

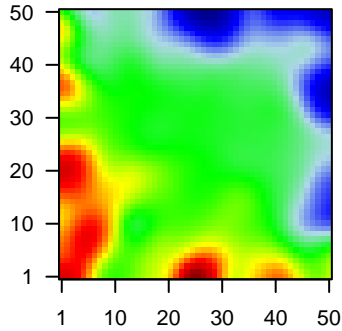
GW_197

Global Summary

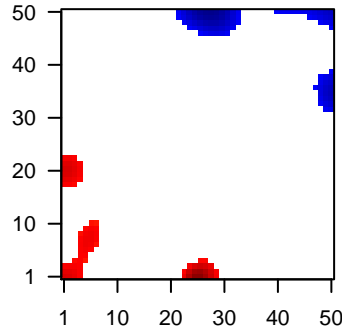
%DE = 0.17
 # genes with $fdr < 0.2$ = 1946 (1055 + / 891 -)
 # genes with $fdr < 0.1$ = 1357 (774 + / 583 -)
 # genes with $fdr < 0.05$ = 1087 (631 + / 456 -)
 # genes with $fdr < 0.01$ = 607 (389 + / 218 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.83

Profile



Regulated Spots



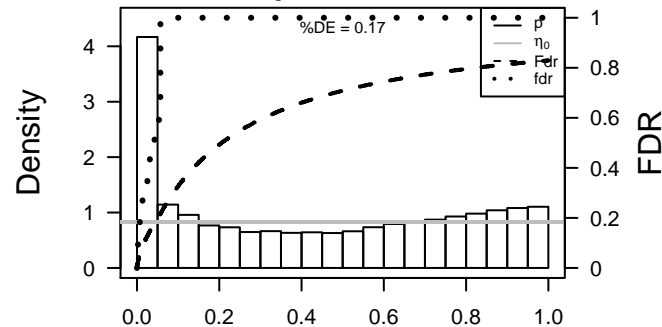
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description	Metagene
1	58	3.96	2e-16	7e-14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.02	2e-16	7e-14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	-2.25	2e-16	7e-14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	218	-2.85	2e-16	7e-14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	242	2.56	2e-16	7e-14	1 x 48	arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
6	151516	2.09	2e-16	7e-14	1 x 46	aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
7	51806	2.12	2e-16	7e-14	4 x 50	calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
8	6366	2.45	2e-16	7e-14	50 x 2	chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
9	1158	2.83	2e-16	7e-14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
10	22802	-2.41	2e-16	7e-14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	54544	2.33	2e-16	7e-14	1 x 50	cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
12	49860	-2.51	2e-16	7e-14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
13	2318	2.08	2e-16	7e-14	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
14	10457	-2.32	2e-16	7e-14	13 x 50	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
15	283120	2.82	2e-16	7e-14	25 x 1	H19, imprinted maternally expressed transcript (non-protein
16	3039	2.82	2e-16	7e-14	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
17	3040	2.66	2e-16	7e-14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
18	3043	2.2	2e-16	7e-14	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
19	3123	2.58	2e-16	7e-14	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
20	3127	2.46	2e-16	7e-14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.69	NULL	36	BP muscle filament sliding
2	13.37	NULL	127	H.Tiss WIRTH_Muscle
3	13.09	NULL	1135	Chr Chr 19
4	11.9	NULL	16	GSEA CRICKMAN_HEAD_AND_NECK_CANCER_F
5	11.66	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
6	11.66	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
7	11.66	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
8	11.66	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
9	11.17	NULL	16	H.Tiss WIRTH_Hippocampus
10	11.02	NULL	21	CC cornified envelope
11	10.91	NULL	42	BP keratinization
12	10.36	NULL	44	MF structural constituent of muscle
13	10.25	NULL	1182	CC extracellular region
14	9.69	NULL	553	Cancer Lembecke_Colonc Inflammation
15	9.52	NULL	84	BP muscle contraction
16	9.28	NULL	683	CC extracellular space
17	8.98	NULL	12	CC myosin filament
18	8.92	NULL	717	Chr Chr 16
19	8.21	NULL	190	CC extracellular matrix
20	8	NULL	76	BP epidermis development
<i>Underexpressed</i>				
1	-11.06	NULL	436	miRNA target starB39a
2	-10.33	NULL	318	miRNA target starB59-3p
3	-10.18	NULL	293	miRNA target starB186
4	-10.16	NULL	618	Chr Chr 4
5	-10.12	NULL	269	miRNA target starB124
6	-10.06	NULL	368	miRNA target starB191
7	-9.72	NULL	463	miRNA target starB39a
8	-9.71	NULL	134	miRNA target starB56
9	-9.65	NULL	534	Chr Chr 8
10	-9.6	NULL	310	miRNA target starB39a
11	-9.59	NULL	315	miRNA target starB39a
12	-9.51	NULL	494	miRNA target starB197
13	-9.36	NULL	495	miRNA target starB183
14	-9.18	NULL	234	miRNA target starB29a
15	-9.04	NULL	456	miRNA target starB190a
16	-9.03	NULL	300	miRNA target starB56
17	-8.98	NULL	449	miRNA target starB190b
18	-8.92	NULL	300	miRNA target starB59c-3p
19	-8.85	NULL	242	miRNA target starB28b
20	-8.85	NULL	171	miRNA target starB59-3p

p-values



GW_197

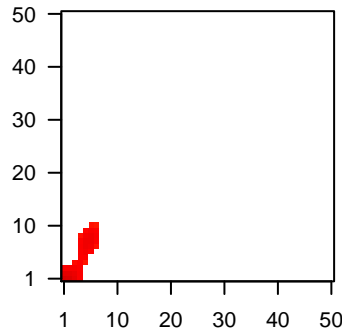
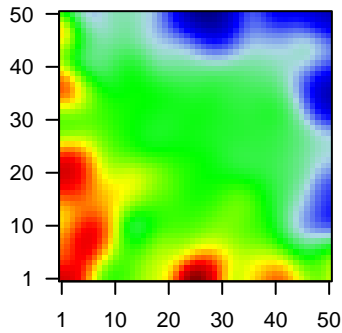
Local Summary

