

GW_250

Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1659 (1073 + / 586 -)
 # genes with fdr < 0.1 = 1348 (914 + / 434 -)
 # genes with fdr < 0.05 = 1019 (734 + / 285 -)
 # genes with fdr < 0.01 = 796 (614 + / 182 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.86

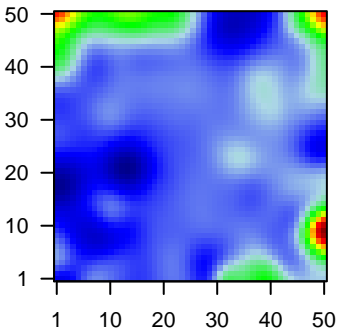
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.59	2e-16	2e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:33188]
2	58	1.73	2e-16	2e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12528]
3	131	1.27	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:HGNC Symbol;Acc:33188]
4	10551	1.66	2e-16	2e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	57016	1.94	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase) [Source:HGNC Symbol;Acc:33188]
6	441282	1.32	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:33188]
7	8644	1.81	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:33188]
8	1109	1.42	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:33188]
9	216	2.11	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:33188]
10	218	2.27	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:33188]
11	401138	1.66	2e-16	2e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
12	55107	2.33	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:33188]
13	200315	1.21	2e-16	2e-14	1 x 40 apolipoprotein B mRNA editing enzyme, catalytic polypeptide [Source:HGNC Symbol;Acc:33188]
14	347	1.78	2e-16	2e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
15	563	1.22	2e-16	2e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol;Acc:33188]
16	2583	1.23	2e-16	2e-14	1 x 9 beta-1,4-N-acetyl-galactosaminyl transferase 1 [Source:HGNC Symbol;Acc:33188]
17	25805	2.02	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC Symbol;Acc:33188]
18	590	1.16	2e-16	2e-14	16 x 50 butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
19	80341	1.9	2e-16	2e-14	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symbol;Acc:33188]
20	283422	1.33	2e-16	2e-14	9 x 50

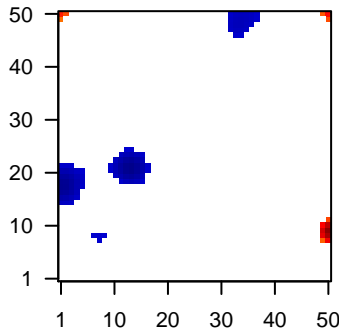
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	20.39	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	15.36	NULL	135	H.Tiss WIRTH_Mucosa
3	12.27	NULL	386	Chr Chr 22
4	11.79	NULL	572	Disease GUDJ_psooriasis up
5	8.93	NULL	13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
6	8.38	NULL	1720	Chr Chr 1
7	8.36	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
8	8.34	NULL	24	TF TissuèAQUERIZAS_Trachea
9	8.06	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
10	8.04	NULL	51	BP type I interferon signaling pathway
11	7.63	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
12	7.6	NULL	1182	CC extracellular region
13	7.45	NULL	7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
14	7.4	NULL	16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
15	7.28	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
16	7.26	NULL	375	Disease GUDJ_psooriasis down
17	7.02	NULL	53	BP keratinocyte differentiation
18	6.97	NULL	123	BP defense response to virus
19	6.82	NULL	9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
20	6.73	NULL	16	TF TissuèAQUERIZAS_Pancreas
<i>Underexpressed</i>				
1	-9.51	NULL	253	BP translation
2	-8.76	NULL	153	MF structural constituent of ribosome
3	-8.58	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
4	-8.2	NULL	167	CC ribosome
5	-8.09	NULL	81	BP viral transcription
6	-8.03	NULL	92	BP translational elongation
7	-8	NULL	649	BP gene expression
8	-7.93	NULL	128	BP translational initiation
9	-7.76	NULL	87	BP translational termination
10	-7.26	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
11	-7.07	NULL	242	BP RNA metabolic process
12	-7.04	NULL	4	MMML C6SCIEJ_MMML 23
13	-6.95	NULL	482	BP cellular protein metabolic process
14	-6.91	NULL	92	BP viral life cycle
15	-6.6	NULL	287	BP viral process
16	-6.24	NULL	219	BP mRNA metabolic process
17	-6.23	NULL	1233	TF KIM_MYC targets
18	-6.1	NULL	51	CC cytosolic large ribosomal subunit
19	-5.91	NULL	37	CC cytosolic small ribosomal subunit
20	-5.85	NULL	1135	Chr Chr 19

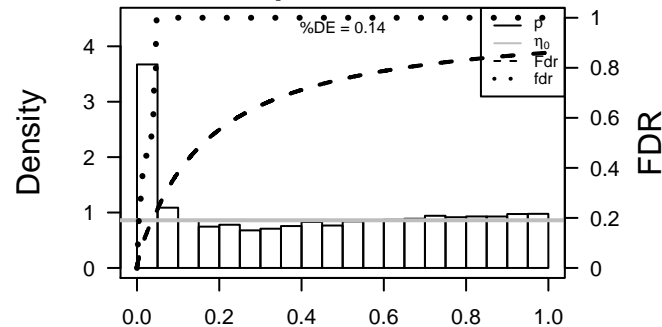
Profile



Regulated Spots



p-values



GW_250

Local Summary

%DE = 0.83
 # metagenes = 9
 # genes = 133
 # genes in genesets = 132

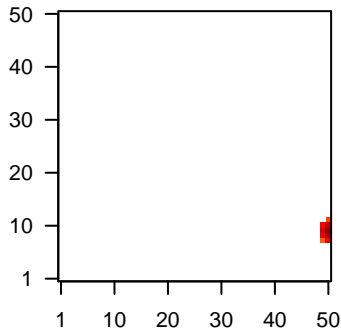
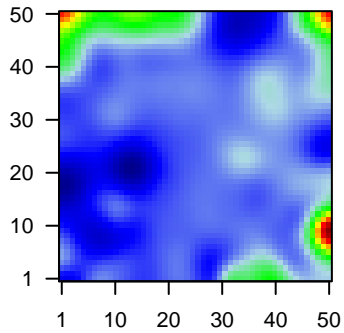
genes with $fdr < 0.1 = 100$ (97 + / 3 -)
 # genes with $fdr < 0.05 = 90$ (89 + / 1 -)
 # genes with $fdr < 0.01 = 78$ (77 + / 1 -)

