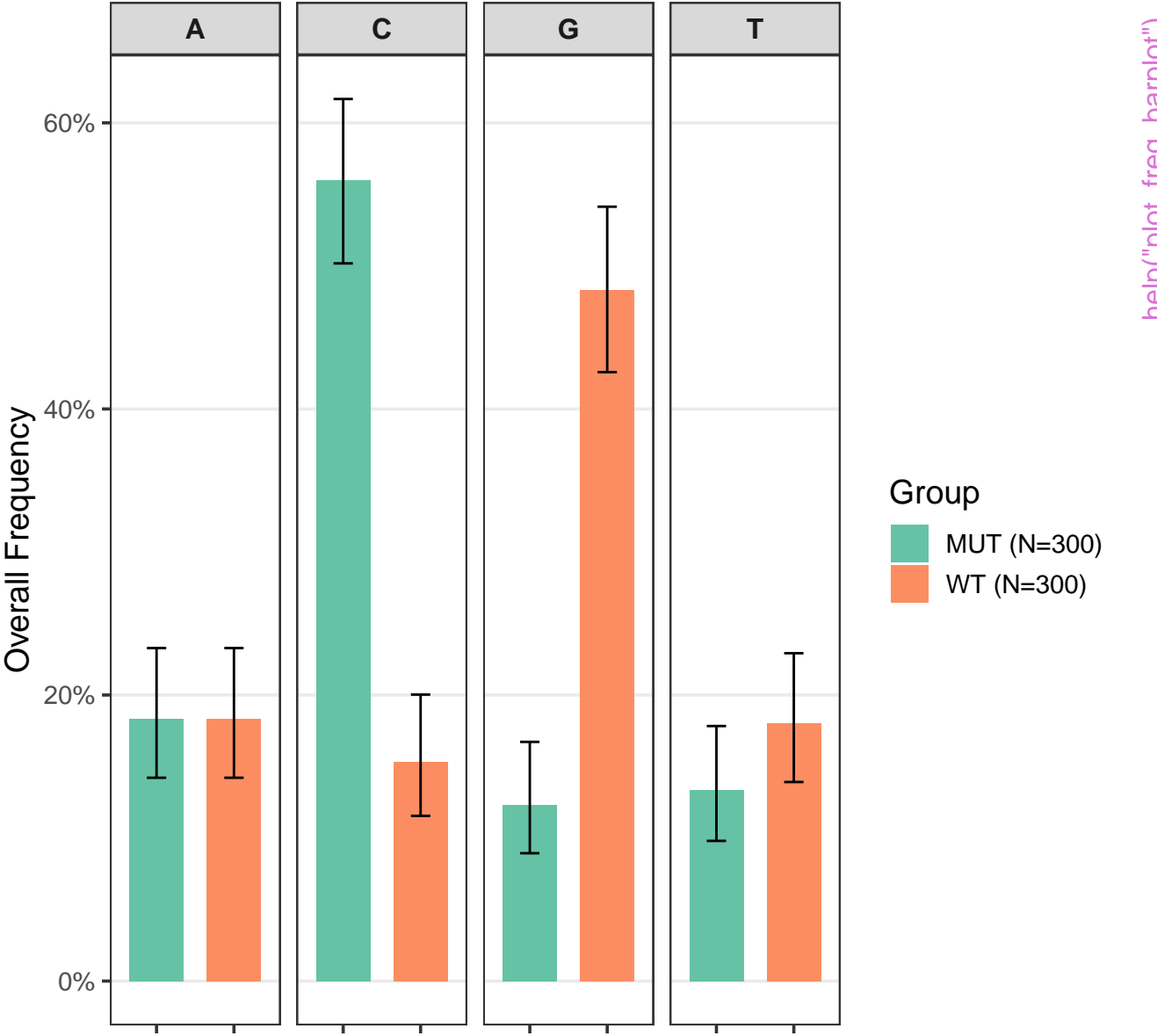
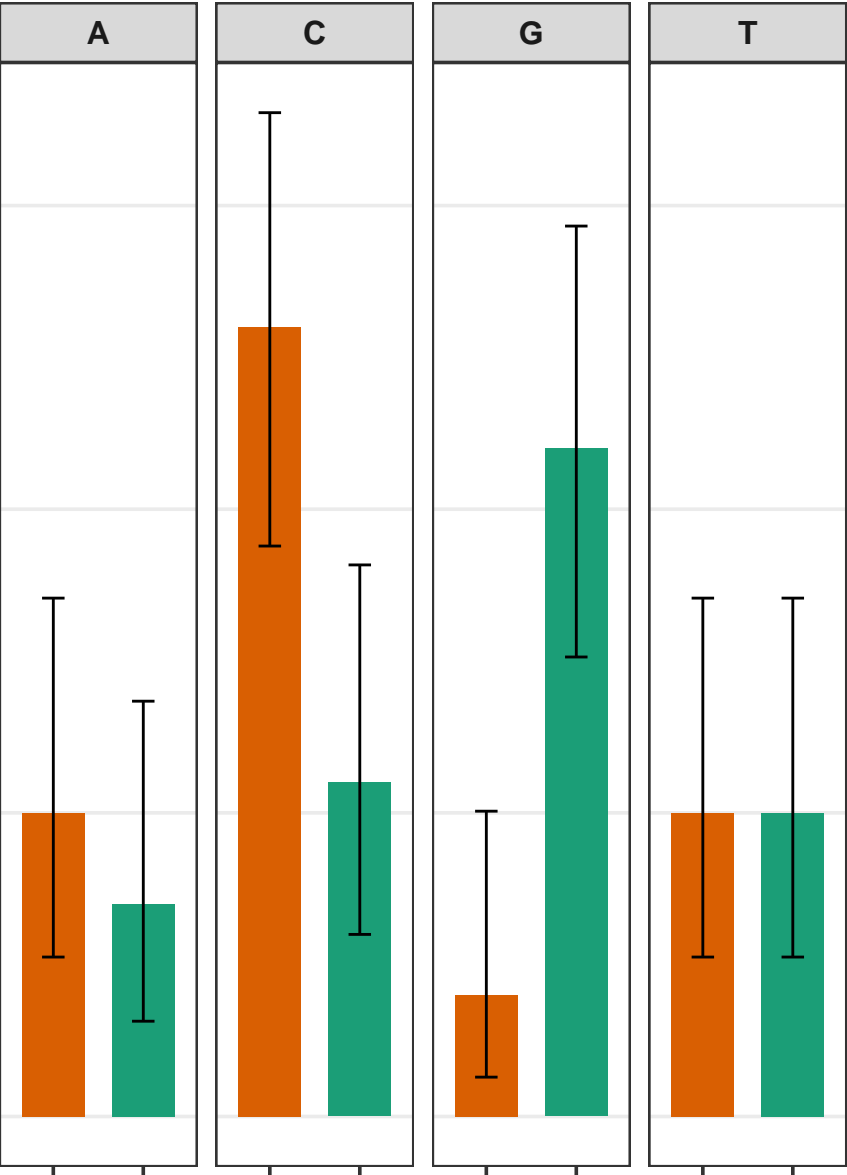


Overall Nucleotide Frequency (3-mers)



Bars represent overall proportion with 95% confidence intervals.
Global comparison (Chi-squared test), $p\text{-value} = <0.001$