%DE = 0.72
 # metagenes = 37
 # genes = 406
 # genes in genesets = 404
 # genes with $fdr < 0.1$ = 214 (200 + / 14 -)
 # genes with $fdr < 0.05$ = 174 (164 + / 10 -)
 # genes with $fdr < 0.01$ = 112 (107 + / 5 -)

$\langle r \rangle$ metagenes = 0.78
 $\langle r \rangle$ genes = 0.27
 $\langle FC \rangle$ = 0.51
 $\langle \text{shrinkage-t} \rangle$ = 17.9
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.51

Profile

Spot



Local Genelist

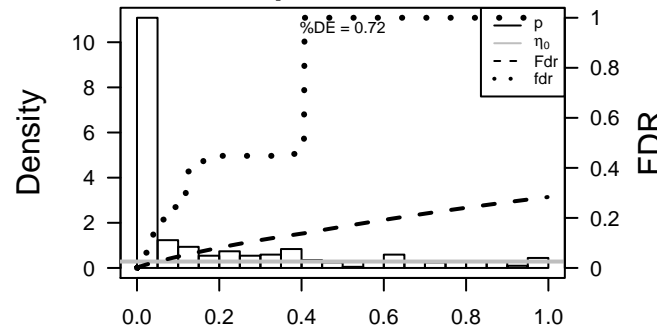
Rank	ID	log(FC)	fdr	p-value	Description
1	3040	2.66	2e-16	5e-15	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	3553	2.07	2e-16	5e-15	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
3	4312	2.35	2e-16	5e-15	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:H
4	4837	2.07	2e-16	5e-15	3 x 1 nicotinamide N-methyltransferase [Source:HGNC Symbol;Ac
5	60675	2.15	2e-16	5e-15	1 x 1 prokineticin 2 [Source:HGNC Symbol;Acc:18455]
6	4314	1.97	2e-15	5e-12	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
7	7169	1.87	5e-14	5e-12	3 x 1 tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
8	871	1.85	8e-14	7e-12	1 x 1 serpin peptidase inhibitor, clade H (heat shock protein 47), m
9	366	1.84	1e-13	1e-09	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
10	50486	1.7	9e-12	9e-09	5 x 4 G0/G1switch 2 [Source:HGNC Symbol;Acc:30229]
11	1291	1.6	1e-10	9e-09	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
12	1277	1.58	2e-10	9e-09	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
13	1441	1.56	3e-10	9e-09	5 x 4 colony stimulating factor 3 receptor (granulocyte) [Source:HG
14	51312	1.56	3e-10	9e-09	5 x 7 solute carrier family 25 (mitochondrial iron transporter), memt
15	8291	1.55	4e-10	2e-08	4 x 2 dysferlin [Source:HGNC Symbol;Acc:3097]
16	80781	1.54	5e-10	2e-08	3 x 1 collagen, type XVIII, alpha 1 [Source:HGNC Symbol;Acc:219
17	1284	1.53	8e-10	2e-08	2 x 1 collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:2203]
18	199675	1.52	9e-10	4e-08	5 x 4 chromosome 19 open reading frame 59 [Source:HGNC Synt
19	4502	1.5	1e-09	4e-08	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
20	6556	1.49	2e-09	4e-08	4 x 3 solute carrier family 11 (proton-coupled divalent metal ion tra

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	19.97	NULL	8 / 11	MF platelet-derived growth factor binding
2	18.96	NULL	32 / 69	BP extracellular matrix disassembly
3	18.68	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
4	17.85	NULL	62 / 242	BP extracellular matrix organization
5	17.36	NULL	59 / 190	CC extracellular matrix
6	17.22	NULL	28 / 64	BP collagen catabolic process
7	16.58	NULL	6 / 11	Glio Phillips MES up vs Prolif & PN
8	15.96	NULL	43 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
9	15.96	NULL	43 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
10	15.96	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	15.96	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
12	15.67	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
13	15.36	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
14	15.07	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
15	14.79	NULL	5 / 10	BP protein heterotrimerization
16	14.49	NULL	14 / 16	MMML C6SCIEJ_MMML 1
17	13.5	NULL	64 / 250	LymphomaENZ_Stromal signature 1
18	13.5	NULL	6 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
19	13.28	NULL	4 / 11	GSEA C2BIOCARTA_PLATELETAPP_PATHWAY
20	13.1	NULL	12 / 35	Glio Colman_survival_associated
21	12.91	NULL	32 / 153	CC endoplasmic reticulum lumen
22	12.83	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
23	12.44	NULL	1 / 4	MMML C6SCIEJ_MMML 23
24	12.42	NULL	4 / 10	GSEA C2KEGG_FOCAL_ADHESION
25	12.28	NULL	2 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
26	12.25	NULL	6 / 15	GSEA C2INDGREN_BLADDER_CANCER_HIGH_RECURRENCE
27	12.24	NULL	3 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
28	12.23	NULL	2 / 6	GSEA C2BIOCARTA_IL5_PATHWAY
29	12.07	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
30	11.98	NULL	6 / 15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
31	11.84	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
32	11.79	NULL	67 / 553	Cancer Lembcke_Colonc Inflammation
33	11.72	NULL	4 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
34	11.65	NULL	15 / 37	BP collagen fibril organization
35	11.52	NULL	8 / 12	miRNA target-29c
36	11.39	NULL	2 / 5	GSEA C2DASU_IL6_SIGNALING_UP
37	11.03	NULL	4 / 12	GSEA C2BIOCARTA_ERYTH_PATHWAY
38	10.92	NULL	16 / 68	CC collagen
39	10.84	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
40	10.8	NULL	105 / 1182	CC extracellular region