<r> metagenes = 0.96
 <r> genes = 0.32

<FC> = 0.79
 <shrinkage-t> = 27.7
 <p-value> = 0
 <fdr> = 0.34

Profile

Spot



Local Genelist

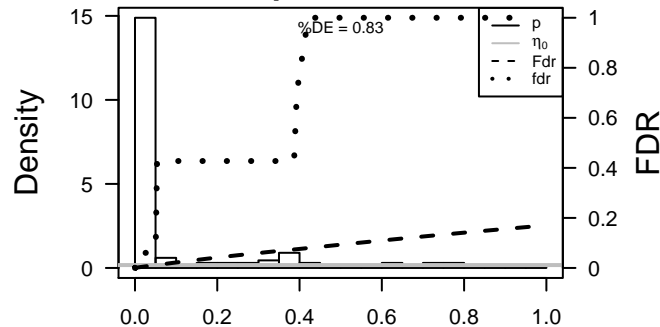
Rank	ID	log(FC)	fdr	p-value	Description
1	10551	1.66	2e-16	2e-16	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	563	1.22	2e-16	2e-16	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol]
3	80341	1.9	2e-16	2e-16	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symb]
4	92747	4.88	2e-16	2e-16	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb]
5	352999	2.69	2e-16	2e-16	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symb]
6	10321	1.15	2e-16	2e-16	50 x 10 cysteine-rich secretory protein 3 [Source:HGNC Symbol;Acc:
7	1755	1.63	2e-16	2e-16	50 x 10 deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
8	2878	1.15	2e-16	2e-16	50 x 9 glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
9	57535	1.98	2e-16	2e-16	50 x 10 KIAA1324 [Source:HGNC Symbol;Acc:29618]
10	124220	2.05	2e-16	2e-16	50 x 10 zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
11	389816	2.32	2e-16	2e-16	50 x 10 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc:
12	4057	1.26	2e-16	2e-16	50 x 10 lactotransferrin [Source:HGNC Symbol;Acc:6720]
13	25840	1.17	2e-16	2e-16	50 x 11 methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
14	79083	1.17	2e-16	2e-16	50 x 10 melanophilin [Source:HGNC Symbol;Acc:29643]
15	4477	3.36	2e-16	2e-16	50 x 11 microseminoprotein, beta- [Source:HGNC Symbol;Acc:7372]
16	4824	1.29	2e-16	2e-16	50 x 10 NK3 homeobox 1 [Source:HGNC Symbol;Acc:7838]
17	5284	2.46	2e-16	2e-16	50 x 10 polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	5304	3.41	2e-16	2e-16	50 x 10 prolactin-induced protein [Source:HGNC Symbol;Acc:8993]
19	51297	1.51	2e-16	2e-16	50 x 10 BPI fold containing family A, member 1 [Source:HGNC Symb]
20	653247	1.99	2e-16	2e-16	50 x 10 proline-rich protein BstNI subfamily 2 [Source:HGNC Symbol]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	52.2	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	20.62	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	17.2	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
4	16.16	NULL	2 / 10	GSEA C2LI_THYROID_CANCER_CLUSTER_5
5	14.26	NULL	1 / 9	GSEA C2SOUYER_TATI_TARGETS_UP
6	13.8	NULL	2 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
7	13.35	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
8	11.43	NULL	1 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
9	11.11	NULL	2 / 15	GSEA C2LOPES_METHYLATED_IN_COLON_CANCER_UP
10	10.02	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_I
11	9.98	NULL	1 / 15	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
12	9.68	NULL	31 / 1182	CC extracellular region
13	8.57	NULL	24 / 683	CC extracellular space
14	8.43	NULL	2 / 16	GSEA C2AIYAR_COBRA1_TARGETS_UP
15	8.27	NULL	2 / 7	TF Tissue/AQUERIZAS_Appendix
16	7.94	NULL	4 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
17	7.63	NULL	2 / 15	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
18	7.12	NULL	2 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
19	7.01	NULL	2 / 37	BP digestion
20	6.97	NULL	5 / 61	CC secretory granule
21	6.7	NULL	1 / 15	GSEA C2HORIUCHI_WTAP_TARGETS_UP
22	6.7	NULL	1 / 15	GSEA C2SENESE_HDAC1_TARGETS_UP
23	6.7	NULL	1 / 15	GSEA C2DOUGLAS_BMI1_TARGETS_DN
24	6.66	NULL	1 / 13	GSEA C2NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
25	6.62	NULL	20 / 375	Disease GUDJ_psooriasis down
26	6.53	NULL	3 / 115	MF lipid binding
27	6.44	NULL	2 / 14	GSEA C2PENG_RAPAMYCIN_RESPONSE_UP
28	6.24	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
29	6.23	NULL	2 / 13	GSEA C2HUANG_DASATINIB_RESISTANCE_DN
30	6.19	NULL	2 / 14	Cancer LIU_LIVER_CANCER
31	5.99	NULL	3 / 53	Glio Christensen_hypermethylated_in_primary_glioblastoma
32	5.88	NULL	1 / 11	GSEA C2PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
33	5.66	NULL	2 / 17	Disease BCHETNIA_EBM up
34	5.58	NULL	1 / 12	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN
35	5.46	NULL	2 / 56	BP response to peptide hormone
36	5.45	NULL	3 / 14	BP negative regulation of epithelial to mesenchymal transition
37	5.42	NULL	2 / 17	BP iron ion transport
38	5.37	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_I
39	5.3	NULL	1 / 13	BP negative regulation of bone mineralization
40	5.17	NULL	2 / 76	BP defense response

p-values



GW_250

Local Summary

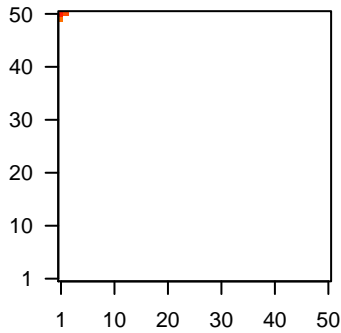
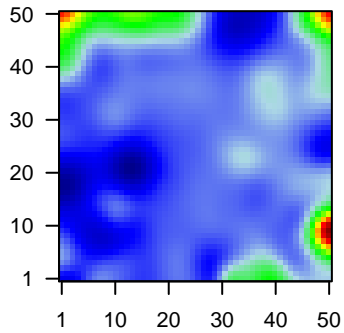
%DE = 0.82
 # metagenes = 3
 # genes = 93
 # genes in genesets = 91
 # genes with $fdr < 0.1$ = 63 (56 + / 7 -)
 # genes with $fdr < 0.05$ = 60 (54 + / 6 -)
 # genes with $fdr < 0.01$ = 56 (51 + / 5 -)

