

GW_087

Global Summary

%DE = 0.15
 # genes with $fdr < 0.2$ = 1780 (987 + / 793 -)
 # genes with $fdr < 0.1$ = 1428 (785 + / 643 -)
 # genes with $fdr < 0.05$ = 986 (529 + / 457 -)
 # genes with $fdr < 0.01$ = 620 (334 + / 286 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.85

Global Genelist

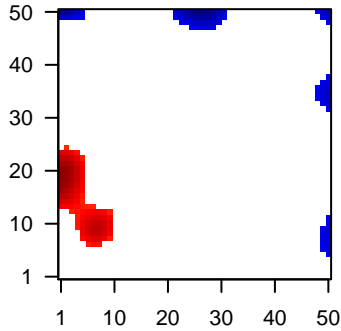
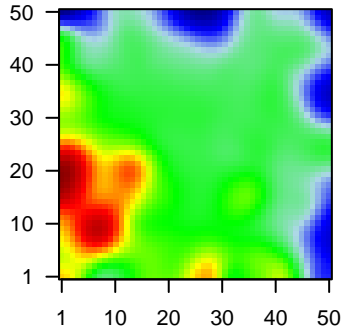
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	131	-1.89	2e-16 1e-13	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	-2.03	2e-16 1e-13	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
3	64207	-2.04	2e-16 1e-13	50 x 40 interferon regulatory factor 2 binding protein-like [Source:HG
4	51806	1.8	2e-16 1e-13	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
5	4680	-2.36	2e-16 1e-13	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
6	10202	2.43	2e-16 1e-13	1 x 15 dehydrogenase/reductase (SDR family) member 2 [Source:H
7	2167	-1.78	2e-16 1e-13	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
8	2318	1.75	2e-16 1e-13	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
9	94234	-1.87	2e-16 1e-13	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
10	163351	-1.92	2e-16 1e-13	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
11	10457	-2.03	2e-16 1e-13	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
12	283120	2.48	2e-16 1e-13	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
13	3485	-1.78	2e-16 1e-13	11 x 50 insulin-like growth factor binding protein 2, 36kDa [Source:HK
14	374918	2.84	2e-16 1e-13	1 x 45 IGF-like family member 1 [Source:HGNC Symbol;Acc:24093]
15	3848	2.38	2e-16 1e-13	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
16	3860	-1.72	2e-16 1e-13	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
17	3866	-2.37	2e-16 1e-13	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
18	3868	1.67	2e-16 1e-13	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
19	3963	1.75	2e-16 1e-13	1 x 47 lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol
20	8581	1.74	2e-16 1e-13	1 x 48 lymphocyte antigen 6 complex, locus D [Source:HGNC Symb

Global Geneset Analysis

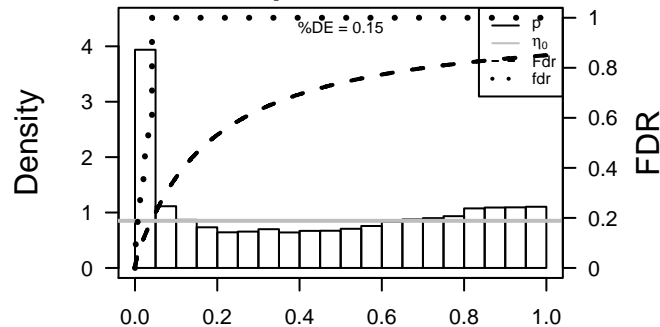
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.77	NULL	717	Chr Chr 16
2	11.99	NULL	1135	Chr Chr 19
3	10.45	NULL	918	Chr Chr 17
4	6.42	NULL	45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
5	5.88	NULL	4	MMML C63CIEJ_MMML 23
6	5.39	NULL	253	BP translation
7	5.32	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
8	5.24	NULL	92	BP translational elongation
9	5.17	NULL	13	BP intermediate filament cytoskeleton organization
10	5.15	NULL	128	BP translational initiation
11	5.14	NULL	36	BP muscle filament sliding
12	5.04	NULL	153	MF structural constituent of ribosome
13	4.92	NULL	8	GSEA C2NKOLSKY_BREAST_CANCER_5P15_AMPLICON
14	4.9	NULL	81	BP viral transcription
15	4.9	NULL	87	BP translational termination
16	4.88	NULL	39	BP glycolysis
17	4.47	NULL	121	CC microtubule cytoskeleton
18	4.46	NULL	13	GSEA C2REACTOME_GLYCOLYSIS
19	4.38	NULL	167	CC ribosome
20	4.38	NULL	92	BP viral life cycle
<i>Underexpressed</i>				
1	-8.84	NULL	633	Chr Chr 9
2	-8.53	NULL	436	miRNA target-miR-34b-3p
3	-8.27	NULL	53	BP keratinocyte differentiation
4	-8.13	NULL	572	Disease GUDJ_psooriasis up
5	-7.88	NULL	269	miRNA target-miR-34a-3p
6	-7.83	NULL	310	miRNA target-miR-34c-3p
7	-7.79	NULL	368	miRNA target-miR-34a-3p
8	-7.7	NULL	318	miRNA target-miR-34b-3p
9	-7.7	NULL	171	miRNA target-miR-34b-3p
10	-7.62	NULL	262	miRNA target-miR-34c-3p
11	-7.61	NULL	134	miRNA target-miR-34c-3p
12	-7.6	NULL	321	miRNA target-miR-34a-5p
13	-7.43	NULL	603	miRNA target-miR-34a-3p
14	-7.34	NULL	198	miRNA target-miR-34a-3p
15	-7.34	NULL	336	miRNA target-miR-34b-5p
16	-7.33	NULL	307	miRNA target-miR-34c-5p
17	-7.3	NULL	271	miRNA target-miR-34b-3p
18	-7.14	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
19	-7.13	NULL	336	miRNA target-miR-34b-5p
20	-7.11	NULL	271	miRNA target-miR-34a-3p

