

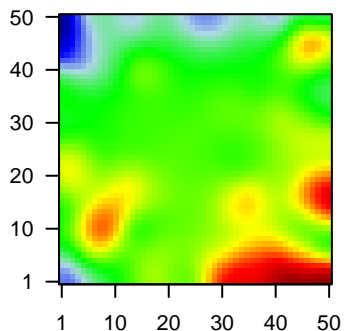
GW_096

Global Summary

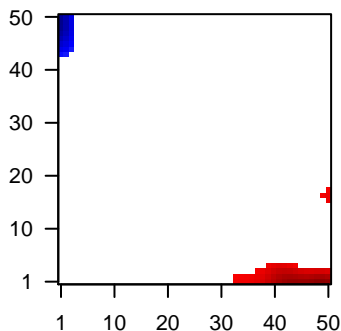
%DE = 0.15
 # genes with $fdr < 0.2$ = 1877 (1066 + / 811 -)
 # genes with $fdr < 0.1$ = 1390 (789 + / 601 -)
 # genes with $fdr < 0.05$ = 1068 (600 + / 468 -)
 # genes with $fdr < 0.01$ = 731 (404 + / 327 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.85

Profile



Regulated Spots



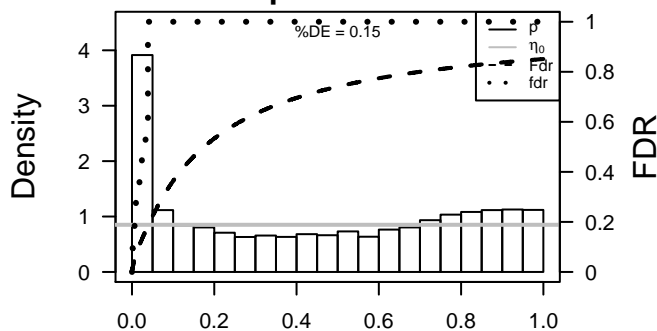
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	21	1.97	2e-16	5e-14	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
2	57016	-2.91	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	8644	-2.62	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym
4	115701	2.21	2e-16	5e-14	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
5	387695	-2.27	2e-16	5e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
6	399948	1.96	2e-16	5e-14	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
7	260436	3.99	2e-16	5e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
8	760	-2.23	2e-16	5e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	57172	2.03	2e-16	5e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
10	875	2.07	2e-16	5e-14	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15
11	4680	-2.13	2e-16	5e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
12	9635	-2.63	2e-16	5e-14	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
13	1365	2	2e-16	5e-14	50 x 15 claudin 3 [Source:HGNC Symbol;Acc:2045]
14	169044	2.59	2e-16	5e-14	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
15	1281	-1.87	2e-16	5e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
16	1593	2.32	2e-16	5e-14	50 x 3 cytochrome P450, family 27, subfamily A, polypeptide 1 [Sou
17	2532	1.94	2e-16	5e-14	50 x 5 Duffy blood group, atypical chemokine receptor [Source:HGNC
18	414325	-2.52	2e-16	5e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	2167	-2.11	2e-16	5e-14	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
20	2171	-2.45	2e-16	5e-14	1 x 46 fatty acid binding protein 5 (psoriasis-associated) [Source:HC

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.28	NULL	417	H.Tiss WIRTH_Immune system
2	11.56	NULL	386	Chr Chr 22
3	10.77	NULL	1135	Chr Chr 19
4	8.19	NULL	51	BP type I interferon signaling pathway
5	8.13	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
6	7.19	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	6.69	NULL	74	BP regulation of immune response
8	6.51	NULL	274	LymphomBPANG_IL21 DN
9	6.38	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
10	6.28	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	6	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
12	5.88	NULL	12	GSEA C2BIOCARTA_CTL_PATHWAY
13	5.73	NULL	14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
14	5.69	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	5.66	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
16	5.61	NULL	1095	TF HEBENSTREIT_high expression TF
17	5.53	NULL	312	BP immune response
18	5.51	NULL	1574	BP transcription, DNA-templated
19	5.48	NULL	11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
20	5.47	NULL	1749	MF DNA binding
<i>Underexpressed</i>				
1	-18.4	NULL	135	H.Tiss WIRTH_Mucosa
2	-13.53	NULL	572	Disease GUDJ_psoriasis up
3	-13.24	NULL	21	CC cornified envelope
4	-10.66	NULL	42	BP keratinization
5	-10.63	NULL	53	BP keratinocyte differentiation
6	-9.9	NULL	76	BP epidermis development
7	-9.34	NULL	16	MMML C6BICIEJ_MMML_1
8	-9.06	NULL	1182	CC extracellular region
9	-9.01	NULL	19	BP peptide cross-linking
10	-8.93	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	-8.69	NULL	190	CC extracellular matrix
12	-8.09	NULL	683	CC extracellular space
13	-7.82	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
14	-7.51	NULL	714	Chr Chr 6
15	-7.31	NULL	280	Chr Chr 13
16	-7.2	NULL	318	miRNA target-miR-590-3p
17	-7.07	NULL	436	miRNA target-miR-34a
18	-6.9	NULL	12	miRNA target-miR-29c
19	-6.75	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	-6.51	NULL	9	GSEA C2WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP

p-values



GW_096

Local Summary

%DE = 0.88
 # metagenes = 56
 # genes = 708
 # genes in genesets = 677

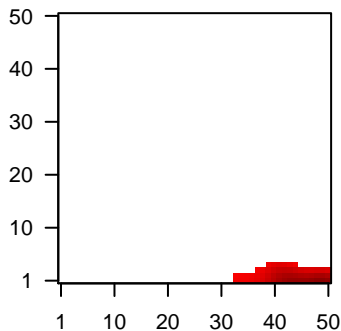
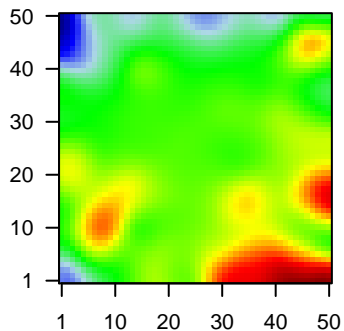
genes with $fdr < 0.1 = 517$ (510 + / 7 -)
 # genes with $fdr < 0.05 = 454$ (447 + / 7 -)
 # genes with $fdr < 0.01 = 326$ (324 + / 2 -)

<r> metagenes = 0.8
 <r> genes = 0.36

<FC> = 0.64
 <shrinkage-t> = 22.49
 <p-value> = 0
 <fdr> = 0.44

Profile

Spot



Local Genelist

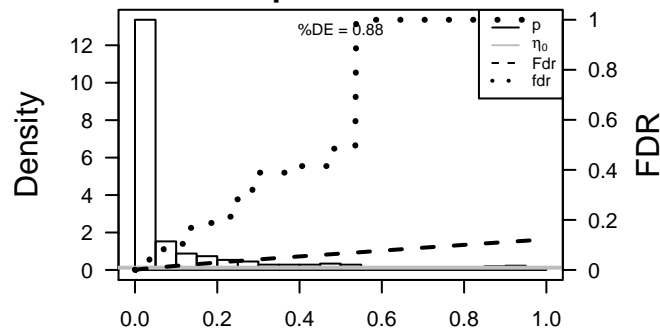
Rank	ID	log(FC)	fdr	p-value	Description
1	115701	2.21	2e-16	2e-15	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
2	260436	3.99	2e-16	2e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
3	57172	2.03	2e-16	2e-15	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
4	169044	2.59	2e-16	2e-15	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
5	1593	2.32	2e-16	2e-15	50 x 3 cytochrome P450, family 27, subfamily A, polypeptide 1 [Sou
6	25849	2.46	2e-16	2e-15	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HK
7	5730	2.78	2e-16	2e-15	50 x 1 prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
8	57484	2.35	2e-16	2e-15	50 x 2 ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
9	9806	2.38	2e-16	2e-15	50 x 1 sparc/osteonectin, cwcv and kazal-like domains proteoglycar
10	10537	1.99	2e-16	2e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
11	7412	2.1	2e-16	2e-15	50 x 1 vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
12	1236	1.91	7e-16	6e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
13	54855	1.89	1e-15	3e-13	49 x 1 family with sequence similarity 46, member C [Source:HGNC
14	22809	1.85	5e-15	9e-13	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:7?
15	8728	1.82	2e-14	1e-12	50 x 3 ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
16	8605	1.79	4e-14	1e-12	50 x 3 phospholipase A2, group IVC (cytosolic, calcium-independe
17	11040	1.79	4e-14	1e-12	49 x 1 pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
18	4248	1.78	5e-14	7e-12	45 x 1 mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucos
19	930	1.75	1e-13	8e-11	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
20	919	1.68	1e-12	8e-11	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	26.21	NULL	122 / 417	H.Tiss WIRTH_Immune system
2	17.1	NULL	104 / 553	Cancer Lembecke_Colonc Inflammation
3	14.65	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
4	14.63	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	14.04	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
6	13.94	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
7	12.9	NULL	10 / 13	Cancer GENTLES_modul18
8	12.47	NULL	7 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
9	12.09	NULL	8 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
10	10.98	NULL	5 / 15	GSEA C2INDGREN_BLADEER_CANCER_HIGH_RECURRENCE
11	10.71	NULL	7 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
12	10.68	NULL	68 / 312	BP immune response
13	10.52	NULL	20 / 74	BP regulation of immune response
14	10.34	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
15	10.32	NULL	31 / 162	CC external side of plasma membrane
16	10.01	NULL	2 / 4	MMML C2SCIEJ_MMML 2
17	9.61	NULL	15 / 45	BP T cell activation
18	9.59	NULL	5 / 10	GSEA C2LEE_EARLY_T_LYMPHOCYTE_DN
19	9.58	NULL	6 / 14	GSEA C2BIOCARTA_IL12_PATHWAY
20	9.55	NULL	5 / 8	GSEA C2BIOCARTA_TCAPOPTOSIS_PATHWAY
21	9.55	NULL	5 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
22	9.49	NULL	10 / 28	LymphonAVE_Immune response 1
23	9.48	NULL	5 / 10	BP negative thymic T cell selection
24	9.26	NULL	34 / 204	BP cell surface receptor signaling pathway
25	9.11	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
26	9.02	NULL	2 / 4	MMML C2SCIEJ_MMML 44
27	8.9	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
28	8.82	NULL	5 / 12	GSEA C2BIOCARTA_CTLA4_PATHWAY
29	8.8	NULL	5 / 11	BP positive regulation of B cell differentiation
30	8.75	NULL	5 / 14	GSEA C2BIOCARTA_STATHMIN_PATHWAY
31	8.69	NULL	6 / 12	CC T cell receptor complex
32	8.62	NULL	9 / 16	GSEA C2SU_THYMUS
33	8.42	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
34	8.41	NULL	4 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
35	8.09	NULL	5 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE
36	8.09	NULL	6 / 13	GSEA C2BIOCARTA_CSK_PATHWAY
37	7.84	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
38	7.64	NULL	5 / 12	BP immunoglobulin mediated immune response
39	7.61	NULL	11 / 43	BP positive regulation of T cell proliferation
40	7.41	NULL	11 / 28	BP B cell receptor signaling pathway

p-values



GW_096

Local Summary

%DE = 0.77
 # metagenes = 4
 # genes = 101
 # genes in genesets = 101

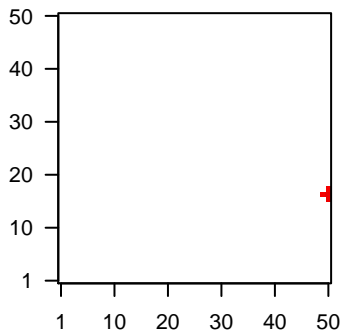
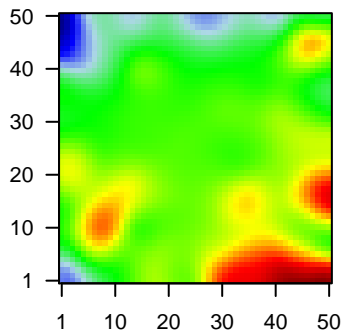
genes with $fdr < 0.1$ = 68 (68 + / 0 -)
 # genes with $fdr < 0.05$ = 56 (56 + / 0 -)
 # genes with $fdr < 0.01$ = 42 (42 + / 0 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.38

$\langle FC \rangle = 0.73$
 $\langle \text{shrinkage-t} \rangle = 25.48$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.45$

Profile

Spot



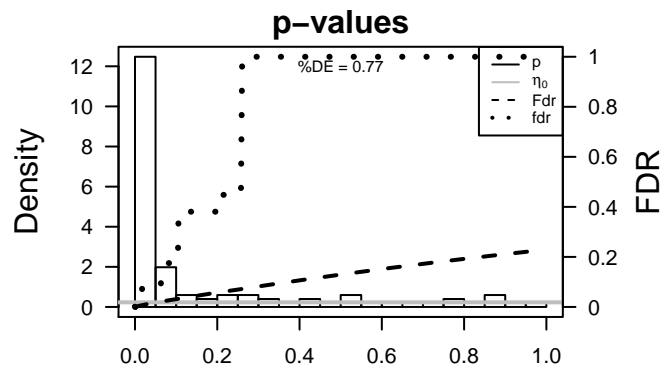
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	21	1.97	2e-16	1e-15	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
2	3670	1.97	2e-16	1e-15	50 x 17 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
3	494470	2.04	2e-16	1e-15	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
4	6263	1.97	2e-16	1e-15	50 x 18 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
5	10439	1.79	4e-14	9e-13	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
6	54959	1.77	8e-14	9e-13	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;
7	728715	1.76	1e-13	1e-10	50 x 18
8	57556	1.63	5e-12	1e-10	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic
9	83988	1.61	9e-12	4e-10	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
10	221061	1.57	3e-11	2e-09	50 x 16 family with sequence similarity 171, member A1 [Source:HG
11	153579	1.52	1e-10	2e-08	50 x 17 butyrophilin-like 9 [Source:HGNC Symbol;Acc:24176]
12	29091	1.45	8e-10	4e-08	50 x 17 syntaxin binding protein 6 (amisyn) [Source:HGNC Symbol;A
13	79924	1.41	2e-09	1e-07	50 x 18 adrenomedullin 2 [Source:HGNC Symbol;Acc:28898]
14	3792	1.36	9e-09	1e-07	50 x 17 Kell blood group, metallo-endopeptidase [Source:HGNC Syrr
15	91461	1.35	1e-08	9e-07	50 x 17 protein kinase domain containing, cytoplasmic [Source:HGNC
16	26002	1.26	9e-08	9e-07	50 x 16 monooxygenase, DBH-like 1 [Source:HGNC Symbol;Acc:211
17	9915	1.25	1e-07	9e-07	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
18	63917	1.24	2e-07	9e-07	50 x 16 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acet
19	10983	1.13	2e-07	9e-07	50 x 17 cyclin I [Source:HGNC Symbol;Acc:1595]
20	23492	1.23	2e-07	5e-06	50 x 16 chromobox homolog 7 [Source:HGNC Symbol;Acc:1557]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.42	NULL	1 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
2	13.19	NULL	4 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
3	12.6	NULL	1 / 2	miRNA target-153
4	11.77	NULL	2 / 15	BP retinal ganglion cell axon guidance
5	11.76	NULL	2 / 9	GSEA C2GOZGIT_ESR1_TARGETS_DN
6	11.35	NULL	2 / 15	BP positive regulation vascular endothelial growth factor production
7	10.31	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_DN
8	9.8	NULL	1 / 10	GSEA C2KEGG_ALZHEIMERS_DISEASE
9	9.64	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
10	9.33	NULL	1 / 3	miRNA target-148a
11	9.25	NULL	1 / 11	GSEA C2HUTTMANN_B CLL_POOR_SURVIVAL_UP
12	9.25	NULL	1 / 11	GSEA C2KEGG_CALCIIUM_SIGNALING_PATHWAY
13	9.25	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
14	9.24	NULL	1 / 11	MF enhancer sequence-specific DNA binding
15	9.24	NULL	1 / 11	BP innervation
16	9.24	NULL	1 / 11	BP negative regulation of intracellular estrogen receptor signaling path
17	9.16	NULL	1 / 8	GSEA C2REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
18	9.1	NULL	3 / 20	MF RNA polymerase II transcription coactivator activity
19	8.97	NULL	5 / 127	miRNA target-212-132
20	8.89	NULL	1 / 10	GSEA C2BROWNE_HCMV_INFECTION_12HR_UP
21	8.89	NULL	1 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
22	8.77	NULL	1 / 12	BP neuron fate specification
23	8.69	NULL	1 / 7	GSEA C2REACTOME_CALCITONIN LIKE_LIGAND_RECEPTORS
24	8.38	NULL	3 / 15	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
25	8.36	NULL	1 / 13	BP cellular response to glucocorticoid stimulus
26	8.35	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
27	8.1	NULL	1 / 10	BP centrosome localization
28	8.09	NULL	1 / 5	GSEA C2PASTURAL_RIZ1_TARGETS_DN
29	8.01	NULL	2 / 13	BP developmental pigmentation
30	8.01	NULL	5 / 139	miRNA target-129
31	8.01	NULL	1 / 14	GSEA C2ROSS_AML_OF_FAB_M7_TYPE
32	7.99	NULL	1 / 14	BP pharyngeal system development
33	7.99	NULL	1 / 14	GSEA C2RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN
34	7.96	NULL	1 / 12	GSEA C2CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
35	7.96	NULL	1 / 12	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_DN
36	7.96	NULL	1 / 12	GSEA C2ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
37	7.76	NULL	5 / 78	BP positive regulation of angiogenesis
38	7.68	NULL	1 / 15	BP striated muscle contraction
39	7.59	NULL	1 / 13	GSEA C2COLDREN_GEFITINIB_RESISTANCE_UP
40	7.59	NULL	1 / 13	GSEA C2STEIN_ESR1_TARGETS



GW_096

Local Summary

%DE = 0.85
 # metagenes = 23
 # genes = 312
 # genes in genesets = 304

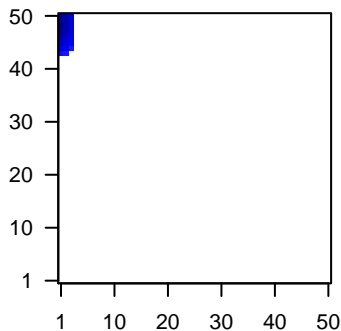
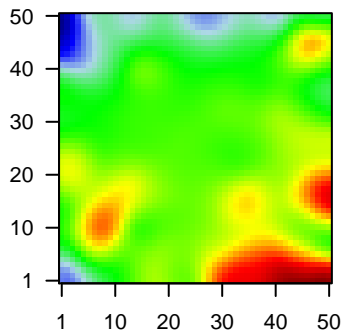
genes with $fdr < 0.1 = 239$ (14 + / 225 -)
 # genes with $fdr < 0.05 = 239$ (14 + / 225 -)
 # genes with $fdr < 0.01 = 195$ (9 + / 186 -)

<r> metagenes = 0.9
 <r> genes = 0.38

<FC> = -0.9
 <shrinkage-t> = -31.56
 <p-value> = 0
 <fdr> = 0.27

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description	
1	57016	-2.91	2e-16	3e-16	1 x 50	aldo-keto reductase family 1, member B10 (aldose reductase)
2	8644	-2.62	2e-16	3e-16	1 x 50	aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
3	387695	-2.27	2e-16	3e-16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Synt
4	760	-2.23	2e-16	3e-16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	4680	-2.13	2e-16	3e-16	1 x 50	carcinoembryonic antigen-related cell adhesion molecule 6 (i
6	9635	-2.63	2e-16	3e-16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
7	414325	-2.52	2e-16	3e-16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	2167	-2.11	2e-16	3e-16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
9	2171	-2.45	2e-16	3e-16	1 x 46	fatty acid binding protein 5 (psoriasis-associated) [Source:HC
10	9982	-2.22	2e-16	3e-16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym]
11	2697	-2.03	2e-16	3e-16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;A
12	2706	-1.77	2e-16	3e-16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
13	10804	-2.75	2e-16	3e-16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
14	2877	-2.8	2e-16	3e-16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy]
15	3861	-2.69	2e-16	3e-16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
16	286887	-2.29	2e-16	3e-16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
17	388533	-3.46	2e-16	3e-16	1 x 49	keratinocyte differentiation-associated protein [Source:HGNC
18	653499	-1.93	2e-16	3e-16	1 x 47	lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol
19	5744	-2.13	2e-16	3e-16	1 x 43	parathyroid hormone-like hormone [Source:HGNC Symbol;A
20	374897	-2.43	2e-16	3e-16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-44.45	NULL	88 / 135	H.Tiss WIRTH_Mucosa
2	-34.49	NULL	18 / 21	CC cornified envelope
3	-28.74	NULL	113 / 572	Disease GUDJ_psoriasis_up
4	-28.02	NULL	20 / 42	BP keratinization
5	-26.54	NULL	27 / 76	BP epidermis development
6	-24.94	NULL	24 / 53	BP keratinocyte differentiation
7	-20.26	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	-17.03	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
9	-15.91	NULL	10 / 19	BP peptide cross-linking
10	-14.24	NULL	4 / 12	H.Tiss WIRTH_Prim_lymphoid organs
11	-14.14	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
12	-13.86	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
13	-12.9	NULL	12 / 21	CC desmosome
14	-12.63	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
15	-12.49	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
16	-12.35	NULL	8 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	-12.2	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
18	-12.07	NULL	5 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
19	-12	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
20	-11.9	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
21	-11.59	NULL	3 / 8	GSEA C2LIU_CDXX2_TARGETS_DN
22	-11.44	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
23	-11.4	NULL	3 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
24	-11.2	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
25	-11.15	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
26	-11.11	NULL	3 / 15	CC connexon complex
27	-10.87	NULL	69 / 1182	CC extracellular region
28	-10.77	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
29	-10.62	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
30	-10.26	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
31	-9.94	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
32	-9.79	NULL	10 / 52	BP negative regulation of endopeptidase activity
33	-9.73	NULL	4 / 21	CC gap junction
34	-9.53	NULL	5 / 25	BP response to zinc ion
35	-9.52	NULL	4 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
36	-9.51	NULL	4 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
37	-9.35	NULL	2 / 9	GSEA C2WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
38	-9.29	NULL	3 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
39	-9.28	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
40	-9.23	NULL	3 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN

