

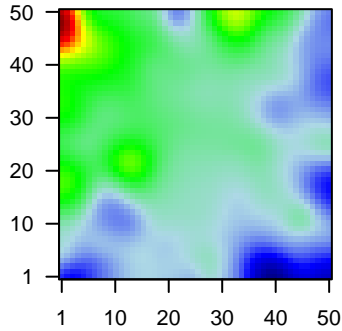
# GW\_139

## Global Summary

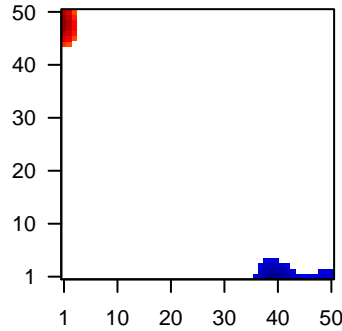
%DE = 0.13  
 # genes with fdr < 0.2 = 1577 ( 852 + / 725 - )  
 # genes with fdr < 0.1 = 1116 ( 625 + / 491 - )  
 # genes with fdr < 0.05 = 854 ( 484 + / 370 - )  
 # genes with fdr < 0.01 = 526 ( 319 + / 207 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.14  
 <fdr> = 0.87

Profile



Regulated Spots



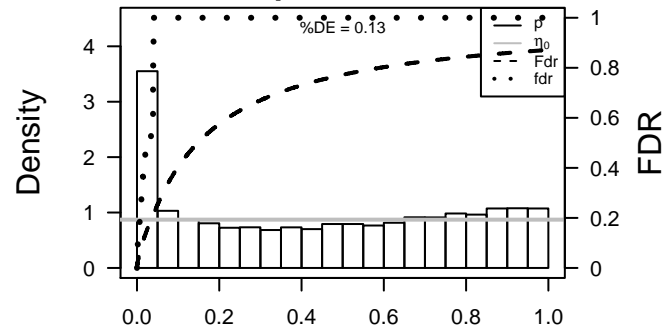
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	222	1.82	2e-16 5e-14 1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC]
2	242	1.62	2e-16 5e-14 1 x 48	arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr]
3	387695	2.19	2e-16 5e-14 1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Synt]
4	760	2.1	2e-16 5e-14 1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	1041	2.16	2e-16 5e-14 1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	84518	1.8	2e-16 5e-14 1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	54544	1.65	2e-16 5e-14 1 x 50	cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
8	1410	1.76	2e-16 5e-14 25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
9	1466	1.67	2e-16 5e-14 5 x 43	cysteine and glycine-rich protein 2 [Source:HGNC Symbol;A]
10	1475	1.75	2e-16 5e-14 1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	9547	1.62	2e-16 5e-14 1 x 46	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A]
12	126410	1.71	2e-16 5e-14 1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour]
13	27065	1.84	2e-16 5e-14 1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1)
14	1672	1.66	2e-16 5e-14 1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
15	55894	3.4	2e-16 5e-14 1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	414325	3.77	2e-16 5e-14 1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	1673	3.84	2e-16 5e-14 1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
18	1823	2.06	2e-16 5e-14 1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
19	1824	1.72	2e-16 5e-14 1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
20	1828	3.1	2e-16 5e-14 1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	21.51	NULL	135	H.Tiss WIRTH_Mucosa
2	19.42	NULL	572	Disease GUDJ_psooriasis up
3	17.35	NULL	21	CC cornified envelope
4	15.61	NULL	42	BP keratinization
5	12.38	NULL	449	Chr Chr 20
6	11.38	NULL	76	BP epidermis development
7	11.3	NULL	53	BP keratinocyte differentiation
8	10.73	NULL	153	MF structural constituent of ribosome
9	10.4	NULL	15	GSEA C2P2YEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	9.47	NULL	44	CC keratin filament
11	9.14	NULL	167	CC ribosome
12	8.98	NULL	1318	CC mitochondrion
13	8.84	NULL	253	BP translation
14	7.91	NULL	83	BP respiratory electron transport chain
15	7.7	NULL	152	BP cellular metabolic process
16	7.68	NULL	16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	7.6	NULL	304	CC mitochondrial inner membrane
18	7.59	NULL	10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
19	7.57	NULL	21	CC desmosome
20	7.39	NULL	82	CC intermediate filament
<i>Underexpressed</i>				
1	-10.52	NULL	8023	MF protein binding
2	-9.82	NULL	553	Cancer Lembecke_Colonc Inflammation
3	-9.25	NULL	417	H.Tiss WIRTH_Immune system
4	-8.92	NULL	1749	MF DNA binding
5	-8.75	NULL	391	miRNA target miR-181A--181B--181C--181D
6	-8.25	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
7	-8.21	NULL	24	TF Tissue/AQUERIZAS_Trachea
8	-8.03	NULL	823	MF sequence-specific DNA binding transcription factor activity
9	-7.95	NULL	4640	CC nucleus
10	-7.74	NULL	504	BP positive regulation of transcription, DNA-dependent
11	-7.68	NULL	1581	BP regulation of transcription, DNA-dependent
12	-7.6	NULL	274	LymphomSPANG_IL21 DN
13	-7.54	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
14	-7.53	NULL	517	miRNA target miR-106a
15	-7.46	NULL	603	miRNA target miR-106a
16	-7.45	NULL	250	LymphomENZ_Stromal signature 1
17	-7.42	NULL	16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
18	-7.36	NULL	1574	BP transcription, DNA-templated
19	-7.35	NULL	538	miRNA target miR-139
20	-7.31	NULL	743	Chr Chr 7

