

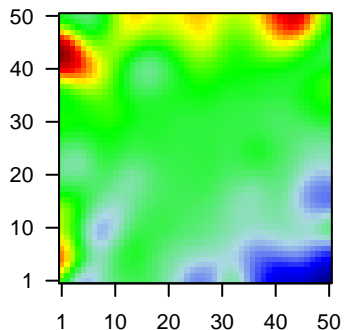
# GW\_184

## Global Summary

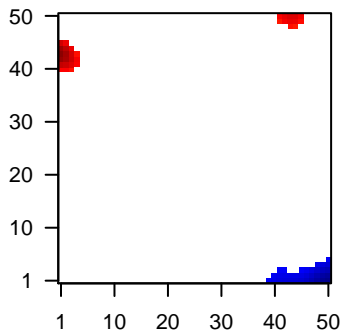
%DE = 0.14  
 # genes with  $fdr < 0.2$  = 1768 ( 1059 + / 709 - )  
 # genes with  $fdr < 0.1$  = 1365 ( 844 + / 521 - )  
 # genes with  $fdr < 0.05$  = 1132 ( 724 + / 408 - )  
 # genes with  $fdr < 0.01$  = 753 ( 515 + / 238 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.12  
 <fdr> = 0.86

Profile



Regulated Spots



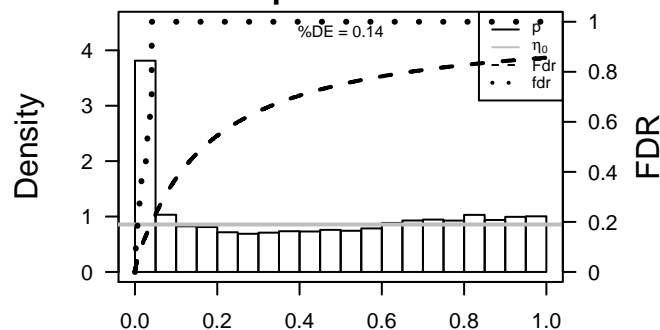
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	147463	1.28	2e-16	5e-14	25 x 50 ankryin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
2	55107	2.19	2e-16	5e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:15777]
3	92747	1.9	2e-16	5e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:15777]
4	768	1.24	2e-16	5e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
5	8900	1.74	2e-16	5e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:15777]
6	595	1.38	2e-16	5e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
7	894	1.24	2e-16	5e-14	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
8	1012	1.38	2e-16	5e-14	1 x 5 cadherin 13 [Source:HGNC Symbol;Acc:1753]
9	1288	1.83	2e-16	5e-14	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
10	1396	1.58	2e-16	5e-14	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:1230]
11	49860	-1.95	2e-16	5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
12	2017	1.29	2e-16	5e-14	1 x 14 cortactin [Source:HGNC Symbol;Acc:3338]
13	9547	1.91	2e-16	5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:31702]
14	285761	1.8	2e-16	5e-14	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC Symbol;Acc:31702]
15	414325	1.65	2e-16	5e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1673	1.52	2e-16	5e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1828	1.82	2e-16	5e-14	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	2167	3.77	2e-16	5e-14	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol;Acc:3048]
19	8772	1.9	2e-16	5e-14	1 x 14 Fas (TNFRSF6)-associated via death domain [Source:HGNC Symbol;Acc:3048]
20	51083	1.33	2e-16	5e-14	1 x 15 galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:417]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	21.92	NULL	519	Chr Chr 14
2	15.2	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
3	15.2	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
4	11.41	NULL	370	BP mitotic cell cycle
5	10.94	NULL	572	Disease GUDJ_psooriasis_up
6	9.94	NULL	530	Cancer Lembcke_Normal vs Adenoma
7	8.22	NULL	232	BP mitosis
8	7.76	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
9	7.62	NULL	15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
10	7.36	NULL	15	GSEA C2REACTOME_CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2
11	7.24	NULL	949	CC nucleoplasm
12	6.9	NULL	68	Glio cultured astroglia vs. in vivo astrocytes
13	6.86	NULL	16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
14	6.82	NULL	148	BP G1/S transition of mitotic cell cycle
15	6.78	NULL	149	BP DNA replication
16	6.76	NULL	12	BP hemidesmosome assembly
17	6.74	NULL	5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
18	6.68	NULL	14	GSEA C2SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
19	6.67	NULL	13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
20	6.45	NULL	1233	TF KIM_MYC targets
<i>Underexpressed</i>				
1	-10.89	NULL	1720	Chr Chr 1
2	-10.28	NULL	15	CC MHC class II protein complex
3	-8.07	NULL	1135	Chr Chr 19
4	-8.01	NULL	714	Chr Chr 6
5	-7.99	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
6	-7.86	NULL	47	BP antigen processing and presentation
7	-7.69	NULL	417	H.Tiss WIRTH_Immune system
8	-7.55	NULL	52	Chr Chr HSCHR6_MHC_QBL
9	-7.06	NULL	11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
10	-6.82	NULL	553	Cancer Lembcke_Colonc Inflammation
11	-6.74	NULL	11	GSEA C2BIOCARTA_THELPER_PATHWAY
12	-6.29	NULL	21	CC clathrin-coated endocytic vesicle membrane
13	-6.23	NULL	84	BP T cell receptor signaling pathway
14	-5.99	NULL	74	BP regulation of immune response
15	-5.84	NULL	21	CC cornified envelope
16	-5.64	NULL	127	H.Tiss WIRTH_Muscle
17	-5.44	NULL	3	MMML C2CACIEJ_MMML 7
18	-5.37	NULL	32	CC ER to Golgi transport vesicle membrane
19	-5.29	NULL	60	BP T cell costimulation
20	-5.24	NULL	10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1

