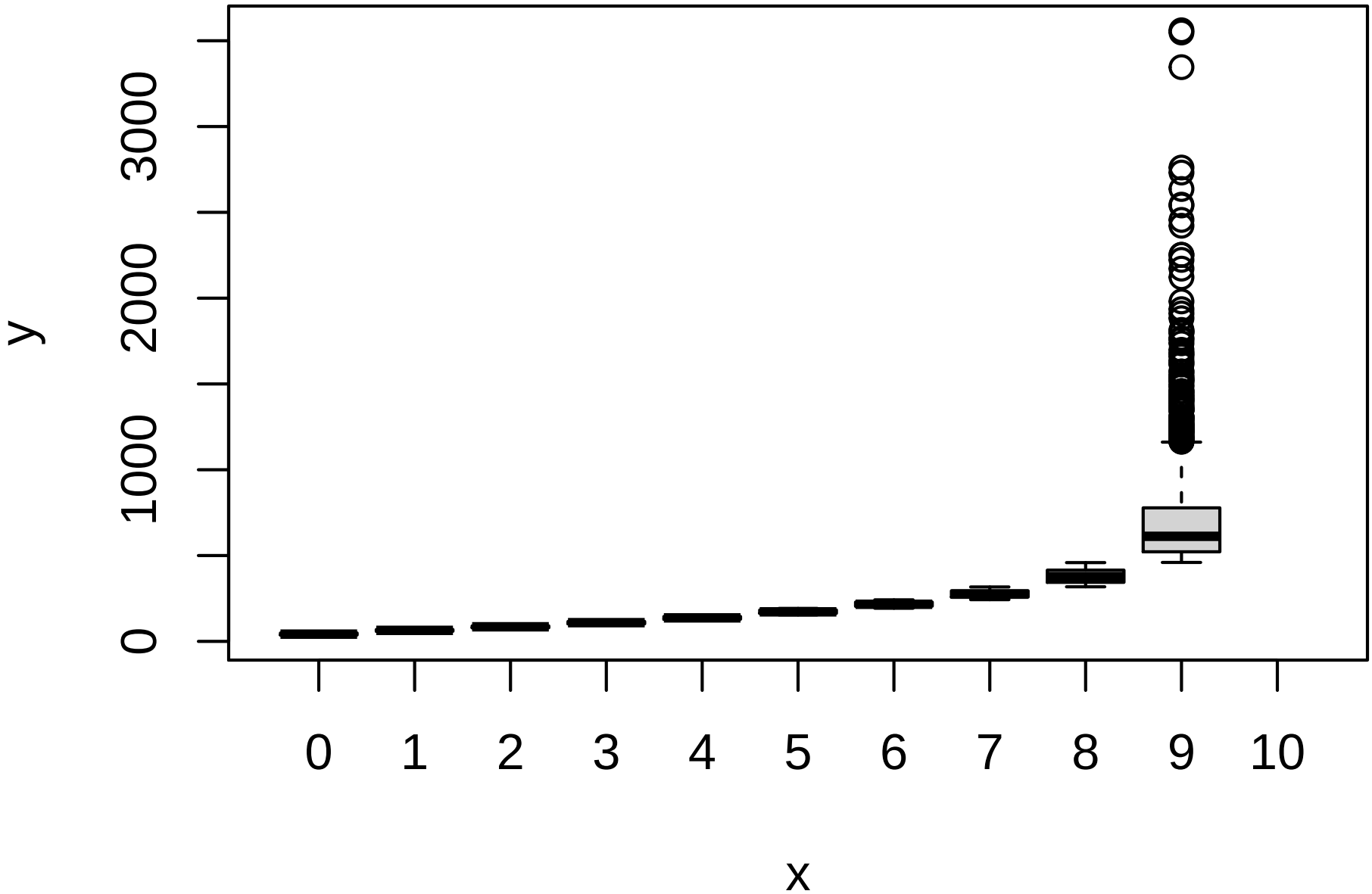
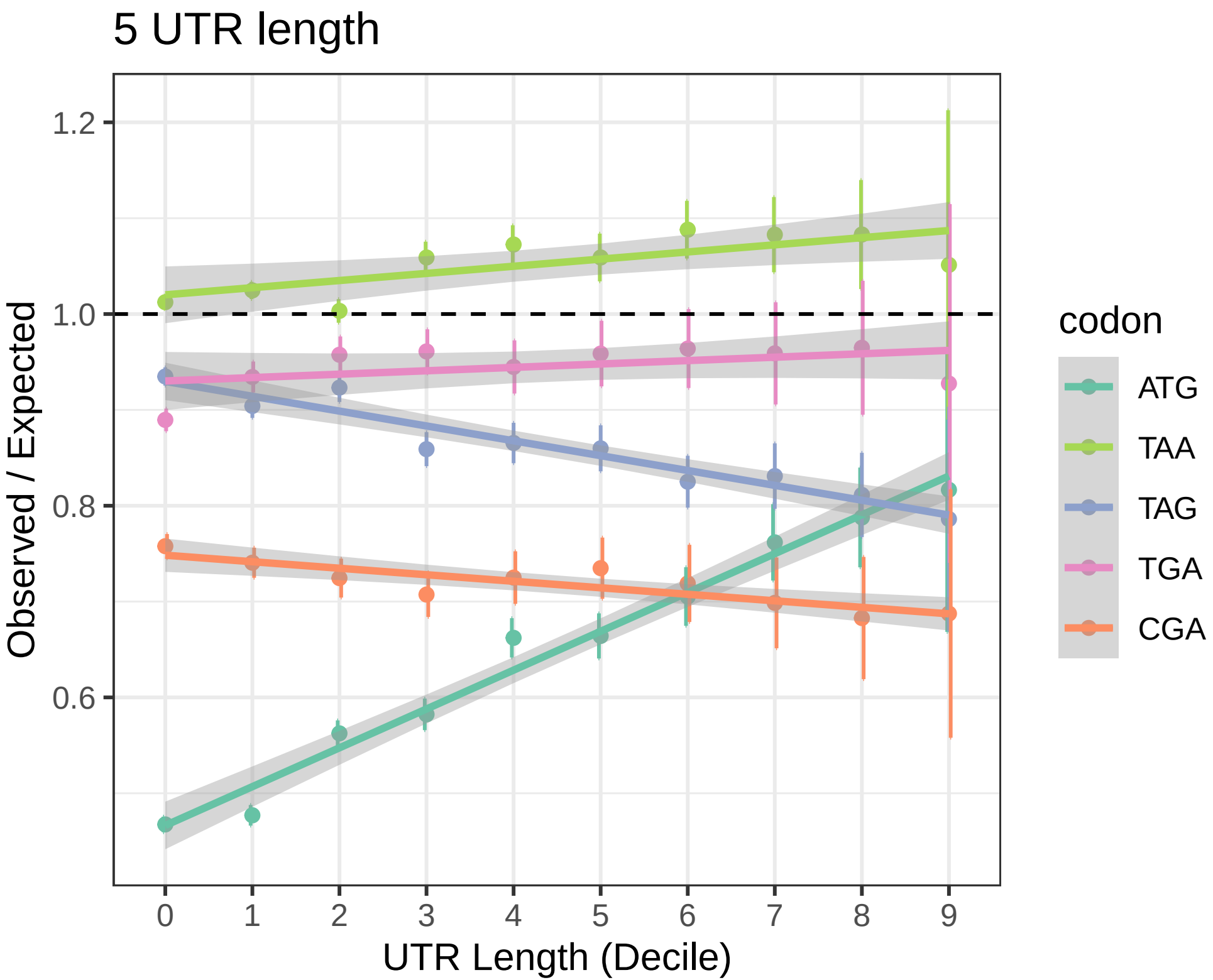
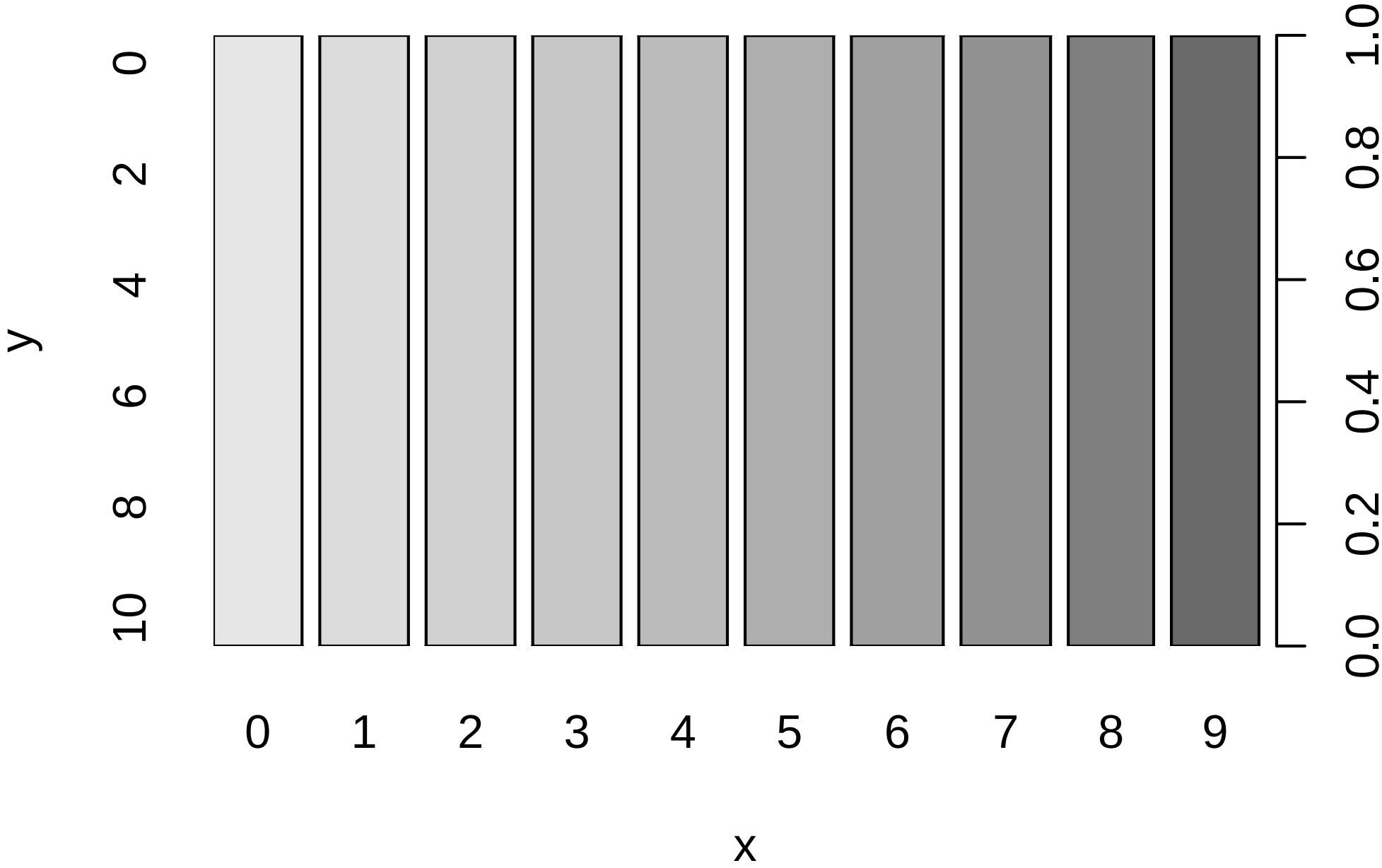
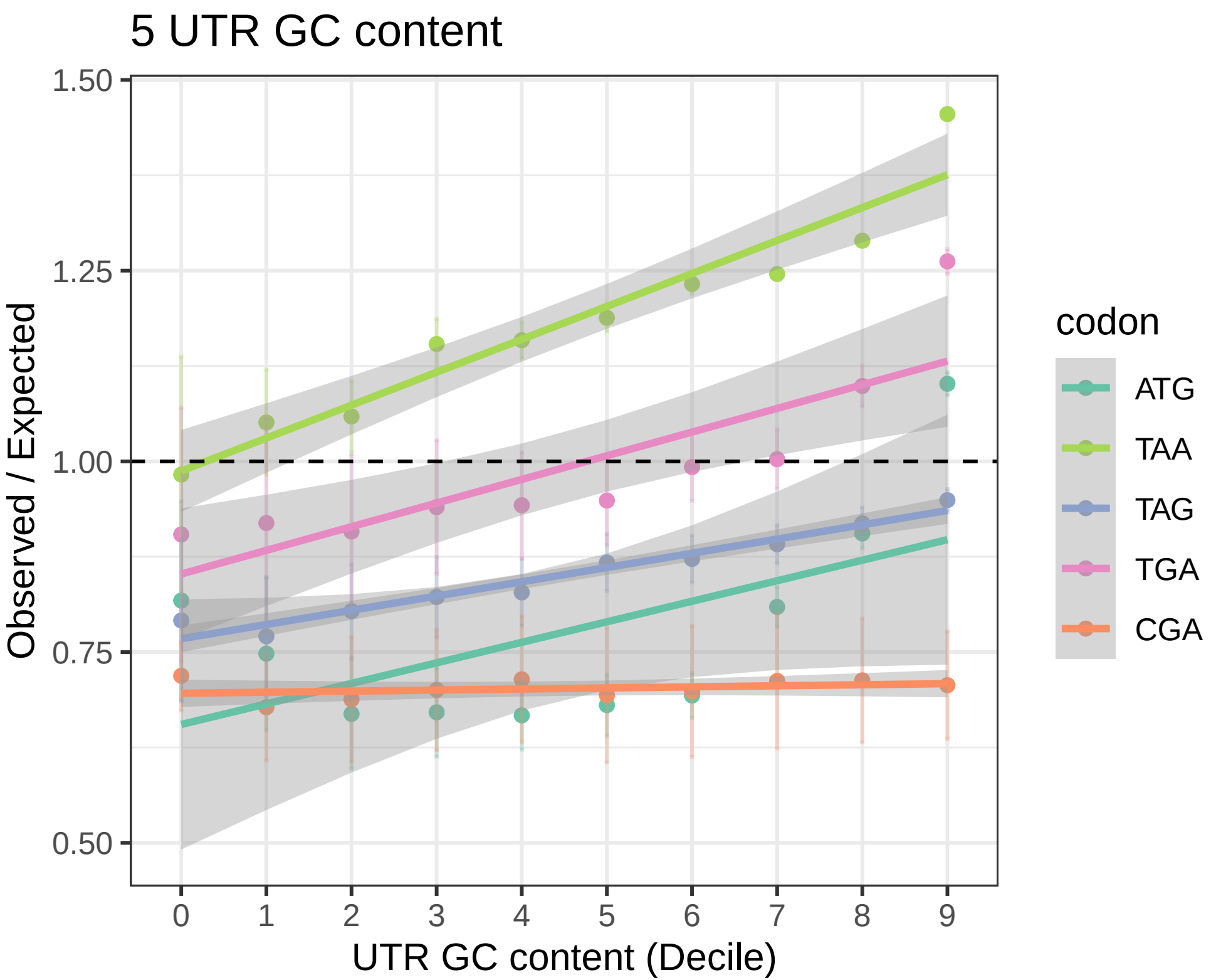
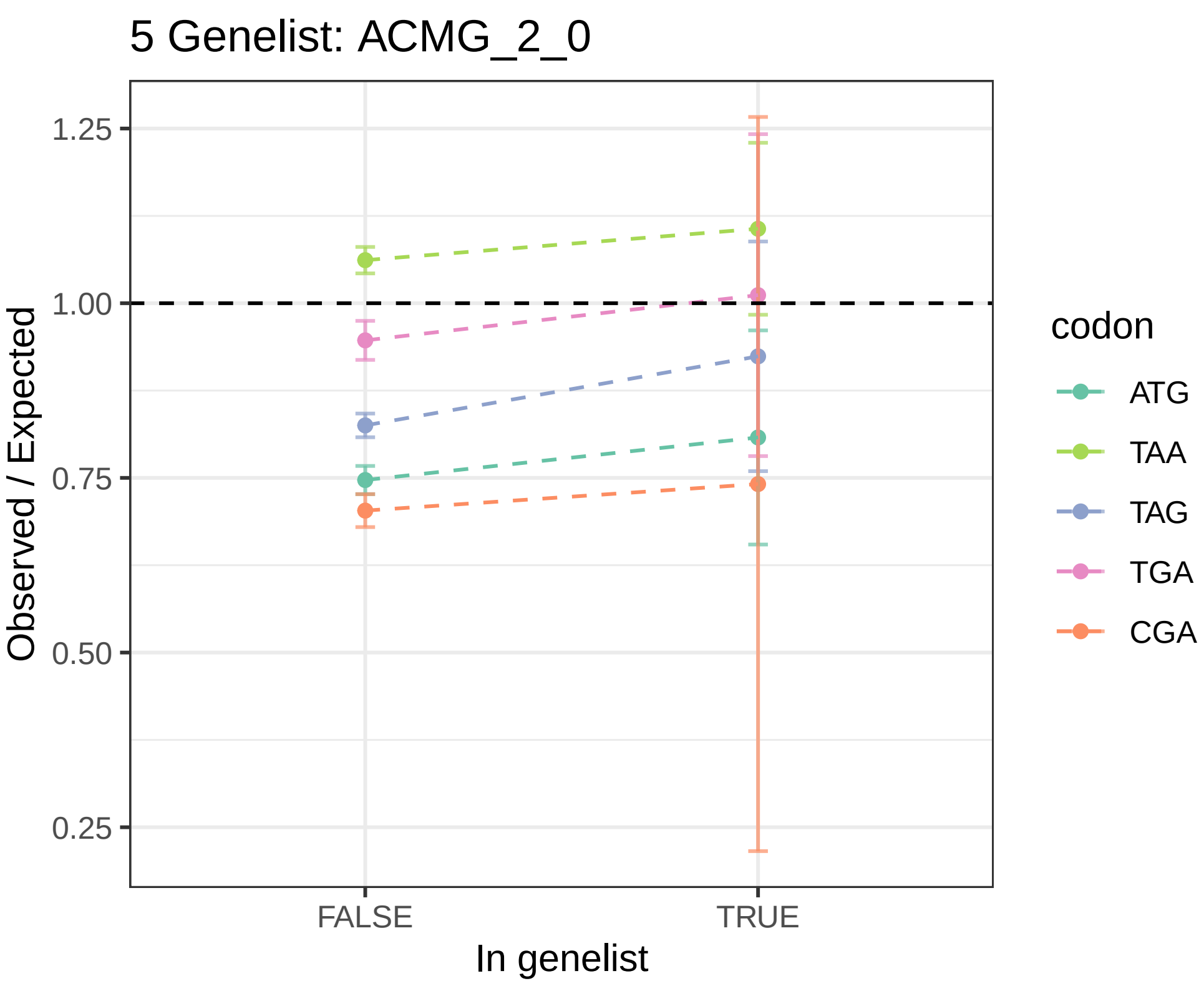
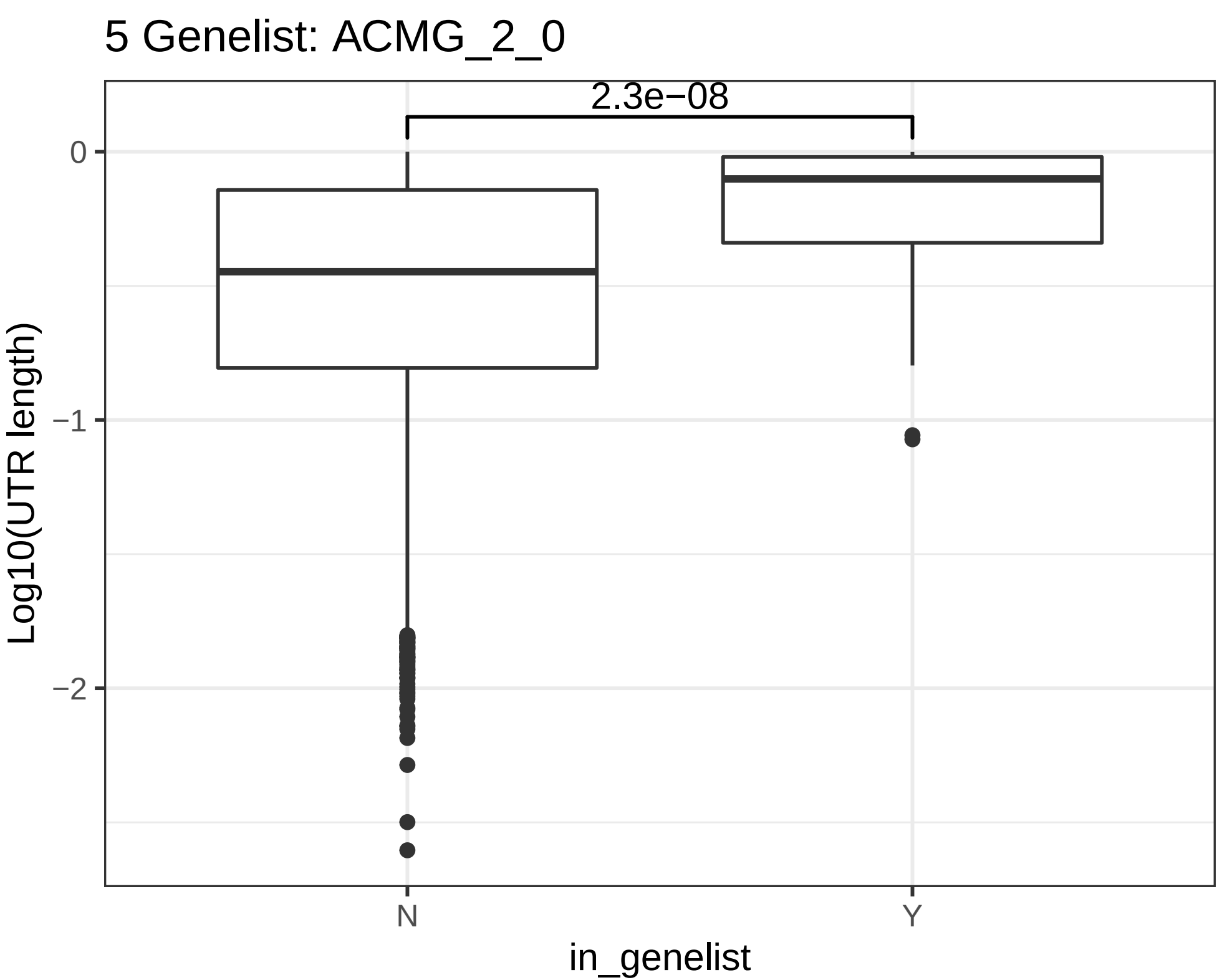

y
0
1000
2000
3000
0
1
2
3
4
5
6
7
8
9
10
x

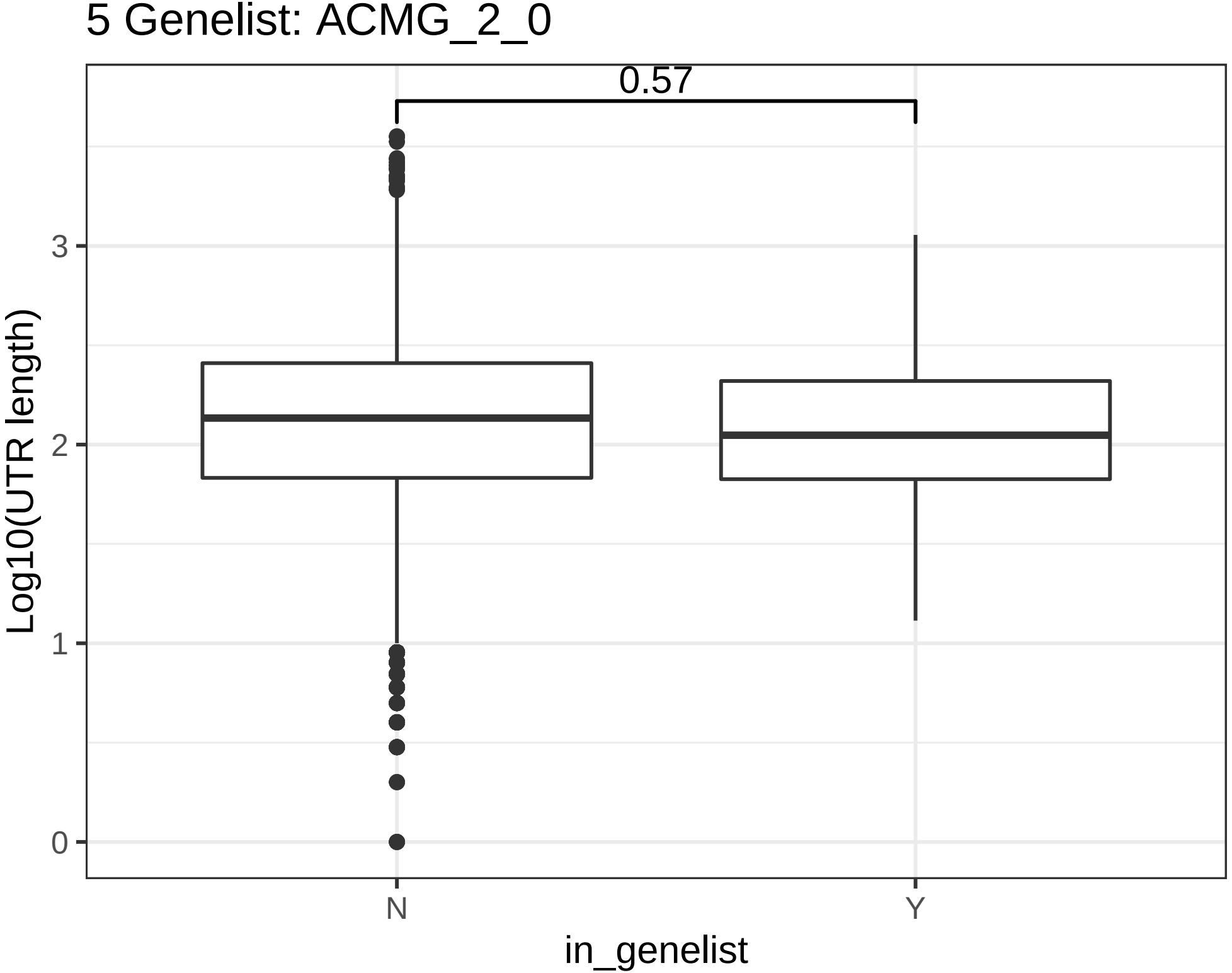

5 UTR length
Observed / Expected
1.2
1.0
0.8
0.6
0
1
2
3
4
5
6
7
8
9
UTR Length (Decile)
codon
ATG
TAA
TAG
TGA
CGA

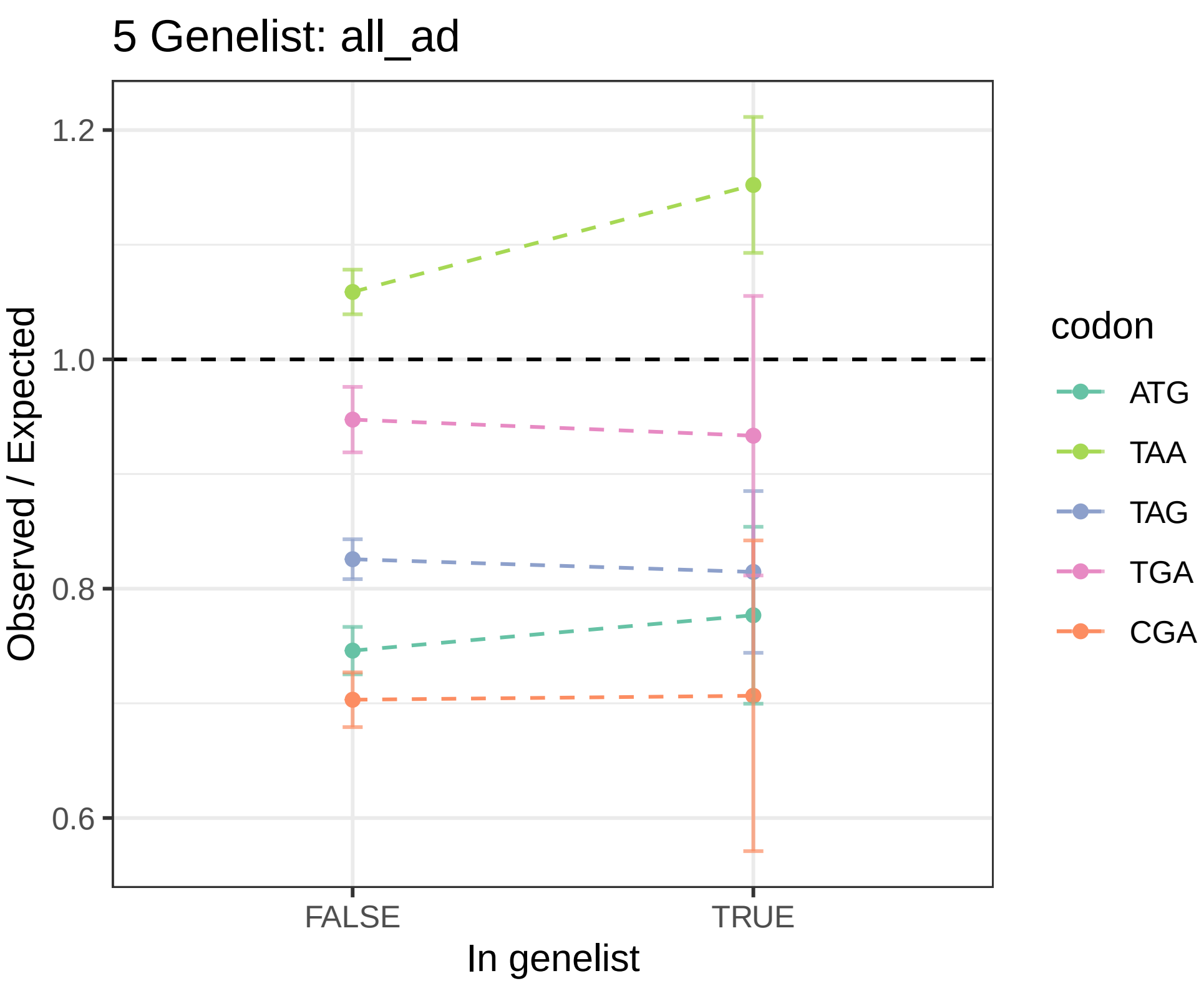

y
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
5
6
7
8
9
x

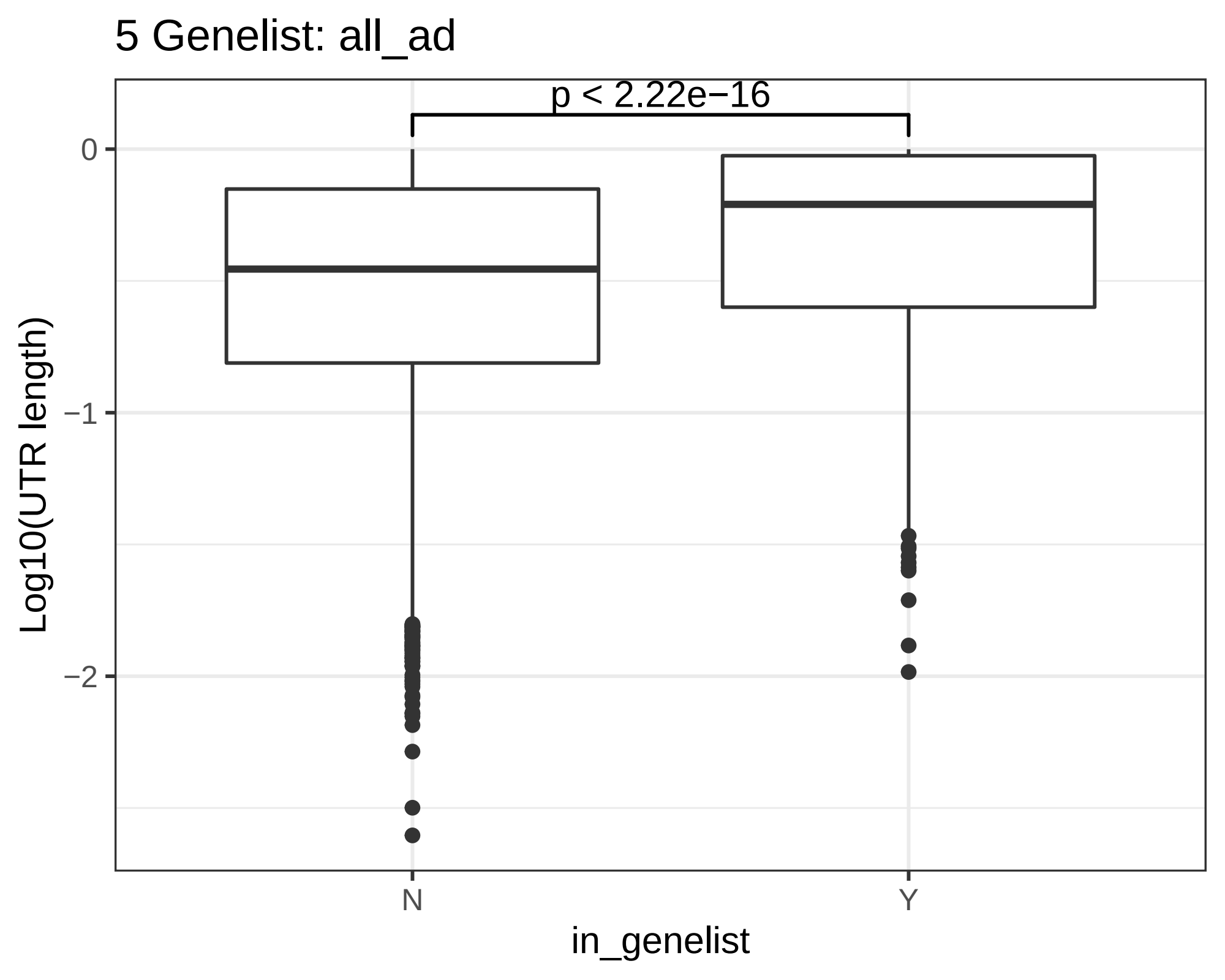

5 UTR GC content
1.50
1.25
1.00
0.75
0.50
Observed / Expected
0
1
2
3
4
5
6
7
8
9
UTR GC content (Decile)
codon
ATG
TAA
TAG
TGA
CGA

