

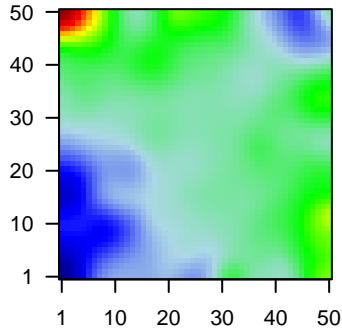
GW_059

Global Summary

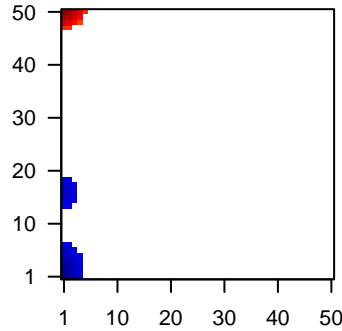
%DE = 0.14
 # genes with fdr < 0.2 = 1940 (1043 + / 897 -)
 # genes with fdr < 0.1 = 1371 (766 + / 605 -)
 # genes with fdr < 0.05 = 1217 (693 + / 524 -)
 # genes with fdr < 0.01 = 769 (468 + / 301 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.86

Profile



Regulated Spots



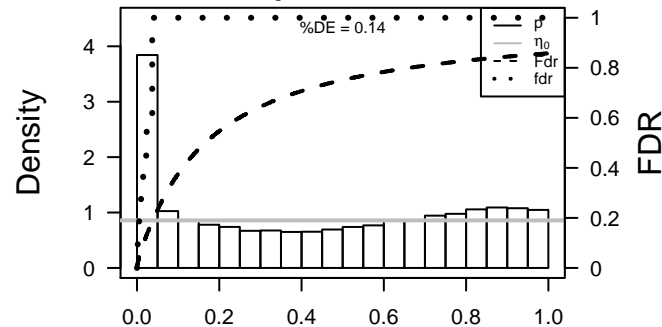
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.67	2e-16	3e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.67	2e-16	3e-14	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.43	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	216	1.84	2e-16	3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	218	1.69	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	80117	1.52	2e-16	3e-14	2 x 40 ADP-ribosylation factor-like 14 [Source:HGNC Symbol;Acc:2
7	23120	1.99	2e-16	3e-14	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
8	387695	1.7	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
9	391267	1.51	2e-16	3e-14	50 x 13 ankyrin repeat domain 20 family, member A11, pseudogene [
10	394263	1.88	2e-16	3e-14	3 x 50
11	375791	1.6	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
12	6363	2.09	2e-16	3e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
13	22802	2.4	2e-16	3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	9071	1.71	2e-16	3e-14	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
15	9022	1.44	2e-16	3e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2t
16	54544	1.46	2e-16	3e-14	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	2.31	2e-16	3e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	1.9	2e-16	3e-14	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	284340	1.42	2e-16	3e-14	6 x 50 chemokine (C-X-C motif) ligand 17 [Source:HGNC Symbol;f
20	1562	1.42	2e-16	3e-14	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	27.23	NULL	135	H.Tiss WIRTH_Mucosa
2	14.53	NULL	572	Disease GUDJ_psooriasis_up
3	10.6	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
4	10.19	NULL	53	BP keratinocyte differentiation
5	9.18	NULL	417	H.Tiss WIRTH_Immune system
6	9.15	NULL	21	CC cornified envelope
7	9.01	NULL	274	LymphomaBPANG_IL21 DN
8	7.96	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
9	7.85	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
10	7.76	NULL	24	TF Tissue/AQUERIZAS_Trachea
11	7.38	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
12	7.18	NULL	8	GSEA C2LIU_CD_X2_TARGETS_DN
13	7.09	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
14	6.97	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
15	6.94	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
16	6.85	NULL	5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
17	6.75	NULL	18	MF aromatase activity
18	6.68	NULL	19	BP peptide cross-linking
19	6.56	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
20	6.49	NULL	4	MMML C6SCIEJ_MMML_47
<i>Underexpressed</i>				
1	-12.13	NULL	242	BP extracellular matrix organization
2	-11.61	NULL	530	Cancer Lembecke_Normal vs Adenoma
3	-11.35	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
4	-11.35	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
5	-10.95	NULL	190	CC extracellular matrix
6	-10.11	NULL	69	BP extracellular matrix disassembly
7	-9.9	NULL	64	BP collagen catabolic process
8	-8.38	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
9	-8.37	NULL	153	CC endoplasmic reticulum lumen
10	-8.01	NULL	83	CC basement membrane
11	-7.41	NULL	183	CC proteinaceous extracellular matrix
12	-7.2	NULL	250	LymphomaL2ENZ_Stromal signature 1
13	-6.79	NULL	57	MF extracellular matrix structural constituent
14	-6.5	NULL	35	Glio Colman_survival_associated
15	-6.47	NULL	72	CC extracellular vesicular exosome
16	-6.34	NULL	386	Chr Chr 22
17	-6.13	NULL	11	MF platelet-derived growth factor binding
18	-6.04	NULL	16	MMML C6SCIEJ_MMML_1
19	-6.03	NULL	717	Chr Chr 16
20	-6.02	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5

