

# GW\_092

## Global Summary

%DE = 0.13  
 # genes with fdr < 0.2 = 1430 ( 800 + / 630 - )  
 # genes with fdr < 0.1 = 904 ( 510 + / 394 - )  
 # genes with fdr < 0.05 = 627 ( 367 + / 260 - )  
 # genes with fdr < 0.01 = 320 ( 210 + / 110 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.18  
 <fdr> = 0.87

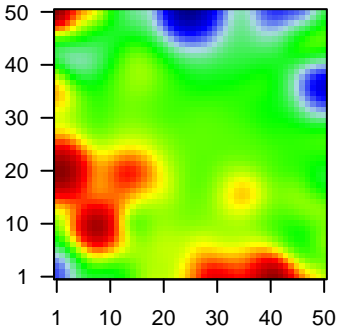
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	339512	2.52	2e-16 4e-13	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
2	49860	2.13	2e-16 4e-13	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
3	26298	-1.96	2e-16 4e-13	4 x 50 ets homologous factor [Source:HGNC Symbol;Acc:3246]
4	2167	2.57	2e-16 4e-13	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
5	2353	-1.84	2e-16 4e-13	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC
6	547	2.01	2e-16 4e-13	12 x 9 kinesin family member 1A [Source:HGNC Symbol;Acc:888]
7	4316	2.8	2e-16 4e-13	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC
8	200958	1.97	2e-16 4e-13	6 x 50 mucin 20, cell surface associated [Source:HGNC Symbol;Acc
9	7053	2.08	2e-16 4e-13	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
10	2877	1.82	1e-15 1e-11	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
11	79852	1.8	2e-15 2e-11	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
12	54414	1.77	5e-15 2e-11	1 x 50 sialic acid acetyltransferase [Source:HGNC Symbol;Acc:18187]
13	655	1.77	6e-15 2e-11	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
14	1830	-1.77	7e-15 1e-10	1 x 48 desmoglein 3 [Source:HGNC Symbol;Acc:3050]
15	7431	-1.73	2e-14 1e-10	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]
16	26239	1.73	2e-14 1e-10	5 x 45 late cornified envelope 2B [Source:HGNC Symbol;Acc:16610]
17	760	-1.72	3e-14 6e-10	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	8644	1.7	7e-14 1e-09	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
19	4014	1.67	2e-13 1e-09	2 x 48 loricrin [Source:HGNC Symbol;Acc:6663]
20	218	1.66	3e-13 3e-09	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC

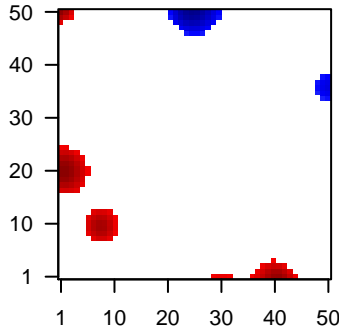
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.08	NULL	1135	Chr Chr 19
2	11.81	NULL	42	BP keratinization
3	10.26	NULL	135	H.Tiss WIRTH_Mucosa
4	8.05	NULL	21	CC cornified envelope
5	7.73	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IFR3
6	7.54	NULL	51	BP type I interferon signaling pathway
7	7.35	NULL	1720	Chr Chr 1
8	6.84	NULL	23	Chr Chr HSCR6_MHC_DBB
9	6.46	NULL	13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
10	6.11	NULL	53	BP keratinocyte differentiation
11	6.05	NULL	717	Chr Chr 16
12	5.93	NULL	918	Chr Chr 17
13	5.86	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
14	5.77	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
15	5.33	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
16	5.32	NULL	16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
17	5.21	NULL	45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
18	5.2	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_JMIQUIMOD
19	5	NULL	31	BP negative regulation of viral genome replication
20	4.97	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
<i>Underexpressed</i>				
1	-11.93	NULL	436	miRNA target-miR-550n
2	-11.09	NULL	262	miRNA target-miR-550l
3	-10.58	NULL	232	Chr Chr 18
4	-10.24	NULL	246	miRNA target-miR-550d-5p
5	-10.16	NULL	335	miRNA target-miR-550e-5p
6	-10.15	NULL	315	miRNA target-miR-550c
7	-9.75	NULL	336	miRNA target-miR-550d-5p
8	-9.67	NULL	603	miRNA target-miR-550a
9	-9.65	NULL	313	miRNA target-miR-550g
10	-9.59	NULL	307	miRNA target-miR-550c-5p
11	-9.58	NULL	494	miRNA target-miR-550f
12	-9.56	NULL	268	miRNA target-miR-550b
13	-9.47	NULL	391	miRNA 3UTRA--181A--181B--181C--181D
14	-9.45	NULL	318	miRNA target-miR-550-3p
15	-9.42	NULL	463	miRNA target-miR-550a
16	-9.37	NULL	300	miRNA target-miR-550e
17	-9.33	NULL	421	miRNA target-miR-550g
18	-9.31	NULL	495	miRNA target-miR-550f
19	-9.26	NULL	217	miRNA target-miR-550m
20	-9.24	NULL	399	miRNA target-miR-550c-3p

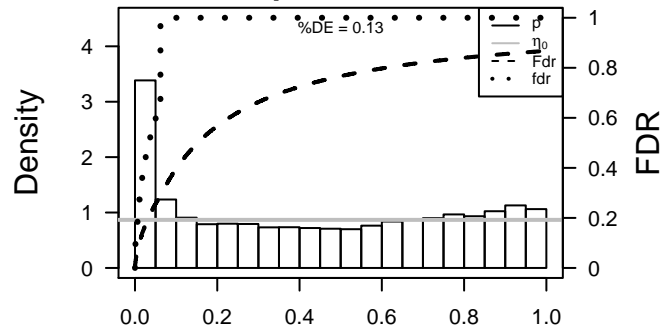
Profile



Regulated Spots



p-values

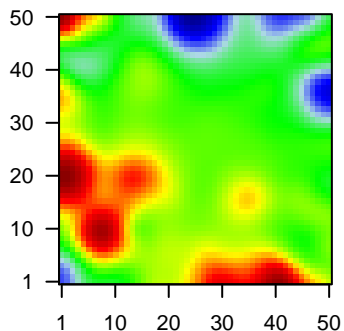


# GW\_092

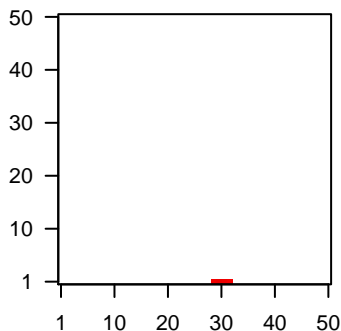
## Local Summary

%DE = 0.7  
 # metagenes = 4  
 # genes = 117  
 # genes in genesets = 115  
  
 # genes with  $fdr < 0.1$  = 53 ( 48 + / 5 - )  
 # genes with  $fdr < 0.05$  = 52 ( 48 + / 4 - )  
 # genes with  $fdr < 0.01$  = 36 ( 33 + / 3 - )  
  
