

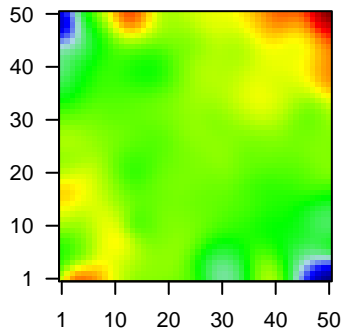
# GW\_249

## Global Summary

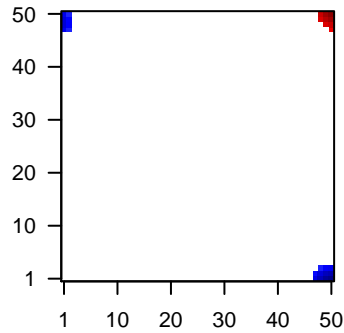
%DE = 0.15  
 # genes with  $fdr < 0.2$  = 1942 ( 973 + / 969 - )  
 # genes with  $fdr < 0.1$  = 1660 ( 812 + / 848 - )  
 # genes with  $fdr < 0.05$  = 1369 ( 672 + / 697 - )  
 # genes with  $fdr < 0.01$  = 1019 ( 488 + / 531 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.08  
 <fdr> = 0.85

Profile



Regulated Spots



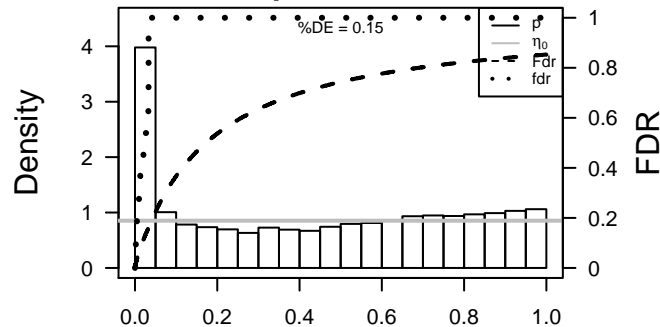
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	8745	1.71	2e-16	2e-14	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	124	1.81	2e-16	2e-14	50 x 11 alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	1.46	2e-16	2e-14	50 x 12 alcohol dehydrogenase 1C (class I), gamma polypeptide [So
4	131	2.04	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	133	1.31	2e-16	2e-14	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
6	154	-1.74	2e-16	2e-14	1 x 40 adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286
7	10551	1.4	2e-16	2e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
8	1646	1.97	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Syr
9	8644	3.27	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
10	1109	3.51	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
11	216	1.61	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
12	220	-2.03	2e-16	2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
13	222	-1.84	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
14	241	-1.65	2e-16	2e-14	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC
15	244	-1.62	2e-16	2e-14	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]
16	360	-1.41	2e-16	2e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
17	151516	1.8	2e-16	2e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
18	344905	1.92	2e-16	2e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
19	84707	-1.6	2e-16	2e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
20	664	1.78	2e-16	2e-14	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.71	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
2	7.46	NULL	1033	Chr Chr 2
3	7.4	NULL	16	MMML C2SCIEJ_MMML_1
4	6.88	NULL	11	MF platelet-derived growth factor binding
5	6.85	NULL	12	miRNA target-29c
6	6.74	NULL	13	GSEA C2SINGH_NFE2L2_TARGETS
7	6.61	NULL	37	BP collagen fibril organization
8	6.57	NULL	190	CC extracellular matrix
9	6.44	NULL	20	TF MYC_Metabolism UP
10	6.26	NULL	9	GSEA C2REACTOME_ETHANOL_OXIDATION
11	6.24	NULL	25	BP glutathione derivative biosynthetic process
12	5.99	NULL	34	BP glutathione metabolic process
13	5.81	NULL	10	BP positive regulation of endothelial cell apoptotic process
14	5.7	NULL	15	GSEA C2REACTOME_Glutathione_Conjugation
15	5.62	NULL	4640	CC nucleus
16	5.53	NULL	7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
17	5.34	NULL	15	GSEA C2KEGG_Glutathione_Metabolism
18	5.27	NULL	10	BP negative regulation of fibroblast growth factor receptor signaling pa
19	5.24	NULL	949	CC nucleoplasm
20	5.23	NULL	57	MF extracellular matrix structural constituent
<i>Underexpressed</i>				
1	-17.68	NULL	135	H.Tiss WIRTH_Mucosa
2	-17.38	NULL	572	Disease GUDJ_psooriasis up
3	-14.92	NULL	312	BP immune response
4	-12.03	NULL	553	Cancer Lembcke_Colonc Inflammation
5	-11.97	NULL	417	H.Tiss WIRTH_Immune system
6	-11.78	NULL	47	BP antigen processing and presentation
7	-10.64	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
8	-10.64	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
9	-10.64	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
10	-10.64	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
11	-10.18	NULL	15	CC MHC class II protein complex
12	-10.07	NULL	316	Cancer SPANG_BCL6-index2
13	-9.65	NULL	269	BP inflammatory response
14	-9.29	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	-9.06	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
16	-8.65	NULL	2659	CC plasma membrane
17	-8.5	NULL	73	BP defense response to bacterium
18	-8.41	NULL	10	MF RAGE receptor binding
19	-8.25	NULL	60	BP interferon-gamma-mediated signaling pathway
20	-7.97	NULL	699	Chr Chr 5

