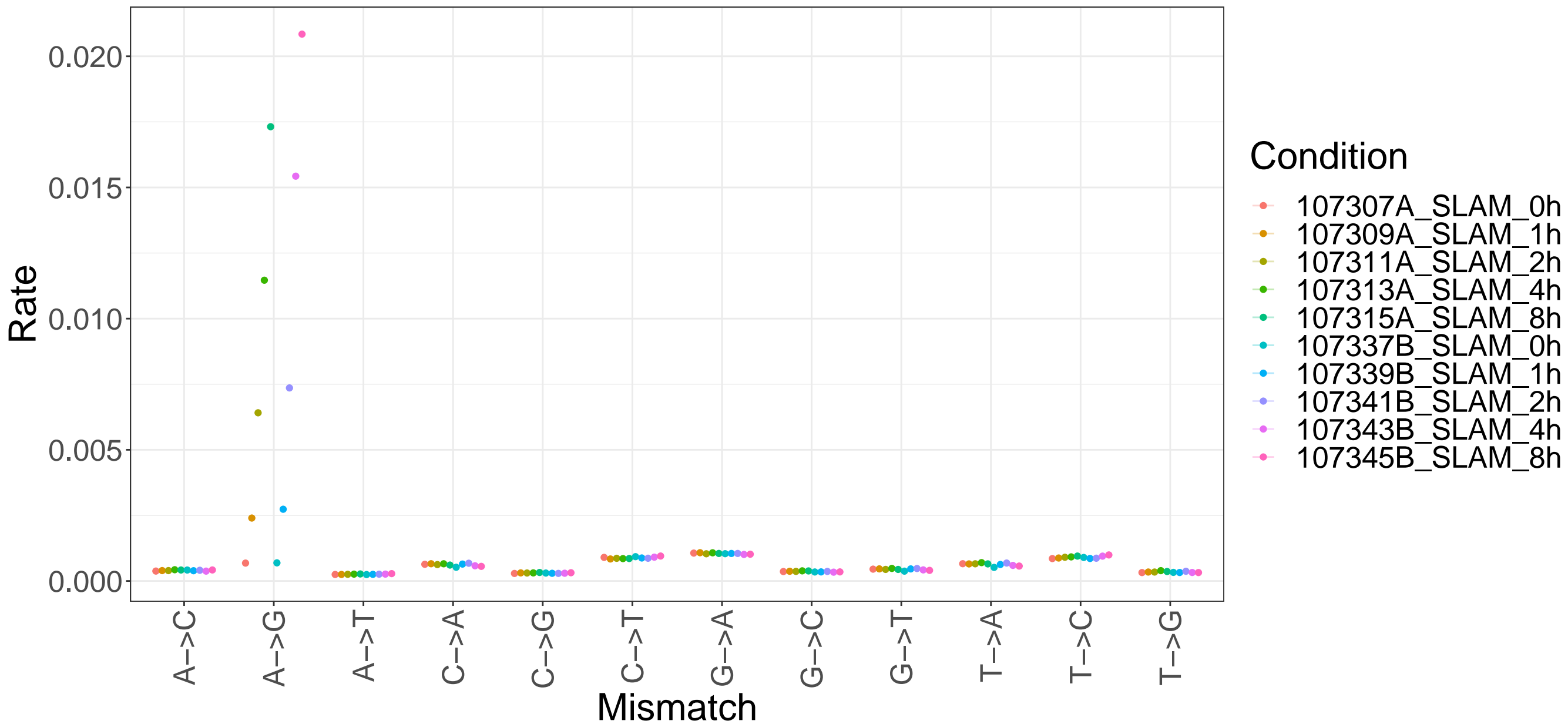


A comparison of metabolic labeling and statistical methods to study genome-wide dynamics of RNA turnover Supplementary File 2

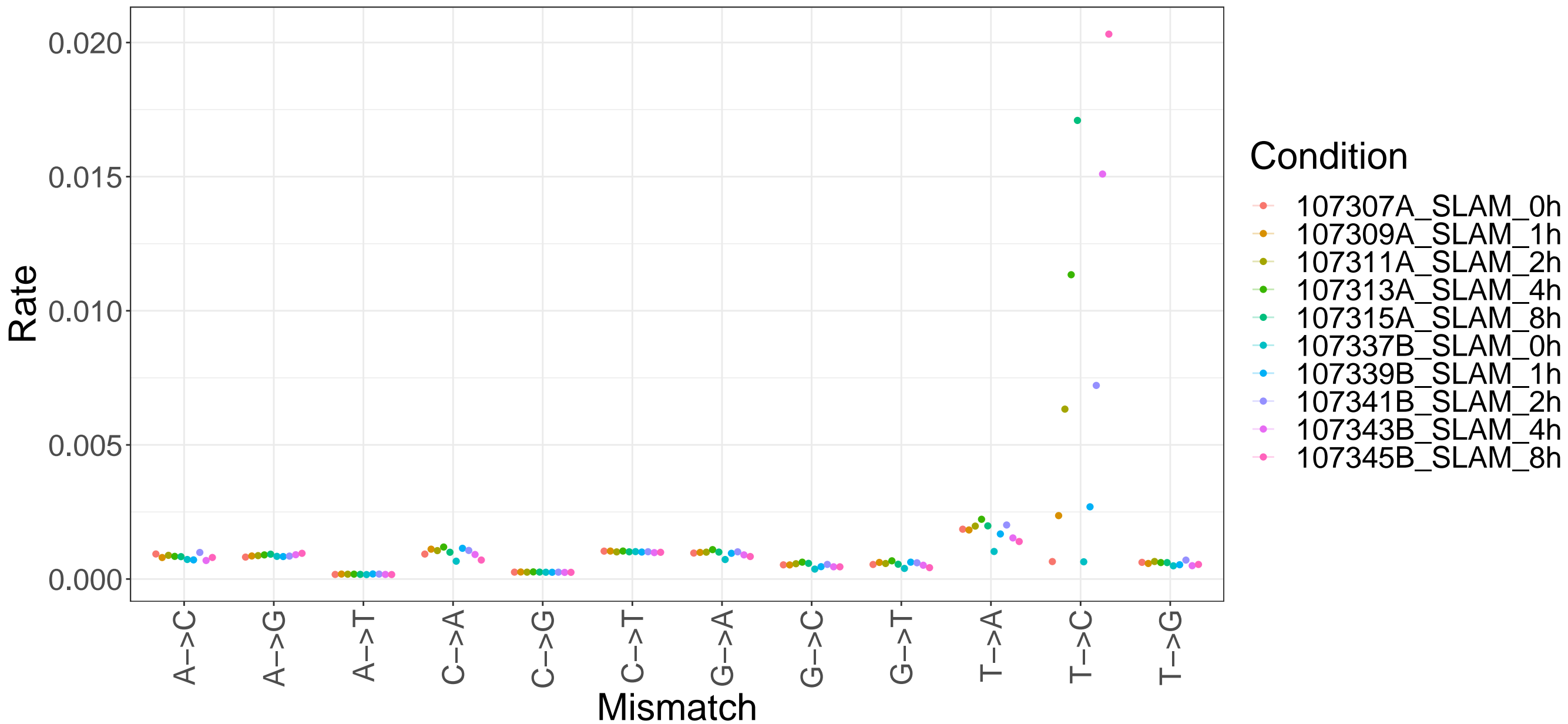
This file includes mismatch statistics for all nucleotide conversion protocols obtained with the ‘pulseR workflow’ (Methods). The first 6 pages include mismatch rates for all first and second reads that are used by featureCounts, per sample. The subsequent pages show mismatches for each position in a read per sample. The first 100 positions correspond to the first read, and positions 100 to 200 to the second read. Genomic bases are on the top, and the color encodes bases in the reads.

See <https://github.com/dieterich-lab/ComparisonOfMetabolicLabeling> under the directory ‘pulseRTc/workflow/mismatches/’ for details.