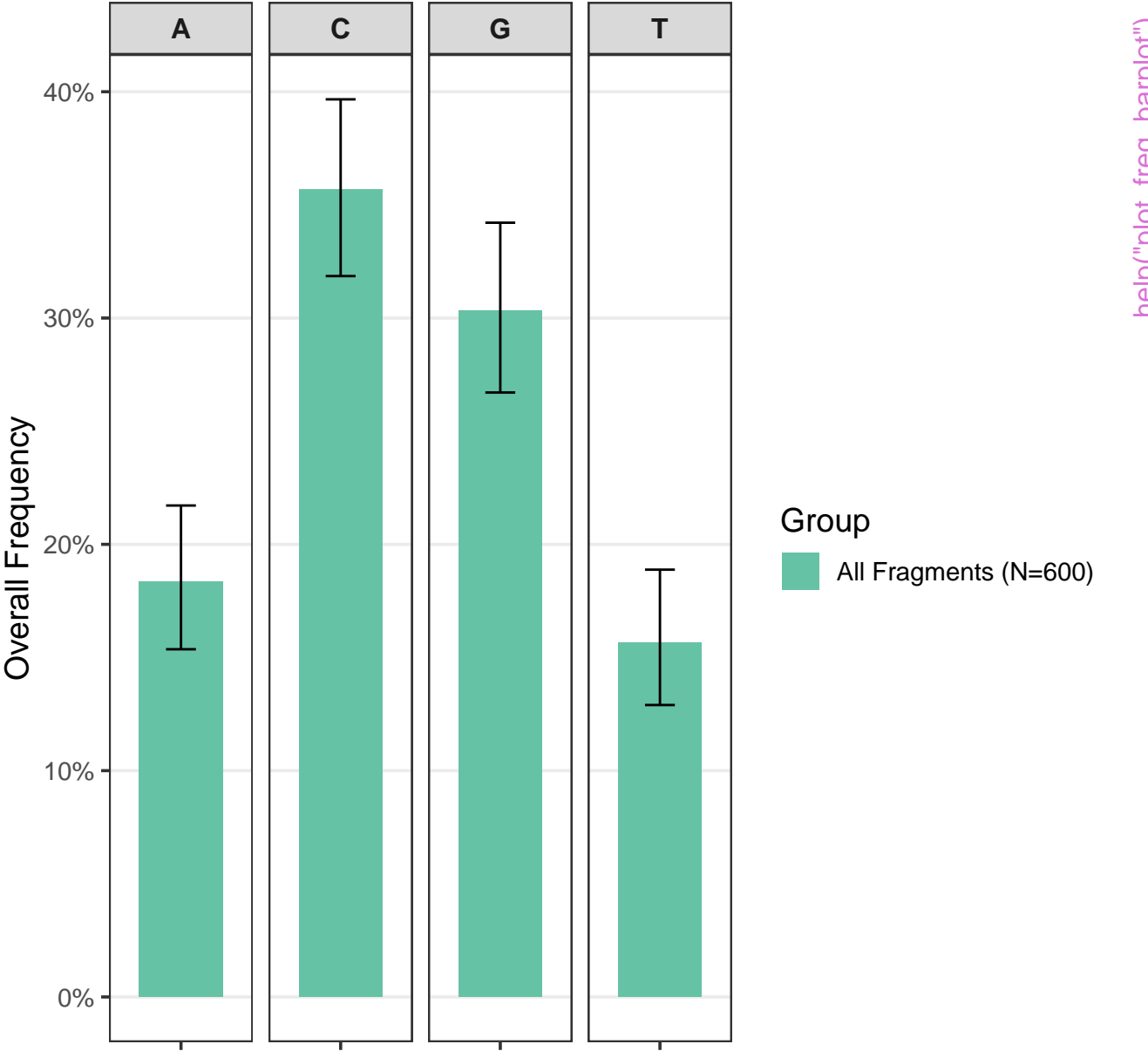
Overall Nucleotide Frequency (1-mers)



Bars represent overall proportion with 95% confidence intervals.
Global comparison (Chi-squared test), $p\text{-value} = <0.001$

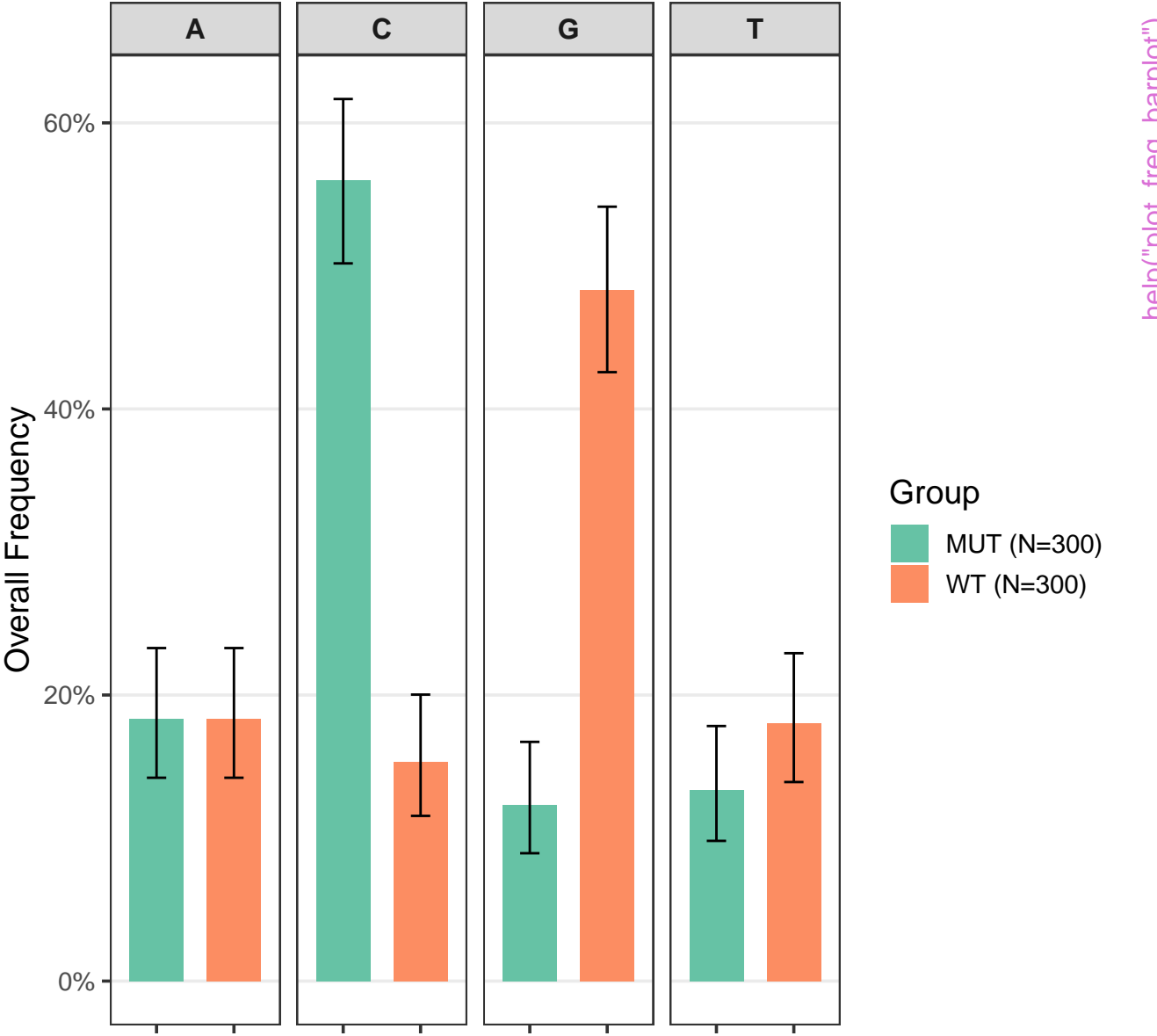
help("plot_freq_barplot")

