

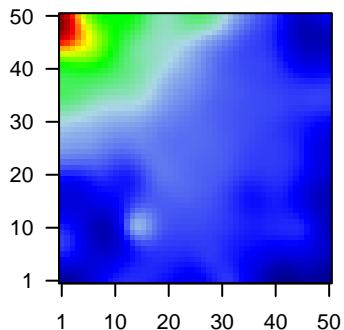
GW_053

Global Summary

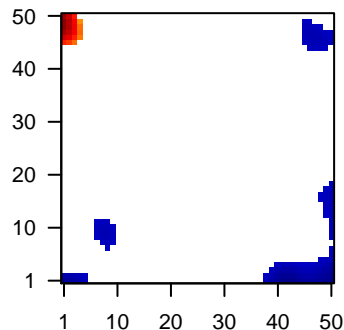
%DE = 0.14
 # genes with $fdr < 0.2$ = 1729 (989 + / 740 -)
 # genes with $fdr < 0.1$ = 1453 (862 + / 591 -)
 # genes with $fdr < 0.05$ = 1195 (730 + / 465 -)
 # genes with $fdr < 0.01$ = 827 (542 + / 285 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.86

Profile



Regulated Spots



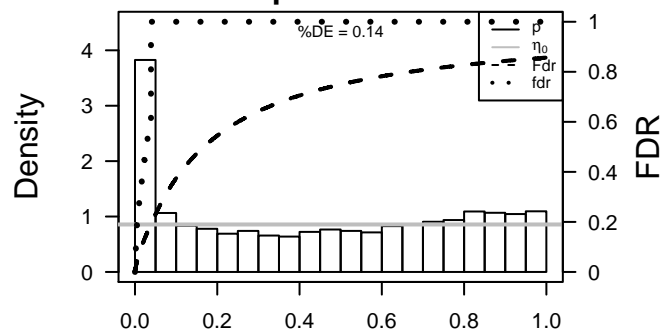
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.08	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	8745	2.16	2e-16	2e-14	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	131	1.87	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	2.49	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
5	441282	2.52	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
6	8644	2.66	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
7	1109	3.04	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
8	222	2.04	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
9	242	2.48	2e-16	2e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
10	151516	2.85	2e-16	2e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
11	84707	-1.89	2e-16	2e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
12	387695	2.36	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
13	260436	-1.73	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
14	375791	1.77	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
15	595	-1.78	2e-16	2e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
16	948	1.8	2e-16	2e-14	6 x 44 CD36 molecule (thrombospondin receptor) [Source:HGNC S
17	1041	3.12	2e-16	2e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
18	4680	2.09	2e-16	2e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
19	1066	2.24	2e-16	2e-14	14 x 50 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
20	9022	1.93	2e-16	2e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.07	NULL	135	H.Tiss WIRTH_Mucosa
2	23.57	NULL	572	Disease GUDJ_psooriasis up
3	19.66	NULL	42	BP keratinization
4	18.01	NULL	21	CC cornified envelope
5	16.44	NULL	53	BP keratinocyte differentiation
6	13.41	NULL	76	BP epidermis development
7	9.68	NULL	19	BP peptide cross-linking
8	9.46	NULL	21	CC desmosome
9	8.98	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	8.33	NULL	13	GSEA C2SINGH_NFE2L2_TARGETS
11	8.16	NULL	186	MF structural molecule activity
12	7.79	NULL	33	BP cholesterol biosynthetic process
13	7.41	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	7.15	NULL	82	CC intermediate filament
15	7.09	NULL	15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
16	7.06	NULL	15	MF retinol dehydrogenase activity
17	7	NULL	44	CC keratin filament
18	6.99	NULL	614	CC endoplasmic reticulum membrane
19	6.95	NULL	29	BP regulation of proteolysis
20	6.94	NULL	16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
<i>Underexpressed</i>				
1	-8.79	NULL	1749	MF DNA binding
2	-8.76	NULL	4640	CC nucleus
3	-8.19	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
4	-8.19	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
5	-7.91	NULL	940	MF nucleic acid binding
6	-7.74	NULL	1574	BP transcription, DNA-templated
7	-7.56	NULL	57	Glio developing astrocytes
8	-7.43	NULL	15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
9	-7.09	NULL	1581	BP regulation of transcription, DNA-dependent
10	-6.83	NULL	417	H.Tiss WIRTH_Immune system
11	-6.57	NULL	949	CC nucleoplasm
12	-6.39	NULL	250	LymphocyteL2ENZ_Stromal signature 1
13	-6.27	NULL	370	BP mitotic cell cycle
14	-6.07	NULL	16	MMML C6SCIEJ_MMML 1
15	-5.99	NULL	7	MMML C6SCIEJ_MMML 13
16	-5.89	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
17	-5.85	NULL	149	BP DNA replication
18	-5.76	NULL	190	CC extracellular matrix
19	-5.75	NULL	553	Cancer Lembecke_Colonc Inflammation
20	-5.69	NULL	10	BP cellular response to zinc ion