p-values



GW_197

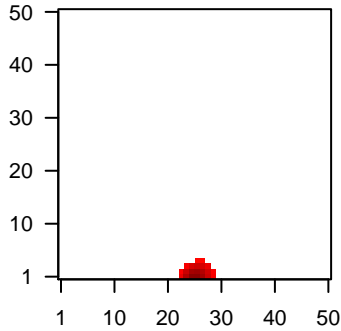
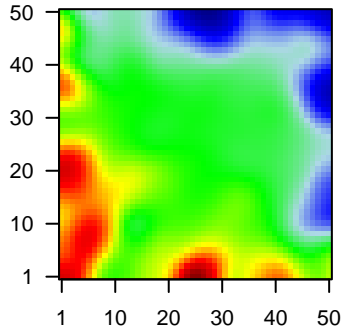
Local Summary

%DE = 0.93
 # metagenes = 21
 # genes = 137
 # genes in genesets = 137
 # genes with $fdr < 0.1 = 104$ (102 + / 2 -)
 # genes with $fdr < 0.05 = 99$ (97 + / 2 -)
 # genes with $fdr < 0.01 = 68$ (67 + / 1 -)

<r> metagenes = 0.89
 <r> genes = 0.46
 <FC> = 0.89
 <shrinkage-t> = 31.01
 <p-value> = 0
 <fdr> = 0.4

Profile

Spot



Local Genelist

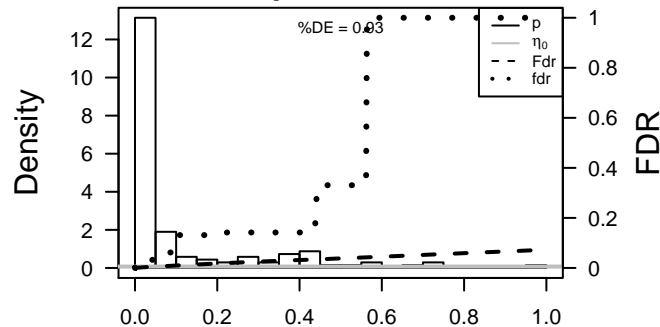
Rank	ID	log(FC)	fdr	p-value	Description
1	58	3.96	2e-16	2e-16	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.02	2e-16	2e-16	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1158	2.83	2e-16	2e-16	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	2318	2.08	2e-16	2e-16	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
5	283120	2.82	2e-16	2e-16	25 x 1 H19, imprinted maternally expressed transcript (non-protein c
6	4608	2.74	2e-16	2e-16	25 x 1 myosin binding protein H [Source:HGNC Symbol;Acc:7552]
7	4620	2.13	2e-16	2e-16	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
8	4625	2.24	2e-16	2e-16	25 x 1 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
9	4633	2.62	2e-16	2e-16	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
10	6588	3.53	2e-16	2e-16	25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]
11	8557	2.32	2e-16	2e-16	25 x 1 titin-cap [Source:HGNC Symbol;Acc:11610]
12	7060	2.52	2e-16	2e-16	25 x 1 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
13	7134	2.43	2e-16	2e-16	25 x 1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
14	7140	2.04	2e-16	2e-16	25 x 1 troponin T type 3 (skeletal, fast) [Source:HGNC Symbol;Acc:1
15	4151	1.97	2e-15	1e-12	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
16	4619	1.84	1e-13	5e-12	25 x 1 myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC
17	1674	1.79	6e-13	5e-10	25 x 1 desmin [Source:HGNC Symbol;Acc:2770]
18	27063	1.63	5e-11	3e-09	25 x 1 ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Syr
19	29895	1.56	3e-10	6e-09	25 x 1 myosin light chain, phosphorylatable, fast skeletal muscle [So
20	27129	1.52	1e-09	6e-09	25 x 1 heat shock 27kDa protein family, member 7 (cardiovascular) [

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	54.96	NULL	24 / 36	BP muscle filament sliding
2	52.38	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
3	48.95	NULL	59 / 127	H.Tiss WIRTH_Muscle
4	47.77	NULL	11 / 16	H.Tiss WIRTH_Hippocampus
5	39.88	NULL	10 / 12	CC myosin filament
6	35.87	NULL	22 / 44	MF structural constituent of muscle
7	29.37	NULL	8 / 13	CC muscle myosin complex
8	28.79	NULL	12 / 37	CC sarcomere
9	28.12	NULL	8 / 14	CC contractile fiber
10	25.28	NULL	16 / 34	CC myofibril
11	25.26	NULL	25 / 84	BP muscle contraction
12	23.9	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
13	23.06	NULL	6 / 12	BP skeletal muscle contraction
14	22.53	NULL	9 / 37	BP cardiac muscle contraction
15	21.97	NULL	9 / 20	CC I band
16	19.53	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
17	19.52	NULL	7 / 18	BP regulation of muscle contraction
18	19.11	NULL	3 / 15	Cancer BEN-PORATH_UP
19	18.7	NULL	2 / 10	BP heart contraction
20	18.18	NULL	7 / 12	MF titin binding
21	17.93	NULL	21 / 88	CC Z disc
22	16.53	NULL	8 / 42	CC myosin complex
23	16.14	NULL	3 / 12	BP muscle fiber development
24	15.73	NULL	5 / 26	BP ventricular cardiac muscle tissue morphogenesis
25	15.55	NULL	2 / 20	MF myosin binding
26	15.34	NULL	4 / 11	CC A band
27	15.16	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
28	15.09	NULL	4 / 16	MF microfilament motor activity
29	14.56	NULL	4 / 14	BP adult heart development
30	13.91	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_UP
31	13.91	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_DN
32	13.78	NULL	8 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
33	13.06	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
34	12.82	NULL	3 / 15	GSEA C2EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
35	12.68	NULL	8 / 16	CC M band
36	12.63	NULL	5 / 29	CC sarcoplasmic reticulum membrane
37	12.59	NULL	7 / 15	BP striated muscle contraction
38	12.5	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
39	12.5	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
40	12.34	NULL	7 / 21	BP sarcomere organization

