

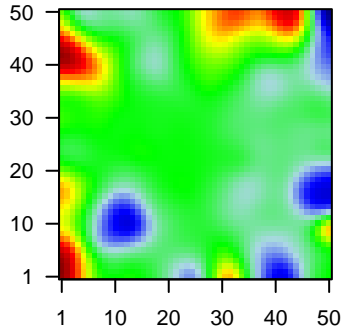
GW_298

Global Summary

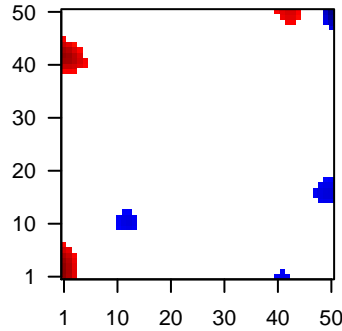
%DE = 0.14
 # genes with fdr < 0.2 = 1753 (1031 + / 722 -)
 # genes with fdr < 0.1 = 1236 (751 + / 485 -)
 # genes with fdr < 0.05 = 1064 (660 + / 404 -)
 # genes with fdr < 0.01 = 650 (435 + / 215 -)
 # genes in genesets = 16332

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

Profile



Regulated Spots



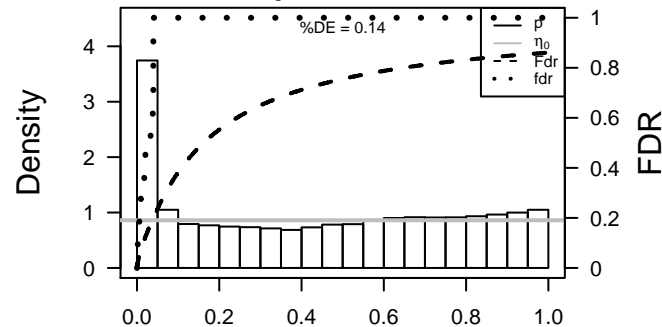
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.65	2e-16	5e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
2	218	-1.16	2e-16	5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
3	80833	1.19	2e-16	5e-14	47 x 1 apolipoprotein L, 3 [Source:HGNC Symbol;Acc:14868]
4	563	1.44	2e-16	5e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol]
5	80115	1.23	2e-16	5e-14	1 x 43 BAI1-associated protein 2-like 2 [Source:HGNC Symbol;Acc:14868]
6	25805	-1.17	2e-16	5e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC Symbol;Acc:14868]
7	8412	1.19	2e-16	5e-14	1 x 5 breast cancer anti-estrogen resistance 3 [Source:HGNC Symbol;Acc:14868]
8	260436	1.71	2e-16	5e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:14868]
9	352999	2.81	2e-16	5e-14	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbol;Acc:14868]
10	760	1.47	2e-16	5e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
11	768	1.33	2e-16	5e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
12	834	1.15	2e-16	5e-14	32 x 1 caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1373]
13	10321	1.48	2e-16	5e-14	50 x 10 cysteine-rich secretory protein 3 [Source:HGNC Symbol;Acc:1373]
14	49860	1.24	2e-16	5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	3627	1.16	2e-16	5e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:1373]
16	6373	1.91	2e-16	5e-14	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:1373]
17	92196	-1.58	2e-16	5e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2]
18	22943	1.22	2e-16	5e-14	1 x 7 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Symbol;Acc:1373]
19	1755	1.85	2e-16	5e-14	50 x 10 deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:1373]
20	2152	1.69	2e-16	5e-14	1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:HGNC Symbol;Acc:1373]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.23	NULL	572	Disease GUDJ_psooriasis up
2	14.64	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
3	12.55	NULL	957	Chr Chr 11
4	12.06	NULL	633	Chr Chr 9
5	10.4	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
6	10.4	NULL	142	Glio wilscher_GBM_Verhaak-PNwt_expression_C_down
7	9.72	NULL	530	Cancer Lembecke_Normal vs Adenoma
8	9.67	NULL	1182	CC extracellular region
9	7.72	NULL	553	Cancer Lembecke_Colonc Inflammation
10	7.49	NULL	123	BP defense response to virus
11	7.36	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
12	7.36	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
13	7.36	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
14	7.36	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
15	7.31	NULL	153	MF structural constituent of ribosome
16	7.31	NULL	13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
17	6.99	NULL	683	CC extracellular space
18	6.75	NULL	253	BP translation
19	6.75	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
20	6.64	NULL	190	CC extracellular matrix
<i>Underexpressed</i>				
1	-8.38	NULL	918	Chr Chr 17
2	-7.66	NULL	914	Chr Chr 3
3	-6.08	NULL	11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
4	-6.04	NULL	13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
5	-5.87	NULL	15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
6	-5.8	NULL	717	Chr Chr 16
7	-5.43	NULL	743	Chr Chr 7
8	-4.96	NULL	119	BP xenobiotic metabolic process
9	-4.93	NULL	14	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B
10	-4.84	NULL	127	H.Tiss WIRTH_Muscle
11	-4.77	NULL	18	MF acyl-CoA dehydrogenase activity
12	-4.73	NULL	20	MF glutathione transferase activity
13	-4.69	NULL	6	GSEA C2KAPOLI_LIVER_CANCER_POOR_SURVIVAL_DN
14	-4.6	NULL	6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
15	-4.55	NULL	25	BP glutathione derivative biosynthetic process
16	-4.5	NULL	11	MF glutathione binding
17	-4.47	NULL	823	MF sequence-specific DNA binding transcription factor activity
18	-4.45	NULL	400	H.Tiss WIRTH_Nervous System
19	-4.32	NULL	36	BP muscle filament sliding
20	-4.19	NULL	618	Chr Chr 4

p-values



GW_298

Local Summary

%DE = 0.69
 # metagenes = 18
 # genes = 296
 # genes in genesets = 294

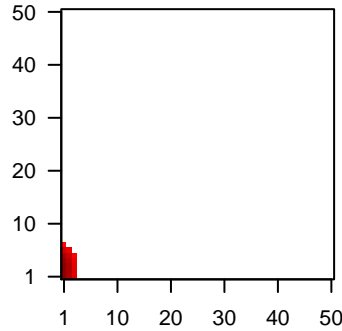
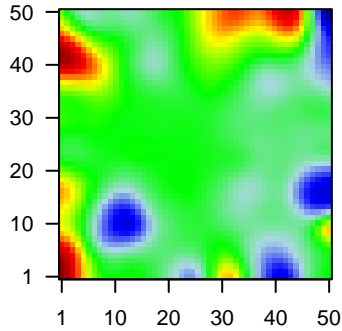
genes with $fdr < 0.1$ = 152 (134 + / 18 -)
 # genes with $fdr < 0.05$ = 148 (131 + / 17 -)
 # genes with $fdr < 0.01$ = 109 (96 + / 13 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.34