p-values



GW_059

Local Summary

%DE = 0.94
 # metagenes = 15
 # genes = 226
 # genes in genesets = 220

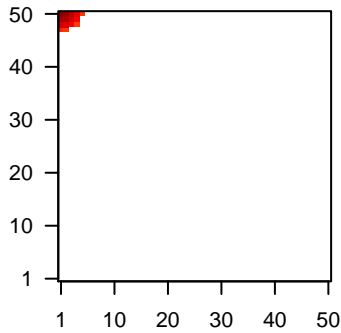
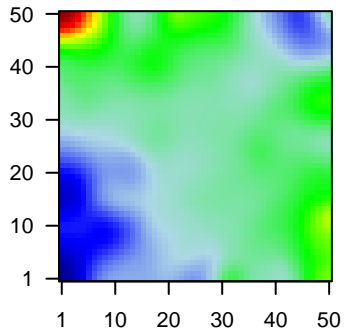
genes with $fdr < 0.1$ = 199 (189 + / 10 -)
 # genes with $fdr < 0.05$ = 186 (179 + / 7 -)
 # genes with $fdr < 0.01$ = 180 (173 + / 7 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.46

$\langle FC \rangle = 0.92$
 $\langle \text{shrinkage-t} \rangle = 32.08$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.19$

Profile

Spot



Local Genelist

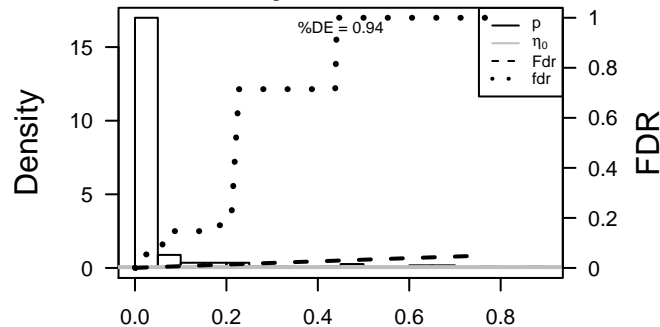
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.67	2e-16	5e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.67	2e-16	5e-17	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.43	2e-16	5e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	218	1.69	2e-16	5e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	23120	1.99	2e-16	5e-17	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
6	387695	1.7	2e-16	5e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	394263	1.88	2e-16	5e-17	3 x 50
8	375791	1.6	2e-16	5e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
9	22802	2.4	2e-16	5e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	9022	1.44	2e-16	5e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
11	54544	1.46	2e-16	5e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
12	49860	2.31	2e-16	5e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	1475	1.9	2e-16	5e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
14	1562	1.42	2e-16	5e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
15	1577	2.26	2e-16	5e-17	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
16	92196	1.66	2e-16	5e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
17	1673	2.3	2e-16	5e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
18	1828	1.79	2e-16	5e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	2012	1.58	2e-16	5e-17	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
20	115572	1.49	2e-16	5e-17	1 x 48 family with sequence similarity 46, member B [Source:HGNC