<r> metagenes = 1
 <r> genes = 0.56

<FC> = 0.55
 <shrinkage-t> = 19.62
 <p-value> = 0
 <fdr> = 0.33

Profile

Spot



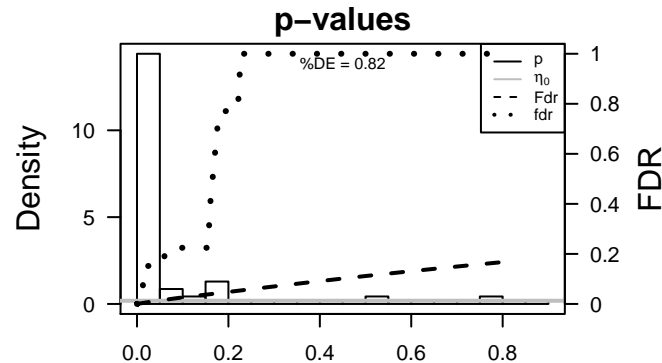
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	1.27	2e-16	2e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.94	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.32	2e-16	2e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	1.81	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
5	218	2.27	2e-16	2e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	4680	1.69	2e-16	2e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
7	22802	2.04	2e-16	2e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	1673	1.19	2e-16	2e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
9	2877	1.65	2e-16	2e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
10	5650	1.19	2e-16	2e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63
11	3860	1.38	2e-16	2e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
12	3851	2.37	2e-16	2e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
13	4118	1.67	2e-16	2e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
14	6700	1.27	2e-16	2e-16	1 x 50 small proline-rich protein 2A [Source:HGNC Symbol;Acc:112
15	6705	1.34	2e-16	2e-16	1 x 50 small proline-rich protein 2F [Source:HGNC Symbol;Acc:112
16	6707	1.28	2e-16	2e-16	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126
17	6947	1.85	2e-16	2e-16	2 x 50 transcobalamin I (vitamin B12 binding protein, R binder family
18	7053	1.21	2e-16	2e-16	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
19	339967	1.8	2e-16	2e-16	2 x 50 transmembrane protease, serine 11A [Source:HGNC Symbol
20	9407	1.61	2e-16	2e-16	1 x 50 transmembrane protease, serine 11D [Source:HGNC Symbol

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	36.98	NULL	45 / 135	H.Tiss WIRTH_Mucosa
2	27.89	NULL	12 / 21	CC cornified envelope
3	26.39	NULL	16 / 53	BP keratinocyte differentiation
4	25.65	NULL	13 / 42	BP keratinization
5	23.43	NULL	3 / 12	BP cellular aldehyde metabolic process
6	20.91	NULL	5 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
7	18.34	NULL	13 / 76	BP epidermis development
8	18.31	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
9	18.04	NULL	4 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
10	17.58	NULL	7 / 19	BP peptide cross-linking
11	17.56	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
12	15.65	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
13	14.72	NULL	4 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
14	14.19	NULL	43 / 572	Disease GUDJ_psooriasis up
15	13.32	NULL	1 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
16	12.56	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
17	12.49	NULL	2 / 14	GSEA C2KEGG_PHENYLALANINE_METABOLISM
18	12.47	NULL	3 / 15	MF retinol dehydrogenase activity
19	12.1	NULL	4 / 39	BP retinoid metabolic process
20	11.56	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_X
21	11.41	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
22	11.39	NULL	1 / 9	GSEA C2GOUYER_TUMOR_INVASIVENESS
23	11.34	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
24	10.84	NULL	2 / 16	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_UP
25	10.67	NULL	1 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
26	10.62	NULL	1 / 13	MF oxidoreductase activity, acting on the aldehyde or oxo group of don
27	10.25	NULL	2 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
28	9.94	NULL	1 / 10	BP positive regulation of endothelial cell apoptotic process
29	9.94	NULL	1 / 10	BP retinal metabolic process
30	9.63	NULL	2 / 14	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
31	9.6	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
32	9.53	NULL	1 / 12	GSEA C2ONDER_CDH1_TARGETS_1_UP
33	9.46	NULL	2 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
34	9.37	NULL	1 / 11	BP prostaglandin metabolic process
35	9.08	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
36	9.07	NULL	1 / 13	GSEA C2BRUECKNER_TARGETS_OF_MIRLET7A3_DN
37	9.07	NULL	1 / 13	GSEA C2KEGG_BUTANOATE_METABOLISM
38	8.91	NULL	10 / 122	MF serine-type endopeptidase activity
39	8.74	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
40	8.73	NULL	1 / 18	MF acyl-CoA dehydrogenase activity



GW_250

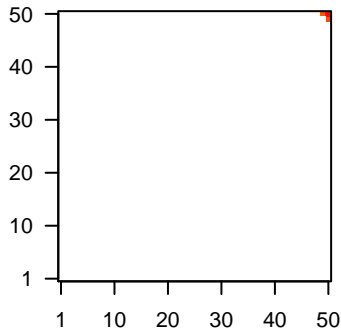
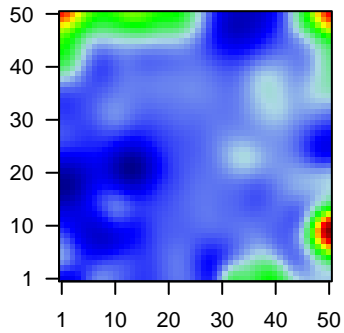
Local Summary

%DE = 0.74
 # metagenes = 3
 # genes = 106
 # genes in genesets = 105
 # genes with $fdr < 0.1 = 62$ (60 + / 2 -)
 # genes with $fdr < 0.05 = 62$ (60 + / 2 -)
 # genes with $fdr < 0.01 = 60$ (58 + / 2 -)

<r> metagenes = 1
 <r> genes = 0.33
 <FC> = 0.55
 <shrinkage-t> = 19.26
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



Local Genelist

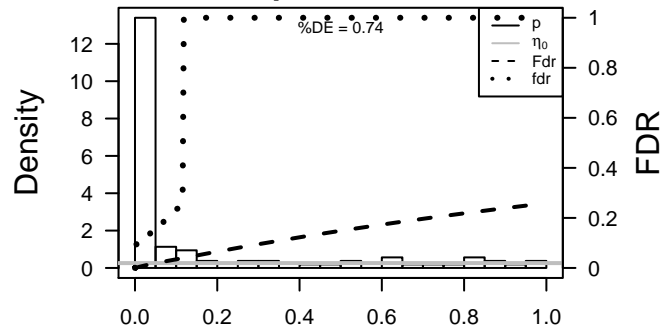
Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.59	2e-16	4e-16	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC]
2	216	2.11	2e-16	4e-16	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
3	339512	1.99	2e-16	4e-16	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt]
4	1592	1.27	2e-16	4e-16	50 x 50 cytochrome P450, family 26, subfamily A, polypeptide 1 [Source:HGNC]
5	10655	1.89	2e-16	4e-16	50 x 50 doublesex and mab-3 related transcription factor 2 [Source:HGNC]
6	2719	1.75	2e-16	4e-16	50 x 50 glypican 3 [Source:HGNC Symbol;Acc:4451]
7	2944	1.44	2e-16	4e-16	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4451]
8	84171	1.41	2e-16	4e-16	50 x 49 lysyl oxidase-like 4 [Source:HGNC Symbol;Acc:17171]
9	4922	3.94	2e-16	4e-16	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
10	9182	1.29	2e-16	4e-16	50 x 50 Ras association (RalGDS/AF-6) domain family (N-terminal) 1 [Source:HGNC]
11	6657	1.27	2e-16	4e-16	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbol;Acc:11166]
12	11166	1.46	2e-16	4e-16	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symbol;Acc:11166]
13	7348	1.9	2e-16	4e-16	50 x 50 uroplakin 1B [Source:HGNC Symbol;Acc:12578]
14	256764	1.41	2e-16	4e-16	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
15	56256	1.14	4e-16	4e-14	50 x 50 SERTA domain containing 4 [Source:HGNC Symbol;Acc:25216]
16	56548	1.11	2e-15	1e-13	50 x 50 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 [Source:HGNC]
17	23321	1.09	6e-15	5e-13	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:15974]
18	26047	1.06	2e-14	3e-12	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Acc:15974]
19	214	1.03	1e-13	3e-11	50 x 50 activated leukocyte cell adhesion molecule [Source:HGNC Symbol;Acc:15974]
20	4915	0.99	1e-12	3e-11	50 x 50 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	34.73	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	22.87	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
3	19.9	NULL	1 / 11	Glio neurons_glio
4	18.57	NULL	3 / 13	BP regulation of blood vessel size
5	17.3	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
6	16.81	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
7	16.56	NULL	1 / 15	MF neuropeptide hormone activity
8	16.16	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
9	15.46	NULL	1 / 6	GSEA C2SAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
10	15.46	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
11	15	NULL	3 / 11	MF glutathione binding
12	15	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	14.01	NULL	1 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
14	13.14	NULL	3 / 16	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G1_DN
15	11.97	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
16	11.97	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
17	11.5	NULL	1 / 8	GSEA C2NIELSEN_LIPOSARCOMA_UP
18	11.22	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
19	11.22	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
20	10.48	NULL	1 / 2	miRNA target-127
21	10.39	NULL	1 / 5	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_DN
22	10.2	NULL	2 / 12	BP cellular aldehyde metabolic process
23	10.04	NULL	1 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY
24	9.94	NULL	11 / 119	BP xenobiotic metabolic process
25	9.93	NULL	2 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
26	9.92	NULL	5 / 20	MF glutathione transferase activity
27	9.77	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
28	9.77	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_E2F1_UP
29	9.55	NULL	6 / 25	BP glutathione derivative biosynthetic process
30	9.47	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
31	9.27	NULL	1 / 41	CC transport vesicle
32	9.15	NULL	1 / 14	MF Ras GTPase activator activity
33	9.15	NULL	1 / 14	GSEA C2TTONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
34	9.15	NULL	1 / 14	GSEA C2MAHADEVAN_IMATINIB_RESISTANCE_UP
35	9.01	NULL	1 / 12	GSEA C2DAZARD_RESPONSE_TO_UV_SCC_UP
36	8.84	NULL	2 / 23	BP stem cell differentiation
37	8.8	NULL	8 / 34	BP glutathione metabolic process
38	8.78	NULL	1 / 15	GSEA C2DORSAM_HOXA9_TARGETS_UP
39	8.47	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
40	8.32	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION

p-values



GW_250

Local Summary

%DE = 0.84
 # metagenes = 4
 # genes = 36
 # genes in genesets = 36

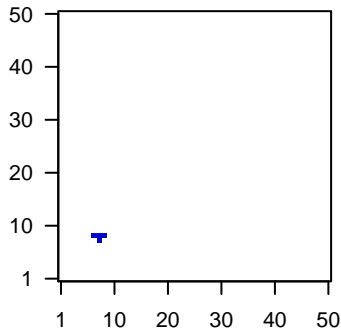
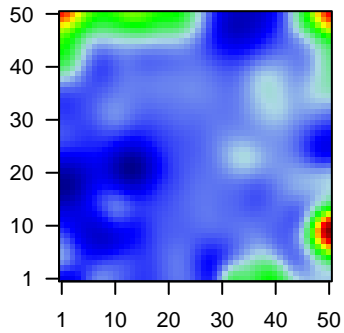
 # genes with $fdr < 0.1 = 17$ (1 + / 16 -)
 # genes with $fdr < 0.05 = 16$ (1 + / 15 -)
 # genes with $fdr < 0.01 = 13$ (1 + / 12 -)

 $\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.33

 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -6.85$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.63$

Profile

Spot



Local Genelist

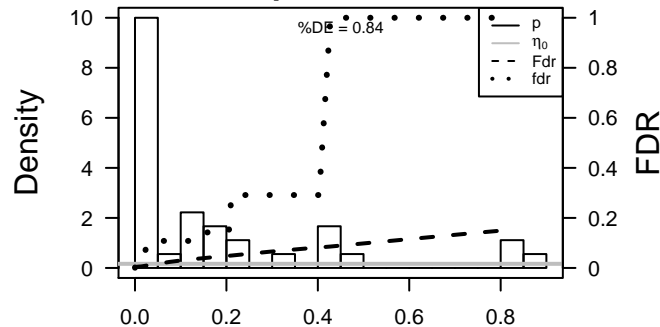
Rank	ID	log(FC)	fdr	p-value	Description
1	3636	0.78	2e-08	9e-04	inositol polyphosphate phosphatase-like 1 [Source:HGNC Sy
2	140465	-0.53	2e-04	5e-03	myosin, light chain 6B, alkali, smooth muscle and non-muscl
3	11018	-0.46	1e-03	7e-03	transmembrane emp24 protein transport domain containing 1
4	83862	-0.41	3e-03	7e-03	transmembrane protein 120A [Source:HGNC Symbol;Acc:21f
5	53635	-0.4	4e-03	7e-03	prostate tumor overexpressed 1 [Source:HGNC Symbol;Acc:f
6	51293	-0.39	5e-03	7e-03	CD320 molecule [Source:HGNC Symbol;Acc:16692]
7	199990	-0.38	6e-03	7e-03	chromosome 1 open reading frame 86 [Source:HGNC Symbc
8	29844	-0.37	9e-03	7e-03	TCF3 (E2A) fusion partner (in childhood Leukemia) [Source:t
9	7466	-0.36	1e-02	7e-03	Wolfram syndrome 1 (wolframin) [Source:HGNC Symbol;Acc:
10	1845	-0.36	1e-02	7e-03	dual specificity phosphatase 3 [Source:HGNC Symbol;Acc:3c
11	7389	-0.36	1e-02	7e-03	uroporphyrinogen decarboxylase [Source:HGNC Symbol;Acc
12	1936	-0.35	1e-02	7e-03	eukaryotic translation elongation factor 1 delta (guanine nucle
13	51507	-0.35	1e-02	7e-03	replication termination factor 2 domain containing 1 [Source:t
14	60673	-0.34	1e-02	1e-02	chromosome 12 open reading frame 44 [Source:HGNC Synt
15	10953	-0.34	2e-02	1e-02	translocase of outer mitochondrial membrane 34 [Source:HG
16	57617	-0.33	2e-02	3e-02	vacuolar protein sorting 18 homolog (S. cerevisiae) [Source:t
17	1155	-0.32	2e-02	6e-02	tubulin folding cofactor B [Source:HGNC Symbol;Acc:1989]
18	10459	-0.29	3e-02	1e-01	MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S
19	54764	-0.24	8e-02	1e-01	zinc finger, RAN-binding domain containing 1 [Source:HGNC
20	4669	-0.23	1e-01	1e-01	N-acetylglucosaminidase, alpha [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.05	NULL	2 / 10	MF K63-linked polyubiquitin binding
2	-12.46	NULL	1 / 5	miRNA 3619-5P
3	-11.92	NULL	1 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
4	-10.33	NULL	1 / 13	CC muscle myosin complex
5	-10.33	NULL	1 / 13	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
6	-9.93	NULL	1 / 14	GSEA C2REACTOME_MUSCLE_CONTRACTION
7	-9.58	NULL	1 / 15	GSEA C2GOLUB_ALL_VS_AML_UP
8	-8.85	NULL	1 / 8	GSEA C2CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN
9	-8.57	NULL	1 / 10	CC Fanconi anaemia nuclear complex
10	-8.1	NULL	1 / 10	BP neurological system process
11	-7.98	NULL	1 / 9	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR
12	-7.84	NULL	2 / 37	CC actin filament
13	-7.69	NULL	1 / 11	BP negative regulation of programmed cell death
14	-7.66	NULL	1 / 11	GSEA C2REACTOME_ERKS_ARE_INACTIVATED
15	-7.61	NULL	1 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
16	-7.54	NULL	1 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
17	-7.31	NULL	1 / 12	BP negative regulation of T cell activation
18	-7.31	NULL	1 / 12	BP negative regulation of T cell receptor signaling pathway
19	-7.26	NULL	1 / 12	BP porphyrin-containing compound biosynthetic process
20	-7.16	NULL	1 / 11	GSEA C2SMITH_TERT_TARGETS_UP
21	-7.13	NULL	2 / 29	BP lysosome organization
22	-7.02	NULL	1 / 11	CC HOPS complex
23	-7	NULL	1 / 13	BP negative regulation of MAPK cascade
24	-6.86	NULL	1 / 16	BP cobalamin metabolic process
25	-6.85	NULL	1 / 14	CC Ino80 complex
26	-6.83	NULL	1 / 12	GSEA C2BENPORATH_CYCLING_GENES
27	-6.83	NULL	1 / 12	GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_UP
28	-6.66	NULL	1 / 16	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_U
29	-6.59	NULL	1 / 10	BP negative regulation of transcription by competitive promoter binding
30	-6.55	NULL	1 / 14	GSEA C2SWEET_KRAS_ONCOGENIC_SIGNATURE
31	-6.54	NULL	1 / 13	GSEA C2FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_UP
32	-6.54	NULL	1 / 13	GSEA C2DOUGLAS_BM1_TARGETS_UP
33	-6.48	NULL	1 / 15	GSEA C2WONG_IFNA2_RESISTANCE_DN
34	-6.45	NULL	1 / 24	CC endoplasmic reticulum-Golgi intermediate compartment membran
35	-6.31	NULL	1 / 15	GSEA C2MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN
36	-6.31	NULL	1 / 15	GSEA C2MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN
37	-6.31	NULL	1 / 15	GSEA C2CHOW_RASSF1_TARGETS_DN
38	-6.31	NULL	1 / 15	GSEA C2FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN
39	-6.31	NULL	1 / 15	GSEA C2ANTVEER_BREAST_CANCER_BRCA1_UP
40	-6.31	NULL	1 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN

p-values



GW_250

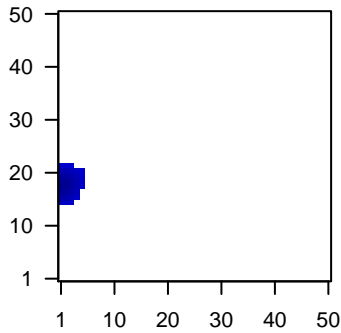
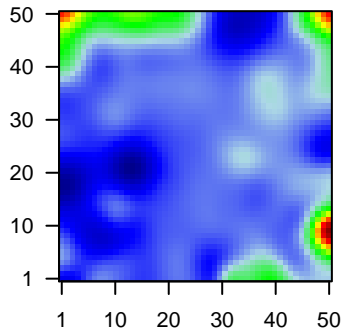
Local Summary

%DE = 0.67
 # metagenes = 34
 # genes = 354
 # genes in genesets = 352
 # genes with $fdr < 0.1$ = 197 (22 + / 175 -)
 # genes with $fdr < 0.05$ = 86 (17 + / 69 -)
 # genes with $fdr < 0.01$ = 38 (10 + / 28 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.28
 $\langle FC \rangle = -0.18$
 $\langle \text{shrinkage-t} \rangle = -6.44$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.7$

