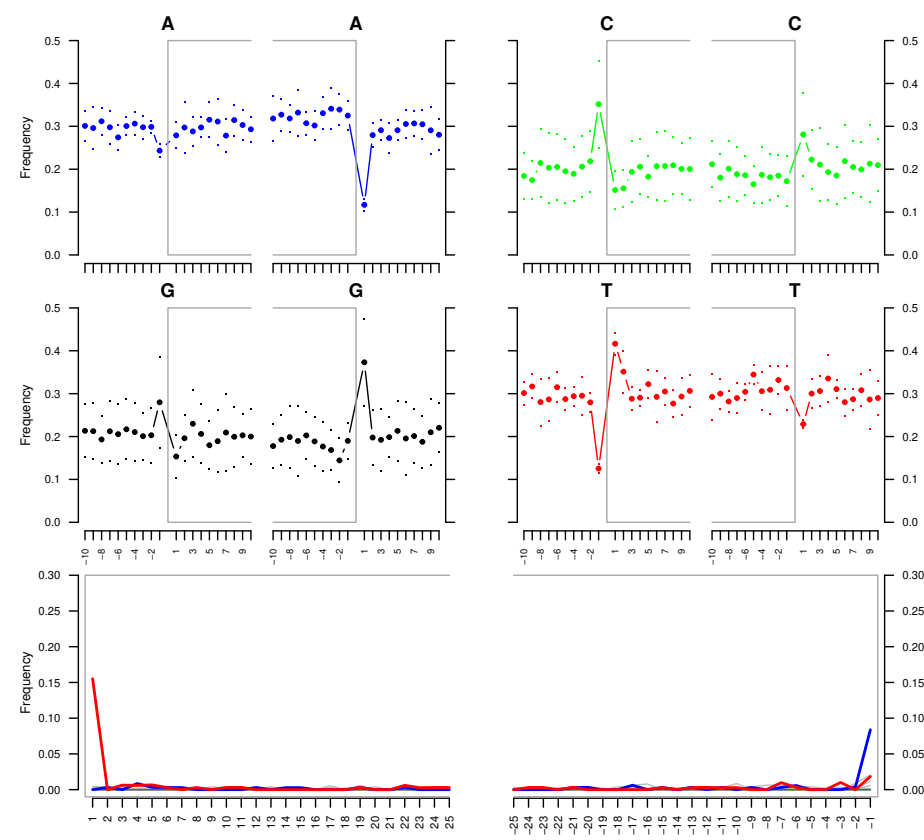
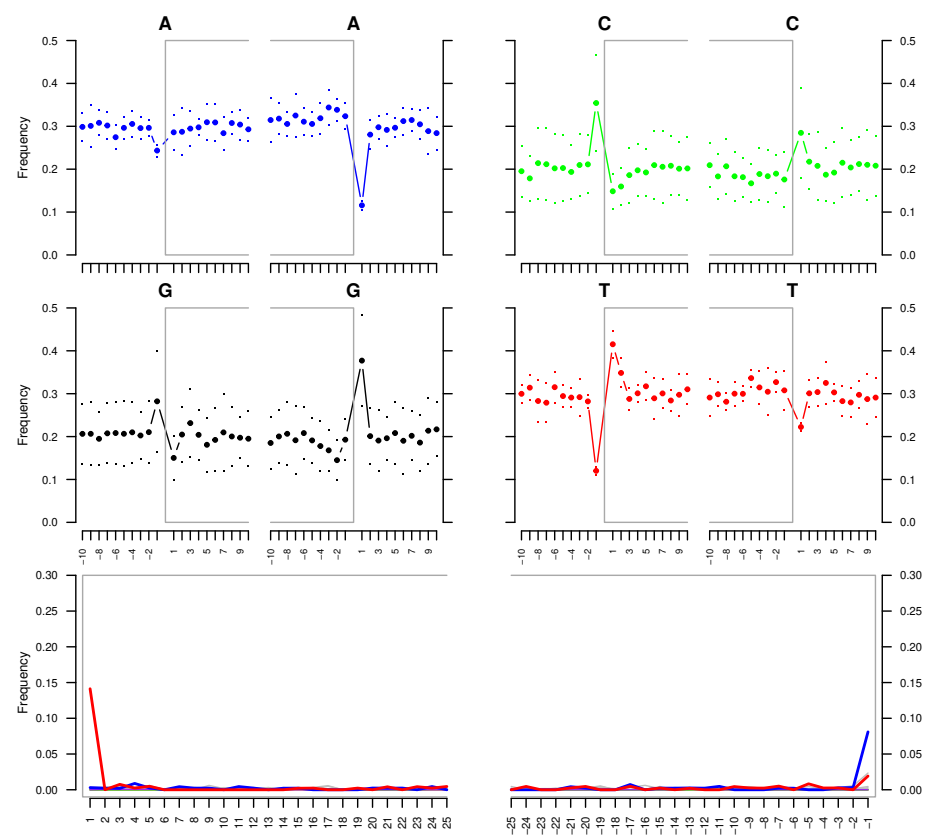


APPENDIX 6. MapDamage report of the BWA iterative mapping using the usual aDNA stringent (STR) and relaxed (REL) mapping parameters to generate the consensus sequences for *Pliomys lenki* sample ZARADNA 219. The top four panels show the frequency of purines and pyrimidines just before and after the reads, respectively. The middle two panels show accumulation of 5' C-to-T (red) and 3' G-to-A (blue) misincorporations. Bottom panel displays the read size distribution of mapped reads.

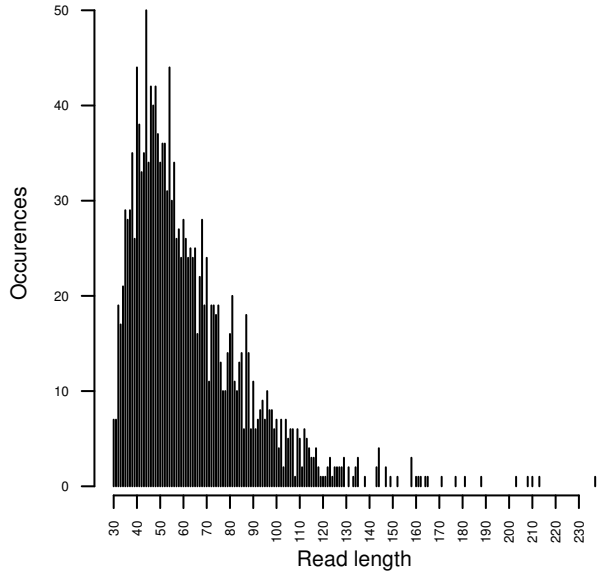
219A *Pliomys* STR



219A *Pliomys* REL



Single-end read length distribution



Single-end read length distribution