Overall Nucleotide Frequency (3-mers)



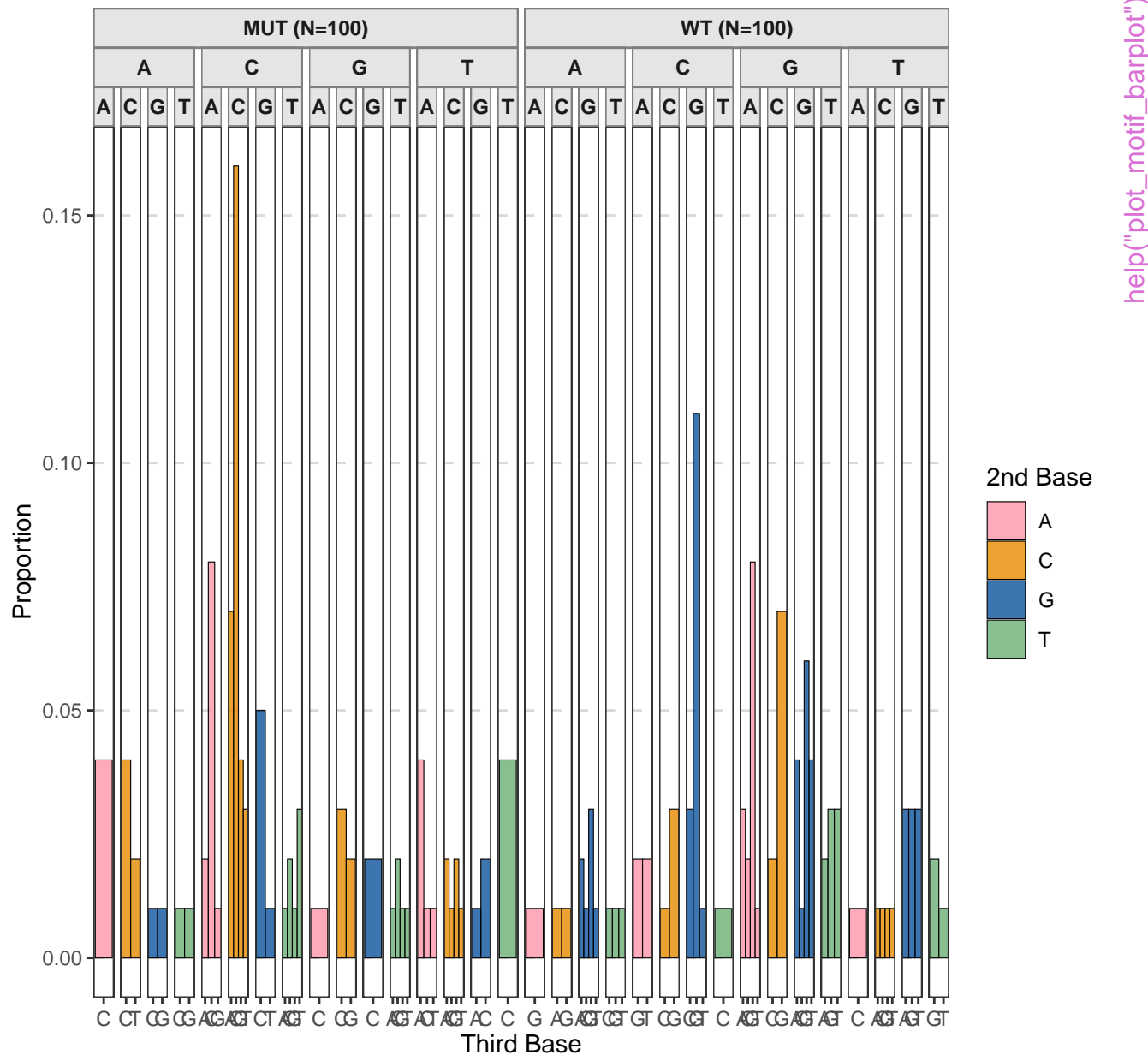
Bars represent overall proportion with 95% confidence intervals.

Overall Nucleotide Frequency (3-mers)



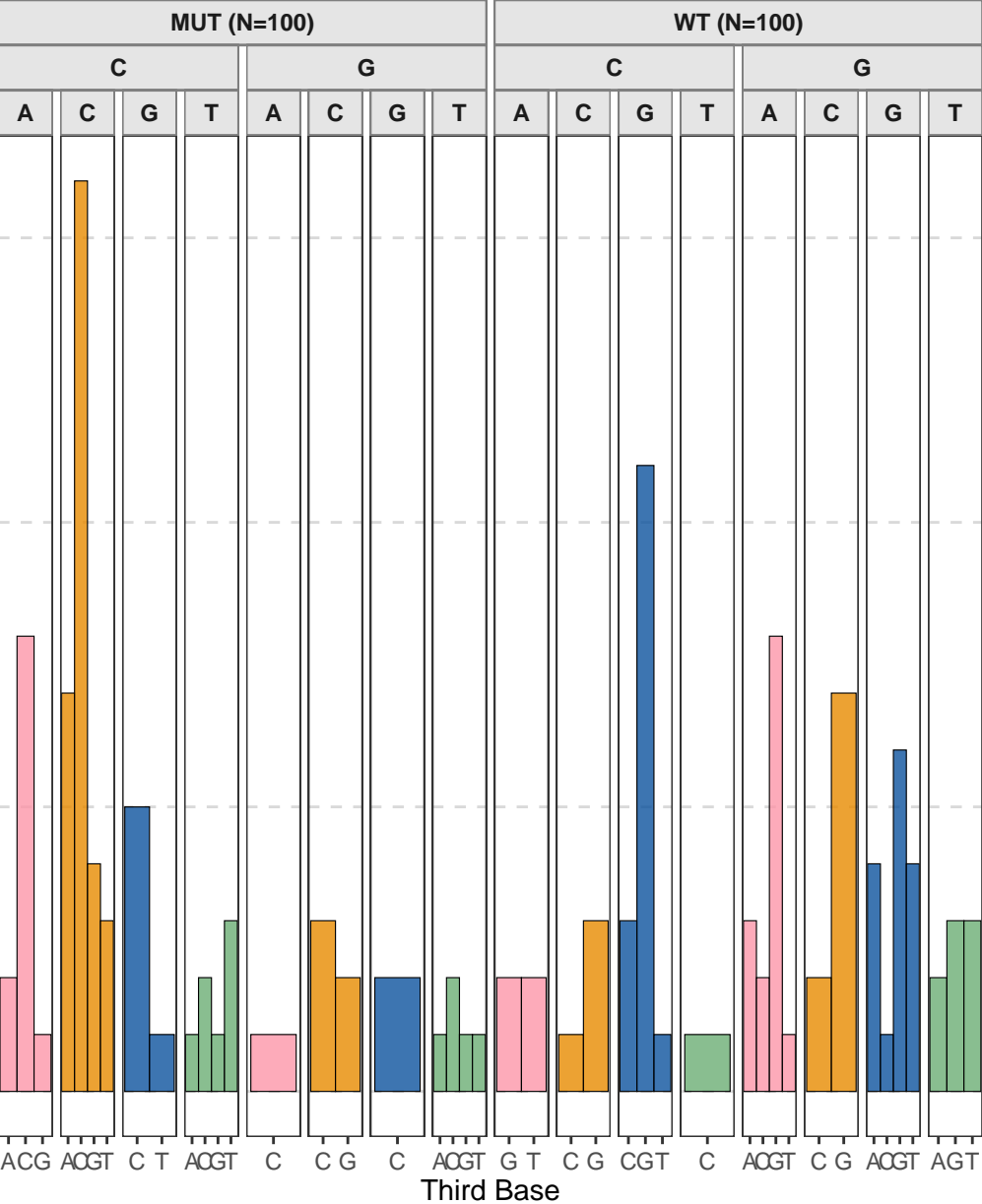
Bars represent overall proportion with 95% confidence intervals.
Global comparison (Chi-squared test), $p\text{-value} = <0.001$

