

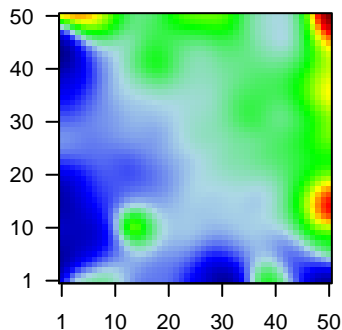
GW_123

Global Summary

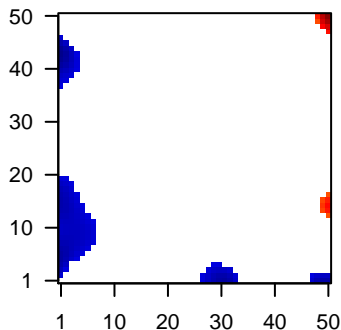
%DE = 0.14
 # genes with fdr < 0.2 = 1726 (1036 + / 690 -)
 # genes with fdr < 0.1 = 1381 (862 + / 519 -)
 # genes with fdr < 0.05 = 1171 (742 + / 429 -)
 # genes with fdr < 0.01 = 804 (529 + / 275 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.86

Profile



Regulated Spots



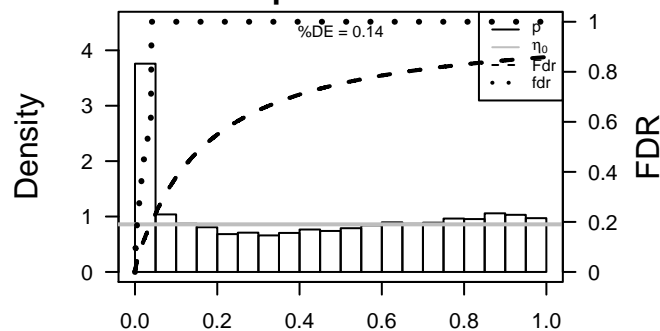
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.34	2e-16	3e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Sou
2	21	1.55	2e-16	3e-14	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
3	131	1.83	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	216	1.84	2e-16	3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	218	1.41	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	401138	1.41	2e-16	3e-14	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
7	55107	-1.48	2e-16	3e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
8	164284	1.86	2e-16	3e-14	1 x 3 adenomatosis polyposis coli down-regulated 1-like [Source:t
9	344905	2	2e-16	3e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
10	375791	1.67	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
11	1056	2.35	2e-16	3e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
12	22802	1.86	2e-16	3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	9076	1.65	2e-16	3e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
14	1277	1.58	2e-16	3e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	1278	1.67	2e-16	3e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
16	1281	1.68	2e-16	3e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
17	49860	2.54	2e-16	3e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	441520	1.47	2e-16	3e-14	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
19	115908	1.56	2e-16	3e-14	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
20	2919	-1.7	2e-16	3e-14	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.84	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
2	9.72	NULL	618	Chr Chr 4
3	9.49	NULL	135	H.Tiss WIRTH_Mucosa
4	7.6	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
5	6.69	NULL	13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
6	6.64	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
7	6.46	NULL	37	BP collagen fibril organization
8	6.44	NULL	9	GSEA C2REACTOME_ETHANOL_OXIDATION
9	6.28	NULL	11	MF platelet-derived growth factor binding
10	6.25	NULL	16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
11	6.14	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
12	6.04	NULL	16	MMML C6CIEJ_MML 1
13	6	NULL	714	Chr Chr 6
14	5.94	NULL	602	Chr Chr 10
15	5.94	NULL	24	TF Tissue/AQUERIZAS_Trachea
16	5.66	NULL	7	MMML C6CIEJ_MML 5
17	5.53	NULL	57	MF extracellular matrix structural constituent
18	5.41	NULL	16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
19	5.39	NULL	16	GSEA C2RODRIGUES_NTN1_TARGETS_UP
20	5.3	NULL	12	miRNA target-29c
<i>Underexpressed</i>				
1	-13.55	NULL	519	Chr Chr 14
2	-11.4	NULL	553	Cancer Lembecke_Colonic Inflammation
3	-11.26	NULL	572	Disease GUDJ_poriasis up
4	-9.12	NULL	312	BP immune response
5	-8.32	NULL	269	BP inflammatory response
6	-8.09	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
7	-7.84	NULL	10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
8	-7.57	NULL	6	Glio Martinez_Glio_hypometh
9	-7.55	NULL	43	MF chemokine activity
10	-7.15	NULL	6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	-7.03	NULL	111	BP chemotaxis
12	-6.76	NULL	957	Chr Chr 11
13	-6.57	NULL	4	MMML C6CIEJ_MML 23
14	-6.47	NULL	417	H.Tiss WIRTH_Immune system
15	-6.26	NULL	918	Chr Chr 17
16	-6.12	NULL	51	BP type I interferon signaling pathway
17	-6.12	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
18	-6.12	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
19	-6.12	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
20	-6.12	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down

p-values



GW_123

Local Summary

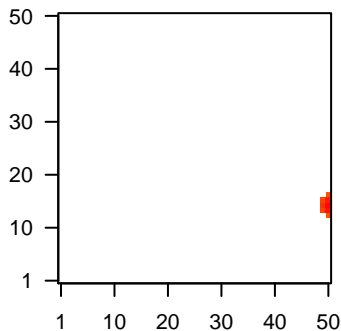
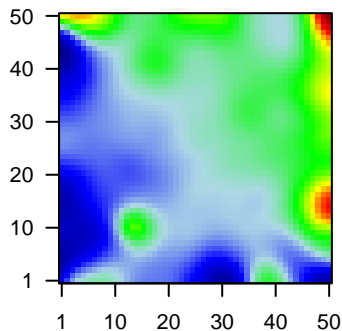
%DE = 0.69
 # metagenes = 8
 # genes = 137
 # genes in genesets = 136
 # genes with $fdr < 0.1$ = 74 (73 + / 1 -)
 # genes with $fdr < 0.05$ = 70 (69 + / 1 -)
 # genes with $fdr < 0.01$ = 61 (61 + / 0 -)

