

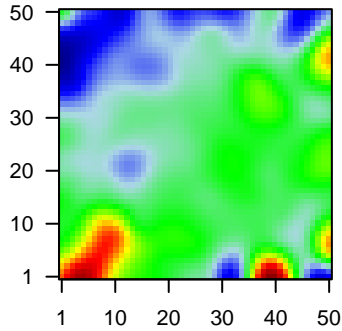
GW_004

Global Summary

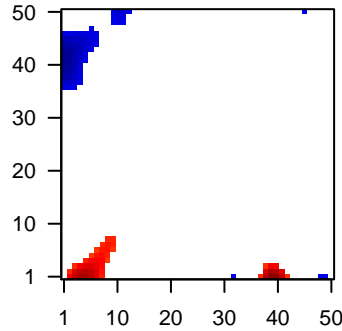
%DE = 0.15
 # genes with fdr < 0.2 = 1947 (1173 + / 774 -)
 # genes with fdr < 0.1 = 1452 (942 + / 510 -)
 # genes with fdr < 0.05 = 1229 (814 + / 415 -)
 # genes with fdr < 0.01 = 863 (587 + / 276 -)
 # genes in genesets = 16332

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

Profile



Regulated Spots



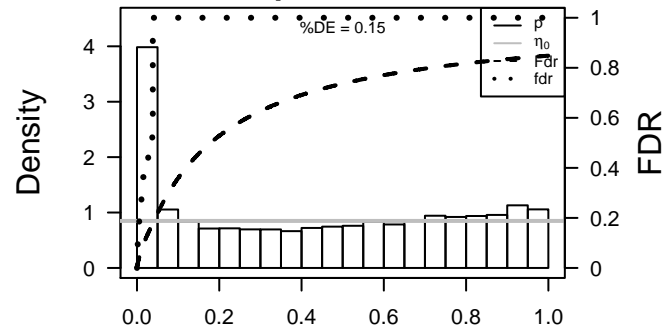
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	24	1.55	2e-16 4e-14	16 x 50 ATP-binding cassette, sub-family A (ABC1), member 4 [Sou
2	220	1.67	2e-16 4e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
3	147495	2.48	2e-16 4e-14	2 x 44 adenomatous polyposis coli down-regulated 1 [Source:HGNC
4	430	1.64	2e-16 4e-14	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HG
5	79058	1.66	2e-16 4e-14	41 x 1 alveolar soft part sarcoma chromosome region, candidate 1 [
6	50617	1.6	2e-16 4e-14	5 x 50 ATPase, H+ transporting, lysosomal V0 subunit a4 [Source:Hi
7	8313	1.74	2e-16 4e-14	50 x 8 axin 2 [Source:HGNC Symbol;Acc:904]
8	25805	2.55	2e-16 4e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
9	586	1.65	2e-16 4e-14	6 x 1 branched chain amino-acid transaminase 1, cytosolic [Source
10	652	1.56	2e-16 4e-14	9 x 1 bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:1C
11	113802	-1.54	2e-16 4e-14	46 x 46 HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:HC
12	260436	-1.62	2e-16 4e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
13	29113	3.02	2e-16 4e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
14	23705	1.7	2e-16 4e-14	50 x 7 cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
15	92291	1.55	2e-16 4e-14	50 x 11 calpain 13 [Source:HGNC Symbol;Acc:16663]
16	1359	1.64	2e-16 4e-14	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
17	1469	2.49	2e-16 4e-14	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
18	27121	2.02	2e-16 4e-14	6 x 50 dickkopf WNT signaling pathway inhibitor 4 [Source:HGNC S
19	10913	1.56	2e-16 4e-14	18 x 42 ectodysplasin A receptor [Source:HGNC Symbol;Acc:2895]
20	4072	1.81	2e-16 4e-14	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.94	NULL	534	Chr Chr 8
2	8.25	NULL	232	Chr Chr 18
3	6.95	NULL	7	MMML C06CIEJ_MMML 13
4	6.6	NULL	13	GSEA C2LINDGREN_BLADEER_CANCER_CLUSTER_2B
5	6.48	NULL	4	MMML C06CIEJ_MMML 23
6	6.47	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_2
7	6.36	NULL	190	CC extracellular matrix
8	6.21	NULL	15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
9	6.1	NULL	13	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
10	6.09	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
11	6.08	NULL	10	BP cellular response to zinc ion
12	6.03	NULL	1182	CC extracellular region
13	6.01	NULL	1146	TF HEBENSTREIT_low expression TF
14	5.91	NULL	13	BP cellular response to cadmium ion
15	5.83	NULL	15	GSEA C2ONDER_CDH1_TARGETS_2_UP
16	5.78	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
17	5.72	NULL	957	Chr Chr 11
18	5.64	NULL	3	GSEA C2BIOCARTA_NEUROTRANSMITTERS_PATHWAY
19	5.59	NULL	9	GSEA C2RODWELL_AGING_KIDNEY_UP
20	5.59	NULL	26	MF Wnt-protein binding
<i>Underexpressed</i>				
1	-8.92	NULL	417	H.Tiss WIRTH_Immune system
2	-8.79	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
3	-8.57	NULL	572	Disease GUDJ_poriasis up
4	-7.93	NULL	504	Chr Chr 15
5	-7.54	NULL	274	Lymphoma SPANG_IL21 DN
6	-6.92	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
7	-6.86	NULL	914	Chr Chr 3
8	-6.68	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
9	-6.58	NULL	204	BP cytokine-mediated signaling pathway
10	-6.09	NULL	15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
11	-6	NULL	312	BP immune response
12	-5.99	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
13	-5.84	NULL	699	Chr Chr 5
14	-5.56	NULL	60	BP interferon-gamma-mediated signaling pathway
15	-5.47	NULL	8	GSEA C2ROETH_TERT_TARGETS_UP
16	-5.41	NULL	51	BP type I interferon signaling pathway
17	-5.37	NULL	7	MMML C06CIEJ_MMML 9
18	-5.35	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
19	-5.33	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
20	-5.33	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down

p-values



GW_004

Local Summary

%DE = 0.56
 # metagenes = 38
 # genes = 422
 # genes in genesets = 416

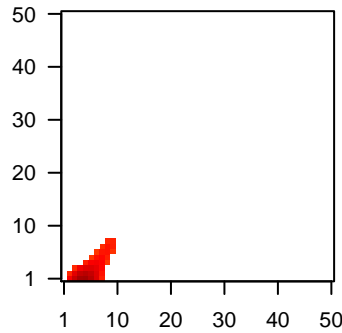
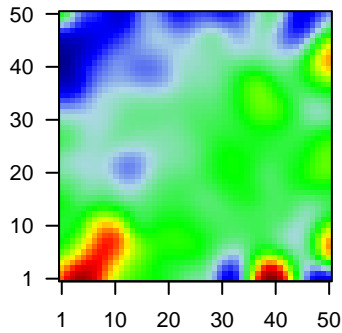
genes with $fdr < 0.1$ = 149 (136 + / 13 -)
 # genes with $fdr < 0.05$ = 141 (131 + / 10 -)
 # genes with $fdr < 0.01$ = 91 (86 + / 5 -)