Profile

Regulated Spots



p-values



GW_087

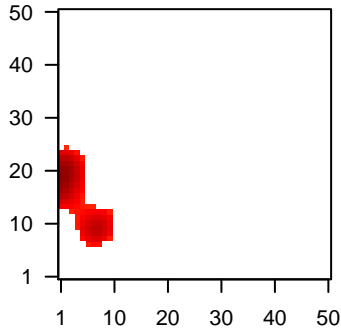
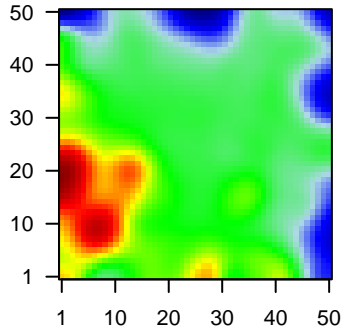
Local Summary

%DE = 0.72
 # metagenes = 101
 # genes = 918
 # genes in genesets = 910
 # genes with $fdr < 0.1$ = 501 (488 + / 13 -)
 # genes with $fdr < 0.05$ = 409 (400 + / 9 -)
 # genes with $fdr < 0.01$ = 272 (270 + / 2 -)

<r> metagenes = 0.78
 <r> genes = 0.21
 <FC> = 0.42
 <shrinkage-t> = 14.59
 <p-value> = 0.01
 <fdr> = 0.56

Profile

Spot



Local Genelist

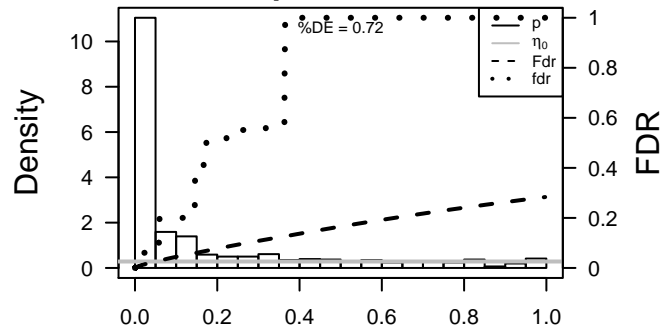
Rank	ID	log(FC)	fdr	p-value	Description
1	10202	2.43	2e-16	6e-14	1 x 15 dehydrogenase/reductase (SDR family) member 2 [Source:HGNC Symbol;Acc:22984]
2	23338	1.43	1e-11	2e-08	10 x 12 jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
3	27161	1.33	2e-10	2e-08	8 x 10 argonaute RISC catalytic component 2 [Source:HGNC Symbol;Acc:22984]
4	23246	1.33	2e-10	3e-07	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
5	131076	1.27	1e-09	6e-07	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:15519]
6	6448	1.22	6e-09	6e-07	6 x 8 N-sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;Acc:15519]
7	3006	-1.21	8e-09	6e-07	5 x 20 histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
8	2288	1.21	8e-09	2e-06	1 x 19 FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:15519]
9	116447	1.18	2e-08	2e-05	1 x 15 topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbol;Acc:15519]
10	64979	1.12	1e-07	2e-05	1 x 16 mitochondrial ribosomal protein L36 [Source:HGNC Symbol;Acc:15519]
11	4715	1.09	2e-07	2e-05	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22 [Source:HGNC Symbol;Acc:15519]
12	4495	1.08	3e-07	2e-05	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
13	2932	1.08	3e-07	2e-05	1 x 17 glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc:15519]
14	142678	1.06	4e-07	2e-05	1 x 17 mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:15519]
15	57407	1.06	4e-07	2e-05	1 x 20 NmrA-like family domain containing 1 [Source:HGNC Symbol;Acc:15519]
16	51629	1.05	5e-07	2e-05	1 x 18 solute carrier family 25, member 39 [Source:HGNC Symbol;Acc:15519]
17	27043	1.05	6e-07	2e-05	9 x 11 proline, glutamate and leucine rich protein 1 [Source:HGNC Symbol;Acc:15519]
18	80728	1.05	6e-07	4e-05	10 x 11 Rho GTPase activating protein 39 [Source:HGNC Symbol;Acc:15519]
19	26470	1.03	8e-07	4e-05	10 x 9 seizure related 6 homolog (mouse)-like 2 [Source:HGNC Symbol;Acc:15519]
20	2597	0.94	1e-06	4e-05	2 x 17 glyceraldehyde-3-phosphate dehydrogenase [Source:HGNC Symbol;Acc:15519]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	10.77	NULL	94 / 717	Chr Chr 16
2	8.72	NULL	3 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
3	8.28	NULL	15 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
4	8.17	NULL	128 / 1135	Chr Chr 19
5	7.45	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
6	7.29	NULL	19 / 96	BP rRNA processing
7	7.18	NULL	6 / 12	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
8	7.07	NULL	131 / 1318	CC mitochondrion
9	6.94	NULL	6 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN
10	6.87	NULL	6 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
11	6.58	NULL	2 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_7
12	6.4	NULL	6 / 16	GSEA C2BIOCARTA_PTIDINS_PATHWAY
13	6.3	NULL	5 / 15	GSEA C2ANTVEER_BREAST_CANCER_BRCA1_UP
14	6.24	NULL	5 / 15	CC mitochondrial large ribosomal subunit
15	6.1	NULL	5 / 14	CC Ino80 complex
16	6.02	NULL	4 / 9	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
17	5.97	NULL	18 / 121	CC microtubule cytoskeleton
18	5.83	NULL	18 / 95	Glio GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
19	5.81	NULL	3 / 15	GSEA C2HU_ANGIOGENESIS_UP
20	5.75	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
21	5.67	NULL	5 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
22	5.61	NULL	5 / 16	GSEA C2JIANG_HYPOXIA_VIA_VHL
23	5.59	NULL	5 / 13	GSEA C2REACTOME_GLYCOLYSIS
24	5.51	NULL	5 / 16	MF Hsp70 protein binding
25	5.49	NULL	41 / 253	BP translation
26	5.44	NULL	12 / 64	BP tRNA processing
27	5.4	NULL	5 / 14	GSEA C2NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
28	5.35	NULL	4 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
29	5.3	NULL	5 / 12	GSEA C2REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA
30	5.22	NULL	4 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
31	5.21	NULL	2 / 9	miRNA 3005G-184
32	5.2	NULL	4 / 14	GSEA C2REACTOME_PI3K_AKT_SIGNALLING
33	5.09	NULL	3 / 10	GSEA C2HONMA_DOCETAXEL_RESISTANCE
34	4.98	NULL	3 / 10	BP chaperone-mediated protein folding
35	4.91	NULL	5 / 22	BP protein export from nucleus
36	4.9	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
37	4.88	NULL	4 / 13	BP ribosomal small subunit biogenesis
38	4.88	NULL	76 / 649	BP gene expression
39	4.85	NULL	3 / 13	CC transcription export complex
40	4.78	NULL	5 / 13	GSEA C2SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY

p-values



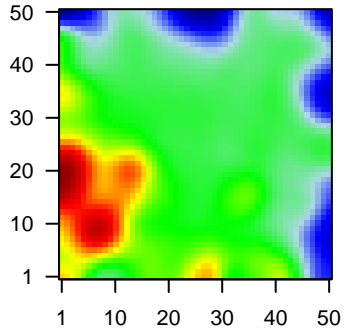
GW_087

Local Summary

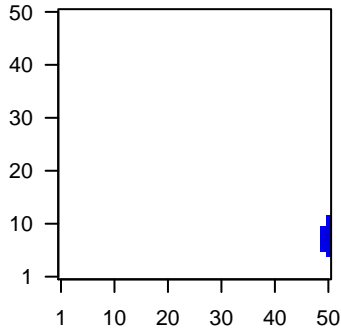
%DE = 0.75
 # metagenes = 13
 # genes = 227
 # genes in genesets = 226
 # genes with $fdr < 0.1$ = 100 (12 + / 88 -)
 # genes with $fdr < 0.05$ = 65 (8 + / 57 -)
 # genes with $fdr < 0.01$ = 35 (4 + / 31 -)

<r> metagenes = 0.9
 <r> genes = 0.29
 <FC> = -0.32
 <shrinkage-t> = -11.1
 <p-value> = 0.02
 <fdr> = 0.67

