

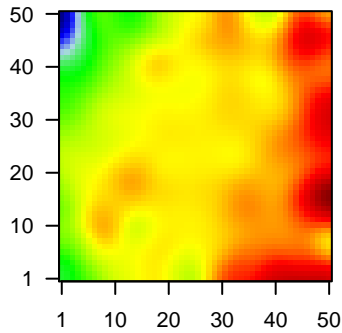
# GW\_003

## Global Summary

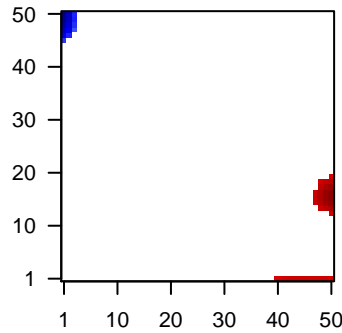
%DE = 0.15  
 # genes with  $fdr < 0.2$  = 1858 ( 994 + / 864 - )  
 # genes with  $fdr < 0.1$  = 1499 ( 789 + / 710 - )  
 # genes with  $fdr < 0.05$  = 1266 ( 675 + / 591 - )  
 # genes with  $fdr < 0.01$  = 869 ( 438 + / 431 - )  
  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.1  
 <fdr> = 0.85

Profile



Regulated Spots



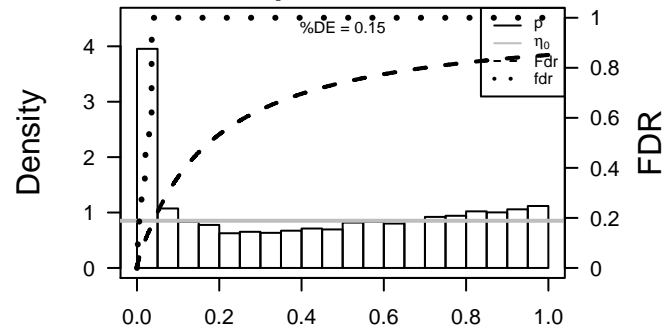
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	21	2	2e-16	3e-14	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Source:HGNC Symbol;Acc:71568]
2	131	-1.66	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:HGNC Symbol;Acc:71568]
3	57016	-2.46	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase) [Source:HGNC Symbol;Acc:71568]
4	441282	-1.77	2e-16	3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:71568]
5	1646	-1.56	2e-16	3e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Symbol;Acc:71568]
6	8644	-1.98	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:71568]
7	1109	-2	2e-16	3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:71568]
8	222	-1.8	2e-16	3e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC Symbol;Acc:71568]
9	9915	1.58	2e-16	3e-14	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HGNC Symbol;Acc:71568]
10	22809	1.89	2e-16	3e-14	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:71568]
11	330	1.57	2e-16	3e-14	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:71568]
12	387695	-2.44	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symbol;Acc:71568]
13	399948	1.71	2e-16	3e-14	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:71568]
14	64207	-1.7	2e-16	3e-14	50 x 40 interferon regulatory factor 2 binding protein-like [Source:HGNC Symbol;Acc:71568]
15	375791	-1.75	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symbol;Acc:71568]
16	760	-1.74	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
17	84290	-1.81	2e-16	3e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
18	6364	2.23	2e-16	3e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:71568]
19	4680	-1.79	2e-16	3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (type 1) [Source:HGNC Symbol;Acc:71568]
20	9635	-3.26	2e-16	3e-14	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20156]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.33	NULL	4640	CC nucleus
2	8.58	NULL	15	CC MHC class II protein complex
3	8.08	NULL	417	H.Tiss WIRTH_Immune system
4	7.87	NULL	1749	MF DNA binding
5	7.47	NULL	1574	BP transcription, DNA-templated
6	7.29	NULL	949	CC nucleoplasm
7	7.27	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
8	7.27	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
9	6.62	NULL	370	BP mitotic cell cycle
10	6.56	NULL	32	CC ER to Golgi transport vesicle membrane
11	6.3	NULL	1581	BP regulation of transcription, DNA-dependent
12	6.17	NULL	28	CC transport vesicle membrane
13	5.95	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
14	5.81	NULL	3	MMML C63CIEJ_MMML 7
15	5.78	NULL	4	MMML C63CIEJ_MMML 23
16	5.75	NULL	1095	TF HEBENSTREIT_high expression TF
17	5.7	NULL	92	BP translational elongation
18	5.66	NULL	21	CC clathrin-coated endocytic vesicle membrane
19	5.47	NULL	60	BP interferon-gamma-mediated signaling pathway
20	5.44	NULL	149	BP DNA replication
<i>Underexpressed</i>				
1	-30.46	NULL	135	H.Tiss WIRTH_Mucosa
2	-21.48	NULL	21	CC cornified envelope
3	-21.27	NULL	572	Disease GUDJ_psooriasis up
4	-18.71	NULL	53	BP keratinocyte differentiation
5	-18.69	NULL	42	BP keratinization
6	-17.22	NULL	76	BP epidermis development
7	-14.18	NULL	19	BP peptide cross-linking
8	-12.42	NULL	16	GSEA C20NDER_CDH1_TARGETS_3_DN
9	-12.31	NULL	1182	CC extracellular region
10	-11.19	NULL	10	MF RAGE receptor binding
11	-11.08	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	-10.57	NULL	44	CC keratin filament
13	-10.39	NULL	82	CC intermediate filament
14	-9.72	NULL	186	MF structural molecule activity
15	-9.23	NULL	683	CC extracellular space
16	-9.23	NULL	10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
17	-8.71	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	-8.49	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
19	-7.53	NULL	190	CC extracellular matrix
20	-7.48	NULL	16	GSEA C2JAEGER_METASTASIS_DN

