

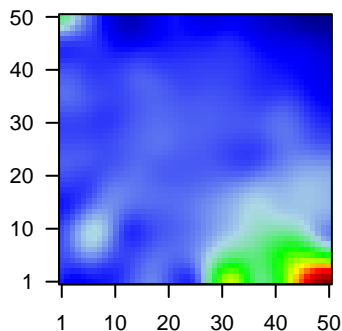
GW_061

Global Summary

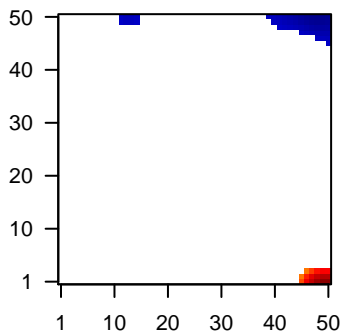
%DE = 0.15
 # genes with fdr < 0.2 = 1723 (1064 + / 659 -)
 # genes with fdr < 0.1 = 1506 (958 + / 548 -)
 # genes with fdr < 0.05 = 1186 (796 + / 390 -)
 # genes with fdr < 0.01 = 849 (598 + / 251 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.09
 <fdr> = 0.85

Profile



Regulated Spots



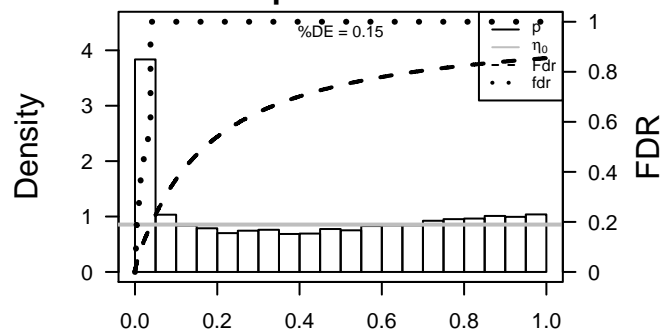
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	9744	1.3	2e-16 2e-14	49 x 1 ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [S
2	218	1.22	2e-16 2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	55107	-1.39	2e-16 2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
4	341	1.23	2e-16 2e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
5	348	1.53	2e-16 2e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
6	80833	1.22	2e-16 2e-14	47 x 1 apolipoprotein L, 3 [Source:HGNC Symbol;Acc:14868]
7	393	1.35	2e-16 2e-14	49 x 1 Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
8	25805	-1.39	2e-16 2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
9	684	1.52	2e-16 2e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	713	1.51	2e-16 2e-14	50 x 1 complement component 1, q subcomponent, B chain [Source
11	260436	3.19	2e-16 2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
12	768	1.24	2e-16 2e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
13	6363	2.15	2e-16 2e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
14	6366	1.72	2e-16 2e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
15	9560	1.46	2e-16 2e-14	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
16	6352	1.49	2e-16 2e-14	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
17	1236	1.88	2e-16 2e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
18	930	2.01	2e-16 2e-14	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
19	914	1.58	2e-16 2e-14	49 x 1 CD2 molecule [Source:HGNC Symbol;Acc:1639]
20	919	1.47	2e-16 2e-14	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	24.69	NULL	417	H.Tiss WIRTH_Immune system
2	23.06	NULL	553	Cancer Lembecke_Colonc Inflammation
3	21.21	NULL	312	BP immune response
4	20.42	NULL	15	CC MHC class II protein complex
5	16.52	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
6	16.46	NULL	47	BP antigen processing and presentation
7	16.14	NULL	60	BP T cell costimulation
8	15.64	NULL	60	BP interferon-gamma-mediated signaling pathway
9	15.21	NULL	51	BP type I interferon signaling pathway
10	15.05	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
11	14.97	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	14.16	NULL	204	BP cytokine-mediated signaling pathway
13	13.68	NULL	32	CC ER to Golgi transport vesicle membrane
14	13.2	NULL	74	BP regulation of immune response
15	13.04	NULL	21	CC clathrin-coated endocytic vesicle membrane
16	12.87	NULL	162	CC external side of plasma membrane
17	12.79	NULL	123	BP defense response to virus
18	12.56	NULL	316	Cancer SPANG_BCL6-index2
19	12.43	NULL	572	Disease GUDJ_poriasis up
20	12.22	NULL	84	BP T cell receptor signaling pathway
<i>Underexpressed</i>				
1	-9.55	NULL	12	miRNA target miR-29c
2	-9.18	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
3	-8.89	NULL	7	MMML C6SCIEJ_MMML 5
4	-8.68	NULL	11	MF platelet-derived growth factor binding
5	-7.1	NULL	57	MF extracellular matrix structural constituent
6	-6.92	NULL	1033	Chr Chr 2
7	-6.88	NULL	37	BP collagen fibril organization
8	-6.78	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
9	-6.54	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
10	-6.54	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
11	-6.52	NULL	15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
12	-6.51	NULL	40	BP cellular response to amino acid stimulus
13	-6.39	NULL	34	Chr Chr Y
14	-6.08	NULL	4	MMML C6SCIEJ_MMML 23
15	-6	NULL	436	miRNA target miR-34a
16	-5.92	NULL	20	Lymphoma BOSOLOWSKI_red UP
17	-5.68	NULL	242	BP extracellular matrix organization
18	-5.67	NULL	190	CC extracellular matrix
19	-5.59	NULL	341	miRNA target miR-34a
20	-5.52	NULL	321	miRNA target miR-52a-5p

p-values



GW_061

Local Summary

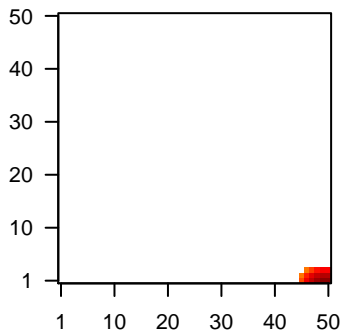
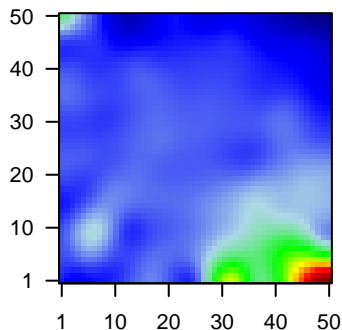
%DE = 0.98
 # metagenes = 17
 # genes = 278
 # genes in genesets = 275

genes with $fdr < 0.1$ = 266 (263 + / 3 -)
 # genes with $fdr < 0.05$ = 266 (263 + / 3 -)
 # genes with $fdr < 0.01$ = 263 (260 + / 3 -)

<r> metagenes = 0.99
 <r> genes = 0.6
 <FC> = 0.92
 <shrinkage-t> = 32.23
 <p-value> = 0
 <fdr> = 0.06

Profile

Spot



Local Genelist

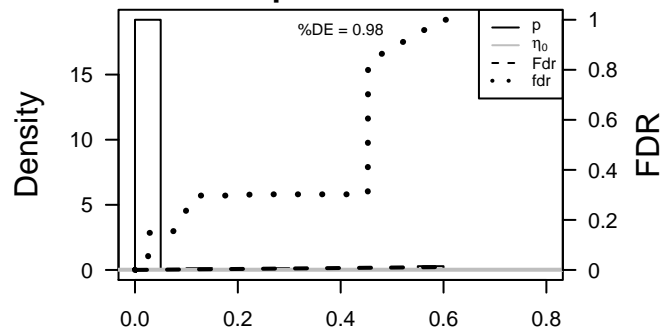
Rank	ID	log(FC)	fdr	p-value	Description
1	9744	1.3	2e-16	1e-17	49 x 1 ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [S
2	341	1.23	2e-16	1e-17	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
3	348	1.53	2e-16	1e-17	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
4	80833	1.22	2e-16	1e-17	47 x 1 apolipoprotein L, 3 [Source:HGNC Symbol;Acc:14868]
5	393	1.35	2e-16	1e-17	49 x 1 Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
6	713	1.51	2e-16	1e-17	50 x 1 complement component 1, q subcomponent, B chain [Source
7	260436	3.19	2e-16	1e-17	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
8	6363	2.15	2e-16	1e-17	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:
9	6366	1.72	2e-16	1e-17	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc:
10	6352	1.49	2e-16	1e-17	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
11	1236	1.88	2e-16	1e-17	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
12	930	2.01	2e-16	1e-17	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
13	914	1.58	2e-16	1e-17	49 x 1 CD2 molecule [Source:HGNC Symbol;Acc:1639]
14	919	1.47	2e-16	1e-17	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
15	915	1.66	2e-16	1e-17	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC S
16	962	1.47	2e-16	1e-17	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
17	923	1.46	2e-16	1e-17	49 x 1 CD6 molecule [Source:HGNC Symbol;Acc:1691]
18	969	1.25	2e-16	1e-17	50 x 1 CD69 molecule [Source:HGNC Symbol;Acc:1694]
19	924	1.49	2e-16	1e-17	49 x 1 CD7 molecule [Source:HGNC Symbol;Acc:1695]
20	972	1.58	2e-16	1e-17	50 x 1 CD74 molecule, major histocompatibility complex, class II inv:

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	37.94	NULL	13 / 15	CC MHC class II protein complex
2	33.53	NULL	98 / 417	H.Tiss WIRTH_Immune system
3	30.5	NULL	3 / 3	MMML C63CIEJ_MMML 7
4	27.92	NULL	95 / 553	Cancer Lembcke_Colonc Inflammation
5	24.18	NULL	56 / 312	BP immune response
6	23.62	NULL	18 / 60	BP T cell costimulation
7	22.25	NULL	15 / 47	BP antigen processing and presentation
8	22.1	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
9	21.7	NULL	8 / 21	CC clathrin-coated endocytic vesicle membrane
10	20.62	NULL	8 / 23	CC integral to luminal side of endoplasmic reticulum membrane
11	20.57	NULL	7 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
12	19.88	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
13	19.05	NULL	2 / 4	MMML C63CIEJ_MMML 2
14	18.89	NULL	8 / 13	Cancer GENTLES_modul18
15	18.46	NULL	8 / 28	BP transport vesicle membrane
16	17.91	NULL	5 / 12	BP dendritic cell chemotaxis
17	17.2	NULL	28 / 162	CC external side of plasma membrane
18	17.12	NULL	8 / 32	CC ER to Golgi transport vesicle membrane
19	17.04	NULL	17 / 84	BP T cell receptor signaling pathway
20	16.92	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
21	16.58	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
22	16.3	NULL	5 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
23	16.27	NULL	8 / 35	CC trans-Golgi network membrane
24	16.01	NULL	6 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
25	15.69	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
26	15.65	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
27	15.15	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
28	14.88	NULL	14 / 87	BP antigen processing and presentation of exogenous peptide antigen
29	14.68	NULL	17 / 74	BP regulation of immune response
30	14.65	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
31	14.47	NULL	12 / 60	BP interferon-gamma-mediated signaling pathway
32	14.43	NULL	9 / 52	Chr Chr HSCHR6_MHC_QBL
33	14.21	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
34	14.05	NULL	6 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
35	13.98	NULL	40 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
36	13.98	NULL	40 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
37	13.98	NULL	40 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
38	13.98	NULL	40 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
39	13.91	NULL	8 / 46	CC endocytic vesicle membrane
40	13.74	NULL	3 / 9	GSEA C2MILIC_FAMILIAL_ADENOMATOUS_POLYPOSIIS_DN

p-values



GW_061

Local Summary

%DE = 0.71
 # metagenes = 43
 # genes = 638
 # genes in genesets = 633
 # genes with $fdr < 0.1 = 282$ (8 + / 274 -)
 # genes with $fdr < 0.05 = 229$ (6 + / 223 -)
 # genes with $fdr < 0.01 = 111$ (4 + / 107 -)

