

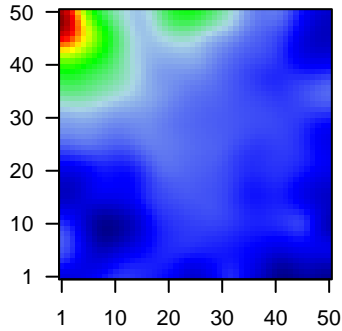
GW_070

Global Summary

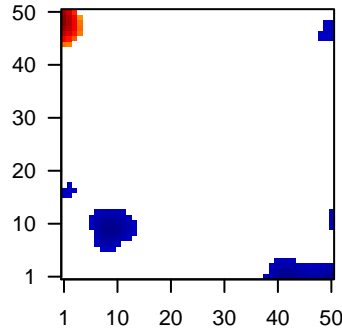
%DE = 0.14
 # genes with fdr < 0.2 = 1819 (1012 + / 807 -)
 # genes with fdr < 0.1 = 1463 (852 + / 611 -)
 # genes with fdr < 0.05 = 1258 (740 + / 518 -)
 # genes with fdr < 0.01 = 823 (515 + / 308 -)
 # genes in genesets = 16332

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

Profile



Regulated Spots



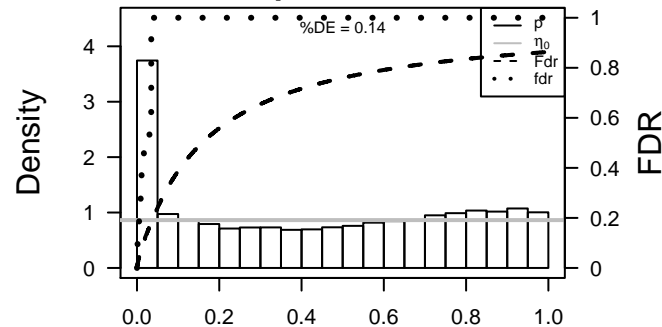
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.68	2e-16	3e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	57016	1.48	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.5	2e-16	3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	242	1.87	2e-16	3e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syn
5	360	1.83	2e-16	3e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	151516	2.53	2e-16	3e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
7	387695	2.1	2e-16	3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
8	260436	-1.5	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
9	375791	1.46	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
10	760	1.56	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
11	810	1.38	2e-16	3e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
12	51806	2.04	2e-16	3e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
13	595	-2.08	2e-16	3e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
14	1041	1.92	2e-16	3e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
15	9022	1.79	2e-16	3e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
16	84518	1.57	2e-16	3e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
17	1410	-1.44	2e-16	3e-14	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
18	3627	1.43	2e-16	3e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
19	1562	2.04	2e-16	3e-14	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
20	126410	1.72	2e-16	3e-14	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.45	NULL	135	H.Tiss WIRTH_Mucosa
2	25.15	NULL	572	Disease GUDJ_psooriasis up
3	16.3	NULL	21	CC cornified envelope
4	15.69	NULL	53	BP keratinocyte differentiation
5	15.42	NULL	1033	Chr Chr 2
6	14.37	NULL	42	BP keratinization
7	11.77	NULL	76	BP epidermis development
8	11.04	NULL	19	BP peptide cross-linking
9	10.7	NULL	21	CC desmosome
10	8.19	NULL	15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
11	7.77	NULL	10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
12	7.5	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
13	7.36	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	6.82	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	6.77	NULL	14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G4
16	6.71	NULL	15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
17	6.45	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
18	6.41	NULL	13	BP negative regulation of peptidase activity
19	6.33	NULL	16	GSEA C2JAEGER_METASTASIS_DN
20	6.23	NULL	15	BP fibrinolysis
<i>Underexpressed</i>				
1	-6.63	NULL	717	Chr Chr 16
2	-6.25	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
3	-6.01	NULL	7	MMML C2SCIEJ_MMML 5
4	-5.94	NULL	940	MF nucleic acid binding
5	-5.82	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
6	-5.79	NULL	918	Chr Chr 17
7	-5.26	NULL	743	Chr Chr 7
8	-5.16	NULL	16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_F
9	-5.05	NULL	1749	MF DNA binding
10	-5.04	NULL	449	Chr Chr 20
11	-4.98	NULL	44	MF structural constituent of muscle
12	-4.68	NULL	36	BP muscle filament sliding
13	-4.63	NULL	127	H.Tiss WIRTH_Muscle
14	-4.62	NULL	386	Chr Chr 22
15	-4.46	NULL	15	GSEA C2ONDER_CDH1_TARGETS_3_UP
16	-4.45	NULL	15	GSEA C2SNIDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
17	-4.45	NULL	16	H.Tiss WIRTH_Hippocampus
18	-4.44	NULL	1574	BP transcription, DNA-templated
19	-4.41	NULL	4	miRNA target-195
20	-4.23	NULL	20	Lymphom BOSOLOWSKI_red UP

p-values



GW_070

Local Summary

%DE = 0.96
 # metagenes = 24
 # genes = 299
 # genes in genesets = 291

genes with $fdr < 0.1 = 280$ (259 + / 21 -)
 # genes with $fdr < 0.05 = 270$ (250 + / 20 -)
 # genes with $fdr < 0.01 = 257$ (240 + / 17 -)