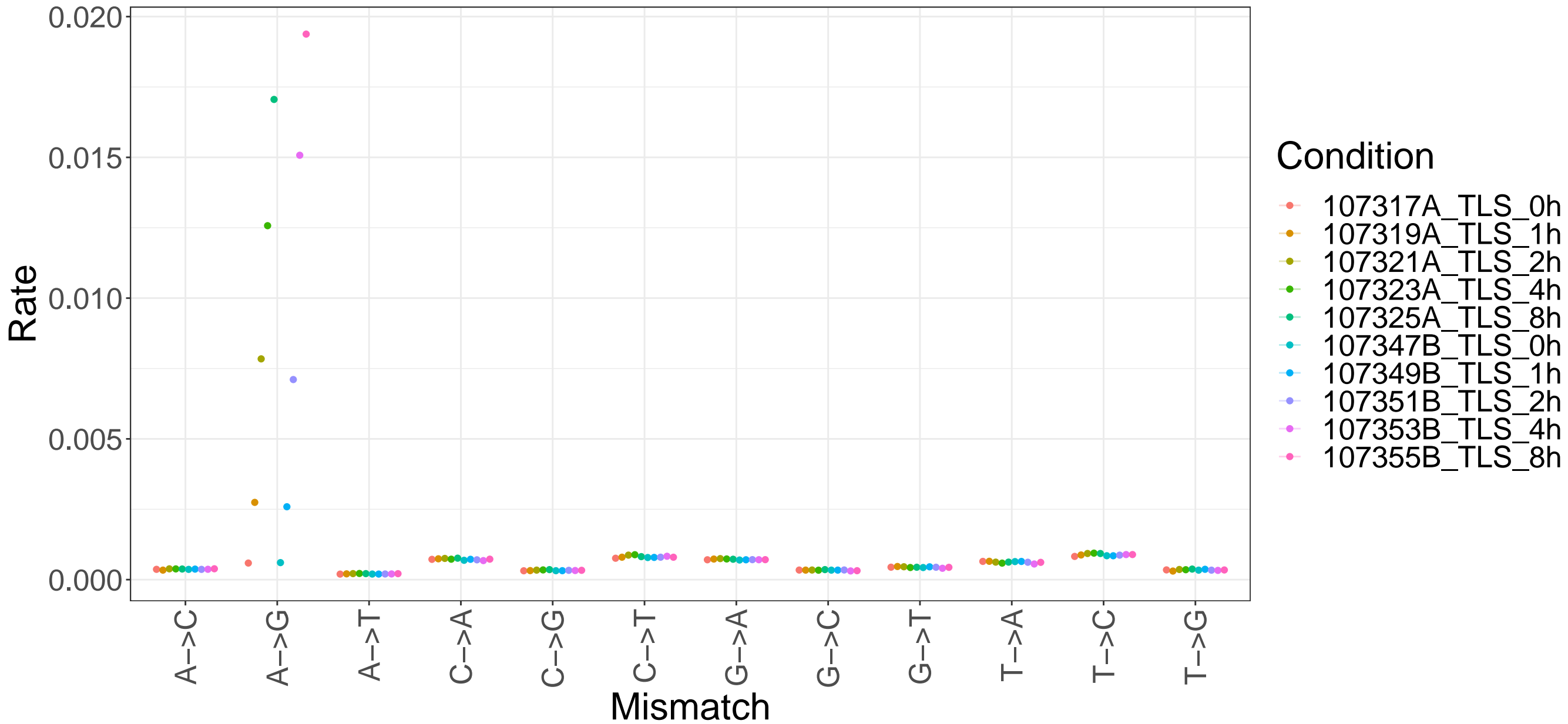
First



Second

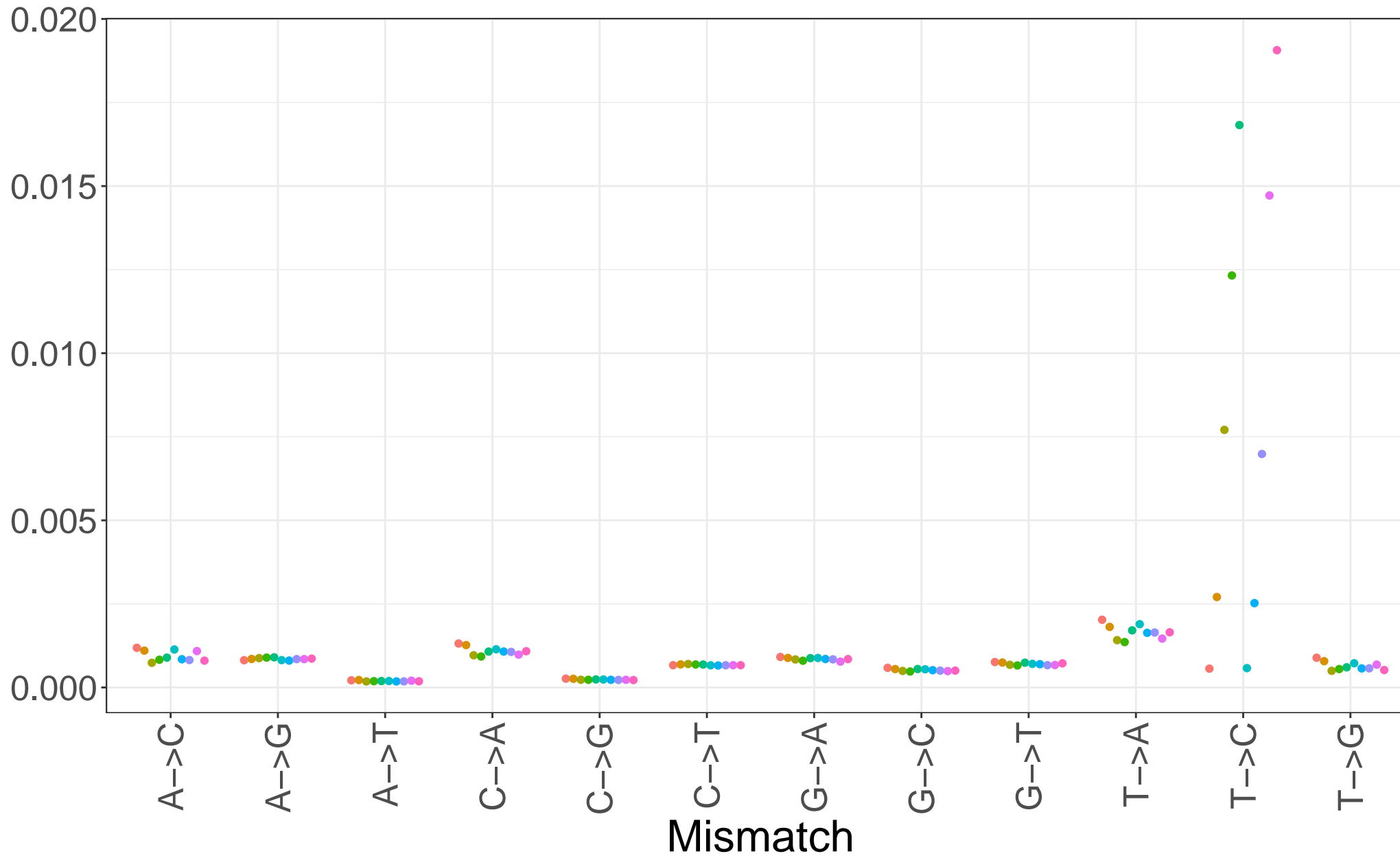


First



Second

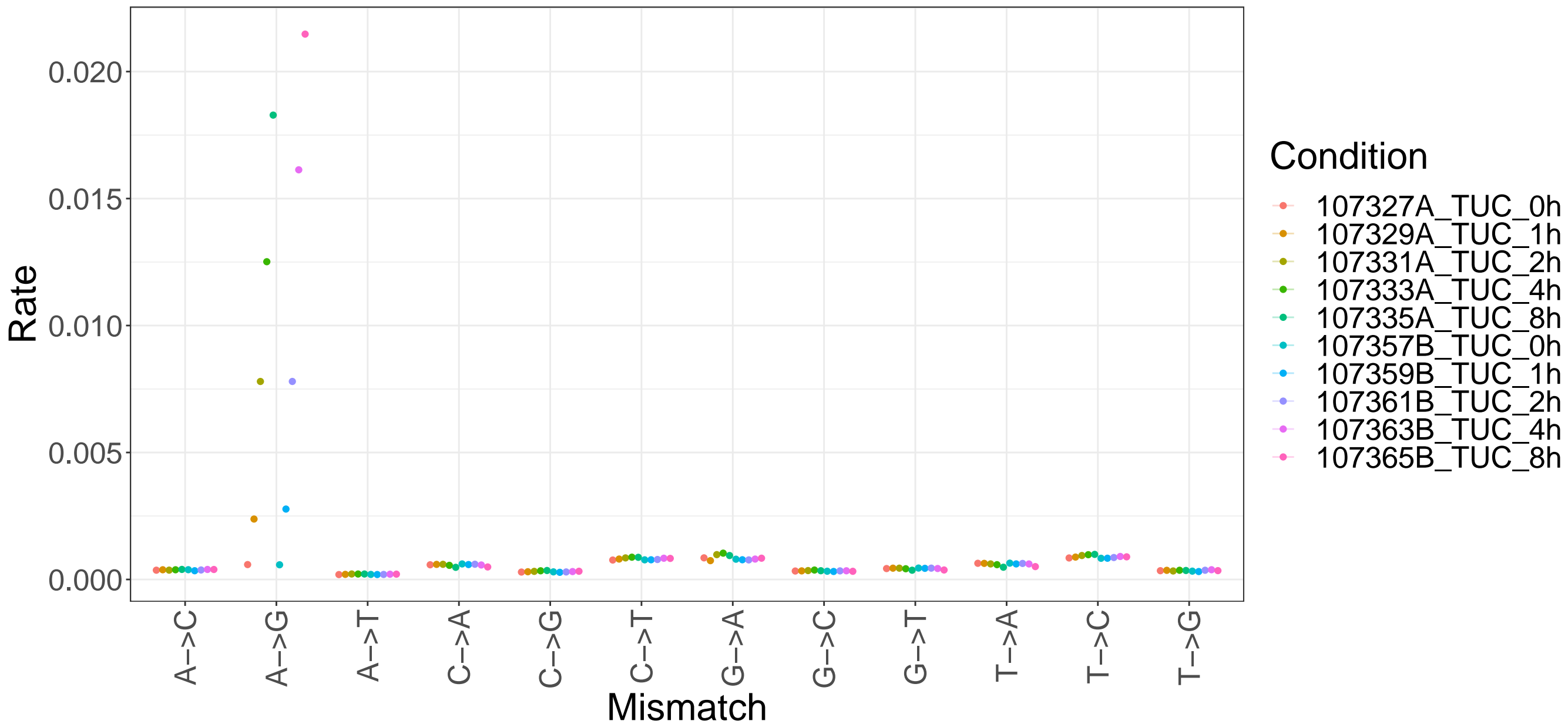
Rate



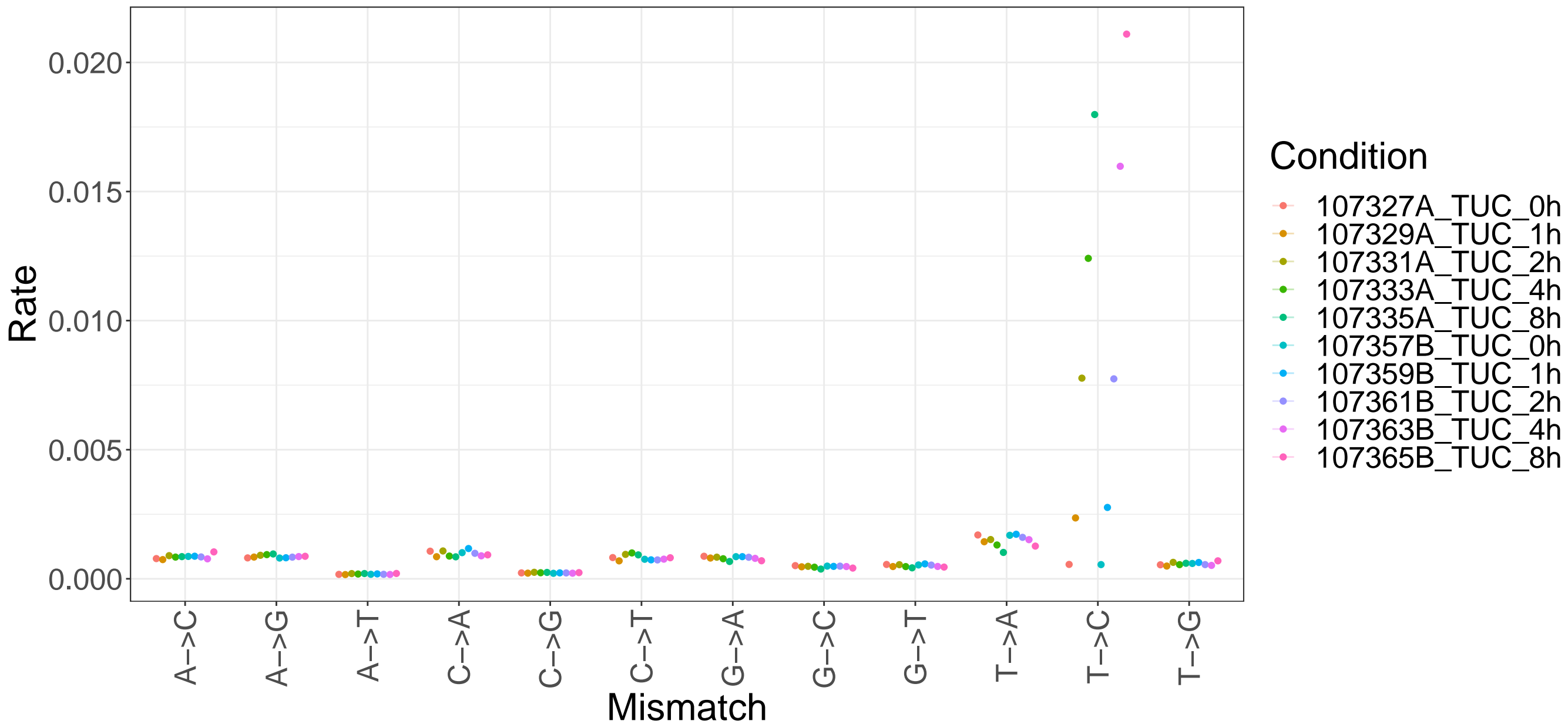
Condition

- 107317A_TLS_0h
- 107319A_TLS_1h
- 107321A_TLS_2h
- 107323A_TLS_4h
- 107325A_TLS_8h
- 107347B_TLS_0h
- 107349B_TLS_1h
- 107351B_TLS_2h
- 107353B_TLS_4h
- 107355B_TLS_8h