$\langle r \rangle$ metagenes = 0.82

$\langle r \rangle$ genes = 0.25

$\langle FC \rangle = -0.26$

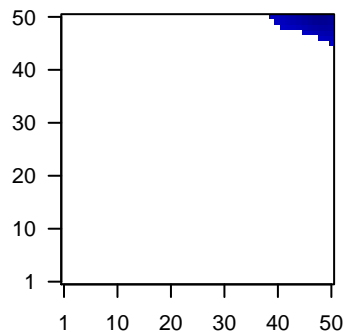
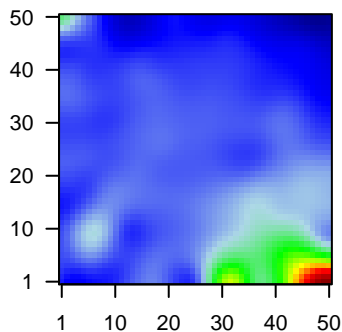
$\langle \text{shrinkage-t} \rangle = -9.26$

$\langle p\text{-value} \rangle = 0.02$

$\langle fdr \rangle = 0.65$

Profile

Spot



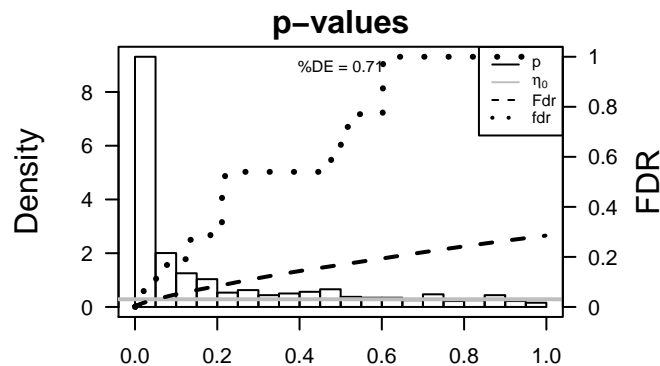
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4072	-1.3	2e-16	1e-14	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:...
2	3880	-1.34	2e-16	1e-14	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
3	4953	-1.38	2e-16	1e-14	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
4	139728	-1.11	2e-14	2e-12	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:HGNC Symbol;Acc:...
5	2944	1.1	2e-14	2e-12	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4...
6	3856	1.09	4e-14	2e-12	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
7	29968	-1.08	5e-14	2e-12	49 x 50 phosphoserine aminotransferase 1 [Source:HGNC Symbol;Acc:...
8	4922	-1.08	6e-14	2e-11	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
9	655	-1.06	2e-13	2e-10	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10...
10	8500	-1.02	2e-12	6e-10	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (PT...
11	79682	-0.99	7e-12	6e-10	46 x 47 centromere protein U [Source:HGNC Symbol;Acc:21348]
12	200634	-0.98	9e-12	1e-08	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc:...
13	26047	-0.94	7e-11	1e-08	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Acc:...
14	4291	-0.92	1e-10	3e-08	46 x 50 myeloid leukemia factor 1 [Source:HGNC Symbol;Acc:7125]
15	7345	-0.91	3e-10	3e-07	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras...
16	86	-0.86	2e-09	4e-07	46 x 50 actin-like 6A [Source:HGNC Symbol;Acc:24124]
17	6657	-0.85	4e-09	4e-07	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbol;Acc:...
18	1056	-0.84	6e-09	2e-06	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
19	28978	-0.82	1e-08	6e-06	49 x 50 transmembrane protein 14A [Source:HGNC Symbol;Acc:2101]
20	26872	-0.78	6e-08	6e-06	40 x 50 six transmembrane epithelial antigen of the prostate 1 [Source:HGNC Symbol;Acc:...