 $\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.44  
  
 $\langle FC \rangle = 0.34$   
 $\langle \text{shrinkage-t} \rangle = 11.94$   
 $\langle p\text{-value} \rangle = 0.01$   
 $\langle fdr \rangle = 0.56$

Profile



Spot



## Local Genelist

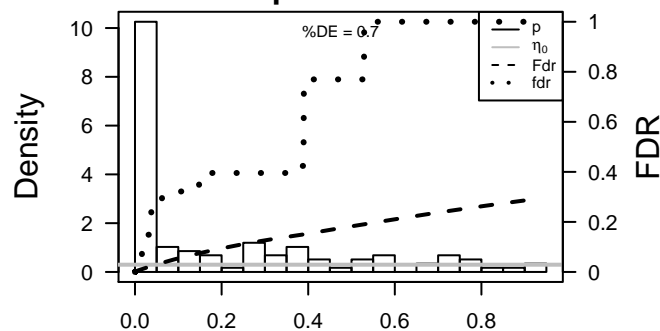
Rank	ID	log(FC)	fdr	p-value	Description
1	4600	1.57	5e-12	3e-08	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HGNC Symbol;Acc:1037]
2	9636	1.39	9e-10	1e-06	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:406]
3	51296	1.24	5e-08	1e-06	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3 [
4	684	1.22	8e-08	3e-06	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
5	10581	1.09	2e-07	1e-05	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC S
6	10410	1.04	6e-07	1e-05	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC S
7	8519	1.12	7e-07	2e-05	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC S
8	2537	1.09	2e-06	2e-05	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;I
9	629	1.08	2e-06	1e-04	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
10	3430	1.01	9e-06	1e-04	32 x 1 interferon-induced protein 35 [Source:HGNC Symbol;Acc:53]
11	54739	1	1e-05	1e-04	32 x 1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
12	4599	0.91	1e-05	2e-04	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible
13	341405	0.97	2e-05	5e-04	30 x 1 ankyrin repeat domain 33 [Source:HGNC Symbol;Acc:13788]
14	5359	-0.94	3e-05	7e-04	32 x 1 phospholipid scramblase 1 [Source:HGNC Symbol;Acc:9092]
15	2633	-0.9	7e-05	7e-04	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HGNC
16	4061	0.89	9e-05	7e-04	32 x 1 lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
17	475	0.89	9e-05	7e-04	29 x 1 antioxidant 1 copper chaperone [Source:HGNC Symbol;Acc:1
18	84875	0.88	1e-04	2e-03	32 x 1 poly (ADP-ribose) polymerase family, member 10 [Source:HC
19	64374	0.86	2e-04	6e-03	29 x 1 SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:
20	3959	0.8	4e-04	6e-03	32 x 1 lectin, galactoside-binding, soluble, 3 binding protein [Source

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	50.42	NULL	7 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
2	47.07	NULL	28 / 51	BP type I interferon signaling pathway
3	44.06	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	40.54	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
5	39.85	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
6	36.14	NULL	10 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	31.56	NULL	13 / 31	BP negative regulation of viral genome replication
8	31.31	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
9	31.3	NULL	10 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQIMOD
10	23.4	NULL	5 / 18	BP response to interferon-gamma
11	22.18	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
12	21.83	NULL	26 / 109	BP response to virus
13	21.76	NULL	33 / 204	BP cytokine-mediated signaling pathway
14	21.72	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
15	21.65	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
16	21.25	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
17	20.34	NULL	3 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
18	19.88	NULL	30 / 123	BP defense response to virus
19	18.12	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
20	17.85	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
21	17.29	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
22	16.86	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
23	16.62	NULL	5 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_LB_DN
24	16.27	NULL	2 / 2	MMML C2BACIEJ_MMML_27
25	16.13	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
26	15.99	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
27	14.16	NULL	30 / 274	Lymphoma C2SPANG_IL21_DN
28	13.92	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
29	13.8	NULL	2 / 11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_UP
30	12.86	NULL	3 / 16	GSEA C2NOJIMA_SFRP2_TARGETS_DN
31	12.37	NULL	2 / 6	GSEA C2SHIKAWA_STING_SIGNALING
32	12.19	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
33	12.01	NULL	5 / 6	Lymphoma C2BAVE_MHCCII_BL_DN
34	11.6	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
35	11.55	NULL	6 / 32	BP negative regulation of type I interferon production
36	11.54	NULL	2 / 15	GSEA C2CHOW_RASSF1_TARGETS_DN
37	11.45	NULL	1 / 6	GSEA C2OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE
38	11.05	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
39	10.75	NULL	2 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
40	10.66	NULL	3 / 15	CC high-density lipoprotein particle

p-values



# GW\_092

## Local Summary

%DE = 0.71  
 # metagenes = 22  
 # genes = 324  
 # genes in genesets = 297

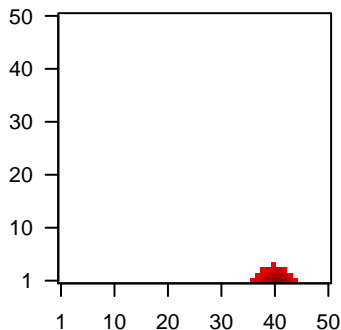
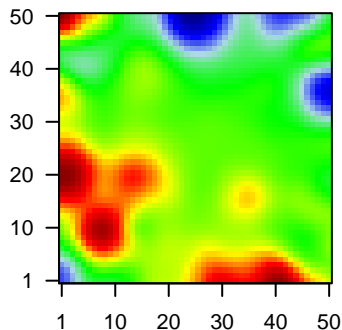
# genes with  $fdr < 0.1 = 150$  ( 148 + / 2 - )  
 # genes with  $fdr < 0.05 = 114$  ( 113 + / 1 - )  
 # genes with  $fdr < 0.01 = 35$  ( 34 + / 1 - )