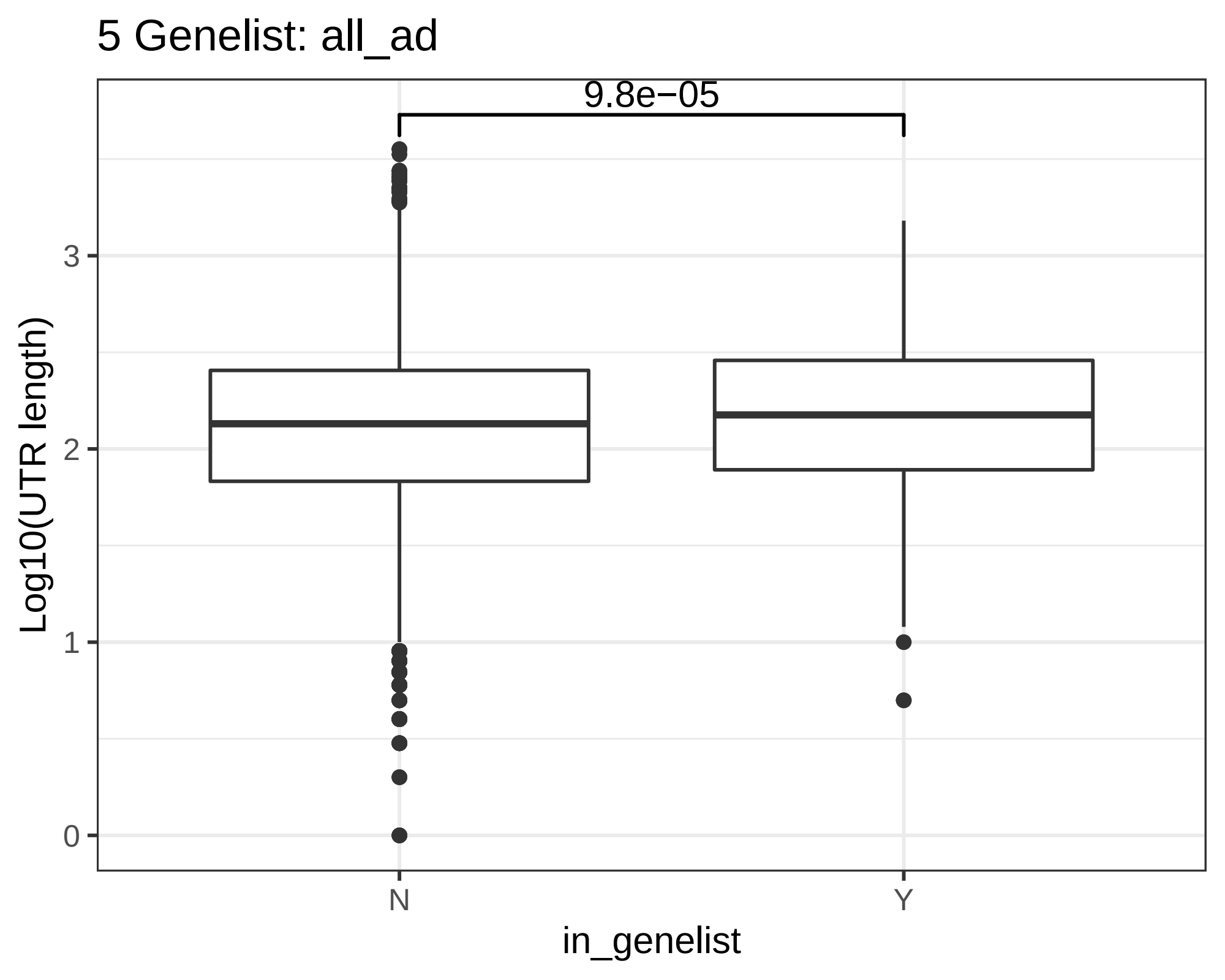

5 Genelist: ACMG_2_0
1.25
1.00
0.75
0.50
0.25
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

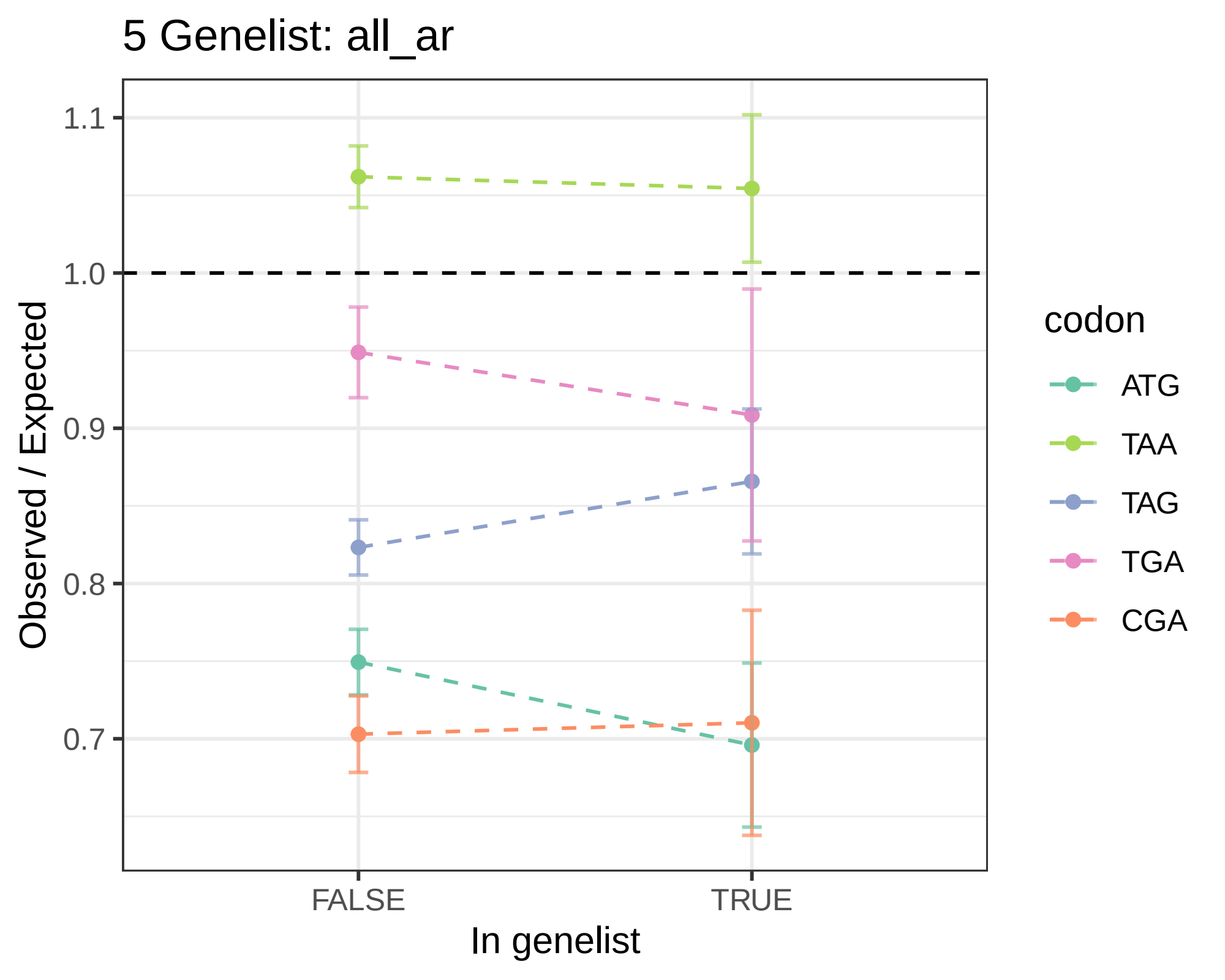

5 Genelist: ACMG_2_0
2.3e−08
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

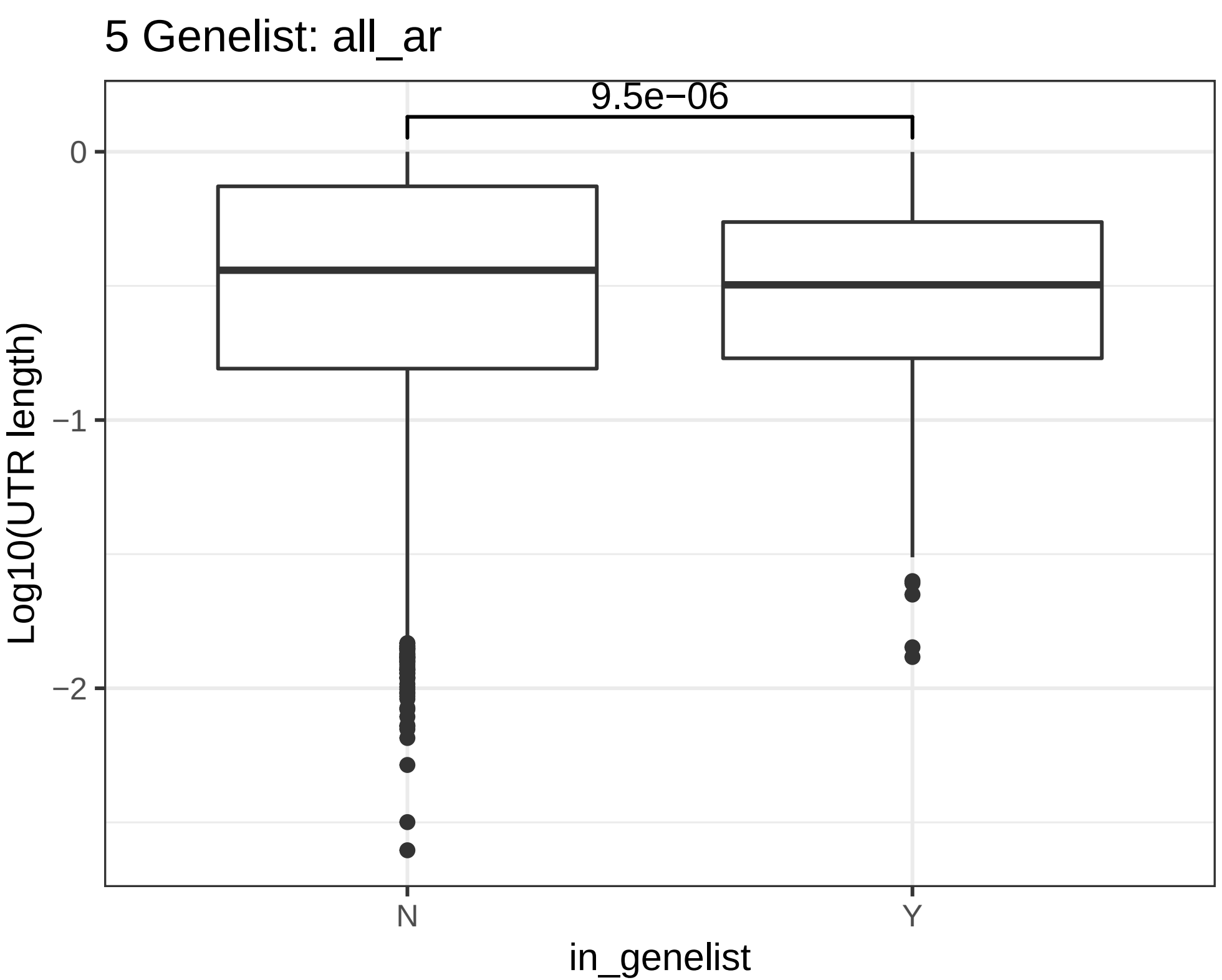

5 Genelist: ACMG_2_0
0.57
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

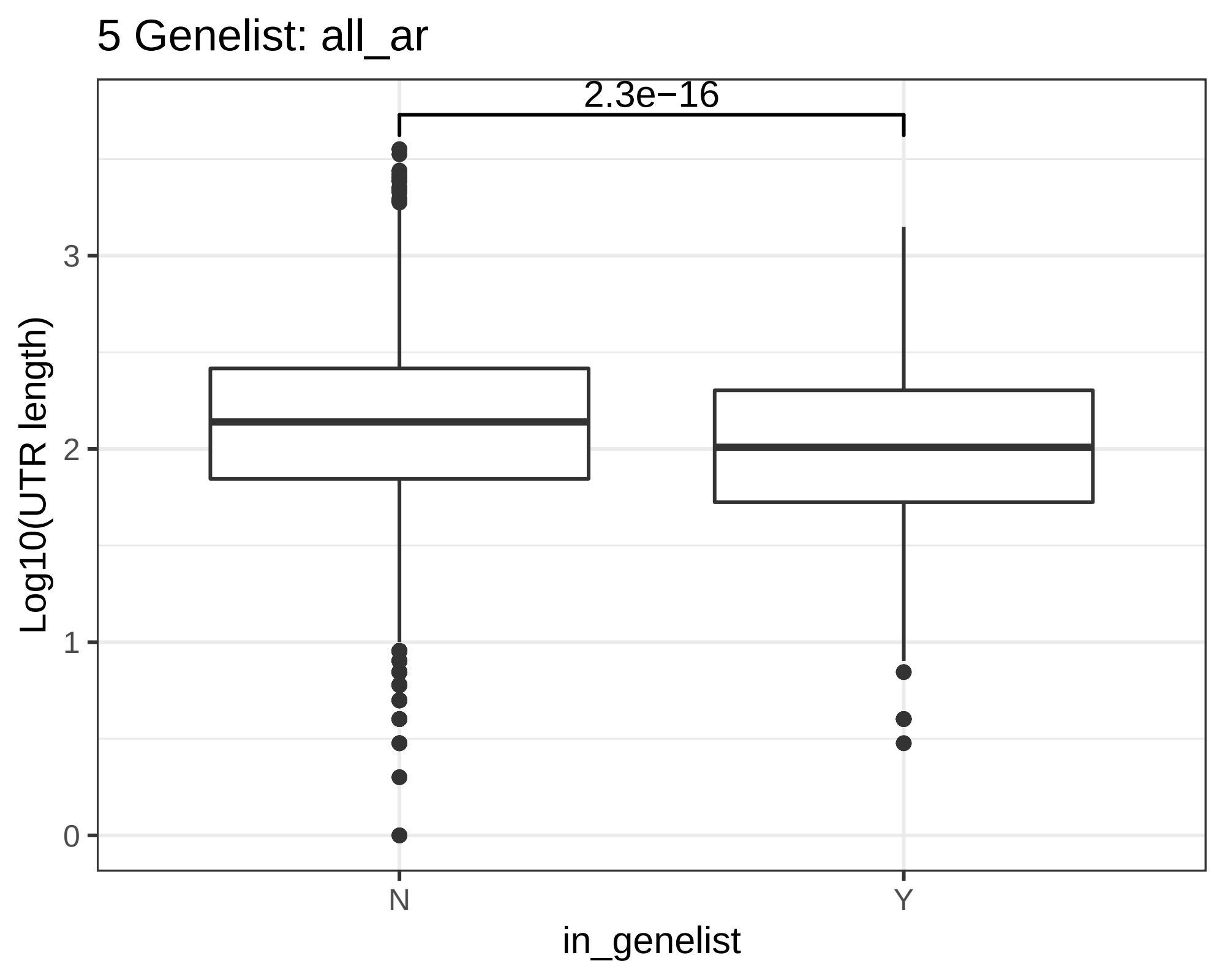

5 Genelist: all_ad
Observed / Expected
1.2
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA


5 Genelist: all_ad
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

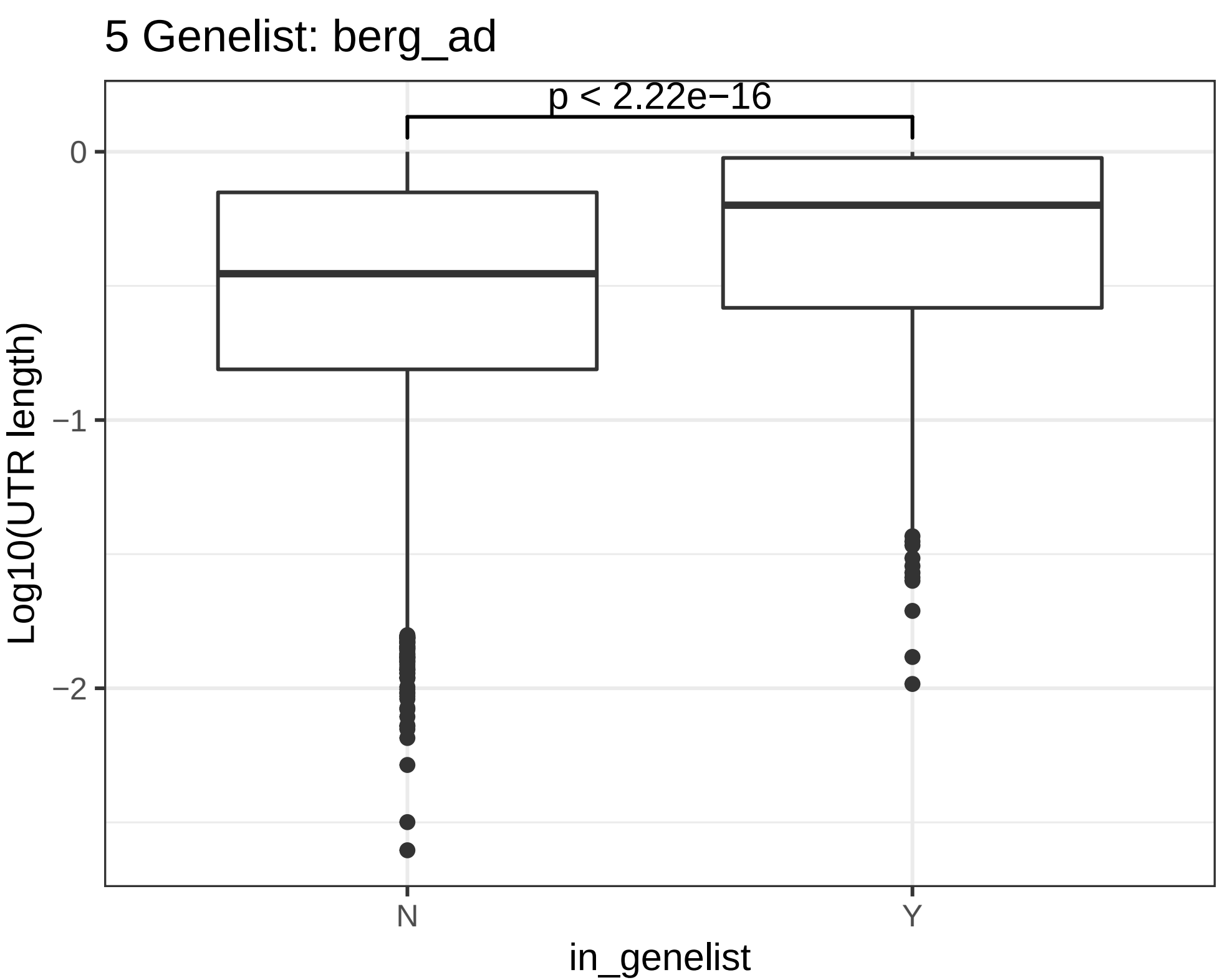

5 Genelist: all_ad
9.8e−05
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

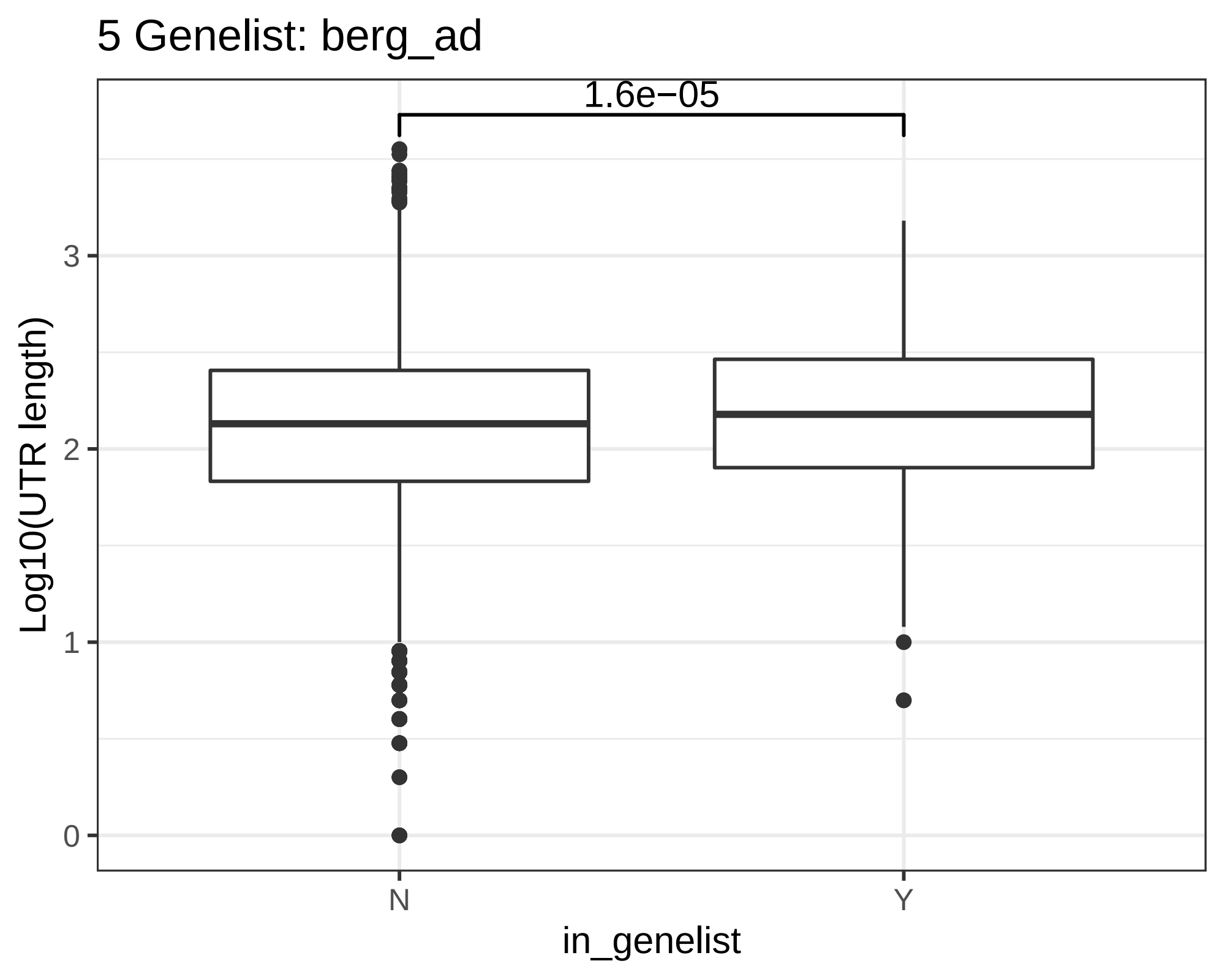

5 Genelist: all_ar
1.1
1.0
0.9
0.8
0.7
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

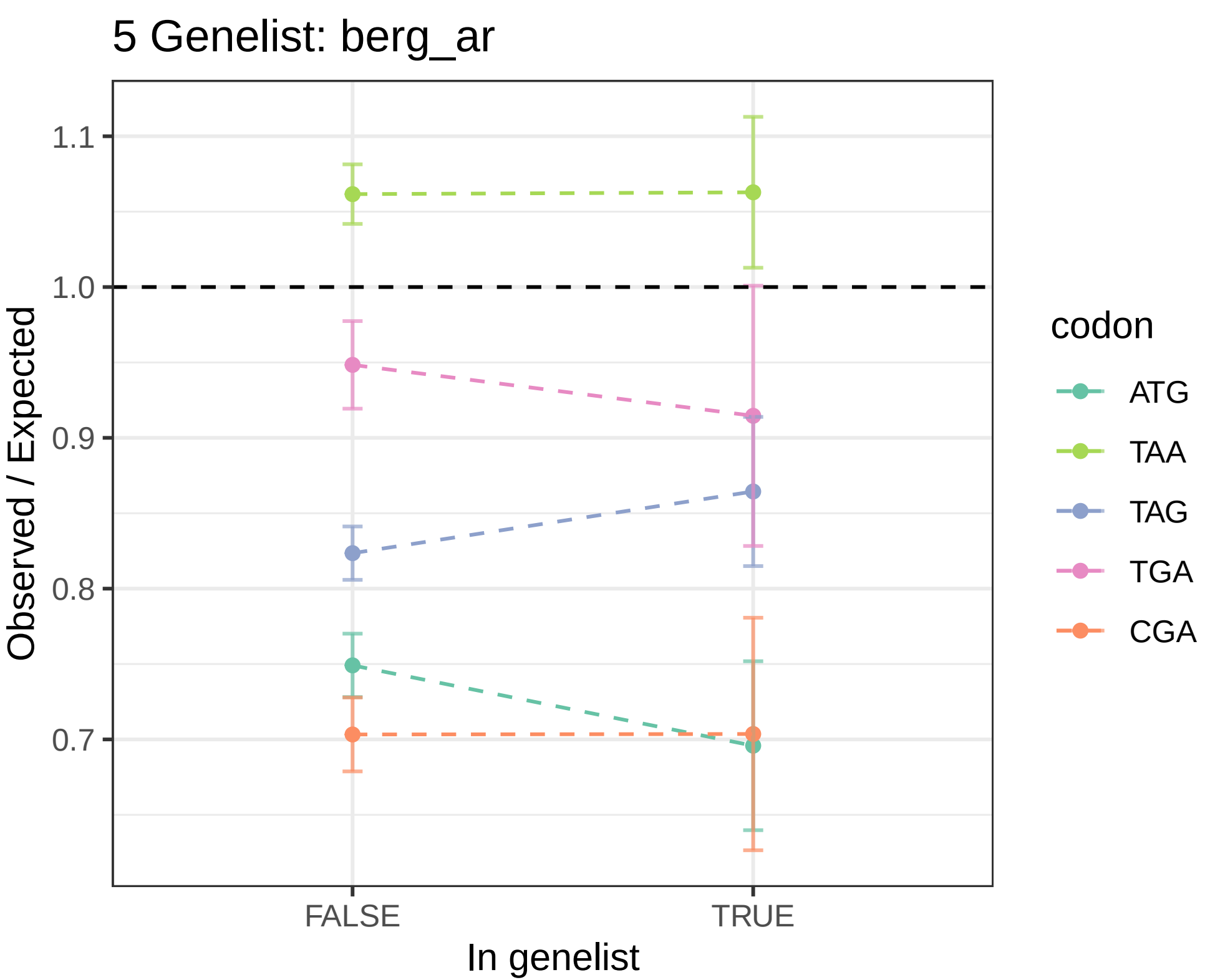

5 Genelist: all_ar
9.5e−06
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

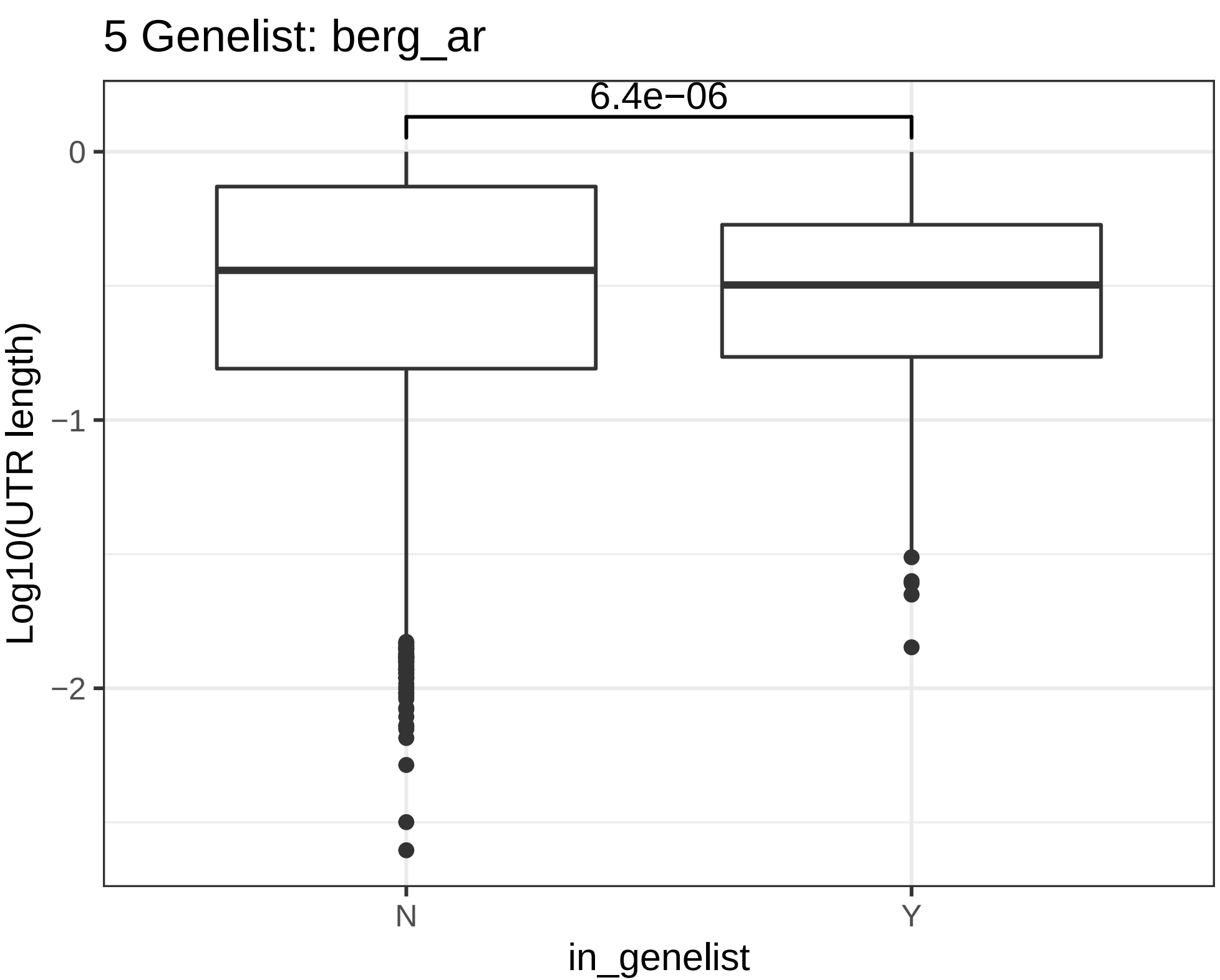

5 Genelist: all_ar
2.3e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

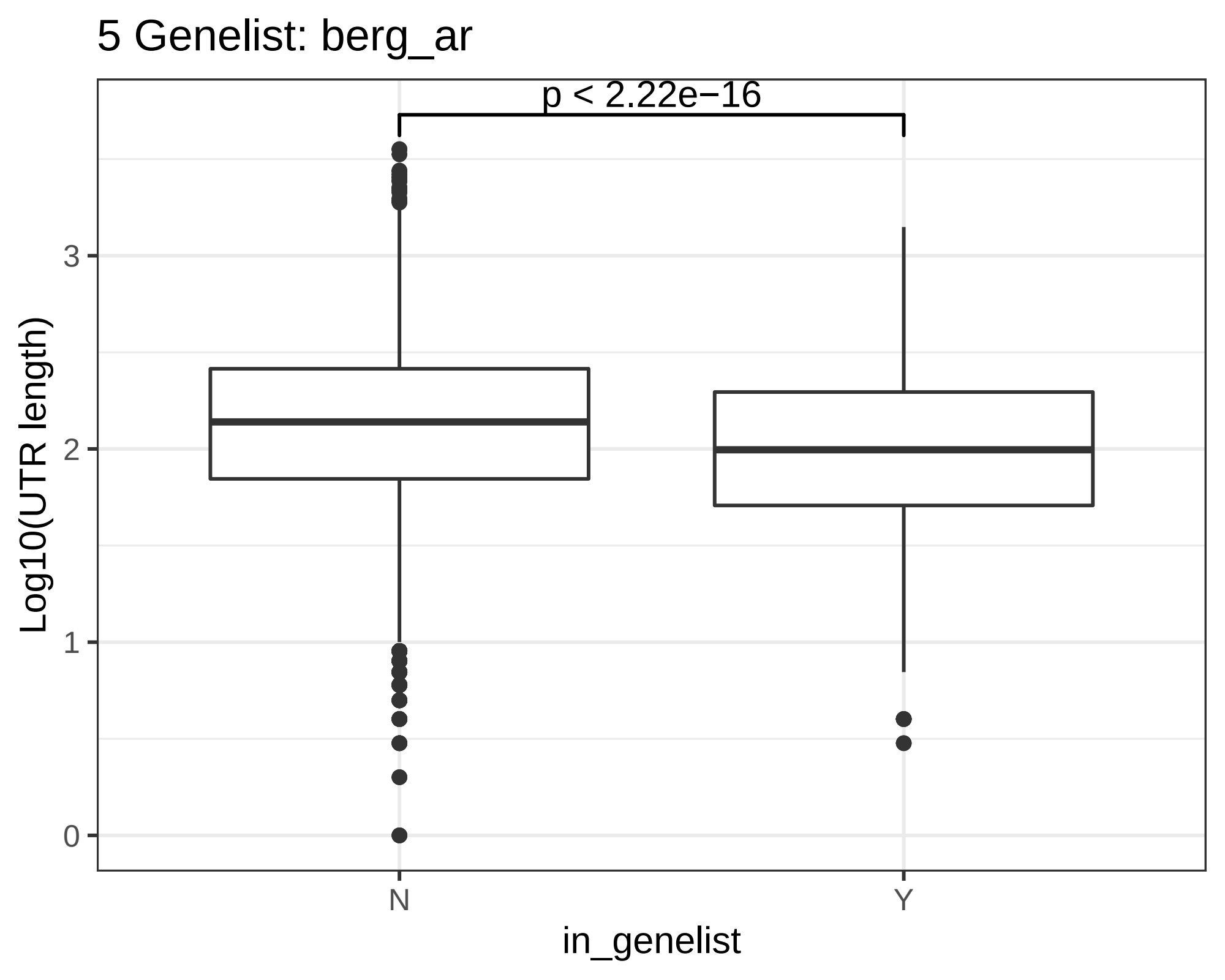
5 Genelist: berg_ad
Observed / Expected
1.1
0.9
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