Hierarchical view by base position



Motif Proportions at Fragment Ends

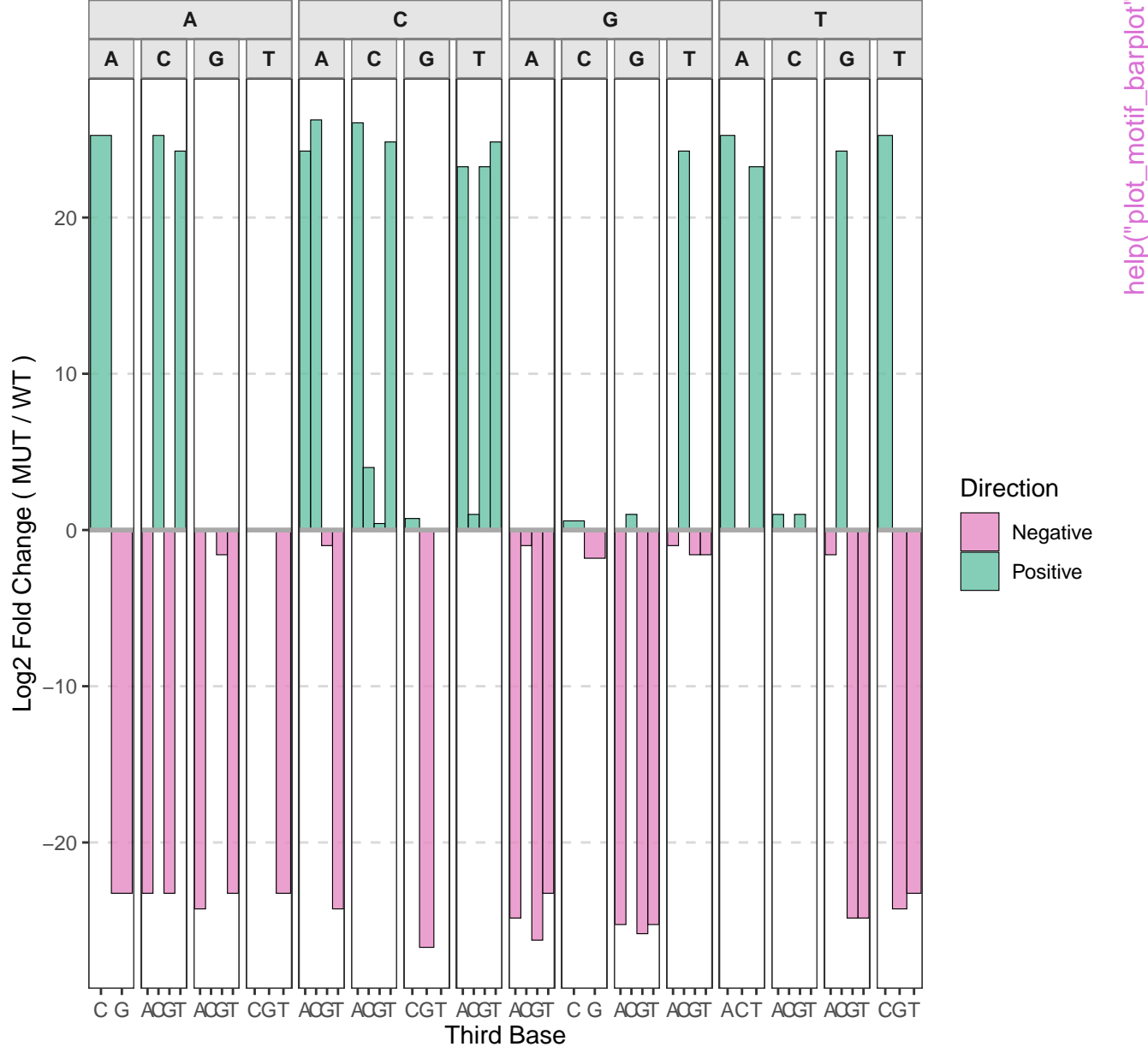
Hierarchical view by base position



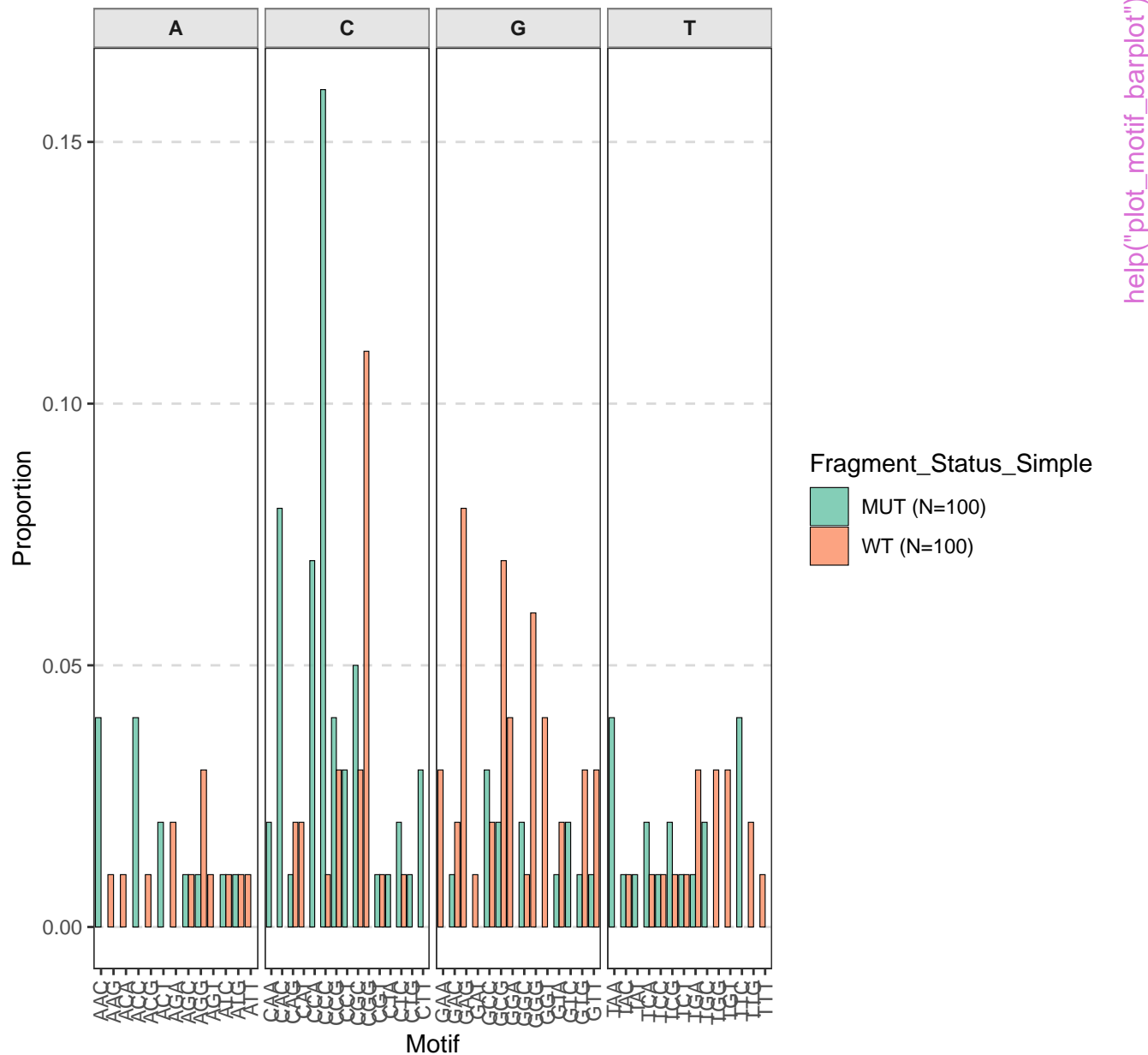
help("plot_motif_barplot")

