

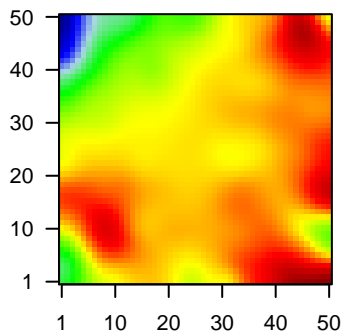
# GW\_178

## Global Summary

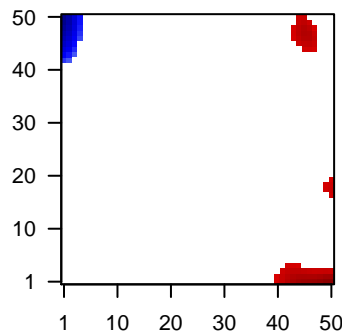
%DE = 0.15  
 # genes with  $fdr < 0.2$  = 1985 ( 979 + / 1006 - )  
 # genes with  $fdr < 0.1$  = 1595 ( 776 + / 819 - )  
 # genes with  $fdr < 0.05$  = 1317 ( 620 + / 697 - )  
 # genes with  $fdr < 0.01$  = 965 ( 434 + / 531 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = -0.01  
 <p-value> = 0.1  
 <fdr> = 0.85

Profile



Regulated Spots



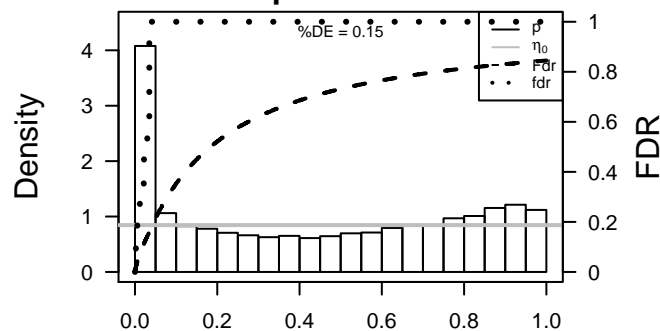
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	72	2.27	2e-16	5e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym]
2	131	-2.47	2e-16	5e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-2.56	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	-2.17	2e-16	5e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Sy]
5	8644	-2.96	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr]
6	1109	-2.74	2e-16	5e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr]
7	115701	2.32	2e-16	5e-14	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
8	10974	-2.17	2e-16	5e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24
9	810	-2	2e-16	5e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
10	1236	2.76	2e-16	5e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
11	970	2.2	2e-16	5e-14	33 x 2 CD70 molecule [Source:HGNC Symbol;Acc:11937]
12	4680	-2.06	2e-16	5e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
13	1116	2.1	2e-16	5e-14	50 x 4 chitinase 3-like 1 (cartilage glycoprotein-39) [Source:HGNC
14	9635	-2.21	2e-16	5e-14	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	22802	-2.23	2e-16	5e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	1308	-2.1	2e-16	5e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
17	1382	-2.03	2e-16	5e-14	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
18	9547	-2	2e-16	5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
19	1673	-2.28	2e-16	5e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	55619	2.17	2e-16	5e-14	50 x 1 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:23479