<r> metagenes = 0.95  
 <r> genes = 0.43

<FC> = 0.4  
 <shrinkage-t> = 13.89  
 <p-value> = 0.04  
 <fdr> = 0.65

Profile

Spot



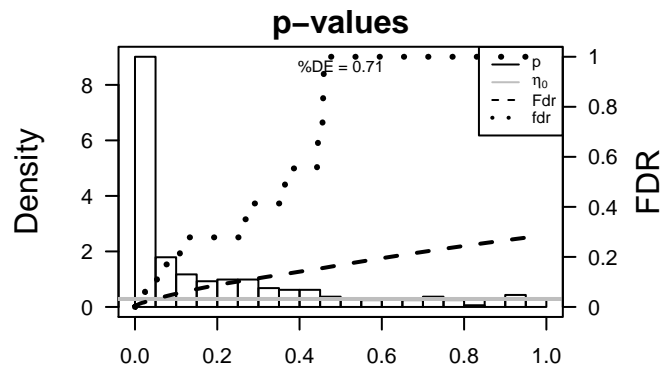
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84446	1.26	3e-08	1e-05	43 x 1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:186
2	22809	1.16	3e-07	1e-05	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:7
3	5152	1.16	3e-07	2e-05	40 x 3 phosphodiesterase 9A [Source:HGNC Symbol;Acc:8795]
4	51326	1.14	5e-07	2e-04	42 x 1 ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc
5	5256	1.04	5e-06	2e-04	40 x 1 phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
6	404093	1.03	5e-06	4e-04	39 x 1 CUE domain containing 1 [Source:HGNC Symbol;Acc:31350]
7	11322	0.99	1e-05	4e-04	44 x 1 transmembrane channel-like 6 [Source:HGNC Symbol;Acc:1
8	79058	0.97	2e-05	4e-04	41 x 1 alveolar soft part sarcoma chromosome region, candidate 1 [
9	90639	0.97	2e-05	4e-04	40 x 1 cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
10	152485	0.96	2e-05	4e-04	41 x 1 zinc finger protein 827 [Source:HGNC Symbol;Acc:27193]
11	374882	0.96	3e-05	1e-03	42 x 1 transmembrane protein 205 [Source:HGNC Symbol;Acc:296
12	51281	0.93	4e-05	1e-03	42 x 1 ankyrin repeat and MYND domain containing 1 [Source:HGN
13	80233	0.92	5e-05	3e-03	41 x 1 chromosome 17 open reading frame 70 [Source:HGNC Symt
14	56834	0.89	9e-05	3e-03	43 x 1 G protein-coupled receptor 137 [Source:HGNC Symbol;Acc:.
15	84893	0.88	1e-04	4e-03	42 x 1 F-box protein, helicase, 18 [Source:HGNC Symbol;Acc:1362
16	9181	0.86	2e-04	4e-03	44 x 1 Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Source
17	1762	0.84	2e-04	4e-03	40 x 1 dystrophia myotonica, WD repeat containing [Source:HGNC
18	80726	0.83	3e-04	4e-03	41 x 2 KIAA1683 [Source:HGNC Symbol;Acc:29350]
19	401261	0.82	3e-04	4e-03	41 x 1
20	3127	-0.82	3e-04	4e-03	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	9.61	NULL	3 / 16	BP negative regulation of neurogenesis
2	8.67	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
3	8.46	NULL	2 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_UP
4	8.23	NULL	1 / 2	miRNA target-193a
5	7.81	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
6	7.14	NULL	3 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
7	6.76	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
8	6.68	NULL	2 / 10	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
9	6.19	NULL	2 / 13	GSEA C2ST_GAQ_PATHWAY
10	6.19	NULL	2 / 13	GSEA C2ST_GA13_PATHWAY
11	6.15	NULL	44 / 1135	Chr Chr 19
12	5.91	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
13	5.91	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
14	5.8	NULL	2 / 10	BP cellular response to peptide hormone stimulus
15	5.76	NULL	1 / 11	MF tau-protein kinase activity
16	5.69	NULL	3 / 15	GSEA C2WANG_CLIM2_TARGETS_UP
17	5.69	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
18	5.67	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
19	5.61	NULL	3 / 23	BP G2 DNA damage checkpoint
20	5.61	NULL	2 / 13	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
21	5.55	NULL	2 / 14	GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_DN
22	5.25	NULL	1 / 11	GSEA C2TRACEY_RESISTANCE_TO_IFNA2_DN
23	5.17	NULL	2 / 19	BP negative regulation of extrinsic apoptotic signaling pathway via dea
24	5.14	NULL	2 / 15	GSEA C2FIRESTEIN_PROLIFERATION
25	5.06	NULL	2 / 19	BP establishment of cell polarity
26	5.03	NULL	2 / 15	GSEA C2ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE
27	5.01	NULL	2 / 19	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
28	5	NULL	2 / 17	BP negative regulation of interleukin-6 production
29	4.99	NULL	1 / 12	GSEA C2PENG_LEUCINE_DEPRIVATION_UP
30	4.98	NULL	1 / 14	BP centrosome duplication
31	4.8	NULL	2 / 28	TF Tissue/AQUERIZAS_Liver
32	4.76	NULL	2 / 29	TF Tissue/AQUERIZAS_Smooth muscle
33	4.75	NULL	1 / 13	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN
34	4.55	NULL	3 / 34	MF hydrolase activity, hydrolyzing O-glycosyl compounds
35	4.54	NULL	1 / 14	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_A
36	4.54	NULL	1 / 14	TF Tissue/AQUERIZAS_Fetal liver
37	4.47	NULL	3 / 24	BP negative regulation of T cell proliferation
38	4.45	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
39	4.43	NULL	3 / 14	MMML C2CIEJ_MMML 8
40	4.35	NULL	1 / 15	GSEA C2GRIGE_AMINO_ACID_DEPRIVATION



# GW\_092

## Local Summary

%DE = 0.77  
 # metagenes = 32  
 # genes = 305  
 # genes in genesets = 303

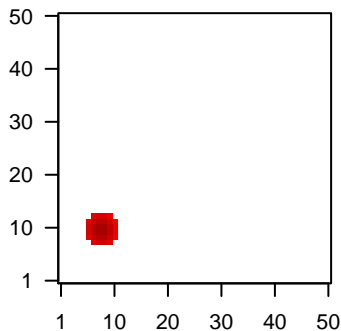
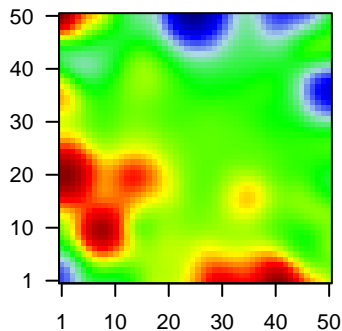
# genes with  $fdr < 0.1 = 180$  ( 180 + / 0 - )  
 # genes with  $fdr < 0.05 = 126$  ( 126 + / 0 - )  
 # genes with  $fdr < 0.01 = 43$  ( 43 + / 0 - )