Differential Motif Usage

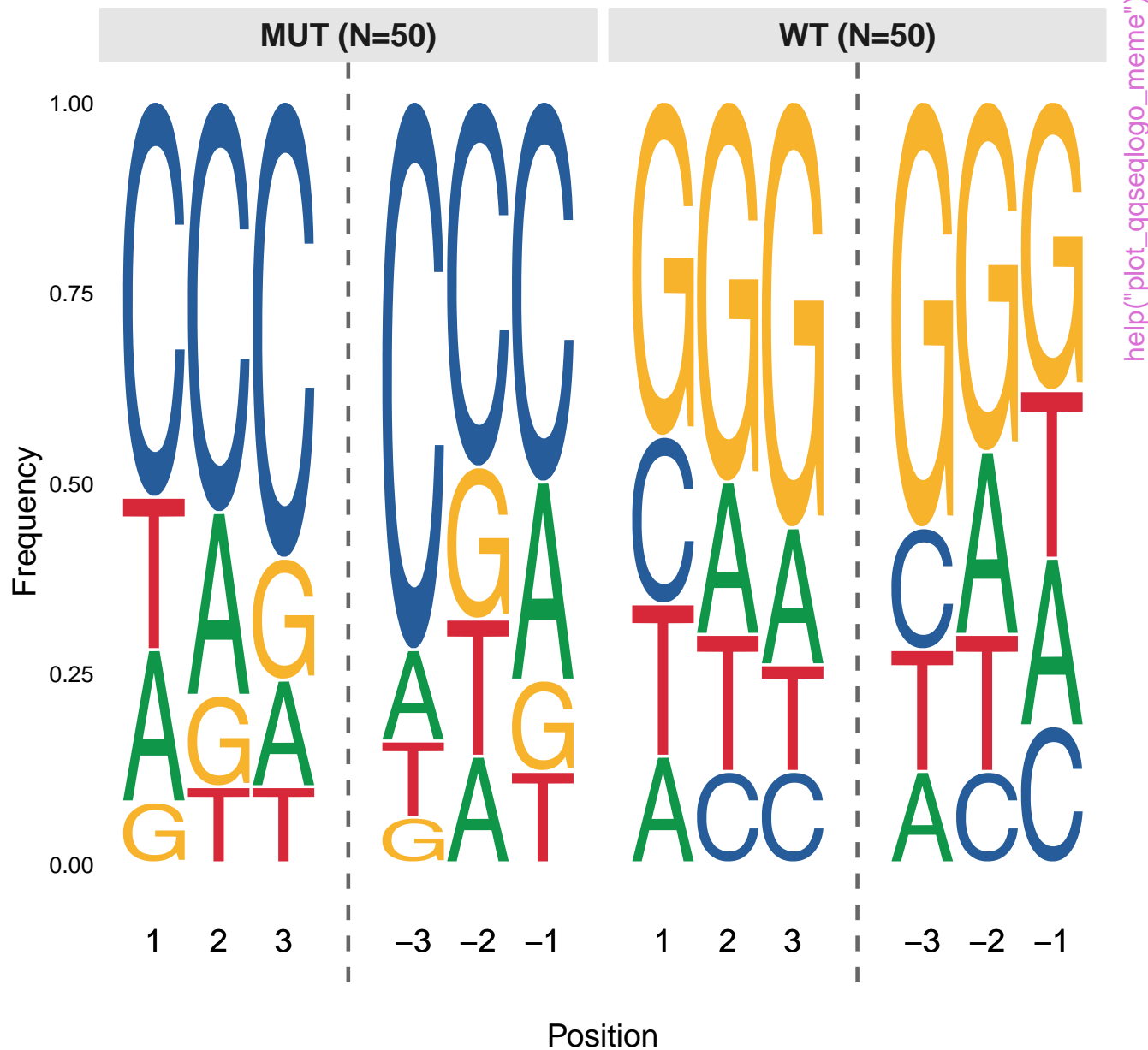
Comparison: MUT vs WT



Grouped by motif



Sequence Motif Composition



Sequence Motif Composition

MUT (N=50)

