

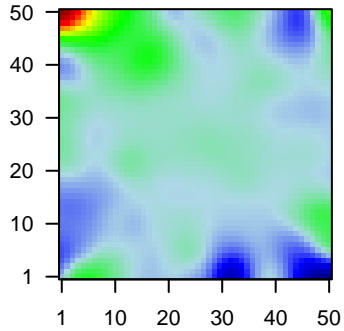
GW_049

Global Summary

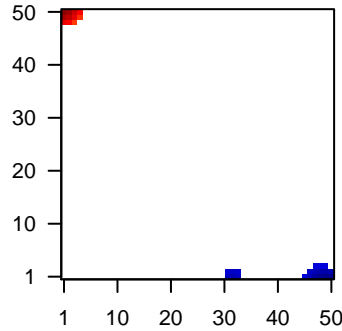
%DE = 0.14
 # genes with fdr < 0.2 = 1808 (999 + / 809 -)
 # genes with fdr < 0.1 = 1529 (881 + / 648 -)
 # genes with fdr < 0.05 = 1332 (767 + / 565 -)
 # genes with fdr < 0.01 = 942 (566 + / 376 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.08
 <fdr> = 0.86

Profile



Regulated Spots



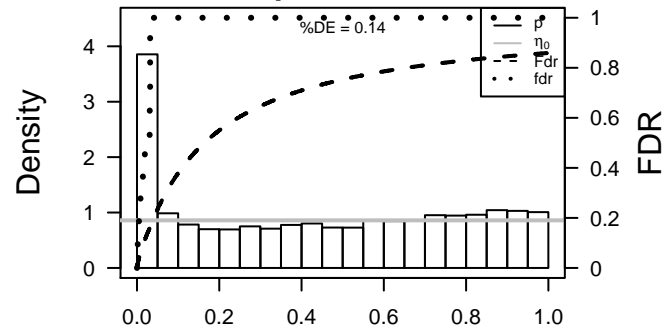
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.29	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.61	2e-16	2e-14	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.58	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.85	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
5	441282	1.62	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Sy
6	8644	1.92	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	1.87	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy
8	216	2.92	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	220	-1.65	2e-16	2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
10	218	2.09	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
11	239	1.59	2e-16	2e-14	5 x 49 arachidonate 12-lipoxygenase [Source:HGNC Symbol;Acc:4:
12	154796	1.35	2e-16	2e-14	50 x 12 angiomin [Source:HGNC Symbol;Acc:17810]
13	353322	1.44	2e-16	2e-14	6 x 48 ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:29593]
14	344905	1.7	2e-16	2e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
15	8424	1.45	2e-16	2e-14	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
16	655	1.65	2e-16	2e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
17	684	-1.95	2e-16	2e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
18	387695	2.15	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
19	64207	-2.1	2e-16	2e-14	50 x 40 interferon regulatory factor 2 binding protein-like [Source:HGI
20	284254	1.37	2e-16	2e-14	6 x 50 dynactin associated protein [Source:HGNC Symbol;Acc:2680

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	27.23	NULL	135	H.Tiss WIRTH_Mucosa
2	15.74	NULL	21	CC cornified envelope
3	14.06	NULL	42	BP keratinization
4	13.17	NULL	53	BP keratinocyte differentiation
5	10.84	NULL	19	BP peptide cross-linking
6	9.45	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
7	9	NULL	8	GSEA C2LJU_CDX2_TARGETS_DN
8	8.95	NULL	190	CC extracellular matrix
9	8.79	NULL	82	CC intermediate filament
10	8.74	NULL	119	BP xenobiotic metabolic process
11	8.64	NULL	12	BP cellular aldehyde metabolic process
12	8.51	NULL	186	MF structural molecule activity
13	8.49	NULL	44	CC keratin filament
14	8.26	NULL	250	LymphomaENZ_Stromal signature 1
15	8.15	NULL	76	BP epidermis development
16	8.11	NULL	10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
17	8.03	NULL	10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
18	7.89	NULL	16	MMML C6SCIEJ_MMML 1
19	7.83	NULL	1146	TF HEBENSTREIT_low expression TF
20	7.64	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
<i>Underexpressed</i>				
1	-16.92	NULL	312	BP immune response
2	-16.88	NULL	417	H.Tiss WIRTH_Immune system
3	-14.43	NULL	204	BP cytokine-mediated signaling pathway
4	-14.29	NULL	51	BP type I interferon signaling pathway
5	-12.89	NULL	60	BP interferon-gamma-mediated signaling pathway
6	-12.31	NULL	123	BP defense response to virus
7	-12.01	NULL	47	BP antigen processing and presentation
8	-11.66	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
9	-11.55	NULL	553	Cancer Lembcke_Colonc Inflammation
10	-11.03	NULL	15	CC MHC class II protein complex
11	-10.98	NULL	316	Cancer SPANG_BCL6-index2
12	-10.95	NULL	274	LymphomaSPANG_IL21 DN
13	-10.89	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
14	-10.69	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
15	-10.33	NULL	16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
16	-10.12	NULL	109	BP response to virus
17	-9.99	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
18	-9.89	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
19	-9.81	NULL	43	MF chemokine activity
20	-9.65	NULL	16	GSEA C2ENAV_INTERFERON_SIGNATURE_IN_CANCER

p-values



GW_049

Local Summary

%DE = 0.98
 # metagenes = 11
 # genes = 168
 # genes in genesets = 165

genes with $fdr < 0.1 = 157$ (149 + / 8 -)
 # genes with $fdr < 0.05 = 157$ (149 + / 8 -)
 # genes with $fdr < 0.01 = 154$ (147 + / 7 -)

<r> metagenes = 0.99
 <r> genes = 0.49

<FC> = 1.16
 <shrinkage-t> = 40.79
 <p-value> = 0
 <fdr> = 0.09

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.29	2e-16	9e-18	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.61	2e-16	9e-18	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.58	2e-16	9e-18	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.85	2e-16	9e-18	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
5	441282	1.62	2e-16	9e-18	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
6	8644	1.92	2e-16	9e-18	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
7	218	2.09	2e-16	9e-18	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	8424	1.45	2e-16	9e-18	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
9	387695	2.15	2e-16	9e-18	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
10	394263	1.83	2e-16	9e-18	3 x 50
11	375791	1.91	2e-16	9e-18	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
12	84290	1.48	2e-16	9e-18	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	9022	1.88	2e-16	9e-18	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:21
14	84518	1.9	2e-16	9e-18	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	54544	2.08	2e-16	9e-18	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
16	49860	3.42	2e-16	9e-18	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	1475	2.22	2e-16	9e-18	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
18	1562	2.01	2e-16	9e-18	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
19	1577	2	2e-16	9e-18	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Sour
20	126410	1.73	2e-16	9e-18	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour

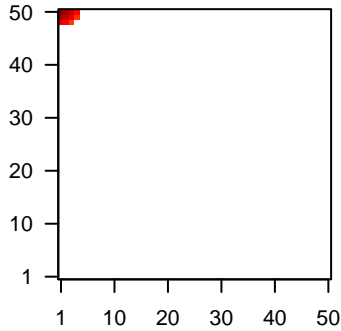
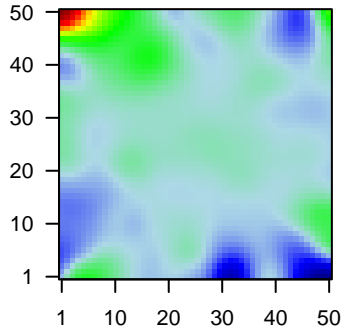
Local Geneset Analysis

Overexpression

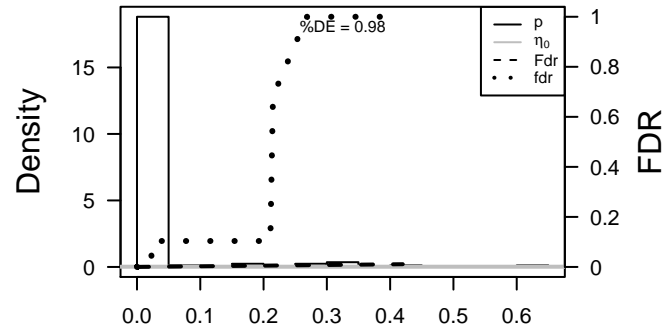
Rank	GSZ	p-value	#in/all	Geneset
1	55.87	NULL	71 / 135	H.Tiss WIRTH_Mucosa
2	38.43	NULL	14 / 21	CC cornified envelope
3	30.77	NULL	16 / 42	BP keratinization
4	30.04	NULL	19 / 53	BP keratinocyte differentiation
5	23.16	NULL	8 / 19	BP peptide cross-linking
6	19.99	NULL	72 / 572	Disease GUDJ_psooriasis up
7	16.89	NULL	18 / 76	BP epidermis development
8	14.72	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	12.9	NULL	4 / 15	MF retinol dehydrogenase activity
10	12.16	NULL	3 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
11	11.87	NULL	6 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	11.63	NULL	6 / 13	BP negative regulation of peptidase activity
13	10.69	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
14	10.51	NULL	3 / 12	BP cellular aldehyde metabolic process
15	10.19	NULL	6 / 38	BP epithelial cell differentiation
16	9.94	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
17	9.9	NULL	5 / 21	CC desmosome
18	9.9	NULL	3 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
19	9.44	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
20	9.4	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
21	9.23	NULL	2 / 11	GSEA C2REACTOME_XENOBIOTICS
22	9.16	NULL	13 / 186	MF structural molecule activity
23	8.91	NULL	4 / 39	BP retinoid metabolic process
24	8.55	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
25	8.53	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
26	8.12	NULL	3 / 18	BP retinol metabolic process
27	7.88	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
28	7.79	NULL	46 / 1182	CC extracellular region
29	7.61	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
30	7.18	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
31	7.11	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
32	7.09	NULL	2 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
33	7.05	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
34	7.05	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
35	6.92	NULL	5 / 51	MF protein binding, bridging
36	6.86	NULL	3 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
37	6.86	NULL	2 / 18	MF aromatase activity
38	6.82	NULL	10 / 122	MF serine-type endopeptidase activity
39	6.8	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
40	6.8	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP

Profile

Spot



p-values



GW_049

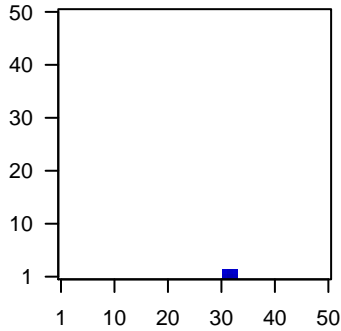
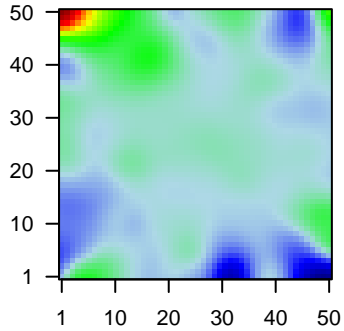
Local Summary

%DE = 0.99
 # metagenes = 6
 # genes = 114
 # genes in genesets = 112
 # genes with $fdr < 0.1 = 111$ (1 + / 110 -)
 # genes with $fdr < 0.05 = 111$ (1 + / 110 -)
 # genes with $fdr < 0.01 = 103$ (0 + / 103 -)

<r> metagenes = 1
 <r> genes = 0.47
 <FC> = -0.79
 <shrinkage-t> = -27.88
 <p-value> = 0
 <fdr> = 0.14

Profile

Spot



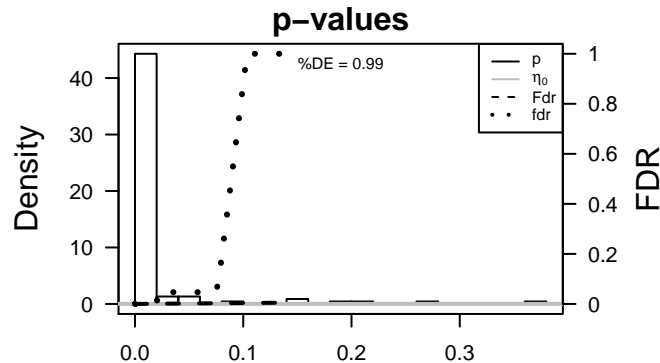
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	684	-1.95	2e-16	3e-17	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	3627	-2.15	2e-16	3e-17	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;A
3	94240	-1.49	2e-16	3e-17	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc
4	2633	-1.49	2e-16	3e-17	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HG
5	115362	-1.39	2e-16	3e-17	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
6	10866	-1.65	2e-16	3e-17	32 x 1 HLA complex P5 (non-protein coding) [Source:HGNC Symbc
7	3106	-1.84	2e-16	3e-17	32 x 1 major histocompatibility complex, class I, B [Source:HGNC S
8	3134	-1.55	2e-16	3e-17	32 x 1 major histocompatibility complex, class I, F [Source:HGNC S
9	3136	-1.59	2e-16	3e-17	32 x 1
10	10964	-1.62	2e-16	3e-17	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
11	9636	-1.64	2e-16	3e-17	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405
12	6772	-1.43	2e-16	3e-17	32 x 1 signal transducer and activator of transcription 1, 91kDa [Sou
13	6890	-1.45	2e-16	3e-17	32 x 1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP
14	7453	-1.27	9e-15	8e-15	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1:
15	10346	-1.25	2e-14	8e-15	32 x 1 tripartite motif containing 22 [Source:HGNC Symbol;Acc:163;
16	219285	-1.25	2e-14	8e-15	32 x 1 sterile alpha motif domain containing 9-like [Source:HGNC S
17	3135	-1.25	2e-14	3e-14	32 x 1 major histocompatibility complex, class I, G [Source:HGNC S
18	10561	-1.23	5e-14	3e-14	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16:
19	629	-1.22	7e-14	3e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
20	55601	-1.22	8e-14	8e-13	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-50.76	NULL	29 / 51	BP type I interferon signaling pathway
2	-49.77	NULL	6 / 6	Lymphocyte activation-induced chemokine (CXCL10) BL DN
3	-49.39	NULL	12 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
4	-43.24	NULL	11 / 16	GSEA C2ENAV_INTERFERON_SIGNATURE_IN_CANCER
5	-41.39	NULL	7 / 10	CC MHC class I protein complex
6	-40.86	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
7	-37.58	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
8	-37.1	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
9	-36.02	NULL	10 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
10	-35.09	NULL	31 / 123	BP defense response to virus
11	-34.57	NULL	2 / 2	MMML C6SCIEJ_MMML_27
12	-34.36	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
13	-34.22	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
14	-32.91	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
15	-32.64	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
16	-31.92	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
17	-31.62	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
18	-30.83	NULL	7 / 18	MF peptide antigen binding
19	-30.74	NULL	27 / 109	BP response to virus
20	-30.41	NULL	13 / 31	BP negative regulation of viral genome replication
21	-29.04	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
22	-28.55	NULL	34 / 204	BP cytokine-mediated signaling pathway
23	-28.52	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
24	-28.37	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
25	-26.15	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
26	-25.94	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
27	-24.03	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
28	-24.03	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
29	-22.75	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
30	-22.59	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
31	-22.59	NULL	6 / 14	Glo Donson-immune cell intra signaling-associated with LTS in HGA
32	-22.43	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION
33	-21.95	NULL	31 / 274	Lymphocyte activation-induced chemokine (CXCL10) BL DN
34	-21.69	NULL	4 / 14	GSEA C2SANA_TNF_SIGNALING_UP
35	-21.15	NULL	12 / 70	BP antigen processing and presentation of exogenous peptide antigen
36	-20.98	NULL	46 / 572	Disease GUDJ_psooriasis up
37	-20.96	NULL	5 / 23	CC integral to luminal side of endoplasmic reticulum membrane
38	-20.53	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
39	-20.51	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
40	-20.51	NULL	12 / 74	BP antigen processing and presentation of exogenous peptide antigen



GW_049

Local Summary

%DE = 0.92
 # metagenes = 14
 # genes = 232
 # genes in genesets = 229

genes with $fdr < 0.1 = 202$ (4 + / 198 -)
 # genes with $fdr < 0.05 = 193$ (3 + / 190 -)
 # genes with $fdr < 0.01 = 159$ (3 + / 156 -)

<r> metagenes = 0.99

<r> genes = 0.61

<FC> = -0.62

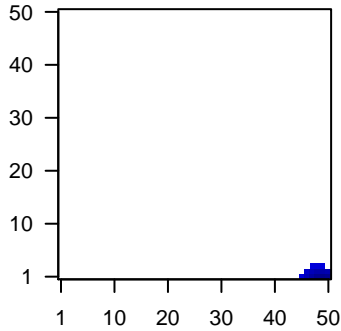
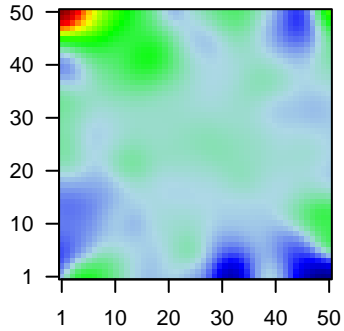
<shrinkage-t> = -21.62

<p-value> = 0

<fdr> = 0.28

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	260436	-1.46	2e-16	3e-16	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
2	6364	-1.68	2e-16	3e-16	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
3	6352	-1.36	2e-16	3e-16	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:'
4	51755	-1.34	2e-16	3e-16	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242;
5	4283	-1.62	2e-16	3e-16	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
6	3001	-1.51	2e-16	3e-16	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
7	3002	-1.75	2e-16	3e-16	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
8	3113	-1.36	2e-16	3e-16	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source
9	3122	-1.53	2e-16	3e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:!
10	3123	-1.81	2e-16	3e-16	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
11	3669	-1.36	2e-16	3e-16	48 x 1 interferon stimulated exonuclease gene 20kDa [Source:HGNC
12	3936	-1.46	2e-16	3e-16	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Syr
13	5880	-1.59	2e-16	3e-16	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small (
14	5552	-1.52	2e-16	3e-16	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
15	10537	-1.47	2e-16	3e-16	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	5996	-1.33	4e-16	4e-14	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc
17	3620	-1.29	2e-15	1e-13	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:!
18	57172	-1.26	1e-14	1e-13	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
19	972	-1.25	2e-14	1e-13	50 x 1 CD74 molecule, major histocompatibility complex, class II inv:
20	3126	-1.25	2e-14	3e-13	50 x 1 major histocompatibility complex, class II, DR beta 4 [Source:

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-42.25	NULL	13 / 15	CC MHC class II protein complex
2	-32.26	NULL	86 / 417	H.Tiss WIRTH_Immune system
3	-26.23	NULL	49 / 312	BP immune response
4	-25.63	NULL	15 / 47	BP antigen processing and presentation
5	-25.21	NULL	3 / 3	MMML C69CIEJ_MMML 7
6	-24.44	NULL	84 / 553	Cancer Lembcke_Colonc Inflammation
7	-23.34	NULL	8 / 21	CC clathrin-coated endocytic vesicle membrane
8	-23.11	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
9	-22.2	NULL	8 / 23	CC integral to luminal side of endoplasmic reticulum membrane
10	-21.71	NULL	17 / 60	BP T cell costimulation
11	-20.84	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
12	-19.91	NULL	8 / 28	CC transport vesicle membrane
13	-18.49	NULL	8 / 32	CC ER to Golgi transport vesicle membrane
14	-18.36	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
15	-18.25	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
16	-18.23	NULL	3 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	-18.23	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
18	-17.89	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
19	-17.58	NULL	8 / 35	CC trans-Golgi network membrane
20	-17.33	NULL	5 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
21	-17.31	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
22	-17.2	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
23	-17.19	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
24	-16.57	NULL	14 / 87	BP antigen processing and presentation of exogenous peptide antigen
25	-16.52	NULL	16 / 84	BP T cell receptor signaling pathway
26	-16.24	NULL	12 / 60	BP interferon-gamma-mediated signaling pathway
27	-15.79	NULL	7 / 13	Cancer GENTLES_modul18
28	-15.31	NULL	9 / 52	Chr Chr HSCHR6_MHC_QBL
29	-15.27	NULL	6 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
30	-15.08	NULL	8 / 46	CC endocytic vesicle membrane
31	-14.91	NULL	2 / 4	MMML C69CIEJ_MMML 2
32	-14.84	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
33	-14.34	NULL	35 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
34	-14.34	NULL	35 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
35	-14.34	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
36	-14.34	NULL	35 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
37	-14.29	NULL	2 / 5	GSEA C2WEST_ADRENOCORITICAL_CARCINOMA_VS_ADENOMA_DN
38	-14.26	NULL	24 / 162	CC external side of plasma membrane
39	-13.62	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
40	-13.52	NULL	5 / 12	BP immunoglobulin mediated immune response

