

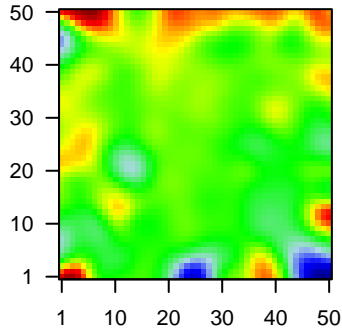
GW_106

Global Summary

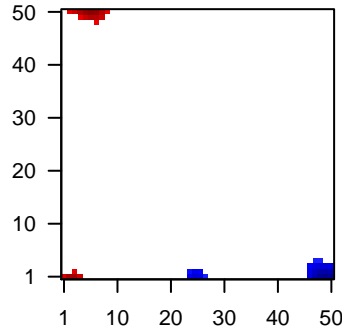
%DE = 0.13
 # genes with fdr < 0.2 = 1602 (921 + / 681 -)
 # genes with fdr < 0.1 = 1277 (768 + / 509 -)
 # genes with fdr < 0.05 = 952 (594 + / 358 -)
 # genes with fdr < 0.01 = 611 (396 + / 215 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.87

Profile



Regulated Spots



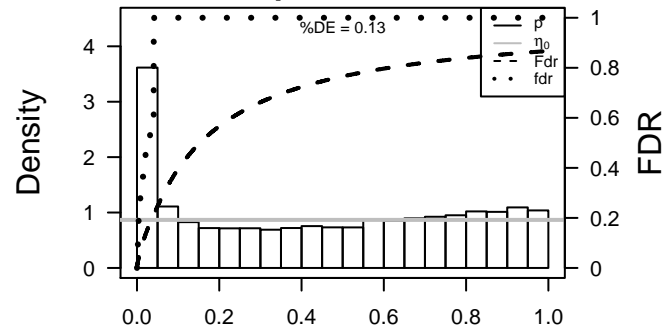
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	220	1.32	2e-16 5e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC]
2	344905	1.32	2e-16 5e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
3	525	1.45	2e-16 5e-14	12 x 8 ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1
4	100133941	1.33	2e-16 5e-14	3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
5	1056	1.69	2e-16 5e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	9073	1.73	2e-16 5e-14	8 x 50 claudin 8 [Source:HGNC Symbol;Acc:2050]
7	1308	-1.3	2e-16 5e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
8	1277	1.45	2e-16 5e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
9	1278	1.68	2e-16 5e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
10	1281	1.72	2e-16 5e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
11	1293	1.34	2e-16 5e-14	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	49860	2.18	2e-16 5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	2919	1.44	2e-16 5e-14	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula
14	9547	-1.79	2e-16 5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
15	1672	1.29	2e-16 5e-14	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
16	1776	1.56	2e-16 5e-14	48 x 12 deoxyribonuclease I-like 3 [Source:HGNC Symbol;Acc:2959]
17	2167	-1.35	2e-16 5e-14	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
18	10457	1.33	2e-16 5e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
19	283120	2.39	2e-16 5e-14	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
20	23593	1.28	2e-16 5e-14	6 x 50 heme binding protein 2 [Source:HGNC Symbol;Acc:15716]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	10.92	NULL	714	Chr Chr 6
2	9.44	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
3	9.35	NULL	37	BP collagen fibril organization
4	9.29	NULL	11	MF platelet-derived growth factor binding
5	8.89	NULL	16	MMML C6SCIEJ_MMML_1
6	7.59	NULL	13	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
7	7.54	NULL	190	CC extracellular matrix
8	7.44	NULL	135	H.Tiss WIRTH_Mucosa
9	7.38	NULL	12	miRNA target 29c
10	7.31	NULL	250	LymphomaENZ_Stromal signature 1
11	7.16	NULL	15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
12	6.79	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
13	6.66	NULL	16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
14	6.57	NULL	957	Chr Chr 11
15	5.97	NULL	10	BP protein heterotrimerization
16	5.75	NULL	119	LymphomaBOSOLOWSKI_green total
17	5.55	NULL	13	GSEA C2REACTOME_FORMATION_OF_PLATELET_PLUG
18	5.55	NULL	13	GSEA C2REACTOME_PLATELET_ACTIVATION
19	5.5	NULL	14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
20	5.47	NULL	15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
<i>Underexpressed</i>				
1	-13.03	NULL	918	Chr Chr 17
2	-11.25	NULL	633	Chr Chr 9
3	-7.44	NULL	699	Chr Chr 5
4	-7	NULL	10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
5	-6.2	NULL	534	Chr Chr 8
6	-6.14	NULL	127	H.Tiss WIRTH_Muscle
7	-6.02	NULL	15	GSEA C2BILD_HRAS_ONCOGENIC_SIGNATURE
8	-5.71	NULL	417	H.Tiss WIRTH_Immune system
9	-5.61	NULL	36	BP muscle filament sliding
10	-5.61	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
11	-5.59	NULL	16	H.Tiss WIRTH_Hippocampus
12	-5.56	NULL	15	CC MHC class II protein complex
13	-4.89	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	-4.71	NULL	8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
15	-4.63	NULL	16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
16	-4.59	NULL	42	BP keratinization
17	-4.59	NULL	23	CC integral to lumenal side of endoplasmic reticulum membrane
18	-4.42	NULL	32	CC ER to Golgi transport vesicle membrane
19	-4.32	NULL	3	MMML C6SCIEJ_MMML_7
20	-4.18	NULL	9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN

p-values



GW_106

Local Summary

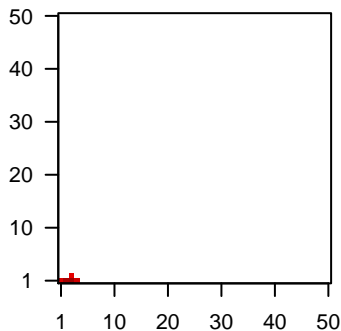
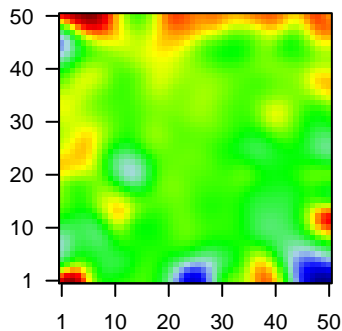
%DE = 0.78
 # metagenes = 5
 # genes = 125
 # genes in genesets = 125
 # genes with $fdr < 0.1$ = 73 (62 + / 11 -)
 # genes with $fdr < 0.05$ = 69 (58 + / 11 -)
 # genes with $fdr < 0.01$ = 52 (44 + / 8 -)

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

<FC> = 0.34
 <shrinkage-t> = 11.84
 <p-value> = 0
 <fdr> = 0.45

Profile

Spot



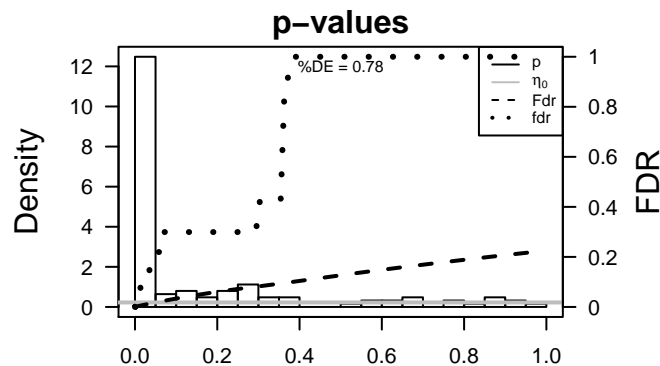
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1277	1.45	2e-16	8e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	1278	1.68	2e-16	8e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	1.72	2e-16	8e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	1293	1.34	2e-16	8e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
5	2919	1.44	2e-16	8e-16	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula
6	3576	1.33	2e-16	8e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
7	4320	1.66	2e-16	8e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
8	10631	2.15	2e-16	8e-16	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
9	26585	1.23	4e-15	2e-13	2 x 1 gremlin 1, DAN family BMP antagonist [Source:HGNC Symbc
10	4318	-1.21	1e-14	8e-12	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9:
11	1290	1.13	5e-13	8e-12	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
12	23213	1.13	6e-13	6e-11	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
13	1289	1.09	3e-12	6e-11	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
14	59	1.08	5e-12	2e-09	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;:
15	1462	1.01	1e-10	2e-09	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
16	1291	1	2e-10	2e-09	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
17	6423	0.99	2e-10	2e-09	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Ac
18	6678	0.99	2e-10	2e-09	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:!
19	633	0.91	3e-10	4e-08	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
20	7857	0.94	2e-09	4e-08	4 x 1 secretogranin II [Source:HGNC Symbol;Acc:10575]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	48.28	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
2	47.98	NULL	7 / 11	MF platelet-derived growth factor binding
3	42.3	NULL	14 / 16	MMML C2SCIEJ_MMML_1