p-values



# GW\_003

## Local Summary

%DE = 0.81  
 # metagenes = 11  
 # genes = 300  
 # genes in genesets = 289

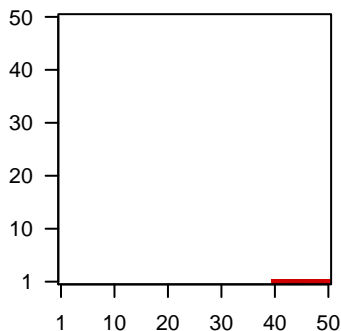
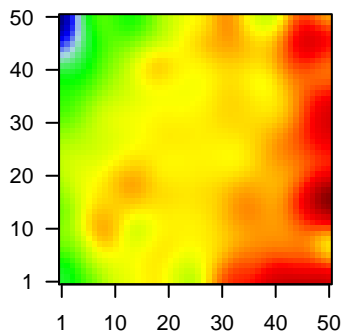
# genes with  $fdr < 0.1 = 167$  ( 160 + / 7 - )  
 # genes with  $fdr < 0.05 = 146$  ( 142 + / 4 - )  
 # genes with  $fdr < 0.01 = 119$  ( 117 + / 2 - )

<r> metagenes = 0.87  
 <r> genes = 0.46

<FC> = 0.47  
 <shrinkage-t> = 16.39  
 <p-value> = 0  
 <fdr> = 0.51

Profile

Spot



## Local Genelist

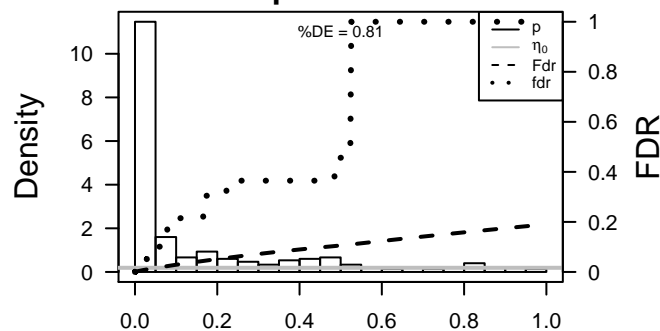
Rank	ID	log(FC)	fdr	p-value	Description
1	22809	1.89	2e-16	1e-15	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:71
2	330	1.57	2e-16	1e-15	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
3	6364	2.23	2e-16	1e-15	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
4	169044	2.13	2e-16	1e-15	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
5	3123	2.29	2e-16	1e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
6	3127	3.13	2e-16	1e-15	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:
7	4248	1.95	2e-16	1e-15	45 x 1 mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucos
8	6689	1.79	2e-16	1e-15	48 x 1 Spi-B transcription factor (Spi-1/PU.1 related) [Source:HGNC
9	10537	2.04	2e-16	1e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
10	260436	1.51	2e-15	2e-13	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
11	972	1.49	4e-15	3e-11	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
12	9806	1.35	1e-12	3e-11	50 x 1 sparc/osteonectin, cwcv and kazal-like domains proteoglycar
13	80162	1.35	1e-12	3e-10	43 x 1 ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;A
14	115361	1.31	6e-12	4e-10	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
15	23062	1.28	1e-11	2e-09	44 x 1 golgi-associated, gamma adaptin ear containing, ARF bindin
16	930	1.25	4e-11	1e-08	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
17	3128	1.2	2e-10	2e-08	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
18	7318	1.17	6e-10	2e-08	48 x 1 ubiquitin-like modifier activating enzyme 7 [Source:HGNC Sy
19	29944	1.16	8e-10	5e-08	42 x 1 paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187
20	3003	1.14	2e-09	5e-08	49 x 1 granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	37.72	NULL	14 / 15	CC MHC class II protein complex