Profile



Spot



Local Genelist

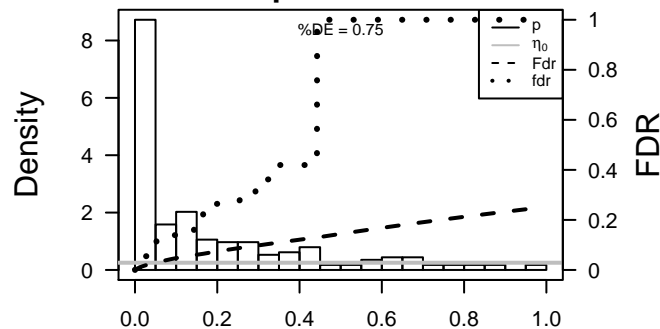
Rank	ID	log(FC)	fdr	p-value	Description
1	10232	1.84	2e-16	1e-14	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
2	1363	-1.4	2e-11	8e-10	50 x 7 carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
3	7033	-1.39	3e-11	2e-07	50 x 10 trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
4	79901	-1.24	3e-09	4e-06	50 x 7 cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797]
5	6867	-1.08	2e-07	4e-06	50 x 6 transforming, acidic coiled-coil containing protein 1 [Source:HGNC Symbol;Acc:11220]
6	1808	-1.08	2e-07	4e-06	50 x 5 dihydropyrimidinase-like 2 [Source:HGNC Symbol;Acc:3014]
7	25840	-1.08	2e-07	4e-06	50 x 11 methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
8	2219	1.07	3e-07	1e-05	50 x 5 ficolin (collagen/fibrinogen domain containing) 1 [Source:HGNC Symbol;Acc:11220]
9	8404	-1.04	6e-07	1e-05	50 x 6 SPARC-like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
10	1266	-1.04	7e-07	3e-05	50 x 6 calponin 3, acidic [Source:HGNC Symbol;Acc:2157]
11	10551	-1.01	1e-06	3e-05	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
12	1359	-0.98	3e-06	3e-05	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:11220]
13	10253	-0.98	3e-06	3e-05	50 x 8 sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11220]
14	1573	-0.97	3e-06	3e-05	50 x 11 cytochrome P450, family 2, subfamily J, polypeptide 2 [Source:HGNC Symbol;Acc:11220]
15	30061	-0.97	4e-06	3e-05	50 x 5 solute carrier family 40 (iron-regulated transporter), member 1 [Source:HGNC Symbol;Acc:11220]
16	2762	-0.97	4e-06	2e-04	50 x 12 GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc:11220]
17	347	-0.93	8e-06	2e-04	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
18	4784	-0.93	9e-06	2e-04	50 x 10 nuclear factor I/X (CCAAT-binding transcription factor) [Source:HGNC Symbol;Acc:11220]
19	3855	0.91	1e-05	2e-04	50 x 11 keratin 7 [Source:HGNC Symbol;Acc:6445]
20	92747	-0.9	2e-05	2e-04	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:11220]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.49	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-15.02	NULL	3 / 13	H.Tiss WIRTH_Sec_lymphoid_organ
3	-13.32	NULL	4 / 17	MF metalloproteinase activity
4	-12.34	NULL	3 / 17	MF carboxypeptidase activity
5	-11.92	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
6	-11.84	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
7	-9.94	NULL	3 / 10	BP germ cell migration
8	-9.57	NULL	35 / 375	Disease GUDJ_psooriasis_down
9	-9.13	NULL	3 / 14	BP regulation of Wnt signaling pathway
10	-9.04	NULL	3 / 15	GSEA C2WONG_LIVER_CANCER_RECURRENCE_DN
11	-9.01	NULL	3 / 15	GSEA C2NADERI_BREAST_CANCER_PROGNOSIS_DN
12	-8.93	NULL	2 / 9	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
13	-8.92	NULL	2 / 12	miRNA target-mir-399
14	-8.71	NULL	3 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
15	-8.65	NULL	2 / 11	MF neurexin family protein binding
16	-8.6	NULL	1 / 2	MMML C2SCIEJ_MMML_32
17	-8.55	NULL	3 / 17	BP iron ion transport
18	-8.23	NULL	1 / 3	miRNA target-miR-210
19	-8.13	NULL	2 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
20	-8.06	NULL	7 / 61	CC secretory granule
21	-7.97	NULL	1 / 9	GSEA C2KANG_GIST_WITH_PDGFR_UP
22	-7.91	NULL	1 / 9	GSEA C2XOUYER_TATI_TARGETS_UP
23	-7.74	NULL	4 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
24	-7.7	NULL	2 / 10	BP angiotensin maturation
25	-7.59	NULL	2 / 12	GSEA C2SHI_SPARC_TARGETS_DN
26	-7.47	NULL	2 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
27	-7.43	NULL	2 / 14	BP tissue regeneration
28	-7.38	NULL	3 / 16	GSEA C2RODRIGUES_NTN1_TARGETS_UP
29	-7.36	NULL	2 / 8	GSEA C2LEE_SP4_THYMOCYTE
30	-7.32	NULL	3 / 13	GSEA C2KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
31	-7.18	NULL	3 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
32	-7.13	NULL	2 / 10	BP response to iron ion
33	-7.01	NULL	1 / 7	GSEA C2OBAYASHI_EGFR_SIGNALING_6HR_UP
34	-6.98	NULL	2 / 15	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_UP
35	-6.83	NULL	4 / 59	BP cellular iron ion homeostasis
36	-6.8	NULL	2 / 13	GSEA C2KAYO_CALORIE_RESTRICTION_MUSCLE_UP
37	-6.73	NULL	6 / 12	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN
38	-6.67	NULL	2 / 12	Lymphoma GAVE_BL_DN
39	-6.67	NULL	3 / 21	MF glycosaminoglycan binding
40	-6.64	NULL	2 / 13	GSEA C2KEGG_RENIN_ANGIOTENSIN_SYSTEM

p-values



GW_087

Local Summary

%DE = 0.72
 # metagenes = 15
 # genes = 280
 # genes in genesets = 280
 # genes with $fdr < 0.1 = 118$ (1 + / 117 -)
 # genes with $fdr < 0.05 = 99$ (1 + / 98 -)
 # genes with $fdr < 0.01 = 31$ (0 + / 31 -)

<r> metagenes = 0.97

<r> genes = 0.3

<FC> = -0.35

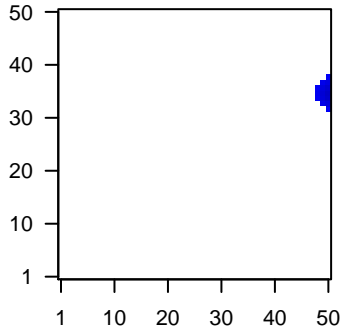
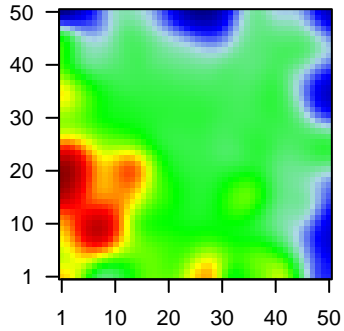
<shrinkage-t> = -12.21