<r> metagenes = 0.96
 <r> genes = 0.34

<FC> = 0.49
 <shrinkage-t> = 17.28
 <p-value> = 0
 <fdr> = 0.46

Profile

Spot



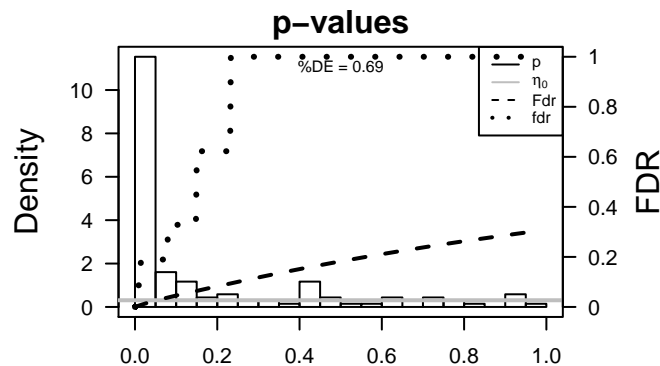
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	21	1.55	2e-16	1e-15	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
2	66002	1.36	2e-16	1e-15	50 x 13 cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
3	2568	2.02	2e-16	1e-15	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HG
4	26002	2.03	2e-16	1e-15	50 x 16 monooxygenase, DBH-like 1 [Source:HGNC Symbol;Acc:216
5	4602	1.86	2e-16	1e-15	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source
6	4948	1.5	2e-16	1e-15	50 x 17 oculocutaneous albinism II [Source:HGNC Symbol;Acc:8101]
7	51316	2.26	2e-16	1e-15	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
8	494470	1.35	2e-16	1e-15	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
9	6542	1.61	2e-16	1e-15	50 x 16 solute carrier family 7 (cationic amino acid transporter, y+ sys
10	221061	1.28	2e-15	1e-11	50 x 16 family with sequence similarity 171, member A1 [Source:HG
11	2205	1.17	6e-13	1e-11	50 x 13 Fc fragment of IgE, high affinity I, receptor for; alpha polypept
12	2628	1.16	7e-13	1e-10	50 x 14 glycine amidinotransferase (L-arginine:glycine amidinotransf
13	162494	1.12	4e-12	4e-10	50 x 17 rhomboid, veinlet-like 3 (Drosophila) [Source:HGNC Symbol;
14	9915	1.1	1e-11	4e-10	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
15	3248	1.08	2e-11	7e-10	50 x 13 hydroxyprostaglandin dehydrogenase 15-(NAD) [Source:HGI
16	8543	1.07	4e-11	7e-10	50 x 15 LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
17	10439	1.06	5e-11	2e-09	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
18	596	1.05	1e-10	5e-08	50 x 17 B-cell CLL/lymphoma 2 [Source:HGNC Symbol;Acc:990]
19	26471	0.98	1e-09	1e-07	49 x 14 nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
20	84532	0.95	4e-09	2e-07	50 x 17 acyl-CoA synthetase short-chain family member 1 [Source:I-

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	31.19	NULL	5 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
2	16.92	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
3	16.15	NULL	1 / 2	miRNA target-153
4	15.95	NULL	2 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
5	15.7	NULL	2 / 4	miRNA target-204
6	15.55	NULL	2 / 12	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
7	12.8	NULL	2 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
8	12.71	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
9	12.35	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
10	12.12	NULL	1 / 3	GSEA C2MYLYKANGAS_AMPLIFICATION_HOT_SPOT_18
11	12.11	NULL	2 / 13	BP developmental pigmentation
12	11.9	NULL	1 / 9	GSEA C2RODWELL_AGING_KIDNEY_UP
13	11.81	NULL	1 / 11	BP negative regulation of multicellular organism growth
14	11.8	NULL	2 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
15	11.8	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
16	11.66	NULL	1 / 8	GSEA C2ADYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
17	11.61	NULL	2 / 11	GSEA C2RIGGI_EWING_SARCOMA_PROGENITOR_DN
18	11.18	NULL	1 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
19	11.16	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_DN
20	11.14	NULL	1 / 10	MF GABA-A receptor activity
21	11.03	NULL	3 / 15	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
22	11.01	NULL	3 / 34	BP thymus development
23	10.87	NULL	1 / 9	GSEA C2BASSO_CD40_SIGNALING_UP
24	10.87	NULL	1 / 9	GSEA C2GUTIERREZ_WALDENSTROMS_MACROGLOBULINEMIA_2
25	10.57	NULL	1 / 11	GSEA C2NUYTEN_EZH2_TARGETS_UP
26	10.53	NULL	1 / 11	GSEA C2AZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
27	10.21	NULL	1 / 10	BP positive regulation of histone H3-K4 methylation
28	10.13	NULL	2 / 10	BP epoxygenase P450 pathway
29	10.05	NULL	1 / 12	GSEA C2PEREZ_TP53_TARGETS
30	10.05	NULL	1 / 12	GSEA C2BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
31	10.01	NULL	1 / 4	miRNA targetc
32	10.01	NULL	1 / 4	miRNA target-34b
33	10.01	NULL	1 / 4	miRNA target-34c
34	9.83	NULL	2 / 14	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
35	9.83	NULL	2 / 14	GSEA C2ANTVEER_BREAST_CANCER_ESR1_UP
36	9.82	NULL	2 / 14	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
37	9.65	NULL	1 / 11	BP homeostasis of number of cells
38	9.65	NULL	1 / 11	Pathw AcBENTINK_e2f3.2
39	9.65	NULL	1 / 11	GSEA C2DOANE_BREAST_CANCER_ESR1_UP
40	9.65	NULL	1 / 11	GSEA C2TURJANSKI_MAPK1_AND_MAPK2_TARGETS