p-values



# GW\_139

## Local Summary

%DE = 0.81  
 # metagenes = 20  
 # genes = 271  
 # genes in genesets = 264

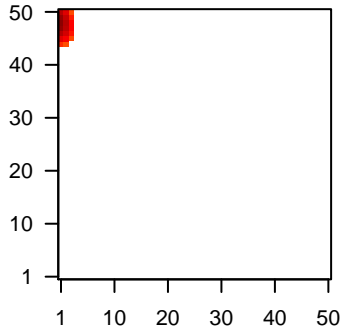
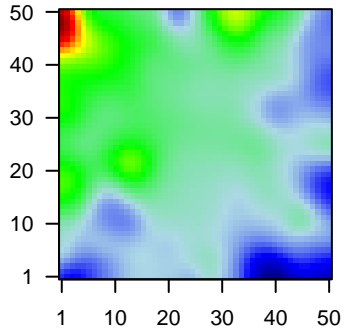
# genes with  $fdr < 0.1 = 195$  ( 190 + / 5 - )  
 # genes with  $fdr < 0.05 = 187$  ( 182 + / 5 - )  
 # genes with  $fdr < 0.01 = 173$  ( 169 + / 4 - )

<r> metagenes = 0.92  
 <r> genes = 0.41

<FC> = 0.98  
 <shrinkage-t> = 34.66  
 <p-value> = 0  
 <fdr> = 0.29

Profile

Spot



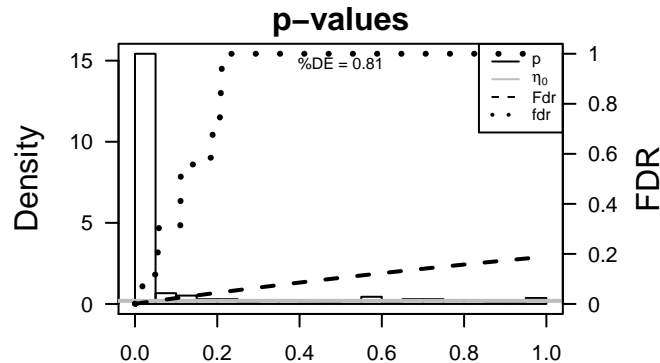
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	222	1.82	2e-16	2e-16	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC]
2	242	1.62	2e-16	2e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr]
3	387695	2.19	2e-16	2e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
4	760	2.1	2e-16	2e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	1041	2.16	2e-16	2e-16	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	84518	1.8	2e-16	2e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
7	54544	1.65	2e-16	2e-16	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
8	1475	1.75	2e-16	2e-16	1 x 50 cystatin A (steffin A) [Source:HGNC Symbol;Acc:2481]
9	9547	1.62	2e-16	2e-16	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;A]
10	126410	1.71	2e-16	2e-16	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour]
11	27065	1.84	2e-16	2e-16	1 x 46 Homo sapiens neuron specific gene family member 1 (NSG1)
12	1672	1.66	2e-16	2e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	55894	3.4	2e-16	2e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	3.77	2e-16	2e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	3.84	2e-16	2e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	1823	2.06	2e-16	2e-16	1 x 45 desmocollin 1 [Source:HGNC Symbol;Acc:3035]
17	1824	1.72	2e-16	2e-16	1 x 48 desmocollin 2 [Source:HGNC Symbol;Acc:3036]
18	1828	3.1	2e-16	2e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
19	2167	3.18	2e-16	2e-16	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
20	220832	1.7	2e-16	2e-16	1 x 45 fatty acid binding protein 5 pseudogene 3 [Source:HGNC Syr]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	41.09	NULL	87 / 135	H.Tiss WIRTH_Mucosa
2	38.87	NULL	18 / 21	CC cornified envelope
3	28.87	NULL	19 / 42	BP keratinization
4	28.7	NULL	104 / 572	Disease GUDJ_psooriasis up
5	26.97	NULL	24 / 53	BP keratinocyte differentiation
6	21.97	NULL	24 / 76	BP epidermis development
7	19.12	NULL	12 / 21	CC desmosome
