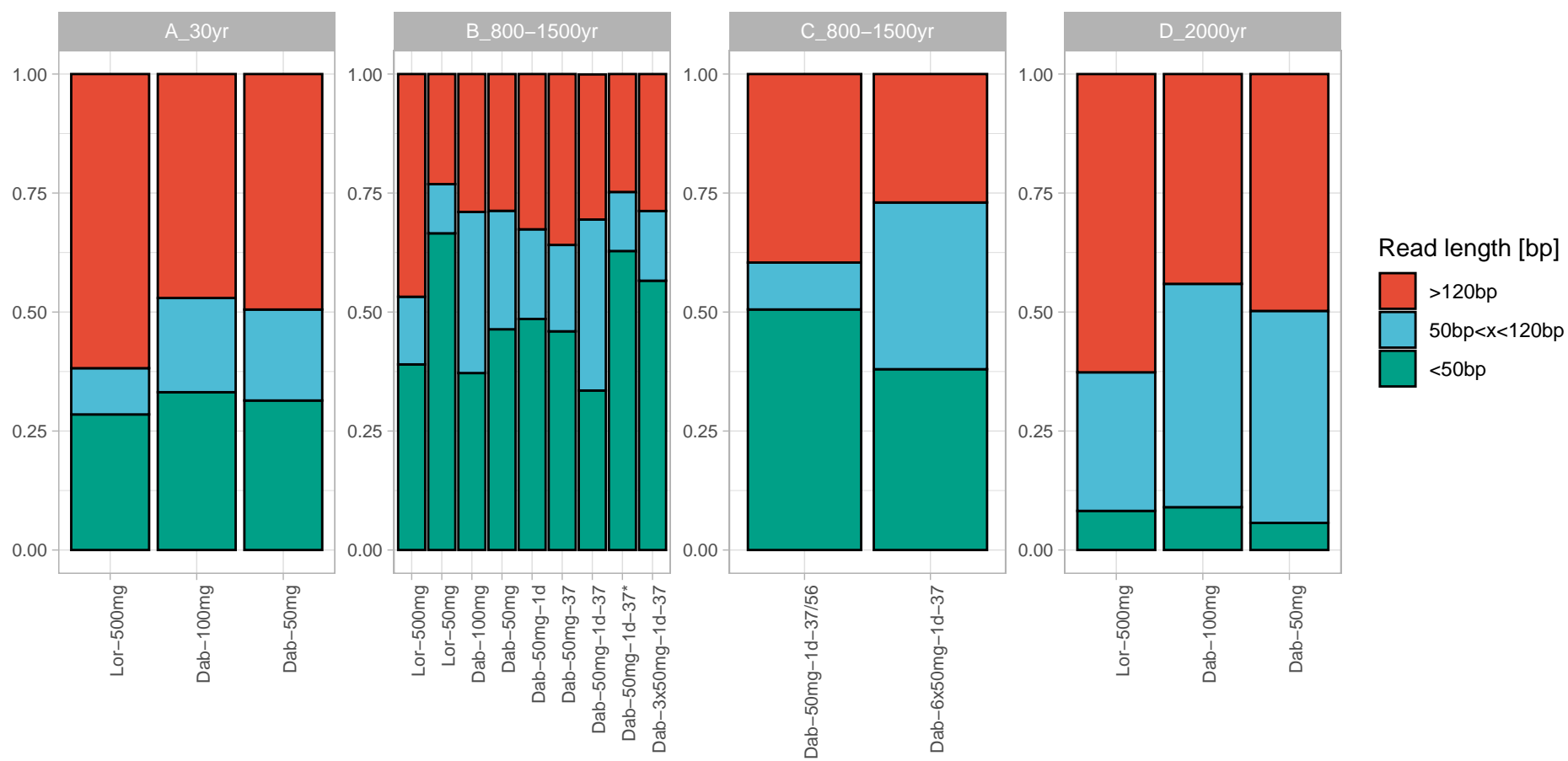
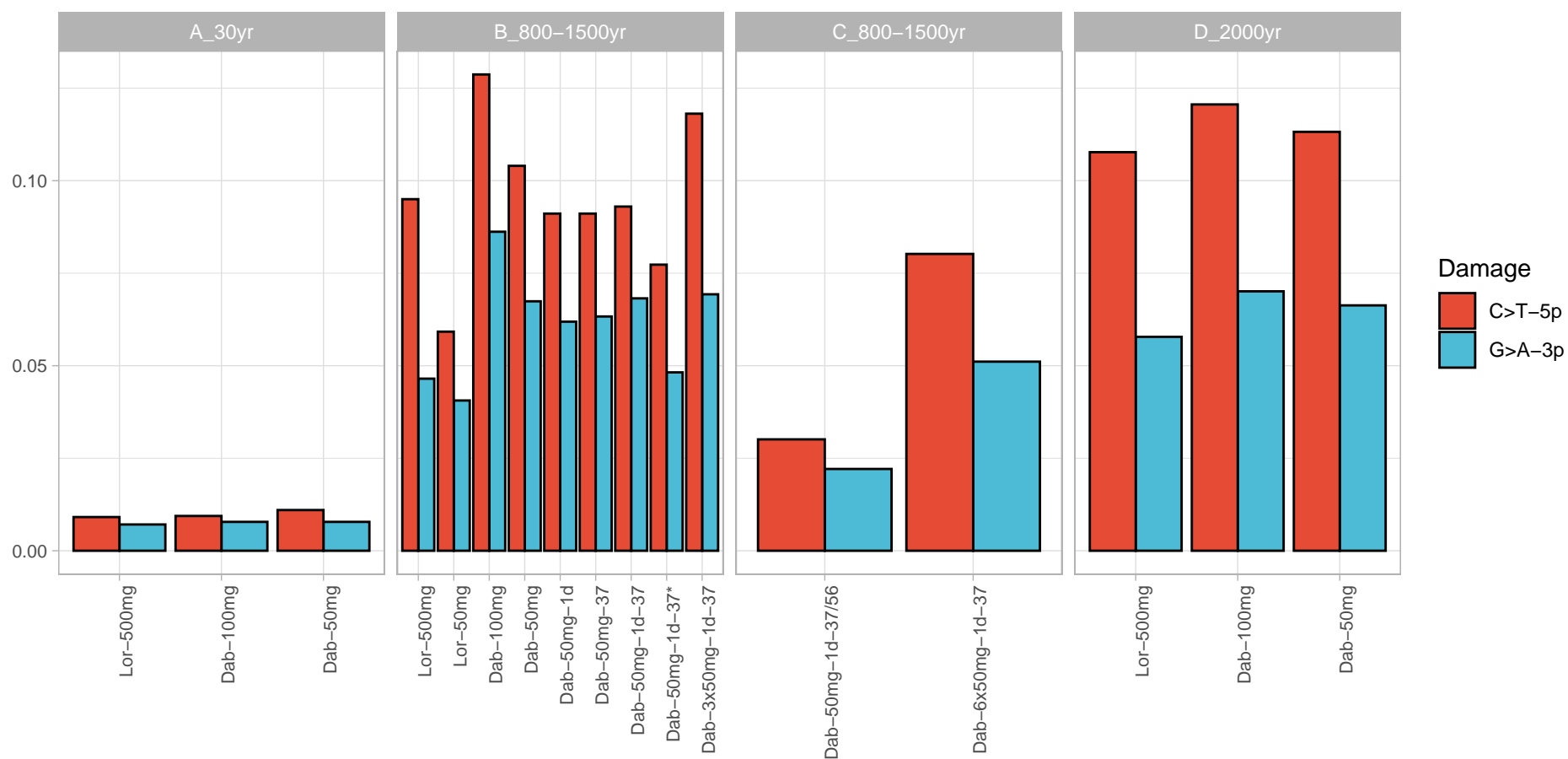


A**B**

Supplementary figure S6 – (A) Normalized read length distribution per method and sample. (B) Mean frequency of the most expected damage patterns (nucleotide substitutions) in ancient DNA data: G>A at the 3' last 25 positions and C>T at the 5' first 25 positions.