4	38.31	NULL	11 / 37	BP collagen fibril organization
5	38.12	NULL	8 / 12	miRNA target-29c
6	31.91	NULL	21 / 64	BP collagen catabolic process
7	31.9	NULL	46 / 190	CC extracellular matrix
8	31.28	NULL	24 / 69	BP extracellular matrix disassembly
9	30.32	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
10	29.22	NULL	4 / 10	BP protein heterotrimerization
11	29	NULL	18 / 57	MF extracellular matrix structural constituent
12	27.88	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
13	27.22	NULL	42 / 242	BP extracellular matrix organization
14	26.39	NULL	48 / 250	LymphomaENZ_Stromal signature 1
15	26.12	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
16	24.71	NULL	4 / 12	GSEA C2ERRRECCHIA_RESPONSE_TO_TGFB1_C2
17	24.52	NULL	5 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NC
18	24.35	NULL	13 / 68	CC collagen
19	24.18	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
20	23.38	NULL	7 / 40	BP cellular response to amino acid stimulus
21	22.96	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
22	22.63	NULL	5 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
23	22.57	NULL	7 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
24	21.8	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
25	21.74	NULL	6 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
26	21.35	NULL	4 / 15	GSEA C2REACTOME_NCAM1_INTERACTIONS
27	21.3	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
28	21.03	NULL	10 / 19	MF extracellular matrix binding
29	20.93	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
30	20.8	NULL	4 / 15	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
31	20.59	NULL	4 / 16	GSEA C2REACTOME_AXON_GUIDANCE
32	20.59	NULL	4 / 16	GSEA C2REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH
33	19.5	NULL	5 / 15	GSEA C2JINDGREN_BLADDER_CANCER_HIGH_RECURRENCE
34	18.58	NULL	2 / 11	GSEA C2REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGE
35	18.19	NULL	17 / 153	CC endoplasmic reticulum lumen
36	17.69	NULL	1 / 3	GSEA C2REN_MIF_TARGETS_DN
37	17.44	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
38	16.8	NULL	4 / 14	GSEA C2WILCOX_RESPONSE_TO_ROGESTERONE_DN
39	16.8	NULL	4 / 15	GSEA C2CHANG_POU5F1_TARGETS_UP
40	16.73	NULL	20 / 119	LymphomaBOSOLOWSKI_green total



GW_106

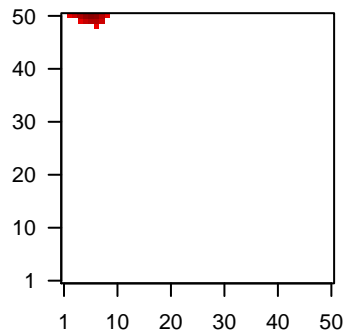
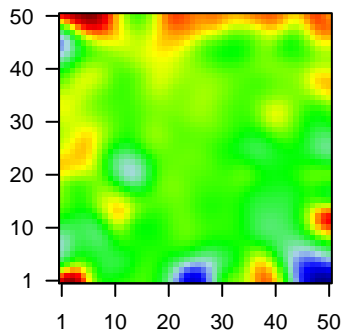
Local Summary