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.97	NULL	15	CC MHC class II protein complex
2	12.06	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
3	12.06	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
4	11.24	NULL	417	H.Tiss WIRTH_Immune system
5	10.68	NULL	4640	CC nucleus
6	10.54	NULL	426	Lymphoma SPANG_CD40 6hrs DN
7	10	NULL	949	CC nucleoplasm
8	9.34	NULL	370	BP mitotic cell cycle
9	9	NULL	1749	MF DNA binding
10	8.73	NULL	298	BP DNA repair
11	8.25	NULL	47	BP antigen processing and presentation
12	8.17	NULL	149	BP DNA replication
13	8.15	NULL	3	MMML C6 CIEJ_MMML 7
14	8.09	NULL	940	MF nucleic acid binding
15	7.92	NULL	1574	BP transcription, DNA-templated
16	7.48	NULL	140	Lymphoma TAVE_BL-vs-DLBCL
17	7.43	NULL	84	BP T cell receptor signaling pathway
18	7.19	NULL	60	BP T cell costimulation
19	6.96	NULL	595	MF RNA binding
20	6.77	NULL	22	Lymphoma TAVE_NFKB BL DN
<i>Underexpressed</i>				
1	-28.06	NULL	135	H.Tiss WIRTH_Mucosa
2	-17.1	NULL	572	Disease GUDJ_pсориаis up
3	-14.61	NULL	1182	CC extracellular region
4	-12.95	NULL	76	BP epidermis development
5	-11.73	NULL	683	CC extracellular space
6	-10.95	NULL	16	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_UP
7	-10.15	NULL	519	Chr Chr 14
8	-10.13	NULL	242	BP extracellular matrix organization
9	-10.07	NULL	633	Chr Chr 9
10	-9.93	NULL	190	CC extracellular matrix
11	-9.92	NULL	250	Lymphoma ENZ_Stromal signature 1
12	-8.97	NULL	186	MF structural molecule activity
13	-8.82	NULL	53	BP keratinocyte differentiation
14	-8.69	NULL	8	GSEA C2 LIU_CD_X2_TARGETS_DN
15	-8.54	NULL	1146	TF HEBENSTREIT_low expression TF
16	-8.42	NULL	12	BP hemidesmosome assembly
17	-8.13	NULL	83	CC basement membrane
18	-8.11	NULL	579	MF calcium ion binding
19	-8.01	NULL	13	H.Tiss WIRTH_Tonsil
20	-7.81	NULL	21	CC cornified envelope

p-values



# GW\_178

## Local Summary

%DE = 0.71  
 # metagenes = 35  
 # genes = 491  
 # genes in genesets = 478  
 # genes with  $fdr < 0.1$  = 239 ( 214 + / 25 - )  
 # genes with  $fdr < 0.05$  = 202 ( 186 + / 16 - )  
 # genes with  $fdr < 0.01$  = 148 ( 137 + / 11 - )

<r> metagenes = 0.9

<r> genes = 0.44

<FC> = 0.54

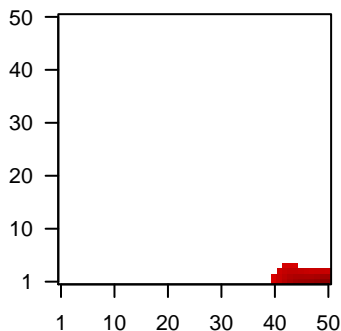
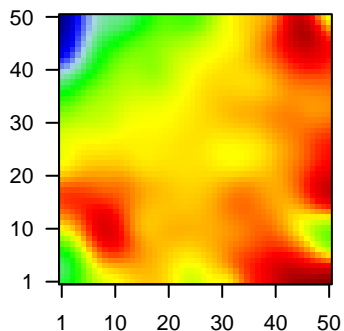
<shrinkage-t> = 18.99