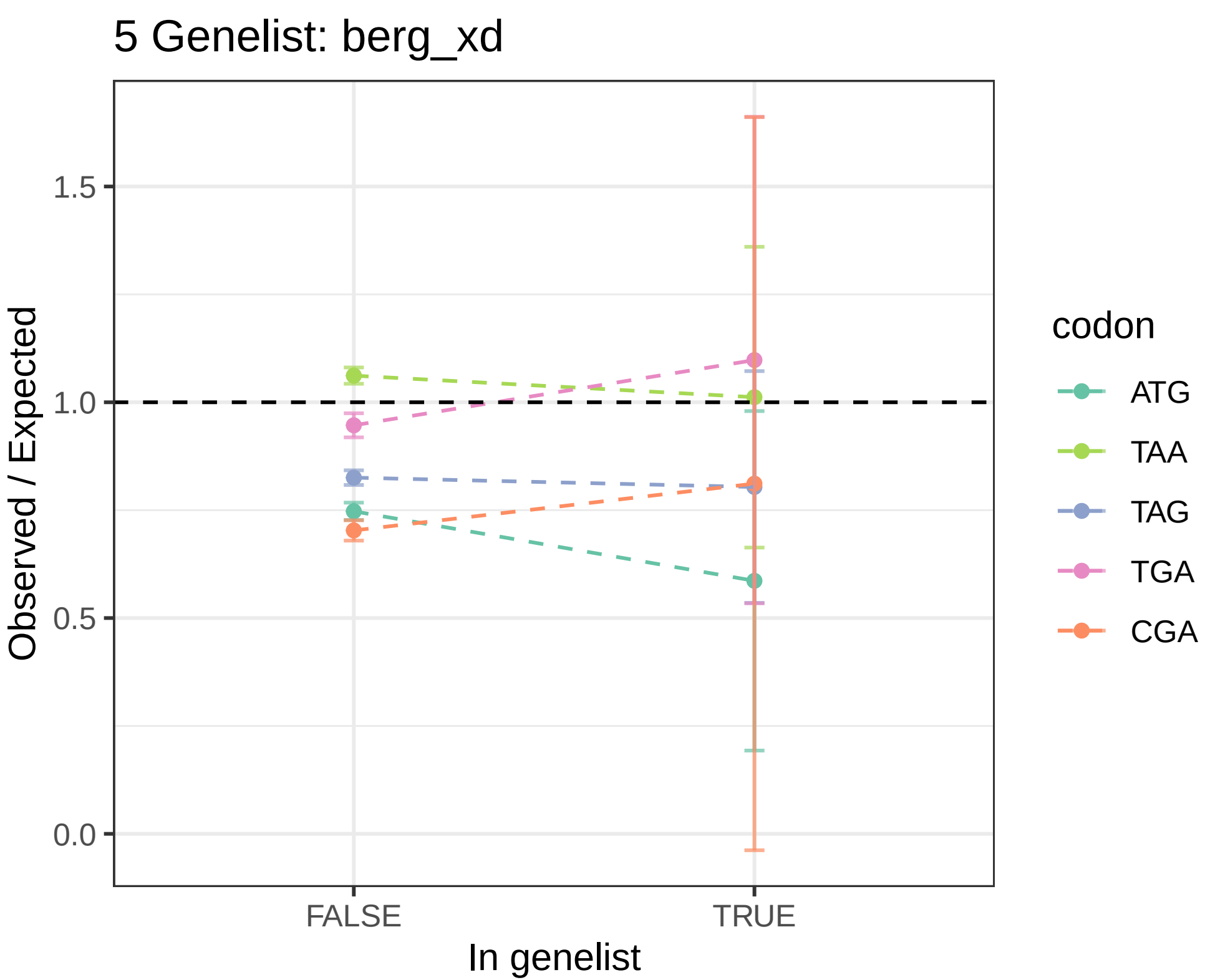

5 Genelist: berg_ad
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

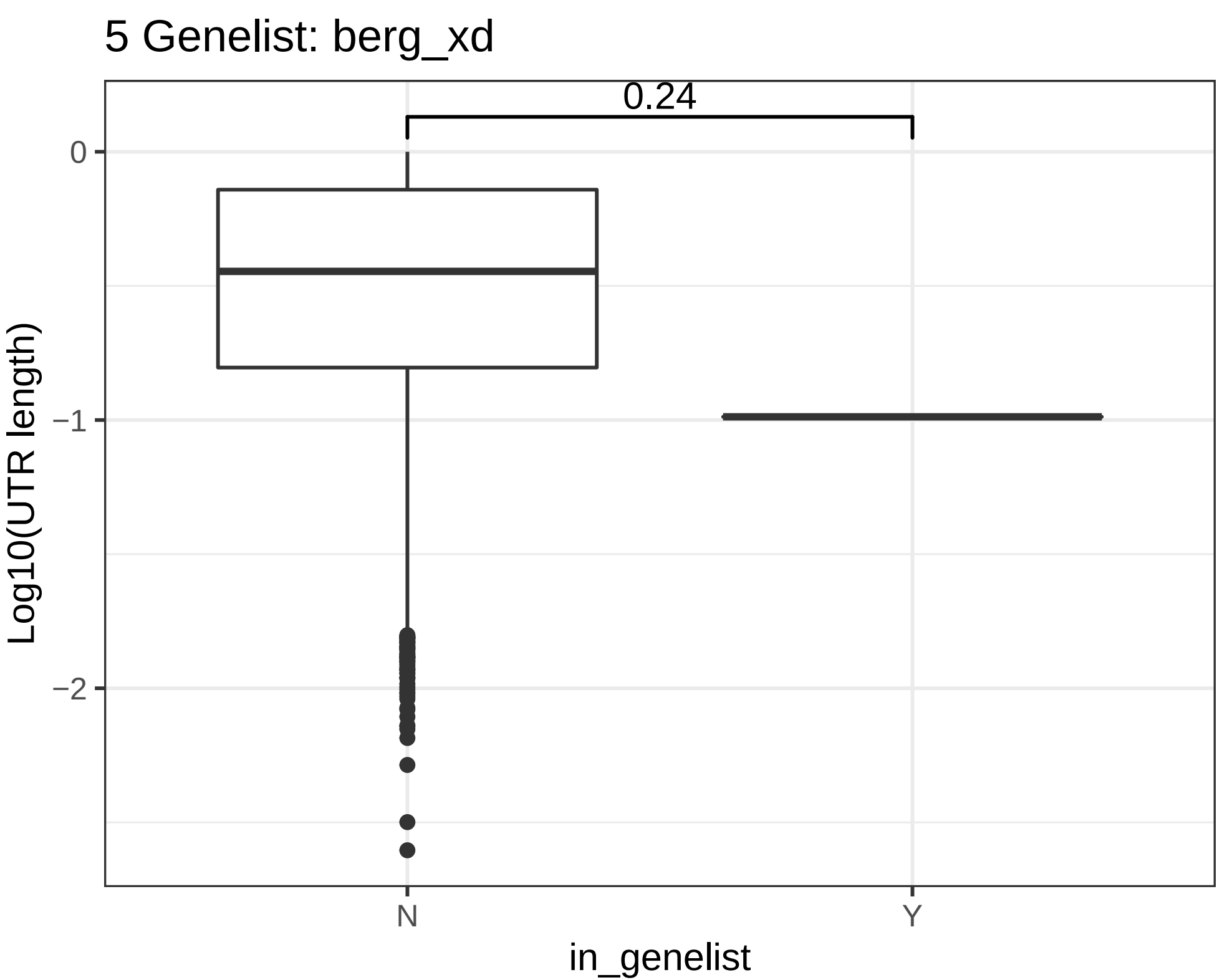

5 Genelist: berg_ad
1.6e−05
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

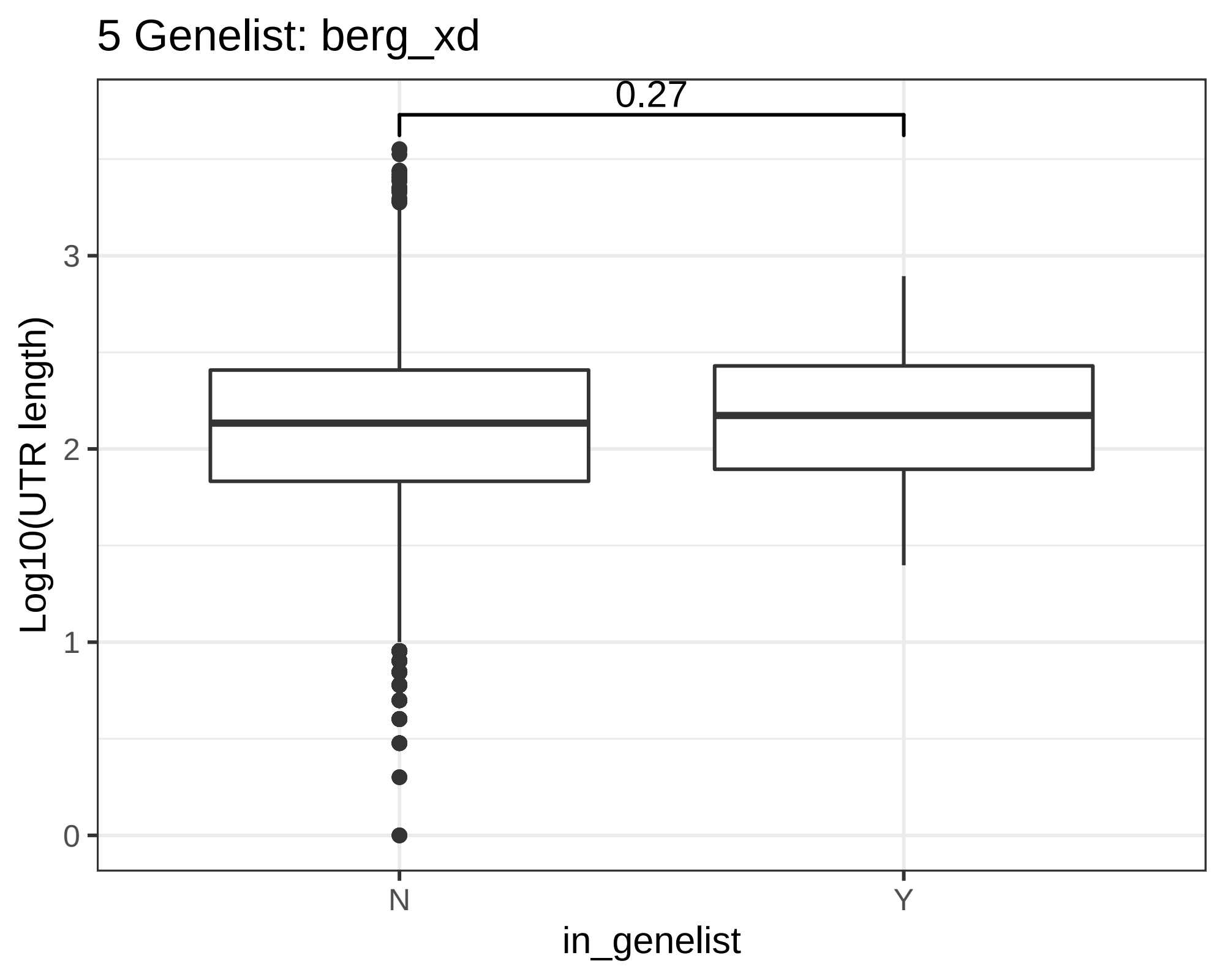

5 Genelist: berg_ar
Observed / Expected
1.1
1.0
0.9
0.8
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

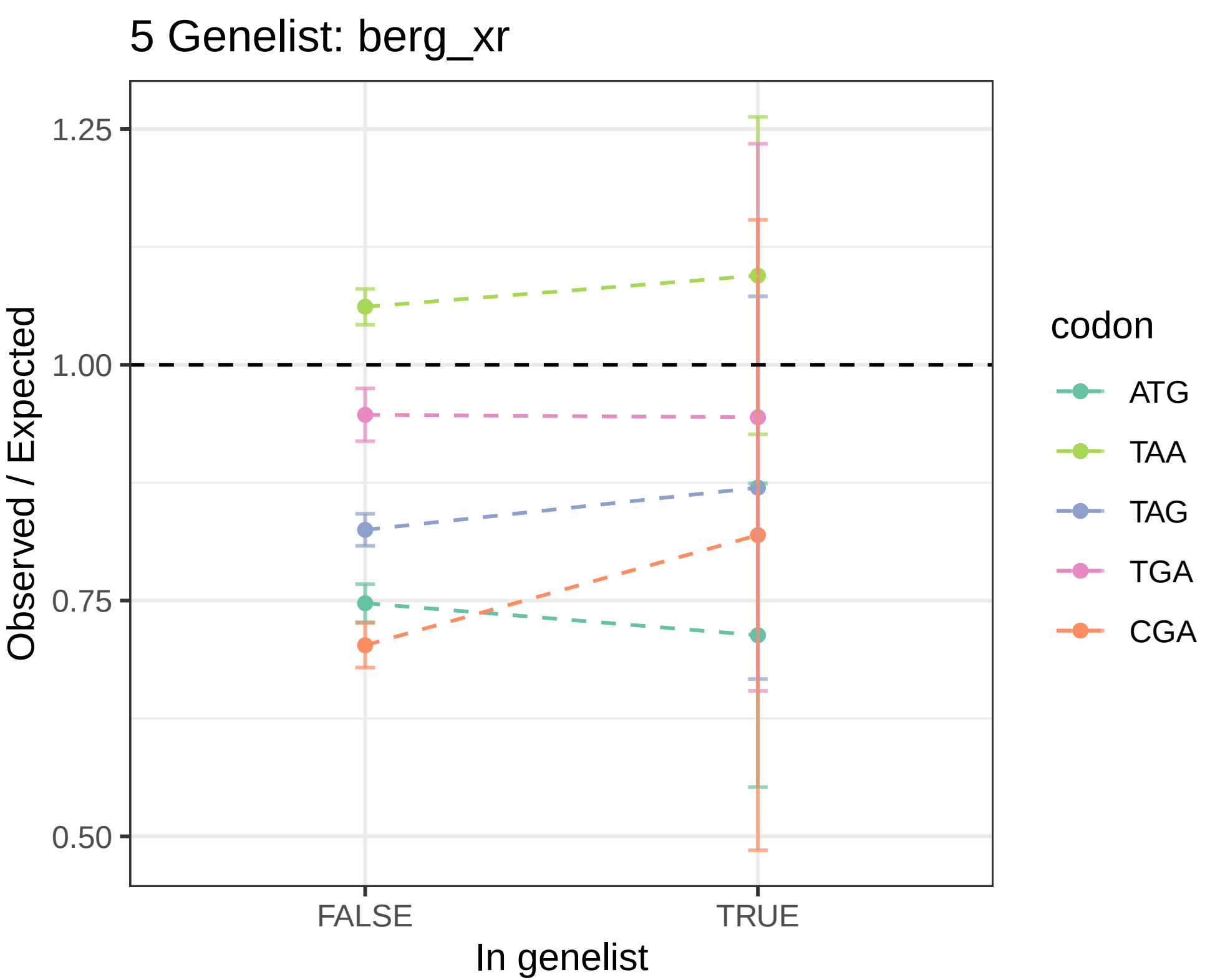

5 Genelist: berg_ar
6.4e−06
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

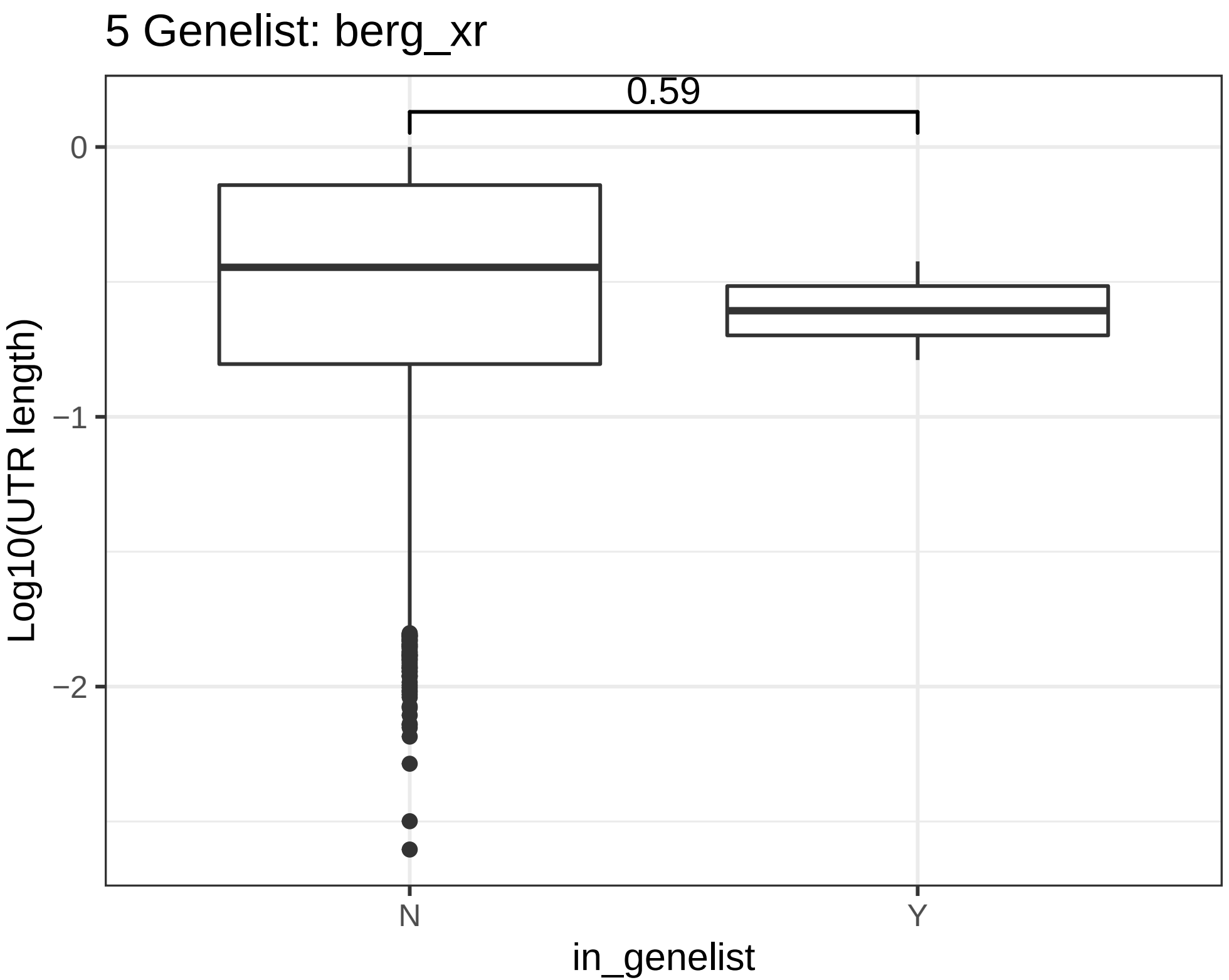

5 Genelist: berg_ar
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

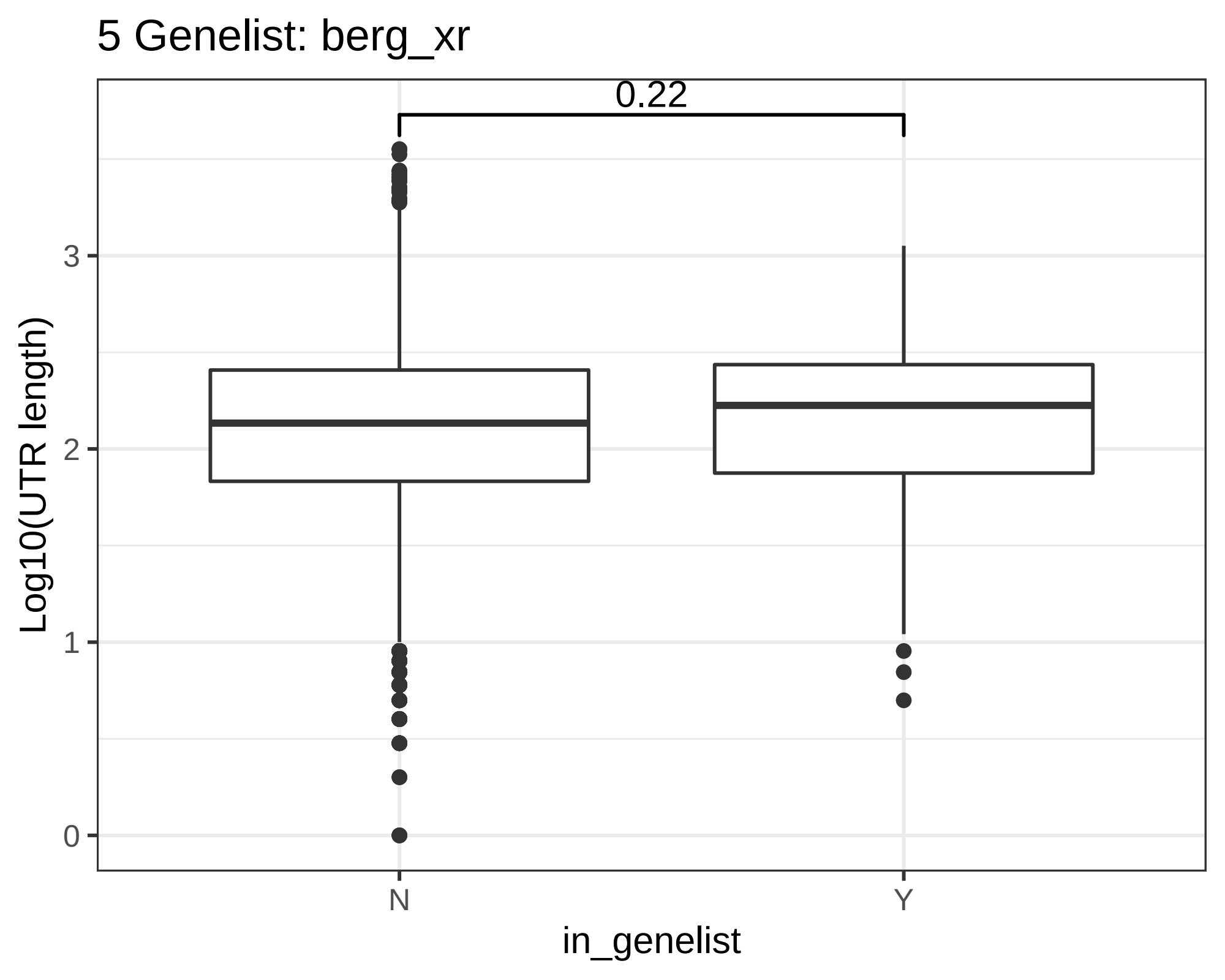

5 Genelist: berg_xd
Observed / Expected
1.5
1.0
0.5
0.0
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

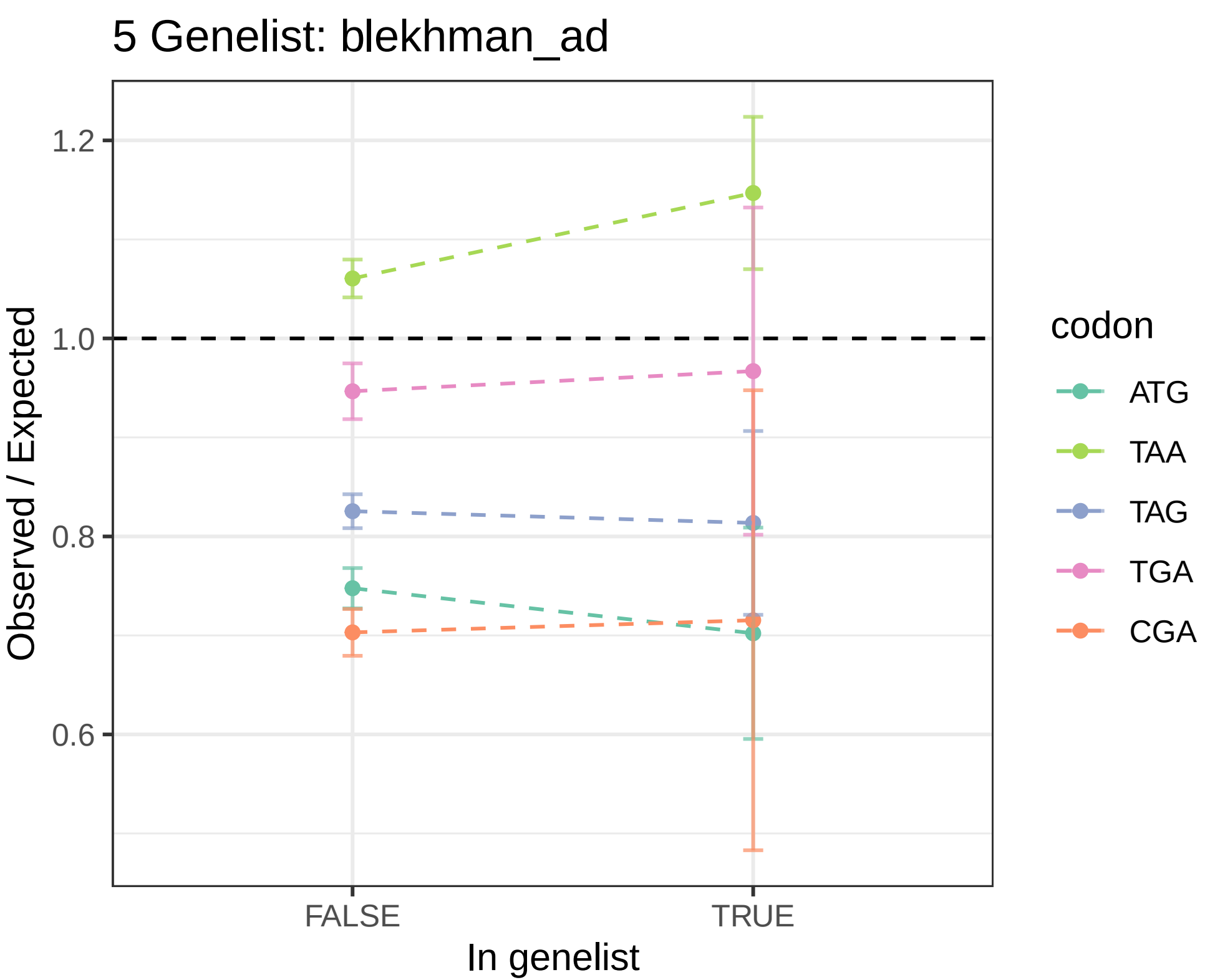

5 Genelist: berg_xd
0.24
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

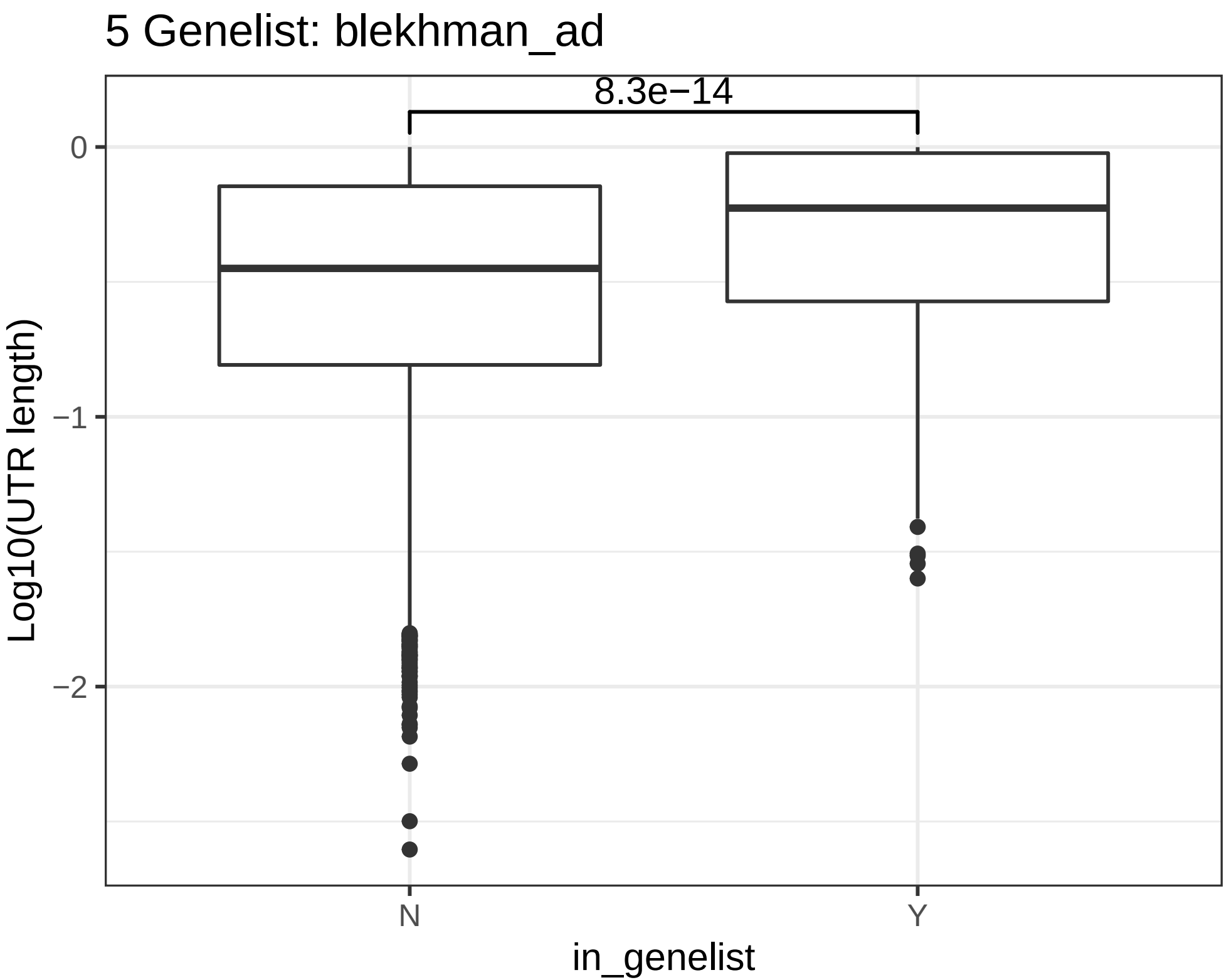

5 Genelist: berg_xd
0.27
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

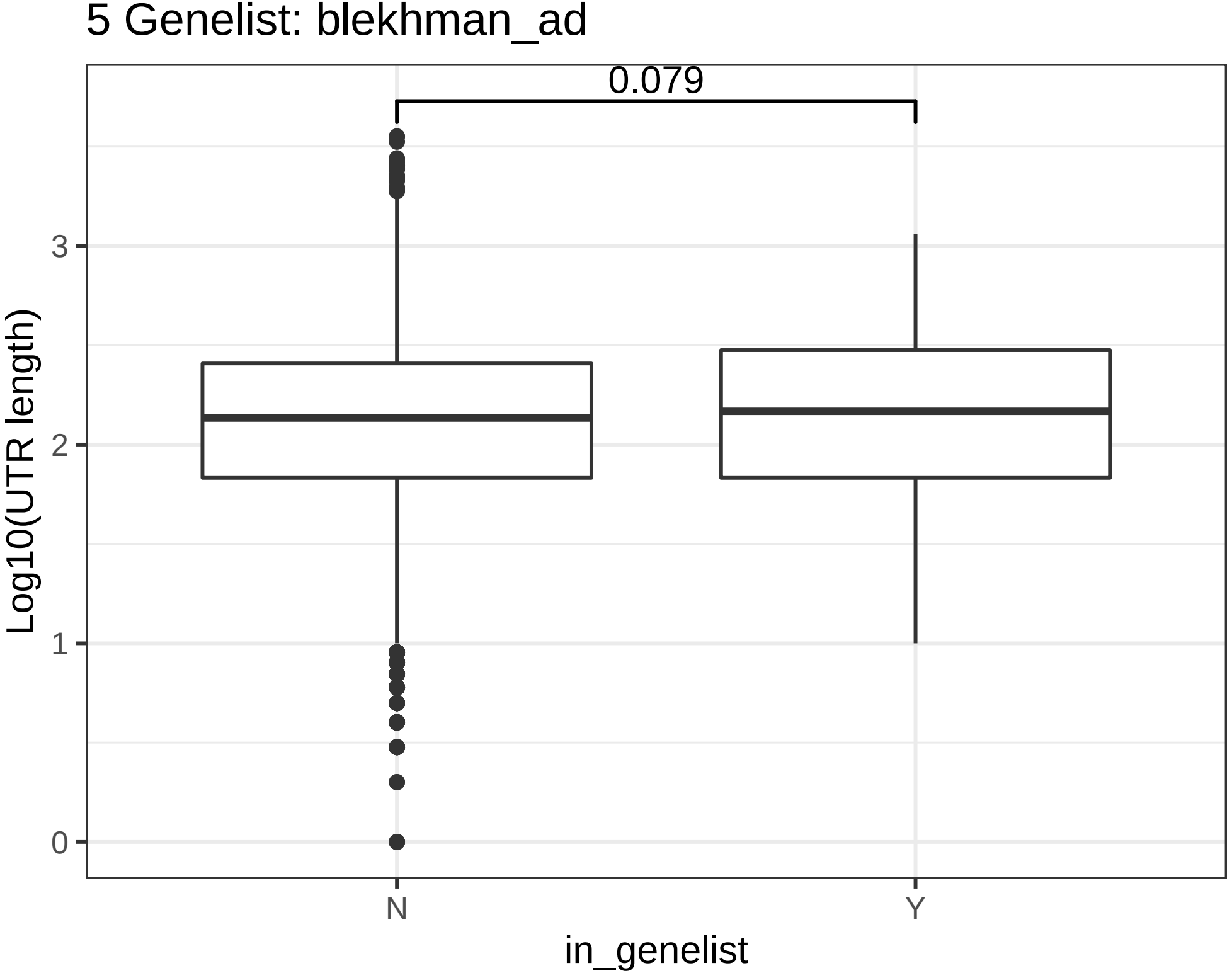

5 Genelist: berg_xr
1.25
1.00
0.75
0.50
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

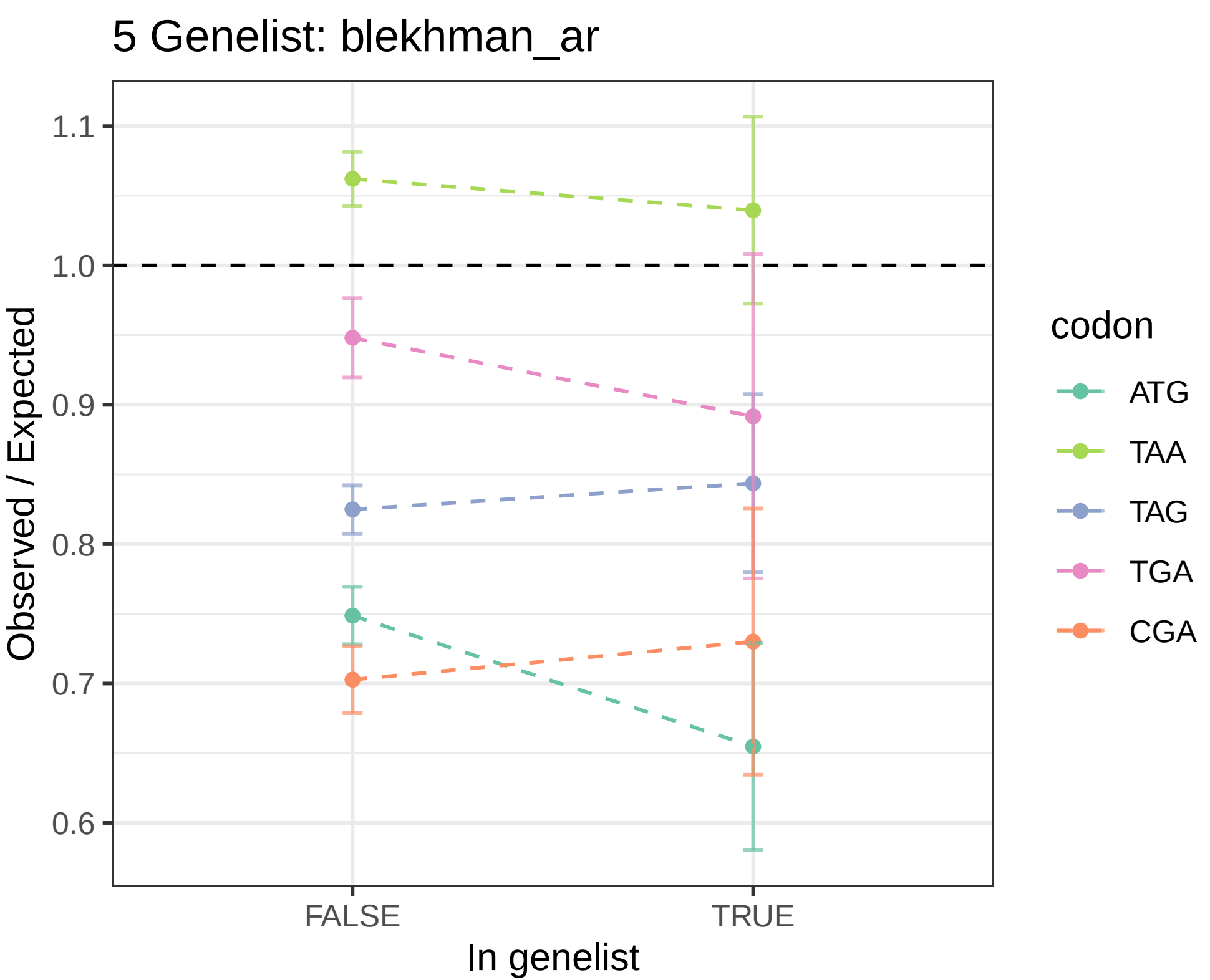

5 Genelist: berg_xr
0.59
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

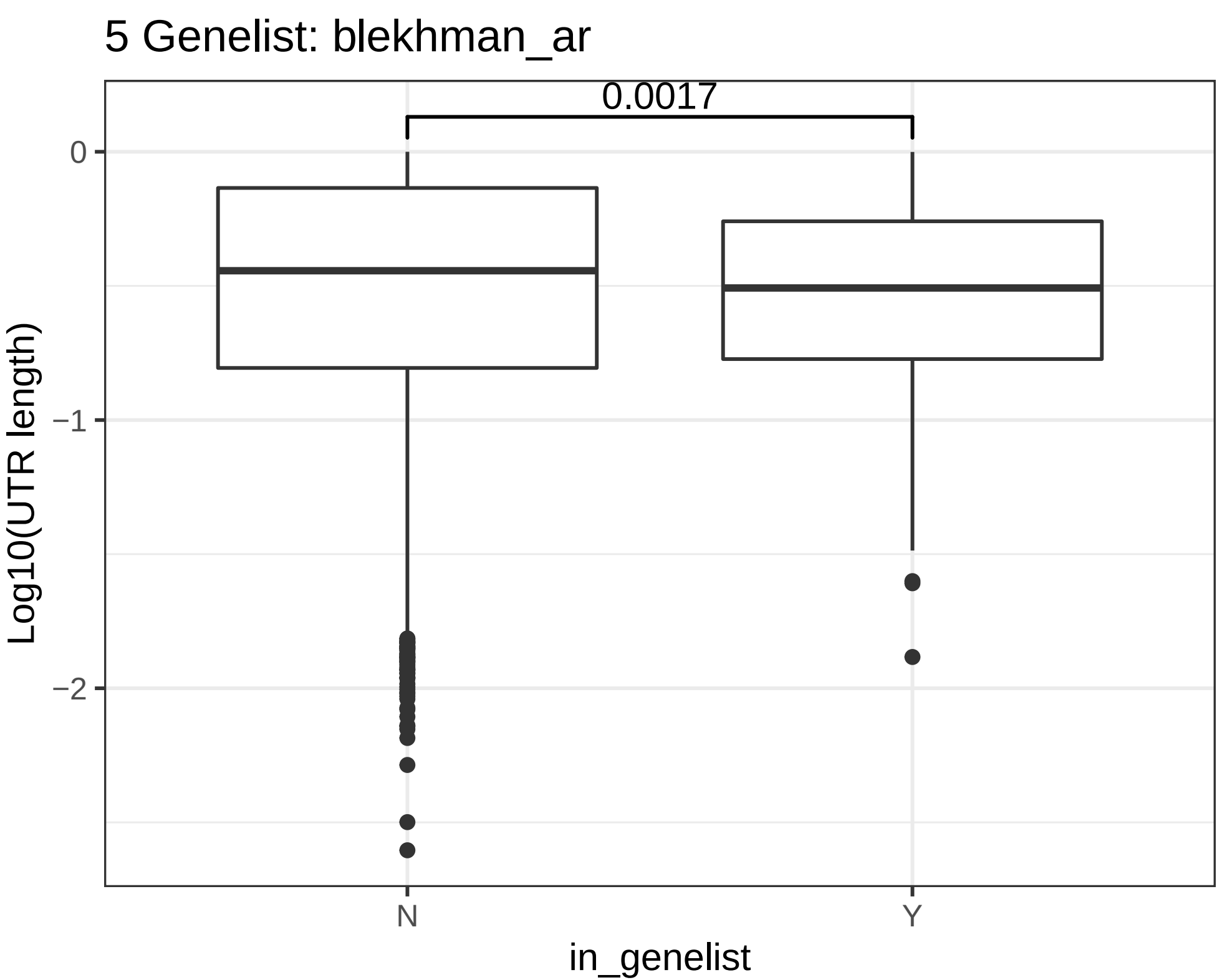

5 Genelist: berg_xr
0.22
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

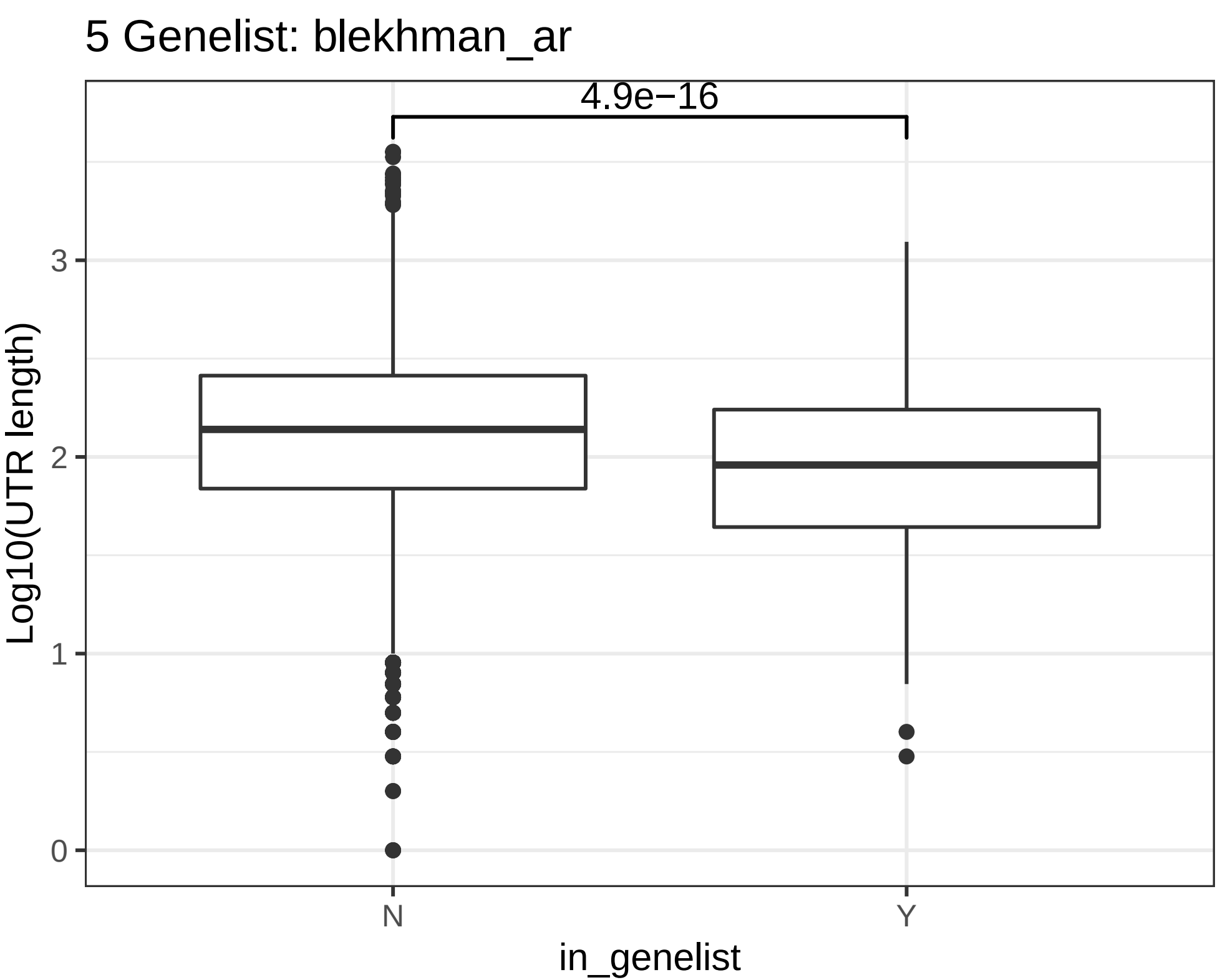

5 Genelist: blekhman_ad
Observed / Expected
1.2
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

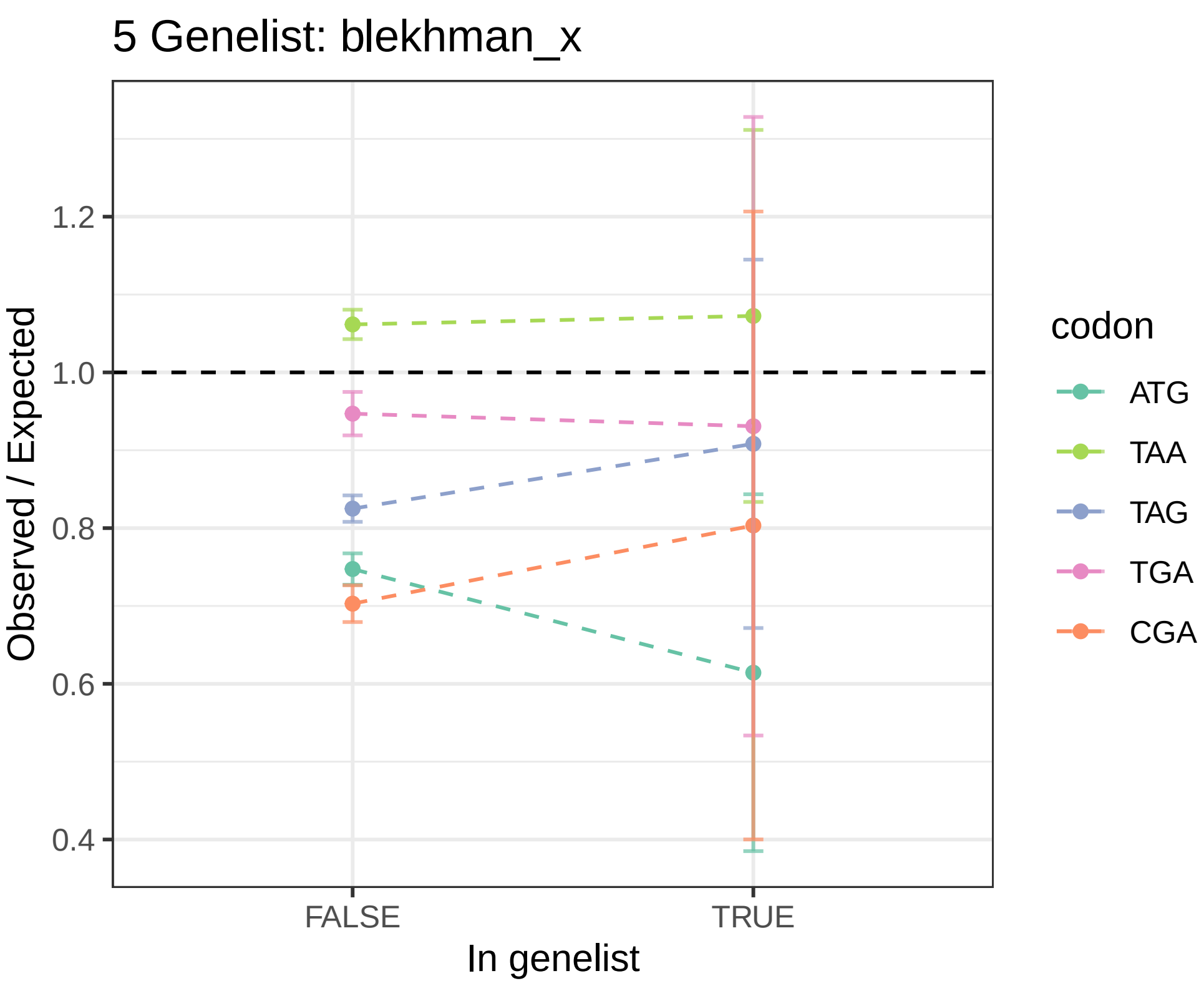

5 Genelist: blekhman_ad
8.3e−14
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

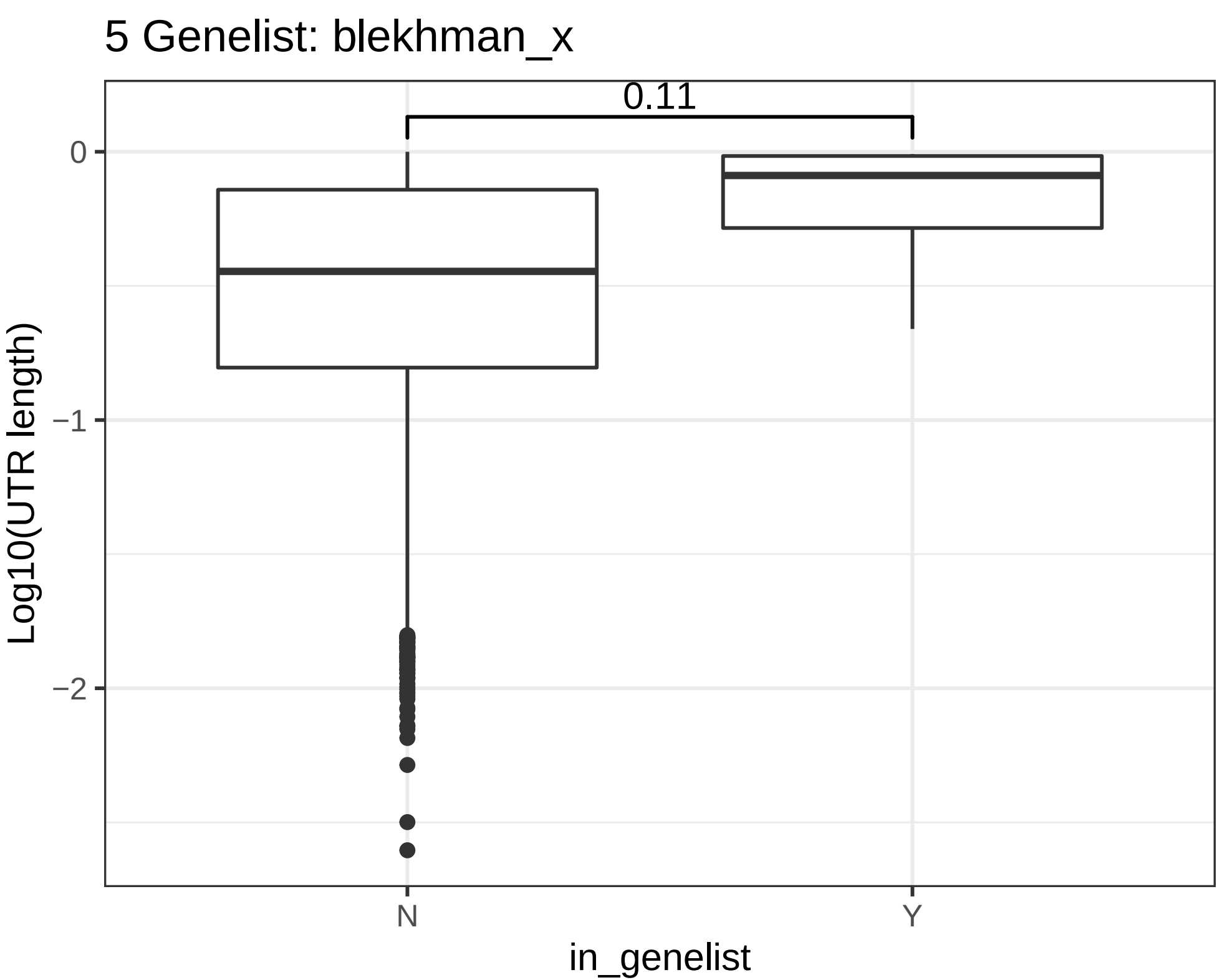

5 Genelist: blekhman_ad
0.079
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

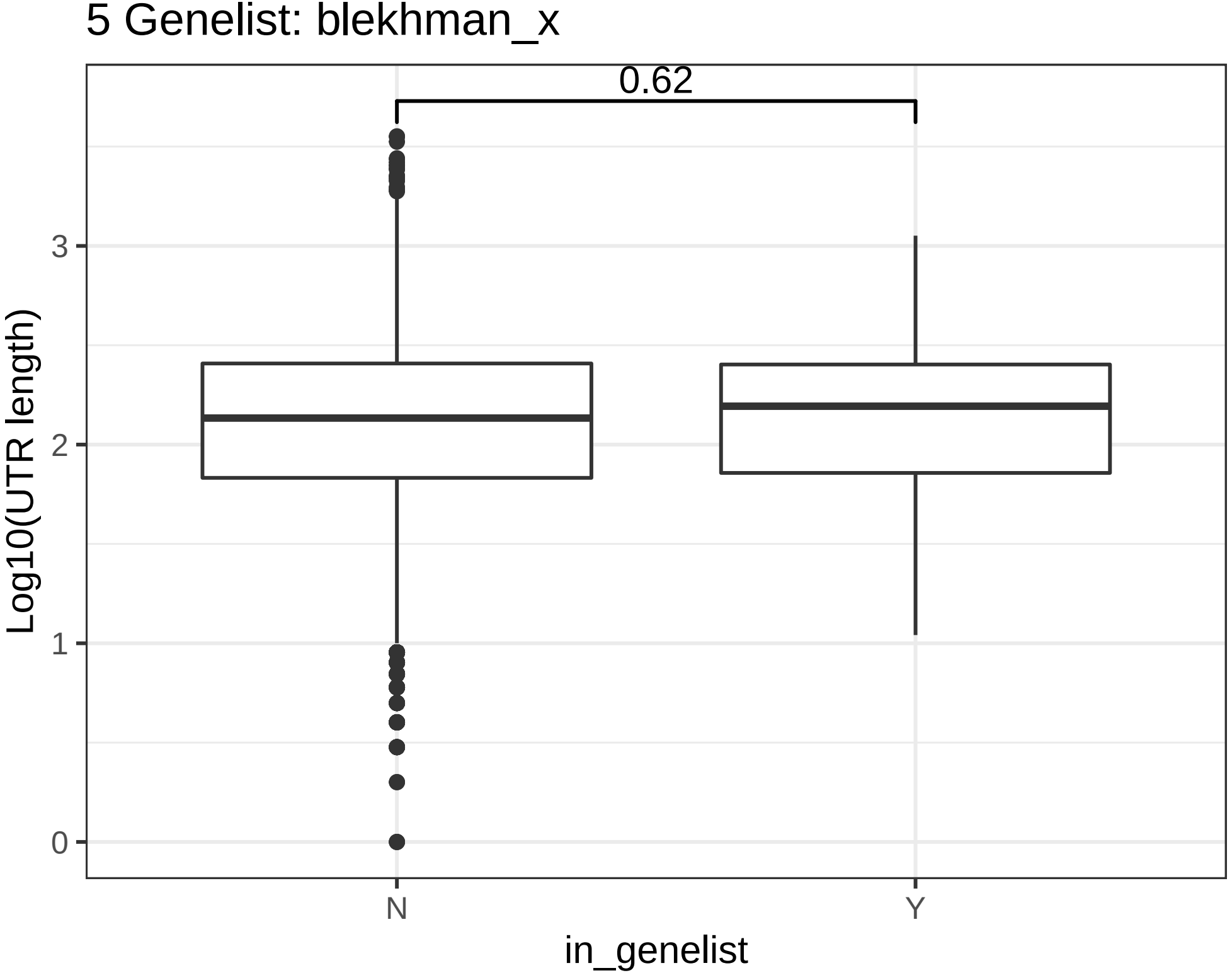

5 Genelist: blekhman_ar
Observed / Expected
1.1
1.0
0.9
0.8
0.7
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

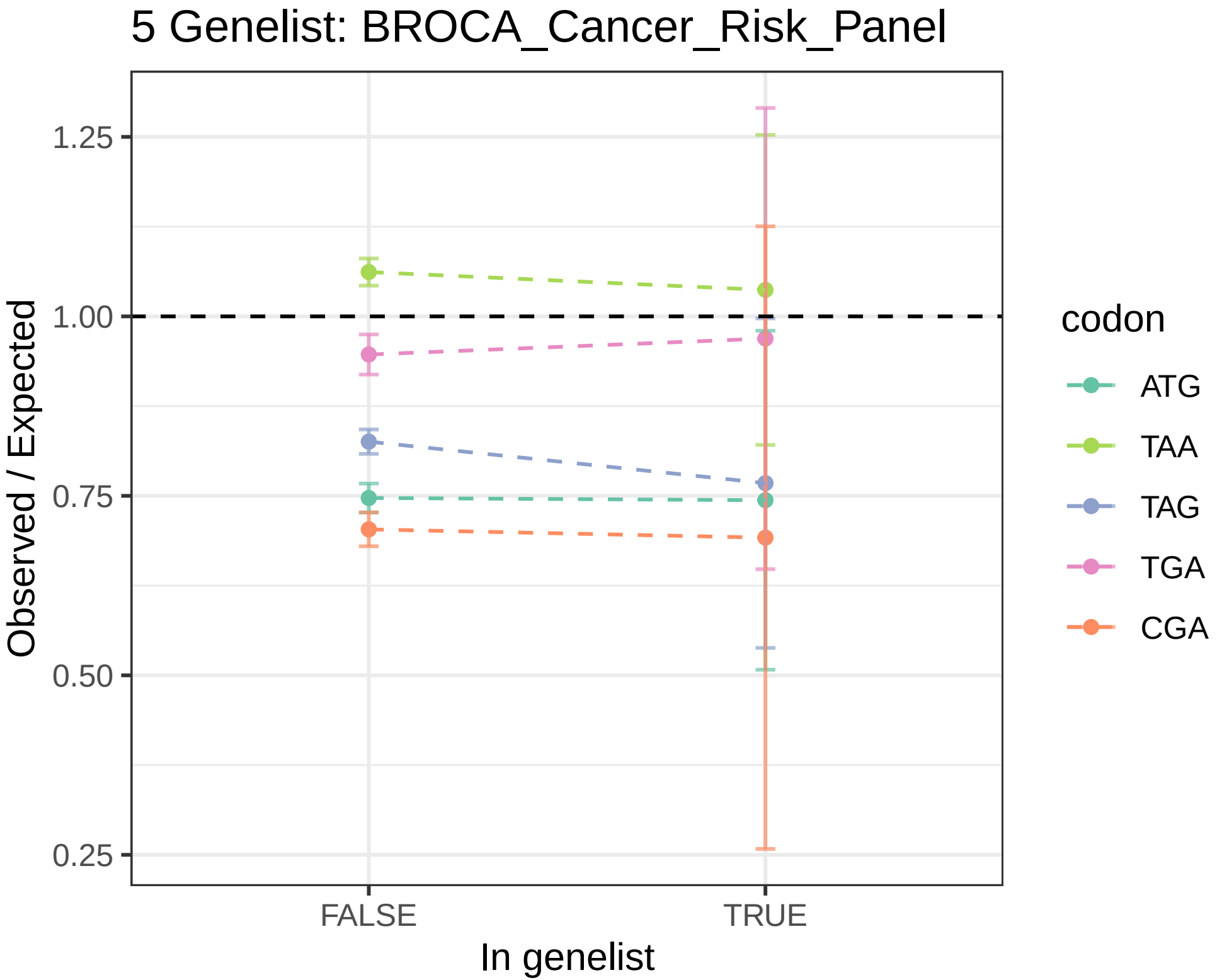

5 Genelist: blekhman_ar
0.0017
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

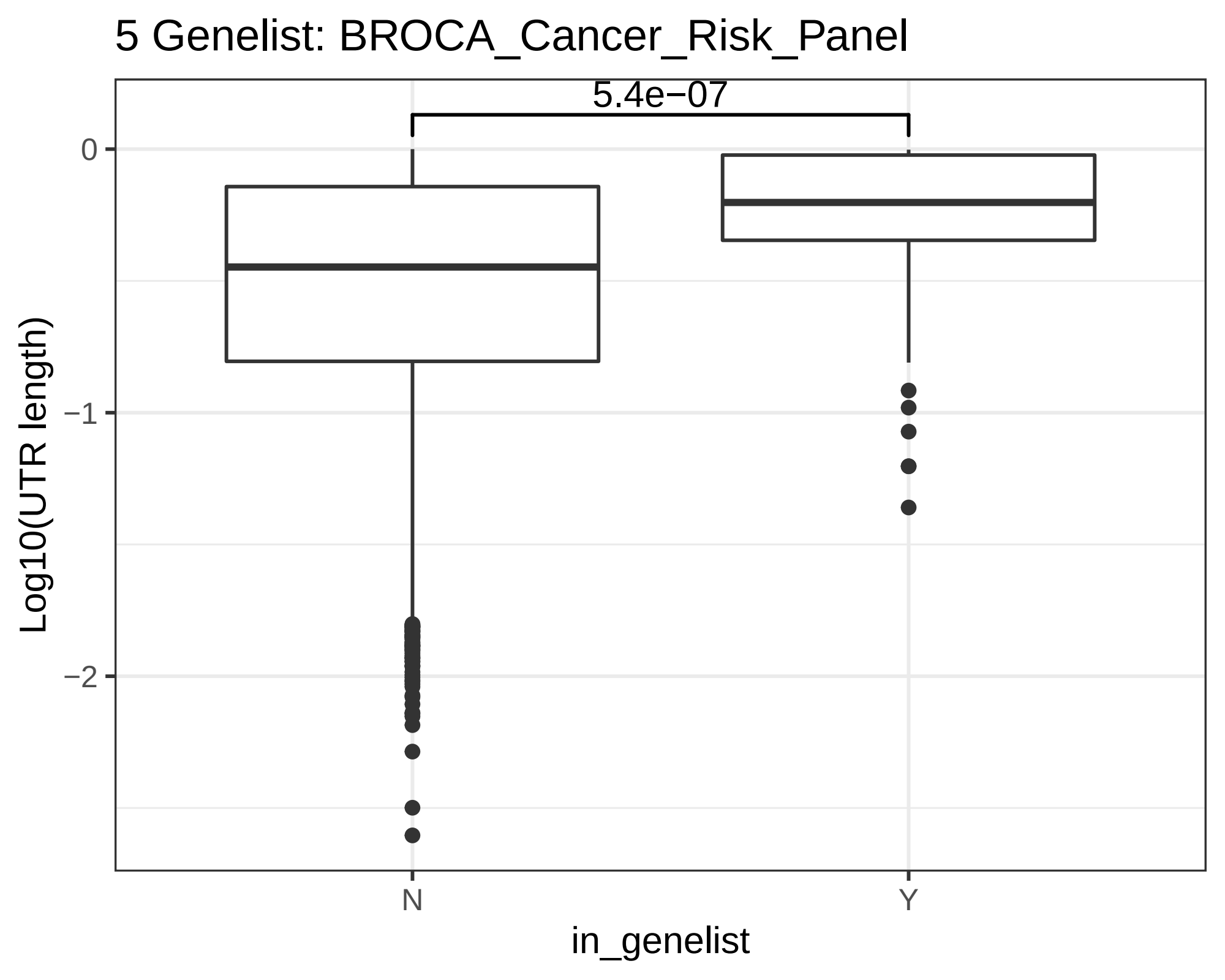

5 Genelist: blekhman_ar
4.9e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

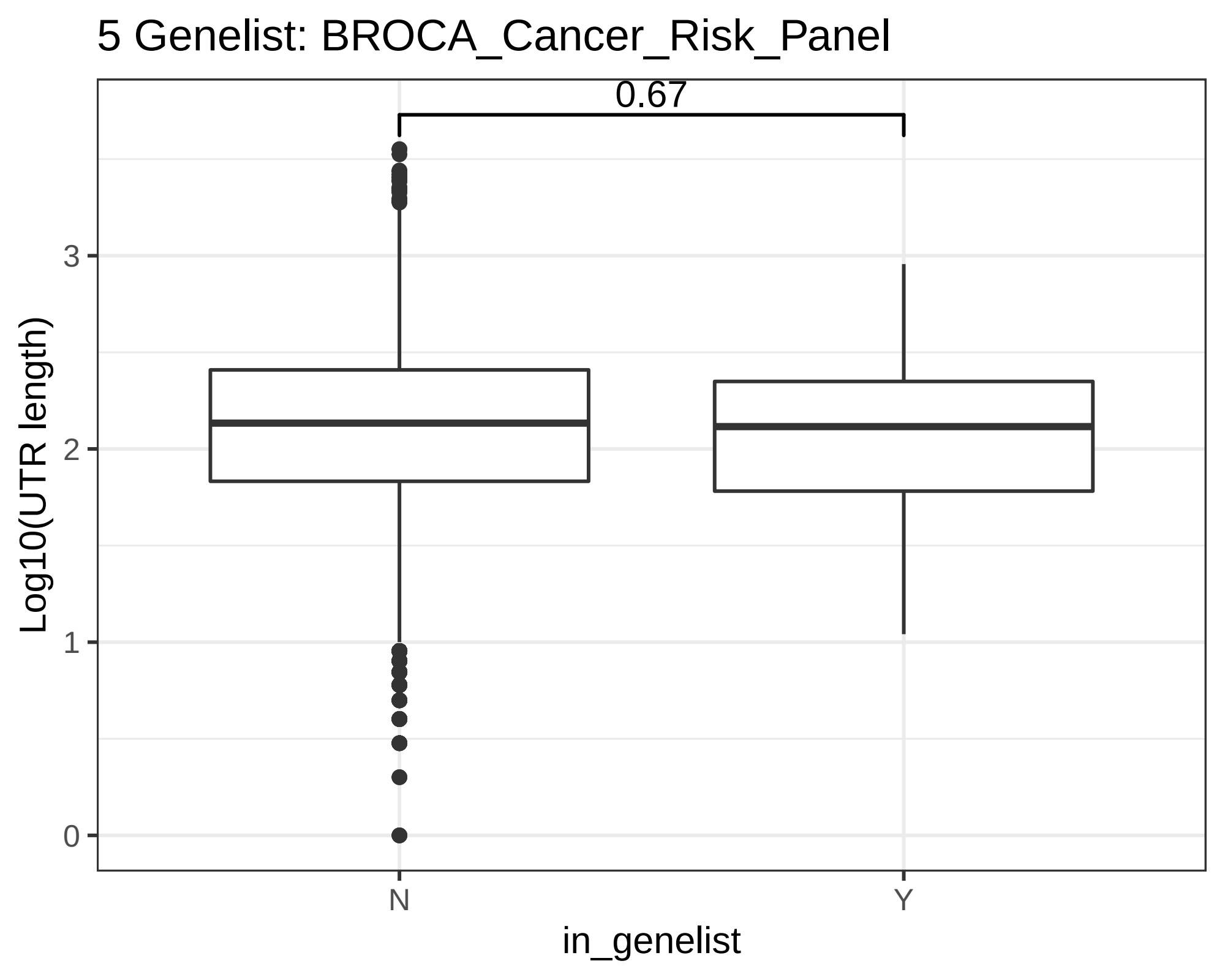

5 Genelist: blekhman_x
Observed / Expected
1.2
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

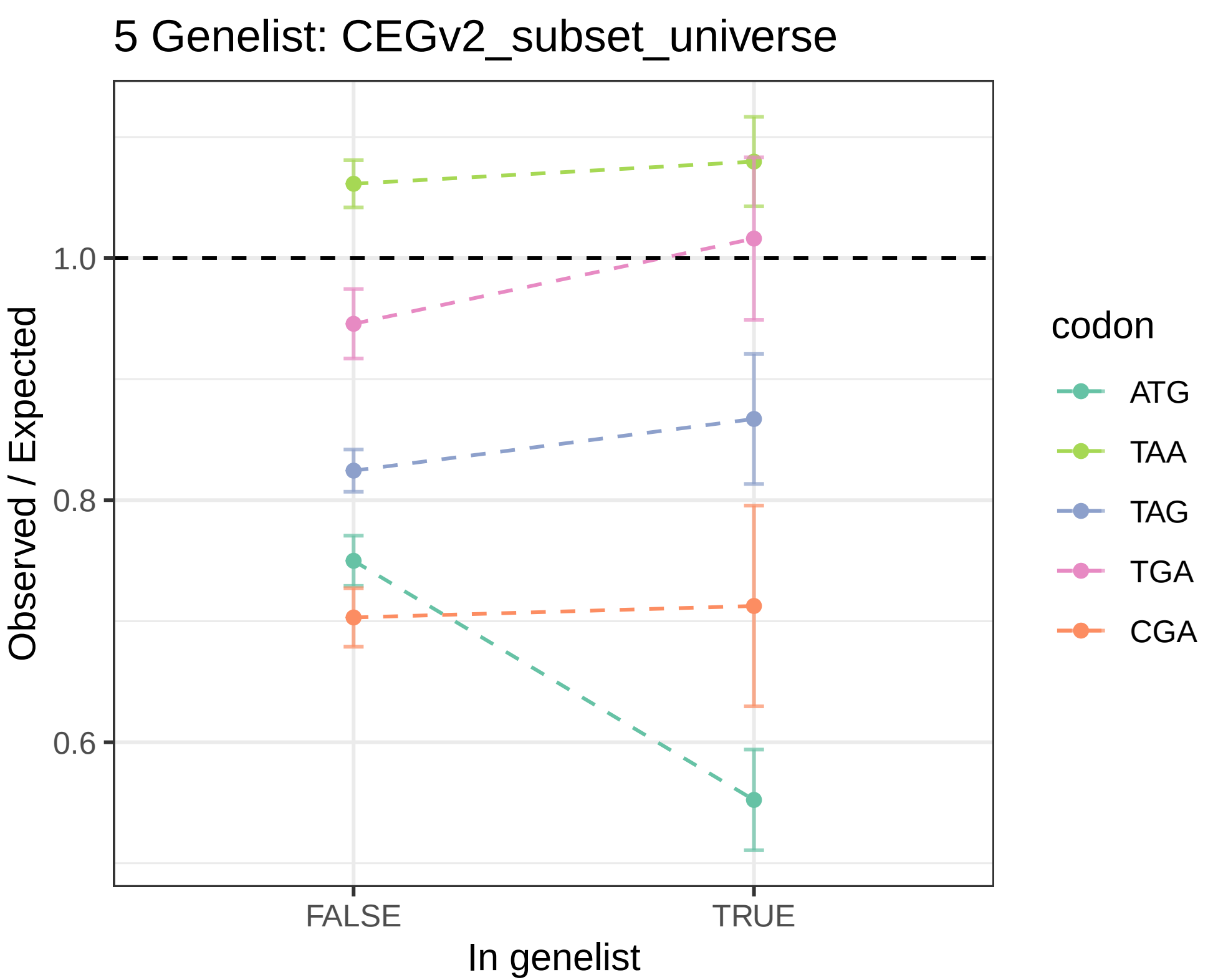

5 Genelist: blekhman_x
0.11
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

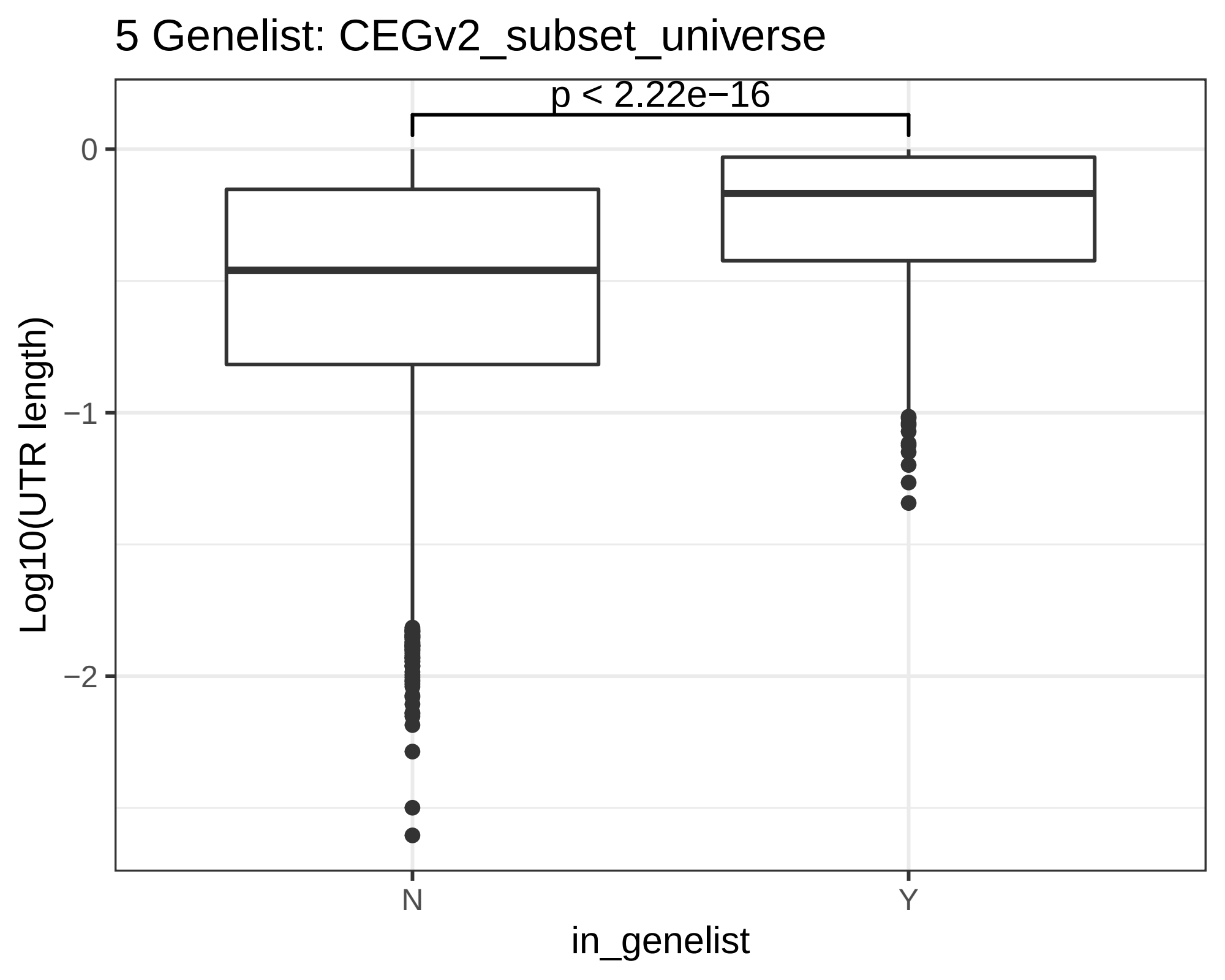

5 Genelist: blekhman_x
0.62
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

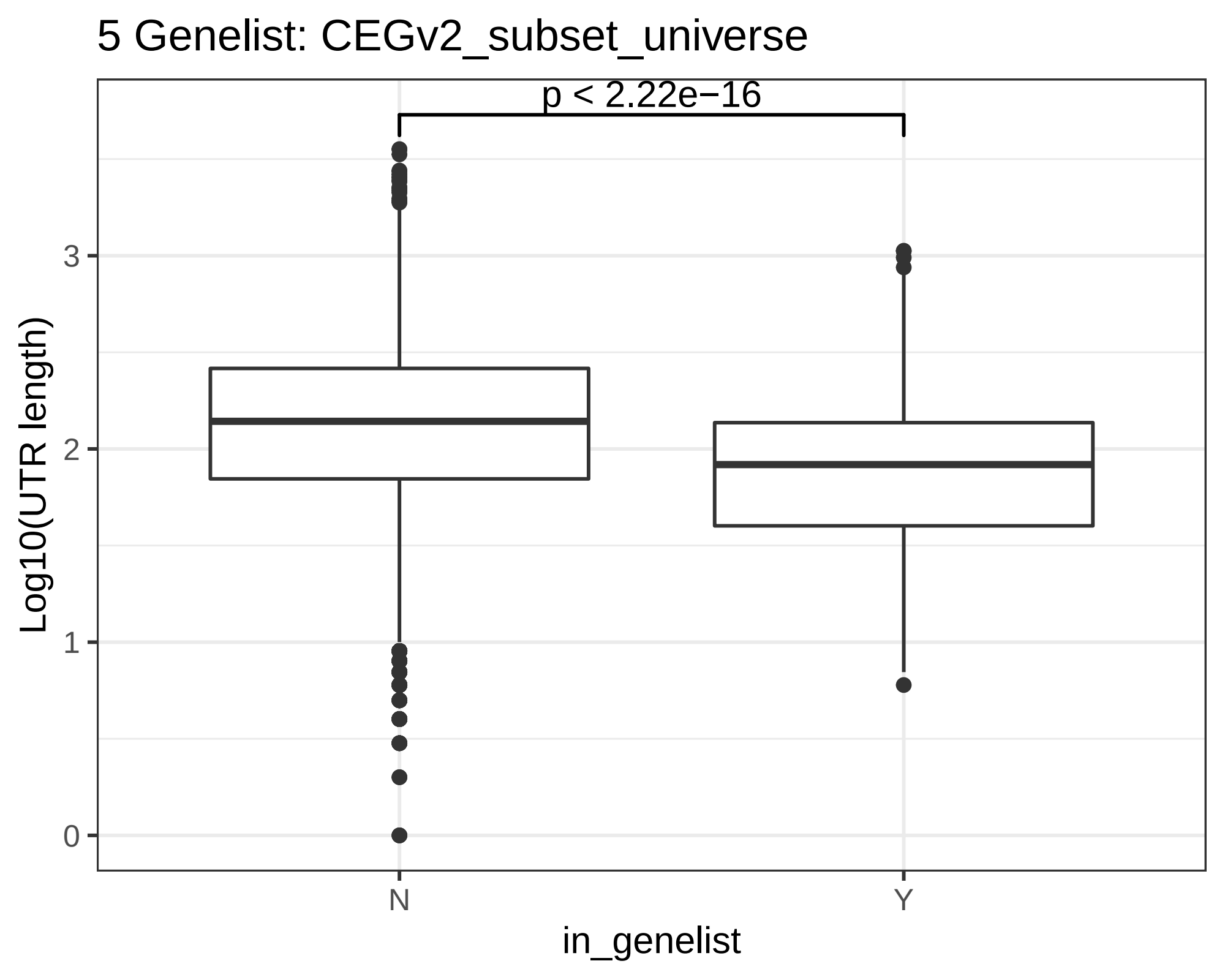

5 Genelist: BROCA_Cancer_Risk_Panel
Observed / Expected
1.25
1.00
0.75
0.50
0.25
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

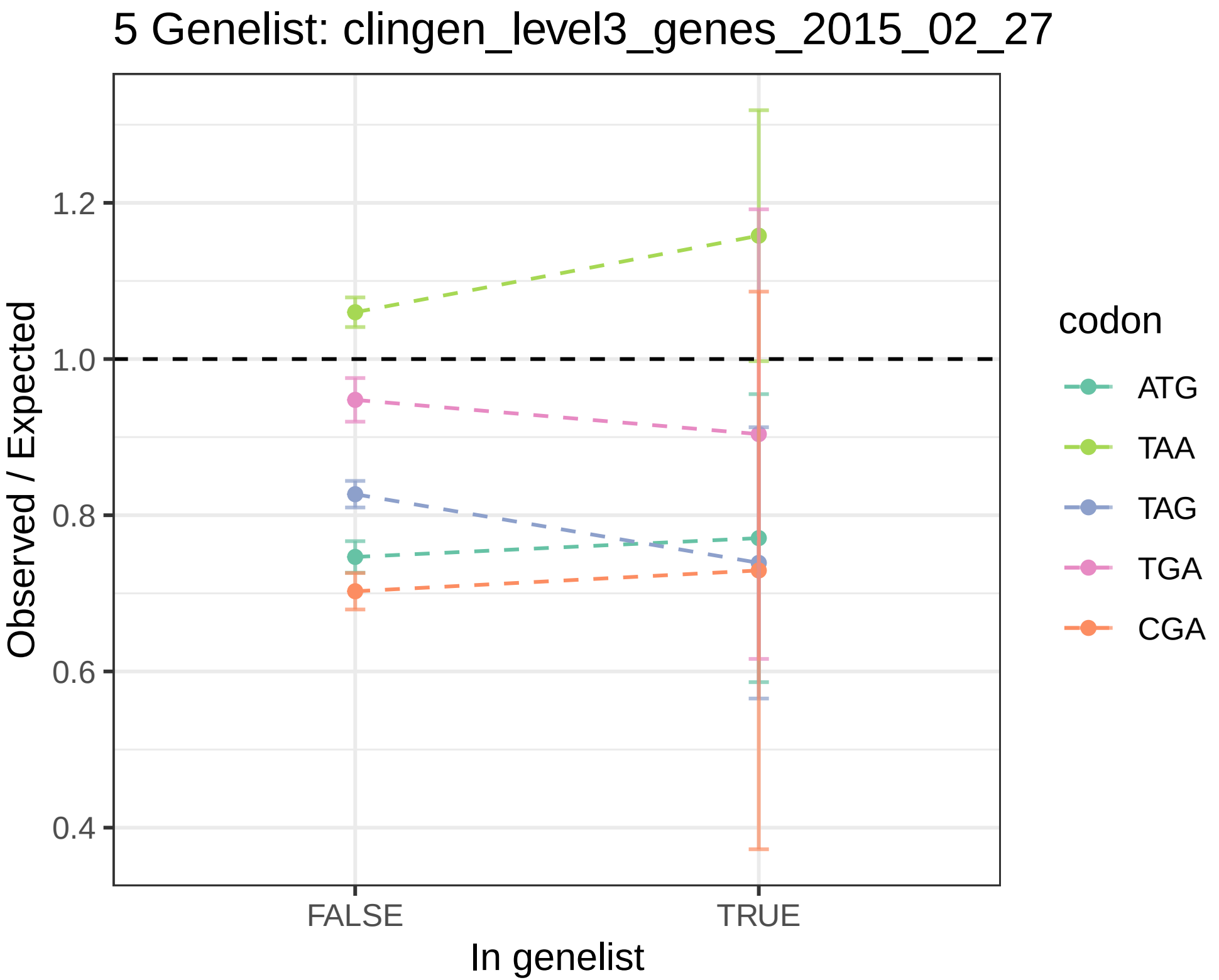

5 Genelist: BROCA_Cancer_Risk_Panel
5.4e−07
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

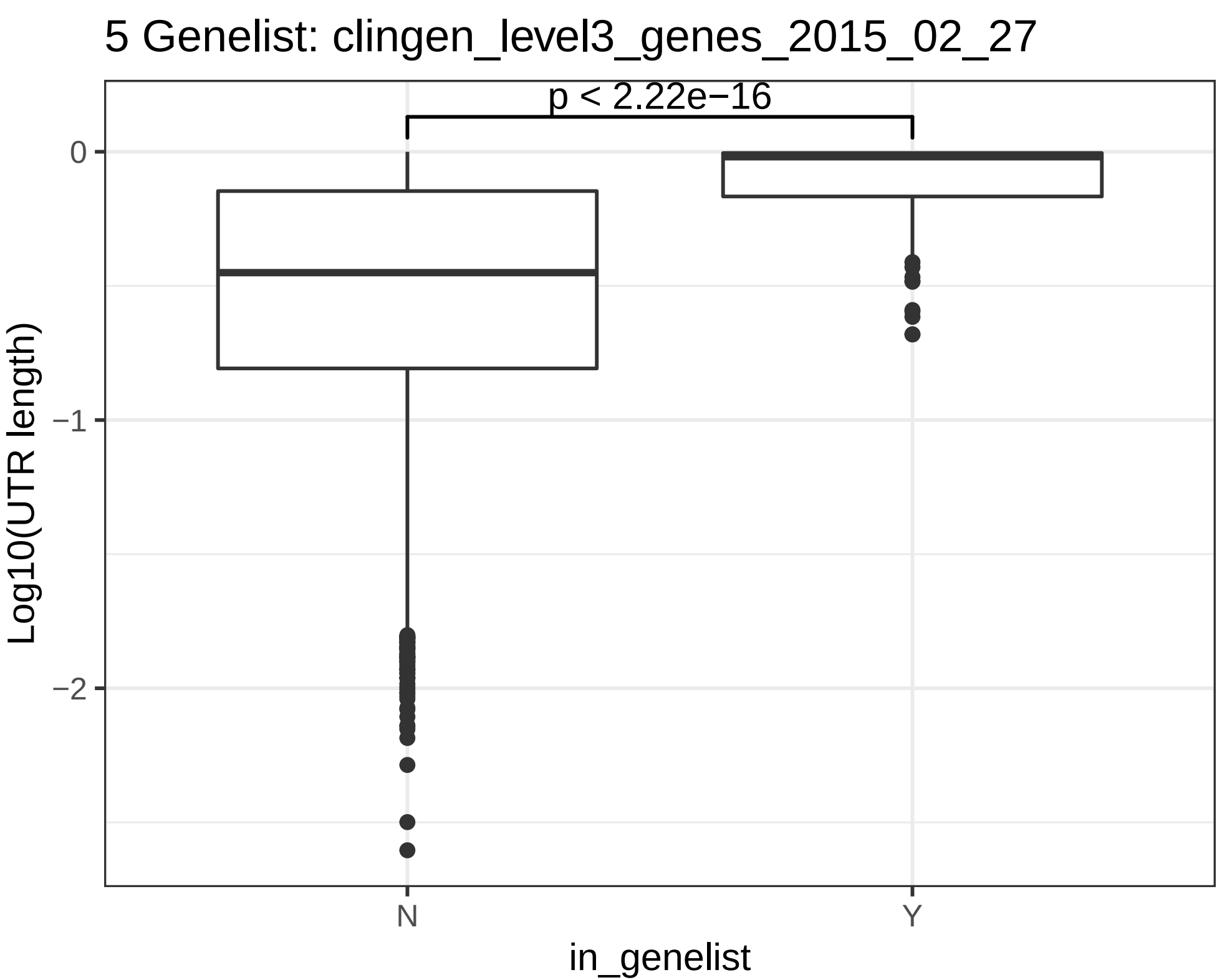

5 Genelist: BROCA_Cancer_Risk_Panel
0.67
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

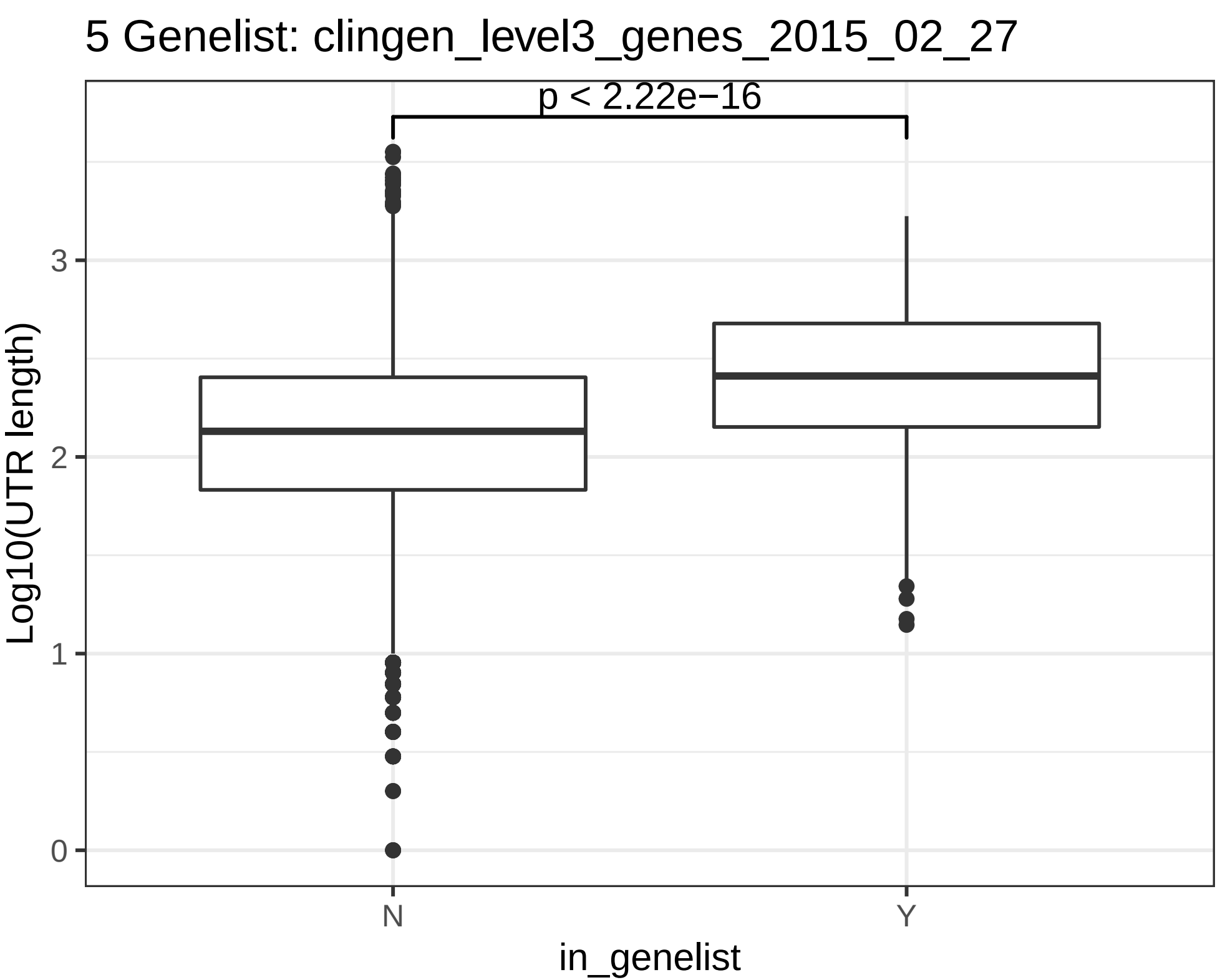

5 Genelist: CEGv2_subset_universe
Observed / Expected
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

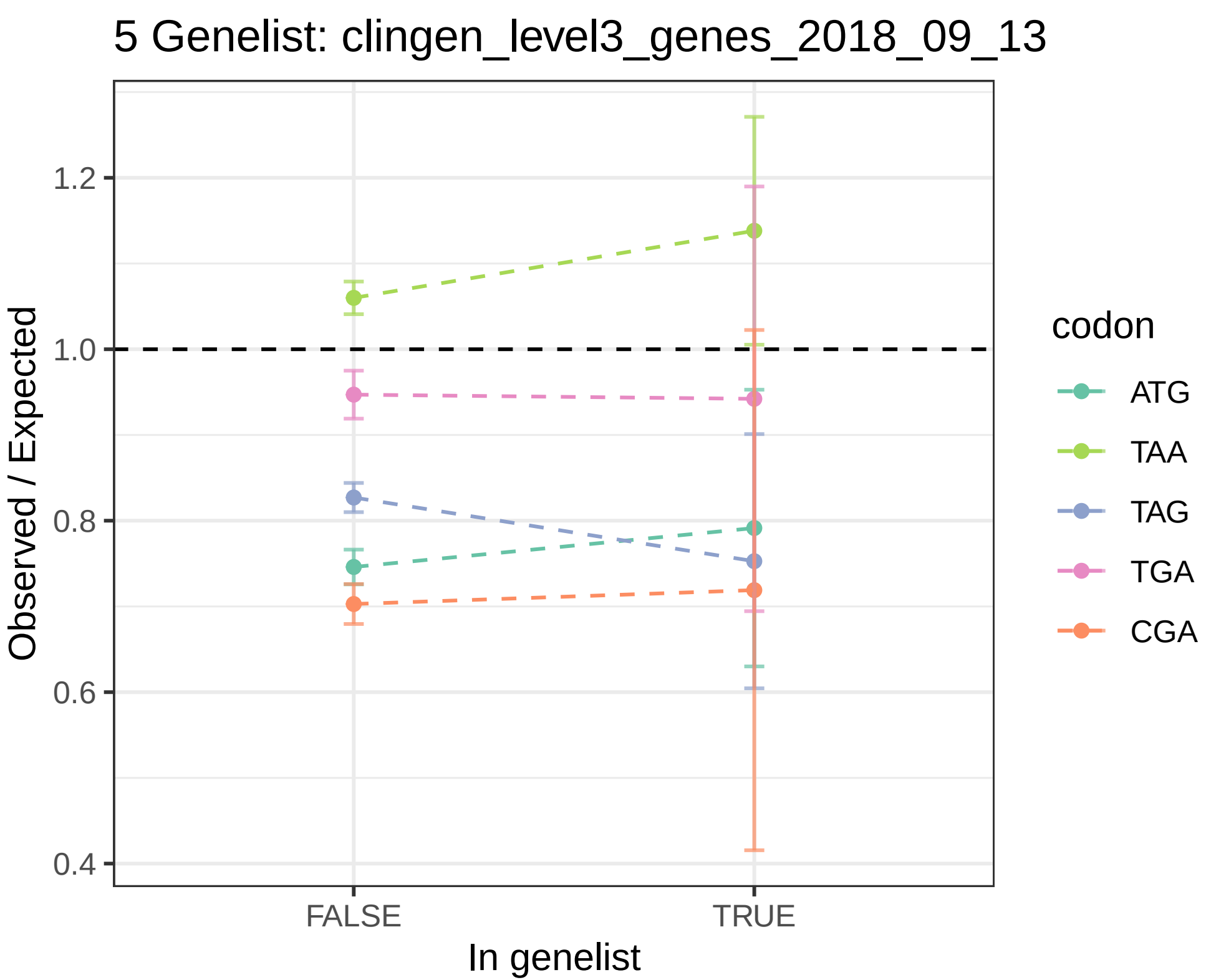

5 Genelist: CEGv2_subset_universe
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

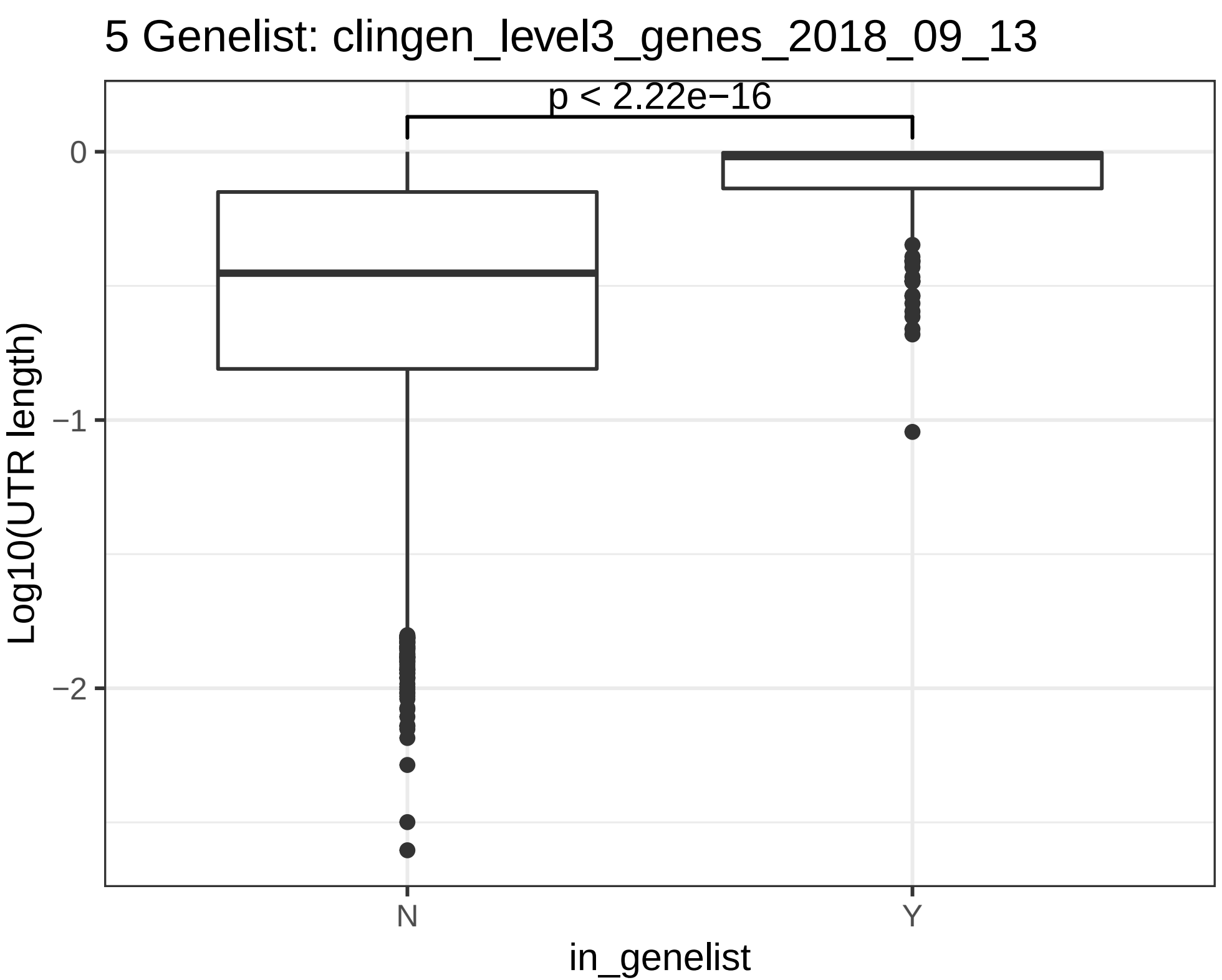

5 Genelist: CEGv2_subset_universe
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

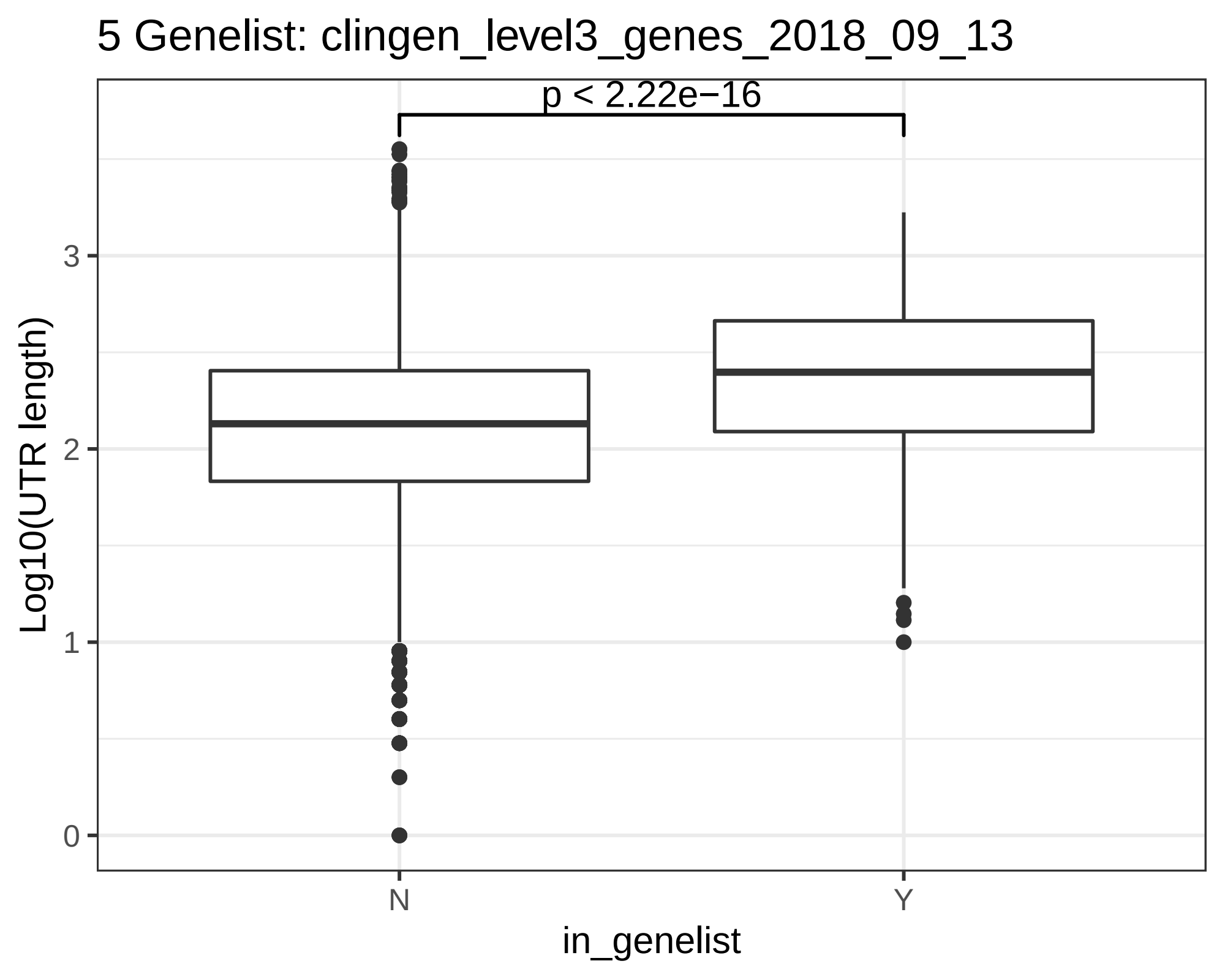

5 Genelist: clingen_level3_genes_2015_02_27
Observed / Expected
1.2
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