p-values



# GW\_184

## Local Summary

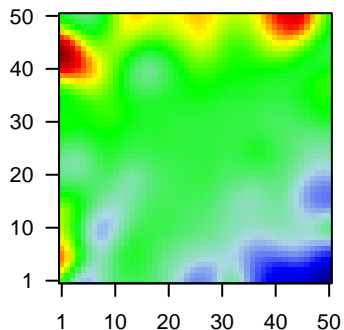
%DE = 0.7  
 # metagenes = 20  
 # genes = 233  
 # genes in genesets = 230

# genes with  $fdr < 0.1 = 140$  ( 137 + / 3 - )  
 # genes with  $fdr < 0.05 = 134$  ( 132 + / 2 - )  
 # genes with  $fdr < 0.01 = 103$  ( 103 + / 0 - )

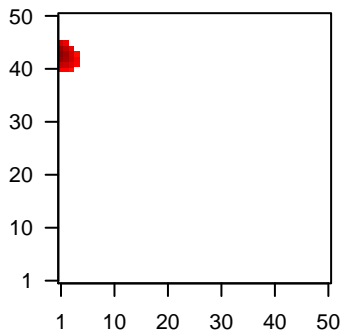
<r> metagenes = 0.97  
 <r> genes = 0.35

<FC> = 0.5  
 <shrinkage-t> = 17.51  
 <p-value> = 0  
 <fdr> = 0.42

Profile



Spot



## Local Genelist

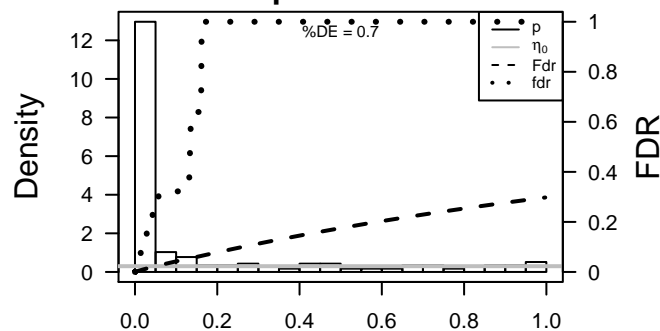
Rank	ID	log(FC)	fdr	p-value	Description
1	8900	1.74	2e-16	1e-15	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
2	1288	1.83	2e-16	1e-15	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
3	2167	3.77	2e-16	1e-15	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
4	3306	1.66	2e-16	1e-15	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]
5	9119	1.68	2e-16	1e-15	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]
6	55214	1.29	2e-16	1e-15	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
7	56901	1.32	2e-16	1e-15	1 x 44 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-li
8	4747	1.26	2e-16	1e-15	1 x 43
9	4753	2.26	2e-16	1e-15	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
10	26499	1.37	2e-16	1e-15	1 x 42 pleckstrin 2 [Source:HGNC Symbol;Acc:19238]
11	5744	2.59	2e-16	1e-15	1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;A
12	5803	1.4	2e-16	1e-15	1 x 45 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
13	5836	1.23	2e-16	1e-15	1 x 44 phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:97
14	404203	2.7	2e-16	1e-15	1 x 43 serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symbo
15	116211	1.64	2e-16	1e-15	1 x 43 Transmembrane 4 L6 family member 19 [Source:UniProtKB/I
16	119548	1.2	2e-15	1e-12	1 x 45 pancreatic lipase-related protein 3 [Source:HGNC Symbol;A
17	3552	1.15	2e-14	1e-12	1 x 43 interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
18	3861	1.05	3e-14	2e-11	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
19	3429	1	4e-13	3e-11	1 x 42 interferon, alpha-inducible protein 27 [Source:HGNC Symbol
20	5947	1.08	7e-13	4e-11	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:1