<p-value> = 0

<fdr> = 0.54

Profile

Spot



## Local Genelist

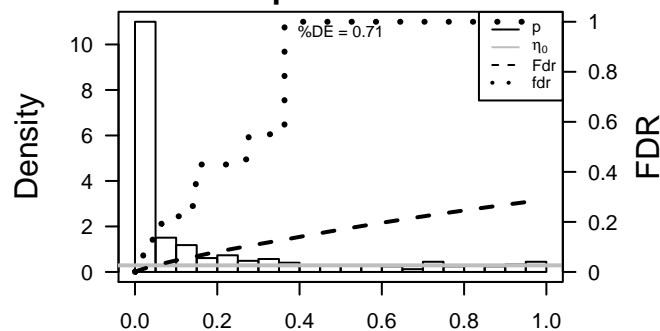
Rank	ID	log(FC)	fdr	p-value	Description
1	115701	2.32	2e-16	2e-15	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
2	1236	2.76	2e-16	2e-15	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:23475]
3	55619	2.17	2e-16	2e-15	50 x 1 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:23475]
4	84824	2.57	2e-16	2e-15	49 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:18504]
5	3111	2.01	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DO alpha [Source:HGNC Symbol;Acc:23475]
6	3113	2.22	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:23475]
7	3119	1.99	2e-16	2e-15	49 x 1 major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:23475]
8	3122	2.02	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:23475]
9	3123	2.69	2e-16	2e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:HGNC Symbol;Acc:23475]
10	3128	2.08	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo)
11	3620	3.29	2e-16	2e-15	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:23475]
12	3936	2.02	2e-16	2e-15	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:23475]
13	25849	2.4	2e-16	2e-15	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HGNC Symbol;Acc:23475]
14	5996	2.11	2e-16	2e-15	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:23475]
15	57484	2.53	2e-16	2e-15	50 x 2 ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
16	9806	3.05	2e-16	2e-15	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycan 1 [Source:HGNC Symbol;Acc:23475]
17	10537	2.15	2e-16	2e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
18	10563	1.93	3e-15	6e-13	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:23475]
19	3512	-1.89	9e-15	6e-13	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin heavy chain [Source:HGNC Symbol;Acc:23475]
20	1512	1.89	1e-14	8e-13	47 x 1 cathepsin H [Source:HGNC Symbol;Acc:2535]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	40.8	NULL	14 / 15	CC MHC class II protein complex
2	27.55	NULL	3 / 3	MMML C6ACIEJ_MMML 7
3	24	NULL	16 / 47	BP antigen processing and presentation
4	21.07	NULL	115 / 417	H.Tiss WIRTH_Immune system
5	20.94	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
6	19.92	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
7	18.47	NULL	10 / 28	CC transport vesicle membrane
8	16.71	NULL	24 / 60	BP T cell costimulation
9	16.63	NULL	9 / 32	CC ER to Golgi transport vesicle membrane
10	15.82	NULL	9 / 35	CC trans-Golgi network membrane
11	15.54	NULL	22 / 84	BP T cell receptor signaling pathway
12	15.06	NULL	9 / 52	Chr Chr HSCHR6_MHC_QBL
13	14.79	NULL	64 / 312	BP immune response
14	14.5	NULL	16 / 87	BP antigen processing and presentation of exogenous peptide antigen
15	14.36	NULL	5 / 10	BP negative thymic T cell selection
16	13.58	NULL	9 / 46	CC endocytic vesicle membrane
17	13.51	NULL	101 / 553	Cancer Lembecke_Colonc Inflammation
18	13.34	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
19	13.31	NULL	3 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
20	13.09	NULL	15 / 60	BP interferon-gamma-mediated signaling pathway
21	12.87	NULL	8 / 14	GSEA C2BIOCARTA_NO2I12_PATHWAY
22	12.62	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
23	11.44	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
24	11.17	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
25	11.15	NULL	15 / 45	BP T cell activation
26	11.08	NULL	5 / 12	BP immunoglobulin mediated immune response
27	10.97	NULL	2 / 5	GSEA C2WEST_ADRENOCORCORTICAL_CARCINOMA_VS_ADENOMA_DN
28	10.89	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
29	10.85	NULL	38 / 426	Lymphom SPANG_CD40 6hrs DN
30	10.73	NULL	9 / 16	GSEA C2SU_THYMUS
31	10.5	NULL	10 / 13	Cancer GENTLES_modul18
32	10.45	NULL	4 / 13	Lymphom BENTINK_mBL DOWN
33	9.91	NULL	5 / 8	GSEA C2BIOCARTA_TCAPOPTOSIS_PATHWAY
34	9.91	NULL	5 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
35	9.87	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
36	9.83	NULL	27 / 204	BP cytokine-mediated signaling pathway
37	9.79	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENT
38	9.76	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
39	9.73	NULL	6 / 22	Lymphom BAVE_NFkB BL DN
40	9.67	NULL	20 / 215	CC lysosomal membrane

