

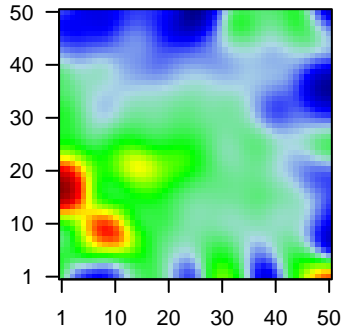
# GW\_235

## Global Summary

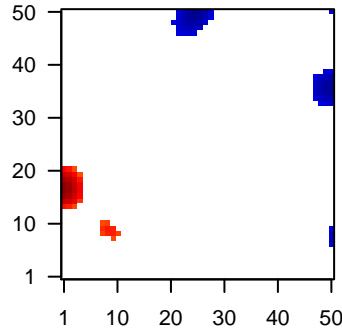
%DE = 0.1  
 # genes with fdr < 0.2 = 999 ( 627 + / 372 - )  
 # genes with fdr < 0.1 = 717 ( 460 + / 257 - )  
 # genes with fdr < 0.05 = 548 ( 359 + / 189 - )  
 # genes with fdr < 0.01 = 399 ( 268 + / 131 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.18  
 <fdr> = 0.9

Profile



Regulated Spots



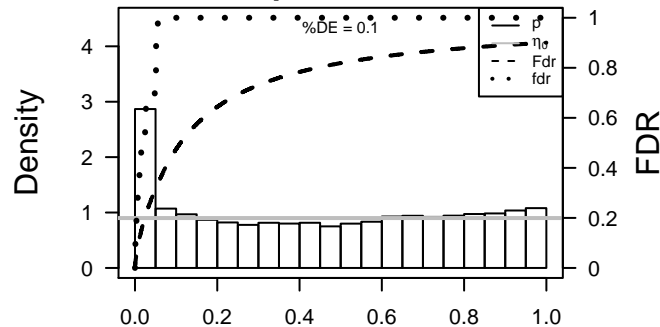
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	164284	1.84	2e-16	1e-13	1 x 3 adenomatosis polyposis coli down-regulated 1-like [Source:HGNC Symbol;Acc:11937]
2	80117	1.81	2e-16	1e-13	2 x 40 ADP-ribosylation factor-like 14 [Source:HGNC Symbol;Acc:11937]
3	140851	1.83	2e-16	1e-13	1 x 5
4	414062	1.89	2e-16	1e-13	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:11937]
5	9560	1.74	2e-16	1e-13	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:11937]
6	970	2.05	2e-16	1e-13	33 x 2 CD70 molecule [Source:HGNC Symbol;Acc:11937]
7	49860	1.73	2e-16	1e-13	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
8	285761	1.66	2e-16	1e-13	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC Symbol;Acc:11937]
9	1673	-1.71	2e-16	1e-13	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	1917	2.06	2e-16	1e-13	25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HGNC Symbol;Acc:11937]
11	2731	1.69	2e-16	1e-13	1 x 38 glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:11937]
12	10457	-1.64	2e-16	1e-13	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;Acc:11937]
13	283120	1.66	2e-16	1e-13	25 x 1 H19, imprinted maternally expressed transcript (non-protein coding) [Source:HGNC Symbol;Acc:11937]
14	3039	3.15	2e-16	1e-13	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
15	3040	3.27	2e-16	1e-13	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
16	3043	3.02	2e-16	1e-13	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
17	3553	2.2	2e-16	1e-13	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
18	3576	2.22	2e-16	1e-13	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
19	192666	1.7	2e-16	1e-13	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
20	3855	1.7	2e-16	1e-13	50 x 11 keratin 7 [Source:HGNC Symbol;Acc:6445]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.03	NULL	4	MMML C6S CIEJ_MMML 23
2	13.44	NULL	717	Chr Chr 16
3	10.67	NULL	10	CC hemoglobin complex
4	10.53	NULL	10	BP cellular response to zinc ion
5	10.3	NULL	7	MMML C6S CIEJ_MMML 13
6	9.08	NULL	11	MF oxygen transporter activity
7	8.04	NULL	11	GSEA C2BIOCARTA_AHSP_PATHWAY
8	7.76	NULL	15	BP negative regulation of growth
9	6.81	NULL	153	MF structural constituent of ribosome
10	6.69	NULL	7	GSEA C2BIOCARTA_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
11	6.65	NULL	36	BP neutrophil chemotaxis
12	6.62	NULL	14	CC endocytic vesicle lumen
13	6.55	NULL	253	BP translation
14	6.48	NULL	92	BP translational elongation
15	6.39	NULL	9	GSEA C2SUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
16	6.15	NULL	16	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
17	6.03	NULL	26	MF oxygen binding
18	5.98	NULL	167	CC ribosome
19	5.87	NULL	417	H.Tiss WIRTH_Immune system
20	5.86	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
<i>Underexpressed</i>				
1	-10.46	NULL	250	Lymphoid ENZ_Stromal signature 1
2	-9.48	NULL	504	Chr Chr 15
3	-8.99	NULL	190	CC extracellular matrix
4	-8.78	NULL	618	Chr Chr 4
5	-7.76	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	-7.5	NULL	1720	Chr Chr 1
7	-6.1	NULL	511	miRNA target-miR-346b
8	-6.03	NULL	16	MMML C6S CIEJ_MMML 1
9	-5.99	NULL	565	miRNA target-miR-326
10	-5.95	NULL	399	miRNA target-miR-548c-3p
11	-5.95	NULL	358	miRNA 3078CA-519C--519B--519A
12	-5.89	NULL	603	miRNA target-miR-326a
13	-5.88	NULL	12	miRNA target-miR-29c
14	-5.88	NULL	457	miRNA 3078CC-124A
15	-5.75	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
16	-5.61	NULL	421	miRNA target-miR-326a
17	-5.61	NULL	127	H.Tiss WIRTH_Muscle
18	-5.48	NULL	318	miRNA target-miR-590-3p
19	-5.39	NULL	69	BP extracellular matrix disassembly
20	-5.36	NULL	517	miRNA target-miR-326a

p-values



# GW\_235

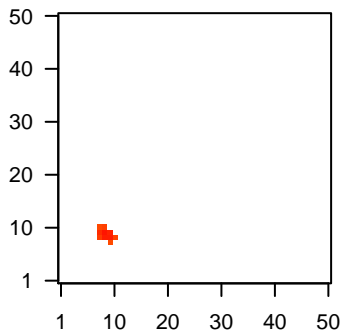
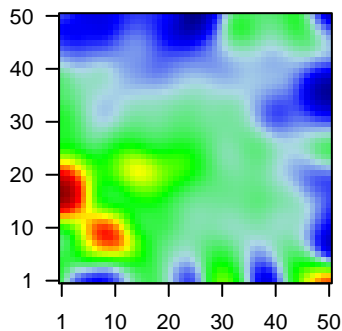
## Local Summary