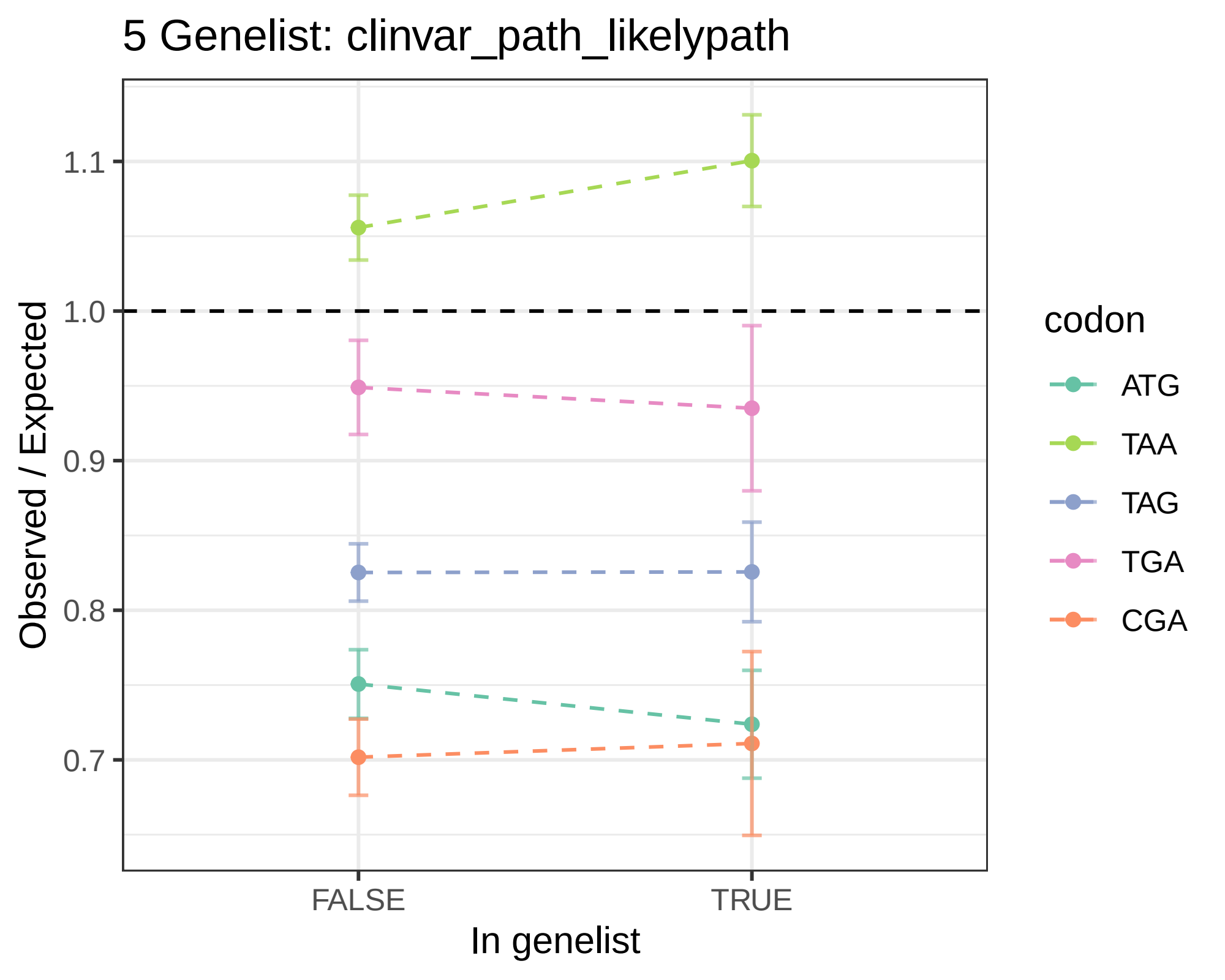

5 Genelist: clingen_level3_genes_2015_02_27
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

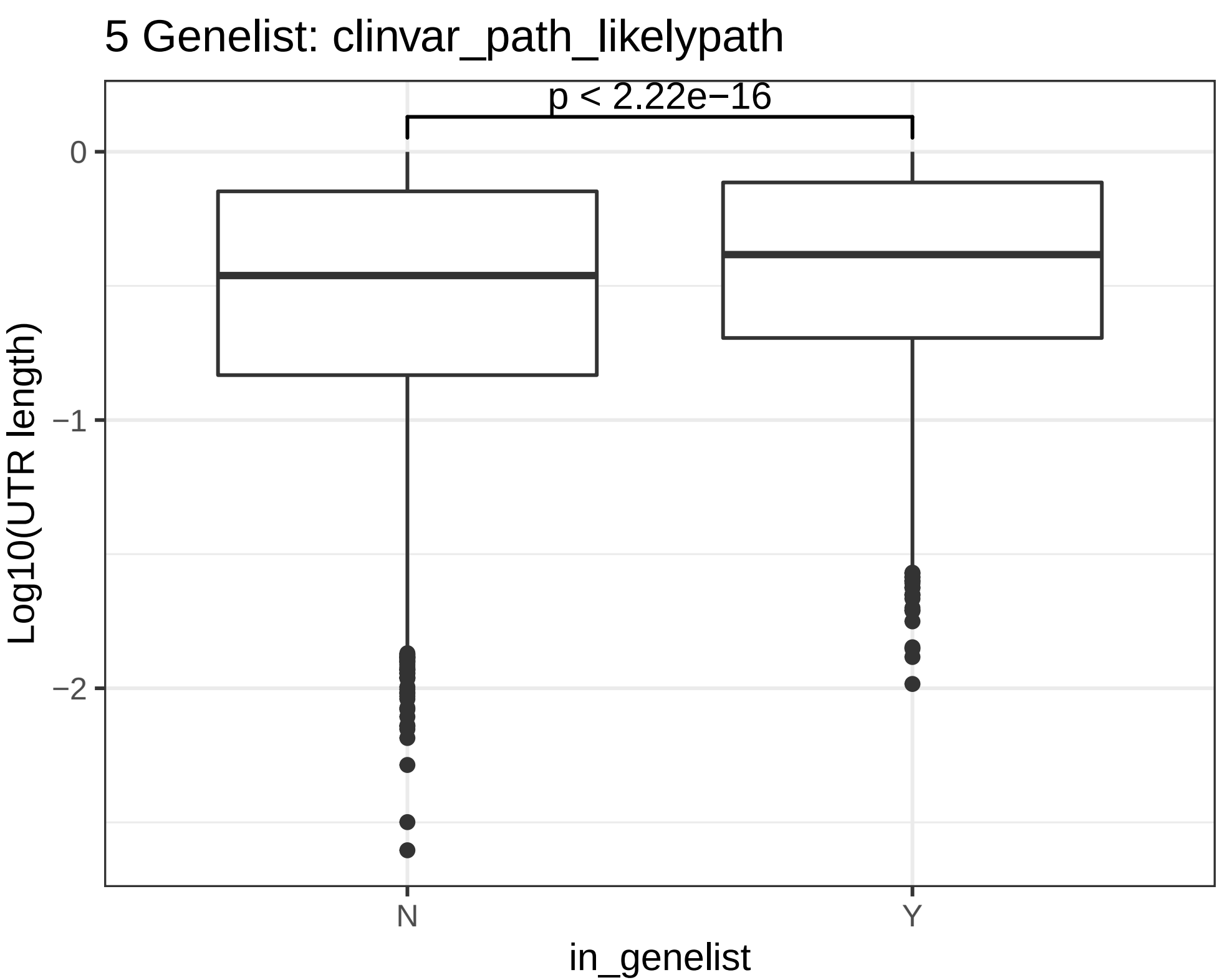

5 Genelist: clingen_level3_genes_2015_02_27
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

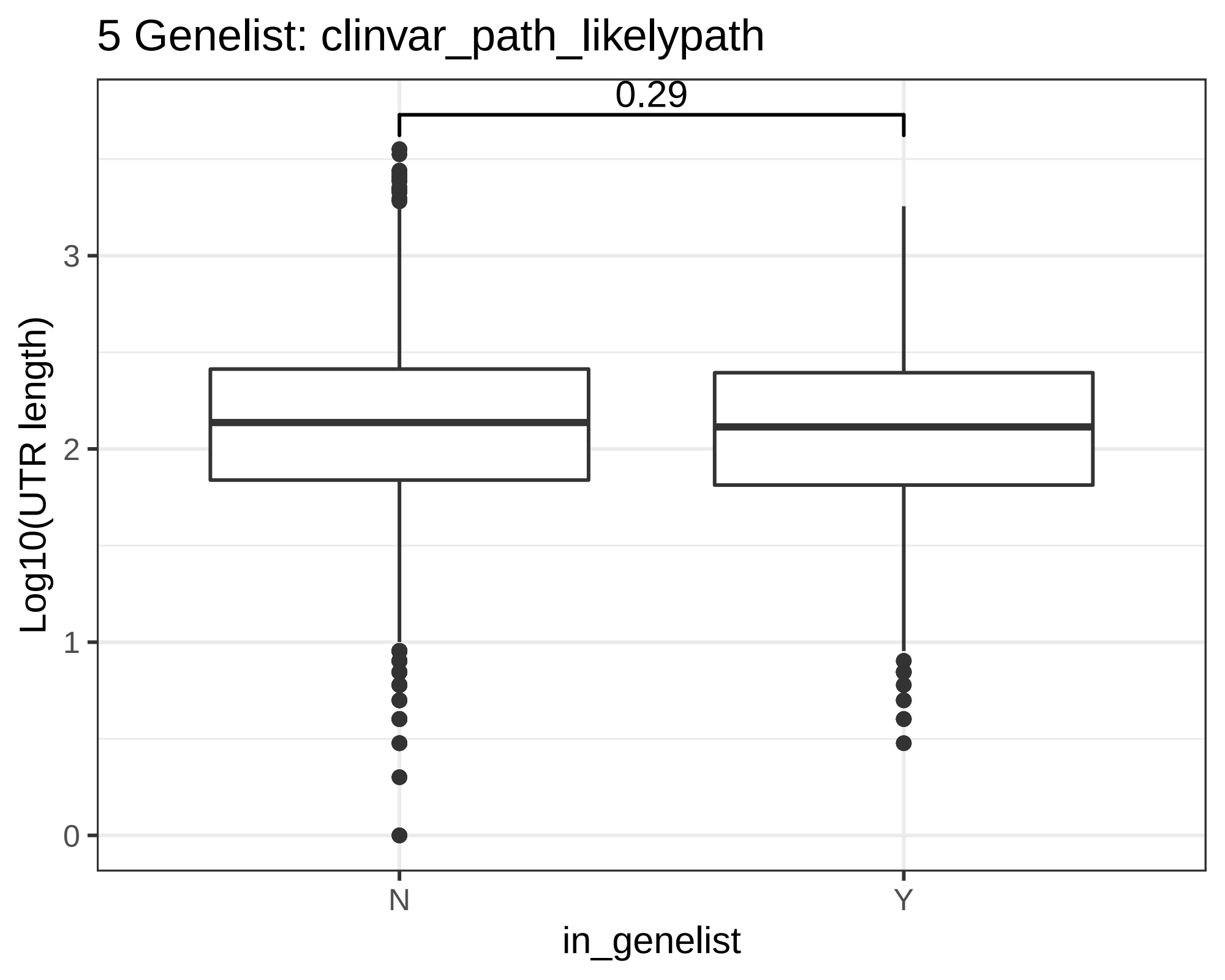

5 Genelist: clingen_level3_genes_2018_09_13
Observed / Expected
1.2
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

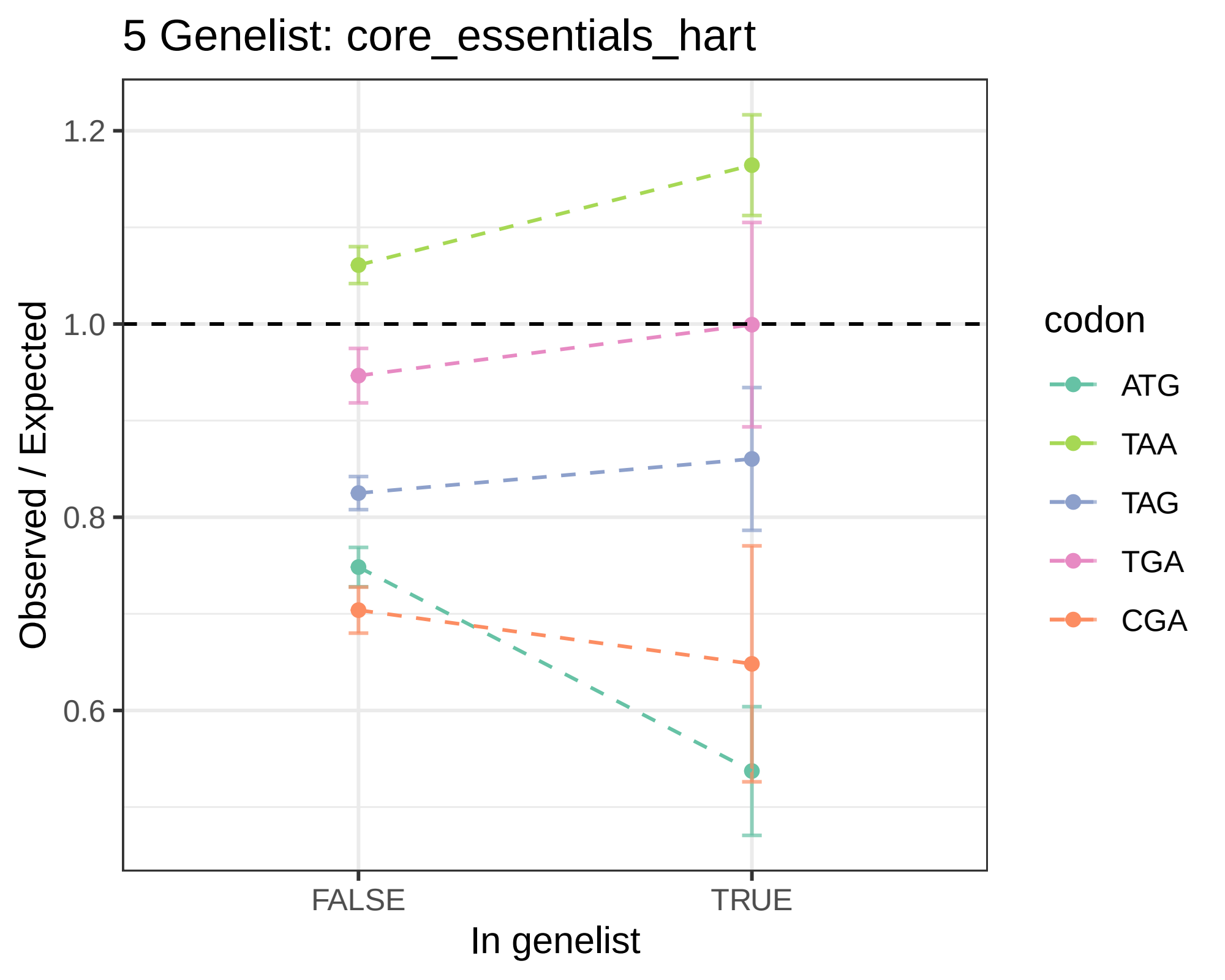

5 Genelist: clingen_level3_genes_2018_09_13
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

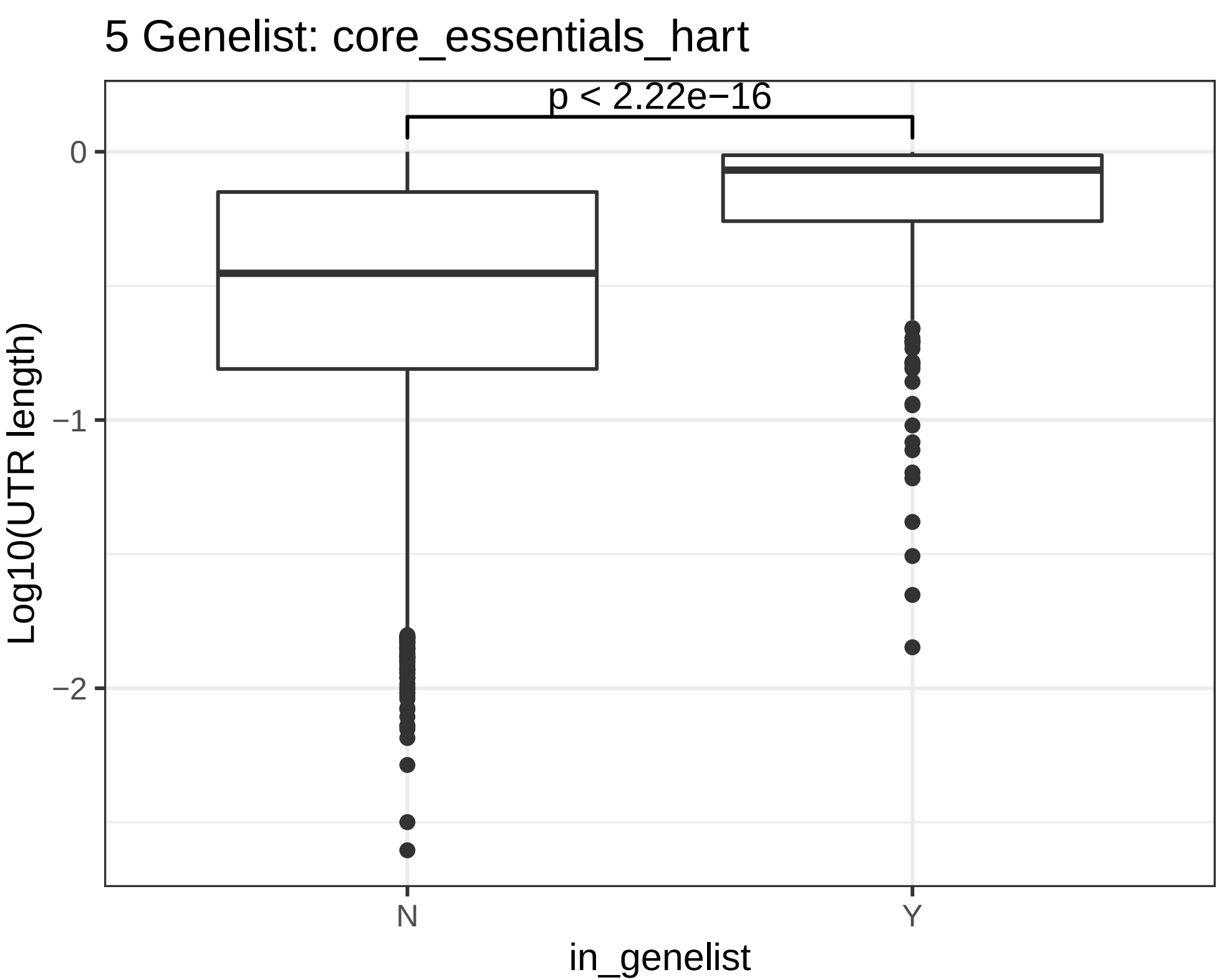

5 Genelist: clingen_level3_genes_2018_09_13
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

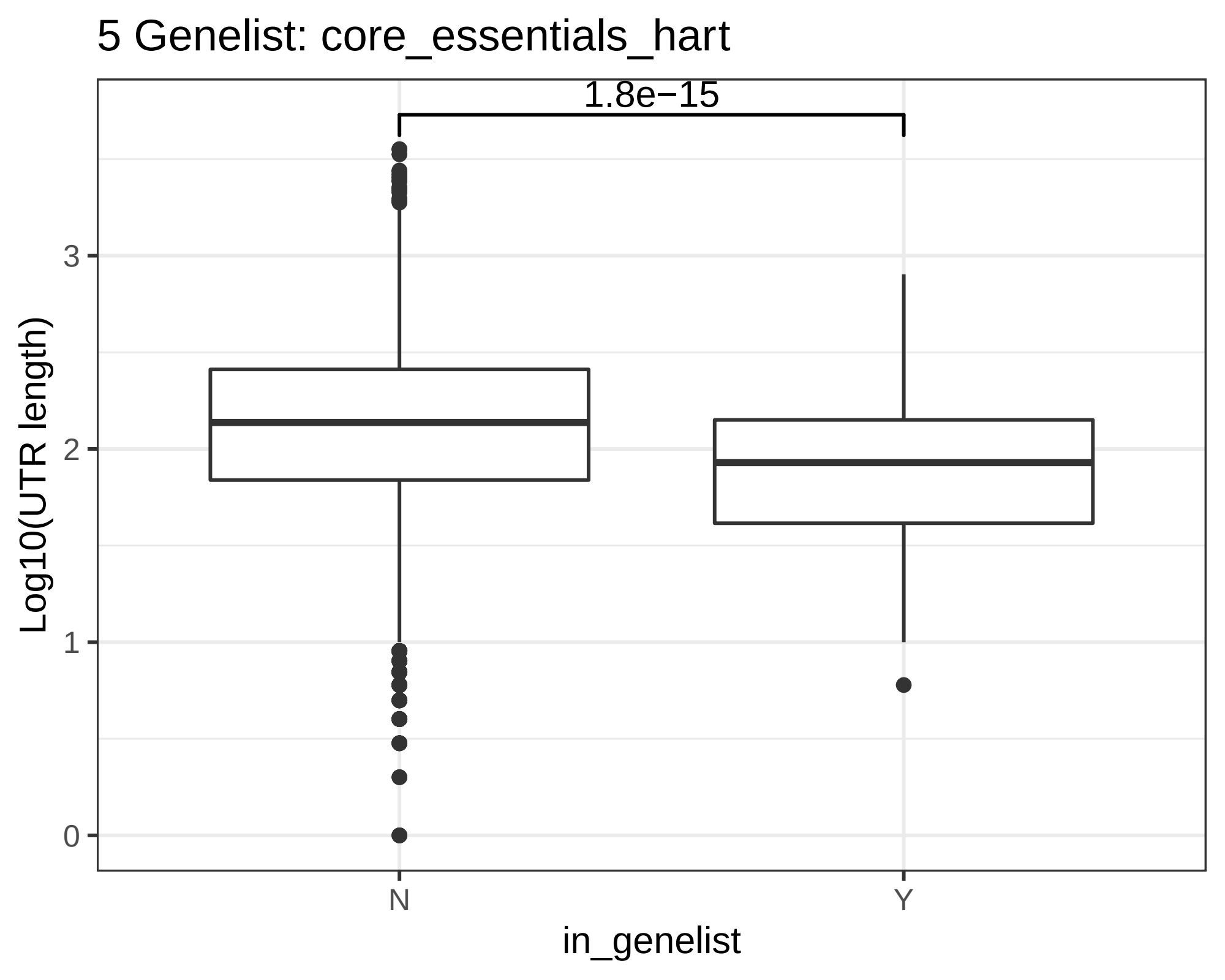

5 Genelist: clinvar_path_likelypath
Observed / Expected
1.1
1.0
0.9
0.8
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