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	15.1	NULL	1 / 10	BP white fat cell differentiation
2	14.3	NULL	1 / 11	GSEA C2REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED
3	13.61	NULL	1 / 12	MF fatty acid binding
4	13.49	NULL	4 / 25	BP brown fat cell differentiation
5	13.36	NULL	5 / 12	BP hemidesmosome assembly
6	13.22	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
7	13	NULL	1 / 13	BP cellular response to lithium ion
8	12.65	NULL	1 / 7	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
9	11.98	NULL	1 / 15	BP triglyceride catabolic process
10	11.63	NULL	2 / 15	GSEA C2NGUYEN_NOTCH1_TARGETS_UP
11	10.97	NULL	5 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	10.27	NULL	1 / 10	BP surfactant homeostasis
13	9.7	NULL	2 / 18	BP male meiosis I
14	9.32	NULL	2 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	9.07	NULL	10 / 76	BP epidermis development
16	8.94	NULL	2 / 11	GSEA C2BIOCARTA_VITCB_PATHWAY
17	8.94	NULL	1 / 25	BP cytokine production
18	8.93	NULL	1 / 10	GSEA C2KIM_MYCL1_AMPLIFICATION_TARGETS_UP
19	8.82	NULL	1 / 13	H.Tiss WIRTH_Thalamus
20	8.72	NULL	3 / 51	CC lipid particle
21	8.67	NULL	1 / 2	miRNA target-346
22	8.44	NULL	1 / 14	BP negative regulation of chondrocyte differentiation
23	8.39	NULL	2 / 15	GSEA C2AMIT_EGF_RESPONSE_240_MCF10A
24	8.31	NULL	12 / 82	CC intermediate filament
25	7.74	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
26	7.68	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
27	7.54	NULL	1 / 17	BP osteoblast development
28	7.5	NULL	2 / 31	BP adenylate cyclase-activating G-protein coupled receptor signaling
29	7.47	NULL	2 / 7	GSEA C2NGO_MALIGNANT_GLIOMA_1P_LOH
30	7.35	NULL	1 / 4	MMML C2SCIEJ_MMML 47
31	7.31	NULL	6 / 83	CC basement membrane
32	7.31	NULL	3 / 15	GSEA C2NAKAMURA_METASTASIS_MODEL_DN
33	7.29	NULL	2 / 14	GSEA C2HOEGERKORP_CD44_TARGETS_DIRECT_UP
34	7.28	NULL	3 / 59	LymphomaL1ENZ_Stromal signature 2
35	7.2	NULL	1 / 10	GSEA C2BIOCARTA_ACE2_PATHWAY
36	7.14	NULL	2 / 47	BP cholesterol homeostasis
37	6.98	NULL	2 / 9	GSEA C2RODWELL_AGING_KIDNEY_UP
38	6.93	NULL	2 / 11	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
39	6.91	NULL	11 / 186	MF structural molecule activity
40	6.9	NULL	2 / 38	BP epithelial cell differentiation