<r> metagenes = 0.93  
 <r> genes = 0.29

<FC> = 0.42  
 <shrinkage-t> = 14.84  
 <p-value> = 0.04  
 <fdr> = 0.64

Profile

Spot



## Local Genelist

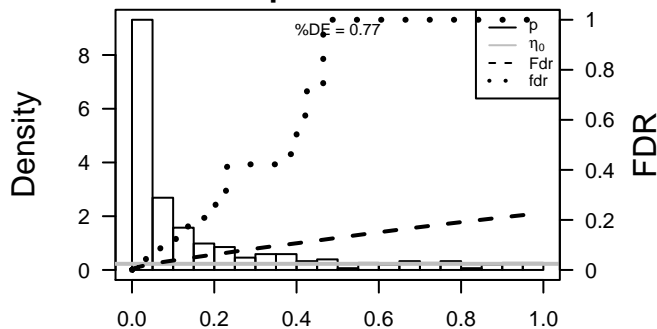
Rank	ID	log(FC)	fdr	p-value	Description
1	64847	1.08	2e-06	7e-05	10 x 9 spermatogenesis associated 20 [Source:HGNC Symbol;Acc:10800]
2	4157	1.08	2e-06	1e-04	10 x 9 melanocortin 1 receptor (alpha melanocyte stimulating hormc
3	692227	1.06	3e-06	3e-04	8 x 11 small nucleolar RNA, C/D box 104 [Source:HGNC Symbol;Acc:10800]
4	57414	1	1e-05	3e-04	9 x 10 rhomboid domain containing 2 [Source:HGNC Symbol;Acc:21522]
5	200185	1	1e-05	3e-04	8 x 10 keratinocyte associated protein 2 [Source:HGNC Symbol;Acc:10800]
6	29937	0.98	2e-05	5e-04	11 x 9 neudesin neurotrophic factor [Source:HGNC Symbol;Acc:30300]
7	23368	0.96	2e-05	6e-04	10 x 12 protein phosphatase 1, regulatory subunit 13B [Source:HGNC Symbol;Acc:10800]
8	56893	0.94	3e-05	6e-04	9 x 12 ubiquitin 4 [Source:HGNC Symbol;Acc:1237]
9	11267	0.93	4e-05	6e-04	9 x 10 SNF8, ESCRT-II complex subunit [Source:HGNC Symbol;Acc:10800]
10	57176	0.92	5e-05	6e-04	9 x 11 Valine--tRNA ligase, mitochondrial [Source:UniProtKB/TrEMBL]
11	10629	0.91	6e-05	6e-04	9 x 11 TAF6-like RNA polymerase II, p300/CBP-associated factor (I
12	140467	0.91	7e-05	2e-03	9 x 8 zinc finger protein 358 [Source:HGNC Symbol;Acc:16838]
13	7466	0.89	1e-04	3e-03	8 x 8 Wolfram syndrome 1 (wolframin) [Source:HGNC Symbol;Acc:10800]
14	55653	0.85	2e-04	3e-03	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Symbol;Acc:10800]
15	79894	0.85	2e-04	6e-03	9 x 12 zinc finger protein 672 [Source:HGNC Symbol;Acc:26179]
16	2794	0.82	3e-04	6e-03	9 x 10 guanine nucleotide binding protein-like 1 [Source:HGNC Symbol;Acc:10800]
17	26262	0.8	4e-04	6e-03	8 x 10 tetraspanin 17 [Source:HGNC Symbol;Acc:13594]
18	10498	0.78	6e-04	6e-03	7 x 11 coactivator-associated arginine methyltransferase 1 [Source:HGNC Symbol;Acc:10800]
19	79414	0.78	6e-04	6e-03	7 x 9 leucine rich repeat and fibronectin type III domain containing 1
20	256281	0.77	7e-04	6e-03	11 x 9 nudix (nucleoside diphosphate linked moiety X)-type motif 14

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	8.45	NULL	62 / 1135	Chr Chr 19
2	7.81	NULL	3 / 10	CC oligosaccharyltransferase complex
3	7.02	NULL	10 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
4	6.78	NULL	4 / 19	MF hydrolase activity, acting on acid anhydrides, in phosphorus-contain
5	6.75	NULL	2 / 13	CC STAGA complex
6	6.66	NULL	3 / 23	Chr Chr HSCHR6_MHC_DBB
7	6.46	NULL	3 / 22	MF polyubiquitin binding
8	6.38	NULL	2 / 12	GSEA C2BROWNE_HCMV_INFECTION_14HR_UP
9	6.29	NULL	1 / 5	GSEA C2NAGY_PCAF_COMPONENTS_HUMAN
10	6.1	NULL	2 / 11	BP UV protection
11	5.84	NULL	2 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
12	5.71	NULL	2 / 11	BP cerebellar Purkinje cell layer development
13	5.54	NULL	3 / 16	BP intracellular steroid hormone receptor signaling pathway
14	5.53	NULL	3 / 15	GSEA C2REACTOME_ERK_MAPK_TARGETS
15	5.53	NULL	3 / 15	GSEA C2REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI
16	5.52	NULL	4 / 15	GSEA C2KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROIT
17	5.45	NULL	4 / 26	BP histone acetylation
18	5.36	NULL	4 / 28	MF ribosome binding
19	5.31	NULL	3 / 16	GSEA C2REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED
20	5.07	NULL	2 / 15	BP intracellular estrogen receptor signaling pathway
21	5.03	NULL	1 / 10	BP melanin biosynthetic process
22	5.01	NULL	2 / 12	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
23	4.98	NULL	2 / 12	GSEA C2KAAB_FAILED_HEART_ATRIUM_UP
24	4.87	NULL	2 / 13	GSEA C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
25	4.81	NULL	2 / 12	GSEA C2TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
26	4.8	NULL	4 / 42	MF ligand-dependent nuclear receptor transcription coactivator activity
27	4.77	NULL	1 / 8	GSEA C2NAGY_STAGA_COMPONENTS_HUMAN
28	4.77	NULL	1 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_20P13_AMPLICON
29	4.76	NULL	2 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
30	4.65	NULL	2 / 14	GSEA C2KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
31	4.65	NULL	2 / 14	GSEA C2REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
32	4.62	NULL	2 / 16	GSEA C2FAELT_B_CLL_WITH_VH3_21_UP
33	4.57	NULL	3 / 12	BP heparan sulfate proteoglycan biosynthetic process
34	4.57	NULL	3 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
35	4.55	NULL	2 / 15	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
36	4.45	NULL	2 / 15	GSEA C2REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
37	4.44	NULL	2 / 15	MF acetylglucosaminyltransferase activity
38	4.4	NULL	1 / 7	miRNA target sites
39	4.38	NULL	2 / 9	miRNA target sites
40	4.36	NULL	3 / 22	MF N-acetyltransferase activity

p-values



# GW\_092

## Local Summary

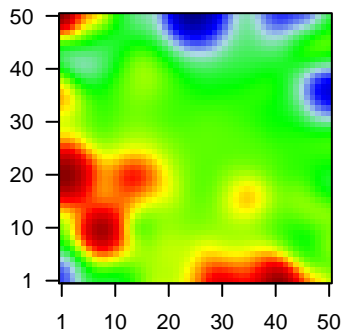
%DE = 0.72  
 # metagenes = 42  
 # genes = 399  
 # genes in genesets = 394