%DE = 0.58  
 # metagenes = 10  
 # genes = 127  
 # genes in genesets = 127  
 # genes with  $fdr < 0.1$  = 43 ( 43 + / 0 - )  
 # genes with  $fdr < 0.05$  = 32 ( 32 + / 0 - )  
 # genes with  $fdr < 0.01$  = 14 ( 14 + / 0 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.32  
 $\langle FC \rangle$  = 0.35  
 $\langle \text{shrinkage-t} \rangle$  = 12.32  
 $\langle p\text{-value} \rangle$  = 0.03  
 $\langle fdr \rangle$  = 0.7

Profile

Spot



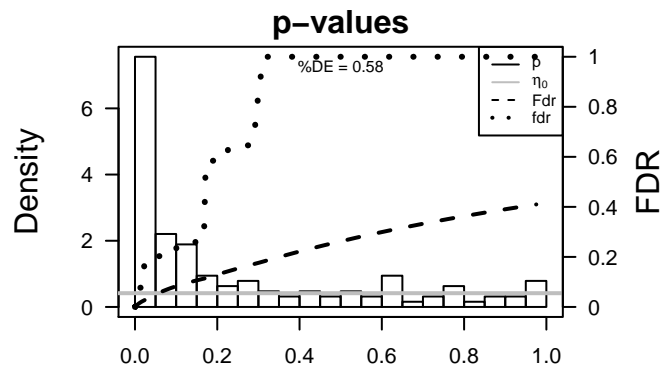
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	55653	1.24	5e-10	3e-06	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Synt
2	339768	1.08	5e-08	2e-05	11 x 9 espin-like [Source:HGNC Symbol;Acc:27937]
3	84080	1.01	4e-07	3e-05	8 x 10 enkurin domain containing 1 [Source:HGNC Symbol;Acc:252
4	2010	0.98	9e-07	4e-05	8 x 10 emerin [Source:HGNC Symbol;Acc:3331]
5	4157	0.95	2e-06	4e-05	10 x 9 melanocortin 1 receptor (alpha melanocyte stimulating hormc
6	51477	0.94	2e-06	5e-05	10 x 10 inositol-3-phosphate synthase 1 [Source:HGNC Symbol;Acc
7	9130	0.93	3e-06	2e-04	8 x 9 family with sequence similarity 50, member A [Source:HGNC
8	57176	0.89	8e-06	3e-04	9 x 11 Valine--tRNA ligase, mitochondrial [Source:UniProtKB/TrEM
9	692227	0.86	2e-05	3e-04	8 x 11 small nucleolar RNA, C/D box 104 [Source:HGNC Symbol;Ac
10	100170841	0.85	2e-05	2e-03	10 x 10 chromosome 17 open reading frame 96 [Source:HGNC Synt
11	64847	0.79	7e-05	2e-03	10 x 9 spermatogenesis associated 20 [Source:HGNC Symbol;Acc:.
12	7390	0.78	9e-05	2e-03	8 x 10 uroporphyrinogen III synthase [Source:HGNC Symbol;Acc:12
13	27043	0.77	1e-04	2e-03	9 x 11 proline, glutamate and leucine rich protein 1 [Source:HGNC S
14	9091	0.76	1e-04	8e-03	9 x 11 phosphatidylinositol glycan anchor biosynthesis, class Q [Sou
15	2794	0.72	3e-04	1e-02	9 x 10 guanine nucleotide binding protein-like 1 [Source:HGNC Syr
16	10953	0.69	5e-04	1e-02	9 x 9 translocase of outer mitochondrial membrane 34 [Source:HGI
17	112752	0.66	8e-04	1e-02	10 x 8 intraflagellar transport 43 homolog (Chlamydomonas) [Source
18	26470	0.66	1e-03	1e-02	10 x 9 seizure related 6 homolog (mouse)-like 2 [Source:HGNC Syr
19	10362	0.65	1e-03	1e-02	9 x 11 high mobility group 20B [Source:HGNC Symbol;Acc:5002]
20	26173	0.63	2e-03	1e-02	8 x 10 integrator complex subunit 1 [Source:HGNC Symbol;Acc:245

