

# GW\_105

## Global Summary

%DE = 0.14  
 # genes with  $fdr < 0.2$  = 1723 ( 877 + / 846 - )  
 # genes with  $fdr < 0.1$  = 1389 ( 706 + / 683 - )  
 # genes with  $fdr < 0.05$  = 1123 ( 566 + / 557 - )  
 # genes with  $fdr < 0.01$  = 715 ( 350 + / 365 - )  
 # genes in genesets = 16332

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

## Global Genelist

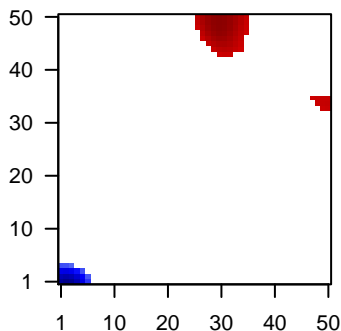
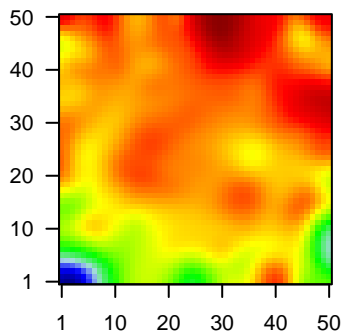
Rank	ID	log(FC)	fdr	p-value	Description
1	59	-1.87	2e-16	6e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	154	-1.7	2e-16	6e-14	1 x 40 adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286]
3	57016	-2.51	2e-16	6e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	8644	2.16	2e-16	6e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
5	1109	2.47	2e-16	6e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy]
6	633	-1.67	2e-16	6e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
7	548596	-1.86	2e-16	6e-14	4 x 50 creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc:
8	9076	-2.9	2e-16	6e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
9	1277	-2.34	2e-16	6e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
10	1288	1.83	2e-16	6e-14	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
11	1289	-1.84	2e-16	6e-14	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
12	1291	-1.71	2e-16	6e-14	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
13	1382	-1.94	2e-16	6e-14	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol]
14	1466	-1.81	2e-16	6e-14	5 x 43 cysteine and glycine-rich protein 2 [Source:HGNC Symbol;A]
15	1475	1.77	2e-16	6e-14	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
16	92196	-1.86	2e-16	6e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
17	54541	-1.99	2e-16	6e-14	1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol;]
18	55894	2.04	2e-16	6e-14	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	414325	2.47	2e-16	6e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	2.23	2e-16	6e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

## Global Geneset Analysis

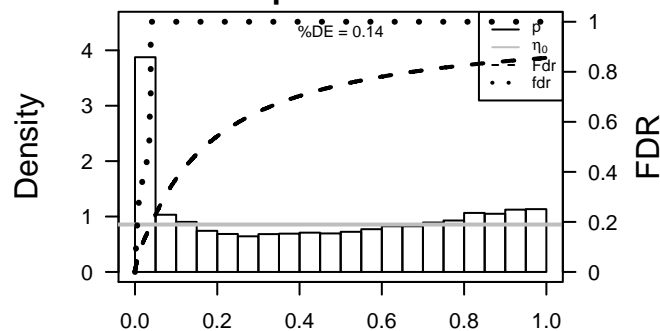
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.22	NULL	940	MF nucleic acid binding
2	8.47	NULL	602	Chr Chr 10
3	8.01	NULL	534	Chr Chr 8
4	7.72	NULL	21	CC cornified envelope
5	6.95	NULL	53	BP keratinocyte differentiation
6	6.48	NULL	633	Chr Chr 9
7	6.24	NULL	1574	BP transcription, DNA-templated
8	6.07	NULL	1749	MF DNA binding
9	5.46	NULL	1142	CC intracellular
10	5.36	NULL	579	CC nucleolus
11	5.23	NULL	1820	MF metal ion binding
12	5.15	NULL	603	miRNA target site
13	5.02	NULL	4640	CC nucleus
14	4.99	NULL	16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
15	4.86	NULL	433	miRNA target site
16	4.83	NULL	618	Chr Chr 4
17	4.79	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	4.77	NULL	76	miRNA target site
19	4.76	NULL	12	GSEA C2BROWNE_HCMV_INFECTION_4HR_UP
20	4.75	NULL	60	miRNA target site
<i>Underexpressed</i>				
1	-13.91	NULL	250	Lymphocyte ENZ_Stromal signature 1
2	-13.1	NULL	190	CC extracellular matrix
3	-11.42	NULL	242	BP extracellular matrix organization
4	-10.19	NULL	683	CC extracellular space
5	-10.1	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
6	-9.74	NULL	16	MMML C6SCIEJ_MMML 1
7	-9.71	NULL	866	Chr Chr 12
8	-9.71	NULL	11	MF platelet-derived growth factor binding
9	-9.28	NULL	699	Chr Chr 5
10	-9.11	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
11	-8.89	NULL	1182	CC extracellular region
12	-8.49	NULL	69	BP extracellular matrix disassembly
13	-8.43	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_HEL4
14	-8.4	NULL	183	CC proteinaceous extracellular matrix
15	-8.34	NULL	16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
16	-8.32	NULL	375	Disease GUDJ_poriasis down
17	-8.11	NULL	403	BP cell adhesion
18	-8.01	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
19	-7.81	NULL	12	miRNA target site
20	-7.44	NULL	37	BP collagen fibril organization