$\langle FC \rangle = 0.29$
 $\langle \text{shrinkage-t} \rangle = 10.33$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.48$

Profile

Spot



Local Genelist

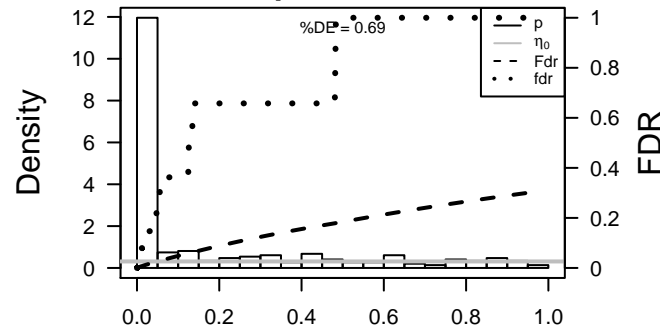
Rank	ID	log(FC)	fdr	p-value	Description
1	8412	1.19	2e-16	2e-15	1 x 5 breast cancer anti-estrogen resistance 3 [Source:HGNC Syrn
2	768	1.33	2e-16	2e-15	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	22943	1.22	2e-16	2e-15	1 x 7 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S;
4	10468	1.26	2e-16	2e-15	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
5	4314	1.2	2e-16	2e-15	1 x 1 matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
6	4502	1.21	2e-16	2e-15	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
7	644314	1.25	2e-16	2e-15	1 x 5
8	12	2.05	2e-16	2e-15	1 x 1
9	7980	1.46	2e-16	2e-15	3 x 5 tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:1
10	7424	1.64	2e-16	2e-15	1 x 3 vascular endothelial growth factor C [Source:HGNC Symbol;f
11	169611	1.12	4e-16	1e-13	1 x 5 olfactomedin-like 2A [Source:HGNC Symbol;Acc:27270]
12	87	1.1	2e-15	1e-13	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
13	4312	1.09	3e-15	1e-13	1 x 1 matrix metallopeptidase 1 (interstitial collagenase) [Source:H
14	8727	1.08	5e-15	1e-13	1 x 5 catenin (cadherin-associated protein), alpha-like 1 [Source:t
15	1594	1.08	8e-15	1e-11	1 x 6 cytochrome P450, family 27, subfamily B, polypeptide 1 [Sou
16	28514	1.08	8e-15	1e-11	1 x 5 delta-like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
17	11009	1.03	1e-13	2e-10	1 x 3 interleukin 24 [Source:HGNC Symbol;Acc:11346]
18	871	0.96	5e-12	2e-10	1 x 1 serpin peptidase inhibitor, clade H (heat shock protein 47), m
19	140851	0.95	6e-12	2e-10	1 x 5
20	4489	0.87	8e-12	2e-10	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	17.77	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
2	17.32	NULL	14 / 16	MMML C6SCIEJ_MMML 1
3	17.26	NULL	7 / 11	MF platelet-derived growth factor binding
4	16.35	NULL	47 / 190	CC extracellular matrix
5	15.28	NULL	3 / 10	BP cellular response to zinc ion
6	15.15	NULL	60 / 242	BP extracellular matrix organization
7	15.11	NULL	7 / 12	miRNA target-29c
8	14.99	NULL	25 / 69	BP extracellular matrix disassembly
9	14.9	NULL	24 / 64	BP collagen catabolic process
10	14.42	NULL	59 / 250	LymphocyteENZ_Stromal signature 1
11	13.65	NULL	17 / 57	MF extracellular matrix structural constituent
12	13.41	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
13	13.37	NULL	38 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
14	13.37	NULL	38 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
15	13.37	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
16	13.37	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
17	13.21	NULL	6 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
18	12.9	NULL	2 / 7	MMML C6SCIEJ_MMML 13
19	12.61	NULL	14 / 37	BP collagen fibril organization
20	12.46	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
21	12.33	NULL	3 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
22	12.19	NULL	3 / 15	BP negative regulation of growth
23	12	NULL	8 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
24	11.98	NULL	6 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
25	11.67	NULL	100 / 1182CC	extracellular region
26	11.28	NULL	2 / 8	GSEA C2SCHLESINGER_METHYLATED_IN_COLON_CANCER
27	10.88	NULL	4 / 16	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHRO
28	10.88	NULL	3 / 16	BP negative regulation of peptidyl-serine phosphorylation
29	10.74	NULL	3 / 16	GSEA C2GU_PDEF_TARGETS_DN
30	10.68	NULL	4 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
31	10.61	NULL	3 / 13	GSEA C2LAMB_CCND1_TARGETS
32	10.6	NULL	1 / 2	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
33	10.5	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER
34	10.5	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER_MARKERS
35	10.5	NULL	1 / 5	GSEA C2LE_SKI_TARGETS_DN
36	10.22	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
37	10.08	NULL	5 / 16	GSEA C2URS_ADIPOCYTE_DIFFERENTIATION_DN
38	10.08	NULL	10 / 40	BP cellular response to amino acid stimulus
39	9.97	NULL	5 / 9	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_DN
40	9.97	NULL	57 / 553	Cancer Lembcke_Colonc Inflammation

p-values



GW_298

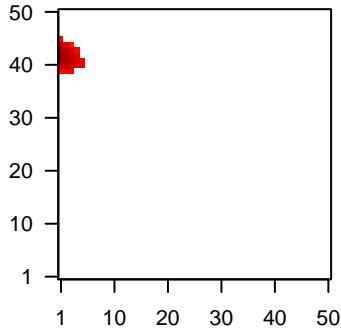
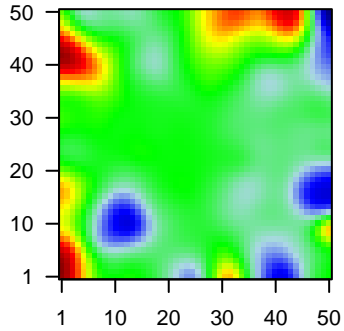
Local Summary

%DE = 0.71
 # metagenes = 25
 # genes = 271
 # genes in genesets = 267
 # genes with $fdr < 0.1 = 140$ (117 + / 23 -)
 # genes with $fdr < 0.05 = 140$ (117 + / 23 -)
 # genes with $fdr < 0.01 = 87$ (77 + / 10 -)

<r> metagenes = 0.97
 <r> genes = 0.34
 <FC> = 0.26
 <shrinkage-t> = 9.16
 <p-value> = 0
 <fdr> = 0.52