%DE = 0.57
 # metagenes = 14
 # genes = 222
 # genes in genesets = 219
 # genes with $fdr < 0.1$ = 81 (67 + / 14 -)
 # genes with $fdr < 0.05$ = 73 (60 + / 13 -)
 # genes with $fdr < 0.01$ = 50 (41 + / 9 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.36
 $\langle FC \rangle = 0.2$
 $\langle \text{shrinkage-t} \rangle = 6.84$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.62$

Profile

Spot



Local Genelist

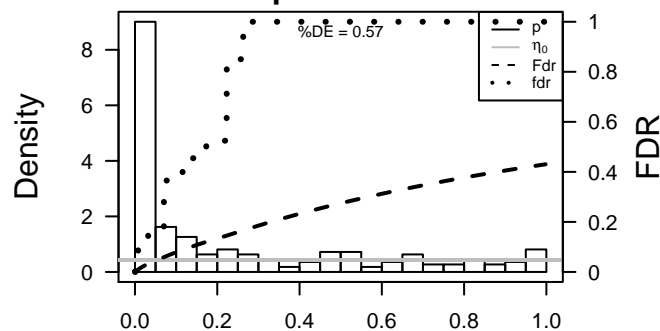
Rank	ID	log(FC)	fdr	p-value	Description
1	100133941	1.33	2e-16	5e-15	3 x 50 CD24 molecule [Source:HGNC Symbol;Acc:1645]
2	9073	1.73	2e-16	5e-15	8 x 50 claudin 8 [Source:HGNC Symbol;Acc:2050]
3	23593	1.28	2e-16	5e-15	6 x 50 heme binding protein 2 [Source:HGNC Symbol;Acc:15716]
4	220963	-1.38	2e-16	5e-15	4 x 50 solute carrier family 16, member 9 [Source:HGNC Symbol;Acc:25422]
5	51806	1.14	3e-13	2e-11	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
6	5627	1.14	4e-13	5e-11	7 x 50 protein S (alpha) [Source:HGNC Symbol;Acc:9456]
7	84239	1.11	1e-12	5e-11	4 x 50 ATPase type 13A4 [Source:HGNC Symbol;Acc:25422]
8	80195	1.11	1e-12	2e-10	7 x 50 transmembrane protein 254 [Source:HGNC Symbol;Acc:2580]
9	6947	1.09	4e-12	4e-10	2 x 50 transcobalamin 1 (vitamin B12 binding protein, R binder family)
10	200958	1.07	8e-12	5e-09	6 x 50 mucin 20, cell surface associated [Source:HGNC Symbol;Acc:2580]
11	154091	1.01	1e-10	5e-09	9 x 50 solute carrier family 2 (facilitated glucose transporter), member 1
12	4582	1	1e-10	5e-09	7 x 50 mucin 1, cell surface associated [Source:HGNC Symbol;Acc:2580]
13	157506	1	2e-10	1e-07	8 x 50 retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:2580]
14	284340	0.93	3e-09	1e-07	6 x 50 chemokine (C-X-C motif) ligand 17 [Source:HGNC Symbol;Acc:2580]
15	157638	0.93	3e-09	2e-06	7 x 49 family with sequence similarity 84, member B [Source:HGNC Symbol;Acc:2580]
16	2012	0.8	2e-08	2e-06	3 x 50 epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33]
17	22837	0.85	5e-08	3e-06	6 x 50 cordon-bleu WH2 repeat protein-like 1 [Source:HGNC Symbol;Acc:2580]
18	1577	0.83	1e-07	3e-06	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Source:HGNC Symbol;Acc:2580]
19	114569	0.82	1e-07	3e-06	4 x 50 mal, T-cell differentiation protein 2 (gene/pseudogene) [Source:HGNC Symbol;Acc:2580]
20	2525	0.82	1e-07	1e-05	3 x 50 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, isoform 1) [Source:HGNC Symbol;Acc:2580]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	12.39	NULL	4 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