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	8.47	NULL	2 / 23	Chr Chr HSCHR6_MHC_DBB
2	8.14	NULL	2 / 9	miRNA target-184
3	8.14	NULL	1 / 10	BP mitotic nuclear envelope reassembly
4	7.9	NULL	1 / 10	BP melanin biosynthetic process
5	7.75	NULL	2 / 11	BP cerebellar Purkinje cell layer development
6	7.52	NULL	1 / 5	miRNA target-205
7	7.47	NULL	1 / 11	BP UV protection
8	7	NULL	1 / 13	BP positive regulation of protein export from nucleus
9	6.6	NULL	1 / 13	GSEA C2WALLACE_JAK2_TARGETS_UP
10	6.17	NULL	1 / 7	GSEA C2BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2
11	6.16	NULL	1 / 15	GSEA C2KEGG_INOSITOL_PHOSPHATE_METABOLISM
12	6.1	NULL	1 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
13	6.07	NULL	1 / 9	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
14	5.99	NULL	3 / 42	BP inositol phosphate metabolic process
15	5.91	NULL	2 / 25	MF phosphatidylinositol-3,4,5-trisphosphate binding
16	5.8	NULL	1 / 12	BP porphyrin-containing compound biosynthetic process
17	5.71	NULL	1 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
18	5.64	NULL	2 / 47	BP skeletal muscle cell differentiation
19	5.61	NULL	1 / 5	miRNA target-196a
20	5.54	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
21	5.54	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
22	5.54	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
23	5.53	NULL	1 / 13	GSEA C2ROVERSI_GLIOMA_COPY_NUMBER_DN
24	5.46	NULL	1 / 9	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
25	5.4	NULL	1 / 11	GSEA C2SMITH_TERT_TARGETS_UP
26	5.35	NULL	1 / 13	GSEA C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
27	5.29	NULL	1 / 14	GSEA C2KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM
28	5.15	NULL	1 / 22	CC nuclear outer membrane
29	5.13	NULL	1 / 21	BP G-protein coupled receptor signaling pathway, coupled to cyclic nu
30	5.13	NULL	1 / 12	GSEA C2BENPORATH_CYCLING_GENES
31	5.13	NULL	1 / 12	GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_UP
32	5.12	NULL	1 / 14	GSEA C2KEGG_GLYCOSYLPHOSPHATIDYLOSITOL_GPI_ANCHOR_BI
33	5.12	NULL	1 / 14	GSEA C2REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
34	5.01	NULL	1 / 23	BP negative regulation of fibroblast proliferation
35	4.92	NULL	1 / 15	GSEA C2REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLOS
36	4.89	NULL	1 / 13	GSEA C2FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_UP
37	4.89	NULL	1 / 13	GSEA C2DOUGLAS_BMI1_TARGETS_UP
38	4.76	NULL	1 / 12	GSEA C2HOSHIDA_LIVER_CANCER_SURVIVAL_UP
39	4.73	NULL	1 / 16	BP preassembly of GPI anchor in ER membrane
40	4.68	NULL	1 / 14	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_1_DN



# GW\_235

## Local Summary

%DE = 0.72  
 # metagenes = 30  
 # genes = 318  
 # genes in genesets = 316

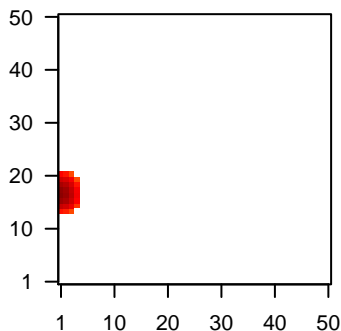
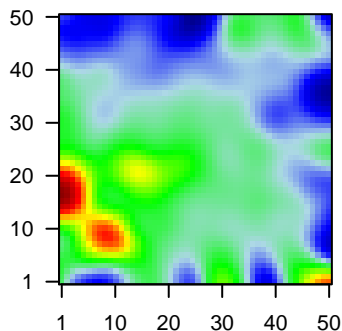
# genes with  $fdr < 0.1 = 152$  ( 151 + / 1 - )  
 # genes with  $fdr < 0.05 = 108$  ( 108 + / 0 - )  
 # genes with  $fdr < 0.01 = 70$  ( 70 + / 0 - )

<r> metagenes = 0.94  
 <r> genes = 0.29

<FC> = 0.38  
 <shrinkage-t> = 13.46  
 <p-value> = 0.02  
 <fdr> = 0.65

Profile

Spot



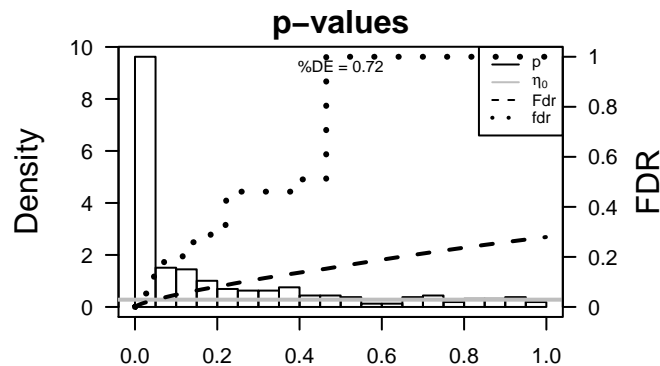
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	283869	1.77	2e-16	2e-14	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	131076	1.59	1e-15	1e-11	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:7399]
3	4495	1.47	1e-13	2e-10	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
4	219931	1.39	3e-12	2e-10	1 x 14 two pore segment channel 2 [Source:HGNC Symbol;Acc:208]
5	51702	1.38	4e-12	2e-07	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;Acc:7399]
6	23246	1.19	2e-09	4e-07	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
7	2194	1.15	7e-09	4e-07	1 x 17 fatty acid synthase [Source:HGNC Symbol;Acc:3594]
8	219927	1.14	1e-08	7e-07	1 x 15 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;Acc:7399]
9	113655	1.12	2e-08	7e-06	1 x 18 major facilitator superfamily domain containing 3 [Source:HGNC Symbol;Acc:7399]
10	8260	1.06	1e-07	7e-06	1 x 20 N(alpha)-acetyltransferase 10, NAtA catalytic subunit [Source:HGNC Symbol;Acc:7399]
11	8270	1.03	2e-07	7e-06	4 x 17 L antigen family, member 3 [Source:HGNC Symbol;Acc:2605]
12	430	1.03	2e-07	7e-06	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:7399]
13	1152	1.01	3e-07	7e-06	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
14	55240	1.01	4e-07	2e-04	3 x 16 STEAP family member 3, metalloredoxase [Source:HGNC Symbol;Acc:7399]
15	57407	0.91	5e-06	2e-04	1 x 20 NmrA-like family domain containing 1 [Source:HGNC Symbol;Acc:7399]
16	10428	0.9	6e-06	2e-04	1 x 15 craniofacial development protein 1 [Source:HGNC Symbol;Acc:7399]
17	51693	0.9	6e-06	2e-04	1 x 21 trafficking protein particle complex 2-like [Source:HGNC Symbol;Acc:7399]
18	3237	0.88	1e-05	2e-04	1 x 16 homeobox D11 [Source:HGNC Symbol;Acc:5134]
19	284085	0.88	1e-05	5e-04	3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]
20	286016	0.85	2e-05	5e-04	1 x 19