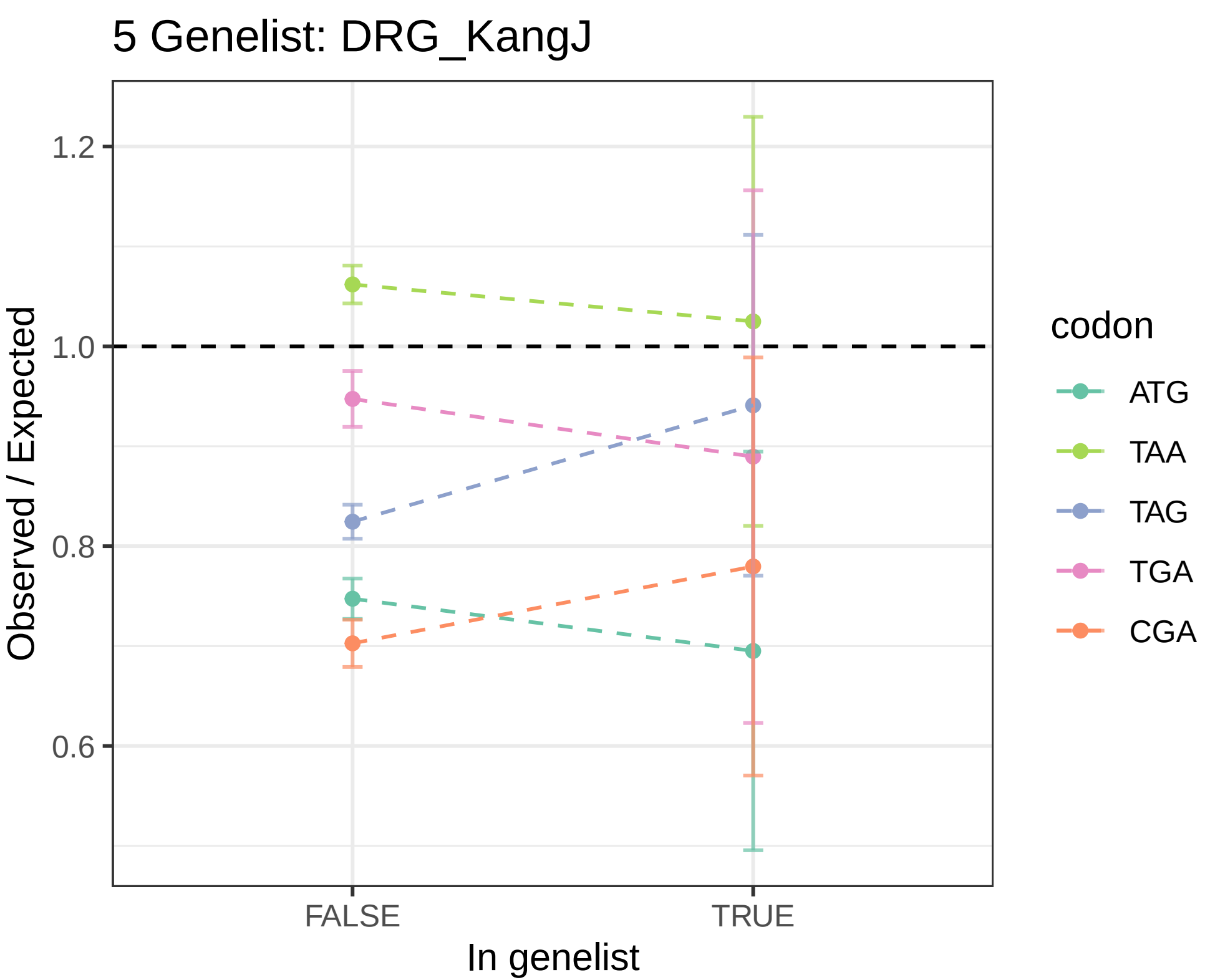

5 Genelist: clinvar_path_likelypath
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

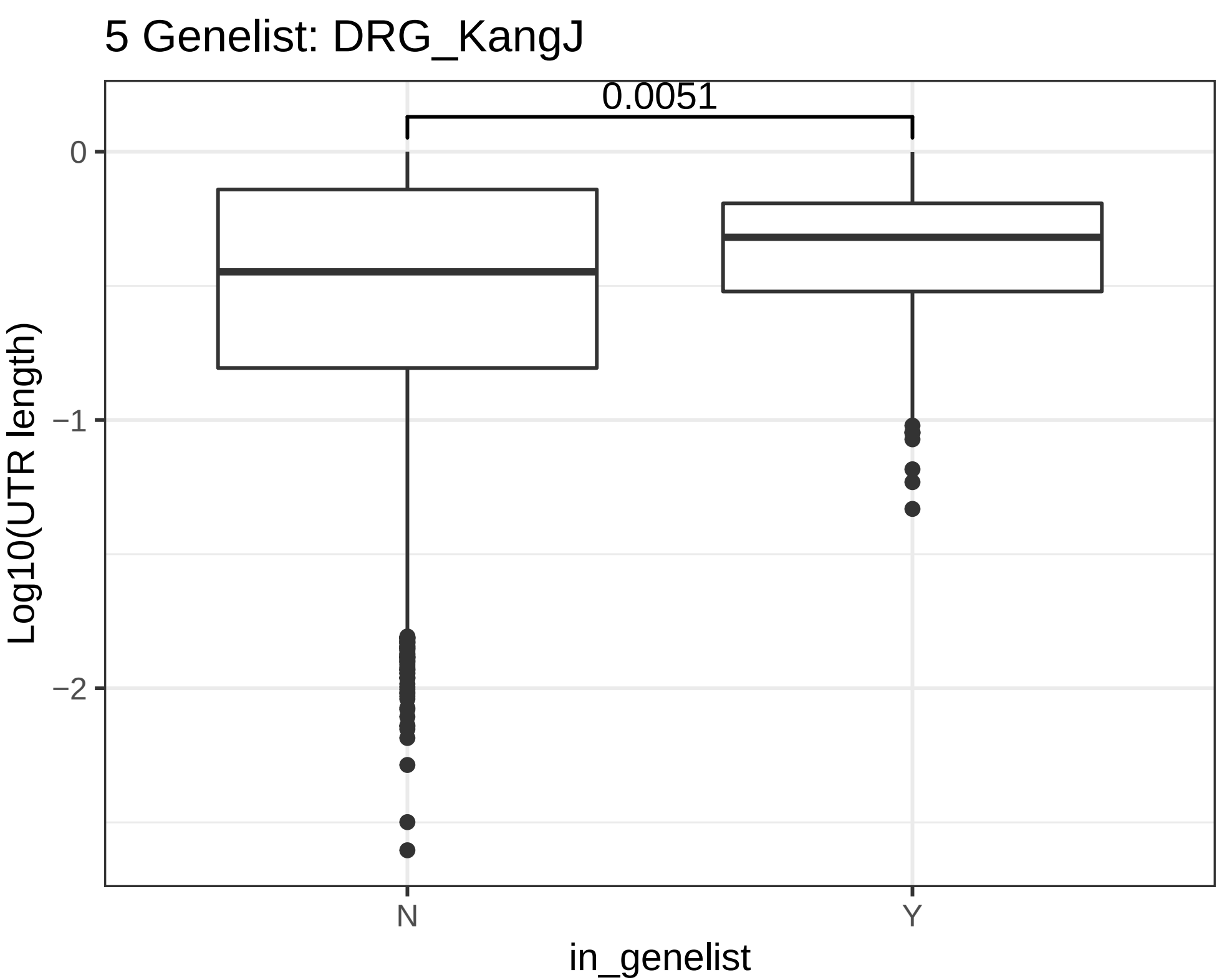

5 Genelist: clinvar_path_likelypath
0.29
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

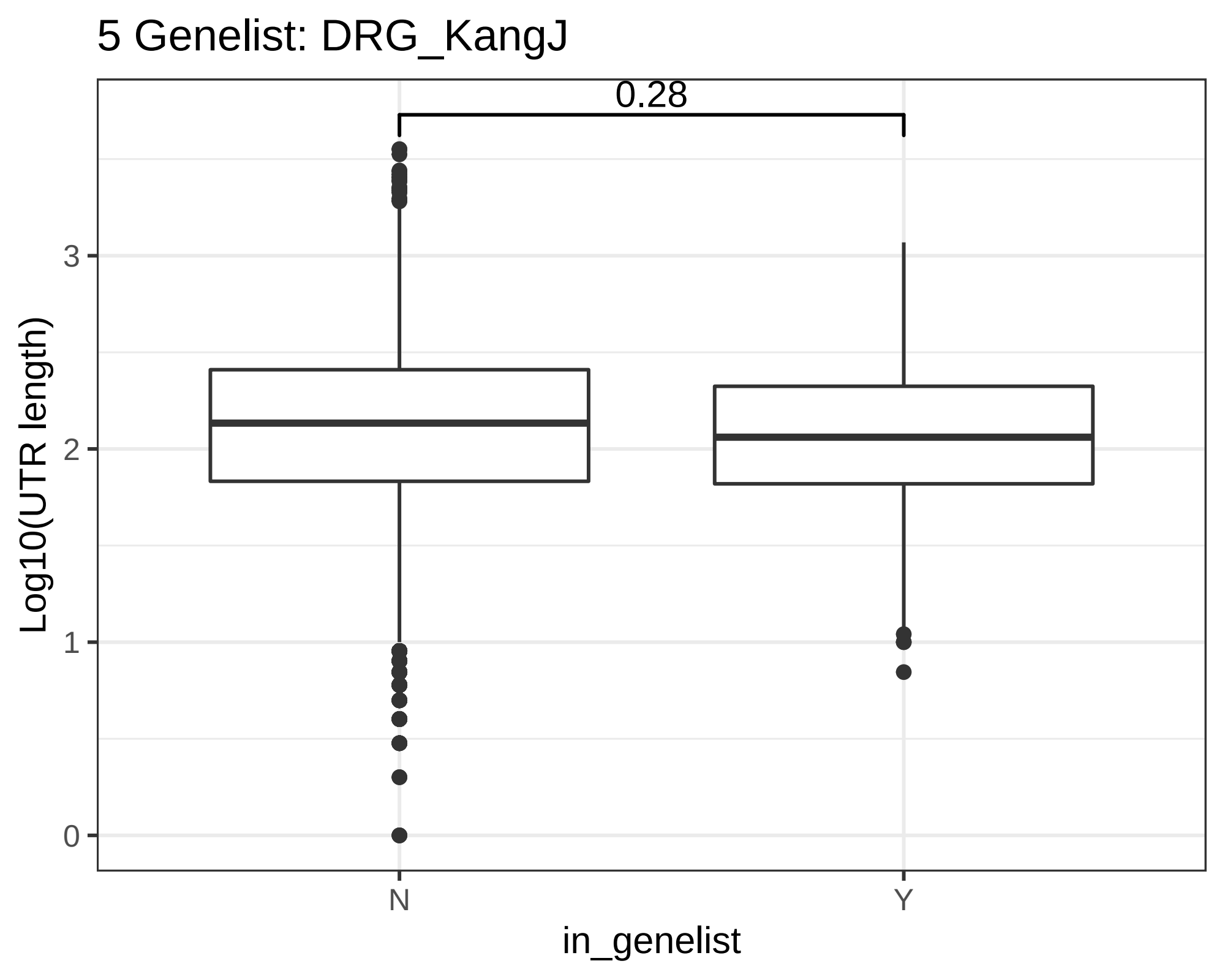

5 Genelist: core_essentials_hart
1.2
1.0
0.8
0.6
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

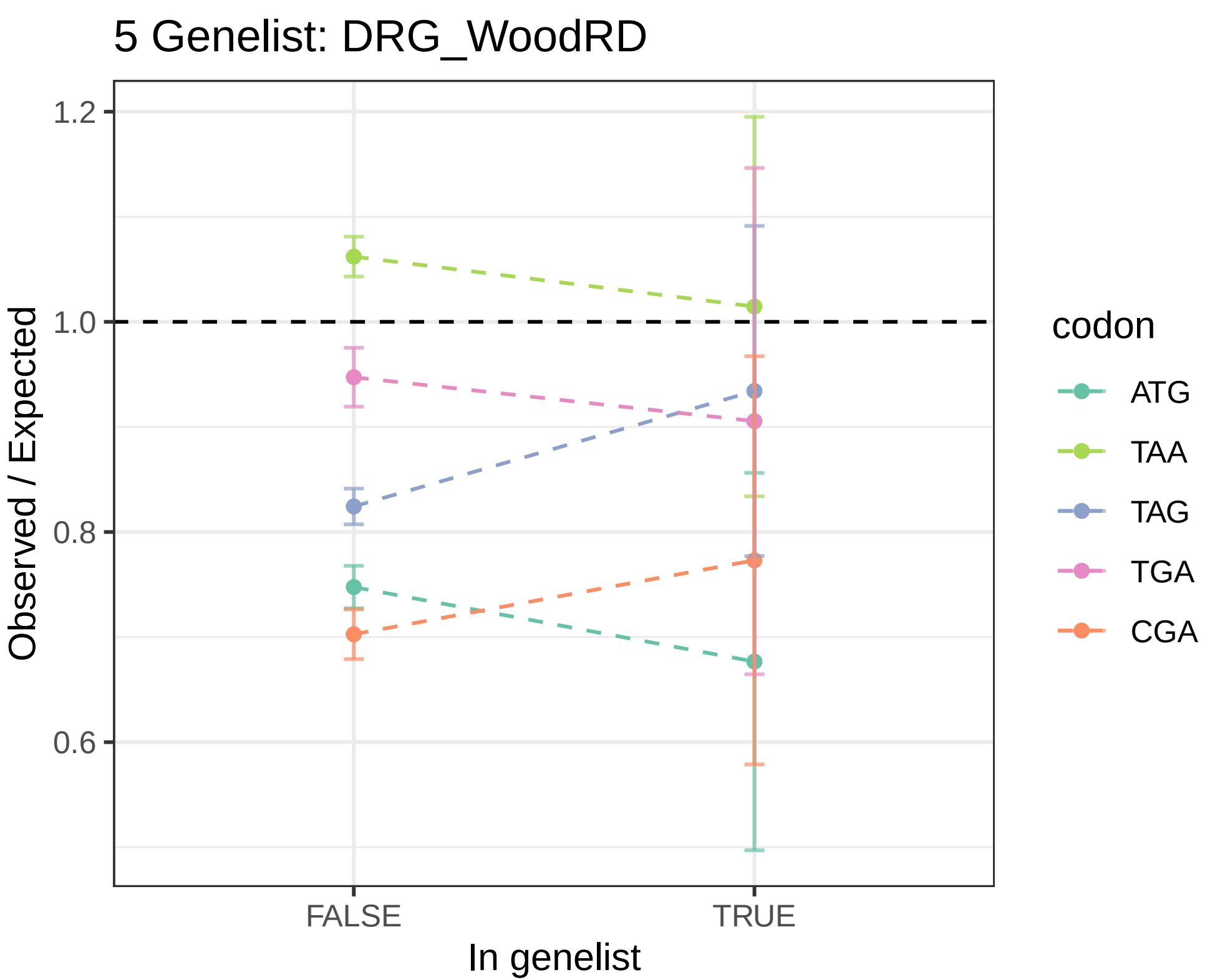

5 Genelist: core_essentials_hart
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

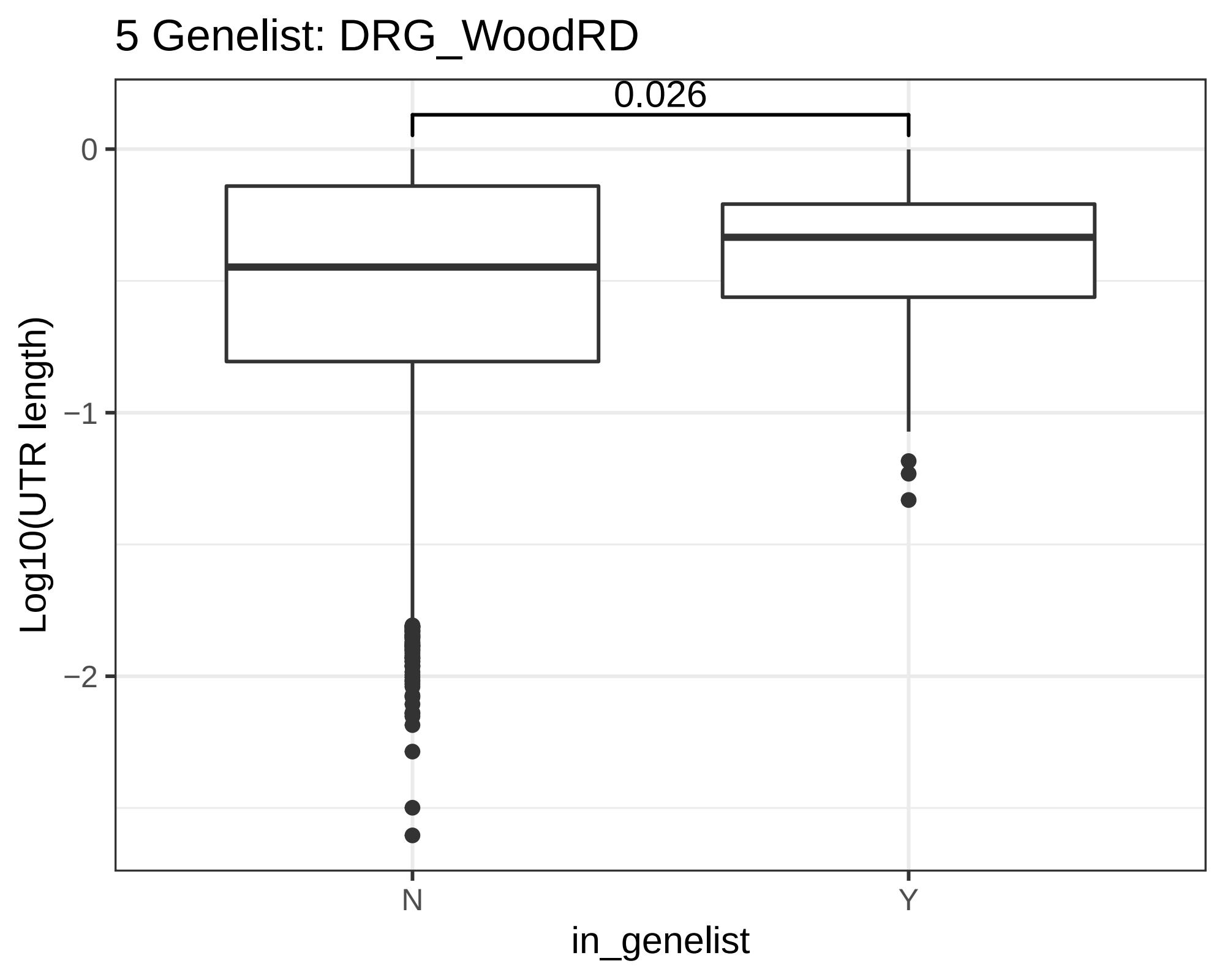

5 Genelist: core_essentials_hart
1.8e−15
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

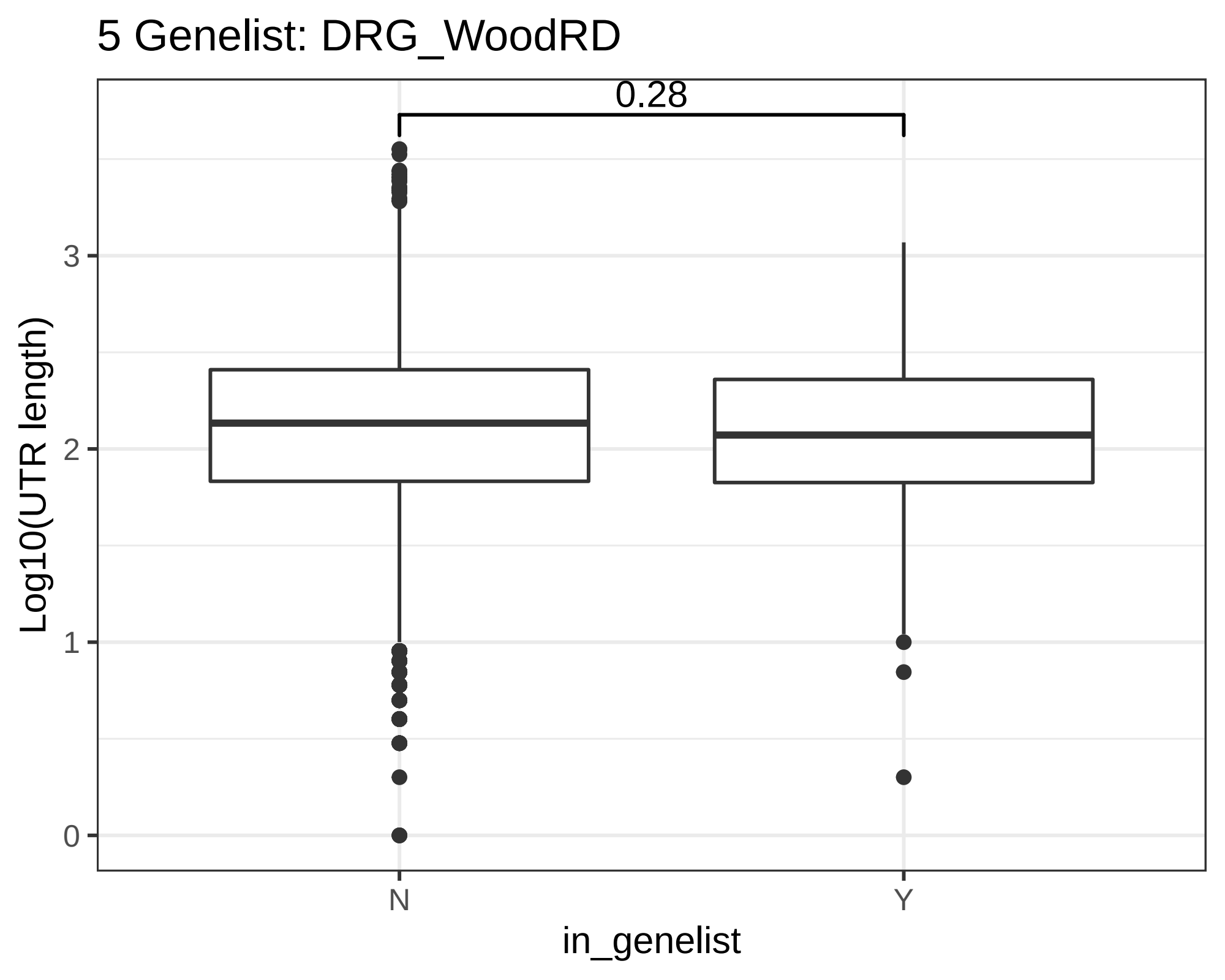

5 Genelist: DRG_KangJ
Observed / Expected
1.2
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

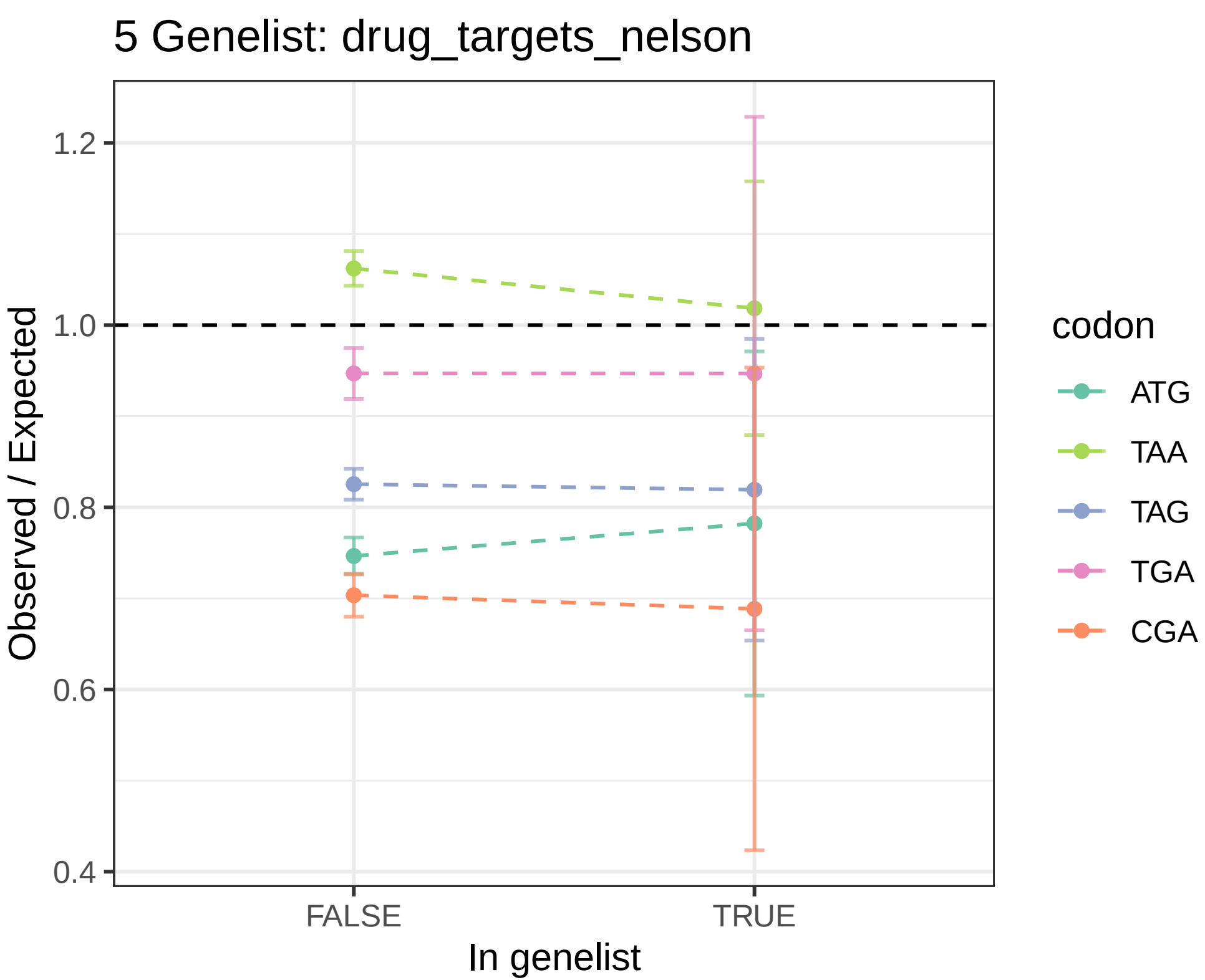

5 Genelist: DRG_KangJ
0.0051
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

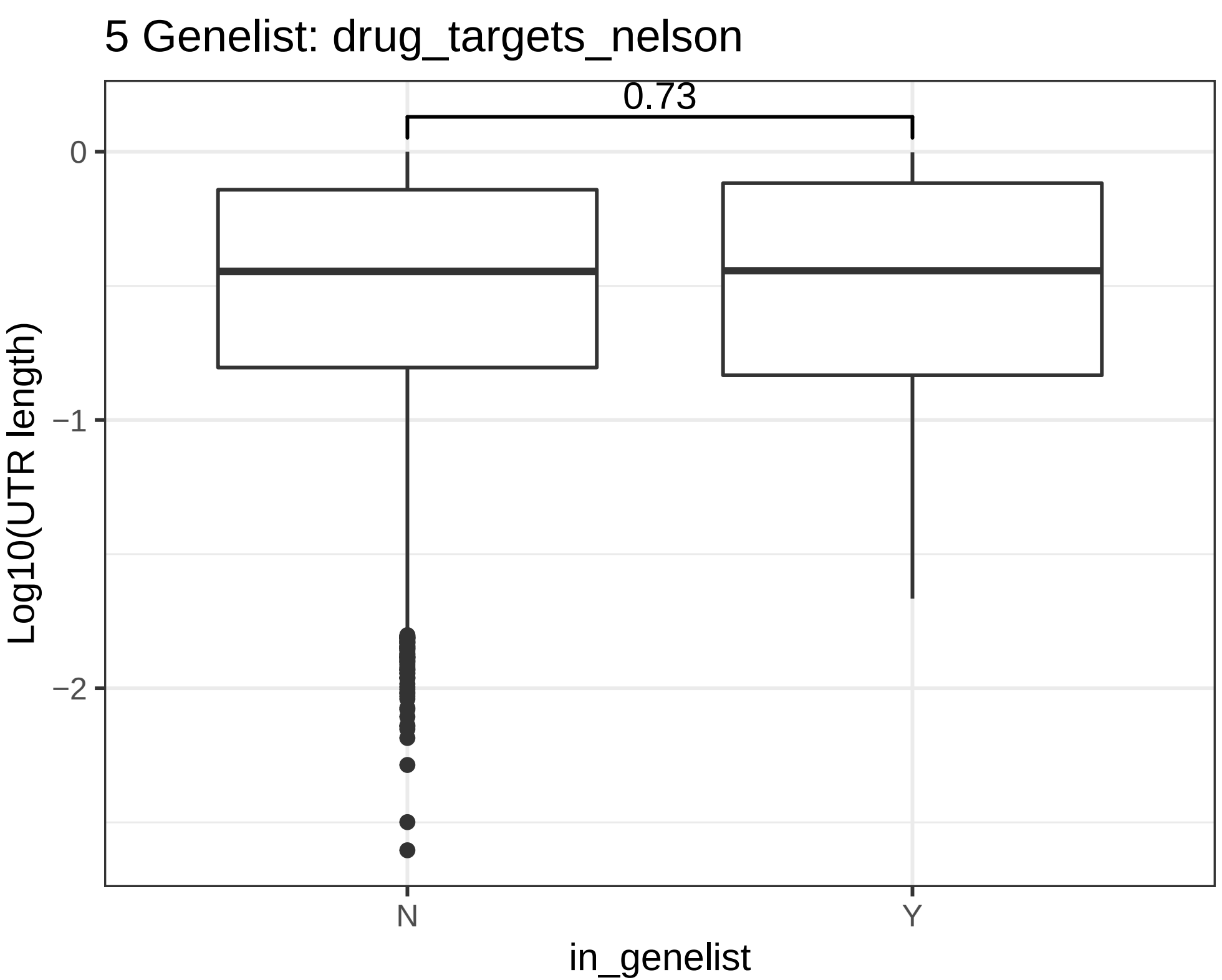

5 Genelist: DRG_KangJ
0.28
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

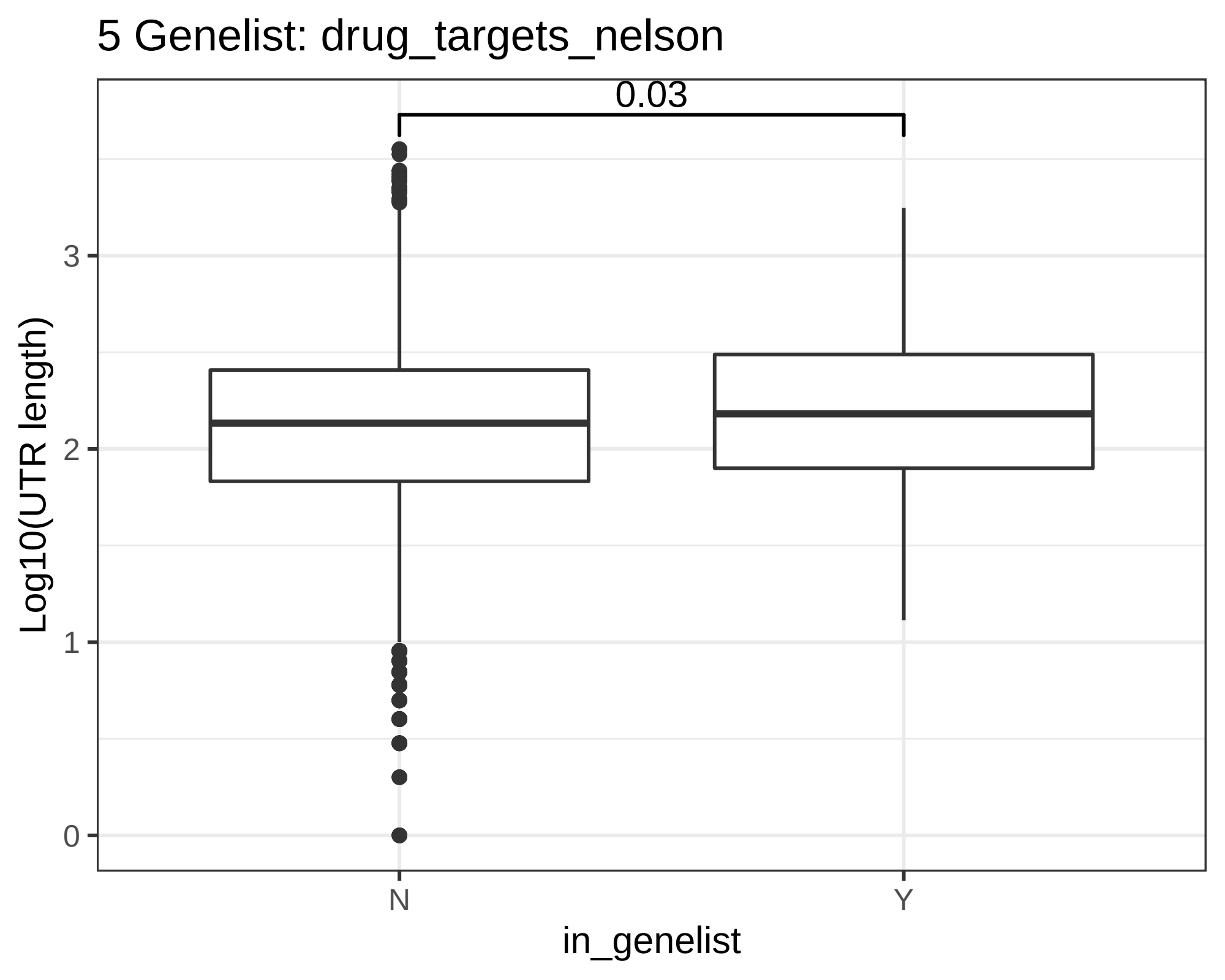

5 Genelist: DRG_WoodRD
1.2
1.0
0.8
0.6
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

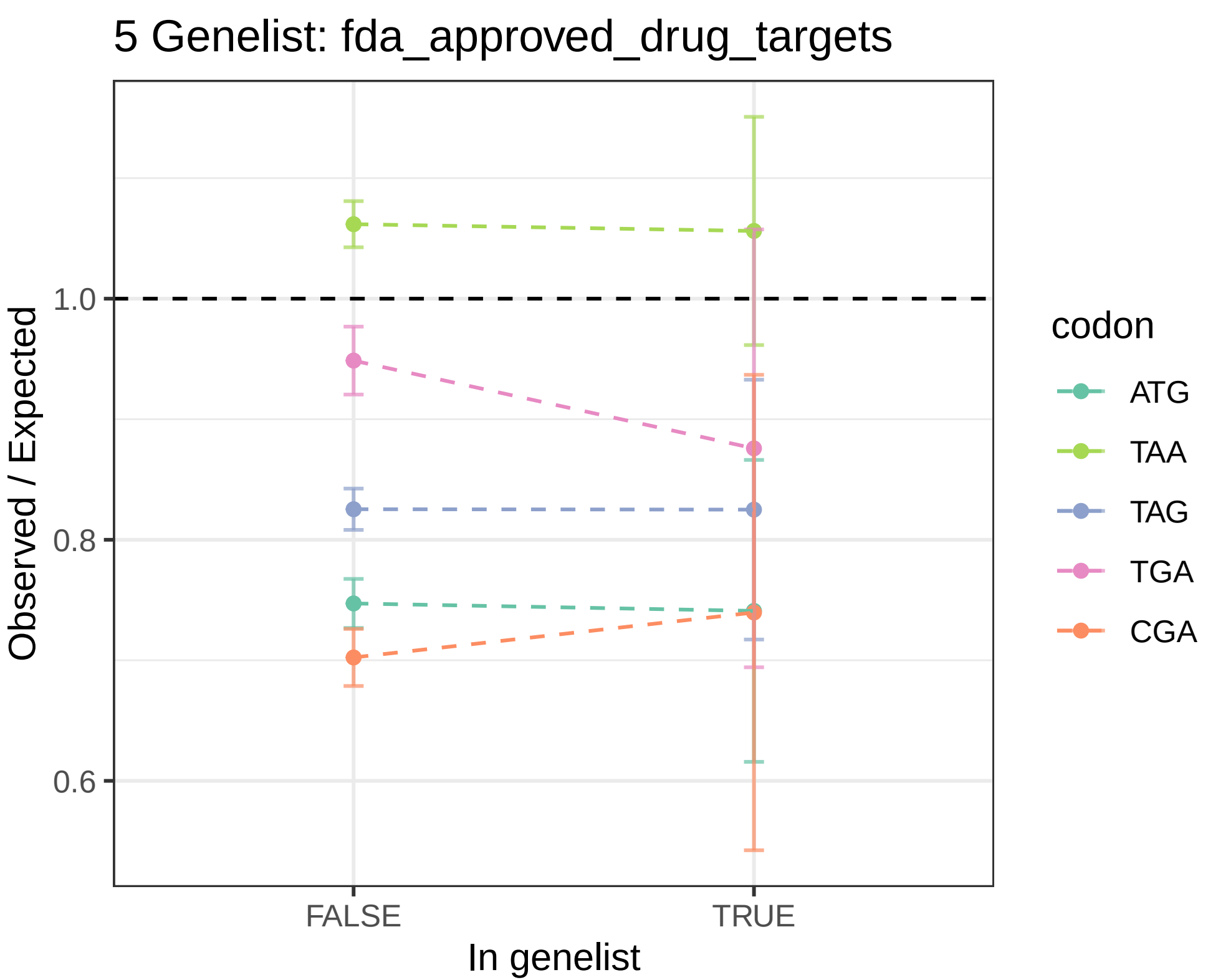

5 Genelist: DRG_WoodRD
0.026
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

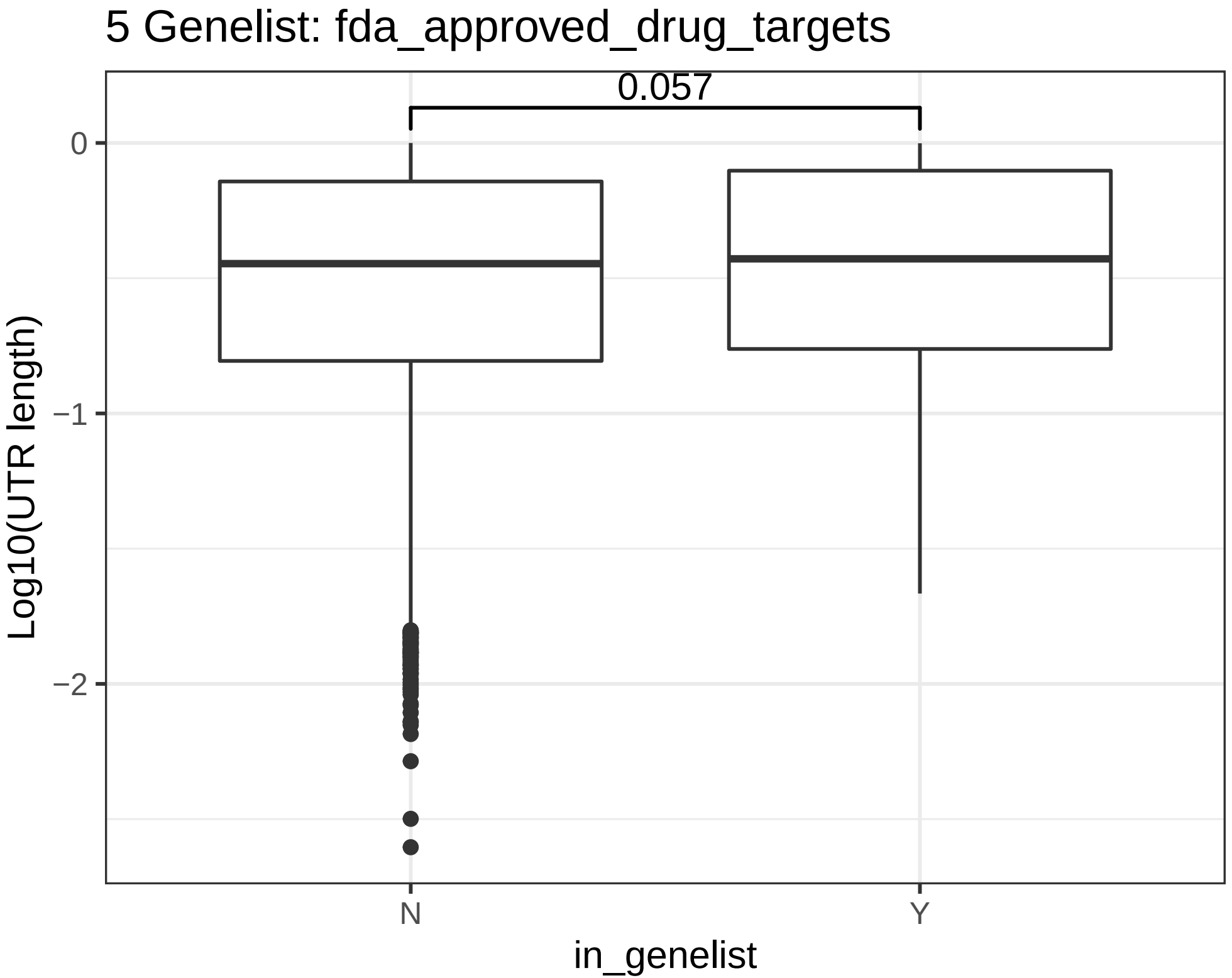

5 Genelist: DRG_WoodRD
0.28
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

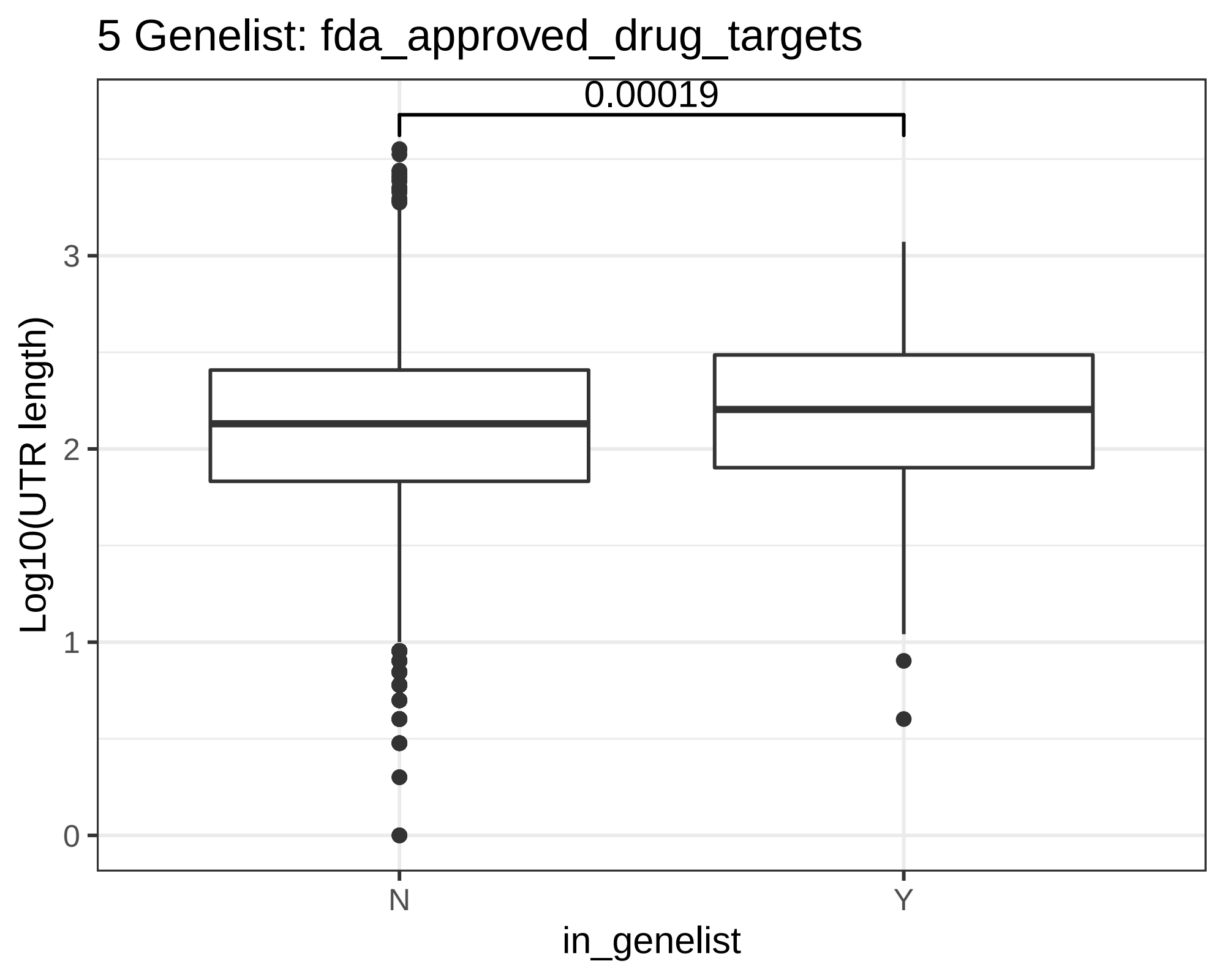

5 Genelist: drug_targets_nelson
Observed / Expected
1.2
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

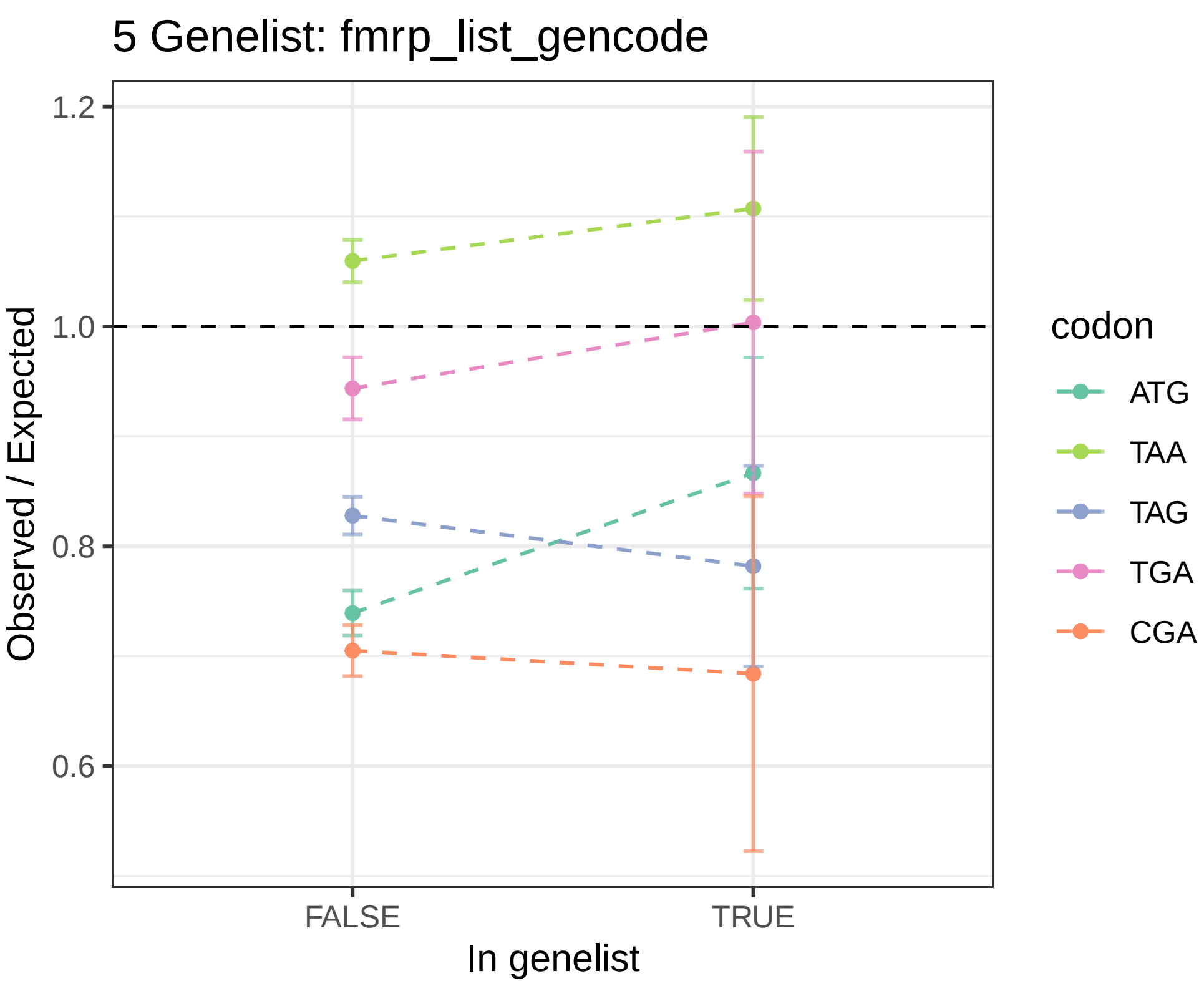

5 Genelist: drug_targets_nelson
0.73
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

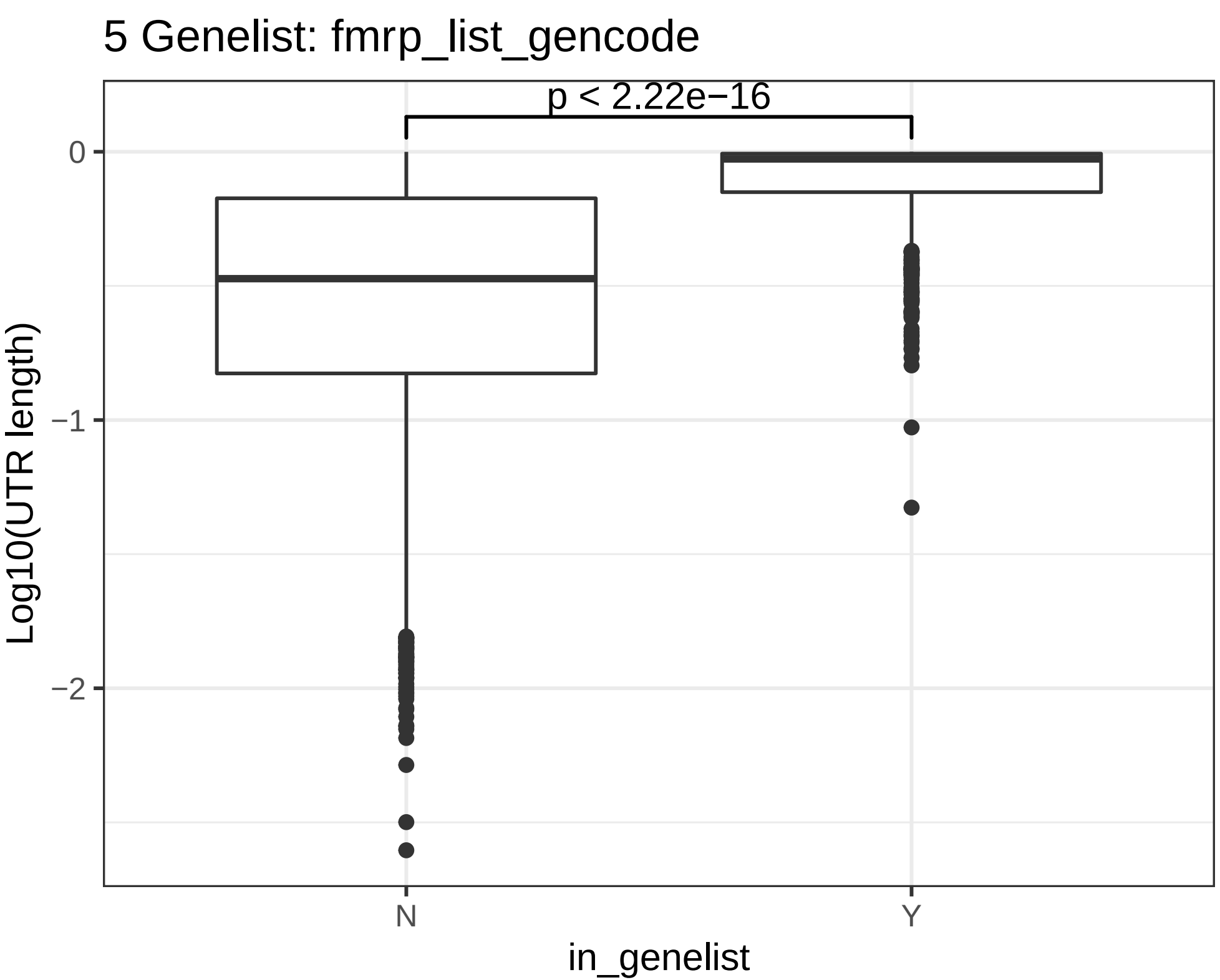

5 Genelist: drug_targets_nelson
0.03
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

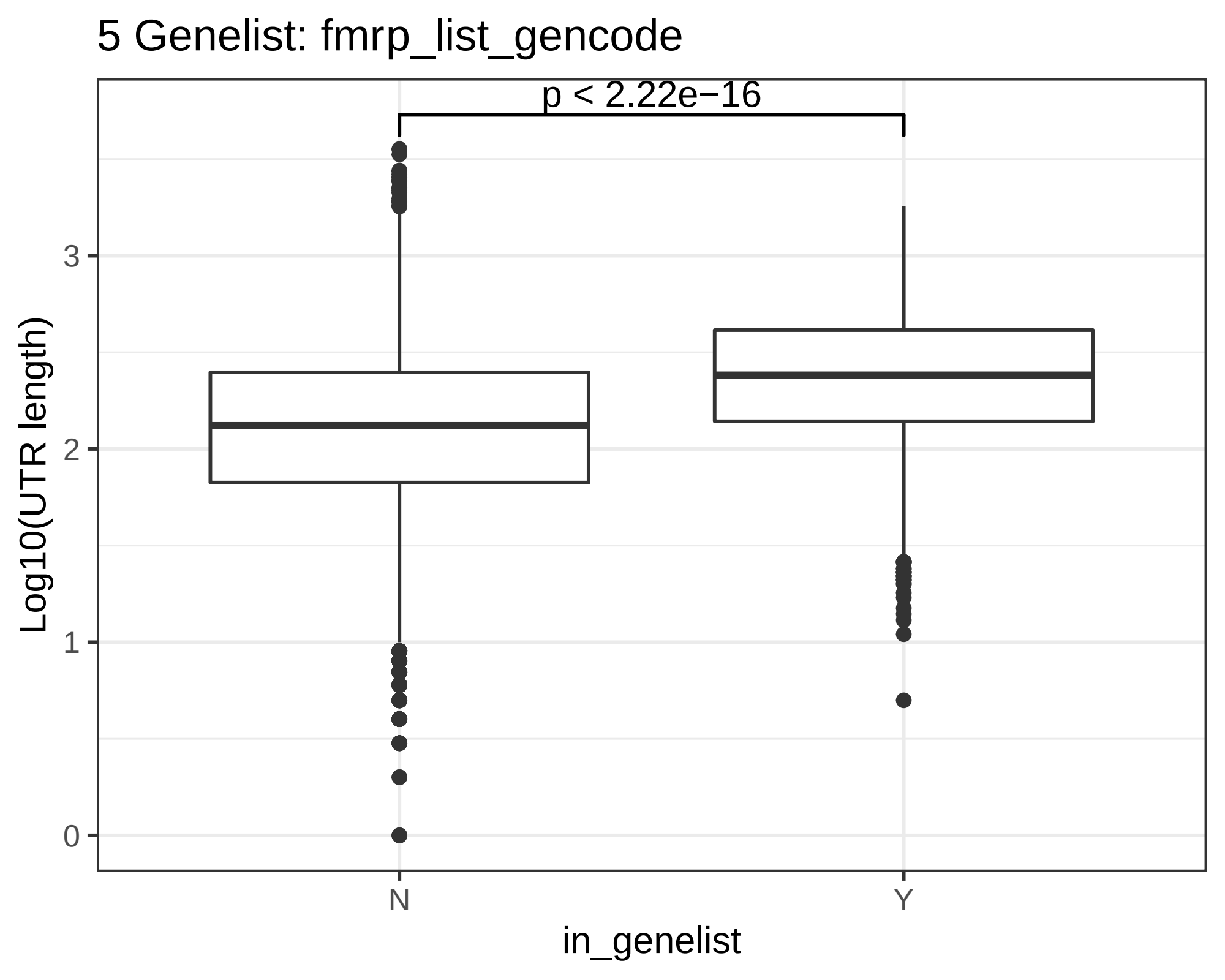

5 Genelist: fda_approved_drug_targets
Observed / Expected
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

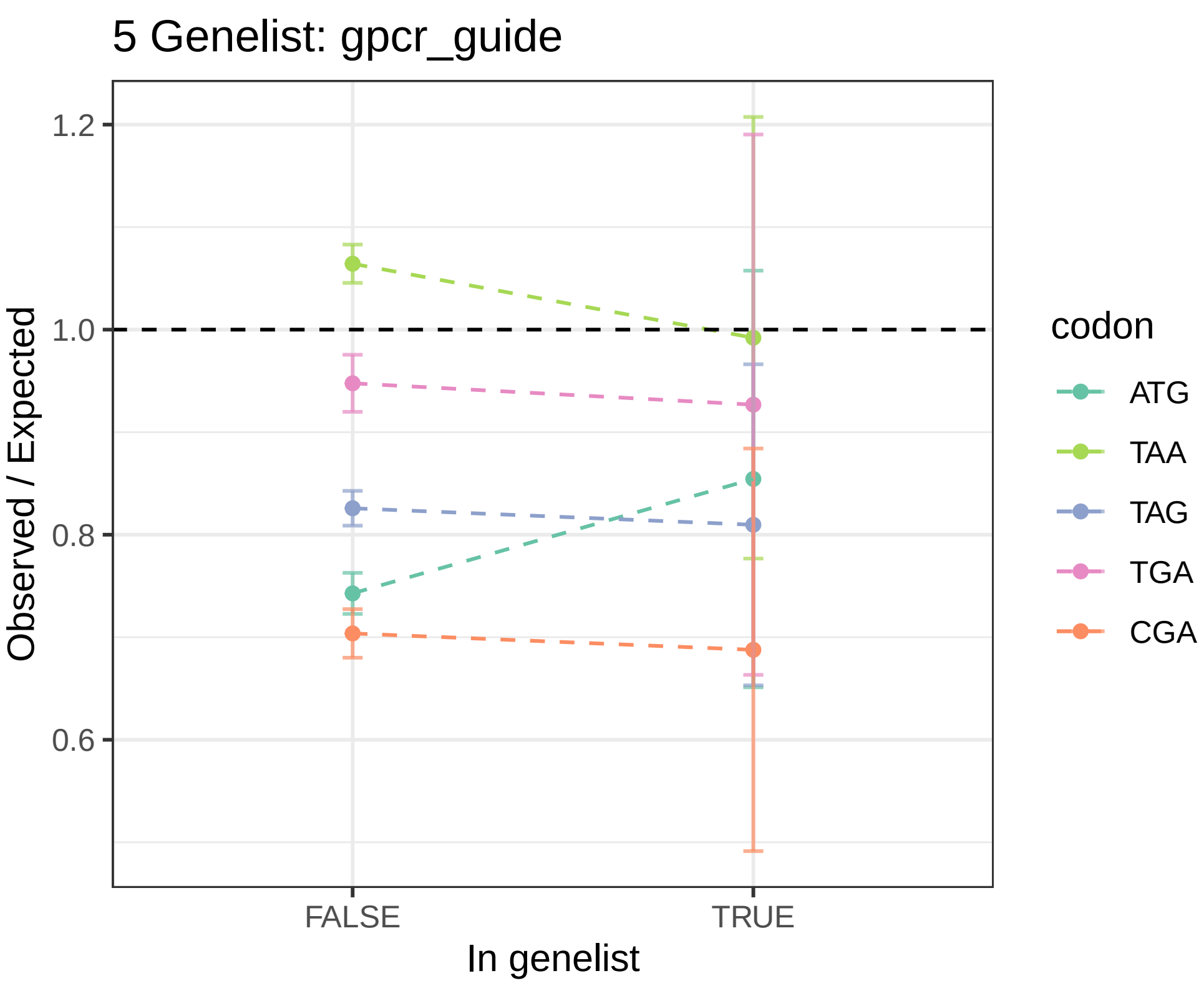

5 Genelist: fda_approved_drug_targets
0.057
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

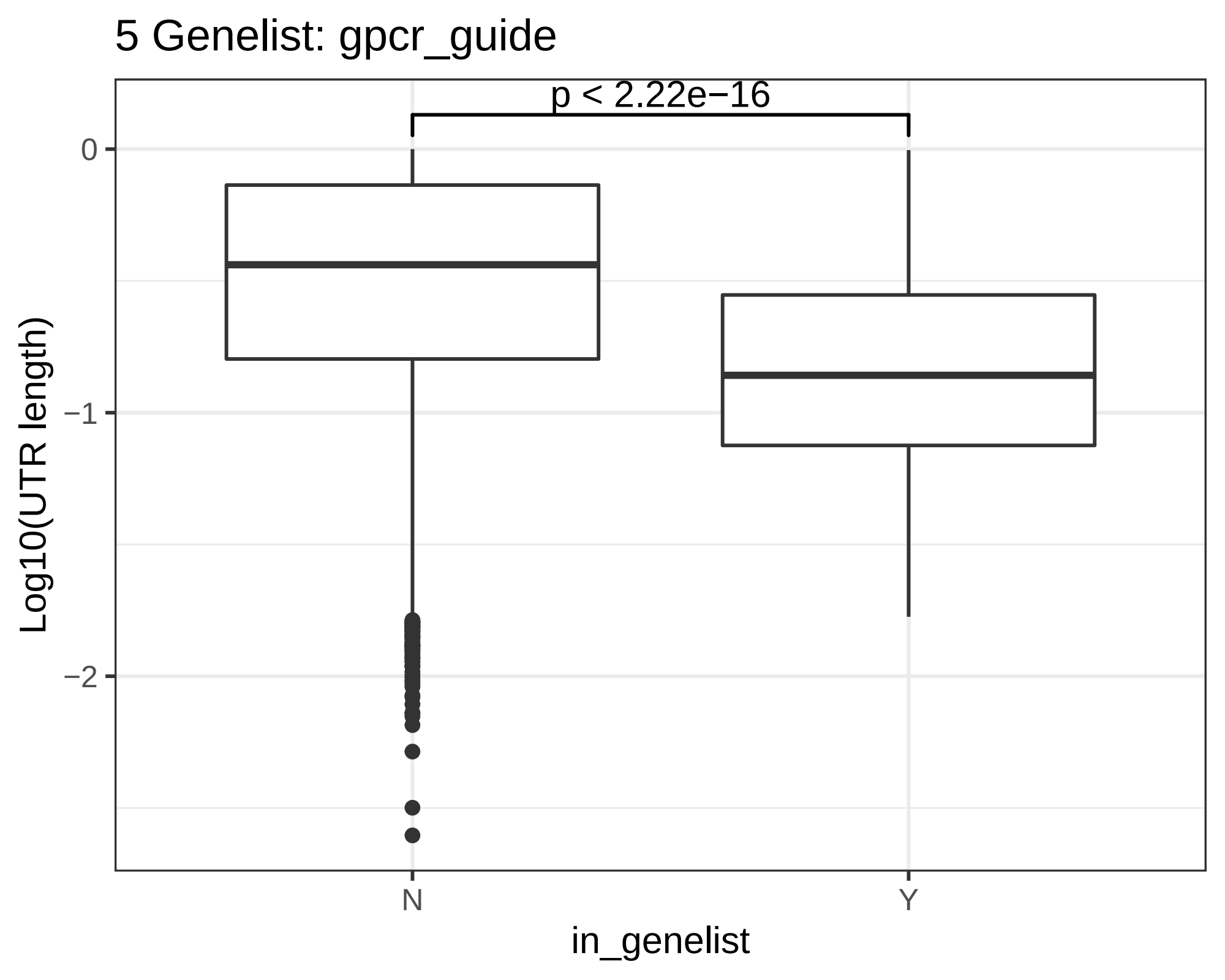

5 Genelist: fda_approved_drug_targets
0.00019
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

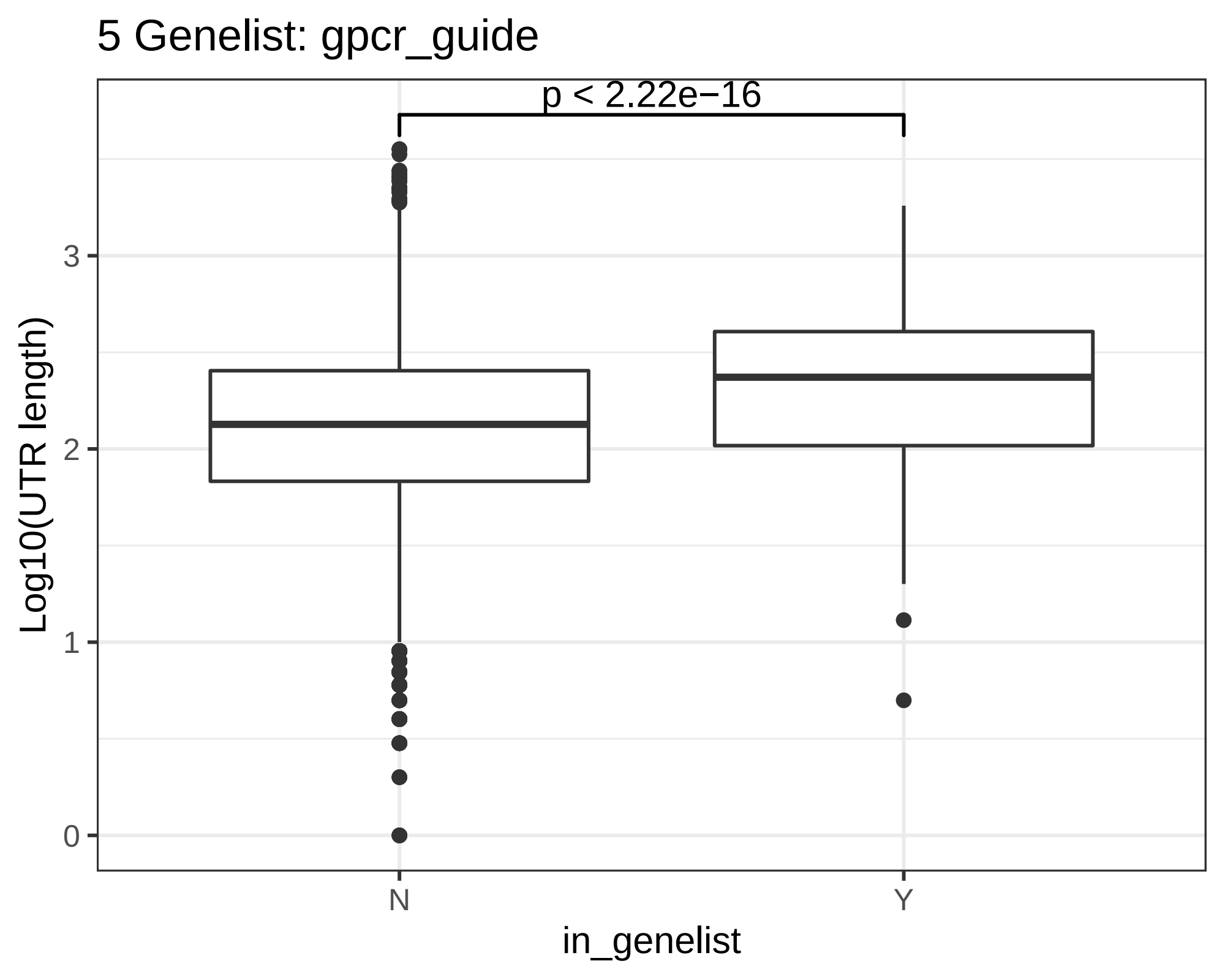

5 Genelist: fmrp_list_gencode
1.2
1.0
0.8
0.6
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

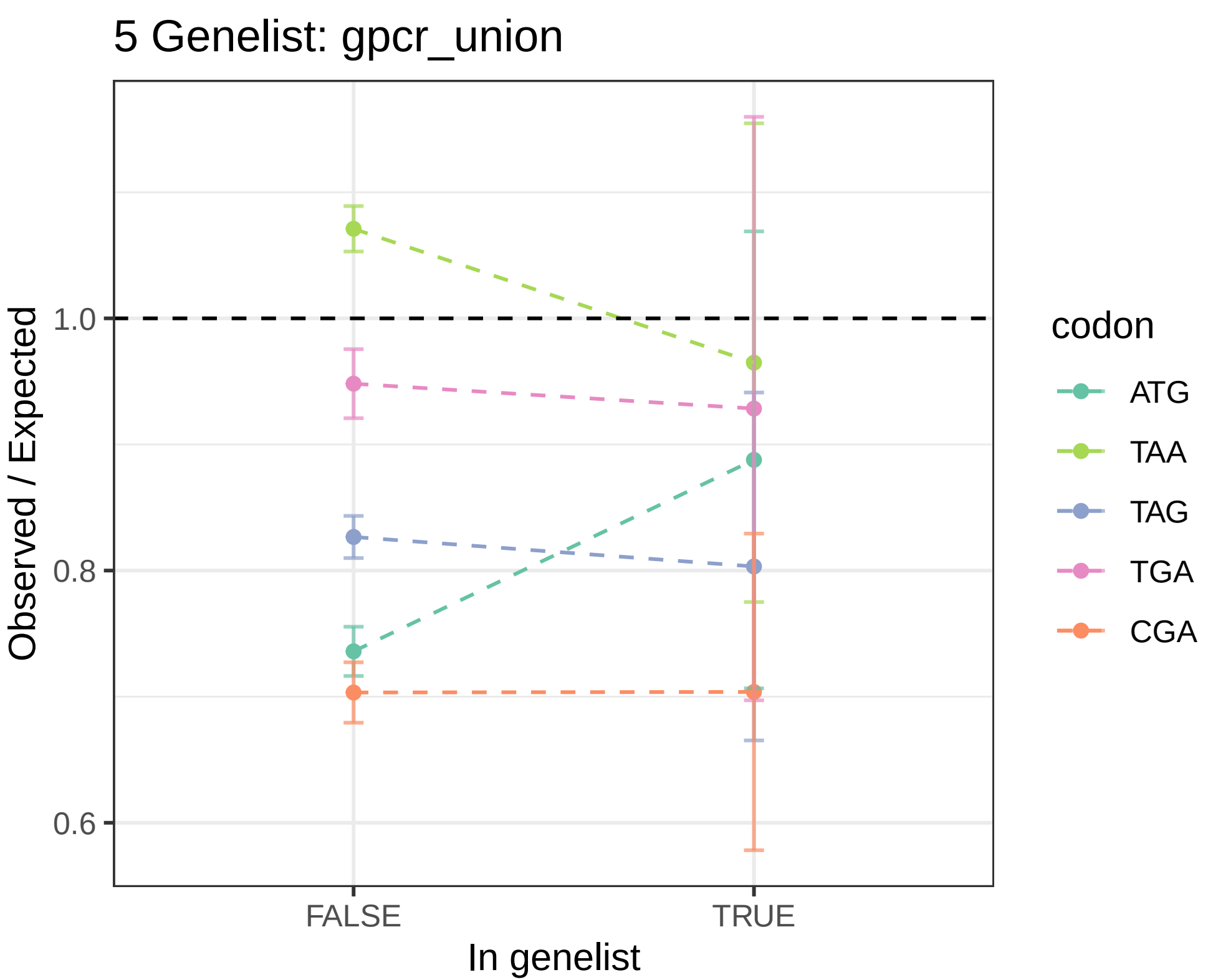

5 Genelist: fmrp_list_gencode
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

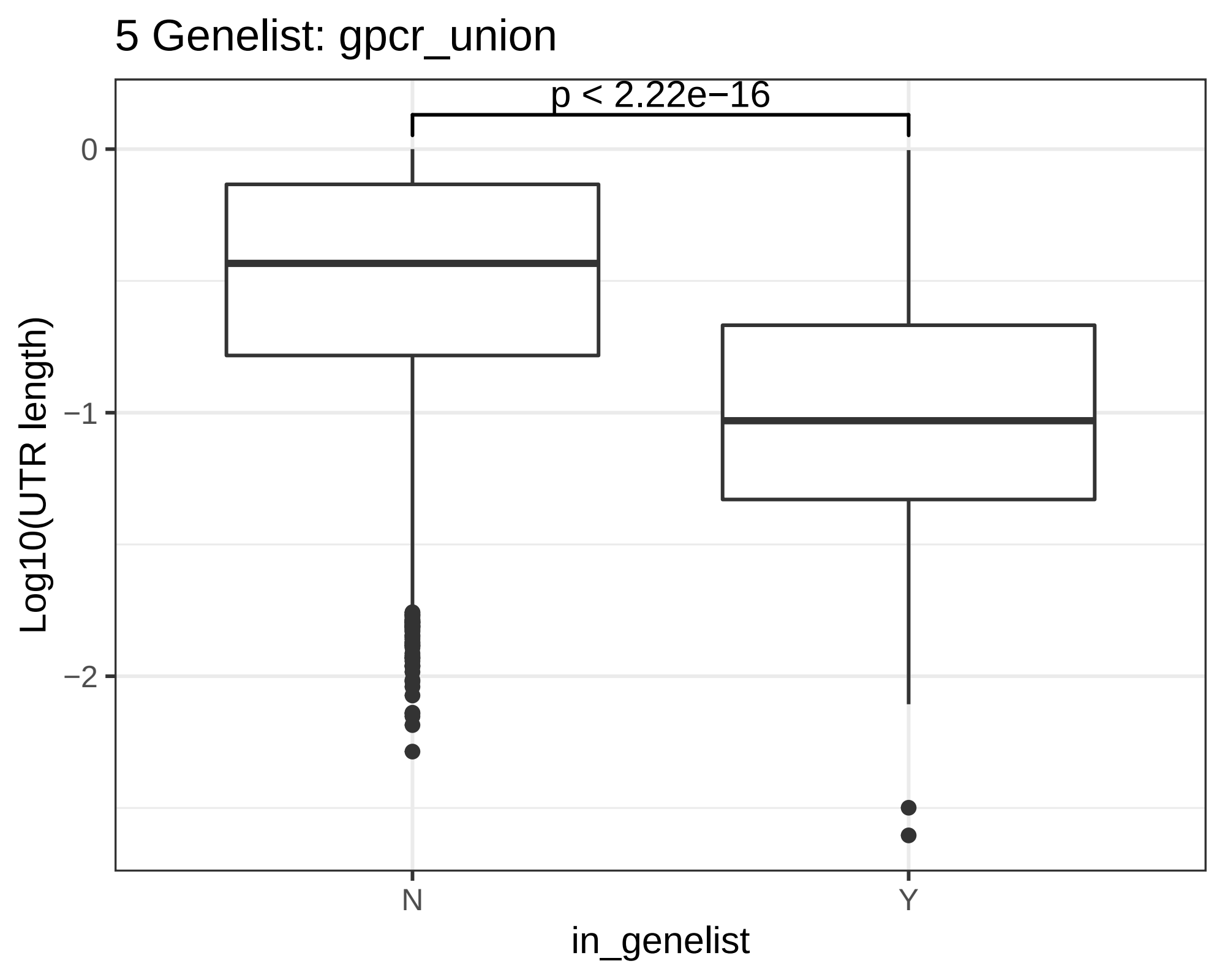

5 Genelist: fmrp_list_gencode
p < 2.22e−16