<r> metagenes = 0.93
 <r> genes = 0.41

<FC> = 0.93
 <shrinkage-t> = 32.68
 <p-value> = 0
 <fdr> = 0.12

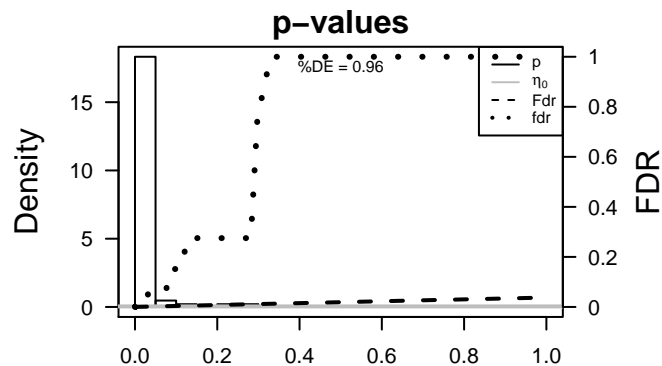
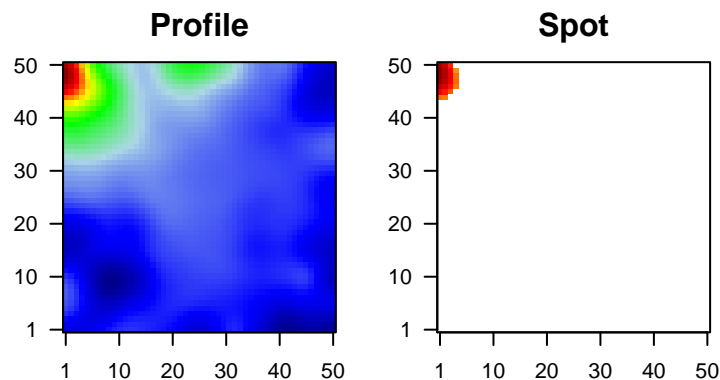
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	1.68	2e-16	3e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	57016	1.48	2e-16	3e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.5	2e-16	3e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	242	1.87	2e-16	3e-17	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syn
5	360	1.83	2e-16	3e-17	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	151516	2.53	2e-16	3e-17	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
7	387695	2.1	2e-16	3e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symt
8	375791	1.46	2e-16	3e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
9	760	1.56	2e-16	3e-17	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
10	810	1.38	2e-16	3e-17	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
11	1041	1.92	2e-16	3e-17	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
12	9022	1.79	2e-16	3e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
13	84518	1.57	2e-16	3e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
14	1562	2.04	2e-16	3e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
15	126410	1.72	2e-16	3e-17	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
16	1672	1.84	2e-16	3e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
17	55894	2.97	2e-16	3e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
18	414325	3.24	2e-16	3e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	1673	2.48	2e-16	3e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	93099	1.59	2e-16	3e-17	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	45.2	NULL	94 / 135	H.Tiss WIRTH_Mucosa
2	33.82	NULL	19 / 21	CC cornified envelope
3	29.49	NULL	110 / 572	Disease GUDJ_pсориаз up
4	29.08	NULL	26 / 53	BP keratinocyte differentiation
5	25.77	NULL	19 / 42	BP keratinization
6	21.2	NULL	12 / 19	BP peptide cross-linking
7	20.56	NULL	26 / 76	BP epidermis development
8	20.19	NULL	12 / 21	CC desmosome
9	15.26	NULL	9 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	15.14	NULL	7 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
11	14.09	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
12	12.63	NULL	5 / 16	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G24
13	12.39	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
14	12.01	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
15	11.96	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
16	11.95	NULL	6 / 13	BP negative regulation of peptidase activity
17	11.48	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	11.23	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
19	10.86	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
20	10.65	NULL	29 / 186	MF structural molecule activity
21	10.39	NULL	7 / 29	BP regulation of proteolysis
22	9.78	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
23	9.78	NULL	10 / 52	BP negative regulation of endopeptidase activity
24	9.72	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
25	9.45	NULL	65 / 1182	CC extracellular region
26	9.38	NULL	7 / 16	GSEA C2JAEGER_METASTASIS_DN
27	9.22	NULL	19 / 82	CC intermediate filament
28	8.94	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
29	8.88	NULL	13 / 79	MF serine-type endopeptidase inhibitor activity
30	8.8	NULL	12 / 44	CC keratin filament
31	8.77	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
32	8.37	NULL	2 / 15	BP fibrinolysis
33	8.24	NULL	9 / 73	BP defense response to bacterium
34	8.19	NULL	5 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
35	8.19	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
36	8.15	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
37	7.83	NULL	5 / 10	MF RAGE receptor binding
38	7.63	NULL	5 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
39	7.58	NULL	4 / 21	CC gap junction
40	7.5	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN



GW_070

Local Summary

%DE = 0.62
 # metagenes = 41
 # genes = 606
 # genes in genesets = 577

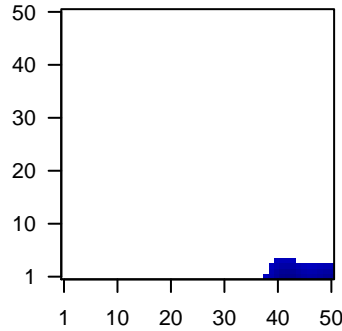
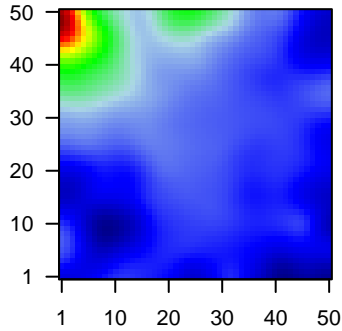
genes with $fdr < 0.1$ = 245 (23 + / 222 -)
 # genes with $fdr < 0.05$ = 181 (13 + / 168 -)
 # genes with $fdr < 0.01$ = 105 (6 + / 99 -)

$\langle r \rangle$ metagenes = 0.86
 $\langle r \rangle$ genes = 0.39

$\langle FC \rangle = -0.27$
 $\langle \text{shrinkage-t} \rangle = -9.41$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.66$