GW_123

Local Summary

%DE = 0.84
 # metagenes = 9
 # genes = 159
 # genes in genesets = 158

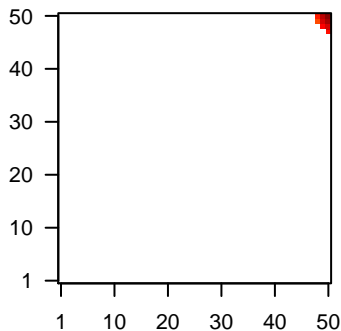
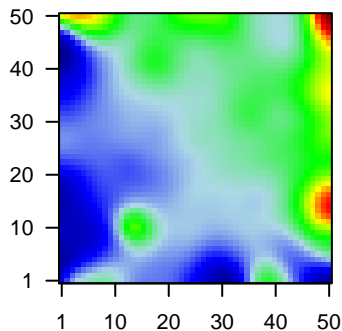
genes with $fdr < 0.1 = 114$ (106 + / 8 -)
 # genes with $fdr < 0.05 = 90$ (88 + / 2 -)
 # genes with $fdr < 0.01 = 83$ (82 + / 1 -)

<r> metagenes = 0.98
 <r> genes = 0.29

<FC> = 0.55
 <shrinkage-t> = 19.4
 <p-value> = 0
 <fdr> = 0.4

Profile

Spot



Local Genelist

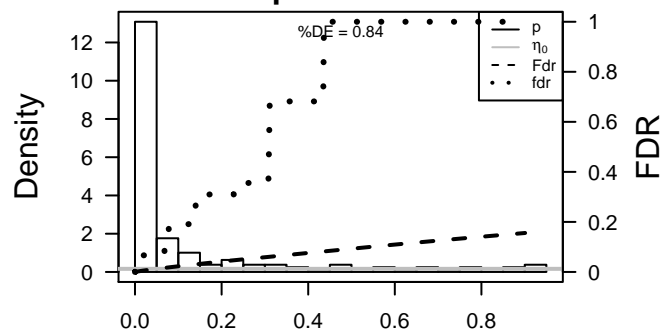
Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.34	2e-16	4e-16	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:31789]
2	216	1.84	2e-16	4e-16	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:31789]
3	344905	2	2e-16	4e-16	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
4	1056	2.35	2e-16	4e-16	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
5	9076	1.65	2e-16	4e-16	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
6	83888	2.37	2e-16	4e-16	50 x 50 fibroblast growth factor binding protein 2 [Source:HGNC Symbol;Acc:2032]
7	2938	1.63	2e-16	4e-16	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc:2032]
8	3866	2.07	2e-16	4e-16	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
9	4922	2.11	2e-16	4e-16	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
10	10966	1.41	2e-16	4e-16	50 x 50 RAB40B, member RAS oncogene family [Source:HGNC Symbol;Acc:26790]
11	6446	1.28	2e-16	4e-16	50 x 50 serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:26790]
12	11166	1.69	2e-16	4e-16	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symbol;Acc:26790]
13	256764	1.41	2e-16	4e-16	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
14	7546	1.68	2e-16	4e-16	48 x 50 Zic family member 2 [Source:HGNC Symbol;Acc:12873]
15	26047	1.29	1e-15	3e-14	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Acc:12873]
16	10643	1.28	2e-15	5e-13	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:HGNC Symbol;Acc:12873]
17	139728	1.24	2e-14	6e-12	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:HGNC Symbol;Acc:12873]
18	79190	1.19	2e-13	3e-11	50 x 47 iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
19	54575	1.15	1e-12	7e-11	50 x 50 UDP glucuronosyltransferase 1 family, polypeptide A10 [Source:HGNC Symbol;Acc:14675]
20	59338	1.11	6e-12	7e-11	50 x 50 pleckstrin homology domain containing, family A (phosphoinositide)