p-values



GW_053

Local Summary

%DE = 0.94
 # metagenes = 22
 # genes = 269
 # genes in genesets = 261

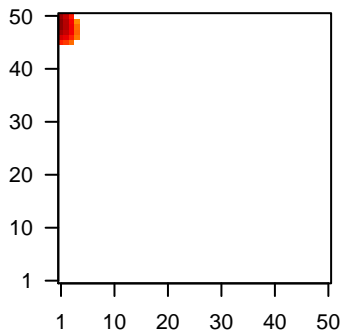
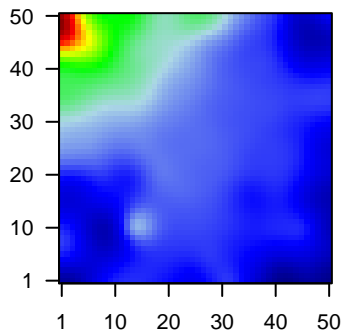
genes with $fdr < 0.1$ = 243 (230 + / 13 -)
 # genes with $fdr < 0.05$ = 237 (225 + / 12 -)
 # genes with $fdr < 0.01$ = 231 (220 + / 11 -)

<r> metagenes = 0.94
 <r> genes = 0.44

<FC> = 1.25
 <shrinkage-t> = 44.12
 <p-value> = 0
 <fdr> = 0.12

Profile

Spot



Local Genelist

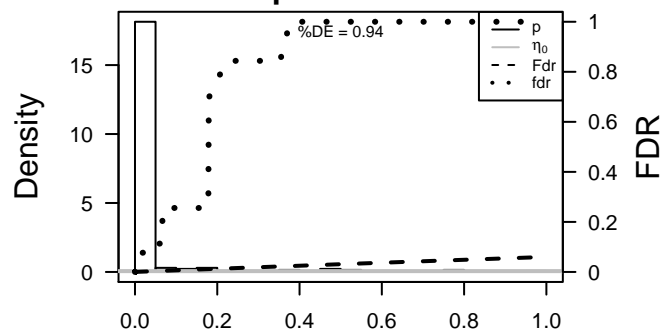
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.08	2e-16	4e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	131	1.87	2e-16	4e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	2.49	2e-16	4e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	2.52	2e-16	4e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	8644	2.66	2e-16	4e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	222	2.04	2e-16	4e-17	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
7	242	2.48	2e-16	4e-17	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syr
8	151516	2.85	2e-16	4e-17	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
9	387695	2.36	2e-16	4e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
10	375791	1.77	2e-16	4e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
11	1041	3.12	2e-16	4e-17	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
12	4680	2.09	2e-16	4e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
13	9022	1.93	2e-16	4e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
14	84518	1.78	2e-16	4e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	1382	1.67	2e-16	4e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
16	54544	1.68	2e-16	4e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:29871
17	1474	2.01	2e-16	4e-17	1 x 47 cystatin E/M [Source:HGNC Symbol;Acc:2478]
18	1475	1.82	2e-16	4e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1562	1.66	2e-16	4e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
20	126410	2.24	2e-16	4e-17	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	45.45	NULL	91 / 135	H.Tiss WIRTH_Mucosa
2	37.3	NULL	19 / 21	CC cornified envelope
3	31.09	NULL	26 / 53	BP keratinocyte differentiation
4	29.55	NULL	105 / 572	Disease GUDJ_psooriasis up
5	26.84	NULL	19 / 42	BP keratinization
6	21.67	NULL	12 / 19	BP peptide cross-linking
7	21.27	NULL	25 / 76	BP epidermis development
8	20.4	NULL	12 / 21	CC desmosome
9	16.64	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	14.93	NULL	7 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
11	13.26	NULL	8 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	13.25	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
13	12.91	NULL	5 / 10	MF RAGE receptor binding
14	12.55	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
15	12.52	NULL	6 / 13	BP negative regulation of peptidase activity
16	11.87	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
17	11.57	NULL	26 / 186	MF structural molecule activity
18	11.57	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	11.35	NULL	13 / 79	MF serine-type endopeptidase inhibitor activity
20	11.27	NULL	7 / 29	BP regulation of proteolysis
21	11.21	NULL	4 / 15	MF retinol dehydrogenase activity
22	11.06	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
23	10.93	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
24	10.29	NULL	10 / 52	BP negative regulation of endopeptidase activity
25	10.24	NULL	16 / 82	CC intermediate filament
26	10.22	NULL	10 / 44	CC keratin filament
27	10.15	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
28	10.06	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
29	9.96	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
30	9.52	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
31	9.45	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
32	9.12	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
33	9.06	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_U
34	8.81	NULL	6 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
35	8.78	NULL	3 / 12	BP cellular aldehyde metabolic process
36	8.76	NULL	60 / 1182	CC extracellular region
37	8.74	NULL	5 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
38	8.34	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
39	8.19	NULL	4 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
40	8.09	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN

p-values



GW_053

Local Summary

%DE = 0.7
 # metagenes = 10
 # genes = 186
 # genes in genesets = 185
 # genes with $fdr < 0.1$ = 97 (8 + / 89 -)
 # genes with $fdr < 0.05$ = 87 (5 + / 82 -)
 # genes with $fdr < 0.01$ = 60 (3 + / 57 -)