p-values



# GW\_178

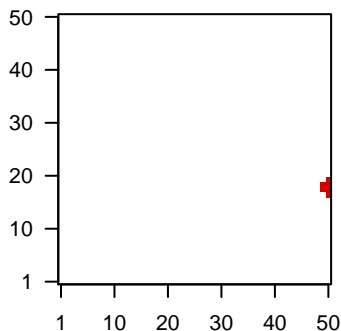
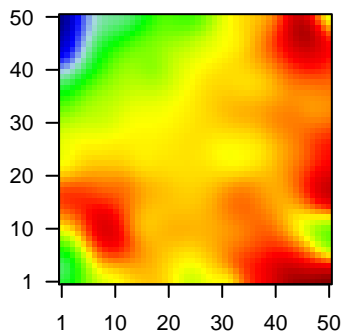
## Local Summary

%DE = 0.62  
 # metagenes = 6  
 # genes = 129  
 # genes in genesets = 128  
 # genes with  $fdr < 0.1$  = 68 ( 66 + / 2 - )  
 # genes with  $fdr < 0.05$  = 53 ( 53 + / 0 - )  
 # genes with  $fdr < 0.01$  = 40 ( 40 + / 0 - )

<r> metagenes = 0.99  
 <r> genes = 0.35  
 <FC> = 0.51  
 <shrinkage-t> = 17.71  
 <p-value> = 0  
 <fdr> = 0.53

Profile

Spot



## Local Genelist

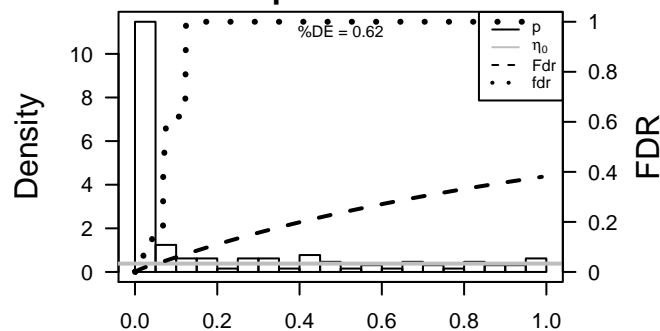
Rank	ID	log(FC)	fdr	p-value	Description
1	83988	2.32	2e-16	1e-14	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
2	21	1.94	2e-15	1e-10	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
3	1298	1.72	2e-12	3e-10	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
4	3792	1.66	9e-12	9e-10	50 x 17 Kell blood group, metallo-endopeptidase [Source:HGNC Syrr
5	9915	1.62	3e-11	4e-09	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
6	79805	1.57	1e-10	3e-07	50 x 18 vasohibin 2 [Source:HGNC Symbol;Acc:25723]
7	112703	1.42	6e-09	3e-07	50 x 18 family with sequence similarity 71, member E1 [Source:HGNC
8	53826	1.39	1e-08	2e-06	50 x 18 FX1D domain containing ion transport regulator 6 [Source:HC
9	79924	1.33	5e-08	9e-06	50 x 18 adrenomedullin 2 [Source:HGNC Symbol;Acc:28898]
10	2047	1.25	3e-07	9e-06	50 x 18 EPH receptor B1 [Source:HGNC Symbol;Acc:3392]
11	596	1.24	4e-07	1e-05	50 x 17 B-cell CLL/lymphoma 2 [Source:HGNC Symbol;Acc:990]
12	9662	1.21	7e-07	1e-04	50 x 19 centrosomal protein 135kDa [Source:HGNC Symbol;Acc:290]
13	2879	1.12	5e-06	1e-04	50 x 18 glutathione peroxidase 4 [Source:HGNC Symbol;Acc:4556]
14	60436	1.1	6e-06	4e-04	50 x 18 TGFB-induced factor homeobox 2 [Source:HGNC Symbol;Ac
15	56983	1.06	1e-05	4e-04	49 x 19 protein O-glucosyltransferase 1 [Source:HGNC Symbol;Acc:1
16	79656	1.04	2e-05	4e-04	50 x 17 BEN domain containing 5 [Source:HGNC Symbol;Acc:25668]
17	3670	1.02	3e-05	6e-04	50 x 17 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
18	55023	0.99	5e-05	6e-04	50 x 17 pleckstrin homology domain interacting protein [Source:HGNC
19	9189	0.98	5e-05	2e-03	50 x 18 zinc finger, BED-type containing 1 [Source:HGNC Symbol;Ac
20	55846	0.93	1e-04	2e-03	50 x 18 integrin alpha FG-GAP repeat containing 2 [Source:HGNC S