p-values



# GW\_249

## Local Summary

%DE = 0.85  
 # metagenes = 9  
 # genes = 159  
 # genes in genesets = 158

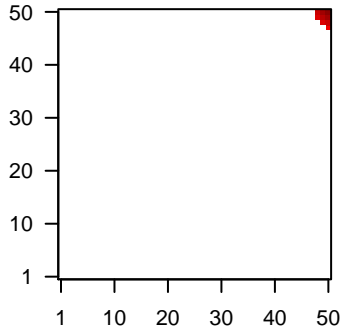
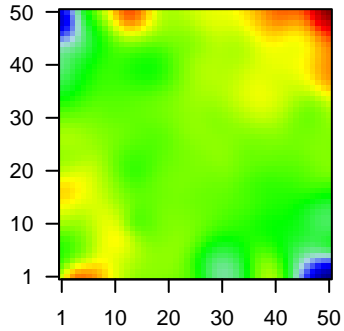
# genes with  $fdr < 0.1 = 116$  ( 97 + / 19 - )  
 # genes with  $fdr < 0.05 = 102$  ( 88 + / 14 - )  
 # genes with  $fdr < 0.01 = 88$  ( 76 + / 12 - )

<r> metagenes = 0.98  
 <r> genes = 0.29

<FC> = 0.55  
 <shrinkage-t> = 19.16  
 <p-value> = 0  
 <fdr> = 0.37

Profile

Spot



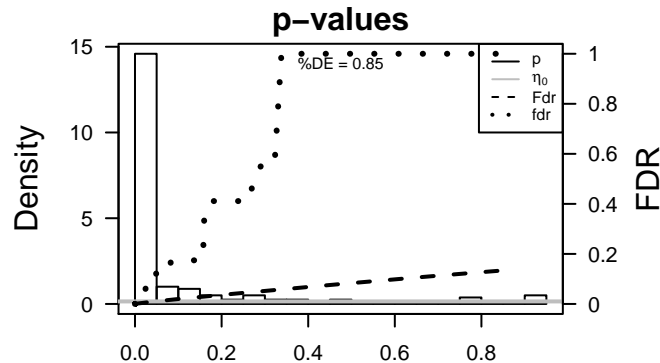
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	8745	1.71	2e-16	2e-16	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	216	1.61	2e-16	2e-16	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	344905	1.92	2e-16	2e-16	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
4	84707	-1.6	2e-16	2e-16	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
5	339512	2.1	2e-16	2e-16	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
6	205428	1.89	2e-16	2e-16	50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbc
7	26256	1.82	2e-16	2e-16	50 x 50 calcium binding tyrosine-(Y)-phosphorylation regulated [Sou
8	1056	2.2	2e-16	2e-16	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
9	4072	2.36	2e-16	2e-16	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
10	83888	2.82	2e-16	2e-16	50 x 50 fibroblast growth factor binding protein 2 [Source:HGNC Syml
11	94234	-1.65	2e-16	2e-16	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
12	2729	1.42	2e-16	2e-16	50 x 50 glutamate-cysteine ligase, catalytic subunit [Source:HGNC S
13	2946	1.41	2e-16	2e-16	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr
14	3856	1.85	2e-16	2e-16	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
15	4922	3.05	2e-16	2e-16	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
16	4953	2.1	2e-16	2e-16	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
17	57526	1.8	2e-16	2e-16	50 x 50 protocadherin 19 [Source:HGNC Symbol;Acc:14270]
18	139728	2.43	2e-16	2e-16	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l
19	10966	1.65	2e-16	2e-16	50 x 50 RAB40B, member RAS oncogene family [Source:HGNC Sym
20	6657	1.38	2e-16	2e-16	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbc

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	20.34	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	17.61	NULL	3 / 13	BP regulation of blood vessel size
3	16.53	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
4	13.71	NULL	1 / 2	miRNA target-127
5	13.11	NULL	6 / 25	BP glutathione derivative biosynthetic process
6	12.66	NULL	8 / 34	BP glutathione metabolic process
7	12.31	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
8	11.72	NULL	2 / 9	GSEA C2REACTOME_GLCUCURONIDATION
9	10.97	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
10	10.67	NULL	1 / 11	Glio neurons_glio
11	10.36	NULL	2 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
12	10.34	NULL	3 / 16	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G1_DN
13	10.26	NULL	11 / 119	BP xenobiotic metabolic process
14	10.17	NULL	5 / 20	MF glutathione transferase activity
15	10.03	NULL	2 / 14	GSEA C2VEI_MYCN_TARGETS_WITH_E_BOX
16	9.88	NULL	1 / 11	GSEA C2YAMANAKA_GLIOMASTOMA_SURVIVAL_UP
17	9.57	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
18	9.55	NULL	1 / 7	GSEA C2REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
19	9.24	NULL	1 / 8	GSEA C2KEGG_GLYCEROLIPID_METABOLISM
20	9.2	NULL	2 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
21	8.91	NULL	1 / 15	MF neuropeptide hormone activity
22	8.86	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
23	8.84	NULL	2 / 13	GSEA C2COLLER_MYC_TARGETS_UP
24	8.81	NULL	1 / 8	GSEA C2PUJANA_CHEK2_PCC_NETWORK
25	8.74	NULL	2 / 20	TF MYC_Metabolism UP
26	8.61	NULL	3 / 11	MF glutathione binding
27	8.61	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
28	8.58	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
29	8.54	NULL	4 / 15	GSEA C2REACTOME_GLUTATHIONE_CONJUGATION
30	8.2	NULL	2 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_U
31	8.16	NULL	2 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
32	8.08	NULL	2 / 12	BP glutamate metabolic process
33	8.02	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
34	8.02	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
35	7.71	NULL	1 / 10	GSEA C2LUI_TARGETS_OF_PAX8_PPARG_FUSION
36	7.71	NULL	1 / 10	GSEA C2PUJANA_ATM_PCC_NETWORK
37	7.71	NULL	1 / 10	GSEA C2HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
38	7.71	NULL	1 / 10	GSEA C2DANG_BOUND_BY_MYC
39	7.71	NULL	2 / 13	GSEA C2SINGH_NFE2L2_TARGETS
40	7.64	NULL	1 / 11	GSEA C2BROWNE_HCMV_INFECTION_10HR_UP



# GW\_249

## Local Summary

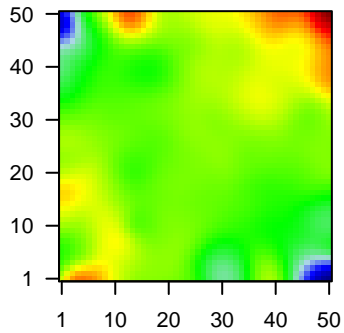
%DE = 0.95  
 # metagenes = 11  
 # genes = 224  
 # genes in genesets = 222

# genes with  $fdr < 0.1 = 205$  ( 8 + / 197 - )  
 # genes with  $fdr < 0.05 = 200$  ( 6 + / 194 - )  
 # genes with  $fdr < 0.01 = 182$  ( 5 + / 177 - )