$\langle r \rangle$ metagenes = 0.98

$\langle r \rangle$ genes = 0.45

$\langle FC \rangle = -0.43$

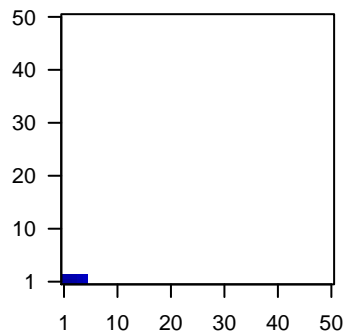
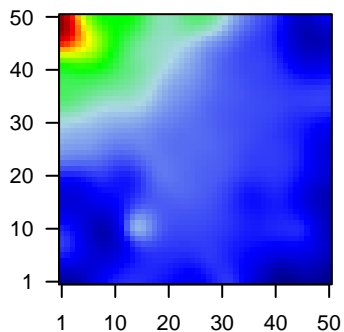
$\langle \text{shrinkage-t} \rangle = -15.18$

$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.52$

Profile

Spot



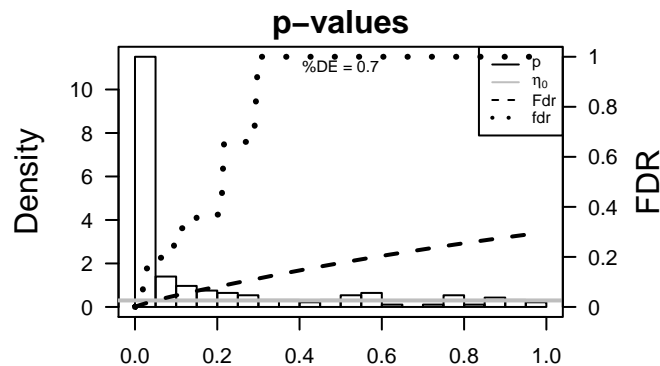
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4316	-1.62	4e-16	4e-14	2 x 1 matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
2	23213	-1.6	1e-15	5e-13	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
3	2919	-1.54	1e-14	2e-12	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula
4	4318	-1.5	7e-14	2e-12	1 x 1 matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9:
5	7076	-1.49	9e-14	8e-12	4 x 1 TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc:
6	6696	1.45	4e-13	8e-12	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125:
7	7070	-1.45	4e-13	9e-12	4 x 1 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:11801
8	4312	-1.44	5e-13	3e-11	1 x 1 matrix metallopeptidase 1 (interstitial collagenase) [Source:Hi
9	3956	-1.42	1e-12	2e-09	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
10	6515	-1.32	4e-11	3e-09	3 x 1 solute carrier family 2 (facilitated glucose transporter), membe
11	1462	-1.29	9e-11	2e-08	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
12	3576	-1.24	5e-10	1e-07	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
13	10630	-1.18	4e-09	1e-07	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]
14	7057	-1.17	5e-09	3e-07	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
15	10631	-1.14	1e-08	4e-07	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
16	1490	-1.13	2e-08	4e-07	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2
17	25878	-1.12	2e-08	6e-07	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:
18	4314	-1.1	3e-08	2e-06	1 x 1 matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
19	1289	-1.08	6e-08	2e-06	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
20	633	-0.99	9e-08	5e-06	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-31.32	NULL	10 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
2	-30.92	NULL	60 / 250	LymphomaENZ_Stromal signature 1
3	-30.1	NULL	57 / 190	CC extracellular matrix
4	-29.62	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
5	-28.96	NULL	14 / 16	MMML C2CIEJ_MMML 1
6	-28.01	NULL	29 / 69	BP extracellular matrix disassembly
7	-25.42	NULL	26 / 64	BP collagen catabolic process
8	-25.34	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
9	-24	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	-23.85	NULL	55 / 242	BP extracellular matrix organization
11	-23.21	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
12	-22.61	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
13	-21.87	NULL	6 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
14	-21.72	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
15	-21.66	NULL	10 / 35	Glio Colman_survival_associated
16	-21.38	NULL	5 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
17	-20.52	NULL	29 / 183	CC proteinaceous extracellular matrix
18	-20.17	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
19	-19.96	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
20	-19.75	NULL	5 / 16	GSEA C2JURS_ADIPOCYTE_DIFFERENTIATION_DN
21	-19.27	NULL	4 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
22	-18.66	NULL	4 / 14	GSEA C2DANG_REGULATED_BY_MYC_DN
23	-18.6	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
24	-17.72	NULL	2 / 6	Glio Martínez_Glio_hypometh
25	-17.52	NULL	6 / 11	Glio Phillips MES up vs Prolif & PN
26	-17.05	NULL	5 / 16	GSEA C2SU_PDEF_TARGETS_UP
27	-17.05	NULL	3 / 7	GSEA C2DASU_IL6_SIGNALING_DN
28	-16.84	NULL	5 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
29	-16.36	NULL	50 / 553	Cancer Lembcke_Colonc Inflammation
30	-16.24	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
31	-16.15	NULL	5 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
32	-16.05	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
33	-16.05	NULL	19 / 57	MF extracellular matrix structural constituent
34	-16.01	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
35	-15.81	NULL	7 / 16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
36	-15.79	NULL	7 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
37	-15.44	NULL	8 / 11	MF platelet-derived growth factor binding
38	-15.42	NULL	3 / 16	GSEA C2KEGG_BLADDER_CANCER
39	-15.36	NULL	4 / 16	GSEA C2U_TUMOR_ENDOTHELIAL_MARKERS_UP
40	-15.36	NULL	3 / 15	GSEA C2WU_HBX_TARGETS_1_UP