<p-value> = 0.05

<fdr> = 0.71

Profile

Spot



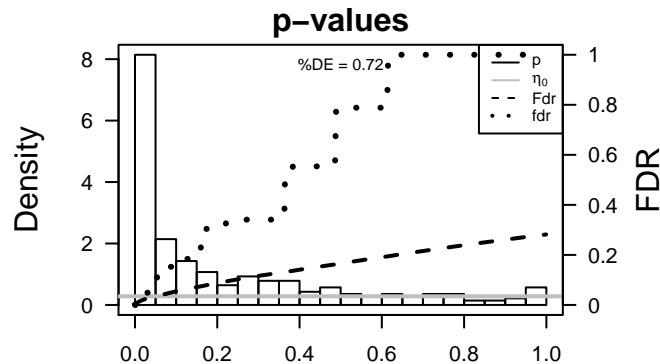
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1429	-1.21	6e-09	2e-05	50 x 34 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
2	60481	-1.08	2e-07	2e-05	50 x 37 ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213
3	27075	-1.06	4e-07	3e-04	50 x 38 tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
4	57223	-0.96	5e-06	3e-04	50 x 36 SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Sourc
5	728026	-0.91	2e-05	3e-04	50 x 35 prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
6	51015	-0.89	2e-05	3e-04	50 x 33 isochorismatase domain containing 1 [Source:HGNC Symbol
7	23588	-0.89	2e-05	3e-04	50 x 33 kelch domain containing 2 [Source:HGNC Symbol;Acc:20231
8	5612	-0.88	2e-05	3e-04	50 x 34 protein-kinase, interferon-inducible double stranded RNA de
9	9061	-0.88	3e-05	5e-04	50 x 34 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Source
10	10923	-0.87	3e-05	5e-04	50 x 32 SUB1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1e
11	310	-0.86	4e-05	2e-03	50 x 35 annexin A7 [Source:HGNC Symbol;Acc:545]
12	1655	-0.77	7e-05	4e-03	50 x 36 DEAD (Asp-Glu-Ala-Asp) box helicase 5 [Source:HGNC Sy
13	84191	-0.81	1e-04	4e-03	50 x 34 family with sequence similarity 96, member A [Source:HGNC
14	3150	-0.79	2e-04	4e-03	50 x 35 high mobility group nucleosome binding domain 1 [Source:HC
15	1859	-0.76	3e-04	4e-03	50 x 35 dual-specificity tyrosine-(Y)-phosphorylation regulated kinas
16	167153	-0.76	3e-04	4e-03	50 x 34 PAP associated domain containing 4 [Source:HGNC Symbol;
17	29058	-0.75	4e-04	4e-03	50 x 38 transmembrane protein 230 [Source:HGNC Symbol;Acc:1587
18	51727	-0.73	5e-04	4e-03	50 x 34 cytidine monophosphate (UMP-CMP) kinase 1, cytosolic [So
19	9528	-0.67	5e-04	4e-03	50 x 34 transmembrane protein 59 [Source:HGNC Symbol;Acc:1239]
20	22887	-0.73	5e-04	4e-03	50 x 38 forkhead box J3 [Source:HGNC Symbol;Acc:29178]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.38	NULL	7 / 54	miRNA target site 3499-5p
2	-9.27	NULL	2 / 16	GSEA C2/YANG_BREAST_CANCER_ESR1_BULK_UP
3	-9.05	NULL	7 / 50	miRNA target site 3498A-508
4	-8.9	NULL	22 / 271	miRNA target site 3499
5	-8.58	NULL	18 / 229	miRNA target site 3499g
6	-8.54	NULL	1 / 2	MMML C6/CIEJ_MMML 38
7	-8.49	NULL	2 / 10	MF NADPH binding
8	-8.34	NULL	16 / 171	miRNA target site 3499-3p
9	-8.31	NULL	23 / 303	miRNA target site 3499b
10	-8.12	NULL	23 / 311	miRNA target site 3499c
11	-8.07	NULL	15 / 186	miRNA target site 3499
12	-7.78	NULL	6 / 45	miRNA target site 3499
13	-7.7	NULL	4 / 27	MF nucleotidyltransferase activity
14	-7.63	NULL	13 / 180	miRNA target site 3499a
15	-7.55	NULL	19 / 215	miRNA target site 3499
16	-7.46	NULL	3 / 11	MF AU-rich element binding
17	-7.35	NULL	9 / 80	miRNA target site 3499*
18	-7.3	NULL	12 / 100	miRNA target site 3499
19	-7.27	NULL	18 / 264	miRNA target site 3499a
20	-7.24	NULL	22 / 325	miRNA target site 3499d
21	-7.23	NULL	17 / 163	BP mRNA splicing, via spliceosome
22	-7.23	NULL	12 / 89	miRNA target site 3499
23	-6.98	NULL	5 / 14	GSEA C2/REACTOME_MRNA_3_END_PROCESSING
24	-6.93	NULL	13 / 155	miRNA target site 3499
25	-6.89	NULL	24 / 396	miRNA target site 3499b
26	-6.86	NULL	11 / 122	miRNA target site 3499
27	-6.82	NULL	25 / 412	miRNA target site 3499
28	-6.8	NULL	26 / 463	miRNA target site 3499a
29	-6.77	NULL	19 / 335	miRNA target site 3499-5p
30	-6.71	NULL	12 / 146	miRNA target site 3499
31	-6.66	NULL	6 / 33	miRNA target site 3499b
32	-6.66	NULL	7 / 55	miRNA target site 3499-3p
33	-6.66	NULL	20 / 318	miRNA target site 3499-3p
34	-6.65	NULL	11 / 108	miRNA target site 3499
35	-6.65	NULL	22 / 315	miRNA target site 3499
36	-6.64	NULL	6 / 46	miRNA target site 3499
37	-6.62	NULL	18 / 321	miRNA target site 3499a-5p
38	-6.59	NULL	10 / 90	miRNA target site 3499-5p
39	-6.57	NULL	29 / 421	miRNA target site 3499
40	-6.53	NULL	7 / 47	miRNA target site 3499*



GW_087

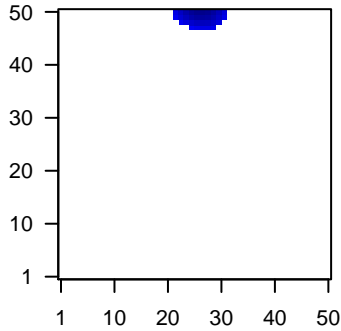
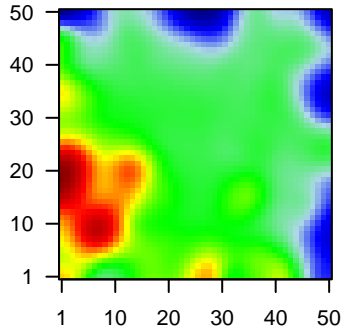
Local Summary

%DE = 0.77
 # metagenes = 33
 # genes = 463
 # genes in genesets = 457
 # genes with $fdr < 0.1 = 225$ (2 + / 223 -)
 # genes with $fdr < 0.05 = 160$ (1 + / 159 -)
 # genes with $fdr < 0.01 = 85$ (1 + / 84 -)

