

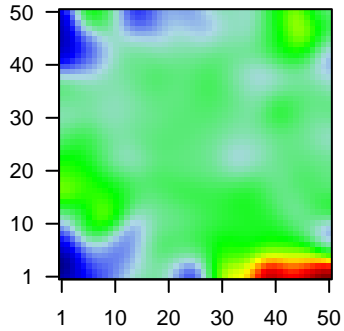
GW_008

Global Summary

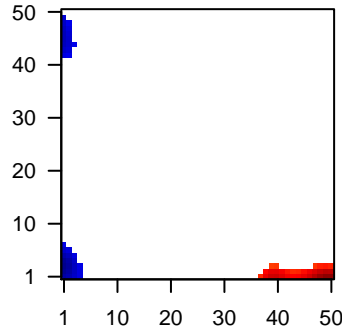
%DE = 0.13
 # genes with fdr < 0.2 = 1558 (893 + / 665 -)
 # genes with fdr < 0.1 = 1284 (747 + / 537 -)
 # genes with fdr < 0.05 = 1078 (648 + / 430 -)
 # genes with fdr < 0.01 = 754 (447 + / 307 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.87

Profile



Regulated Spots



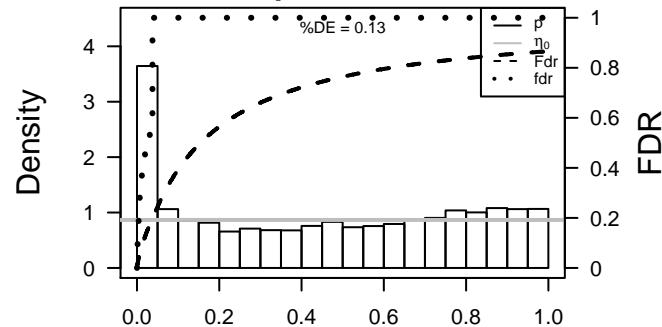
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	124	1.57	2e-16	5e-14	50 x 11 alcohol dehydrogenase 1A (class I), alpha polypeptide [Source:HGNC Symbol;Acc:20125]
2	126	1.45	2e-16	5e-14	50 x 12 alcohol dehydrogenase 1C (class I), gamma polypeptide [Source:HGNC Symbol;Acc:20125]
3	113146	-1.53	2e-16	5e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	1109	-1.43	2e-16	5e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:20125]
5	218	-1.5	2e-16	5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:20125]
6	501	-1.56	2e-16	5e-14	6 x 46 aldehyde dehydrogenase 7 family, member A1 [Source:HGNC Symbol;Acc:20125]
7	55107	-1.4	2e-16	5e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:20125]
8	341	1.96	2e-16	5e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
9	348	1.69	2e-16	5e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	10974	1.64	2e-16	5e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:20125]
11	339512	1.5	2e-16	5e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:20125]
12	875	1.55	2e-16	5e-14	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:151]
13	414062	1.43	2e-16	5e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:20125]
14	9560	1.39	2e-16	5e-14	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:20125]
15	26047	-1.39	2e-16	5e-14	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Acc:20125]
16	49860	-1.55	2e-16	5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1410	-1.44	2e-16	5e-14	25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
18	3627	1.92	2e-16	5e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:20125]
19	9547	-1.98	2e-16	5e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:20125]
20	284340	1.4	2e-16	5e-14	6 x 50 chemokine (C-X-C motif) ligand 17 [Source:HGNC Symbol;Acc:20125]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.51	NULL	417	H.Tiss WIRTH_Immune system
2	13.24	NULL	534	Chr Chr 8
3	12.43	NULL	1135	Chr Chr 19
4	10.3	NULL	618	Chr Chr 4
5	10.05	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
6	9.49	NULL	7	MMML C6SCIEJ_MMML 5
7	9.15	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
8	9.15	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
9	7.66	NULL	595	MF RNA binding
10	7.2	NULL	34	Chr Chr Y
11	6.7	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
12	6.67	NULL	187	Chr Chr 21
13	6.64	NULL	15	CC MHC class II protein complex
14	6.43	NULL	20	Lymphoma OSOLOWSKI_red UP
15	6.31	NULL	553	Cancer Lembcke_Colonc Inflammation
16	6.22	NULL	7	MMML C6SCIEJ_MMML 9
17	6.17	NULL	11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
18	6.16	NULL	312	BP immune response
19	6.07	NULL	11	GSEA C2BIOCARTA_THelper_PATHWAY
20	6	NULL	717	Chr Chr 16
<i>Underexpressed</i>				
1	-11.03	NULL	1033	Chr Chr 2
2	-9.1	NULL	449	Chr Chr 20
3	-8.5	NULL	375	Disease GUDJ_poriasis down
4	-8.06	NULL	242	BP extracellular matrix organization
5	-7.6	NULL	12	BP hemidesmosome assembly
6	-7.47	NULL	914	Chr Chr 3
7	-7.31	NULL	630	Chr Chr X
8	-7.11	NULL	76	BP epidermis development
9	-7.09	NULL	4	MMML C6SCIEJ_MMML 23
10	-7.07	NULL	699	Chr Chr 5
11	-6.97	NULL	250	Lymphoma ENZ_Stromal signature 1
12	-6.91	NULL	42	BP keratinization
13	-6.88	NULL	519	Chr Chr 14
14	-6.83	NULL	183	CC proteinaceous extracellular matrix
15	-6.72	NULL	1182	CC extracellular region
16	-6.57	NULL	190	CC extracellular matrix
17	-5.97	NULL	83	CC basement membrane
18	-5.84	NULL	53	BP keratinocyte differentiation
19	-5.74	NULL	6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
20	-5.59	NULL	10	CC hemoglobin complex