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

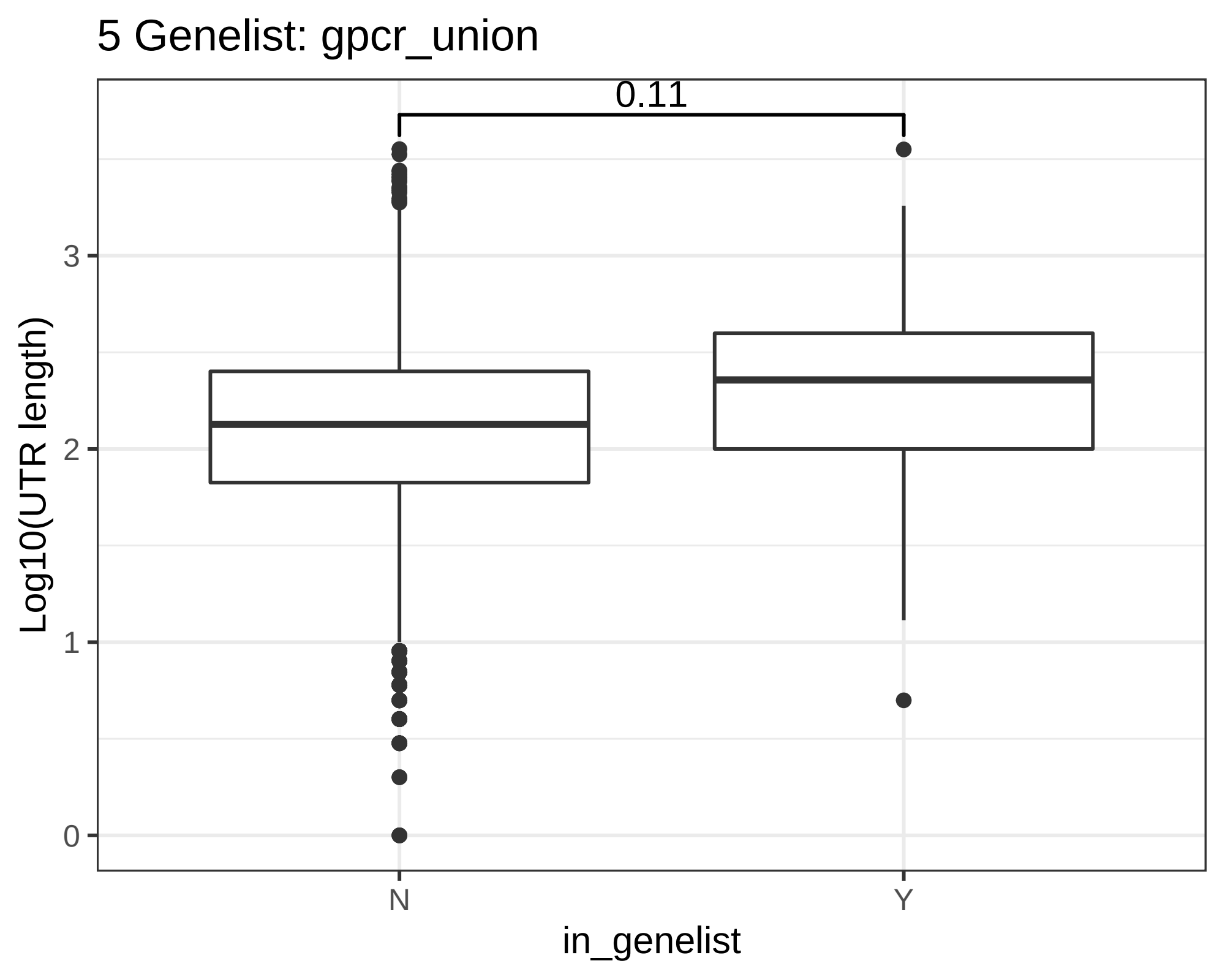

5 Genelist: gpcr_guide
1.2
1.0
0.8
0.6
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

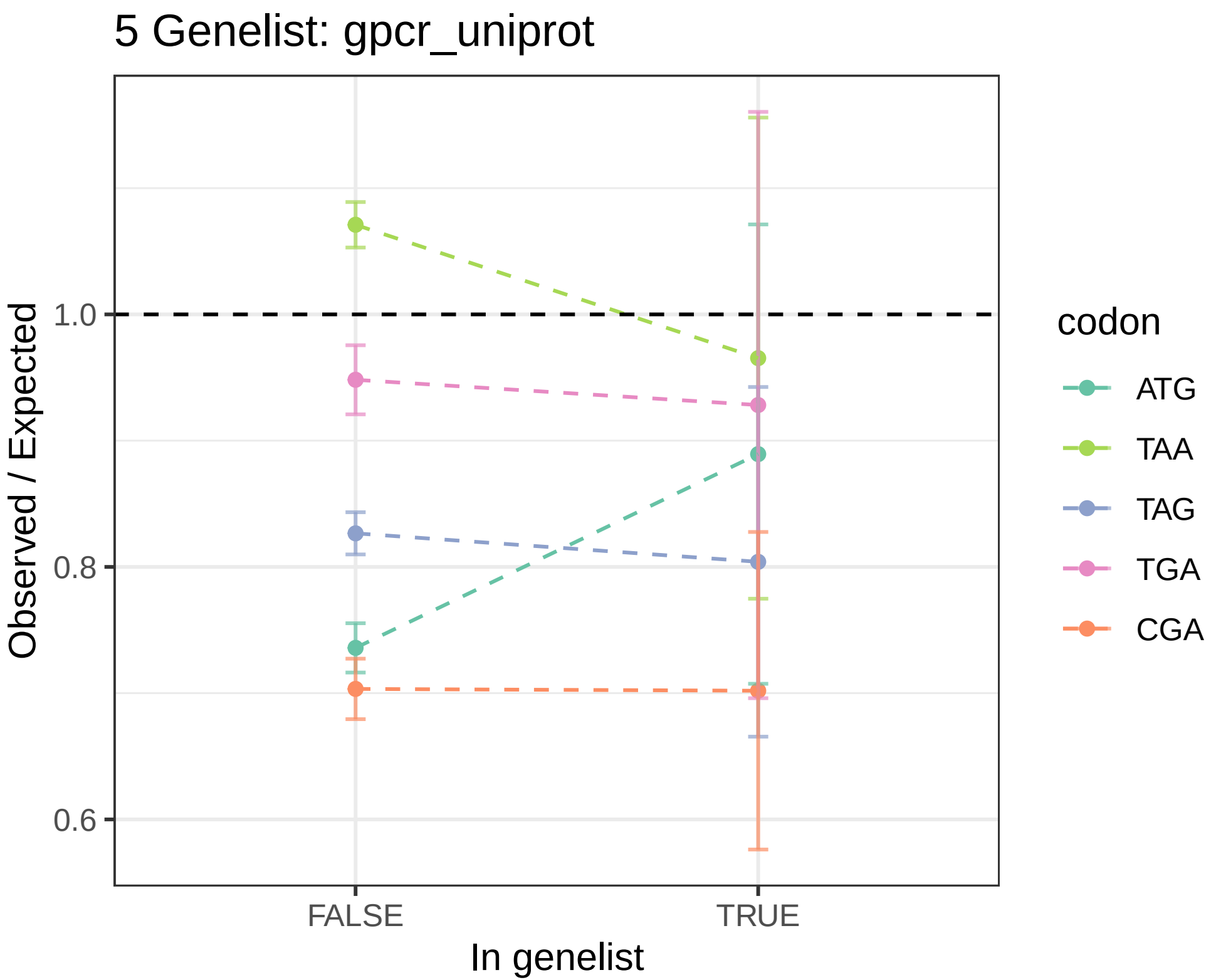

5 Genelist: gpcr_guide
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

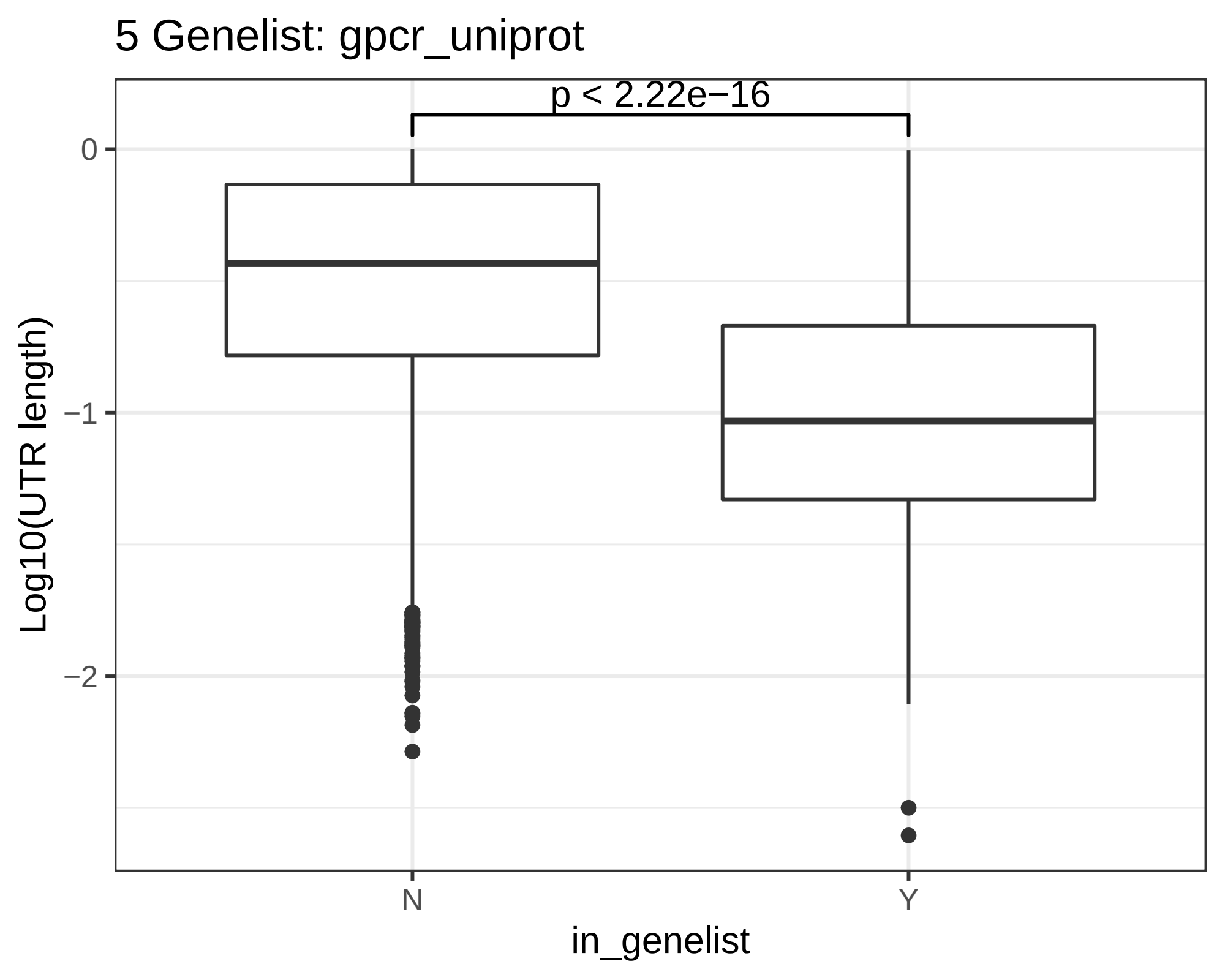

5 Genelist: gpcr_guide
p < 2.22e−16
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

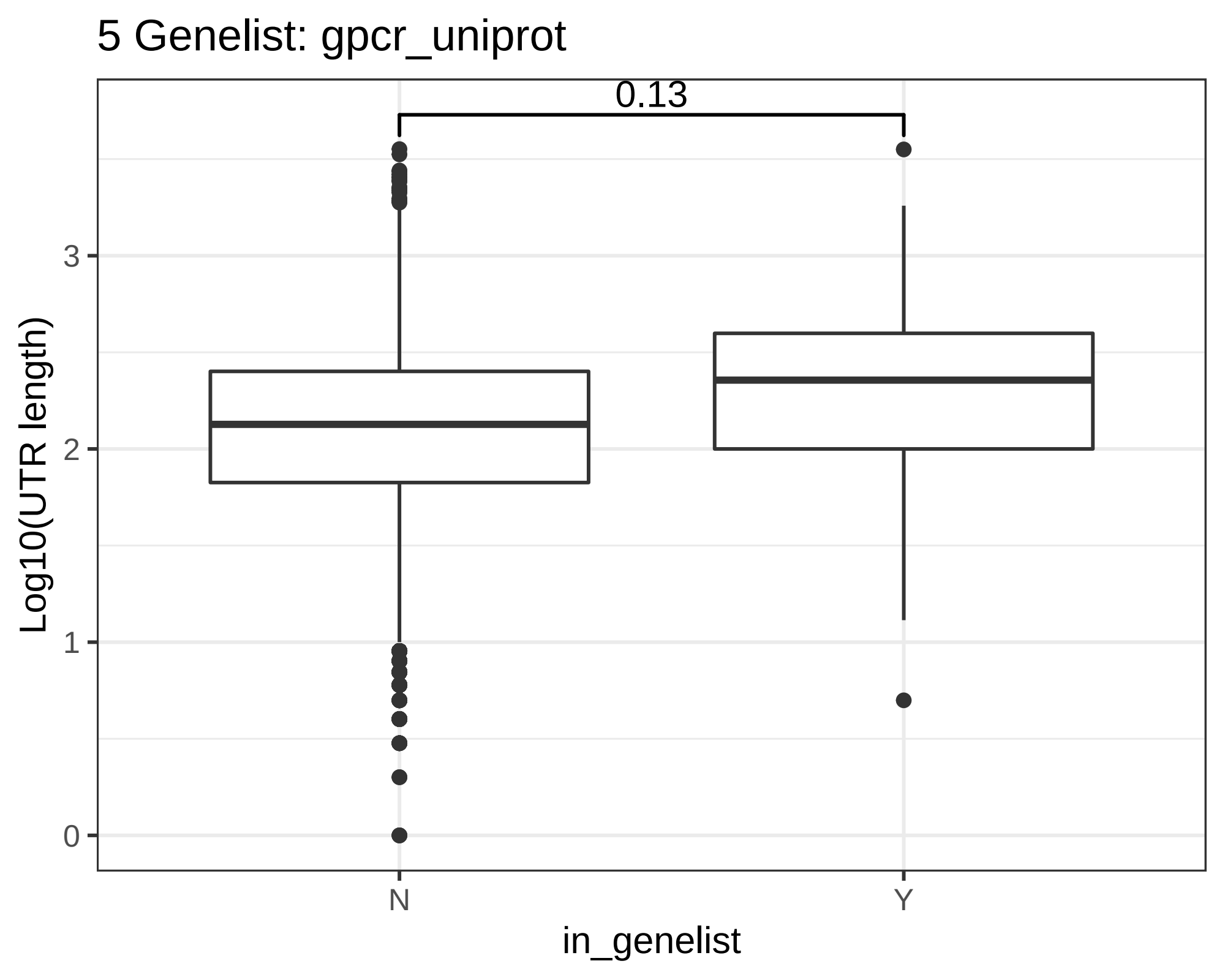

5 Genelist: gpcr_union
Observed / Expected
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

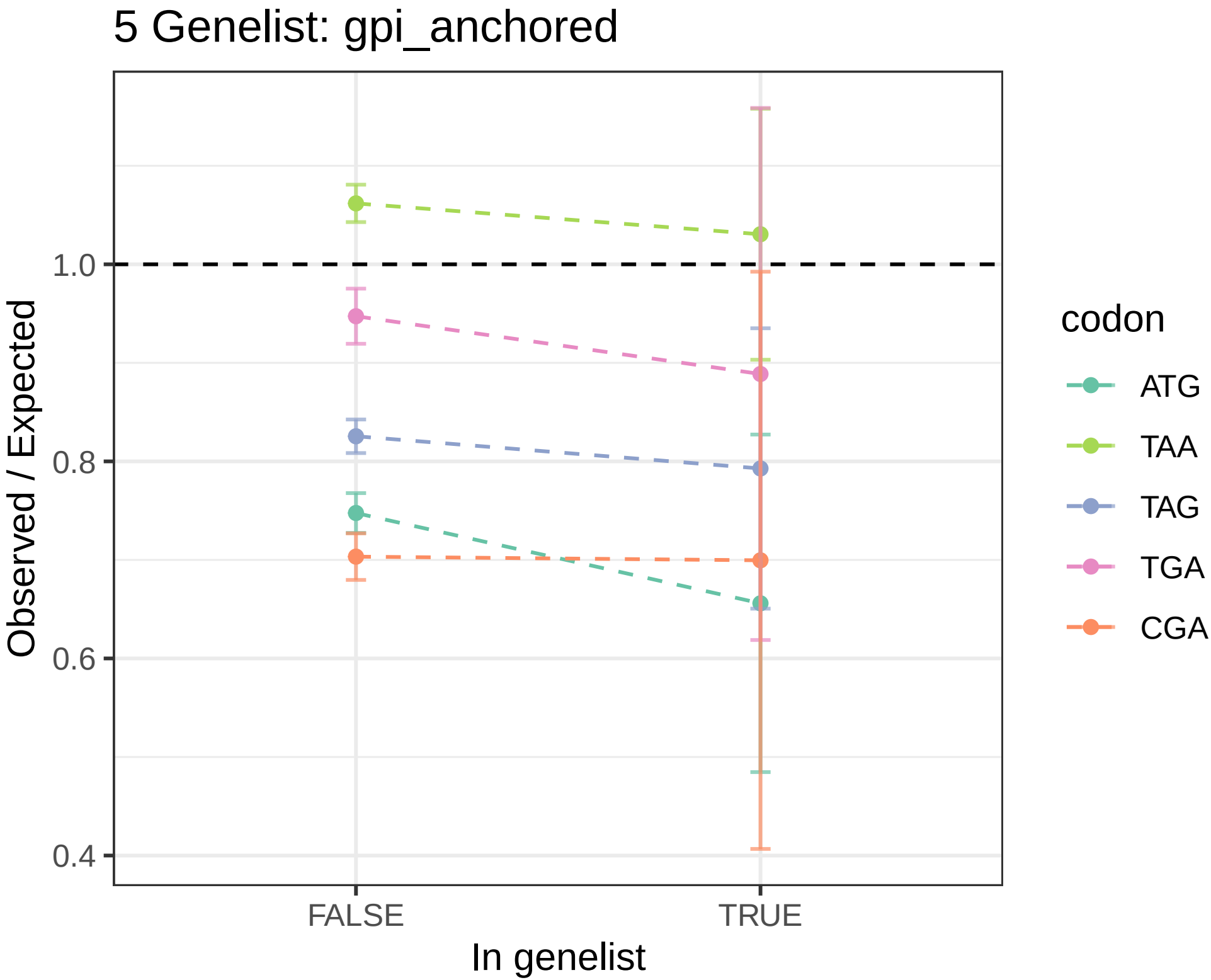

5 Genelist: gpcr_union
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

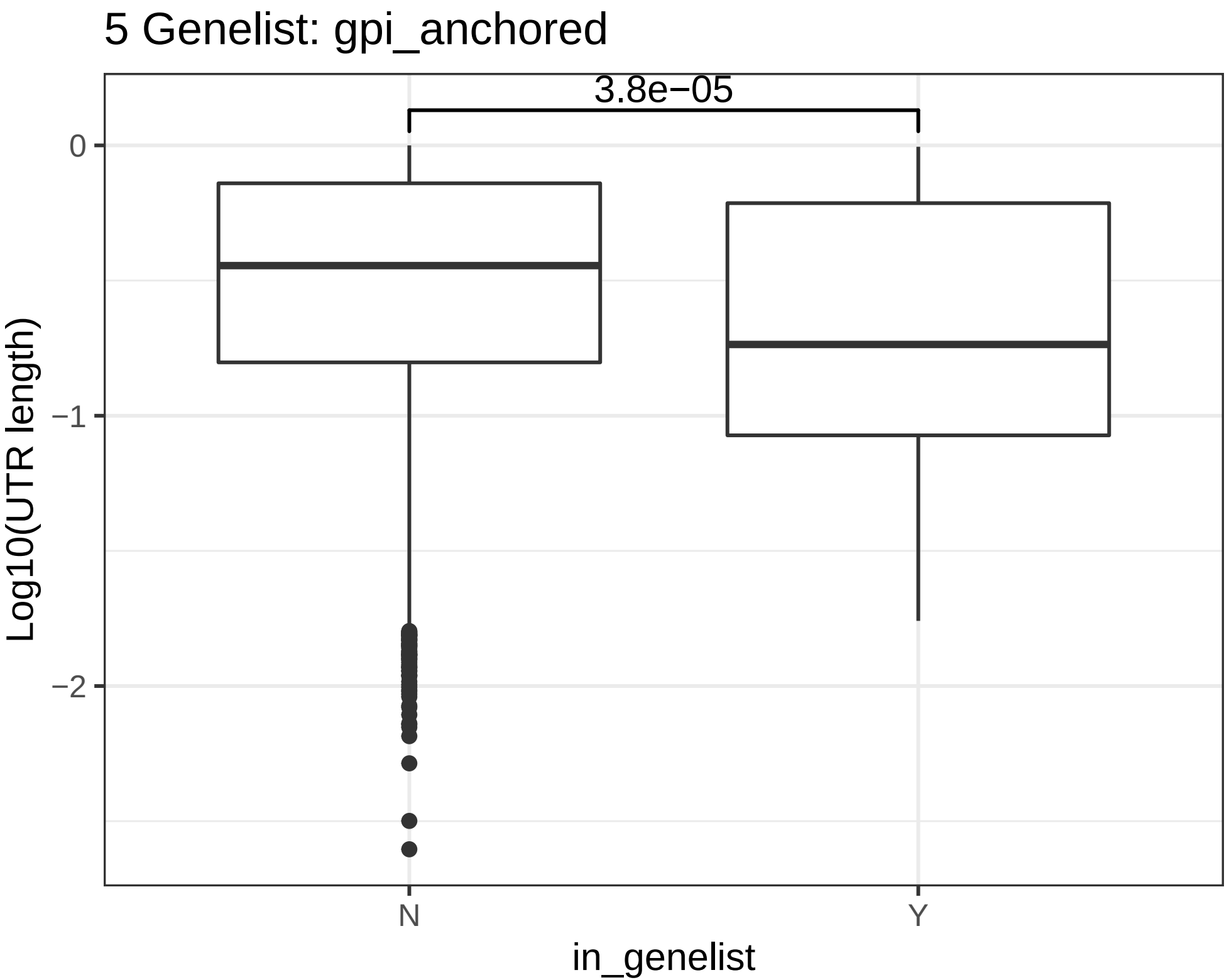

5 Genelist: gpcr_union
0.11
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

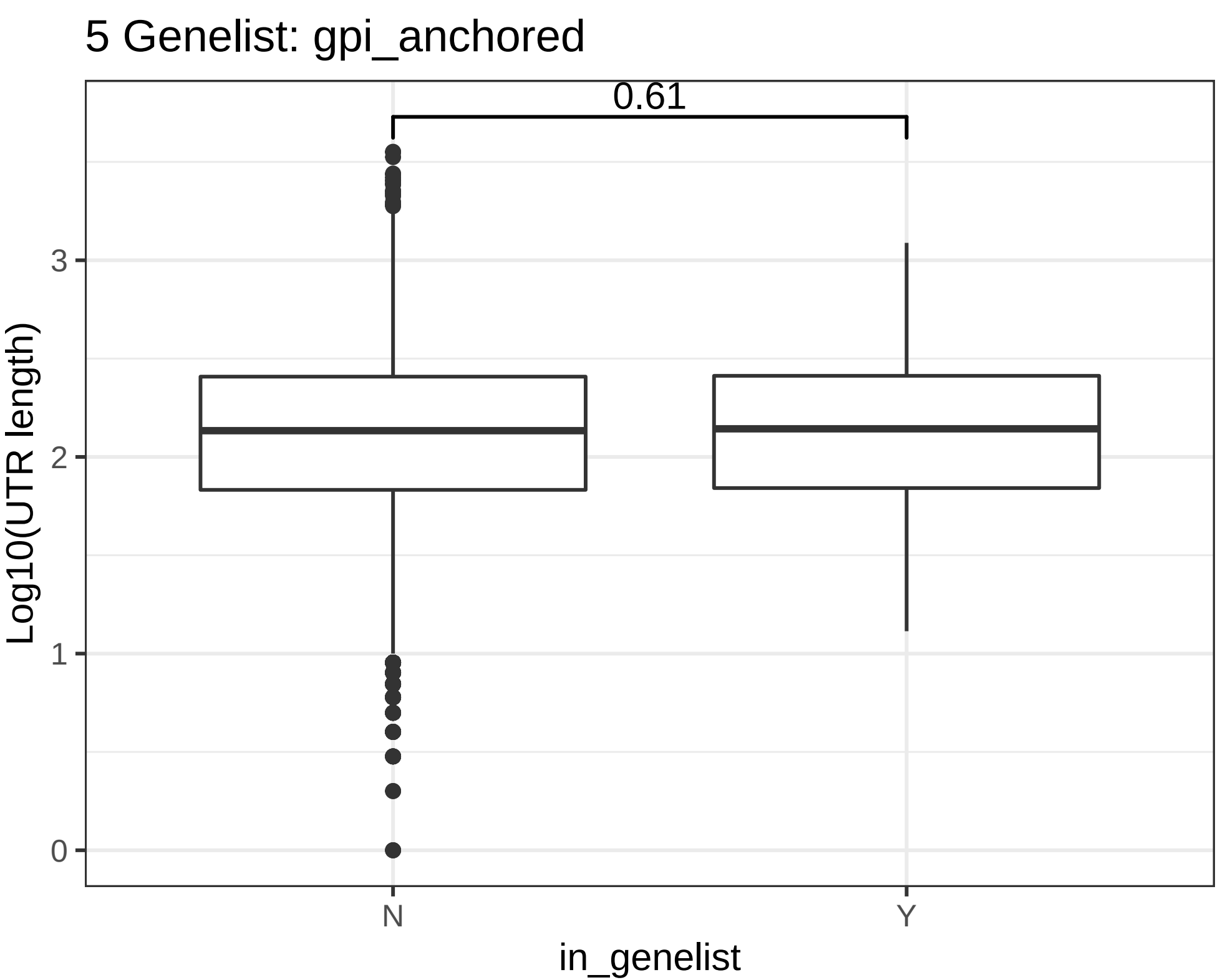

5 Genelist: gpcr_uniprot
Observed / Expected
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

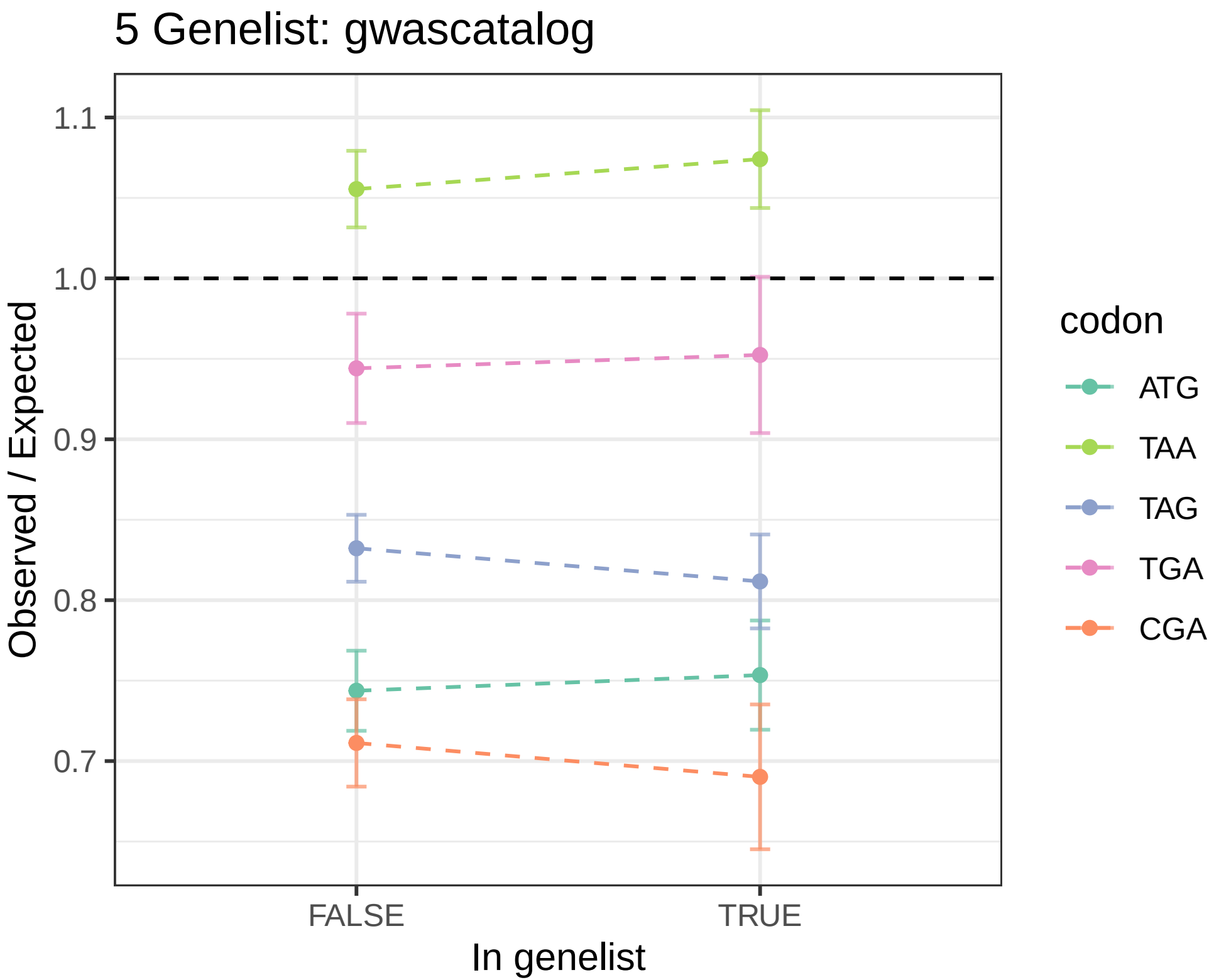

5 Genelist: gpcr_uniprot
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

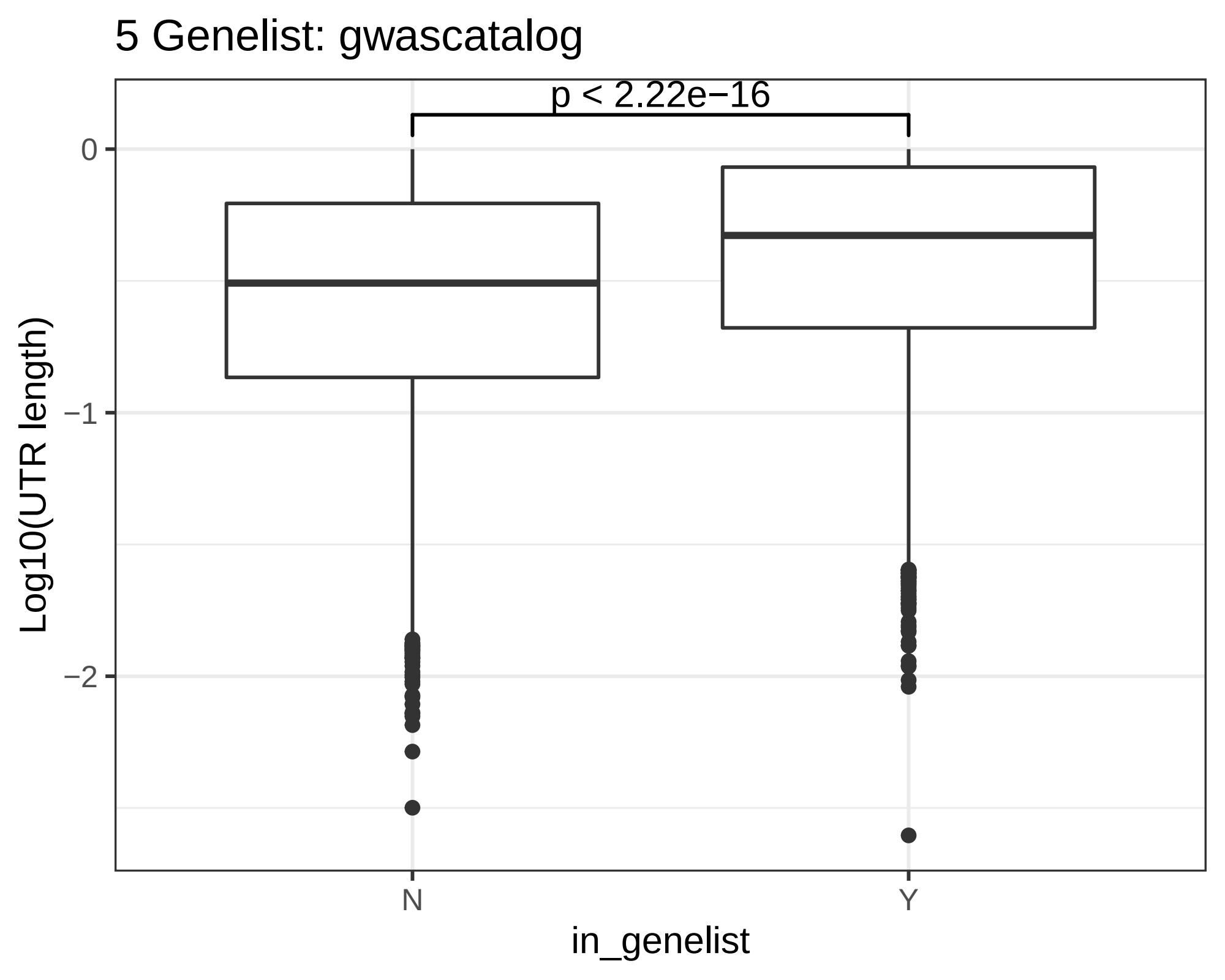

5 Genelist: gpcr_uniprot
0.13
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

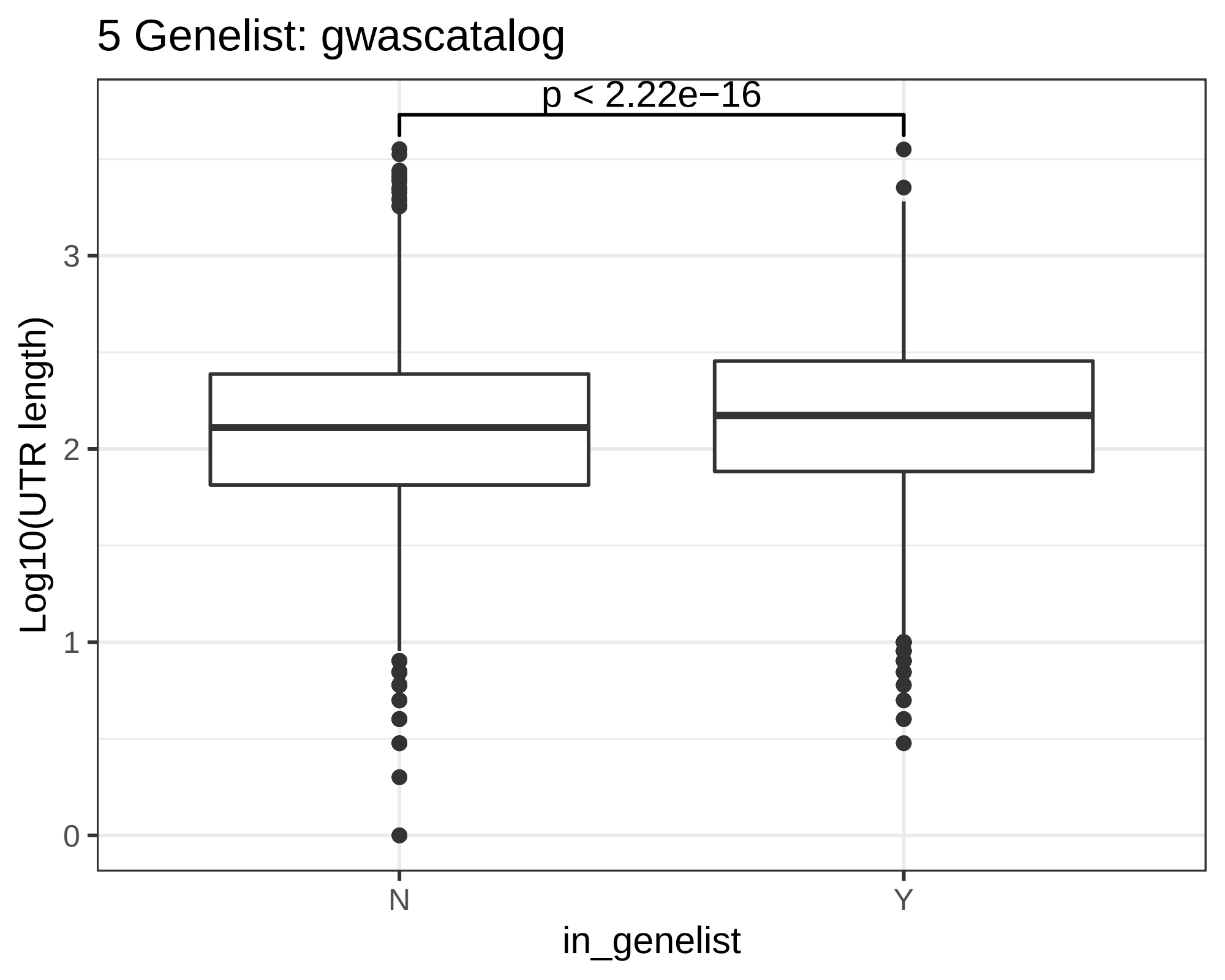

5 Genelist: gpi_anchored
Observed / Expected
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

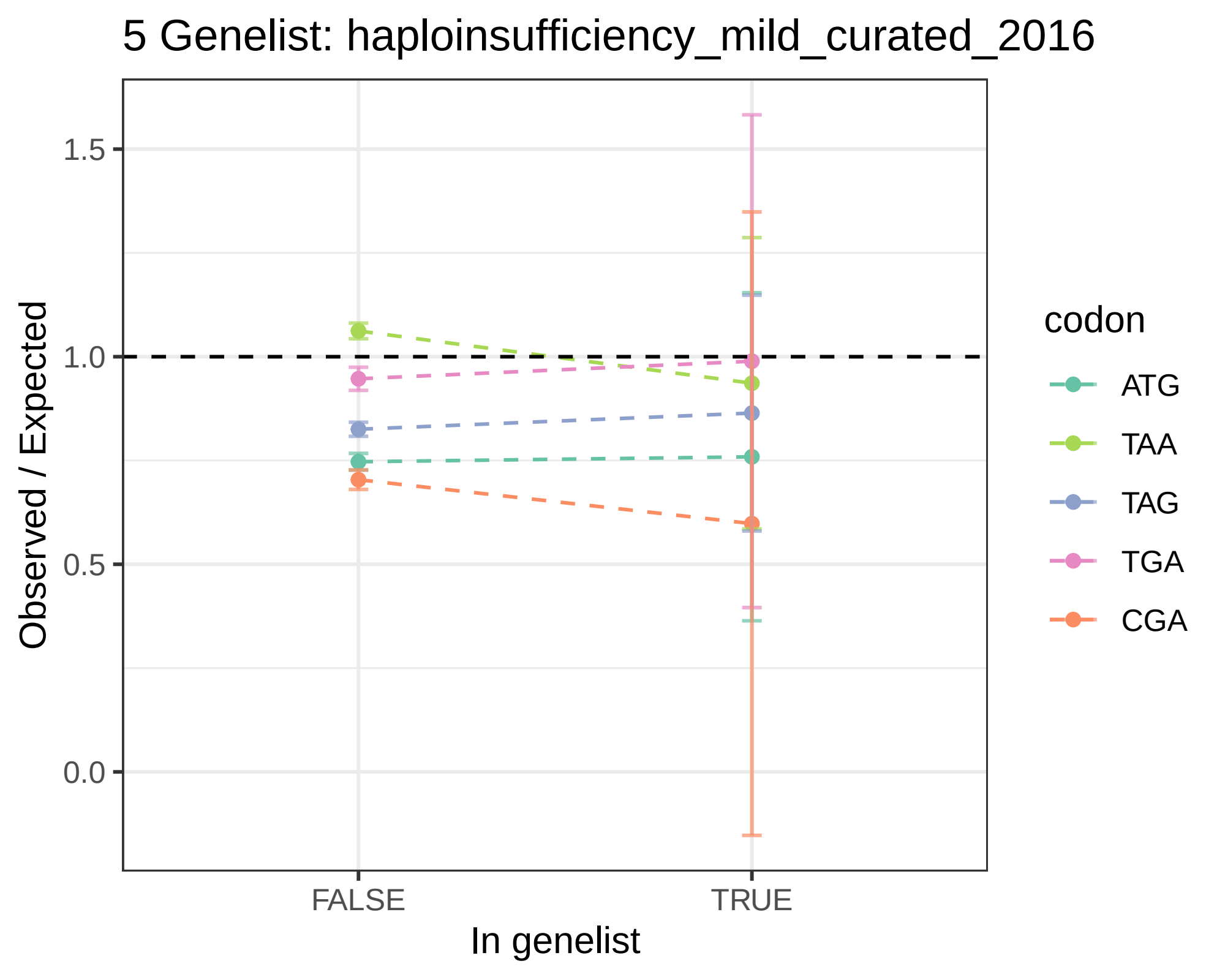

5 Genelist: gpi_anchored
3.8e−05
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

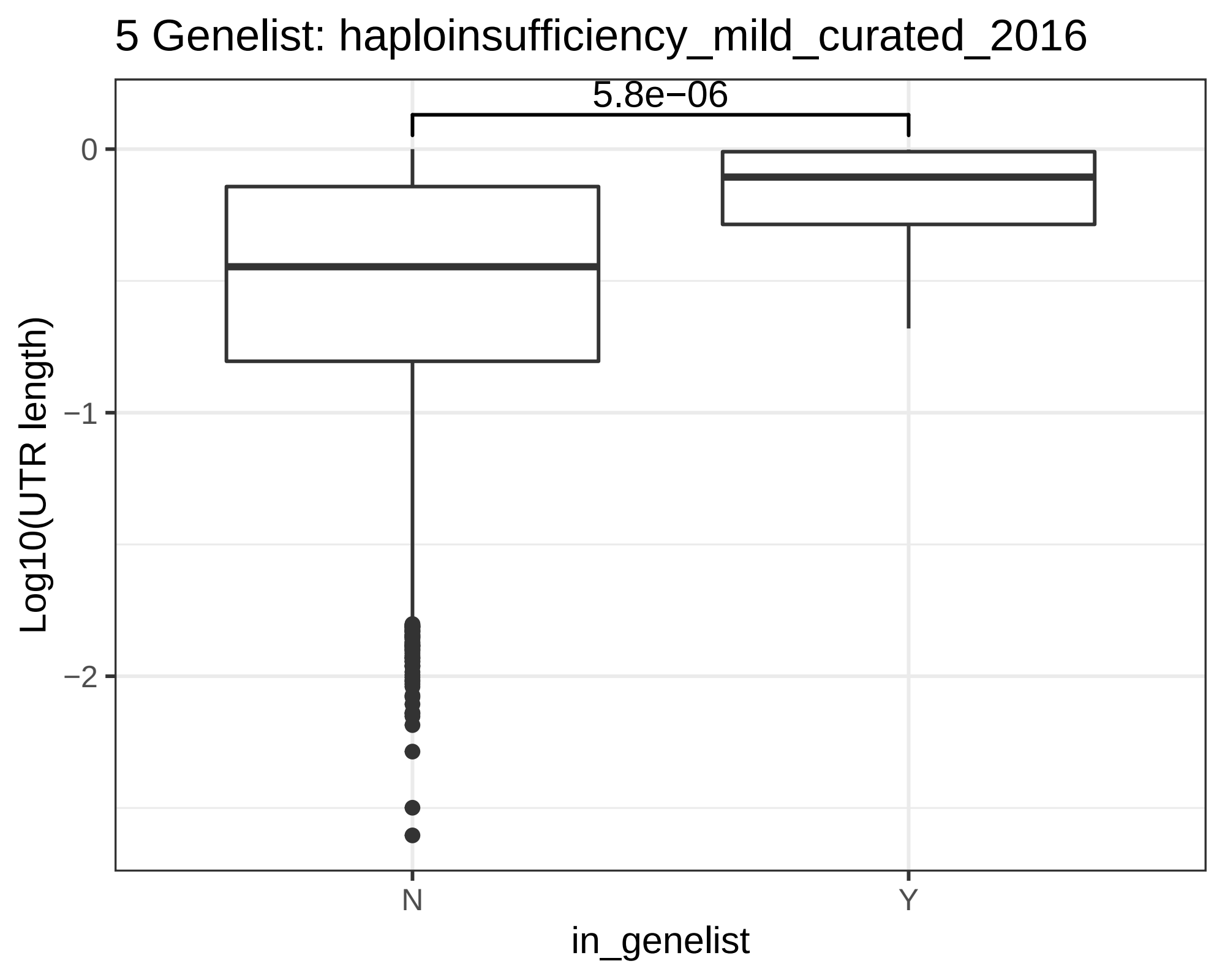

5 Genelist: gpi_anchored
0.61
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

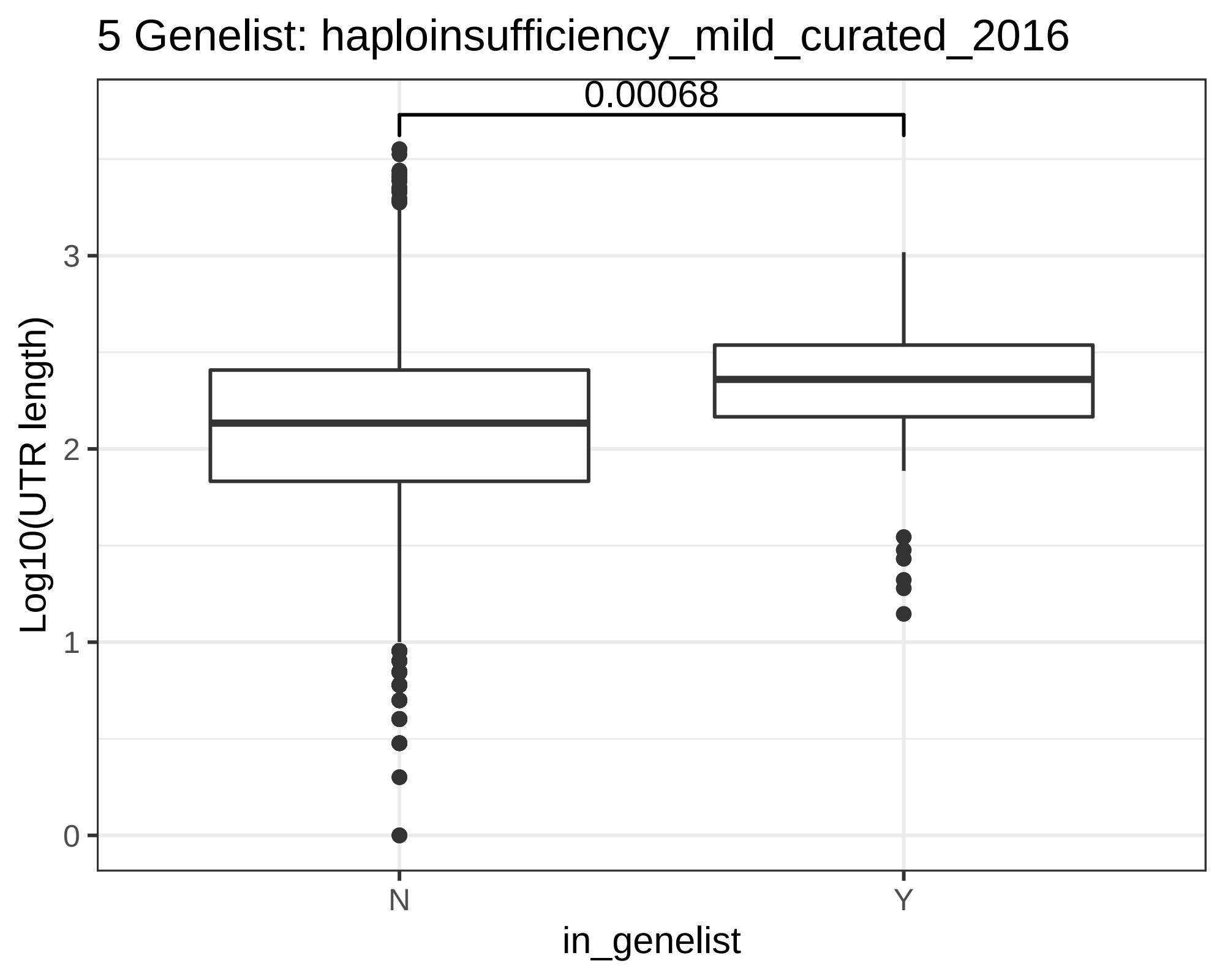

5 Genelist: gwascatalog
Observed / Expected
1.1
1.0
0.9
0.8
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

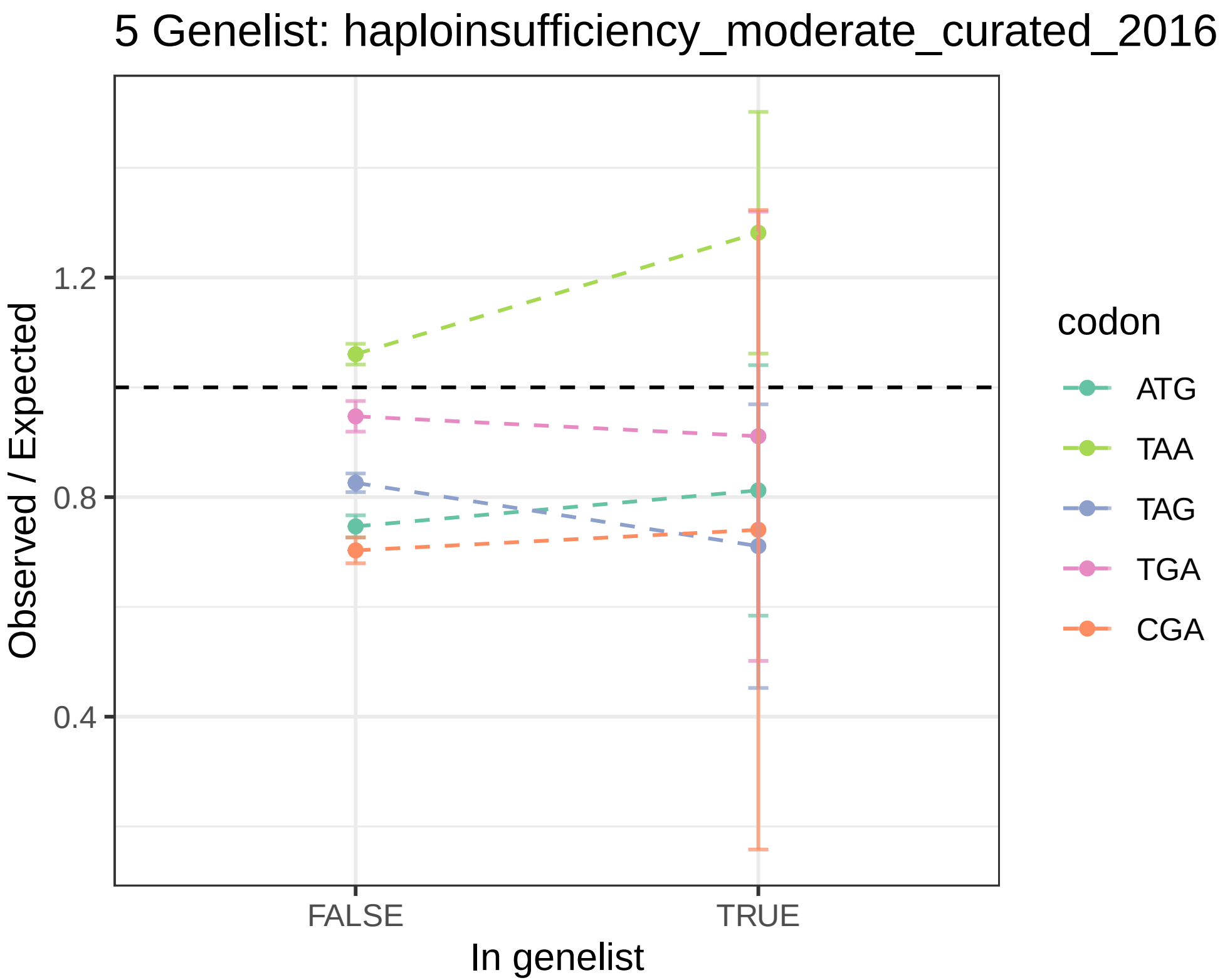

5 Genelist: gwascatalog
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

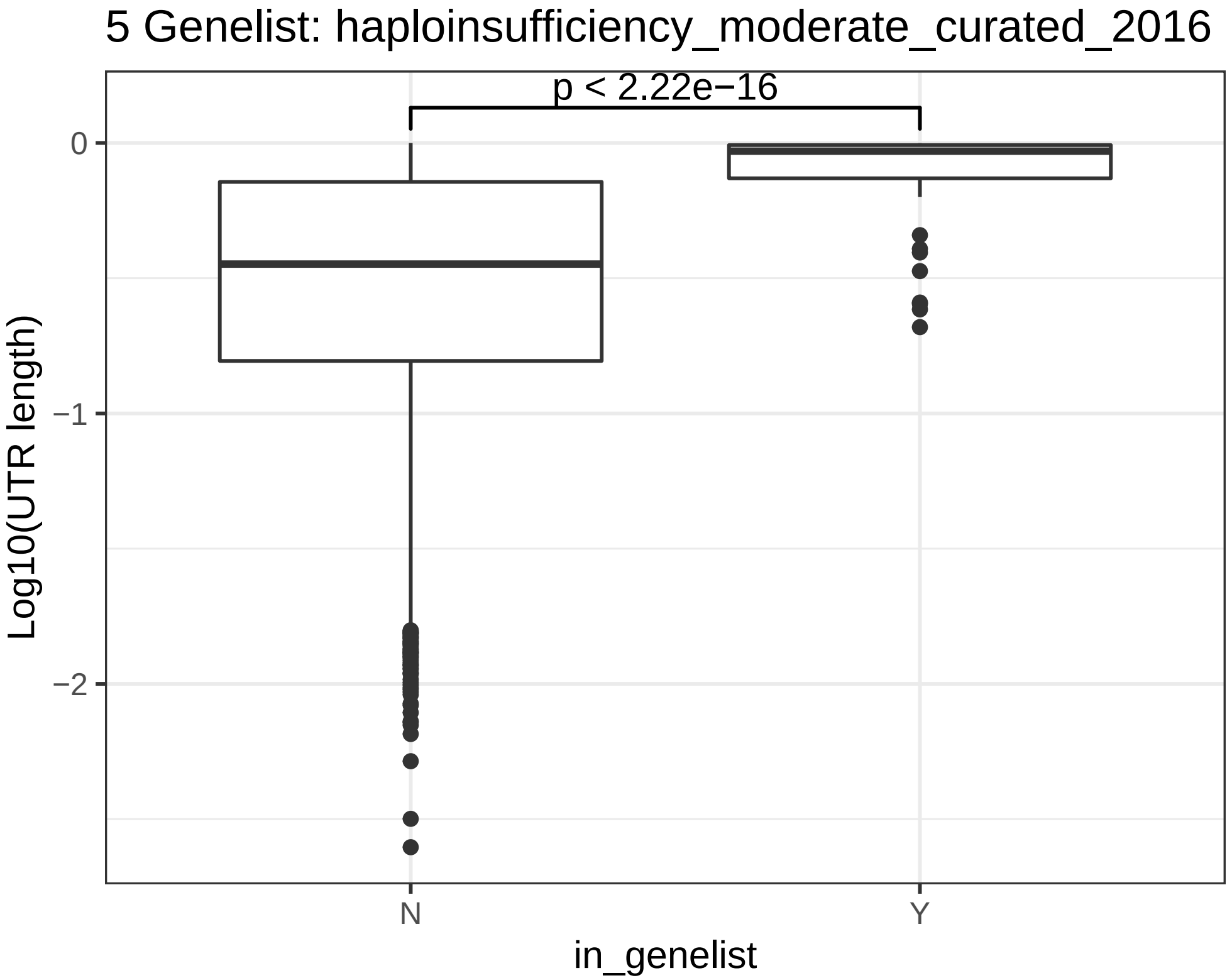

5 Genelist: gwascatalog
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

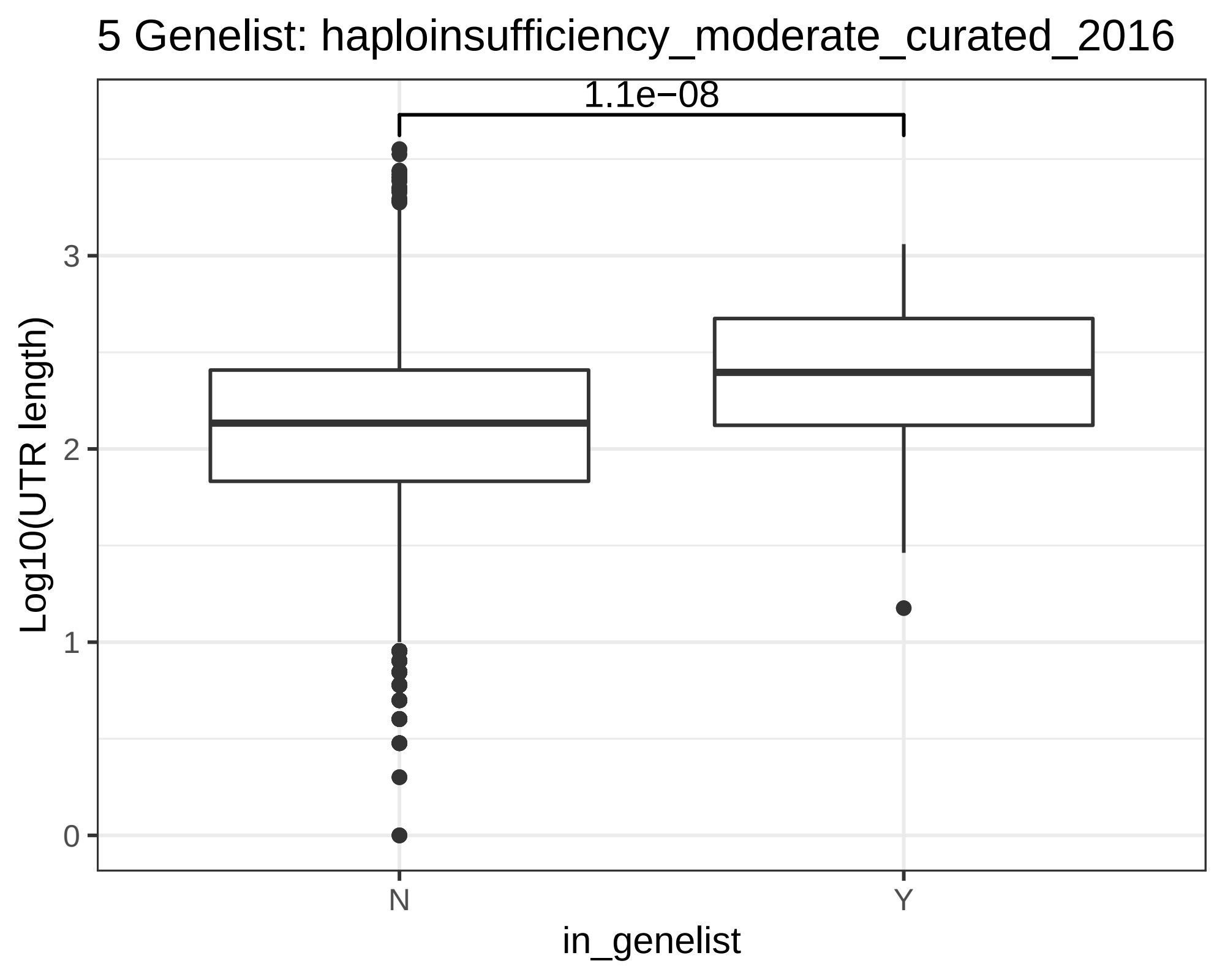

5 Genelist: haploinsufficiency_mild_curated_2016
Observed / Expected
1.5
1.0
0.5
0.0
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

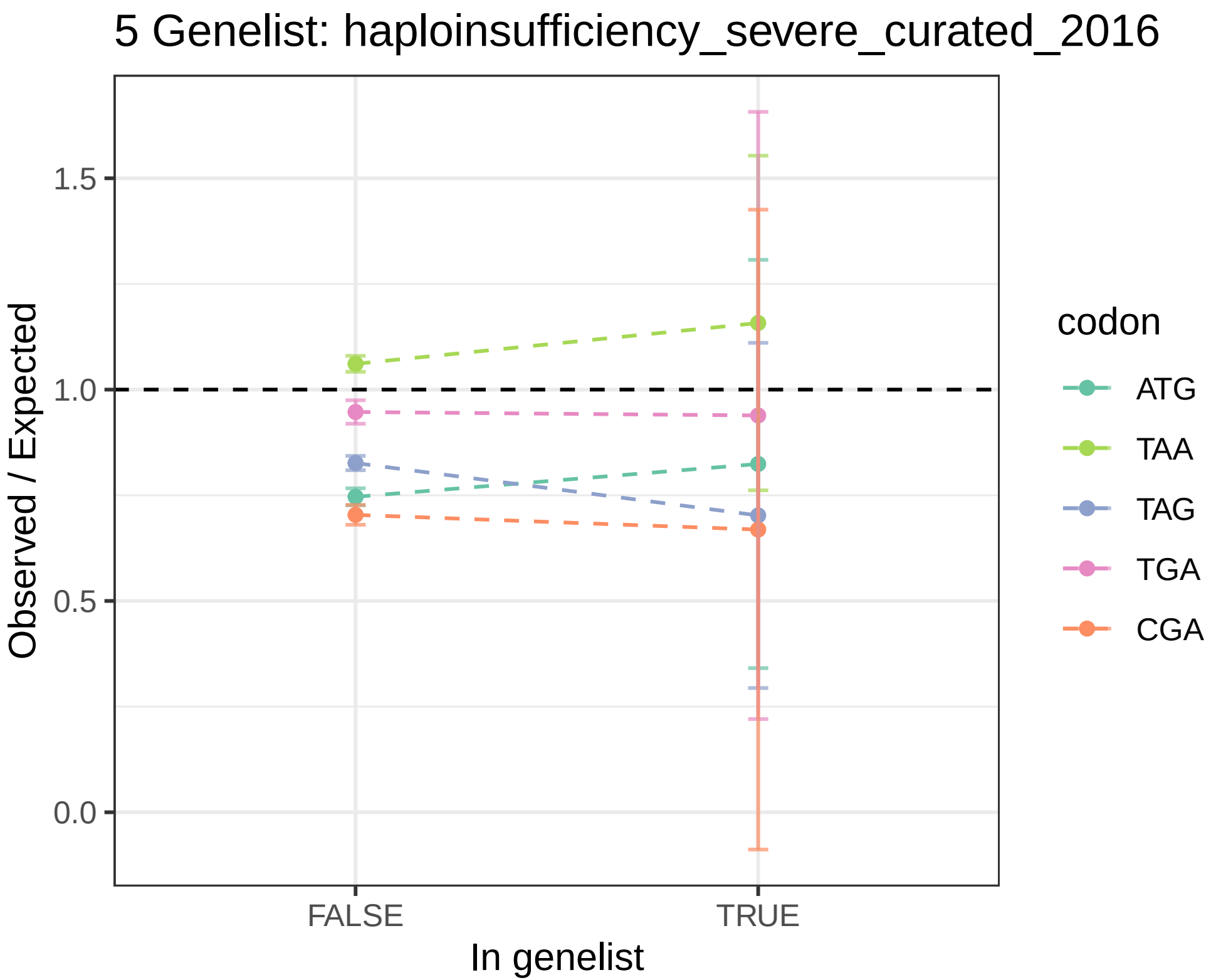

5 Genelist: haploinsufficiency_mild_curated_2016
5.8e−06
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

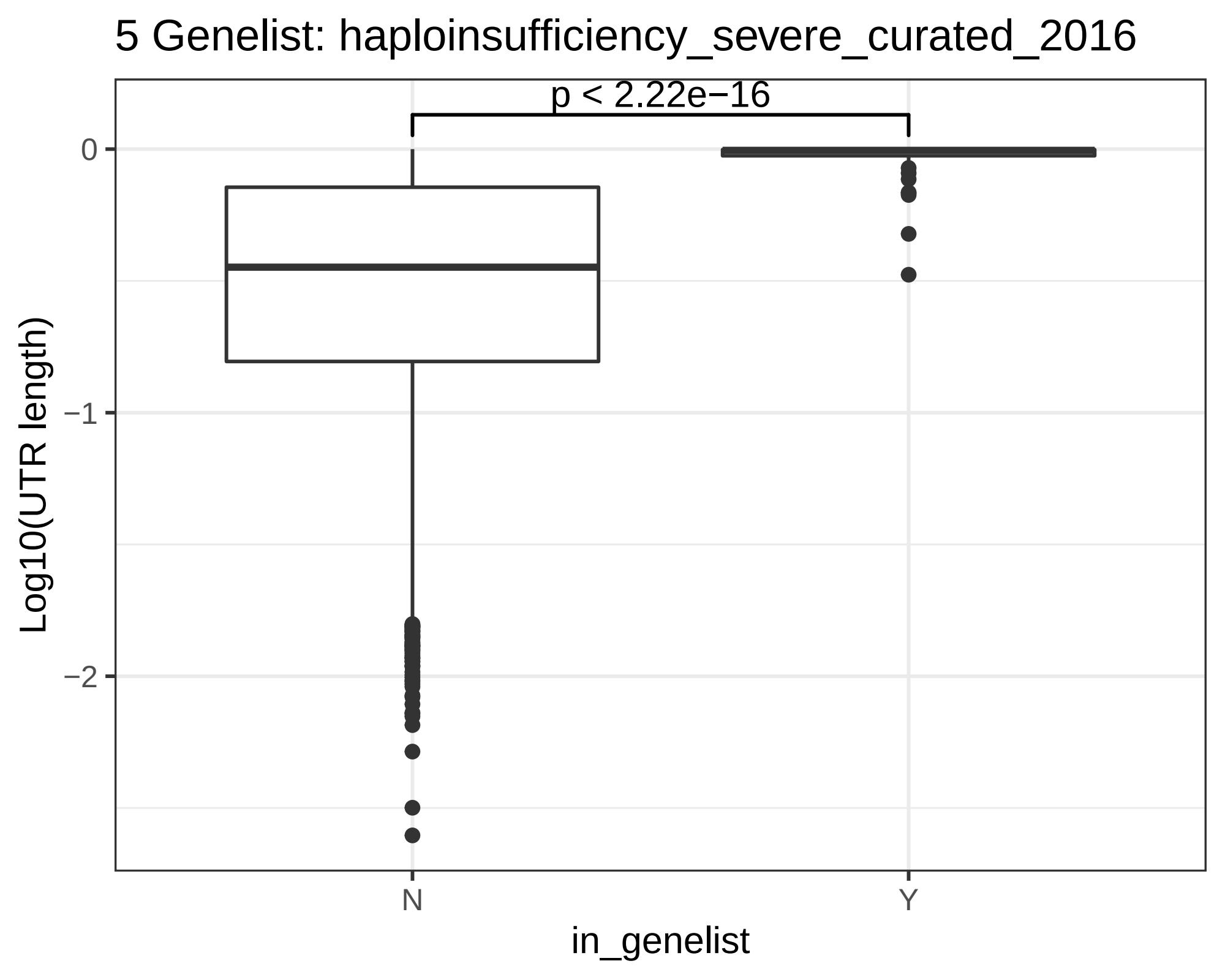

5 Genelist: haploinsufficiency_mild_curated_2016
0.00068
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

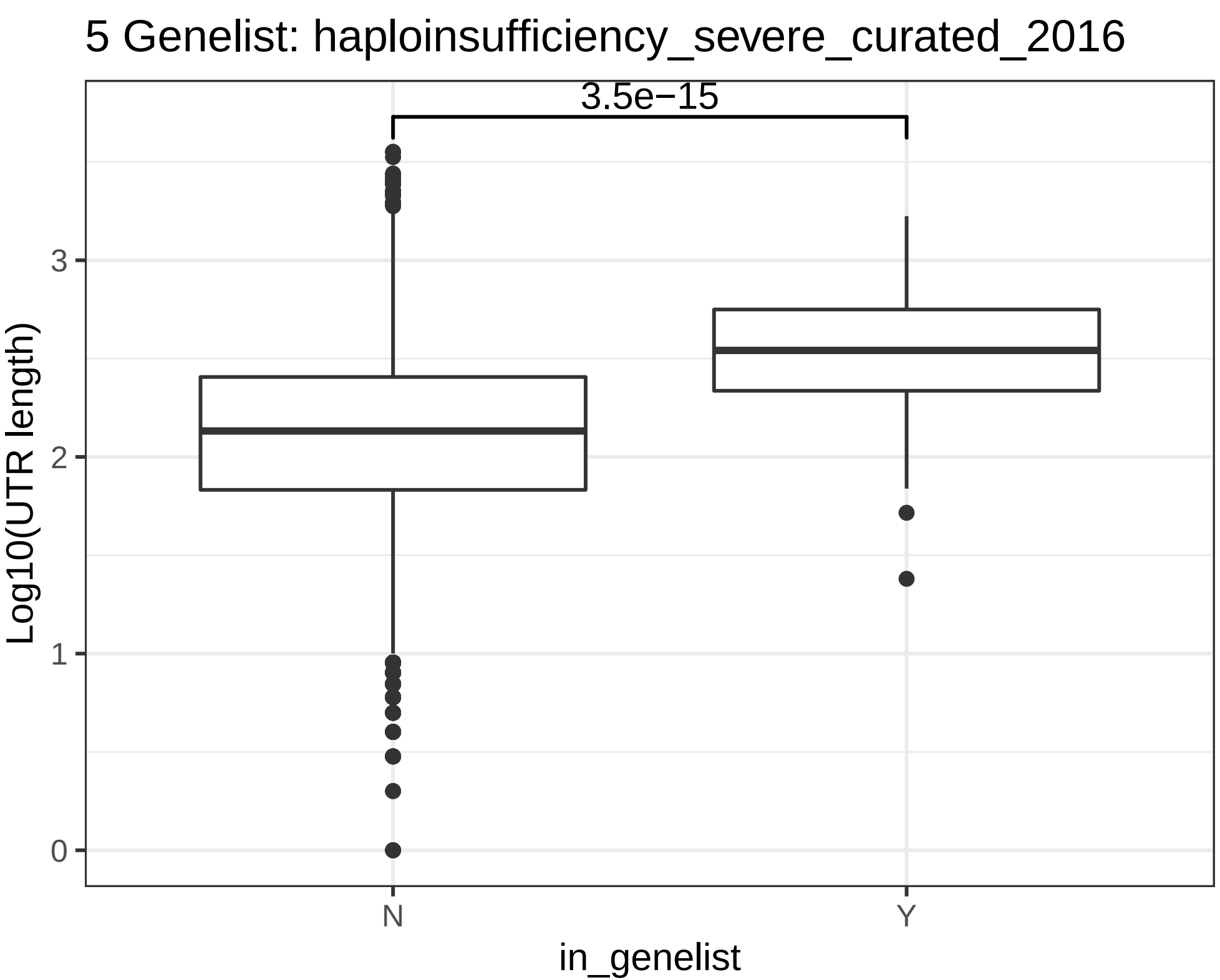

5 Genelist: haploinsufficiency_moderate_curated_2016
Observed / Expected
1.2
0.8
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