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	54.96	NULL	80 / 135	H.Tiss WIRTH_Mucosa
2	21.45	NULL	17 / 21	CC cornified envelope
3	21.15	NULL	88 / 572	Disease GUDJ_psooriasis up
4	19.16	NULL	22 / 53	BP keratinocyte differentiation
5	16.9	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
6	15.39	NULL	10 / 19	BP peptide cross-linking
7	15.24	NULL	19 / 42	BP keratinization
8	14.9	NULL	5 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
9	14.74	NULL	8 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	14.38	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	13.8	NULL	6 / 13	BP negative regulation of peptidase activity
12	13.45	NULL	21 / 76	BP epidermis development
13	12.64	NULL	8 / 44	CC keratin filament
14	12.56	NULL	8 / 38	BP epithelial cell differentiation
15	12.13	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
16	11.65	NULL	10 / 82	CC intermediate filament
17	11.49	NULL	3 / 11	GSEA C2REACTOME_XENOBIOTICS
18	11.39	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	10.97	NULL	20 / 186	MF structural molecule activity
20	10.33	NULL	3 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
21	10.04	NULL	15 / 122	MF serine-type endopeptidase activity
22	9.93	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
23	9.61	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
24	9.59	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
25	9.39	NULL	3 / 12	BP cellular aldehyde metabolic process
26	9.25	NULL	5 / 21	CC desmosome
27	9.08	NULL	55 / 1182	CC extracellular region
28	9.02	NULL	2 / 9	GSEA C2REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
29	9.02	NULL	2 / 9	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
30	8.84	NULL	4 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
31	8.69	NULL	11 / 79	MF serine-type endopeptidase inhibitor activity
32	8.59	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
33	8.55	NULL	2 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
34	8.5	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
35	8.29	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_U
36	8.28	NULL	4 / 27	BP response to bacterium
37	8.21	NULL	1 / 6	GSEA C2SAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
38	8.11	NULL	5 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
39	8	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
40	7.99	NULL	2 / 11	GSEA C2REACTOME_BIOLOGICAL_OXIDATIONS

p-values



GW_059

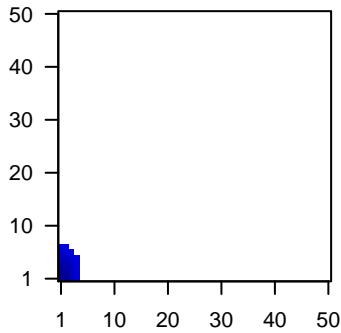
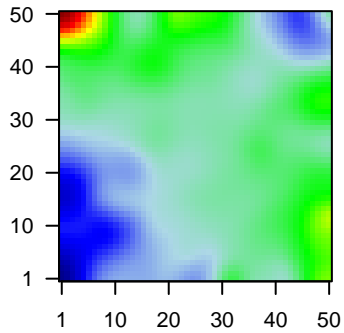
Local Summary

%DE = 0.84
 # metagenes = 25
 # genes = 367
 # genes in genesets = 364
 # genes with $fdr < 0.1$ = 263 (8 + / 255 -)
 # genes with $fdr < 0.05$ = 239 (7 + / 232 -)
 # genes with $fdr < 0.01$ = 200 (7 + / 193 -)

<r> metagenes = 0.93
 <r> genes = 0.33
 <FC> = -0.52
 <shrinkage-t> = -18.25
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



