

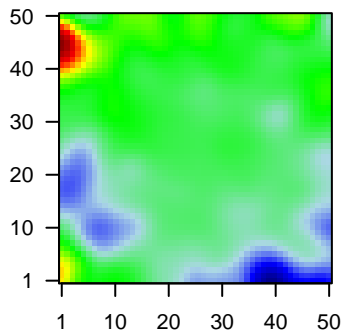
# GW\_134

## Global Summary

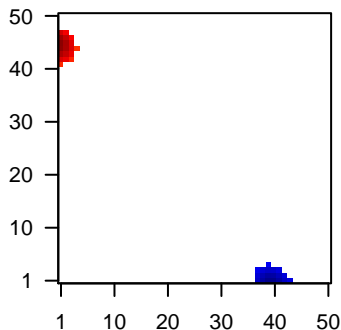
%DE = 0.17  
 # genes with fdr < 0.2 = 1976 ( 1075 + / 901 - )  
 # genes with fdr < 0.1 = 1630 ( 895 + / 735 - )  
 # genes with fdr < 0.05 = 1331 ( 744 + / 587 - )  
 # genes with fdr < 0.01 = 877 ( 488 + / 389 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.09  
 <fdr> = 0.83

Profile



Regulated Spots



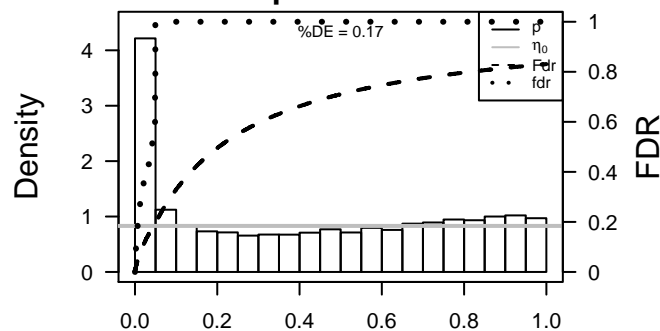
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.89	2e-16	4e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
2	441282	1.67	2e-16	4e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	1109	-1.77	2e-16	4e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy]
4	220	1.63	2e-16	4e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
5	218	-1.64	2e-16	4e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	401138	3.58	2e-16	4e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
7	147463	1.54	2e-16	4e-14	25 x 50 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
8	366	1.65	2e-16	4e-14	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
9	684	-1.86	2e-16	4e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	387695	1.55	2e-16	4e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
11	64207	-1.56	2e-16	4e-14	50 x 40 interferon regulatory factor 2 binding protein-like [Source:HG
12	148304	1.78	2e-16	4e-14	1 x 41 chromosome 1 open reading frame 74 [Source:HGNC Symbc
13	771	1.63	2e-16	4e-14	1 x 44 carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
14	760	2.7	2e-16	4e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	51806	-1.71	2e-16	4e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
16	51755	-1.55	2e-16	4e-14	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
17	49860	-2.33	2e-16	4e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	3627	-1.81	2e-16	4e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
19	9547	2.09	2e-16	4e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
20	56603	1.57	2e-16	4e-14	1 x 4 cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.93	NULL	572	Disease GUDJ_psooriasis up
2	11.38	NULL	1720	Chr Chr 1
3	11.18	NULL	386	Chr Chr 22
4	9.75	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	9.07	NULL	232	Chr Chr 18
6	7.55	NULL	21	CC cornified envelope
7	6.82	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
8	6.63	NULL	12	H.Tiss WIRTH_Prim. lymphoid organs
9	6.42	NULL	15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
10	6.27	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
11	6.26	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
12	6.11	NULL	10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
13	6.01	NULL	76	BP epidermis development
14	5.9	NULL	52	BP negative regulation of endopeptidase activity
15	5.79	NULL	16	GSEA C2JAEGER_METASTASIS_DN
16	5.7	NULL	6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
17	5.62	NULL	534	Chr Chr 8
18	5.47	NULL	1182	CC extracellular region
19	5.4	NULL	79	MF serine-type endopeptidase inhibitor activity
20	5.37	NULL	13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
<i>Underexpressed</i>				
1	-8.78	NULL	602	Chr Chr 10
2	-8.65	NULL	1135	Chr Chr 19
3	-7.18	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
4	-7.04	NULL	92	BP translational elongation
5	-7.01	NULL	92	BP viral life cycle
6	-7	NULL	153	MF structural constituent of ribosome
7	-6.8	NULL	81	BP viral transcription
8	-6.71	NULL	253	BP translation
9	-6.69	NULL	167	CC ribosome
10	-6.47	NULL	87	BP translational termination
11	-6.25	NULL	957	Chr Chr 11
12	-5.98	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
13	-5.86	NULL	128	BP translational initiation
14	-5.85	NULL	595	MF RNA binding
15	-5.79	NULL	918	Chr Chr 17
16	-5.65	NULL	11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN
17	-5.51	NULL	5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
18	-5.16	NULL	649	BP gene expression
19	-5.05	NULL	25	CC small ribosomal subunit
20	-4.95	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated

p-values



# GW\_134

## Local Summary

%DE = 0.82  
 # metagenes = 19  
 # genes = 237  
 # genes in genesets = 233

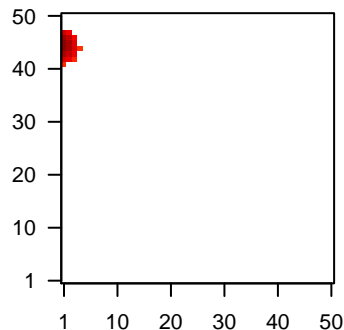
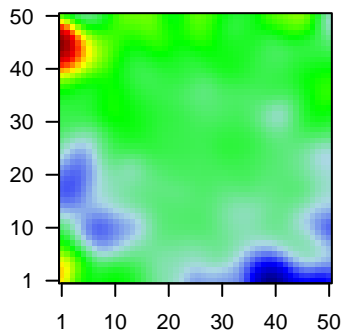
# genes with  $fdr < 0.1$  = 182 ( 162 + / 20 - )  
 # genes with  $fdr < 0.05$  = 156 ( 143 + / 13 - )  
 # genes with  $fdr < 0.01$  = 144 ( 131 + / 13 - )

<r> metagenes = 0.94  
 <r> genes = 0.39

<FC> = 0.62  
 <shrinkage-t> = 21.67  
 <p-value> = 0  
 <fdr> = 0.3

Profile

Spot



## Local Genelist

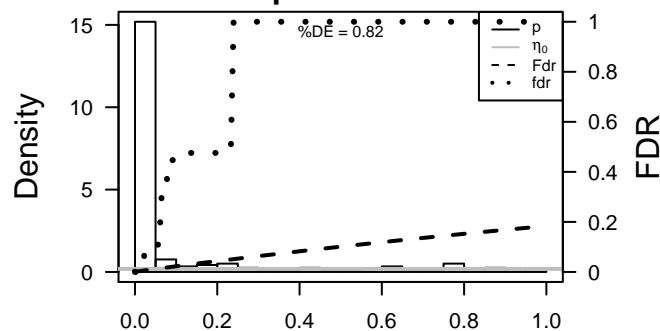
Rank	ID	log(FC)	fdr	p-value	Description
1	148304	1.78	2e-16	5e-16	1 x 41 chromosome 1 open reading frame 74 [Source:HGNC Symbc
2	771	1.63	2e-16	5e-16	1 x 44 carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
3	760	2.7	2e-16	5e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
4	9547	2.09	2e-16	5e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
5	55894	2.2	2e-16	5e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
6	2697	1.77	2e-16	5e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;v
7	10804	1.66	2e-16	5e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
8	56300	2.48	2e-16	5e-16	1 x 47 interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
9	9119	2.38	2e-16	5e-16	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]
10	353145	1.95	2e-16	5e-16	1 x 47 late cornified envelope 3E [Source:HGNC Symbol;Acc:29463]
11	55214	1.59	2e-16	5e-16	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
12	118430	2.74	2e-16	5e-16	2 x 44 mucin-like 1 [Source:HGNC Symbol;Acc:30588]
13	4753	1.62	2e-16	5e-16	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
14	81706	1.53	2e-16	5e-16	1 x 43 protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou
15	8710	1.88	2e-16	5e-16	1 x 46 serpin peptidase inhibitor, clade B (ovalbumin), member 7 [Sc
16	404203	2.71	2e-16	5e-16	1 x 43 serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
17	116211	1.58	2e-16	5e-16	1 x 43 Transmembrane 4 L6 family member 19 [Source:UniProtKB/!
18	51673	1.83	2e-16	5e-16	2 x 46 tubulin polymerization-promoting protein family member 3 [Si
19	10158	1.5	7e-16	3e-14	1 x 47 PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:1686
20	5268	1.49	1e-15	4e-14	1 x 46 serpin peptidase inhibitor, clade B (ovalbumin), member 5 [Sc