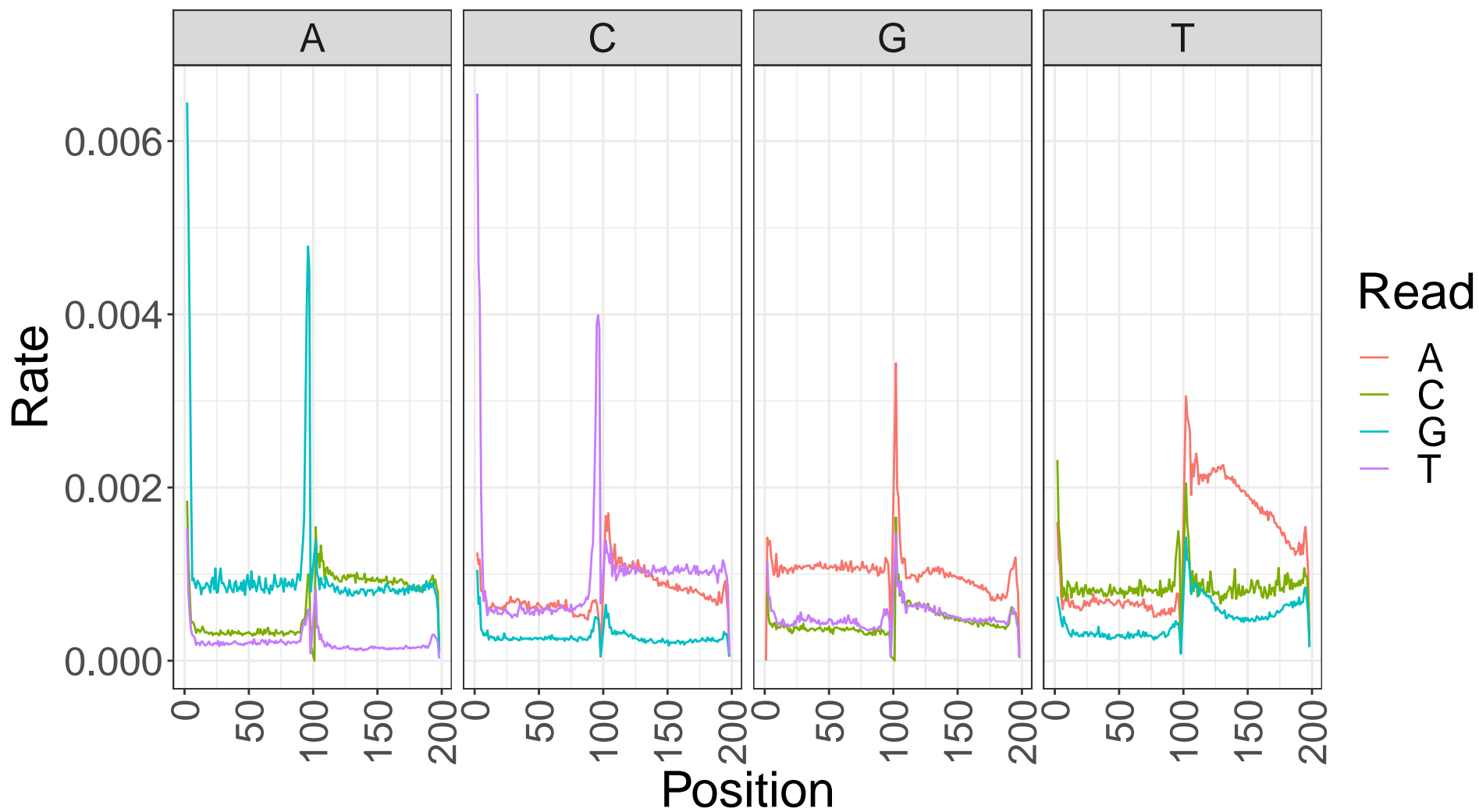
First



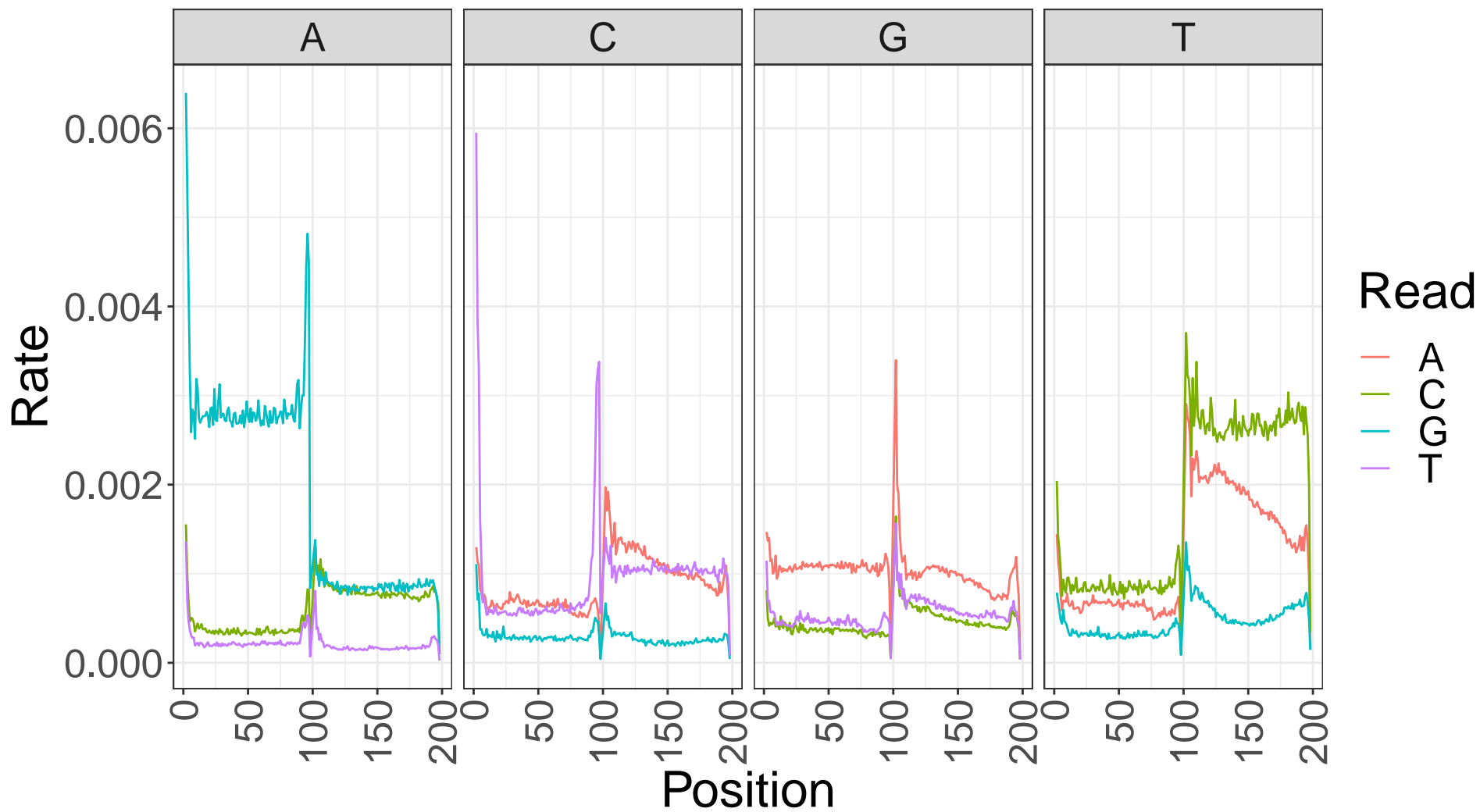
Second



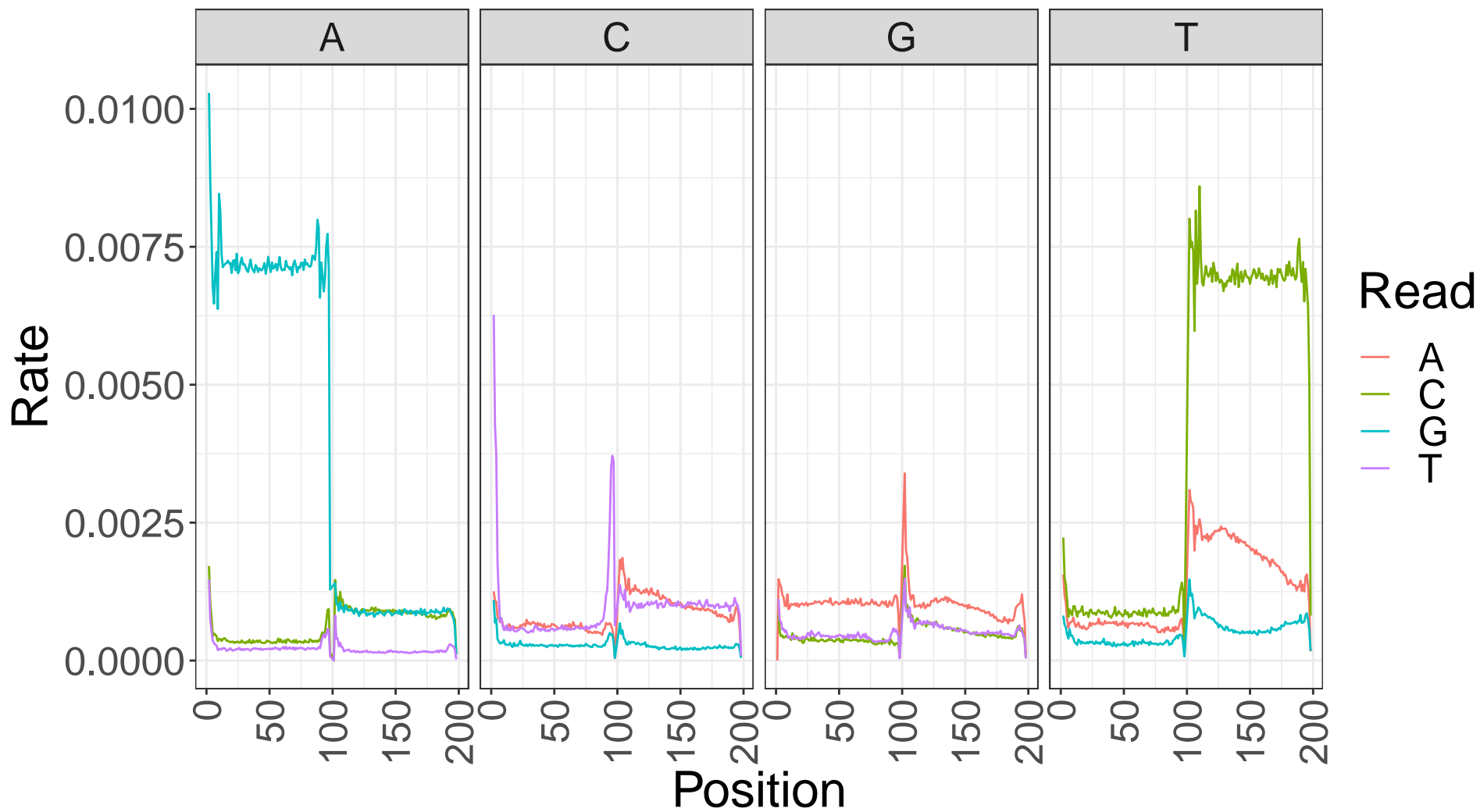
107307A_SLAM_0h



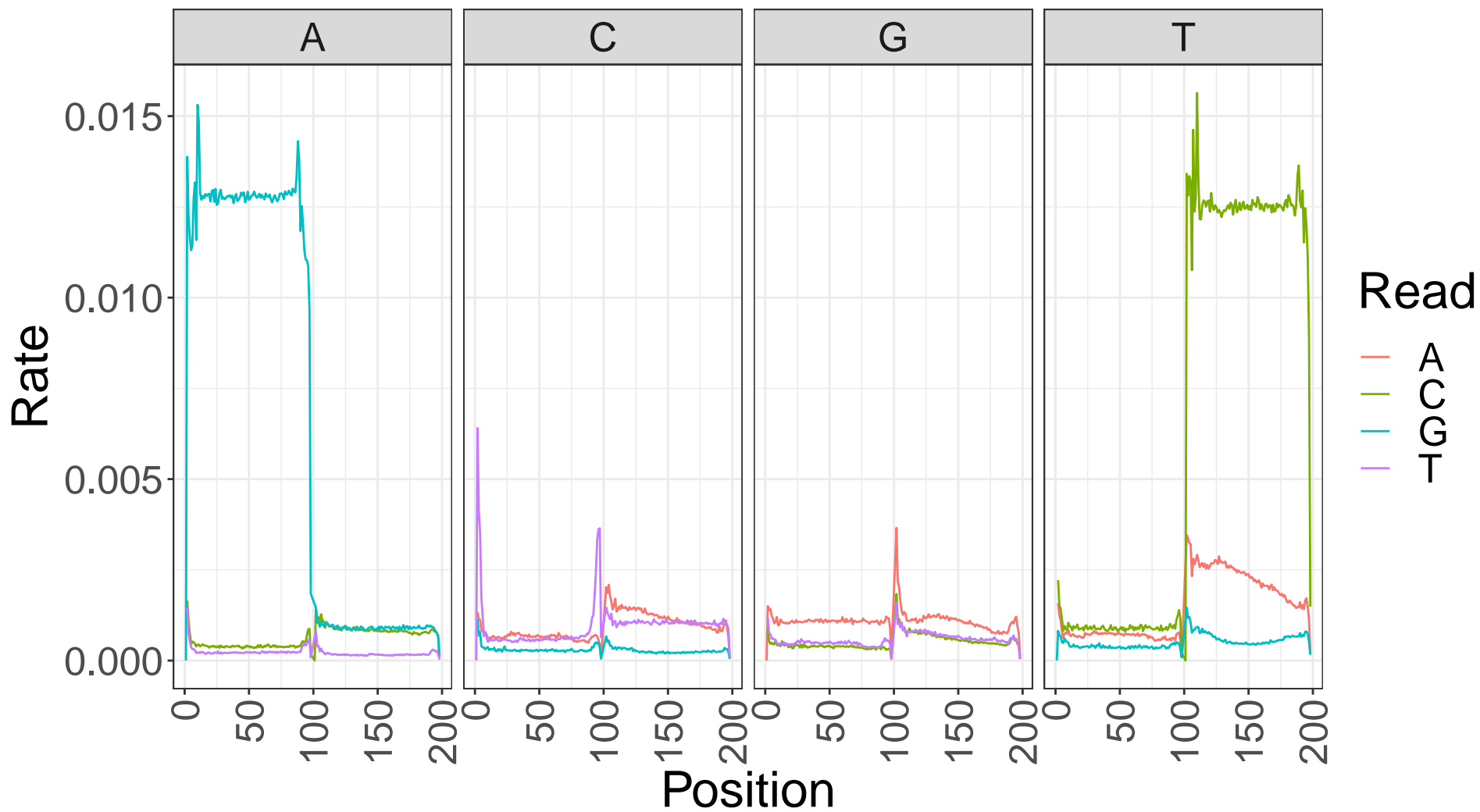
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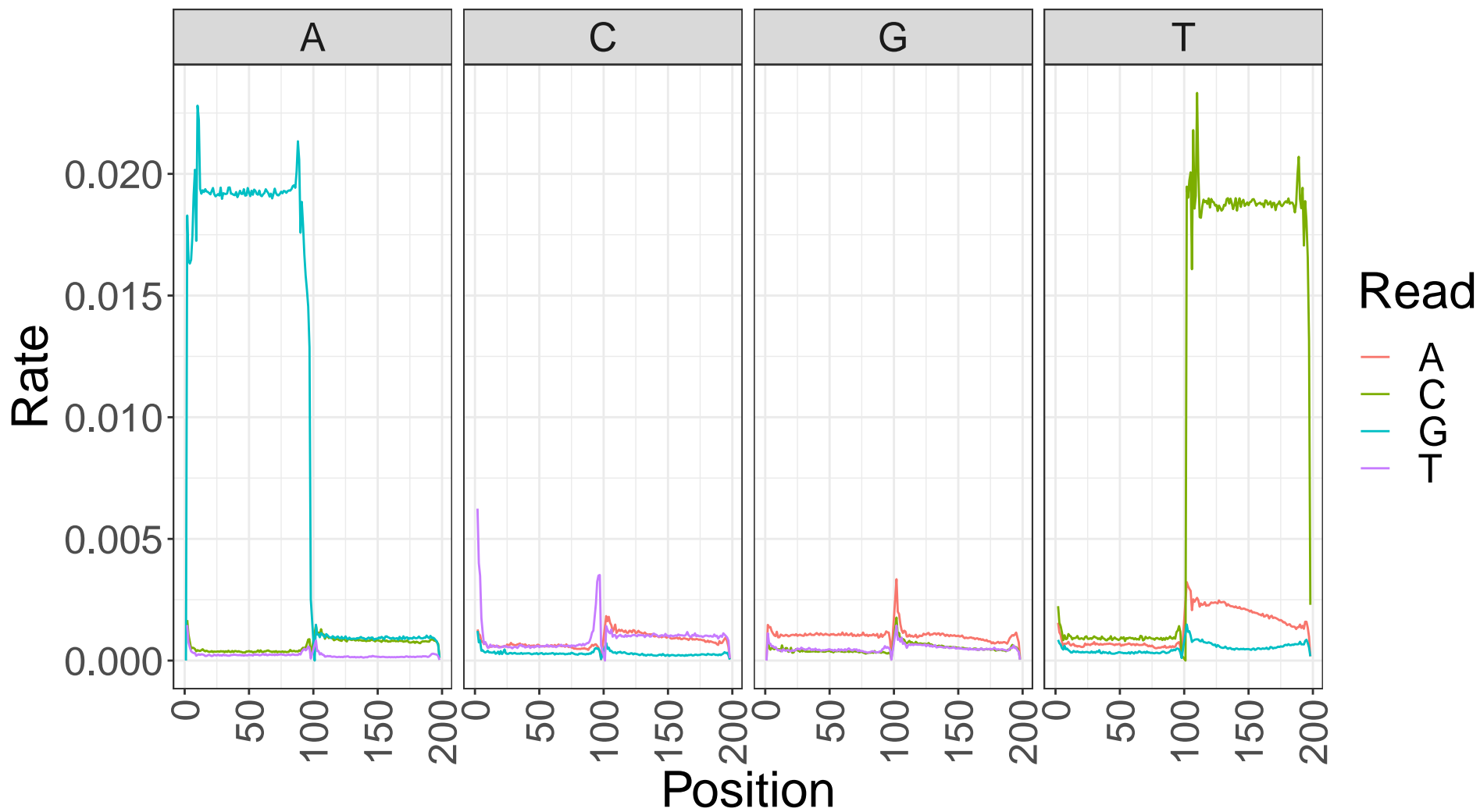
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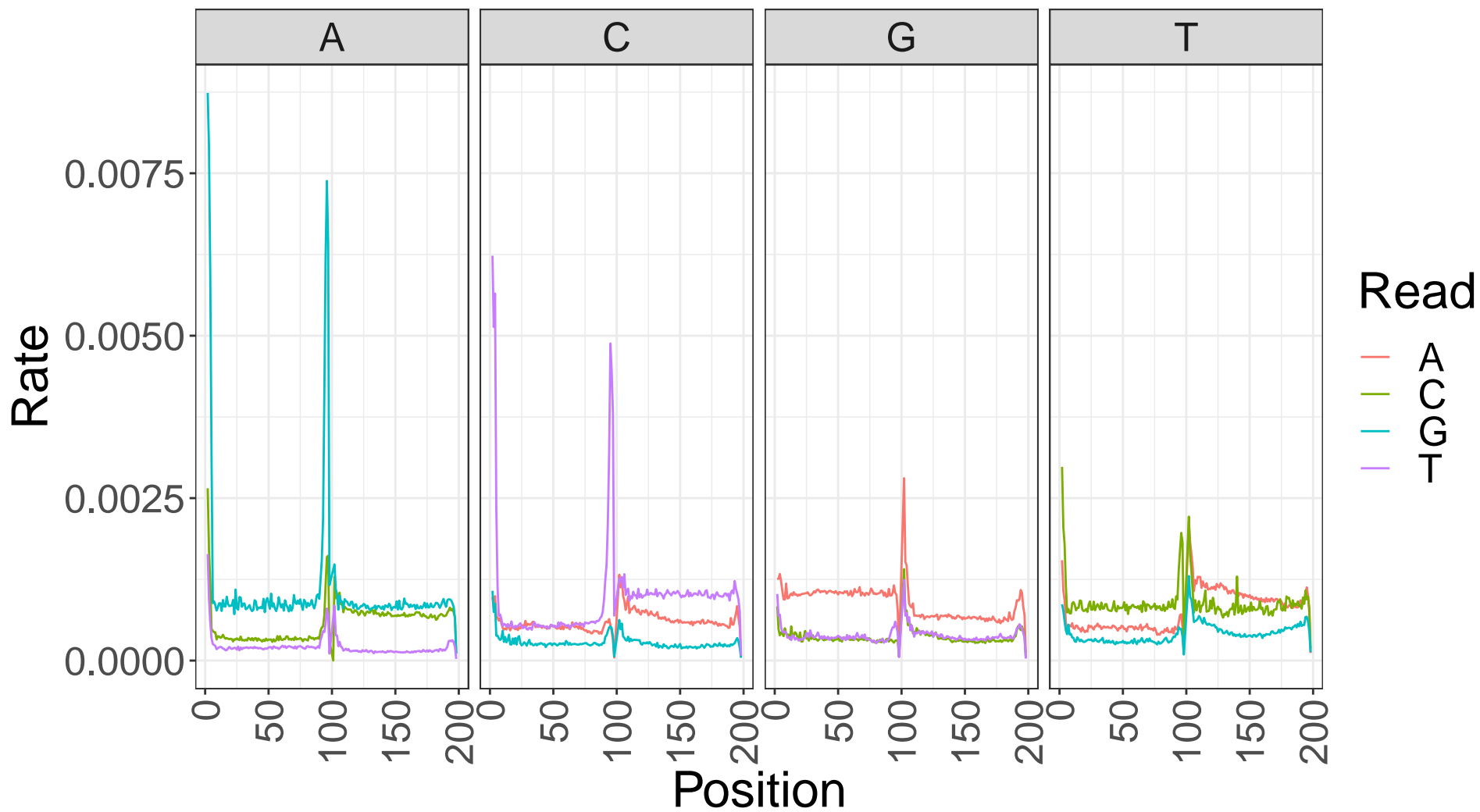