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	18.27	NULL	3 / 8	GSEA C2JUCDX2_TARGETS_DN
2	16.12	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	15.97	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
4	14.32	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
5	12.26	NULL	1 / 8	GSEA C2KEGG_GLYCEROLIPID_METABOLISM
6	11.33	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
7	11.33	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
8	11.03	NULL	2 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
9	10.42	NULL	3 / 13	BP regulation of blood vessel size
10	10.21	NULL	1 / 11	GSEA C2YAMANAKA_GLIOMASTOMA_SURVIVAL_UP
11	10.16	NULL	1 / 11	GSEA C2BROWNE_HCMV_INFECTION_10HR_UP
12	10.12	NULL	3 / 16	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G1_DN
13	9.99	NULL	2 / 16	GSEA C2KEGG_STEROID_BIOSYNTHESIS
14	9.34	NULL	3 / 15	BP lipid glycosylation
15	9.21	NULL	1 / 13	MF triglyceride lipase activity
16	9.06	NULL	1 / 11	Glio neurons_glio
17	9.01	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
18	8.92	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
19	8.86	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
20	8.86	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
21	8.82	NULL	1 / 14	GSEA C2WATANABE_COLON_CANCER_MSI_VS_MSS_DN
22	8.34	NULL	4 / 15	GSEA C2REACTOME_Glutathione_CONJUGATION
23	8.33	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
24	8.32	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
25	8.32	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
26	8.14	NULL	2 / 16	GSEA C2WILCOX_PRESPONSE_TO_ROGESTERONE_UP
27	8.14	NULL	2 / 16	GSEA C2NAKAYAMA_FRA2_TARGETS
28	8.08	NULL	2 / 12	BP cellular aldehyde metabolic process
29	7.85	NULL	2 / 16	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP
30	7.68	NULL	8 / 34	BP glutathione metabolic process
31	7.54	NULL	1 / 15	MF neuropeptide hormone activity
32	7.39	NULL	1 / 15	H Tiss WIRTH_Cerebellum
33	7.34	NULL	1 / 5	GSEA C2TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR
34	7.19	NULL	2 / 9	GSEA C2REACTOME_GLUCCURONIDATION
35	7.11	NULL	1 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
36	7.11	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
37	6.86	NULL	2 / 13	GSEA C2BROWNE_HCMV_INFECTION_6HR_DN
38	6.85	NULL	5 / 20	MF glutathione transferase activity
39	6.82	NULL	2 / 23	BP stem cell differentiation
40	6.81	NULL	1 / 14	MF Ras GTPase activator activity

p-values



GW_123

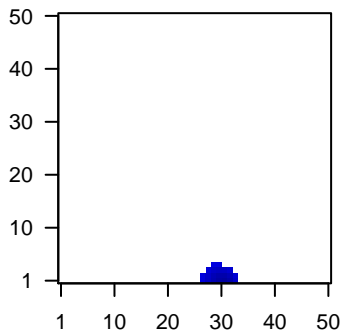
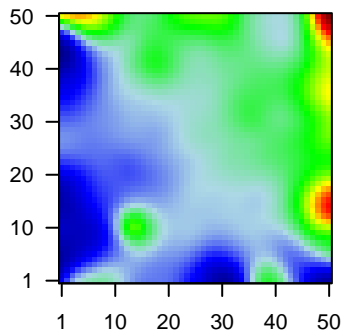
Local Summary

%DE = 0.77
 # metagenes = 21
 # genes = 187
 # genes in genesets = 184
 # genes with fdr < 0.1 = 101 (10 + / 91 -)
 # genes with fdr < 0.05 = 82 (6 + / 76 -)
 # genes with fdr < 0.01 = 52 (3 + / 49 -)

<r> metagenes = 0.87
 <r> genes = 0.32
 <FC> = -0.3
 <shrinkage-t> = -10.71
 <p-value> = 0.01
 <fdr> = 0.59

Profile

Spot



Local Genelist

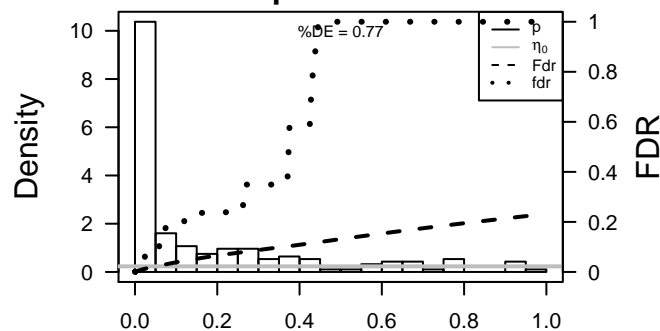
Rank	ID	log(FC)	fdr	p-value	Description
1	3627	-1.62	2e-16	5e-15	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:10040]
2	7453	-1.35	2e-16	5e-15	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:10040]
3	10410	-1.1	1e-13	3e-11	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC Symbol;Acc:10040]
4	115362	-1.16	9e-13	1e-09	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989]
5	629	-1.08	3e-11	7e-09	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
6	6355	-1.03	2e-10	7e-09	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:10040]
7	9636	-1.02	3e-10	2e-08	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405]
8	9560	-0.99	9e-10	2e-08	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:10040]
9	4321	-0.98	2e-09	2e-08	32 x 1 matrix metalloproteinase 12 (macrophage elastase) [Source:HGNC Symbol;Acc:10040]
10	10581	-0.9	2e-09	2e-06	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:10040]
11	8519	-0.89	4e-08	6e-06	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC Symbol;Acc:10040]
12	3628	0.84	2e-07	6e-06	33 x 1 inositol polyphosphate-1-phosphatase [Source:HGNC Symbol;Acc:10040]
13	1591	-0.83	3e-07	2e-05	33 x 2 cytochrome P450, family 24, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:10040]
14	10866	-0.8	8e-07	2e-05	32 x 1 HLA complex P5 (non-protein coding) [Source:HGNC Symbol;Acc:10040]
15	4814	0.79	1e-06	7e-05	32 x 3 ninjurin 1 [Source:HGNC Symbol;Acc:7824]
16	1200	-0.76	3e-06	7e-05	29 x 1 tripeptidyl peptidase I [Source:HGNC Symbol;Acc:2073]
17	391	-0.74	5e-06	1e-04	29 x 2 ras homolog family member G [Source:HGNC Symbol;Acc:67]
18	6289	-0.73	7e-06	2e-04	29 x 1 serum amyloid A2 [Source:HGNC Symbol;Acc:10514]
19	3133	-0.7	1e-05	2e-04	32 x 1 major histocompatibility complex, class I, E [Source:HGNC Symbol;Acc:10040]
20	6890	-0.7	2e-05	2e-04	32 x 1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Source:HGNC Symbol;Acc:10040]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-35.62	NULL	29 / 51	BP type I interferon signaling pathway
2	-33.26	NULL	11 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
3	-29.24	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	-28.42	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
5	-27.71	NULL	6 / 6	Lymphonoma_AVE_MHCCII_BL_DN
6	-26.46	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	-24.28	NULL	14 / 31	BP negative regulation of viral genome replication
8	-22.98	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
9	-22.47	NULL	2 / 2	MMML C2SCIEJ_MMML_27
10	-22.31	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
11	-21.76	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
12	-20.82	NULL	7 / 10	CC MHC class I protein complex
13	-20.68	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
14	-19.81	NULL	32 / 123	BP defense response to virus
15	-19.3	NULL	27 / 109	BP response to virus
16	-18.99	NULL	7 / 18	MF peptide antigen binding
17	-18.93	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
18	-18.35	NULL	34 / 204	BP cytokine-mediated signaling pathway
19	-17.64	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
20	-16.78	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
21	-16.75	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
22	-16.75	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
23	-16.7	NULL	5 / 18	BP response to interferon-gamma
24	-16.09	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
25	-15.3	NULL	3 / 16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
26	-15.2	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
27	-15.06	NULL	2 / 10	BP positive regulation of cAMP-mediated signaling
28	-15.02	NULL	3 / 14	GSEA C2LINDSTEDT_DENDRITIC_CELL_MATURATION_A
29	-14.57	NULL	33 / 312	BP immune response
30	-14.34	NULL	2 / 13	BP response to vitamin D
31	-14.18	NULL	34 / 274	Lymphonoma_SPANG_IL21_DN
32	-13.61	NULL	2 / 12	BP positive regulation of leukocyte chemotaxis
33	-13.37	NULL	12 / 70	BP antigen processing and presentation of exogenous peptide antigen
34	-13.34	NULL	19 / 185	Cancer SPANG_LPS-index2
35	-13.24	NULL	10 / 52	Chr Chr HSCHR6_MHC_QBL
36	-13.09	NULL	3 / 14	GSEA C2REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
37	-13.06	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
38	-12.97	NULL	3 / 8	GSEA C2KEGG_PRIMARY_IMMUNODEFICIENCY
39	-12.96	NULL	12 / 74	BP antigen processing and presentation of exogenous peptide antigen
40	-12.9	NULL	9 / 47	BP antigen processing and presentation

p-values



GW_123

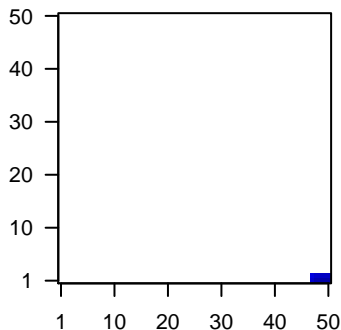
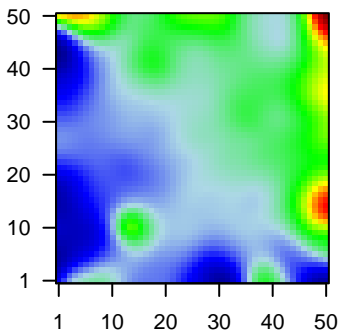
Local Summary

%DE = 0.78
 # metagenes = 8
 # genes = 186
 # genes in genesets = 184
 # genes with fdr < 0.1 = 119 (15 + / 104 -)
 # genes with fdr < 0.05 = 95 (11 + / 84 -)
 # genes with fdr < 0.01 = 50 (10 + / 40 -)

<r> metagenes = 1
 <r> genes = 0.65
 <FC> = -0.24
 <shrinkage-t> = -8.46
 <p-value> = 0.01
 <fdr> = 0.56

