

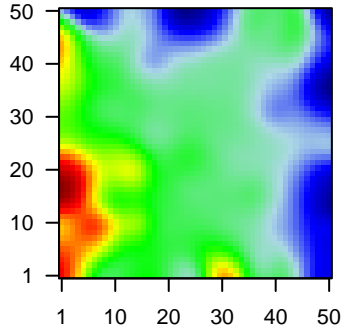
GW_207

Global Summary

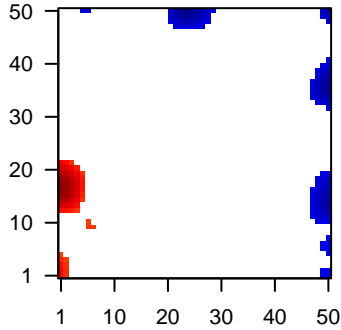
%DE = 0.13
 # genes with fdr < 0.2 = 1318 (764 + / 554 -)
 # genes with fdr < 0.1 = 1068 (623 + / 445 -)
 # genes with fdr < 0.05 = 785 (464 + / 321 -)
 # genes with fdr < 0.01 = 486 (303 + / 183 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.15
 <fdr> = 0.87

Profile



Regulated Spots



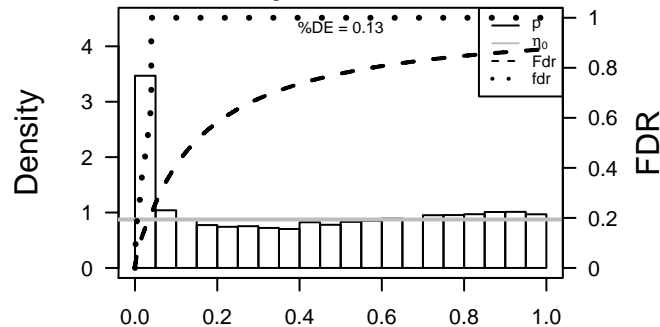
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	218	-1.54	2e-16	7e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
2	23246	1.67	2e-16	7e-14	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
3	92747	1.56	2e-16	7e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
4	8900	1.64	2e-16	7e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
5	49860	-2.35	2e-16	7e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
6	441520	2.13	2e-16	7e-14	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
7	55894	1.81	2e-16	7e-14	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	414325	2.02	2e-16	7e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	1843	-1.61	2e-16	7e-14	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30
10	2353	-1.74	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:+
11	2354	-2.15	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source
12	10457	-1.7	2e-16	7e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
13	121355	2.23	2e-16	7e-14	14 x 11 gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
14	3039	2.18	2e-16	7e-14	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
15	3040	2.31	2e-16	7e-14	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
16	3043	2.31	2e-16	7e-14	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
17	3553	1.73	2e-16	7e-14	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
18	26525	2.04	2e-16	7e-14	1 x 49 interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
19	3576	1.84	2e-16	7e-14	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
20	3665	1.88	2e-16	7e-14	32 x 1 interferon regulatory factor 7 [Source:HGNC Symbol;Acc:612

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.17	NULL	918	Chr Chr 17
2	9.02	NULL	530	Cancer Lembecke_Normal vs Adenoma
3	8.83	NULL	572	Disease GUDJ_psooriasis up
4	7.92	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
5	7.54	NULL	4	MMML C6SCIEJ_MMML_23
6	7.42	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	7.41	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	7.24	NULL	51	BP type I interferon signaling pathway
9	6.93	NULL	31	BP negative regulation of viral genome replication
10	6.82	NULL	6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	6.78	NULL	1135	Chr Chr 19
12	6.64	NULL	16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
13	6.21	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
14	5.91	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
15	5.91	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
16	5.91	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
17	5.91	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
18	5.8	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
19	5.79	NULL	15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
20	5.78	NULL	1182	CC extracellular region
<i>Underexpressed</i>				
1	-8.22	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-7.44	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
3	-7.36	NULL	463	miRNA target-miR-33a
4	-7.12	NULL	335	miRNA target-miR-342-5p
5	-6.9	NULL	24	TF Tissu/AQUERIZAS_Trachea
6	-6.57	NULL	456	miRNA target-miR-349a
7	-6.56	NULL	368	miRNA target-miR-344a
8	-6.4	NULL	358	miRNA target-miR-519C--519B--519A
9	-6.29	NULL	198	miRNA target-miR-33a
10	-6.28	NULL	415	miRNA target-miR-19A--19B
11	-6.17	NULL	399	miRNA target-miR-549c-3p
12	-6.16	NULL	15	CC MHC class II protein complex
13	-6.14	NULL	9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
14	-6.11	NULL	545	miRNA target-miR-33a
15	-6.11	NULL	310	miRNA target-miR-33a
16	-6.1	NULL	246	miRNA target-miR-551-5p
17	-6.03	NULL	433	miRNA target-miR-349b
18	-6.01	NULL	449	miRNA target-miR-349b
19	-5.98	NULL	184	miRNA target-miR-33b
20	-5.94	NULL	303	miRNA target-miR-33b

p-values



GW_207

Local Summary

%DE = 0.67
 # metagenes = 9
 # genes = 171
 # genes in genesets = 169

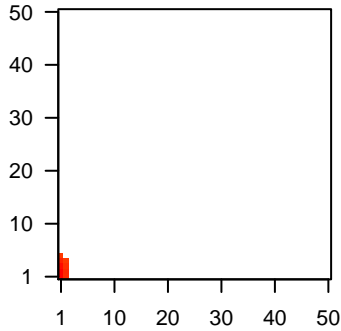
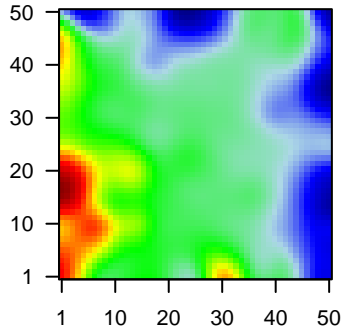
genes with $fdr < 0.1 = 84$ (76 + / 8 -)
 # genes with $fdr < 0.05 = 66$ (60 + / 6 -)
 # genes with $fdr < 0.01 = 53$ (47 + / 6 -)

<r> metagenes = 0.98
 <r> genes = 0.38

<FC> = 0.34
 <shrinkage-t> = 11.98
 <p-value> = 0
 <fdr> = 0.55

Profile

Spot



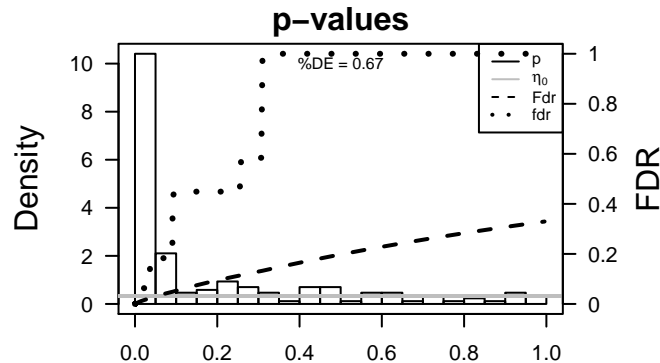
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3553	1.73	2e-16	4e-15	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
2	3576	1.84	2e-16	4e-15	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
3	12	1.71	2e-16	4e-15	1 x 1
4	60675	1.42	6e-15	3e-12	1 x 1 prokineticin 2 [Source:HGNC Symbol;Acc:18455]
5	5008	1.37	5e-14	1e-11	1 x 1 oncostatin M [Source:HGNC Symbol;Acc:8506]
6	4502	1.33	3e-13	3e-11	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
7	55107	1.3	8e-13	4e-10	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:10468]
8	3956	1.23	1e-11	4e-10	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:3956]
9	1464	1.23	1e-11	6e-10	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:1464]
10	5054	1.21	3e-11	6e-10	1 x 2 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) [Source:HGNC Symbol;Acc:5054]
11	10468	1.21	3e-11	1e-09	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
12	285761	1.19	5e-11	6e-09	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC Symbol;Acc:285761]
13	1277	1.16	2e-10	6e-09	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
14	1291	1.14	3e-10	6e-09	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
15	3918	1.14	4e-10	1e-07	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
16	366	1.08	3e-09	1e-07	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
17	4489	0.98	4e-09	9e-07	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
18	3678	1	3e-08	9e-07	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Source:HGNC Symbol;Acc:3678]
19	2195	-1	4e-08	1e-06	1 x 5 FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
20	4319	-0.99	6e-08	9e-06	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:4319]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	27.2	NULL	2 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
2	24.54	NULL	6 / 11	MF platelet-derived growth factor binding
3	21.23	NULL	1 / 3	GSEA C2REN_MIF_TARGETS_DN
4	19.55	NULL	4 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
5	18.04	NULL	2 / 6	Glio Martinez_Glio_hypometh
6	17.34	NULL	6 / 12	miRNA target-29c
7	17.23	NULL	45 / 242	BP extracellular matrix organization
8	17.09	NULL	5 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
9	16.91	NULL	10 / 40	BP cellular response to amino acid stimulus
10	16.7	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
11	16.41	NULL	3 / 10	BP protein heterotrimerization
12	16.13	NULL	19 / 64	BP collagen catabolic process
13	16.1	NULL	4 / 11	Glio Phillips MES up vs Prolif & PN
14	15.94	NULL	3 / 10	BP cellular response to zinc ion
15	15.67	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
16	15.65	NULL	20 / 69	BP extracellular matrix disassembly
17	15.6	NULL	2 / 16	GSEA C2GRAHAM_CML QUIESCENT_VS_CML_DIVIDING_UP
18	15.53	NULL	1 / 5	GSEA C2DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCCOC
19	15.46	NULL	33 / 190	CC extracellular matrix
20	15.36	NULL	3 / 11	GSEA C2BIOCARTA_STEM_PATHWAY
21	15.34	NULL	29 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
22	15.34	NULL	29 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
23	15.34	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
24	15.34	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
25	15.26	NULL	10 / 37	BP collagen fibril organization
26	14.98	NULL	2 / 6	GSEA C2BIOCARTA_IL5_PATHWAY
27	14.31	NULL	4 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
28	14.11	NULL	10 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
29	13.94	NULL	1 / 6	GSEA C2MIZUKAMI_HYPOXIA_DN
30	13.94	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
31	13.93	NULL	2 / 5	GSEA C2DASU_IL6_SIGNALING_UP
32	13.58	NULL	10 / 16	MMML C6CIEJ_MMML 1
33	13.48	NULL	9 / 35	Glio Colman_survival_associated
34	13.44	NULL	3 / 10	BP negative regulation of cell-substrate adhesion
35	13.36	NULL	2 / 13	BP positive regulation of vascular endothelial growth factor receptor signaling pathway
36	13.06	NULL	72 / 1182	CC extracellular region
37	12.99	NULL	4 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
38	12.82	NULL	7 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
39	12.81	NULL	53 / 683	CC extracellular space
40	12.74	NULL	1 / 7	GSEA C2BIOCARTA_FREE_PATHWAY



