < 0.05 = 219$  ( 21 + / 198 - )  
 # genes with  $fdr < 0.01 = 160$  ( 12 + / 148 - )

<r> metagenes = 0.94

<r> genes = 0.35

<FC> = -0.36

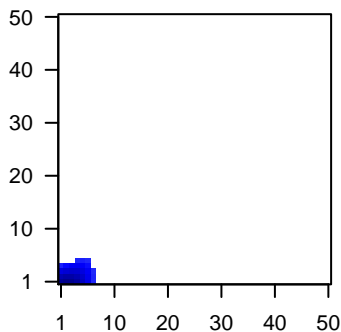
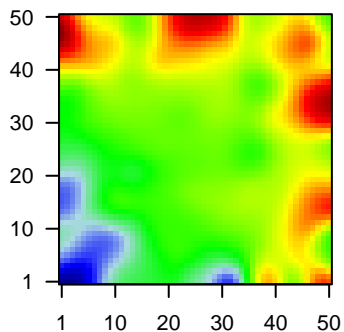
<shrinkage-t> = -12.45

<p-value> = 0

<fdr> = 0.51

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4316	-1.86	2e-16	2e-14	2 x 1 matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
2	4320	-1.32	4e-16	2e-14	3 x 1 matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
3	3553	-1.3	7e-16	4e-14	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
4	6696	-1.29	1e-15	1e-11	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125]
5	26064	-1.19	2e-13	2e-11	4 x 1 retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
6	3040	-1.17	5e-13	2e-11	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
7	7076	-1.16	7e-13	2e-11	4 x 1 TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
8	10630	-1.15	1e-12	5e-11	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]
9	1462	-1.14	2e-12	5e-11	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
10	23213	-1.13	2e-12	8e-11	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
11	57124	1.13	3e-12	8e-11	3 x 1 CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
12	72	-1.12	4e-12	8e-11	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
13	3043	-1.12	5e-12	4e-10	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
14	4319	1.1	9e-12	4e-10	1 x 3 matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
15	414062	-1.09	1e-11	8e-10	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
16	2296	-1.08	2e-11	1e-09	7 x 3 forkhead box C1 [Source:HGNC Symbol;Acc:3800]
17	27122	-1.07	4e-11	1e-09	1 x 3 dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
18	2919	-1.06	4e-11	1e-09	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimule
19	3678	-1.06	6e-11	1e-09	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [So
20	10631	-1.05	8e-11	2e-09	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Ac

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-28.49	NULL	91 / 250	Lymphoma_TENZ_Stromal signature 1
2	-24.17	NULL	71 / 190	CC extracellular matrix
3	-19.43	NULL	74 / 242	BP extracellular matrix organization
4	-18.83	NULL	6 / 10	GSEA C2JLEON_SMAD6_TARGETS_UP
5	-18.59	NULL	9 / 11	MF platelet-derived growth factor binding
6	-18.41	NULL	7 / 11	Glio Phillips MES up vs Prolif & PN
7	-18.26	NULL	101 / 683	CC extracellular space
8	-18.24	NULL	92 / 553	Cancer Lembcke_Colonc Inflammation
9	-18.08	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
10	-18.06	NULL	15 / 16	MMML C6SCIEJ_MMML 1
11	-17.98	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
12	-17.85	NULL	16 / 37	BP collagen fibril organization
13	-17.75	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
14	-17.05	NULL	8 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
15	-16.99	NULL	51 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	-16.99	NULL	51 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	-16.99	NULL	51 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	-16.99	NULL	51 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
19	-16.86	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
20	-16.78	NULL	134 / 1182	CC extracellular region
21	-16.61	NULL	11 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
22	-16.49	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
23	-15.83	NULL	34 / 69	BP extracellular matrix disassembly
24	-15.77	NULL	5 / 7	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_UP
25	-14.91	NULL	12 / 35	Glio Colman_survival_associated
26	-14.72	NULL	22 / 57	MF extracellular matrix structural constituent
27	-14.24	NULL	8 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
28	-13.92	NULL	2 / 4	MMML C6SCIEJ_MMML 23
29	-13.81	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
30	-13.75	NULL	8 / 12	miRNA target-29c
31	-13.69	NULL	29 / 64	BP collagen catabolic process
32	-13.66	NULL	7 / 16	GSEA C2ZHU_CMV_ALL_DN
33	-13.23	NULL	6 / 16	GSEA C2ZHU_CMV_24_HR_DN
34	-13.12	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
35	-12.93	NULL	5 / 10	BP protein heterotrimerization
36	-12.91	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
37	-12.89	NULL	4 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
38	-12.78	NULL	31 / 269	BP inflammatory response
39	-12.05	NULL	7 / 16	GSEA C2SU_PDEF_TARGETS_UP
40	-12.05	NULL	5 / 10	BP negative regulation of fibroblast growth factor receptor signaling pa