2	27.89	NULL	3 / 3	MMML C6ACIEJ_MMML 7
3	27.09	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
4	25.79	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
5	23.19	NULL	9 / 28	CC transport vesicle membrane
6	21.82	NULL	16 / 47	BP antigen processing and presentation
7	21.56	NULL	9 / 32	CC ER to Golgi transport vesicle membrane
8	20.54	NULL	9 / 35	CC trans-Golgi network membrane
9	18.53	NULL	17 / 60	BP T cell costimulation
10	17.68	NULL	9 / 46	CC endocytic vesicle membrane
11	17.3	NULL	50 / 312	BP immune response
12	17.07	NULL	2 / 4	MMML C6ACIEJ_MMML 2
13	16.72	NULL	75 / 417	H.Tiss WIRTH_Immune system
14	15.72	NULL	12 / 60	BP interferon-gamma-mediated signaling pathway
15	15.34	NULL	16 / 87	BP antigen processing and presentation of exogenous peptide antigen
16	14.15	NULL	14 / 84	BP T cell receptor signaling pathway
17	12.92	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
18	12.35	NULL	1 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
19	11.97	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
20	11.73	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDP_SIGNATURE
21	11.55	NULL	8 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
22	11.54	NULL	7 / 77	CC late endosome membrane
23	11.43	NULL	4 / 10	BP negative thymic T cell selection
24	11.28	NULL	69 / 553	Cancer Lembecke_Colonc Inflammation
25	10.71	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
26	10.66	NULL	9 / 52	Chr Chr HSCR6_MHC_QBL
27	10.37	NULL	19 / 215	CC lysosomal membrane
28	10.01	NULL	20 / 204	BP cytokine-mediated signaling pathway
29	9.8	NULL	21 / 162	CC external side of plasma membrane
30	9.77	NULL	4 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
31	9.5	NULL	3 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
32	9.21	NULL	2 / 9	GSEA C2BIOCARTA_SODD_PATHWAY
33	9.01	NULL	5 / 12	BP immunoglobulin mediated immune response
34	8.74	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
35	8.46	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
36	8.45	NULL	2 / 5	GSEA C2WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
37	8.31	NULL	3 / 14	GSEA C2MAYBURD_RESPONSE_TO_L663536_UP
38	8.27	NULL	5 / 13	Cancer GENTLES_modul18
39	8.26	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
40	8.1	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY

p-values



# GW\_003

## Local Summary

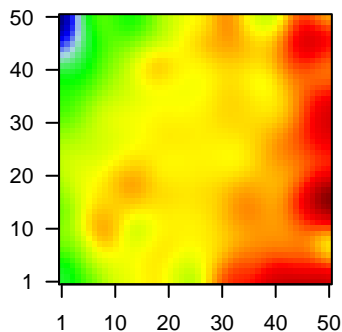
%DE = 0.85  
 # metagenes = 23  
 # genes = 274  
 # genes in genesets = 272

# genes with  $fdr < 0.1$  = 193 ( 187 + / 6 - )  
 # genes with  $fdr < 0.05$  = 169 ( 167 + / 2 - )  
 # genes with  $fdr < 0.01$  = 141 ( 140 + / 1 - )

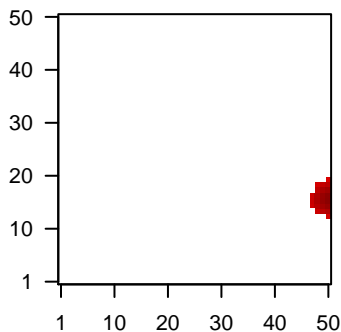
$\langle r \rangle$  metagenes = 0.95  
 $\langle r \rangle$  genes = 0.3

$\langle FC \rangle = 0.57$   
 $\langle \text{shrinkage-t} \rangle = 19.89$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.4$

Profile



Spot



## Local Genelist

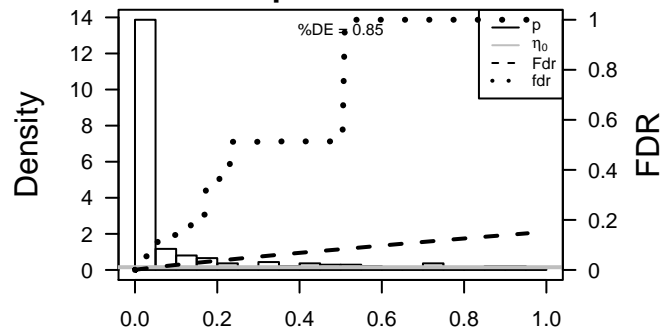
Rank	ID	log(FC)	fdr	p-value	Description
1	21	2	2e-16	9e-16	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
2	9915	1.58	2e-16	9e-16	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
3	399948	1.71	2e-16	9e-16	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
4	1365	2.03	2e-16	9e-16	50 x 15 claudin 3 [Source:HGNC Symbol;Acc:2045]
5	3670	1.58	2e-16	9e-16	50 x 17 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
6	4602	1.66	2e-16	9e-16	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source
7	83988	1.56	2e-16	9e-16	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
8	10439	2.3	2e-16	9e-16	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
9	494470	1.94	2e-16	9e-16	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
10	6263	1.84	2e-16	9e-16	50 x 18 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
11	57556	1.46	2e-14	5e-13	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic
12	9603	1.44	3e-14	5e-13	50 x 18 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:
13	221061	1.44	3e-14	1e-10	50 x 16 family with sequence similarity 171, member A1 [Source:HG
14	66002	1.31	5e-12	1e-10	50 x 13 cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
15	217	1.3	8e-12	1e-10	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HC
16	4774	1.29	1e-11	1e-10	50 x 13 nuclear factor I/A [Source:HGNC Symbol;Acc:7784]
17	3792	1.28	1e-11	1e-10	50 x 17 Kell blood group, metallo-endopeptidase [Source:HGNC Syrr
18	6091	1.28	1e-11	8e-10	50 x 17 roundabout, axon guidance receptor, homolog 1 (Drosophila)
19	6228	1.26	3e-11	1e-09	50 x 14 ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
20	112703	1.24	7e-11	1e-09	50 x 18 family with sequence similarity 71, member E1 [Source:HGNC