GW_207

Local Summary

%DE = 0.84
 # metagenes = 3
 # genes = 37
 # genes in genesets = 36

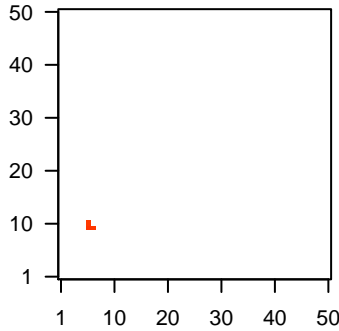
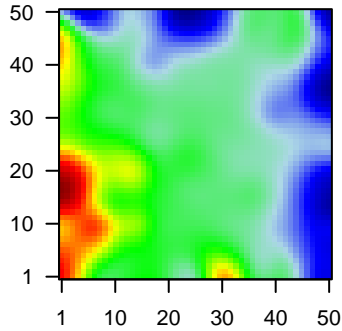
 # genes with $fdr < 0.1 = 24$ (24 + / 0 -)
 # genes with $fdr < 0.05 = 21$ (21 + / 0 -)
 # genes with $fdr < 0.01 = 9$ (9 + / 0 -)

 $\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.37

 $\langle FC \rangle = 0.39$
 $\langle \text{shrinkage-t} \rangle = 13.72$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.57$

Profile

Spot



Local Genelist

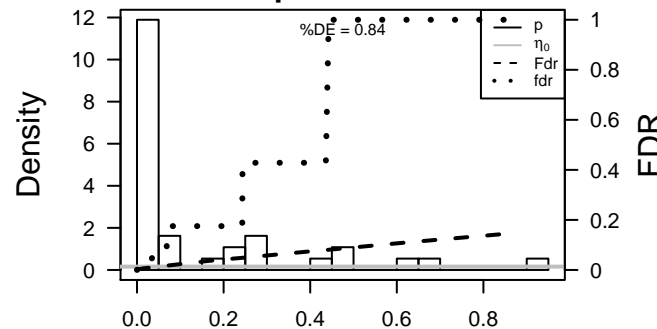
Rank	ID	log(FC)	fdr	p-value	Description
1	55291	1.29	1e-12	6e-05	6 x 11 protein phosphatase 6, regulatory subunit 3 [Source:HGNC S
2	23144	0.8	1e-05	2e-04	6 x 10 zinc finger CCH-type containing 3 [Source:HGNC Symbol;/
3	9277	0.72	7e-05	2e-04	7 x 10 WD repeat domain 46 [Source:HGNC Symbol;Acc:13923]
4	126208	0.71	9e-05	4e-03	7 x 10 zinc finger protein 787 [Source:HGNC Symbol;Acc:26998]
5	22870	0.57	2e-03	4e-03	7 x 10 protein phosphatase 6, regulatory subunit 1 [Source:HGNC S
6	6195	0.56	2e-03	4e-03	7 x 10 ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:H
7	83985	0.55	3e-03	4e-03	7 x 10 spinster homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:
8	11140	0.5	3e-03	4e-03	7 x 10 cell division cycle 37 [Source:HGNC Symbol;Acc:1735]
9	5518	0.53	3e-03	7e-03	6 x 10 protein phosphatase 2, regulatory subunit A, alpha [Source:H
10	29928	0.52	5e-03	1e-02	6 x 11 translocase of inner mitochondrial membrane 22 homolog (ye
11	90678	0.49	7e-03	2e-02	6 x 10 leucine rich repeat and sterile alpha motif containing 1 [Sourc
12	10078	0.46	1e-02	2e-02	7 x 10 tumor suppressing subtransferable candidate 4 [Source:HGN
13	23193	0.45	1e-02	2e-02	6 x 11 glucosidase, alpha; neutral AB [Source:HGNC Symbol;Acc:4'
14	9146	0.44	1e-02	2e-02	6 x 10 hepatocyte growth factor-regulated tyrosine kinase substrate
15	29115	0.42	2e-02	2e-02	6 x 11 SAP30 binding protein [Source:HGNC Symbol;Acc:30785]
16	10844	0.42	2e-02	2e-02	7 x 10 tubulin, gamma complex associated protein 2 [Source:HGNC
17	64210	0.41	2e-02	2e-02	6 x 10 MMS19 nucleotide excision repair homolog (S. cerevisiae) [S
18	1616	0.41	2e-02	2e-02	6 x 11 death-domain associated protein [Source:HGNC Symbol;Acc
19	54662	0.39	3e-02	2e-02	6 x 11 TBC1 domain family, member 13 [Source:HGNC Symbol;Acc
20	79446	0.39	3e-02	2e-02	6 x 10 WD repeat domain 25 [Source:HGNC Symbol;Acc:21064]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	17.31	NULL	1 / 15	GSEA C2WANG_CLIM2_TARGETS_UP
2	14.53	NULL	2 / 15	GSEA C2REACTOME_ERK_MAPK_TARGETS
3	14.53	NULL	2 / 15	GSEA C2REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPT
4	14.11	NULL	2 / 16	GSEA C2SCHEIDERIT_IKK_INTERACTING_PROTEINS
5	13.99	NULL	2 / 16	GSEA C2REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED
6	12.03	NULL	1 / 5	miRNA target set miR-3199-3p
7	11.85	NULL	2 / 11	CC holo TFIIH complex
8	11.46	NULL	2 / 59	MF protein phosphatase binding
9	9.63	NULL	1 / 9	GSEA C2REACTOME_PP2A_MEDIATED_DEPHOSPHORYLATION_OF_KI
10	9.42	NULL	1 / 43	miRNA target set miR-3199-3p
11	9.22	NULL	2 / 34	miRNA target set miR-3199-3p
12	9.17	NULL	1 / 10	MF protein kinase B binding
13	9.08	NULL	4 / 67	BP chromosome segregation
14	9.01	NULL	1 / 10	BP mitotic nuclear envelope reassembly
15	8.84	NULL	1 / 48	miRNA target set miR-3199-3p
16	8.49	NULL	1 / 11	BP regulation of DNA replication
17	8.49	NULL	1 / 11	GSEA C2REACTOME_BETACATENIN_PHOSPHORYLATION_CASCADE
18	8.49	NULL	1 / 11	GSEA C2REACTOME_ERKS_ARE_INACTIVATED
19	8.29	NULL	1 / 23	BP mRNA polyadenylation
20	8.19	NULL	1 / 12	miRNA target set miR-3199-3p
21	8	NULL	1 / 13	GSEA C2AMB_CCND1_TARGETS
22	8	NULL	1 / 13	GSEA C2REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACT
23	7.79	NULL	1 / 12	GSEA C2LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
24	7.66	NULL	1 / 13	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
25	7.65	NULL	1 / 14	GSEA C2BIOCARTA_ERK5_PATHWAY
26	7.63	NULL	1 / 10	GSEA C2JISON_SICKLE_CELL_DISEASE_DN
27	7.45	NULL	1 / 14	MF Hsp90 protein binding
28	7.33	NULL	1 / 15	GSEA C2FIRESTEIN_CTNNB1_PATHWAY
29	7.33	NULL	1 / 15	GSEA C2BIOCARTA_G2_PATHWAY
30	7.33	NULL	1 / 15	GSEA C2BIOCARTA_GH_PATHWAY
31	7.33	NULL	1 / 15	GSEA C2BIOCARTA_IGF1R_PATHWAY
32	7.33	NULL	1 / 15	GSEA C2BIOCARTA_BAD_PATHWAY
33	7.33	NULL	1 / 15	GSEA C2BIOCARTA_CREB_PATHWAY
34	7.33	NULL	1 / 15	GSEA C2SA_B_CELL_RECEPTOR_COMPLEXES
35	7.32	NULL	1 / 14	BP positive regulation of extrinsic apoptotic signaling pathway in abse
36	7.32	NULL	1 / 14	BP regulation of Wnt signaling pathway
37	7.32	NULL	1 / 14	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G4
38	7.18	NULL	1 / 69	miRNA target set miR-562-5p
39	7.14	NULL	1 / 15	GSEA C2ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN
40	7.11	NULL	5 / 361	MF binding

p-values



GW_207

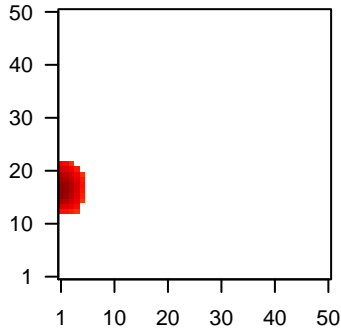
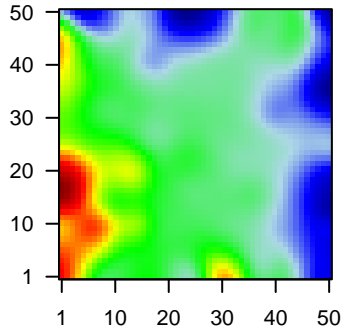
Local Summary