<r> metagenes = 0.85
 <r> genes = 0.33

<FC> = 0.32
 <shrinkage-t> = 11.17
 <p-value> = 0
 <fdr> = 0.62

Profile

Spot



Local Genelist

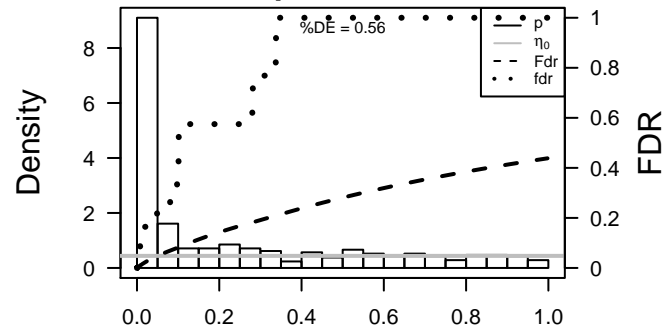
Rank	ID	log(FC)	fdr	p-value	Description
1	25805	2.55	2e-16	3e-15	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
2	586	1.65	2e-16	3e-15	6 x 1 branched chain amino-acid transaminase 1, cytosolic [Sourc
3	1469	2.49	2e-16	3e-15	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
4	3039	1.94	2e-16	3e-15	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3040	2.28	2e-16	3e-15	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
6	3043	2.11	2e-16	3e-15	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
7	10962	1.87	2e-16	3e-15	5 x 1 myeloid/lymphoid or mixed-lineage leukemia (trithorax homol
8	4311	1.76	2e-16	3e-15	2 x 1 membrane metallo-endopeptidase [Source:HGNC Symbol;A
9	4487	1.58	2e-16	3e-15	5 x 2 msh homeobox 1 [Source:HGNC Symbol;Acc:7391]
10	85409	2.01	2e-16	3e-15	8 x 4 naked cuticle homolog 2 (Drosophila) [Source:HGNC Symbol
11	4885	1.88	2e-16	3e-15	5 x 1 neuronal pentraxin II [Source:HGNC Symbol;Acc:7953]
12	5954	1.54	2e-16	3e-15	7 x 4 reticulocalbin 1, EF-hand calcium binding domain [Source:HK
13	56241	1.56	2e-16	3e-15	5 x 1 sushi domain containing 2 [Source:HGNC Symbol;Acc:30667
14	7076	1.77	2e-16	3e-15	4 x 1 TIMP metalloproteinase inhibitor 1 [Source:HGNC Symbol;Acc
15	2296	1.53	4e-16	1e-13	7 x 3 forkhead box C1 [Source:HGNC Symbol;Acc:3800]
16	115908	1.51	1e-15	2e-13	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
17	10449	1.49	2e-15	9e-13	8 x 1 acetyl-CoA acyltransferase 2 [Source:HGNC Symbol;Acc:83]
18	23670	1.46	1e-14	9e-13	3 x 3 transmembrane protein 2 [Source:HGNC Symbol;Acc:11869]
19	55321	1.45	2e-14	9e-13	8 x 5 transmembrane protein 74B [Source:HGNC Symbol;Acc:158
20	10395	1.44	2e-14	2e-12	5 x 1 deleted in liver cancer 1 [Source:HGNC Symbol;Acc:2897]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	22.72	NULL	2 / 4	MMML C6SCIEJ_MMML 23
2	17.17	NULL	3 / 11	MF oxygen transporter activity
3	16.09	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
4	15.29	NULL	4 / 19	MF peroxidase activity
5	13.91	NULL	83 / 250	LymphocyteENZ_Stromal signature 1
6	13.7	NULL	2 / 10	CC hemoglobin complex
7	13.68	NULL	9 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
8	13.04	NULL	63 / 190	CC extracellular matrix
9	13	NULL	2 / 11	GSEA C2IOACARTA_AHSP_PATHWAY
10	12.79	NULL	5 / 11	MMML C6SCIEJ_MMML 31
11	12.52	NULL	1 / 2	GSEA C2TESAR_ALK_TARGETS_HUMAN_ES_5D_UP
12	12.46	NULL	4 / 13	BP regulation of blood vessel size
13	12.16	NULL	3 / 19	BP hydrogen peroxide catabolic process
14	12.03	NULL	6 / 8	GSEA C2YAGUE_PRETUMOR_DRUG_RESISTANCE_DN
15	11.95	NULL	3 / 14	CC endocytic vesicle lumen
16	10.71	NULL	3 / 26	MF oxygen binding
17	10.65	NULL	5 / 15	Cancer LIU_PROSTATE_CANCER_DN
18	10.55	NULL	3 / 15	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
19	10.14	NULL	2 / 6	GSEA C2TSAI_DNAJB4_TARGETS_DN
20	10.1	NULL	6 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
21	10.06	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
22	10.04	NULL	3 / 10	BP negative regulation of fibroblast growth factor receptor signaling pa
23	9.55	NULL	6 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
24	9.45	NULL	23 / 57	MF extracellular matrix structural constituent
25	9.42	NULL	6 / 22	BP positive regulation of BMP signaling pathway
26	9.35	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
27	9.23	NULL	6 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
28	9.17	NULL	13 / 16	MMML C6SCIEJ_MMML 1
29	9.05	NULL	3 / 29	BP positive regulation of cell death
30	9.04	NULL	3 / 31	MF frizzled binding
31	9.02	NULL	4 / 11	Glio Phillips MES vs Prolif & PN
32	8.85	NULL	2 / 22	BP bicarbonate transport
33	8.82	NULL	53 / 242	BP extracellular matrix organization
34	8.78	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
35	8.67	NULL	2 / 13	MF transmembrane receptor protein serine/threonine kinase activity
36	8.64	NULL	8 / 11	MF platelet-derived growth factor binding
37	8.56	NULL	3 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
38	8.52	NULL	3 / 18	MF transforming growth factor beta-activated receptor activity
39	8.41	NULL	25 / 69	BP extracellular matrix disassembly
40	8.29	NULL	6 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN

p-values



GW_004

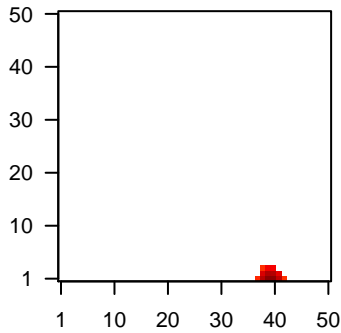
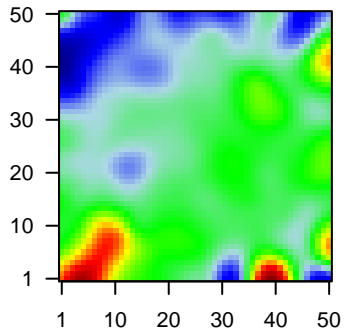
Local Summary

%DE = 0.75
 # metagenes = 13
 # genes = 230
 # genes in genesets = 204
 # genes with $fdr < 0.1 = 151$ (146 + / 5 -)
 # genes with $fdr < 0.05 = 110$ (106 + / 4 -)
 # genes with $fdr < 0.01 = 73$ (71 + / 2 -)

<r> metagenes = 0.99
 <r> genes = 0.5
 <FC> = 0.41
 <shrinkage-t> = 14.55
 <p-value> = 0.01
 <fdr> = 0.54

Profile

Spot



Local Genelist

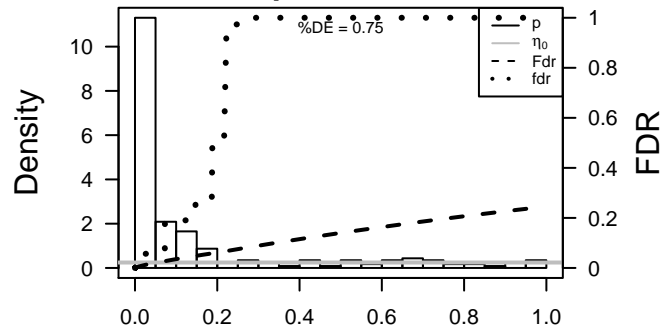
Rank	ID	log(FC)	fdr	p-value	Description
1	79058	1.66	2e-16	1e-14	41 x 1 alveolar soft part sarcoma chromosome region, candidate 1 [
2	28996	1.14	1e-09	8e-07	40 x 1 homeodomain interacting protein kinase 2 [Source:HGNC Sy
3	400818	1.06	2e-08	8e-07	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
4	202134	1.05	3e-08	4e-06	40 x 1 family with sequence similarity 153, member B [Source:HGNC
5	26040	1	1e-07	4e-06	40 x 3 SET binding protein 1 [Source:HGNC Symbol;Acc:15573]
6	85452	0.98	2e-07	4e-06	39 x 1 chromosome 1 open reading frame 222 [Source:HGNC Synt
7	55333	0.98	2e-07	3e-05	40 x 1 synaptojanin 2 binding protein [Source:HGNC Symbol;Acc:18
8	126205	0.93	7e-07	3e-05	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbo
9	136051	0.9	2e-06	3e-05	40 x 1 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
10	319085	0.89	2e-06	3e-05	39 x 1 ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
11	80224	0.89	3e-06	3e-05	40 x 1 nucleotide binding protein-like [Source:HGNC Symbol;Acc:20
12	25862	0.89	3e-06	3e-05	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
13	440275	0.87	4e-06	3e-05	40 x 1 eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
14	401494	0.87	4e-06	3e-05	40 x 1 protein tyrosine phosphatase-like A domain containing 2 [Sou
15	90586	0.87	4e-06	3e-05	39 x 1 amine oxidase, copper containing 4, pseudogene [Source:HC
16	56203	0.87	4e-06	1e-04	39 x 1 leiomodlin 3 (fetal) [Source:HGNC Symbol;Acc:6649]
17	91368	0.77	8e-06	1e-04	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC S
18	5900	-0.84	9e-06	1e-04	39 x 2 ral guanine nucleotide dissociation stimulator [Source:HGNC
19	27148	0.83	1e-05	1e-04	41 x 1 serine/threonine kinase 36 [Source:HGNC Symbol;Acc:17206
20	399761	0.82	1e-05	1e-04	39 x 1 BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	15.91	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
2	9.5	NULL	1 / 10	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
3	9.29	NULL	2 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
4	8.4	NULL	3 / 14	MMML C2SCIEJ_MMML_8
5	8.2	NULL	1 / 13	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
6	7.62	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
7	7.55	NULL	1 / 15	CC vesicle membrane
8	7.33	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
9	6.88	NULL	1 / 9	GSEA C2BROWNE_HCMV_INFECTION_1HR_DN
10	6.39	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
11	6.23	NULL	2 / 14	BP mitochondrion morphogenesis
12	6.18	NULL	2 / 13	GSEA C2ST_GAQ_PATHWAY
13	6.18	NULL	2 / 13	GSEA C2ST_GA13_PATHWAY
14	5.82	NULL	1 / 12	BP retina layer formation
15	5.56	NULL	1 / 13	BP DNA damage response, signal transduction by p53 class mediator
16	5.56	NULL	1 / 13	BP SMAD protein signal transduction
17	5.47	NULL	2 / 15	GSEA C2FIRESTEIN_PROLIFERATION
18	5.44	NULL	2 / 38	CC cytoplasmic side of plasma membrane
19	5.32	NULL	1 / 14	GSEA C2MILCOX_PRESPONSE_TO_ROGESTERONE_DN
20	5.11	NULL	1 / 15	GSEA C2WANG_LMO4_TARGETS_UP
21	5.11	NULL	1 / 15	GSEA C2ODONNELL_TFRC_TARGETS_UP
22	5.11	NULL	1 / 15	GSEA C2RODRIGUES_THYROID_CARCINOMA_DN
23	5.11	NULL	1 / 15	GSEA C2SUNG_METASTASIS_STROMA_DN
24	5.11	NULL	1 / 15	GSEA C2LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP
25	5.11	NULL	1 / 15	GSEA C2DE_YY1_TARGETS_DN
26	5.11	NULL	1 / 15	GSEA C2BROWNE_HCMV_INFECTION_24HR_DN
27	5.02	NULL	2 / 16	GSEA C2YANAGIHARA_ESX1_TARGETS
28	5.02	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
29	5.01	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
30	4.98	NULL	2 / 40	CC extrinsic to membrane
31	4.91	NULL	1 / 16	BP embryonic camera-type eye morphogenesis
32	4.91	NULL	1 / 16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
33	4.91	NULL	1 / 16	GSEA C2BILD_CTNNB1_ONCOGENIC_SIGNATURE
34	4.91	NULL	1 / 16	GSEA C2COULOUARN_TEMPORAL_TGFB1_SIGNATURE_DN
35	4.63	NULL	2 / 14	BP cellular response to estradiol stimulus
36	4.61	NULL	1 / 11	GSEA C2BIOCARTA_EIF2_PATHWAY
37	4.49	NULL	1 / 14	CC integral to mitochondrial outer membrane
38	4.41	NULL	1 / 10	BP negative regulation of cell-matrix adhesion
39	4.38	NULL	1 / 10	BP negative regulation of JUN kinase activity
40	4.29	NULL	1 / 20	BP positive regulation of transforming growth factor beta receptor sign

p-values



GW_004

Local Summary

%DE = 0.73
 # metagenes = 1
 # genes = 96
 # genes in genesets = 94
 # genes with fdr < 0.1 = 62 (10 + / 52 -)
 # genes with fdr < 0.05 = 46 (8 + / 38 -)
 # genes with fdr < 0.01 = 40 (8 + / 32 -)

