

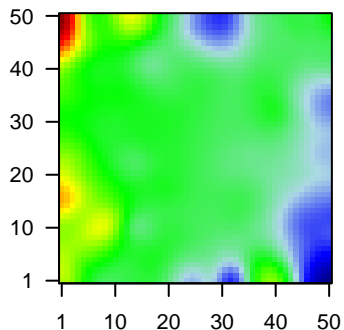
GW_022

Global Summary

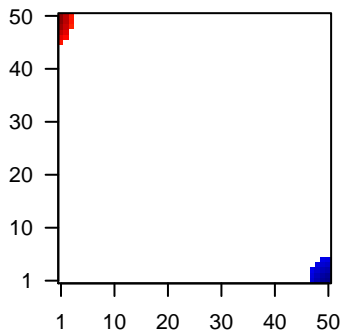
%DE = 0.14
 # genes with $fdr < 0.2$ = 1678 (959 + / 719 -)
 # genes with $fdr < 0.1$ = 1273 (786 + / 487 -)
 # genes with $fdr < 0.05$ = 1040 (664 + / 376 -)
 # genes with $fdr < 0.01$ = 680 (475 + / 205 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.86

Profile



Regulated Spots



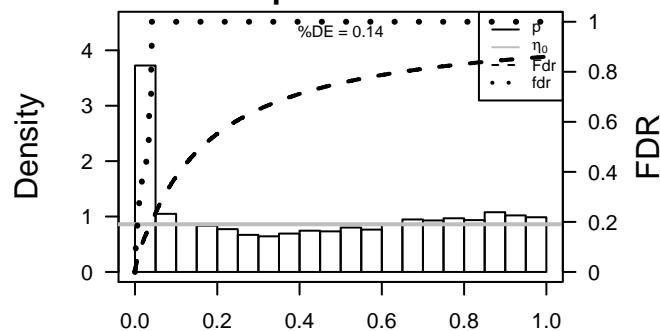
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	154664	1.49	2e-16 4e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:20125]
2	113146	1.51	2e-16 4e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	1.65	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	1.46	2e-16 4e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:20125]
5	1646	1.38	2e-16 4e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Symbol;Acc:20125]
6	8644	2.35	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:20125]
7	1109	2.41	2e-16 4e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:20125]
8	218	1.56	2e-16 4e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:20125]
9	55107	1.53	2e-16 4e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:20125]
10	339512	2.3	2e-16 4e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:20125]
11	8900	1.6	2e-16 4e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
12	595	1.46	2e-16 4e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
13	84518	1.9	2e-16 4e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
14	1277	1.38	2e-16 4e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	169044	1.67	2e-16 4e-14	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298]
16	49860	1.4	2e-16 4e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1469	2.19	2e-16 4e-14	9 x 6 cystatin SN [Source:HGNC Symbol;Acc:2473]
18	1525	1.67	2e-16 4e-14	10 x 50 coxsackie virus and adenovirus receptor [Source:HGNC Symbol;Acc:20125]
19	3627	-1.63	2e-16 4e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:20125]
20	9547	1.45	2e-16 4e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:20125]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.87	NULL	42	BP keratinization
2	16.8	NULL	135	H.Tiss WIRTH_Mucosa
3	14.36	NULL	21	CC cornified envelope
4	12.84	NULL	53	BP keratinocyte differentiation
5	11.05	NULL	1135	Chr Chr 19
6	10.93	NULL	76	BP epidermis development
7	10.75	NULL	14	GSEA C2NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON
8	10.38	NULL	572	Disease GUDJ_psooriasis up
9	8.52	NULL	19	BP peptide cross-linking
10	8.41	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	7.82	NULL	15	GSEA C2NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON
12	7.7	NULL	530	Cancer Lembcke_Normal vs Adenoma
13	7.28	NULL	64	BP collagen catabolic process
14	7	NULL	504	Chr Chr 15
15	6.85	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
16	6.69	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
17	6.31	NULL	449	Chr Chr 20
18	6.27	NULL	717	Chr Chr 16
19	6.24	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
20	6.17	NULL	14	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G4
<i>Underexpressed</i>				
1	-11.1	NULL	417	H.Tiss WIRTH_Immune system
2	-9.62	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
3	-8.37	NULL	51	BP type I interferon signaling pathway
4	-8.28	NULL	633	Chr Chr 9
5	-7.78	NULL	312	BP immune response
6	-7.62	NULL	185	Cancer SPANG_LPS-index2
7	-7.11	NULL	204	BP cytokine-mediated signaling pathway
8	-6.75	NULL	316	Cancer SPANG_BCL6-index2
9	-6.58	NULL	47	BP antigen processing and presentation
10	-6.52	NULL	60	BP interferon-gamma-mediated signaling pathway
11	-6.48	NULL	957	Chr Chr 11
12	-6.42	NULL	274	Lymphoma SPANG_IL21 DN
13	-6.16	NULL	602	Chr Chr 10
14	-6.06	NULL	6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
15	-6.02	NULL	6	Lymphoma SAVA_MHCCII BL DN
16	-5.99	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
17	-5.9	NULL	10	CC MHC class I protein complex
18	-5.79	NULL	123	BP defense response to virus
19	-5.79	NULL	14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
20	-5.56	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1

p-values



GW_022

Local Summary

%DE = 0.79
 # metagenes = 14
 # genes = 216
 # genes in genesets = 210

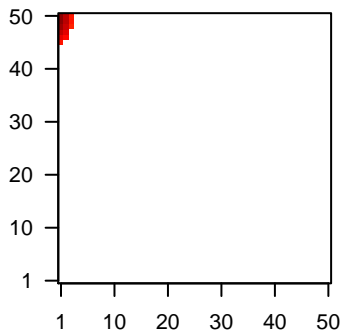
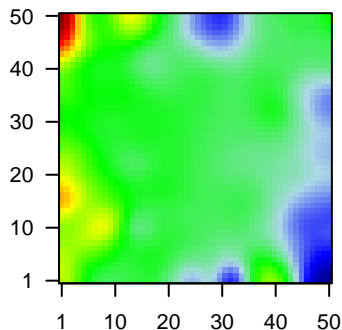
genes with $fdr < 0.1$ = 148 (135 + / 13 -)
 # genes with $fdr < 0.05$ = 135 (124 + / 11 -)
 # genes with $fdr < 0.01$ = 119 (111 + / 8 -)

<r> metagenes = 0.95
 <r> genes = 0.45

<FC> = 0.62
 <shrinkage-t> = 21.97
 <p-value> = 0
 <fdr> = 0.36

Profile

Spot



Local Genelist

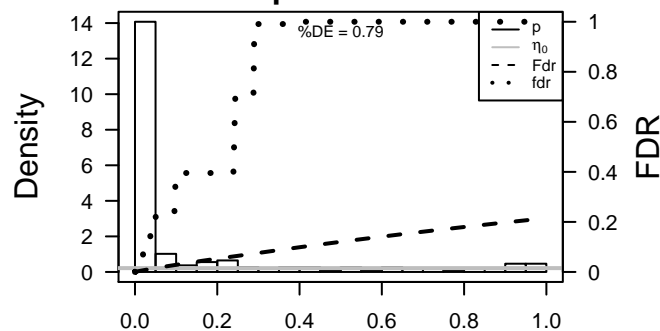
Rank	ID	log(FC)	fdr	p-value	Description
1	57016	1.65	2e-16	3e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
2	441282	1.46	2e-16	3e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	2.35	2e-16	3e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
4	218	1.56	2e-16	3e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	84518	1.9	2e-16	3e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
6	49860	1.4	2e-16	3e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
7	9547	1.45	2e-16	3e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
8	55894	1.64	2e-16	3e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	414325	1.92	2e-16	3e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	1673	1.91	2e-16	3e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	93099	1.46	2e-16	3e-16	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
12	1828	1.48	2e-16	3e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	10804	1.59	2e-16	3e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
14	2877	1.99	2e-16	3e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
15	26525	1.46	2e-16	3e-16	1 x 49 interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
16	56300	1.41	2e-16	3e-16	1 x 47 interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
17	43849	1.91	2e-16	3e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6
18	5653	1.54	2e-16	3e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
19	5650	2.06	2e-16	3e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63
20	388533	2.93	2e-16	3e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	44.6	NULL	81 / 135	H.Tiss WIRTH_Mucosa
2	43.45	NULL	18 / 21	CC cornified envelope
3	41.14	NULL	19 / 42	BP keratinization
4	34.4	NULL	24 / 53	BP keratinocyte differentiation
5	26.94	NULL	91 / 572	Disease GUDJ_psooriasis up
6	25.92	NULL	23 / 76	BP epidermis development
7	23.35	NULL	10 / 19	BP peptide cross-linking
8	19.43	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	15.28	NULL	7 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
10	15.28	NULL	12 / 21	CC desmosome
11	15.03	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
12	14.41	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
13	14.06	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
14	13.36	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
15	12.51	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	11.95	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
17	11.25	NULL	5 / 10	MF RAGE receptor binding
18	11.15	NULL	2 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
19	10.57	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
20	10.55	NULL	3 / 12	BP cellular aldehyde metabolic process
21	10.38	NULL	4 / 16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
22	10.11	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
23	9.89	NULL	2 / 17	Disease BCHETNIA_EBM up
24	9.83	NULL	23 / 186	MF structural molecule activity
25	9.32	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HP31_DN
26	9.11	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
27	8.92	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
28	8.27	NULL	12 / 122	MF serine-type endopeptidase activity
29	8.13	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
30	7.91	NULL	6 / 53	MF serine-type peptidase activity
31	7.83	NULL	2 / 11	GSEA C2LEI_MYB_TARGETS
32	7.78	NULL	7 / 51	MF protein binding, bridging
33	7.78	NULL	8 / 73	BP defense response to bacterium
34	7.56	NULL	1 / 10	BP positive regulation of endothelial cell apoptotic process
35	7.56	NULL	1 / 10	BP retinal metabolic process
36	7.53	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
37	7.34	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
38	7.32	NULL	2 / 15	MF interleukin-1 receptor binding
39	7.25	NULL	2 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
40	7.17	NULL	16 / 82	CC intermediate filament

p-values



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Local Summary

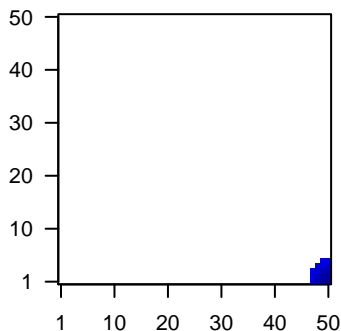
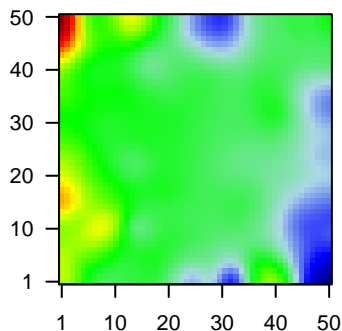
%DE = 0.81
 # metagenes = 17
 # genes = 283
 # genes in genesets = 281
 # genes with $fdr < 0.1 = 180$ (10 + / 170 -)
 # genes with $fdr < 0.05 = 180$ (10 + / 170 -)
 # genes with $fdr < 0.01 = 127$ (5 + / 122 -)

<r> metagenes = 0.98
 <r> genes = 0.56

<FC> = -0.4
 <shrinkage-t> = -14.04
 <p-value> = 0
 <fdr> = 0.45

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	10628	-1.28	6e-15	8e-13	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
2	2634	-1.27	2e-14	3e-12	guanylate binding protein 2, interferon-inducible [Source:HG
3	5920	-1.25	8e-14	4e-10	retinoic acid receptor responder (tazarotene induced) 3 [Sour
4	3126	-1.14	9e-12	4e-10	major histocompatibility complex, class II, DR beta 4 [Source:
5	8764	-1.12	2e-11	4e-10	tumor necrosis factor receptor superfamily, member 14 [Sourc
6	5880	-1.11	2e-11	1e-09	ras-related C3 botulinum toxin substrate 2 (rho family, small G
7	115361	-1.09	5e-11	1e-09	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
8	5552	-1.09	7e-11	2e-08	serglycin [Source:HGNC Symbol;Acc:9361]
9	3122	-0.97	4e-10	2e-08	major histocompatibility complex, class II, DR alpha [Source:G
10	4283	-1.02	9e-10	2e-08	chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:
11	80833	-1.02	9e-10	7e-08	apolipoprotein L 3 [Source:HGNC Symbol;Acc:14868]
12	7318	-0.98	4e-09	7e-08	ubiquitin-like modifier activating enzyme 7 [Source:HGNC Sy
13	3113	-0.98	4e-09	7e-08	major histocompatibility complex, class II, DP alpha 1 [Source
14	54504	-0.97	5e-09	4e-07	carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;Acc:
15	3109	-0.94	1e-08	4e-07	major histocompatibility complex, class II, DM beta [Source:H
16	10550	-0.94	2e-08	9e-07	ADP-ribosylation-like factor 6 interacting protein 5 [Source:H
17	6347	-0.91	5e-08	9e-07	chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:1
18	3398	-0.9	6e-08	9e-07	inhibitor of DNA binding 2, dominant negative helix-loop-heli
19	3001	-0.89	8e-08	9e-07	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
20	5341	-0.89	9e-08	9e-07	pleckstrin [Source:HGNC Symbol;Acc:9070]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-31.32	NULL	12 / 15	CC MHC class II protein complex
2	-26.43	NULL	89 / 417	H.Tiss WIRTH_Immune system
3	-20.46	NULL	15 / 47	BP antigen processing and presentation
4	-19.74	NULL	92 / 553	Cancer Lembcke_Colonin Inflammation
5	-19.47	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
6	-18.48	NULL	50 / 312	BP immune response
7	-17.35	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
8	-16.76	NULL	2 / 4	MMML C2SCIEJ_MMML 2
9	-16.55	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
10	-16.37	NULL	43 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
11	-16.37	NULL	43 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
12	-16.37	NULL	43 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
13	-16.37	NULL	43 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
14	-16.04	NULL	14 / 60	BP T cell costimulation
15	-15.87	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
16	-15.64	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
17	-15.5	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
18	-15.12	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
19	-14.76	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
20	-14.37	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
21	-14.31	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
22	-14.01	NULL	5 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
23	-13.78	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
24	-13.6	NULL	17 / 74	BP regulation of immune response
25	-13.58	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
26	-13.37	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
27	-13.35	NULL	29 / 316	Cancer SPANG_BCL6-index2
28	-13	NULL	6 / 13	Cancer GENTLES_modul18
29	-12.92	NULL	5 / 12	BP immunoglobulin mediated immune response
30	-12.87	NULL	7 / 28	CC transport vesicle membrane
31	-12.71	NULL	6 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
32	-12.67	NULL	5 / 14	GSEA C2WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
33	-12.48	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
34	-12.38	NULL	13 / 87	BP antigen processing and presentation of exogenous peptide antigen
35	-12.34	NULL	9 / 35	CC trans-Golgi network membrane
36	-12.08	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
37	-11.95	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
38	-11.94	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
39	-11.73	NULL	23 / 162	CC external side of plasma membrane
40	-11.41	NULL	4 / 13	GSEA C2BIOCARTA_IL17_PATHWAY