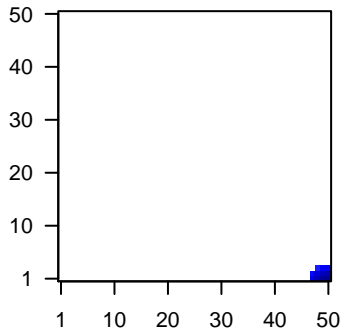
<r> metagenes = 1  
 <r> genes = 0.63

<FC> = -0.69  
 <shrinkage-t> = -24.12  
 <p-value> = 0  
 <fdr> = 0.18

Profile



Spot



## Local Genelist

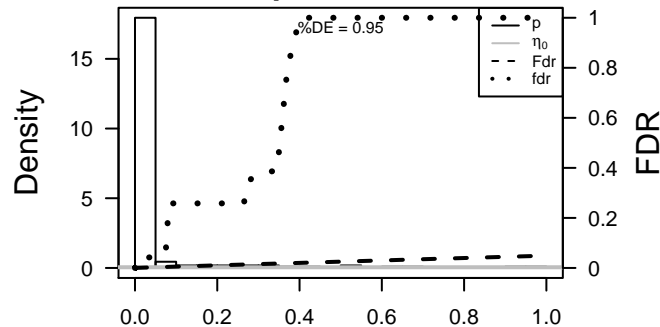
Rank	ID	log(FC)	fdr	p-value	Description
1	241	-1.65	2e-16	2e-16	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC]
2	260436	-1.42	2e-16	2e-16	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc]
3	972	-1.61	2e-16	2e-16	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
4	3059	-1.48	2e-16	2e-16	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC S]
5	3109	-1.51	2e-16	2e-16	50 x 1 major histocompatibility complex, class II, DM beta [Source:H]
6	3113	-1.75	2e-16	2e-16	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:
7	3122	-1.82	2e-16	2e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:t
8	3128	-1.47	2e-16	2e-16	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
9	3689	-1.51	2e-16	2e-16	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 s
10	3936	-1.75	2e-16	2e-16	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Syr
11	5341	-1.61	2e-16	2e-16	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
12	5880	-1.96	2e-16	2e-16	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small C
13	10537	-1.47	2e-16	2e-16	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
14	4050	-1.36	4e-16	2e-14	50 x 1 lymphotoxin beta (TNF superfamily, member 3) [Source:HGNC]
15	3120	-1.32	2e-15	4e-14	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:
16	5996	-1.29	8e-15	4e-14	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc
17	3001	-1.28	1e-14	4e-14	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
18	962	-1.28	1e-14	4e-14	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
19	4069	-1.28	2e-14	1e-13	50 x 2 lysozyme [Source:HGNC Symbol;Acc:6740]
20	3108	-1.26	3e-14	1e-13	50 x 1 major histocompatibility complex, class II, DM alpha [Source:l

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-38.76	NULL	12 / 15	CC MHC class II protein complex
2	-29.1	NULL	84 / 417	H.Tiss WIRTH_Immune system
3	-23.66	NULL	45 / 312	BP immune response
4	-23.2	NULL	14 / 47	BP antigen processing and presentation
5	-21.98	NULL	81 / 553	Cancer Lembecke_Colonic Inflammation
6	-21.05	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
7	-20.11	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
8	-20.01	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
9	-18.99	NULL	35 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
10	-18.99	NULL	35 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
11	-18.99	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
12	-18.99	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
13	-18.99	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
14	-18.92	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
15	-17.93	NULL	7 / 28	CC transport vesicle membrane
16	-16.84	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
17	-16.64	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
18	-16.61	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
19	-16.46	NULL	13 / 60	BP T cell costimulation
20	-16.08	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
21	-15.82	NULL	7 / 35	CC trans-Golgi network membrane
22	-15.32	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
23	-15.18	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
24	-14.88	NULL	3 / 8	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_D
25	-14.86	NULL	12 / 87	BP antigen processing and presentation of exogenous peptide antigen
26	-14.79	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
27	-14.6	NULL	2 / 5	GSEA C2WEST_ADRENOCORITICAL_CARCINOMA_VS_ADENOMA_DN
28	-14.59	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
29	-14.54	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
30	-14.52	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
31	-14.38	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
32	-14.31	NULL	4 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
33	-14.3	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
34	-14.25	NULL	8 / 16	GSEA C2SU_THYMUS
35	-13.69	NULL	8 / 52	Chr Chr HSCHR6_MHC_QBL
36	-13.67	NULL	3 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE
37	-13.55	NULL	7 / 46	CC endocytic vesicle membrane
38	-13.49	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
39	-13.47	NULL	27 / 316	Cancer SPANG_BCL6-index2
40	-13.46	NULL	16 / 74	BP regulation of immune response

