

Mitochondrial genomes from New Zealand's extinct adzebills (Aves: Aptornithidae: *Aptornis*) support a sister-taxon relationship with the Afro-Madagascan Sarothruridae

Supplementary Figures

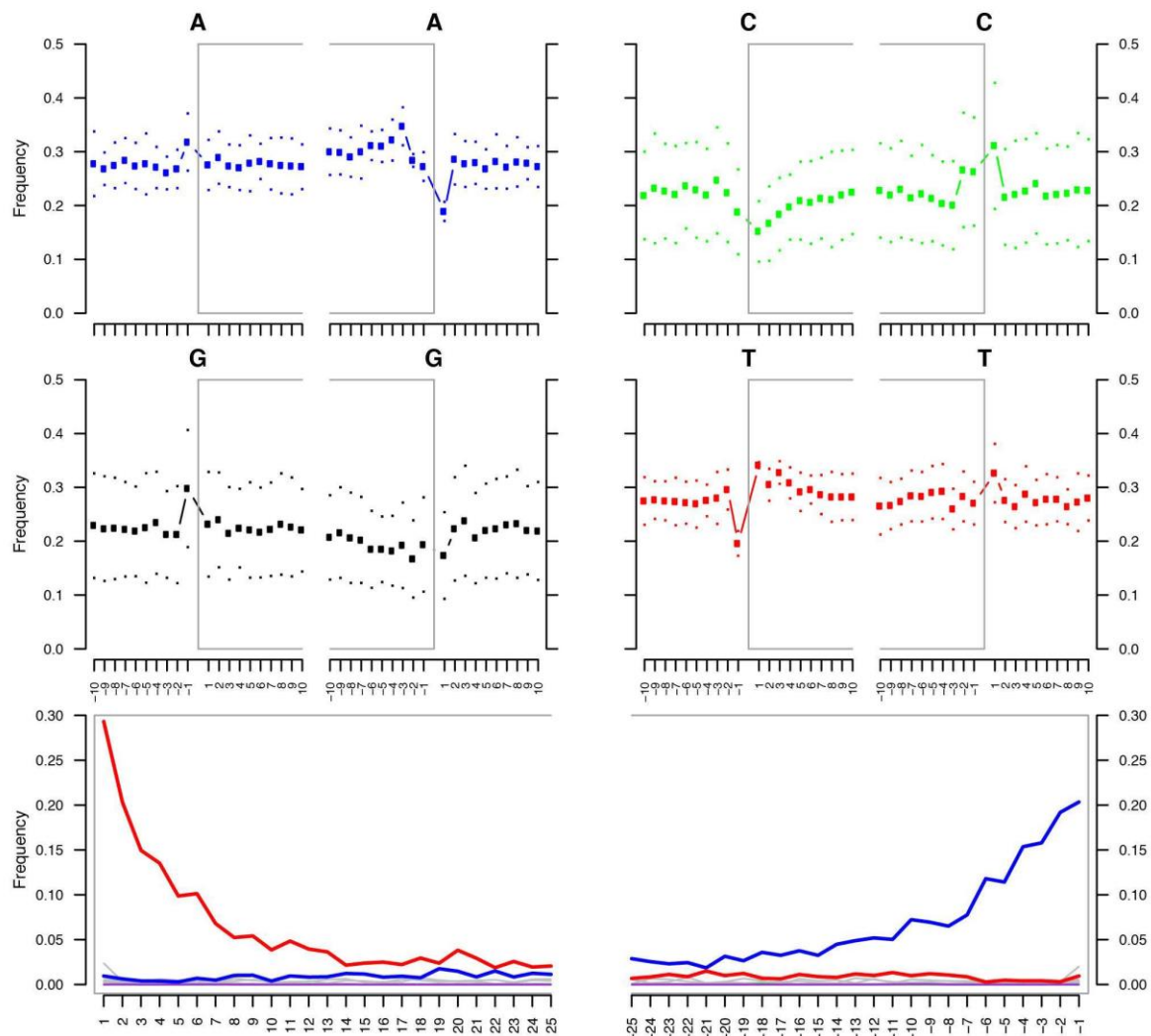


Figure S1: MapDamage report for the final round of mapping reads from DM8046 against the DM8046 majority-rule consensus. The top panels show the characteristic high frequency of purines (A and G) immediately before the reads. The two lower panels show the accumulation of 5' C-to-T (red) and 3' G-to-A (blue) misincorporations characteristic of ancient DNA.