<r> metagenes = NA

<r> genes = 0.52

<FC> = -0.34

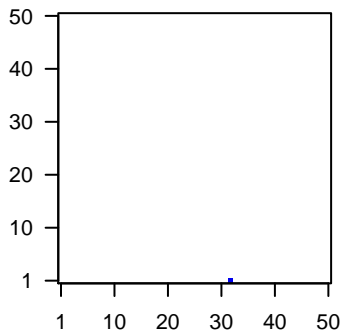
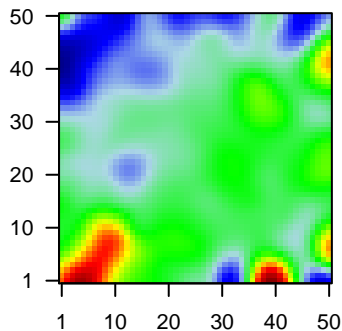
<shrinkage-t> = -11.99

<p-value> = 0

<fdr> = 0.48

Profile

Spot



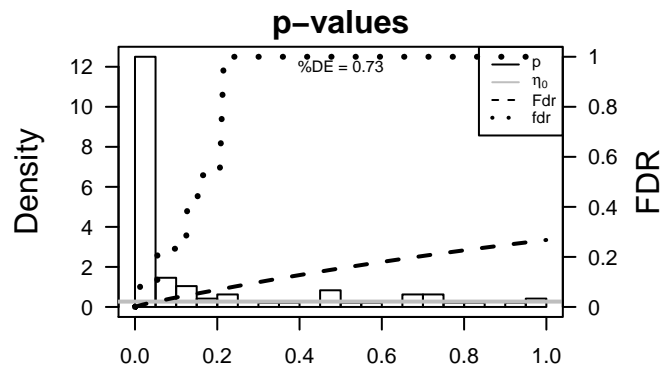
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3627	-1.48	5e-15	3e-10	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:1037]
2	629	1.28	1e-11	1e-07	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
3	10561	-1.11	5e-09	1e-07	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16899]
4	2633	-1.09	8e-09	3e-07	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:1037]
5	27074	-1.06	2e-08	5e-07	32 x 1 lysosomal-associated membrane protein 3 [Source:HGNC Symbol;Acc:1037]
6	8743	-1.04	4e-08	8e-07	32 x 1 tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:1037]
7	10964	-1.02	7e-08	1e-06	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Acc:1037]
8	115362	-0.99	1e-07	1e-06	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:19899]
9	3433	-0.99	2e-07	4e-05	32 x 1 interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:1037]
10	64761	0.9	2e-06	4e-05	32 x 1 poly (ADP-ribose) polymerase family, member 12 [Source:HGNC Symbol;Acc:1037]
11	64135	-0.85	7e-06	4e-05	32 x 1 interferon induced with helicase C domain 1 [Source:HGNC Symbol;Acc:1037]
12	8519	0.85	7e-06	4e-05	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC Symbol;Acc:1037]
13	9560	-0.84	8e-06	4e-05	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:1037]
14	5551	0.83	1e-05	4e-05	32 x 1 perforin 1 (pore forming protein) [Source:HGNC Symbol;Acc:1037]
15	834	-0.83	1e-05	1e-04	32 x 1 caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1037]
16	388372	-0.81	2e-05	1e-04	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:1037]
17	2537	-0.8	2e-05	1e-04	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:1037]
18	4599	-0.73	3e-05	1e-04	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible [Source:HGNC Symbol;Acc:1037]
19	55601	-0.79	3e-05	1e-04	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC Symbol;Acc:1037]
20	4600	-0.79	3e-05	1e-04	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HGNC Symbol;Acc:1037]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-63.6	NULL	12 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
2	-41.92	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
3	-34.1	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
4	-32.06	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
5	-31.18	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
6	-28.68	NULL	10 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	-28.65	NULL	3 / 4	MMML C2SCIEJ_MMML_47
8	-28.13	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
9	-26.37	NULL	28 / 51	BP type I interferon signaling pathway
10	-26.16	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
11	-25.06	NULL	30 / 123	BP defense response to virus
12	-24.88	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
13	-24.57	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
14	-23.56	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
15	-23.33	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_1
16	-23.14	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
17	-22.88	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
18	-22.3	NULL	26 / 109	BP response to virus
19	-22.17	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
20	-22.07	NULL	45 / 572	Disease GUDJ_poriasis up
21	-21.25	NULL	4 / 14	GSEA C2SANA_TNF_SIGNALING_UP
22	-19.28	NULL	4 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_UP
23	-19.27	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
24	-18.88	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
25	-18.31	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
26	-18.31	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
27	-17.15	NULL	33 / 204	BP cytokine-mediated signaling pathway
28	-16.95	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
29	-16.65	NULL	3 / 15	GSEA C2JIANG_SILENCED_BY_METHYLATION_2
30	-16.5	NULL	10 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
31	-16.11	NULL	30 / 274	Lymphoma SPANG_IL21 DN
32	-15.83	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
33	-15.6	NULL	2 / 10	BP positive regulation of cAMP-mediated signaling
34	-15.58	NULL	3 / 5	GSEA C2BROWNE_INTERFERON_RESPONSIVE_GENES
35	-15.24	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
36	-15.08	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
37	-14.65	NULL	2 / 12	GSEA C2KONUMA_COLON_CANCER_MSI_DN
38	-14.34	NULL	3 / 16	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
39	-14.05	NULL	2 / 12	BP positive regulation of leukocyte chemotaxis
40	-13.71	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP



GW_004

Local Summary

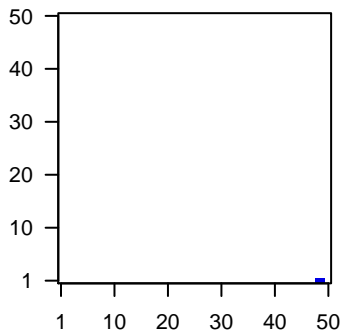
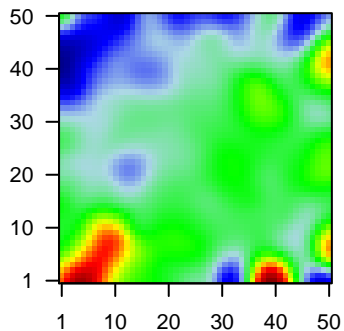
%DE = 0.76
 # metagenes = 2
 # genes = 70
 # genes in genesets = 69
 # genes with $fdr < 0.1 = 48$ (2 + / 46 -)
 # genes with $fdr < 0.05 = 41$ (1 + / 40 -)
 # genes with $fdr < 0.01 = 27$ (1 + / 26 -)

