

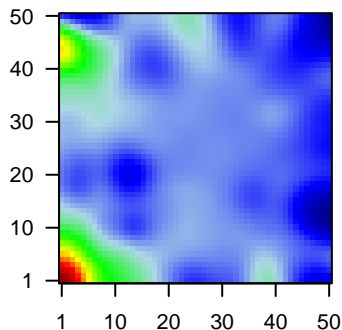
GW_251

Global Summary

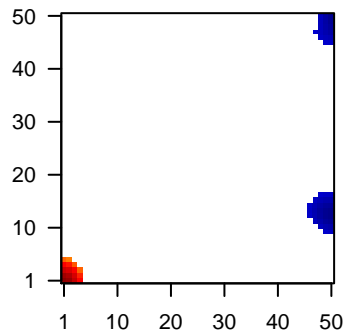
%DE = 0.14
 # genes with fdr < 0.2 = 1794 (1002 + / 792 -)
 # genes with fdr < 0.1 = 1364 (800 + / 564 -)
 # genes with fdr < 0.05 = 1120 (668 + / 452 -)
 # genes with fdr < 0.01 = 739 (472 + / 267 -)
 # genes in genesets = 16332

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

Profile



Regulated Spots



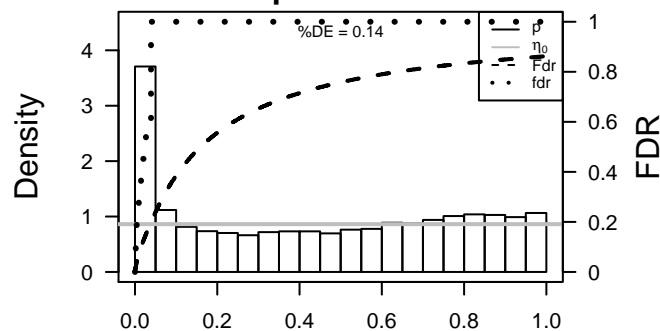
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	72	1.33	2e-16	3e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	131	-1.67	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	-1.51	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	-1.66	2e-16	3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy
5	216	-1.66	2e-16	3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	220	2	2e-16	3e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
7	218	-1.33	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	9823	1.49	2e-16	3e-14	7 x 1 armadillo repeat containing, X-linked 2 [Source:HGNC Symb
9	655	-1.45	2e-16	3e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
10	260436	-1.33	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
11	760	1.58	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	414062	1.6	2e-16	3e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
13	1041	1.76	2e-16	3e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
14	4680	-1.47	2e-16	3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
15	8837	1.5	2e-16	3e-14	44 x 1 CASP8 and FADD-like apoptosis regulator [Source:HGNC S
16	22802	-2.26	2e-16	3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	1306	1.4	2e-16	3e-14	4 x 1 collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
18	1277	1.84	2e-16	3e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
19	1278	1.42	2e-16	3e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
20	1281	1.37	2e-16	3e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	17.49	NULL	250	Lympho
2	16.94	NULL	242	BP extracellular matrix organization
3	16.29	NULL	190	CC extracellular matrix
4	14.87	NULL	69	BP extracellular matrix disassembly
5	14.31	NULL	64	BP collagen catabolic process
6	13.29	NULL	16	MMML C63CIEJ_MMML 1
7	11.54	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
8	11.49	NULL	11	MF platelet-derived growth factor binding
9	11.41	NULL	57	MF extracellular matrix structural constituent
10	10.44	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
11	10.34	NULL	12	miRNA tagR-29c
12	10.29	NULL	1182	CC extracellular region
13	10.19	NULL	553	Cancer Lembecke_Colonc Inflammation
14	9.86	NULL	83	CC basement membrane
15	9.64	NULL	403	BP cell adhesion
16	9.54	NULL	683	CC extracellular space
17	9.46	NULL	183	CC proteinaceous extracellular matrix
18	9.16	NULL	37	BP collagen fibril organization
19	9.13	NULL	10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
20	8.77	NULL	40	BP cellular response to amino acid stimulus
<i>Underexpressed</i>				
1	-8.77	NULL	866	Chr Chr 12
2	-8.18	NULL	1318	CC mitochondrion
3	-7.33	NULL	15	CC MHC class II protein complex
4	-7	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
5	-6.84	NULL	83	BP respiratory electron transport chain
6	-6.82	NULL	52	Chr H5CHR6_MHC_QBL
7	-6.76	NULL	304	CC mitochondrial inner membrane
8	-6.32	NULL	220	CC mitochondrial matrix
9	-6.15	NULL	9	GSEA C2REACTOME_ETHANOL_OXIDATION
10	-5.98	NULL	92	BP viral life cycle
11	-5.95	NULL	153	MF structural constituent of ribosome
12	-5.91	NULL	81	BP viral transcription
13	-5.85	NULL	128	BP translational initiation
14	-5.7	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
15	-5.65	NULL	87	BP translational termination
16	-5.63	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
17	-5.63	NULL	253	BP translation
18	-5.57	NULL	152	BP cellular metabolic process
19	-5.46	NULL	167	CC ribosome
20	-5.38	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated

p-values



GW_251

Local Summary

%DE = 0.93
 # metagenes = 17
 # genes = 263
 # genes in genesets = 261

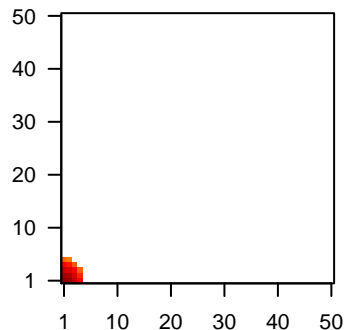
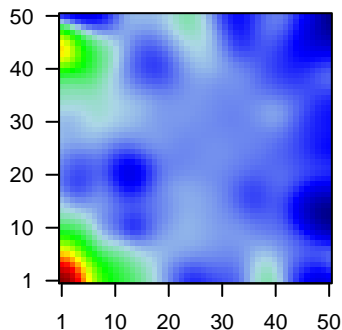
genes with $fdr < 0.1 = 224$ (221 + / 3 -)
 # genes with $fdr < 0.05 = 220$ (217 + / 3 -)
 # genes with $fdr < 0.01 = 194$ (191 + / 3 -)

<r> metagenes = 0.96
 <r> genes = 0.38

<FC> = 0.76
 <shrinkage-t> = 26.66
 <p-value> = 0
 <fdr> = 0.2

Profile

Spot



Local Genelist

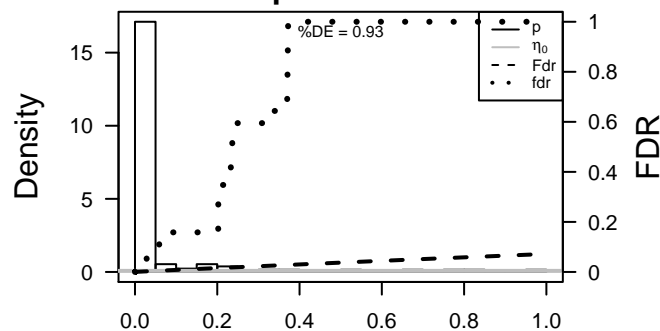
Rank	ID	log(FC)	fdr	p-value	Description
1	72	1.33	2e-16	1e-16	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	414062	1.6	2e-16	1e-16	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
3	1306	1.4	2e-16	1e-16	4 x 1 collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
4	1277	1.84	2e-16	1e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	1.42	2e-16	1e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1281	1.37	2e-16	1e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
7	1282	1.36	2e-16	1e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
8	1289	1.38	2e-16	1e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
9	1290	1.3	2e-16	1e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
10	1291	1.43	2e-16	1e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
11	1293	1.59	2e-16	1e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	6372	1.41	2e-16	1e-16	1 x 1 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Ac
13	285761	1.37	2e-16	1e-16	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC
14	27122	1.31	2e-16	1e-16	1 x 3 dickkopf1 WNT signaling pathway inhibitor 3 [Source:HGNC S
15	28514	1.38	2e-16	1e-16	1 x 5 delta-like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
16	26585	1.3	2e-16	1e-16	2 x 1 gremlin 1, DAN family BMP antagonist [Source:HGNC Symbc
17	3553	1.54	2e-16	1e-16	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
18	11009	1.65	2e-16	1e-16	1 x 3 interleukin 24 [Source:HGNC Symbol;Acc:11346]
19	3569	1.99	2e-16	1e-16	1 x 1 interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:f
20	3576	2.4	2e-16	1e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	37.29	NULL	15 / 16	MMML C6SCIEJ_MMML 1
2	36.73	NULL	59 / 190	CC extracellular matrix
3	34.38	NULL	32 / 69	BP extracellular matrix disassembly
4	33.4	NULL	69 / 242	BP extracellular matrix organization
5	33.24	NULL	69 / 250	Lymphom1ENZ_Stromal signature 1
6	32.73	NULL	29 / 64	BP collagen catabolic process
7	30.77	NULL	12 / 16	FARMER_BREAST_CANCER_CLUSTER_5
8	29.45	NULL	7 / 11	MF platelet-derived growth factor binding
9	29.23	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
10	28.95	NULL	8 / 12	miRNA target-29c
11	25.22	NULL	20 / 57	MF extracellular matrix structural constituent
12	24.82	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
13	24.09	NULL	15 / 37	BP collagen fibril organization
14	23.46	NULL	4 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
15	22.27	NULL	73 / 683	CC extracellular space
16	21.58	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
17	21.27	NULL	12 / 19	MF extracellular matrix binding
18	21.11	NULL	37 / 183	CC proteinaceous extracellular matrix
19	21.02	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
20	20.43	NULL	100 / 1182	CC extracellular region
21	20.1	NULL	11 / 40	BP cellular response to amino acid stimulus
22	19.42	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
23	19.41	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
24	19.31	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
25	19.18	NULL	23 / 83	CC basement membrane
26	19.16	NULL	61 / 553	Cancer Lembcke_Colonc Inflammation
27	19.09	NULL	41 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
28	19.09	NULL	41 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
29	19.09	NULL	41 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
30	19.09	NULL	41 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
31	18.95	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
32	18.55	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
33	18.25	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
34	18.07	NULL	23 / 119	Lymphom1BOSOLOWSKI_green total
35	17.56	NULL	12 / 35	Glio Colman_survival_associated
36	17.37	NULL	16 / 68	CC collagen
37	17.11	NULL	52 / 403	BP cell adhesion
38	17.09	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
39	16.94	NULL	5 / 12	GSEA C2Y_AGING_MIDDLE_UP
40	16.92	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN

p-values



GW_251

Local Summary

%DE = 0.83
 # metagenes = 31
 # genes = 337
 # genes in genesets = 332

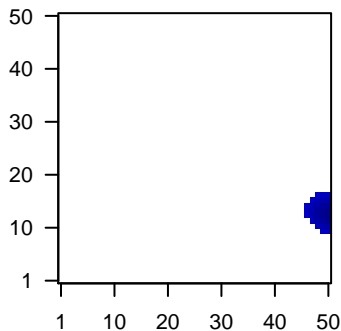
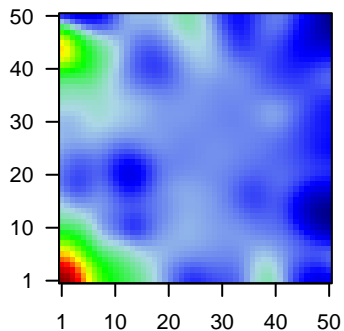
genes with $fdr < 0.1$ = 218 (16 + / 202 -)
 # genes with $fdr < 0.05$ = 173 (15 + / 158 -)
 # genes with $fdr < 0.01$ = 96 (8 + / 88 -)

<r> metagenes = 0.91
 <r> genes = 0.25

<FC> = -0.3
 <shrinkage-t> = -10.7
 <p-value> = 0.01
 <fdr> = 0.57

Profile

Spot



Local Genelist

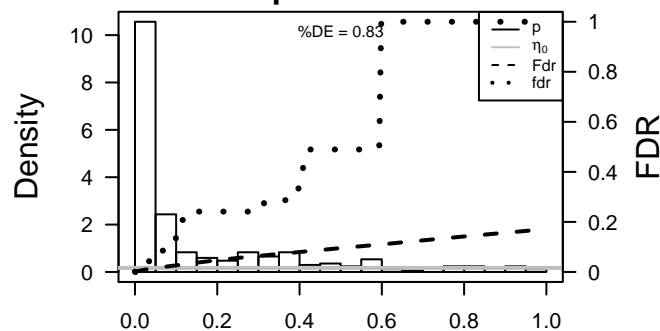
Rank	ID	log(FC)	fdr	p-value	Description
1	3169	-1.49	2e-16	1e-14	50 x 12 forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	2568	-1.21	3e-14	5e-11	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:15254]
3	55268	-1.14	9e-13	3e-10	50 x 14 enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:15254]
4	10232	-1.09	6e-12	1e-09	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
5	51316	-1.06	3e-11	2e-09	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
6	79191	1.04	6e-11	4e-08	50 x 15 iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
7	83699	-0.97	9e-10	4e-08	50 x 11 SH3 domain binding glutamic acid-rich protein like 2 [Source:HGNC Symbol;Acc:14360]
8	27347	0.96	1e-09	6e-08	49 x 11 serine threonine kinase 39 [Source:HGNC Symbol;Acc:17717]
9	10439	-0.95	2e-09	9e-08	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
10	293	-0.93	4e-09	9e-08	50 x 15 solute carrier family 25 (mitochondrial carrier; adenine nucleotide) member 1 [Source:HGNC Symbol;Acc:17187]
11	217	-0.93	6e-09	1e-07	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:17187]
12	2762	-0.92	8e-09	1e-07	50 x 12 GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc:17187]
13	28958	-0.91	9e-09	4e-07	49 x 13 cytochrome c oxidase assembly factor 3 [Source:HGNC Symbol;Acc:17187]
14	10551	-0.9	2e-08	9e-07	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
15	23171	-0.88	3e-08	2e-06	50 x 12 glycerol-3-phosphate dehydrogenase 1-like [Source:HGNC Symbol;Acc:328]
16	92747	-0.86	7e-08	2e-06	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:328]
17	4602	-0.85	1e-07	2e-06	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:328]
18	260293	-0.84	1e-07	2e-06	50 x 14 cytochrome P450, family 4, subfamily X, polypeptide 1 [Source:HGNC Symbol;Acc:328]
19	7018	-0.82	2e-07	2e-06	50 x 10 transferrin [Source:HGNC Symbol;Acc:11740]
20	8857	-0.82	2e-07	2e-06	50 x 13 Fc fragment of IgG binding protein [Source:HGNC Symbol;Acc:11740]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-17.53	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-14.86	NULL	5 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