GW_053

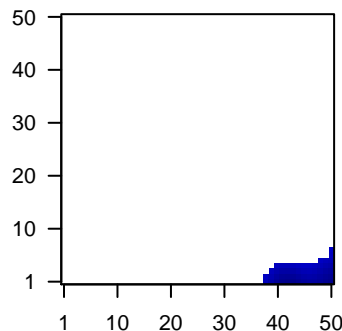
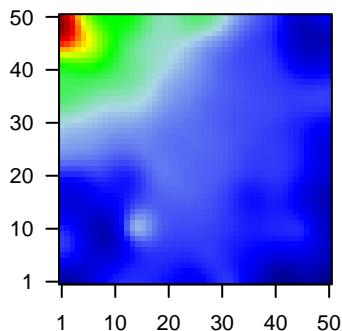
Local Summary

%DE = 0.74
 # metagenes = 54
 # genes = 801
 # genes in genesets = 771
 # genes with $fdr < 0.1$ = 349 (18 + / 331 -)
 # genes with $fdr < 0.05$ = 225 (13 + / 212 -)
 # genes with $fdr < 0.01$ = 146 (9 + / 137 -)

$\langle r \rangle$ metagenes = 0.84
 $\langle r \rangle$ genes = 0.36
 $\langle FC \rangle = -0.33$
 $\langle \text{shrinkage-t} \rangle = -11.56$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.67$

Profile

Spot



Local Genelist

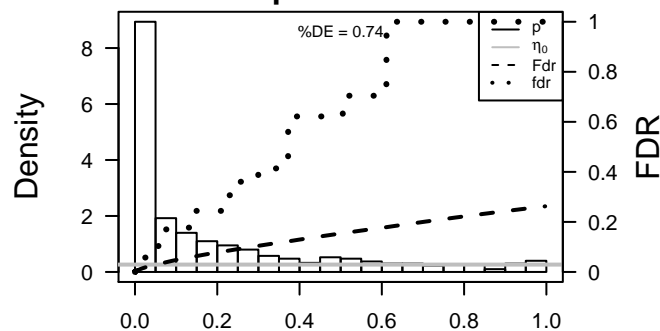
Rank	ID	log(FC)	fdr	p-value	Description
1	260436	-1.73	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
2	2745	1.67	2e-16	2e-14	50 x 3 glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
3	3488	-1.76	2e-16	2e-14	50 x 7 insulin-like growth factor binding protein 5 [Source:HGNC Sy
4	1396	-1.62	4e-16	2e-11	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
5	3123	1.49	8e-14	2e-08	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
6	6376	-1.3	8e-11	2e-08	44 x 1 chemokine (C-X3-C motif) ligand 1 [Source:HGNC Symbol;#
7	6352	-1.27	2e-10	2e-08	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
8	10537	-1.26	3e-10	6e-08	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	23466	-1.24	5e-10	1e-07	41 x 1 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
10	347733	-1.21	1e-09	2e-07	50 x 5 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
11	6363	-1.2	2e-09	1e-06	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
12	3512	1.16	7e-09	1e-06	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglo
13	338773	-1.13	1e-08	1e-06	50 x 5 transmembrane protein 119 [Source:HGNC Symbol;Acc:278
14	3543	1.03	2e-08	6e-06	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
15	3575	-1.08	7e-08	6e-06	50 x 2 interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
16	10628	-1.06	7e-08	8e-06	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
17	51466	-1.05	1e-07	8e-06	48 x 1 Enah/Vasp-like [Source:HGNC Symbol;Acc:20234]
18	81618	-1.05	2e-07	8e-06	48 x 5 integral membrane protein 2C [Source:HGNC Symbol;Acc:61
19	5900	-1.04	2e-07	2e-05	39 x 2 ral guanine nucleotide dissociation stimulator [Source:HGNC
20	8764	-1	6e-07	2e-05	50 x 1 tumor necrosis factor receptor superfamily, member 14 [Sour

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.96	NULL	126 / 417	H.Tiss WIRTH_Immune system
2	-15.86	NULL	137 / 553	Cancer Lembcke_Colonc Inflammation
3	-14.75	NULL	83 / 312	BP immune response
4	-12.92	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
5	-12.45	NULL	9 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
6	-12.25	NULL	5 / 12	BP dendritic cell chemotaxis
7	-10.95	NULL	12 / 43	MF chemokine activity
8	-10.27	NULL	61 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
9	-10.27	NULL	61 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
10	-10.27	NULL	61 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	-10.27	NULL	61 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
12	-9.91	NULL	8 / 15	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOC
13	-9.82	NULL	12 / 28	LymphomaAVE_Immune response 1
14	-9.71	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
15	-9.7	NULL	26 / 60	BP T cell costimulation
16	-9.42	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
17	-9.37	NULL	14 / 15	CC MHC class II protein complex
18	-9.13	NULL	3 / 12	BP macrophage chemotaxis
19	-9.05	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
20	-9.01	NULL	4 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
21	-8.99	NULL	36 / 204	BP cell surface receptor signaling pathway
22	-8.87	NULL	7 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
23	-8.79	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
24	-8.63	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
25	-8.56	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
26	-8.36	NULL	6 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
27	-8.34	NULL	6 / 8	GSEA C2BIOCARTA_TCR_PATHWAY
28	-8.33	NULL	6 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
29	-8.3	NULL	12 / 43	BP positive regulation of T cell proliferation
30	-8.26	NULL	4 / 10	BP positive regulation of chemotaxis
31	-8.25	NULL	37 / 162	CC external side of plasma membrane
32	-8.25	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
33	-8.22	NULL	5 / 13	BP lymph node development
34	-8.21	NULL	6 / 10	GSEA C2DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
35	-8.06	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
36	-8.04	NULL	10 / 13	Cancer GENTLES_modul18
37	-8.02	NULL	22 / 74	BP regulation of immune response
38	-7.89	NULL	3 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
39	-7.83	NULL	4 / 12	GSEA C2REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
40	-7.8	NULL	9 / 14	GSEA C2BIOCARTA_N02L12_PATHWAY

p-values



GW_053

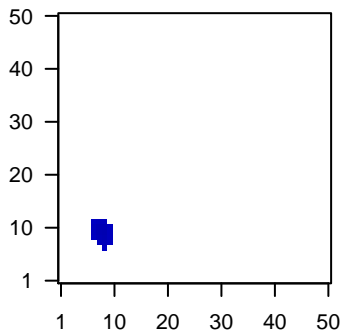
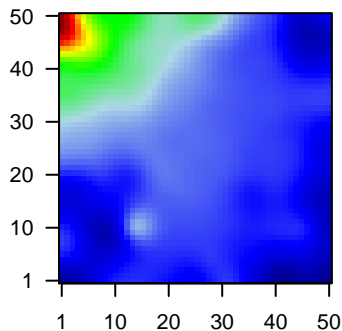
Local Summary

%DE = 0.8
 # metagenes = 19
 # genes = 208
 # genes in genesets = 208
 # genes with $fdr < 0.1$ = 111 (2 + / 109 -)
 # genes with $fdr < 0.05$ = 63 (2 + / 61 -)
 # genes with $fdr < 0.01$ = 21 (0 + / 21 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.32
 $\langle FC \rangle = -0.34$
 $\langle \text{shrinkage-t} \rangle = -12.03$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.72$

Profile

Spot



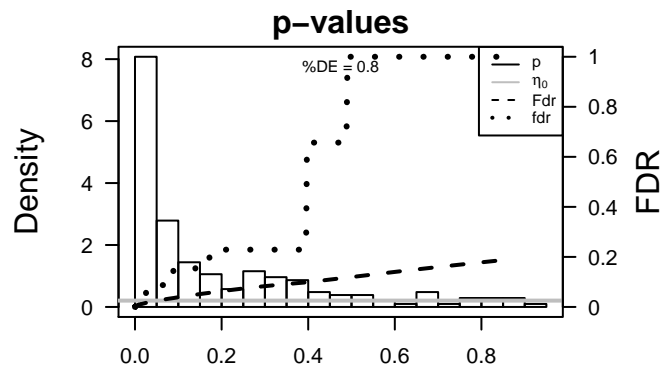
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	140465	-1.05	1e-07	4e-05	9 x 9 myosin, light chain 6B, alkali, smooth muscle and non-muscl
2	7389	-0.97	1e-06	1e-04	7 x 9 uroporphyrinogen decarboxylase [Source:HGNC Symbol;Acc
3	2026	-0.93	4e-06	3e-04	10 x 10 enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
4	65980	-0.83	3e-05	3e-04	9 x 10 bromodomain containing 9 [Source:HGNC Symbol;Acc:2581f
5	11033	-0.83	3e-05	3e-04	9 x 9 ArfGAP with dual PH domains 1 [Source:HGNC Symbol;Acc:
6	55146	-0.82	4e-05	3e-04	10 x 8 zinc finger, DHHC-type containing 4 [Source:HGNC Symbol;
7	55653	-0.82	4e-05	3e-04	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Symb
8	64710	-0.82	4e-05	4e-04	9 x 11 nuclear casein kinase and cyclin-dependent kinase substrate
9	9130	-0.81	5e-05	1e-03	8 x 9 family with sequence similarity 50, member A [Source:HGNC
10	10946	-0.79	8e-05	3e-03	8 x 12 splicing factor 3a, subunit 3, 60kDa [Source:HGNC Symbol;A
11	140467	-0.76	1e-04	4e-03	9 x 8 zinc finger protein 358 [Source:HGNC Symbol;Acc:16838]
12	93643	-0.73	2e-04	5e-03	9 x 11 tight junction associated protein 1 (peripheral) [Source:HGNC
13	221927	-0.7	4e-04	5e-03	9 x 11 BRCA1-associated ATM activator 1 [Source:HGNC Symbol;f
14	29894	-0.69	6e-04	5e-03	8 x 10 cleavage and polyadenylation specific factor 1, 160kDa [Sour
15	26470	-0.68	6e-04	5e-03	10 x 9 seizure related 6 homolog (mouse)-like 2 [Source:HGNC Syr
16	23644	-0.67	7e-04	8e-03	8 x 11 enhancer of mRNA decapping 4 [Source:HGNC Symbol;Acc:
17	6621	-0.65	1e-03	8e-03	8 x 11 small nuclear RNA activating complex, polypeptide 4, 190kDa
18	57190	-0.64	1e-03	8e-03	9 x 7 selenoprotein N, 1 [Source:HGNC Symbol;Acc:15999]
19	10459	-0.64	1e-03	8e-03	8 x 9 MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S
20	3636	-0.63	1e-03	8e-03	8 x 9 inositol polyphosphate phosphatase-like 1 [Source:HGNC Sy