p-values



# GW\_184

## Local Summary

%DE = 0.78  
 # metagenes = 12  
 # genes = 185  
 # genes in genesets = 184

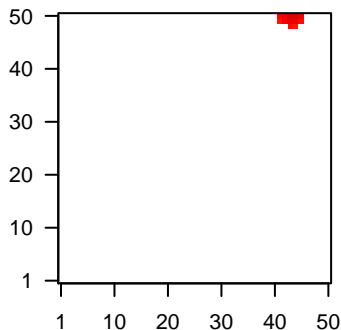
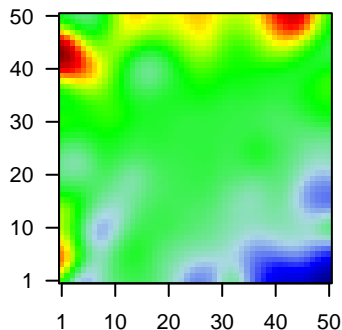
# genes with  $fdr < 0.1 = 117$  ( 117 + / 0 - )  
 # genes with  $fdr < 0.05 = 111$  ( 111 + / 0 - )  
 # genes with  $fdr < 0.01 = 74$  ( 74 + / 0 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.44

$\langle FC \rangle = 0.41$   
 $\langle \text{shrinkage-t} \rangle = 14.5$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.46$

Profile

Spot



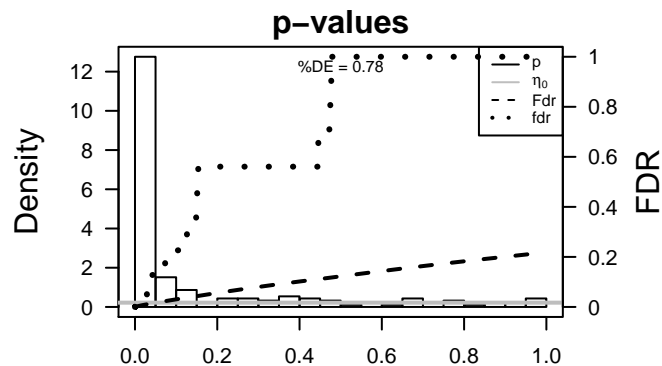
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4173	1.4	2e-16	4e-15	44 x 50 minichromosome maintenance complex component 4 [Source:HGNC Symbol;Acc:10000]
2	8500	1.61	2e-16	4e-15	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (P1)
3	136	1.14	3e-14	4e-12	41 x 50 adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
4	3161	1.11	1e-13	4e-12	43 x 50 hyaluronan-mediated motility receptor (RHAMM) [Source:HGNC Symbol;Acc:10000]
5	1033	1.1	2e-13	4e-11	43 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:10000]
6	10635	1.06	2e-12	4e-11	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169]
7	55839	1.06	2e-12	4e-10	44 x 50 centromere protein N [Source:HGNC Symbol;Acc:30873]
8	5427	1.02	1e-11	7e-10	44 x 49 polymerase (DNA directed), epsilon 2, accessory subunit (So)
9	9787	1	3e-11	1e-09	43 x 50 discs, large (Drosophila) homolog-associated protein 5 [Source:HGNC Symbol;Acc:10000]
10	1894	0.99	6e-11	4e-09	45 x 50 epithelial cell transforming sequence 2 oncogene [Source:HGNC Symbol;Acc:10000]
11	890	0.96	2e-10	6e-09	44 x 50 cyclin A2 [Source:HGNC Symbol;Acc:1578]
12	81831	0.95	3e-10	1e-08	42 x 50 neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Symbol;Acc:10000]
13	9133	0.93	6e-10	1e-08	45 x 49 cyclin B2 [Source:HGNC Symbol;Acc:1580]
14	5591	0.92	1e-09	1e-08	41 x 50 protein kinase, DNA-activated, catalytic polypeptide [Source:HGNC Symbol;Acc:10000]
15	8487	0.92	1e-09	5e-08	41 x 50 gem (nuclear organelle) associated protein 2 [Source:HGNC Symbol;Acc:10000]
16	3251	0.9	3e-09	5e-08	42 x 50 hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Symbol;Acc:10000]
17	9918	0.89	4e-09	1e-07	45 x 49 non-SMC condensin I complex, subunit D2 [Source:HGNC Symbol;Acc:10000]
18	51659	0.87	6e-09	3e-07	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Symbol;Acc:10000]
19	29028	0.86	1e-08	3e-06	44 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Symbol;Acc:10000]
20	259266	0.8	9e-08	4e-06	45 x 49 asp (abnormal spindle) homolog, microcephaly associated (D)