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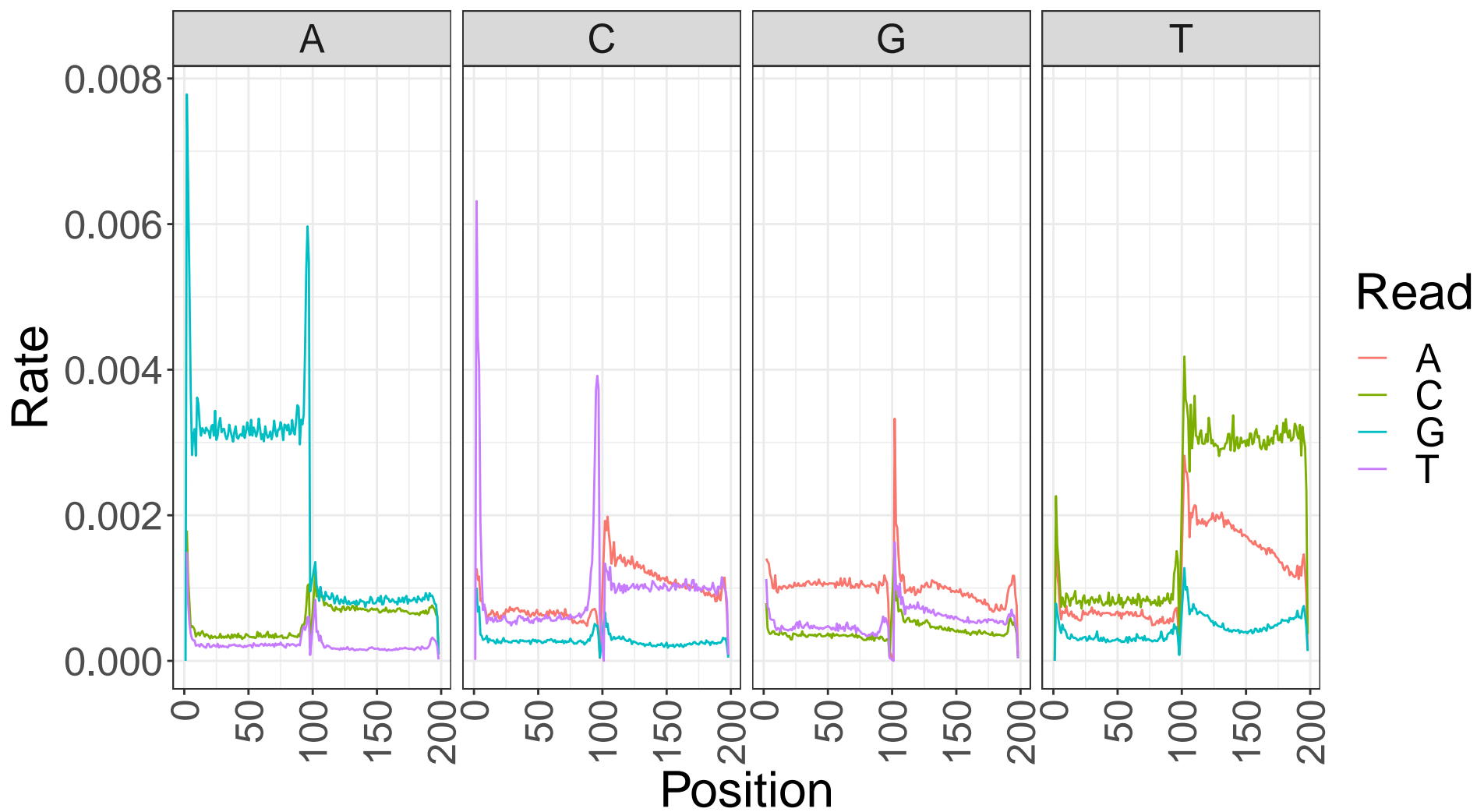
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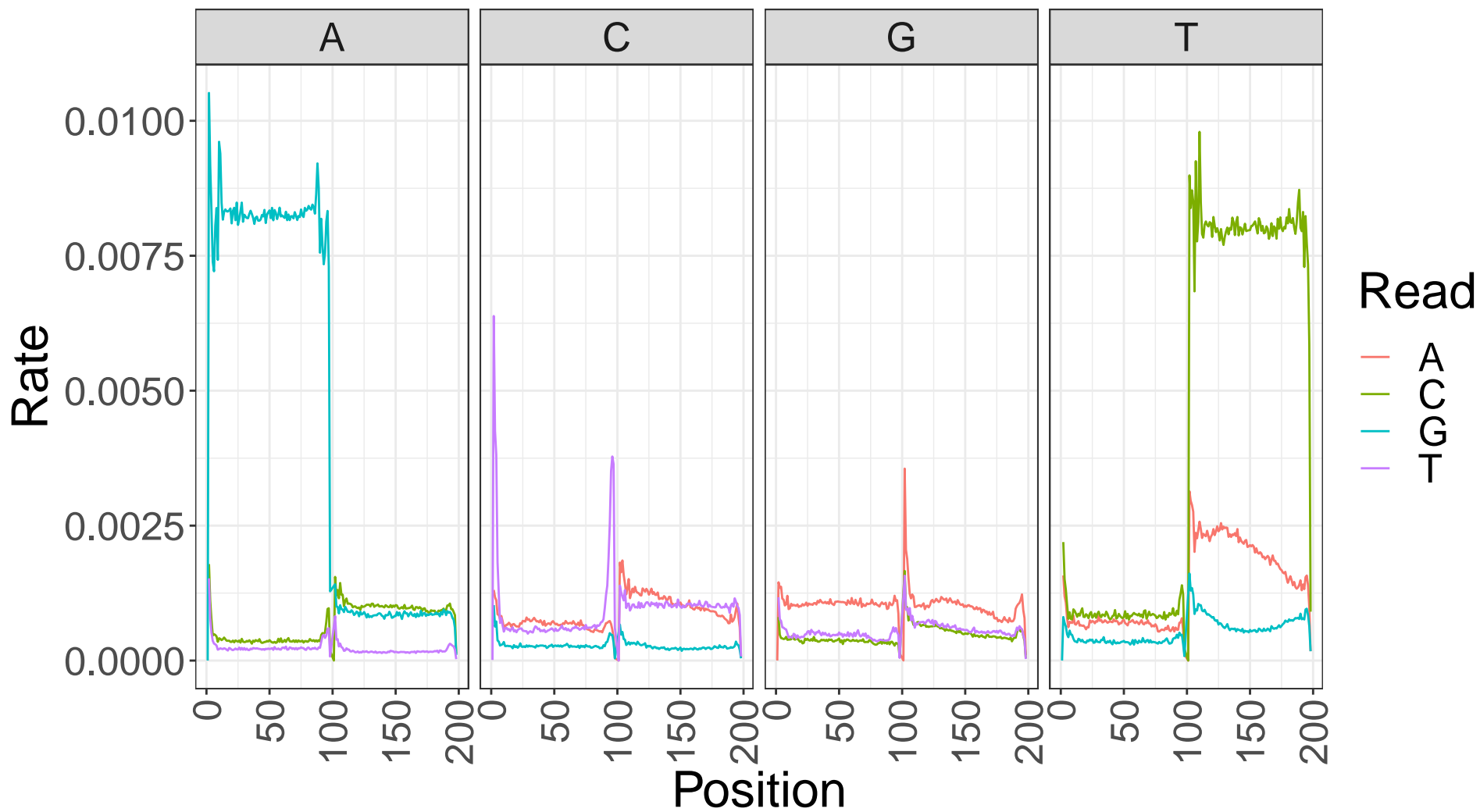
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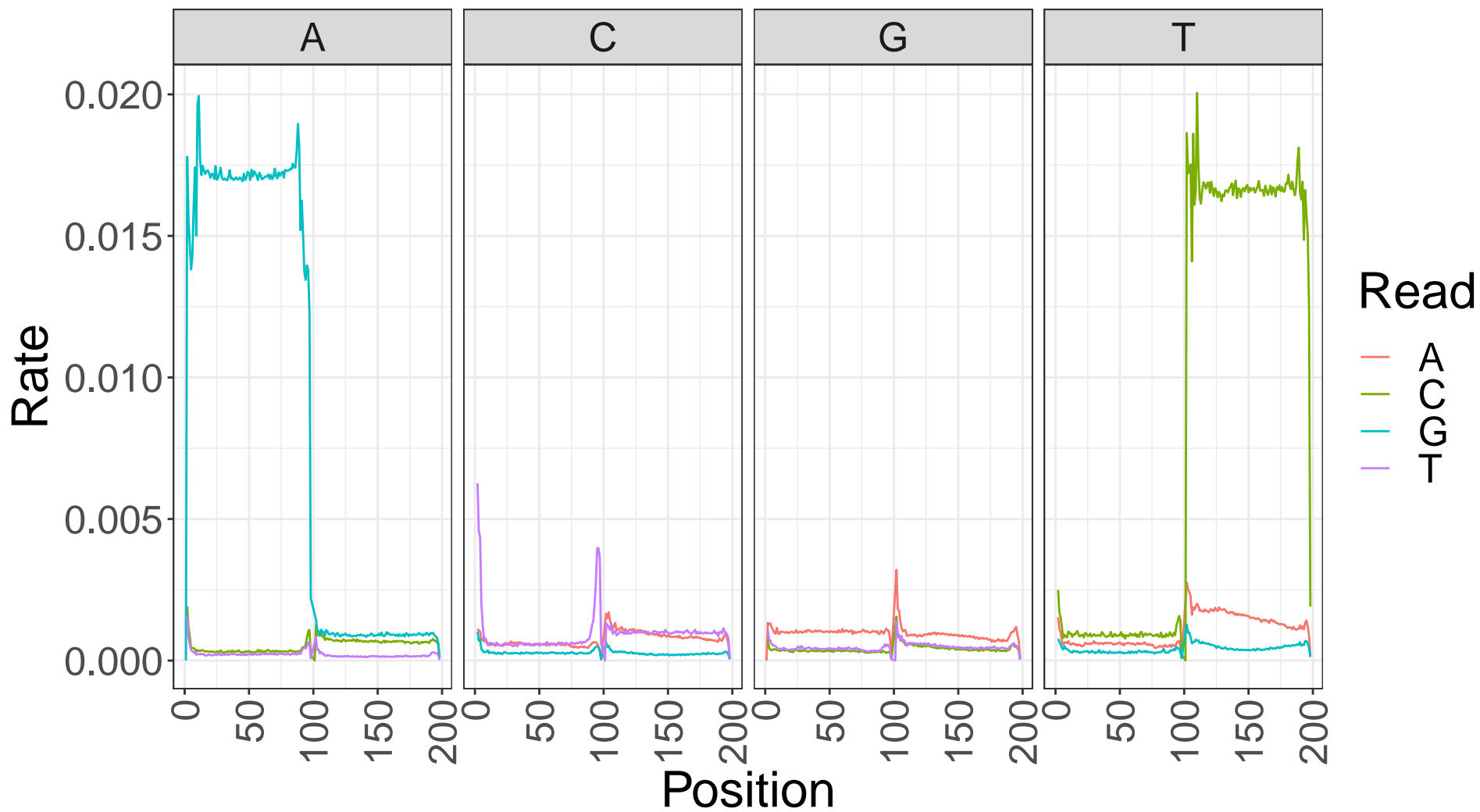