p-values



GW_197

Local Summary

%DE = 0.67
 # metagenes = 22
 # genes = 249
 # genes in genesets = 244

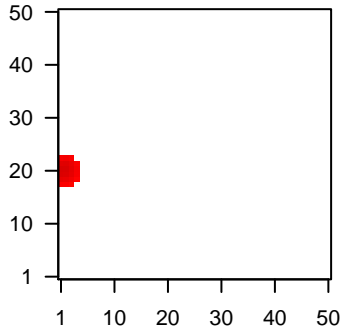
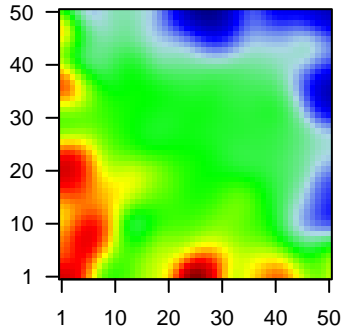
genes with $fdr < 0.1 = 135$ (132 + / 3 -)
 # genes with $fdr < 0.05 = 94$ (93 + / 1 -)
 # genes with $fdr < 0.01 = 56$ (56 + / 0 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.29

$\langle FC \rangle = 0.47$
 $\langle \text{shrinkage-t} \rangle = 16.53$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.54$

Profile

Spot



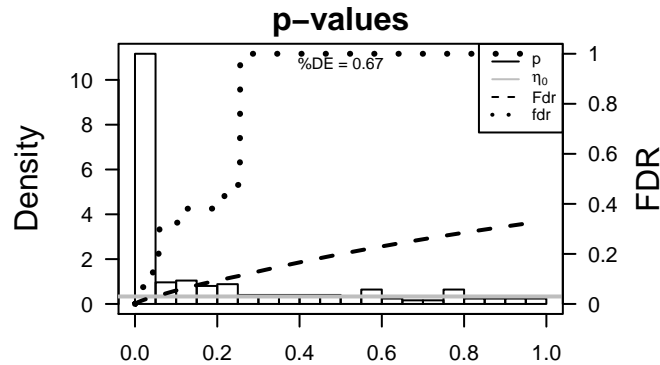
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	6884	1.41	1e-08	7e-05	1 x 22 TAF13 RNA polymerase II, TATA box binding protein (TBP)-a
2	118881	1.2	1e-06	7e-05	1 x 22 catechol-O-methyltransferase domain containing 1 [Source:HGNC]
3	1173	1.19	2e-06	8e-05	1 x 20 adaptor-related protein complex 2, mu 1 subunit [Source:HGNC]
4	51079	1.15	4e-06	8e-05	2 x 21 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 [Source:HGNC]
5	64975	1.14	4e-06	8e-05	3 x 21 mitochondrial ribosomal protein L41 [Source:HGNC Symbol;Acc:9491]
6	5652	1.13	6e-06	8e-05	1 x 22 protease, serine, 8 [Source:HGNC Symbol;Acc:9491]
7	8260	1.13	6e-06	2e-04	1 x 20 N(alpha)-acetyltransferase 10, NaaA catalytic subunit [Source:HGNC]
8	8045	1.1	9e-06	2e-04	2 x 22 Ras association (RalGDS/AF-6) domain family (N-terminal) 1 [Source:HGNC]
9	51042	1.1	1e-05	4e-04	1 x 19 zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
10	57407	1.07	2e-05	4e-04	1 x 20 NmrA-like family domain containing 1 [Source:HGNC Symbol;Acc:30943]
11	29763	1.05	2e-05	4e-04	1 x 20 protein kinase C and casein kinase substrate in neurons 3 [Source:HGNC]
12	84300	1.04	3e-05	4e-04	2 x 18 ubiquinol-cytochrome c reductase complex assembly factor 2 [Source:HGNC]
13	389541	1.04	3e-05	4e-04	3 x 19 late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [Source:HGNC]
14	5211	1.03	3e-05	4e-04	2 x 22 phosphofructokinase, liver [Source:HGNC Symbol;Acc:8876]
15	10273	1.02	4e-05	4e-04	3 x 22 STIP1 homology and U-box containing protein 1, E3 ubiquitin ligase [Source:HGNC]
16	25796	1.02	4e-05	7e-04	2 x 23 6-phosphogluconolactonase [Source:HGNC Symbol;Acc:8900]
17	375757	1.01	5e-05	2e-03	1 x 21 SWI5 recombination repair homolog (yeast) [Source:HGNC Symbol;Acc:30943]
18	8568	0.96	1e-04	2e-03	2 x 21 ribosomal RNA processing 1 [Source:HGNC Symbol;Acc:187]
19	112724	0.96	1e-04	2e-03	1 x 23 retinol dehydrogenase 13 (all-trans/9-cis) [Source:HGNC Symbol;Acc:187]
20	3028	0.94	1e-04	2e-03	3 x 21 hydroxysteroid (17-beta) dehydrogenase 10 [Source:HGNC Symbol;Acc:187]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	10.5	NULL	3 / 15	GSEA C2VANTVEER_BREAST_CANCER_BRCA1_UP
2	9.57	NULL	3 / 12	BP apoptotic nuclear changes
3	9.05	NULL	2 / 10	MF monosaccharide binding
4	8.71	NULL	3 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN
5	8.07	NULL	2 / 13	GSEA C2REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSE
6	7.98	NULL	3 / 10	MF NADH dehydrogenase activity
7	7.74	NULL	2 / 14	GSEA C2REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND
8	7.53	NULL	3 / 15	CC mitochondrial large ribosomal subunit
9	7.53	NULL	2 / 16	GSEA C2BIOCARTA_PTIDINS_PATHWAY
10	7.44	NULL	32 / 717	Chr Chr 16
11	7.37	NULL	3 / 16	GSEA C2MOOHTHA_FFA_OXYDATION
12	7.21	NULL	1 / 5	GSEA C2ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
13	7.19	NULL	2 / 15	GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY
14	7.07	NULL	2 / 9	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
15	7.02	NULL	3 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
16	6.98	NULL	2 / 10	GSEA C2REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS
17	6.93	NULL	3 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
18	6.84	NULL	2 / 10	H Tiss WIRTH_B-cells
19	6.78	NULL	64 / 1318	CC mitochondrion
20	6.76	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
21	6.67	NULL	2 / 13	CC mitochondrial respiratory chain
22	6.61	NULL	2 / 11	GSEA C2REACTOME_HIV_INFECTION
23	6.26	NULL	2 / 13	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
24	6.23	NULL	2 / 12	GSEA C2WANG_SMARCE1_TARGETS_DN
25	6.13	NULL	1 / 10	GSEA C2REACTOME_HIV1_TRANSCRIPTION_INITIATION
26	6.04	NULL	3 / 15	GSEA C2REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL
27	6.02	NULL	3 / 14	GSEA C2ELVIDGE_HYPOXIA_DN
28	5.84	NULL	2 / 16	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_L
29	5.8	NULL	1 / 11	GSEA C2KEGG_BASAL_TRANSCRIPTION_FACTORS
30	5.79	NULL	3 / 13	GSEA C2MOOHTHA_VOXPPOS
31	5.79	NULL	2 / 12	BP oxidative phosphorylation
32	5.76	NULL	2 / 11	GSEA C2REACTOME_RETROGRADE_NEUROTROPIN_SIGNALLING
33	5.64	NULL	2 / 16	BP positive regulation of TOR signaling
34	5.53	NULL	3 / 37	CC mitochondrial nucleoid
35	5.52	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
36	5.52	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF
37	5.52	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
38	5.52	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
39	5.51	NULL	1 / 12	GSEA C2CAMP5_COLON_CANCER_COPY_NUMBER_DN
40	5.47	NULL	2 / 12	GSEA C2REACTOME_TRAFFICKING_OF_GLR2_CONTAINING_AMPA_R