3	-13.72	NULL	4 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
4	-13.07	NULL	3 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
5	-12.97	NULL	4 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
6	-12.2	NULL	3 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
7	-10.79	NULL	3 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
8	-9.76	NULL	6 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
9	-9.5	NULL	2 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
10	-9.36	NULL	1 / 4	GSEA C2NICK_RESPONSE_TO_PROC_TREATMENT_UP
11	-9.05	NULL	1 / 7	GSEA C2NEBEN_AML_WITH_FLT3_OR_NRAS_UP
12	-8.82	NULL	3 / 10	GSEA C2YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
13	-8.49	NULL	1 / 3	miRNA 3408C-210
14	-8.08	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_BULK_UP
15	-8.06	NULL	4 / 21	BP drug metabolic process
16	-7.93	NULL	2 / 15	BP hormone metabolic process
17	-7.92	NULL	2 / 14	GSEA C2WANG_BARRETTES_ESOPHAGUS_UP
18	-7.89	NULL	1 / 3	GSEA C2RUNNE_GENDER_EFFECT_DN
19	-7.78	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
20	-7.63	NULL	5 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
21	-7.41	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_UP
22	-7.4	NULL	1 / 10	BP prostate gland epithelium morphogenesis
23	-7.39	NULL	2 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
24	-7.11	NULL	2 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
25	-7.03	NULL	2 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
26	-7.03	NULL	2 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
27	-6.94	NULL	2 / 9	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
28	-6.85	NULL	2 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_DN
29	-6.74	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
30	-6.66	NULL	2 / 11	BP neurotransmitter biosynthetic process
31	-6.51	NULL	3 / 9	GSEA C2GOZGIT_ESR1_TARGETS_DN
32	-6.36	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
33	-6.24	NULL	4 / 39	MF NAD binding
34	-6.24	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_UP
35	-6.24	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_UP
36	-6.09	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition
37	-5.93	NULL	1 / 10	MF GABA-A receptor activity
38	-5.91	NULL	2 / 14	GSEA C2VANTVEER_BREAST_CANCER_ESR1_UP
39	-5.88	NULL	2 / 12	Pathway Ac:BENTINK_ras.1
40	-5.81	NULL	2 / 12	BP nitric oxide biosynthetic process

p-values



GW_251

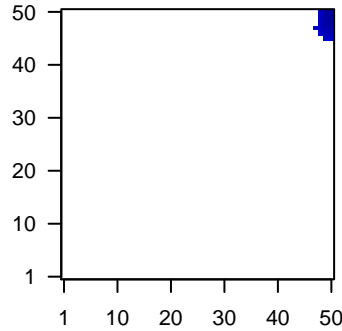
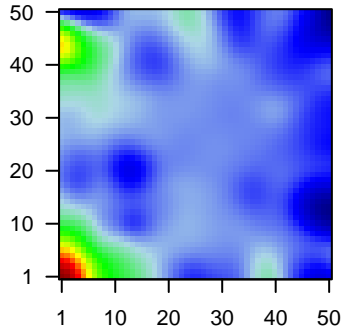
Local Summary