%DE = 0.73
 # metagenes = 45
 # genes = 444
 # genes in genesets = 441
 # genes with $fdr < 0.1$ = 229 (225 + / 4 -)
 # genes with $fdr < 0.05$ = 190 (186 + / 4 -)
 # genes with $fdr < 0.01$ = 121 (119 + / 2 -)

<r> metagenes = 0.92
 <r> genes = 0.26
 <FC> = 0.39
 <shrinkage-t> = 13.62
 <p-value> = 0.01
 <fdr> = 0.57

Profile

Spot



Local Genelist

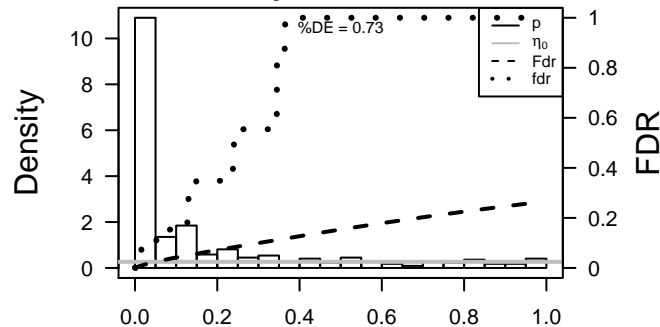
Rank	ID	log(FC)	fdr	p-value	Description
1	23246	1.67	2e-16	3e-14	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
2	8772	1.35	1e-13	1e-11	1 x 14 Fas (TNFRSF6)--associated via death domain [Source:HGNC
3	8045	1.34	2e-13	1e-11	2 x 22 Ras association (RalGDS/AF-6) domain family (N-terminal)
4	4728	1.33	3e-13	5e-09	2 x 17 NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (†
5	79581	1.2	4e-11	5e-09	1 x 15 solute carrier family 52 (riboflavin transporter), member 2 [So
6	113655	1.18	8e-11	1e-08	1 x 18 major facilitator superfamily domain containing 3 [Source:HGI
7	220064	1.16	2e-10	1e-08	1 x 14 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
8	2017	1.15	3e-10	3e-08	1 x 14 cortactin [Source:HGNC Symbol;Acc:3338]
9	57761	1.13	5e-10	1e-07	1 x 17 tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]
10	22827	1.1	2e-09	3e-07	1 x 16 poly-U binding splicing factor 60kDa [Source:HGNC Symbol;
11	10467	1.06	5e-09	3e-07	2 x 18 zinc finger, HIT-type containing 1 [Source:HGNC Symbol;Acc
12	54512	1.05	8e-09	3e-07	1 x 16 exosome component 4 [Source:HGNC Symbol;Acc:18189]
13	389541	1.04	1e-08	4e-07	3 x 19 late endosomal/lysosomal adaptor, MAPK and MTOR activat
14	283869	1.03	1e-08	4e-07	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
15	131076	-1.02	2e-08	4e-07	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
16	2050	1.02	2e-08	4e-07	1 x 15 EPH receptor B4 [Source:HGNC Symbol;Acc:3395]
17	7936	1.01	2e-08	2e-06	1 x 19 negative elongation factor complex member E [Source:HGNC
18	10248	1	4e-08	7e-06	1 x 16 processing of precursor 7, ribonuclease P/MRP subunit (S. ce
19	26519	-0.96	1e-07	7e-06	1 x 19 translocase of inner mitochondrial membrane 10 homolog (ye
20	26233	0.96	1e-07	7e-06	1 x 15 F-box and leucine-rich repeat protein 6 [Source:HGNC Syml

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	11.6	NULL	20 / 96	BP rRNA processing
2	10.71	NULL	2 / 5	GSEA C2REACTOME_ELECTRON_TRANSPORT_CHAIN
3	10.16	NULL	5 / 10	GSEA C2REACTOME_HIV_LIFE_CYCLE
4	10.12	NULL	1 / 3	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
5	10.12	NULL	1 / 3	GSEA C2KEGG_PARKINSONS_DISEASE
6	9.71	NULL	3 / 9	GSEA C2REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE
7	9.55	NULL	4 / 10	MF NADH dehydrogenase activity
8	9.28	NULL	25 / 153	MF structural constituent of ribosome
9	9.06	NULL	47 / 579	CC nucleolus
10	8.89	NULL	3 / 8	GSEA C2MUELLER_PLURINET
11	8.84	NULL	3 / 13	GSEA C2MOOHA_VOXPPOS
12	8.59	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
13	8.57	NULL	1 / 4	GSEA C2REACTOME_GLUCCOSE_REGULATION_OF_INSULIN_SECRETI
14	8.57	NULL	1 / 4	GSEA C2REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
15	8.57	NULL	1 / 4	GSEA C2REACTOME_REGULATION_OF_INSULIN_SECRETION
16	8.5	NULL	3 / 10	GSEA C2KEGG_HUNTINGTONS_DISEASE
17	8.17	NULL	4 / 18	MF ribonucleoprotein complex binding
18	8.05	NULL	4 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
19	7.83	NULL	98 / 1318	CC mitochondrion
20	7.73	NULL	2 / 8	GSEA C2REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
21	7.71	NULL	5 / 16	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
22	7.56	NULL	30 / 253	BP translation
23	7.45	NULL	21 / 167	CC ribosome
24	7.42	NULL	2 / 8	GSEA C2REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
25	7.37	NULL	4 / 14	CC exosome (RNase complex)
26	7.25	NULL	6 / 19	CC mitochondrial small ribosomal subunit
27	7.22	NULL	2 / 9	GSEA C2REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_CO
28	7.22	NULL	2 / 9	GSEA C2REACTOME_HIV1_TRANSCRIPTION_ELONGATION
29	7.22	NULL	2 / 9	GSEA C2REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME
30	7.19	NULL	2 / 10	MF oxidoreductase activity, acting on NAD(P)H
31	7.14	NULL	7 / 34	MF NADH dehydrogenase (ubiquinone) activity
32	7.06	NULL	41 / 530	Cancer Lembcke_Normal vs Adenoma
33	7.05	NULL	6 / 37	CC mitochondrial nucleoid
34	6.96	NULL	5 / 16	GSEA C2MOOHA_HUMAN_MITODB_6_2002
35	6.9	NULL	1 / 6	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_DN
36	6.89	NULL	7 / 36	CC mitochondrial respiratory chain complex I
37	6.88	NULL	2 / 10	GSEA C2YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_DN
38	6.84	NULL	5 / 36	BP ribosome biogenesis
39	6.78	NULL	2 / 10	GSEA C2REACTOME_TRANSCRIPTION
40	6.78	NULL	2 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP

p-values



GW_207

Local Summary

%DE = 0.7
 # metagenes = 4
 # genes = 125
 # genes in genesets = 124

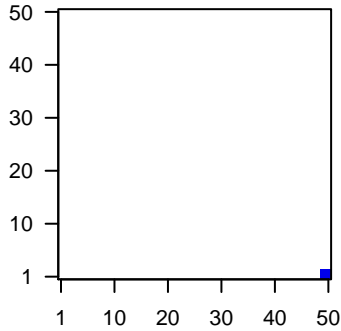
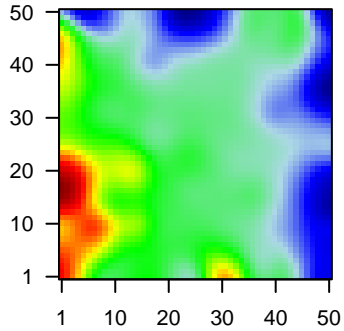
 # genes with $fdr < 0.1$ = 57 (8 + / 49 -)
 # genes with $fdr < 0.05$ = 51 (8 + / 43 -)
 # genes with $fdr < 0.01$ = 31 (4 + / 27 -)

 $\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.68

 $\langle FC \rangle = -0.25$
 $\langle \text{shrinkage-t} \rangle = -8.93$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.58$