2	10.2	NULL	3 / 15	GSEA C2REACTOME_TIGHT_JUNCTION_INTERACTIONS
3	9.71	NULL	3 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
4	9.37	NULL	2 / 15	GSEA C2FAELT_B CLL_WITH_VH3_21_DN
5	9.05	NULL	2 / 12	GSEA C2RUTELLA_RESPONSE_TO_HGF_DN
6	9.01	NULL	4 / 13	H.Tiss WIRTH_Tonsil
7	8.96	NULL	2 / 19	BP calcium-independent cell-cell adhesion
8	8.54	NULL	2 / 9	GSEA C2REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE
9	8.54	NULL	2 / 9	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
10	8.23	NULL	1 / 6	GSEA C2REACTOME_GLUCOSE_AND_OTHER_SUGAR_SLC_TRANSPORT
11	8.21	NULL	2 / 15	GSEA C2STOSSI_RESPONSE_TO ESTRADIOL
12	8.19	NULL	1 / 6	GSEA C2GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION
13	8.1	NULL	5 / 63	CC Golgi lumen
14	7.89	NULL	1 / 8	GSEA C2REACTOME_GAMMA_CARBOXYLATION_TRANSPORT_AND_A
15	7.85	NULL	2 / 16	CC microvillus membrane
16	7.84	NULL	3 / 16	miRNA target-mir-1498
17	7.72	NULL	24 / 135	H.Tiss WIRTH_Mucosa
18	7.63	NULL	2 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	7.63	NULL	2 / 11	GSEA C2REACTOME_BIOLOGICAL_OXIDATIONS
20	7.63	NULL	2 / 11	GSEA C2REACTOME_XENOBIOTICS
21	7.47	NULL	5 / 38	BP epithelial cell differentiation
22	7.39	NULL	1 / 9	GSEA C2REACTOME_COMMON_PATHWAY
23	7.29	NULL	2 / 15	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP
24	7.16	NULL	2 / 15	GSEA C2BEIER_GLIOMA_STEM_CELL_UP
25	7.05	NULL	2 / 7	GSEA C2REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
26	6.99	NULL	1 / 8	GSEA C2REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TRANSPORT
27	6.96	NULL	1 / 10	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
28	6.95	NULL	1 / 8	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24
29	6.59	NULL	1 / 11	GSEA C2BIOCARTA_EXTRINSIC_PATHWAY
30	6.51	NULL	1 / 4	GSEA C2GRAHAM_CML QUIESCENT_VS_NORMAL QUIESCENT_DN
31	6.38	NULL	2 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
32	6.31	NULL	4 / 45	BP O-glycan processing
33	6.27	NULL	3 / 16	GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP
34	6.21	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
35	6.21	NULL	2 / 12	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION
36	6.14	NULL	4 / 70	CC endomembrane system
37	6.11	NULL	2 / 9	GSEA C2REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES
38	6.1	NULL	1 / 10	BP embryonic camera-type eye development
39	6.1	NULL	1 / 10	BP retinal metabolic process
40	6.1	NULL	1 / 6	Glio Martinez_Glio_hypometh

p-values



GW_106

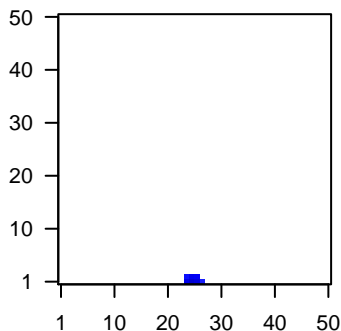
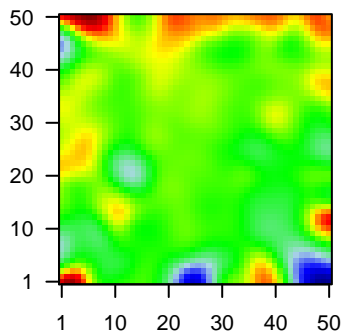
Local Summary