%DE = 0.69
 # metagenes = 18
 # genes = 232
 # genes in genesets = 231
 # genes with $fdr < 0.1$ = 107 (11 + / 96 -)
 # genes with $fdr < 0.05$ = 99 (10 + / 89 -)
 # genes with $fdr < 0.01$ = 54 (5 + / 49 -)

<r> metagenes = 0.95
 <r> genes = 0.26
 <FC> = -0.3
 <shrinkage-t> = -10.65
 <p-value> = 0
 <fdr> = 0.59

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.66	2e-16	4e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
2	655	-1.45	2e-16	4e-15	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C]
3	3856	-1.71	2e-16	4e-15	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
4	11166	-1.48	2e-16	4e-15	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt]
5	5625	-1.29	4e-16	2e-14	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ar]
6	445	-1.29	7e-16	6e-13	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75]
7	4922	-1.23	9e-15	9e-13	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
8	3866	-1.22	2e-14	1e-12	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
9	928	-1.2	4e-14	2e-12	50 x 50 CD9 molecule [Source:HGNC Symbol;Acc:1709]
10	1056	-1.19	6e-14	9e-11	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
11	214	-1.13	1e-12	2e-10	50 x 50 activated leukocyte cell adhesion molecule [Source:HGNC Sy]
12	26227	-1.1	4e-12	2e-09	50 x 46 phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac]
13	26047	-1.05	3e-11	9e-09	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ar]
14	339512	-1.02	2e-10	2e-06	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt]
15	56256	-0.88	3e-08	2e-06	50 x 50 SERTA domain containing 4 [Source:HGNC Symbol;Acc:252]
16	80896	-0.87	5e-08	2e-06	50 x 50 N-acetylneuraminatase pyruvate lyase (dihydrodipicolinate synt
17	440	-0.86	7e-08	5e-06	50 x 46 asparagine synthetase (glutamine-hydrolyzing) [Source:HGN]
18	79844	-0.84	1e-07	1e-05	50 x 50 zinc finger, DHHC-type containing 11 [Source:HGNC Symbo]
19	7345	0.8	5e-07	1e-05	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
20	200634	-0.8	5e-07	1e-04	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-15.23	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
2	-14.81	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
3	-14.58	NULL	2 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
4	-12.51	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
5	-11.58	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
6	-11.48	NULL	4 / 19	BP cellular amino acid biosynthetic process
7	-11.39	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
8	-11.34	NULL	2 / 12	BP cellular aldehyde metabolic process
9	-10.7	NULL	1 / 5	GSEA C2NIELSEN_SCHWANNOMA_DN
10	-10.28	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
11	-10.14	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
12	-9.96	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
13	-9.96	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
14	-9.46	NULL	3 / 19	BP anatomical structure formation involved in morphogenesis
15	-9.39	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
16	-9.39	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
17	-9.24	NULL	1 / 8	GSEA C2MCCABE_HOXC6_TARGETS_UP
18	-9.14	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
19	-9.04	NULL	2 / 18	MF acyl-CoA dehydrogenase activity
20	-9.01	NULL	1 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP
21	-8.97	NULL	2 / 14	GSEA C2SILIGAN_TARGETS_OF_EWS_FL11_FUSION_DN
22	-8.81	NULL	3 / 8	GSEA C2LIU_CD2_TARGETS_DN
23	-8.54	NULL	2 / 16	GSEA C2PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
24	-8.54	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
25	-8.49	NULL	2 / 14	CC membrane-bounded vesicle
26	-8.14	NULL	1 / 10	BP branching involved in salivary gland morphogenesis
27	-8.14	NULL	1 / 10	BP mesonephros development
28	-8.02	NULL	2 / 16	GSEA C2GOUYER_TATI_TARGETS_DN
29	-8.01	NULL	2 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
30	-7.99	NULL	2 / 18	BP glutamine metabolic process
31	-7.76	NULL	1 / 14	MF Ras GTPase activator activity
32	-7.76	NULL	1 / 14	GSEA C2MAHADEVAN_IMATINIB_RESISTANCE_UP
33	-7.73	NULL	2 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
34	-7.57	NULL	1 / 8	GSEA C2KEGG_GLYCEROLIPID_METABOLISM
35	-7.46	NULL	1 / 15	GSEA C2DORSAM_HOXA9_TARGETS_UP
36	-7.41	NULL	2 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
37	-7.39	NULL	3 / 14	GSEA C2VANTVEER_BREAST_CANCER_METASTASIS_DN
38	-7.34	NULL	1 / 12	BP positive regulation of peptidyl-threonine phosphorylation
39	-7.34	NULL	1 / 12	LymphomRAVE_BL_UP
40	-7.21	NULL	1 / 10	BP urea cycle

