

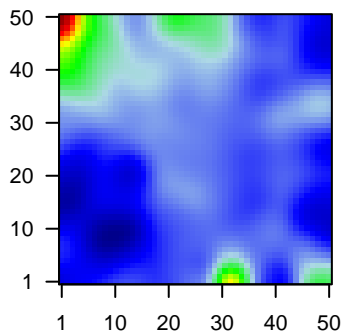
GW_074

Global Summary

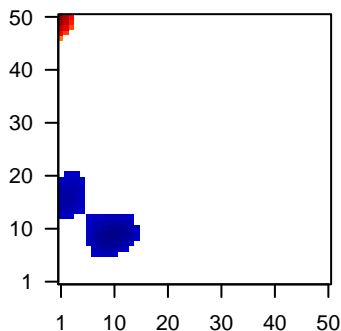
%DE = 0.12
 # genes with $fdr < 0.2$ = 1471 (853 + / 618 -)
 # genes with $fdr < 0.1$ = 1170 (718 + / 452 -)
 # genes with $fdr < 0.05$ = 969 (618 + / 351 -)
 # genes with $fdr < 0.01$ = 603 (434 + / 169 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.88

Profile



Regulated Spots



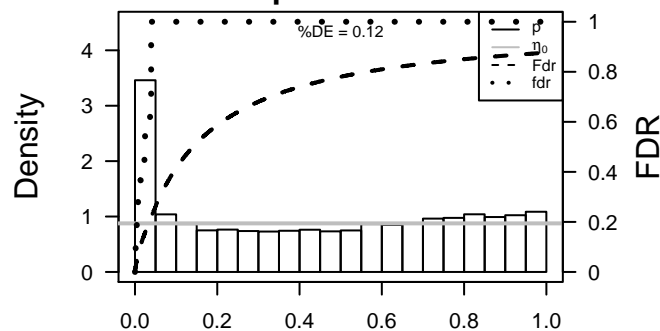
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	133	1.34	2e-16 4e-14	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
2	1646	-1.72	2e-16 4e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Syri
3	8644	-2.15	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syri
4	1109	-2.52	2e-16 4e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syri
5	200315	2.02	2e-16 4e-14	1 x 40 apolipoprotein B mRNA editing enzyme, catalytic polypeptide
6	23780	1.39	2e-16 4e-14	32 x 1 apolipoprotein L 2 [Source:HGNC Symbol;Acc:619]
7	445	1.66	2e-16 4e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75f
8	25805	1.37	2e-16 4e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
9	8424	1.63	2e-16 4e-14	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
10	387695	1.99	2e-16 4e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
11	440712	1.43	2e-16 4e-14	1 x 39 chromosome 1 open reading frame 186 [Source:HGNC Symt
12	260436	-1.46	2e-16 4e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
13	375791	1.72	2e-16 4e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
14	6364	-1.43	2e-16 4e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
15	894	1.68	2e-16 4e-14	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
16	26047	1.51	2e-16 4e-14	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ar
17	49860	3.38	2e-16 4e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1410	1.45	2e-16 4e-14	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
19	3627	2.66	2e-16 4e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
20	6373	2.12	2e-16 4e-14	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;f

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	24.83	NULL	135	H.Tiss WIRTH_Mucosa
2	20	NULL	572	Disease GUDJ_psooriasis up
3	16.09	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
4	15.39	NULL	51	BP type I interferon signaling pathway
5	15.27	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
6	14.91	NULL	123	BP defense response to virus
7	13.68	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
8	13.51	NULL	957	Chr Chr 11
9	13	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
10	12.96	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	12.9	NULL	31	BP negative regulation of viral genome replication
12	12.68	NULL	274	Lymphocyte SPANG_IL21 DN
13	12.31	NULL	21	CC cornified envelope
14	12.28	NULL	866	Chr Chr 12
15	12.08	NULL	76	BP epidermis development
16	11.27	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
17	11.24	NULL	204	BP cytokine-mediated signaling pathway
18	11.24	NULL	53	BP keratinocyte differentiation
19	10.72	NULL	16	GSEA C2ZINAV_INTERFERON_SIGNATURE_IN_CANCER
20	10.56	NULL	633	Chr Chr 9
<i>Underexpressed</i>				
1	-8.21	NULL	717	Chr Chr 16
2	-8.06	NULL	449	Chr Chr 20
3	-6.69	NULL	482	BP cellular protein metabolic process
4	-6.66	NULL	1135	Chr Chr 19
5	-6.04	NULL	253	BP translation
6	-5.95	NULL	630	Chr Chr X
7	-5.68	NULL	743	Chr Chr 7
8	-5.62	NULL	153	MF structural constituent of ribosome
9	-5.61	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
10	-5.49	NULL	92	BP translational elongation
11	-5.45	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
12	-5.42	NULL	1253	BP small molecule metabolic process
13	-5.18	NULL	13	GSEA C2MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP
14	-5.07	NULL	918	Chr Chr 17
15	-5.01	NULL	87	BP translational termination
16	-4.98	NULL	81	BP viral transcription
17	-4.96	NULL	167	CC ribosome
18	-4.78	NULL	1318	CC mitochondrion
19	-4.74	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
20	-4.74	NULL	914	Chr Chr 3

