

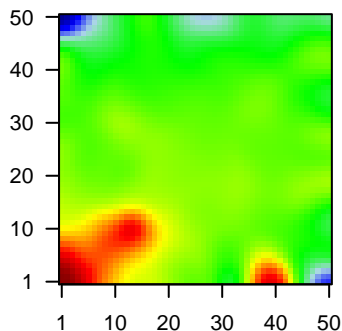
GW_103

Global Summary

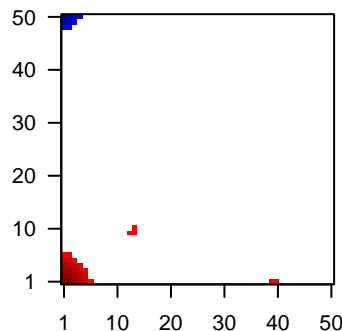
%DE = 0.14
 # genes with fdr < 0.2 = 1801 (971 + / 830 -)
 # genes with fdr < 0.1 = 1376 (762 + / 614 -)
 # genes with fdr < 0.05 = 1057 (597 + / 460 -)
 # genes with fdr < 0.01 = 720 (428 + / 292 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.12
 <fdr> = 0.86

Profile



Regulated Spots



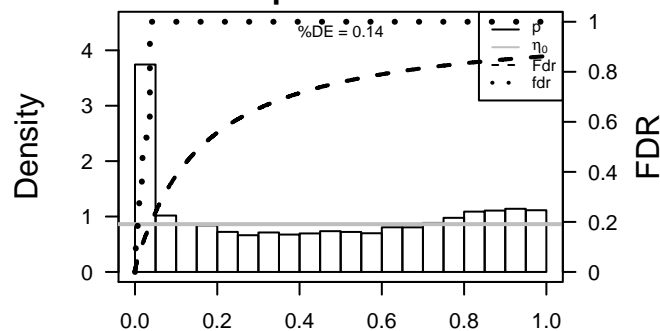
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.59	2e-16	5e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.52	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-2.11	2e-16	5e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	216	-2.07	2e-16	5e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	218	-3.4	2e-16	5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	401138	3.29	2e-16	5e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
7	375791	-2.23	2e-16	5e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
8	57172	-2.15	2e-16	5e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
9	4680	-2.18	2e-16	5e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	1152	2.07	2e-16	5e-14	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
11	22802	-2.59	2e-16	5e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	1277	2.19	2e-16	5e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
13	1290	2.31	2e-16	5e-14	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
14	1298	2.13	2e-16	5e-14	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
15	51755	-2.17	2e-16	5e-14	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
16	49860	-3.13	2e-16	5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1475	-2.17	2e-16	5e-14	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
18	9547	2.41	2e-16	5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A
19	10202	2.38	2e-16	5e-14	1 x 15 dehydrogenase/reductase (SDR family) member 2 [Source:H
20	1809	2.08	2e-16	5e-14	6 x 1 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:3015]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.87	NULL	250	LymphomaTENZ_Stromal signature 1
2	13.59	NULL	242	BP extracellular matrix organization
3	12.82	NULL	190	CC extracellular matrix
4	11.05	NULL	183	CC proteinaceous extracellular matrix
5	10.72	NULL	69	BP extracellular matrix disassembly
6	10.28	NULL	83	CC basement membrane
7	9.81	NULL	64	BP collagen catabolic process
8	9.75	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
9	9.51	NULL	153	CC endoplasmic reticulum lumen
10	9.39	NULL	386	Chr Chr 22
11	9.15	NULL	16	MMML C6SCIEJ_MMML 1
12	8.85	NULL	15	GSEA C2ONDER_CDH1_TARGETS_2_UP
13	8.36	NULL	11	MF platelet-derived growth factor binding
14	8.15	NULL	57	MF extracellular matrix structural constituent
15	7.32	NULL	68	CC collagen
16	7.22	NULL	403	BP cell adhesion
17	7.17	NULL	37	BP collagen fibril organization
18	7.16	NULL	400	H.Tiss WIRTH_Nervous System
19	6.96	NULL	699	Chr Chr 5
20	6.92	NULL	37	BP embryonic skeletal system development
<i>Underexpressed</i>				
1	-22.54	NULL	135	H.Tiss WIRTH_Mucosa
2	-20.86	NULL	572	Disease GUDJ_psooriasis up
3	-14.04	NULL	417	H.Tiss WIRTH_Immune system
4	-11.45	NULL	21	CC cornified envelope
5	-11.36	NULL	42	BP keratinization
6	-10.8	NULL	53	BP keratinocyte differentiation
7	-10.41	NULL	2378	CC cytosol
8	-9.85	NULL	19	BP peptide cross-linking
9	-9.34	NULL	8	GSEA C2LIU_CD_X2_TARGETS_DN
10	-9.04	NULL	312	BP immune response
11	-8.49	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
12	-6.94	NULL	316	Cancer SPANG_BCL6-index2
13	-6.85	NULL	204	BP cytokine-mediated signaling pathway
14	-6.67	NULL	287	BP viral process
15	-6.66	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
16	-6.58	NULL	76	BP epidermis development
17	-6.5	NULL	15	GSEA C2AIGNER_ZEB1_TARGETS
18	-6.42	NULL	530	BP innate immune response
19	-6.42	NULL	15	CC MHC class II protein complex
20	-6.4	NULL	232	Chr Chr 18