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	12.92	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
2	12.64	NULL	6 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
3	10.87	NULL	2 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
4	10.41	NULL	2 / 9	GSEA C2GOZGIT_ESR1_TARGETS_DN
5	9.32	NULL	2 / 4	miRNA target-204
6	9.08	NULL	1 / 3	miRNA target-223
7	8.81	NULL	1 / 2	miRNA target-153
8	8.43	NULL	3 / 12	GSEA C2PROVENZANI_METASTASIS_UP
9	8.08	NULL	1 / 10	GSEA C2BROWNE_HCMV_INFECTION_12HR_UP
10	8.08	NULL	1 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
11	7.99	NULL	2 / 10	GSEA C2REACTOME_INNATE_IMMUNITY_SIGNALING
12	7.9	NULL	1 / 3	miRNA target-148a
13	7.77	NULL	2 / 10	BP positive regulation of histone H3-K4 methylation
14	7.69	NULL	2 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
15	7.68	NULL	2 / 15	BP retinal ganglion cell axon guidance
16	7.61	NULL	2 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
17	7.61	NULL	2 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
18	7.51	NULL	2 / 15	BP embryonic digestive tract development
19	7.47	NULL	2 / 16	GSEA C2BROWNE_HCMV_INFECTION_24HR_UP
20	7.4	NULL	2 / 16	GSEA C2WU_HBX_TARGETS_3_UP
21	7.4	NULL	4 / 20	MF RNA polymerase II transcription coactivator activity
22	7.31	NULL	2 / 11	MF enhancer sequence-specific DNA binding
23	7.26	NULL	1 / 12	GSEA C2CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
24	7.26	NULL	1 / 12	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_DN
25	7.26	NULL	1 / 12	GSEA C2ZHANG_TARGETS_OF_EWSR1_FL1_FUSION
26	7.2	NULL	2 / 11	BP neurotransmitter biosynthetic process
27	7.08	NULL	7 / 127	miRNA target-212-132
28	6.93	NULL	1 / 13	GSEA C2COLDREN_GEFITINIB_RESISTANCE_UP
29	6.93	NULL	1 / 13	GSEA C2STEIN_ESR1_TARGETS
30	6.86	NULL	8 / 139	miRNA target-129
31	6.85	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
32	6.63	NULL	1 / 14	GSEA C2POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASS
33	6.63	NULL	1 / 14	GSEA C2POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASS
34	6.63	NULL	1 / 14	GSEA C2MASSARWEH_TAMOXIFEN_RESISTANCE_DN
35	6.63	NULL	1 / 14	GSEA C2STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA
36	6.63	NULL	1 / 14	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
37	6.63	NULL	1 / 14	GSEA C2BROWNE_HCMV_INFECTION_16HR_UP
38	6.63	NULL	1 / 14	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_DN
39	6.63	NULL	1 / 5	GSEA C2WALK_AML_WITH_T_8_21_TRANSLOCATION
40	6.57	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN

p-values



# GW\_003

## Local Summary

%DE = 0.96  
 # metagenes = 15  
 # genes = 222  
 # genes in genesets = 216

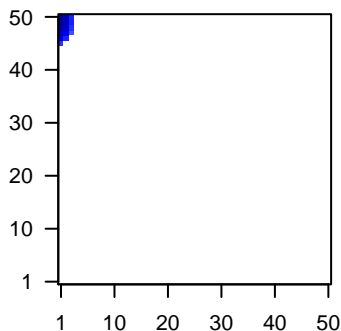
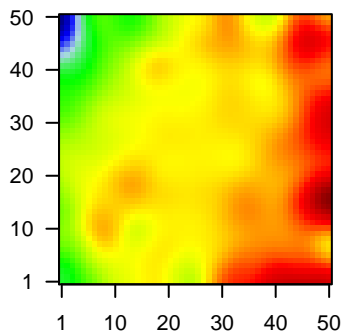
# genes with  $fdr < 0.1$  = 211 ( 6 + / 205 - )  
 # genes with  $fdr < 0.05$  = 203 ( 4 + / 199 - )  
 # genes with  $fdr < 0.01$  = 195 ( 3 + / 192 - )