p-values



GW_074

Local Summary

%DE = 0.89
 # metagenes = 12
 # genes = 187
 # genes in genesets = 182

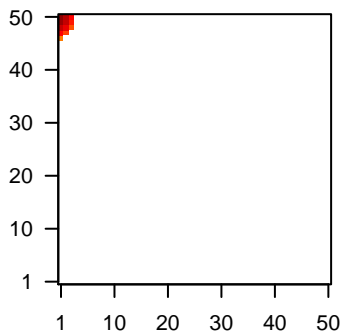
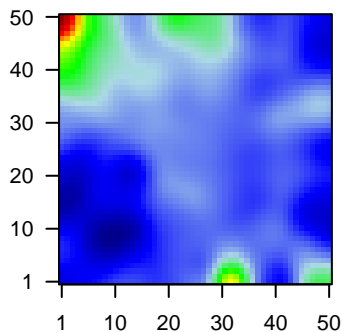
genes with $fdr < 0.1$ = 143 (130 + / 13 -)
 # genes with $fdr < 0.05$ = 142 (129 + / 13 -)
 # genes with $fdr < 0.01$ = 133 (122 + / 11 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.47

$\langle FC \rangle = 0.76$
 $\langle \text{shrinkage-t} \rangle = 26.74$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.26$

Profile

Spot



Local Genelist

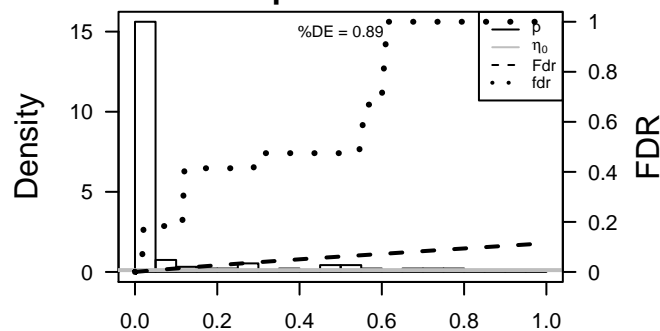
Rank	ID	log(FC)	fdr	p-value	Description
1	8644	-2.15	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym]
2	8424	1.63	2e-16	1e-16	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxxygenase (gamma)
3	387695	1.99	2e-16	1e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
4	375791	1.72	2e-16	1e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
5	49860	3.38	2e-16	1e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
6	1562	1.53	2e-16	1e-16	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
7	27065	1.5	2e-16	1e-16	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1)
8	414325	1.49	2e-16	1e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	1673	1.6	2e-16	1e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	1828	1.76	2e-16	1e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
11	2012	1.46	2e-16	1e-16	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
12	115572	1.52	2e-16	1e-16	1 x 48 family with sequence similarity 46, member B [Source:HGNC
13	163351	1.86	2e-16	1e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S]
14	10804	1.43	2e-16	1e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
15	43849	1.54	2e-16	1e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6:
16	26085	1.73	2e-16	1e-16	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6:
17	5650	1.43	2e-16	1e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63]
18	3848	2.65	2e-16	1e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
19	3860	1.89	2e-16	1e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
20	192666	2.58	2e-16	1e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	52.31	NULL	77 / 135	H.Tiss WIRTH_Mucosa
2	31.74	NULL	18 / 21	CC cornified envelope
3	25.69	NULL	19 / 42	BP keratinization
4	24.81	NULL	23 / 53	BP keratinocyte differentiation
5	23.26	NULL	22 / 76	BP epidermis development
6	22.41	NULL	85 / 572	Disease GUDJ_psooriasis up
7	21.3	NULL	10 / 19	BP peptide cross-linking
8	17.05	NULL	9 / 44	CC keratin filament
9	16.93	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
10	16.21	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
11	16.13	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
12	15.74	NULL	13 / 82	CC intermediate filament
13	15.43	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
14	14.4	NULL	20 / 186	MF structural molecule activity
15	12.47	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
16	12.15	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
17	11.85	NULL	3 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
18	11.84	NULL	6 / 13	BP negative regulation of peptidase activity
19	10.8	NULL	8 / 21	CC desmosome
20	10.79	NULL	12 / 122	MF serine-type endopeptidase activity
21	9.69	NULL	12 / 79	MF serine-type endopeptidase inhibitor activity
22	9.53	NULL	2 / 15	BP fibrinolysis
23	9.48	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
24	9.44	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
25	9.28	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
26	9.03	NULL	50 / 1182	CC extracellular region
27	8.83	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
28	8.65	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
29	8.64	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
30	8.42	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
31	8.3	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
32	8.28	NULL	7 / 29	BP regulation of proteolysis
33	8.26	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
34	8.23	NULL	6 / 38	BP epithelial cell differentiation
35	8.09	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
36	7.51	NULL	4 / 15	GSEA C2AIGNER_ZEB1_TARGETS
37	7.03	NULL	1 / 12	GSEA C2ODDONNELL_METASTASIS_DN
38	7.03	NULL	1 / 12	GSEA C2SYED ESTRADIOL_RESPONSE
39	6.89	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
40	6.81	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY

p-values



GW_074

Local Summary

%DE = 0.68
 # metagenes = 69
 # genes = 524
 # genes in genesets = 500

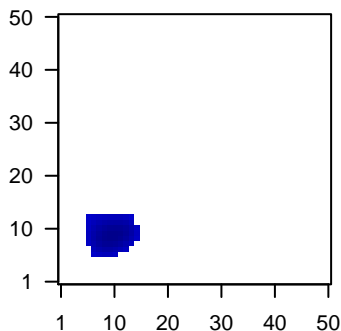
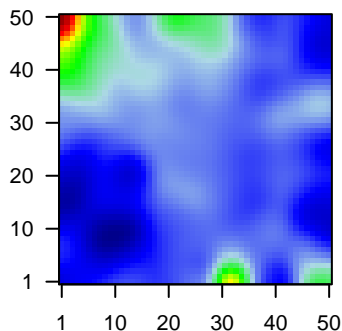
genes with $fdr < 0.1$ = 149 (11 + / 138 -)
 # genes with $fdr < 0.05$ = 142 (10 + / 132 -)
 # genes with $fdr < 0.01$ = 52 (4 + / 48 -)