p-values



GW_103

Local Summary

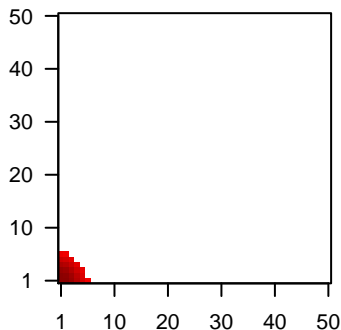
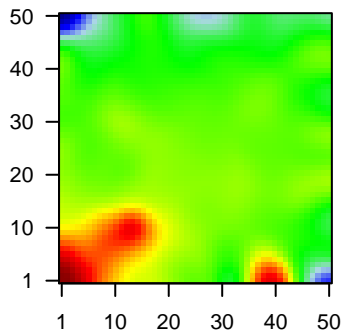
%DE = 0.75
 # metagenes = 25
 # genes = 387
 # genes in genesets = 384
 # genes with $fdr < 0.1$ = 253 (237 + / 16 -)
 # genes with $fdr < 0.05$ = 242 (227 + / 15 -)
 # genes with $fdr < 0.01$ = 208 (198 + / 10 -)

<r> metagenes = 0.93
 <r> genes = 0.33

<FC> = 0.75
 <shrinkage-t> = 26.38
 <p-value> = 0
 <fdr> = 0.36

Profile

Spot



Local Genelist

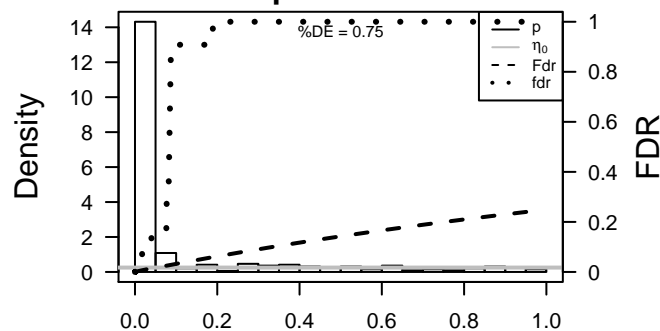
Rank	ID	log(FC)	fdr	p-value	Description
1	401138	3.29	2e-16	1e-15	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
2	1277	2.19	2e-16	1e-15	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1290	2.31	2e-16	1e-15	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
4	1809	2.08	2e-16	1e-15	6 x 1 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:3015]
5	3043	-2.52	2e-16	1e-15	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
6	8988	2.66	2e-16	1e-15	1 x 4 heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248]
7	3486	2.44	2e-16	1e-15	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Sy
8	10962	2.19	2e-16	1e-15	5 x 1 myeloid/lymphoid or mixed-lineage leukemia (trithorax homol
9	4319	2.59	2e-16	1e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
10	4316	2.46	2e-16	1e-15	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC
11	25878	2.66	2e-16	1e-15	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:
12	4885	2.39	2e-16	1e-15	5 x 1 neuronal pentraxin II [Source:HGNC Symbol;Acc:7953]
13	6695	2.17	2e-16	1e-15	1 x 2 sparco/osteonectin, cwcv and kazal-like domains proteoglycar
14	7045	2	2e-16	1e-15	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG
15	7078	2.1	2e-16	1e-15	2 x 1 TIMP metalloproteinase inhibitor 3 [Source:HGNC Symbol;Acc:
16	1289	2.01	1e-15	1e-13	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
17	83700	1.99	2e-15	2e-13	5 x 1 junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:1
18	11167	1.97	4e-15	5e-13	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
19	633	1.78	2e-14	5e-13	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
20	1464	1.92	2e-14	5e-13	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	31.91	NULL	87 / 250	Lymphoma_TENZ_Stromal signature 1
2	31.22	NULL	70 / 190	CC extracellular matrix
3	27.61	NULL	15 / 16	MMML C2GSCIEJ_MMML 1
4	27.44	NULL	76 / 242	BP extracellular matrix organization
