

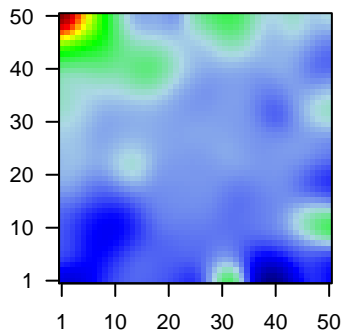
# GW\_185

## Global Summary

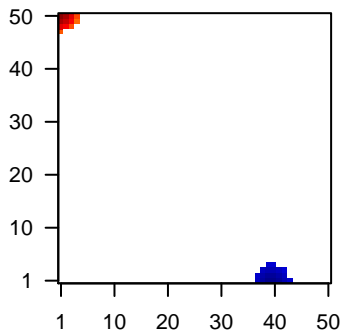
%DE = 0.12  
 # genes with fdr < 0.2 = 1581 ( 892 + / 689 - )  
 # genes with fdr < 0.1 = 1213 ( 709 + / 504 - )  
 # genes with fdr < 0.05 = 1003 ( 592 + / 411 - )  
 # genes with fdr < 0.01 = 776 ( 489 + / 287 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.11  
 <fdr> = 0.88

Profile



Regulated Spots



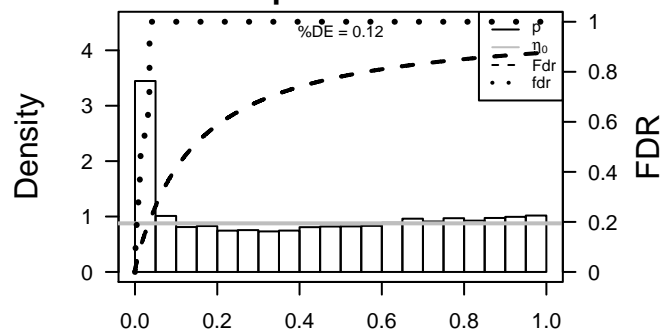
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	79852	1.36	2e-16 2e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	1.7	2e-16 2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.45	2e-16 2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
4	441282	1.2	2e-16 2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
5	8644	1.13	2e-16 2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr]
6	1109	1.14	2e-16 2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr]
7	220	1.41	2e-16 2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC]
8	218	1.4	2e-16 2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
9	348	-1.33	2e-16 2e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	360	1.48	2e-16 2e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63]
11	23120	1.16	2e-16 2e-14	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543]
12	633	-0.99	2e-16 2e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
13	84419	1.22	2e-16 2e-14	5 x 50 chromosome 15 open reading frame 48 [Source:HGNC Symt]
14	92747	2.38	2e-16 2e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb]
15	375791	1.9	2e-16 2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt]
16	760	1.32	2e-16 2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
17	768	1.11	2e-16 2e-14	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
18	8900	1.1	2e-16 2e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
19	1048	1.21	2e-16 2e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
20	4680	1.54	2e-16 2e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	35.4	NULL	135	H.Tiss WIRTH_Mucosa
2	29.84	NULL	572	Disease GUDJ_psooriasis up
3	13.63	NULL	21	CC cornified envelope
4	13.5	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
5	13.02	NULL	53	BP keratinocyte differentiation
6	11.92	NULL	76	BP epidermis development
7	11.25	NULL	16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
8	10.42	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
9	10.27	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	10.21	NULL	42	BP keratinization
11	9.94	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	9.75	NULL	186	MF structural molecule activity
13	9.48	NULL	123	BP defense response to virus
14	9.28	NULL	82	CC intermediate filament
15	9.2	NULL	15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	9.16	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
17	9.13	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD
18	9.12	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
19	9.12	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
20	9.1	NULL	31	BP negative regulation of viral genome replication
<i>Underexpressed</i>				
1	-12.49	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-9.04	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
3	-8.32	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
4	-7.94	NULL	190	CC extracellular matrix
5	-7.91	NULL	717	Chr Chr 16
6	-7.59	NULL	11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
7	-7.57	NULL	250	LymphontLEN_Stromal signature 1
8	-7.56	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
9	-7.53	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
10	-7.49	NULL	16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_DN
11	-7.48	NULL	9	GSEA C2XUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
12	-7.18	NULL	16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
13	-7.03	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
14	-6.87	NULL	14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
15	-6.54	NULL	56	BP response to mechanical stimulus
16	-6.43	NULL	19	MF extracellular matrix binding
17	-6.41	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
18	-6.4	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
19	-6.24	NULL	30	BP cellular response to hormone stimulus
20	-6.18	NULL	15	BP response to corticosterone

p-values



# GW\_185

## Local Summary

%DE = 0.98  
 # metagenes = 12  
 # genes = 189  
 # genes in genesets = 184

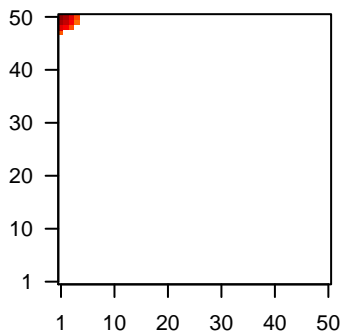
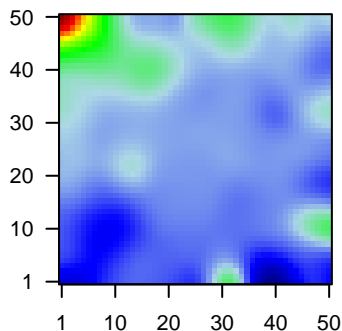
# genes with  $fdr < 0.1 = 180$  ( 177 + / 3 - )  
 # genes with  $fdr < 0.05 = 176$  ( 175 + / 1 - )  
 # genes with  $fdr < 0.01 = 173$  ( 172 + / 1 - )