Profile

Regulated Spots



p-values



# GW\_105

## Local Summary

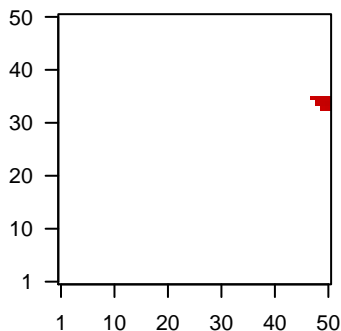
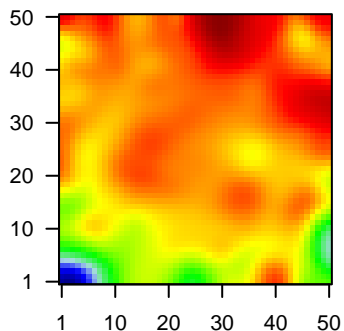
%DE = 0.47  
 # metagenes = 9  
 # genes = 135  
 # genes in genesets = 135  
 # genes with  $fdr < 0.1$  = 35 ( 28 + / 7 - )  
 # genes with  $fdr < 0.05$  = 19 ( 16 + / 3 - )  
 # genes with  $fdr < 0.01$  = 10 ( 8 + / 2 - )

<r> metagenes = 0.99  
 <r> genes = 0.33

<FC> = 0.18  
 <shrinkage-t> = 6.31  
 <p-value> = 0.06  
 <fdr> = 0.76

Profile

Spot



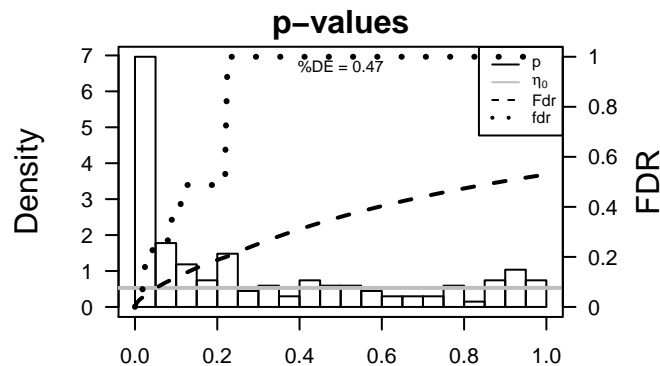
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5612	1.08	2e-07	2e-04	50 x 34 protein-kinase, interferon-inducible double stranded RNA de
2	9849	0.94	6e-06	2e-04	50 x 35 zinc finger protein 518A [Source:HGNC Symbol;Acc:29009]
3	143684	0.94	7e-06	4e-04	50 x 35 family with sequence similarity 76, member B [Source:HGNC
4	34	0.91	1e-05	5e-03	50 x 34 acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Sourc
5	58527	-0.81	1e-04	5e-03	50 x 33 ABRA C-terminal like [Source:HGNC Symbol;Acc:21230]
6	9857	0.77	2e-04	5e-03	48 x 35 centrosomal protein 350kDa [Source:HGNC Symbol;Acc:242
7	3187	-0.75	3e-04	5e-03	50 x 35 heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
8	9774	0.74	4e-04	5e-03	50 x 35 BCL2-associated transcription factor 1 [Source:HGNC Symb
9	29110	0.74	4e-04	5e-03	48 x 35 TANK-binding kinase 1 [Source:HGNC Symbol;Acc:11584]
10	54665	0.73	4e-04	5e-03	50 x 33 round spermatid basic protein 1 [Source:HGNC Symbol;Acc:
11	51322	0.73	5e-04	1e-02	47 x 35 WW domain containing adaptor with coiled-coil [Source:HGN
12	23592	0.71	7e-04	1e-02	49 x 35 LEM domain containing 3 [Source:HGNC Symbol;Acc:28887]
13	221294	0.7	8e-04	1e-02	50 x 33 5'-nucleotidase domain containing 1 [Source:HGNC Symbol;
14	10314	0.69	9e-04	1e-02	50 x 35 LanC lantibiotic synthetase component C-like 1 (bacterial) [S
15	10473	0.68	1e-03	4e-02	50 x 33 high mobility group nucleosomal binding domain 4 [Source:Hi
16	310	0.61	3e-03	4e-02	50 x 35 annexin A7 [Source:HGNC Symbol;Acc:545]
17	149420	0.61	3e-03	4e-02	50 x 34 PDLIM1 interacting kinase 1 like [Source:HGNC Symbol;Acc:
18	9685	-0.61	3e-03	4e-02	50 x 34 clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
19	84146	0.61	3e-03	4e-02	49 x 34 zinc finger protein 644 [Source:HGNC Symbol;Acc:29222]