<r> metagenes = 1
 <r> genes = 0.68

<FC> = -0.42
 <shrinkage-t> = -14.59
 <p-value> = 0
 <fdr> = 0.46

Profile

Spot



Local Genelist

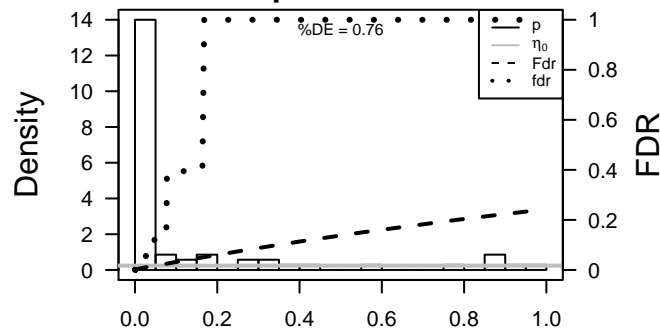
Rank	ID	log(FC)	fdr	p-value	Description
1	54855	1.44	2e-14	3e-07	49 x 1 family with sequence similarity 46, member C [Source:HGNC
2	930	-1.06	2e-08	6e-07	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
3	4283	-1.02	6e-08	6e-07	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:
4	57172	-1.01	9e-08	1e-06	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
5	255231	-0.98	2e-07	1e-06	49 x 1 mucolin 2 [Source:HGNC Symbol;Acc:13357]
6	3003	-0.97	2e-07	1e-05	49 x 1 granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol
7	6352	-0.93	9e-07	8e-05	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
8	11040	-0.84	8e-06	8e-05	49 x 1 pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
9	3669	-0.81	2e-05	8e-05	48 x 1 interferon stimulated exonuclease gene 20kDa [Source:HGNC
10	51755	-0.8	2e-05	8e-05	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	84824	-0.8	2e-05	8e-05	49 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:18504]
12	3112	-0.79	3e-05	2e-04	48 x 1 major histocompatibility complex, class II, DO beta [Source:H
13	3702	-0.78	4e-05	6e-04	49 x 1 IL2-inducible T-cell kinase [Source:HGNC Symbol;Acc:6171
14	5790	-0.75	8e-05	6e-04	49 x 1 protein tyrosine phosphatase, receptor type, C-associated pr
15	29851	-0.73	1e-04	9e-04	48 x 1 inducible T-cell co-stimulator [Source:HGNC Symbol;Acc:53
16	23048	-0.71	2e-04	3e-03	49 x 1 formin binding protein 1 [Source:HGNC Symbol;Acc:17069]
17	91353	-0.66	5e-04	3e-03	48 x 1
18	939	-0.65	6e-04	3e-03	49 x 1 CD27 molecule [Source:HGNC Symbol;Acc:11922]
19	5450	-0.64	6e-04	5e-03	48 x 1 POU class 2 associating factor 1 [Source:HGNC Symbol;Acc:
20	3001	-0.61	1e-03	5e-03	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associat

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-22.58	NULL	5 / 13	Cancer GENTLES_modul18
2	-22.02	NULL	3 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
3	-21.9	NULL	35 / 417	H.Tiss WIRTH_Immune system
4	-21.63	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	-17.92	NULL	1 / 2	GSEA C2SUTIERREZ_MULTIPLE_MYELOMA_UP
6	-17.44	NULL	4 / 14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
7	-16.51	NULL	1 / 4	GSEA C2ROETH_TERT_TARGETS_DN
8	-16.08	NULL	5 / 45	BP cellular defense response
9	-16.03	NULL	2 / 10	GSEA C2SIG_BCR_SIGNALING_PATHWAY
10	-16	NULL	4 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
11	-15.99	NULL	30 / 553	Cancer Lembcke_Colonc Inflammation
12	-14.96	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
13	-13.99	NULL	11 / 162	CC external side of plasma membrane
14	-13.41	NULL	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
15	-13.27	NULL	3 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
16	-12.33	NULL	3 / 15	GSEA C2HAHTOLA_SEZARY_SYNDROM_DN
17	-12.14	NULL	3 / 16	GSEA C2SU_THYMUS
18	-12.11	NULL	1 / 6	GSEA C2RAY_ALZHEIMERS_DISEASE
19	-11.72	NULL	2 / 12	GSEA C2BIOCARTA_CTLA4_PATHWAY
20	-11.26	NULL	3 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
21	-10.74	NULL	3 / 13	GSEA C2HAHTOLA_CTL_PATHOGENESIS
22	-10.57	NULL	4 / 28	BP B cell receptor signaling pathway
23	-10.49	NULL	3 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
24	-10.49	NULL	1 / 6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
25	-10.3	NULL	2 / 15	GSEA C2ST_T_CELL_SIGNAL_TRANSDUCTION
26	-10.22	NULL	1 / 10	GSEA C2KIM_MYCL1_AMPLIFICATION_TARGETS_UP
27	-10.22	NULL	1 / 10	GSEA C2SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES
28	-10.04	NULL	1 / 7	GSEA C2IZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN
29	-9.96	NULL	2 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
30	-9.93	NULL	3 / 43	MF chemokine activity
31	-9.85	NULL	1 / 10	BP positive regulation of cAMP-mediated signaling
32	-9.85	NULL	1 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
33	-9.61	NULL	2 / 10	MF small GTPase binding
34	-9.59	NULL	2 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
35	-9.56	NULL	10 / 204	BP cell surface receptor signaling pathway
36	-9.2	NULL	2 / 12	GSEA C2MCCABE_HOXC6_TARGETS_CANCER_UP
37	-9.18	NULL	1 / 12	GSEA C2KLEIN_TARGETS_OF_BCR_ABL1_FUSION
38	-9.18	NULL	1 / 11	GSEA C2BIOCARTA_CACAM_PATHWAY
39	-9.15	NULL	14 / 312	BP immune response
40	-8.89	NULL	1 / 10	BP negative regulation of G-protein coupled receptor protein signaling

p-values



GW_004

Local Summary

%DE = 0.64
 # metagenes = 57
 # genes = 568
 # genes in genesets = 558

genes with $fdr < 0.1$ = 213 (47 + / 166 -)
 # genes with $fdr < 0.05$ = 165 (39 + / 126 -)
 # genes with $fdr < 0.01$ = 102 (25 + / 77 -)

<r> metagenes = 0.9

<r> genes = 0.28

<FC> = -0.22

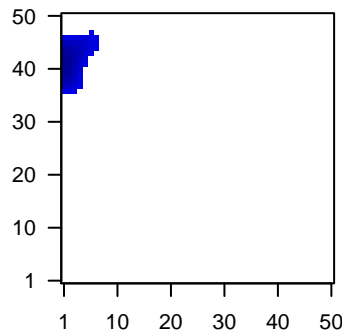
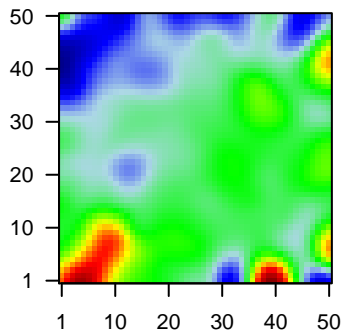
<shrinkage-t> = -7.54

<p-value> = 0.01

<fdr> = 0.66

Profile

Spot



Local Genelist

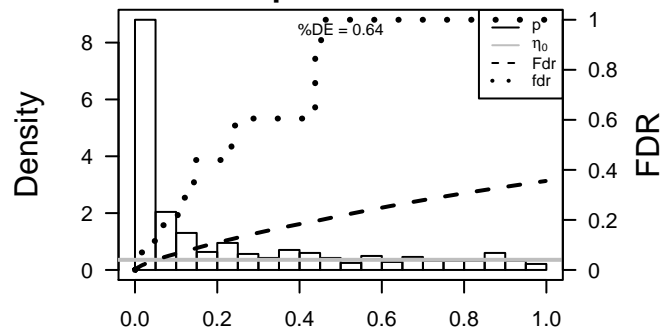
Rank	ID	log(FC)	fdr	p-value	Description
1	220	1.67	2e-16	7e-15	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
2	147495	2.48	2e-16	7e-15	2 x 44 adenomatosis polyposis coli down-regulated 1 [Source:HGNC
3	2731	1.81	2e-16	7e-15	1 x 38 glycine dehydrogenase (decarboxylating) [Source:HGNC Syn
4	118430	1.75	2e-16	7e-15	2 x 44 mucin-like 1 [Source:HGNC Symbol;Acc:30588]
5	4753	1.95	2e-16	7e-15	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
6	5947	2.61	2e-16	7e-15	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
7	55214	-1.51	1e-15	9e-13	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
8	8140	1.47	6e-15	1e-12	1 x 43 solute carrier family 7 (amino acid transporter light chain, L s
9	84632	1.45	2e-14	1e-12	1 x 41 actin filament associated protein 1-like 2 [Source:HGNC Syrr
10	3552	-1.45	2e-14	2e-12	1 x 43 interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
11	5317	-1.44	3e-14	2e-11	1 x 46 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
12	388585	1.39	2e-13	2e-11	3 x 46 hes family bHLH transcription factor 5 [Source:HGNC Symbol
13	780854	-1.39	2e-13	4e-11	2 x 39 small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
14	6274	1.37	4e-13	5e-10	1 x 43 S100 calcium binding protein A3 [Source:HGNC Symbol;Acc:
15	1825	-1.32	3e-12	2e-09	1 x 45 desmocollin 3 [Source:HGNC Symbol;Acc:3037]
16	338382	-1.27	2e-11	2e-09	1 x 40
17	387882	-1.26	3e-11	1e-08	2 x 41 chromosome 12 open reading frame 75 [Source:HGNC Symt
18	3775	-1.22	9e-11	1e-08	1 x 43 potassium channel, subfamily K, member 1 [Source:HGNC S
19	723790	-1.21	1e-10	1e-08	2 x 38 histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
20	64919	-1.2	2e-10	1e-08	7 x 44 B-cell CLL/lymphoma 11B (zinc finger protein) [Source:HGNI

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.97	NULL	8 / 21	CC desmosome
2	-10.56	NULL	29 / 135	H.Tiss WIRTH_Mucosa
3	-9.97	NULL	4 / 7	MMML C63CIEJ_MMML 9
4	-9.21	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	-7.79	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
6	-7.4	NULL	3 / 10	GSEA C2NIELSEN_MALIGNANT_FIBROUS_HISTIOCYTOMA_UP
7	-7.26	NULL	1 / 2	MMML C63CIEJ_MMML 43
8	-7.13	NULL	1 / 2	miRNA target-346
9	-7.11	NULL	3 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
10	-7.08	NULL	2 / 2	miRNA target-199a*
11	-6.35	NULL	10 / 44	BP skin development
12	-6.29	NULL	4 / 21	BP filopodium assembly
13	-6.22	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
14	-6.04	NULL	4 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
15	-5.98	NULL	1 / 3	GSEA C2VICENT_METASTASIS_DN
16	-5.89	NULL	3 / 14	GSEA C2REACTOME_GENES_INVOLVED_IN_APOPTOTIC_CLEAVAGE_E
17	-5.89	NULL	2 / 13	GSEA C2REACTOME_PACKAGING_OF_TELOMERE_ENDS
18	-5.86	NULL	10 / 86	Lymphoma ROSOLOWSKI_green UP
19	-5.78	NULL	3 / 13	GSEA C2COLLER_MYC_TARGETS_UP
20	-5.76	NULL	2 / 12	MF fatty acid binding
21	-5.73	NULL	3 / 15	BP positive regulation vascular endothelial growth factor production
22	-5.67	NULL	3 / 15	GSEA C2REACTOME_APOPTOTIC_EXECUTION_PHASE
23	-5.61	NULL	3 / 10	GSEA C2XU_RESPONSE_TO_TRETINOIN_DN
24	-5.46	NULL	3 / 11	MMML C63CIEJ_MMML 3
25	-5.4	NULL	2 / 14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G4
26	-5.39	NULL	5 / 12	BP hemidesmosome assembly
27	-5.38	NULL	101 / 572	Disease GUDJ_psooriasis up
28	-5.32	NULL	2 / 13	H.Tiss WIRTH_Tonsil
29	-5.29	NULL	7 / 47	CC nucleosome
30	-5.18	NULL	1 / 5	miRNA target-196a
31	-5.16	NULL	4 / 12	BP keratinocyte proliferation
32	-5.15	NULL	3 / 9	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP
33	-5.1	NULL	5 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
34	-5.06	NULL	1 / 5	GSEA C2ELVIDGE_HIF2A_TARGETS_UP
35	-5.05	NULL	2 / 15	MF cytoskeletal adaptor activity
36	-5.01	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_120_MCF10A
37	-4.96	NULL	3 / 13	GSEA C2CHIBA_RESPONSE_TO_TSA_UP
38	-4.95	NULL	2 / 14	MF actin monomer binding
39	-4.92	NULL	2 / 15	GSEA C2WANG_RECURRENT_LIVER_CANCER_DN
40	-4.86	NULL	6 / 32	CC cell-cell adherens junction

p-values



GW_004

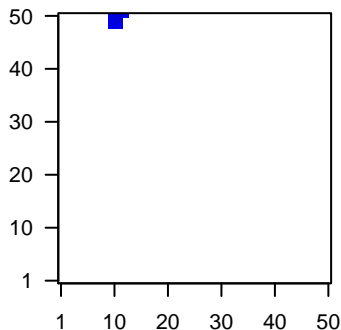
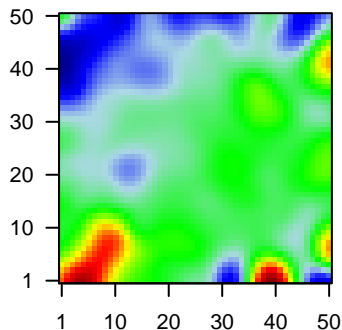
Local Summary