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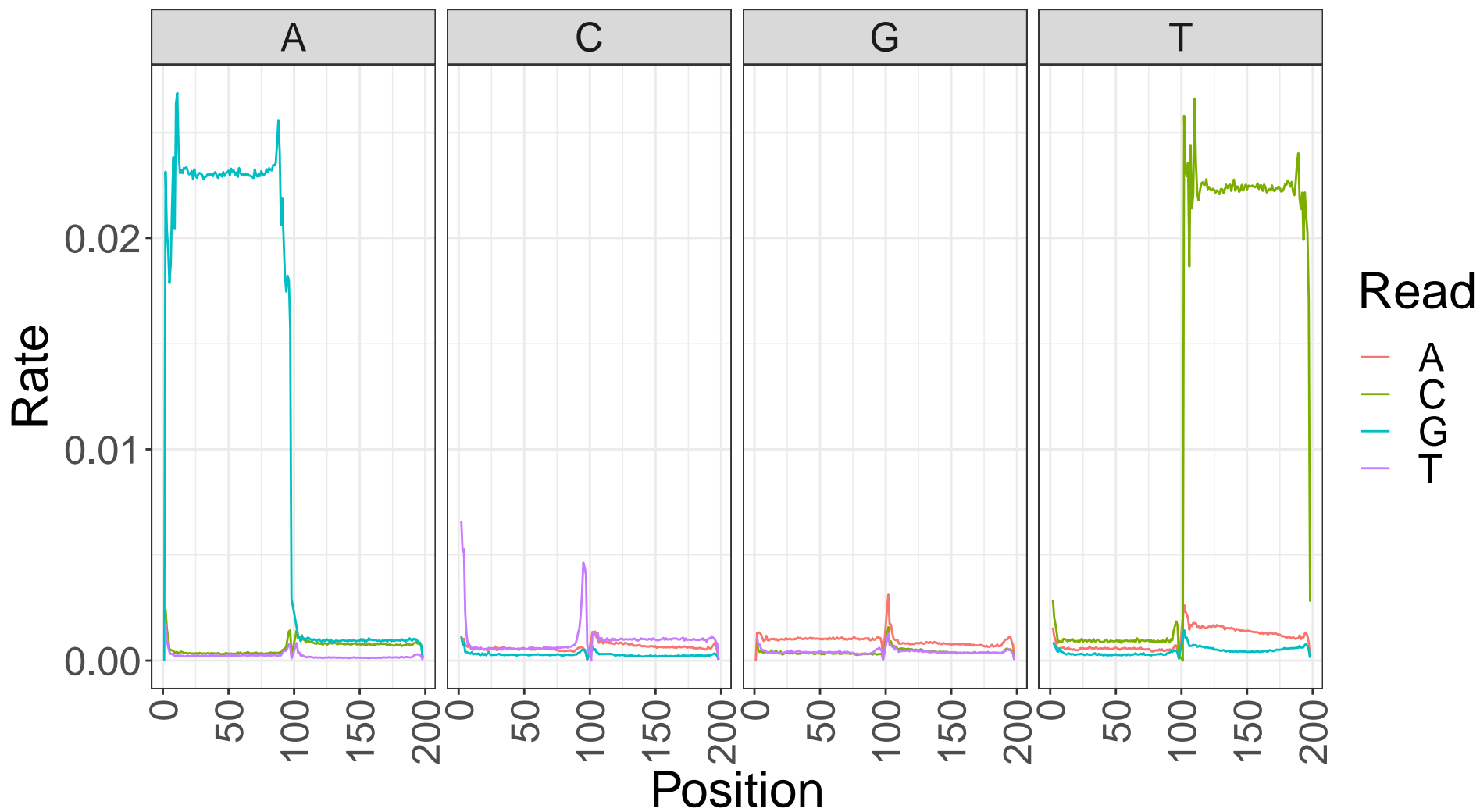
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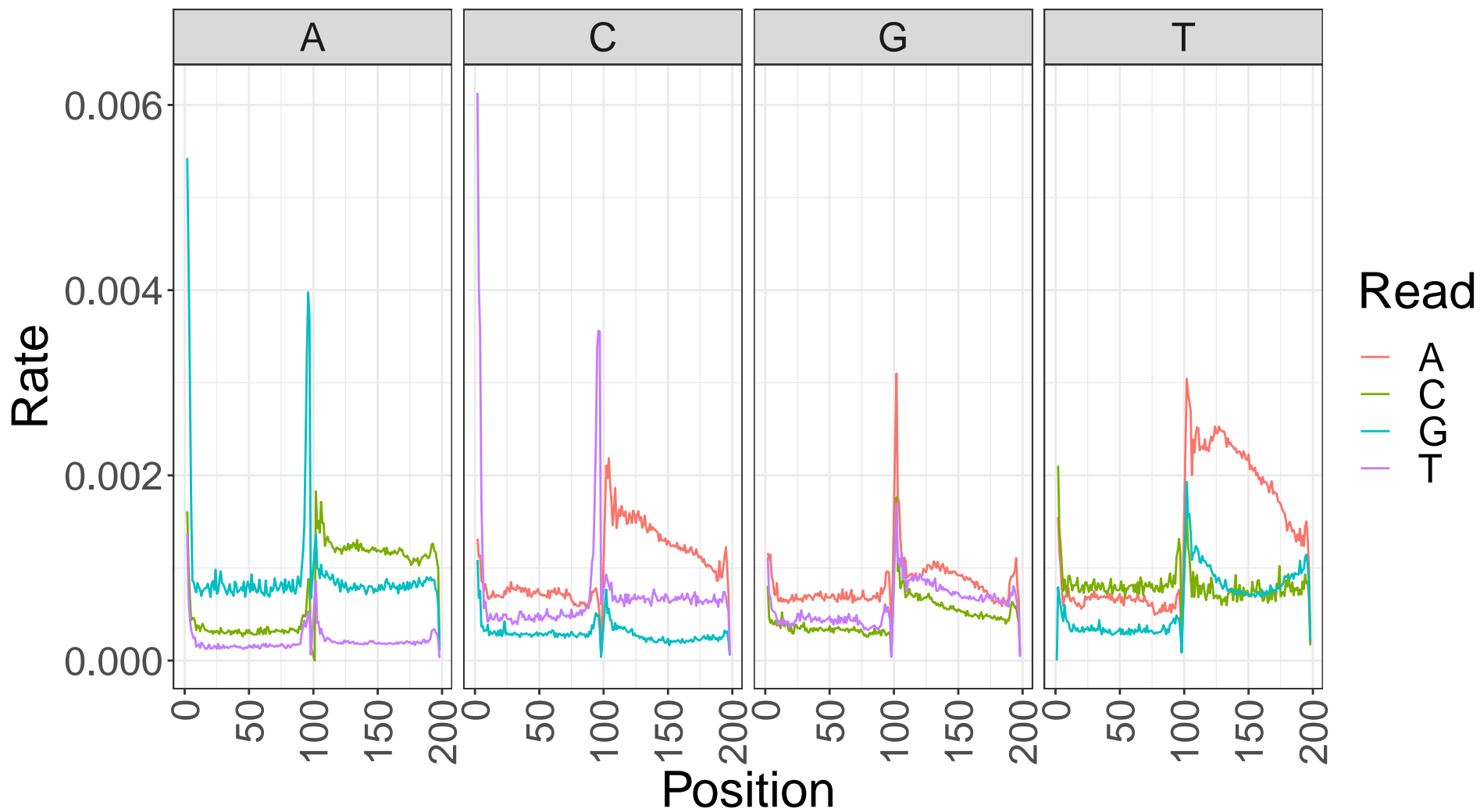
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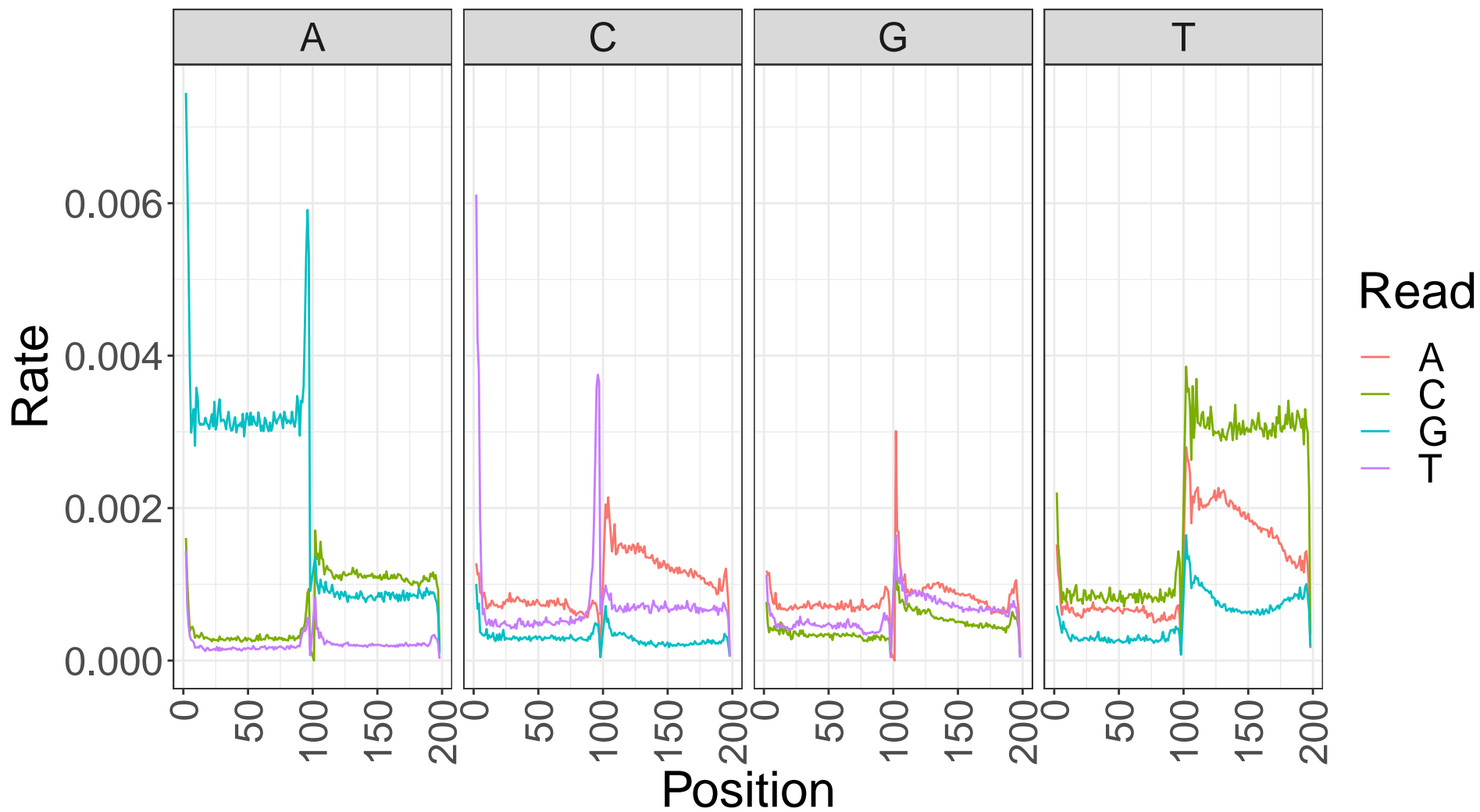
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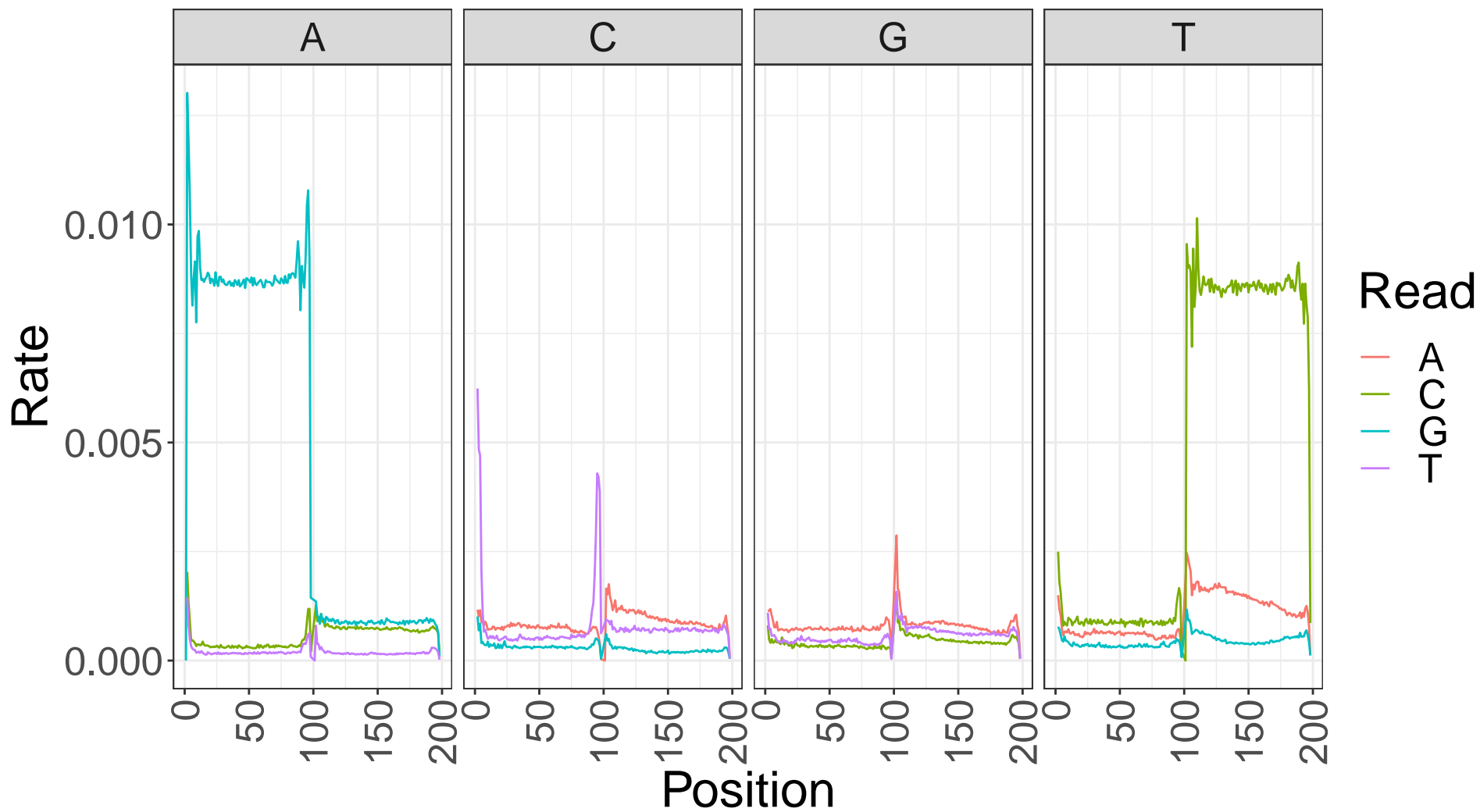
107317A_TLS_0h