Profile

Spot



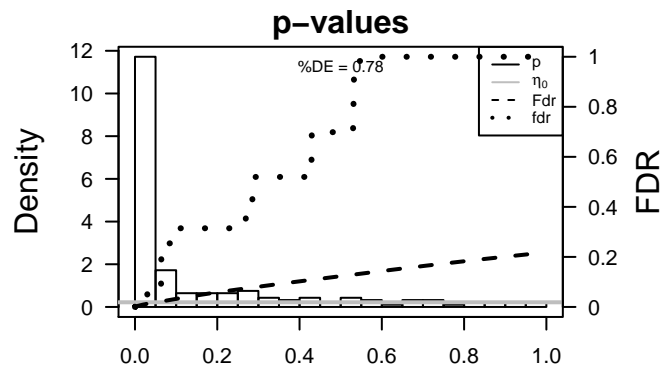
Local Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	3120	2	2e-16 3e-15	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:HGNC Symbol;Acc:23138]
2	25849	1.85	2e-16 3e-15	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HGNC Symbol;Acc:23138]
3	57484	1.95	2e-16 3e-15	50 x 2 ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
4	55619	1.2	1e-13 2e-10	50 x 1 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:23471]
5	4283	-1.12	4e-12 5e-10	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:23138]
6	3620	-1.08	2e-11 5e-10	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:23138]
7	5880	-1.08	3e-11 7e-09	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP-binding protein RhoC) [Source:HGNC Symbol;Acc:23138]
8	23231	-1.02	3e-10 7e-09	48 x 2 sel-1 suppressor of lin-12-like 3 (C. elegans) [Source:HGNC Symbol;Acc:23138]
9	3128	-1.01	4e-10 6e-07	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene) [Source:HGNC Symbol;Acc:23138]
10	3059	-0.92	1e-08 2e-05	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:23138]
11	3575	-0.82	4e-07 3e-05	50 x 2 interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
12	9214	-0.79	1e-06 7e-05	49 x 1 Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;Acc:23138]
13	126306	-0.75	3e-06 7e-05	49 x 1 junctional sarcoplasmic reticulum protein 1 [Source:HGNC Symbol;Acc:23138]
14	23180	-0.74	5e-06 7e-05	50 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
15	260436	-0.73	6e-06 2e-04	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:23138]
16	1236	-0.69	2e-05 2e-04	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:23138]
17	3512	0.69	2e-05 2e-04	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin heavy chain [Source:HGNC Symbol;Acc:23138]
18	255231	-0.69	2e-05 3e-04	49 x 1 mucolin 2 [Source:HGNC Symbol;Acc:13357]
19	8320	-0.67	3e-05 3e-04	48 x 1 eomesodermin [Source:HGNC Symbol;Acc:3372]
20	54923	0.67	4e-05 3e-04	47 x 1

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-25.74	NULL	79 / 417	H.Tiss WIRTH_Immune system
2	-19.48	NULL	70 / 553	Cancer Lembocke_Colonic Inflammation
3	-14.12	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
4	-13.09	NULL	4 / 13	BP lymph node development
5	-12.38	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
6	-11.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
7	-11.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
8	-11.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
9	-11.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
10	-11.58	NULL	4 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
11	-11.47	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
12	-11.38	NULL	7 / 16	GSEA C2SU_THYMUS
13	-11.38	NULL	5 / 12	BP immunoglobulin mediated immune response
14	-11.28	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
15	-11.13	NULL	6 / 28	LymphomaSAVE_Immune response 1
16	-11.06	NULL	3 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
17	-10.85	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
18	-10.74	NULL	6 / 45	BP cellular defense response
19	-10.72	NULL	16 / 74	BP regulation of immune response
20	-10.39	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDP_SIGNATURE
21	-10.32	NULL	4 / 22	BP positive regulation of interleukin-12 production
22	-10.1	NULL	21 / 162	CC external side of plasma membrane
23	-10.05	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
24	-9.89	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
25	-9.45	NULL	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
26	-9.34	NULL	19 / 204	BP cell surface receptor signaling pathway
27	-9.03	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
28	-8.67	NULL	3 / 10	BP negative thymic T cell selection
29	-8.59	NULL	1 / 6	GSEA C2TRAYNOR_RETT_SYNDROM_DN
30	-8.38	NULL	8 / 45	BP T cell activation
31	-8.12	NULL	6 / 24	CC immunological synapse
32	-8.02	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
33	-7.95	NULL	3 / 8	GSEA C2BIOCARTA_GRANULOCYTES_PATHWAY
34	-7.88	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
35	-7.88	NULL	5 / 11	BP positive regulation of B cell differentiation
36	-7.81	NULL	1 / 2	GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IIGA_PRODUC
37	-7.81	NULL	1 / 2	GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE
38	-7.81	NULL	1 / 2	GSEA C2KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
39	-7.75	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
40	-7.65	NULL	2 / 11	GSEA C2CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN



GW_123

Local Summary

%DE = 0.7
 # metagenes = 87
 # genes = 925
 # genes in genesets = 919

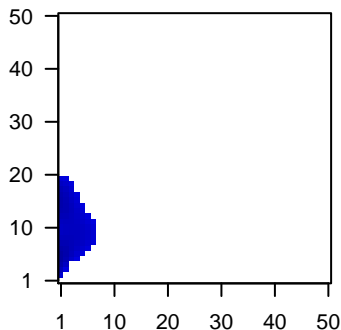
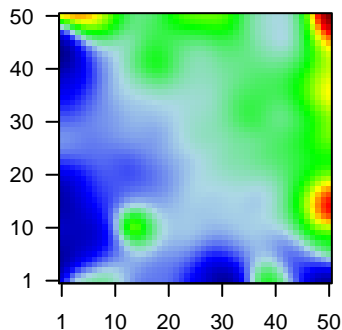
 # genes with $fdr < 0.1$ = 346 (47 + / 299 -)
 # genes with $fdr < 0.05$ = 213 (33 + / 180 -)
 # genes with $fdr < 0.01$ = 119 (21 + / 98 -)

 $\langle r \rangle$ metagenes = 0.72
 $\langle r \rangle$ genes = 0.2

 $\langle FC \rangle = -0.21$
 $\langle \text{shrinkage-t} \rangle = -7.44$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.72$