8	16.69	NULL	3 / 8	GSEA C2LJU_CDX2_TARGETS_DN
9	16.68	NULL	10 / 19	BP peptide cross-linking
10	16.62	NULL	12 / 44	CC keratin filament
11	14.71	NULL	5 / 10	MF RAGE receptor binding
12	14.6	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
13	13.99	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
14	13.57	NULL	27 / 186	MF structural molecule activity
15	12.85	NULL	19 / 82	CC intermediate filament
16	12.33	NULL	8 / 15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	12.22	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
18	12.01	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	11.87	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
20	11.62	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
21	11.19	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
22	10.76	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
23	10.23	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
24	10.15	NULL	8 / 73	BP defense response to bacterium
25	10.09	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
26	9.97	NULL	3 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
27	9.81	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
28	9.74	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
29	9.37	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
30	9.33	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
31	9.06	NULL	5 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
32	8.8	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
33	8.78	NULL	2 / 12	MF fatty acid binding
34	8.71	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
35	8.64	NULL	62 / 1182	CC extracellular region
36	8.57	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
37	8.52	NULL	6 / 13	BP negative regulation of peptidase activity
38	8.46	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
39	8.43	NULL	4 / 21	CC gap junction
40	8.4	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP



# GW\_139

## Local Summary

%DE = 0.87  
 # metagenes = 34  
 # genes = 554  
 # genes in genesets = 523  
 # genes with  $fdr < 0.1$  = 422 ( 8 + / 414 - )  
 # genes with  $fdr < 0.05$  = 379 ( 6 + / 373 - )  
 # genes with  $fdr < 0.01$  = 266 ( 5 + / 261 - )

$\langle r \rangle$  metagenes = 0.84

$\langle r \rangle$  genes = 0.37

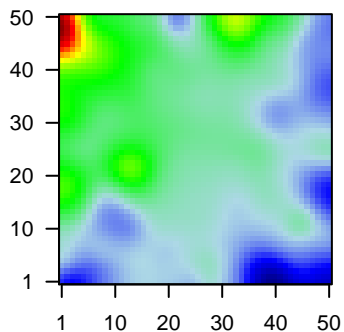
$\langle FC \rangle = -0.48$

$\langle \text{shrinkage-t} \rangle = -17.07$

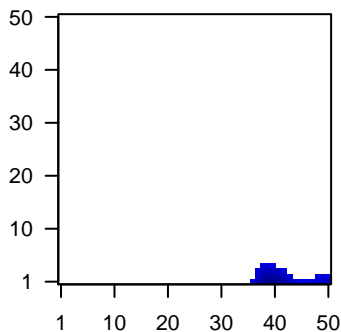
$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.48$