Profile

Spot



Local Genelist

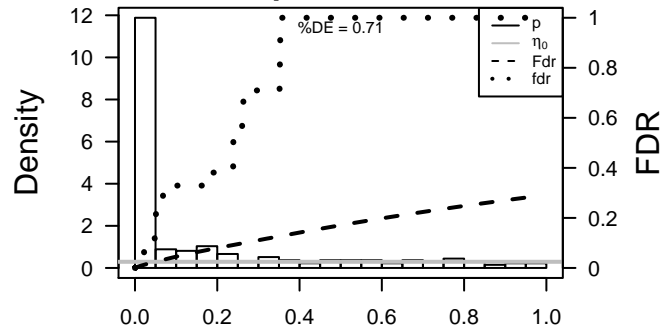
Rank	ID	log(FC)	fdr	p-value	Description
1	80115	1.23	2e-16	2e-15	1 x 43 BAI1-associated protein 2-like 2 [Source:HGNC Symbol;Acc:1373]
2	760	1.47	2e-16	2e-15	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	2152	1.69	2e-16	2e-15	1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:H
4	3489	2.22	2e-16	2e-15	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
5	3552	1.23	2e-16	2e-15	1 x 43 interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
6	8942	1.15	2e-16	2e-15	1 x 40 kynureninase [Source:HGNC Symbol;Acc:6469]
7	26499	1.22	2e-16	2e-15	1 x 42 pleckstrin 2 [Source:HGNC Symbol;Acc:19238]
8	22800	1.28	2e-16	2e-15	3 x 41 related RAS viral (r-ras) oncogene homolog 2 [Source:HGNC
9	6713	1.13	4e-16	1e-13	2 x 43 squalene epoxidase [Source:HGNC Symbol;Acc:11279]
10	3861	1.01	2e-15	5e-13	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
11	1288	1.08	8e-15	2e-12	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
12	374918	1.05	3e-14	1e-11	1 x 45 IGF-like family member 1 [Source:HGNC Symbol;Acc:24093]
13	664	1.02	2e-13	2e-11	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK
14	24145	1	5e-13	9e-11	3 x 41 pannexin 1 [Source:HGNC Symbol;Acc:8599]
15	3885	0.97	2e-12	9e-11	4 x 42 keratin 34 [Source:HGNC Symbol;Acc:6452]
16	8986	0.97	3e-12	9e-11	1 x 40 ribosomal protein S6 kinase, 90kDa, polypeptide 4 [Source:H
17	1308	0.96	4e-12	7e-10	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
18	154	0.94	1e-11	1e-09	1 x 40 adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286
19	3949	0.92	3e-11	1e-08	1 x 41 low density lipoprotein receptor [Source:HGNC Symbol;Acc:6
20	3084	0.88	3e-10	1e-08	3 x 40 neuregulin 1 [Source:HGNC Symbol;Acc:7997]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	17.38	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
2	16.03	NULL	5 / 12	BP hemidesmosome assembly
3	14.35	NULL	1 / 7	GSEA C2YE_METASTASIS_LIVER_CANCER
4	13.69	NULL	3 / 16	GSEA C2LEONARD_HYPOXIA
5	12.77	NULL	2 / 2	miRNA target-199a*
6	12.76	NULL	3 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
7	12.67	NULL	49 / 572	Disease GUDJ_psooriasis up
8	12.13	NULL	3 / 16	GSEA C2HARRIS_HYPOXIA
9	11.89	NULL	2 / 14	GSEA C2MAINA_VHL_TARGETS_DN
10	11.84	NULL	1 / 6	GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP
11	11.7	NULL	3 / 13	GSEA C2WANG_METHYLATED_IN_BREAST_CANCER
12	11.53	NULL	2 / 11	BP positive regulation of positive chemotaxis
13	11	NULL	3 / 15	GSEA C2BROWNE_HCMV_INFECTION_2HR_DN
14	10.88	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
15	10.59	NULL	1 / 12	GSEA C2SANCHEZ_MDM2_TARGETS
16	10.37	NULL	3 / 15	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_DN
17	10.13	NULL	1 / 13	GSEA C2REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
18	9.91	NULL	3 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
19	9.71	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
20	9.68	NULL	2 / 14	BP positive regulation of osteoclast differentiation
21	9.56	NULL	3 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
22	9.5	NULL	2 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP
23	9.39	NULL	3 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
24	9.34	NULL	1 / 15	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_UP
25	8.85	NULL	1 / 10	GSEA C2REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASO
26	8.79	NULL	6 / 78	BP positive regulation of angiogenesis
27	8.59	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
28	8.5	NULL	3 / 15	GSEA C2PRAMONJAGO_SOX4_TARGETS_UP
29	8.38	NULL	1 / 11	GSEA C2BIOCARTA_EXTRINSIC_PATHWAY
30	8.31	NULL	2 / 10	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G3
31	8.25	NULL	10 / 76	BP epidermis development
32	8.18	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
33	8.15	NULL	1 / 9	GSEA C2HEDVAT_ELF4_TARGETS_UP
34	8.13	NULL	2 / 25	BP response to zinc ion
35	8.04	NULL	1 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
36	7.89	NULL	2 / 13	BP response to copper ion
37	7.84	NULL	1 / 6	GSEA C2OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_
38	7.75	NULL	12 / 82	CC intermediate filament
39	7.7	NULL	2 / 17	BP morphogenesis of an epithelium
40	7.62	NULL	1 / 13	GSEA C2FRIDMAN_SENESCENCE_UP

p-values



GW_298

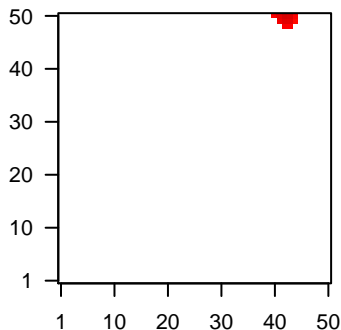
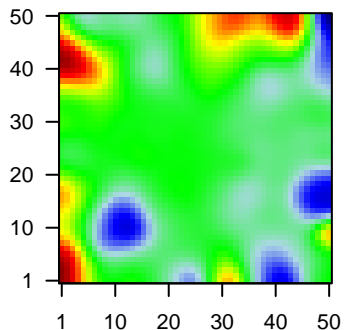
Local Summary

%DE = 0.7
 # metagenes = 11
 # genes = 206
 # genes in genesets = 204
 # genes with $fdr < 0.1 = 104$ (100 + / 4 -)
 # genes with $fdr < 0.05 = 85$ (83 + / 2 -)
 # genes with $fdr < 0.01 = 49$ (49 + / 0 -)

<r> metagenes = 0.97
 <r> genes = 0.4
 <FC> = 0.27
 <shrinkage-t> = 9.37
 <p-value> = 0.01
 <fdr> = 0.59