<r> metagenes = 0.8
 <r> genes = 0.2

<FC> = -0.23
 <shrinkage-t> = -8.09
 <p-value> = 0.05
 <fdr> = 0.75

Profile

Spot



Local Genelist

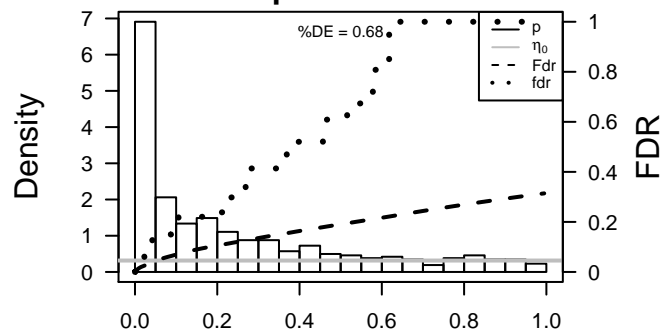
Rank	ID	log(FC)	fdr	p-value	Description
1	4833	-1.26	4e-14	3e-07	9 x 6 NME/NM23 nucleoside diphosphate kinase 4 [Source:HGNC
2	4037	-1.01	2e-09	4e-05	10 x 7 low density lipoprotein receptor-related protein 3 [Source:HG
3	64943	-0.87	2e-07	1e-04	9 x 8 5'-nucleotidase domain containing 2 [Source:HGNC Symbol;
4	55506	-0.81	1e-06	1e-04	12 x 9 H2A histone family, member Y2 [Source:HGNC Symbol;Acc:1
5	10459	-0.79	2e-06	2e-04	8 x 9 MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S
6	3303	-0.77	3e-06	7e-04	11 x 12 heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
7	53635	-0.73	1e-05	7e-04	9 x 9 prostate tumor overexpressed 1 [Source:HGNC Symbol;Acc:1
8	1469	-0.73	1e-05	7e-04	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
9	57190	-0.71	2e-05	7e-04	9 x 7 selenoprotein N, 1 [Source:HGNC Symbol;Acc:15999]
10	51614	-0.71	2e-05	1e-03	9 x 8 ERGIC and golgi 3 [Source:HGNC Symbol;Acc:15927]
11	146754	0.7	3e-05	1e-03	13 x 10 dynein, axonemal, heavy chain 2 [Source:HGNC Symbol;Acc
12	23344	-0.68	4e-05	1e-03	8 x 10 extended synaptotagmin-like protein 1 [Source:HGNC Symb
13	441520	-0.68	5e-05	1e-03	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
14	9627	-0.66	7e-05	1e-03	13 x 9 synuclein, alpha interacting protein [Source:HGNC Symbol;A
15	22913	-0.66	8e-05	1e-03	8 x 11 RALY heterogeneous nuclear ribonucleoprotein [Source:HGNC
16	51477	-0.66	8e-05	1e-03	10 x 10 inositol-3-phosphate synthase 1 [Source:HGNC Symbol;Acc
17	83985	-0.65	1e-04	1e-03	7 x 10 spinster homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:
18	10587	-0.65	1e-04	1e-03	8 x 9 thioredoxin reductase 2 [Source:HGNC Symbol;Acc:18155]
19	645037	-0.64	1e-04	1e-03	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
20	22859	-0.64	1e-04	1e-03	12 x 10 latrophilin 1 [Source:HGNC Symbol;Acc:20973]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.88	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
2	-9.81	NULL	2 / 5	GSEA C2DASU_IL6_SIGNALING_UP
3	-8.78	NULL	2 / 10	BP GTP biosynthetic process
4	-8.33	NULL	2 / 11	BP CTP biosynthetic process