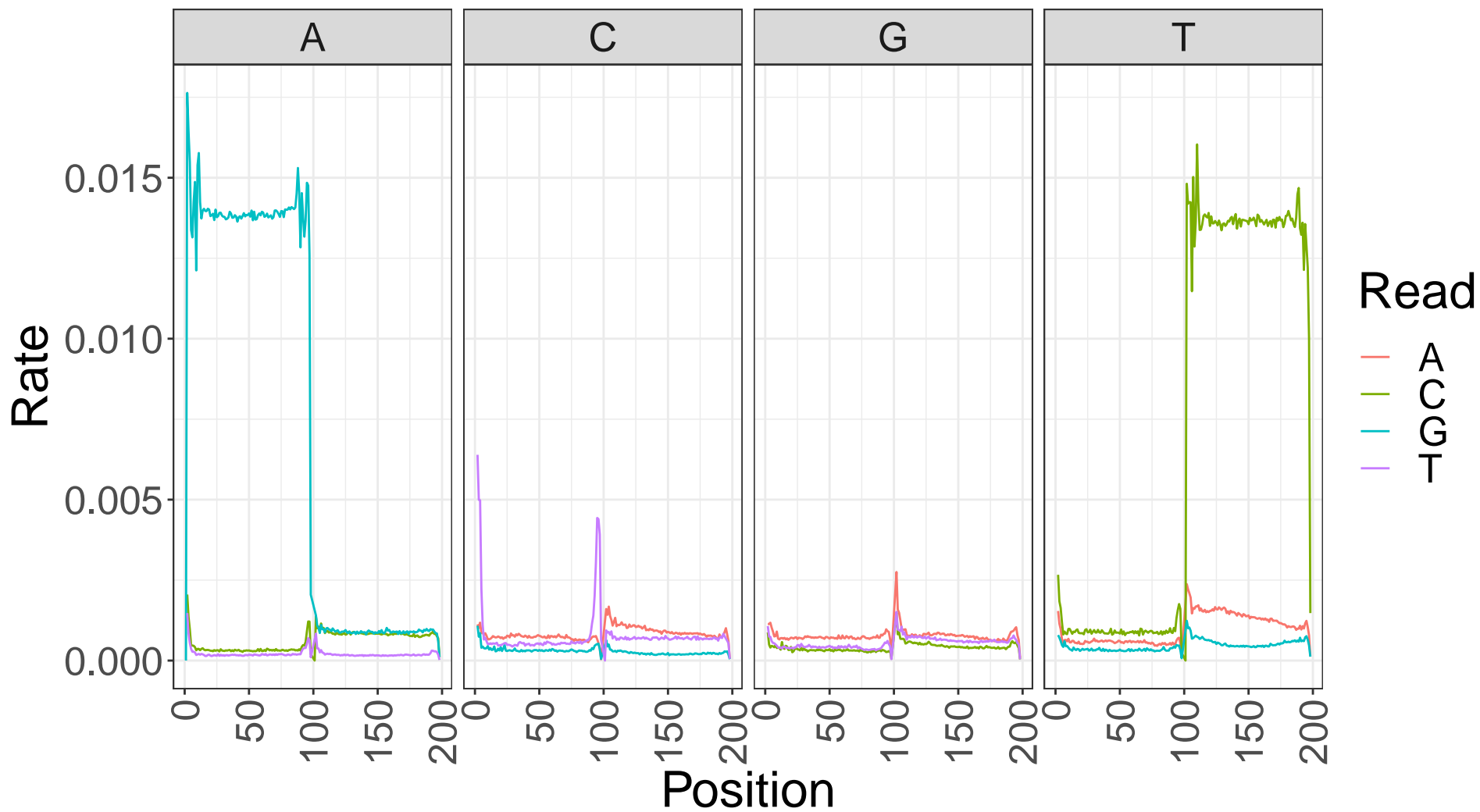
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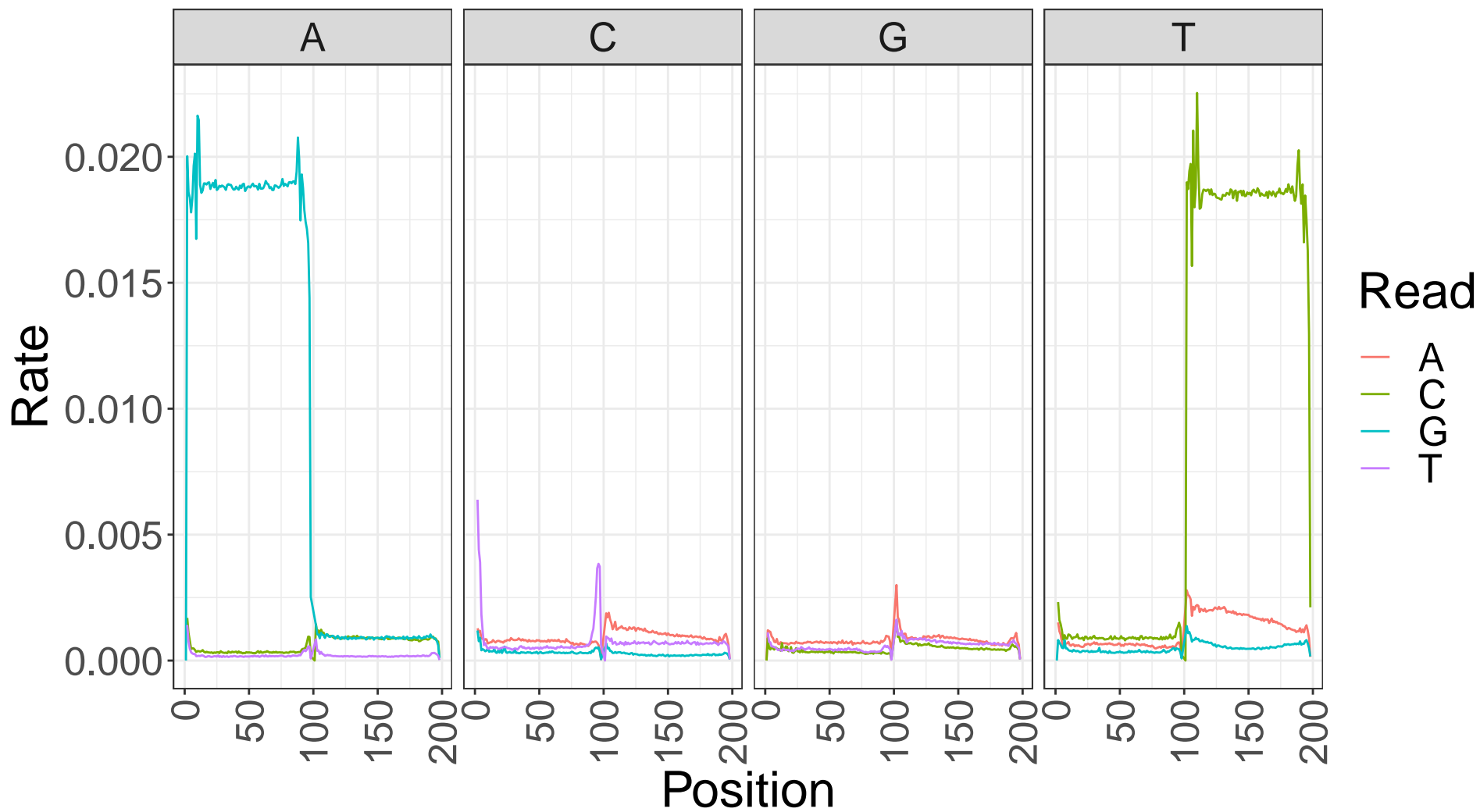
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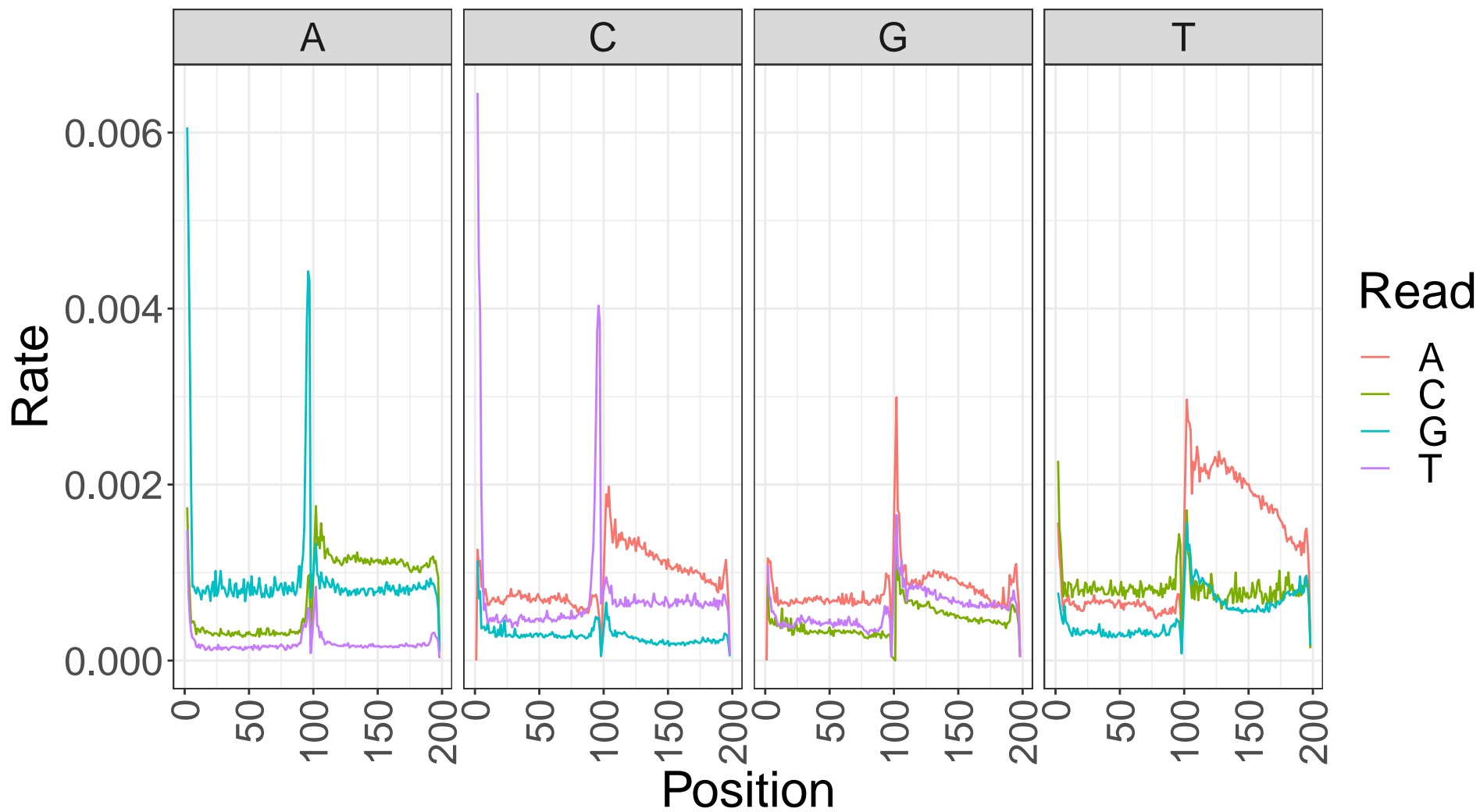
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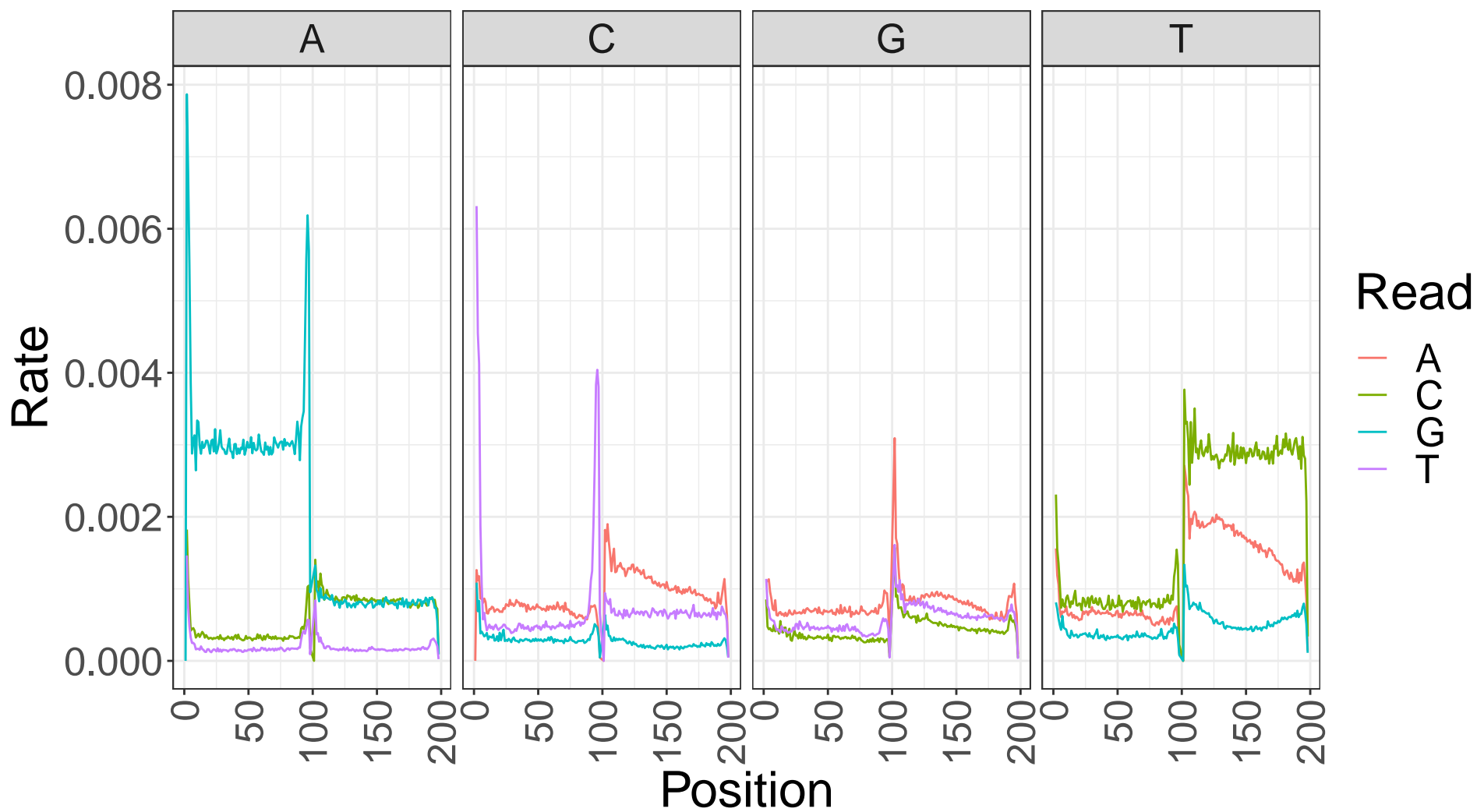
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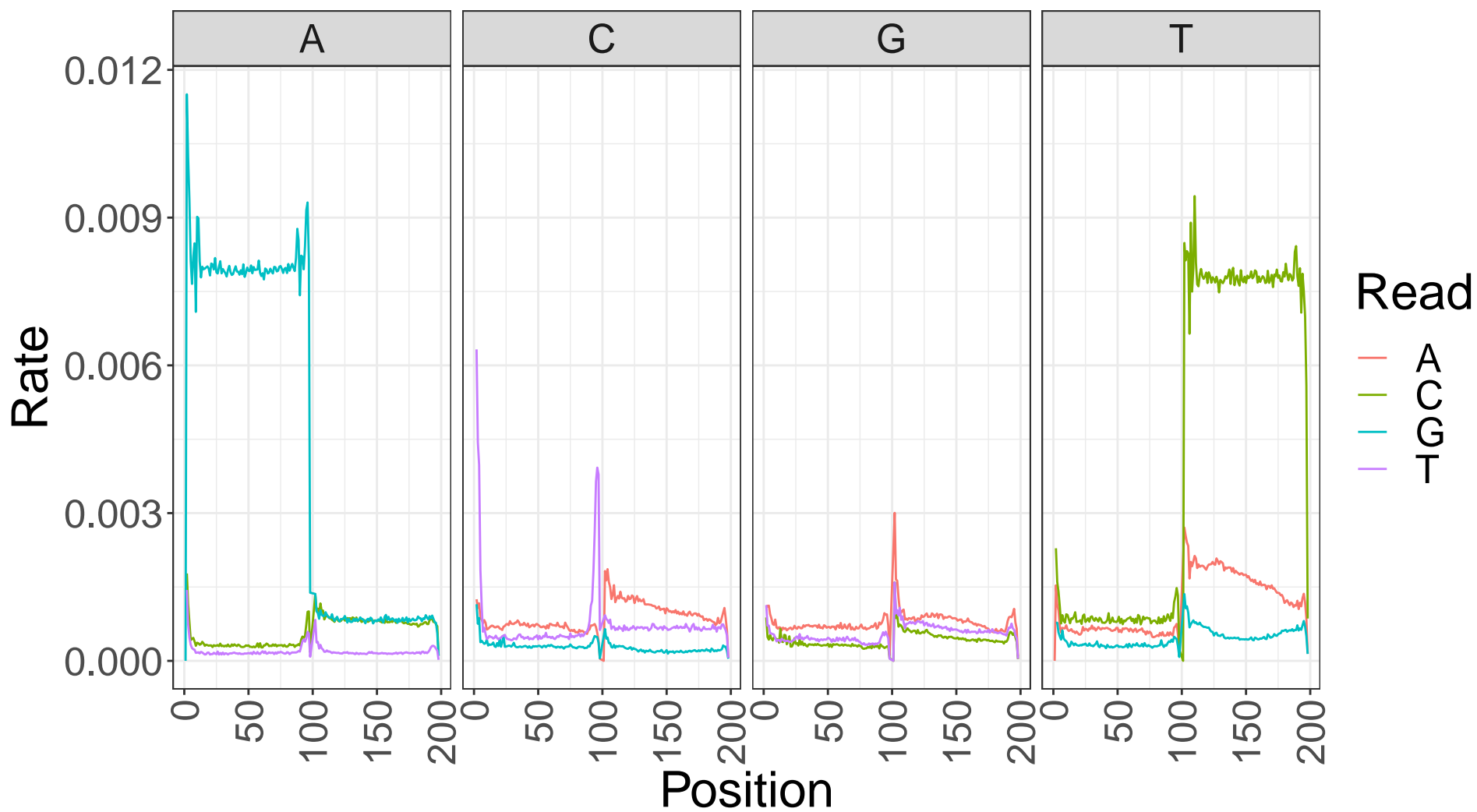
107347B_TLS_0h