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	9.93	NULL	15 / 96	BP rRNA processing
2	9.02	NULL	23 / 153	MF structural constituent of ribosome
3	8.38	NULL	1 / 7	MMML C2GACIEJ_MMML_13
4	8.27	NULL	3 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
5	8.23	NULL	3 / 18	MF ribonucleoprotein complex binding
6	8.01	NULL	27 / 253	BP translation
7	7.95	NULL	32 / 717	Chr Chr 16
8	7.66	NULL	1 / 5	GSEA C2NIELSEN_LIPOSARCOMA_DN
9	7.56	NULL	20 / 167	CC ribosome
10	7.53	NULL	8 / 63	TF MYC_Targets UP
11	7.37	NULL	76 / 1318	CC mitochondrion
12	7.25	NULL	2 / 10	BP creatine metabolic process
13	7	NULL	3 / 13	BP ribosomal small subunit biogenesis
14	6.93	NULL	3 / 15	GSEA C2REACTOME_REMOVAL_OF_DNA_PATCH_CONTAINING_ABASIN
15	6.89	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
16	6.82	NULL	1 / 10	BP cellular response to zinc ion
17	6.73	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
18	6.65	NULL	2 / 21	BP feeding behavior
19	6.61	NULL	2 / 7	GSEA C2REACTOME_SIGNALING_BY_WNT
20	6.55	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
21	6.39	NULL	4 / 10	MF NADH dehydrogenase activity
22	6.29	NULL	1 / 7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
23	6.29	NULL	1 / 7	GSEA C2NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP
24	6.29	NULL	2 / 16	GSEA C2WALLACE_PROSTATE_CANCER_UP
25	6.22	NULL	2 / 16	BP monocyte differentiation
26	6.15	NULL	6 / 19	CC mitochondrial small ribosomal subunit
27	5.92	NULL	2 / 18	BP smooth muscle contraction
28	5.87	NULL	1 / 2	TF MYC_Chromatin_modification UP
29	5.84	NULL	1 / 13	BP cellular response to cadmium ion
30	5.83	NULL	5 / 36	BP ribosome biogenesis
31	5.79	NULL	35 / 579	CC nucleolus
32	5.75	NULL	2 / 10	GSEA C2REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_V
33	5.7	NULL	9 / 118	CC ribonucleoprotein complex
34	5.69	NULL	2 / 16	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
35	5.64	NULL	4 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
36	5.6	NULL	1 / 3	TF MYC_DNA replication UP
37	5.58	NULL	3 / 15	GSEA C2Y_AGING_MIDDLE_DN
38	5.54	NULL	4 / 15	GSEA C2REACTOME_EXTENSION_OF_TELOMERES
39	5.51	NULL	6 / 34	MF NADH dehydrogenase (ubiquinone) activity
40	5.51	NULL	2 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP



# GW\_235

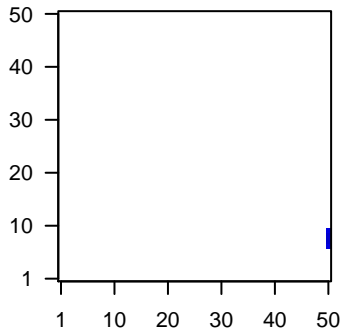
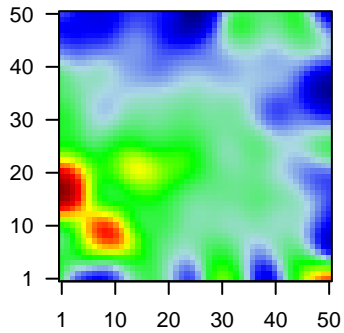
## Local Summary

%DE = 0.62  
 # metagenes = 4  
 # genes = 124  
 # genes in genesets = 123  
 # genes with fdr < 0.1 = 59 ( 5 + / 54 - )  
 # genes with fdr < 0.05 = 41 ( 3 + / 38 - )  
 # genes with fdr < 0.01 = 23 ( 2 + / 21 - )

<r> metagenes = 0.96  
 <r> genes = 0.33  
 <FC> = -0.32  
 <shrinkage-t> = -11.15  
 <p-value> = 0.02  
 <fdr> = 0.65

Profile

Spot



## Local Genelist

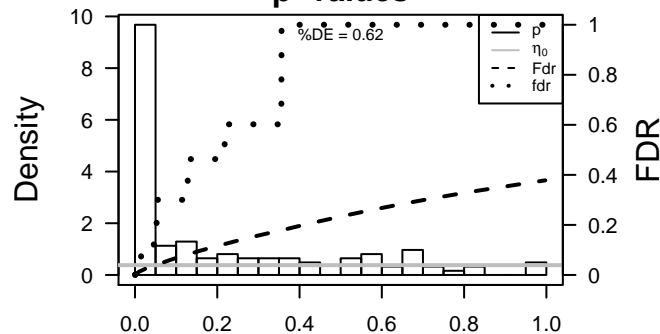
Rank	ID	log(FC)	fdr	p-value	Description
1	347	-1.25	4e-10	2e-07	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
2	92747	-1.17	4e-09	1e-05	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
3	11272	-1.03	2e-07	1e-05	50 x 10 proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
4	7033	-1	4e-07	1e-05	50 x 10 trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
5	7177	-0.99	7e-07	1e-05	50 x 7 tryptase alpha/beta 1 [Source:HGNC Symbol;Acc:12019]
6	92304	-0.98	9e-07	4e-04	50 x 10 secretoglobulin, family 3A, member 1 [Source:HGNC Symbol;A
7	8842	-0.88	1e-05	4e-04	50 x 10 prominin 1 [Source:HGNC Symbol;Acc:9454]
8	3488	-0.85	2e-05	4e-04	50 x 7 insulin-like growth factor binding protein 5 [Source:HGNC Sy
9	58480	-0.84	3e-05	4e-04	50 x 8 ras homolog family member U [Source:HGNC Symbol;Acc:17
10	5918	-0.83	3e-05	1e-03	50 x 9 retinoic acid receptor responder (tazarotene induced) 1 [Sou
11	64284	0.8	6e-05	2e-03	50 x 10 RAB17, member RAS oncogene family [Source:HGNC Symb
12	1359	-0.78	9e-05	2e-03	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
13	79901	-0.74	2e-04	2e-03	50 x 7 cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797]
14	124220	-0.74	2e-04	2e-03	50 x 10 zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
15	8613	-0.73	2e-04	4e-03	50 x 7 phosphatidic acid phosphatase type 2B [Source:HGNC Symb
16	4629	-0.71	3e-04	4e-03	50 x 9 myosin, heavy chain 11, smooth muscle [Source:HGNC Symb
17	1675	0.7	4e-04	4e-03	50 x 9 complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
18	56892	-0.69	5e-04	4e-03	50 x 7 chromosome 8 open reading frame 4 [Source:HGNC Symbol
19	5304	-0.68	7e-04	4e-03	50 x 10 prolactin-induced protein [Source:HGNC Symbol;Acc:8993]
20	6358	-0.67	7e-04	4e-03	50 x 7 chemokine (C-C motif) ligand 14 [Source:HGNC Symbol;Acc