# genes with  $fdr < 0.1$  = 196 ( 195 + / 1 - )  
 # genes with  $fdr < 0.05$  = 116 ( 115 + / 1 - )  
 # genes with  $fdr < 0.01$  = 44 ( 43 + / 1 - )

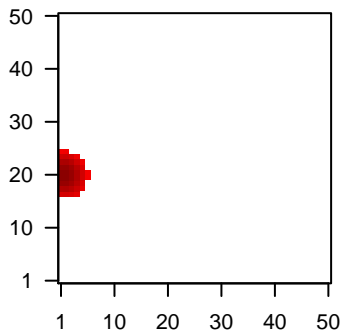
$\langle r \rangle$  metagenes = 0.94  
 $\langle r \rangle$  genes = 0.26

$\langle FC \rangle = 0.4$   
 $\langle \text{shrinkage-t} \rangle = 14.06$   
 $\langle p\text{-value} \rangle = 0.04$   
 $\langle fdr \rangle = 0.67$

Profile



Spot



## Local Genelist

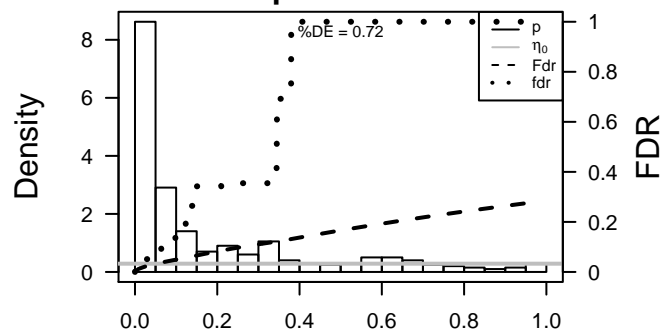
Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	80154	1.25	3e-08	5e-05	1 x 23
2	2194	1.14	5e-07	5e-05	1 x 17
3	51181	1.11	9e-07	7e-05	2 x 21
4	230	1.09	2e-06	3e-04	2 x 17
5	2288	1.04	5e-06	3e-04	1 x 19
6	118881	1.02	7e-06	2e-03	1 x 22
7	284085	0.95	3e-05	2e-03	3 x 18
8	25845	0.94	4e-05	2e-03	2 x 23
9	5639	0.92	5e-05	2e-03	1 x 22
10	27237	0.9	8e-05	2e-03	2 x 20
11	23623	0.89	9e-05	2e-03	2 x 23
12	8570	0.89	9e-05	4e-03	2 x 19
13	286016	0.86	1e-04	4e-03	1 x 19
14	51693	0.81	4e-04	4e-03	1 x 21
15	85359	0.81	4e-04	4e-03	2 x 20
16	10489	0.8	4e-04	4e-03	1 x 25
17	113655	0.8	4e-04	4e-03	1 x 18
18	85014	0.8	4e-04	4e-03	1 x 21
19	2224	0.8	4e-04	4e-03	4 x 20
20	5652	0.8	4e-04	4e-03	1 x 22

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.23	NULL	5 / 10	MF NADH dehydrogenase activity
2	13.13	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
3	11.03	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
4	10.13	NULL	93 / 1318	CC mitochondrion
5	9.41	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
6	8.77	NULL	4 / 13	GSEA C2MOOTHA_VOXPHOS
7	8.23	NULL	21 / 153	MF structural constituent of ribosome
8	8.06	NULL	3 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
9	7.72	NULL	7 / 34	MF NADH dehydrogenase (ubiquinone) activity
10	7.45	NULL	7 / 36	CC mitochondrial respiratory chain complex I
11	7.42	NULL	3 / 10	MF monosaccharide binding
12	7.34	NULL	2 / 10	BP pantothenate metabolic process
13	7.34	NULL	2 / 10	GSEA C2REACTOME_VITAMIN_B5_(PANTOTHENATE)_METABOLISM
14	7.3	NULL	31 / 304	CC mitochondrial inner membrane
15	7.22	NULL	5 / 16	GSEA C2BIOCARTA_PTDINS_PATHWAY
16	7.12	NULL	3 / 16	GSEA C2WALLACE_PROSTATE_CANCER_UP
17	7.06	NULL	2 / 10	GSEA C2REACTOME_TRIACYLGLYCERIDE_BIOSYNTHESIS
18	6.98	NULL	3 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
19	6.97	NULL	2 / 7	GSEA C2PARK_HSC_MARKERS
20	6.69	NULL	5 / 50	BP protein homotetramerization
21	6.66	NULL	2 / 15	GSEA C2JI_RESPONSE_TO_FSH_UP
22	6.58	NULL	4 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN
23	6.51	NULL	14 / 83	BP respiratory electron transport chain
24	6.51	NULL	3 / 13	GSEA C2REACTOME_GLYCOLYSIS
25	6.49	NULL	3 / 14	GSEA C2PENG_RAPAMYCIN_RESPONSE_DN
26	6.48	NULL	18 / 167	CC ribosome
27	6.42	NULL	4 / 16	GSEA C2GRADE_METASTASIS_DN
28	6.41	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
29	6.41	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_P27
30	6.41	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
31	6.41	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
32	6.37	NULL	4 / 15	CC mitochondrial large ribosomal subunit
33	6.3	NULL	3 / 12	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
34	6.21	NULL	24 / 253	BP translation
35	6.2	NULL	3 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
36	6.11	NULL	2 / 10	BP chaperone-mediated protein folding
37	6.09	NULL	3 / 15	GSEA C2VANTVEER_BREAST_CANCER_BRCA1_UP
38	5.97	NULL	6 / 35	BP mitochondrial electron transport, NADH to ubiquinone
39	5.95	NULL	3 / 16	GSEA C2MOOTHA_FFA_OXYDATION
40	5.84	NULL	3 / 15	GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY

p-values



# GW\_092

## Local Summary

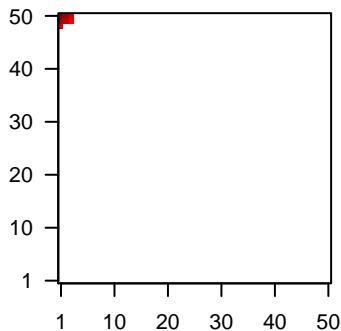
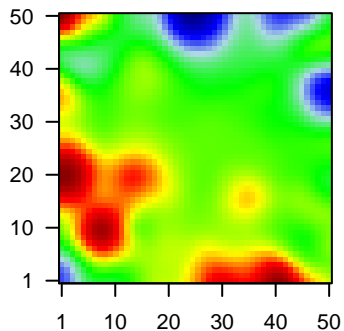
%DE = 0.77  
 # metagenes = 7  
 # genes = 132  
 # genes in genesets = 129  
 # genes with  $fdr < 0.1$  = 90 ( 81 + / 9 - )  
 # genes with  $fdr < 0.05$  = 89 ( 80 + / 9 - )  
 # genes with  $fdr < 0.01$  = 72 ( 65 + / 7 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.52

$\langle FC \rangle = 0.63$   
 $\langle \text{shrinkage-t} \rangle = 22.19$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.33$

Profile

Spot



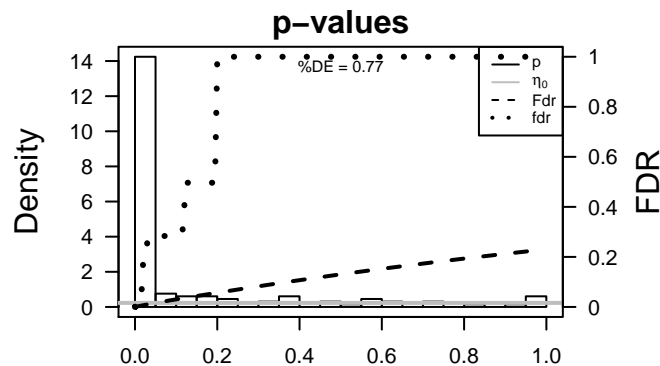
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	49860	2.13	2e-16	3e-15	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
2	7053	2.08	2e-16	3e-15	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
3	2877	1.82	1e-15	3e-14	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
4	79852	1.8	2e-15	7e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
5	54414	1.77	5e-15	7e-14	1 x 50 sialic acid acetyltransferase [Source:HGNC Symbol;Acc:18187]
6	1830	-1.77	7e-15	2e-12	1 x 48 desmoglein 3 [Source:HGNC Symbol;Acc:3050]
7	8644	1.7	7e-14	6e-12	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
8	218	1.66	3e-13	2e-11	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
9	375791	1.62	9e-13	6e-11	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
10	6286	1.59	3e-12	7e-11	1 x 50 S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
11	3934	1.57	5e-12	1e-10	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]
12	6337	1.55	1e-11	4e-09	3 x 50 sodium channel, non-voltage-gated 1 alpha subunit [Source:
13	388533	1.44	2e-10	4e-09	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
14	5653	1.43	3e-10	1e-08	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:630
15	5307	1.33	7e-10	1e-08	3 x 50 paired-like homeodomain 1 [Source:HGNC Symbol;Acc:9004
16	54544	1.37	1e-09	1e-08	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:29871
17	6704	1.37	2e-09	5e-08	1 x 50 small proline-rich protein 2E [Source:HGNC Symbol;Acc:112
18	374897	1.35	3e-09	5e-08	1 x 49 suprabasin [Source:HGNC Symbol;Acc:24950]
19	57152	1.33	5e-09	1e-07	1 x 50 secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
20	1475	1.29	1e-08	1e-07	1 x 50 cystatin A (steffin A) [Source:HGNC Symbol;Acc:2481]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	39.92	NULL	62 / 135	H.Tiss WIRTH_Mucosa
2	30.51	NULL	13 / 21	CC cornified envelope
3	28.64	NULL	15 / 42	BP keratinization
4	28	NULL	17 / 53	BP keratinocyte differentiation
5	23.96	NULL	7 / 19	BP peptide cross-linking
6	21.28	NULL	64 / 572	Disease GUDJ_psooriasis up
7	18.5	NULL	6 / 13	BP negative regulation of peptidase activity
8	16.49	NULL	4 / 10	MF RAGE receptor binding
9	15.51	NULL	16 / 76	BP epidermis development
10	12.38	NULL	4 / 15	MF retinol dehydrogenase activity
11	11.45	NULL	5 / 16	GSEA C2WNDER_CDH1_TARGETS_3_DN
12	11.4	NULL	5 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	10.69	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
14	10.62	NULL	2 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
15	10.48	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
16	10.2	NULL	3 / 12	BP cellular aldehyde metabolic process
17	9.92	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	9.85	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
19	9.58	NULL	4 / 27	BP response to bacterium
20	9.57	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
21	9.28	NULL	41 / 1182	CC extracellular region
22	8.86	NULL	2 / 14	GSEA C2KEGG_PHENYLALANINE_METABOLISM
23	8.85	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
24	8.82	NULL	12 / 186	MF structural molecule activity
25	8.78	NULL	3 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
26	8.57	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
27	8.57	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_CIPROFIBRATE_UP
28	8.57	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_DENA_UP
29	8.41	NULL	1 / 8	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
30	8.27	NULL	2 / 17	Disease BCHETNIA_EBM up
31	8.12	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
32	7.91	NULL	2 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
33	7.87	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
34	7.74	NULL	1 / 12	GSEA C2ODONNELL_METASTASIS_DN
35	7.74	NULL	1 / 12	GSEA C2SYED ESTRADIOL_RESPONSE
36	7.59	NULL	3 / 16	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G24
37	7.4	NULL	1 / 8	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
38	7.4	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
39	7.37	NULL	2 / 10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING
40	7.34	NULL	1 / 10	GSEA C2NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN



# GW\_092

## Local Summary

%DE = 0.91  
 # metagenes = 13  
 # genes = 217  
 # genes in genesets = 217  
 # genes with  $fdr < 0.1$  = 180 ( 0 + / 180 - )  
 # genes with  $fdr < 0.05$  = 148 ( 0 + / 148 - )  
 # genes with  $fdr < 0.01$  = 73 ( 0 + / 73 - )