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	17.07	NULL	1 / 2	miRNA target-153
2	13.93	NULL	1 / 8	GSEA C2REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTOR
3	13.18	NULL	1 / 3	GSEA C2MYLLKANGAS_AMPLIFICATION_HOT_SPOT_18
4	11.72	NULL	1 / 3	miRNA target-148a
5	11.08	NULL	1 / 7	GSEA C2KANG_CISPLATIN_RESISTANCE_DN
6	11.05	NULL	1 / 4	miRNA target-c
7	11.05	NULL	1 / 4	miRNA target-204
8	11.05	NULL	1 / 4	miRNA target-34b
9	11.05	NULL	1 / 4	miRNA target-34c
10	10.45	NULL	2 / 5	LymphomaASCQUE_mBL UP
11	10.14	NULL	1 / 14	GSEA C2VALK_AML_CLUSTER_13
12	9.94	NULL	2 / 13	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G3_DN
13	9.75	NULL	1 / 15	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G56_DN
14	9.7	NULL	1 / 8	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
15	9.67	NULL	1 / 5	miRNA target-15a
16	9.67	NULL	1 / 5	miRNA target-320
17	9.54	NULL	2 / 15	BP retinal ganglion cell axon guidance
18	9.38	NULL	1 / 2	TF MYC_Chromatin_modification UP
19	9.38	NULL	3 / 15	GSEA C2XOLUB_ALL_VS_AML_UP
20	9.08	NULL	1 / 17	MF clathrin binding
21	8.76	NULL	3 / 16	GSEA C2BILBAN_B_CLL_LPL_DN
22	8.68	NULL	1 / 6	GSEA C2SA_FAS_SIGNALING
23	8.68	NULL	1 / 6	miRNA target-d
24	8.68	NULL	1 / 6	miRNA target-15b
25	8.54	NULL	1 / 7	GSEA C2REACTOME_CALCITONIN_LIKE_LIGAND_RECEPTORS
26	8.29	NULL	1 / 8	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP
27	8.24	NULL	1 / 4	GSEA C2GARASHI_ATF4_TARGETS_UP
28	8.07	NULL	5 / 78	BP positive regulation of angiogenesis
29	7.68	NULL	1 / 12	TF Tissue/AQUERIZAS_Kidney
30	7.65	NULL	1 / 23	MF alpha-tubulin binding
31	7.61	NULL	3 / 30	BP extrinsic apoptotic signaling pathway in absence of ligand
32	7.21	NULL	1 / 14	BP vasoconstriction
33	7.04	NULL	3 / 65	BP response to glucocorticoid
34	6.95	NULL	3 / 29	TF Tissue/AQUERIZAS_Lymph node
35	6.86	NULL	1 / 4	GSEA C2MYLLKANGAS_AMPLIFICATION_HOT_SPOT_27
36	6.85	NULL	1 / 9	GSEA C2MARKS_HDAC_TARGETS_DN
37	6.85	NULL	1 / 9	GSEA C2SA_PROGRAMMED_CELL_DEATH
38	6.85	NULL	1 / 9	miRNA target-348
39	6.73	NULL	2 / 13	Cancer GENTLES_modul12
40	6.62	NULL	2 / 19	BP negative regulation of G1/S transition of mitotic cell cycle