<r> metagenes = 0.9
 <r> genes = 0.26
 <FC> = -0.39
 <shrinkage-t> = -13.55
 <p-value> = 0.03
 <fdr> = 0.65

Profile

Spot



Local Genelist

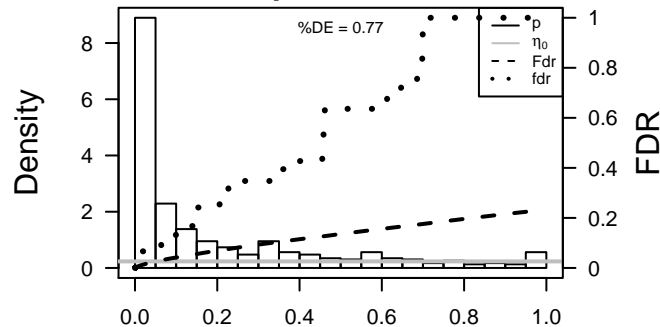
Rank	ID	log(FC)	fdr	p-value	Description
1	10413	-1.54	2e-13	2e-09	26 x 50 Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
2	3725	-1.4	2e-11	3e-07	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
3	114908	-1.24	3e-09	2e-06	26 x 50 transmembrane protein 123 [Source:HGNC Symbol;Acc:3013]
4	1843	-1.06	3e-08	2e-06	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3013]
5	147463	-1.14	5e-08	6e-06	25 x 50 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
6	85461	-1.11	1e-07	7e-06	24 x 50 tetratricopeptide repeat, ankyrin repeat and coiled-coil contain
7	27020	-1.09	2e-07	7e-06	25 x 50 neuroplastin [Source:HGNC Symbol;Acc:17867]
8	2353	-0.99	2e-07	5e-05	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:17867]
9	55013	-1.04	7e-07	5e-05	26 x 47 coiled-coil domain containing 109B [Source:HGNC Symbol;Acc:27110]
10	1958	-1.01	1e-06	5e-05	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
11	6392	-0.99	2e-06	5e-05	31 x 50 succinate dehydrogenase complex, subunit D, integral membrane
12	100008589	-0.99	2e-06	5e-05	23 x 50 RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
13	114884	-0.99	2e-06	2e-04	25 x 50 oxysterol binding protein-like 10 [Source:HGNC Symbol;Acc:27110]
14	7385	-0.95	5e-06	2e-04	31 x 50 ubiquinol-cytochrome c reductase core protein II [Source:HGNC Symbol;Acc:17867]
15	51014	-0.95	6e-06	2e-04	26 x 50 transmembrane emp24 protein transport domain containing 7
16	10196	-0.94	7e-06	4e-04	29 x 50 protein arginine methyltransferase 3 [Source:HGNC Symbol;Acc:17867]
17	7465	-0.9	2e-05	4e-04	23 x 50 WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:12710]
18	10190	-0.9	2e-05	4e-04	31 x 50 thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:17867]
19	9197	-0.89	2e-05	4e-04	26 x 50 solute carrier family 33 (acetyl-CoA transporter), member 1 [Source:HGNC Symbol;Acc:17867]
20	25978	-0.89	2e-05	4e-04	26 x 50 charged multivesicular body protein 2B [Source:HGNC Symbol;Acc:17867]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.37	NULL	5 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	-12.6	NULL	6 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
3	-12.46	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
4	-12.12	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
5	-11.42	NULL	6 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
6	-10.89	NULL	38 / 269	miRNA target set miR-394
7	-10.69	NULL	2 / 8	GSEA C2EMELYANOV_GR_TARGETS_DN
8	-10.28	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
9	-10.13	NULL	4 / 11	miRNA target set miR-399-5p
10	-9.97	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
11	-9.78	NULL	3 / 12	GSEA C2BIOCARTA_DREAM_PATHWAY
12	-9.72	NULL	2 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCRIPTION_FACTORS
13	-9.66	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY
14	-9.66	NULL	3 / 15	GSEA C2BIOCARTA_TPO_PATHWAY
15	-9.65	NULL	24 / 169	miRNA target set miR-394b
16	-9.64	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
17	-9.62	NULL	21 / 151	miRNA target set miR-399
18	-9.31	NULL	3 / 16	GSEA C2BIOCARTA_EPO_PATHWAY
19	-9.31	NULL	3 / 16	GSEA C2BIOCARTA_IGF1_PATHWAY
20	-9.31	NULL	3 / 16	GSEA C2BIOCARTA_GLEEVEC_PATHWAY
21	-9.31	NULL	3 / 16	GSEA C2BIOCARTA_NGF_PATHWAY
22	-9.27	NULL	52 / 436	miRNA target set miR-396n
23	-9.27	NULL	4 / 16	GSEA C2BIOCARTA_ETS_PATHWAY
24	-9.22	NULL	25 / 155	miRNA target set miR-392
25	-9.05	NULL	21 / 155	miRNA target set miR-392b
26	-9.04	NULL	2 / 12	BP cellular response to gamma radiation
27	-9.01	NULL	3 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
28	-8.76	NULL	2 / 12	GSEA C2BIOCARTA_ARENERF2_PATHWAY
29	-8.76	NULL	4 / 15	BP long-term synaptic potentiation
30	-8.68	NULL	7 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
31	-8.65	NULL	4 / 14	BP response to light stimulus
32	-8.47	NULL	5 / 8	MMML C6CIEJ_MMML_50
33	-8.46	NULL	44 / 511	miRNA target set miR-396b
34	-8.4	NULL	3 / 15	GSEA C2BIOCARTA_IL6_PATHWAY
35	-8.37	NULL	2 / 13	BP SMAD protein signal transduction
36	-8.35	NULL	20 / 150	miRNA target set miR-396c
37	-8.28	NULL	2 / 10	BP notochord development
38	-8.28	NULL	2 / 10	BP paraxial mesoderm development
39	-8.26	NULL	25 / 198	miRNA target set miR-396a
40	-8.23	NULL	38 / 310	miRNA target set miR-396