Profile

Spot



Local Genelist

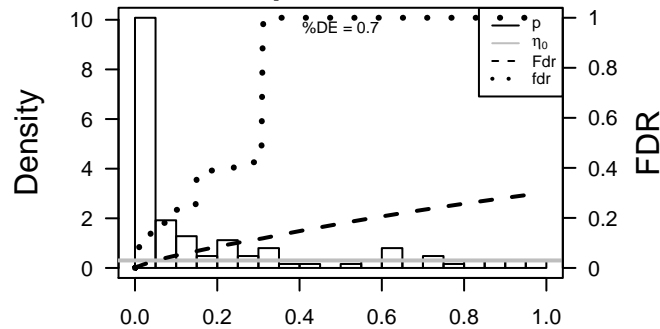
Rank	ID	log(FC)	fdr	p-value	Description
1	3512	-1.45	1e-15	5e-09	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
2	5996	-1.17	1e-10	2e-07	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:10000]
3	57172	-1.05	7e-09	6e-06	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HGNC Symbol;Acc:10000]
4	3543	-0.87	2e-07	6e-06	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:10000]
5	5341	0.93	3e-07	9e-06	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
6	255231	-0.91	5e-07	1e-05	49 x 1 mucopolipin 2 [Source:HGNC Symbol;Acc:13357]
7	9806	-0.89	9e-07	4e-05	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycan 1
8	54855	-0.85	3e-06	4e-05	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:10000]
9	341	0.85	3e-06	2e-04	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
10	6363	-0.81	9e-06	3e-04	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:10000]
11	51755	-0.77	2e-05	3e-04	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242]
12	930	-0.76	3e-05	3e-04	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
13	3113	-0.75	4e-05	3e-04	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:10000]
14	241	0.74	5e-05	3e-04	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:10000]
15	3128	-0.74	5e-05	5e-04	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo)
16	3820	-0.72	7e-05	5e-04	50 x 1 killer cell lectin-like receptor subfamily B, member 1 [Source:HGNC Symbol;Acc:10000]
17	25849	-0.71	1e-04	5e-04	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HGNC Symbol;Acc:10000]
18	81704	-0.7	1e-04	5e-04	50 x 1 dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:19191]
19	9404	-0.7	1e-04	5e-04	50 x 1 leupaxin [Source:HGNC Symbol;Acc:14061]
20	3702	-0.7	1e-04	5e-04	49 x 1 IL2-inducible T-cell kinase [Source:HGNC Symbol;Acc:6171]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-31.79	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
2	-27.23	NULL	10 / 15	CC MHC class II protein complex
3	-17.58	NULL	5 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
4	-17.58	NULL	5 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
5	-15.39	NULL	54 / 417	H.Tiss WIRTH_Immune system
6	-15.29	NULL	3 / 16	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
7	-15.01	NULL	3 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
8	-14.64	NULL	10 / 47	BP antigen processing and presentation
9	-14.57	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
10	-14.29	NULL	6 / 21	CC clathrin-coated endocytic vesicle membrane
11	-14.15	NULL	31 / 312	BP immune response
12	-14.02	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
13	-13.6	NULL	6 / 23	CC integral to luminal side of endoplasmic reticulum membrane
14	-13.18	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
15	-13.14	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
16	-12.78	NULL	1 / 2	GSEA C2GUTIERREZ_MULTIPLE_MYELOMA_UP
17	-12.66	NULL	7 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
18	-12.42	NULL	3 / 12	GSEA C2BIOCARTA_CTLA4_PATHWAY
19	-12.2	NULL	6 / 28	CC transport vesicle membrane
20	-12.15	NULL	4 / 13	Cancer GENTLES_modul18
21	-12.03	NULL	50 / 553	Cancer Lembecke_Colonc Inflammation
22	-11.34	NULL	3 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
23	-11.34	NULL	6 / 32	CC ER to Golgi transport vesicle membrane
24	-11.32	NULL	3 / 10	BP negative thymic T cell selection
25	-11.18	NULL	11 / 60	BP T cell costimulation
26	-11.14	NULL	1 / 11	GSEA C2GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
27	-10.94	NULL	3 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
28	-10.93	NULL	3 / 14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
29	-10.86	NULL	2 / 8	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
30	-10.79	NULL	6 / 35	CC trans-Golgi network membrane
31	-10.79	NULL	2 / 13	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_DN
32	-10.54	NULL	9 / 84	BP T cell receptor signaling pathway
33	-10.49	NULL	3 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
34	-10.49	NULL	3 / 14	GSEA C2BIOCARTA_STATHMIN_PATHWAY
35	-10.3	NULL	3 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
36	-10.3	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
37	-10.21	NULL	1 / 6	H.Tiss WIRTH_Bone marrow
38	-10.14	NULL	1 / 13	GSEA C2LEE_INTRATHYMIC_T_PROGENITOR
39	-9.69	NULL	2 / 5	GSEA C2WEST_ADRENOCHROMAL_CARCINOMA_VS_ADENOMA_DN
40	-9.55	NULL	2 / 7	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G5_DN

p-values



GW_207

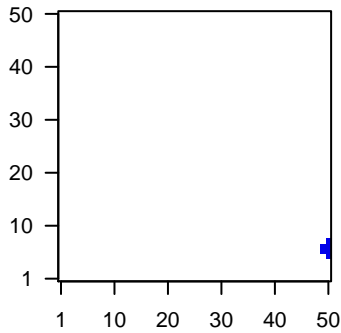
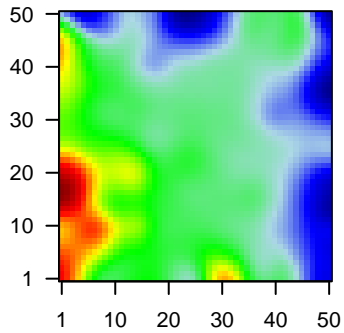
Local Summary

%DE = 0.68
 # metagenes = 6
 # genes = 114
 # genes in genesets = 114
 # genes with fdr < 0.1 = 49 (10 + / 39 -)
 # genes with fdr < 0.05 = 38 (9 + / 29 -)
 # genes with fdr < 0.01 = 19 (3 + / 16 -)

<r> metagenes = 0.97
 <r> genes = 0.4
 <FC> = -0.22
 <shrinkage-t> = -7.55
 <p-value> = 0.02
 <fdr> = 0.66

Profile

Spot



Local Genelist

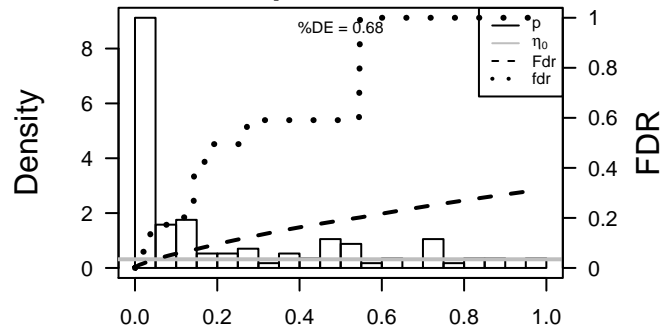
Rank	ID	log(FC)	fdr	p-value	Description
1	1359	-1.31	6e-13	2e-09	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:...
2	7832	-1.19	5e-11	4e-07	49 x 6 BTG family, member 2 [Source:HGNC Symbol;Acc:1131]
3	79901	-1.04	1e-08	3e-05	50 x 7 cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797]
4	7177	-0.9	7e-07	3e-04	50 x 7 tryptase alpha/beta 1 [Source:HGNC Symbol;Acc:12019]
5	51176	-0.78	2e-05	3e-04	50 x 5 lymphoid enhancer-binding factor 1 [Source:HGNC Symbol;A...
6	64499	-0.77	2e-05	3e-04	50 x 7 tryptase beta 2 (gene/pseudogene) [Source:HGNC Symbol;A...
7	7450	0.76	3e-05	2e-03	50 x 6 von Willebrand factor [Source:HGNC Symbol;Acc:12726]
8	30061	-0.7	1e-04	2e-03	50 x 5 solute carrier family 40 (iron-regulated transporter), member
9	2532	-0.69	2e-04	2e-03	50 x 5 Duffy blood group, atypical chemokine receptor [Source:HGNC...
10	1363	-0.68	2e-04	2e-03	50 x 7 carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
11	90865	-0.67	2e-04	2e-03	50 x 7 interleukin 33 [Source:HGNC Symbol;Acc:16028]
12	23136	-0.65	3e-04	2e-03	50 x 8 erythrocyte membrane protein band 4.1-like 3 [Source:HGNC...
13	7122	0.65	4e-04	2e-03	50 x 6 claudin 5 [Source:HGNC Symbol;Acc:2047]
14	6867	-0.65	4e-04	2e-03	50 x 6 transforming, acidic coiled-coil containing protein 1 [Source:HGNC...
15	8404	-0.64	4e-04	5e-03	50 x 6 SPARC-like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
16	641700	0.62	7e-04	5e-03	50 x 6 endothelial cell surface expressed chemotaxis and apoptosis
17	3815	-0.6	1e-03	5e-03	50 x 7 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hom
18	399959	-0.59	1e-03	5e-03	50 x 6
19	56892	-0.59	1e-03	5e-03	50 x 7 chromosome 8 open reading frame 4 [Source:HGNC Symbol...
20	347	-0.59	1e-03	3e-02	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.76	NULL	3 / 7	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
2	-18.17	NULL	3 / 12	BP dentate gyrus development
3	-16.73	NULL	1 / 5	GSEA C2DONATO_CELL_CYCLE_TRETINOIN
4	-16.37	NULL	2 / 10	BP angiotensin maturation
5	-15.16	NULL	1 / 7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
6	-14.6	NULL	3 / 17	MF metalloproteinase activity
7	-14.17	NULL	2 / 13	GSEA C2KEGG_RENIN_ANGIOTENSIN_SYSTEM
8	-14.16	NULL	2 / 17	MF carboxypeptidase activity
9	-14.06	NULL	1 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
10	-13.82	NULL	1 / 7	GSEA C2GENTILE_UV_LOW_DOSE_DN
11	-13.82	NULL	1 / 7	GSEA C2GENTILE_UV_LOW_DOSE_UP
12	-13.17	NULL	1 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
13	-13.16	NULL	2 / 15	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO...
14	-12.84	NULL	3 / 14	BP regulation of Wnt signaling pathway
15	-12.26	NULL	2 / 16	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP
16	-12.01	NULL	3 / 10	BP germ cell migration
17	-12	NULL	1 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP
18	-11.81	NULL	2 / 15	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
19	-11.44	NULL	2 / 12	GSEA C2EHRlich_ICF_SYNDROM_DN
20	-11.32	NULL	1 / 10	GSEA C2BASSO_CD40_SIGNALING_DN
21	-11.22	NULL	3 / 16	GSEA C2CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
22	-10.84	NULL	2 / 13	H.Tiss WIRTH_Sec_lymphoid_organ
23	-10.73	NULL	1 / 11	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
24	-10.73	NULL	1 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
25	-10.68	NULL	2 / 12	miRNA target set 205
26	-10.62	NULL	2 / 12	GSEA C2SHI_SPARC_TARGETS_DN
27	-10.45	NULL	2 / 10	MF armadillo repeat domain binding
28	-9.82	NULL	1 / 10	BP response to iron ion
29	-9.78	NULL	1 / 13	BP response to electrical stimulus
30	-9.78	NULL	1 / 13	GSEA C2KANNAN_TP53_TARGETS_UP
31	-9.76	NULL	4 / 19	BP positive regulation of epithelial to mesenchymal transition
32	-9.57	NULL	1 / 16	GSEA C2L1_PROSTATE_CANCER_EPIGENETIC
33	-9.57	NULL	1 / 5	miRNA target set 205
34	-9.56	NULL	2 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
35	-9.39	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT...
36	-9.39	NULL	1 / 14	GSEA C2WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
37	-9.39	NULL	1 / 14	GSEA C2VANTVEER_BREAST_CANCER_METASTASIS_UP
38	-9.39	NULL	1 / 14	GSEA C2TAVOR_CEBPA_TARGETS_UP
39	-9.39	NULL	1 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
40	-9.39	NULL	1 / 14	GSEA C2BONCI_TARGETS_OF_MIR15A_AND_MIR16_1

p-values



GW_207

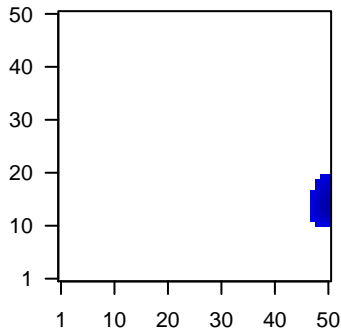
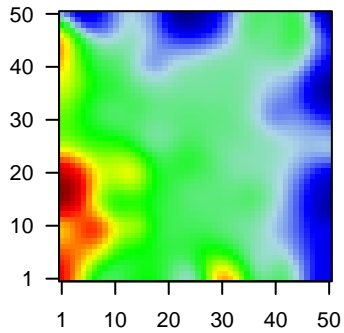
Local Summary

%DE = 0.58
 # metagenes = 35
 # genes = 373
 # genes in genesets = 369
 # genes with $fdr < 0.1$ = 86 (6 + / 80 -)
 # genes with $fdr < 0.05$ = 82 (6 + / 76 -)
 # genes with $fdr < 0.01$ = 48 (2 + / 46 -)

$\langle r \rangle$ metagenes = 0.89
 $\langle r \rangle$ genes = 0.26
 $\langle FC \rangle = -0.26$
 $\langle \text{shrinkage-t} \rangle = -9.11$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.72$

Profile

Spot



Local Genelist

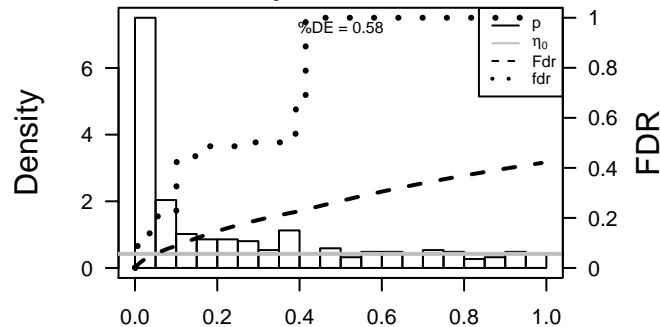
Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	343990	-1.33	2e-13	3e-08	50 x 12 KIAA1211-like [Source:HGNC Symbol;Acc:33454]
2	26751	-1.16	2e-10	2e-07	49 x 13 SH3 and SYLF domain containing 1 [Source:HGNC Symbol;Acc:33454]
3	10232	-1.1	1e-09	2e-07	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
4	57556	1.08	3e-09	4e-06	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic
5	55268	-1	4e-08	4e-06	50 x 14 enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:31696]
6	26018	-0.99	5e-08	2e-05	50 x 16 leucine-rich repeats and immunoglobulin-like domains 1 [Source:HGNC Symbol;Acc:31696]
7	494470	-0.93	4e-07	2e-05	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
8	2205	-0.92	5e-07	2e-05	50 x 13 Fc fragment of IgE, high affinity I, receptor for; alpha polypept
9	4774	-0.91	5e-07	4e-05	50 x 13 nuclear factor I/A [Source:HGNC Symbol;Acc:7784]
10	10439	-0.9	8e-07	2e-04	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
11	1776	-0.86	2e-06	5e-04	48 x 12 deoxyribonuclease I-like 3 [Source:HGNC Symbol;Acc:2959]
12	135112	-0.8	1e-05	5e-04	50 x 13 nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21696]
13	57035	-0.79	1e-05	5e-04	49 x 19 chromosome 1 open reading frame 63 [Source:HGNC Symbol;Acc:21696]
14	2053	-0.79	1e-05	5e-04	50 x 14 epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc:21696]
15	84159	-0.79	1e-05	5e-04	50 x 17 AT rich interactive domain 5B (MRF1-like) [Source:HGNC Symbol;Acc:21696]
16	10020	-0.78	2e-05	5e-04	49 x 11 glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosaminidase 1 [Source:HGNC Symbol;Acc:21696]
17	29116	-0.77	2e-05	7e-04	50 x 14 myosin regulatory light chain interacting protein [Source:HGNC Symbol;Acc:21696]
18	5860	-0.75	3e-05	7e-04	48 x 17 quinoid dihydropteridine reductase [Source:HGNC Symbol;Acc:21696]
19	694	-0.69	4e-05	7e-04	50 x 18 B-cell translocation gene 1, anti-proliferative [Source:HGNC Symbol;Acc:21696]
20	7155	-0.75	4e-05	7e-04	50 x 15 topoisomerase (DNA) II beta 180kDa [Source:HGNC Symbol;Acc:21696]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.29	NULL	3 / 10	BP epoxygenase P450 pathway
2	-9.3	NULL	1 / 3	miRNA target-223
3	-8.67	NULL	1 / 4	GSEA C2NICK_RESPONSE_TO_PROC_TREATMENT_UP
4	-8.49	NULL	2 / 16	GSEA C2HATADA_METHYLATED_IN_LUNG_CANCER_UP
5	-8.15	NULL	3 / 11	BP DNA integration
6	-8.13	NULL	2 / 6	GSEA C2KAPOLI_LIVER_CANCER_POOR_SURVIVAL_DN
7	-8.07	NULL	6 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
8	-7.99	NULL	5 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	-7.9	NULL	3 / 16	GSEA C2ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR
10	-7.62	NULL	1 / 3	GSEA C2MYLYKANGAS_AMPLIFICATION_HOT_SPOT_30
11	-7.39	NULL	2 / 10	GSEA C2YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
12	-7.37	NULL	3 / 14	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G12_DN
13	-6.97	NULL	2 / 11	MF enhancer sequence-specific DNA binding
14	-6.91	NULL	4 / 21	BP drug metabolic process
15	-6.43	NULL	1 / 9	GSEA C2HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP
16	-6.36	NULL	4 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
17	-6.33	NULL	2 / 21	BP pancreas development
18	-6.32	NULL	3 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
19	-6.31	NULL	1 / 6	GSEA C2KAUFFMANN_MELANOMA_RELAPSE_DN
20	-6.14	NULL	2 / 15	GSEA C2CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS
21	-6.01	NULL	2 / 16	GSEA C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
22	-6	NULL	2 / 16	GSEA C2MANN_RESPONSE_TO_AMIFOSTINE_UP
23	-5.99	NULL	2 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
24	-5.99	NULL	2 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
25	-5.98	NULL	2 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
26	-5.9	NULL	2 / 16	GSEA C2BROWNE_HCMV_INFECTION_24HR_UP
27	-5.86	NULL	2 / 15	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
28	-5.84	NULL	2 / 12	MF NAD+ binding
29	-5.82	NULL	6 / 48	BP negative regulation of neuron differentiation
30	-5.81	NULL	1 / 7	GSEA C2TOMKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
31	-5.74	NULL	2 / 11	GSEA C2BIOCARTA_ETC_PATHWAY
32	-5.72	NULL	5 / 32	miRNA target-510
33	-5.69	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
34	-5.68	NULL	3 / 18	MF aromatase activity
35	-5.64	NULL	3 / 15	GSEA C2NAKAJIMA_MAST_CELL
36	-5.5	NULL	2 / 10	GSEA C2KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
37	-5.5	NULL	2 / 10	GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION
38	-5.47	NULL	3 / 16	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G1_UP
39	-5.43	NULL	3 / 15	GSEA C2DOANE_BREAST_CANCER_CLASSES_UP
40	-5.43	NULL	3 / 16	GSEA C2BILBAN_B_CLL_LPL_DN

p-values



GW_207

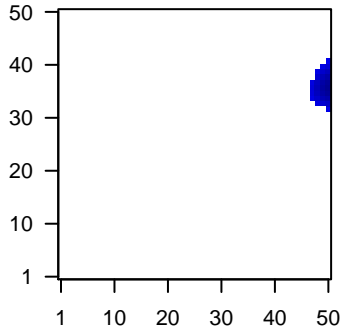
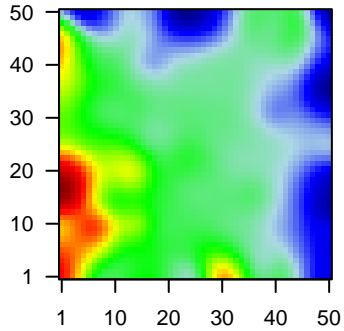
Local Summary

%DE = 0.68
 # metagenes = 29
 # genes = 409
 # genes in genesets = 408
 # genes with $fdr < 0.1 = 134$ (4 + / 130 -)
 # genes with $fdr < 0.05 = 92$ (3 + / 89 -)
 # genes with $fdr < 0.01 = 17$ (2 + / 15 -)

$\langle r \rangle$ metagenes = 0.92
 $\langle r \rangle$ genes = 0.25
 $\langle FC \rangle = -0.28$
 $\langle \text{shrinkage-t} \rangle = -9.71$
 $\langle p\text{-value} \rangle = 0.06$
 $\langle fdr \rangle = 0.75$

Profile

Spot



Local Genelist

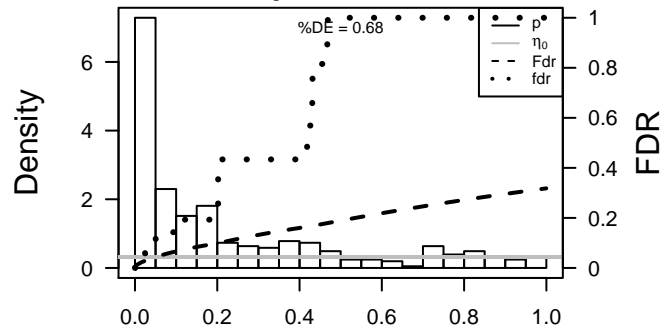
Rank	ID	log(FC)	fdr	p-value	Description
1	7763	-0.98	5e-08	5e-05	50 x 36 zinc finger, AN1-type domain 5 [Source:HGNC Symbol;Acc:1
2	9908	-0.92	4e-07	1e-04	50 x 36 GTPase activating protein (SH3 domain) binding protein 2 [Sc
3	4942	-0.88	1e-06	1e-03	50 x 35 ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
4	55556	-0.77	2e-05	1e-03	50 x 37 enolase superfamily member 1 [Source:HGNC Symbol;Acc:3
5	9284	-0.76	3e-05	1e-03	50 x 40 nuclear pore complex interacting protein family, member A1 [S
6	1953	-0.74	4e-05	1e-03	50 x 41 multiple EGF-like-domains 6 [Source:HGNC Symbol;Acc:32
7	3181	-0.74	5e-05	1e-03	49 x 39 heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HG
8	10159	-0.73	5e-05	1e-03	50 x 36 ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
9	10099	-0.73	6e-05	1e-03	50 x 37 tetraspanin 3 [Source:HGNC Symbol;Acc:17752]
10	5311	-0.73	6e-05	1e-03	50 x 38 polycystic kidney disease 2 (autosomal dominant) [Source:HK
11	27031	-0.72	7e-05	3e-03	50 x 38 nephronophthisis 3 (adolescent) [Source:HGNC Symbol;Acc:
12	167153	-0.71	1e-04	3e-03	50 x 34 PAP associated domain containing 4 [Source:HGNC Symbol;
13	9512	0.7	1e-04	3e-03	50 x 38 peptidase (mitochondrial processing) beta [Source:HGNC Sy
14	23505	-0.69	2e-04	3e-03	50 x 37 transmembrane protein 131 [Source:HGNC Symbol;Acc:3036
15	1429	0.69	2e-04	4e-03	50 x 34 crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
16	6146	-0.68	2e-04	6e-03	50 x 34 ribosomal protein L22 [Source:HGNC Symbol;Acc:10315]
17	57092	-0.66	3e-04	6e-03	50 x 35 PEST proteolytic signal containing nuclear protein [Source:HK
18	7844	-0.66	3e-04	1e-02	50 x 37 RNF103-CHMP3 readthrough [Source:HGNC Symbol;Acc:38
19	5934	-0.62	6e-04	1e-02	50 x 36 retinoblastoma-like 2 (p130) [Source:HGNC Symbol;Acc:989
20	10015	-0.62	7e-04	1e-02	50 x 34 programmed cell death 6 interacting protein [Source:HGNC S

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.64	NULL	1 / 2	miRNA target-miR-98
2	-10.04	NULL	37 / 433	miRNA target-miR-319b
3	-9.5	NULL	15 / 100	miRNA target-miR-354d
4	-9.06	NULL	20 / 171	miRNA target-miR-3669-3p
5	-8.47	NULL	26 / 271	miRNA target-miR-319d
6	-8.39	NULL	35 / 440	miRNA target-miR-319e
7	-8.37	NULL	13 / 89	miRNA target-miR-595
8	-8.33	NULL	19 / 180	miRNA target-miR-374a
9	-8.12	NULL	9 / 47	miRNA target-miR-392*
10	-8.05	NULL	37 / 463	miRNA target-miR-391a
11	-7.98	NULL	1 / 4	miRNA target-miR-7c
12	-7.98	NULL	1 / 4	miRNA target-miR-7g
13	-7.96	NULL	11 / 80	miRNA target-miR-390a*
14	-7.91	NULL	15 / 146	miRNA target-miR-992
15	-7.91	NULL	6 / 46	miRNA target-miR-399
16	-7.89	NULL	9 / 49	miRNA target-miR-154-487
17	-7.82	NULL	23 / 215	miRNA target-miR-393
18	-7.73	NULL	1 / 3	miRNA target-miR-197
19	-7.67	NULL	36 / 421	miRNA target-miR-295e
20	-7.6	NULL	9 / 63	miRNA target-miR-896
21	-7.56	NULL	26 / 303	miRNA target-miR-392b
22	-7.56	NULL	21 / 186	miRNA target-miR-392
23	-7.52	NULL	25 / 325	miRNA target-miR-392d
24	-7.48	NULL	21 / 189	miRNA target-miR-4283
25	-7.44	NULL	20 / 172	miRNA target-miR-897
26	-7.39	NULL	9 / 58	miRNA target-miR-155-5p
27	-7.37	NULL	7 / 48	miRNA target-miR-298b
28	-7.28	NULL	8 / 50	miRNA target-miR-508
29	-7.19	NULL	9 / 51	miRNA target-miR-556-3p
30	-7.18	NULL	25 / 300	miRNA target-miR-561
31	-7.13	NULL	19 / 153	miRNA target-miR-450b-5p
32	-7.08	NULL	17 / 121	miRNA target-miR-543
33	-7.07	NULL	25 / 311	miRNA target-miR-392c
34	-7.06	NULL	21 / 229	miRNA target-miR-590g
35	-7.05	NULL	5 / 33	miRNA target-miR-147b
36	-7.03	NULL	26 / 321	miRNA target-miR-295e
37	-7.01	NULL	33 / 412	miRNA target-miR-397
38	-6.98	NULL	13 / 169	miRNA target-miR-374b
39	-6.95	NULL	13 / 122	miRNA target-miR-149b
40	-6.92	NULL	20 / 163	BP mRNA splicing, via spliceosome

p-values



GW_207

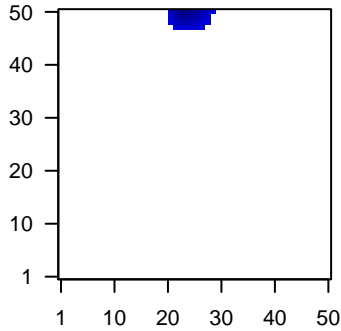
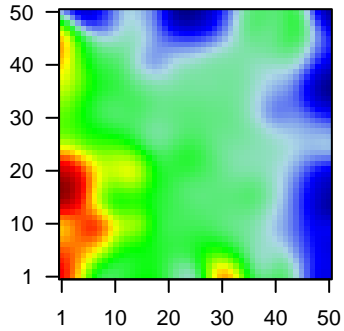
Local Summary

%DE = 0.61
 # metagenes = 31
 # genes = 407
 # genes in genesets = 401
 # genes with $fdr < 0.1 = 105$ (1 + / 104 -)
 # genes with $fdr < 0.05 = 49$ (1 + / 48 -)
 # genes with $fdr < 0.01 = 32$ (1 + / 31 -)

<r> metagenes = 0.93
 <r> genes = 0.27
 <FC> = -0.29
 <shrinkage-t> = -10.14
 <p-value> = 0.04
 <fdr> = 0.77

Profile

Spot



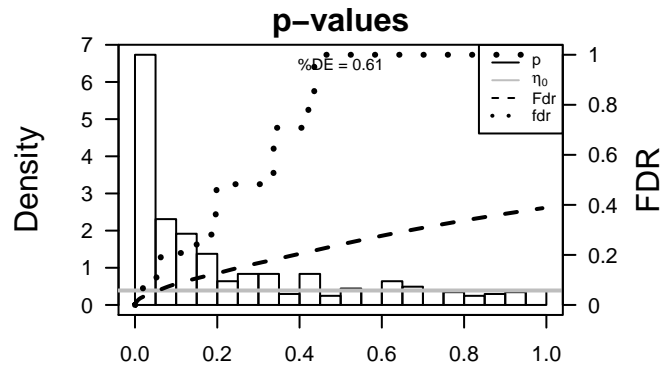
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	1843	-1.61	2e-16	1e-14	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30
2	2353	-1.74	2e-16	1e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:l
3	2354	-2.15	2e-16	1e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source
4	1958	-1.31	7e-13	1e-08	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
5	5573	-1.18	9e-11	4e-08	24 x 50 protein kinase, cAMP-dependent, regulatory, type I, alpha [S
6	3725	-1.14	4e-10	1e-07	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
7	100008589	-1.11	1e-09	2e-05	23 x 50 RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
8	467	-0.97	1e-07	4e-04	22 x 50 activating transcription factor 3 [Source:HGNC Symbol;Acc:71
9	1997	-0.82	6e-06	4e-04	24 x 49 E74-like factor 1 (ets domain transcription factor) [Source:HC
10	653566	-0.79	1e-05	4e-04	28 x 49
11	8553	-0.72	2e-05	4e-04	22 x 50 basic helix-loop-helix family, member e40 [Source:HGNC Sy
12	2117	-0.79	2e-05	4e-04	22 x 50 ets variant 3 [Source:HGNC Symbol;Acc:3492]
13	220869	-0.78	2e-05	4e-04	29 x 50 COBW domain containing 1 [Source:HGNC Symbol;Acc:171:
14	57162	-0.78	2e-05	4e-04	23 x 50 pellino E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;A
15	23353	-0.77	2e-05	4e-04	24 x 50 Sad1 and UNC84 domain containing 1 [Source:HGNC Symb
16	678	-0.77	2e-05	6e-04	23 x 50 ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:1
17	2970	-0.76	3e-05	3e-03	23 x 50
18	25831	-0.74	5e-05	3e-03	25 x 50 HECT domain containing E3 ubiquitin protein ligase 1 [Source
19	8895	-0.71	9e-05	3e-03	27 x 50 copine III [Source:HGNC Symbol;Acc:2316]
20	9991	0.7	1e-04	3e-03	21 x 50 polypyrimidine tract binding protein 3 [Source:HGNC Symbol;

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-36.41	NULL	6 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	-29.12	NULL	7 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
3	-25.41	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
4	-23.69	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
5	-21.77	NULL	2 / 9	GSEA C2JUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
6	-20.86	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
7	-20.27	NULL	4 / 14	BP response to light stimulus
8	-20.14	NULL	6 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HEL4
9	-20.08	NULL	3 / 12	GSEA C2BIOCARTA_DREAM_PATHWAY
10	-18.35	NULL	4 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
11	-18.26	NULL	5 / 39	BP response to cAMP
12	-17.92	NULL	3 / 15	BP response to corticosterone
13	-17.85	NULL	6 / 16	TF Tissue/AQUERIZAS_Pancreas
14	-17.59	NULL	4 / 30	BP cellular response to hormone stimulus
15	-16.93	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
16	-16.88	NULL	2 / 5	miRNA target-101
17	-16.62	NULL	5 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
18	-16.56	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
19	-16.33	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
20	-16.19	NULL	3 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
21	-16.15	NULL	5 / 39	TF Tissue/AQUERIZAS_Thyroid
22	-15.85	NULL	2 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSC
23	-15.81	NULL	4 / 16	GSEA C2BIOCARTA_ETS_PATHWAY
24	-15.73	NULL	4 / 14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
25	-15.72	NULL	4 / 30	BP cellular response to calcium ion
26	-15.31	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HEL4
27	-14.32	NULL	2 / 8	GSEA C2EMELYANOV_GR_TARGETS_DN
28	-14.28	NULL	1 / 5	GSEA C2TURJANSKI_MAPK11_TARGETS
29	-13.91	NULL	4 / 19	MF R-SMAD binding
30	-13.75	NULL	2 / 13	BP SMAD protein signal transduction
31	-13.64	NULL	3 / 12	GSEA C2BIOCARTA_ARENR2_PATHWAY
32	-13.1	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY
33	-13.1	NULL	3 / 15	GSEA C2BIOCARTA_TPO_PATHWAY
34	-12.91	NULL	3 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
35	-12.65	NULL	3 / 16	GSEA C2BIOCARTA_EPO_PATHWAY
36	-12.65	NULL	3 / 16	GSEA C2BIOCARTA_IGF1_PATHWAY
37	-12.65	NULL	3 / 16	GSEA C2BIOCARTA_GLEEVEC_PATHWAY
38	-12.65	NULL	3 / 16	GSEA C2BIOCARTA_NGF_PATHWAY
39	-12.34	NULL	3 / 15	GSEA C2NGA_TP53_TARGETS
40	-12.27	NULL	2 / 16	GSEA C2BIOCARTA_CARDIACEGF_PATHWAY



GW_207

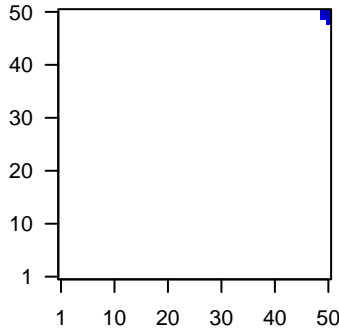
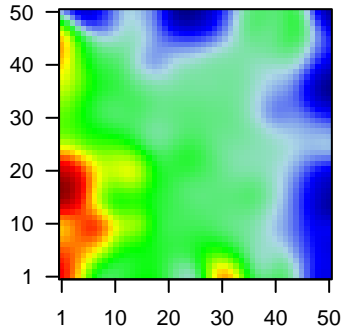
Local Summary

%DE = 0.73
 # metagenes = 5
 # genes = 119
 # genes in genesets = 118
 # genes with $fdr < 0.1$ = 63 (6 + / 57 -)
 # genes with $fdr < 0.05$ = 58 (5 + / 53 -)
 # genes with $fdr < 0.01$ = 37 (2 + / 35 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.31
 $\langle FC \rangle = -0.37$
 $\langle \text{shrinkage-t} \rangle = -13.07$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.54$

Profile

Spot



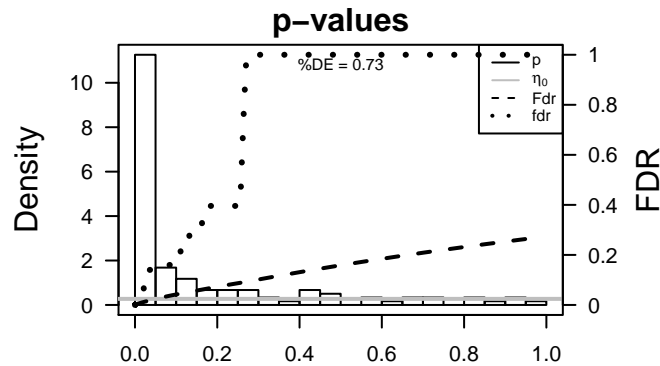
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	57216	-1.54	2e-16	7e-15	50 x 48 VANGL planar cell polarity protein 2 [Source:HGNC Symbol;Acc:26790]
2	256764	1.2	5e-11	2e-09	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
3	4922	-1.18	9e-11	7e-09	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
4	6446	-1.05	3e-10	3e-08	50 x 50 serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym]
5	3866	-1.11	1e-09	4e-08	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
6	154664	-1.08	2e-09	1e-07	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [So]
7	6657	-1.04	1e-08	1e-07	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symb]
8	928	-1.04	1e-08	3e-07	50 x 50 CD9 molecule [Source:HGNC Symbol;Acc:1709]
9	79844	-1.01	2e-08	3e-07	50 x 50 zinc finger, DHHC-type containing 11 [Source:HGNC Symbo]
10	339512	-1.01	3e-08	2e-06	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt]
11	8544	-0.97	8e-08	5e-06	50 x 50 pirin (iron-binding nuclear protein) [Source:HGNC Symbol;Ac
12	11166	-0.94	2e-07	8e-06	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symt]
13	26047	-0.92	5e-07	8e-06	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
14	1056	-0.9	7e-07	8e-06	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
15	3856	-0.89	9e-07	2e-05	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
16	56963	-0.87	2e-06	1e-04	50 x 50 repulsive guidance molecule family member a [Source:HGNC
17	2944	-0.82	7e-06	1e-04	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
18	54800	-0.81	9e-06	1e-04	50 x 48 kelch-like family member 24 [Source:HGNC Symbol;Acc:259
19	120	-0.78	2e-05	1e-04	50 x 50 adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]
20	8745	-0.78	2e-05	1e-04	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-22.36	NULL	3 / 8	GSEA C2JUCDX2_TARGETS_DN
2	-20.18	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	-15.46	NULL	2 / 11	BP planar cell polarity pathway involved in neural tube closure
4	-15.35	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
5	-14.78	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
6	-14.71	NULL	2 / 12	BP Wnt signaling pathway, planar cell polarity pathway
7	-12.97	NULL	3 / 11	MF glutathione binding
8	-12.97	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
9	-11.78	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
10	-11.64	NULL	2 / 13	GSEA C2BROWNE_HCMV_INFECTION_6HR_DN
11	-11.35	NULL	1 / 10	BP somatic stem cell division
12	-11.23	NULL	5 / 20	MF glutathione transferase activity
13	-11.23	NULL	8 / 34	BP glutathione metabolic process
14	-11	NULL	2 / 20	BP cochlea morphogenesis
15	-10.99	NULL	2 / 16	GSEA C2WILCOX_PRESPONSE_TO_ROGESTERONE_UP
16	-10.99	NULL	2 / 16	GSEA C2NAKAYAMA_FRA2_TARGETS
17	-10.89	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
18	-10.31	NULL	6 / 25	BP glutathione derivative biosynthetic process
19	-10.28	NULL	1 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP
20	-10.18	NULL	2 / 16	GSEA C2ENGELMANN_CANCER_PROGENITORS_DN
21	-9.74	NULL	1 / 13	GSEA C2GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP
22	-9.72	NULL	2 / 15	GSEA C2BIOCARTA_ACTININ_PATHWAY
23	-9.56	NULL	2 / 34	BP somatic stem cell maintenance
24	-9.37	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
25	-9.37	NULL	1 / 7	miRNA target-145
26	-9.29	NULL	2 / 16	GSEA C2KEGG_STEROID_BIOSYNTHESIS
27	-9.25	NULL	2 / 20	BP long-term memory
28	-9.07	NULL	2 / 23	BP stem cell differentiation
29	-9.03	NULL	2 / 35	BP hair follicle development
30	-8.97	NULL	1 / 15	BP digestive tract morphogenesis
31	-8.9	NULL	2 / 29	BP positive regulation of JUN kinase activity
32	-8.86	NULL	4 / 15	GSEA C2REACTOME_GLUTATHIONE_CONJUGATION
33	-8.78	NULL	2 / 16	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP
34	-8.65	NULL	1 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
35	-8.65	NULL	1 / 8	miRNA target-450
36	-8.64	NULL	1 / 16	BP post-anal tail morphogenesis
37	-8.51	NULL	3 / 13	BP regulation of blood vessel size
38	-8.39	NULL	1 / 2	miRNA target-127
39	-8.36	NULL	1 / 10	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_DN
40	-8.36	NULL	1 / 10	GSEA C2MOHANKUMAR_TLX1_TARGETS_DN