p-values



# GW\_178

## Local Summary

%DE = 0.76  
 # metagenes = 27  
 # genes = 300  
 # genes in genesets = 298

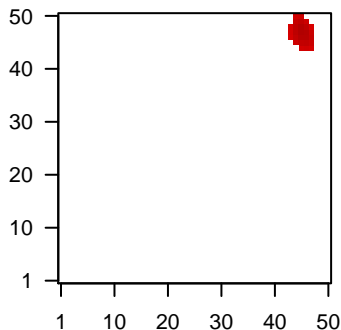
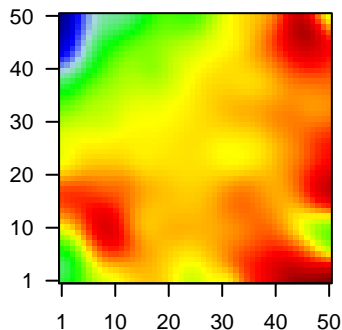
# genes with  $fdr < 0.1$  = 173 ( 168 + / 5 - )  
 # genes with  $fdr < 0.05$  = 166 ( 162 + / 4 - )  
 # genes with  $fdr < 0.01$  = 99 ( 98 + / 1 - )

<r> metagenes = 0.94  
 <r> genes = 0.38

<FC> = 0.54  
 <shrinkage-t> = 18.99  
 <p-value> = 0.01  
 <fdr> = 0.52

Profile

Spot



## Local Genelist

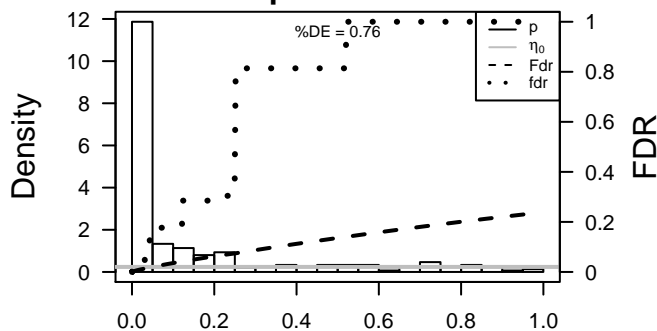
Rank	ID	log(FC)	fdr	p-value	Description
1	9355	1.74	1e-12	2e-09	LIM homeobox 2 [Source:HGNC Symbol;Acc:6594]
2	4171	1.63	2e-11	7e-09	minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:1211]
3	84223	1.55	2e-10	7e-09	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
4	3148	1.55	2e-10	3e-08	high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
5	9070	1.51	6e-10	8e-08	ash2 (absent, small, or homeotic)-like (Drosophila) [Source:HGNC Symbol;Acc:1211]
6	128178	1.47	2e-09	4e-07	EDAR-associated death domain [Source:HGNC Symbol;Acc:1211]
7	51087	1.37	2e-08	4e-07	Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
8	4172	1.36	2e-08	4e-07	minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:1211]
9	79682	1.36	2e-08	4e-07	centromere protein U [Source:HGNC Symbol;Acc:21348]
10	699	1.36	3e-08	4e-07	BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:1211]
11	55215	1.35	3e-08	4e-07	Fanconi anemia, complementation group I [Source:HGNC Symbol;Acc:1211]
12	116028	1.35	3e-08	2e-06	RecQ mediated genome instability 2 [Source:HGNC Symbol;Acc:1211]
13	113130	1.32	7e-08	2e-06	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1211]
14	7153	1.3	1e-07	2e-06	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbol;Acc:1211]
15	2956	1.29	1e-07	3e-06	mutS homolog 6 [Source:HGNC Symbol;Acc:7329]
16	4175	1.27	2e-07	3e-06	minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:1211]
17	8438	1.25	3e-07	3e-06	RAD54-like (S. cerevisiae) [Source:HGNC Symbol;Acc:9826]
18	10024	1.25	3e-07	3e-06	trophinin associated protein [Source:HGNC Symbol;Acc:1232]
19	899	1.25	3e-07	4e-06	cyclin F [Source:HGNC Symbol;Acc:1591]
20	78995	1.23	4e-07	4e-06	chromosome 17 open reading frame 53 [Source:HGNC Symbol;Acc:1211]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	48.78	NULL	83 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	48.78	NULL	83 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	28.61	NULL	86 / 370	BP mitotic cell cycle
4	28.48	NULL	15 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