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	53.82	NULL	66 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	53.82	NULL	66 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	32.25	NULL	10 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
4	31.9	NULL	11 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
5	29.63	NULL	8 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
6	29.26	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	27.83	NULL	11 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
8	27.53	NULL	9 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
9	27.4	NULL	8 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	27.06	NULL	7 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
11	26.54	NULL	9 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
12	26.29	NULL	8 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
13	25.4	NULL	19 / 57	Glio developing astrocytes
14	25.31	NULL	10 / 14	MMLL C6S3CIEJ_MMLL_4
15	24.98	NULL	9 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
16	23.81	NULL	8 / 13	GSEA C2WINNEPENNING_MELANOMA_METASTASIS_UP
17	23.36	NULL	8 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	23.12	NULL	53 / 370	BP mitotic cell cycle
19	23.03	NULL	8 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	22.52	NULL	6 / 15	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
21	21.38	NULL	54 / 572	Disease GUDJ_poriasis up
22	21.25	NULL	11 / 18	BP spindle organization
23	21.17	NULL	60 / 530	Cancer Lembcke_Normal vs Adenoma
24	20.84	NULL	4 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
25	20.48	NULL	36 / 232	BP mitosis
26	19.91	NULL	8 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
27	19.5	NULL	6 / 13	GSEA C2CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP
28	19.44	NULL	5 / 11	GSEA C2ODONNELL_TFRC_TARGETS_DN
29	19.43	NULL	7 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
30	19.41	NULL	4 / 15	GSEA C2FERRANDO_HOX11_NEIGHBORS
31	19.28	NULL	6 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
32	18.17	NULL	6 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
33	17.67	NULL	7 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
34	17.66	NULL	4 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
35	17.48	NULL	6 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
36	17.38	NULL	7 / 15	GSEA C2Y_AGING_MIDDLE_DN
37	17.24	NULL	6 / 15	GSEA C2TANG_SENESCENCE_TP53_TARGETS_DN
38	17.17	NULL	2 / 5	Glio Phillips Prolif up vs PN & MES
39	16.99	NULL	5 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
40	16.52	NULL	3 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA



# GW\_184

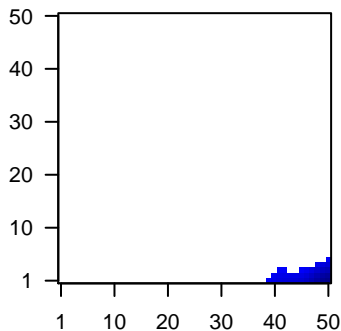
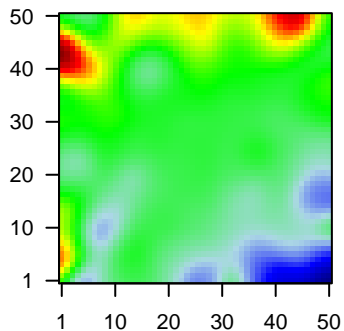
## Local Summary

%DE = 0.83  
 # metagenes = 35  
 # genes = 559  
 # genes in genesets = 532  
 # genes with  $fdr < 0.1$  = 367 ( 14 + / 353 - )  
 # genes with  $fdr < 0.05$  = 334 ( 13 + / 321 - )  
 # genes with  $fdr < 0.01$  = 224 ( 7 + / 217 - )