GW_207

Local Summary

%DE = 0.82
 # metagenes = 2
 # genes = 63
 # genes in genesets = 63
 # genes with fdr < 0.1 = 35 (3 + / 32 -)
 # genes with fdr < 0.05 = 35 (3 + / 32 -)
 # genes with fdr < 0.01 = 18 (2 + / 16 -)

<r> metagenes = 1

<r> genes = 0.41

<FC> = -0.32

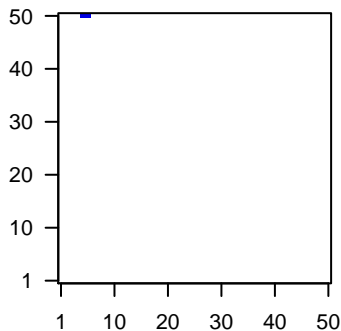
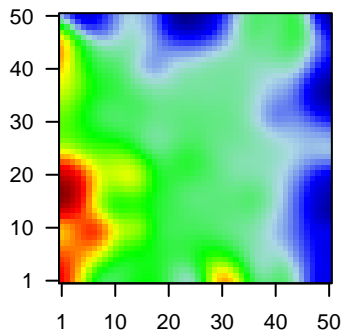
<shrinkage-t> = -11.09

<p-value> = 0.01

<fdr> = 0.64

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	22949	-1.35	1e-13	7e-10	5 x 50 prostaglandin reductase 1 [Source:HGNC Symbol;Acc:18429]
2	26353	-1.19	6e-11	5e-05	5 x 50 heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:3017]
3	5083	-0.83	5e-06	5e-05	5 x 50 paired box 9 [Source:HGNC Symbol;Acc:8623]
4	1571	-0.8	1e-05	5e-05	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Source:HGNC Symbol;Acc:18429]
5	22837	-0.8	1e-05	9e-05	6 x 50 cordon-bleu WH2 repeat protein-like 1 [Source:HGNC Symbol;Acc:18429]
6	51195	-0.78	2e-05	3e-04	5 x 50 Rap guanine nucleotide exchange factor (GEF)-like 1 [Source:HGNC Symbol;Acc:18429]
7	1622	-0.73	5e-05	3e-04	6 x 50 diazepam binding inhibitor (GABA receptor modulator, acyl-CoA oxidase) [Source:HGNC Symbol;Acc:18429]
8	7113	-0.71	9e-05	3e-04	5 x 50 transmembrane protease, serine 2 [Source:HGNC Symbol;Acc:18429]
9	58528	-0.71	1e-04	5e-04	6 x 50 Ras-related GTP binding D [Source:HGNC Symbol;Acc:1990]
10	23593	-0.69	1e-04	2e-03	6 x 50 heme binding protein 2 [Source:HGNC Symbol;Acc:15716]
11	10974	0.65	4e-04	2e-03	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:249]
12	26578	-0.64	5e-04	2e-03	6 x 50 osteoclast stimulating factor 1 [Source:HGNC Symbol;Acc:85]
13	1999	-0.62	7e-04	2e-03	5 x 50 E74-like factor 3 (ets domain transcription factor, epithelial-specific) [Source:HGNC Symbol;Acc:18429]
14	57579	-0.6	9e-04	2e-03	5 x 50 family with sequence similarity 135, member A [Source:HGNC Symbol;Acc:18429]
15	10161	-0.59	1e-03	8e-03	6 x 50 lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:18429]
16	1366	0.57	2e-03	8e-03	6 x 50 claudin 7 [Source:HGNC Symbol;Acc:2049]
17	57447	-0.55	2e-03	9e-03	5 x 50 NDRG family member 2 [Source:HGNC Symbol;Acc:14460]
18	6338	-0.54	3e-03	9e-03	5 x 50 sodium channel, non-voltage-gated 1, beta subunit [Source:HGNC Symbol;Acc:18429]
19	148741	-0.52	4e-03	4e-02	5 x 50 ankyrin repeat domain 35 [Source:HGNC Symbol;Acc:26323]
20	79007	0.46	1e-02	4e-02	6 x 50 dysbindin (dystrobrein binding protein 1) domain containing

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.42	NULL	1 / 10	GSEA C2TSUDA_ALVEOLAR_SOFT_PART_SARCOMA
2	-14.33	NULL	2 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
3	-13.44	NULL	1 / 14	BP cyclooxygenase pathway
4	-12.92	NULL	1 / 15	BP leukotriene metabolic process
5	-12.24	NULL	2 / 16	GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP
6	-11.84	NULL	2 / 12	Pathw AcBENTINK_e2f3.1
7	-11.39	NULL	1 / 15	GSEA C2WILLIAMS_ESR1_TARGETS_UP
8	-11.39	NULL	1 / 15	GSEA C2E_SKI_TARGETS_UP
9	-11.33	NULL	3 / 21	BP drug metabolic process
10	-11.05	NULL	1 / 8	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP
11	-10.97	NULL	1 / 16	GSEA C2RUGO_RESPONSE_TO_4NQO
12	-10.97	NULL	1 / 16	GSEA C2KYNG_DNA_DAMAGE_BY_4NQO
13	-10.76	NULL	2 / 11	GSEA C2KEGG_ARACHIDONIC_ACID_METABOLISM
14	-10.29	NULL	1 / 9	GSEA C2EE_LIVER_CANCER
15	-10.29	NULL	1 / 9	GSEA C2EE_LIVER_CANCER_TOP50
16	-10.29	NULL	1 / 9	GSEA C2BROWNE_HCMV_INFECTION_18HR_UP
17	-10.29	NULL	1 / 9	GSEA C2BIOCARTA_NUCLEAR_PATHWAY
18	-10.29	NULL	1 / 9	GSEA C2REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE
19	-10.29	NULL	1 / 9	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUNDS
20	-10.12	NULL	1 / 8	LymphomaBASCQUE_GCB_UP
21	-9.78	NULL	2 / 31	BP triglyceride metabolic process
22	-9.59	NULL	1 / 10	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G23_DN
23	-9.13	NULL	1 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
24	-9.13	NULL	1 / 11	GSEA C2REACTOME_BIOLOGICAL_OXIDATIONS
25	-9.13	NULL	1 / 11	GSEA C2REACTOME_XENOBIOTICS
26	-8.68	NULL	1 / 12	GSEA C2EE_LIVER_CANCER_E2F1_DN
27	-8.68	NULL	1 / 12	GSEA C2SIAO_LIVER_SPECIFIC_GENES
28	-8.68	NULL	1 / 12	GSEA C2VERHAAK_AML_WITH_NPM1_MUTATED_DN
29	-8.68	NULL	1 / 12	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP
30	-8.68	NULL	1 / 12	GSEA C2SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
31	-8.68	NULL	1 / 12	GSEA C2YAGI_AML_WITH_T_9_11_TRANSLOCATION
32	-8.68	NULL	1 / 12	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION
33	-8.53	NULL	2 / 49	BP arachidonic acid metabolic process
34	-8.5	NULL	1 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
35	-8.28	NULL	1 / 13	GSEA C2EE_LIVER_CANCER_CIPROFIBRATE_DN
36	-8.28	NULL	1 / 13	GSEA C2EE_LIVER_CANCER_MYC_E2F1_DN
37	-8.28	NULL	1 / 13	GSEA C2EE_LIVER_CANCER_DENA_DN
38	-8.28	NULL	1 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
39	-8.17	NULL	3 / 30	BP excretion
40	-8.02	NULL	1 / 13	miRNA 3063-517A--517C