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	23.58	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
2	21.44	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	12.86	NULL	27 / 135	H.Tiss WIRTH_Mucosa
4	12.5	NULL	17 / 82	CC intermediate filament
5	12.12	NULL	60 / 572	Disease GUDJ_psooriasis up
6	11.88	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
7	11.73	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
8	10.92	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
9	10.79	NULL	3 / 17	BP morphogenesis of an epithelium
10	10.32	NULL	3 / 15	CC connexon complex
11	10.13	NULL	9 / 44	CC keratin filament
12	10	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
13	9.99	NULL	4 / 12	BP hemidesmosome assembly
14	9.9	NULL	4 / 21	CC gap junction
15	9.82	NULL	3 / 25	BP response to zinc ion
16	9.63	NULL	3 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
17	9.24	NULL	13 / 76	BP epidermis development
18	8.7	NULL	1 / 9	GSEA C2HEDVAT_ELF4_TARGETS_UP
19	8.68	NULL	3 / 15	GSEA C2FRIDMAN_IMMORTALIZATION_DN
20	8.54	NULL	3 / 10	BP negative regulation of interleukin-2 production
21	8.45	NULL	2 / 22	BP bicarbonate transport
22	8.21	NULL	2 / 15	GSEA C2STOSSI_RESPONSE_TO ESTRADIOL
23	7.84	NULL	2 / 25	BP one-carbon metabolic process
24	7.82	NULL	2 / 10	MF gap junction channel activity
25	7.78	NULL	8 / 21	CC desmosome
26	7.75	NULL	2 / 10	GSEA C2KIM_MYCL1_AMPLIFICATION_TARGETS_UP
27	7.74	NULL	1 / 11	BP positive regulation of bone resorption
28	7.55	NULL	4 / 16	GSEA C2ZELVIDGE_HIF1A_TARGETS_DN
29	7.5	NULL	1 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
30	7.44	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
31	7.38	NULL	2 / 21	BP positive regulation of cytokine production
32	7.35	NULL	1 / 12	GSEA C2HO_LIVER_CANCER_VASCULAR_INVASION
33	7.22	NULL	3 / 16	GSEA C2ZELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
34	7.14	NULL	18 / 186	MF structural molecule activity
35	6.92	NULL	2 / 16	GSEA C2BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
36	6.9	NULL	3 / 13	BP intermediate filament cytoskeleton organization
37	6.9	NULL	2 / 16	GSEA C2MILLERT_WNT_SIGNALING
38	6.82	NULL	4 / 38	BP epithelial cell differentiation
39	6.8	NULL	2 / 15	Pathw AcGUSTAFSON_PI3K_DN
40	6.76	NULL	3 / 11	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP

p-values



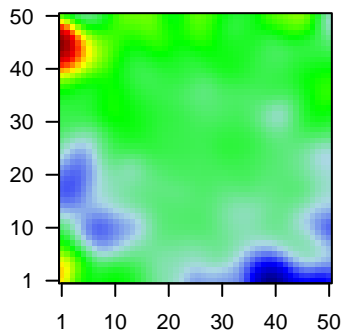
# GW\_134

## Local Summary

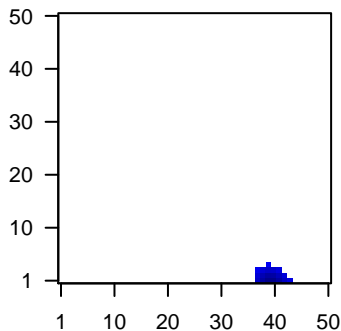
%DE = 0.86  
 # metagenes = 19  
 # genes = 300  
 # genes in genesets = 273  
 # genes with  $fdr < 0.1$  = 202 ( 8 + / 194 - )  
 # genes with  $fdr < 0.05$  = 177 ( 7 + / 170 - )  
 # genes with  $fdr < 0.01$  = 102 ( 5 + / 97 - )