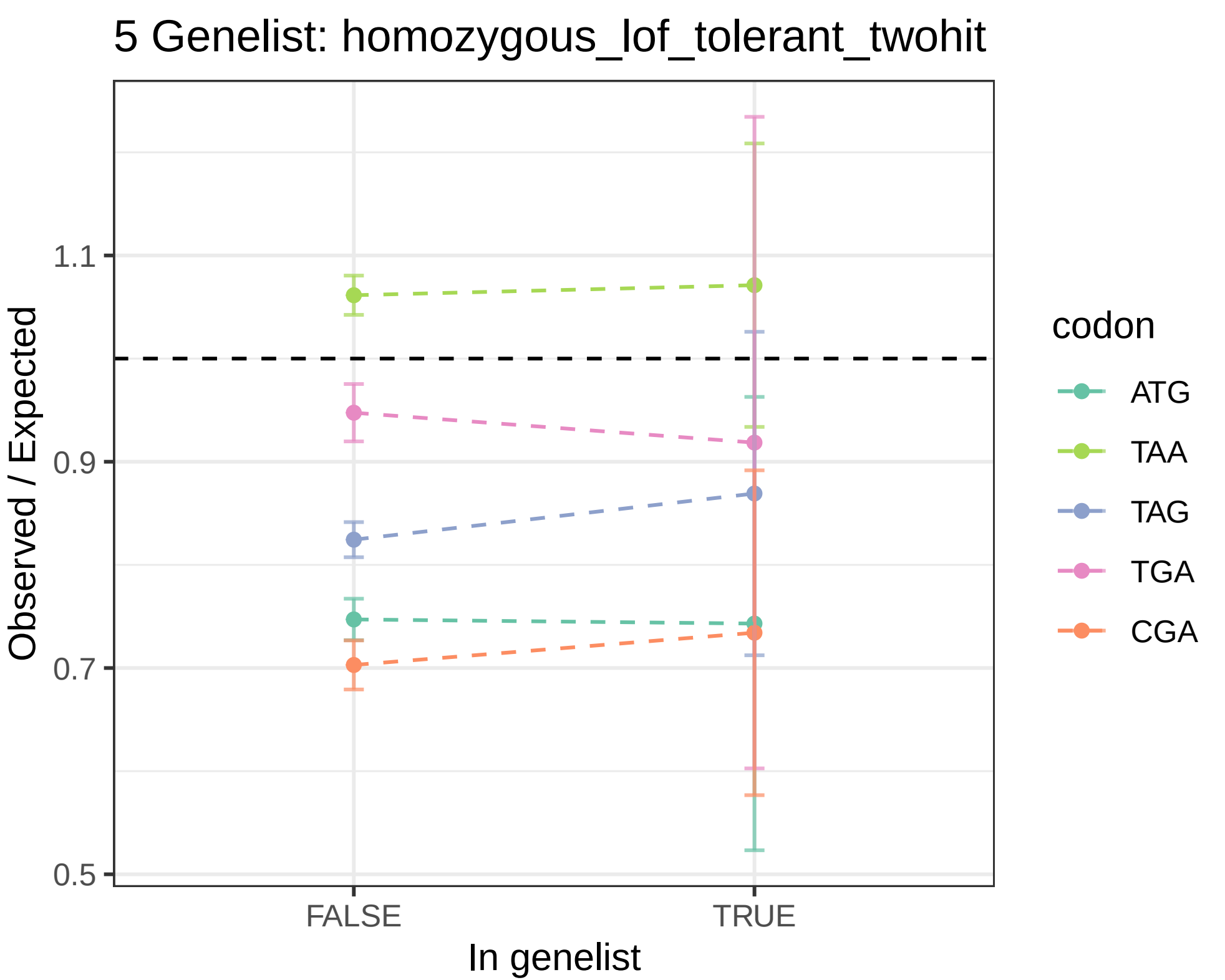

5 Genelist: haploinsufficiency_moderate_curated_2016
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

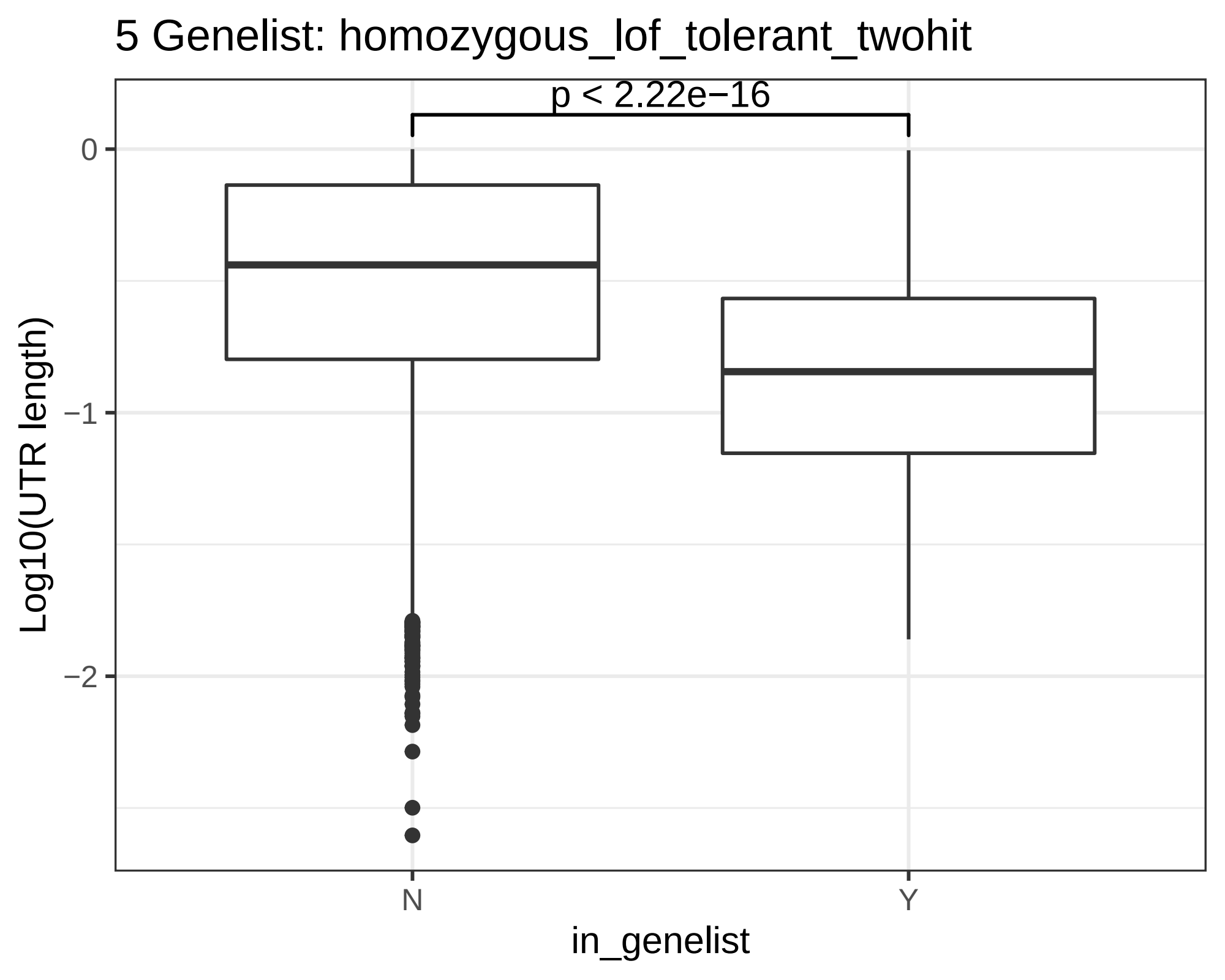

5 Genelist: haploinsufficiency_moderate_curated_2016
1.1e−08
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

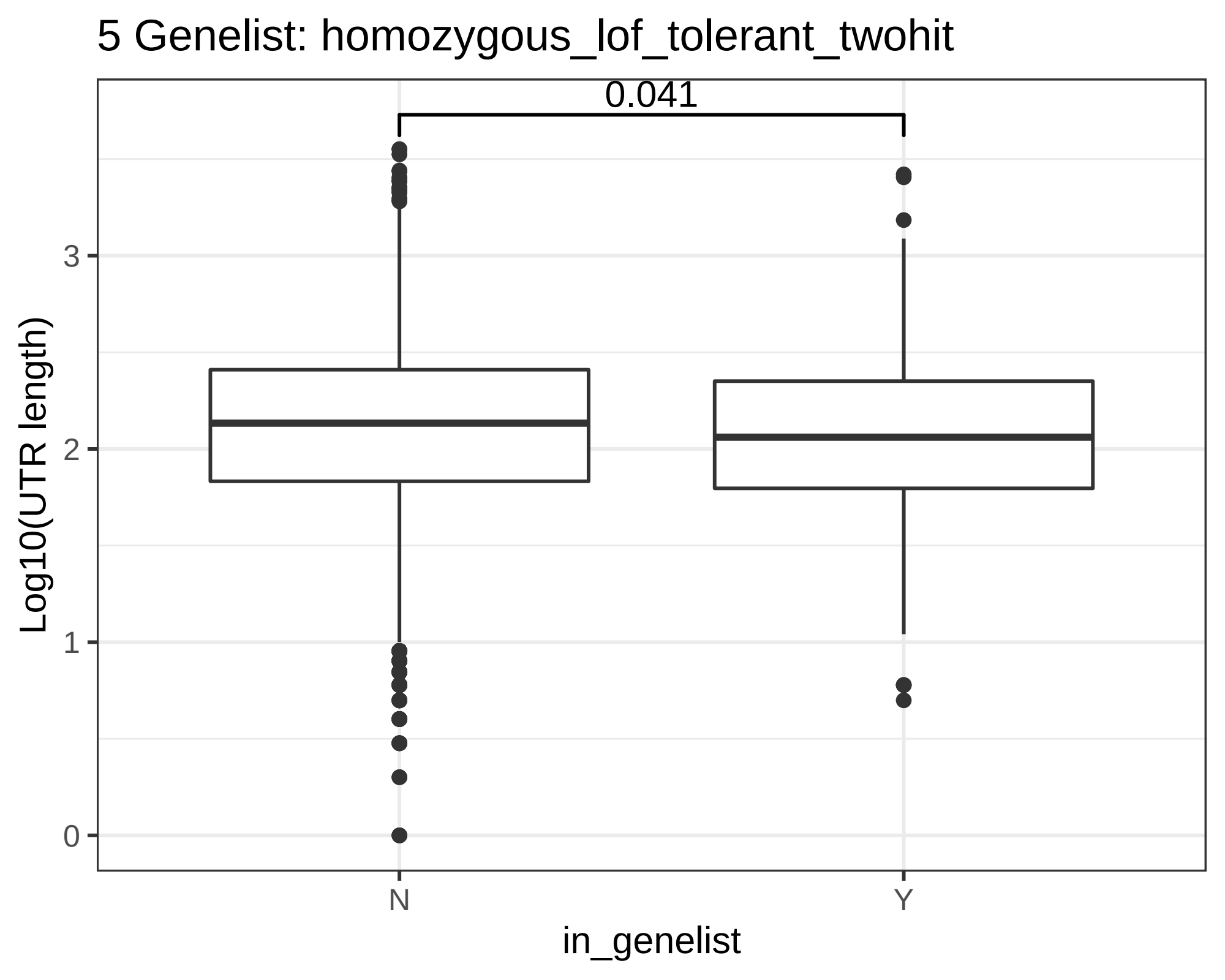

5 Genelist: haploinsufficiency_severe_curated_2016
Observed / Expected
1.5
1.0
0.5
0.0
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

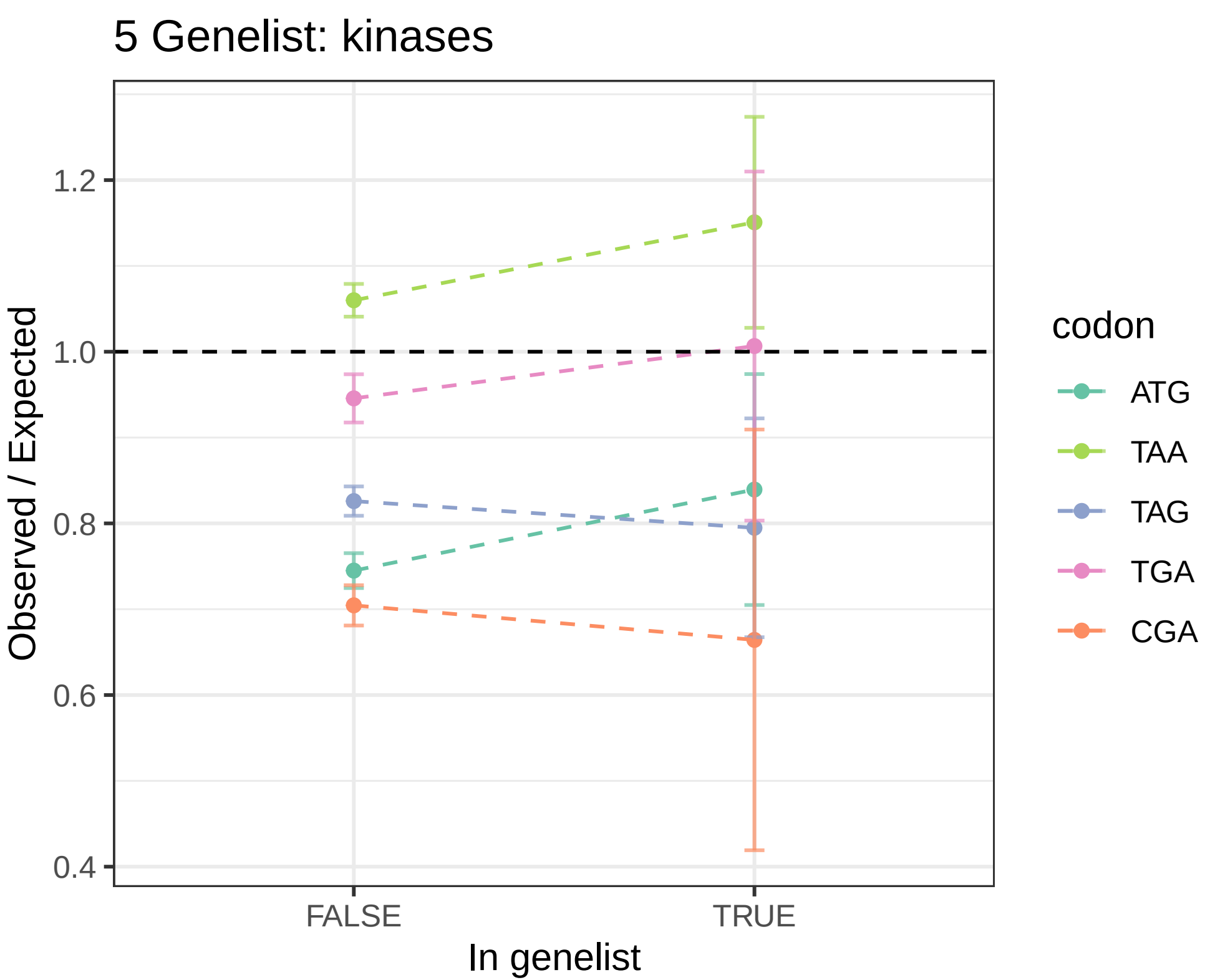

5 Genelist: haploinsufficiency_severe_curated_2016
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

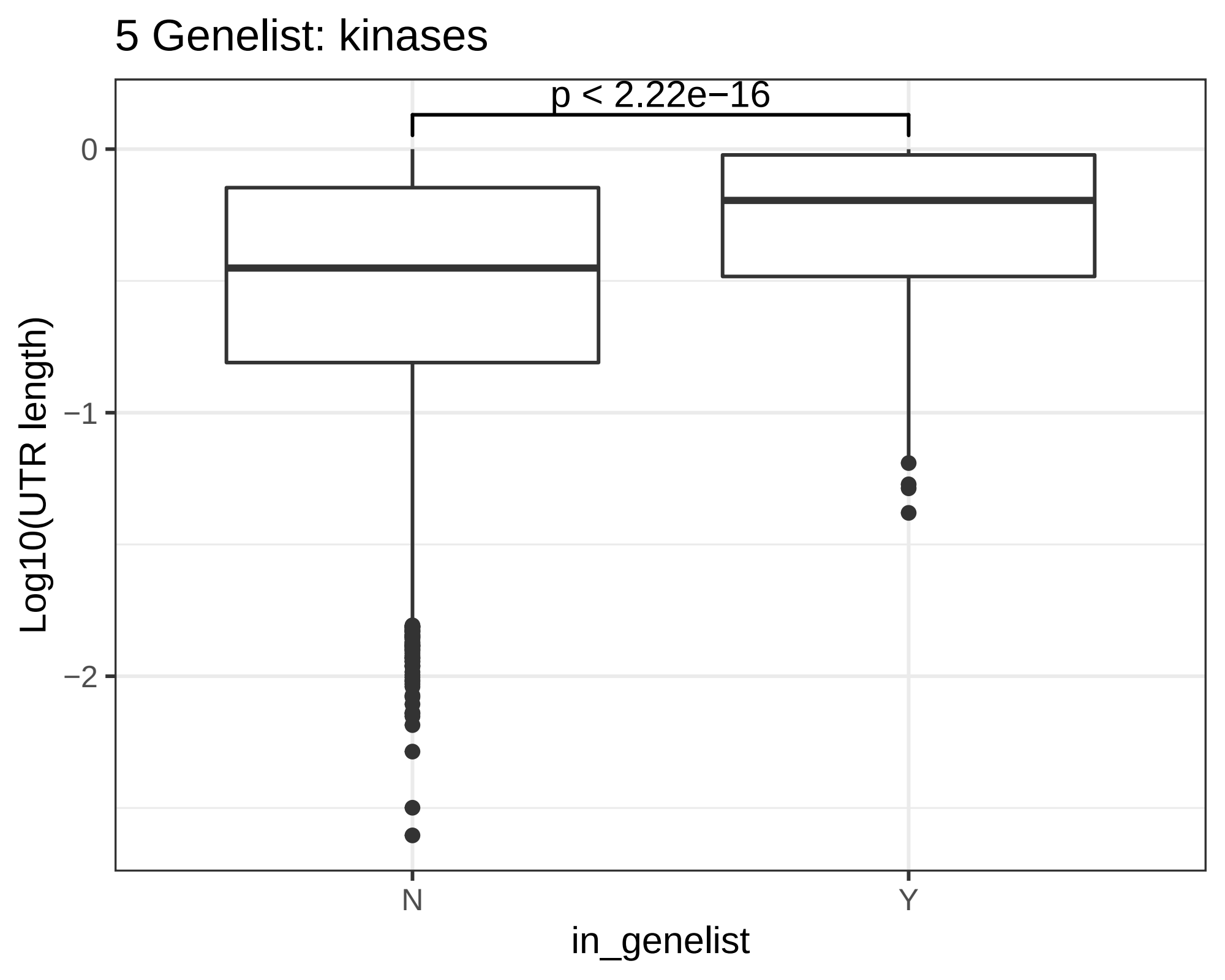

5 Genelist: haploinsufficiency_severe_curated_2016
3.5e−15
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

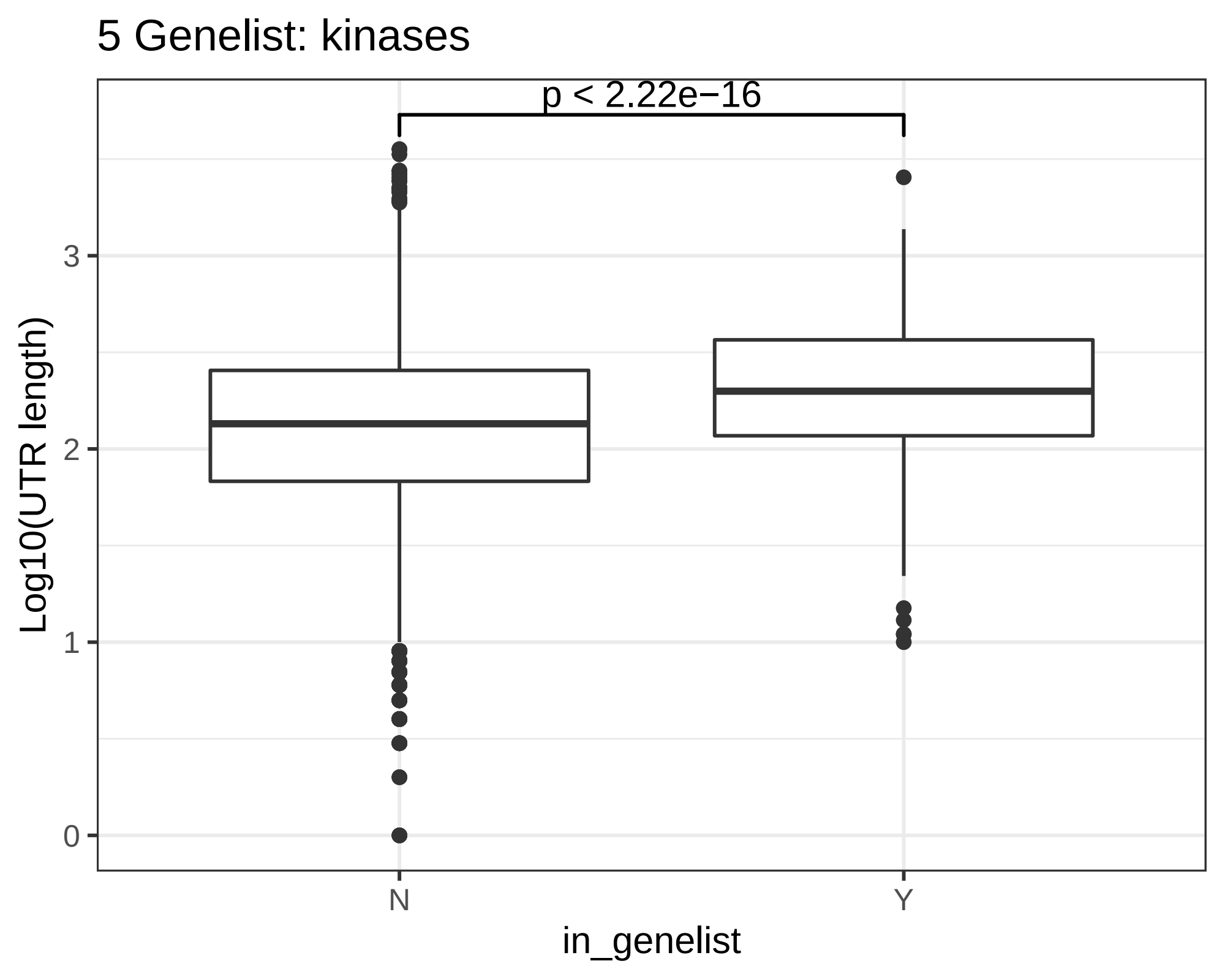

5 Genelist: homozygous_lof_tolerant_twohit
Observed / Expected
1.1
0.9
0.7
0.5
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA


5 Genelist: homozygous_lof_tolerant_twohit
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

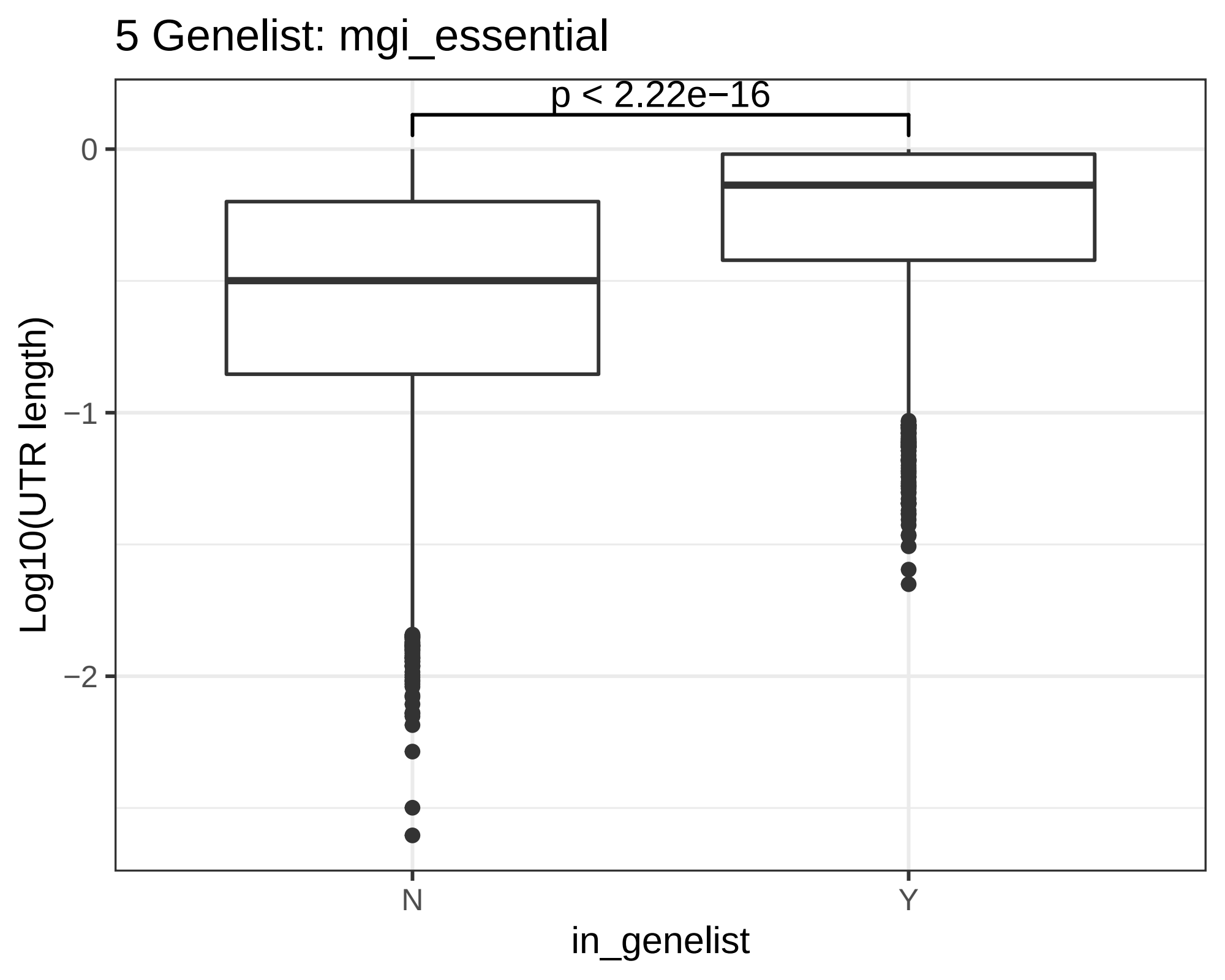

5 Genelist: homozygous_lof_tolerant_twohit
0.041
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

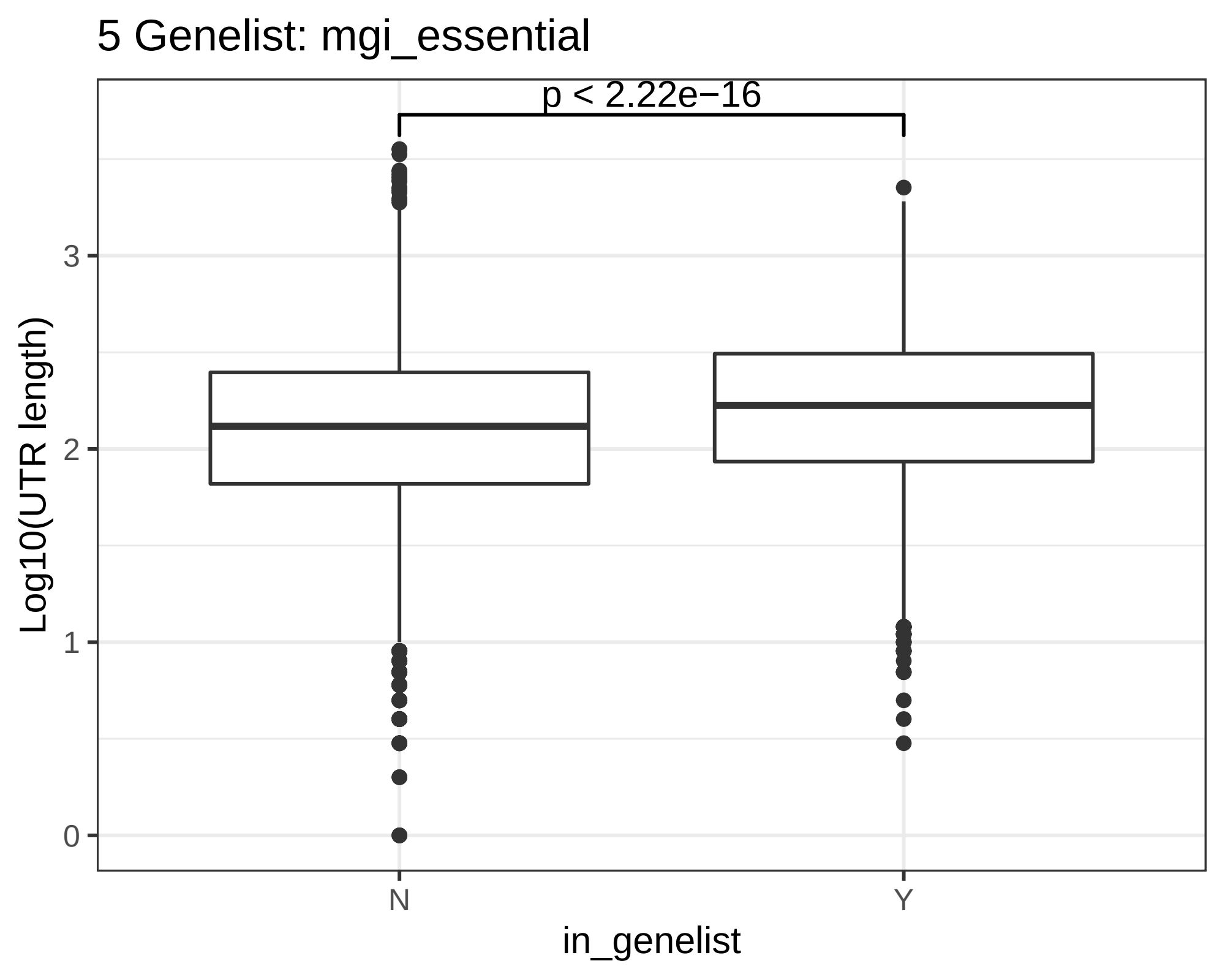

5 Genelist: kinases
Observed / Expected
1.2
1.0
0.8
0.6
0.4
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

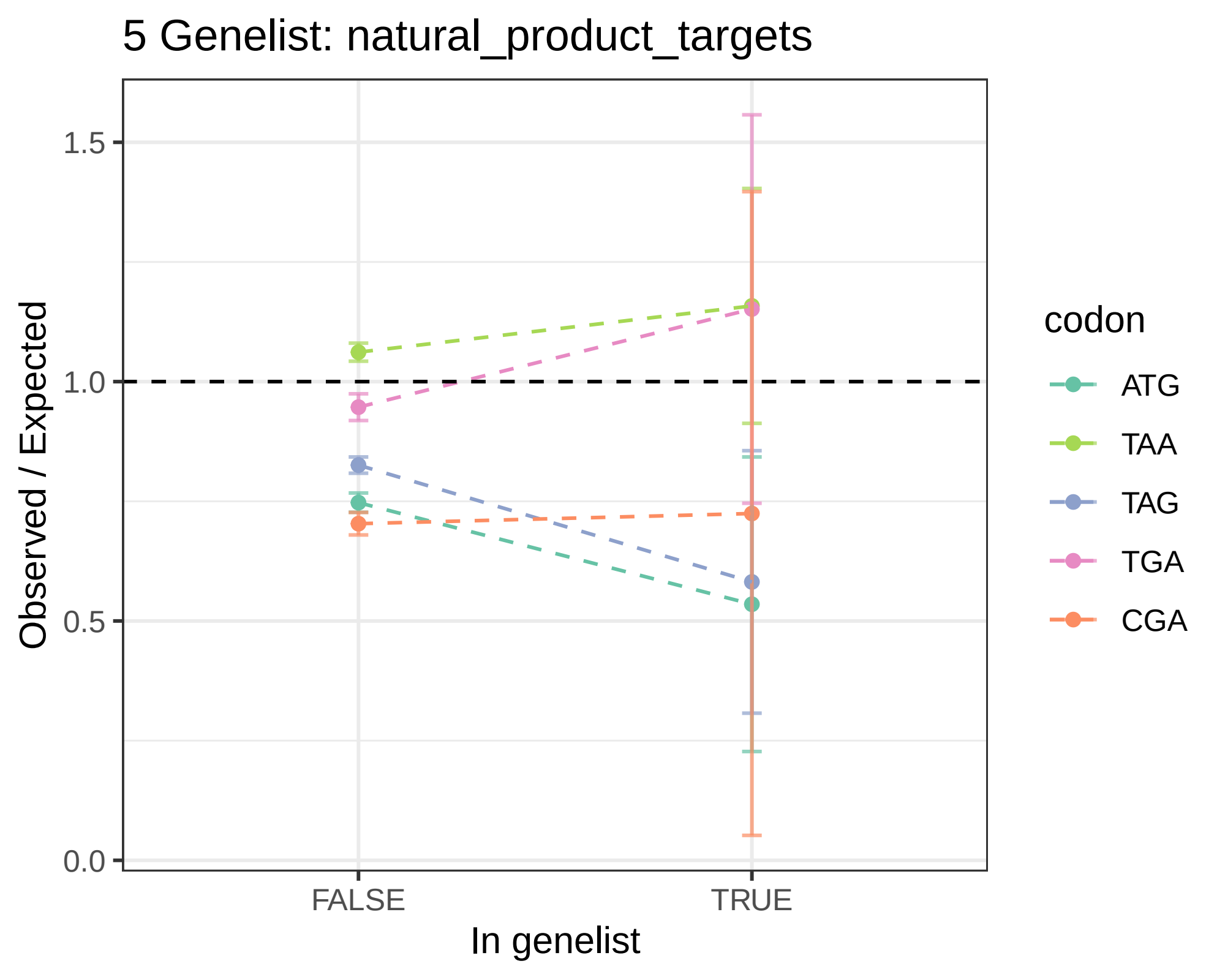

5 Genelist: kinases
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

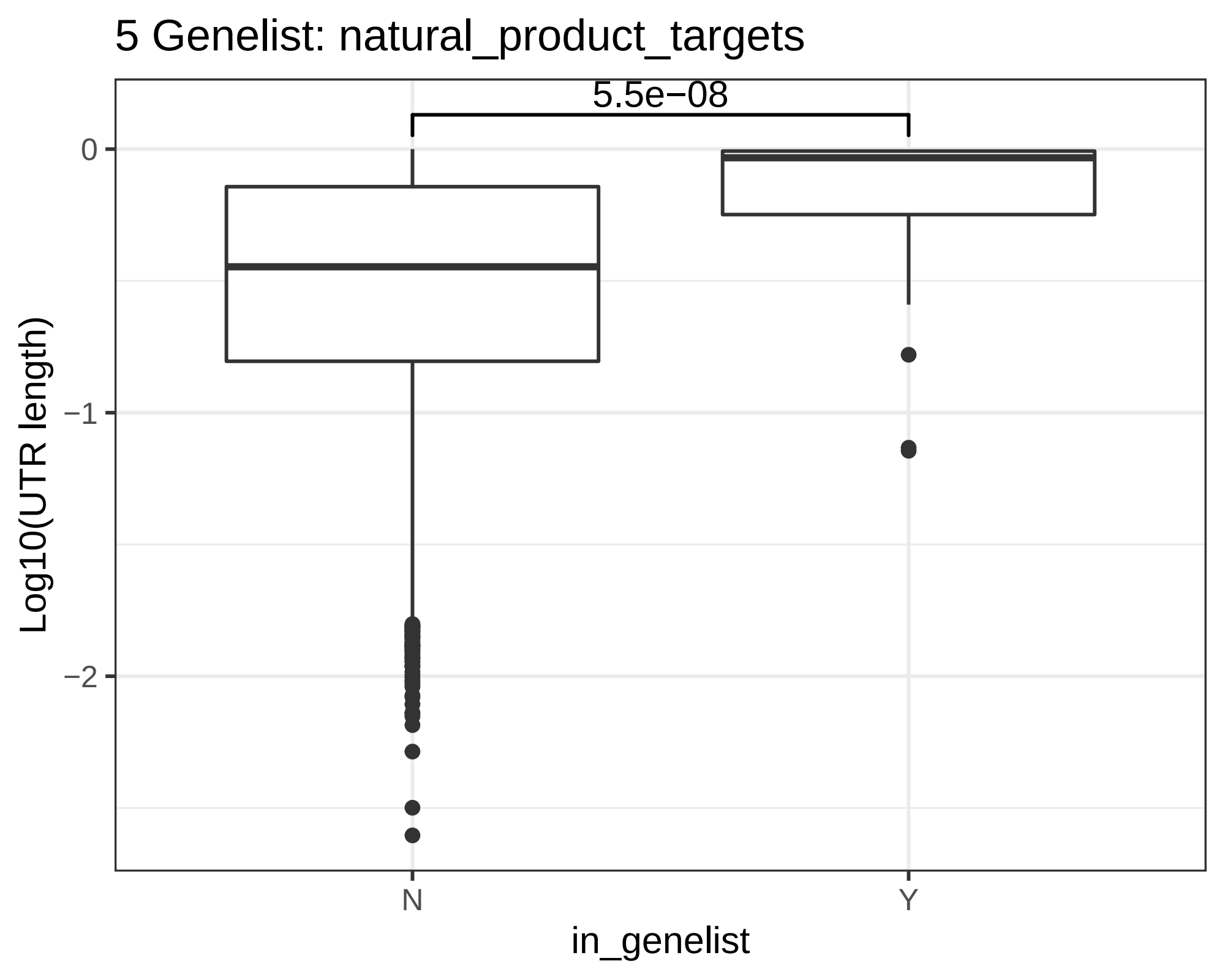

5 Genelist: kinases
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

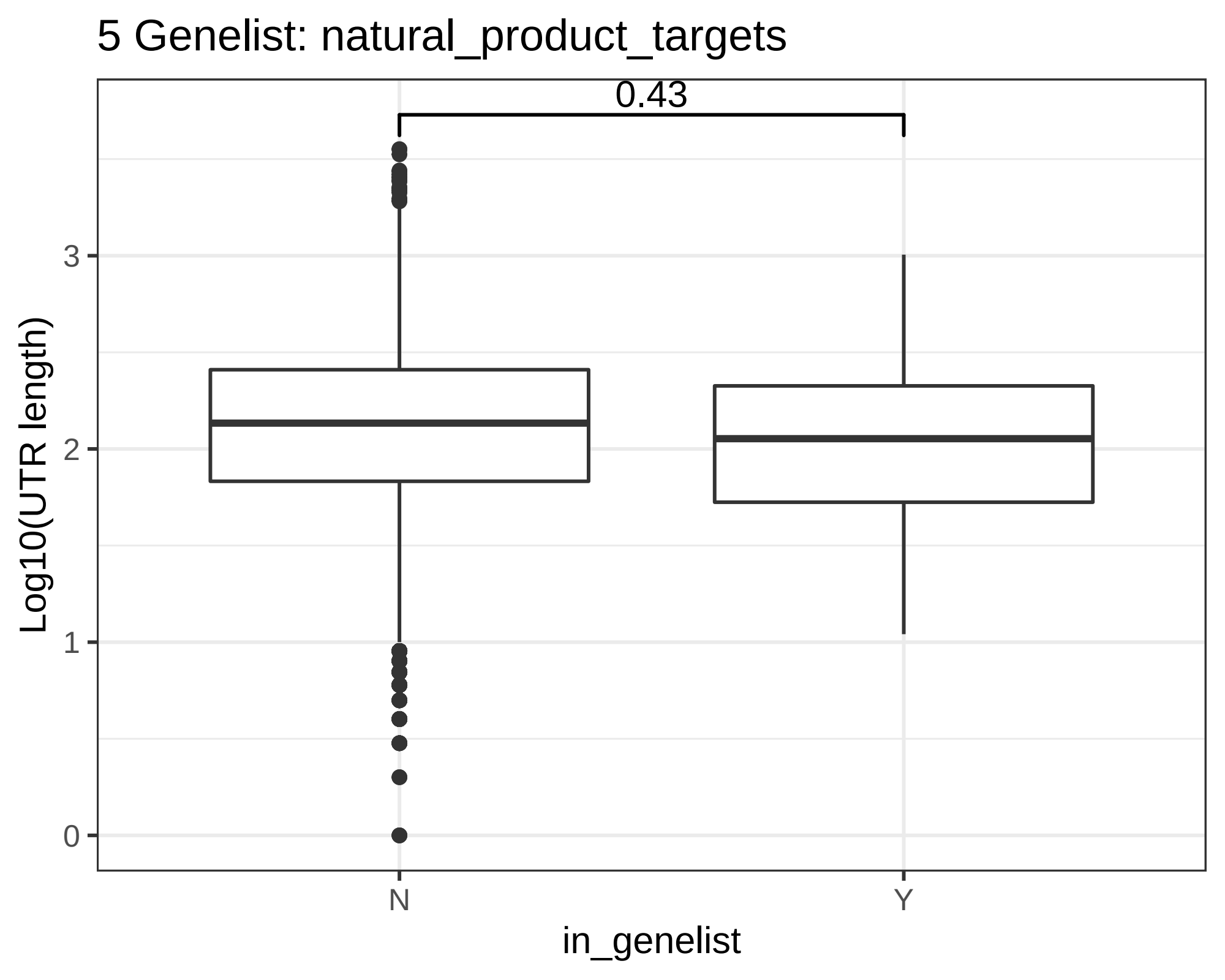
5 Genelist: mgi_essential
Observed / Expected
1.1
1.0
0.9
0.8
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

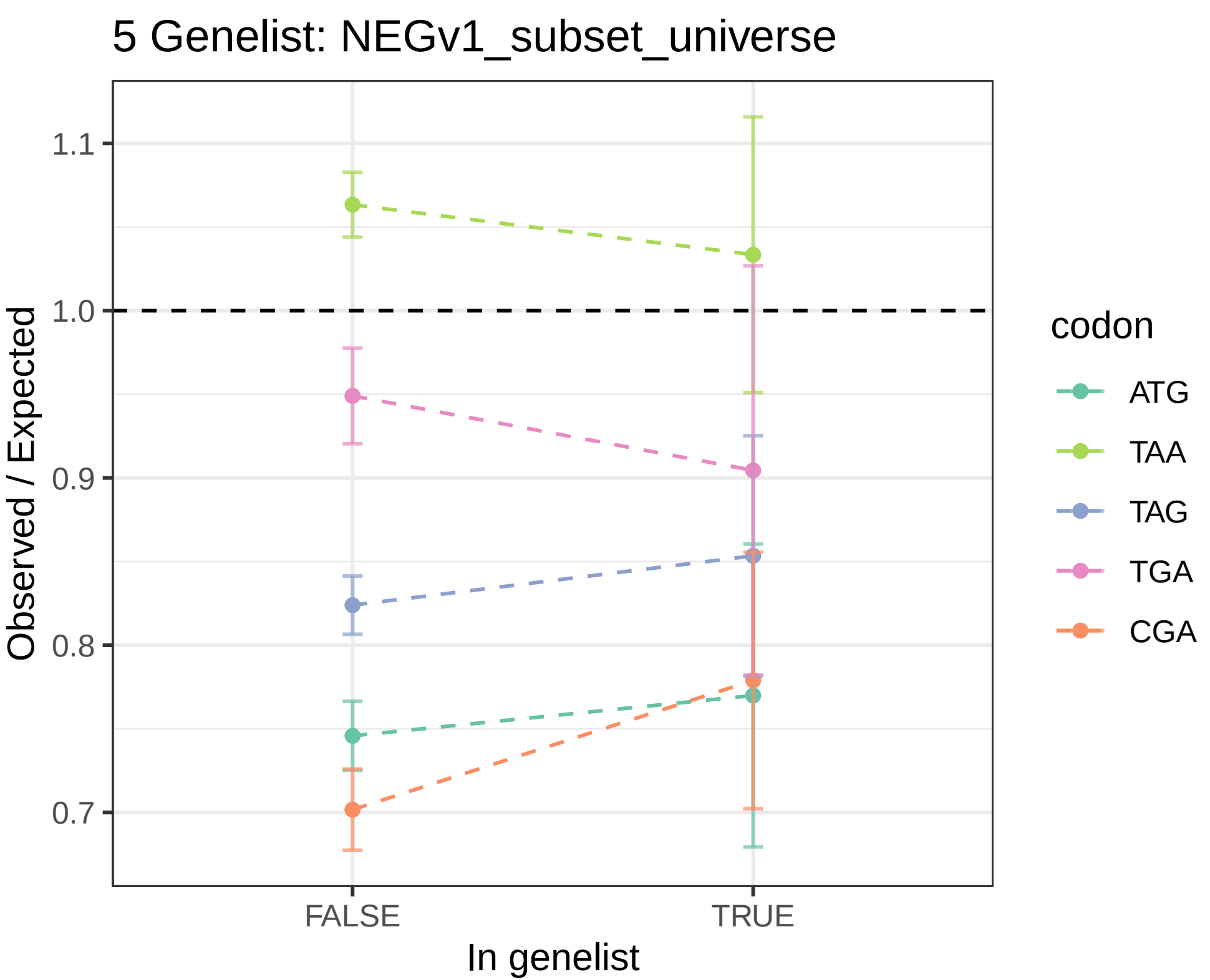

5 Genelist: mgi_essential
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

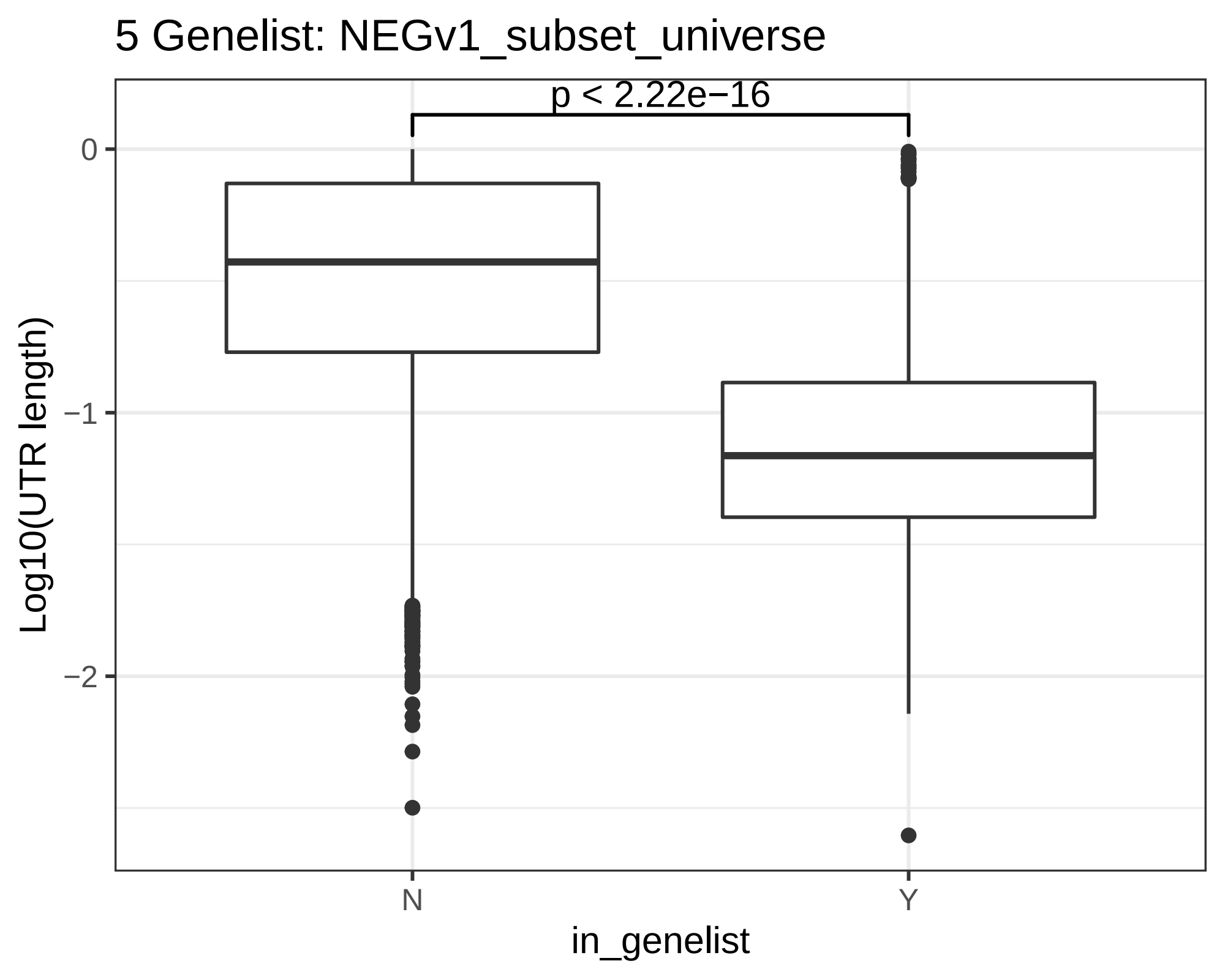

5 Genelist: mgi_essential
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

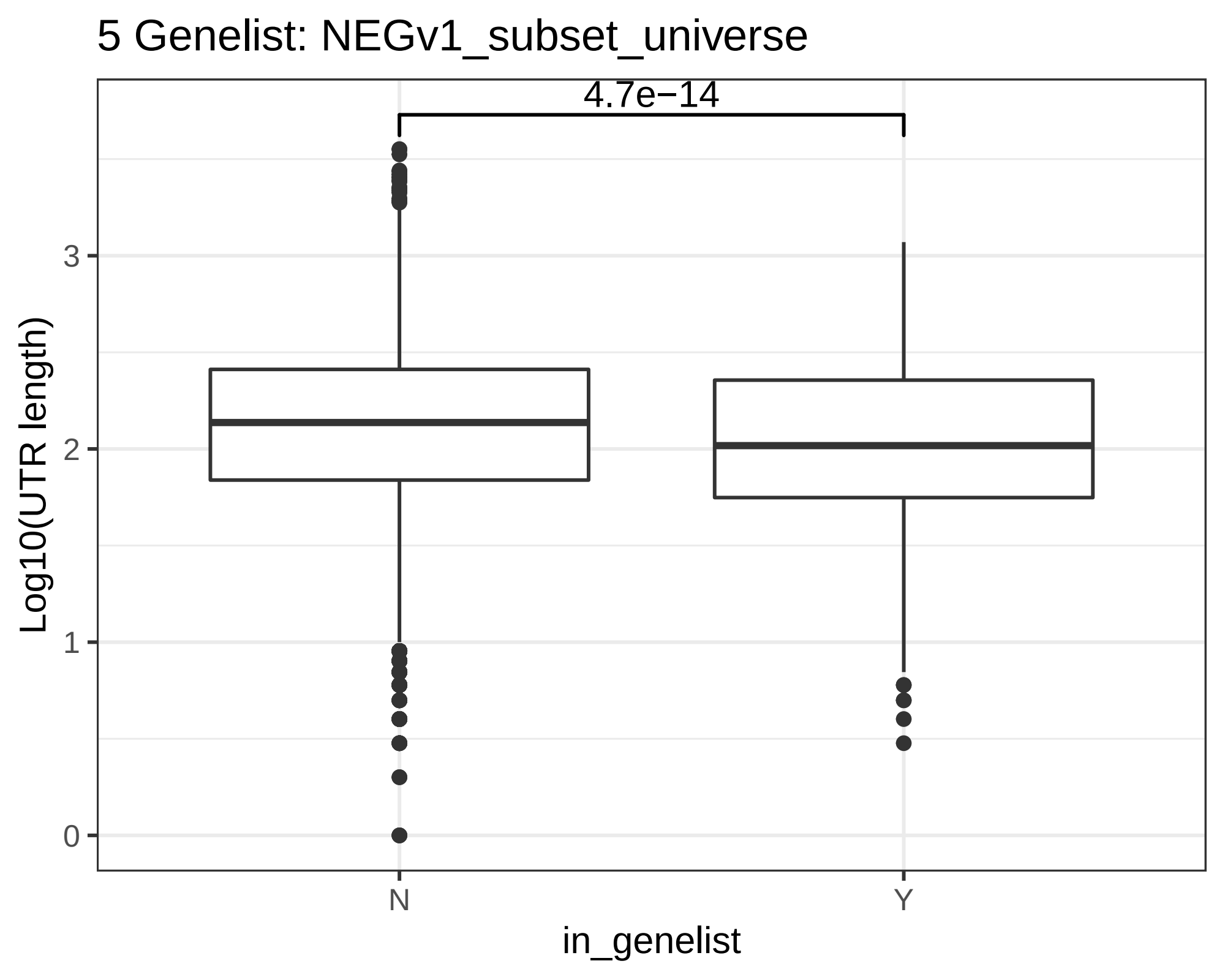

5 Genelist: natural_product_targets
Observed / Expected
1.5
1.0
0.5
0.0
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