<r> metagenes = 0.98

<r> genes = 0.31

<FC> = -0.47

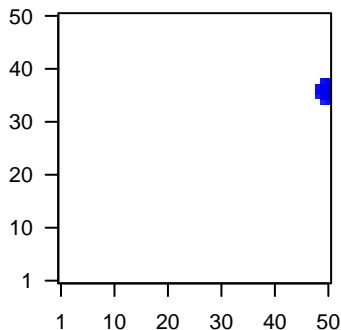
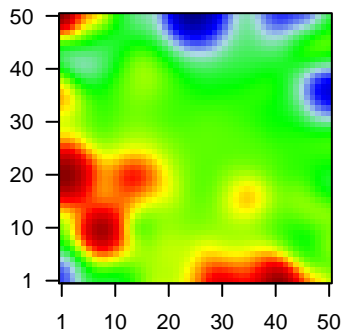
<shrinkage-t> = -16.54

<p-value> = 0.03

<fdr> = 0.6

Profile

Spot



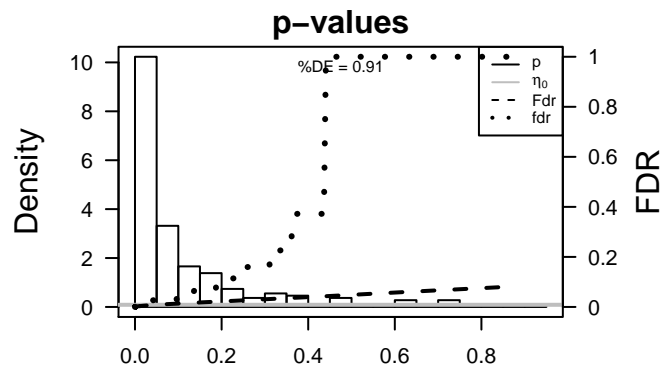
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4089	-1.06	3e-06	1e-04	50 x 35 SMAD family member 4 [Source:HGNC Symbol;Acc:6770]
2	7764	-0.97	2e-05	1e-04	50 x 37 zinc finger protein 217 [Source:HGNC Symbol;Acc:13009]
3	84928	-0.96	2e-05	1e-04	50 x 37 transmembrane protein 209 [Source:HGNC Symbol;Acc:2185]
4	10015	-0.95	3e-05	1e-04	50 x 34 programmed cell death 6 interacting protein [Source:HGNC S
5	1429	-0.95	3e-05	1e-04	50 x 34 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
6	64083	-0.94	3e-05	1e-04	50 x 37 golgi phosphoprotein 3 (coat-protein) [Source:HGNC Symbol
7	9908	-0.94	4e-05	6e-04	50 x 36 GTPase activating protein (SH3 domain) binding protein 2 [S
8	23215	-0.89	8e-05	6e-04	50 x 37 proline-rich coiled-coil 2C [Source:HGNC Symbol;Acc:2490]
9	55251	-0.87	1e-04	6e-04	50 x 37 protein-L-isoaspartate (D-aspartate) O-methyltransferase d
10	1195	-0.86	2e-04	6e-04	50 x 35 CDC-like kinase 1 [Source:HGNC Symbol;Acc:2068]
11	27075	-0.86	2e-04	6e-04	50 x 38 tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
12	85440	-0.85	2e-04	8e-04	50 x 38 dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:19190]
13	3187	-0.81	3e-04	8e-04	50 x 35 heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
14	5431	-0.8	4e-04	8e-04	50 x 37 polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [
15	4200	-0.8	4e-04	8e-04	50 x 35 malic enzyme 2, NAD(+)-dependent, mitochondrial [Source:G
16	171586	-0.8	5e-04	8e-04	50 x 37 abhydrolase domain containing 3 [Source:HGNC Symbol;Acc
17	9685	-0.79	5e-04	8e-04	50 x 34 clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
18	10159	-0.79	5e-04	8e-04	50 x 36 ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
19	64112	-0.78	6e-04	8e-04	50 x 37 modulator of apoptosis 1 [Source:HGNC Symbol;Acc:16658]
20	23505	-0.77	7e-04	8e-04	50 x 37 transmembrane protein 131 [Source:HGNC Symbol;Acc:3036]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.3	NULL	3 / 11	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
2	-10.75	NULL	14 / 121	miRNA target set miR-343
3	-10.6	NULL	1 / 2	MMML C06CIEJ_MMML_38
4	-9.94	NULL	21 / 271	miRNA target set miR-344
5	-9.41	NULL	8 / 58	miRNA target set miR-345-5p
6	-8.91	NULL	2 / 10	MF NADPH binding
7	-8.82	NULL	14 / 189	miRNA target set miR-345-3
8	-8.75	NULL	7 / 51	miRNA target set miR-346-3p
9	-8.7	NULL	27 / 421	miRNA target set miR-347
10	-8.62	NULL	17 / 215	miRNA target set miR-348
11	-8.56	NULL	2 / 10	GSEA C2CROONQUIST_STROMAL_STIMULATION_DN
12	-8.2	NULL	1 / 3	miRNA target set miR-197
13	-8.15	NULL	12 / 155	miRNA target set miR-349
14	-8.11	NULL	2 / 10	BP positive regulation of SMAD protein import into nucleus
15	-8.08	NULL	5 / 38	miRNA target set miR-3497
16	-8.01	NULL	14 / 163	BP mRNA splicing, via spliceosome
17	-7.87	NULL	22 / 440	miRNA target set miR-349a
18	-7.84	NULL	7 / 49	miRNA target set miR-349b-154-487
19	-7.81	NULL	23 / 433	miRNA target set miR-349b
20	-7.76	NULL	10 / 100	miRNA target set miR-349c
21	-7.76	NULL	9 / 157	miRNA target set miR-349c-3p
22	-7.74	NULL	1 / 2	miRNA target set miR-98
23	-7.73	NULL	5 / 46	miRNA target set miR-349d
24	-7.71	NULL	3 / 20	BP protein secretion
25	-7.58	NULL	5 / 63	miRNA target set miR-349e
26	-7.55	NULL	9 / 98	miRNA target set miR-349e-3p
27	-7.52	NULL	14 / 153	miRNA target set miR-349e-5p
28	-7.5	NULL	3 / 16	Cancer GENTLES_modul14
29	-7.5	NULL	3 / 26	miRNA target set miR-349f-5p
30	-7.5	NULL	13 / 229	miRNA target set miR-349g
31	-7.47	NULL	5 / 45	miRNA target set miR-349g
32	-7.46	NULL	20 / 303	miRNA target set miR-349h
33	-7.37	NULL	22 / 463	miRNA target set miR-349i
34	-7.34	NULL	13 / 232	Chr Chr 18
35	-7.34	NULL	11 / 146	miRNA target set miR-349j
36	-7.33	NULL	2 / 10	BP negative regulation of DNA damage response, signal transduction
37	-7.33	NULL	23 / 512	miRNA target set miR-349k
38	-7.25	NULL	20 / 396	miRNA target set miR-349l
39	-7.23	NULL	22 / 381	miRNA target set miR-349m
40	-7.21	NULL	20 / 311	miRNA target set miR-349n