5	26.15	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	25.87	NULL	34 / 69	BP extracellular matrix disassembly
7	24.21	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
8	23.83	NULL	29 / 64	BP collagen catabolic process
9	21.94	NULL	44 / 183	CC proteinaceous extracellular matrix
10	21.86	NULL	8 / 11	MF platelet-derived growth factor binding
11	19.26	NULL	13 / 35	Glio Colman_survival_associated
12	19.15	NULL	26 / 83	CC basement membrane
13	17.6	NULL	22 / 57	MF extracellular matrix structural constituent
14	17.37	NULL	8 / 12	miRNA target-29c
15	17	NULL	50 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	17	NULL	50 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	17	NULL	50 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	17	NULL	50 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
19	16.73	NULL	16 / 37	BP collagen fibril organization
20	16.72	NULL	62 / 403	BP cell adhesion
21	16.55	NULL	96 / 683	CC extracellular space
22	15.99	NULL	8 / 11	Glio Phillips MES up vs Prolif & PN
23	15.89	NULL	12 / 19	MF extracellular matrix binding
24	15.84	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
25	15.12	NULL	80 / 553	Cancer Lembcke_Colonc Inflammation
26	14.91	NULL	18 / 68	CC collagen
27	14.55	NULL	131 / 1182	CC extracellular region
28	14.4	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
29	14.27	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
30	14.05	NULL	28 / 153	CC endoplasmic reticulum lumen
31	13.96	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
32	13.88	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
33	13.71	NULL	4 / 10	BP negative regulation of cell-substrate adhesion
34	13.45	NULL	21 / 85	MF integrin binding
35	13.08	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
36	12.91	NULL	18 / 68	Glio cultured astroglia vs. in vivo astrocytes
37	12.72	NULL	5 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
38	12.71	NULL	7 / 16	GSEA C2GU_PDEF_TARGETS_UP
39	12.69	NULL	12 / 40	BP cellular response to amino acid stimulus
40	12.67	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN

p-values



GW_103

Local Summary

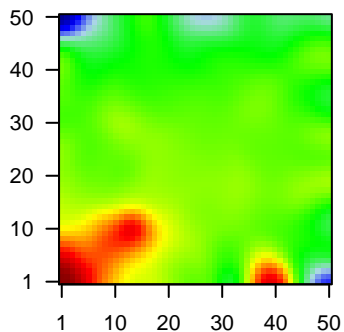
%DE = 0.95
 # metagenes = 2
 # genes = 106
 # genes in genesets = 86

 # genes with $fdr < 0.1 = 92$ (90 + / 2 -)
 # genes with $fdr < 0.05 = 89$ (87 + / 2 -)
 # genes with $fdr < 0.01 = 86$ (84 + / 2 -)

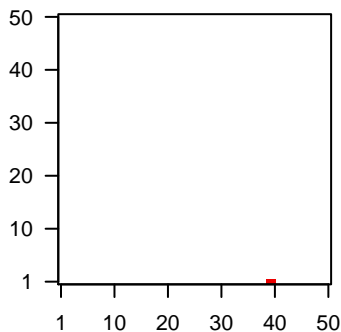
 $\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.66