p-values



GW_008

Local Summary

%DE = 0.84
 # metagenes = 33
 # genes = 549
 # genes in genesets = 520
 # genes with $fdr < 0.1$ = 397 (385 + / 12 -)
 # genes with $fdr < 0.05$ = 358 (350 + / 8 -)
 # genes with $fdr < 0.01$ = 272 (267 + / 5 -)

<r> metagenes = 0.82

<r> genes = 0.39

<FC> = 0.46

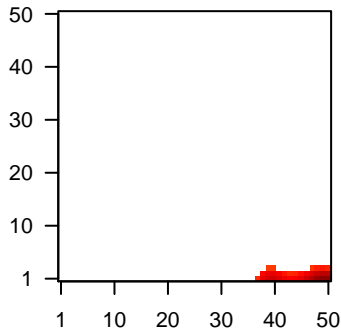
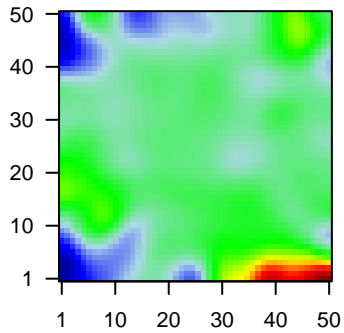
<shrinkage-t> = 16.22

