



Supplemental Fig S1. mapDamage results for the Ata specimen. A. This plot illustrates frequency of each nucleotide from -10 to -1 (in the reference genome) to +1 to +10 (in sequenced reads) with grey brackets denoting the 5' and 3' paired ends of the sequenced reads. B. This plot indicates the positions' specific substitution rates from the 5' (left) and 3' (right) ends. Red is C->T substitutions, blue is G->A substitutions, and all possible misincorporations are plotted in grey.