GW_197

Local Summary

%DE = 0.91
 # metagenes = 22
 # genes = 335
 # genes in genesets = 335
 # genes with $fdr < 0.1 = 261$ (2 + / 259 -)
 # genes with $fdr < 0.05 = 233$ (2 + / 231 -)
 # genes with $fdr < 0.01 = 91$ (0 + / 91 -)

<r> metagenes = 0.95

<r> genes = 0.28

<FC> = -0.48

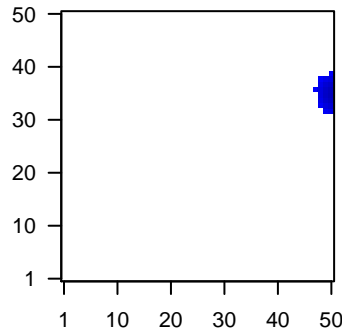
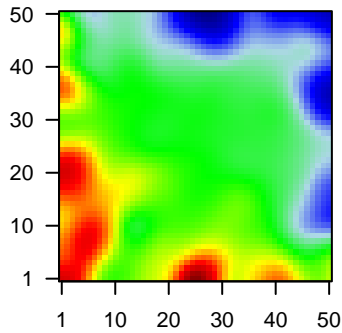
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<p-value> = 0.03

<fdr> = 0.61

Profile

Spot



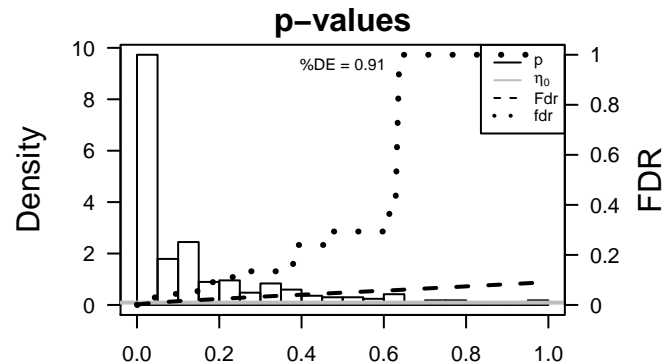
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5612	-1.18	2e-06	2e-04	50 x 34 protein-kinase, interferon-inducible double stranded RNA de
2	64083	-1.11	8e-06	2e-04	50 x 37 golgi phosphoprotein 3 (coat-protein) [Source:HGNC Symbol
3	84928	-1.08	1e-05	2e-04	50 x 37 transmembrane protein 209 [Source:HGNC Symbol;Acc:2185
4	1655	-0.97	2e-05	2e-04	50 x 36 DEAD (Asp-Glu-Ala-Asp) box helicase 5 [Source:HGNC Sy
5	23588	-1.03	4e-05	2e-04	50 x 33 kelch domain containing 2 [Source:HGNC Symbol;Acc:20231
6	57223	-1.02	4e-05	2e-04	50 x 36 SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Sourc
7	7334	-1	5e-05	2e-04	50 x 33 ubiquitin-conjugating enzyme E2N [Source:HGNC Symbol;A
8	5934	-0.98	8e-05	2e-04	50 x 36 retinoblastoma-like 2 (p130) [Source:HGNC Symbol;Acc:989
9	728026	-0.98	8e-05	2e-04	50 x 35 prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
10	22887	-0.97	9e-05	2e-04	50 x 38 forkhead box J3 [Source:HGNC Symbol;Acc:29178]
11	79139	-0.97	9e-05	2e-04	48 x 37 derlin 1 [Source:HGNC Symbol;Acc:28454]
12	26135	-0.97	9e-05	2e-04	50 x 32 SERPINE1 mRNA binding protein 1 [Source:HGNC Symbol;f
13	7764	-0.97	9e-05	6e-04	50 x 37 zinc finger protein 217 [Source:HGNC Symbol;Acc:13009]
14	6427	-0.92	1e-04	6e-04	50 x 38 serine/arginine-rich splicing factor 2 [Source:HGNC Symbol;v
15	29058	-0.95	1e-04	1e-03	50 x 38 transmembrane protein 230 [Source:HGNC Symbol;Acc:1587
16	10914	-0.92	2e-04	1e-03	50 x 33 poly(A) polymerase alpha [Source:HGNC Symbol;Acc:14981]
17	84191	-0.91	3e-04	1e-03	50 x 34 family with sequence similarity 96, member A [Source:HGNC
18	5311	-0.9	3e-04	1e-03	50 x 38 polycystic kidney disease 2 (autosomal dominant) [Source:HC
19	7342	-0.88	4e-04	1e-03	50 x 35 upstream binding protein 1 (LBP-1a) [Source:HGNC Symbol;
20	22862	-0.87	4e-04	1e-03	50 x 35 fibronectin type III domain containing 3A [Source:HGNC Sym