Profile

Spot



Local Genelist

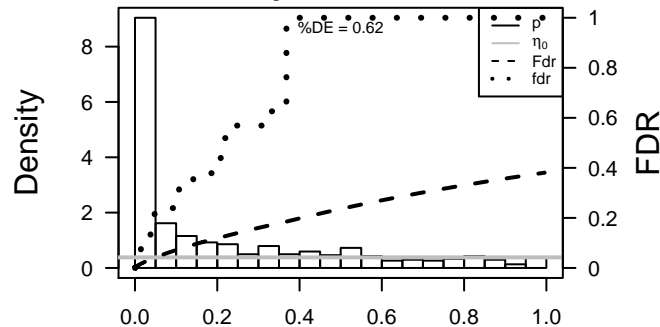
Rank	ID	log(FC)	fdr	p-value	Description
1	260436	-1.5	2e-16	1e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
2	3120	1.72	2e-16	1e-14	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:
3	3127	2.44	2e-16	1e-14	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:
4	3543	-1.89	2e-16	1e-14	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
5	57172	-1.32	6e-15	5e-11	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
6	51755	-1.24	2e-13	5e-11	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
7	4283	1.22	4e-13	2e-10	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
8	54855	-1.2	1e-12	2e-09	49 x 1 family with sequence similarity 46, member C [Source:HGNC
9	1512	-1.15	9e-12	3e-09	47 x 1 cathepsin H [Source:HGNC Symbol;Acc:2535]
10	6363	-1.13	2e-11	8e-09	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
11	23466	-1.11	5e-11	8e-09	41 x 1 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
12	10628	-1.07	1e-10	8e-09	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
13	374882	-1.08	2e-10	8e-09	42 x 1 transmembrane protein 205 [Source:HGNC Symbol;Acc:296
14	83641	-1.08	2e-10	5e-08	50 x 1 family with sequence similarity 107, member B [Source:HGNC
15	3512	-1.05	4e-10	5e-08	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobu
16	2120	-1.04	6e-10	1e-07	44 x 1 ets variant 6 [Source:HGNC Symbol;Acc:3495]
17	1535	-1.03	1e-09	3e-07	47 x 1 cytochrome b-245, alpha polypeptide [Source:HGNC Symb
18	10537	-1	3e-09	3e-07	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
19	3123	0.99	4e-09	3e-07	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
20	26580	-0.99	5e-09	2e-06	43 x 1 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-15.7	NULL	110 / 417	H.Tiss WIRTH_Immune system
2	-11.34	NULL	101 / 553	Cancer Lembcke_Colonic Inflammation
3	-10.27	NULL	1 / 6	H.Tiss WIRTH_Bone marrow
4	-9.19	NULL	2 / 6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
5	-8.96	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
6	-8.95	NULL	3 / 12	GSEA C2MCCABE_HOXC6_TARGETS_CANCER_UP
7	-8.31	NULL	4 / 13	BP lymph node development
8	-8.25	NULL	2 / 7	GSEA C2IZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN
9	-8.18	NULL	31 / 204	BP cell surface receptor signaling pathway
10	-7.96	NULL	4 / 11	GSEA C2APPEL_IMATINIB_RESPONSE
11	-7.6	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
12	-7.54	NULL	44 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
13	-7.54	NULL	44 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
14	-7.54	NULL	44 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
15	-7.54	NULL	44 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
16	-7.06	NULL	1 / 4	LymphomaASCQUE_mBL_DOWN
17	-7.05	NULL	9 / 28	LymphomaDAVE_Immune response 1
18	-7.01	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
19	-6.84	NULL	19 / 74	BP regulation of immune response
20	-6.73	NULL	11 / 43	BP positive regulation of T cell proliferation
21	-6.55	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
22	-6.52	NULL	5 / 12	BP dendritic cell chemotaxis
23	-6.5	NULL	9 / 28	BP B cell receptor signaling pathway
24	-6.43	NULL	3 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
25	-6.39	NULL	7 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
26	-6.37	NULL	3 / 11	BP negative regulation of lipid catabolic process
27	-6.36	NULL	2 / 4	MMLL C2SCICJ_MMLL 44
28	-6.23	NULL	3 / 13	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_DN
29	-6.16	NULL	1 / 2	GSEA C2GUTIERREZ_MULTIPLE_MYELOMA_UP
30	-6.04	NULL	2 / 4	MMLL C2SCICJ_MMLL 2
31	-6.01	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
32	-5.95	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
33	-5.95	NULL	3 / 18	miRNA target-miR-551a
34	-5.83	NULL	6 / 16	LymphomaWRIGHT_ABC_UP
35	-5.71	NULL	5 / 27	MF antigen binding
36	-5.7	NULL	3 / 14	GSEA C2WINNENPENNINCKX_MELANOMA_METASTASIS_DN
37	-5.66	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
38	-5.54	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
39	-5.44	NULL	39 / 316	Cancer SPANG_BCL6-index2
40	-5.4	NULL	2 / 9	GSEA C2BIOCARTA_SODD_PATHWAY

p-values



GW_070

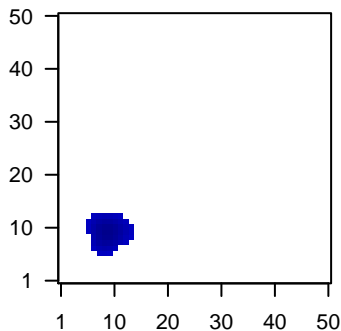
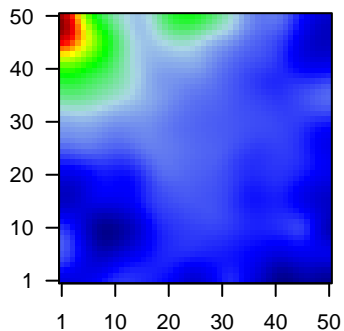
Local Summary