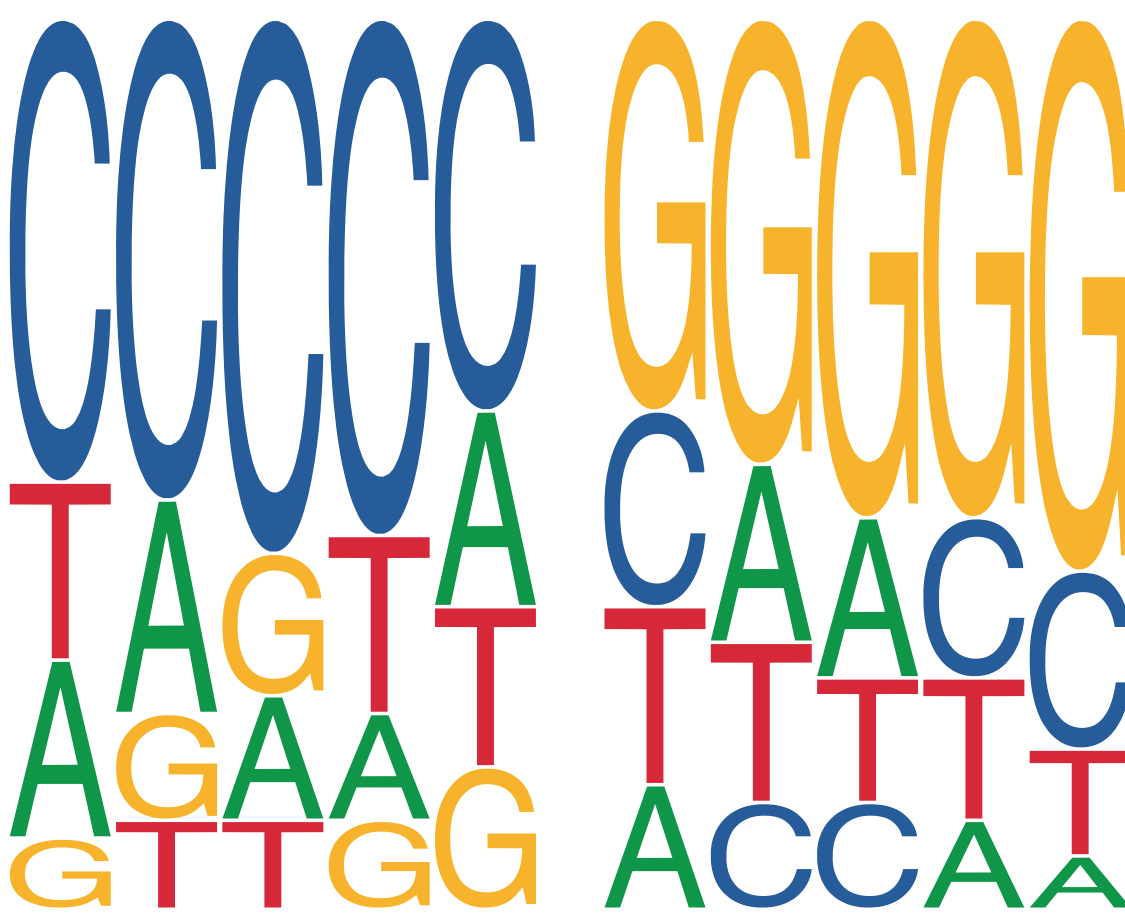
WT (N=50)

Frequency

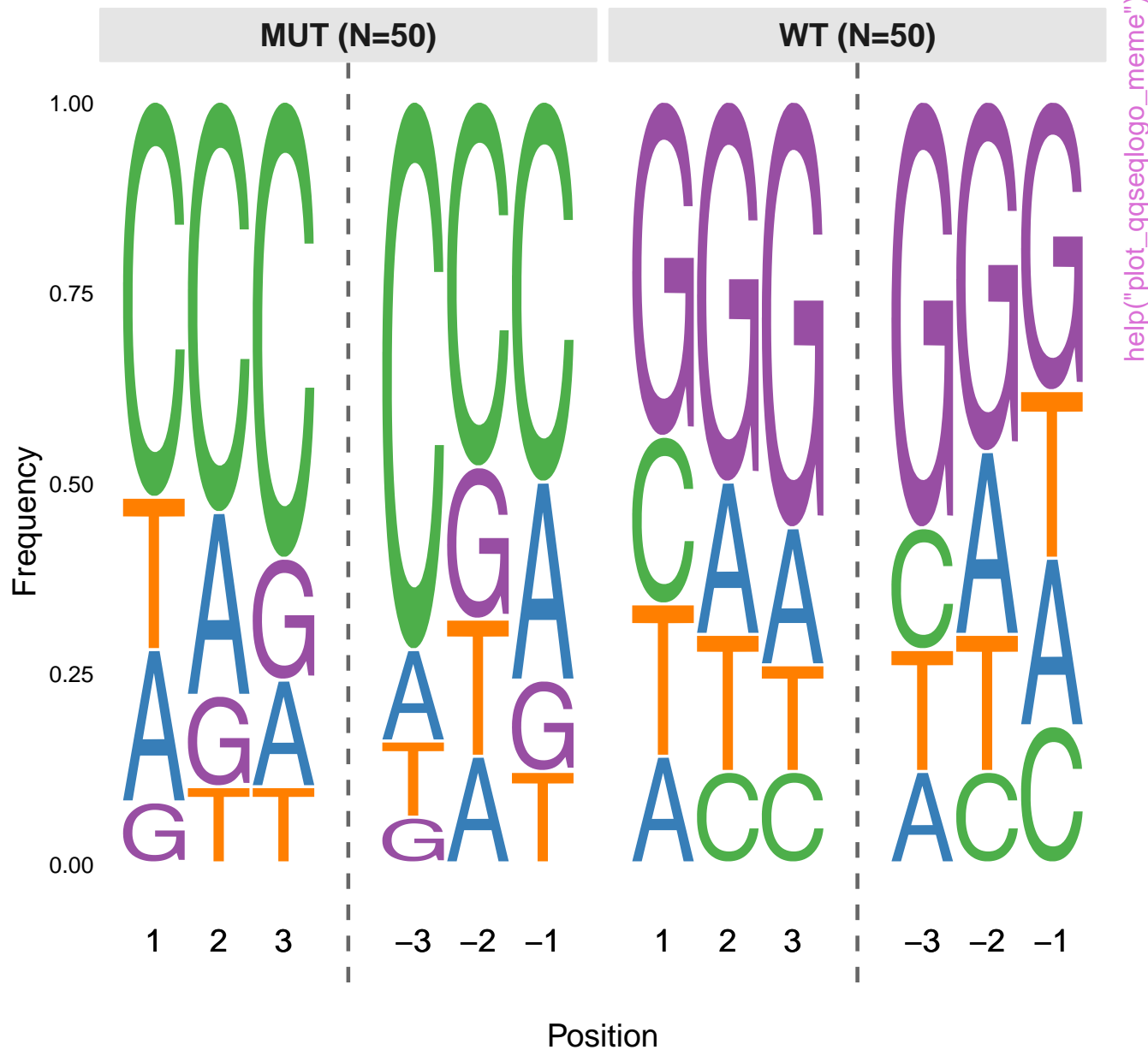
1 2 3 4 5 1 2 3 4 5

Position

help("plot_qqseqlogo_meme")



Sequence Motif Composition



Sequence Motif Composition

MUT (N=50)

WT (N=50)

Frequency

1

2

3

1

2

3

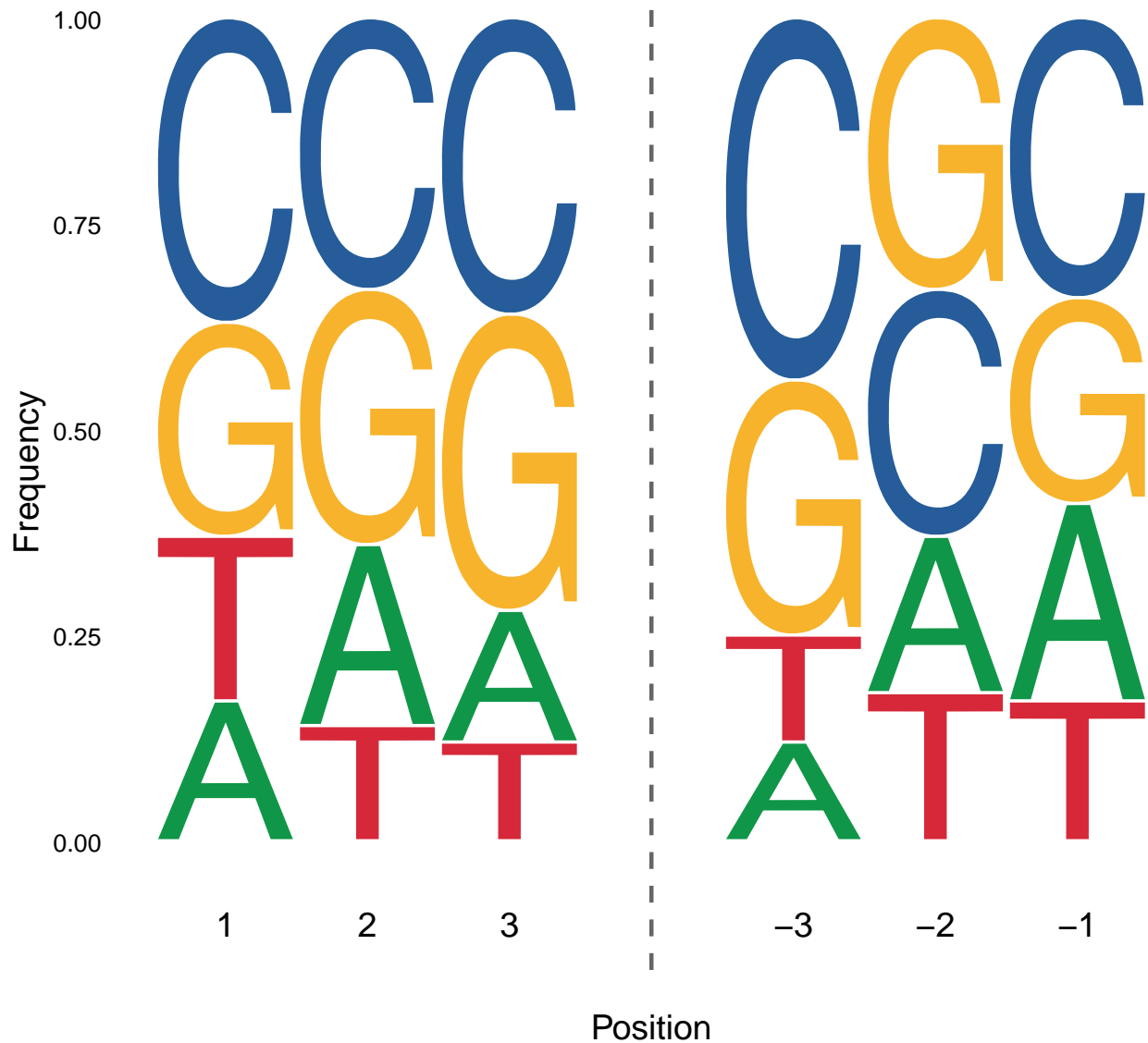
Position

help("plot_qqseqlogo_meme")



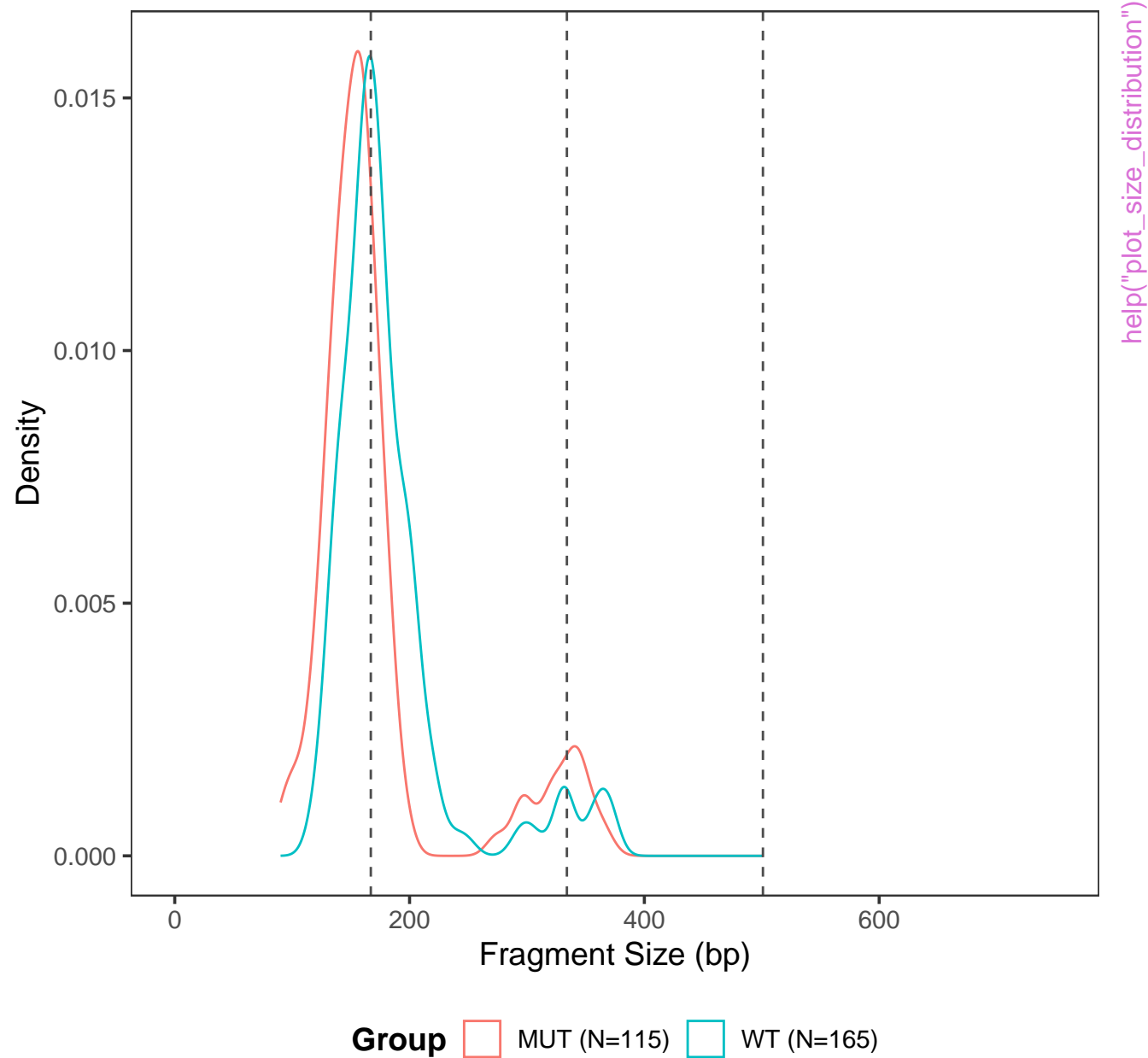
Sequence Motif Composition

All Fragments (N=100)