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-22.49	NULL	85 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-22.49	NULL	85 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-14.14	NULL	10 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
4	-13.73	NULL	93 / 370	BP mitotic cell cycle
5	-13.47	NULL	8 / 11	GSEA C2ODONNELL_TFRC_TARGETS_DN
6	-12.91	NULL	11 / 16	Cancer WOLFER_overlap genes
7	-12.34	NULL	88 / 914	Chr Chr 3
8	-11.99	NULL	10 / 14	GSEA CZZHAN_MULTIPLE_MYELOMA_PR_UP
9	-11.94	NULL	5 / 13	GSEA C2LEE_LIVER_CANCER_SURVIVAL_DN
10	-11.74	NULL	12 / 16	GSEA C2GUCHI_CELL_CYCLE_RB1_TARGETS
11	-11.62	NULL	6 / 14	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_2
12	-11.5	NULL	10 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
13	-10.55	NULL	10 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
14	-10.5	NULL	9 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
15	-10.45	NULL	8 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
16	-10.43	NULL	6 / 16	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
17	-10.39	NULL	7 / 15	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
18	-10.36	NULL	22 / 66	CC condensed chromosome kinetochores
19	-10.33	NULL	3 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
20	-10.18	NULL	11 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
21	-10.12	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
22	-10.07	NULL	23 / 57	Glio developing astrocytes
23	-9.96	NULL	7 / 16	GSEA C2BIDUS_METASTASIS_UP
24	-9.91	NULL	3 / 7	GSEA C2REACTOME_G1_S_TRANSITION
25	-9.91	NULL	5 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
26	-9.71	NULL	93 / 530	Cancer Lembcke_Normal vs Adenoma
27	-9.7	NULL	6 / 14	GSEA C2RUIZ_TNC_TARGETS_DN
28	-9.67	NULL	8 / 12	GSEA C2I_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
29	-9.62	NULL	7 / 16	GSEA C2FUJII_YBX1_TARGETS_DN
30	-9.51	NULL	8 / 15	GSEA C2ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
31	-9.5	NULL	3 / 12	GSEA C2CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
32	-9.49	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
33	-9.41	NULL	8 / 14	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
34	-9.17	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
35	-8.97	NULL	6 / 11	GSEA C2REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION
36	-8.95	NULL	7 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
37	-8.9	NULL	5 / 16	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
38	-8.83	NULL	2 / 8	GSEA C2PUJANA_CHEK2_PCC_NETWORK
39	-8.82	NULL	13 / 30	BP DNA strand elongation involved in DNA replication
40	-8.76	NULL	106 / 949	CC nucleoplasm



GW_061

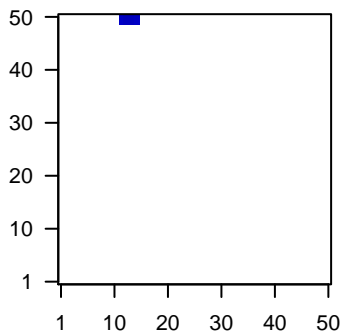
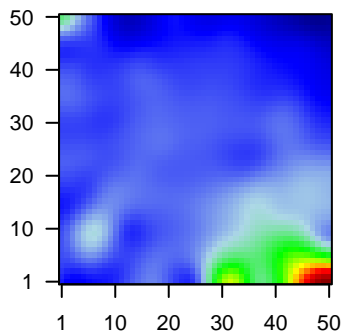
Local Summary