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.33	NULL	5 / 14	GSEA C2REACTOME_MRNA_3_END_PROCESSING
2	-9.63	NULL	9 / 51	miRNA target set miR-5566-3p
3	-9.18	NULL	13 / 89	miRNA target set miR-5565
4	-9.04	NULL	17 / 171	miRNA target set miR-3669-3p
5	-8.86	NULL	25 / 303	miRNA target set miR-3692b
6	-8.66	NULL	14 / 100	miRNA target set miR-3694
7	-8.42	NULL	23 / 271	miRNA target set miR-3691
8	-8.38	NULL	6 / 33	miRNA target set miR-3692b
9	-8.19	NULL	17 / 186	miRNA target set miR-3692
10	-8.06	NULL	1 / 2	MMML C63CIEJ_MMML 38
11	-8	NULL	11 / 108	miRNA target set miR-449b
12	-7.95	NULL	36 / 421	miRNA target set miR-795e
13	-7.86	NULL	24 / 311	miRNA target set miR-3692c
14	-7.67	NULL	17 / 153	miRNA target set miR-450b-5p
15	-7.54	NULL	8 / 47	miRNA target set miR-3692*
16	-7.52	NULL	25 / 318	miRNA target set miR-5560-3p
17	-7.47	NULL	18 / 172	miRNA target set miR-607
18	-7.41	NULL	21 / 215	miRNA target set miR-293
19	-7.26	NULL	23 / 325	miRNA target set miR-3692d
20	-7.23	NULL	8 / 63	miRNA target set miR-606
21	-7.22	NULL	16 / 181	miRNA target set miR-3691
22	-7.21	NULL	22 / 264	miRNA target set miR-449a
23	-7.21	NULL	23 / 315	miRNA target set miR-369e
24	-7.2	NULL	8 / 41	BP mRNA 3'-end processing
25	-7.15	NULL	8 / 55	miRNA target set miR-29e-3p
26	-7.12	NULL	2 / 10	GSEA C2CROONQUIST_STROMAL_STIMULATION_DN
27	-7.09	NULL	25 / 311	miRNA target set miR-369e
28	-7.07	NULL	11 / 113	miRNA target set miR-3697
29	-7.03	NULL	8 / 49	miRNA target set miR-154-487
30	-7.02	NULL	29 / 381	miRNA target set miR-369e
31	-7.02	NULL	12 / 142	miRNA target set miR-469-3p
32	-6.96	NULL	13 / 157	miRNA target set miR-5560c
33	-6.95	NULL	29 / 433	miRNA target set miR-450b
34	-6.93	NULL	9 / 85	miRNA target set miR-607
35	-6.92	NULL	19 / 281	miRNA target set miR-369e
36	-6.91	NULL	15 / 121	miRNA target set miR-5563
37	-6.91	NULL	26 / 412	miRNA target set miR-3692
38	-6.89	NULL	8 / 44	BP termination of RNA polymerase II transcription
39	-6.87	NULL	3 / 16	GSEA C2CHOL_ATL_CHRONIC_VS_ACUTE_DN
40	-6.86	NULL	13 / 146	miRNA target set miR-607



GW_197

Local Summary

%DE = 0.86
 # metagenes = 50
 # genes = 633
 # genes in genesets = 624
 # genes with $fdr < 0.1$ = 455 (5 + / 450 -)
 # genes with $fdr < 0.05$ = 298 (2 + / 296 -)
 # genes with $fdr < 0.01$ = 146 (1 + / 145 -)

<r> metagenes = 0.85

<r> genes = 0.23

<FC> = -0.48

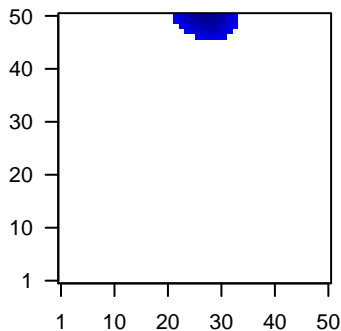
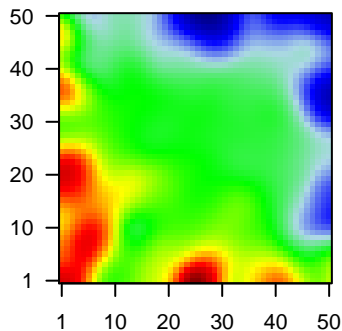
<shrinkage-t> = -16.93