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-28.31	NULL	10 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-15.39	NULL	3 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
3	-13.86	NULL	4 / 17	MF metalloproteinase activity
4	-12.26	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
5	-11.99	NULL	4 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
6	-11.18	NULL	4 / 15	GSEA C2ZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
7	-11.04	NULL	23 / 375	Disease GUDDJ_psooriasis down
8	-10.87	NULL	3 / 27	BP negative regulation of smooth muscle cell proliferation
9	-10.67	NULL	2 / 10	BP angiotensin maturation
10	-10.27	NULL	2 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
11	-10.13	NULL	2 / 11	BP negative regulation of smooth muscle cell migration
12	-10.13	NULL	2 / 14	BP tissue regeneration
13	-9.81	NULL	3 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_I
14	-9.72	NULL	2 / 15	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
15	-9.68	NULL	28 / 683	CC extracellular space
16	-9.6	NULL	38 / 1182	CC extracellular region
17	-9.53	NULL	5 / 61	CC secretory granule
18	-9.34	NULL	2 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
19	-9.33	NULL	1 / 6	GSEA C2TRAYNOR_RETT_SYNDROM_DN
20	-9.22	NULL	2 / 10	BP germ cell migration
21	-9.19	NULL	2 / 13	GSEA C2KEGG_RENIN_ANGIOTENSIN_SYSTEM
22	-9.14	NULL	1 / 2	MMML C2CIEJ_MMML_32
23	-8.96	NULL	2 / 14	BP regulation of Wnt signaling pathway
24	-8.86	NULL	1 / 5	GSEA C2DER_IFN_ALPHA_RESPONSE_DN
25	-8.85	NULL	2 / 12	BP regulation of glucose metabolic process
26	-8.76	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
27	-8.71	NULL	1 / 9	GSEA C2SOUYER_TATI_TARGETS_UP
28	-8.64	NULL	1 / 5	GSEA C2WALK_AML_WITH_T_8_21_TRANSLOCATION
29	-8.48	NULL	3 / 21	MF glycosaminoglycan binding
30	-8.43	NULL	1 / 14	MF lipid transporter activity
31	-8.26	NULL	5 / 115	MF lipid binding
32	-8.26	NULL	2 / 15	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_UP
33	-8.1	NULL	1 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
34	-8.1	NULL	1 / 15	GSEA C2ABE_INNER_EAR
35	-7.98	NULL	9 / 112	MF heparin binding
36	-7.96	NULL	2 / 16	GSEA C2GRAHAM_CML QUIESCENT_VS_NORMAL_DIVIDING_UP
37	-7.95	NULL	1 / 6	GSEA C2DER_IFN_BETA_RESPONSE_DN
38	-7.81	NULL	1 / 16	BP response to reactive oxygen species
39	-7.81	NULL	1 / 16	GSEA C2WILLIAMS_ESR2_TARGETS_UP
40	-7.76	NULL	3 / 28	BP branching morphogenesis of an epithelial tube

p-values



# GW\_235

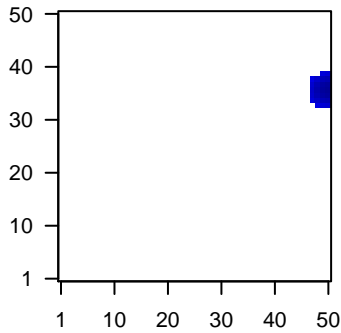
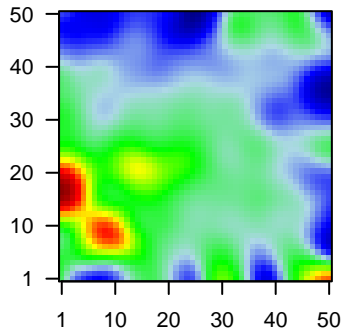
## Local Summary

%DE = 0.56  
 # metagenes = 25  
 # genes = 325  
 # genes in genesets = 324  
 # genes with  $fdr < 0.1$  = 34 ( 2 + / 32 - )  
 # genes with  $fdr < 0.05$  = 14 ( 0 + / 14 - )  
 # genes with  $fdr < 0.01$  = 1 ( 0 + / 1 - )

<r> metagenes = 0.96  
 <r> genes = 0.28  
 <FC> = -0.22  
 <shrinkage-t> = -7.86  
 <p-value> = 0.14  
 <fdr> = 0.87