%DE = 0.74
 # metagenes = 8
 # genes = 114
 # genes in genesets = 113
 # genes with $fdr < 0.1$ = 51 (6 + / 45 -)
 # genes with $fdr < 0.05$ = 48 (6 + / 42 -)
 # genes with $fdr < 0.01$ = 41 (5 + / 36 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.28
 $\langle FC \rangle = -0.25$
 $\langle \text{shrinkage-t} \rangle = -8.89$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.56$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	56666	-1.11	1e-14	2e-12	14 x 50 pannexin 2 [Source:HGNC Symbol;Acc:8600]
2	1109	1.07	9e-14	3e-12	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sym]
3	1749	-1.06	2e-13	5e-11	13 x 50 distal-less homeobox 5 [Source:HGNC Symbol;Acc:2918]
4	10457	-1.01	3e-12	5e-11	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
5	57007	-1	3e-12	6e-07	14 x 50 atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
6	4828	-0.81	2e-08	4e-06	13 x 50 neuromedin B [Source:HGNC Symbol;Acc:7842]
7	65055	-0.76	1e-07	6e-06	14 x 50 receptor accessory protein 1 [Source:HGNC Symbol;Acc:257
8	483	-0.73	4e-07	6e-06	13 x 50 ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
9	1646	0.72	5e-07	7e-06	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Sym]
10	2817	-0.71	8e-07	3e-04	14 x 50 glypican 1 [Source:HGNC Symbol;Acc:4449]
11	23446	-0.62	1e-05	3e-04	15 x 50 solute carrier family 44 (choline transporter), member 1 [Sour
12	79850	-0.6	3e-05	3e-04	13 x 50 family with sequence similarity 57, member A [Source:HGNC
13	51071	-0.6	3e-05	4e-04	13 x 50 deoxyribose-phosphate aldolase (putative) [Source:HGNC S
14	8626	-0.59	5e-05	4e-04	13 x 50 tumor protein p63 [Source:HGNC Symbol;Acc:15979]
15	493861	0.57	7e-05	4e-04	14 x 50 EP300 interacting inhibitor of differentiation 3 [Source:HGNC
16	4071	-0.52	8e-05	4e-04	12 x 50 transmembrane 4 L six family member 1 [Source:HGNC Sym
17	55971	-0.57	9e-05	4e-04	13 x 50 BAI1-associated protein 2-like 1 [Source:HGNC Symbol;Acc
18	9069	-0.56	1e-04	5e-04	14 x 50 claudin 12 [Source:HGNC Symbol;Acc:2034]
19	3836	-0.55	1e-04	5e-04	14 x 50 karyopherin alpha 1 (importin alpha 5) [Source:HGNC Symbc
20	23108	-0.55	1e-04	5e-04	15 x 50 RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-13.62	NULL	1 / 6	GSEA C2ZAIID_OSTEOBLAST_TRANSCRIPTION_FACTORS
2	-13.62	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
3	-12.92	NULL	2 / 14	GSEA C2MAYBURD_RESPONSE_TO_L663536_DN
4	-11.99	NULL	3 / 19	BP anatomical structure formation involved in morphogenesis
5	-10.33	NULL	2 / 15	GSEA C2KANG_FLUOROURACIL_RESISTANCE_UP
6	-10.28	NULL	1 / 9	Glio Colman_survival_robust
7	-10.26	NULL	2 / 12	BP head development
8	-9.69	NULL	1 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
9	-9.65	NULL	1 / 11	BP ear development
10	-9.65	NULL	1 / 11	GSEA C2SU_PLACENTA
11	-9.64	NULL	1 / 12	MF channel activity
12	-9.47	NULL	2 / 12	BP positive regulation of protein import into nucleus
13	-9.22	NULL	1 / 13	BP response to ischemia
14	-9.18	NULL	1 / 11	GSEA C2TO_PTTG1_TARGETS_UP
15	-9.11	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
16	-8.84	NULL	1 / 14	GSEA C2NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON
17	-8.79	NULL	1 / 13	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
18	-8.72	NULL	3 / 38	BP epithelial cell differentiation
19	-8.71	NULL	2 / 16	GSEA C2REACTOME_BASIGIN_INTERACTIONS
20	-8.7	NULL	1 / 12	BP negative regulation of intrinsic apoptotic signaling pathway in respo
21	-8.66	NULL	3 / 51	BP osteoblast differentiation
22	-8.43	NULL	1 / 14	GSEA C2ENK_UV_RESPONSE_EPIDERMIS_UP
23	-8.35	NULL	1 / 13	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
24	-8.11	NULL	1 / 15	BP cellular response to BMP stimulus
25	-8.11	NULL	1 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
26	-8.02	NULL	2 / 13	GSEA C2KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
27	-7.82	NULL	1 / 16	MF HMG box domain binding
28	-7.78	NULL	2 / 15	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
29	-7.72	NULL	1 / 10	BP arachidonic acid secretion
30	-7.72	NULL	1 / 10	BP positive regulation of hormone secretion
31	-7.45	NULL	2 / 11	GSEA C2REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION
32	-7.4	NULL	2 / 15	GSEA C2KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTIO
33	-7.31	NULL	1 / 11	BP negative regulation of hormone secretion
34	-7.07	NULL	2 / 15	GSEA C2JEON_SMAD6_TARGETS_DN
35	-7.04	NULL	1 / 21	CC gap junction
36	-6.97	NULL	1 / 10	GSEA C2TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
37	-6.97	NULL	1 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
38	-6.83	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C7
39	-6.79	NULL	1 / 10	BP negative regulation of fibroblast growth factor receptor signaling pa
40	-6.71	NULL	1 / 21	BP bone morphogenesis