<r> metagenes = 0.98  
 <r> genes = 0.48

<FC> = 1.04  
 <shrinkage-t> = 36.69  
 <p-value> = 0  
 <fdr> = 0.08

Profile

Spot



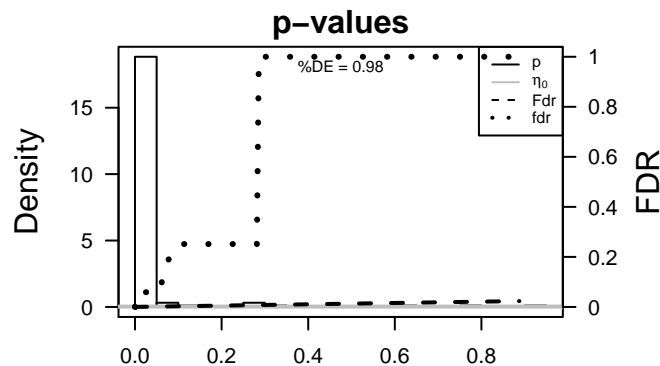
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	79852	1.36	2e-16	1e-17	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	1.7	2e-16	1e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.45	2e-16	1e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	1.2	2e-16	1e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	8644	1.13	2e-16	1e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	218	1.4	2e-16	1e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
7	360	1.48	2e-16	1e-17	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
8	23120	1.16	2e-16	1e-17	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
9	375791	1.9	2e-16	1e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
10	1048	1.21	2e-16	1e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
11	4680	1.54	2e-16	1e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
12	22802	1.8	2e-16	1e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	9022	1.58	2e-16	1e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
14	84518	1.78	2e-16	1e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
15	1382	1.29	2e-16	1e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
16	54544	1.82	2e-16	1e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	3.17	2e-16	1e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1562	1.28	2e-16	1e-17	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
19	1672	1.1	2e-16	1e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
20	55894	1.93	2e-16	1e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	57.69	NULL	75 / 135	H.Tiss WIRTH_Mucosa
2	27.67	NULL	15 / 21	CC cornified envelope
3	26.25	NULL	80 / 572	Disease GUDJ_pсорiasis up
4	24.24	NULL	20 / 53	BP keratinocyte differentiation
5	21.68	NULL	18 / 42	BP keratinization
6	20.5	NULL	20 / 76	BP epidermis development
7	19.73	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	19.69	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	18.65	NULL	6 / 13	BP negative regulation of peptidase activity
10	18.64	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
11	17.71	NULL	8 / 19	BP peptide cross-linking
12	15.25	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	14.51	NULL	5 / 10	MF RAGE receptor binding
14	14.22	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
15	13.44	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	12.39	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
17	12.05	NULL	49 / 1182	CC extracellular region
18	11.93	NULL	11 / 122	MF serine-type endopeptidase activity
19	11.8	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
20	11.62	NULL	8 / 44	CC keratin filament
21	11.55	NULL	10 / 82	CC intermediate filament
22	11.05	NULL	8 / 52	BP negative regulation of endopeptidase activity
23	11.05	NULL	17 / 186	MF structural molecule activity
24	10.48	NULL	4 / 15	MF retinol dehydrogenase activity
25	10.03	NULL	7 / 38	BP epithelial cell differentiation
26	9.98	NULL	4 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
27	9.79	NULL	4 / 23	MF peptidase inhibitor activity
28	9.73	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
29	9.52	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
30	9.38	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
31	9.35	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
32	9.35	NULL	5 / 29	BP regulation of proteolysis
33	9.31	NULL	4 / 13	H.Tiss WIRTH_Tonsil
34	8.91	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
35	8.88	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
36	8.85	NULL	3 / 10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING
37	8.83	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
38	8.83	NULL	3 / 16	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G24
39	8.8	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
40	8.7	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN



# GW\_185

## Local Summary

%DE = 0.92  
 # metagenes = 20  
 # genes = 301  
 # genes in genesets = 274  
 # genes with  $fdr < 0.1$  = 257 ( 2 + / 255 - )  
 # genes with  $fdr < 0.05$  = 224 ( 1 + / 223 - )  
 # genes with  $fdr < 0.01$  = 189 ( 0 + / 189 - )

<r> metagenes = 0.97

<r> genes = 0.44

<FC> = -0.41

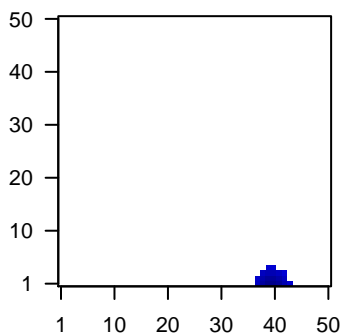
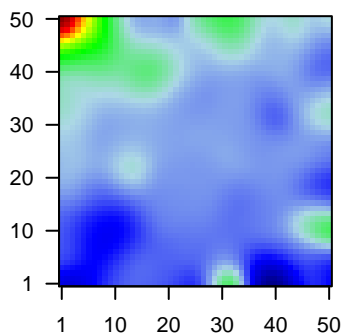
<shrinkage-t> = -14.43

<p-value> = 0

<fdr> = 0.39

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
1	641737	-1.02	2e-16	3e-15	40 x 1	
2	440157	-1.22	2e-16	3e-15	39 x 1	
3	84061	-1.04	7e-16	6e-14	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
4	81033	-0.93	3e-15	7e-14	39 x 1	potassium voltage-gated channel, subfamily H (eag-related).
5	91368	-0.92	6e-15	3e-13	39 x 1	CDKN2A interacting protein N-terminal like [Source:HGNC S
6	399900	-0.9	2e-14	1e-12	39 x 1	
7	3127	-0.96	8e-14	2e-12	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
8	90586	-0.95	2e-13	8e-12	39 x 1	amine oxidase, copper containing 4, pseudogene [Source:HC
9	400866	-0.92	1e-12	8e-12	39 x 1	long intergenic non-protein coding RNA 114 [Source:HGNC :
10	250	-0.91	1e-12	8e-12	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:4
11	319085	-0.9	1e-12	2e-11	39 x 1	ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
12	25862	-0.9	2e-12	2e-11	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
13	9747	-0.82	3e-12	2e-11	39 x 1	family with sequence similarity 115, member A [Source:HGNC
14	126205	-0.89	3e-12	2e-11	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
15	401494	-0.89	4e-12	3e-11	40 x 1	protein tyrosine phosphatase-like A domain containing 2 [Soi
16	255031	-0.89	5e-12	8e-11	40 x 1	long intergenic non-protein coding RNA 957 [Source:HGNC :
17	22834	-0.87	1e-11	8e-11	40 x 1	zinc finger protein 652 [Source:HGNC Symbol;Acc:29147]
18	85452	-0.86	2e-11	8e-11	39 x 1	chromosome 1 open reading frame 222 [Source:HGNC Symt
19	5143	-0.79	2e-11	8e-11	39 x 1	phosphodiesterase 4C, cAMP-specific [Source:HGNC Symbi
20	374860	-0.85	2e-11	8e-11	40 x 1	ankyrin repeat domain 30B [Source:HGNC Symbol;Acc:2416

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-13.12	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-12.14	NULL	3 / 14	MMML C6ACIEJ_MMML 8
3	-9.28	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
4	-7.25	NULL	2 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
5	-6.81	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
6	-6.11	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
7	-6.11	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
8	-6.05	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
9	-6.04	NULL	2 / 14	BP cellular response to estradiol stimulus
10	-5.97	NULL	2 / 16	BP cognition
11	-5.77	NULL	3 / 24	BP negative regulation of T cell proliferation
12	-5.65	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
13	-5.61	NULL	1 / 10	CC oligosaccharyltransferase complex
14	-5.14	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
15	-5.09	NULL	1 / 4	MMML C6ACIEJ_MMML 44
16	-5.07	NULL	2 / 14	BP mitochondrion morphogenesis
17	-4.97	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
18	-4.88	NULL	3 / 23	BP G2 DNA damage checkpoint
19	-4.86	NULL	3 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
20	-4.77	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
21	-4.73	NULL	2 / 11	GSEA C2KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
22	-4.6	NULL	1 / 11	GSEA C2KEGG_FOLATE_BIOSYNTHESIS
23	-4.56	NULL	1 / 14	BP magnesium ion transport
24	-4.55	NULL	1 / 14	Cancer LIU_COMMON_CANCER_GENES
25	-4.54	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
26	-4.48	NULL	2 / 19	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
27	-4.48	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process
28	-4.48	NULL	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
29	-4.29	NULL	2 / 19	MF mitogen-activated protein kinase kinase kinase binding
30	-4.22	NULL	1 / 11	BP negative regulation of interleukin-12 production
31	-4.22	NULL	1 / 11	GSEA C2SU_PANCREAS
32	-4.16	NULL	2 / 10	MF endodeoxyribonuclease activity
33	-4.09	NULL	1 / 12	BP cAMP catabolic process
34	-4	NULL	1 / 15	CC MHC class II protein complex
35	-3.99	NULL	1 / 12	BP negative regulation of growth of symbiont in host
36	-3.98	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
37	-3.94	NULL	42 / 1135	Chr Chr 19
38	-3.86	NULL	4 / 100	Lymphomonocytosis BOSOLOWSKI_blue total
39	-3.84	NULL	2 / 22	BP negative regulation of interferon-gamma production
40	-3.81	NULL	2 / 15	BP female gamete generation

p-values