p-values



# GW\_249

## Local Summary

%DE = 0.9  
 # metagenes = 8  
 # genes = 143  
 # genes in genesets = 139

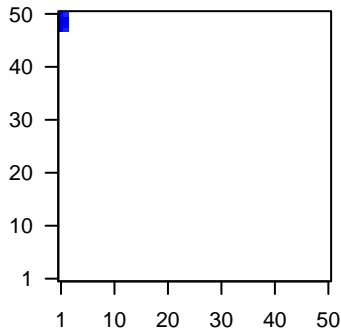
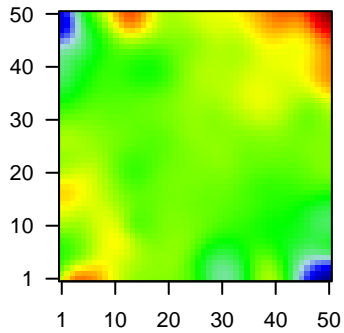
# genes with  $fdr < 0.1 = 120$  ( 10 + / 110 - )  
 # genes with  $fdr < 0.05 = 120$  ( 10 + / 110 - )  
 # genes with  $fdr < 0.01 = 107$  ( 9 + / 98 - )

<r> metagenes = 0.98  
 <r> genes = 0.51

<FC> = -0.84  
 <shrinkage-t> = -29.51  
 <p-value> = 0  
 <fdr> = 0.21

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	2.04	2e-16	8e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	3.27	2e-16	8e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:16371]
3	222	-1.84	2e-16	8e-17	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC Symbol;Acc:16371]
4	360	-1.41	2e-16	8e-17	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:6371]
5	84290	-1.51	2e-16	8e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	22802	-1.7	2e-16	8e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:2071]
7	84518	-1.51	2e-16	8e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	1382	-1.94	2e-16	8e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol;Acc:1230]
9	49860	-1.74	2e-16	8e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
10	1672	-1.89	2e-16	8e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	55894	-1.54	2e-16	8e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	414325	-2.03	2e-16	8e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	1673	-2.52	2e-16	8e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	115572	-1.52	2e-16	8e-17	1 x 48 family with sequence similarity 46, member B [Source:HGNC Symbol;Acc:31702]
15	2706	-3.34	2e-16	8e-17	1 x 47 gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;Acc:31702]
16	10804	-3.24	2e-16	8e-17	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;Acc:31702]
17	2877	2.91	2e-16	8e-17	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Symbol;Acc:31702]
18	3848	-1.59	2e-16	8e-17	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
19	3860	-1.99	2e-16	8e-17	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
20	388533	-1.46	2e-16	8e-17	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC Symbol;Acc:31702]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-40.43	NULL	63 / 135	H.Tiss WIRTH_Mucosa
2	-24.61	NULL	69 / 572	Disease GUDJ_psooriasis up
3	-21.17	NULL	4 / 10	MF RAGE receptor binding
4	-21	NULL	16 / 21	CC cornified envelope
5	-19.17	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
6	-18.3	NULL	2 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
7	-17.78	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
8	-16.84	NULL	2 / 15	CC connexon complex
9	-16.54	NULL	19 / 42	BP keratinization
10	-16.18	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
11	-16.08	NULL	5 / 13	BP negative regulation of peptidase activity
12	-14.9	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
13	-14.67	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
14	-13.87	NULL	2 / 21	CC gap junction
15	-13.09	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
16	-13.09	NULL	6 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	-12.96	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
18	-12.83	NULL	21 / 53	BP keratinocyte differentiation
19	-12.65	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	-12.41	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
21	-12.36	NULL	1 / 7	GSEA C2KONDO_PROSTATE_CANCER_WITH_H3K27ME3
22	-12.19	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
23	-12.06	NULL	8 / 52	BP negative regulation of endopeptidase activity
24	-11.95	NULL	17 / 76	BP epidermis development
25	-11.89	NULL	6 / 73	BP defense response to bacterium
26	-11.69	NULL	3 / 15	GSEA C2AIGNER_ZEB1_TARGETS
27	-11.65	NULL	1 / 5	miRNA target-196a
28	-11.48	NULL	8 / 44	CC keratin filament
29	-11.28	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
30	-11.28	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
31	-11.19	NULL	1 / 10	MF gap junction channel activity
32	-11.11	NULL	2 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
33	-11.09	NULL	5 / 29	BP regulation of proteolysis
34	-10.99	NULL	3 / 16	GSEA C2JAEGER_METASTASIS_DN
35	-10.88	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
36	-10.63	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
37	-10.44	NULL	2 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
38	-10.11	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
39	-10.03	NULL	1 / 12	GSEA C2SCHLESINGER METHYLATED_DE_NOVO_IN_CANCER
40	-10.01	NULL	2 / 8	GSEA C2MCLAHLAN_DENTAL_CARIES_UP