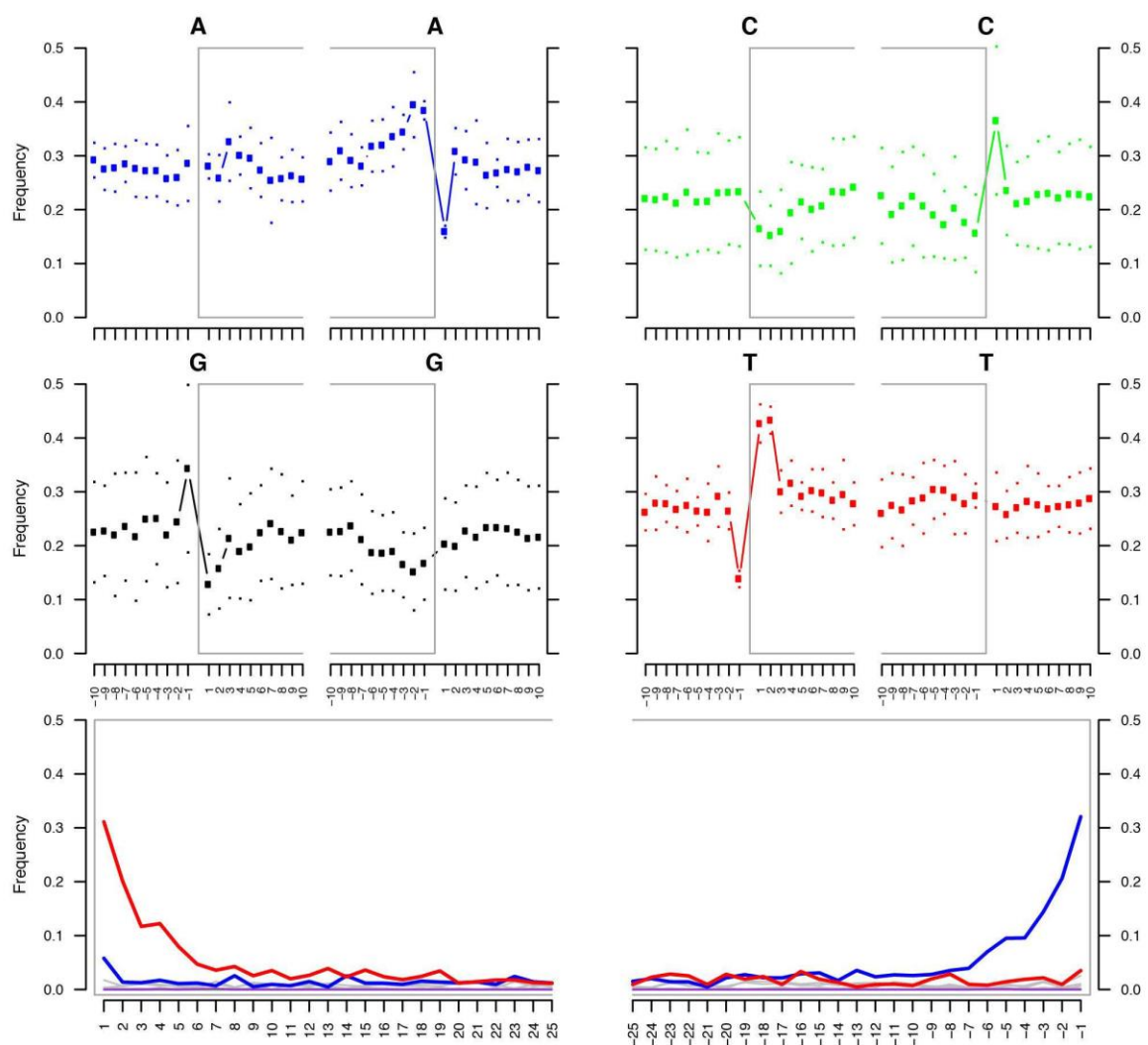


Figure S2: MapDamage report for the final round of mapping reads from S23033 against the DM8046 majority-rule consensus. The top panels show the characteristic high frequency of purines (A and G) immediately before the reads. The two lower panels show the accumulation of 5' C-to-T (red) and 3' G-to-A (blue) misincorporations characteristic of ancient DNA.