Profile

Spot



## Local Genelist

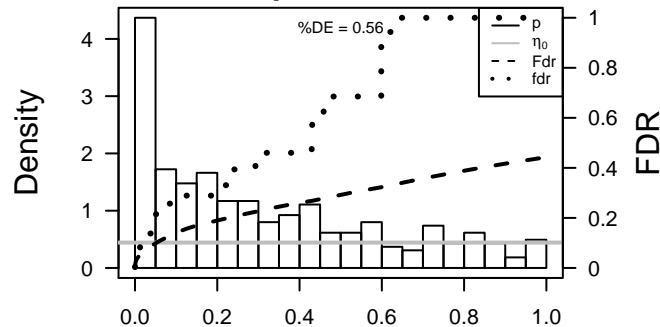
Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	4089	-1.02	3e-07	0.004 50 x 35 SMAD family member 4 [Source:HGNC Symbol;Acc:6770]
2	64083	-0.84	3e-05	0.012 50 x 37 golgi phosphoprotein 3 (coat-protein) [Source:HGNC Symbol]
3	22889	-0.76	1e-04	0.012 50 x 37 KIAA0907 [Source:HGNC Symbol;Acc:29145]
4	4254	-0.73	2e-04	0.012 50 x 36 KIT ligand [Source:HGNC Symbol;Acc:6343]
5	23530	-0.72	3e-04	0.020 50 x 36 nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
6	115426	-0.7	4e-04	0.046 48 x 34 ubiquitin-like with PHD and ring finger domains 2, E3 ubiquiti
7	6429	-0.65	1e-03	0.046 49 x 37 serine/arginine-rich splicing factor 4 [Source:HGNC Symbol;
8	400657	-0.65	1e-03	0.046 49 x 33 long intergenic non-protein coding RNA 909 [Source:HGNC :
9	285636	-0.63	2e-03	0.046 50 x 39 chromosome 5 open reading frame 51 [Source:HGNC Symbc
10	10159	-0.61	2e-03	0.046 50 x 36 ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
11	56947	-0.6	2e-03	0.046 50 x 33 mitochondrial fission factor [Source:HGNC Symbol;Acc:2485f
12	10194	-0.6	3e-03	0.046 50 x 36 teashirt zinc finger homeobox 1 [Source:HGNC Symbol;Acc:1
13	51000	-0.59	3e-03	0.046 50 x 34 solute carrier family 35 (adenosine 3'-phospho 5'-phospho
14	7763	-0.58	3e-03	0.046 50 x 36 zinc finger, AN1-type domain 5 [Source:HGNC Symbol;Acc:1
15	80208	-0.58	3e-03	0.056 50 x 35 spastic paraplegia 11 (autosomal recessive) [Source:HGNC f
16	54495	-0.58	4e-03	0.056 50 x 34 thioredoxin-related transmembrane protein 3 [Source:HGNC
17	6139	0.57	4e-03	0.056 50 x 33 RPL17-C18orf32 readthrough [Source:HGNC Symbol;Acc:4f
18	22862	-0.57	4e-03	0.058 50 x 35 fibronectin type III domain containing 3A [Source:HGNC Sym
19	5612	0.55	5e-03	0.058 50 x 34 protein-kinase, interferon-inducible double stranded RNA de
20	23215	-0.55	5e-03	0.058 50 x 37 proline-rich coiled-coil 2C [Source:HGNC Symbol;Acc:2490c

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.68	NULL	8 / 58	miRNA target set miR-455-5p
2	-9.41	NULL	7 / 45	miRNA target set miR-434
3	-8.74	NULL	5 / 37	miRNA target set miR-3700
4	-8.7	NULL	2 / 10	BP positive regulation of SMAD protein import into nucleus
5	-8.69	NULL	4 / 20	BP protein secretion
6	-8.56	NULL	4 / 15	GSEA C2ZOUILLETTE CLL_13Q14_DELETION_UP
7	-8.52	NULL	16 / 121	miRNA target set miR-5393
8	-8.44	NULL	18 / 186	miRNA target set miR-332
9	-8.41	NULL	3 / 13	MF core promoter proximal region sequence-specific DNA binding
10	-8.29	NULL	16 / 181	miRNA target set miR-3391
11	-8.2	NULL	36 / 421	miRNA target set miR-205e
12	-8.15	NULL	18 / 189	miRNA target set miR-4283
13	-8.15	NULL	15 / 177	miRNA target set miR-3300
14	-7.93	NULL	32 / 463	miRNA target set miR-3301a
15	-7.9	NULL	10 / 80	miRNA target set miR-3301*
16	-7.89	NULL	7 / 57	miRNA target set miR-639
17	-7.86	NULL	9 / 63	miRNA target set miR-606
18	-7.7	NULL	12 / 100	miRNA target set miR-334
19	-7.66	NULL	25 / 303	miRNA target set miR-332b
20	-7.54	NULL	11 / 90	miRNA target set miR-332-5p
21	-7.49	NULL	24 / 311	miRNA target set miR-332c
22	-7.46	NULL	5 / 48	miRNA target set miR-208b
23	-7.44	NULL	4 / 33	miRNA target set miR-332b
24	-7.42	NULL	12 / 122	miRNA target set miR-424b
25	-7.34	NULL	17 / 180	miRNA target set miR-334a
26	-7.27	NULL	31 / 381	miRNA target set miR-205e
27	-7.26	NULL	2 / 13	BP regulation of transforming growth factor beta receptor signaling pat
28	-7.25	NULL	3 / 11	GSEA C2ZARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
29	-7.25	NULL	25 / 311	miRNA target set miR-330
30	-7.21	NULL	2 / 11	GSEA C2ZROZANOV_MMP14_CORRELATED
31	-7.2	NULL	1 / 2	MMML C65CIEJ_MMML_38
32	-7.19	NULL	23 / 325	miRNA target set miR-332d
33	-7.11	NULL	1 / 10	MF RNA polymerase II transcription factor binding transcription factor
34	-7.08	NULL	12 / 114	miRNA target set miR-297
35	-7.08	NULL	4 / 16	Cancer GENTLES_modul14
36	-6.97	NULL	2 / 22	BP positive regulation of BMP signaling pathway
37	-6.94	NULL	20 / 246	miRNA target set miR-551-5p
38	-6.91	NULL	25 / 321	miRNA target set miR-205e
39	-6.89	NULL	14 / 146	miRNA target set miR-332
40	-6.84	NULL	27 / 440	miRNA target set miR-205a

p-values



# GW\_235

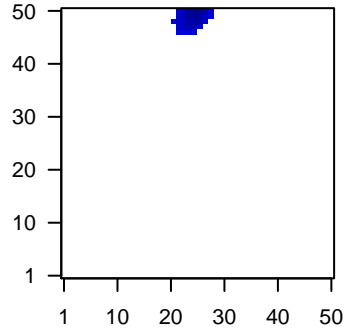
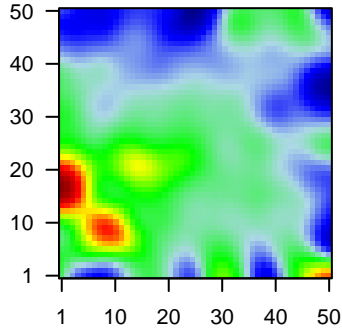
## Local Summary

%DE = 0.59  
 # metagenes = 30  
 # genes = 352  
 # genes in genesets = 347  
 # genes with  $fdr < 0.1$  = 48 ( 9 + / 39 - )  
 # genes with  $fdr < 0.05$  = 19 ( 8 + / 11 - )  
 # genes with  $fdr < 0.01$  = 5 ( 4 + / 1 - )

<r> metagenes = 0.95  
 <r> genes = 0.27  
 <FC> = -0.2  
 <shrinkage-t> = -7.01  
 <p-value> = 0.1  
 <fdr> = 0.85

Profile

Spot



## Local Genelist

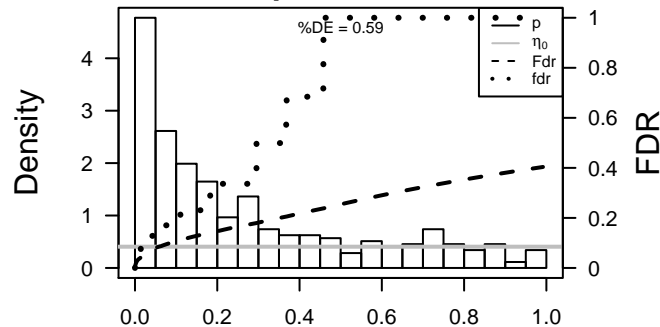
Rank	ID	log(FC)	fdr	p-value	Description
1	2354	1.5	2e-14	5e-07	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:3238]
2	1958	1.17	4e-09	2e-03	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
3	467	0.84	2e-05	2e-03	22 x 50 activating transcription factor 3 [Source:HGNC Symbol;Acc:71]
4	10787	-0.84	3e-05	2e-03	25 x 50 NCK-associated protein 1 [Source:HGNC Symbol;Acc:7666]
5	3725	0.81	4e-05	2e-03	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
6	1843	0.74	5e-05	2e-02	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30]
7	163126	-0.71	3e-04	2e-02	25 x 49 EP300 interacting inhibitor of differentiation 2 [Source:HGNC Symbol;Acc:12862]
8	2353	0.65	4e-04	2e-02	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3238]
9	7538	0.69	5e-04	3e-02	22 x 50 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
10	23191	-0.67	7e-04	3e-02	26 x 50 cytoplasmic FMR1 interacting protein 1 [Source:HGNC Symbol;Acc:12862]
11	22931	-0.66	9e-04	3e-02	26 x 50 RAB18, member RAS oncogene family [Source:HGNC Symbol;Acc:12862]
12	23022	-0.65	1e-03	3e-02	24 x 50 palladin, cytoskeletal associated protein [Source:HGNC Symbol;Acc:12862]
13	11260	-0.64	1e-03	3e-02	25 x 50 exportin, tRNA [Source:HGNC Symbol;Acc:12862]
14	23645	0.63	1e-03	3e-02	22 x 50 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:12862]
15	55013	-0.62	2e-03	3e-02	26 x 47 coiled-coil domain containing 109B [Source:HGNC Symbol;Acc:12862]
16	2970	-0.62	2e-03	4e-02	23 x 50
17	1793	-0.59	3e-03	4e-02	22 x 48 dedicator of cytokinesis 1 [Source:HGNC Symbol;Acc:2987]
18	10413	-0.59	3e-03	4e-02	26 x 50 Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
19	147463	-0.59	3e-03	4e-02	25 x 50 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
20	5604	-0.59	3e-03	5e-02	24 x 50 mitogen-activated protein kinase kinase 1 [Source:HGNC Symbol;Acc:12862]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.93	NULL	24 / 167	miRNA target set miR-548g
2	-9.61	NULL	50 / 436	miRNA target set miR-548n
3	-9.32	NULL	38 / 310	miRNA target set miR-548c
4	-9.01	NULL	33 / 324	miRNA target set miR-548a
5	-8.97	NULL	2 / 10	BP notochord development
6	-8.97	NULL	2 / 10	BP paraxial mesoderm development
7	-8.77	NULL	3 / 10	MF lamin binding
8	-8.39	NULL	29 / 301	miRNA target set miR-548b
9	-8.3	NULL	31 / 313	Glio willscher_GBM_Verhaak-CL_expression_D_up
10	-8.3	NULL	31 / 313	Glio willscher_GBM_Verhaak-MES_expression_D_down
11	-8.3	NULL	31 / 313	Glio willscher_GBM_Verhaak-PNwt_expression_D_up
12	-7.94	NULL	3 / 13	MMML C63CIEJ_MMML 10
13	-7.66	NULL	15 / 99	miRNA target set miR-548e
14	-7.36	NULL	18 / 146	miRNA target set miR-548d
15	-7.18	NULL	16 / 119	miRNA target set miR-548f
16	-7.17	NULL	3 / 16	CC lamellipodium membrane
17	-7.14	NULL	12 / 81	miRNA target set miR-548t-223
18	-7.13	NULL	26 / 217	miRNA target set miR-548m
19	-7.04	NULL	33 / 335	miRNA target set miR-548l-5p
20	-7	NULL	8 / 35	miRNA target set miR-548f-4b
21	-6.78	NULL	12 / 86	miRNA target set miR-548s
22	-6.76	NULL	30 / 284	miRNA target set miR-548g
23	-6.75	NULL	44 / 517	miRNA target set miR-548a
24	-6.75	NULL	2 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
25	-6.68	NULL	21 / 169	miRNA target set miR-548b
26	-6.66	NULL	3 / 15	GSEA C2REACTOME_SIGNALING_BY_EGFR
27	-6.52	NULL	34 / 336	miRNA target set miR-548d-5p
28	-6.48	NULL	16 / 130	miRNA target set miR-548s
29	-6.43	NULL	28 / 271	miRNA target set miR-548n
30	-6.42	NULL	30 / 364	miRNA target set miR-548b-3p
31	-6.41	NULL	31 / 318	miRNA target set miR-548c-3p
32	-6.4	NULL	30 / 321	miRNA target set miR-548a-5p
33	-6.35	NULL	17 / 134	miRNA target set miR-548e
34	-6.33	NULL	34 / 399	miRNA target set miR-548c-3p
35	-6.29	NULL	5 / 14	GSEA C2CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN
36	-6.28	NULL	19 / 185	Cancer SPANG_LPS-index2
37	-6.25	NULL	3 / 11	BP nuclear envelope organization
38	-6.21	NULL	10 / 74	miRNA target set miR-548f
39	-6.18	NULL	4 / 15	BP COPII vesicle coating
40	-6.17	NULL	32 / 387	miRNA target set miR-548a

p-values



# GW\_235

## Local Summary

%DE = 0.81  
 # metagenes = 1  
 # genes = 81  
 # genes in genesets = 80  
 # genes with fdr < 0.1 = 40 ( 3 + / 37 - )  
 # genes with fdr < 0.05 = 31 ( 3 + / 28 - )  
 # genes with fdr < 0.01 = 19 ( 3 + / 16 - )