20	1429	0.6	4e-03	7e-02	50 x 34 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	9.86	NULL	2 / 15	BP glyco
2	8.79	NULL	1 / 2	miRNA target-mir-98
3	8.77	NULL	4 / 60	miRNA target-mir-349
4	8.73	NULL	2 / 10	BP positive regulation of macroautophagy
5	8.46	NULL	8 / 90	miRNA target-mir-362-5p
6	8.01	NULL	9 / 153	miRNA target-mir-146b-5p
7	7.87	NULL	1 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
8	7.87	NULL	1 / 10	GSEA C2REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
9	7.86	NULL	3 / 38	miRNA target-mir-397
10	7.4	NULL	5 / 69	miRNA target-mir-299-5p
11	7.31	NULL	1 / 16	GSEA C2SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN
12	7.31	NULL	1 / 16	miRNA target-mir-391a
13	7.14	NULL	1 / 12	GSEA C2KEGG_PPAR_SIGNALING_PATHWAY
14	7.1	NULL	2 / 15	GSEA C2ONDER_CDH1_TARGETS_1_DN
15	6.7	NULL	10 / 264	miRNA target-mir-349a
16	6.7	NULL	12 / 294	miRNA target-mir-202
17	6.57	NULL	3 / 15	GSEA C2OUILLETTE_CLL_13Q14_DELETION_UP
18	6.51	NULL	10 / 172	miRNA target-mir-307
19	6.41	NULL	7 / 89	miRNA target-mir-305
20	6.39	NULL	1 / 5	miRNA target-mir-305
21	6.38	NULL	3 / 39	miRNA target-mir-125b
22	6.36	NULL	7 / 215	miRNA target-mir-199a-3p
23	6.35	NULL	1 / 10	BP positive regulation of interferon-alpha production
24	6.34	NULL	1 / 15	GSEA C2KEGG_BETA_ALANINE_METABOLISM
25	6.34	NULL	1 / 15	GSEA C2KEGG_PROPANOATE_METABOLISM
26	6.34	NULL	1 / 15	GSEA C2REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PERC
27	6.31	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
28	6.31	NULL	5 / 82	miRNA target-mir-307
29	6.27	NULL	1 / 10	BP histone monoubiquitination
30	6.27	NULL	1 / 10	BP negative regulation of proteasomal ubiquitin-dependent protein cat
31	6.27	NULL	1 / 10	MF RNA polymerase II core binding
32	6.13	NULL	2 / 11	GSEA C2FINETTI_BREAST_CANCERS_KINOME_GRAY
33	6.13	NULL	1 / 16	GSEA C2OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP
34	6.13	NULL	1 / 16	GSEA C2MOOTHA_FFA_OXYDATION
35	6.13	NULL	1 / 16	GSEA C2KEGG_FATTY_ACID_METABOLISM
36	6.13	NULL	1 / 16	GSEA C2KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
37	6.12	NULL	19 / 463	miRNA target-mir-391a
38	6.07	NULL	1 / 4	miRNA target-mir-7c
39	6.07	NULL	1 / 4	miRNA target-mir-7g
40	6.05	NULL	3 / 50	miRNA target-mir-391a



# GW\_105

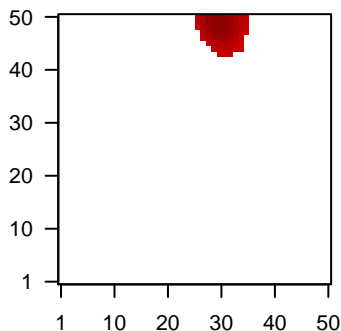
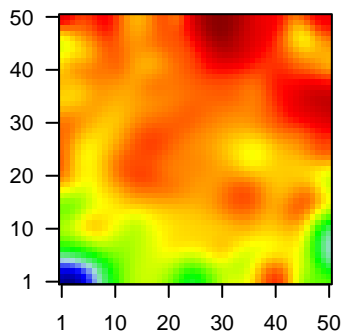
## Local Summary

%DE = 0.41  
 # metagenes = 63  
 # genes = 693  
 # genes in genesets = 682  
 # genes with  $fdr < 0.1$  = 85 ( 78 + / 7 - )  
 # genes with  $fdr < 0.05$  = 68 ( 63 + / 5 - )  
 # genes with  $fdr < 0.01$  = 30 ( 29 + / 1 - )

$\langle r \rangle$  metagenes = 0.88  
 $\langle r \rangle$  genes = 0.21  
 $\langle FC \rangle$  = 0.19  
 $\langle \text{shrinkage-t} \rangle$  = 6.81  
 $\langle p\text{-value} \rangle$  = 0.09  
 $\langle fdr \rangle$  = 0.81

