

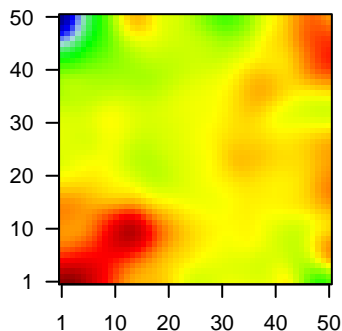
# GW\_169

## Global Summary

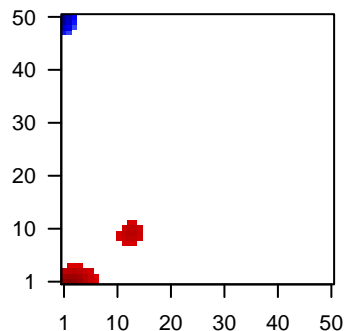
%DE = 0.18  
 # genes with  $fdr < 0.2$  = 2194 ( 1328 + / 866 - )  
 # genes with  $fdr < 0.1$  = 1872 ( 1137 + / 735 - )  
 # genes with  $fdr < 0.05$  = 1612 ( 997 + / 615 - )  
 # genes with  $fdr < 0.01$  = 1184 ( 746 + / 438 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = -0.01  
 <p-value> = 0.07  
 <fdr> = 0.82

Profile



Regulated Spots



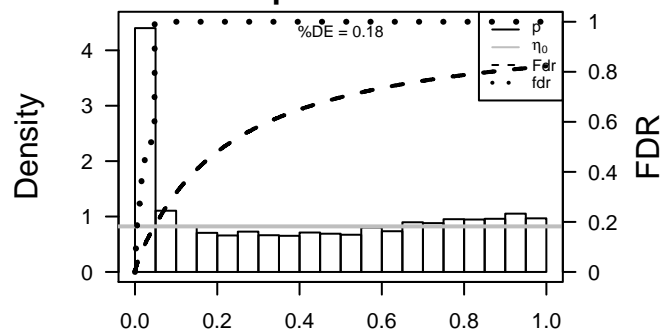
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	72	1.87	2e-16	2e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym]
2	131	-2.55	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-3.25	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	-2.33	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
5	8644	-1.86	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr]
6	1109	-1.88	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr]
7	218	-1.6	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	244	-1.84	2e-16	2e-14	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]
9	9823	1.6	2e-16	2e-14	7 x 1 armadillo repeat containing, X-linked 2 [Source:HGNC Symb
10	25805	1.73	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
11	84707	1.8	2e-16	2e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
12	633	1.78	2e-16	2e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
13	10974	-1.58	2e-16	2e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24
14	387695	-2.03	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
15	64073	-1.59	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Symt
16	375791	-2.18	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
17	768	2.41	2e-16	2e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
18	810	-1.76	2e-16	2e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
19	51806	-1.61	2e-16	2e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
20	875	1.56	2e-16	2e-14	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:151

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.63	NULL	190	CC extracellular matrix
2	12.48	NULL	242	BP extracellular matrix organization
3	11.1	NULL	153	CC endoplasmic reticulum lumen
4	10.81	NULL	57	MF extracellular matrix structural constituent
5	10.58	NULL	717	Chr Chr 16
6	9.69	NULL	183	CC proteinaceous extracellular matrix
7	9.49	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
8	9.18	NULL	250	LymphoIntENZ_Stromal signature 1
9	9.09	NULL	16	MMML C6CIEJ_MMML 1
10	8.99	NULL	519	Chr Chr 14
11	8.53	NULL	69	BP extracellular matrix disassembly
12	8.04	NULL	683	CC extracellular space
13	7.81	NULL	64	BP collagen catabolic process
14	7.39	NULL	11	MF platelet-derived growth factor binding
15	7.33	NULL	83	CC basement membrane
16	7.26	NULL	534	Chr Chr 8
17	7.07	NULL	3274	CC integral to membrane
18	6.99	NULL	500	MF sequence-specific DNA binding
19	6.94	NULL	112	MF heparin binding
20	6.9	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
<i>Underexpressed</i>				
1	-31.72	NULL	135	H.Tiss WIRTH_Mucosa
2	-22.97	NULL	21	CC cornified envelope
3	-19.97	NULL	53	BP keratinocyte differentiation
4	-19.46	NULL	572	Disease GUDJ_psooriasis up
5	-18.95	NULL	42	BP keratinization
6	-15.54	NULL	76	BP epidermis development
7	-13.36	NULL	19	BP peptide cross-linking
8	-12.38	NULL	957	Chr Chr 11
9	-9.38	NULL	44	CC keratin filament
10	-8.9	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
11	-8.89	NULL	82	CC intermediate filament
12	-8.68	NULL	186	MF structural molecule activity
13	-8.64	NULL	1720	Chr Chr 1
14	-8.53	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
15	-8.44	NULL	417	H.Tiss WIRTH_Immune system
16	-7.99	NULL	10	MF RAGE receptor binding
17	-7.34	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	-7.28	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
19	-7.23	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
20	-6.99	NULL	15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN

p-values



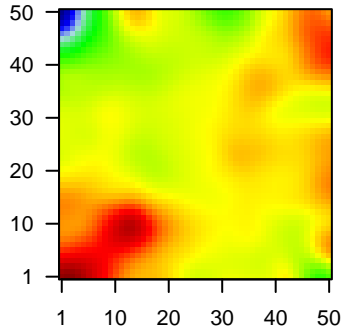
# GW\_169

## Local Summary

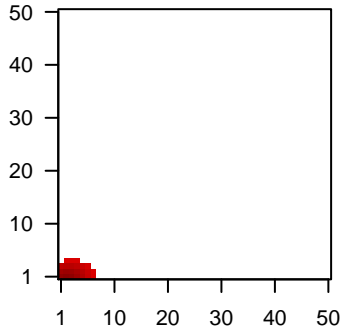
%DE = 0.7  
 # metagenes = 23  
 # genes = 329  
 # genes in genesets = 328  
 # genes with  $fdr < 0.1 = 172$  ( 167 + / 5 - )  
 # genes with  $fdr < 0.05 = 168$  ( 163 + / 5 - )  
 # genes with  $fdr < 0.01 = 148$  ( 144 + / 4 - )

$\langle r \rangle$  metagenes = 0.95  
 $\langle r \rangle$  genes = 0.39  
 $\langle FC \rangle = 0.57$   
 $\langle \text{shrinkage-t} \rangle = 19.84$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.44$

Profile



Spot



## Local Genelist

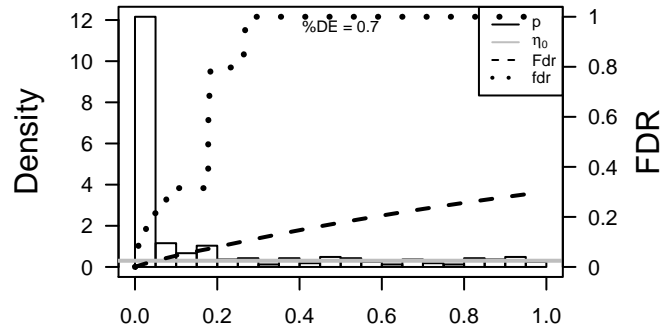
Rank	ID	log(FC)	fdr	p-value	Description
1	72	1.87	2e-16	8e-16	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	9823	1.6	2e-16	8e-16	7 x 1 armadillo repeat containing, X-linked 2 [Source:HGNC Symb
3	633	1.78	2e-16	8e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
4	414062	1.7	2e-16	8e-16	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
5	1306	1.56	2e-16	8e-16	4 x 1 collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
6	1289	2.09	2e-16	8e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1397	1.55	2e-16	8e-16	4 x 3 cysteine-rich protein 2 [Source:HGNC Symbol;Acc:2361]
8	3491	1.52	2e-16	8e-16	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
9	10979	1.5	2e-16	8e-16	4 x 1 fermitin family member 2 [Source:HGNC Symbol;Acc:15767]
10	64778	1.69	2e-16	8e-16	4 x 3 fibronectin type III domain containing 3B [Source:HGNC Sym
11	11167	2.35	2e-16	8e-16	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
12	2882	1.56	2e-16	8e-16	6 x 1 glutathione peroxidase 7 [Source:HGNC Symbol;Acc:4559]
13	3487	1.82	2e-16	8e-16	5 x 1 insulin-like growth factor binding protein 4 [Source:HGNC Sy
14	3553	2.23	2e-16	8e-16	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
15	3576	2.32	2e-16	8e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
16	83700	1.93	2e-16	8e-16	5 x 1 junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:1
17	55384	2.06	2e-16	8e-16	4 x 1 maternally expressed 3 (non-protein coding) [Source:HGNC
18	4319	2.66	2e-16	8e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
19	4316	1.54	2e-16	8e-16	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC
20	4692	1.55	2e-16	8e-16	5 x 1 neccdin, melanoma antigen (MAGE) family member [Source:H

