

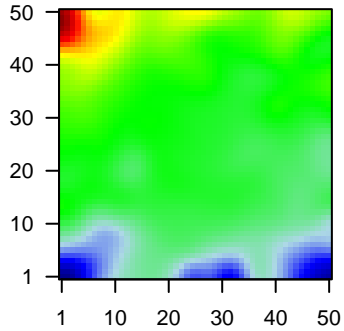
GW_077

Global Summary

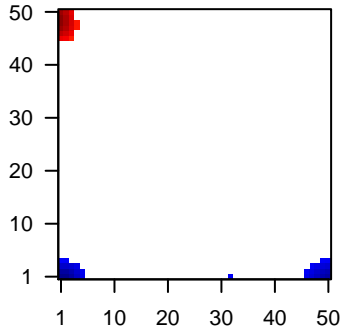
%DE = 0.13
 # genes with fdr < 0.2 = 1746 (860 + / 886 -)
 # genes with fdr < 0.1 = 1333 (659 + / 674 -)
 # genes with fdr < 0.05 = 1068 (531 + / 537 -)
 # genes with fdr < 0.01 = 713 (367 + / 346 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.87

Profile



Regulated Spots



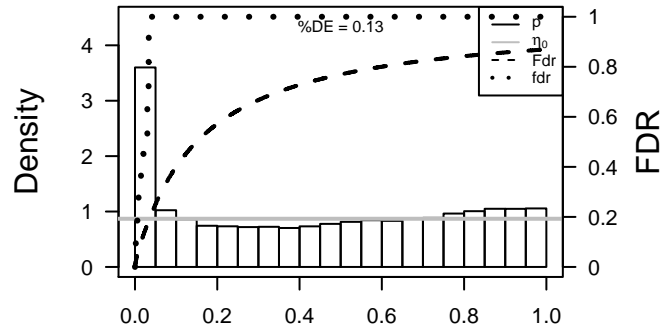
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	58	-1.38	2e-16	4e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	57016	1.48	2e-16	4e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	218	1.86	2e-16	4e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	242	1.85	2e-16	4e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syn
5	55107	1.71	2e-16	4e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
6	348	-1.41	2e-16	4e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	684	-1.64	2e-16	4e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
8	387695	1.31	2e-16	4e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
9	713	-1.54	2e-16	4e-14	50 x 1 complement component 1, q subcomponent, B chain [Source
10	1041	1.46	2e-16	4e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
11	1277	-1.34	2e-16	4e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	1475	1.43	2e-16	4e-14	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
13	115908	-1.55	2e-16	4e-14	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
14	9547	1.47	2e-16	4e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
15	1562	1.4	2e-16	4e-14	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
16	260293	1.43	2e-16	4e-14	50 x 14 cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
17	92196	2.29	2e-16	4e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
18	55894	1.42	2e-16	4e-14	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	414325	1.91	2e-16	4e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	2.19	2e-16	4e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	20.72	NULL	135	H.Tiss WIRTH_Mucosa
2	12.3	NULL	53	BP keratinocyte differentiation
3	11.31	NULL	21	CC cornified envelope
4	10.34	NULL	572	Disease GUDJ_poriasis up
5	9.53	NULL	76	BP epidermis development
6	8.89	NULL	504	Chr Chr 15
7	8.62	NULL	8	GSEA C2LJU_CDX2_TARGETS_DN
8	8.55	NULL	4	MMML C6S CIEJ_MMML 23
9	8.42	NULL	42	BP keratinization
10	6.83	NULL	7	MMML C6S CIEJ_MMML 9
11	6.77	NULL	918	Chr Chr 17
12	6.6	NULL	19	BP peptide cross-linking
13	6.33	NULL	9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
14	6.02	NULL	370	BP mitotic cell cycle
15	5.99	NULL	949	CC nucleoplasm
16	5.86	NULL	1233	TF KIM_MYC targets
17	5.79	NULL	30	BP cellular response to calcium ion
18	5.68	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	5.59	NULL	44	CC keratin filament
20	5.56	NULL	12	BP cellular aldehyde metabolic process
<i>Underexpressed</i>				
1	-14.43	NULL	553	Cancer Lembecke_Colonc Inflammation
2	-12.05	NULL	242	BP extracellular matrix organization
3	-11.75	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
4	-11.75	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
5	-11.75	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
6	-11.75	NULL	265	Glio willscher_GBM_Verhaak-PNmt_expression_B_down
7	-11.74	NULL	250	LymphontL2N_Stromal signature 1
8	-10.96	NULL	51	BP type I interferon signaling pathway
9	-10.89	NULL	190	CC extracellular matrix
10	-10.45	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
11	-10.4	NULL	69	BP extracellular matrix disassembly
12	-9.7	NULL	123	BP defense response to virus
13	-9.62	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
14	-9.53	NULL	64	BP collagen catabolic process
15	-9.35	NULL	683	CC extracellular space
16	-8.92	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
17	-8.9	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
18	-8.58	NULL	16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
19	-8.53	NULL	312	BP immune response
20	-8.52	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD

p-values



GW_077

Local Summary

%DE = 0.83
 # metagenes = 20
 # genes = 256
 # genes in genesets = 248
 # genes with $fdr < 0.1$ = 196 (167 + / 29 -)
 # genes with $fdr < 0.05$ = 191 (163 + / 28 -)
 # genes with $fdr < 0.01$ = 172 (147 + / 25 -)

<r> metagenes = 0.94

<r> genes = 0.44

<FC> = 0.54

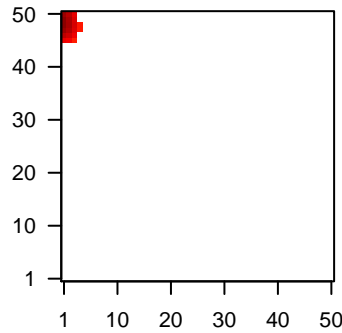
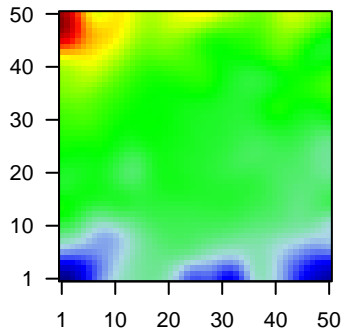
<shrinkage-t> = 19.08

<p-value> = 0

<fdr> = 0.28

Profile

Spot



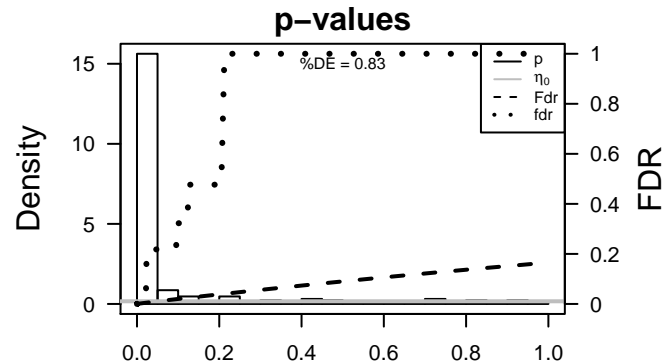
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.48	2e-16	3e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
2	218	1.86	2e-16	3e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	242	1.85	2e-16	3e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
4	387695	1.31	2e-16	3e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
5	1041	1.46	2e-16	3e-16	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	1475	1.43	2e-16	3e-16	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
7	9547	1.47	2e-16	3e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;/
8	1562	1.4	2e-16	3e-16	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
9	92196	2.29	2e-16	3e-16	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
10	55894	1.42	2e-16	3e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	1.91	2e-16	3e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	2.19	2e-16	3e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1828	1.84	2e-16	3e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	10804	1.74	2e-16	3e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	2941	1.44	2e-16	3e-16	3 x 50 glutathione S-transferase alpha 4 [Source:HGNC Symbol;Ac
16	43849	1.41	2e-16	3e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6:
17	26085	2.33	2e-16	3e-16	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6:
18	3848	3.01	2e-16	3e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
19	3858	2.07	2e-16	3e-16	1 x 47 keratin 10 [Source:HGNC Symbol;Acc:6413]
20	3868	1.33	2e-16	3e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	42.81	NULL	88 / 135	H.Tiss WIRTH_Mucosa
2	30.84	NULL	19 / 21	CC cornified envelope
3	29.93	NULL	26 / 53	BP keratinocyte differentiation
4	23.69	NULL	12 / 19	BP peptide cross-linking
5	22.87	NULL	102 / 572	Disease GUDJ_psooriasis up
6	20.59	NULL	19 / 42	BP keratinization
7	19.69	NULL	25 / 76	BP epidermis development
8	18.71	NULL	12 / 21	CC desmosome
9	16.42	NULL	3 / 8	GSEA C2LUCDX2_TARGETS_DN
10	15.07	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	13.74	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
12	13.74	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
13	13.73	NULL	10 / 44	CC keratin filament
14	13.25	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
15	12.32	NULL	26 / 186	MF structural molecule activity
16	12.31	NULL	7 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
17	11.79	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
18	11.56	NULL	3 / 12	BP cellular aldehyde metabolic process
19	11.24	NULL	16 / 82	CC intermediate filament
20	10.49	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
21	10.37	NULL	2 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
22	10.35	NULL	8 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
23	9.82	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
24	9.79	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
25	9.71	NULL	2 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
26	9.22	NULL	8 / 51	MF protein binding, bridging
27	9.06	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
28	8.98	NULL	5 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HP31_DN
29	8.88	NULL	3 / 13	BP intermediate filament cytoskeleton organization
30	8.76	NULL	2 / 13	GSEA C2CHEN_LUNG_CANCER_SURVIVAL
31	8.3	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
32	8.1	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
33	8.04	NULL	5 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
34	8	NULL	3 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
35	7.93	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
36	7.91	NULL	14 / 122	MF serine-type endopeptidase activity
37	7.9	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
38	7.89	NULL	3 / 26	BP regulation of angiogenesis
39	7.84	NULL	5 / 58	Glio Christensen_hypomethylated_in_secondary_glioblastoma
40	7.8	NULL	4 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN



GW_077

Local Summary

%DE = 0.84
 # metagenes = 16
 # genes = 258
 # genes in genesets = 257

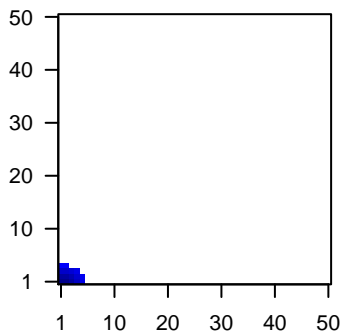
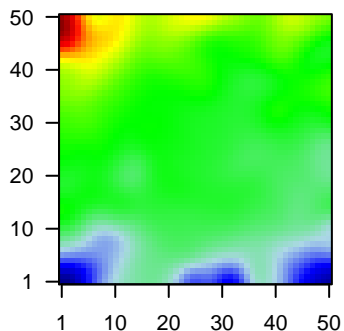
genes with $fdr < 0.1$ = 197 (11 + / 186 -)
 # genes with $fdr < 0.05$ = 165 (7 + / 158 -)
 # genes with $fdr < 0.01$ = 150 (6 + / 144 -)

$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.4

$\langle FC \rangle = -0.47$
 $\langle \text{shrinkage-t} \rangle = -16.4$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.37$

Profile

Spot



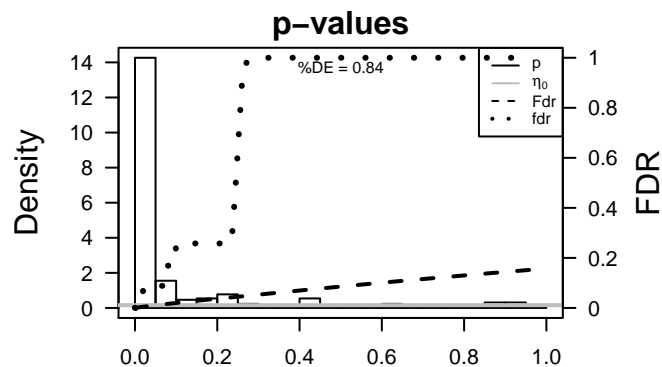
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1277	-1.34	2e-16	6e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	115908	-1.55	2e-16	6e-16	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
3	3039	2.04	2e-16	6e-16	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3040	2.22	2e-16	6e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3043	2.07	2e-16	6e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
6	3576	-1.38	2e-16	6e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
7	4319	-1.62	2e-16	6e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
8	4320	-1.36	2e-16	6e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
9	4316	-1.79	2e-16	6e-16	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC
10	4318	-1.69	2e-16	6e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9:
11	26064	-1.4	2e-16	6e-16	4 x 1 retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
12	6696	-1.32	2e-16	6e-16	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125:
13	23213	-1.62	2e-16	6e-16	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
14	7045	-2.28	2e-16	6e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG
15	55714	-1.26	3e-15	1e-12	1 x 1 teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
16	55450	-1.21	3e-14	2e-11	1 x 4 calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
17	6781	1.14	6e-13	9e-11	1 x 3 stanniocalcin 1 [Source:HGNC Symbol;Acc:11373]
18	5066	-1.11	3e-12	9e-11	2 x 3 peptidylglycine alpha-amidating monooxygenase [Source:HC
19	3491	-1.1	5e-12	1e-10	2 x 1 cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol
20	3678	-1.08	9e-12	1e-10	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [So