<p-value> = 0

<fdr> = 0.4

Profile

Spot



Local Genelist

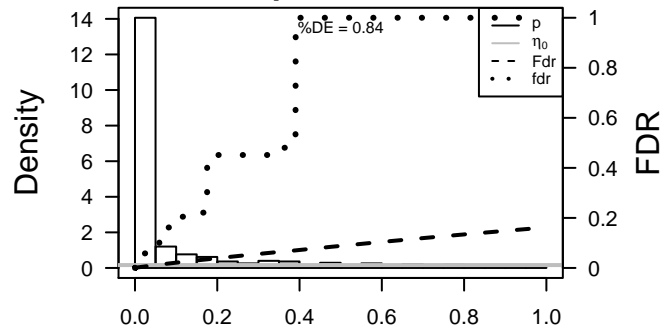
Rank	ID	log(FC)	fdr	p-value	Description
1	341	1.96	2e-16	3e-15	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
2	348	1.69	2e-16	3e-15	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	4283	1.53	2e-16	3e-15	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:613]
4	115361	1.6	2e-16	3e-15	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048]
5	3123	1.97	2e-16	3e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:HGNC Symbol;Acc:613]
6	10537	1.63	2e-16	3e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
7	8320	1.17	3e-12	2e-10	48 x 1 eomesodermin [Source:HGNC Symbol;Acc:3372]
8	9806	1.15	8e-12	2e-10	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycan
9	919	1.15	8e-12	2e-10	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
10	84061	1.15	9e-12	2e-10	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
11	64170	1.14	1e-11	9e-10	45 x 1 caspase recruitment domain family, member 9 [Source:HGNC Symbol;Acc:613]
12	126205	1.12	3e-11	9e-10	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbol;Acc:613]
13	442578	1.11	4e-11	9e-10	39 x 1
14	4050	1.11	4e-11	4e-09	50 x 1 lymphotoxin beta (TNF superfamily, member 3) [Source:HGNC Symbol;Acc:613]
15	136051	1.08	1e-10	4e-09	40 x 1 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
16	7454	1.07	2e-10	4e-09	50 x 1 Wiskott-Aldrich syndrome [Source:HGNC Symbol;Acc:12731]
17	25862	1.07	2e-10	4e-09	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2048]
18	440157	1.07	2e-10	8e-09	39 x 1
19	57835	1.05	3e-10	8e-09	40 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7I]
20	113277	1.05	4e-10	8e-09	40 x 1 transmembrane protein 106A [Source:HGNC Symbol;Acc:28880]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	26.4	NULL	100 / 417	H.Tiss WIRTH_Immune system
2	19.92	NULL	100 / 553	Cancer Lembecke_Colonc Inflammation
3	19.53	NULL	14 / 15	CC MHC class II protein complex
4	18.82	NULL	3 / 3	MMML C6S CIEJ_MMML 7
5	16.9	NULL	63 / 312	BP immune response
6	15.97	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
7	14.58	NULL	6 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
8	13.39	NULL	20 / 60	BP T cell costimulation
9	13.16	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
10	13.13	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
11	12.99	NULL	7 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
12	12.55	NULL	19 / 74	BP regulation of immune response
13	12.44	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
14	12.26	NULL	5 / 13	MMML C6S CIEJ_MMML 6
15	12.01	NULL	43 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	12.01	NULL	43 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	12.01	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	12.01	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
19	11.96	NULL	7 / 13	Cancer GENTLES_modul18
20	11.5	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
21	11.14	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
22	10.87	NULL	2 / 11	BP high-density lipoprotein particle remodeling
23	10.64	NULL	16 / 47	BP antigen processing and presentation
24	10.46	NULL	28 / 162	CC external side of plasma membrane
25	10.31	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
26	10.24	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
27	10.02	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
28	9.83	NULL	6 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
29	9.79	NULL	2 / 4	MMML C6S CIEJ_MMML 2
30	9.73	NULL	9 / 52	Chr HSCR6_MHC_QBL
31	9.71	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
32	9.59	NULL	4 / 11	GSEA C2APPEL_IMATINIB_RESPONSE
33	9.55	NULL	4 / 10	BP negative thymic T cell selection
34	9.46	NULL	2 / 14	CC very-low-density lipoprotein particle
35	9.41	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
36	9.25	NULL	5 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
37	9.24	NULL	4 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
38	9.15	NULL	3 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
39	9.11	NULL	10 / 43	BP positive regulation of T cell proliferation
40	9.09	NULL	2 / 15	BP cholesterol efflux

p-values



GW_008

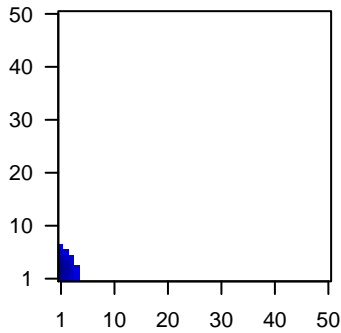
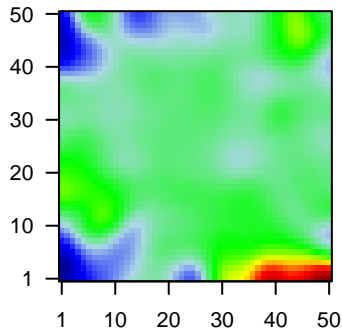
Local Summary

%DE = 0.69
 # metagenes = 21
 # genes = 338
 # genes in genesets = 336
 # genes with $fdr < 0.1$ = 176 (15 + / 161 -)
 # genes with $fdr < 0.05$ = 129 (10 + / 119 -)
 # genes with $fdr < 0.01$ = 119 (10 + / 109 -)

<r> metagenes = 0.94
 <r> genes = 0.34
 <FC> = -0.31
 <shrinkage-t> = -10.74
 <p-value> = 0
 <fdr> = 0.56