%DE = 0.69
 # metagenes = 55
 # genes = 452
 # genes in genesets = 431
 # genes with $fdr < 0.1$ = 175 (6 + / 169 -)
 # genes with $fdr < 0.05$ = 123 (5 + / 118 -)
 # genes with $fdr < 0.01$ = 70 (2 + / 68 -)

$\langle r \rangle$ metagenes = 0.83
 $\langle r \rangle$ genes = 0.21
 $\langle FC \rangle = -0.29$
 $\langle \text{shrinkage-t} \rangle = -10.02$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.7$

Profile

Spot



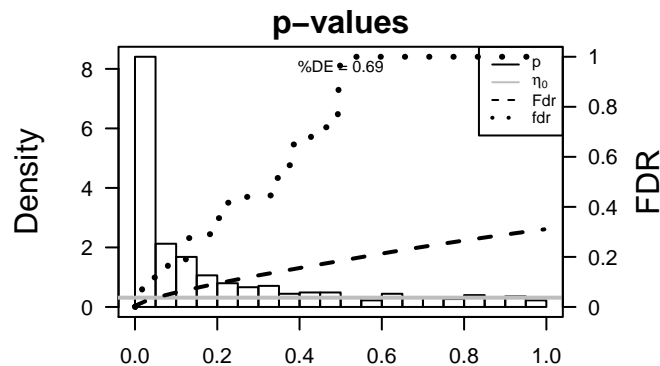
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	23338	-1.11	5e-11	4e-07	10 x 12 jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
2	23753	-0.98	6e-09	4e-07	8 x 9 stromal cell-derived factor 2-like 1 [Source:HGNC Symbol;Acc:22984]
3	4037	-0.97	7e-09	4e-07	10 x 7 low density lipoprotein receptor-related protein 3 [Source:HGNC Symbol;Acc:22984]
4	5891	-0.96	1e-08	4e-07	13 x 10 MOK protein kinase [Source:HGNC Symbol;Acc:9833]
5	4103	0.96	1e-08	3e-06	14 x 10 melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68]
6	65980	-0.93	3e-08	4e-05	9 x 10 bromodomain containing 9 [Source:HGNC Symbol;Acc:2581]
7	6184	-0.81	3e-07	6e-05	11 x 10 ribophorin I [Source:HGNC Symbol;Acc:10381]
8	29927	-0.83	7e-07	2e-04	9 x 10 Sec61 alpha 1 subunit (S. cerevisiae) [Source:HGNC Symbol;Acc:22984]
9	55653	-0.79	2e-06	2e-04	9 x 10 breast carcinoma amplified sequence 4 [Source:HGNC Symbol;Acc:22984]
10	2026	-0.78	3e-06	3e-04	10 x 10 enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33]
11	11033	-0.76	6e-06	3e-04	9 x 9 ArfGAP with dual PH domains 1 [Source:HGNC Symbol;Acc:22984]
12	1649	-0.75	8e-06	3e-04	8 x 6 DNA-damage-inducible transcript 3 [Source:HGNC Symbol;Acc:22984]
13	1469	-0.74	1e-05	3e-04	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
14	2648	-0.73	2e-05	3e-04	11 x 11 K(lysine) acetyltransferase 2A [Source:HGNC Symbol;Acc:42]
15	402	-0.72	2e-05	3e-04	8 x 10 ADP-ribosylation factor-like 2 [Source:HGNC Symbol;Acc:65]
16	64847	-0.72	2e-05	3e-04	10 x 9 spermatogenesis associated 20 [Source:HGNC Symbol;Acc:22984]
17	525	-0.72	2e-05	5e-04	12 x 8 ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1
18	84310	-0.7	3e-05	5e-04	6 x 10 chromosome 7 open reading frame 50 [Source:HGNC Symbol;Acc:22984]
19	112770	-0.7	3e-05	5e-04	8 x 8 chromosome 1 open reading frame 85 [Source:HGNC Symbol;Acc:22984]
20	404217	-0.7	3e-05	1e-03	10 x 9 cortixin 1 [Source:HGNC Symbol;Acc:31108]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.02	NULL	3 / 10	CC oligosaccharyltransferase complex
2	-7.84	NULL	2 / 12	GSEA C2REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
3	-7.47	NULL	11 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
4	-7.27	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
5	-6.16	NULL	2 / 15	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
6	-6.13	NULL	3 / 30	CC rough endoplasmic reticulum
7	-5.85	NULL	4 / 28	MF ribosome binding
8	-5.67	NULL	1 / 6	miRNA target-200c
9	-5.57	NULL	2 / 13	CC STAGA complex
10	-5.56	NULL	3 / 40	BP histone H3 acetylation
11	-5.55	NULL	2 / 15	GSEA C2BIOCARTA_PROTEASOME_PATHWAY
12	-5.54	NULL	4 / 15	GSEA C2KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN
13	-5.5	NULL	1 / 6	GSEA C2AFFAREL_RESPONSE_TO_THC_24HR_3_UP
14	-5.47	NULL	3 / 16	GSEA C2JURS_ADIPOCYTE_DIFFERENTIATION_DN
15	-5.43	NULL	2 / 12	BP mRNA transcription from RNA polymerase II promoter
16	-5.39	NULL	27 / 449	Chr Chr 20
17	-5.25	NULL	1 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
18	-4.92	NULL	1 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_21
19	-4.87	NULL	3 / 38	BP response to endoplasmic reticulum stress
20	-4.81	NULL	2 / 13	BP inner cell mass cell proliferation
21	-4.75	NULL	1 / 10	GSEA C2KU_RESPONSE_TO_TRETINOIN_DN
22	-4.72	NULL	3 / 24	miRNA target-302
23	-4.68	NULL	3 / 22	MF N-acetyltransferase activity
24	-4.66	NULL	4 / 19	MF hydrolase activity, acting on acid anhydrides, in phosphorus-contain
25	-4.63	NULL	2 / 9	miRNA target-184
26	-4.59	NULL	70 / 1135	Chr Chr 19
27	-4.57	NULL	2 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
28	-4.55	NULL	3 / 12	BP mRNA cleavage
29	-4.49	NULL	2 / 16	GSEA C2LIU_SOX4_TARGETS_DN
30	-4.48	NULL	1 / 9	GSEA C2ACOSTA_UV_RESPONSE_VIA_ERCC3_UP
31	-4.48	NULL	1 / 9	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
32	-4.48	NULL	1 / 9	GSEA C2BRODWELL_AGING_KIDNEY_UP
33	-4.42	NULL	2 / 11	BP maintenance of protein location in nucleus
34	-4.39	NULL	1 / 4	GSEA C2NICK_RESPONSE_TO_PROC_TREATMENT_UP
35	-4.37	NULL	2 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
36	-4.35	NULL	1 / 15	BP histone H4-K5 acetylation
37	-4.35	NULL	1 / 15	BP histone H4-K8 acetylation
38	-4.35	NULL	1 / 15	GSEA C2HU_ANGIOGENESIS_UP
39	-4.32	NULL	2 / 13	GSEA C2ENK_UV_RESPONSE_KERATINOCYTE_UP
40	-4.27	NULL	2 / 13	GSEA C2REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION



GW_070

Local Summary

%DE = 0.81
 # metagenes = 4
 # genes = 107
 # genes in genesets = 106

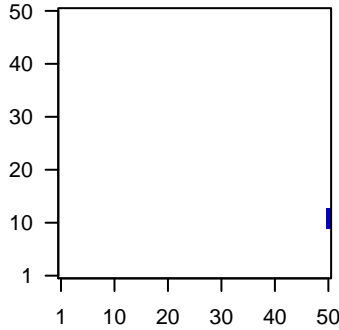
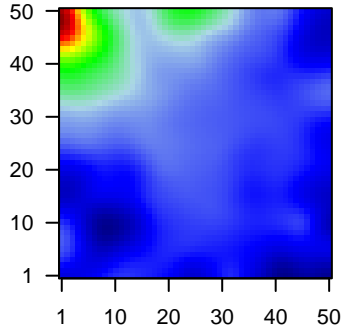
genes with $fdr < 0.1 = 69$ (9 + / 60 -)
 # genes with $fdr < 0.05 = 46$ (5 + / 41 -)
 # genes with $fdr < 0.01 = 44$ (5 + / 39 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.35

$\langle FC \rangle = -0.35$
 $\langle \text{shrinkage-t} \rangle = -12.36$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.55$

Profile

Spot



Local Genelist

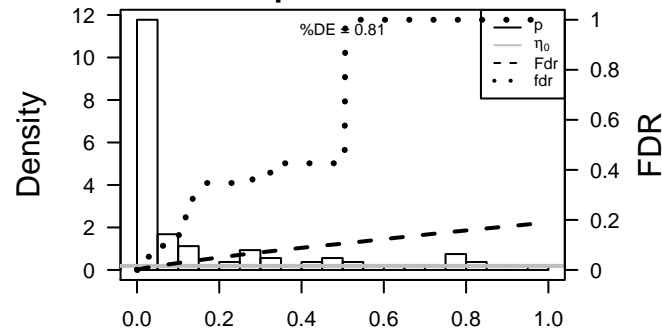
Rank	ID	log(FC)	fdr	p-value	Description
1	2568	-1.29	2e-14	2e-11	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:11740]
2	9249	-1.2	1e-12	4e-11	50 x 13 dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:11740]
3	10232	-1.18	3e-12	2e-10	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
4	3169	-1.14	1e-11	4e-09	50 x 12 forkhead box A1 [Source:HGNC Symbol;Acc:5021]
5	51316	-1.07	2e-10	3e-08	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
6	92747	-1.02	1e-09	3e-07	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:11740]
7	7018	-0.96	1e-08	1e-06	50 x 10 transferrin [Source:HGNC Symbol;Acc:11740]
8	11272	-0.89	1e-07	1e-06	50 x 10 proline rich 4 (lacrima) [Source:HGNC Symbol;Acc:18020]
9	7033	-0.88	2e-07	1e-06	50 x 10 trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
10	27134	-0.88	2e-07	2e-06	50 x 12 tight junction protein 3 [Source:HGNC Symbol;Acc:11829]
11	8842	-0.86	3e-07	4e-06	50 x 10 prominin 1 [Source:HGNC Symbol;Acc:9454]
12	2327	-0.85	5e-07	5e-06	50 x 11 flavin containing monooxygenase 2 (non-functional) [Source:HGNC Symbol;Acc:11740]
13	64284	-0.83	7e-07	1e-05	50 x 10 RAB17, member RAS oncogene family [Source:HGNC Symbol;Acc:11740]
14	84952	-0.81	1e-06	2e-05	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]
15	9071	-0.79	3e-06	2e-05	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
16	94025	-0.78	3e-06	7e-05	50 x 11 mucin 16, cell surface associated [Source:HGNC Symbol;Acc:11740]
17	2139	-0.76	7e-06	2e-04	50 x 13 eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11740]
18	56271	-0.71	2e-05	2e-04	50 x 12 brain expressed, X-linked 4 [Source:HGNC Symbol;Acc:254]
19	54102	-0.7	4e-05	2e-04	50 x 10 chloride intracellular channel 6 [Source:HGNC Symbol;Acc:21]
20	283229	-0.68	6e-05	2e-04	50 x 10 EF-hand calcium binding domain 4A [Source:HGNC Symbol;Acc:11740]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-30.3	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-24	NULL	3 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	-19.81	NULL	3 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
4	-17.1	NULL	3 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
5	-16.02	NULL	2 / 11	CC photoreceptor outer segment membrane
6	-15.79	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
7	-15.54	NULL	2 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
8	-14.59	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_T
9	-14.59	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
10	-13.55	NULL	2 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
11	-12.87	NULL	3 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
12	-12	NULL	2 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_T
13	-11.96	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
14	-11.4	NULL	1 / 7	GSEA C2NEBEN_AML_WITH_FLT3_OR_NRAS_UP
15	-11.39	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_BULK_UP
16	-10.73	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
17	-10.51	NULL	1 / 10	MF GABA-A receptor activity
18	-10.03	NULL	3 / 21	BP drug metabolic process
19	-9.95	NULL	1 / 11	GSEA C2IAZARI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
20	-9.74	NULL	2 / 15	GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
21	-9.59	NULL	2 / 12	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
22	-9.26	NULL	1 / 10	BP prostate gland epithelium morphogenesis
23	-8.66	NULL	1 / 14	GSEA C2TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
24	-8.66	NULL	1 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
25	-8.59	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
26	-8.53	NULL	2 / 10	BP negative regulation of blood coagulation
27	-8.39	NULL	1 / 13	GSEA C2ZIRN_TRETINOIN_RESPONSE_UP
28	-8.33	NULL	1 / 12	BP neuron fate specification
29	-8.21	NULL	1 / 11	BP negative regulation of multicellular organism growth
30	-8.16	NULL	2 / 34	CC chloride channel complex
31	-8.16	NULL	2 / 10	GSEA C2JUI_THYROID_CANCER_CLUSTER_5
32	-8.11	NULL	2 / 17	BP iron ion transport
33	-8.03	NULL	1 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
34	-8.03	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
35	-7.96	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
36	-7.94	NULL	2 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
37	-7.86	NULL	1 / 14	GSEA C2WALK_AML_WITH_11Q23_REARRANGED
38	-7.78	NULL	2 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
39	-7.72	NULL	1 / 15	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_UP
40	-7.62	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition

p-values



GW_070

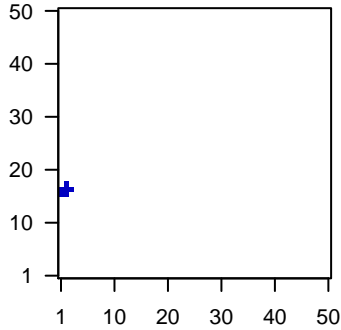
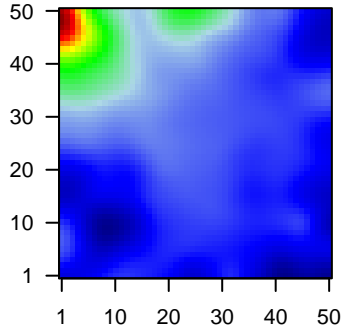
Local Summary

%DE = 0.6
 # metagenes = 6
 # genes = 79
 # genes in genesets = 79
 # genes with $fdr < 0.1 = 25$ (0 + / 25 -)
 # genes with $fdr < 0.05 = 15$ (0 + / 15 -)
 # genes with $fdr < 0.01 = 7$ (0 + / 7 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.35
 $\langle FC \rangle = -0.26$
 $\langle \text{shrinkage-t} \rangle = -9.2$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.75$

Profile

Spot



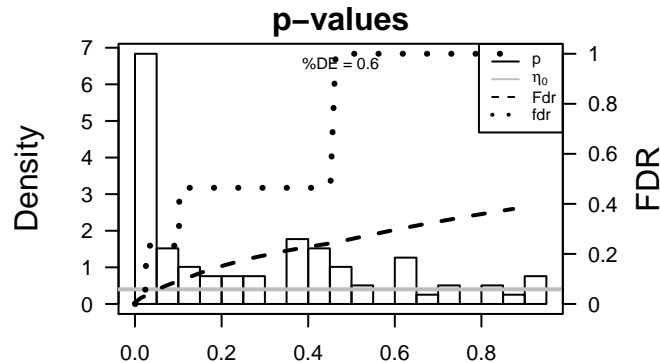
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131076	-1.21	9e-13	2e-11	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:30509]
2	1152	-1.2	1e-12	3e-09	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
3	283869	-1.09	1e-10	4e-07	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
4	4495	-0.96	1e-08	2e-04	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
5	51069	-0.76	6e-06	2e-04	2 x 18 mitochondrial ribosomal protein L2 [Source:HGNC Symbol;Acc:30509]
6	26873	-0.73	1e-05	2e-04	1 x 17 5-oxoprolinase (ATP-hydrolysing) [Source:HGNC Symbol;Acc:30509]
7	3237	-0.73	2e-05	4e-03	1 x 16 homeobox D11 [Source:HGNC Symbol;Acc:5134]
8	2932	-0.64	2e-04	1e-02	1 x 17 glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc:30509]
9	283643	-0.57	8e-04	1e-02	2 x 17 chromosome 14 open reading frame 80 [Source:HGNC Symbol;Acc:30509]
10	4728	-0.55	1e-03	1e-02	2 x 17 NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (beta) [Source:HGNC Symbol;Acc:30509]
11	3276	-0.55	1e-03	5e-02	3 x 17 protein arginine methyltransferase 1 [Source:HGNC Symbol;Acc:30509]
12	4715	-0.49	4e-03	5e-02	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22 kDa [Source:HGNC Symbol;Acc:30509]
13	10131	-0.45	7e-03	5e-02	2 x 17 TNF receptor-associated protein 1 [Source:HGNC Symbol;Acc:30509]
14	8607	-0.44	8e-03	5e-02	2 x 16 RuvB-like AAA ATPase 1 [Source:HGNC Symbol;Acc:10474]
15	22827	-0.44	8e-03	5e-02	1 x 16 poly-U binding splicing factor 60kDa [Source:HGNC Symbol;Acc:30509]
16	64979	-0.44	9e-03	6e-02	1 x 16 mitochondrial ribosomal protein L36 [Source:HGNC Symbol;Acc:30509]
17	55039	-0.43	1e-02	6e-02	1 x 16 tRNA methyltransferase 12 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:30509]
18	10436	-0.41	1e-02	6e-02	1 x 17 Ribosomal RNA small subunit methyltransferase NEP1 [Source:HGNC Symbol;Acc:30509]
19	230	-0.41	1e-02	6e-02	2 x 17 aldolase C, fructose-bisphosphate [Source:HGNC Symbol;Acc:30509]
20	84916	-0.4	2e-02	6e-02	1 x 16 cirrhosis, autosomal recessive 1A (cirhin) [Source:HGNC Symbol;Acc:30509]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-15.45	NULL	1 / 9	GSEA C2GOUYER_TUMOR_INVASIVENESS
2	-14.2	NULL	1 / 7	MMML C6ACIEJ_MMML_13
3	-13.01	NULL	2 / 10	BP creatine metabolic process
4	-12.99	NULL	1 / 3	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
5	-12.99	NULL	1 / 3	GSEA C2KEGG_PARKINSONS_DISEASE
6	-12.62	NULL	2 / 16	BP monocyte differentiation
7	-11.76	NULL	3 / 14	GSEA C2STEIN_ESRRA_TARGETS_UP
8	-11.68	NULL	1 / 10	BP cellular response to zinc ion
9	-11.44	NULL	2 / 10	GSEA C2STEIN_ESRRA_TARGETS
10	-11.31	NULL	1 / 16	GSEA C2DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN
11	-11.31	NULL	1 / 16	GSEA C2WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP
12	-11.02	NULL	1 / 4	GSEA C2REACTOME_GLYCOSE_REGULATION_OF_INSULIN_SECRETION
13	-11.02	NULL	1 / 4	GSEA C2REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
14	-11.02	NULL	1 / 4	GSEA C2REACTOME_REGULATION_OF_INSULIN_SECRETION
15	-10.55	NULL	2 / 15	GSEA C2KEGG_WNT_SIGNALING_PATHWAY
16	-10.12	NULL	1 / 13	BP cellular response to cadmium ion
17	-9.93	NULL	1 / 8	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
18	-9.72	NULL	1 / 5	GSEA C2REACTOME_ELECTRON_TRANSPORT_CHAIN
19	-9.42	NULL	2 / 14	Pathw AcBENTINK_myc.1
20	-9.38	NULL	1 / 7	GSEA C2REACTOME_SIGNALING_BY_WNT
21	-9.36	NULL	1 / 15	BP negative regulation of growth
22	-8.85	NULL	2 / 16	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
23	-8.85	NULL	2 / 16	GSEA C2MOOHA_HUMAN_MITODB_6_2002
24	-8.85	NULL	2 / 16	GSEA C2MOOHA_MITOCHONDRIA
25	-8.84	NULL	1 / 21	BP feeding behavior
26	-8.74	NULL	1 / 17	BP cellular response to vascular endothelial growth factor stimulus
27	-8.71	NULL	1 / 8	GSEA C2CHANDRAN_METASTASIS_UP
28	-8.39	NULL	2 / 10	GSEA C2KEGG_HUNTINGTONS_DISEASE
29	-7.94	NULL	1 / 12	BP organ induction
30	-7.84	NULL	2 / 16	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
31	-7.7	NULL	1 / 27	MF G-protein coupled receptor binding
32	-7.7	NULL	1 / 10	BP myotube differentiation
33	-7.7	NULL	1 / 10	GSEA C2BIOCARTA_P35ALZHEIMERS_PATHWAY
34	-7.7	NULL	1 / 10	GSEA C2SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES
35	-7.7	NULL	1 / 10	GSEA C2SIG_BCR_SIGNALING_PATHWAY
36	-7.65	NULL	2 / 16	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
37	-7.3	NULL	1 / 11	MF ionotropic glutamate receptor binding
38	-7.3	NULL	1 / 11	MF positive regulation of protein complex assembly
39	-7.3	NULL	1 / 11	MF protein kinase A catalytic subunit binding
40	-7.3	NULL	1 / 11	MF tau-protein kinase activity



GW_070

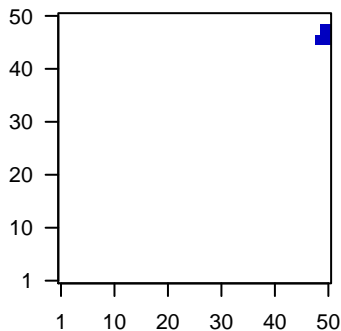
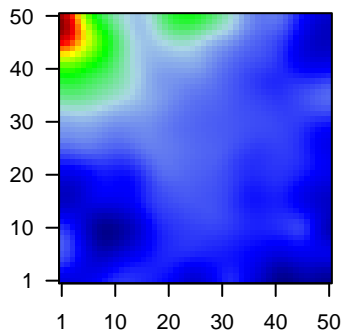
Local Summary

%DE = 0.58
 # metagenes = 10
 # genes = 83
 # genes in genesets = 83
 # genes with $fdr < 0.1 = 32$ (5 + / 27 -)
 # genes with $fdr < 0.05 = 23$ (4 + / 19 -)
 # genes with $fdr < 0.01 = 11$ (2 + / 9 -)

<r> metagenes = 0.97
 <r> genes = 0.26
 <FC> = -0.22
 <shrinkage-t> = -7.85
 <p-value> = 0.02
 <fdr> = 0.68

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3856	-1.42	2e-16	8e-15	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
2	84707	-1.1	6e-11	5e-06	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
3	54800	-0.89	1e-07	7e-06	50 x 48 kelch-like family member 24 [Source:HGNC Symbol;Acc:259]
4	7345	-0.86	3e-07	8e-05	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
5	1974	-0.71	5e-06	8e-05	49 x 47 eukaryotic translation initiation factor 4A2 [Source:HGNC Syn
6	51804	-0.77	5e-06	4e-04	50 x 46 SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
7	6659	-0.73	2e-05	3e-03	50 x 45 SRY (sex determining region Y)-box 4 [Source:HGNC Symb
8	56704	-0.66	1e-04	6e-03	50 x 47 junctophilin 1 [Source:HGNC Symbol;Acc:14201]
9	5625	0.62	3e-04	8e-03	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ac
10	291	-0.57	7e-04	8e-03	50 x 46 solute carrier family 25 (mitochondrial carrier; adenine nucleo
11	445	0.56	9e-04	8e-03	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75f
12	11138	0.56	1e-03	1e-02	50 x 47 TBC1 domain family, member 8 (with GRAM domain) [Source
13	219736	0.54	1e-03	1e-02	50 x 45 storkhead box 1 [Source:HGNC Symbol;Acc:23508]
14	6261	-0.52	2e-03	1e-02	49 x 46 ryanodine receptor 1 (skeletal) [Source:HGNC Symbol;Acc:1f
15	59342	-0.51	3e-03	1e-02	50 x 47 serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
16	26024	-0.5	3e-03	1e-02	49 x 48 pentatricopeptide repeat domain 1 [Source:HGNC Symbol;Ac
17	3177	-0.5	3e-03	1e-02	49 x 46 solute carrier family 29 (equilibrative nucleoside transporter),
18	80258	-0.49	3e-03	1e-02	50 x 45 EF-hand domain (C-terminal) containing 2 [Source:HGNC S
19	3202	-0.49	4e-03	1e-02	49 x 47 homeobox A5 [Source:HGNC Symbol;Acc:5106]
20	253782	-0.48	4e-03	1e-02	50 x 47 ceramide synthase 6 [Source:HGNC Symbol;Acc:23826]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.92	NULL	1 / 2	miRNA target set 129
2	-13.56	NULL	2 / 10	CC junctional sarcoplasmic reticulum membrane
3	-12.49	NULL	1 / 7	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_UP
4	-11.45	NULL	2 / 12	GSEA C2ZONDER_CDH1_TARGETS_1_UP
5	-11.22	NULL	1 / 8	GSEA C2MUNSHI_MULTIPLE_MYELOMA_DN
6	-10.54	NULL	2 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
7	-9.92	NULL	1 / 10	MF omega peptidase activity
8	-9.74	NULL	1 / 11	GSEA C2LIU_SOX4_TARGETS_UP
9	-9.74	NULL	1 / 11	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
10	-8.97	NULL	1 / 12	BP muscle fiber development
11	-8.97	NULL	1 / 12	GSEA C2CHANG_IMMORTALIZED_BY_HP131_UP
12	-8.84	NULL	1 / 10	BP anatomical structure development
13	-8.79	NULL	2 / 35	miRNA target set 127 4b
14	-8.71	NULL	3 / 30	TF Tissue/AQUERIZAS_Fetal Lung
15	-8.59	NULL	1 / 13	BP response to ischemia
16	-8.59	NULL	1 / 13	Lymphocyte/BENTINK_mBL UP
17	-8.53	NULL	1 / 14	MMML C2SCIEJ_MMMML 8
18	-8.35	NULL	1 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
19	-8.22	NULL	1 / 15	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
20	-8.22	NULL	1 / 15	GSEA C2RUIZ_TNC_TARGETS_UP
21	-7.94	NULL	1 / 15	GSEA C2ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN
22	-7.93	NULL	1 / 16	GSEA C2MILCOX_PRESPONSE_TO_ROGESTERONE_UP
23	-7.93	NULL	1 / 16	GSEA C2ELVIDGE_HYPOXIA_UP
24	-7.93	NULL	1 / 16	GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP
25	-7.93	NULL	1 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_DN
26	-7.93	NULL	1 / 16	GSEA C2NAKAYAMA_FRA2_TARGETS
27	-7.93	NULL	1 / 16	GSEA C2MENSE_HYPOXIA_UP
28	-7.93	NULL	1 / 16	GSEA C2MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_UP
29	-7.93	NULL	1 / 16	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_UP
30	-7.93	NULL	1 / 16	GSEA C2RODWELL_AGING_KIDNEY_DN
31	-7.93	NULL	1 / 16	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_DN
32	-7.92	NULL	1 / 11	GSEA C2CLAUS_PGR_POSITIVE_MENINGIOMA_DN
33	-7.92	NULL	1 / 11	GSEA C2PARK_APL_PATHOGENESIS_UP
34	-7.91	NULL	2 / 15	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_E2
35	-7.76	NULL	3 / 21	Glio Martinez_Glio_hypermeth
36	-7.66	NULL	1 / 16	BP eating behavior
37	-7.65	NULL	1 / 6	miRNA target set 128 1
38	-7.55	NULL	1 / 12	miRNA target set 128 2
39	-7.35	NULL	1 / 14	miRNA target set 128 3
40	-7.22	NULL	1 / 13	MF core promoter sequence-specific DNA binding