 $\langle FC \rangle = 0.88$
 $\langle \text{shrinkage-t} \rangle = 31.05$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.21$

Profile



Spot



Local Genelist

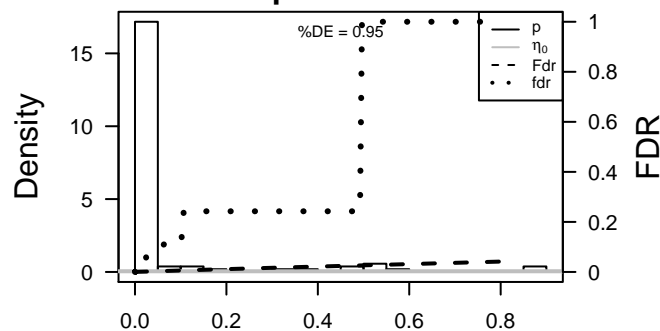
Rank	ID	log(FC)	fdr	p-value	Description
1	84061	1.78	1e-12	5e-12	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
2	126205	1.77	2e-12	2e-09	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbo
3	618	1.56	5e-10	3e-09	39 x 1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
4	25862	1.53	1e-09	8e-09	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2c
5	85452	1.49	3e-09	8e-09	39 x 1 chromosome 1 open reading frame 222 [Source:HGNC Synt
6	80224	1.47	4e-09	1e-08	40 x 1 nucleotide binding protein-like [Source:HGNC Symbol;Acc:2f
7	728903	1.45	7e-09	2e-08	39 x 1
8	399761	1.43	1e-08	2e-08	39 x 1 BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653]
9	90586	1.41	2e-08	2e-08	39 x 1 amine oxidase, copper containing 4, pseudogene [Source:HC
10	100128288	1.4	2e-08	3e-08	39 x 1
11	113277	1.39	3e-08	5e-08	40 x 1 transmembrane protein 106A [Source:HGNC Symbol;Acc:28;
12	399900	1.26	4e-08	5e-08	39 x 1
13	56203	1.37	5e-08	5e-08	39 x 1 leiomodlin 3 (fetal) [Source:HGNC Symbol;Acc:6649]
14	441087	1.34	8e-08	5e-08	39 x 1
15	84278	1.34	8e-08	5e-08	39 x 1
16	26279	1.34	1e-07	5e-08	40 x 1 phospholipase A2, group IID [Source:HGNC Symbol;Acc:903
17	319085	1.32	1e-07	5e-08	39 x 1 ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
18	91368	1.22	1e-07	5e-08	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC S
19	158399	1.33	1e-07	9e-08	39 x 1 zinc finger protein 483 [Source:HGNC Symbol;Acc:23384]
20	2204	1.32	2e-07	9e-08	39 x 1 Fc fragment of IgA, receptor for [Source:HGNC Symbol;Acc:3

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	15.71	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	11.7	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
3	10.4	NULL	3 / 14	MMML C6SCIEJ_MMML_8
4	9.84	NULL	2 / 14	BP cellular response to estradiol stimulus
5	8.86	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
6	8.74	NULL	2 / 14	BP mitochondrion morphogenesis
7	8.66	NULL	1 / 10	CC oligosaccharyltransferase complex
8	7.86	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
9	7.84	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
10	7.84	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	7.37	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
12	7.08	NULL	2 / 24	BP negative regulation of T cell proliferation
13	7.04	NULL	1 / 14	BP magnesium ion transport
14	6.95	NULL	1 / 4	GSEA C2KORKOLA_CHORIOCARCINOMA
15	6.73	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
16	6.55	NULL	1 / 9	GSEA C2SA_MMP_CYTOKINE_CONNECTION
17	6.5	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
18	6.49	NULL	1 / 16	BP cognition
19	6.26	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
20	6.2	NULL	1 / 14	Cancer LIU_COMMON_CANCER_GENES
21	6.18	NULL	1 / 10	MF endodeoxyribonuclease activity
22	6.18	NULL	1 / 10	GSEA C2REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_VI
23	6.12	NULL	1 / 10	BP negative thymic T cell selection
24	5.87	NULL	1 / 11	GSEA C2KEGG_FOLATE_BIOSYNTHESIS
25	5.82	NULL	1 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
26	5.77	NULL	2 / 15	GSEA C2THUM_SYSTOLIC_HEART_FAILURE_DN
27	5.74	NULL	1 / 12	BP phosphatidylinositol acyl-chain remodeling
28	5.64	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process
29	5.64	NULL	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
30	5.51	NULL	1 / 12	GSEA C2GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
31	5.51	NULL	1 / 12	GSEA C2REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE
32	5.46	NULL	1 / 13	BP phosphatidylserine acyl-chain remodeling
33	5.46	NULL	1 / 12	BP negative regulation of T cell activation
34	5.4	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
35	5.33	NULL	1 / 6	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_DN
36	5.33	NULL	1 / 14	MF tropomyosin binding
37	5.31	NULL	1 / 11	BP negative regulation of interleukin-12 production
38	5.31	NULL	1 / 11	GSEA C2SU_PANCREAS
39	5.3	NULL	1 / 16	BP mitochondrial respiratory chain complex I assembly
40	5.26	NULL	1 / 13	BP cellular response to glucocorticoid stimulus

p-values



GW_103

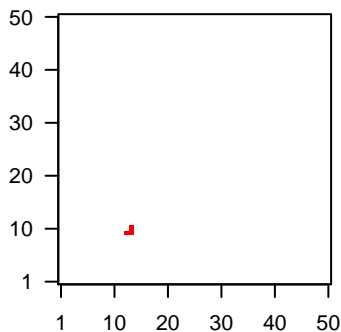
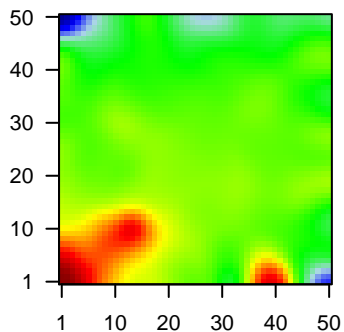
Local Summary

%DE = 0.96
 # metagenes = 3
 # genes = 44
 # genes in genesets = 29
 # genes with $fdr < 0.1$ = 36 (34 + / 2 -)
 # genes with $fdr < 0.05$ = 36 (34 + / 2 -)
 # genes with $fdr < 0.01$ = 30 (30 + / 0 -)

<r> metagenes = 0.99
 <r> genes = 0.46
 <FC> = 1.19
 <shrinkage-t> = 41.57
 <p-value> = 0
 <fdr> = 0.26

Profile

Spot



Local Genelist

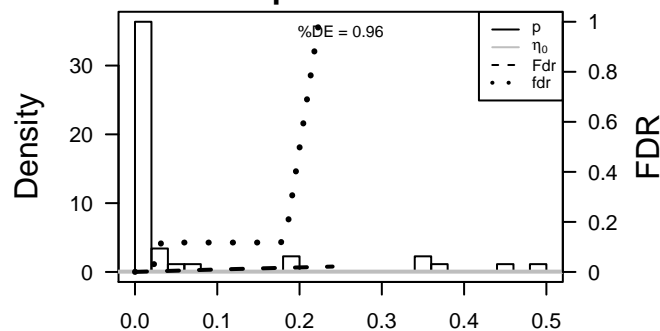
Rank	ID	log(FC)	fdr	p-value	Description
1	729428	2.37	2e-16	4e-17	14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	2.64	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100008586	2.23	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	645073	2.06	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	729442	2.51	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	26748	2.57	2e-16	4e-17	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
7	645037	2.67	2e-16	4e-17	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
8	2576	2.2	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	2577	2.47	2e-16	4e-17	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	2579	2.54	2e-16	4e-17	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
11	24150	1.94	1e-14	5e-14	14 x 11 TP53 target 3D [Source:HGNC Symbol;Acc:44657]
12	441520	1.9	3e-14	9e-12	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
13	653219	1.73	5e-12	3e-11	14 x 11 X antigen family, member 1B [Source:HGNC Symbol;Acc:254
14	26749	1.66	4e-11	3e-11	14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960]
15	729447	1.66	4e-11	1e-10	14 x 11 G antigen 2A [Source:HGNC Symbol;Acc:4099]
16	8277	1.61	1e-10	1e-10	14 x 10 transketolase-like 1 [Source:HGNC Symbol;Acc:11835]
17	146754	1.6	2e-10	5e-10	13 x 10 dynein, axonemal, heavy chain 2 [Source:HGNC Symbol;Acc
18	729396	1.56	5e-10	4e-09	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	5446	1.49	3e-09	1e-08	13 x 10 paraoxonase 3 [Source:HGNC Symbol;Acc:9206]
20	2578	1.44	9e-09	2e-07	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	19.4	NULL	1 / 12	GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
2	15.1	NULL	1 / 9	GSEA C2ABE_VEGFA_TARGETS_30MIN
3	12.94	NULL	1 / 11	GSEA C2ABE_VEGFA_TARGETS_2HR
4	12.89	NULL	1 / 10	GSEA C2NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
5	12.68	NULL	1 / 4	GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_DN
6	11.99	NULL	1 / 11	GSEA C2NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
7	11.55	NULL	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
8	11.5	NULL	16 / 630	Chr Chr X
9	11.39	NULL	1 / 13	CC axonemal dynein complex
10	11.25	NULL	1 / 12	GSEA C2HSIAO_LIVER_SPECIFIC_GENES
11	10.86	NULL	1 / 14	GSEA C2WALK_AML_WITH_11Q23_REARRANGED
12	10.61	NULL	1 / 13	GSEA C2HOSHIDA_LIVER_CANCER_SURVIVAL_DN
13	10.35	NULL	1 / 15	GSEA C2WALK_AML_CLUSTER_16
14	10.35	NULL	1 / 15	GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY
15	9.85	NULL	1 / 16	BP ciliary or bacterial-type flagellar motility
16	9.69	NULL	1 / 10	GSEA C2XU_RESPONSE_TO_TRETINOIN_DN
17	9.6	NULL	1 / 15	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
18	9.6	NULL	1 / 15	GSEA C2AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
19	9.6	NULL	1 / 15	GSEA C2SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4
20	9.6	NULL	1 / 15	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S3
21	9.18	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
22	9.18	NULL	1 / 16	GSEA C2JI_METASTASIS_REPRESSED_BY_STK11
23	8.48	NULL	1 / 20	CC dynein complex
24	7.75	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
25	6.69	NULL	1 / 7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
26	6.39	NULL	3 / 120	H.Tiss WIRTH_Testis
27	5.95	NULL	1 / 8	GSEA C2WEBER_METHYLATED_ICP_IN_FIBROBLAST
28	4.98	NULL	1 / 26	MF cyclin-dependent protein serine/threonine kinase activity
29	4.06	NULL	1 / 13	GSEA C2HATADA_METHYLATED_IN_LUNG_CANCER_DN
30	4.06	NULL	1 / 13	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
31	3.98	NULL	1 / 21	BP negative regulation of Notch signaling pathway
32	3.92	NULL	1 / 68	BP microtubule-based movement
33	3.85	NULL	1 / 14	BP negative regulation of retinoic acid receptor signaling pathway
34	3.85	NULL	1 / 14	GSEA C2KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN
35	3.81	NULL	1 / 71	MF microtubule motor activity
36	3.71	NULL	1 / 66	BP biosynthetic process
37	3.66	NULL	1 / 15	GSEA C2L_WILMS_TUMOR
38	3.5	NULL	1 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
39	3.1	NULL	1 / 19	MF retinoic acid receptor binding
40	2.59	NULL	1 / 7	GSEA C2REACTOME_AMINE_LIGAND_BINDING_RECEPTORS

p-values



GW_103

Local Summary

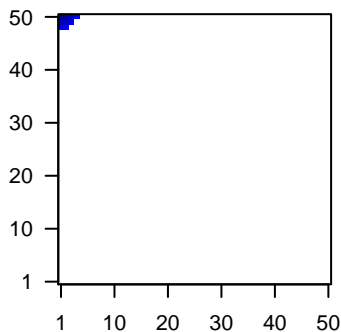
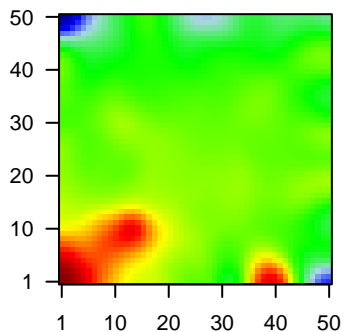
%DE = 0.88
 # metagenes = 9
 # genes = 159
 # genes in genesets = 156

genes with $fdr < 0.1$ = 136 (6 + / 130 -)
 # genes with $fdr < 0.05$ = 129 (5 + / 124 -)
 # genes with $fdr < 0.01$ = 117 (3 + / 114 -)

<r> metagenes = 0.99
 <r> genes = 0.5
 <FC> = -1.19
 <shrinkage-t> = -41.88
 <p-value> = 0
 <fdr> = 0.2

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.59	2e-16	2e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.52	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-2.11	2e-16	2e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	218	-3.4	2e-16	2e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	375791	-2.23	2e-16	2e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
6	4680	-2.18	2e-16	2e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
7	22802	-2.59	2e-16	2e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	49860	-3.13	2e-16	2e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
9	1475	-2.17	2e-16	2e-16	1 x 50 cystatin A (steфин A) [Source:HGNC Symbol;Acc:2481]
10	1824	-2.4	2e-16	2e-16	1 x 48 desmocollin 2 [Source:HGNC Symbol;Acc:3036]
11	163351	-2.43	2e-16	2e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
12	2877	-2.42	2e-16	2e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
13	26085	-2.14	2e-16	2e-16	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6
14	5653	-2.2	2e-16	2e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
15	3860	-2.91	2e-16	2e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	-2.21	2e-16	2e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
17	3851	-3.03	2e-16	2e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
18	4118	-2.82	2e-16	2e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
19	51458	-2.07	2e-16	2e-16	1 x 50 Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
20	6286	-3.16	2e-16	2e-16	1 x 50 S100 calcium binding protein P [Source:HGNC Symbol;Acc:1

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-55.9	NULL	67 / 135	H.Tiss WIRTH_Mucosa
2	-32.33	NULL	14 / 21	CC cornified envelope
3	-30.66	NULL	16 / 42	BP keratinization
4	-30.21	NULL	19 / 53	BP keratinocyte differentiation
5	-29.11	NULL	8 / 19	BP peptide cross-linking
6	-24.45	NULL	70 / 572	Disease GUDJ_psooriasis up
7	-21.87	NULL	5 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
8	-18.98	NULL	18 / 76	BP epidermis development
9	-17.19	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
10	-16.94	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
11	-16.23	NULL	3 / 12	BP cellular aldehyde metabolic process
12	-15.29	NULL	6 / 13	BP negative regulation of peptidase activity
13	-15.02	NULL	4 / 10	MF RAGE receptor binding
14	-14.49	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	-14.21	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
16	-14.01	NULL	5 / 21	CC desmosome
17	-13.99	NULL	8 / 52	BP negative regulation of endopeptidase activity
18	-13.29	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
19	-13.05	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
20	-12.93	NULL	5 / 29	BP regulation of proteolysis
21	-12.83	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
22	-12.67	NULL	2 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
23	-12.17	NULL	13 / 186	MF structural molecule activity
24	-11.26	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
25	-11.19	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
26	-10.95	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
27	-10.74	NULL	6 / 38	BP epithelial cell differentiation
28	-10.64	NULL	4 / 15	MF retinol dehydrogenase activity
29	-10.47	NULL	2 / 14	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
30	-10.31	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
31	-10.24	NULL	4 / 16	GSEA C2JAEGER_METASTASIS_DN
32	-9.78	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
33	-9.71	NULL	2 / 14	GSEA C2KEGG_PHENYLALANINE_METABOLISM
34	-9.64	NULL	4 / 23	MF peptidase inhibitor activity
35	-9.49	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
36	-9.44	NULL	3 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
37	-9.41	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
38	-9.2	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
39	-9.05	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_
40	-9.03	NULL	1 / 6	GSEA C2CLAUS_PGR_POSITIVE_MENINGIOMA_UP

p-values