p-values



GW_087

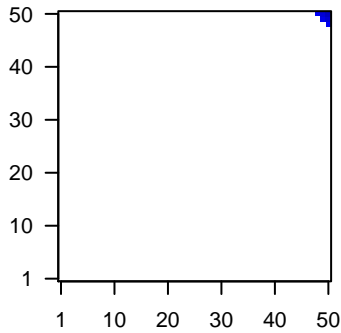
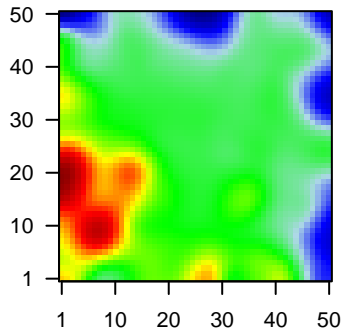
Local Summary

%DE = 0.71
 # metagenes = 6
 # genes = 140
 # genes in genesets = 139
 # genes with $fdr < 0.1$ = 60 (9 + / 51 -)
 # genes with $fdr < 0.05$ = 60 (9 + / 51 -)
 # genes with $fdr < 0.01$ = 40 (6 + / 34 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.31
 $\langle FC \rangle = -0.39$
 $\langle \text{shrinkage-t} \rangle = -13.86$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.57$

Profile

Spot



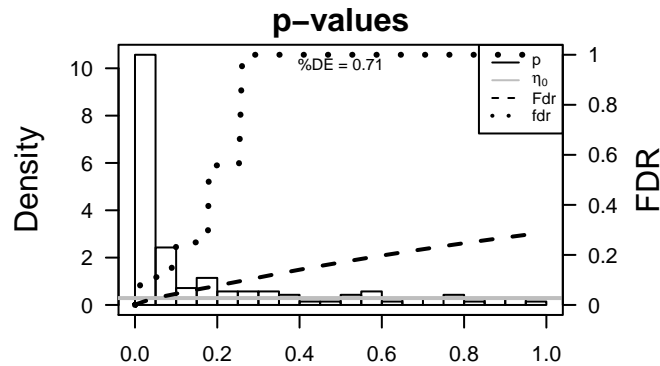
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	94234	-1.87	2e-16	5e-15	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
2	3866	-2.37	2e-16	5e-15	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
3	655	-1.56	8e-14	2e-12	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1038]
4	4922	-1.56	8e-14	3e-12	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
5	11166	-1.55	2e-13	7e-12	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt
6	216	-1.52	3e-13	2e-11	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
7	23321	-1.49	9e-13	7e-09	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:15972
8	3304	-1.22	2e-10	8e-08	49 x 49 heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:521
9	256764	-1.24	3e-09	8e-08	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
10	6657	-1.23	4e-09	4e-07	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symb
11	29968	-1.19	1e-08	2e-06	49 x 50 phosphoserine aminotransferase 1 [Source:HGNC Symbol;Ac
12	26047	-1.12	8e-08	2e-06	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
13	154664	-1.12	9e-08	9e-06	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [So
14	120	-1.07	3e-07	1e-05	50 x 50 adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]
15	6446	-0.95	7e-07	1e-05	50 x 50 serum/glucocorticoid regulated kinase 1 [Source:HGNC Syml
16	10643	-1.02	1e-06	6e-05	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:t
17	339512	0.97	4e-06	6e-05	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
18	5955	-0.96	4e-06	8e-05	48 x 50 reticulocalbin 2, EF-hand calcium binding domain [Source:H
19	4711	-0.94	6e-06	1e-04	48 x 50 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16
20	200810	0.91	1e-05	1e-04	49 x 50 ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferas

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-23.7	NULL	3 / 8	GSEA C2JUCDX2_TARGETS_DN
2	-19.49	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	-16.08	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
4	-14.45	NULL	3 / 16	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G1_DN
5	-13.11	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
6	-12.33	NULL	3 / 13	BP regulation of blood vessel size
7	-12.19	NULL	5 / 15	GSEA C2KEGG_Glutathione_Metabolism
8	-11.85	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
9	-11.57	NULL	1 / 6	GSEA C2SAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
10	-11.57	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
11	-11.05	NULL	2 / 19	BP anatomical structure formation involved in morphogenesis
12	-10.66	NULL	3 / 33	BP regulation of sequence-specific DNA binding transcription factor ac
13	-10.66	NULL	1 / 15	H.Tiss WIRTH_Cerebellum
14	-10.37	NULL	8 / 34	BP glutathione metabolic process
15	-10.27	NULL	1 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
16	-10.17	NULL	2 / 22	BP eye development
17	-10.03	NULL	1 / 8	GSEA C2MCCABE_HOXC6_TARGETS_UP
18	-9.85	NULL	2 / 23	BP stem cell differentiation
19	-9.73	NULL	2 / 16	GSEA C2SOUYER_TATI_TARGETS_DN
20	-9.72	NULL	2 / 12	BP cellular aldehyde metabolic process
21	-9.69	NULL	6 / 25	BP glutathione derivative biosynthetic process
22	-9.43	NULL	2 / 10	GSEA C2ZHANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
23	-9.29	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
24	-9.24	NULL	2 / 23	BP hair follicle morphogenesis
25	-9.24	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
26	-9.15	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME
27	-9.12	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
28	-9.12	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
29	-9.05	NULL	1 / 20	MF scaffold protein binding
30	-8.87	NULL	11 / 119	BP xenobiotic metabolic process
31	-8.81	NULL	1 / 10	BP branching involved in salivary gland morphogenesis
32	-8.81	NULL	1 / 10	BP mesonephros development
33	-8.63	NULL	3 / 19	miRNA target-380-5P
34	-8.58	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
35	-8.58	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENT_DN
36	-8.49	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
37	-8.49	NULL	1 / 7	miRNA target-145
38	-8.47	NULL	3 / 30	BP negative regulation of cell death
39	-8.45	NULL	2 / 14	CC membrane-bounded vesicle
40	-8.45	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS



GW_087

Local Summary

%DE = 0.83
 # metagenes = 10
 # genes = 171
 # genes in genesets = 167

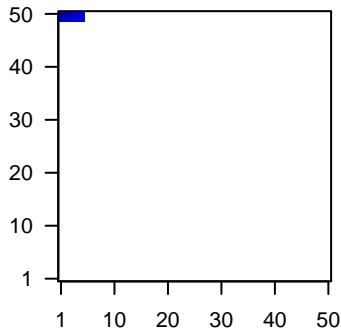
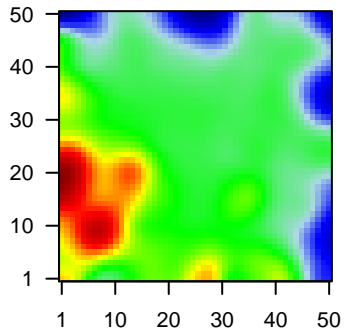
genes with $fdr < 0.1$ = 139 (18 + / 121 -)
 # genes with $fdr < 0.05$ = 113 (14 + / 99 -)
 # genes with $fdr < 0.01$ = 89 (10 + / 79 -)

<r> metagenes = 0.99
 <r> genes = 0.49

<FC> = -0.55
 <shrinkage-t> = -19.45
 <p-value> = 0
 <fdr> = 0.33

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-1.89	2e-16	8e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	-2.03	2e-16	8e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
3	51806	1.8	2e-16	8e-16	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
4	4680	-2.36	2e-16	8e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
5	163351	-1.92	2e-16	8e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
6	3860	-1.72	2e-16	8e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
7	6698	-1.57	2e-16	8e-16	1 x 50 small proline-rich protein 1A [Source:HGNC Symbol;Acc:112
8	9407	-1.72	2e-16	8e-16	1 x 50 transmembrane protease, serine 11D [Source:HGNC Symbol
9	92196	-1.65	4e-15	2e-12	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
10	1672	1.57	6e-14	3e-12	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	26298	-1.54	2e-13	3e-12	4 x 50 ets homologous factor [Source:HGNC Symbol;Acc:3246]
12	11045	1.53	2e-13	1e-11	4 x 50 uroplakin 1A [Source:HGNC Symbol;Acc:12577]
13	9314	-1.49	9e-13	1e-11	4 x 50 Kruppel-like factor 4 (gut) [Source:HGNC Symbol;Acc:6348]
14	339967	-1.49	1e-12	3e-11	2 x 50 transmembrane protease, serine 11A [Source:HGNC Symbol
15	192666	-1.47	2e-12	3e-11	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
16	114569	-1.46	3e-12	8e-11	4 x 50 mal, T-cell differentiation protein 2 (gene/pseudogene) [Sour
17	22802	-1.44	6e-12	8e-11	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	388533	-1.43	9e-12	1e-10	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
19	3934	-1.42	1e-11	5e-10	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]
20	218	-1.39	3e-11	1e-09	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-34.5	NULL	63 / 135	H.Tiss WIRTH_Mucosa
2	-22.76	NULL	12 / 21	CC cornified envelope
3	-21.03	NULL	16 / 53	BP keratinocyte differentiation
4	-20.78	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
5	-17.9	NULL	13 / 42	BP keratinization
6	-16.49	NULL	5 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
7	-15.69	NULL	4 / 15	MF retinol dehydrogenase activity
8	-13.85	NULL	17 / 76	BP epidermis development
9	-13.67	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_1
10	-13.51	NULL	5 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
11	-13.48	NULL	61 / 572	Disease GUDJ_psooriasis_up
12	-12.71	NULL	7 / 19	BP peptide cross-linking
13	-12.21	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
14	-11.8	NULL	12 / 122	MF serine-type endopeptidase activity
15	-10.5	NULL	2 / 14	BP cyclooxygenase pathway
16	-10.21	NULL	4 / 24	TF Tissue/AQUERIZAS_Trachea
17	-9.63	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
18	-9.6	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
19	-9.52	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
20	-9.52	NULL	5 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
21	-9.47	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
22	-9.22	NULL	4 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
23	-9.02	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
24	-8.86	NULL	4 / 39	BP retinoid metabolic process
25	-8.64	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
26	-8.54	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HP31_DN
27	-8.52	NULL	3 / 18	BP retinol metabolic process
28	-8.23	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
29	-8.06	NULL	5 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
30	-7.98	NULL	46 / 1182	CC extracellular region
31	-7.88	NULL	7 / 38	BP epithelial cell differentiation
32	-7.64	NULL	2 / 13	MF RNA polymerase II transcription factor binding transcription factor
33	-7.63	NULL	2 / 15	GSEA C2ORKOLA_TERATOMA
34	-7.57	NULL	1 / 10	BP positive regulation of endothelial cell apoptotic process
35	-7.57	NULL	1 / 10	BP retinal metabolic process
36	-7.52	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
37	-7.5	NULL	6 / 82	CC intermediate filament
38	-7.49	NULL	4 / 49	BP arachidonic acid metabolic process
39	-7.45	NULL	12 / 186	MF structural molecule activity
40	-7.39	NULL	2 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP

