

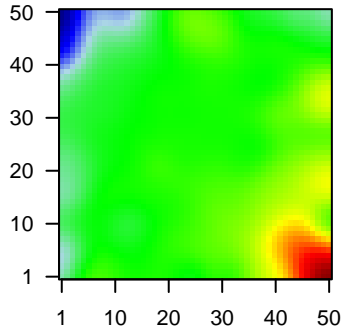
GW_258

Global Summary

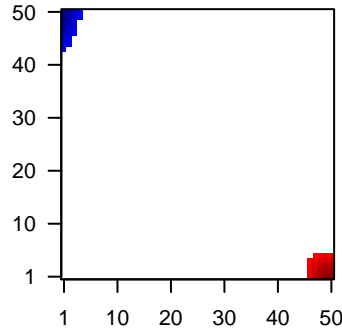
%DE = 0.16
 # genes with $fdr < 0.2$ = 2259 (1123 + / 1136 -)
 # genes with $fdr < 0.1$ = 1912 (941 + / 971 -)
 # genes with $fdr < 0.05$ = 1576 (752 + / 824 -)
 # genes with $fdr < 0.01$ = 1188 (551 + / 637 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.06
 <fdr> = 0.84

Profile



Regulated Spots



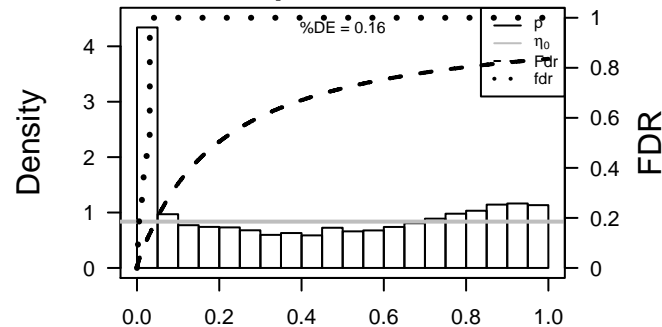
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.67	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	113146	-2.39	2e-16	2e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	-2.9	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	-1.96	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
5	8644	-1.98	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr]
6	1109	-2.27	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr]
7	218	-2.82	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
8	222	-2.12	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC]
9	55107	-2.03	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG]
10	244	-2.18	2e-16	2e-14	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]
11	341	1.94	2e-16	2e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
12	348	2.18	2e-16	2e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
13	92591	2	2e-16	2e-14	48 x 2 ankyrin repeat and SOCS box containing 16 [Source:HGNC S]
14	387695	-2.17	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
15	64073	-2.21	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt]
16	260436	2.89	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc]
17	810	-3.65	2e-16	2e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
18	57172	2.92	2e-16	2e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG]
19	84290	-2.11	2e-16	2e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
20	6363	3.14	2e-16	2e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	25.53	NULL	417	H.Tiss WIRTH_Immune system
2	13.87	NULL	553	Cancer Lembcke_Colonc Inflammation
3	11.82	NULL	15	CC MHC class II protein complex
4	11.55	NULL	312	BP immune response
5	10.85	NULL	316	Cancer SPANG_BCL6-index2
6	9.68	NULL	60	BP T cell costimulation
7	9.61	NULL	28	BP B cell receptor signaling pathway
8	9.51	NULL	327	Lymphom SPANG_CD40 6hrs UP
9	9.06	NULL	84	BP T cell receptor signaling pathway
10	8.17	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
11	8.09	NULL	47	BP antigen processing and presentation
12	7.78	NULL	162	CC external side of plasma membrane
13	7.71	NULL	852	Lymphom SPANG_BCR DN
14	7.5	NULL	74	BP regulation of immune response
15	7.5	NULL	8	Glio Donson-migration tethering and rolling-associated with LTS in HG
16	7.43	NULL	28	BP B cell activation
17	7.42	NULL	16	GSEA C2SU_THYMUS
18	7.36	NULL	14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
19	7.34	NULL	45	BP T cell activation
20	7.31	NULL	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
<i>Underexpressed</i>				
1	-39.2	NULL	135	H.Tiss WIRTH_Mucosa
2	-23.39	NULL	572	Disease GUDJ_psooriasis up
3	-19.94	NULL	76	BP epidermis development
4	-16.15	NULL	21	CC cornified envelope
5	-15.31	NULL	53	BP keratinocyte differentiation
6	-14.58	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
7	-14.34	NULL	42	BP keratinization
8	-13.61	NULL	15	GSEA C2AIGNER_ZEB1_TARGETS
9	-13.1	NULL	186	MF structural molecule activity
10	-12.69	NULL	82	CC intermediate filament
11	-12.17	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
12	-12.08	NULL	530	Cancer Lembcke_Normal vs Adenoma
13	-11.54	NULL	13	H.Tiss WIRTH_Tonsil
14	-10.96	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
15	-10.21	NULL	21	CC desmosome
16	-10.17	NULL	19	BP peptide cross-linking
17	-10.16	NULL	12	BP hemidesmosome assembly
18	-9.96	NULL	44	CC keratin filament
19	-9.79	NULL	242	BP extracellular matrix organization
20	-9.74	NULL	16	GSEA C2JAEGER_METASTASIS_DN

p-values



GW_258

Local Summary

%DE = 0.97
 # metagenes = 24
 # genes = 354
 # genes in genesets = 352

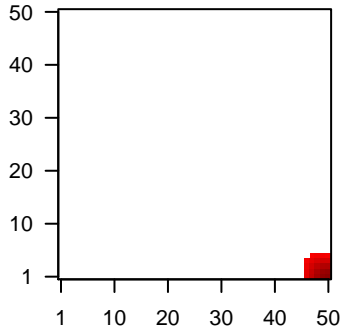
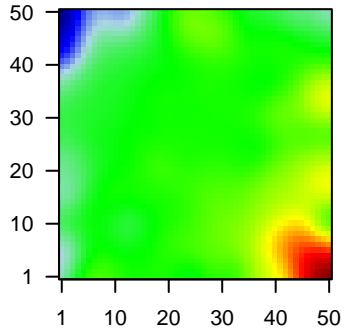
 # genes with $fdr < 0.1$ = 343 (339 + / 4 -)
 # genes with $fdr < 0.05$ = 331 (328 + / 3 -)
 # genes with $fdr < 0.01$ = 321 (320 + / 1 -)

 $\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.55

 $\langle FC \rangle$ = 1.32
 $\langle \text{shrinkage-t} \rangle$ = 46.23
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.08

Profile

Spot



Local Genelist

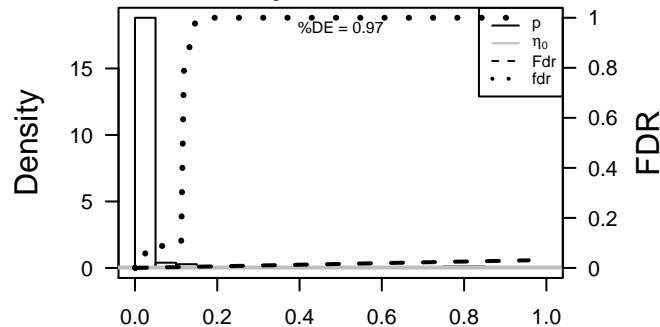
Rank	ID	log(FC)	fdr	p-value	Description
1	341	1.94	2e-16	5e-17	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
2	348	2.18	2e-16	5e-17	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	92591	2	2e-16	5e-17	48 x 2 ankyrin repeat and SOCS box containing 16 [Source:HGNC S
4	260436	2.89	2e-16	5e-17	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
5	57172	2.92	2e-16	5e-17	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
6	6363	3.14	2e-16	5e-17	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
7	6347	2.01	2e-16	5e-17	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:
8	6366	3.13	2e-16	5e-17	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
9	1236	2.19	2e-16	5e-17	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
10	930	2.75	2e-16	5e-17	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
11	962	2.53	2e-16	5e-17	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
12	1043	2.07	2e-16	5e-17	50 x 1 CD52 molecule [Source:HGNC Symbol;Acc:1804]
13	969	1.95	2e-16	5e-17	50 x 1 CD69 molecule [Source:HGNC Symbol;Acc:1694]
14	11151	2.01	2e-16	5e-17	50 x 1 coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
15	51755	2.6	2e-16	5e-17	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
16	55619	2.18	2e-16	5e-17	50 x 1 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:2347
17	1794	2.12	2e-16	5e-17	50 x 1 dedicator of cytokinesis 2 [Source:HGNC Symbol;Acc:2988]
18	81704	1.92	2e-16	5e-17	50 x 1 dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:19191]
19	5168	2.11	2e-16	5e-17	50 x 2 ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
20	9214	2.24	2e-16	5e-17	49 x 1 Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	33.05	NULL	105 / 417	H Tiss WIRTH_Immune system
2	31.88	NULL	117 / 553	Cancer Lembecke_Colonc Inflammation
3	22.73	NULL	12 / 15	CC MHC class II protein complex
4	20.41	NULL	9 / 16	GSEA C27FARMER_BREAST_CANCER_CLUSTER_1
5	20.17	NULL	64 / 312	BP immune response
6	18	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
7	16.49	NULL	12 / 28	BP B cell receptor signaling pathway
8	16.34	NULL	7 / 15	GSEA C27FINAK_BREAST_CANCER_SDPP_SIGNATURE
9	16.28	NULL	54 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
10	16.28	NULL	54 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
11	16.28	NULL	54 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
12	16.28	NULL	54 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
13	16.21	NULL	3 / 5	GSEA C27WONG_ENDOMETRIAL_CANCER_LATE
14	15.79	NULL	4 / 9	GSEA C27MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
15	15.76	NULL	7 / 11	GSEA C27BIOCARTA_TCYTOTOXIC_PATHWAY
16	15.64	NULL	8 / 16	GSEA C27SU_THYMUS
17	15.52	NULL	19 / 60	BP T cell costimulation
18	15.5	NULL	7 / 11	GSEA C27BIOCARTA_THELPER_PATHWAY
19	14.88	NULL	5 / 12	BP dendritic cell chemotaxis
20	13.75	NULL	5 / 10	GSEA C27LEE_DIFFERENTIATING_T_LYMPHOCYTE
21	13.64	NULL	15 / 47	BP antigen processing and presentation
22	13.63	NULL	8 / 13	Cancer GENTLES_modul18
23	13.51	NULL	6 / 10	GSEA C27LECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
24	13.51	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
25	13.15	NULL	3 / 7	GSEA C27GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
26	12.94	NULL	28 / 162	CC external side of plasma membrane
27	12.89	NULL	4 / 8	GSEA C27GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
28	12.79	NULL	18 / 74	BP regulation of immune response
29	12.76	NULL	6 / 12	GSEA C27BIOCARTA_CTL_PATHWAY
30	12.09	NULL	6 / 12	GSEA C27ZHAN_MULTIPLE_MYELOMA_DN
31	11.85	NULL	19 / 84	BP T cell receptor signaling pathway
32	11.81	NULL	7 / 16	Lymphoma7RIGHT_ABC UP
33	11.57	NULL	6 / 14	GSEA C27FINETTI_BREAST_CANCER_KINOME_GREEN
34	11.46	NULL	5 / 8	GSEA C27BIOCARTA_TCRA_PATHWAY
35	11.31	NULL	35 / 316	Cancer SPANG_BCL6-index2
36	11.31	NULL	4 / 14	BP ruffle organization
37	11.31	NULL	35 / 327	Lymphoma8SPANG_CD40 6hrs UP
38	10.96	NULL	6 / 13	GSEA C27BIOCARTA_IL17_PATHWAY
39	10.94	NULL	2 / 3	GSEA C27KEGG_VIRAL_MYOCARDITIS
40	10.8	NULL	6 / 13	GSEA C27HAHTOLA_CTCL_PATHOGENESIS

p-values



GW_258

Local Summary

%DE = 0.97
 # metagenes = 22
 # genes = 319
 # genes in genesets = 312

genes with $fdr < 0.1 = 305$ (1 + / 304 -)
 # genes with $fdr < 0.05 = 297$ (1 + / 296 -)
 # genes with $fdr < 0.01 = 284$ (1 + / 283 -)

<r> metagenes = 0.9

<r> genes = 0.38

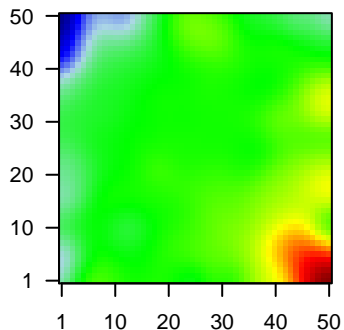
<FC> = -1.54

<shrinkage-t> = -54.59

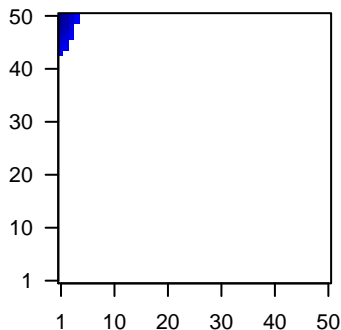
<p-value> = 0

<fdr> = 0.09

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.67	2e-16	2e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	113146	-2.39	2e-16	2e-17	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	-2.9	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	-1.96	2e-16	2e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:20125]
5	8644	-1.98	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:20125]
6	218	-2.82	2e-16	2e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:20125]
7	222	-2.12	2e-16	2e-17	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC Symbol;Acc:20125]
8	244	-2.18	2e-16	2e-17	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]
9	387695	-2.17	2e-16	2e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symbol;Acc:20125]
10	64073	-2.21	2e-16	2e-17	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Symbol;Acc:20125]
11	810	-3.65	2e-16	2e-17	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
12	84290	-2.11	2e-16	2e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	1001	-2.43	2e-16	2e-17	1 x 43 cadherin 3, type 1, P-cadherin (placental) [Source:HGNC Symbol;Acc:20125]
14	4680	-2.53	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (type 1)
15	548596	-1.99	2e-16	2e-17	4 x 50 creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc:20125]
16	9635	-3.41	2e-16	2e-17	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20125]
17	22802	-2.18	2e-16	2e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20125]
18	84518	-2.72	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
19	1308	-2.89	2e-16	2e-17	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
20	1382	-2.46	2e-16	2e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol;Acc:20125]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-68.37	NULL	94 / 135	H.Tiss WIRTH_Mucosa
2	-33.11	NULL	115 / 572	Disease GUDJ_psooriasis_up
3	-33.03	NULL	18 / 21	CC cornified envelope
4	-32.68	NULL	29 / 76	BP epidermis development
5	-28.15	NULL	20 / 42	BP keratinization
6	-27.82	NULL	24 / 53	BP keratinocyte differentiation
7	-22.02	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	-20.73	NULL	21 / 82	CC intermediate filament
9	-20.13	NULL	10 / 19	BP peptide cross-linking
10	-20.08	NULL	13 / 44	CC keratin filament
11	-19.98	NULL	12 / 21	CC desmosome
12	-19.54	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
13	-17.4	NULL	29 / 186	MF structural molecule activity
14	-17.23	NULL	5 / 10	MF RAGE receptor binding
15	-16.92	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	-16.66	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
17	-16.5	NULL	8 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	-14.54	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
19	-14.47	NULL	6 / 16	GSEA C2JAEGER_METASTASIS_DN
20	-13.87	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
21	-13.47	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
22	-13	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
23	-12.91	NULL	10 / 52	BP negative regulation of endopeptidase activity
24	-12.28	NULL	5 / 13	H.Tiss WIRTH_Tonsil
25	-12.24	NULL	2 / 5	miRNA target-196a
26	-12.12	NULL	3 / 12	BP hemidesmosome assembly
27	-12.01	NULL	4 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
28	-11.79	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
29	-11.57	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
30	-11.54	NULL	6 / 13	BP negative regulation of peptidase activity
31	-11.52	NULL	5 / 25	BP response to zinc ion
32	-11.51	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
33	-11.51	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
34	-11.48	NULL	10 / 38	BP epithelial cell differentiation
35	-11.31	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
36	-11.27	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
37	-11.25	NULL	3 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
38	-11.12	NULL	7 / 29	BP regulation of proteolysis
39	-11.11	NULL	2 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
40	-10.79	NULL	11 / 82	MF structural constituent of cytoskeleton

p-values