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-33.81	NULL	62 / 190	CC extracellular matrix
2	-32.36	NULL	30 / 69	BP extracellular matrix disassembly
3	-32.35	NULL	65 / 242	BP extracellular matrix organization
4	-31.38	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
5	-31.28	NULL	71 / 250	LymphocyteENZ_Stromal signature 1
6	-30.77	NULL	27 / 64	BP collagen catabolic process
7	-27.62	NULL	15 / 16	MMML C6SCIEJ_MMML 1
8	-24.97	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
9	-24.69	NULL	8 / 11	MF platelet-derived growth factor binding
10	-23.17	NULL	11 / 19	MF extracellular matrix binding
11	-22.85	NULL	12 / 35	Glio Colman_survival_associated
12	-21.6	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
13	-21.29	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
14	-21.09	NULL	35 / 183	CC proteinaceous extracellular matrix
15	-19.98	NULL	14 / 37	BP collagen fibril organization
16	-19.7	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
17	-18.76	NULL	8 / 12	miRNA target-29c
18	-18.57	NULL	76 / 683	CC extracellular space
19	-18.02	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
20	-18.01	NULL	61 / 553	Cancer Lembecke_Colonc Inflammation
21	-17.77	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
22	-17.16	NULL	6 / 11	Glio Phillips MES up vs Prolif & PN
23	-17.06	NULL	19 / 57	MF extracellular matrix structural constituent
24	-16.69	NULL	39 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
25	-16.69	NULL	39 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
26	-16.69	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
27	-16.69	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
28	-16.65	NULL	3 / 7	GSEA C2DASU_IL6_SIGNALING_DN
29	-16.61	NULL	17 / 68	CC collagen
30	-16.46	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
31	-16.35	NULL	2 / 6	Glio Martinez_Glio_hypometh
32	-16.29	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
33	-16	NULL	6 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
34	-15.4	NULL	17 / 85	MF integrin binding
35	-15.3	NULL	4 / 7	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_UP
36	-15.24	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
37	-15.23	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
38	-15.19	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
39	-15.06	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
40	-14.85	NULL	102 / 1182	CC extracellular region



GW_077

Local Summary

%DE = 0.83
 # metagenes = 1
 # genes = 96
 # genes in genesets = 94
 # genes with $fdr < 0.1 = 72$ (1 + / 71 -)
 # genes with $fdr < 0.05 = 58$ (0 + / 58 -)
 # genes with $fdr < 0.01 = 54$ (0 + / 54 -)

<r> metagenes = NA

<r> genes = 0.52

<FC> = -0.56

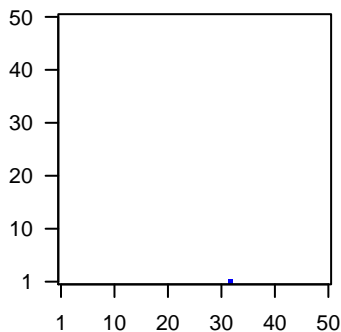
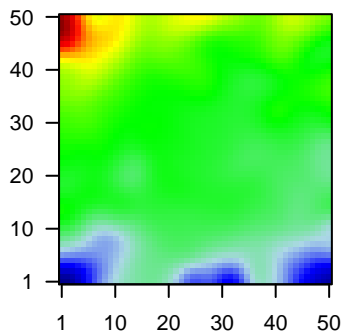
<shrinkage-t> = -19.77

<p-value> = 0

<fdr> = 0.38

Profile

Spot



Local Genelist

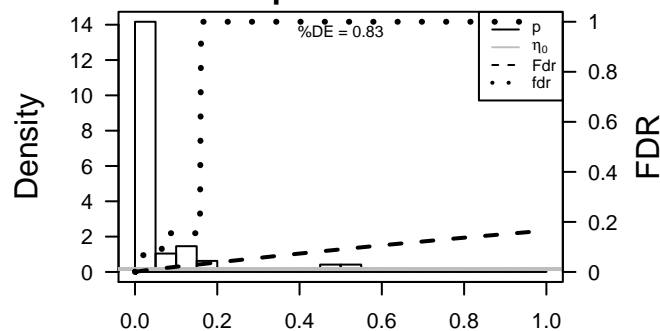
Rank	ID	log(FC)	fdr	p-value	Description
1	684	-1.64	2e-16	6e-16	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	94240	-1.4	2e-16	6e-16	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc
3	10964	-1.34	2e-16	6e-16	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Acc
4	2537	-1.6	2e-16	6e-16	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;f
5	9636	-1.62	2e-16	6e-16	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:40E
6	4599	-1.46	2e-16	6e-16	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible
7	64135	-1.17	2e-13	9e-12	32 x 1 interferon induced with helicase C domain 1 [Source:HGNC S
8	4600	-1.14	8e-13	5e-11	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
9	10561	-1.1	5e-12	5e-11	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16
10	6772	-1.09	6e-12	2e-10	32 x 1 signal transducer and activator of transcription 1, 91kDa [Sou
11	51296	-1.07	2e-11	3e-10	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3
12	55008	-1.05	4e-11	3e-10	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
13	3627	-1.04	5e-11	5e-09	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
14	5610	-1	4e-10	8e-09	32 x 1 eukaryotic translation initiation factor 2-alpha kinase 2 [Sourc
15	3433	-0.98	8e-10	4e-08	32 x 1 interferon-induced protein with tetratricopeptide repeats 2 [Sc
16	51191	-0.94	3e-09	4e-08	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
17	115362	-0.93	5e-09	5e-08	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
18	4321	-0.91	9e-09	9e-08	32 x 1 matrix metalloproteinase 12 (macrophage elastase) [Source:H
19	2633	-0.9	1e-08	2e-07	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HG
20	3430	-0.89	2e-08	2e-07	32 x 1 interferon-induced protein 35 [Source:HGNC Symbol;Acc:53

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-57.5	NULL	10 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
2	-55.19	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
3	-54.26	NULL	12 / 16	GSEA C2MOSEERLE_IFNA_RESPONSE
4	-50.43	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
5	-50.36	NULL	28 / 51	BP type I interferon signaling pathway
6	-48.96	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
7	-47.25	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
8	-38.99	NULL	30 / 123	BP defense response to virus
9	-38.7	NULL	10 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
10	-38.47	NULL	13 / 31	BP negative regulation of viral genome replication
11	-36.29	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	-35.44	NULL	7 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
13	-35.27	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
14	-34.31	NULL	26 / 109	BP response to virus
15	-33.5	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
16	-33.19	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
17	-31.35	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
18	-30.38	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
19	-29.65	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
20	-29.1	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
21	-28.55	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
22	-28.32	NULL	3 / 4	MMML C2CIEJ_MMML_47
23	-27.61	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
24	-27.11	NULL	33 / 204	BP cytokine-mediated signaling pathway
25	-27.03	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
26	-26.53	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
27	-26.41	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
28	-26.08	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION
29	-24.04	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
30	-23.81	NULL	30 / 274	Lymphom C2PANG_IL21 DN
31	-23.17	NULL	45 / 572	Disease GUDJ_psooriasis up
32	-21.92	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
33	-21.5	NULL	3 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
34	-21.17	NULL	4 / 14	GSEA C2SANA_TNF_SIGNALING_UP
35	-21.14	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
36	-20.16	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
37	-20.16	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
38	-19.4	NULL	5 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_LB_DN
39	-18.03	NULL	4 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_UP
40	-17.53	NULL	6 / 32	BP negative regulation of type I interferon production

p-values



GW_077

Local Summary

%DE = 0.85
 # metagenes = 16
 # genes = 268
 # genes in genesets = 266

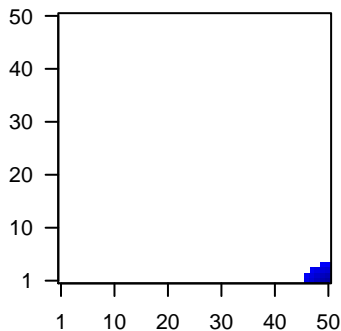
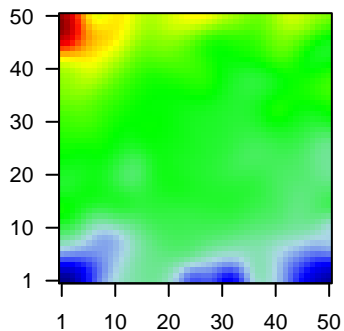
genes with $fdr < 0.1 = 181$ (8 + / 173 -)
 # genes with $fdr < 0.05 = 178$ (8 + / 170 -)
 # genes with $fdr < 0.01 = 107$ (5 + / 102 -)

<r> metagenes = 0.99
 <r> genes = 0.6

<FC> = -0.39
 <shrinkage-t> = -13.62
 <p-value> = 0
 <fdr> = 0.48

Profile

Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	348	-1.41	2e-16	4e-15	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	713	-1.54	2e-16	4e-15	50 x 1 complement component 1, q subcomponent, B chain [Source
3	260436	-1.27	1e-15	7e-13	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
4	714	-1.22	2e-14	1e-12	50 x 1 complement component 1, q subcomponent, C chain [Source
5	341	-1.2	5e-14	1e-09	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
6	25849	1.05	4e-11	2e-09	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HC
7	5341	-1.02	1e-10	2e-09	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
8	3109	-1.02	1e-10	8e-09	50 x 1 major histocompatibility complex, class II, DM beta [Source:H
9	4283	-1	3e-10	1e-08	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
10	3122	-0.92	6e-10	3e-08	50 x 1 major histocompatibility complex, class II, DR alpha [Source:t
11	1436	-0.95	2e-09	3e-08	50 x 1 colony stimulating factor 1 receptor [Source:HGNC Symbol;A
12	3059	-0.95	3e-09	3e-08	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC S
13	7305	-0.94	3e-09	3e-08	50 x 1 TYRO protein tyrosine kinase binding protein [Source:HGNC
14	5920	-0.94	3e-09	4e-07	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Sour
15	115361	-0.88	3e-08	4e-07	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
16	894	-0.88	3e-08	4e-07	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
17	2517	-0.88	3e-08	9e-07	48 x 3 fucosidase, alpha-L- 1, tissue [Source:HGNC Symbol;Acc:4
18	54504	-0.86	7e-08	9e-07	50 x 4 carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;A
19	155038	0.85	8e-08	1e-06	50 x 3 GTPase, IMAP family member 8 [Source:HGNC Symbol;Acc:
20	10563	-0.84	1e-07	1e-06	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-25.68	NULL	12 / 15	CC MHC class II protein complex
2	-23.59	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
3	-23.01	NULL	91 / 417	H.Tiss WIRTH_Immune system
4	-20.4	NULL	94 / 553	Cancer Lembcke_Colonc Inflammation
5	-19.64	NULL	4 / 11	GSEA C2APPEL_IMATINIB_RESPONSE
6	-18.33	NULL	43 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
7	-18.33	NULL	43 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
8	-18.33	NULL	43 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
9	-18.33	NULL	43 / 265	Glio wilscher_GBM_Verhaak-PNmt_expression_B_down
10	-17.77	NULL	15 / 47	BP antigen processing and presentation
11	-17.61	NULL	52 / 312	BP immune response
12	-17.16	NULL	2 / 7	GSEA C2BIOCARTA_COMP_PATHWAY
13	-16.52	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
14	-15.92	NULL	2 / 8	GSEA C2BIOCARTA_CLASSIC_PATHWAY
15	-15.92	NULL	2 / 8	GSEA C2REACTOME_COMPLEMENT_CASCADE
16	-15.92	NULL	2 / 8	GSEA C2REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
17	-15.44	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
18	-14.71	NULL	2 / 4	MMML C6SCIEJ_MMML 2
19	-14.28	NULL	4 / 13	MMML C6SCIEJ_MMML 6
20	-14.22	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
21	-14.12	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
22	-13.68	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
23	-13.66	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
24	-13.51	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
25	-13.5	NULL	18 / 74	BP regulation of immune response
26	-13.18	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
27	-13.04	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
28	-12.9	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
29	-12.76	NULL	30 / 316	Cancer SPANG_BCL6-index2
30	-12.75	NULL	4 / 14	GSEA C2WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
31	-12.57	NULL	2 / 11	BP high-density lipoprotein particle remodeling
32	-12.43	NULL	2 / 3	MMML C6SCIEJ_MMML 7
33	-12.42	NULL	8 / 35	CC trans-Golgi network membrane
34	-12.4	NULL	16 / 60	BP T cell costimulation
35	-12.23	NULL	4 / 14	BP ruffle organization
36	-12.2	NULL	5 / 12	BP immunoglobulin mediated immune response
37	-12.1	NULL	7 / 28	CC transport vesicle membrane
38	-11.99	NULL	25 / 162	CC external side of plasma membrane
39	-11.97	NULL	2 / 10	GSEA C2AMUNDSON_GAMMA_RADIATION_RESISTANCE
40	-11.89	NULL	13 / 87	BP antigen processing and presentation of exogenous peptide antigen