Profile

Spot



Local Genelist

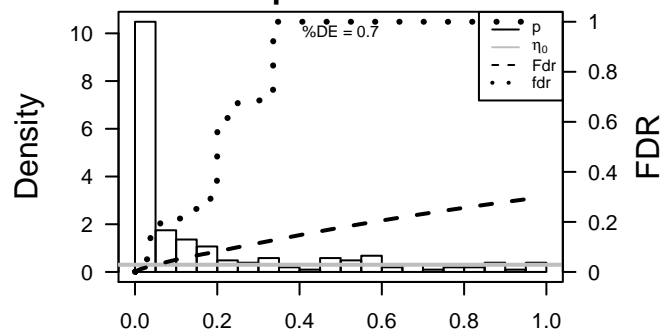
Rank	ID	log(FC)	fdr	p-value	Description
1	55165	0.91	5e-11	4e-09	44 x 50 centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161]
2	39	0.88	2e-10	4e-09	42 x 48 acetyl-CoA acetyltransferase 2 [Source:HGNC Symbol;Acc:9
3	220042	0.88	2e-10	5e-08	42 x 50 chromosome 11 open reading frame 82 [Source:HGNC Synt
4	9833	0.84	1e-09	5e-08	44 x 50 maternal embryonic leucine zipper kinase [Source:HGNC Syr
5	3336	0.84	2e-09	5e-08	42 x 50 heat shock 10kDa protein 1 [Source:HGNC Symbol;Acc:5268
6	51010	0.83	2e-09	2e-06	41 x 50 exosome component 3 [Source:HGNC Symbol;Acc:17944]
7	1033	0.75	5e-08	2e-06	43 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	55353	0.74	8e-08	2e-05	42 x 50 lysosomal protein transmembrane 4 beta [Source:HGNC Syrr
9	1164	0.69	6e-07	2e-05	44 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
10	113130	0.69	7e-07	3e-05	44 x 49 cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
11	5684	0.67	1e-06	5e-05	40 x 50 proteasome (prosome, macropain) subunit, alpha type, 3 [Sou
12	29128	0.66	2e-06	1e-04	44 x 49
13	6611	0.64	4e-06	1e-04	42 x 50 spermine synthase [Source:HGNC Symbol;Acc:11123]
14	9221	0.63	6e-06	2e-04	40 x 50 nucleolar and coiled-body phosphoprotein 1 [Source:HGNC :
15	51001	0.61	9e-06	2e-04	41 x 50 MTERF domain containing 1 [Source:HGNC Symbol;Acc:242
16	6636	0.61	1e-05	2e-04	43 x 48 small nuclear ribonucleoprotein polypeptide F [Source:HGNC
17	983	0.6	2e-05	2e-04	44 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:1722]
18	23212	0.6	2e-05	3e-04	40 x 50 RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
19	2739	0.58	3e-05	3e-04	40 x 50 glyoxalase I [Source:HGNC Symbol;Acc:4323]
20	9787	0.57	4e-05	3e-04	43 x 50 discs, large (Drosophila) homolog-associated protein 5 [Sour

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	35.31	NULL	46 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	35.31	NULL	46 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	25.18	NULL	10 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	24.05	NULL	10 / 18	BP spindle organization
5	22.02	NULL	9 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
6	19.08	NULL	7 / 11	BP mitotic metaphase plate congression
7	17.91	NULL	4 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
8	17.88	NULL	12 / 57	Glio developing astrocytes
9	17.65	NULL	6 / 14	MMML C2SCIEJ_MMML_4
10	17.63	NULL	8 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
11	17.28	NULL	7 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
12	16.95	NULL	7 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
13	15.74	NULL	5 / 9	GSEA C2BIOCARTA_RANMS_PATHWAY
14	15.64	NULL	6 / 16	Cancer WOLFER_overlap genes
15	15.57	NULL	46 / 370	BP mitotic cell cycle
16	15.44	NULL	48 / 530	Cancer Lembcke_Normal vs Adenoma
17	15.07	NULL	6 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
18	14.66	NULL	26 / 232	BP mitosis
19	14.6	NULL	6 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
20	14.58	NULL	6 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
21	14.55	NULL	5 / 18	LymphomaBAVE_c-myc BL UP
22	14.08	NULL	38 / 572	Disease GUDJ_psooriasis up
23	13.07	NULL	6 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
24	12.89	NULL	4 / 14	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
25	12.79	NULL	13 / 56	CC chromosome, centromeric region
26	12.72	NULL	6 / 13	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_UP
27	11.76	NULL	17 / 148	BP G1/S transition of mitotic cell cycle
28	11.62	NULL	3 / 10	GSEA C2BIOCARTA_PTC1_PATHWAY
29	11.55	NULL	6 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
30	11.51	NULL	4 / 15	GSEA C2REACTOME_CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2
31	11.4	NULL	5 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
32	11.27	NULL	4 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
33	11.15	NULL	4 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
34	10.9	NULL	4 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
35	10.8	NULL	5 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
36	10.64	NULL	2 / 10	GSEA C2REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE
37	10.53	NULL	4 / 14	GSEA C2MAYBURD_RESPONSE_TO_L663536_DN
38	10.48	NULL	6 / 15	GSEA C2LY_AGING_MIDDLE_DN
39	10.47	NULL	9 / 63	TF MYC_Targets UP
40	10.38	NULL	12 / 66	CC condensed chromosome kinetochore

p-values



GW_298

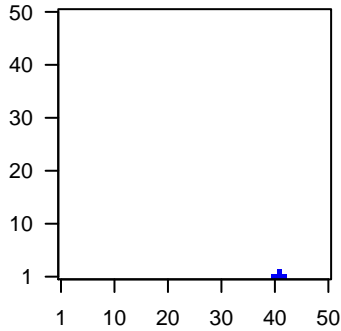
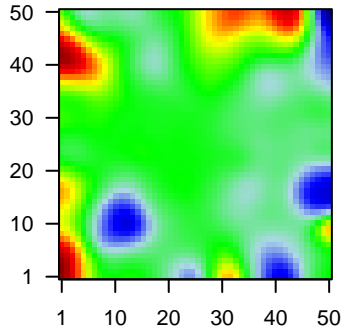
Local Summary

%DE = 0.88
 # metagenes = 4
 # genes = 94
 # genes in genesets = 86
 # genes with fdr < 0.1 = 75 (1 + / 74 -)
 # genes with fdr < 0.05 = 53 (1 + / 52 -)
 # genes with fdr < 0.01 = 16 (0 + / 16 -)

<r> metagenes = 0.99
 <r> genes = 0.51
 <FC> = -0.27
 <shrinkage-t> = -9.37
 <p-value> = 0.02
 <fdr> = 0.7