Profile

Spot



Local Genelist

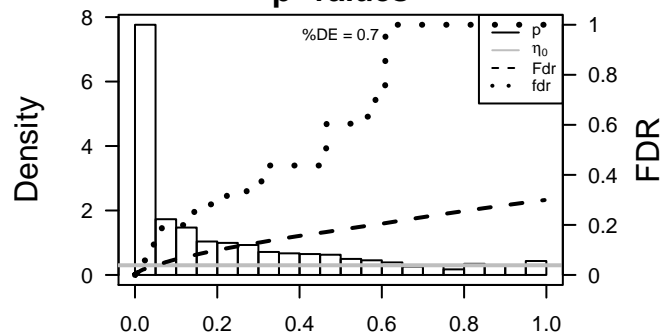
Rank	ID	log(FC)	fdr	p-value	Description
1	401138	1.41	2e-16	9e-15	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
2	55107	-1.48	2e-16	9e-15	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
3	164284	1.86	2e-16	9e-15	1 x 3 adenomatosis polyposis coli down-regulated 1-like [Source:HGNC]
4	4319	-1.67	2e-16	9e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol]
5	4502	-1.36	2e-16	9e-15	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
6	4628	-1.33	2e-16	9e-15	1 x 5 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol]
7	5054	-1.43	2e-16	9e-15	1 x 2 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1)
8	87	-1.3	1e-15	2e-12	1 x 3 actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
9	5328	-1.25	1e-14	2e-11	1 x 3 plasminogen activator, urokinase [Source:HGNC Symbol;Acc:163]
10	4495	1.21	8e-14	3e-10	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
11	11031	-1.15	1e-12	2e-09	1 x 3 RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:11031]
12	857	-1.1	9e-12	9e-09	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:857]
13	2274	-1.05	9e-11	9e-09	1 x 4 four and a half LIM domains 2 [Source:HGNC Symbol;Acc:37]
14	3486	-1.04	1e-10	9e-09	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Symbol;Acc:3486]
15	131076	-1.04	1e-10	9e-09	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:131076]
16	10409	-1.04	1e-10	3e-08	1 x 2 brain abundant, membrane attached signal protein 1 [Source:HGNC Symbol;Acc:10409]
17	1051	-0.93	4e-10	3e-08	1 x 4 CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:1051]
18	55240	1.01	5e-10	3e-08	3 x 16 STEAP family member 3, metalloreductase [Source:HGNC Symbol;Acc:55240]
19	1021	-1.01	5e-10	9e-08	1 x 6 cyclin-dependent kinase 6 [Source:HGNC Symbol;Acc:1777]
20	11009	-0.99	1e-09	9e-08	1 x 3 interleukin 24 [Source:HGNC Symbol;Acc:11346]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.5	NULL	10 / 35	Glio Colman_survival_associated
2	-11.18	NULL	3 / 11	GSEA C2BIOCARTA_PLATELETAPP_PATHWAY
3	-11.05	NULL	4 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
4	-10.49	NULL	2 / 6	GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP
5	-10.39	NULL	4 / 13	GSEA C2LAMB_CCND1_TARGETS
6	-9.79	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
7	-9.78	NULL	4 / 16	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_UP
8	-9.45	NULL	5 / 16	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C1
9	-9.26	NULL	3 / 15	BP fibrinolysis
10	-9.15	NULL	2 / 10	BP regulation of receptor activity
11	-9.15	NULL	2 / 10	GSEA C2BIOCARTA_FIBRINOLYSIS_PATHWAY
12	-8.93	NULL	4 / 15	GSEA C2SEMENZA_HIF1_TARGETS
13	-8.92	NULL	2 / 4	GSEA C2ACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
14	-8.77	NULL	3 / 14	GSEA C2DANG_MYC_TARGETS_DN
15	-8.77	NULL	5 / 10	GSEA C2BIOCARTA_CELL2CELL_PATHWAY
16	-8.69	NULL	5 / 11	Glio Phillips MES up vs Prolif & PN
17	-8.67	NULL	15 / 72	CC extracellular vesicular exosome
18	-8.13	NULL	12 / 74	BP platelet degranulation
19	-8.11	NULL	3 / 11	BP cellular copper ion homeostasis
20	-8.05	NULL	1 / 2	miRNA target-124a
21	-7.95	NULL	2 / 11	BP negative regulation of smooth muscle cell migration
22	-7.95	NULL	4 / 11	GSEA C2PARK_APL_PATHOGENESIS_DN
23	-7.94	NULL	2 / 10	BP lateral ventricle development
24	-7.85	NULL	2 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
25	-7.82	NULL	6 / 16	GSEA C2ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
26	-7.66	NULL	5 / 14	GSEA C2PROVENZANI_METASTASIS_DN
27	-7.39	NULL	4 / 15	GSEA C2RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
28	-7.28	NULL	6 / 12	BP hemidesmosome assembly
29	-7.26	NULL	6 / 43	CC platelet alpha granule lumen
30	-7.17	NULL	8 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
31	-7.16	NULL	4 / 9	GSEA C2REACTOME_SIGNALING_BY_VEGF
32	-7.14	NULL	7 / 16	MF fibronectin binding
33	-7.14	NULL	4 / 16	GSEA C2LEONARD_HYPOXIA
34	-7.13	NULL	2 / 9	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_UP
35	-7.13	NULL	5 / 16	GSEA C2REACTOME_CELLEXTRACELLULAR_MATRIX_INTERACTIONS
36	-7.02	NULL	3 / 13	GSEA C2AMIT_EGF_RESPONSE_480_HEL4
37	-6.98	NULL	4 / 13	GSEA C2LUNG_GASTRIC_CANCER
38	-6.98	NULL	4 / 8	GSEA C2SASAKI_TARGETS_OF_TP73_AND_TP63
39	-6.96	NULL	4 / 9	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_DN
40	-6.9	NULL	45 / 242	BP extracellular matrix organization