Profile

Spot



## Local Genelist

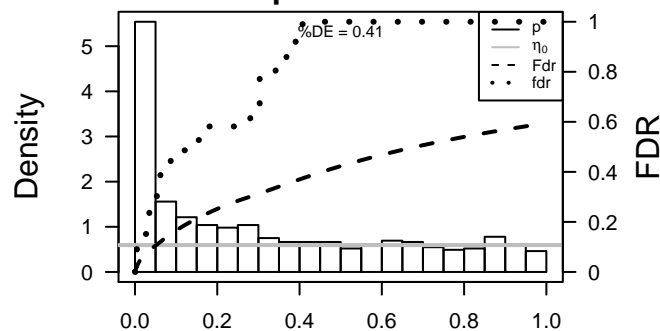
Rank	ID	log(FC)	fdr	p-value	Description
1	5321	1.38	3e-11	2e-05	35 x 50 phospholipase A2, group IVA (cytosolic, calcium-dependent)
2	684959	1.14	4e-08	8e-05	29 x 46 small nucleolar RNA, H/ACA box 25 [Source:HGNC Symbol;Acc:16262]
3	10413	1.08	2e-07	2e-04	26 x 50 Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
4	80110	1.02	1e-06	2e-04	31 x 46 zinc finger protein 614 [Source:HGNC Symbol;Acc:24722]
5	692063	0.98	2e-06	2e-04	28 x 47 small nucleolar RNA, H/ACA box 32 [Source:HGNC Symbol;Acc:16262]
6	8895	0.98	2e-06	2e-04	27 x 50 copine III [Source:HGNC Symbol;Acc:2316]
7	9550	0.98	2e-06	2e-04	29 x 49 ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1 [S]
8	329	0.98	3e-06	9e-04	27 x 46 baculoviral IAP repeat containing 2 [Source:HGNC Symbol;Acc:16262]
9	55246	0.93	8e-06	9e-04	34 x 44 coiled-coil domain containing 25 [Source:HGNC Symbol;Acc:16262]
10	965	0.92	9e-06	9e-04	28 x 50 CD58 molecule [Source:HGNC Symbol;Acc:1688]
11	3460	0.92	1e-05	9e-04	28 x 45 interferon gamma receptor 2 (interferon gamma transducer 1)
12	8065	0.91	1e-05	9e-04	30 x 48 cullin 5 [Source:HGNC Symbol;Acc:2556]
13	509	0.91	1e-05	2e-03	31 x 50 ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit [Source:HGNC Symbol;Acc:16262]
14	10694	0.87	3e-05	2e-03	30 x 48 chaperonin containing TCP1, subunit 8 (theta) [Source:HGNC Symbol;Acc:16262]
15	5423	0.87	3e-05	2e-03	34 x 50 polymerase (DNA directed), beta [Source:HGNC Symbol;Acc:16262]
16	1207	0.86	4e-05	2e-03	31 x 49 chloride channel, nucleotide-sensitive, 1A [Source:HGNC Symbol;Acc:16262]
17	6622	-0.85	4e-05	2e-03	27 x 50 synuclein, alpha (non A4 component of amyloid precursor) [S]
18	2764	0.85	5e-05	2e-03	29 x 45 glia maturation factor, beta [Source:HGNC Symbol;Acc:4373]
19	9821	0.84	5e-05	4e-03	27 x 49 RB1-inducible coiled-coil 1 [Source:HGNC Symbol;Acc:1557]
20	10730	0.84	6e-05	4e-03	27 x 50 YME1-like 1 ATPase [Source:HGNC Symbol;Acc:12843]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	10.52	NULL	5 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_MS_DN
2	9.94	NULL	4 / 5	MMML C6ACIEJ_MMML 28
3	9.56	NULL	5 / 16	GSEA C2MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
4	8.28	NULL	3 / 11	GSEA C2DEURIG_T_CELL_PROLYMPHOCTIC_LEUKEMIA_DN
5	8.12	NULL	82 / 957	Chr Chr 11
6	8.07	NULL	3 / 12	MF lysophospholipase activity
7	7.95	NULL	30 / 109	BP SRP-dependent cotranslational protein targeting to membrane
8	7.71	NULL	2 / 14	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_A
9	7.65	NULL	4 / 15	GSEA C2HASLINGER_B_CLL_WITH_11Q23_DELETION
10	7.37	NULL	5 / 15	GSEA C2BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP
11	7	NULL	3 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
12	6.94	NULL	15 / 51	CC cytosolic large ribosomal subunit
13	6.72	NULL	48 / 253	BP translation
14	6.71	NULL	6 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
15	6.57	NULL	2 / 15	GSEA C2SNIJNDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
16	6.56	NULL	7 / 27	BP DNA-dependent transcription, initiation
17	6.55	NULL	3 / 8	GSEA C2DER_IFN_GAMMA_RESPONSE_DN
18	6.44	NULL	6 / 14	BP mitochondrial ATP synthesis coupled proton transport
19	6.42	NULL	23 / 81	BP viral transcription
20	6.42	NULL	3 / 27	MF calcium-dependent phospholipid binding
21	6.36	NULL	7 / 11	MMML C6ACIEJ_MMML 49
22	6.36	NULL	35 / 153	MF structural constituent of ribosome
23	6.31	NULL	25 / 87	BP translational termination
24	6.23	NULL	3 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
25	6.19	NULL	105 / 1233TF	KIM_MYC targets
26	6.16	NULL	56 / 618	Chr Chr 4
27	6.08	NULL	24 / 92	BP translational elongation
28	5.99	NULL	7 / 15	BP ATP synthesis coupled proton transport
29	5.91	NULL	23 / 92	BP viral life cycle
30	5.9	NULL	3 / 16	GSEA C2WANG_HCP_PROSTATE_CANCER
31	5.9	NULL	9 / 19	CC mitochondrial proton-transporting ATP synthase complex
32	5.74	NULL	5 / 12	BP oxidative phosphorylation
33	5.74	NULL	1 / 9	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_DN
34	5.7	NULL	3 / 10	MF RNA helicase activity
35	5.67	NULL	4 / 13	CC cullin-RING ubiquitin ligase complex
36	5.65	NULL	41 / 534	Chr Chr 8
37	5.64	NULL	3 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_DN
38	5.41	NULL	1 / 10	BP arachidonic acid secretion
39	5.41	NULL	1 / 10	BP cellular response to antibiotic
40	5.41	NULL	1 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM

p-values



# GW\_105

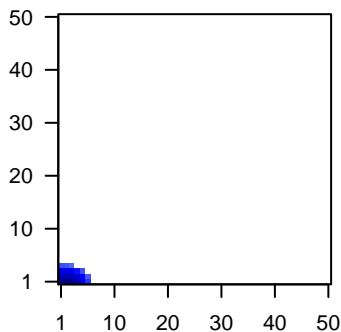
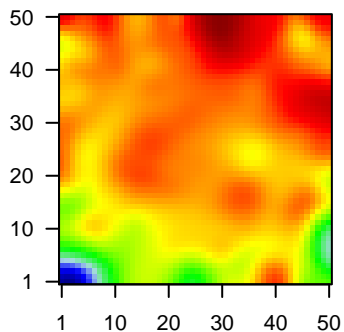
## Local Summary