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.03	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
2	-7.28	NULL	2 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
3	-7.16	NULL	2 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
4	-6.94	NULL	2 / 12	BP porphyrin-containing compound biosynthetic process
5	-6.73	NULL	5 / 45	Glio wilscher_GBM_Verhaak-PNwt_expression_J_up
6	-6.18	NULL	2 / 9	miRNA target-184
7	-6.12	NULL	1 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
8	-6.01	NULL	1 / 13	CC muscle myosin complex
9	-6.01	NULL	1 / 13	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
10	-6	NULL	1 / 5	miRNA target-205
11	-5.87	NULL	2 / 25	MF phosphatidylinositol-3,4,5-trisphosphate binding
12	-5.87	NULL	2 / 16	GSEA C2ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN
13	-5.77	NULL	1 / 14	GSEA C2REACTOME_MUSCLE_CONTRACTION
14	-5.64	NULL	2 / 12	GSEA C2TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
15	-5.61	NULL	2 / 11	BP maintenance of protein location in nucleus
16	-5.57	NULL	2 / 11	BP cerebellar Purkinje cell layer development
17	-5.55	NULL	1 / 15	GSEA C2GOLUB_ALL_VS_AML_UP
18	-5.52	NULL	2 / 18	BP porphyrin-containing compound metabolic process
19	-5.43	NULL	43 / 1135	Chr Chr 19
20	-5.25	NULL	1 / 13	GSEA C2REACTOME_GLYCOLYSIS
21	-5.2	NULL	3 / 24	MF translation factor activity, nucleic acid binding
22	-5.2	NULL	2 / 20	BP heme biosynthetic process
23	-5.15	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
24	-5.15	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
25	-5.15	NULL	2 / 15	GSEA C2REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
26	-5.03	NULL	1 / 14	GSEA C2TOMIDA_METASTASIS_DN
27	-4.98	NULL	1 / 7	GSEA C2BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2
28	-4.94	NULL	2 / 16	MF histone acetyl-lysine binding
29	-4.9	NULL	1 / 5	GSEA C2NAGY_PCAF_COMPONENTS_HUMAN
30	-4.88	NULL	3 / 24	BP centrosome organization
31	-4.83	NULL	1 / 15	GSEA C2SMOOTHA_GLYCOLYSIS
32	-4.83	NULL	1 / 15	GSEA C2REACTOME_GLUCCONEOGENESIS
33	-4.78	NULL	2 / 15	MF acetylglucosaminyltransferase activity
34	-4.73	NULL	1 / 6	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
35	-4.66	NULL	1 / 16	CC photoreceptor inner segment
36	-4.66	NULL	1 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
37	-4.66	NULL	1 / 16	GSEA C2SMOOTHA_GLUCCONEOGENESIS
38	-4.66	NULL	1 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
39	-4.63	NULL	3 / 26	BP histone acetylation
40	-4.63	NULL	3 / 24	miRNA target-184



GW_053

Local Summary

%DE = 0.67
 # metagenes = 19
 # genes = 317
 # genes in genesets = 315

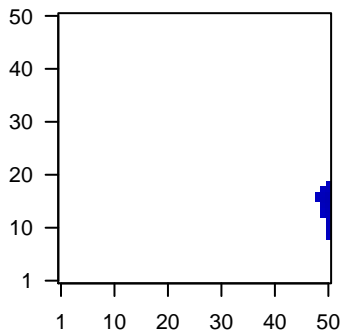
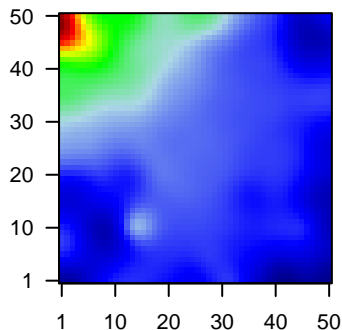
 # genes with $fdr < 0.1 = 135$ (15 + / 120 -)
 # genes with $fdr < 0.05 = 117$ (13 + / 104 -)
 # genes with $fdr < 0.01 = 70$ (9 + / 61 -)

 $\langle r \rangle$ metagenes = 0.87
 $\langle r \rangle$ genes = 0.24

 $\langle FC \rangle = -0.34$
 $\langle \text{shrinkage-t} \rangle = -12.07$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.61$