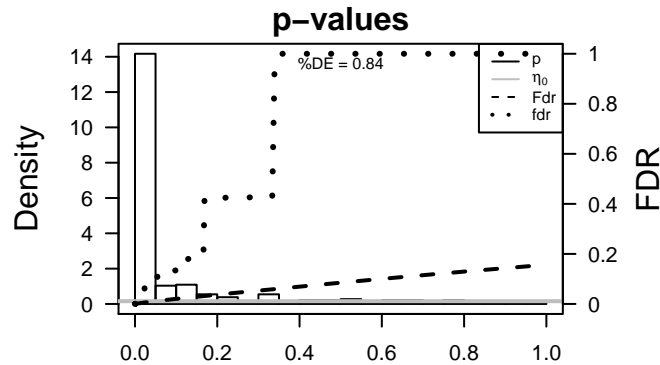
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1687	-1.56	2e-16	1e-15	1 x 4 deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc:6493]
2	3918	-1.69	2e-16	1e-15	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
3	3956	-1.86	2e-16	1e-15	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6493]
4	4312	-2.63	2e-16	1e-15	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:6493]
5	4319	-2.03	2e-16	1e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:6493]
6	4314	-2.46	2e-16	1e-15	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:6493]
7	4316	-1.4	2e-16	1e-15	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC Symbol;Acc:6493]
8	284119	-1.61	2e-16	1e-15	1 x 3 polymerase I and transcript release factor [Source:HGNC Symbol;Acc:6493]
9	12	-1.84	2e-16	1e-15	1 x 1
10	7045	-2.13	2e-16	1e-15	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:6493]
11	10381	-1.45	2e-16	1e-15	1 x 4 tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
12	6696	-1.38	9e-16	4e-14	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:11257]
13	7070	-1.37	2e-15	3e-13	4 x 1 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:11801]
14	871	-1.34	6e-15	4e-12	1 x 1 serpin peptidase inhibitor, clade H (heat shock protein 47), member 1 [Source:HGNC Symbol;Acc:11801]
15	10468	-1.29	7e-14	1e-11	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
16	51330	-1.25	4e-13	1e-11	1 x 4 tumor necrosis factor receptor superfamily, member 12A [Source:HGNC Symbol;Acc:3971]
17	10644	-1.24	5e-13	4e-11	1 x 6 insulin-like growth factor 2 mRNA binding protein 2 [Source:HGNC Symbol;Acc:3971]
18	3576	-1.22	1e-12	4e-11	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
19	26064	-1.2	2e-12	4e-11	4 x 1 retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
20	25907	-1.19	4e-12	4e-11	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:14873]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-30.99	NULL	75 / 242	BP extracellular matrix organization
2	-30.94	NULL	60 / 190	CC extracellular matrix
3	-28.55	NULL	33 / 69	BP extracellular matrix disassembly
4	-27.85	NULL	29 / 64	BP collagen catabolic process
5	-26.51	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
6	-25.09	NULL	73 / 250	LymphocyteENZ_Stromal signature 1
7	-24.06	NULL	15 / 16	MMML C6SCIEJ_MMML 1
8	-21.9	NULL	38 / 183	CC proteinaceous extracellular matrix
9	-19.74	NULL	13 / 35	Glio Colman_survival_associated
10	-18.78	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
11	-18.57	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
12	-18.28	NULL	9 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
13	-17.74	NULL	122 / 1182	CC extracellular region
14	-17.64	NULL	7 / 11	MF platelet-derived growth factor binding
15	-17.47	NULL	25 / 83	CC basement membrane
16	-17.26	NULL	85 / 683	CC extracellular space
17	-16.91	NULL	12 / 19	MF extracellular matrix binding
18	-16.83	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
19	-16.76	NULL	70 / 553	Cancer Lembcke_Colonc Inflammation
20	-16.13	NULL	6 / 10	GSEA C2LEON_SMAD6_TARGETS_UP
21	-16.08	NULL	45 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
22	-16.08	NULL	45 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
23	-16.08	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
24	-16.08	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
25	-16.03	NULL	21 / 57	MF extracellular matrix structural constituent
26	-15.45	NULL	7 / 11	Glio Phillips MES vs Prolif & PN
27	-15.04	NULL	16 / 68	Glio cultured astroglia vs. in vivo astrocytes
28	-14.82	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
29	-14.8	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
30	-14.8	NULL	61 / 403	BP cell adhesion
31	-14.79	NULL	16 / 37	BP collagen fibril organization
32	-14.45	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
33	-14.28	NULL	6 / 16	GSEA C2HENDRICKS_SMARCA4_TARGETS_UP
34	-14.26	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
35	-14.09	NULL	7 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
36	-13.73	NULL	6 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
37	-13.65	NULL	4 / 15	GSEA C2ROY_WOUND_BLOOD_VESSEL_UP
38	-13.46	NULL	5 / 14	GSEA C2HUANG_FOXA2_TARGETS_DN
39	-13.19	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
40	-13.13	NULL	6 / 12	BP hemidesmosome assembly



GW_059

Local Summary

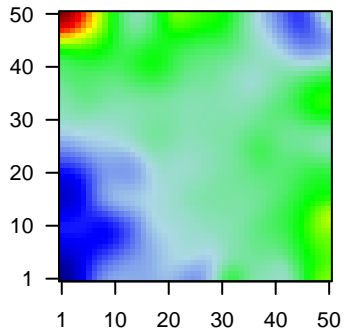
%DE = 0.95
 # metagenes = 16
 # genes = 199
 # genes in genesets = 198

genes with $fdr < 0.1 = 180$ (2 + / 178 -)
 # genes with $fdr < 0.05 = 161$ (1 + / 160 -)
 # genes with $fdr < 0.01 = 131$ (1 + / 130 -)

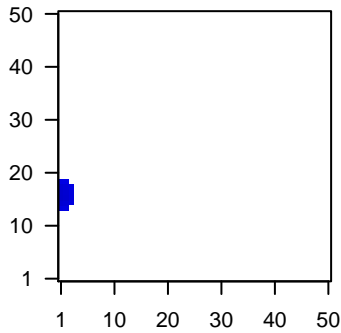
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.31

$\langle FC \rangle = -0.45$
 $\langle \text{shrinkage-t} \rangle = -15.64$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.47$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	283869	-1.37	2e-15	7e-11	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	1152	-1.17	8e-12	1e-08	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
3	131076	-1.02	2e-09	1e-08	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:26519]
4	26519	-1.02	3e-09	3e-08	1 x 19 translocase of inner mitochondrial membrane 10 homolog (ye
5	51373	-0.99	7e-09	3e-08	1 x 16 28S ribosomal protein S17, mitochondrial; HCG1984214, isof
6	8772	-0.99	9e-09	2e-07	1 x 14 Fas (TNFRSF6)-associated via death domain [Source:HGNC
7	220064	-0.95	3e-08	5e-07	1 x 14 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
8	284085	-0.92	8e-08	8e-07	3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
9	10963	-0.9	2e-07	3e-06	1 x 16 stress-induced-phosphoprotein 1 [Source:HGNC Symbol;Ac
10	2194	-0.85	7e-07	3e-06	1 x 17 fatty acid synthase [Source:HGNC Symbol;Acc:3594]
11	79077	-0.84	9e-07	3e-06	3 x 17 dCTP pyrophosphatase 1 [Source:HGNC Symbol;Acc:28777]
12	10552	-0.84	1e-06	3e-06	1 x 15 actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
13	81037	-0.83	1e-06	1e-05	1 x 14 CLPTM1-like [Source:HGNC Symbol;Acc:24308]
14	25886	-0.81	3e-06	2e-05	3 x 17 POC1 centriolar protein A [Source:HGNC Symbol;Acc:24488
15	10598	-0.76	9e-06	2e-05	1 x 14 AHA1, activator of heat shock 90kDa protein ATPase homolo
16	6510	-0.75	1e-05	2e-05	2 x 19 solute carrier family 1 (neutral amino acid transporter), memb
17	2821	-0.75	1e-05	2e-05	3 x 17 glucose-6-phosphate isomerase [Source:HGNC Symbol;Acc
18	80028	-0.75	1e-05	2e-05	1 x 14 F-box and leucine-rich repeat protein 18 [Source:HGNC Syn
19	23246	-0.75	1e-05	2e-05	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
20	203068	-0.74	2e-05	4e-05	3 x 15 tubulin, beta class I [Source:HGNC Symbol;Acc:20778]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.66	NULL	2 / 10	BP creatine metabolic process
2	-10.42	NULL	2 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
3	-10.35	NULL	2 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
4	-10.03	NULL	4 / 13	GSEA C2XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
5	-9.96	NULL	17 / 153	MF structural constituent of ribosome
6	-9.57	NULL	5 / 43	MF chaperone binding
7	-9.46	NULL	2 / 10	GSEA C2ZHU_CMV_24_HR_UP
8	-9.46	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP
9	-9.13	NULL	2 / 7	GSEA C2PARK_HSC_MARKERS
10	-9.06	NULL	3 / 15	GSEA C2NAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
11	-8.99	NULL	3 / 15	GSEA C2Y_AGING_MIDDLE_DN
12	-8.76	NULL	3 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
13	-8.65	NULL	16 / 167	CC ribosome
14	-8.51	NULL	2 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_OUTLIN_3A_DN
15	-8.3	NULL	11 / 96	BP rRNA processing
16	-8.24	NULL	2 / 15	GSEA C2DIRMEIER_LMP1_RESPONSE_LATE_UP
17	-8.22	NULL	20 / 253	BP translation
18	-8.15	NULL	3 / 10	GSEA C2REACTOME_HIV_LIFE_CYCLE
19	-8.07	NULL	2 / 21	BP feeding behavior
20	-8.04	NULL	2 / 11	GSEA C2SCIBETTA_KDM5B_TARGETS_DN
21	-8.04	NULL	2 / 13	GSEA C2KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
22	-7.97	NULL	3 / 15	CC mitochondrial large ribosomal subunit
23	-7.79	NULL	4 / 19	CC mitochondrial small ribosomal subunit
24	-7.73	NULL	1 / 6	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_DN
25	-7.69	NULL	3 / 10	GSEA C2TOMIDA_METASTASIS_UP
26	-7.64	NULL	2 / 12	GSEA C2BHATTACHARYA_EMBRYONIC_STEM_CELL
27	-7.42	NULL	3 / 16	GSEA C2GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
28	-7.31	NULL	1 / 9	GSEA C2GOUYER_TUMOR_INVASIVENESS
29	-7.3	NULL	1 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
30	-7.21	NULL	3 / 15	GSEA C2MATTIOLI_MGUS_VS_PCL
31	-7.2	NULL	3 / 13	GSEA C2AUNG_GASTRIC_CANCER
32	-7.08	NULL	3 / 13	GSEA C2REACTOME_GLYCOLYSIS
33	-7.05	NULL	3 / 26	MF virus receptor activity
34	-7.02	NULL	3 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
35	-6.87	NULL	3 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
36	-6.86	NULL	5 / 44	BP positive regulation of viral transcription
37	-6.86	NULL	1 / 3	GSEA C2WEBER_METHYLATED_LCP_IN_SPERM_DN
38	-6.79	NULL	3 / 14	Pathw AcBENTINK_myc.1
39	-6.77	NULL	3 / 14	GSEA C2KEGG_COLORECTAL_CANCER
40	-6.69	NULL	2 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_7

p-values