<r> metagenes = 0.97  
 <r> genes = 0.45  
 <FC> = -0.41  
 <shrinkage-t> = -14.43  
 <p-value> = 0  
 <fdr> = 0.51

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	100132406	-1.6	2e-16	5e-15	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
2	400818	-1.77	2e-16	5e-15	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
3	641737	-1.3	7e-14	5e-10	40 x 1
4	10299	-1.26	1e-11	2e-08	40 x 1 membrane-associated ring finger (C3HC4) 6, E3 ubiquitin pr
5	399900	-1.04	9e-10	2e-08	39 x 1
6	100190986	-1.13	1e-09	2e-08	39 x 1
7	91368	-1.03	2e-09	1e-07	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC S
8	84061	-1.09	5e-09	5e-07	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
9	28996	-1.05	2e-08	5e-07	40 x 1 homeodomain interacting protein kinase 2 [Source:HGNC Sy
10	250	-1.02	4e-08	5e-07	40 x 1 alkaline phosphatase, placental [Source:HGNC Symbol;Acc:4
11	8019	-1.02	4e-08	1e-06	38 x 1 bromodomain containing 3 [Source:HGNC Symbol;Acc:1104]
12	387700	-0.92	8e-08	1e-06	40 x 1 solute carrier family 16, member 12 [Source:HGNC Symbol;A
13	319085	-0.98	1e-07	1e-06	39 x 1 ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
14	84278	-0.98	1e-07	1e-06	39 x 1
15	442578	-0.98	1e-07	1e-06	39 x 1
16	25862	-0.97	2e-07	1e-06	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2c
17	399761	-0.97	2e-07	2e-06	39 x 1 BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653]
18	126205	-0.96	3e-07	2e-06	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbo
19	3586	-0.88	3e-07	2e-06	40 x 1 interleukin 10 [Source:HGNC Symbol;Acc:5962]
20	3127	-0.95	4e-07	2e-06	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.33	NULL	3 / 14	MMML C69CIEJ_MMML 8
2	-9.48	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
3	-9.31	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
4	-8.74	NULL	2 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
5	-7.87	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
6	-7.28	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
7	-6.6	NULL	2 / 15	GSEA C2IL_RESPONSE_TO_FSH_UP
8	-6.5	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
9	-6.36	NULL	2 / 16	GSEA C2SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
10	-5.98	NULL	2 / 14	BP cellular response to estradiol stimulus
11	-5.84	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
12	-5.84	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
13	-5.51	NULL	2 / 15	GSEA C2THUM_SYSTOLIC_HEART_FAILURE_DN
14	-5.3	NULL	2 / 16	BP cognition
15	-5.29	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
16	-5.11	NULL	1 / 9	GSEA C2BROWNE_HCMV_INFECTION_1HR_DN
17	-4.99	NULL	1 / 10	CC oligosaccharyltransferase complex
18	-4.98	NULL	2 / 19	MF mitogen-activated protein kinase kinase binding
19	-4.94	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
20	-4.73	NULL	3 / 24	BP negative regulation of T cell proliferation
21	-4.67	NULL	1 / 10	GSEA C2STEIN_ESRRA_TARGETS
22	-4.55	NULL	3 / 15	GSEA C2WANG_CLIM2_TARGETS_UP
23	-4.43	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
24	-4.42	NULL	1 / 11	GSEA C2KEGG_FOLATE_BIOSYNTHESIS
25	-4.41	NULL	1 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
26	-4.41	NULL	1 / 11	GSEA C2TARTE_PLASMA_CELL_VS_PLASMABLAST_UP
27	-4.39	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
28	-4.37	NULL	2 / 14	BP mitochondrion morphogenesis
29	-4.32	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process
30	-4.32	NULL	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
31	-4.3	NULL	1 / 12	BP retina layer formation
32	-4.28	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
33	-4.26	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
34	-4.26	NULL	4 / 105	miRNA target site B76b
35	-4.18	NULL	1 / 12	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_1_UP
36	-4.18	NULL	1 / 12	GSEA C2KAAB_FAILED_HEART_ATRIUM_UP
37	-4.16	NULL	3 / 38	MF methylated histone residue binding
38	-4.11	NULL	3 / 23	BP G2 DNA damage checkpoint
39	-4.1	NULL	1 / 13	BP DNA damage response, signal transduction by p53 class mediator
40	-4.1	NULL	1 / 13	BP SMAD protein signal transduction

p-values