<p-value> = 0.03

<fdr> = 0.6

Profile

Spot



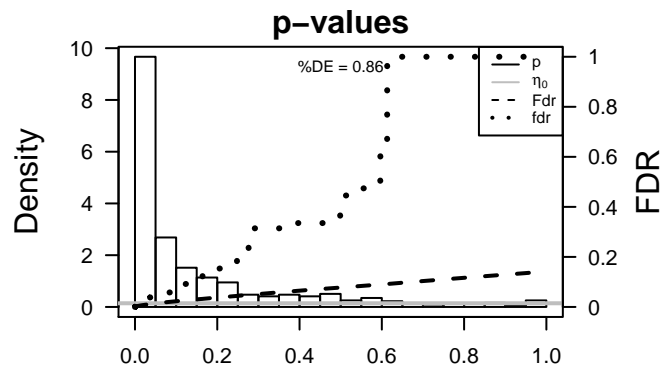
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	114908	-1.52	1e-09	2e-07	26 x 50 transmembrane protein 123 [Source:HGNC Symbol;Acc:30131]
2	4609	-1.46	4e-09	4e-06	22 x 50 v-myc avian myelocytomatosis viral oncogene homolog [Sou
3	1207	-1.35	5e-08	2e-05	31 x 49 chloride channel, nucleotide-sensitive, 1A [Source:HGNC Sy
4	81853	-1.25	5e-07	2e-05	32 x 50 transmembrane protein 14B [Source:HGNC Symbol;Acc:2131
5	81542	-1.24	6e-07	4e-05	30 x 47 thioredoxin-related transmembrane protein 1 [Source:HGNC
6	1958	-1.21	1e-06	5e-05	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
7	7465	-1.18	2e-06	5e-05	23 x 50 WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:127
8	2353	-1.08	2e-06	1e-04	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:+
9	51119	-1.14	4e-06	1e-04	27 x 50 Shwachman-Bodian-Diamond syndrome [Source:HGNC Syr
10	23471	-1.03	6e-06	1e-04	28 x 46 translocation associated membrane protein 1 [Source:HGNC
11	1665	-1.12	7e-06	1e-04	27 x 50 DEAH (Asp-Glu-Ala-His) box helicase 15 [Source:HGNC Sy
12	60592	-1.12	7e-06	2e-04	28 x 50 short coiled-coil protein [Source:HGNC Symbol;Acc:20335]
13	25831	-1.1	1e-05	2e-04	25 x 50 HECT domain containing E3 ubiquitin protein ligase 1 [Sourc
14	8065	-1.09	1e-05	2e-04	30 x 48 cullin 5 [Source:HGNC Symbol;Acc:2556]
15	55854	-1.08	1e-05	2e-04	28 x 50 zinc finger CCCH-type containing 15 [Source:HGNC Symbol
16	10492	-1.08	1e-05	2e-04	26 x 50 synaptotagmin binding, cytoplasmic RNA interacting protein [
17	91612	-1.07	2e-05	3e-04	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:20
18	653566	-1.06	2e-05	3e-04	28 x 49
19	6129	-1.05	2e-05	5e-04	32 x 48 ribosomal protein L7 [Source:HGNC Symbol;Acc:10363]
20	10196	-1.03	4e-05	5e-04	29 x 50 protein arginine methyltransferase 3 [Source:HGNC Symbol;+

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.92	NULL	41 / 269	miRNA target set B124
2	-9.9	NULL	1 / 2	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
3	-9.8	NULL	61 / 436	miRNA target set B124
4	-9.7	NULL	23 / 130	miRNA target set B124
5	-9.45	NULL	29 / 155	miRNA target set B124
6	-9.34	NULL	5 / 10	GSEA C2CHASSOT_SKIN_WOUND
7	-9.19	NULL	45 / 310	miRNA target set B124
8	-9.18	NULL	11 / 61	miRNA target set B124
9	-9.04	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
10	-9.03	NULL	6 / 16	TF Tissue/AQUERIZAS_Pancreas
11	-8.7	NULL	32 / 217	miRNA target set B124
12	-8.69	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
13	-8.62	NULL	23 / 109	BP SRP-dependent cotranslational protein targeting to membrane
14	-8.44	NULL	39 / 324	miRNA target set B124
15	-8.37	NULL	5 / 8	MMML C2CIEJ_MMML_50
16	-8.11	NULL	42 / 300	miRNA target set B124
17	-8.11	NULL	4 / 11	BP ribosomal large subunit biogenesis
18	-8.09	NULL	27 / 198	miRNA target set B124
19	-7.86	NULL	26 / 157	miRNA target set B124
20	-7.83	NULL	4 / 15	BP long-term synaptic potentiation
21	-7.79	NULL	23 / 151	miRNA target set B124
22	-7.7	NULL	38 / 280	miRNA target set B124
23	-7.65	NULL	24 / 173	miRNA target set B124
24	-7.6	NULL	25 / 169	miRNA target set B124
25	-7.57	NULL	23 / 155	miRNA target set B124
26	-7.53	NULL	7 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
27	-7.52	NULL	34 / 328	Glio Up
28	-7.51	NULL	4 / 16	GSEA C2BIOCARTA_ETS_PATHWAY
29	-7.48	NULL	26 / 187	miRNA target set B124
30	-7.45	NULL	36 / 262	miRNA target set B124
31	-7.39	NULL	27 / 189	miRNA target set B124
32	-7.39	NULL	19 / 130	miRNA target set B124
33	-7.31	NULL	5 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_MS_DN
34	-7.29	NULL	2 / 5	miRNA target set B124
35	-7.16	NULL	22 / 150	miRNA target set B124
36	-7.08	NULL	52 / 565	miRNA target set B124
37	-7.06	NULL	15 / 95	miRNA target set B124
38	-7.05	NULL	33 / 253	BP translation
39	-7	NULL	7 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
40	-6.99	NULL	25 / 184	miRNA target set B124



GW_197

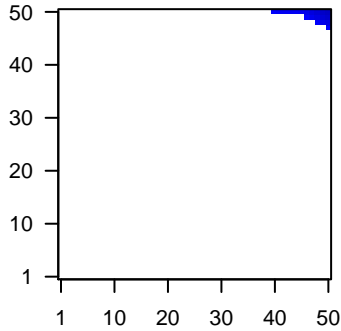
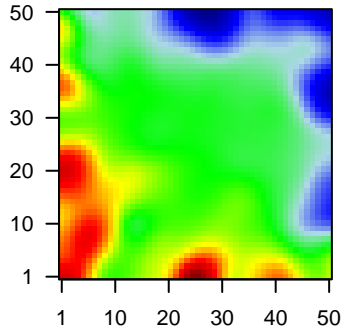
Local Summary

%DE = 0.73
 # metagenes = 20
 # genes = 393
 # genes in genesets = 391
 # genes with fdr < 0.1 = 195 (9 + / 186 -)
 # genes with fdr < 0.05 = 126 (3 + / 123 -)
 # genes with fdr < 0.01 = 79 (3 + / 76 -)

<r> metagenes = 0.83
 <r> genes = 0.25
 <FC> = -0.44
 <shrinkage-t> = -15.48
 <p-value> = 0.02
 <fdr> = 0.6

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.93	9e-15	7e-11	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	94234	-1.78	7e-13	9e-11	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
3	11166	-1.76	1e-12	4e-09	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt
4	23321	-1.63	5e-11	4e-09	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:1597
5	26047	-1.61	8e-11	7e-08	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
6	57216	-1.53	7e-10	3e-06	50 x 48 VANGL planar cell polarity protein 2 [Source:HGNC Symbol;f
7	1894	-1.36	5e-08	3e-06	45 x 50 epithelial cell transforming sequence 2 oncogene [Source:HG
8	6657	-1.33	8e-08	3e-06	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symb
9	3428	-1.33	9e-08	3e-06	45 x 50 interferon, gamma-inducible protein 16 [Source:HGNC Symb
10	4780	-1.32	1e-07	1e-05	50 x 50 nuclear factor, erythroid 2-like 2 [Source:HGNC Symbol;Acc:
11	9076	-1.28	2e-07	2e-05	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
12	139728	-1.26	4e-07	2e-05	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l
13	4072	-1.24	5e-07	4e-05	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
14	8500	-1.22	1e-06	4e-05	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (P1
15	84171	-1.19	2e-06	4e-05	50 x 49 lysyl oxidase-like 4 [Source:HGNC Symbol;Acc:17171]
16	81831	-1.18	2e-06	4e-05	42 x 50 neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Sym
17	7514	-1.17	2e-06	4e-05	47 x 49 exportin 1 (CRM1 homolog, yeast) [Source:HGNC Symbol;Ac
18	79866	-1.17	3e-06	4e-05	43 x 50 bora, aurora kinase A activator [Source:HGNC Symbol;Acc:2
19	655	-1.16	3e-06	1e-04	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
20	4922	-1.15	4e-06	2e-04	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.27	NULL	38 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-11.27	NULL	38 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-10.82	NULL	4 / 11	GSEA C2REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE
4	-10.26	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
5	-10.05	NULL	3 / 16	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G1_DN
6	-9.88	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
7	-9.7	NULL	5 / 26	BP cellular response to ionizing radiation
8	-9.45	NULL	4 / 14	BP purine ribonucleoside monophosphate biosynthetic process
9	-9.23	NULL	2 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
10	-8.64	NULL	4 / 15	GSEA C2REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_E
11	-8.62	NULL	6 / 16	Cancer WOLFER_overlap genes
12	-8.62	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
13	-8.62	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
14	-8.44	NULL	50 / 530	Cancer Lembcke_Normal vs Adenoma
15	-8.32	NULL	6 / 15	GSEA C2MMS_MOUSE_LYMPH_HIGH_4HRS_UP
16	-8.31	NULL	8 / 18	BP spindle organization
17	-8.16	NULL	5 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
18	-8.06	NULL	9 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
19	-8.02	NULL	2 / 5	Glio Phillips Prolif up vs PN & MES
20	-7.96	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
21	-7.77	NULL	3 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
22	-7.63	NULL	4 / 14	GSEA C2MAYBURD_RESPONSE_TO_L663536_DN
23	-7.48	NULL	4 / 14	BP purine nucleotide biosynthetic process
24	-7.41	NULL	4 / 37	CC lateral plasma membrane
25	-7.35	NULL	6 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
26	-7.23	NULL	7 / 25	BP glutathione derivative biosynthetic process
27	-7.19	NULL	4 / 16	GSEA C2WILCOX_PRESPONSE_TO_ROGESTERONE_UP
28	-7.17	NULL	4 / 12	BP regulation of double-strand break repair via homologous recomb
29	-7.17	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
30	-7.16	NULL	2 / 10	GSEA C2SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN
31	-7.14	NULL	3 / 14	GSEA C2REACTOME_PURINE_METABOLISM
32	-7.12	NULL	5 / 15	GSEA C2TIEN_INTESTINE_PROBIOTICS_24HR_UP
33	-7.11	NULL	5 / 15	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
34	-7.01	NULL	2 / 12	BP cellular aldehyde metabolic process
35	-6.85	NULL	5 / 16	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
36	-6.85	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
37	-6.85	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
38	-6.82	NULL	6 / 14	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
39	-6.8	NULL	8 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
40	-6.78	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS

p-values