5	27.49	NULL	8 / 11	GSEA C2KALMA_E2F1_TARGETS
6	27.47	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
7	26.53	NULL	25 / 57	Glio developing astrocytes
8	26.1	NULL	44 / 149	BP DNA replication
9	25.83	NULL	16 / 30	BP DNA strand elongation involved in DNA replication
10	25.8	NULL	11 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
11	24.66	NULL	10 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
12	24.09	NULL	89 / 530	Cancer Lembcke_Normal vs Adenoma
13	23.75	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
14	22.85	NULL	12 / 22	BP DNA replication initiation
15	22.82	NULL	11 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
16	22.71	NULL	7 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
17	22.4	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	22.39	NULL	9 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
19	21.99	NULL	10 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
20	21.79	NULL	10 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
21	21.61	NULL	12 / 15	GSEA C2ZHANG_CYCLING_GENES
22	21.37	NULL	9 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
23	20.8	NULL	10 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
24	20.51	NULL	9 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
25	19.72	NULL	10 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
26	19.67	NULL	12 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
27	19.36	NULL	8 / 15	GSEA C2KEGG_DNA_REPLICATION
28	19.35	NULL	10 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
29	18.99	NULL	9 / 15	GSEA C2Y_AGING_MIDDLE_DN
30	18.93	NULL	21 / 56	CC chromosome, centromeric region
31	18.84	NULL	7 / 16	GSEA C2Y_AGING_PREMATURE_DN
32	18.71	NULL	6 / 14	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
33	18.52	NULL	8 / 16	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
34	18.21	NULL	47 / 232	BP mitosis
35	18.09	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
36	18.06	NULL	7 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
37	17.94	NULL	7 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
38	17.78	NULL	7 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
39	17.52	NULL	7 / 15	GSEA C2Y_AGING_OLD_DN
40	17.02	NULL	10 / 14	MMLL C2SCIEJ_MMLL_4

p-values



# GW\_178

## Local Summary

%DE = 0.94  
 # metagenes = 31  
 # genes = 405  
 # genes in genesets = 396

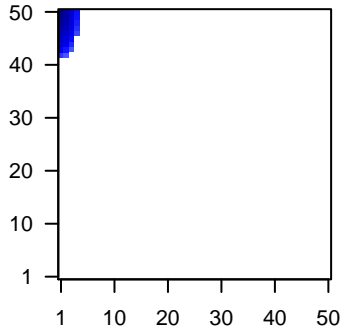
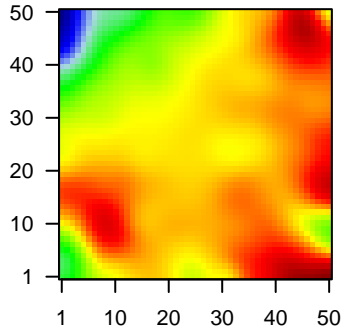
# genes with  $fdr < 0.1 = 374$  ( 6 + / 368 - )  
 # genes with  $fdr < 0.05 = 360$  ( 5 + / 355 - )  
 # genes with  $fdr < 0.01 = 324$  ( 5 + / 319 - )