# GW\_092

## Local Summary

%DE = 0.85  
 # metagenes = 38  
 # genes = 497  
 # genes in genesets = 489  
 # genes with fdr < 0.1 = 344 ( 0 + / 344 - )  
 # genes with fdr < 0.05 = 293 ( 0 + / 293 - )  
 # genes with fdr < 0.01 = 111 ( 0 + / 111 - )

<r> metagenes = 0.91

<r> genes = 0.25

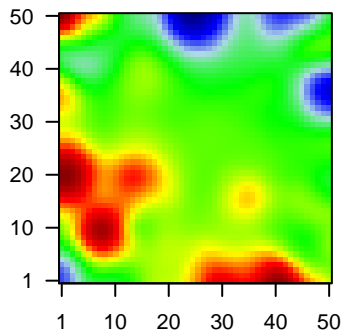
<FC> = -0.45

<shrinkage-t> = -15.93

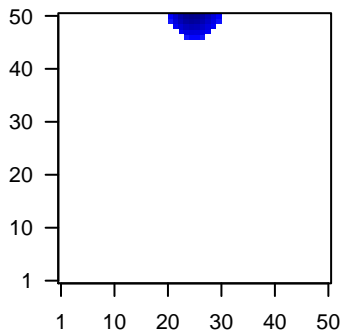
<p-value> = 0.03

<fdr> = 0.63

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	2353	-1.84	2e-16	2e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3238]
2	1843	-1.41	1e-11	7e-07	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3238]
3	3725	-1.28	2e-08	7e-07	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
4	57162	-1.28	2e-08	8e-06	23 x 50 pellino E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:3238]
5	25800	-1.2	1e-07	8e-06	25 x 50 solute carrier family 39 (zinc transporter), member 6 [Source:HGNC Symbol;Acc:3238]
6	1958	-1.17	2e-07	2e-04	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
7	3716	-1.06	3e-06	2e-04	25 x 49 Janus kinase 1 [Source:HGNC Symbol;Acc:6190]
8	51030	-1.02	6e-06	2e-04	26 x 50 trans-golgi network vesicle protein 23 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:3238]
9	7465	-1.01	8e-06	2e-04	23 x 50 WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:127]
10	2632	-0.99	1e-05	2e-04	25 x 50 glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Symbol;Acc:3238]
11	5782	-0.98	1e-05	2e-04	25 x 50 protein tyrosine phosphatase, non-receptor type 12 [Source:HGNC Symbol;Acc:3238]
12	10972	-0.98	2e-05	2e-04	25 x 50 transmembrane emp24-like trafficking protein 10 (yeast) [Source:HGNC Symbol;Acc:3238]
13	1326	-0.97	2e-05	4e-04	22 x 50 mitogen-activated protein kinase kinase kinase 8 [Source:HGNC Symbol;Acc:3238]
14	9643	-0.95	3e-05	4e-04	26 x 50 mortality factor 4 like 2 [Source:HGNC Symbol;Acc:16849]
15	71	-0.86	3e-05	4e-04	24 x 50 actin, gamma 1 [Source:HGNC Symbol;Acc:144]
16	147463	-0.94	3e-05	4e-04	25 x 50 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
17	114908	-0.93	4e-05	1e-03	26 x 50 transmembrane protein 123 [Source:HGNC Symbol;Acc:3013]
18	91612	-0.92	6e-05	1e-03	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:20000]
19	5868	-0.9	7e-05	1e-03	25 x 50 RAB5A, member RAS oncogene family [Source:HGNC Symbol;Acc:3238]
20	960	-0.89	9e-05	1e-03	24 x 50 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:3238]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.78	NULL	6 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	-17.73	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
3	-16.2	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
4	-14.66	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
5	-14.37	NULL	7 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
6	-14.11	NULL	4 / 14	BP response to light stimulus
7	-13.95	NULL	6 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
8	-13.66	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
9	-13.44	NULL	3 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCRIPTION_FACTORS
10	-13.05	NULL	5 / 8	MMML C2CIEJ_MMML50
11	-12.85	NULL	63 / 436	miRNA target set miR-346
12	-12.47	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
13	-12.46	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
14	-12.19	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
15	-12.1	NULL	3 / 12	GSEA C2BIOCARTA_DREAM_PATHWAY
16	-11.79	NULL	4 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
17	-11.69	NULL	45 / 269	miRNA target set miR-344
18	-11.51	NULL	3 / 12	GSEA C2BIOCARTA_ARENERF2_PATHWAY
19	-11.41	NULL	44 / 310	miRNA target set miR-346
20	-11.36	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
21	-11.35	NULL	6 / 16	TF Tissue/AQUERIZAS_Pancreas
22	-11.27	NULL	2 / 5	miRNA target set miR-101
23	-10.86	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY
24	-10.86	NULL	3 / 15	GSEA C2BIOCARTA_TPO_PATHWAY
25	-10.83	NULL	30 / 169	miRNA target set miR-374b
26	-10.68	NULL	5 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
27	-10.61	NULL	4 / 11	miRNA target set miR-346-5p
28	-10.54	NULL	1 / 5	GSEA C2TURJANSKI_MAPK11_TARGETS
29	-10.51	NULL	30 / 180	miRNA target set miR-374a
30	-10.47	NULL	3 / 16	GSEA C2BIOCARTA_EPO_PATHWAY
31	-10.47	NULL	3 / 16	GSEA C2BIOCARTA_IGF1_PATHWAY
32	-10.47	NULL	3 / 16	GSEA C2BIOCARTA_GLEEVEC_PATHWAY
33	-10.47	NULL	3 / 16	GSEA C2BIOCARTA_NGF_PATHWAY
34	-10.3	NULL	3 / 16	GSEA C2ST_GRANULE_CELL_SURVIVAL_PATHWAY
35	-10.28	NULL	21 / 114	miRNA target set miR-346
36	-10.25	NULL	2 / 13	BP SMAD protein signal transduction
37	-10.22	NULL	6 / 39	BP response to cAMP
38	-10.05	NULL	7 / 16	GSEA C2AMIT_DELAYED_EARLY_GENES
39	-10.03	NULL	25 / 151	miRNA target set miR-346
40	-10.01	NULL	37 / 262	miRNA target set miR-346

p-values