Profile

Spot



Local Genelist

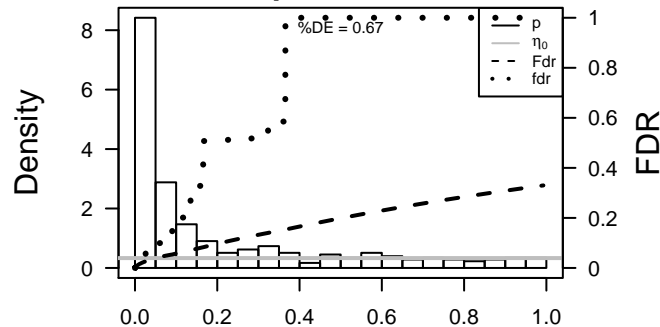
Rank	ID	log(FC)	fdr	p-value	Description
1	219927	1.02	2e-13	5e-11	1 x 15 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;]
2	27237	1	7e-13	8e-07	2 x 20 Rho guanine nucleotide exchange factor (GEF) 16 [Source:HGNC Symbol;]
3	51702	0.81	7e-09	5e-06	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;]
4	3237	-0.76	5e-08	4e-05	1 x 16 homeobox D11 [Source:HGNC Symbol;Acc:5134]
5	63875	-0.71	4e-07	4e-05	1 x 18 mitochondrial ribosomal protein L17 [Source:HGNC Symbol;]
6	7965	-0.69	7e-07	1e-04	1 x 15 aminoacyl tRNA synthetase complex-interacting multifunctional
7	64979	-0.66	2e-06	2e-04	1 x 16 mitochondrial ribosomal protein L36 [Source:HGNC Symbol;]
8	131076	0.64	5e-06	2e-04	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:30943]
9	375757	-0.64	5e-06	3e-04	1 x 21 SWI5 recombination repair homolog (yeast) [Source:HGNC Symbol;]
10	388581	0.62	8e-06	3e-04	1 x 15 family with sequence similarity 132, member A [Source:HGNC Symbol;]
11	26873	0.61	1e-05	3e-04	1 x 17 5-oxoprolinase (ATP-hydrolysing) [Source:HGNC Symbol;]
12	2597	-0.56	1e-05	5e-04	2 x 17 glyceraldehyde-3-phosphate dehydrogenase [Source:HGNC Symbol;]
13	51042	-0.6	2e-05	5e-04	1 x 19 zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
14	51373	-0.59	2e-05	5e-04	1 x 16 28S ribosomal protein S17, mitochondrial; HCG1984214, isoform
15	51400	0.59	3e-05	9e-04	1 x 18 protein phosphatase methylesterase 1 [Source:HGNC Symbol;]
16	230	-0.58	3e-05	1e-03	2 x 17 aldolase C, fructose-bisphosphate [Source:HGNC Symbol;]
17	10428	-0.57	4e-05	1e-03	1 x 15 craniofacial development protein 1 [Source:HGNC Symbol;]
18	57109	-0.56	6e-05	1e-03	1 x 20 REX4, RNA exonuclease 4 homolog (S. cerevisiae) [Source:HGNC Symbol;]
19	8045	-0.56	6e-05	1e-03	2 x 22 Ras association (RalGDS/AF-6) domain family (N-terminal) member
20	3276	-0.55	7e-05	1e-03	3 x 17 protein arginine methyltransferase 1 [Source:HGNC Symbol;]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.09	NULL	3 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
2	-9.88	NULL	18 / 96	BP rRNA processing
3	-9.49	NULL	25 / 153	MF structural constituent of ribosome
4	-8.65	NULL	4 / 13	BP ribosomal small subunit biogenesis
5	-8.47	NULL	6 / 19	CC mitochondrial small ribosomal subunit
6	-8.29	NULL	21 / 167	CC ribosome
7	-8.28	NULL	3 / 13	GSEA C2REACTOME_GLYCOLYSIS
8	-8.13	NULL	4 / 13	GSEA C2XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
9	-8.03	NULL	2 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP
10	-7.95	NULL	4 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
11	-7.67	NULL	28 / 253	BP translation
12	-7.47	NULL	5 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN
13	-7.38	NULL	3 / 15	GSEA C2KORKOLA_YOLK_SAC_TUMOR_UP
14	-7.31	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
15	-6.78	NULL	3 / 15	GSEA C2MULLIGHAN_MLL_SIGNATURE_1_UP
16	-6.74	NULL	38 / 579	CC nucleolus
17	-6.73	NULL	1 / 4	GSEA C2ACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_DN
18	-6.66	NULL	2 / 12	GSEA C2WANG_SMARCE1_TARGETS_DN
19	-6.63	NULL	3 / 14	Pathw AcBENTINK_myc.1
20	-6.59	NULL	3 / 12	BP apoptotic nuclear changes
21	-6.48	NULL	4 / 39	BP glycolysis
22	-6.41	NULL	3 / 7	GSEA C2PARK_HSC_MARKERS
23	-6.4	NULL	5 / 15	CC mitochondrial large ribosomal subunit
24	-6.35	NULL	3 / 16	GSEA C2KORKOLA_SEMINOMA_UP
25	-6.28	NULL	3 / 13	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
26	-6.25	NULL	3 / 11	MMML C2SCIEJ_MMML_15
27	-6.25	NULL	4 / 14	GSEA C2LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
28	-6.22	NULL	2 / 15	GSEA C2SEMENZA_HIF1_TARGETS
29	-6.2	NULL	2 / 10	GSEA C2HONMA_DOCETAXEL_RESISTANCE
30	-6.19	NULL	3 / 14	MF snoRNA binding
31	-6.19	NULL	88 / 1318	CC mitochondrion
32	-6.01	NULL	3 / 12	GSEA C2KEGG_PYRIMIDINE_METABOLISM
33	-5.83	NULL	1 / 8	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
34	-5.77	NULL	2 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
35	-5.68	NULL	1 / 7	TF MYC_DNA repair UP
36	-5.49	NULL	7 / 63	TF MYC_Targets UP
37	-5.42	NULL	6 / 37	CC mitochondrial nucleoid
38	-5.36	NULL	2 / 8	GSEA C2REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
39	-5.32	NULL	2 / 9	GSEA C2ACOSTA_UV_RESPONSE_VIA_ERCC3_UP
40	-5.28	NULL	4 / 16	GSEA C2MOOTHA_HUMAN_MITODB_6_2002

p-values



GW_250

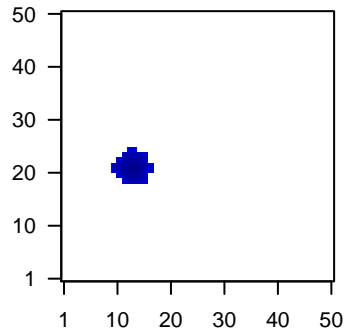
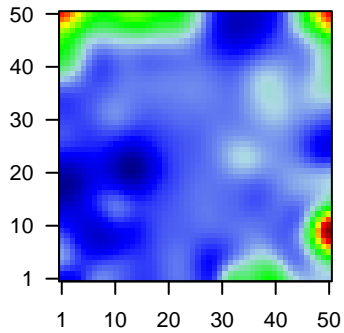
Local Summary

%DE = 0.74
 # metagenes = 40
 # genes = 319
 # genes in genesets = 311
 # genes with $fdr < 0.1$ = 121 (3 + / 118 -)
 # genes with $fdr < 0.05$ = 40 (2 + / 38 -)
 # genes with $fdr < 0.01$ = 30 (1 + / 29 -)

$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.19
 $\langle FC \rangle = -0.21$
 $\langle \text{shrinkage-t} \rangle = -7.28$
 $\langle p\text{-value} \rangle = 0.07$
 $\langle fdr \rangle = 0.79$