<r> metagenes = 0.87  
 <r> genes = 0.4  
 <FC> = -0.34  
 <shrinkage-t> = -11.88  
 <p-value> = 0  
 <fdr> = 0.49

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	894	1.24	2e-16	4e-15	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
2	1396	1.58	2e-16	4e-15	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:1583]
3	3123	-1.34	2e-16	4e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:HGNC Symbol;Acc:1583]
4	3128	-1.77	2e-16	4e-15	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo)
5	3512	1.5	2e-16	4e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
6	3120	-1.12	1e-13	8e-12	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:HGNC Symbol;Acc:1583]
7	3113	-1.11	2e-13	1e-10	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:1583]
8	3127	-1.07	1e-12	1e-10	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:1583]
9	3122	-0.99	2e-12	2e-10	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:1583]
10	9404	1.05	4e-12	4e-09	50 x 1 leupaxin [Source:HGNC Symbol;Acc:14061]
11	3108	-0.99	5e-11	4e-09	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:1583]
12	3109	-0.98	8e-11	2e-08	50 x 1 major histocompatibility complex, class II, DM beta [Source:HGNC Symbol;Acc:1583]
13	3689	-0.93	6e-10	2e-08	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 s)
14	972	-0.93	6e-10	2e-08	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain
15	919	-0.93	7e-10	3e-08	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
16	6352	-0.92	1e-09	3e-08	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:1583]
17	3001	-0.91	2e-09	3e-08	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated protein 10)
18	2532	-0.91	2e-09	9e-08	50 x 5 Duffy blood group, atypical chemokine receptor [Source:HGNC Symbol;Acc:1583]
19	3936	-0.9	3e-09	1e-07	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:1583]
20	221472	-0.89	4e-09	8e-07	49 x 1 FYVE, RhoGEF and PH domain containing 2 [Source:HGNC Symbol;Acc:1583]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-34.62	NULL	14 / 15	CC MHC class II protein complex
2	-22.85	NULL	109 / 417	H.Tiss WIRTH_Immune system
3	-21.44	NULL	17 / 47	BP antigen processing and presentation
4	-20.73	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
5	-19.72	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
6	-19.61	NULL	24 / 60	BP T cell costimulation
7	-19.58	NULL	3 / 3	MMML C5CIEJ_MMML 7
8	-19.25	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
9	-18.11	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
10	-18.06	NULL	10 / 28	CC transport vesicle membrane
11	-17.41	NULL	11 / 35	CC trans-Golgi network membrane
12	-16.58	NULL	22 / 84	BP T cell receptor signaling pathway
13	-16.43	NULL	9 / 32	CC ER to Golgi transport vesicle membrane
14	-16.34	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGS
15	-15.56	NULL	67 / 312	BP immune response
16	-15.35	NULL	108 / 553	Cancer Lembecke_Colonc Inflammation
17	-14.89	NULL	17 / 87	BP antigen processing and presentation of exogenous peptide antigen
18	-14.68	NULL	11 / 46	CC endocytic vesicle membrane
19	-14.66	NULL	20 / 74	BP regulation of immune response
20	-14.55	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
21	-14.55	NULL	48 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
22	-14.55	NULL	48 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
23	-14.55	NULL	48 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
24	-14.55	NULL	48 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
25	-14.16	NULL	9 / 13	Cancer GENTLES_modul18
26	-14.09	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
27	-13.86	NULL	8 / 14	GSEA C2BIOCARTA_NO2112_PATHWAY
28	-13.85	NULL	14 / 60	BP interferon-gamma-mediated signaling pathway
29	-12.99	NULL	7 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
30	-12.96	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
31	-12.75	NULL	6 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
32	-12.49	NULL	7 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
33	-12.44	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
34	-12.37	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTIO
35	-11.97	NULL	6 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
36	-11.88	NULL	9 / 52	Chr Chr HSCR6_MHC_QBL
37	-11.5	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
38	-11.44	NULL	5 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN
39	-11.41	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
40	-11.15	NULL	5 / 12	BP immunoglobulin mediated immune response

p-values