%DE = 0.8  
 # metagenes = 20  
 # genes = 309  
 # genes in genesets = 308  
 # genes with  $fdr < 0.1$  = 215 ( 19 + / 196 - )  
 # genes with  $fdr < 0.05$  = 176 ( 12 + / 164 - )  
 # genes with  $fdr < 0.01$  = 159 ( 12 + / 147 - )

<r> metagenes = 0.95  
 <r> genes = 0.38  
 <FC> = -0.56  
 <shrinkage-t> = -19.62  
 <p-value> = 0  
 <fdr> = 0.4

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	-1.87	2e-16	2e-15	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	633	-1.67	2e-16	2e-15	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	1277	-2.34	2e-16	2e-15	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1289	-1.84	2e-16	2e-15	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	1291	-1.71	2e-16	2e-15	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
6	54541	-1.99	2e-16	2e-15	1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol;]
7	4489	-1.56	2e-16	2e-15	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
8	5743	2.28	2e-16	2e-15	1 x 1 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H s
9	4320	-1.64	3e-15	1e-13	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
10	1293	-1.62	6e-15	1e-13	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	165	-1.62	6e-15	3e-13	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
12	10409	-1.61	1e-14	3e-13	1 x 2 brain abundant, membrane attached signal protein 1 [Source:
13	4502	-1.59	2e-14	3e-13	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
14	1278	-1.59	2e-14	7e-13	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
15	3040	-1.58	3e-14	6e-12	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
16	6678	-1.54	1e-13	2e-11	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:]
17	3490	-1.51	4e-13	2e-11	3 x 1 insulin-like growth factor binding protein 7 [Source:HGNC Sy
18	7057	-1.49	8e-13	7e-11	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
19	6423	-1.45	3e-12	7e-11	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Ac
20	4312	-1.44	4e-12	7e-11	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-33.89	NULL	68 / 190	CC extracellular matrix
2	-33.37	NULL	8 / 11	MF platelet-derived growth factor binding
3	-33.36	NULL	82 / 250	LymphomL1ENZ_Stromal signature 1
4	-33.07	NULL	15 / 16	MMML C63CIEJ_MMML 1
5	-28.54	NULL	32 / 69	BP extracellular matrix disassembly
6	-27.71	NULL	68 / 242	BP extracellular matrix organization
7	-27.33	NULL	8 / 12	miRNA target-29c
8	-27.27	NULL	28 / 64	BP collagen catabolic process
9	-23.65	NULL	20 / 57	MF extracellular matrix structural constituent
10	-22.56	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
11	-22.45	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
12	-22.33	NULL	15 / 37	BP collagen fibril organization
13	-21.66	NULL	8 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
14	-21.54	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
15	-20.56	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
16	-20.27	NULL	11 / 19	MF extracellular matrix binding
17	-20.21	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
18	-20.2	NULL	12 / 40	BP cellular response to amino acid stimulus
19	-20.19	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
20	-19.73	NULL	7 / 16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
21	-19.43	NULL	4 / 10	BP protein heterotrimerization
22	-19.13	NULL	6 / 13	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
23	-18.27	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
24	-18.12	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
25	-18.12	NULL	18 / 68	CC collagen
26	-18.04	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
27	-17.96	NULL	5 / 7	GSEA C2SUNODA_CISPLATIN_RESISTANCE_UP
28	-17.76	NULL	7 / 16	GSEA C2ROONQUIST_STROMAL_STIMULATION_UP
29	-17.3	NULL	88 / 683	CC extracellular space
30	-17.3	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
31	-17.2	NULL	7 / 16	GSEA C2GU_PDEF_TARGETS_UP
32	-17.03	NULL	5 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
33	-16.66	NULL	7 / 16	GSEA C2ZHU_CMV_ALL_DN
34	-16	NULL	115 / 1182	CC extracellular region
35	-15.85	NULL	7 / 11	MMML C63CIEJ_MMML 31
36	-15.7	NULL	41 / 183	CC proteinaceous extracellular matrix
37	-15.37	NULL	24 / 119	LymphomBOSOLOWSKI_green total
38	-15.37	NULL	5 / 10	BP negative regulation of fibroblast growth factor receptor signaling pa
39	-14.87	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
40	-14.79	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA

p-values