<r> metagenes = 0.87  
 <r> genes = 0.35

<FC> = -1.06  
 <shrinkage-t> = -37.46  
 <p-value> = 0  
 <fdr> = 0.16

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.47	2e-16	2e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.56	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-2.17	2e-16	2e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
4	8644	-2.96	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
5	810	-2	2e-16	2e-16	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
6	4680	-2.06	2e-16	2e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
7	9635	-2.21	2e-16	2e-16	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
8	22802	-2.23	2e-16	2e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	1308	-2.1	2e-16	2e-16	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
10	1382	-2.03	2e-16	2e-16	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
11	9547	-2	2e-16	2e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
12	1673	-2.28	2e-16	2e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	2012	-2	2e-16	2e-16	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
14	2697	-2.21	2e-16	2e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;v
15	3429	-1.9	2e-16	2e-16	1 x 42 interferon, alpha-inducible protein 27 [Source:HGNC Symbol
16	3489	-2.13	2e-16	2e-16	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
17	3860	-2.33	2e-16	2e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
18	3851	-2.52	2e-16	2e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
19	3852	-1.83	2e-16	2e-16	1 x 44 keratin 5 [Source:HGNC Symbol;Acc:6442]
20	3934	-2.5	2e-16	2e-16	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-58.05	NULL	101 / 135	H.Tiss WIRTH_Mucosa
2	-31.71	NULL	133 / 572	Disease GUDJ_psooriasis up
3	-22.97	NULL	32 / 76	BP epidermis development
4	-21.66	NULL	10 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	-19.36	NULL	19 / 21	CC cornified envelope
6	-18.4	NULL	26 / 53	BP keratinocyte differentiation
7	-17.06	NULL	5 / 10	MF RAGE receptor binding
8	-16.75	NULL	8 / 16	GSEA C2WNDER_CDH1_TARGETS_3_DN
9	-15.12	NULL	8 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
10	-15.05	NULL	20 / 42	BP keratinization
11	-15.05	NULL	9 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	-14.89	NULL	8 / 16	GSEA C2JAEGER_METASTASIS_DN
13	-14.78	NULL	12 / 21	CC desmosome
14	-14.58	NULL	22 / 82	CC intermediate filament
15	-14.41	NULL	3 / 5	miRNA target-196a
16	-13.69	NULL	13 / 44	CC keratin filament
17	-13.13	NULL	6 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
18	-12.97	NULL	5 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
19	-12.83	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
20	-12.6	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
21	-11.95	NULL	3 / 10	BP chronic inflammatory response
22	-11.55	NULL	4 / 12	H.Tiss WIRTH_Prim. lymphoid organs
23	-11.53	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
24	-11.38	NULL	7 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
25	-11.3	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
26	-11.1	NULL	32 / 186	MF structural molecule activity
27	-11.06	NULL	10 / 38	BP epithelial cell differentiation
28	-11.01	NULL	8 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
29	-10.95	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
30	-10.88	NULL	10 / 52	BP negative regulation of endopeptidase activity
31	-10.7	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
32	-10.63	NULL	5 / 13	H.Tiss WIRTH_Tonsil
33	-10.57	NULL	7 / 29	BP regulation of proteolysis
34	-10.55	NULL	12 / 19	BP peptide cross-linking
35	-10.51	NULL	4 / 12	BP hemidesmosome assembly
36	-10.4	NULL	5 / 25	BP response to zinc ion
37	-10.36	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
38	-10.32	NULL	4 / 13	BP retinoic acid metabolic process
39	-10.32	NULL	5 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
40	-10.27	NULL	78 / 1182	CC extracellular region

p-values