<r> metagenes = NA

<r> genes = 0.35

<FC> = -0.35

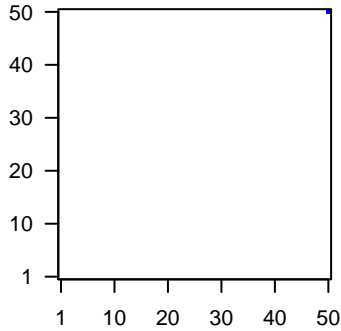
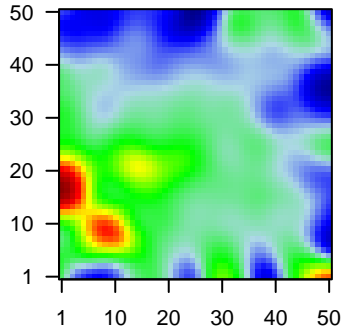
<shrinkage-t> = -12.24

<p-value> = 0.01

<fdr> = 0.62

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4922	-1.52	2e-14	2e-08	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
2	23321	-1.21	1e-09	3e-08	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:15974]
3	339512	-1.18	3e-09	6e-06	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
4	154664	-1.01	4e-07	2e-05	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Sou
5	26256	0.95	2e-06	3e-04	50 x 50 calcium binding tyrosine-(Y)-phosphorylation regulated [Sou
6	7358	-0.82	4e-05	3e-04	50 x 50 UDP-glucose 6-dehydrogenase [Source:HGNC Symbol;Acc:
7	29785	-0.81	5e-05	3e-04	50 x 50 cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc
8	216	-0.81	5e-05	4e-04	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	56548	-0.78	1e-04	4e-04	50 x 50 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 [
10	6446	-0.7	1e-04	4e-04	50 x 50 serum/glucocorticoid regulated kinase 1 [Source:HGNC Syml
11	6657	-0.76	1e-04	1e-03	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbx
12	256764	0.73	2e-04	1e-03	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
13	2719	-0.72	3e-04	2e-03	50 x 50 glypican 3 [Source:HGNC Symbol;Acc:4451]
14	1056	0.7	4e-04	3e-03	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
15	94234	-0.67	8e-04	3e-03	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
16	10655	-0.65	1e-03	3e-03	50 x 50 doublesex and mab-3 related transcription factor 2 [Source:H
17	8745	-0.64	1e-03	3e-03	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
18	3790	-0.64	1e-03	3e-03	50 x 50 potassium voltage-gated channel, delayed-rectifier, subfamil
19	80896	-0.63	1e-03	5e-03	50 x 50 N-acetylneuraminate pyruvate lyase (dihydropicolinate synt
20	2730	-0.62	2e-03	1e-02	50 x 50 glutamate-cysteine ligase, modifier subunit [Source:HGNC S

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-27.68	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	-21.96	NULL	3 / 13	BP regulation of blood vessel size
3	-19.79	NULL	3 / 16	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G1_DN
4	-14.06	NULL	1 / 11	Glio neurons_glio
5	-13.85	NULL	4 / 15	GSEA C2REACTOME_GlutATHIONE_CONJUGATION
6	-13.43	NULL	2 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
7	-12.25	NULL	1 / 4	GSEA C2MYLYKANGAS_AMPLIFICATION_HOT_SPOT_13
8	-12.04	NULL	8 / 34	BP glutathione metabolic process
9	-12.02	NULL	11 / 119	BP xenobiotic metabolic process
10	-11.75	NULL	1 / 15	MF neuropeptide hormone activity
11	-11.49	NULL	6 / 25	BP glutathione derivative biosynthetic process
12	-11.38	NULL	5 / 15	GSEA C2KEGG_GlutATHIONE_METABOLISM
13	-11.2	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
14	-10.67	NULL	2 / 10	GSEA C2ONRAD_STEM_CELL
15	-10.64	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
16	-10.64	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
17	-10.44	NULL	2 / 16	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP
18	-10.31	NULL	2 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
19	-10.15	NULL	2 / 9	GSEA C2REACTOME_GLUcURONIDATION
20	-9.97	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
21	-9.96	NULL	2 / 15	GSEA C2ODONNELL_TFRC_TARGETS_UP
22	-9.68	NULL	1 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
23	-9.44	NULL	2 / 12	BP glutamate metabolic process
24	-9.41	NULL	2 / 15	GSEA C2REACTOME_PHASE_II_CONJUGATION
25	-9.3	NULL	1 / 15	GSEA C2BARRIER_COLON_CANCER_RECURRENCE_UP
26	-9.25	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
27	-9.14	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
28	-9.14	NULL	1 / 7	miRNA target-145
29	-9.01	NULL	2 / 13	GSEA C2SINGH_NFE2L2_TARGETS
30	-8.96	NULL	1 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
31	-8.95	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
32	-8.54	NULL	2 / 20	BP long-term memory
33	-8.43	NULL	1 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
34	-8.43	NULL	1 / 8	miRNA target-450
35	-8.33	NULL	1 / 9	GSEA C2REACTOME_CytoCHROME_P450_ARRANGED_BY_SUBSTRAT
36	-8.31	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
37	-8.31	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
38	-8.11	NULL	1 / 19	miRNA target-380-5P
39	-7.98	NULL	2 / 16	BP glutathione biosynthetic process
40	-7.9	NULL	2 / 23	BP stem cell differentiation

