Supplemental Figure 1. *Mycobacterium tuberculosis* (Mtb) and *Mycobacterium smegmatis* contain two \( \epsilon \) (dnaQ) exonuclease homologues.

(A) Sequence alignment of \( \epsilon \)-exonuclease homologues from four different species. Conserved catalytic residues of \( \epsilon \) are indicated by blue triangles below the sequences. The clamp binding motif of \( \epsilon \) is boxed in green. (B) Active site of the \( \epsilon \) exonuclease. (C) Computational model of the active site of Mtb Rv3711c. (D) Computational model of the active site of Mtb Rv2191.