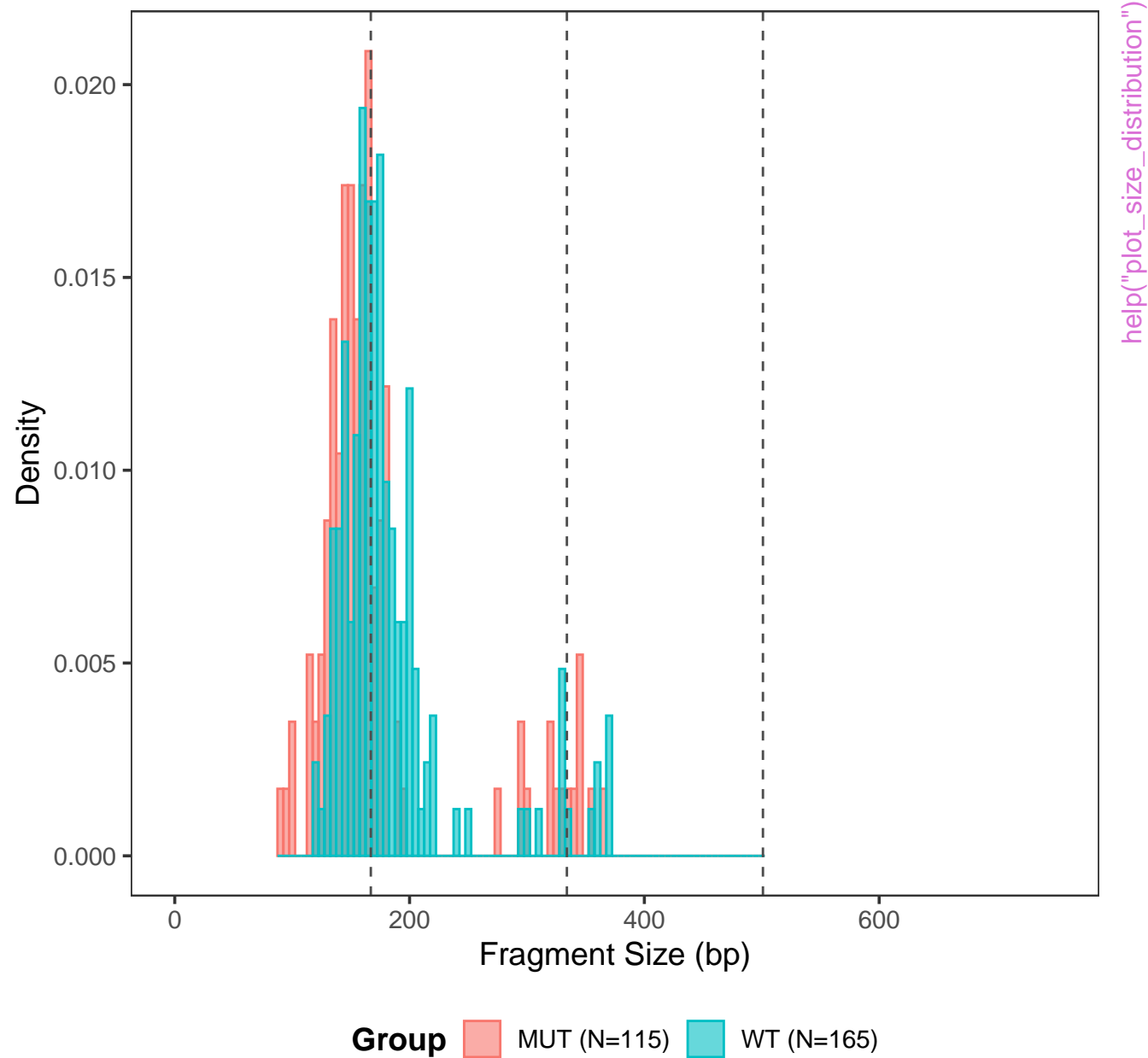


help("plot_qqseqlogo_meme")

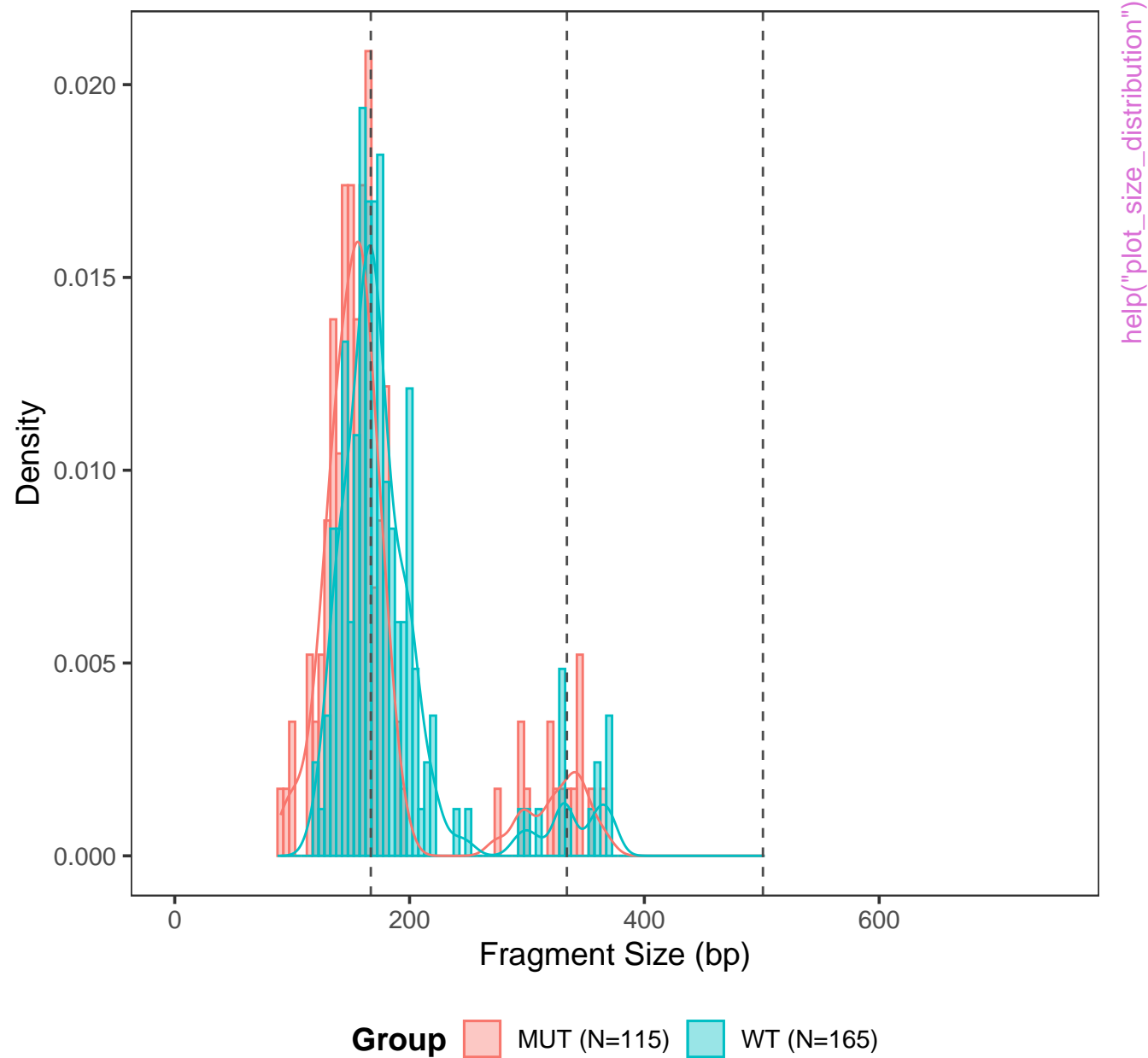
Fragment Size Distribution



Fragment Size Distribution



Fragment Size Distribution



Fragment Size Distribution