Profile

Spot



Local Genelist

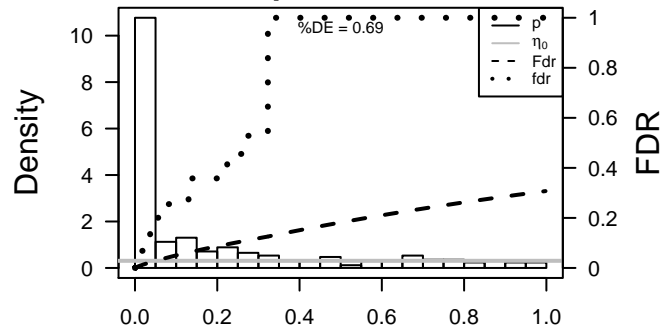
Rank	ID	log(FC)	fdr	p-value	Description
1	55107	-1.4	2e-16	3e-15	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
2	414062	1.43	2e-16	3e-15	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc]
3	131566	-1.39	2e-16	3e-15	1 x 4 discoidin, CUB and LCCL domain containing 2 [Source:HGNC]
4	3040	-1.75	2e-16	3e-15	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	4319	-1.77	2e-16	3e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy]
6	4316	-1.44	2e-16	3e-15	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC]
7	4973	1.75	2e-16	3e-15	1 x 1 oxidized low density lipoprotein (lectin-like) receptor 1 [Sourc]
8	3371	-1.65	2e-16	3e-15	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
9	7045	-1.17	3e-14	3e-12	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG]
10	12	-1.26	6e-14	4e-12	1 x 1
11	7057	-1.25	1e-13	4e-12	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
12	4314	-1.24	1e-13	2e-11	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou]
13	8406	-1.22	4e-13	2e-10	2 x 1 sushi-repeat containing protein, X-linked [Source:HGNC Syr]
14	10630	-1.17	4e-12	2e-10	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]
15	3918	-1.17	4e-12	6e-10	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
16	27253	1.14	1e-11	7e-10	4 x 1 protocadherin 17 [Source:HGNC Symbol;Acc:14267]
17	6696	1.13	2e-11	2e-08	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125]
18	857	-1.07	2e-10	2e-08	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A]
19	9805	-1.05	5e-10	2e-08	1 x 7 secernin 1 [Source:HGNC Symbol;Acc:22192]
20	90	-1.04	6e-10	4e-08	2 x 4 activin A receptor, type I [Source:HGNC Symbol;Acc:171]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.04	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
2	-19.46	NULL	73 / 242	BP extracellular matrix organization
3	-18.09	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
4	-17.81	NULL	60 / 190	CC extracellular matrix
5	-16.75	NULL	13 / 35	Glio Colman_survival_associated
6	-15.38	NULL	8 / 16	MF fibronectin binding
7	-15.04	NULL	70 / 250	LymphomaENZ_Stromal signature 1
8	-14.51	NULL	7 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
9	-13.88	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
10	-13.86	NULL	38 / 183	CC proteinaceous extracellular matrix
11	-13.83	NULL	60 / 403	BP cell adhesion
12	-13.67	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
13	-13.45	NULL	15 / 16	MMML C6CIEJ_MMML 1
14	-13.04	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
15	-12.94	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
16	-12.85	NULL	6 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
17	-12.77	NULL	4 / 12	MF transforming growth factor beta binding
18	-12.69	NULL	79 / 683	CC extracellular space
19	-12.68	NULL	32 / 69	BP extracellular matrix disassembly
20	-12.61	NULL	25 / 83	CC basement membrane
21	-12.36	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
22	-12.3	NULL	29 / 64	BP collagen catabolic process
23	-12.16	NULL	5 / 12	BP hemidesmosome assembly
24	-11.81	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
25	-11.8	NULL	1 / 3	Glio wilscher_GBM_Verhaak-PNwt_expression_N_down
26	-11.8	NULL	1 / 3	Glio wilscher_GBM_Verhaak-PNmut_expression_N_up
27	-11.71	NULL	4 / 16	GSEA C2I_PROSTATE_CANCER_EPIGENETIC
28	-11.64	NULL	3 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
29	-11.3	NULL	6 / 11	MMML C6CIEJ_MMML 31
30	-11.16	NULL	6 / 37	Glio Christensen_hypomethylated_in_ependymoma
31	-11.1	NULL	2 / 8	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
32	-10.91	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
33	-10.78	NULL	6 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
34	-10.72	NULL	4 / 13	Cancer GENTLES_modul17
35	-10.72	NULL	1 / 4	MMML C6CIEJ_MMML 23
36	-10.66	NULL	6 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
37	-10.62	NULL	114 / 1182	CC extracellular region
38	-10.44	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
39	-10.43	NULL	5 / 14	GSEA C2SIMBLAN_UV_RESPONSE_IMMORTALIZED_DN
40	-10.3	NULL	8 / 51	BP regulation of cell migration

p-values



GW_008

Local Summary

%DE = 0.78
 # metagenes = 16
 # genes = 236
 # genes in genesets = 231

 # genes with $fdr < 0.1$ = 146 (26 + / 120 -)
 # genes with $fdr < 0.05$ = 143 (25 + / 118 -)
 # genes with $fdr < 0.01$ = 105 (17 + / 88 -)

 $\langle r \rangle$ metagenes = 0.91
 $\langle r \rangle$ genes = 0.4

 $\langle FC \rangle = -0.38$
 $\langle \text{shrinkage-t} \rangle = -13.51$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.42$