Profile

Spot



Local Genelist

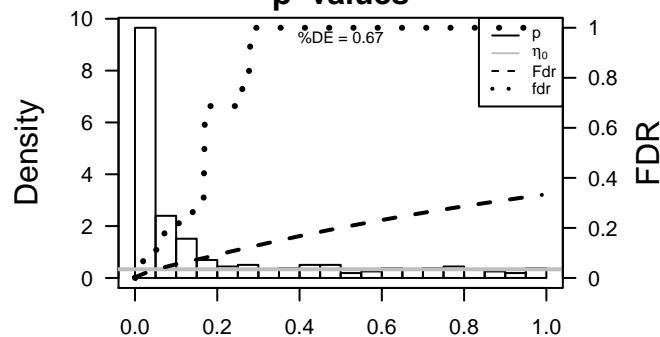
Rank	ID	log(FC)	fdr	p-value	Description
1	6920	-1.7	2e-16	2e-14	50 x 13 transcription elongation factor A (SII), 3 [Source:HGNC Symb
2	10232	-1.51	5e-14	2e-10	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
3	3248	1.41	2e-12	1e-09	50 x 13 hydroxyprostaglandin dehydrogenase 15-(NAD) [Source:HGI
4	51316	-1.35	2e-11	1e-08	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
5	217	1.27	2e-10	1e-08	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HC
6	7033	-1.26	3e-10	1e-08	50 x 10 trefol factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
7	2568	-1.26	3e-10	2e-07	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HG
8	92747	-1.2	2e-09	4e-07	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
9	494470	-1.15	9e-09	4e-07	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
10	155066	-1.14	1e-08	1e-06	50 x 15 ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
11	84952	-1.12	2e-08	2e-06	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]
12	9071	-1.09	4e-08	2e-06	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
13	2878	-1.08	7e-08	4e-06	50 x 9 glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
14	728715	-1.05	1e-07	4e-06	50 x 18
15	83988	-1.05	1e-07	5e-06	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
16	148170	-1.03	2e-07	5e-06	50 x 9 CDC42 effector protein (Rho GTPase binding) 5 [Source:HGI
17	8857	-1.03	2e-07	2e-05	50 x 13 Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
18	7716	-1.01	4e-07	5e-05	50 x 16 vascular endothelial zinc finger 1 [Source:HGNC Symbol;Acc
19	29116	-0.98	1e-06	5e-05	50 x 14 myosin regulatory light chain interacting protein [Source:HGN
20	634	-0.96	1e-06	5e-05	50 x 12 carcinoembryonic antigen-related cell adhesion molecule 1 (I

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.94	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-12.68	NULL	3 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	-12.13	NULL	4 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
4	-10.64	NULL	3 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
5	-10.34	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_F
6	-9.18	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
7	-9.14	NULL	2 / 14	GSEA C2WANG_BARRETTES_ESOPHAGUS_UP
8	-8.42	NULL	4 / 13	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G3_DN
9	-8.23	NULL	6 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
10	-7.89	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
11	-7.86	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
12	-7.39	NULL	4 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
13	-6.97	NULL	4 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
14	-6.95	NULL	3 / 10	Cancer LIU_BREAST_CANCER
15	-6.9	NULL	2 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
16	-6.68	NULL	2 / 16	GSEA C2ALK_AML_CLUSTER_9
17	-6.56	NULL	1 / 12	BP regulation of DNA-dependent transcription, elongation
18	-6.43	NULL	5 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
19	-6.37	NULL	4 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
20	-6.06	NULL	3 / 14	GSEA C2VANTVEER_BREAST_CANCER_METASTASIS_UP
21	-6.04	NULL	2 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
22	-6.03	NULL	2 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
23	-6.03	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
24	-6.01	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
25	-5.87	NULL	2 / 21	BP pancreas development
26	-5.66	NULL	1 / 9	GSEA C2SOUYER_TATL_TARGETS_UP
27	-5.57	NULL	3 / 14	MF selenium binding
28	-5.56	NULL	28 / 375	Disease GUDJ_psooriasis down
29	-5.47	NULL	5 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
30	-5.47	NULL	3 / 4	miRNA target-204
31	-5.47	NULL	2 / 10	BP regulation of dendrite development
32	-5.45	NULL	3 / 14	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
33	-5.4	NULL	1 / 11	BP negative regulation of multicellular organism growth
34	-5.39	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
35	-5.36	NULL	9 / 116	miRNA target-219
36	-5.3	NULL	1 / 10	MF GABA-A receptor activity
37	-5.28	NULL	1 / 14	GSEA C2WALK_AML_WITH_11Q23_REARRANGED
38	-5.22	NULL	2 / 14	GSEA C2VANTVEER_BREAST_CANCER_ESR1_UP
39	-5.18	NULL	2 / 10	BP positive regulation of histone H3-K4 methylation
40	-5.11	NULL	1 / 3	miRNA target-148a

p-values



GW_053

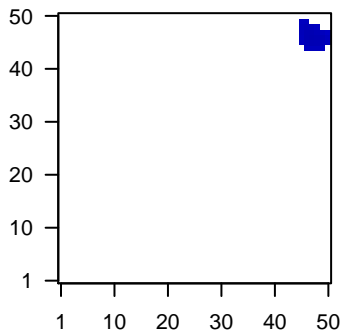
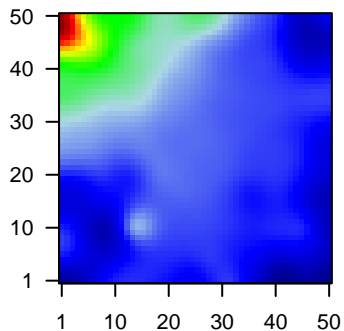
Local Summary

%DE = 0.75
 # metagenes = 28
 # genes = 260
 # genes in genesets = 258
 # genes with $fdr < 0.1$ = 119 (6 + / 113 -)
 # genes with $fdr < 0.05$ = 85 (4 + / 81 -)
 # genes with $fdr < 0.01$ = 56 (2 + / 54 -)

$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.3
 $\langle FC \rangle = -0.36$
 $\langle \text{shrinkage-t} \rangle = -12.48$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.65$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	23580	-1.23	7e-10	1e-05	47 x 45 CDC42 effector protein (Rho GTPase binding) 4 [Source:HGNC]
2	142	-1.03	3e-07	1e-05	47 x 46 poly (ADP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:23141]
3	26227	-0.99	6e-07	1e-05	50 x 46 phosphoglycerate dehydrogenase [Source:HGNC Symbol;Acc:23141]
4	116028	-0.99	7e-07	1e-05	46 x 47 RecQ mediated genome instability 2 [Source:HGNC Symbol;Acc:23141]
5	7083	-0.98	8e-07	1e-05	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183]
6	5050	-0.97	1e-06	1e-05	47 x 45 platelet-activating factor acetylhydrolase 1b, catalytic subunit
7	57570	-0.96	1e-06	1e-05	46 x 45 tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141]
8	51804	-0.96	1e-06	3e-05	50 x 46 SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
9	4171	-0.95	2e-06	4e-05	46 x 48 minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:15]
10	875	-0.94	3e-06	4e-05	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15]
11	2091	-0.93	3e-06	2e-04	47 x 45 fibrillarin [Source:HGNC Symbol;Acc:3599]
12	51259	-0.9	7e-06	2e-04	50 x 45 transmembrane protein 216 [Source:HGNC Symbol;Acc:2501]
13	1974	-0.8	1e-05	2e-04	49 x 47 eukaryotic translation initiation factor 4A2 [Source:HGNC Symbol;Acc:5106]
14	3202	-0.87	1e-05	6e-04	49 x 47 homeobox A5 [Source:HGNC Symbol;Acc:5106]
15	3148	-0.84	3e-05	6e-04	46 x 46 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
16	1019	-0.83	4e-05	6e-04	46 x 47 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:1773]
17	92370	-0.8	6e-05	6e-04	50 x 46 acid phosphatase-like 2 [Source:HGNC Symbol;Acc:26303]
18	23306	-0.8	6e-05	6e-04	46 x 47 transmembrane protein 194A [Source:HGNC Symbol;Acc:29]
19	9133	-0.78	9e-05	6e-04	45 x 49 cyclin B2 [Source:HGNC Symbol;Acc:1580]
20	78995	-0.78	9e-05	6e-04	46 x 46 chromosome 17 open reading frame 53 [Source:HGNC Symt]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.72	NULL	9 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
2	-20.08	NULL	35 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
3	-20.08	NULL	35 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
4	-18.93	NULL	6 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
5	-17.59	NULL	31 / 149	BP DNA replication
6	-17.41	NULL	12 / 57	Glio developing astrocytes
7	-16.98	NULL	5 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
8	-16.85	NULL	7 / 11	GSEA C2KALMA_E2F1_TARGETS
9	-15.97	NULL	11 / 30	BP DNA strand elongation involved in DNA replication
10	-15.39	NULL	7 / 16	GSEA C2FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
11	-15.21	NULL	5 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
12	-14.73	NULL	5 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
13	-14.59	NULL	4 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
14	-14.59	NULL	6 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
15	-14.44	NULL	5 / 14	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
16	-14.09	NULL	6 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
17	-13.89	NULL	6 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
18	-13.81	NULL	4 / 16	GSEA C2Y_AGING_PREMATURE_DN
19	-13.65	NULL	4 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
20	-13.61	NULL	7 / 15	GSEA C2KEGG_DNA_REPLICATION
21	-13.48	NULL	4 / 9	miRNA target-24
22	-13.4	NULL	8 / 22	BP DNA replication initiation
23	-13.26	NULL	5 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
24	-13.2	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
25	-13.06	NULL	45 / 370	BP mitotic cell cycle
26	-13.05	NULL	4 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
27	-12.78	NULL	4 / 12	GSEA C2L_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
28	-12.48	NULL	6 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
29	-12.29	NULL	4 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
30	-12.03	NULL	6 / 24	MF DNA helicase activity
31	-12.02	NULL	5 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
32	-11.99	NULL	3 / 9	GSEA C2REACTOME_CELL_CYCLE_CHECKPOINTS
33	-11.86	NULL	4 / 15	GSEA C2KAUFFMANN_DNA_REPLICATION_GENES
34	-11.79	NULL	5 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
35	-11.69	NULL	5 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
36	-11.66	NULL	4 / 16	GSEA C2KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN
37	-11.42	NULL	46 / 530	Cancer Lembecke_Normal vs Adenoma
38	-11.26	NULL	3 / 15	GSEA C2Y_AGING_OLD_DN
39	-11.18	NULL	4 / 13	Pathw Ac:GUSTAFSON_PI3K_UP
40	-11.1	NULL	3 / 14	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM

p-values