5	-8.33	NULL	2 / 11	BP UTP biosynthetic process
6	-6.9	NULL	2 / 13	GSEA C2SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY
7	-6.74	NULL	2 / 16	BP nucleoside diphosphate phosphorylation
8	-6.66	NULL	2 / 12	Glio willscher_GBM_LTSmut_proteomics-B_UP
9	-6.66	NULL	2 / 12	Glio willscher_GBM_STSwt_proteomics-B_DOWN
10	-6.58	NULL	1 / 10	GSEA C2POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN
11	-6.51	NULL	2 / 17	MF nucleoside diphosphate kinase activity
12	-6.42	NULL	3 / 8	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
13	-6.39	NULL	4 / 16	CC photoreceptor inner segment
14	-6.23	NULL	1 / 11	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C5
15	-6.23	NULL	1 / 11	GSEA C2VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
16	-6	NULL	1 / 6	GSEA C2SESTO_RESPONSE_TO_UV_C0
17	-6	NULL	1 / 6	GSEA C2BIOCARTA_TID_PATHWAY
18	-5.87	NULL	80 / 1135	Chr Chr 19
19	-5.82	NULL	11 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
20	-5.68	NULL	3 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
21	-5.59	NULL	4 / 15	BP semaphorin-plexin signaling pathway
22	-5.5	NULL	1 / 7	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_UP
23	-5.41	NULL	1 / 14	GSEA C2SMITH_TERT_TARGETS_DN
24	-5.41	NULL	1 / 14	GSEA C2REACTOME_METABLISM_OF_NUCLEOTIDES
25	-5.41	NULL	1 / 14	GSEA C2REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUC
26	-5.41	NULL	5 / 24	BP tissue development
27	-5.33	NULL	2 / 8	GSEA C2WEBER_METHYLATED_ICP_IN_FIBROBLAST
28	-5.21	NULL	5 / 44	CC presynaptic membrane
29	-5.12	NULL	2 / 12	GSEA C2KIM_WT1_TARGETS_12HR_UP
30	-5.1	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
31	-5.1	NULL	1 / 8	GSEA C2CHANDRAN_METASTASIS_UP
32	-5.1	NULL	1 / 8	GSEA C2WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53
33	-5.1	NULL	1 / 8	GSEA C2SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
34	-5.1	NULL	1 / 8	GSEA C2KEGG_PRION_DISEASES
35	-5.1	NULL	1 / 8	GSEA C2REACTOME_INFLUENZA_LIFE_CYCLE
36	-5.02	NULL	39 / 630	Chr Chr X
37	-5	NULL	1 / 16	BP nucleoside metabolic process
38	-5	NULL	1 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN
39	-4.85	NULL	1 / 4	GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_DN
40	-4.82	NULL	1 / 17	BP nucleobase-containing small molecule interconversion

p-values



GW_074

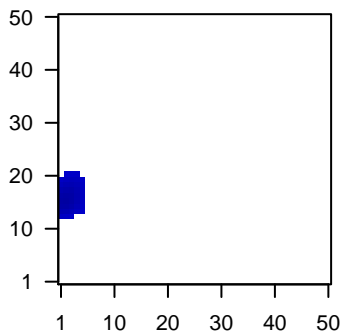
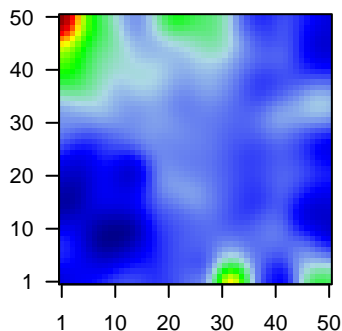
Local Summary

%DE = 0.61
 # metagenes = 41
 # genes = 388
 # genes in genesets = 386
 # genes with $fdr < 0.1$ = 84 (5 + / 79 -)
 # genes with $fdr < 0.05$ = 51 (4 + / 47 -)
 # genes with $fdr < 0.01$ = 23 (2 + / 21 -)

$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.27
 $\langle FC \rangle = -0.19$
 $\langle \text{shrinkage-t} \rangle = -6.59$
 $\langle p\text{-value} \rangle = 0.07$
 $\langle fdr \rangle = 0.8$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	430	1.03	7e-10	9e-05	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:10204]
2	131076	-0.83	6e-07	3e-04	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:131076]
3	389541	-0.77	5e-06	3e-04	3 x 19 late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [Source:HGNC Symbol;Acc:389541]
4	81037	-0.76	6e-06	3e-04	1 x 14 CLPTM1-like [Source:HGNC Symbol;Acc:24308]
5	8772	-0.76	6e-06	6e-04	1 x 14 Fas (TNFRSF6)-associated via death domain [Source:HGNC Symbol;Acc:8772]
6	2194	-0.74	1e-05	8e-04	1 x 17 fatty acid synthase [Source:HGNC Symbol;Acc:3594]
7	85359	-0.72	2e-05	8e-04	2 x 20 DiGeorge syndrome critical region gene 6-like [Source:HGNC Symbol;Acc:85359]
8	10204	-0.71	2e-05	8e-04	1 x 14 nuclear transport factor 2 [Source:HGNC Symbol;Acc:13722]
9	10467	-0.7	2e-05	2e-03	2 x 18 zinc finger, HIT-type containing 1 [Source:HGNC Symbol;Acc:10467]
10	5435	-0.68	4e-05	2e-03	3 x 17 polymerase (RNA) II (DNA directed) polypeptide F [Source:HGNC Symbol;Acc:5435]
11	27341	0.67	6e-05	2e-03	1 x 19 ribosomal RNA processing 7 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:27341]
12	64951	-0.66	7e-05	2e-03	2 x 18 mitochondrial ribosomal protein S24 [Source:HGNC Symbol;Acc:64951]
13	51181	-0.66	8e-05	2e-03	2 x 21 dicarbonyl/L-xylulose reductase [Source:HGNC Symbol;Acc:51181]
14	51069	-0.66	8e-05	4e-03	2 x 18 mitochondrial ribosomal protein L2 [Source:HGNC Symbol;Acc:51069]
15	283869	-0.63	1e-04	4e-03	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
16	3326	-0.62	2e-04	4e-03	1 x 14 heat shock protein 90kDa alpha (cytosolic), class B member 1 [Source:HGNC Symbol;Acc:3326]
17	230	-0.62	2e-04	4e-03	2 x 17 aldolase C, fructose-bisphosphate [Source:HGNC Symbol;Acc:230]
18	203068	-0.62	2e-04	5e-03	3 x 15 tubulin, beta class I [Source:HGNC Symbol;Acc:20778]
19	7384	-0.61	2e-04	5e-03	3 x 21 ubiquinol-cytochrome c reductase core protein I [Source:HGNC Symbol;Acc:7384]
20	8270	-0.61	3e-04	7e-03	4 x 17 L antigen family, member 3 [Source:HGNC Symbol;Acc:2605]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.7	NULL	2 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
2	-9.32	NULL	4 / 10	GSEA C2REACTOME_HIV_LIFE_CYCLE
3	-8.98	NULL	5 / 15	CC mitochondrial large ribosomal subunit
4	-7.89	NULL	6 / 19	CC mitochondrial small ribosomal subunit
5	-7.37	NULL	91 / 1318	CC mitochondrion
6	-6.87	NULL	24 / 153	MF structural constituent of ribosome
7	-6.71	NULL	3 / 16	GSEA C2REACTOME_MICRORNA_BIOGENESIS
8	-6.66	NULL	2 / 13	GSEA C2KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
9	-6.48	NULL	2 / 10	CC DNA-directed RNA polymerase I complex
10	-6.47	NULL	29 / 253	BP translation
11	-6.35	NULL	1 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
12	-6.34	NULL	3 / 11	MF telomeric DNA binding
13	-6.28	NULL	2 / 14	GSEA C2REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS
14	-6.25	NULL	1 / 6	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_DN
15	-6.23	NULL	5 / 39	BP gluconeogenesis
16	-6.19	NULL	4 / 16	GSEA C2OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP
17	-6.15	NULL	2 / 10	GSEA C2HONMA_DOCETAXEL_RESISTANCE
18	-6.08	NULL	3 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
19	-6.04	NULL	2 / 15	CC DNA-directed RNA polymerase II, core complex
20	-6.03	NULL	3 / 15	CC DNA-directed RNA polymerase III complex
21	-6.03	NULL	1 / 3	GSEA C2WEBER_METHYLATED_LCP_IN_SPERM_DN
22	-6.02	NULL	4 / 48	CC cell body
23	-5.99	NULL	10 / 63	TF MYC_Targets_UP
24	-5.96	NULL	3 / 7	GSEA C2PARK_HSC_MARKERS
25	-5.96	NULL	3 / 10	GSEA C2REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE
26	-5.92	NULL	2 / 17	BP long-chain fatty-acyl-CoA biosynthetic process
27	-5.88	NULL	3 / 14	GSEA C2PROVENZANI_METASTASIS_DN
28	-5.82	NULL	3 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
29	-5.8	NULL	4 / 50	BP protein homotetramerization
30	-5.79	NULL	3 / 16	Cancer GENTLES_modul7
31	-5.78	NULL	1 / 2	GSEA C2PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN
32	-5.78	NULL	1 / 2	GSEA C2REACTOME_DIABETES_PATHWAYS
33	-5.78	NULL	2 / 11	GSEA C2KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS
34	-5.76	NULL	4 / 13	GSEA C2XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
35	-5.72	NULL	1 / 4	Glio wilscher_GBM_STSwt_proteomics-L_UP
36	-5.63	NULL	3 / 11	MMML C6CIEJ_MMML_15
37	-5.62	NULL	4 / 34	BP extrinsic apoptotic signaling pathway
38	-5.58	NULL	6 / 44	BP positive regulation of viral transcription
39	-5.51	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
40	-5.5	NULL	3 / 11	GSEA C2REACTOME_CHAPERONIN_MEDIATED_PROTEIN_FOLDING

p-values