%DE = 0.61
 # metagenes = 10
 # genes = 121
 # genes in genesets = 121
 # genes with $fdr < 0.1$ = 48 (8 + / 40 -)
 # genes with $fdr < 0.05$ = 48 (8 + / 40 -)
 # genes with $fdr < 0.01$ = 19 (2 + / 17 -)

$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.29
 $\langle FC \rangle = -0.27$
 $\langle \text{shrinkage-t} \rangle = -9.61$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.61$

Profile

Spot



Local Genelist

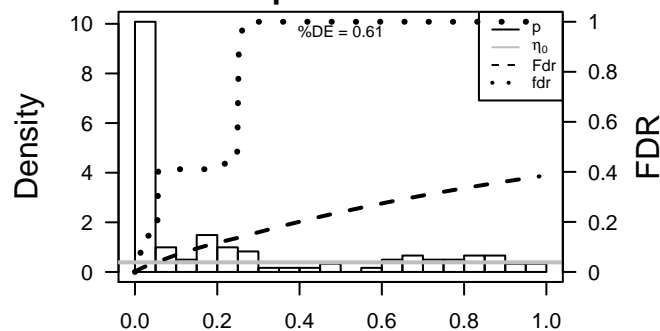
Rank	ID	log(FC)	fdr	p-value	Description
1	10457	-2	2e-16	1e-14	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
2	85236	-1.12	3e-09	2e-07	histone cluster 1, H2bk [Source:HGNC Symbol;Acc:13954]
3	8626	-1.09	8e-09	8e-06	tumor protein p63 [Source:HGNC Symbol;Acc:15979]
4	79850	-0.99	2e-07	8e-05	family with sequence similarity 57, member A [Source:HGNC
5	3280	-0.9	2e-06	1e-03	hes family bHLH transcription factor 1 [Source:HGNC Symbol
6	57609	-0.77	5e-05	1e-03	DIP2 disco-interacting protein 2 homolog B (Drosophila) [So
7	55605	-0.74	8e-05	1e-03	kinesin family member 21A [Source:HGNC Symbol;Acc:1934
8	53637	-0.74	9e-05	1e-03	sphingosine-1-phosphate receptor 5 [Source:HGNC Symbol
9	5349	-0.72	1e-04	1e-03	FX1D domain containing ion transport regulator 3 [Source:HC
10	2049	-0.72	1e-04	1e-03	EPH receptor B3 [Source:HGNC Symbol;Acc:3394]
11	9121	0.71	2e-04	3e-03	solute carrier family 16 (monocarboxylate transporter), memb
12	2950	-0.63	2e-04	3e-03	glutathione S-transferase pi 1 [Source:HGNC Symbol;Acc:46
13	4071	-0.61	4e-04	3e-03	transmembrane 4 L six family member 1 [Source:HGNC Sym
14	144402	-0.66	4e-04	3e-03	copine VIII [Source:HGNC Symbol;Acc:23498]
15	481	0.66	5e-04	3e-03	ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:HG
16	7086	-0.65	5e-04	3e-03	transketolase [Source:HGNC Symbol;Acc:11834]
17	10610	-0.65	5e-04	7e-03	ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-
18	6840	-0.63	9e-04	7e-03	supervillin [Source:HGNC Symbol;Acc:11480]
19	57834	-0.63	9e-04	7e-03	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
20	6319	0.62	1e-03	1e-02	stearoyl-CoA desaturase (delta-9-desaturase) [Source:HGNC

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-18.37	NULL	2 / 8	TF Tissue/AQUERIZAS_Tongue
2	-16.3	NULL	1 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
3	-15.47	NULL	1 / 11	GSEA C2TO_PTTG1_TARGETS_UP
4	-14.12	NULL	1 / 13	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
5	-14.08	NULL	2 / 13	TF Tissue/AQUERIZAS_Skin
6	-13.77	NULL	2 / 15	GSEA C2KANG_FLUOROURACIL_RESISTANCE_UP
7	-12.24	NULL	2 / 9	Glio Colman_survival_robust
8	-11.79	NULL	2 / 18	BP positive regulation of Notch signaling pathway
9	-11.1	NULL	1 / 7	MMML C2SCIEJ_MMML_9
10	-11.1	NULL	1 / 7	GSEA C2DAVIES_MULTIPLE_TARGETS_MYELOMA_VS_MGUS_UP
11	-10	NULL	2 / 10	H.Tiss WIRTH_B-cells
12	-9.65	NULL	1 / 9	GSEA C2DORN_ADENOVIRUS_INFECTION_32HR_UP
13	-9.47	NULL	3 / 12	GSEA C2DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
14	-9.15	NULL	2 / 12	GSEA C2TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
15	-9.15	NULL	2 / 12	GSEA C2L_LUNG_CANCER
16	-9.11	NULL	1 / 29	BP bone mineralization
17	-9.1	NULL	1 / 10	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
18	-9.1	NULL	1 / 10	GSEA C2REACTOME_RNA_POLYMERASE_L_PROMOTER_OPENING
19	-8.84	NULL	3 / 14	GSEA C2AIYAR_COBRA1_TARGETS_DN
20	-8.63	NULL	1 / 11	GSEA C2BOYALTI_LIVER_CANCER_SUBCLASS_G56_UP
21	-8.55	NULL	2 / 13	BP smooth muscle tissue development
22	-8.26	NULL	2 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
23	-8.23	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
24	-8.22	NULL	1 / 12	GSEA C2DORN_ADENOVIRUS_INFECTION_48HR_UP
25	-8.2	NULL	1 / 5	GSEA C2OHM_EMBRYONIC_CARCINOMA_UP
26	-7.97	NULL	1 / 12	BP keratinocyte proliferation
27	-7.97	NULL	1 / 12	GSEA C2HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_DN
28	-7.86	NULL	1 / 13	Pathw AcGUSTAFSON_PI3K_UP
29	-7.86	NULL	1 / 13	GSEA C2REACTOME_PACKAGING_OF_TELOMERE_ENDS
30	-7.8	NULL	2 / 16	GSEA C2KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP
31	-7.8	NULL	2 / 16	GSEA C2KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_UP
32	-7.8	NULL	2 / 16	GSEA C2ZHANG_PROLIFERATING_VS_QUIESCENT
33	-7.67	NULL	2 / 16	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
34	-7.62	NULL	1 / 13	BP DNA damage response, signal transduction by p53 class mediator
35	-7.31	NULL	1 / 14	BP multicellular organismal aging
36	-7.26	NULL	1 / 10	BP auditory receptor cell differentiation
37	-7.15	NULL	4 / 88	CC melanosome
38	-7.04	NULL	1 / 15	GSEA C2HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN
39	-7	NULL	1 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_UP
40	-7	NULL	1 / 16	GSEA C2ZHUNG_BLISTER_CYTOTOXICITY_DN

p-values



GW_004

Local Summary

%DE = 0.66
 # metagenes = 1
 # genes = 12
 # genes in genesets = 12
 # genes with $fdr < 0.1 = 6$ (0 + / 6 -)
 # genes with $fdr < 0.05 = 6$ (0 + / 6 -)
 # genes with $fdr < 0.01 = 1$ (0 + / 1 -)

<r> metagenes = NA

<r> genes = 0.52

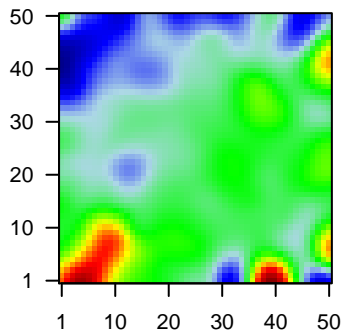
<FC> = -0.3

<shrinkage-t> = -10.6

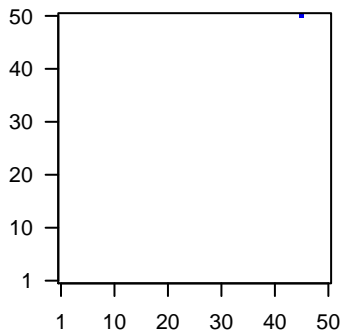
<p-value> = 0.02

<fdr> = 0.58

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3428	-0.94	6e-07	7e-04	45 x 50 interferon, gamma-inducible protein 16 [Source:HGNC Symb
2	56945	-0.71	2e-04	1e-02	45 x 50 mitochondrial ribosomal protein S22 [Source:HGNC Symbol;]
3	8833	-0.55	3e-03	3e-02	45 x 50 guanine monophosphate synthase [Source:HGNC Symbol;Acc
4	10728	-0.48	1e-02	3e-02	45 x 50 prostaglandin E synthase 3 (cytosolic) [Source:HGNC Symbc
5	63979	-0.43	2e-02	3e-02	45 x 50 fidgetin-like 1 [Source:HGNC Symbol;Acc:13286]
6	144455	-0.4	3e-02	3e-02	45 x 50 E2F transcription factor 7 [Source:HGNC Symbol;Acc:23820]
7	3992	0.39	4e-02	6e-01	45 x 50 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
8	83540	-0.16	4e-01	6e-01	45 x 50 NUF2, NDC80 kinetochore complex component [Source:HG
9	10635	-0.15	4e-01	6e-01	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169]
10	23350	-0.14	5e-01	1e+00	45 x 50 U2 snRNP-associated SURP domain containing [Source:HG
11	1894	-0.06	7e-01	1e+00	45 x 50 epithelial cell transforming sequence 2 oncogene [Source:HG
12	23204	-0.01	9e-01	1e+00	45 x 50 ADP-ribosylation factor-like 6 interacting protein 1 [Source:H

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-37.17	NULL	1 / 7	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G5_DN
2	-30.21	NULL	1 / 10	GSEA C2SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN
3	-30.21	NULL	1 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	-28.43	NULL	4 / 26	BP cellular response to ionizing radiation
5	-28.42	NULL	1 / 11	BP activation of innate immune response
6	-25.58	NULL	1 / 13	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
7	-25.58	NULL	1 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
8	-24.44	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
9	-24.44	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
10	-23.43	NULL	1 / 15	GSEA C2FRIDMAN_IMMORTALIZATION_DN
11	-23.43	NULL	1 / 15	GSEA C2GILDEA_METASTASIS
12	-22.75	NULL	1 / 10	GSEA C2TOMIDA_METASTASIS_UP
13	-22.75	NULL	1 / 10	GSEA C2STEIN_ESRRA_TARGETS
14	-22.53	NULL	1 / 16	BP monocyte differentiation
15	-22.53	NULL	1 / 16	GSEA C2DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN
16	-22.53	NULL	1 / 16	GSEA C2MOSELERLE_IFNA_RESPONSE
17	-22.53	NULL	1 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
18	-21.72	NULL	1 / 17	BP cellular response to glucose starvation
19	-21.72	NULL	1 / 17	BP regulation of autophagy
20	-19.27	NULL	1 / 13	GSEA C2ALONSO_METASTASIS_UP
21	-19.15	NULL	1 / 21	BP positive regulation of cytokine production
22	-19.15	NULL	1 / 21	TF Tissue/AQUERIZAS_Tonsil
23	-18.71	NULL	1 / 5	Glio Phillips Prolif up vs PN & MES
24	-18.64	NULL	1 / 22	BP myeloid cell differentiation
25	-18.4	NULL	1 / 14	GSEA C2HOLLMAN_APOPTOSIS_VIA_CD40_UP
26	-18.4	NULL	1 / 14	GSEA C2STEIN_ESRRA_TARGETS_UP
27	-18.16	NULL	1 / 23	BP intrinsic apoptotic signaling pathway by p53 class mediator
28	-17.64	NULL	1 / 15	GSEA C2MULLIGHAN_MLL_SIGNATURE_1_DN
29	-17.64	NULL	1 / 15	GSEA C2TIEN_INTESTINE_PROBIOTICS_24HR_UP
30	-16.96	NULL	1 / 16	GSEA C2MULLIGHAN_MLL_SIGNATURE_2_DN
31	-16.96	NULL	1 / 16	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
32	-16.96	NULL	1 / 16	GSEA C2MOOTHA_MITOCHONDRIA
33	-16.64	NULL	1 / 11	GSEA C2REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE
34	-16.54	NULL	1 / 27	BP negative regulation of DNA binding
35	-16.46	NULL	2 / 12	BP regulation of double-strand break repair via homologous recomb
36	-15.88	NULL	1 / 29	BP intrinsic apoptotic signaling pathway in response to DNA damage b
37	-15.88	NULL	1 / 29	TF Tissue/AQUERIZAS_Smooth muscle
38	-15.88	NULL	1 / 29	TF Tissue/AQUERIZAS_Lymph node
39	-15.57	NULL	1 / 30	TF Tissue/AQUERIZAS_Fetal lung
40	-15.32	NULL	1 / 10	GSEA C2REACTOME_PROSTANOID_HORMONES

p-values