%DE = 0.74
 # metagenes = 7
 # genes = 89
 # genes in genesets = 89
 # genes with $fdr < 0.1$ = 37 (5 + / 32 -)
 # genes with $fdr < 0.05$ = 33 (4 + / 29 -)
 # genes with $fdr < 0.01$ = 25 (4 + / 21 -)

<r> metagenes = 0.99
 <r> genes = 0.65
 <FC> = -0.26
 <shrinkage-t> = -9.08
 <p-value> = 0.01
 <fdr> = 0.61

Profile

Spot



Local Genelist

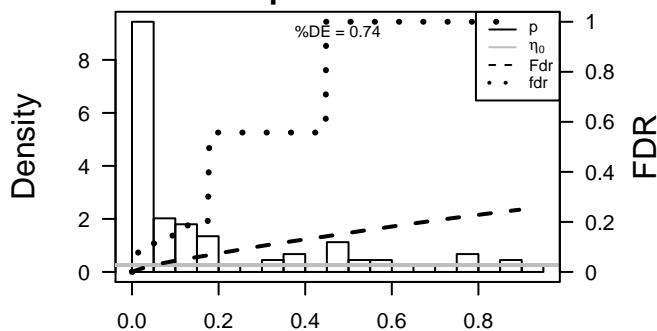
Rank	ID	log(FC)	fdr	p-value	Description
1	283120	2.39	2e-16	5e-15	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
2	58	-1.21	1e-14	3e-10	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	1410	1.06	1e-11	2e-09	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
4	6588	-1.01	9e-11	2e-08	25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]
5	7060	-0.96	9e-10	4e-07	25 x 1 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
6	274	-0.88	2e-08	3e-05	26 x 1 bridging integrator 1 [Source:HGNC Symbol;Acc:1052]
7	1158	-0.75	1e-06	4e-05	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
8	4151	-0.72	4e-06	4e-05	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
9	70	-0.71	5e-06	1e-04	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
10	2273	-0.69	1e-05	4e-04	25 x 1 four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
11	7138	-0.66	3e-05	5e-04	25 x 1 troponin T type 1 (skeletal, slow) [Source:HGNC Symbol;Acc:
12	388115	0.62	7e-05	5e-04	26 x 2 chromosome 15 open reading frame 52 [Source:HGNC Synt
13	4620	-0.62	7e-05	6e-04	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
14	1917	-0.6	1e-04	6e-04	25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
15	22998	0.6	1e-04	9e-04	24 x 1 LIM and calponin homology domains 1 [Source:HGNC Symb
16	2318	-0.59	2e-04	3e-03	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
17	10324	-0.56	4e-04	3e-03	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
18	202333	-0.55	5e-04	3e-03	25 x 1 cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
19	7134	-0.52	9e-04	3e-03	25 x 1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
20	8557	-0.52	9e-04	3e-03	25 x 1 titin-cap [Source:HGNC Symbol;Acc:11610]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-45.54	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
2	-44.72	NULL	22 / 36	BP muscle filament sliding
3	-41	NULL	47 / 127	H.Tiss WIRTH_Muscle
4	-38.47	NULL	9 / 16	H.Tiss WIRTH_Hippocampus
5	-29.35	NULL	21 / 44	MF structural constituent of muscle
6	-27.92	NULL	9 / 12	CC myosin filament
7	-22.91	NULL	11 / 37	CC sarcomere
8	-20.78	NULL	6 / 12	BP skeletal muscle contraction
9	-20.3	NULL	7 / 13	CC muscle myosin complex
10	-17.29	NULL	7 / 16	CC M band
11	-16.56	NULL	13 / 34	CC myofibril
12	-16.52	NULL	6 / 18	BP regulation of muscle contraction
13	-16.05	NULL	21 / 84	BP muscle contraction
14	-15.39	NULL	9 / 37	BP cardiac muscle contraction
15	-15.36	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
16	-15.33	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
17	-15.15	NULL	3 / 15	Cancer BEN-PORATH_UP
18	-14.53	NULL	6 / 12	MF titin binding
19	-14.37	NULL	6 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
20	-12.56	NULL	2 / 20	MF myosin binding
21	-12.46	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
22	-12.46	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
23	-11.85	NULL	2 / 10	BP heart contraction
24	-11.71	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
25	-11.64	NULL	2 / 14	GSEA C2BIOCARTA_UCALPAIN_PATHWAY
26	-11.42	NULL	3 / 16	MF microfilament motor activity
27	-11.26	NULL	18 / 88	CC Z disc
28	-11.2	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
29	-11.2	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
30	-11.19	NULL	2 / 15	GSEA C2BIOCARTA_INTEGRIN_PATHWAY
31	-11.05	NULL	7 / 42	CC myosin complex
32	-10.62	NULL	4 / 14	MF tropomyosin binding
33	-10.52	NULL	1 / 12	GSEA C2BIOCARTA_NO1_PATHWAY
34	-10.52	NULL	1 / 12	GSEA C2BIOCARTA_RAB_PATHWAY
35	-10.45	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
36	-10.22	NULL	4 / 36	CC sarcoplasmic reticulum
37	-10.17	NULL	2 / 15	BP skeletal muscle fiber development
38	-10.12	NULL	1 / 5	GSEA C2LE_SKI_TARGETS_DN
39	-10.08	NULL	3 / 37	CC actin filament
40	-10.05	NULL	1 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP

p-values



GW_106

Local Summary

%DE = 0.61
 # metagenes = 17
 # genes = 274
 # genes in genesets = 272

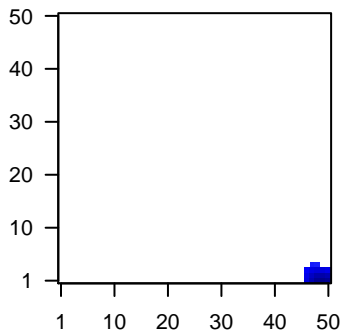
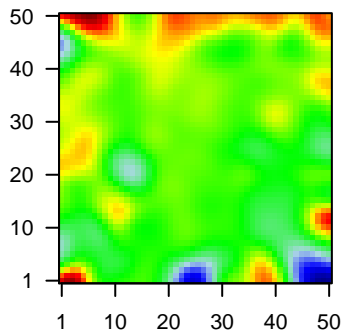
genes with $fdr < 0.1$ = 82 (14 + / 68 -)
 # genes with $fdr < 0.05$ = 73 (13 + / 60 -)
 # genes with $fdr < 0.01$ = 28 (10 + / 18 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.61

$\langle FC \rangle = -0.17$
 $\langle \text{shrinkage-t} \rangle = -6.07$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.71$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5996	1.39	2e-16	2e-14	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:2663]
2	692084	1	1e-10	1e-08	48 x 4 small nucleolar RNA, C/D box 13 [Source:HGNC Symbol;Acc:2663]
3	4283	0.99	3e-10	1e-07	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:2663]
4	341	0.95	1e-09	3e-07	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
5	441168	0.91	5e-09	3e-07	46 x 1 family with sequence similarity 26, member F [Source:HGNC Symbol;Acc:2663]
6	89846	-0.91	7e-09	2e-06	48 x 1 FYVE, RhoGEF and PH domain containing 3 [Source:HGNC Symbol;Acc:2663]
7	8635	0.86	4e-08	2e-06	46 x 1 ribonuclease T2 [Source:HGNC Symbol;Acc:21686]
8	115701	0.85	5e-08	3e-04	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
9	23231	-0.72	5e-06	3e-04	48 x 2 sel-1 suppressor of lin-12-like 3 (C. elegans) [Source:HGNC Symbol;Acc:2663]
10	54855	-0.71	6e-06	3e-04	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:2663]
11	10563	-0.7	9e-06	3e-04	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:2663]
12	91607	-0.69	1e-05	3e-04	48 x 4 schlafen family member 11 [Source:HGNC Symbol;Acc:2663]
13	5920	-0.68	1e-05	7e-04	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC Symbol;Acc:2663]
14	8605	-0.66	2e-05	7e-04	50 x 3 phospholipase A2, group IVC (cytosolic, calcium-independent) [Source:HGNC Symbol;Acc:2663]
15	4050	-0.65	3e-05	7e-04	50 x 1 lymphotoxin beta (TNF superfamily, member 3) [Source:HGNC Symbol;Acc:2663]
16	9308	-0.65	4e-05	7e-04	50 x 3 CD83 molecule [Source:HGNC Symbol;Acc:1703]
17	3820	-0.64	4e-05	1e-03	50 x 1 killer cell lectin-like receptor subfamily B, member 1 [Source:HGNC Symbol;Acc:2663]
18	3001	-0.63	6e-05	1e-03	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated protein 10) [Source:HGNC Symbol;Acc:2663]
19	3108	-0.62	7e-05	5e-03	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:2663]