p-values



GW_123

Local Summary

%DE = 0.67
 # metagenes = 28
 # genes = 335
 # genes in genesets = 330

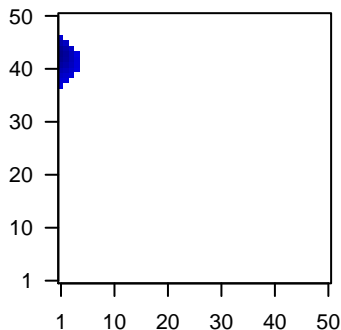
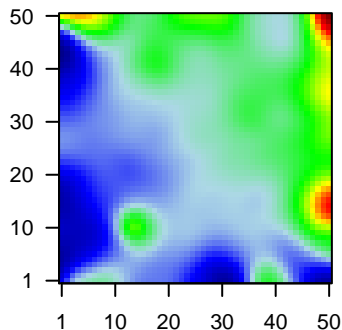
genes with $fdr < 0.1 = 157$ (33 + / 124 -)
 # genes with $fdr < 0.05 = 129$ (22 + / 107 -)
 # genes with $fdr < 0.01 = 113$ (20 + / 93 -)

<r> metagenes = 0.96
 <r> genes = 0.32

<FC> = -0.23
 <shrinkage-t> = -8.15
 <p-value> = 0
 <fdr> = 0.56

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	2152	-1.51	2e-16	3e-15	1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:HGNC Symbol;Acc:10000]
2	2167	-1.48	2e-16	3e-15	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol;Acc:10000]
3	3489	-1.34	2e-16	3e-15	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Symbol;Acc:10000]
4	3868	-1.47	2e-16	3e-15	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
5	3872	-1.61	2e-16	3e-15	1 x 43 keratin 17 [Source:HGNC Symbol;Acc:6427]
6	55214	1.45	2e-16	3e-15	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
7	6273	-1.56	2e-16	3e-15	1 x 44 S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:10000]
8	780851	1.47	2e-16	3e-15	2 x 39 small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc:10000]
9	780854	1.31	4e-16	4e-13	2 x 39 small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc:10000]
10	780853	1.27	4e-15	8e-13	2 x 39 small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc:10000]
11	4753	1.25	1e-14	2e-12	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
12	3552	-1.23	3e-14	2e-11	1 x 43 interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
13	5836	-1.19	2e-13	2e-11	1 x 44 phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:9700]
14	2810	-1.08	3e-13	5e-10	1 x 45 stratifin [Source:HGNC Symbol;Acc:10773]
15	7280	-1.12	5e-12	9e-10	1 x 45 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
16	27065	1.09	2e-11	9e-10	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1) [Source:HGNC Symbol;Acc:10000]
17	1515	-1.08	2e-11	2e-09	1 x 44 cathepsin V [Source:HGNC Symbol;Acc:2538]
18	760	-1.07	4e-11	1e-08	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
19	1288	1.03	2e-10	1e-08	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
20	3306	-1.03	2e-10	1e-08	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-13.53	NULL	63 / 572	Disease GUDJ_psooriasis up
2	-10.65	NULL	4 / 15	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_DN
3	-10.48	NULL	3 / 17	BP morphogenesis of an epithelium
4	-9.61	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
5	-9.03	NULL	1 / 6	Glio Martinez_Glio_hypometh
6	-9.03	NULL	15 / 76	BP epidermis development
7	-9.02	NULL	2 / 7	GSEA C2YE_METASTATIC_LIVER_CANCER
8	-8.89	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
9	-8.81	NULL	3 / 13	GSEA C2WANG_METHYLATED_IN_BREAST_CANCER
10	-8.77	NULL	1 / 2	miRNA target-346
11	-8.7	NULL	1 / 6	GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP
12	-8.65	NULL	11 / 82	MF structural constituent of cytoskeleton
13	-8.59	NULL	4 / 13	BP intermediate filament cytoskeleton organization
14	-8.56	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
15	-8.55	NULL	2 / 2	miRNA target-199a*
16	-8.52	NULL	3 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
17	-8.41	NULL	3 / 35	CC cell periphery
18	-8.25	NULL	3 / 25	BP response to zinc ion
19	-8.14	NULL	2 / 9	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP
20	-7.98	NULL	3 / 15	GSEA C2BROWNE_HCMV_INFECTION_2HR_DN
21	-7.9	NULL	3 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
22	-7.82	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C2
23	-7.59	NULL	2 / 12	GSEA C2SANCHEZ_MDM2_TARGETS
24	-7.47	NULL	3 / 16	GSEA C2LEONARD_HYPOXIA
25	-7.44	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_120_MCF10A
26	-7.3	NULL	2 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP
27	-7.2	NULL	2 / 12	MF fatty acid binding
28	-7.2	NULL	5 / 65	BP positive regulation of cell growth
29	-7.14	NULL	3 / 16	GSEA C2SCHAVOLT_TARGETS_OF_TP53_AND_TP63
30	-7.06	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
31	-7.01	NULL	2 / 14	GSEA C2NATSUME_RESPONSE_TO_INTERFERON_BETA_DN
32	-6.96	NULL	2 / 8	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
33	-6.94	NULL	20 / 135	H.Tiss WIRTH_Mucosa
34	-6.82	NULL	3 / 15	GSEA C2AIGNER_ZEB1_TARGETS
35	-6.75	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
36	-6.57	NULL	2 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
37	-6.53	NULL	1 / 10	GSEA C2REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASE
38	-6.5	NULL	15 / 82	CC intermediate filament
39	-6.41	NULL	1 / 10	BP white fat cell differentiation
40	-6.39	NULL	3 / 15	GSEA C2REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED