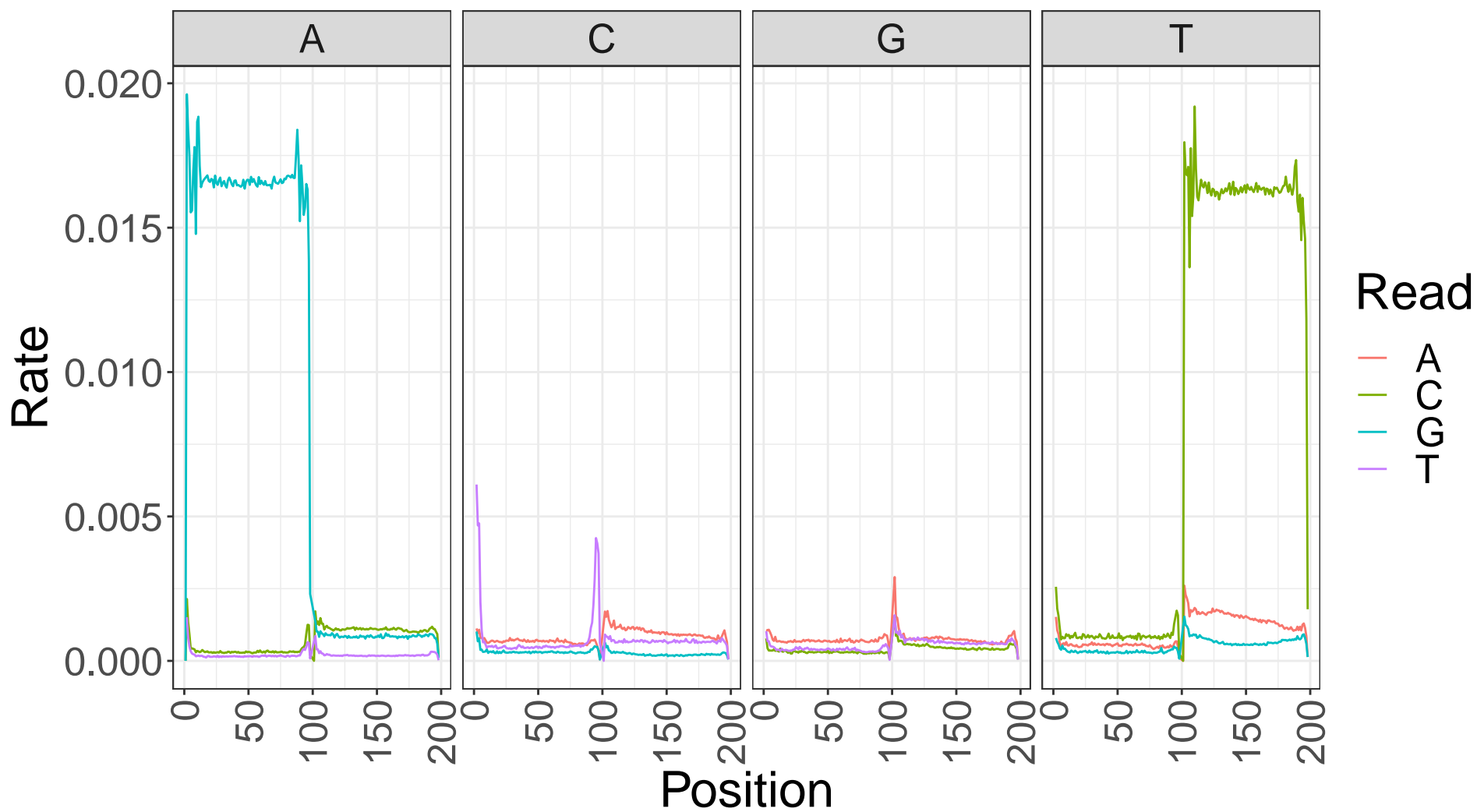
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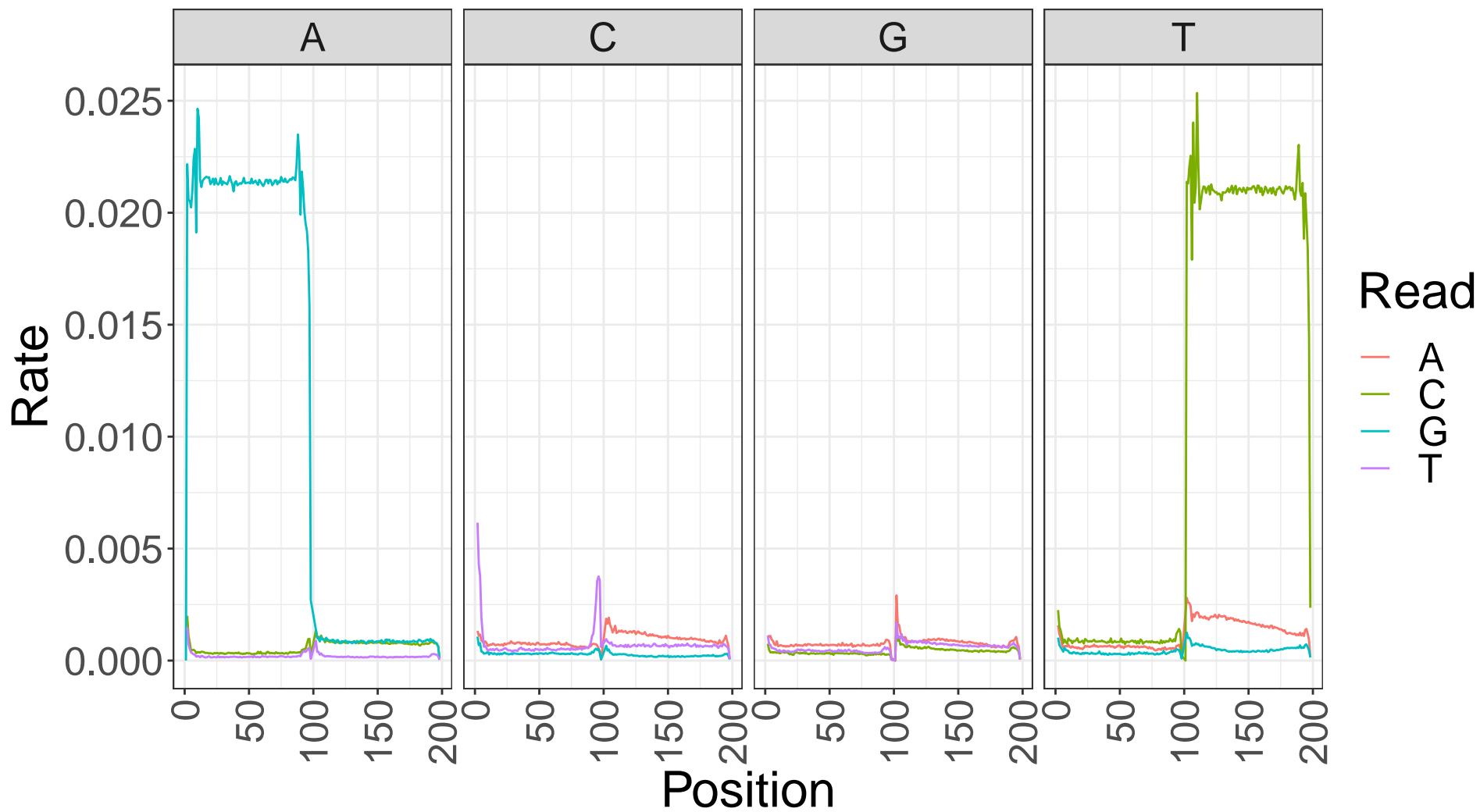
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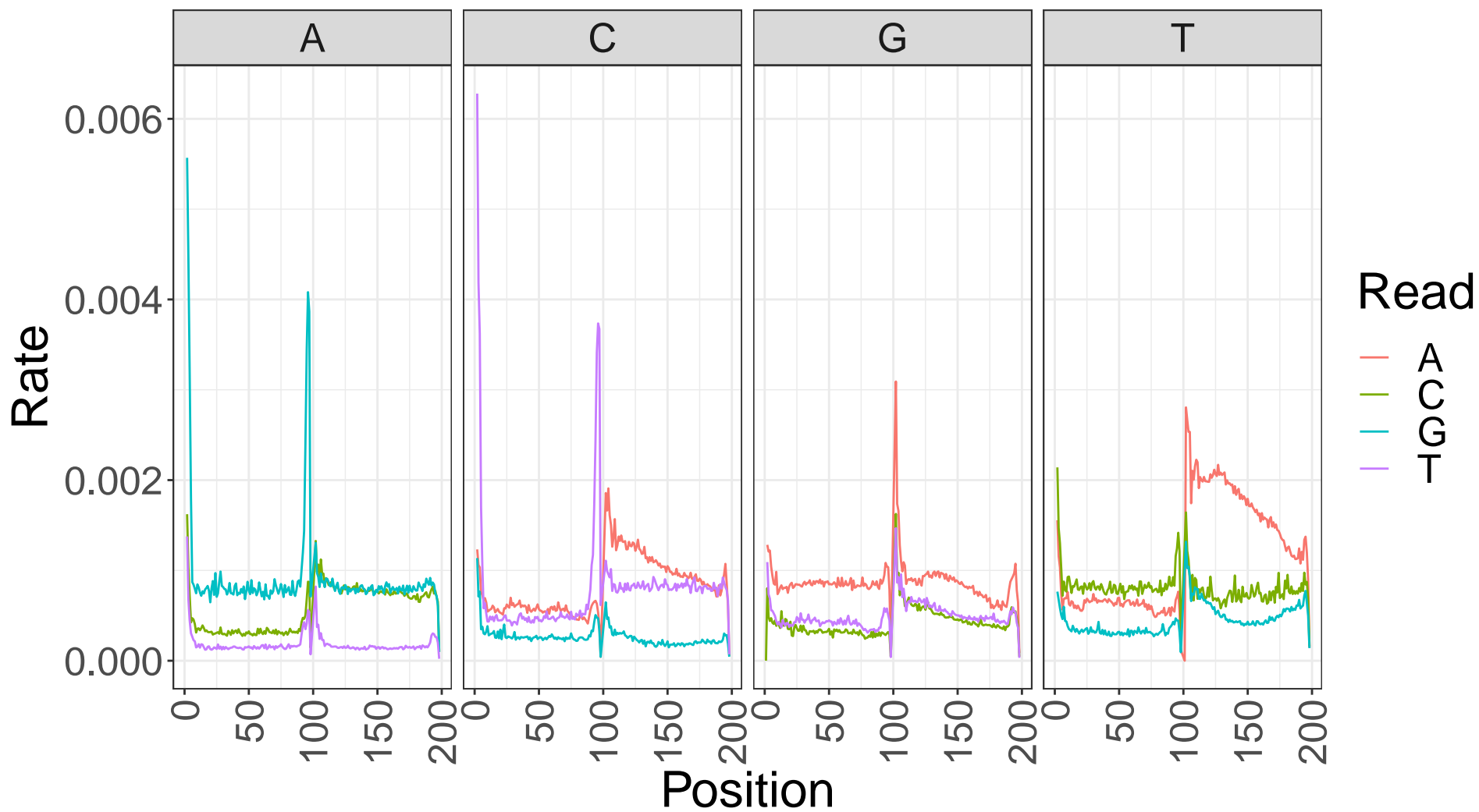
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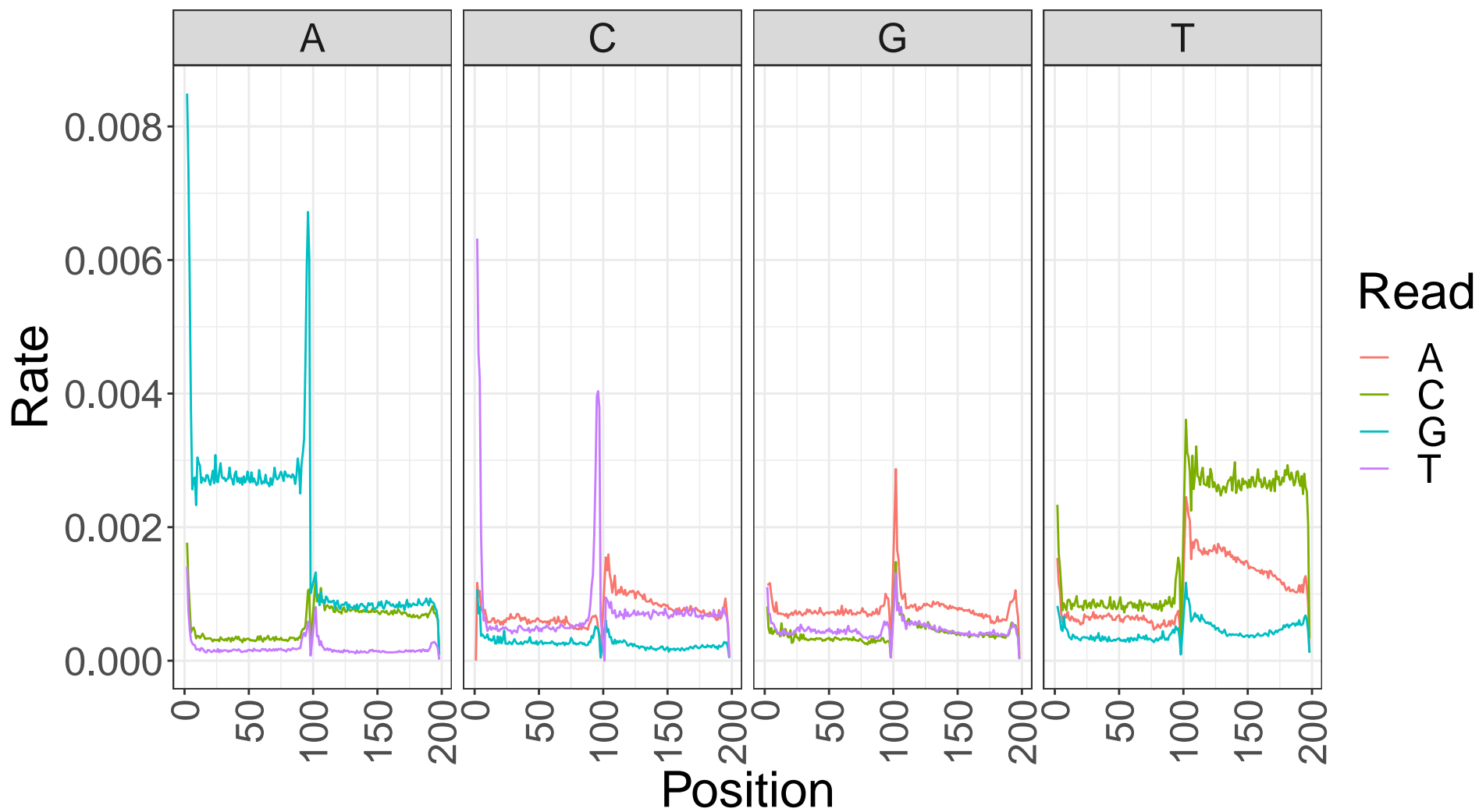
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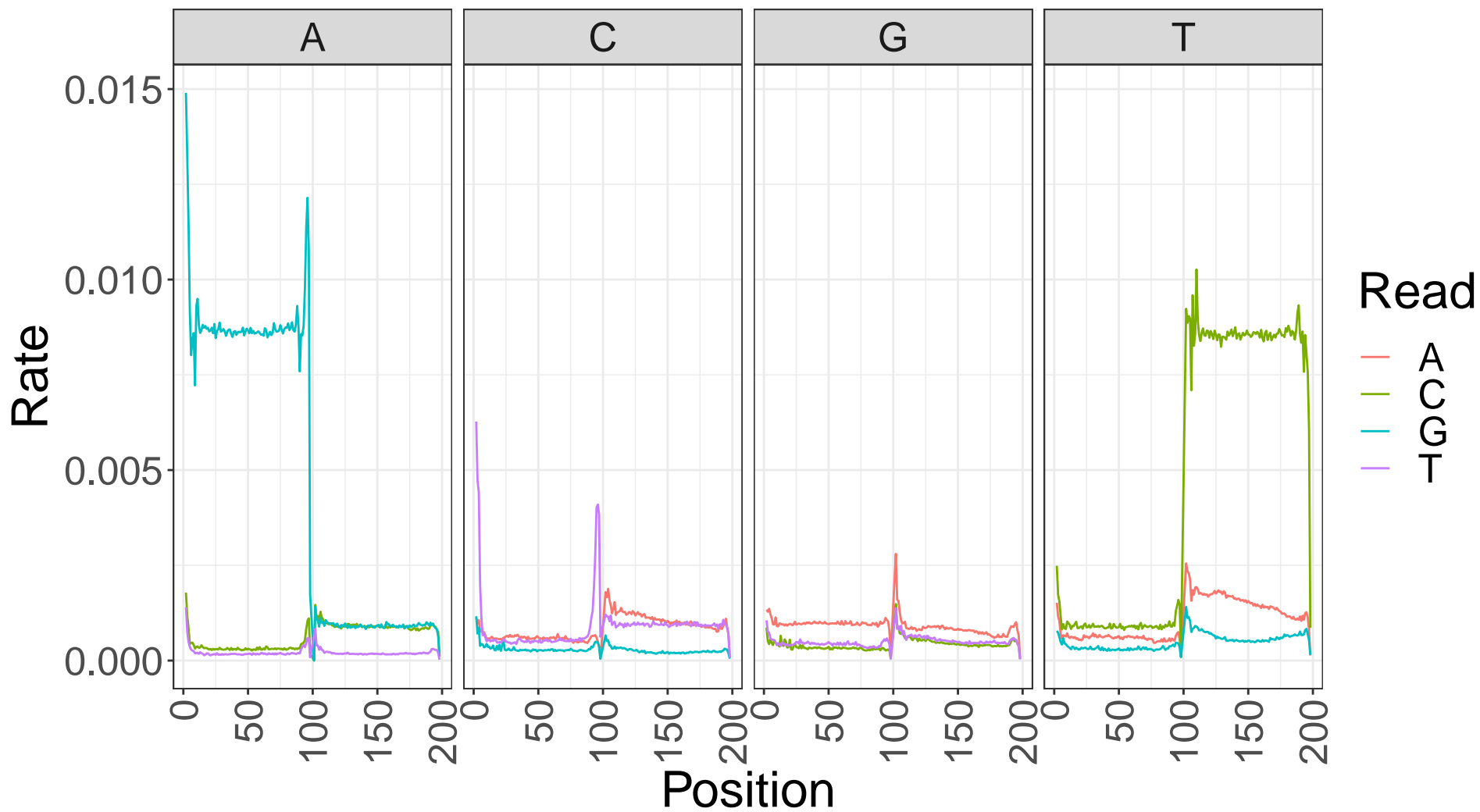
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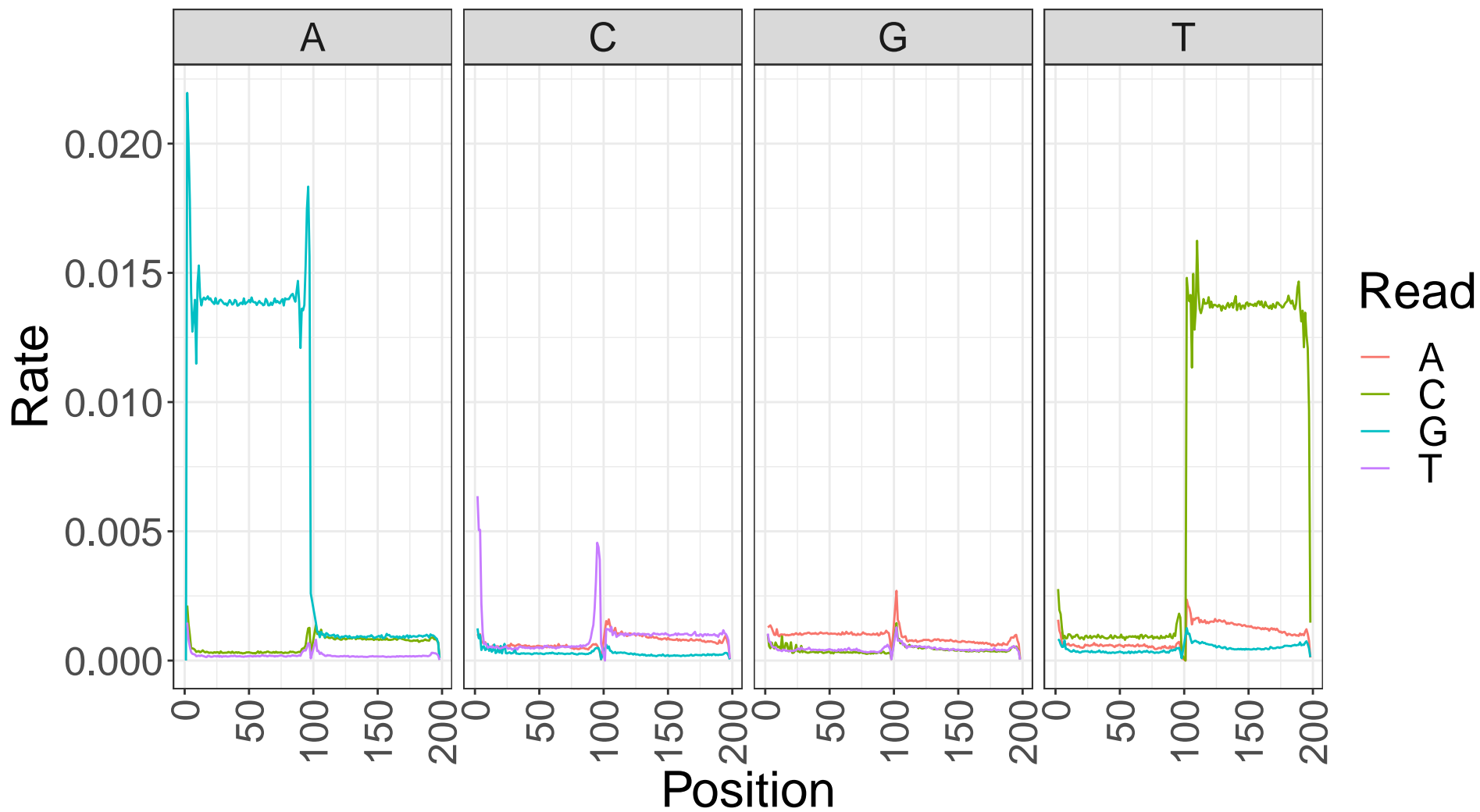