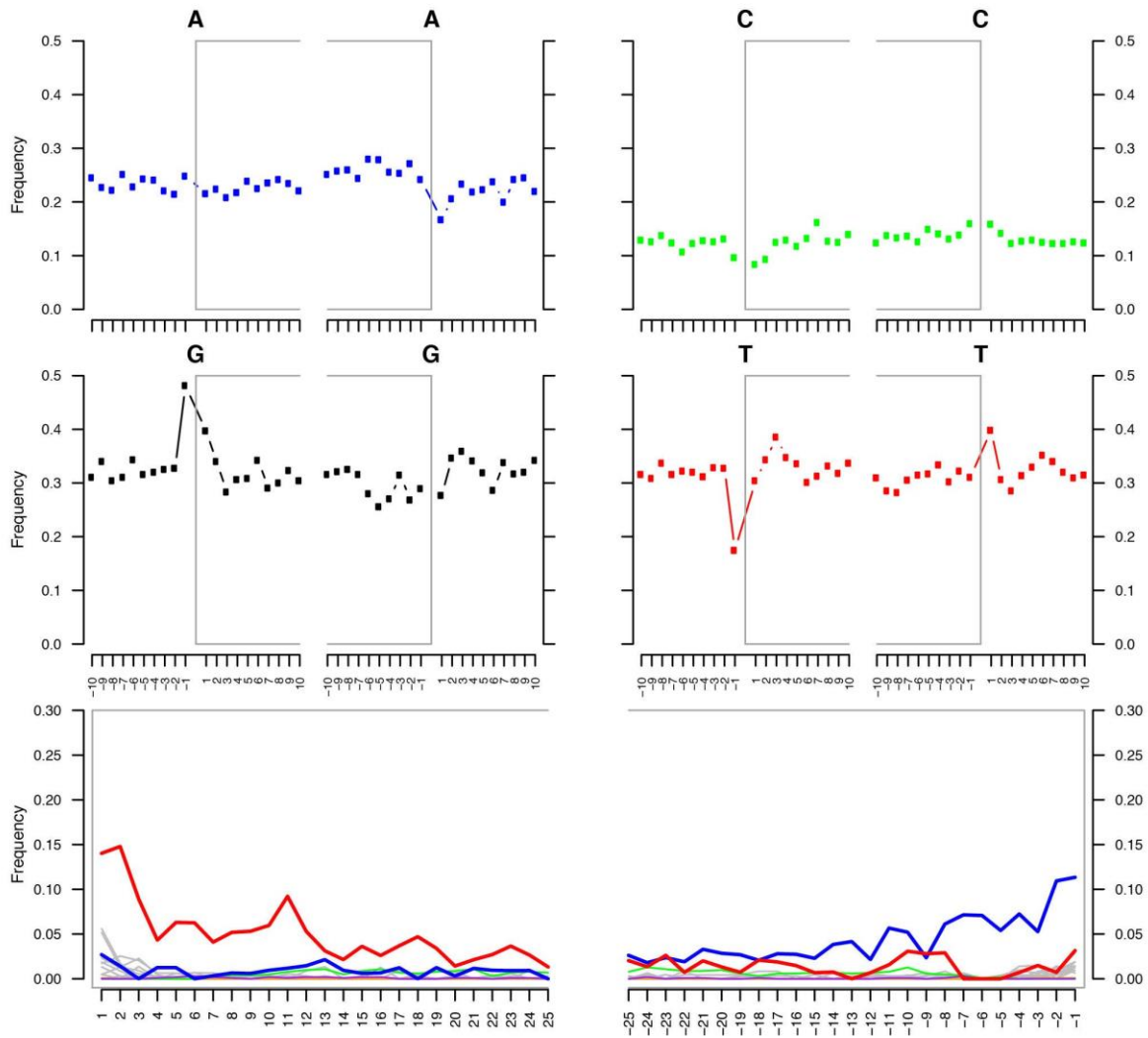


Figure S3: MapDamage report for the final round of mapping reads from CM AV.18536 against the DM8046 majority-rule consensus. The top panels show the characteristic high frequency of purines (A and G) immediately before the reads. The two lower panels show the accumulation of 5' C-to-T (red) and 3' G-to-A (blue) misincorporations characteristic of ancient DNA.

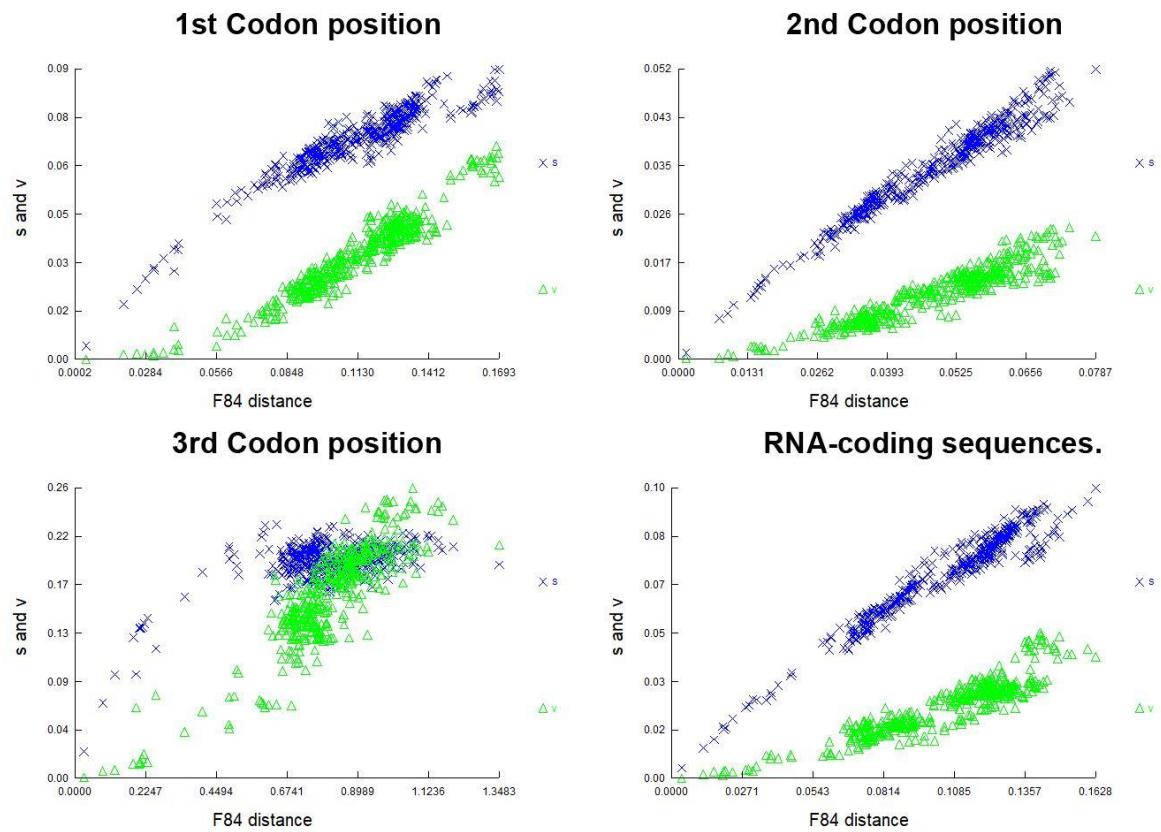


Figure S4: Saturation plots of the primary alignment (predominantly complete mitochondrial genomes) generated using DAMBE. Blue points represent transitions (s), green points represent transversions (v).