<r> metagenes = 0.95  
 <r> genes = 0.45

<FC> = -1.28  
 <shrinkage-t> = -45.59  
 <p-value> = 0  
 <fdr> = 0.12

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-1.66	2e-16	3e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.46	2e-16	3e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.77	2e-16	3e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	-1.98	2e-16	3e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
5	222	-1.8	2e-16	3e-17	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
6	387695	-2.44	2e-16	3e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	375791	-1.75	2e-16	3e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
8	84290	-1.81	2e-16	3e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	4680	-1.79	2e-16	3e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	9635	-3.26	2e-16	3e-17	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
11	22802	-1.84	2e-16	3e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	84518	-2.57	2e-16	3e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
13	49860	-2.43	2e-16	3e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
14	9547	-1.75	2e-16	3e-17	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
15	1672	-1.71	2e-16	3e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
16	1673	-2.17	2e-16	3e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1830	-2.14	2e-16	3e-17	1 x 48 desmoglein 3 [Source:HGNC Symbol;Acc:3050]
18	2012	-1.6	2e-16	3e-17	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
19	2125	-1.58	2e-16	3e-17	1 x 50 envoplakin [Source:HGNC Symbol;Acc:3503]
20	2171	-2.24	2e-16	3e-17	1 x 46 fatty acid binding protein 5 (psoriasis-associated) [Source:HC

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-56.97	NULL	82 / 135	H.Tiss WIRTH_Mucosa
2	-45.91	NULL	18 / 21	CC cornified envelope
3	-38.16	NULL	24 / 53	BP keratinocyte differentiation
4	-36.27	NULL	19 / 42	BP keratinization
5	-32.57	NULL	23 / 76	BP epidermis development
6	-32.18	NULL	93 / 572	Disease GUDJ_pсориаз up
7	-26.83	NULL	5 / 10	MF RAGE receptor binding
8	-25.63	NULL	8 / 16	GSEA C2WNDER_CDH1_TARGETS_3_DN
9	-25.57	NULL	10 / 19	BP peptide cross-linking
10	-18.17	NULL	10 / 44	CC keratin filament
11	-18	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
12	-17.14	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
13	-16.94	NULL	23 / 186	MF structural molecule activity
14	-16.76	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
15	-16.53	NULL	3 / 10	GSEA C2AJJLA_IL22_AND_IL17A_SIGNALING
16	-16.02	NULL	16 / 82	CC intermediate filament
17	-14.75	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	-13.7	NULL	12 / 21	CC desmosome
19	-13.7	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
20	-13.13	NULL	4 / 25	BP response to zinc ion
21	-13.06	NULL	4 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HP31_DN
22	-12.37	NULL	6 / 13	BP negative regulation of peptidase activity
23	-12.31	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
24	-12.04	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
25	-11.44	NULL	7 / 38	BP epithelial cell differentiation
26	-11.25	NULL	3 / 14	BP defense response to fungus
27	-10.84	NULL	55 / 1182	CC extracellular region
28	-10.63	NULL	3 / 13	BP intermediate filament cytoskeleton organization
29	-10.08	NULL	2 / 10	BP chronic inflammatory response
30	-10.05	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
31	-9.93	NULL	4 / 15	GSEA C2IN_SILENCED_BY_TUMOR_MICROENVIRONMENT
32	-9.88	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
33	-9.83	NULL	2 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
34	-9.78	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
35	-9.59	NULL	2 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
36	-9.57	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
37	-9.54	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
38	-9.5	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
39	-9.4	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX
40	-9.35	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN

p-values