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	641737	-1.55	2e-16	5e-15	40 x 1
2	3127	2.35	2e-16	5e-15	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:UniProt]
3	3543	-1.54	2e-16	5e-15	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC S]
4	400818	-1.56	3e-15	2e-12	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt]
5	100132406	-1.5	3e-14	1e-10	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC]
6	3123	1.4	1e-12	1e-10	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:UniProt]
7	84061	-1.38	3e-12	1e-09	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
8	25862	-1.33	2e-11	1e-09	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20000]
9	3512	-1.3	5e-11	1e-09	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin heavy chain [Source:UniProt]
10	6376	-1.3	6e-11	1e-09	44 x 1 chemokine (C-X3-C motif) ligand 1 [Source:HGNC Symbol;Acc:10000]
11	399900	-1.18	8e-11	1e-09	39 x 1
12	65108	-1.28	9e-11	3e-09	44 x 1 MARCKS-like 1 [Source:HGNC Symbol;Acc:7142]
13	9747	-1.17	1e-10	3e-09	39 x 1 family with sequence similarity 115, member A [Source:HGNC Symbol;Acc:10000]
14	5996	-1.26	2e-10	1e-08	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:10000]
15	260436	-1.24	3e-10	1e-08	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:10000]
16	54855	-1.22	6e-10	1e-08	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:10000]
17	442578	-1.22	7e-10	3e-07	39 x 1
18	11040	-1.16	4e-09	3e-07	49 x 1 pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
19	126205	-1.14	8e-09	8e-07	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbol;Acc:10000]
20	136051	-1.1	3e-08	8e-07	40 x 1 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.27	NULL	83 / 417	H.Tiss WIRTH_Immune system
2	-11.4	NULL	56 / 312	BP immune response
3	-10.97	NULL	7 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
4	-10.85	NULL	77 / 553	Cancer Lembcke_Colonin Inflammation
5	-10.65	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
6	-9.91	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
7	-9.65	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
8	-8.84	NULL	3 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
9	-8.79	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
10	-8.66	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
11	-8.54	NULL	4 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
12	-8.54	NULL	4 / 13	BP lymph node development
13	-8.23	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
14	-8.15	NULL	4 / 12	BP dendritic cell chemotaxis
15	-7.93	NULL	4 / 14	MMML C2SCIEJ_MMML_8
16	-7.9	NULL	4 / 10	BP negative thymic T cell selection
17	-7.89	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
18	-7.77	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
19	-7.76	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
20	-7.63	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
21	-7.48	NULL	4 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
22	-7.36	NULL	3 / 12	GSEA C2MCCABE_HOX6_TARGETS_CANCER_UP
23	-7.31	NULL	25 / 162	CC external side of plasma membrane
24	-7.19	NULL	2 / 6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
25	-7.14	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
26	-6.95	NULL	4 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
27	-6.86	NULL	17 / 74	BP regulation of immune response
28	-6.73	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
29	-6.72	NULL	30 / 316	Cancer SPANG_BCL6-index2
30	-6.71	NULL	3 / 8	GSEA C2BIOCARTA_GRANULOCYTES_PATHWAY
31	-6.68	NULL	1 / 6	H.Tiss WIRTH_Bone marrow
32	-6.68	NULL	3 / 16	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
33	-6.59	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
34	-6.55	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
35	-6.54	NULL	3 / 12	BP macrophage chemotaxis
36	-6.42	NULL	4 / 16	GSEA C2PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
37	-6.32	NULL	3 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
38	-6.29	NULL	9 / 43	BP positive regulation of T cell proliferation
39	-6.28	NULL	4 / 14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
40	-6.16	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS

p-values