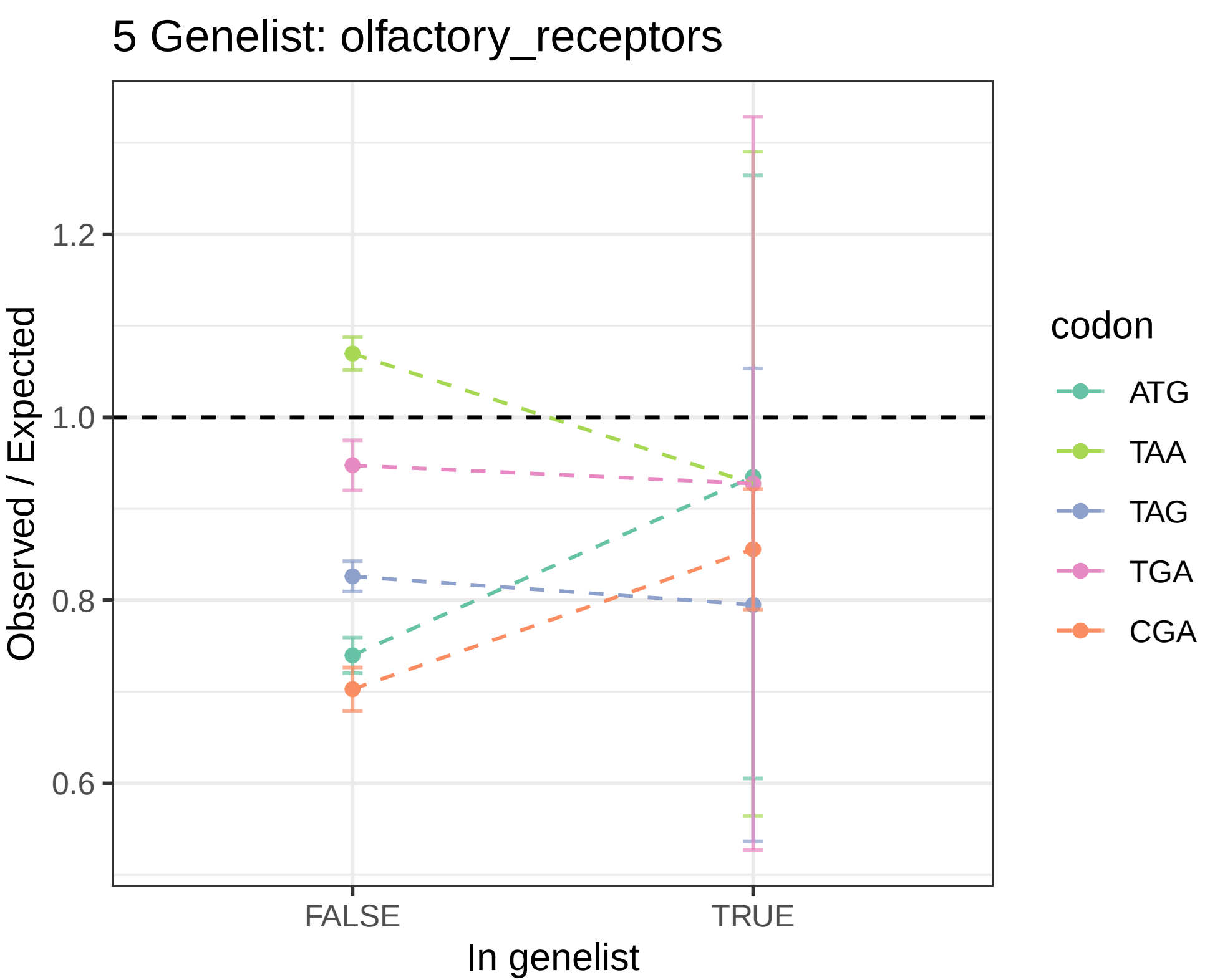

5 Genelist: natural_product_targets
5.5e−08
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

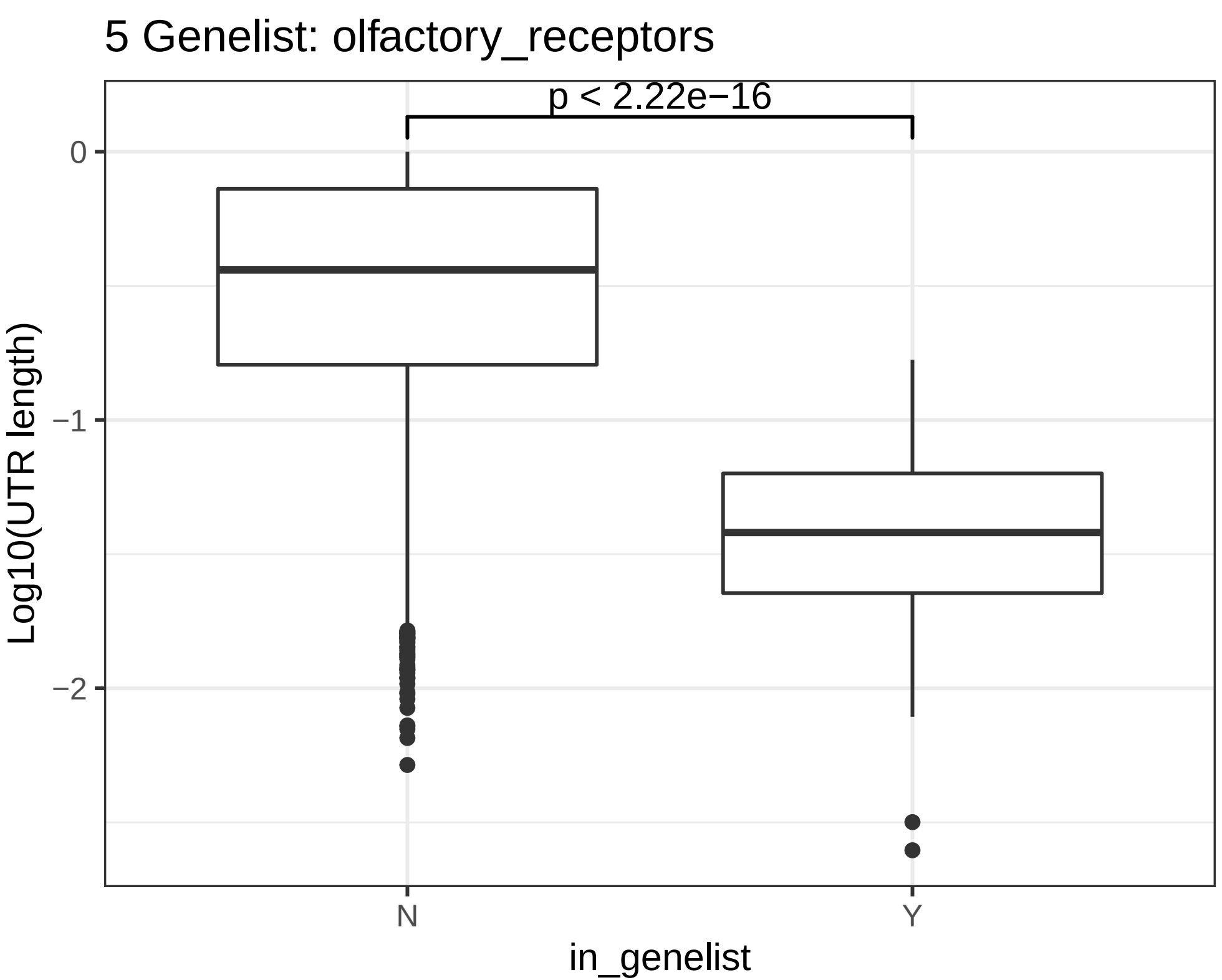

5 Genelist: natural_product_targets
0.43
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

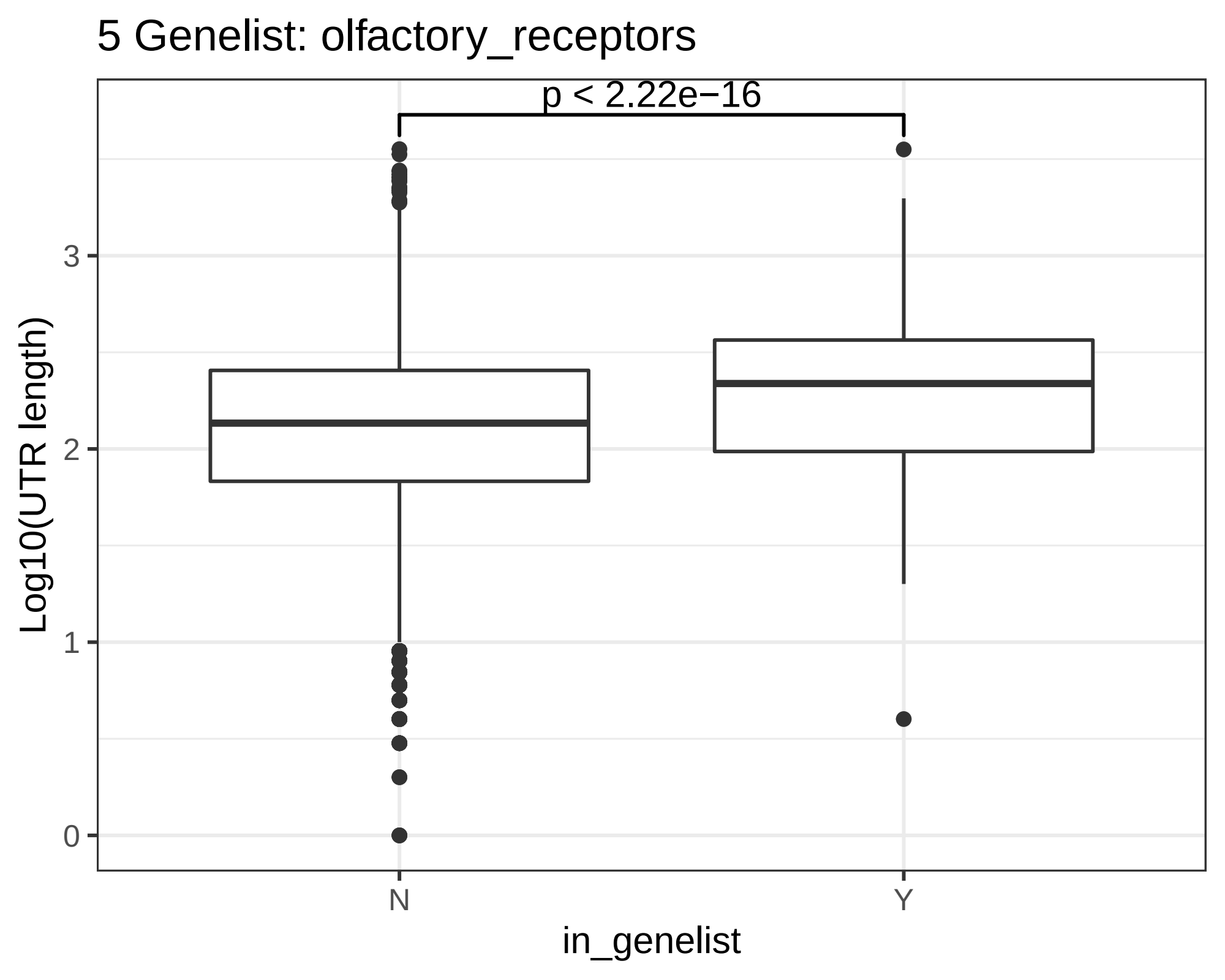

5 Genelist: NEGv1_subset_universe
Observed / Expected
1.1
1.0
0.9
0.8
0.7
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

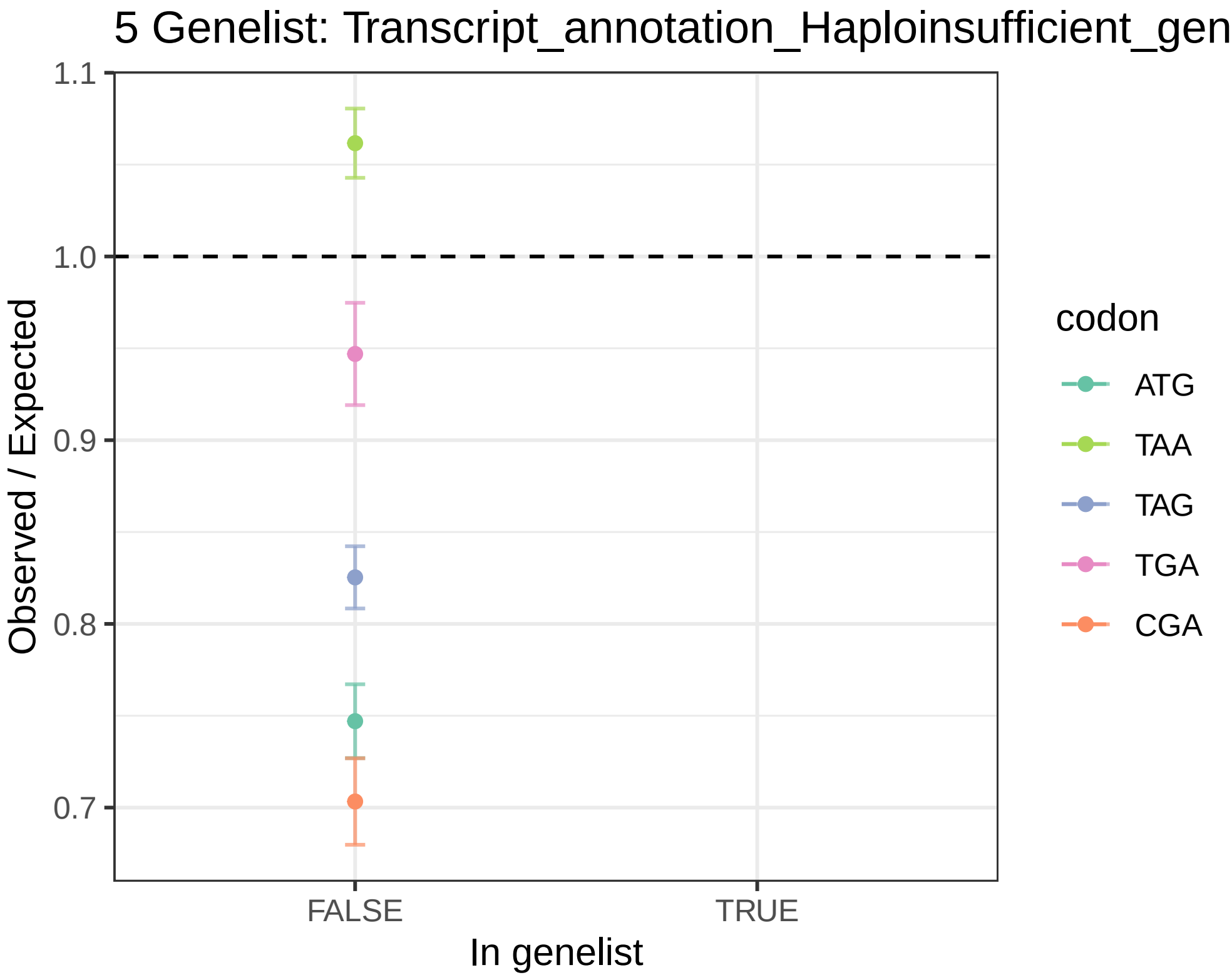

5 Genelist: NEGv1_subset_universe
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

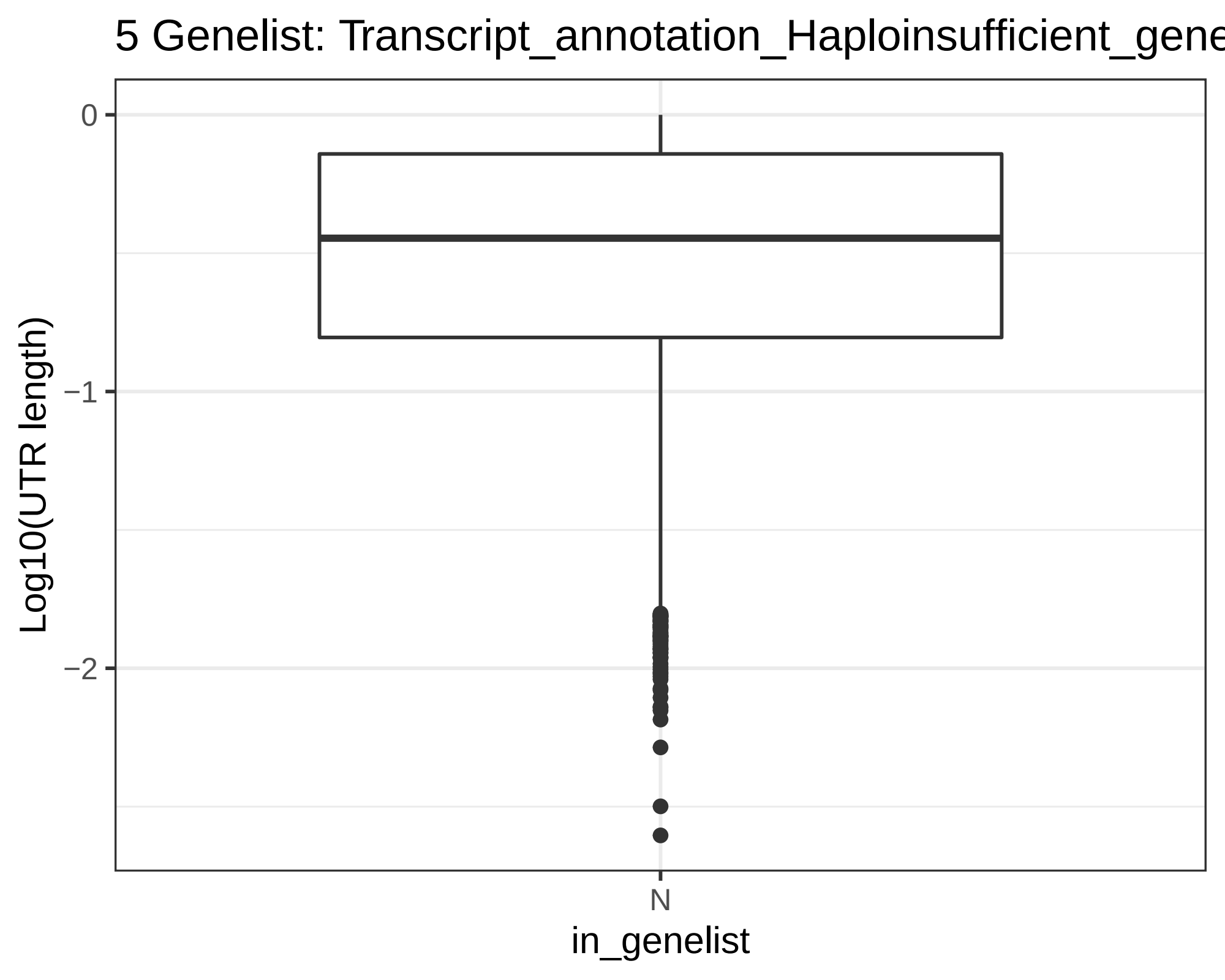

5 Genelist: NEGv1_subset_universe
4.7e−14
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

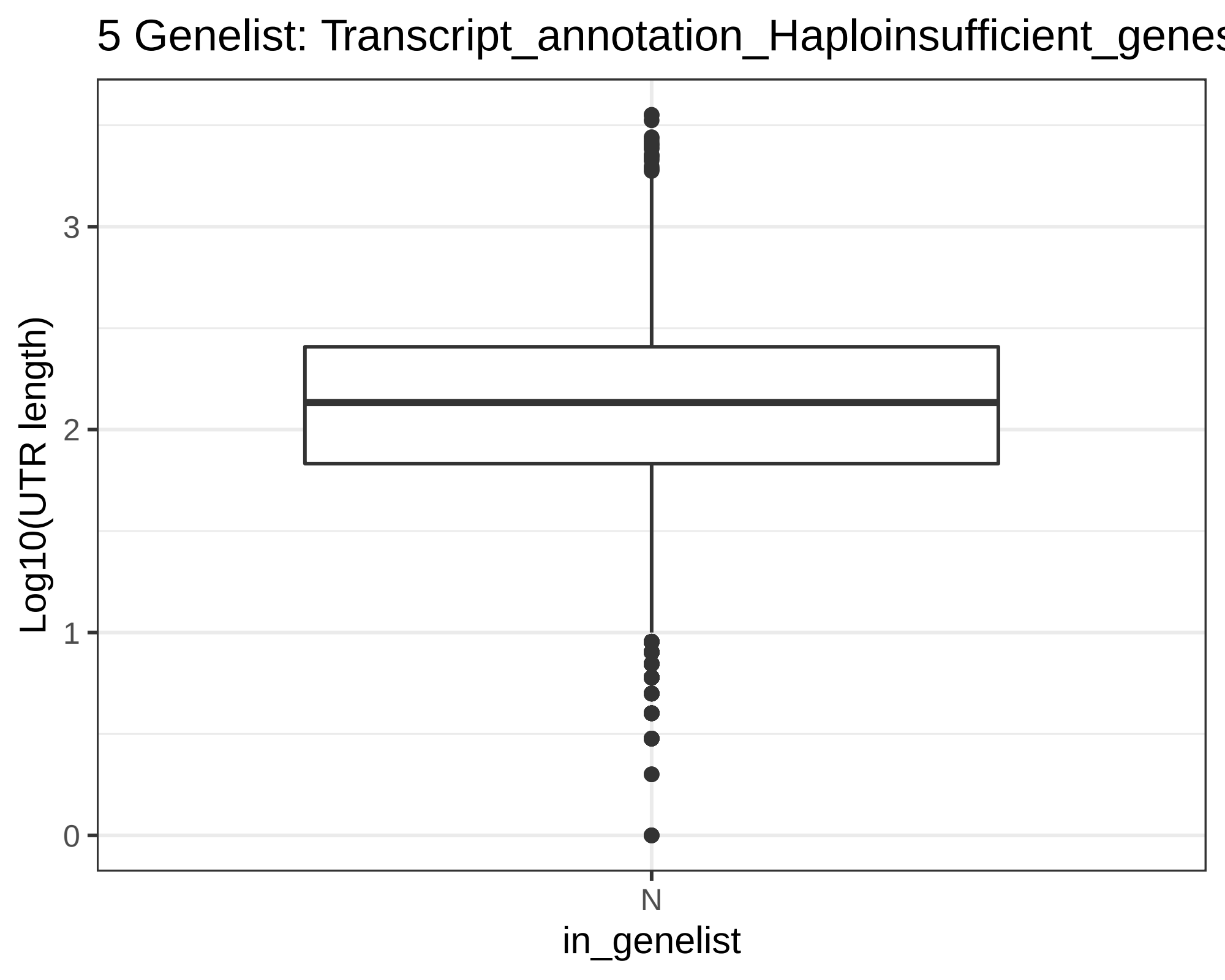

5 Genelist: olfactory_receptors
Observed / Expected
1.2
1.0
0.8
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

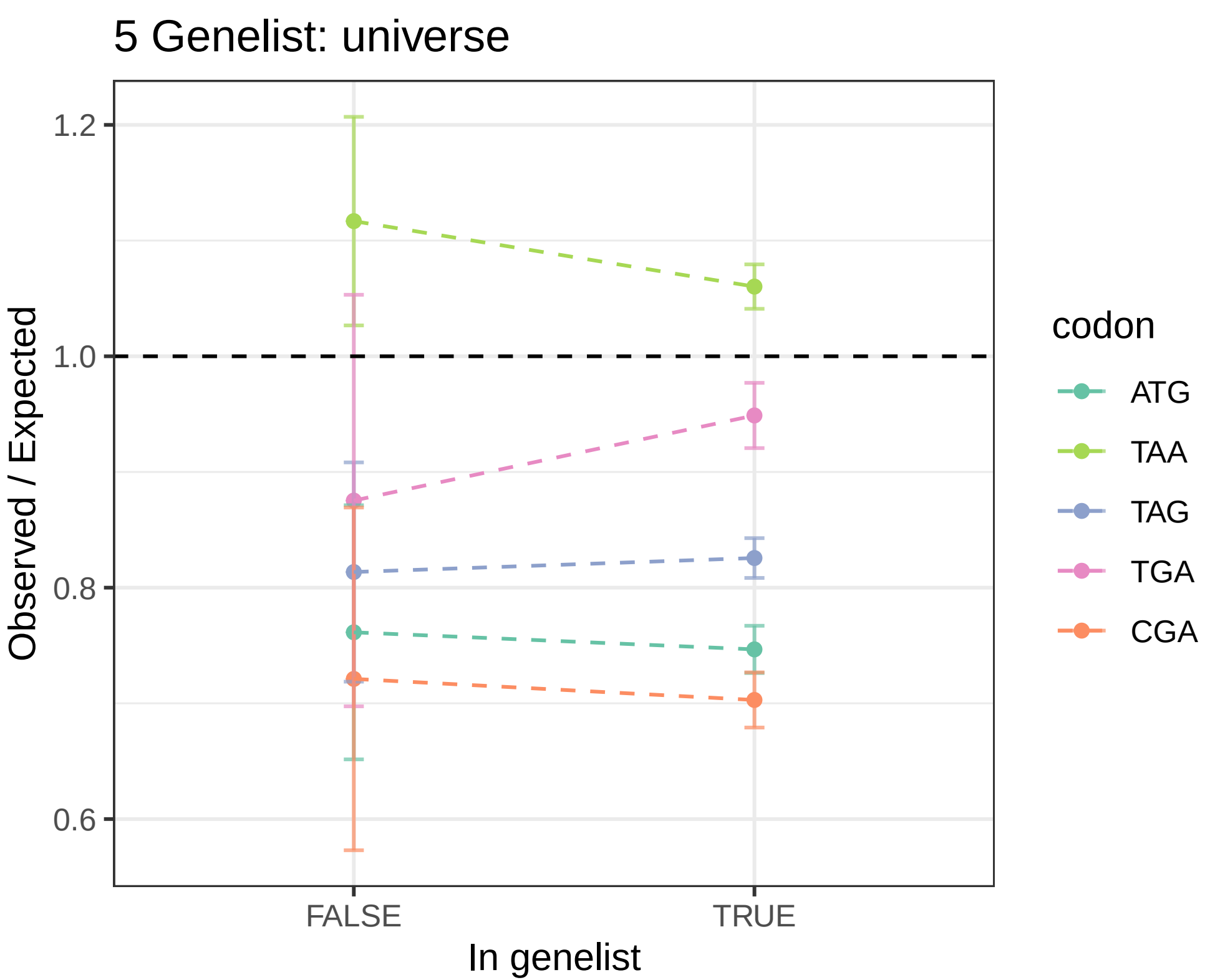

5 Genelist: olfactory_receptors
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

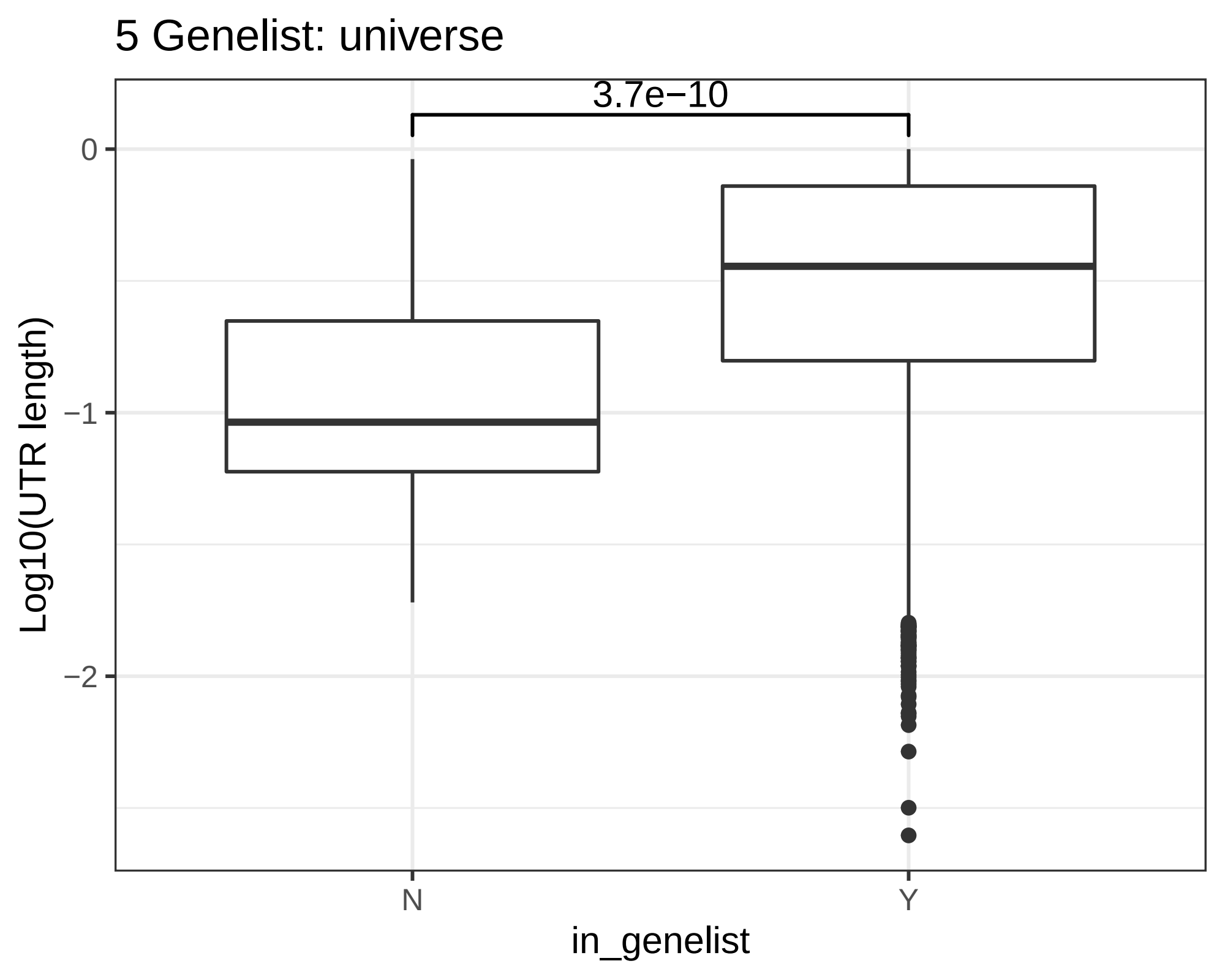

5 Genelist: olfactory_receptors
p < 2.22e−16
Log10(UTR length)
3
2
1
0
N
Y
in_genelist

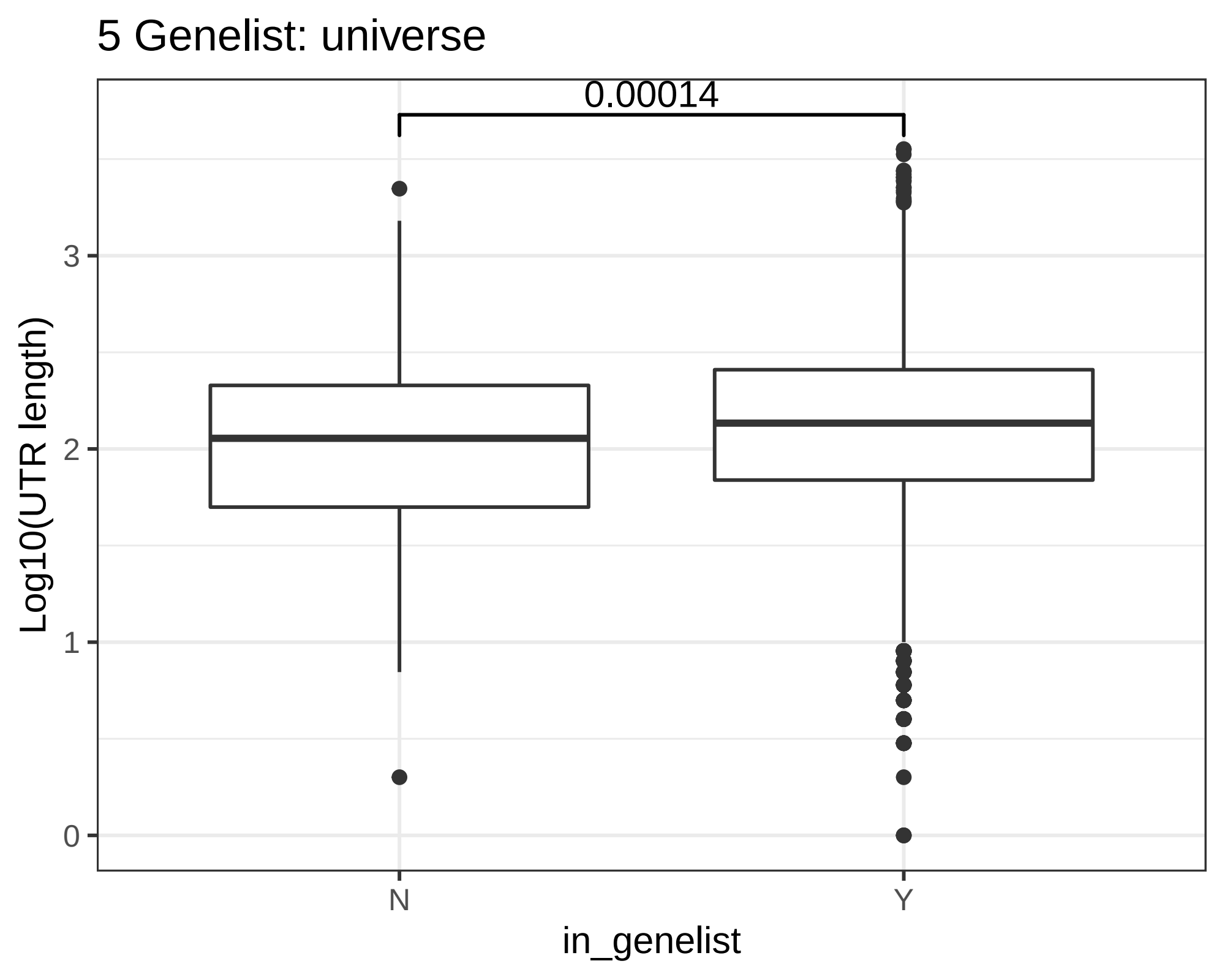

5 Genelist: Transcript_annotation_Haploinsufficient_gene
1.1
1.0
0.9
0.8
0.7
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

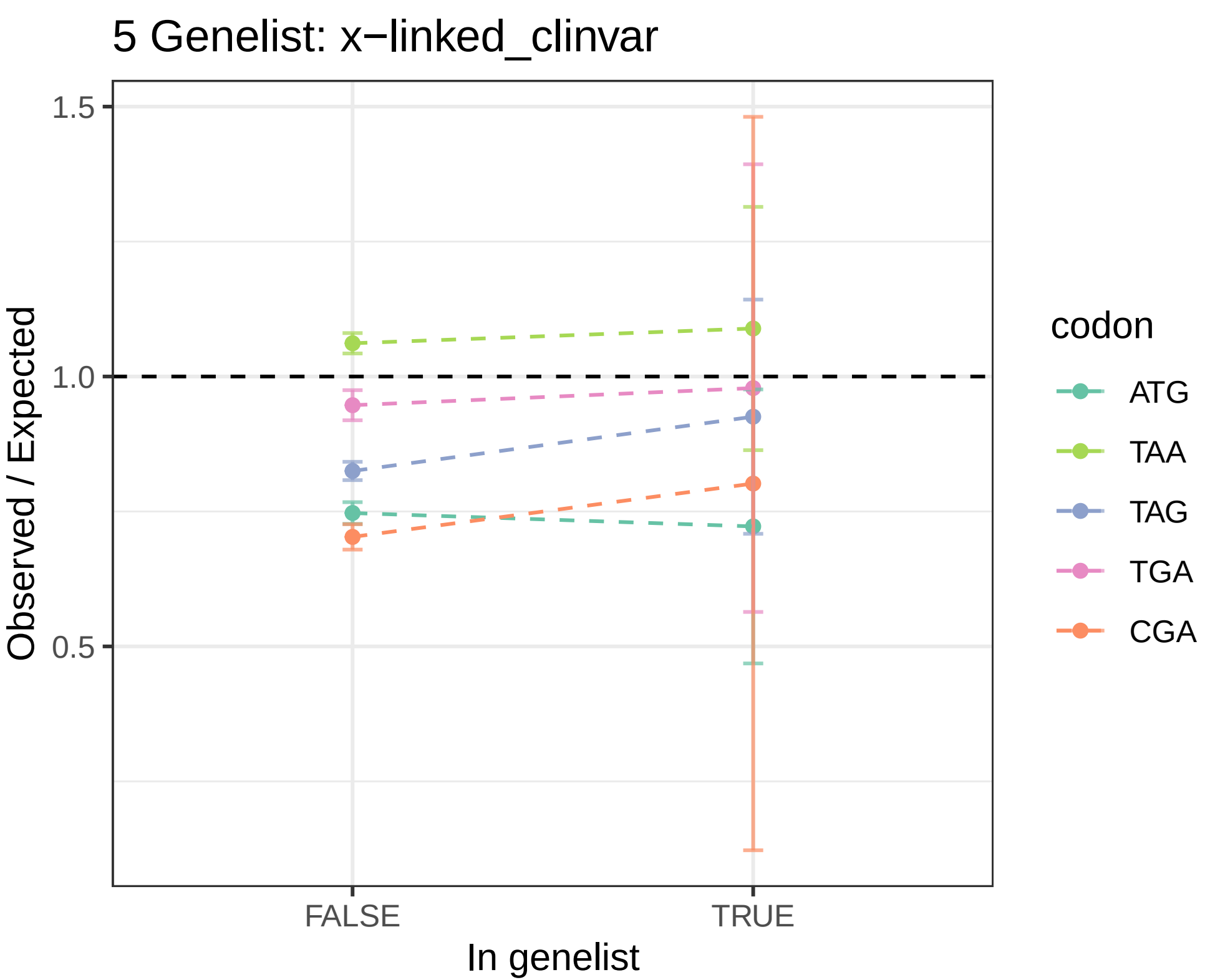

5 Genelist: Transcript_annotation_Haploinsufficient_gene
0
−1
−2
Log10(UTR length)
N
in_genelist

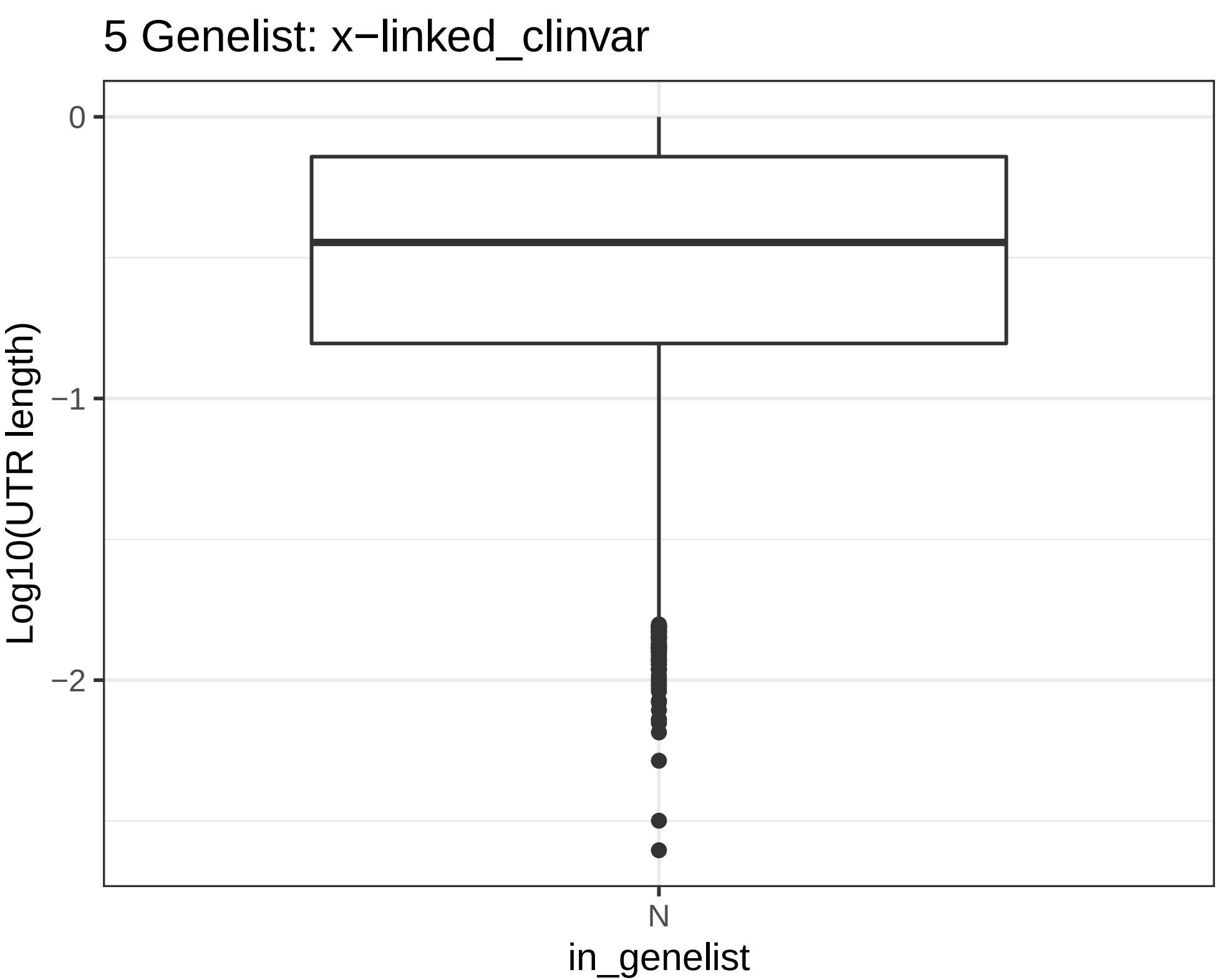

5 Genelist: Transcript_annotation_Haploinsufficient_genes
Log10(UTR length)
3
2
1
0
N
in_genelist

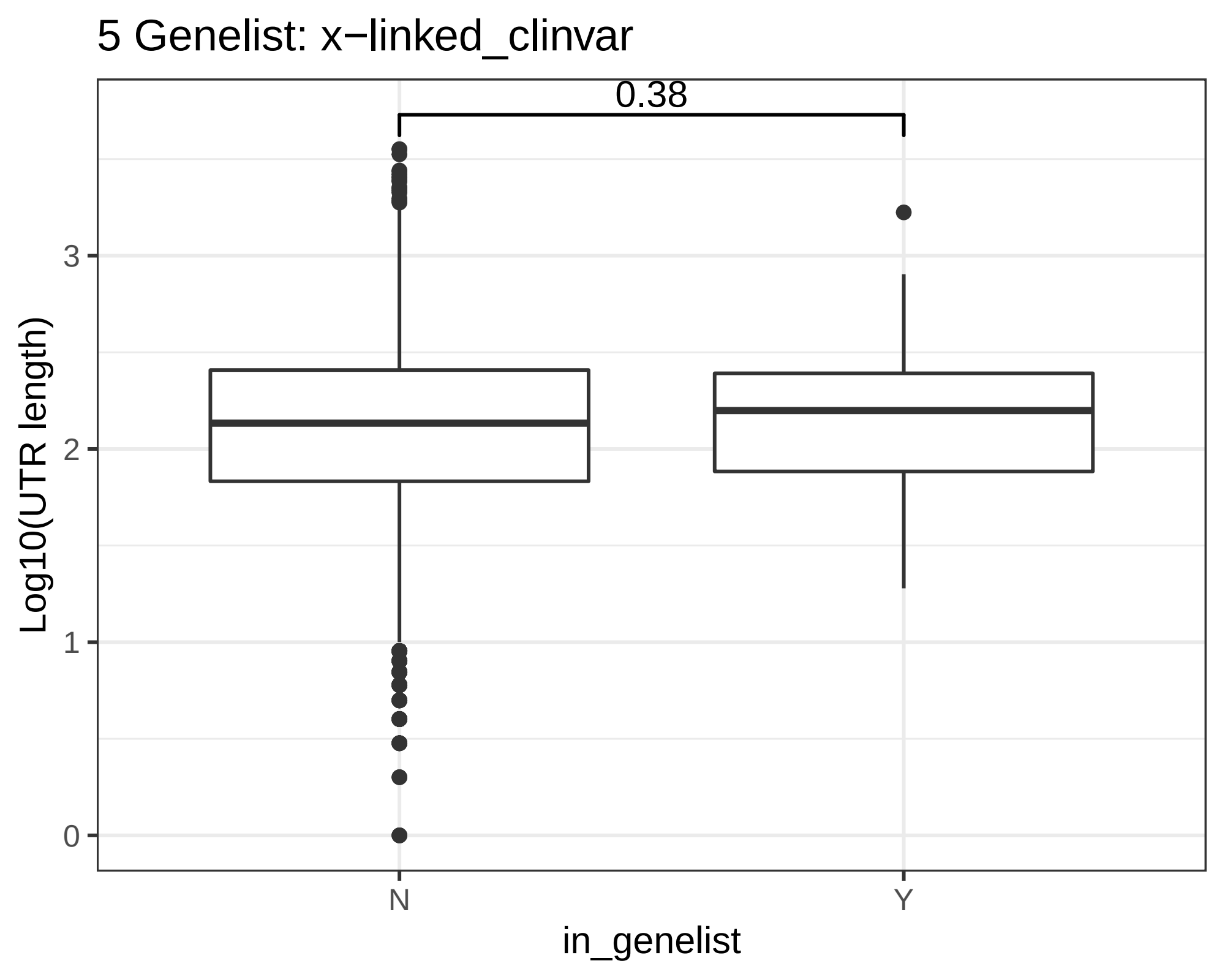

5 Genelist: universe
1.2
1.0
0.8
0.6
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA

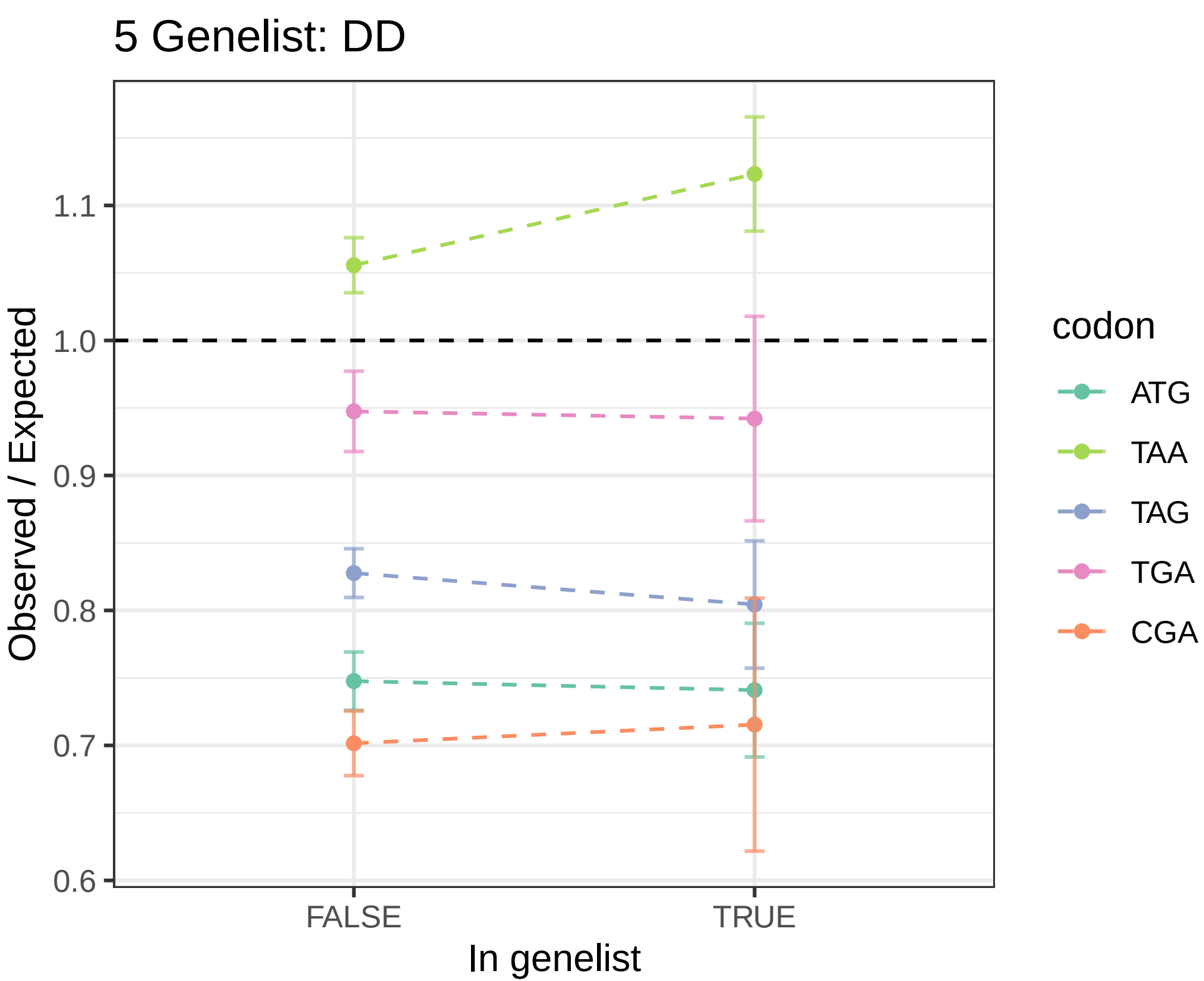

5 Genelist: universe
3.7e−10
0
−1
−2
Log10(UTR length)
N
Y
in_genelist

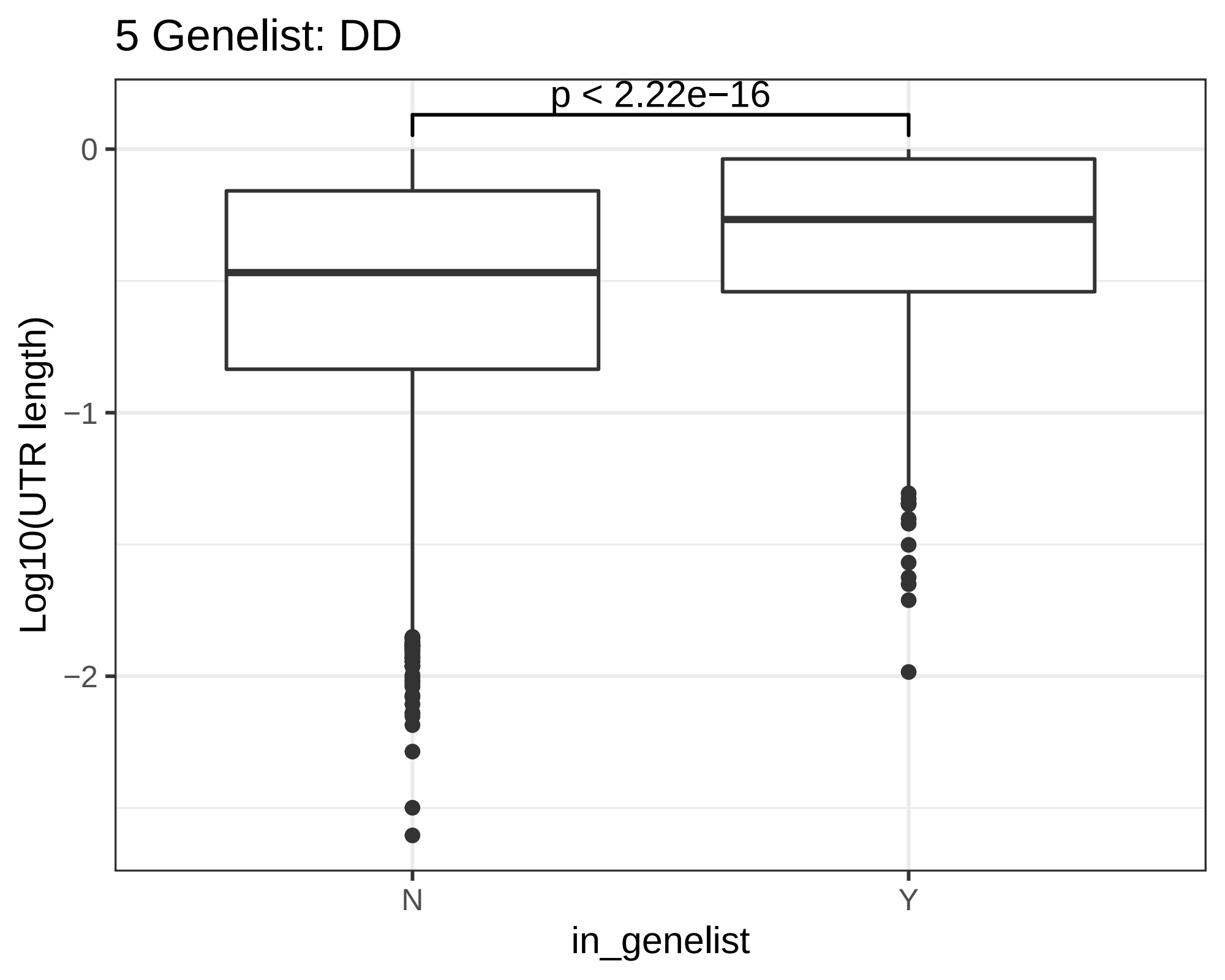

5 Genelist: universe
0.00014
Log10(UTR length)
0
1
2
3
N
Y
in_genelist

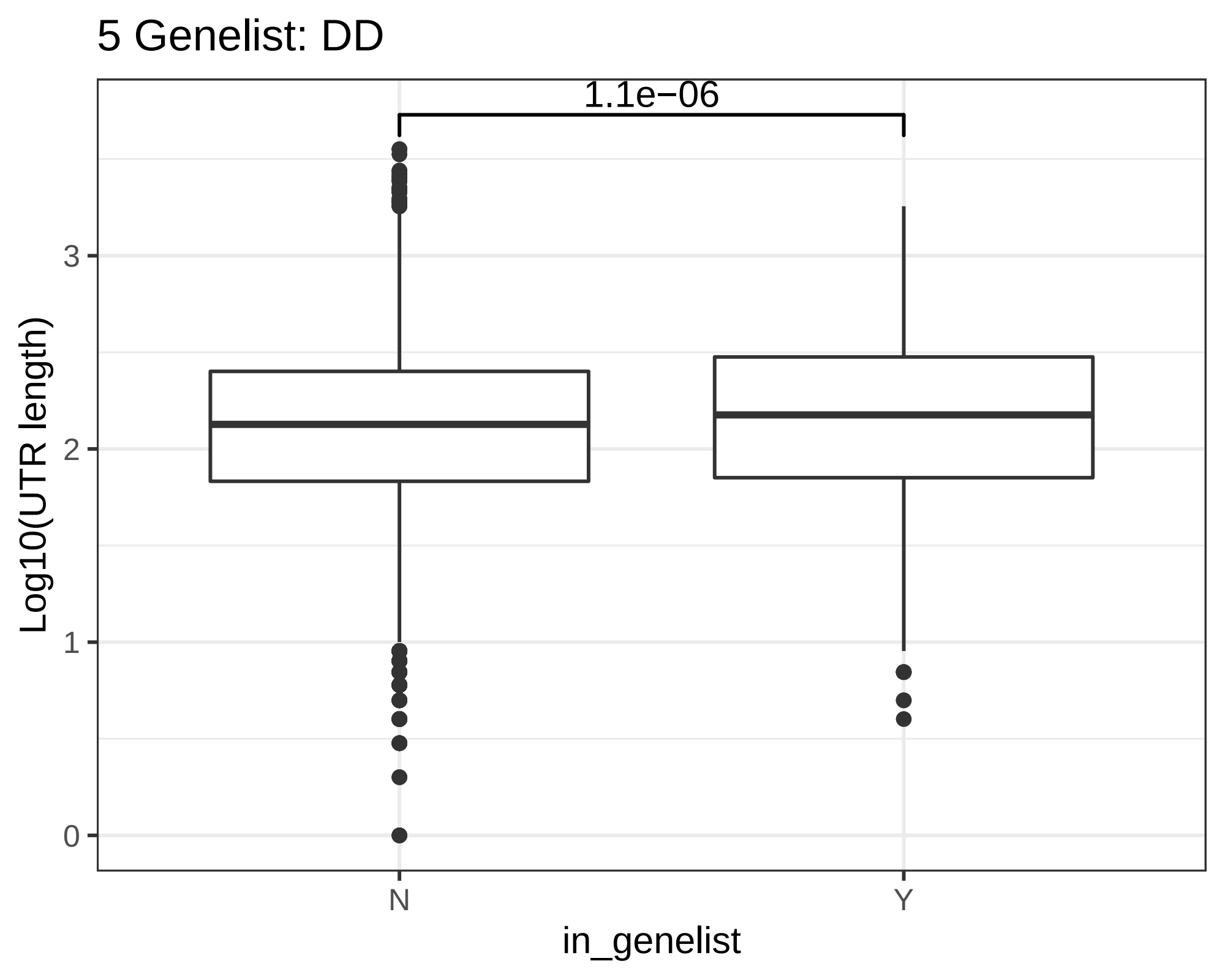

5 Genelist: x−linked_clinvar
1.5
1.0
0.5
Observed / Expected
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA


5 Genelist: x−linked_clinvar
0
−1
−2
Log10(UTR length)
N
in_genelist


5 Genelist: x−linked_clinvar
0.38
Log10(UTR length)
3
2
1
0
N
Y
in_genelist


5 Genelist: DD
Observed / Expected
1.1
1.0
0.9
0.8
0.7
0.6
FALSE
TRUE
In genelist
codon
ATG
TAA
TAG
TGA
CGA


5 Genelist: DD
p < 2.22e−16
0
−1
−2
Log10(UTR length)
N
Y
in_genelist


5 Genelist: DD
1.1e−06
Log10(UTR length)
3
2
1
0
N
Y
in_genelist