Profile

Spot



Local Genelist

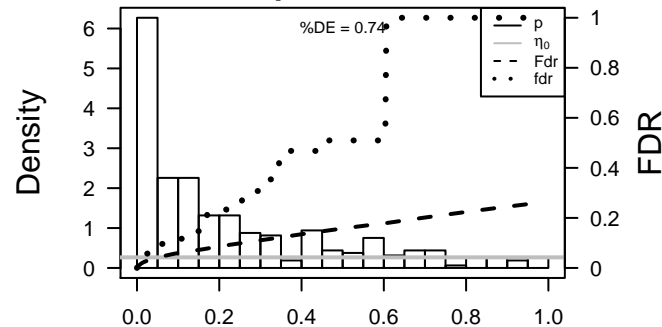
Rank	ID	log(FC)	fdr	p-value	Description
1	6302	0.64	5e-06	2e-04	tetraspanin 31 [Source:HGNC Symbol;Acc:10539]
2	79078	-0.63	5e-06	2e-04	chromosome 1 open reading frame 50 [Source:HGNC Symb
3	100128731	-0.62	8e-06	2e-04	oligosaccharyltransferase 4 homolog (S. cerevisiae) [Source:l
4	150684	-0.62	9e-06	4e-04	copper metabolism (Murr1) domain containing 1 [Source:HGf
5	6881	-0.61	1e-05	4e-03	TAF10 RNA polymerase II, TATA box binding protein (TBP)-a
6	28974	-0.54	1e-04	4e-03	chromosome 19 open reading frame 53 [Source:HGNC Synt
7	51255	-0.53	1e-04	4e-03	ring finger protein 181 [Source:HGNC Symbol;Acc:28037]
8	3615	-0.52	2e-04	4e-03	IMP (inosine 5'-monophosphate) dehydrogenase 2 [Source:l
9	29964	-0.51	2e-04	4e-03	prickle homolog 4 (Drosophila) [Source:HGNC Symbol;Acc:1
10	140823	-0.51	3e-04	4e-03	reactive oxygen species modulator 1 [Source:HGNC Symbol;
11	56655	-0.5	3e-04	4e-03	polymerase (DNA-directed), epsilon 4, accessory subunit [Sc
12	327	-0.5	3e-04	4e-03	acylaminoacyl-peptide hydrolase [Source:HGNC Symbol;Acc
13	4713	-0.5	4e-04	4e-03	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 1e
14	28971	-0.49	4e-04	5e-03	adipogenesis associated, Mth938 domain containing [Source
15	100188893	-0.48	5e-04	5e-03	prickle homolog 4 (Drosophila) [Source:HGNC Symbol;Acc:1
16	6640	-0.48	5e-04	5e-03	syntrophin, alpha 1 [Source:HGNC Symbol;Acc:11167]
17	27090	-0.48	6e-04	5e-03	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-
18	55100	-0.47	7e-04	5e-03	WD repeat domain 70 [Source:HGNC Symbol;Acc:25495]
19	6150	-0.47	8e-04	5e-03	mitochondrial ribosomal protein L23 [Source:HGNC Symbol;f
20	6155	-0.43	9e-04	5e-03	ribosomal protein L27 [Source:HGNC Symbol;Acc:10328]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.35	NULL	4 / 15	GSEA C2REACTOME_MRNA_SPLICING_MINOR_PATHWAY
2	-8.22	NULL	2 / 4	MMML C6SCIEJ_MMML 23
3	-7.86	NULL	3 / 12	GSEA C2REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED
4	-7.77	NULL	3 / 9	GSEA C2KEGG_RNA_POLYMERASE
5	-7.52	NULL	3 / 13	GSEA C2REACTOME_FORMATION_AND_MATURATION_OF_MRNA_TRA
6	-7.41	NULL	58 / 1233	TF KIM_MYC targets
7	-7.24	NULL	6 / 38	MF DNA-directed RNA polymerase activity
8	-7.22	NULL	3 / 14	GSEA C2REACTOME_MRNA_SPLICING
9	-7.22	NULL	3 / 14	GSEA C2REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAININ
10	-7.18	NULL	2 / 7	MMML C6SCIEJ_MMML 48
11	-7.16	NULL	1 / 5	GSEA C2NAGY_PCAF_COMPONENTS_HUMAN
12	-7.03	NULL	2 / 13	CC STAGA complex
13	-6.75	NULL	2 / 14	CC transcription factor TF1C complex
14	-6.42	NULL	68 / 1318	CC mitochondrion
15	-6.29	NULL	3 / 15	CC mitochondrial large ribosomal subunit
16	-6.19	NULL	3 / 10	MF NADH dehydrogenase activity
17	-6.12	NULL	3 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
18	-6.02	NULL	4 / 16	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN
19	-6.01	NULL	2 / 9	GSEA C2REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_CO
20	-6.01	NULL	2 / 9	GSEA C2REACTOME_HIV1_TRANSCRIPTION_ELONGATION
21	-5.89	NULL	1 / 4	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G5_UP
22	-5.88	NULL	3 / 14	BP mitochondrial ATP synthesis coupled proton transport
23	-5.77	NULL	3 / 40	BP histone H3 acetylation
24	-5.67	NULL	2 / 10	GSEA C2REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
25	-5.67	NULL	2 / 10	GSEA C2REACTOME_HIV1_TRANSCRIPTION_INITIATION
26	-5.67	NULL	2 / 10	GSEA C2REACTOME_MRNA_PROCESSING
27	-5.67	NULL	2 / 10	GSEA C2REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INT
28	-5.65	NULL	3 / 15	BP ATP synthesis coupled proton transport
29	-5.57	NULL	1 / 8	GSEA C2NAGY_STAGA_COMPONENTS_HUMAN
30	-5.57	NULL	14 / 167	CC ribosome
31	-5.57	NULL	3 / 12	GSEA C2REACTOME_NUCLEOTIDE_EXCISION_REPAIR
32	-5.55	NULL	2 / 16	CC Ada2/Gcn5/Ada3 transcription activator complex
33	-5.38	NULL	2 / 13	BP vesicle fusion
34	-5.38	NULL	2 / 11	GSEA C2REACTOME_TRANSCRIPTION_COUPLED_NER
35	-5.36	NULL	2 / 10	BP peroxisome fission
36	-5.34	NULL	2 / 15	BP cellular response to reactive oxygen species
37	-5.3	NULL	6 / 51	CC cytosolic large ribosomal subunit
38	-5.12	NULL	2 / 12	GSEA C2KEGG_PYRIDIMINE_METABOLISM
39	-5.12	NULL	2 / 12	GSEA C2REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIP
40	-5.07	NULL	3 / 21	CC transcription factor TF1D complex

p-values



GW_250

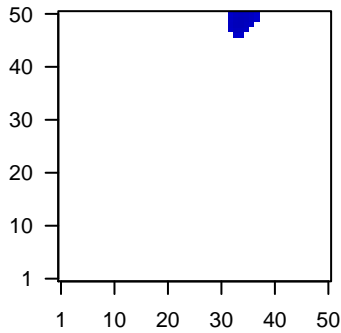
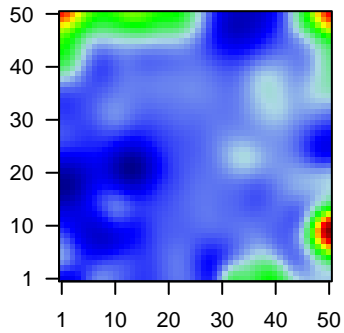
Local Summary

%DE = 0.59
 # metagenes = 23
 # genes = 272
 # genes in genesets = 262
 # genes with $fdr < 0.1$ = 55 (5 + / 50 -)
 # genes with $fdr < 0.05$ = 32 (5 + / 27 -)
 # genes with $fdr < 0.01$ = 7 (1 + / 6 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.25
 $\langle FC \rangle = -0.17$
 $\langle \text{shrinkage-t} \rangle = -6$
 $\langle p\text{-value} \rangle = 0.08$
 $\langle fdr \rangle = 0.8$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	51642	0.88	2e-10	1e-04	34 x 49 mitochondrial ribosomal protein L48 [Source:HGNC Symbol;]
2	26156	-0.68	1e-06	9e-04	37 x 50 ribosomal L1 domain containing 1 [Source:HGNC Symbol;Ac
3	64776	-0.61	1e-05	9e-04	32 x 49 chromosome 11 open reading frame 1 [Source:HGNC Symbc
4	6147	-0.6	2e-05	2e-03	33 x 49 ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
5	1069	-0.58	3e-05	5e-03	35 x 47 centrin, EF-hand protein, 2 [Source:HGNC Symbol;Acc:1867
6	4725	-0.55	7e-05	5e-03	34 x 50 NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (†
7	51406	-0.54	1e-04	6e-03	32 x 47 nucleolar protein 7, 27kDa [Source:HGNC Symbol;Acc:2104C
8	80306	-0.52	2e-04	2e-02	32 x 48 mediator complex subunit 28 [Source:HGNC Symbol;Acc:246
9	2271	0.49	5e-04	2e-02	35 x 50 fumarate hydratase [Source:HGNC Symbol;Acc:3700]
10	79035	-0.47	7e-04	2e-02	35 x 48 nucleic acid binding protein 2 [Source:HGNC Symbol;Acc:284
11	55505	-0.47	7e-04	2e-02	34 x 50 NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:14378]
12	51258	-0.46	9e-04	2e-02	36 x 49 mitochondrial ribosomal protein L51 [Source:HGNC Symbol;]
13	401505	-0.46	1e-03	2e-02	33 x 50 translocase of outer mitochondrial membrane 5 homolog (yea
14	6629	-0.45	1e-03	2e-02	34 x 46 small nuclear ribonucleoprotein polypeptide B [Source:HGNC
15	51260	-0.45	1e-03	2e-02	32 x 47 polysaccharide biosynthesis domain containing 1 [Source:HG
16	6133	-0.45	1e-03	3e-02	32 x 48 ribosomal protein L9 [Source:HGNC Symbol;Acc:10369]
17	654364	-0.44	2e-03	3e-02	36 x 50 NME1-NME2 readthrough [Source:HGNC Symbol;Acc:3353
18	80273	-0.43	2e-03	4e-02	35 x 50 GrpE-like 1, mitochondrial (E. coli) [Source:HGNC Symbol;A
19	10799	-0.43	2e-03	4e-02	34 x 50 ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;]
20	51611	-0.42	3e-03	4e-02	34 x 48 diphthamide biosynthesis 5 [Source:HGNC Symbol;Acc:2427

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-21.23	NULL	39 / 153	MF structural constituent of ribosome
2	-17.81	NULL	22 / 87	BP translational termination
3	-17.81	NULL	33 / 167	CC ribosome
4	-17.51	NULL	21 / 81	BP viral transcription
5	-17.2	NULL	22 / 92	BP translational elongation
6	-17.09	NULL	44 / 253	BP translation
7	-16.35	NULL	21 / 92	BP viral life cycle
8	-15.27	NULL	14 / 51	CC cytosolic large ribosomal subunit
9	-15.27	NULL	22 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
10	-15.16	NULL	22 / 109	BP SRP-dependent cotranslational protein targeting to membrane
11	-13.88	NULL	24 / 128	BP translational initiation
12	-12.7	NULL	27 / 242	BP RNA metabolic process
13	-12.66	NULL	26 / 219	BP mRNA metabolic process
14	-12.47	NULL	7 / 10	CC large ribosomal subunit
15	-12.33	NULL	12 / 36	CC mitochondrial respiratory chain complex I
16	-12.15	NULL	25 / 83	BP respiratory electron transport chain
17	-11.56	NULL	11 / 35	BP mitochondrial electron transport, NADH to ubiquinone
18	-11.48	NULL	11 / 34	MF NADH dehydrogenase (ubiquinone) activity
19	-11.27	NULL	2 / 7	GSEA C2WALK_AML_CLUSTER_6
20	-10.88	NULL	6 / 27	MF rRNA binding
21	-9.42	NULL	91 / 1318	CC mitochondrion
22	-9.34	NULL	26 / 287	BP viral process
23	-9.29	NULL	41 / 649	BP gene expression
24	-9.16	NULL	4 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
25	-8.88	NULL	32 / 482	BP cellular protein metabolic process
26	-8.62	NULL	4 / 9	GSEA C2KEGG_RIBOSOME
27	-8.62	NULL	4 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
28	-8.62	NULL	4 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
29	-8.62	NULL	4 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
30	-8.62	NULL	4 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
31	-8.62	NULL	4 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
32	-8.62	NULL	4 / 9	GSEA C2REACTOME_VIRAL_MRNA_TRANSLATION
33	-8.44	NULL	38 / 304	CC mitochondrial inner membrane
34	-8.33	NULL	2 / 15	GSEA C2GARCIA_TARGETS_OF_FL1_AND_DAX1_DN
35	-8.16	NULL	4 / 10	GSEA C2REACTOME_TRANSLATION
36	-8.01	NULL	6 / 11	Cancer GENTLES_modul5
37	-7.56	NULL	5 / 39	Cancer ZHANG_MM up
38	-7.31	NULL	26 / 152	BP cellular metabolic process
39	-7.27	NULL	4 / 11	BP ribosomal large subunit biogenesis
40	-7.01	NULL	4 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU

p-values