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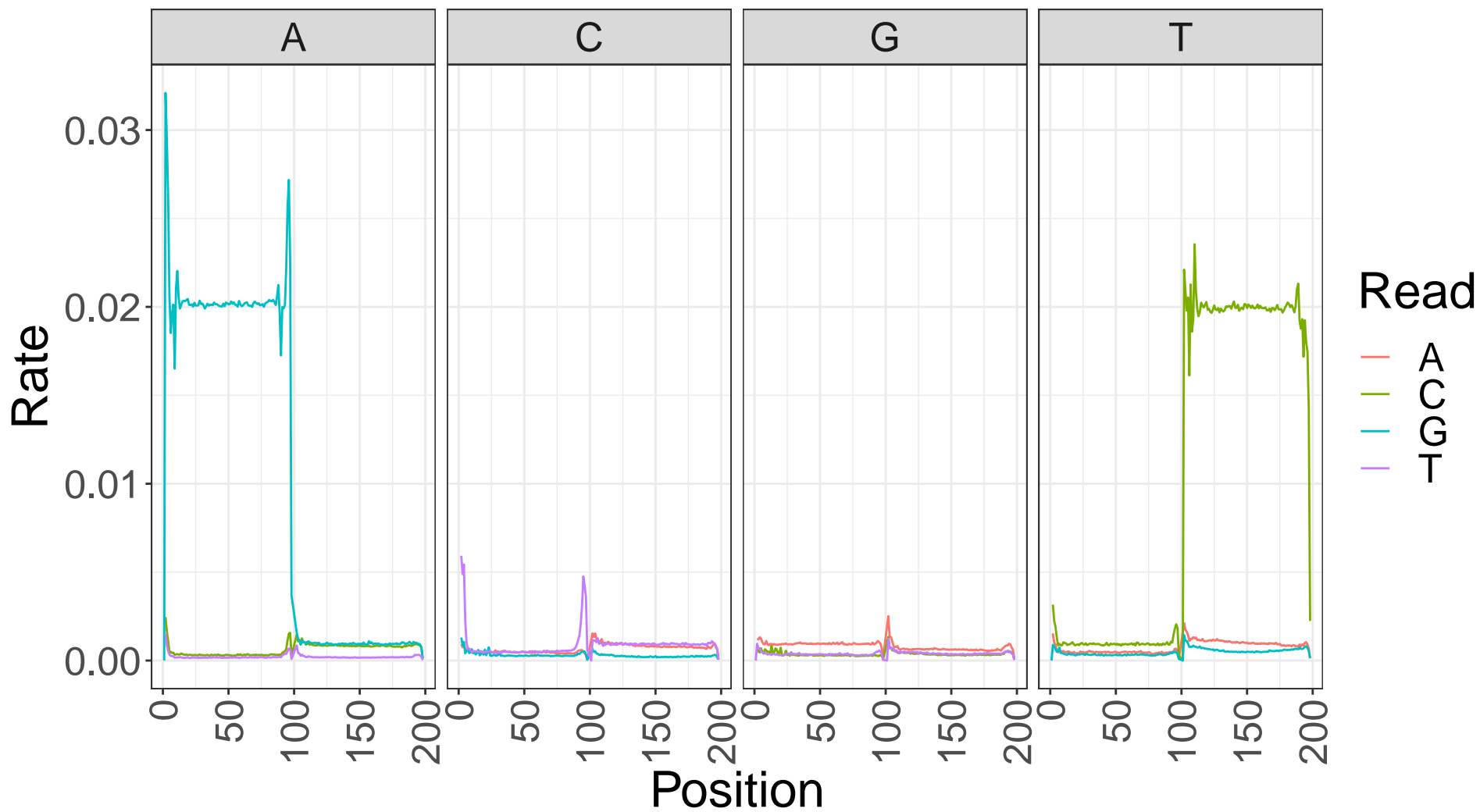
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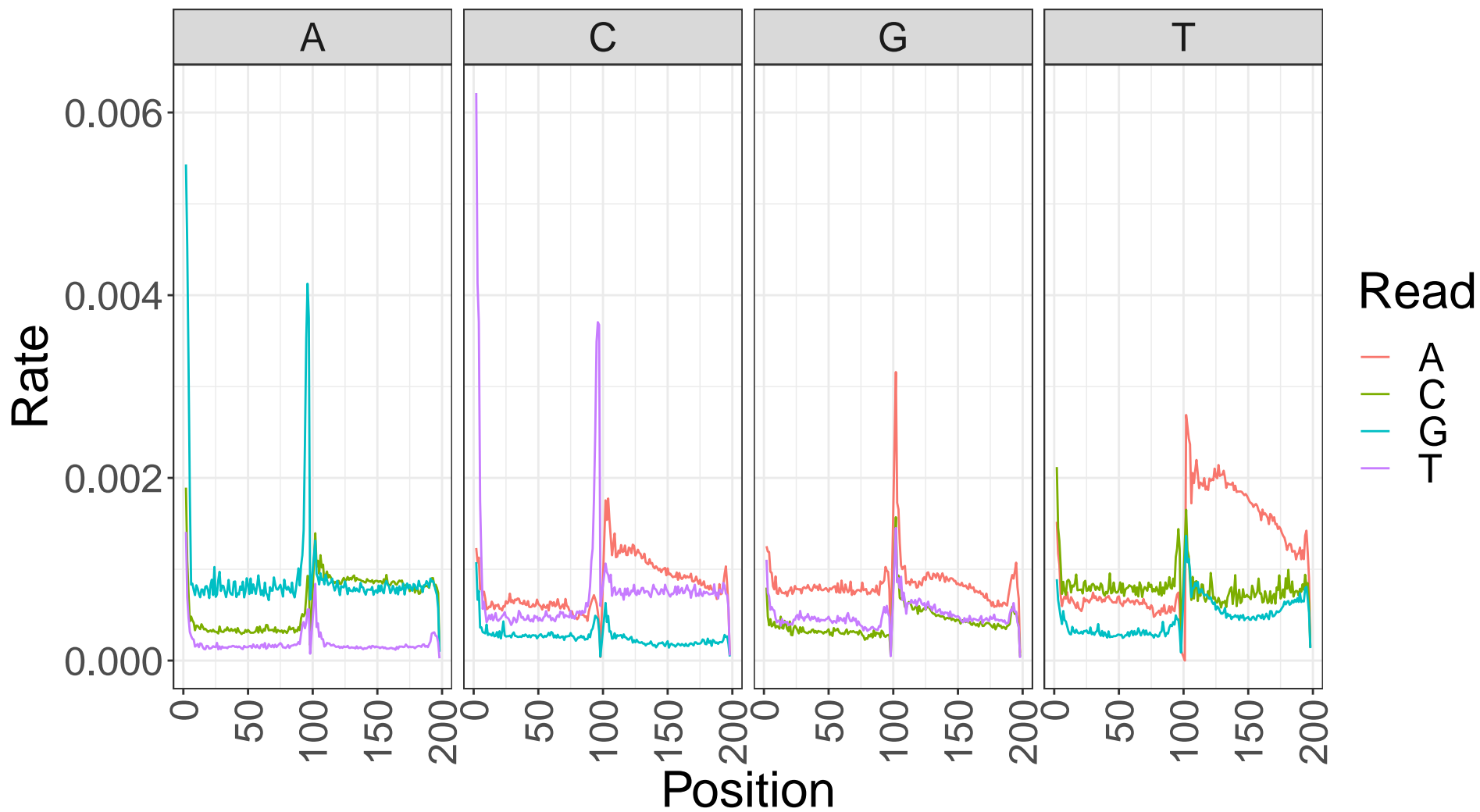
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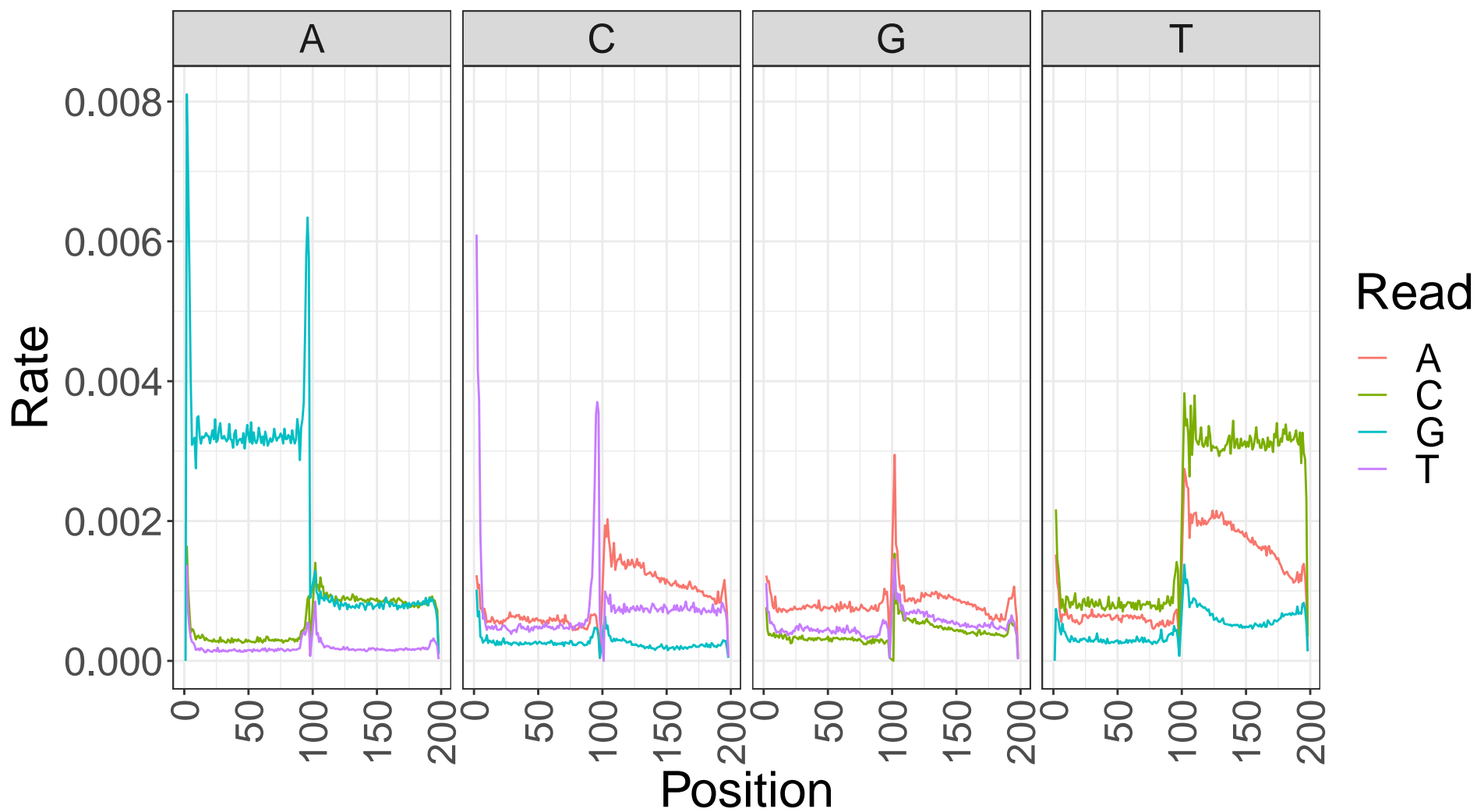
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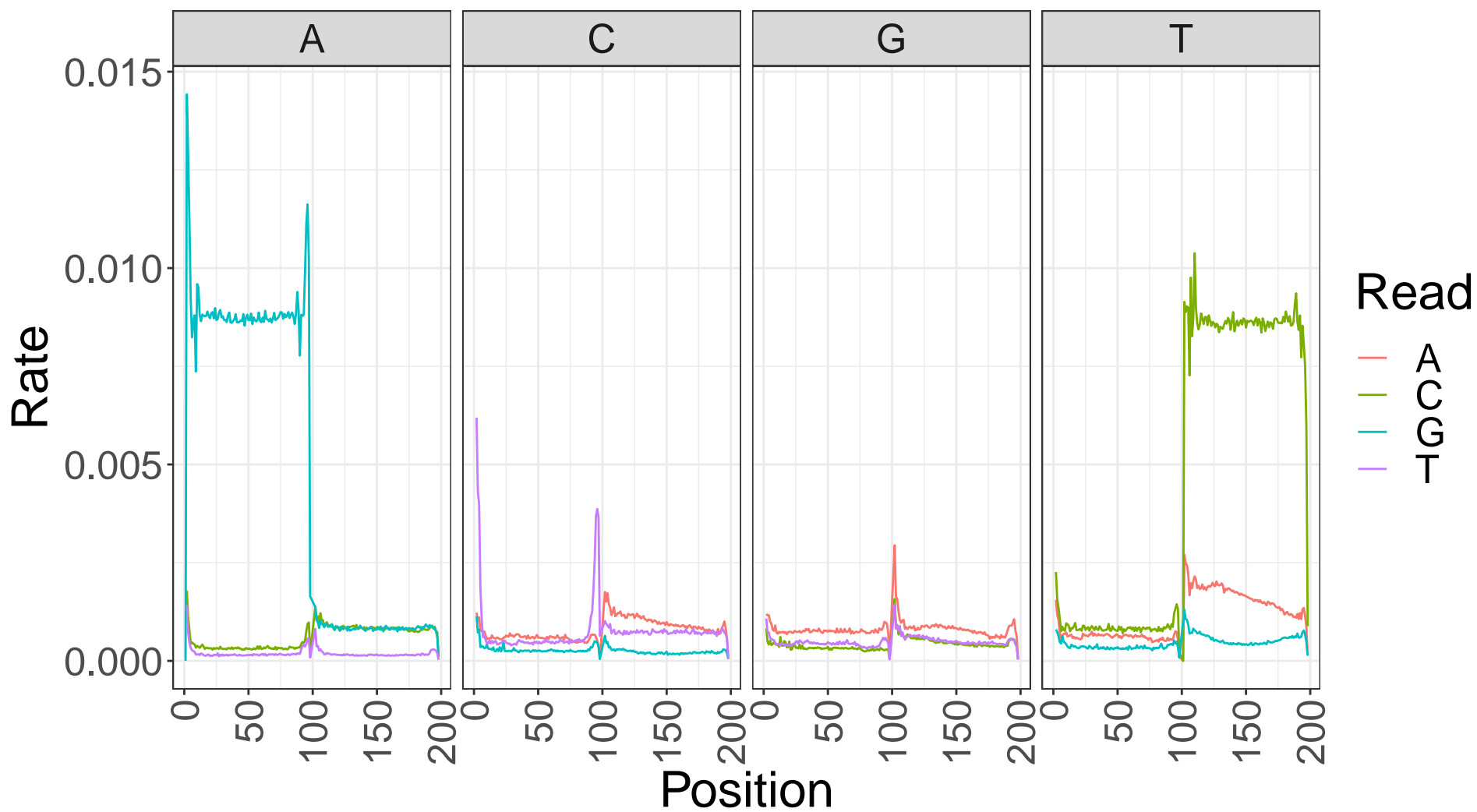
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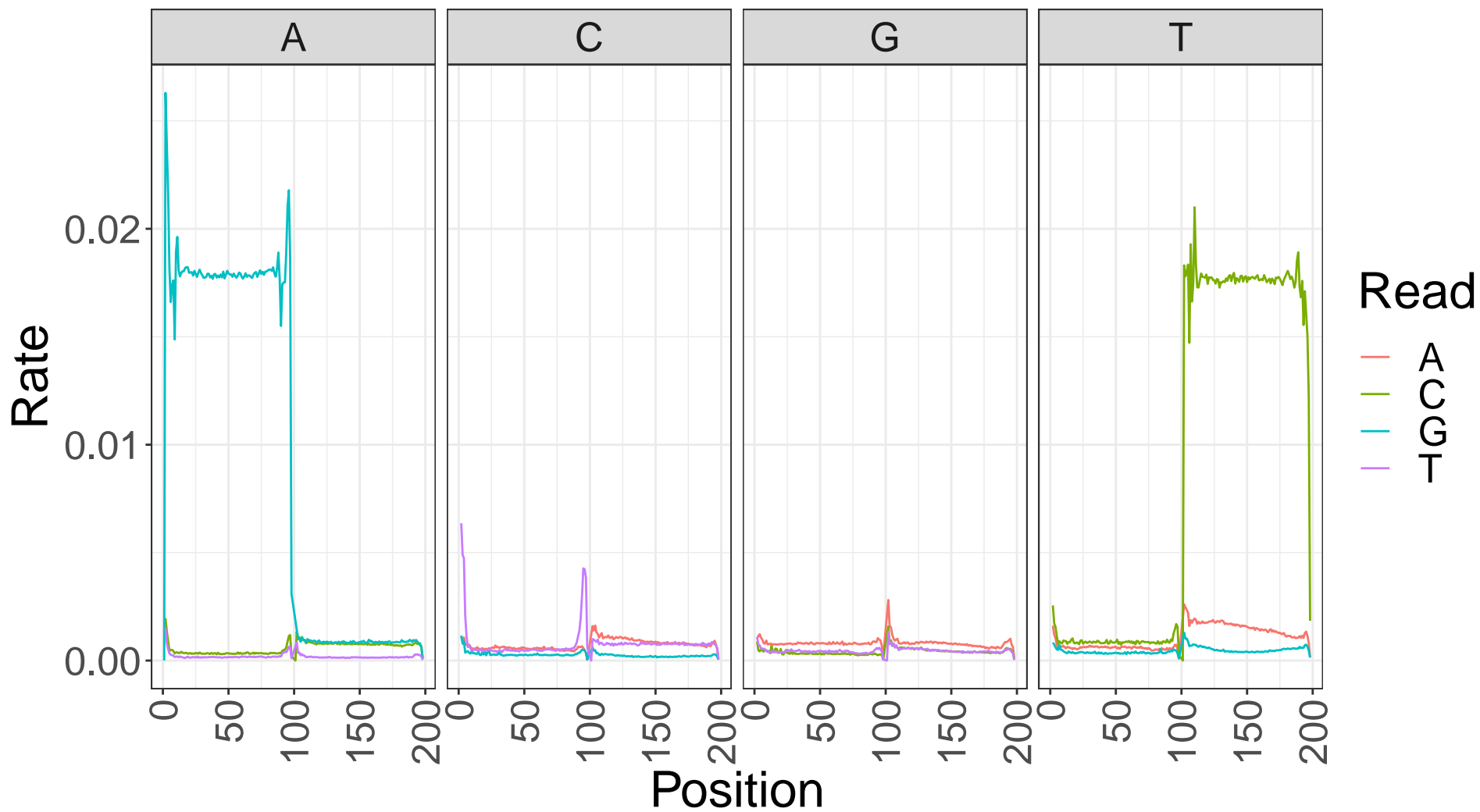
107359B_TUC_1h



107361B_TUC_2h



107363B_TUC_4h



107365B_TUC_8h