20	6366	0.59	2e-04	5e-03	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc:2663]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-24.59	NULL	97 / 417	H.Tiss WIRTH_Immune system
2	-23.13	NULL	12 / 15	CC MHC class II protein complex
3	-17.58	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
4	-16.03	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
5	-14.38	NULL	2 / 4	MMML C6BACIEJ_MMML 2
6	-13.8	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
7	-13.13	NULL	8 / 13	Cancer GENTLES_modul18
8	-12.66	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
9	-12.52	NULL	100 / 553	Cancer Lembcke_Colonc Inflammation
10	-12.41	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
11	-12.3	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
12	-12.26	NULL	4 / 13	BP lymph node development
13	-12.18	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
14	-11.73	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
15	-11.73	NULL	17 / 84	BP T cell receptor signaling pathway
16	-11.71	NULL	7 / 23	CC integral to lumenal side of endoplasmic reticulum membrane
17	-11.56	NULL	14 / 47	BP antigen processing and presentation
18	-11.53	NULL	2 / 5	GSEA C2WEST_ADRENOCORITICAL_CARINOMA_VS_ADENOMA_DN
19	-11.31	NULL	2 / 3	MMML C6BACIEJ_MMML 7
20	-11.28	NULL	7 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
21	-11.09	NULL	17 / 74	BP regulation of immune response
22	-11.07	NULL	5 / 8	GSEA C2BIOCARTA_TCR_PATHWAY
23	-11.04	NULL	8 / 16	GSEA C2S_THYMUS
24	-10.85	NULL	53 / 312	BP immune response
25	-10.54	NULL	7 / 28	LymphonodeAVE_Immune response 1
26	-10.53	NULL	7 / 28	CC transport vesicle membrane
27	-10.49	NULL	1 / 2	GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
28	-10.49	NULL	1 / 2	GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE
29	-10.49	NULL	1 / 2	GSEA C2KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
30	-10.39	NULL	4 / 16	BP cytolysis
31	-10.23	NULL	12 / 60	BP interferon-gamma-mediated signaling pathway
32	-10.18	NULL	4 / 12	GSEA C2BIOCARTA_CTLA4_PATHWAY
33	-9.79	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
34	-9.32	NULL	6 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
35	-9.32	NULL	7 / 35	CC trans-Golgi network membrane
36	-9.29	NULL	18 / 60	BP T cell costimulation
37	-9.27	NULL	5 / 15	GSEA C2BIOCARTA_TCR_PATHWAY
38	-9.23	NULL	45 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
39	-9.23	NULL	45 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
40	-9.23	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down