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	32.3	NULL	70 / 190	CC extracellular matrix
2	32.1	NULL	14 / 16	MMML C6ACIEJ_MMML 1
3	25.8	NULL	84 / 250	LymphomaL1ENZ_Stromal signature 1
4	25.67	NULL	67 / 242	BP extracellular matrix organization
5	25.04	NULL	8 / 11	MF platelet-derived growth factor binding
6	24.62	NULL	33 / 69	BP extracellular matrix disassembly
7	24.09	NULL	22 / 57	MF extracellular matrix structural constituent
8	23.56	NULL	8 / 12	miRNA target-29c
9	23.19	NULL	28 / 64	BP collagen catabolic process
10	20.73	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
11	20.57	NULL	88 / 683	CC extracellular space
12	20.36	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
13	19.26	NULL	7 / 12	GSEA C2Y_AGING_MIDDLE_UP
14	19.01	NULL	79 / 553	Cancer Lembcke_Colonc Inflammation
15	18.27	NULL	11 / 19	MF extracellular matrix binding
16	17.93	NULL	119 / 1182	CC extracellular region
17	17.43	NULL	42 / 183	CC proteinaceous extracellular matrix
18	17.19	NULL	2 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
19	17.09	NULL	15 / 37	BP collagen fibril organization
20	16.18	NULL	11 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
21	16.17	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
22	16.04	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
23	15.92	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
24	15.88	NULL	5 / 7	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_UP
25	15.65	NULL	44 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
26	15.65	NULL	44 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
27	15.65	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
28	15.65	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
29	15.29	NULL	7 / 11	Glio Phillips MES up vs Prolif & PN
30	15.25	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
31	15.22	NULL	22 / 83	CC basement membrane
32	14.99	NULL	4 / 15	BP positive regulation vascular endothelial growth factor production
33	14.84	NULL	17 / 68	CC collagen
34	14.66	NULL	5 / 15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
35	14.35	NULL	8 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
36	14.12	NULL	21 / 119	LymphomaL1OSOLOWSKI_green total
37	14.04	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
38	13.93	NULL	11 / 36	BP embryo implantation
39	13.92	NULL	3 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
40	13.84	NULL	25 / 153	CC endoplasmic reticulum lumen

p-values



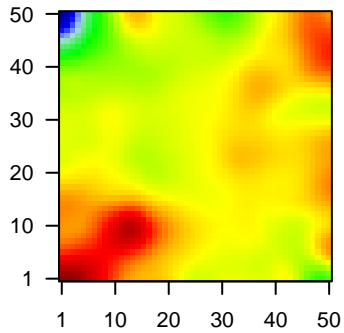
# GW\_169

## Local Summary

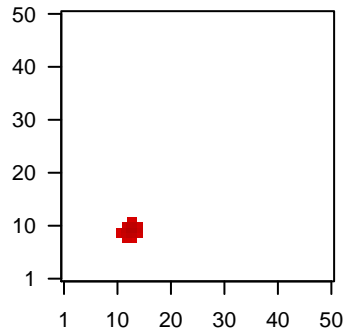
%DE = 0.81  
 # metagenes = 19  
 # genes = 107  
 # genes in genesets = 90  
 # genes with fdr < 0.1 = 74 ( 74 + / 0 - )  
 # genes with fdr < 0.05 = 74 ( 74 + / 0 - )  
 # genes with fdr < 0.01 = 70 ( 70 + / 0 - )

<r> metagenes = 0.94  
 <r> genes = 0.25  
 <FC> = 0.78  
 <shrinkage-t> = 27.17  
 <p-value> = 0  
 <fdr> = 0.28

Profile



Spot



## Local Genelist

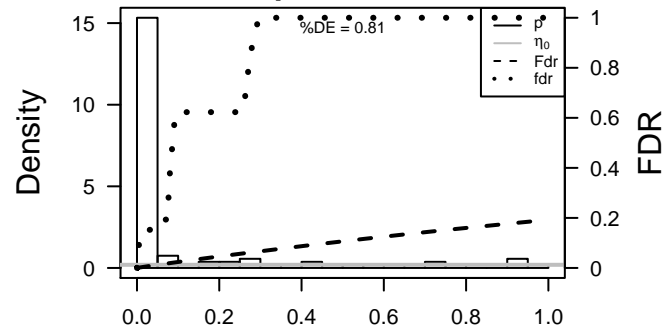
Rank	ID	log(FC)	fdr	p-value	Description
1	441520	2.32	2e-16	4e-16	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
2	729422	2	2e-16	4e-16	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	645073	1.66	2e-16	4e-16	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	729442	1.77	2e-16	4e-16	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645037	2.06	2e-16	4e-16	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
6	2576	1.73	2e-16	4e-16	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	121355	2.07	2e-16	4e-16	14 x 11 gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
8	4100	2.36	2e-16	4e-16	14 x 11 melanoma antigen family A, 1 (directs expression of antigen I
9	4109	2.47	2e-16	4e-16	14 x 11 melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
10	4103	2.21	2e-16	4e-16	14 x 10 melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
11	728269	1.49	2e-16	4e-16	14 x 10 melanoma antigen family A, 9B [Source:HGNC Symbol;Acc:3
12	5746	1.58	2e-16	4e-16	14 x 10 parathyroid hormone 2 receptor [Source:HGNC Symbol;Acc:5
13	24150	1.89	2e-16	4e-16	14 x 11 TP53 target 3D [Source:HGNC Symbol;Acc:44657]
14	729428	1.49	4e-16	2e-12	14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402]
15	5891	1.35	1e-13	3e-11	13 x 10 MOK protein kinase [Source:HGNC Symbol;Acc:9833]
16	55859	1.29	1e-12	5e-11	13 x 8 brain expressed, X-linked 1 [Source:HGNC Symbol;Acc:103
17	29801	1.26	4e-12	9e-11	13 x 8 zinc finger, DHHC-type containing 8 [Source:HGNC Symbol;
18	729396	1.24	9e-12	2e-09	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	440905	1.18	1e-10	3e-09	14 x 10 fatty acyl CoA reductase 2 pseudogene 1 [Source:HGNC Syr
20	10570	1.15	3e-10	3e-09	12 x 8 dihydropyrimidinase-like 4 [Source:HGNC Symbol;Acc:3016]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	14.39	NULL	1 / 2	miRNA target-107
2	12.78	NULL	2 / 8	GSEA C2WEBER_METHYLATED_ICP_IN_FIBROBLAST
3	12.36	NULL	1 / 11	GSEA C2SU_PLACENTA
4	11.44	NULL	26 / 630	Chr Chr X
5	10.69	NULL	1 / 14	GSEA C2NIELSEN_GIST
6	10.48	NULL	1 / 4	GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_DN
7	10.26	NULL	1 / 15	GSEA C2BROWNE_HCMV_INFECTION_8HR_DN
8	9.54	NULL	1 / 14	GSEA C2CRICKMAN_HEAD_AND_NECK_CANCER_B
9	9.49	NULL	1 / 4	GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_UP
10	8.69	NULL	3 / 15	GSEA C2MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
11	8.46	NULL	1 / 7	GSEA C2NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP
12	8.01	NULL	1 / 21	BP negative regulation of Notch signaling pathway
13	7.96	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
14	7.27	NULL	2 / 16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
15	7.27	NULL	2 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
16	7.26	NULL	2 / 16	GSEA C2REACTOME_CRMP5_IN_SEMA3A_SIGNALING
17	7.2	NULL	1 / 7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
18	7.17	NULL	1 / 5	miRNA target-181a
19	7.09	NULL	1 / 7	GSEA C2KONDO_PROSTATE_CANCER_WITH_H3K27ME3
20	7.08	NULL	1 / 10	GSEA C2XU_RESPONSE_TO_TRETINOIN_DN
21	7	NULL	1 / 12	GSEA C2HO_LIVER_CANCER_VASCULAR_INVASION
22	6.34	NULL	1 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16
23	6.34	NULL	1 / 6	miRNA target-181b
24	5.79	NULL	1 / 10	GSEA C2CONRAD_GERMLINE_STEM_CELL
25	5.77	NULL	2 / 24	BP tissue development
26	5.73	NULL	1 / 7	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9
27	5.67	NULL	1 / 6	GSEA C2DER_IFN_BETA_RESPONSE_DN
28	5.64	NULL	1 / 10	GSEA C2BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1
29	5.64	NULL	1 / 10	GSEA C2CONRAD_STEM_CELL
30	5.6	NULL	1 / 7	GSEA C2NEBEN_AML_WITH_FLT3_OR_NRAS_UP
31	5.53	NULL	7 / 120	H.Tiss WIRTH_Testis
32	5.5	NULL	1 / 10	BP branching involved in salivary gland morphogenesis
33	5.47	NULL	2 / 27	Glio WIRTH_PN subtype
34	5.33	NULL	1 / 5	GSEA C2CHOI_ATL_ACUTE_STAGE
35	5.32	NULL	10 / 481	BP biological_process
36	5.31	NULL	1 / 11	GSEA C2ODONNELL_TFRC_TARGETS_DN
37	5.16	NULL	1 / 12	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
38	5.08	NULL	2 / 17	BP calcium ion homeostasis
39	4.99	NULL	1 / 10	BP paraxial mesoderm development
40	4.9	NULL	1 / 12	BP regulation of embryonic development

p-values



# GW\_169

## Local Summary

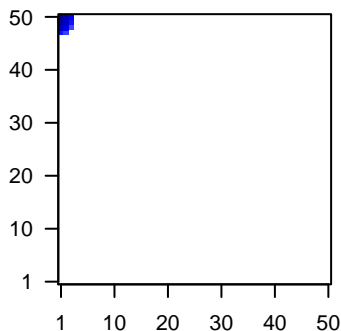
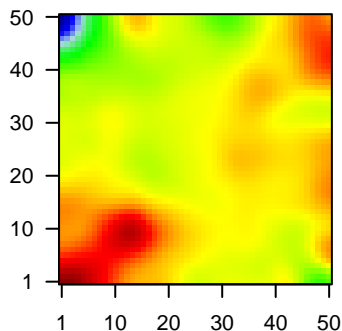
%DE = 0.97  
 # metagenes = 11  
 # genes = 165  
 # genes in genesets = 160  
 # genes with  $fdr < 0.1$  = 156 ( 2 + / 154 - )  
 # genes with  $fdr < 0.05$  = 151 ( 2 + / 149 - )  
 # genes with  $fdr < 0.01$  = 151 ( 2 + / 149 - )

$\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.49

$\langle FC \rangle = -1.44$   
 $\langle \text{shrinkage-t} \rangle = -51.2$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.08$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.55	2e-16	2e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-3.25	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-2.33	2e-16	2e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	-1.86	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
5	218	-1.6	2e-16	2e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	387695	-2.03	2e-16	2e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	375791	-2.18	2e-16	2e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
8	810	-1.76	2e-16	2e-17	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
9	4680	-1.8	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	22802	-2.03	2e-16	2e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	9022	-1.55	2e-16	2e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2i
12	84518	-2.57	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
13	54544	-1.77	2e-16	2e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987:
14	49860	-2.04	2e-16	2e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	1475	-2.52	2e-16	2e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
16	1476	-1.55	2e-16	2e-17	1 x 50 cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
17	414325	-1.82	2e-16	2e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
18	1673	-2.51	2e-16	2e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
19	1824	-1.8	2e-16	2e-17	1 x 48 desmocollin 2 [Source:HGNC Symbol;Acc:3036]
20	1828	-1.58	2e-16	2e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-55.67	NULL	70 / 135	H.Tiss WIRTH_Mucosa
2	-53.95	NULL	16 / 21	CC cornified envelope
3	-42.76	NULL	19 / 42	BP keratinization
4	-42.44	NULL	21 / 53	BP keratinocyte differentiation
5	-32.54	NULL	9 / 19	BP peptide cross-linking
6	-29.86	NULL	18 / 76	BP epidermis development
7	-28.75	NULL	76 / 572	Disease GUDJ_pсориазis up
8	-23.64	NULL	5 / 10	MF RAGE receptor binding
9	-21.63	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	-21.07	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
11	-16.69	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	-16.1	NULL	18 / 186	MF structural molecule activity
13	-15.81	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
14	-15.44	NULL	6 / 13	BP negative regulation of peptidase activity
15	-15.01	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
16	-14.24	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
17	-13.6	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	-13.15	NULL	8 / 44	CC keratin filament
19	-13.06	NULL	6 / 16	GSEA C2XROMER_TUMORIGENESIS_DN
20	-13	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HP31_DN
21	-12.16	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
22	-11.92	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
23	-11.2	NULL	6 / 51	MF protein binding, bridging
24	-11.19	NULL	10 / 82	CC intermediate filament
25	-11.12	NULL	5 / 21	CC desmosome
26	-10.83	NULL	46 / 1182	CC extracellular region
27	-10.53	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
28	-10.53	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
29	-10.47	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	-10.21	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
31	-10.01	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
32	-9.97	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
33	-9.91	NULL	3 / 14	BP defense response to fungus
34	-9.9	NULL	4 / 15	MF retinol dehydrogenase activity
35	-9.57	NULL	3 / 12	BP cellular aldehyde metabolic process
36	-9.4	NULL	12 / 122	MF serine-type endopeptidase activity
37	-9.15	NULL	4 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
38	-9.12	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
39	-8.95	NULL	2 / 10	BP chronic inflammatory response
40	-8.51	NULL	4 / 27	BP response to bacterium

p-values