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	113146	-1.53	2e-16	8e-16	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	9547	-1.98	2e-16	8e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:10122]
3	414325	-1.46	2e-16	8e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
4	1673	-2.23	2e-16	8e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
5	9982	-1.3	2e-16	8e-16	1 x 47 fibroblast growth factor binding protein 1 [Source:HGNC Symbol;Acc:10122]
6	3848	-1.6	2e-16	8e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
7	3861	-2.71	2e-16	8e-16	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
8	388533	-1.86	2e-16	8e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC Symbol;Acc:31702]
9	84648	-1.64	2e-16	8e-16	1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615]
10	55214	-1.99	2e-16	8e-16	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
11	5266	-2.11	2e-16	8e-16	1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Acc:10122]
12	5744	-1.42	2e-16	8e-16	1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;Acc:10122]
13	338324	-1.56	2e-16	8e-16	1 x 48 S100 calcium binding protein A7A [Source:HGNC Symbol;Acc:10122]
14	6701	-1.57	2e-16	8e-16	1 x 49 small proline-rich protein 2B [Source:HGNC Symbol;Acc:112]
15	6706	-2.28	2e-16	8e-16	1 x 48 small proline-rich protein 2G [Source:HGNC Symbol;Acc:112]
16	3306	-1.36	7e-16	6e-14	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]
17	1308	-1.33	3e-15	6e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
18	1828	-1.32	4e-15	6e-14	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	1382	1.32	5e-15	6e-14	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol;Acc:10122]
20	2167	-1.32	5e-15	2e-12	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol;Acc:10122]

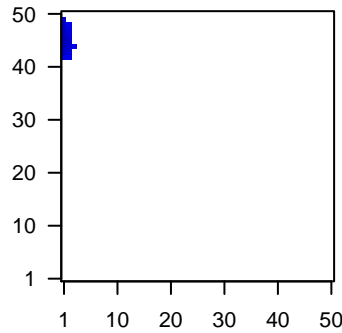
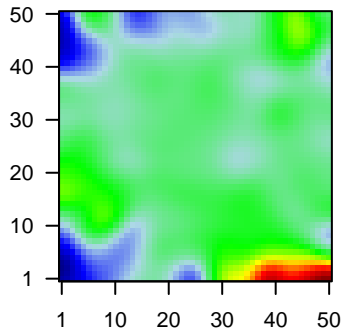
Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.17	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
2	-19.8	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
3	-17.78	NULL	18 / 76	BP epidermis development
4	-15.68	NULL	4 / 12	BP hemidesmosome assembly
5	-15.48	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
6	-14.83	NULL	3 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
7	-14.53	NULL	9 / 42	BP keratinization
8	-13.93	NULL	3 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
9	-13.87	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
10	-13.67	NULL	8 / 21	CC cornified envelope
11	-13.65	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
12	-13.56	NULL	18 / 82	CC intermediate filament
13	-13.3	NULL	10 / 44	CC keratin filament
14	-12.76	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
15	-12.65	NULL	5 / 16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
16	-12.41	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
17	-12.02	NULL	4 / 38	BP epithelial cell differentiation
18	-11.93	NULL	3 / 13	BP intermediate filament cytoskeleton organization
19	-11.92	NULL	12 / 53	BP keratinocyte differentiation
20	-10.49	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
21	-10.37	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
22	-10.37	NULL	79 / 572	Disease GUDJ_psooriasis up
23	-10.35	NULL	2 / 13	GSEA C2HAN_SATB1_TARGETS_DN
24	-10.13	NULL	2 / 15	GSEA C2FRIDMAN_IMMORTALIZATION_DN
25	-9.93	NULL	2 / 11	GSEA C2LEI_MYB_TARGETS
26	-9.71	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
27	-9.54	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_B_DN
28	-9.22	NULL	3 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
29	-9.01	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	-8.92	NULL	19 / 186	MF structural molecule activity
31	-8.9	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
32	-8.86	NULL	3 / 35	CC cell periphery
33	-8.74	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
34	-8.7	NULL	1 / 10	GSEA C2THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
35	-8.7	NULL	3 / 23	MF peptidase inhibitor activity
36	-8.49	NULL	5 / 49	Glio Christensen_hypomethylated_in_primary_glioblastoma
37	-8.36	NULL	2 / 11	BP positive regulation of positive chemotaxis
38	-8.35	NULL	2 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_UP
39	-8.32	NULL	42 / 1182	CC extracellular region
40	-8.29	NULL	2 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP

Profile

Spot



p-values