Profile

Spot



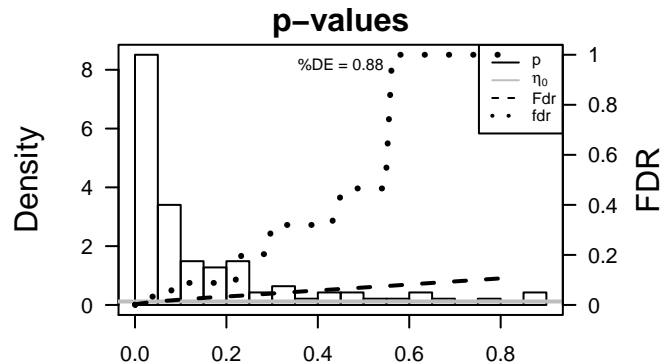
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	728294	-1	5e-13	2e-05	40 x 1 D-2-hydroxyglutarate dehydrogenase [Source:HGNC Symbc
2	51326	-0.66	2e-06	3e-05	42 x 1 ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc
3	152485	-0.63	5e-06	3e-05	41 x 1 zinc finger protein 827 [Source:HGNC Symbol;Acc:27193]
4	23646	-0.62	9e-06	3e-05	42 x 1 phospholipase D family, member 3 [Source:HGNC Symbol;Ac
5	1455	-0.61	1e-05	1e-04	41 x 2 casein kinase 1, gamma 2 [Source:HGNC Symbol;Acc:2455]
6	115703	-0.59	2e-05	2e-04	41 x 1 Rho GTPase activating protein 33 [Source:HGNC Symbol;Ac
7	2319	-0.57	4e-05	2e-04	42 x 1 flotillin 2 [Source:HGNC Symbol;Acc:3758]
8	27148	-0.56	5e-05	2e-04	41 x 1 serine/threonine kinase 36 [Source:HGNC Symbol;Acc:17205]
9	22980	-0.55	7e-05	7e-04	41 x 2 transcription factor 25 (basic helix-loop-helix) [Source:HGNC
10	23524	-0.53	1e-04	7e-04	40 x 1 serine/arginine repetitive matrix 2 [Source:HGNC Symbol;Acc
11	440353	-0.51	2e-04	1e-03	40 x 1
12	51281	-0.5	3e-04	6e-03	42 x 1 ankyrin repeat and MYND domain containing 1 [Source:HGNC
13	23466	-0.46	1e-03	6e-03	41 x 1 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
14	90639	-0.44	1e-03	9e-03	40 x 1 cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [S
15	401261	-0.41	3e-03	9e-03	41 x 1
16	23468	-0.41	3e-03	9e-03	40 x 1 chromobox homolog 5 [Source:HGNC Symbol;Acc:1555]
17	57130	0.4	4e-03	1e-02	41 x 2 ATPase type 13A1 [Source:HGNC Symbol;Acc:24215]
18	79716	-0.38	6e-03	1e-02	41 x 2 aminopeptidase-like 1 [Source:HGNC Symbol;Acc:16244]
19	79058	-0.38	7e-03	1e-02	41 x 1 alveolar soft part sarcoma chromosome region, candidate 1 [
20	80233	-0.37	8e-03	1e-02	41 x 1 chromosome 17 open reading frame 70 [Source:HGNC Synt

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.59	NULL	1 / 15	BP 2-oxoglutarate metabolic process
2	-11.01	NULL	2 / 15	GSEA C2REACTOME_SPHINGOLIPID_METABOLISM
3	-10.74	NULL	1 / 7	GSEA C2GENTILE_UV_LOW_DOSE_DN
4	-10.74	NULL	1 / 7	GSEA C2GENTILE_UV_LOW_DOSE_UP
5	-9.97	NULL	1 / 8	GSEA C2BARRIER_COLON_CANCER_RELAPSE_NORMAL_SAMPLE_DN
6	-9.19	NULL	2 / 13	GSEA C2ST_GAQ_PATHWAY
7	-9.19	NULL	2 / 13	GSEA C2ST_GA13_PATHWAY
8	-9.18	NULL	1 / 7	GSEA C2LIU_CMYB_TARGETS_DN
9	-8.99	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
10	-8.74	NULL	1 / 25	BP response to zinc ion
11	-8.6	NULL	2 / 12	GSEA C2BARRIER_COLON_CANCER_RECURRENCE_DN
12	-8.21	NULL	1 / 10	CC acrosomal membrane
13	-8.04	NULL	2 / 22	CC heterochromatin
14	-7.78	NULL	1 / 11	MF ionotropic glutamate receptor binding
15	-7.66	NULL	1 / 12	MF Rac GTPase activator activity
16	-7.66	NULL	1 / 12	GSEA C2MCCABE_HOXC6_TARGETS_CANCER_UP
17	-7.6	NULL	1 / 13	GSEA C2WU_HBX_TARGETS_1_DN
18	-7.54	NULL	1 / 14	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
19	-7.32	NULL	1 / 14	GSEA C2ROSS_AML_WITH_MLL_FUSIONS
20	-7.29	NULL	1 / 14	GSEA C2GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
21	-7.29	NULL	1 / 14	GSEA C2WU_HBX_TARGETS_2_UP
22	-7.29	NULL	1 / 14	GSEA C2KEGG_HEDGEHOG_SIGNALING_PATHWAY
23	-7.12	NULL	1 / 11	MF C2H2 zinc finger domain binding
24	-7.09	NULL	2 / 33	BP sphingolipid biosynthetic process
25	-7.04	NULL	1 / 15	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
26	-7.04	NULL	1 / 15	GSEA C2ST_GA12_PATHWAY
27	-6.79	NULL	1 / 14	miRNA target sites
28	-6.79	NULL	1 / 16	GSEA C2LIU_THYROID_CANCER_CLUSTER_1
29	-6.78	NULL	1 / 12	Glio Phillips PN up vs MES & Prolif
30	-6.78	NULL	1 / 12	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
31	-6.76	NULL	1 / 16	GSEA C2WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2
32	-6.75	NULL	1 / 15	GSEA C2ODONNELL_METASTASIS_UP
33	-6.55	NULL	1 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
34	-6.09	NULL	1 / 18	BP positive regulation of Rac GTPase activity
35	-5.97	NULL	1 / 15	GSEA C2JIANG_TIP30_TARGETS_DN
36	-5.84	NULL	1 / 7	GSEA C2KEGG_SPHINGOLIPID_METABOLISM
37	-5.59	NULL	1 / 19	BP positive regulation of smoothed signaling pathway
38	-5.42	NULL	1 / 20	miRNA target sites
39	-5.31	NULL	1 / 10	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
40	-5.04	NULL	1 / 25	MF Rho GTPase activator activity



GW_298

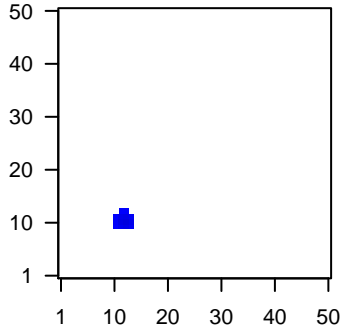
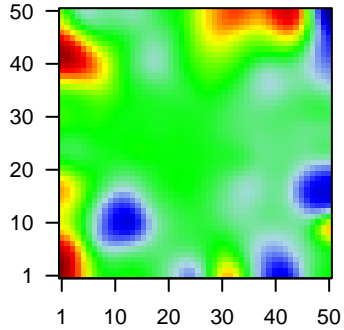
Local Summary

%DE = 0.9
 # metagenes = 14
 # genes = 74
 # genes in genesets = 58
 # genes with $fdr < 0.1 = 60$ (1 + / 59 -)
 # genes with $fdr < 0.05 = 42$ (0 + / 42 -)
 # genes with $fdr < 0.01 = 35$ (0 + / 35 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.3
 $\langle FC \rangle = -0.33$
 $\langle \text{shrinkage-t} \rangle = -11.67$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.47$

Profile

Spot



Local Genelist

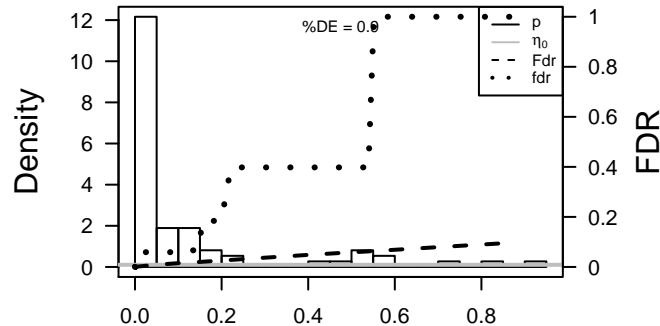
Rank	ID	log(FC)	fdr	p-value	Description
1	4103	-0.71	3e-07	2e-05	14 x 10 melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68]
2	26609	-0.65	2e-06	2e-05	13 x 11 variable charge, X-linked [Source:HGNC Symbol;Acc:12667]
3	425054	-0.63	5e-06	2e-05	13 x 11 variable charge, X-linked 3B [Source:HGNC Symbol;Acc:318]
4	25894	-0.62	7e-06	6e-05	12 x 11 pleckstrin homology domain containing, family G (with RhoGe
5	441520	-0.57	3e-05	6e-05	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
6	729422	-0.57	4e-05	6e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	24150	-0.57	4e-05	6e-05	14 x 11 TP53 target 3D [Source:HGNC Symbol;Acc:44657]
8	4485	-0.57	4e-05	2e-04	12 x 12 macrophage stimulating 1 (hepatocyte growth factor-like) [Sc
9	645037	-0.55	7e-05	2e-04	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
10	51481	-0.54	1e-04	2e-04	13 x 11 variable charge, X-linked 3A [Source:HGNC Symbol;Acc:181
11	6015	-0.53	1e-04	2e-04	11 x 12 ring finger protein 1 [Source:HGNC Symbol;Acc:10018]
12	4109	-0.52	2e-04	2e-04	14 x 11 melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
13	729442	-0.52	2e-04	2e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	23532	-0.52	2e-04	2e-04	13 x 10 preferentially expressed antigen in melanoma [Source:HGNC
15	4100	-0.52	2e-04	5e-04	14 x 11 melanoma antigen family A, 1 (directs expression of antigen I
16	8408	-0.5	3e-04	5e-04	11 x 12 unc-51 like autophagy activating kinase 1 [Source:HGNC Sy
17	26748	-0.5	3e-04	1e-03	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
18	2577	-0.48	5e-04	1e-03	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	22859	-0.48	6e-04	1e-03	12 x 10 latrophilin 1 [Source:HGNC Symbol;Acc:20973]
20	729428	-0.47	7e-04	1e-03	14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.3	NULL	1 / 4	GSEA C2WBEVER_METHYLATED_ICP_IN_SPERM_DN
2	-12.66	NULL	1 / 5	GSEA C2NGUYEN_NOTCH1_TARGETS_DN
3	-12.49	NULL	19 / 630	Chr Chr X
4	-11.4	NULL	2 / 16	GSEA C2LANDEMAINE_LUNG_METASTASIS
5	-11.29	NULL	1 / 6	GSEA C2LOPEZ_MBD_TARGETS
6	-11.04	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
7	-10.92	NULL	2 / 8	GSEA C2WBEVER_METHYLATED_ICP_IN_FIBROBLAST
8	-10.04	NULL	1 / 7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
9	-9.4	NULL	2 / 15	GSEA C2BROWNE_HCMV_INFECTION_8HR_DN
10	-9.14	NULL	1 / 14	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B
11	-8.81	NULL	1 / 9	GSEA C2DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
12	-8.34	NULL	1 / 9	GSEA C2SOZGIT_ESR1_TARGETS_DN
13	-8.28	NULL	2 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
14	-7.82	NULL	1 / 10	BP positive regulation of macroautophagy
15	-7.82	NULL	1 / 10	GSEA C2STEIN_ESRRA_TARGETS
16	-7.82	NULL	1 / 10	GSEA C2KEGG_REGULATION_OF_AUTOPHAGY
17	-7.81	NULL	1 / 11	GSEA C2STEGMEIER_PRE-MITOTIC_CELL_CYCLE_REGULATORS
18	-7.78	NULL	1 / 11	GSEA C2SU_PLACENTA
19	-7.42	NULL	1 / 12	CC PRC1 complex
20	-7.42	NULL	1 / 12	GSEA C2OSMAN_BLADDER_CANCER_UP
21	-7.39	NULL	1 / 11	CC pre-autophagosomal structure membrane
22	-7.39	NULL	1 / 11	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
23	-7.39	NULL	1 / 11	GSEA C2FUJII_YBX1_TARGETS_UP
24	-7.32	NULL	2 / 27	BP response to starvation
25	-7.11	NULL	2 / 13	GSEA C2ENK_UV_RESPONSE KERATINOCYTE_UP
26	-7.04	NULL	1 / 11	BP positive regulation of synapse maturation
27	-7.02	NULL	1 / 12	GSEA C2PEREZ_TP53_TARGETS
28	-7.02	NULL	1 / 12	GSEA C2BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
29	-7.02	NULL	1 / 12	GSEA C2NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
30	-7.02	NULL	1 / 12	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
31	-6.91	NULL	1 / 13	GSEA C2HATADA_METHYLATED_IN_LUNG_CANCER_DN
32	-6.91	NULL	1 / 13	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
33	-6.74	NULL	1 / 14	GSEA C2NIELSEN_GIST
34	-6.69	NULL	1 / 13	BP axon extension
35	-6.69	NULL	1 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
36	-6.69	NULL	1 / 13	GSEA C2DOUGLAS_BMI1_TARGETS_UP
37	-6.69	NULL	1 / 13	GSEA C2MOOHTA_PGC
38	-6.68	NULL	1 / 12	BP calcium-mediated signaling using intracellular calcium source
39	-6.68	NULL	1 / 12	GSEA C2PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
40	-6.66	NULL	1 / 21	BP chromatin organization

p-values



GW_298

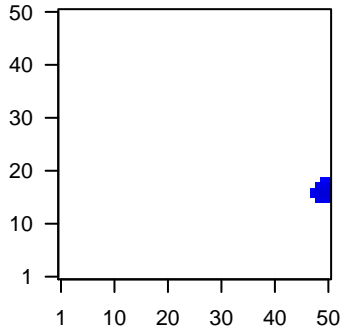
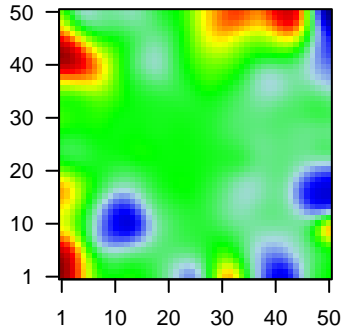
Local Summary

%DE = 0.61
 # metagenes = 16
 # genes = 192
 # genes in genesets = 191
 # genes with fdr < 0.1 = 61 (5 + / 56 -)
 # genes with fdr < 0.05 = 59 (5 + / 54 -)
 # genes with fdr < 0.01 = 28 (2 + / 26 -)

<r> metagenes = 0.98
 <r> genes = 0.34
 <FC> = -0.21
 <shrinkage-t> = -7.23
 <p-value> = 0.03
 <fdr> = 0.68

Profile

Spot



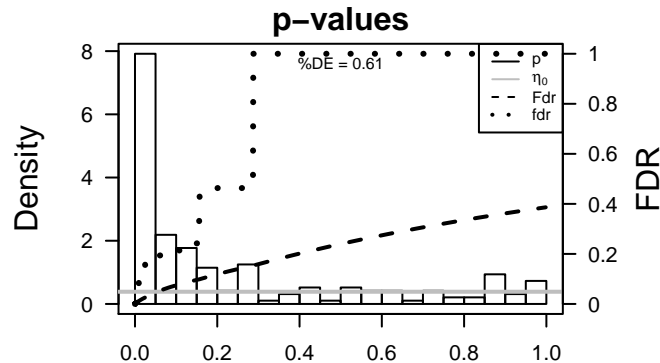
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	54959	1.11	9e-16	4e-07	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:10439]
2	55063	-0.81	5e-09	3e-06	50 x 16 zinc finger, CW type with PWWP domain 1 [Source:HGNC Symbol;Acc:10439]
3	217	-0.76	4e-08	5e-06	50 x 15 aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:10439]
4	2879	-0.73	1e-07	5e-06	50 x 18 glutathione peroxidase 4 [Source:HGNC Symbol;Acc:4556]
5	1153	-0.72	2e-07	9e-05	50 x 15 cold inducible RNA binding protein [Source:HGNC Symbol;Acc:10439]
6	8543	-0.64	4e-06	9e-05	50 x 15 LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
7	79191	-0.64	4e-06	9e-05	50 x 15 iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
8	23113	-0.63	5e-06	9e-05	48 x 17 cullin 9 [Source:HGNC Symbol;Acc:15982]
9	1959	-0.63	5e-06	4e-04	50 x 19 early growth response 2 [Source:HGNC Symbol;Acc:3239]
10	63917	-0.6	1e-05	4e-04	50 x 16 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase 1 [Source:HGNC Symbol;Acc:10439]
11	1298	-0.6	2e-05	5e-04	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
12	155066	-0.59	2e-05	2e-03	50 x 15 ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symbol;Acc:10439]
13	10439	-0.57	4e-05	2e-03	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
14	4255	-0.55	7e-05	3e-03	48 x 15 O-6-methylguanine-DNA methyltransferase [Source:HGNC Symbol;Acc:10439]
15	694	-0.49	1e-04	3e-03	50 x 18 B-cell translocation gene 1, anti-proliferative [Source:HGNC Symbol;Acc:10439]
16	6263	-0.51	2e-04	3e-03	50 x 18 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
17	9110	-0.51	2e-04	3e-03	49 x 17 myotubularin related protein 4 [Source:HGNC Symbol;Acc:74]
18	221061	-0.51	2e-04	3e-03	50 x 16 family with sequence similarity 171, member A1 [Source:HGNC Symbol;Acc:10439]
19	6431	-0.47	3e-04	3e-03	50 x 18 serine/arginine-rich splicing factor 6 [Source:HGNC Symbol;Acc:10439]
20	3021	-0.5	3e-04	4e-03	50 x 18 H3 histone, family 3B (H3.3B) [Source:HGNC Symbol;Acc:47]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.54	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30
2	-9.25	NULL	2 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
3	-8.88	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
4	-8.57	NULL	1 / 7	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
5	-8.56	NULL	1 / 5	GSEA C2STAEGE_EWING_FAMILY_TUMOR
6	-7.87	NULL	2 / 14	GSEA C2CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL
7	-7.86	NULL	3 / 15	GSEA C2FAELT_B CLL_WITH_VH3_21_DN
8	-7.76	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY
9	-7.2	NULL	2 / 16	GSEA C2TOOKER_GEMCITABINE_RESISTANCE_UP
10	-7.2	NULL	2 / 16	GSEA C2TOOKER_RESPONSE_TO_BEXAROTENE_DN
11	-7.15	NULL	4 / 34	BP thymus development
12	-7.03	NULL	1 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
13	-7.03	NULL	1 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
14	-6.78	NULL	1 / 12	GSEA C2INDGREN_BLADDER_CANCER_CLUSTER_1_UP
15	-6.76	NULL	1 / 10	BP lipoxygenase pathway
16	-6.72	NULL	1 / 7	GSEA C2KANG_CISPLATIN_RESISTANCE_DN
17	-6.69	NULL	1 / 10	GSEA C2OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
18	-6.66	NULL	1 / 11	BP neurotransmitter biosynthetic process
19	-6.41	NULL	1 / 11	MF glutathione binding
20	-6.4	NULL	2 / 13	Cancer GENTLES_modul12
21	-6.29	NULL	2 / 16	GSEA C2BROWNE_HCMV_INFECTION_24HR_UP
22	-6.28	NULL	3 / 30	BP negative regulation of cell death
23	-6.24	NULL	1 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
24	-6.2	NULL	2 / 9	GSEA C2ZOZIGT_ESR1_TARGETS_DN
25	-6.16	NULL	1 / 9	GSEA C2ABE_VEGFA_TARGETS_30MIN
26	-6.16	NULL	2 / 12	CC PRC1 complex
27	-6.04	NULL	1 / 12	BP mRNA stabilization
28	-6.01	NULL	1 / 2	miRNA target-153
29	-5.95	NULL	3 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
30	-5.86	NULL	2 / 15	GSEA C2SHIPP_DLCL_VS_FOLLICULAR_LYMPHOMA_DN
31	-5.81	NULL	1 / 10	BP cellular response to gonadotropin stimulus
32	-5.81	NULL	1 / 10	BP regulation of ossification
33	-5.81	NULL	1 / 10	GSEA C2CHASSOT_SKIN_WOUND
34	-5.81	NULL	1 / 10	GSEA C2ABE_VEGFA_TARGETS
35	-5.8	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
36	-5.77	NULL	1 / 13	GSEA C2ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
37	-5.77	NULL	1 / 13	GSEA C2CHANDRAN_METASTASIS_TOP50_DN
38	-5.77	NULL	1 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
39	-5.7	NULL	1 / 8	GSEA C2SCHLESINGER_METHYLATED_IN_COLON_CANCER
40	-5.7	NULL	2 / 12	GSEA C2PROVENZANI_METASTASIS_UP



GW_298

Local Summary

%DE = 0.74
 # metagenes = 7
 # genes = 134
 # genes in genesets = 133

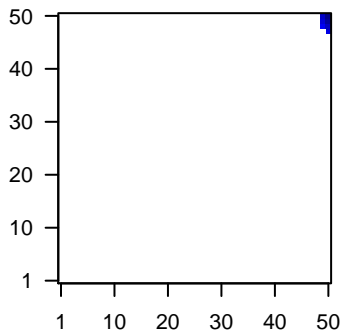
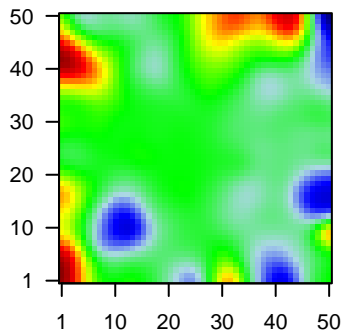
genes with $fdr < 0.1 = 82$ (8 + / 74 -)
 # genes with $fdr < 0.05 = 74$ (7 + / 67 -)
 # genes with $fdr < 0.01 = 60$ (4 + / 56 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.3

$\langle FC \rangle = -0.37$
 $\langle \text{shrinkage-t} \rangle = -13.04$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.43$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.65	2e-16	1e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
2	2944	-1.36	2e-16	1e-15	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4]
3	2946	-1.16	2e-16	1e-15	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr]
4	3880	-1.46	2e-16	1e-15	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
5	6657	-1.29	2e-16	1e-15	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbx]
6	11166	-1.38	2e-16	1e-15	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt]
7	256764	-1.87	2e-16	1e-15	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
8	4953	-1.08	6e-15	5e-12	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
9	139728	-1.02	2e-13	5e-12	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:l]
10	445	1	4e-13	5e-12	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75f]
11	56977	-1	4e-13	6e-11	50 x 49 storkhead box 2 [Source:HGNC Symbol;Acc:25450]
12	4922	-0.97	2e-12	6e-11	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
13	339512	-0.96	4e-12	2e-09	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt]
14	4915	-0.91	7e-11	2e-09	50 x 50 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC]
15	655	-0.89	1e-10	3e-09	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1f]
16	26047	-0.88	2e-10	9e-09	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac]
17	56922	-0.86	6e-10	9e-09	50 x 50 methylcrotonoyl-CoA carboxylase 1 (alpha) [Source:HGNC S]
18	84707	-0.85	1e-09	9e-09	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
19	57216	-0.85	1e-09	5e-08	50 x 48 VANGL planar cell polarity protein 2 [Source:HGNC Symbol;f]
20	154664	-0.83	3e-09	2e-07	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Sou]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-24.92	NULL	5 / 15	GSEA C2KEGG_Glutathione_Metabolism
2	-22.66	NULL	3 / 8	GSEA C2LJU_CDX2_TARGETS_DN
3	-19.93	NULL	3 / 11	MF glutathione binding
4	-19.93	NULL	3 / 11	GSEA C2KEGG_DRUG_Metabolism_Cytochrome_P450
5	-19	NULL	2 / 7	GSEA C2MCCOLLUM_Geldanamycin_Resistance_DN
6	-17.17	NULL	4 / 13	GSEA C2KEGG_Metabolism_of_Xenobiotics_by_Cytochrome_P
7	-15.17	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_Fusion_Targets_D_DN
8	-15.17	NULL	1 / 6	GSEA C2KAPOSI_Liver_Cancer_Poor_Survival_DN
9	-15.11	NULL	5 / 20	MF glutathione transferase activity
10	-14.72	NULL	6 / 25	BP glutathione derivative biosynthetic process
11	-14.02	NULL	2 / 9	GSEA C2REACTOME_Metabolism_of_Amino_Acids
12	-13.82	NULL	1 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
13	-13.57	NULL	2 / 15	GSEA C2LEE_Liver_Cancer_MYC_UP
14	-13.57	NULL	2 / 15	GSEA C2LEE_Liver_Cancer_E2F1_UP
15	-13.41	NULL	3 / 16	GSEA C2BOYALT_Liver_Cancer_Subclass_G1_DN
16	-12.92	NULL	8 / 34	BP glutathione metabolic process
17	-11.89	NULL	1 / 9	GSEA C2ABDULRAHMAN_Kidney_Cancer_VHL_DN
18	-11.89	NULL	1 / 9	GSEA C2REACTOME_Ethanol_Oxidation
19	-11.66	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
20	-11.52	NULL	2 / 12	BP cellular aldehyde metabolic process
21	-11.4	NULL	2 / 11	GSEA C2SMID_Breast_Cancer_Basal_UP
22	-11.3	NULL	2 / 23	BP stem cell differentiation
23	-11.17	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
24	-11.17	NULL	1 / 10	GSEA C2FRIDMAN_Senescence_DN
25	-10.8	NULL	11 / 119	BP xenobiotic metabolic process
26	-10.75	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
27	-10.75	NULL	1 / 7	miRNA target-145
28	-10.61	NULL	4 / 15	GSEA C2REACTOME_Glutathione_Conjugation
29	-10.56	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
30	-10.4	NULL	2 / 15	GSEA C2YANG_Breast_Cancer_ESR1_LASER_DN
31	-10.27	NULL	2 / 11	BP planar cell polarity pathway involved in neural tube closure
32	-10.23	NULL	2 / 19	BP anatomical structure formation involved in morphogenesis
33	-10.02	NULL	1 / 15	GSEA C2SABATES_Colorectal_Adenoma_UP
34	-9.92	NULL	1 / 8	GSEA C2REACTOME_E2F_Transcriptional_Targets_At_G1_S
35	-9.92	NULL	1 / 8	miRNA target-450
36	-9.91	NULL	2 / 16	GSEA C2KOKKINAKIS_Methionine_Deprivation_48HR_DN
37	-9.76	NULL	2 / 12	BP Wnt signaling pathway, planar cell polarity pathway
38	-9.73	NULL	1 / 9	GSEA C2GOERING_Blood_HDL_Cholesterol_QTL_CIS
39	-9.5	NULL	2 / 15	GSEA C2REACTOME_Phase_II_Conjugation
40	-9.4	NULL	2 / 22	BP eye development

