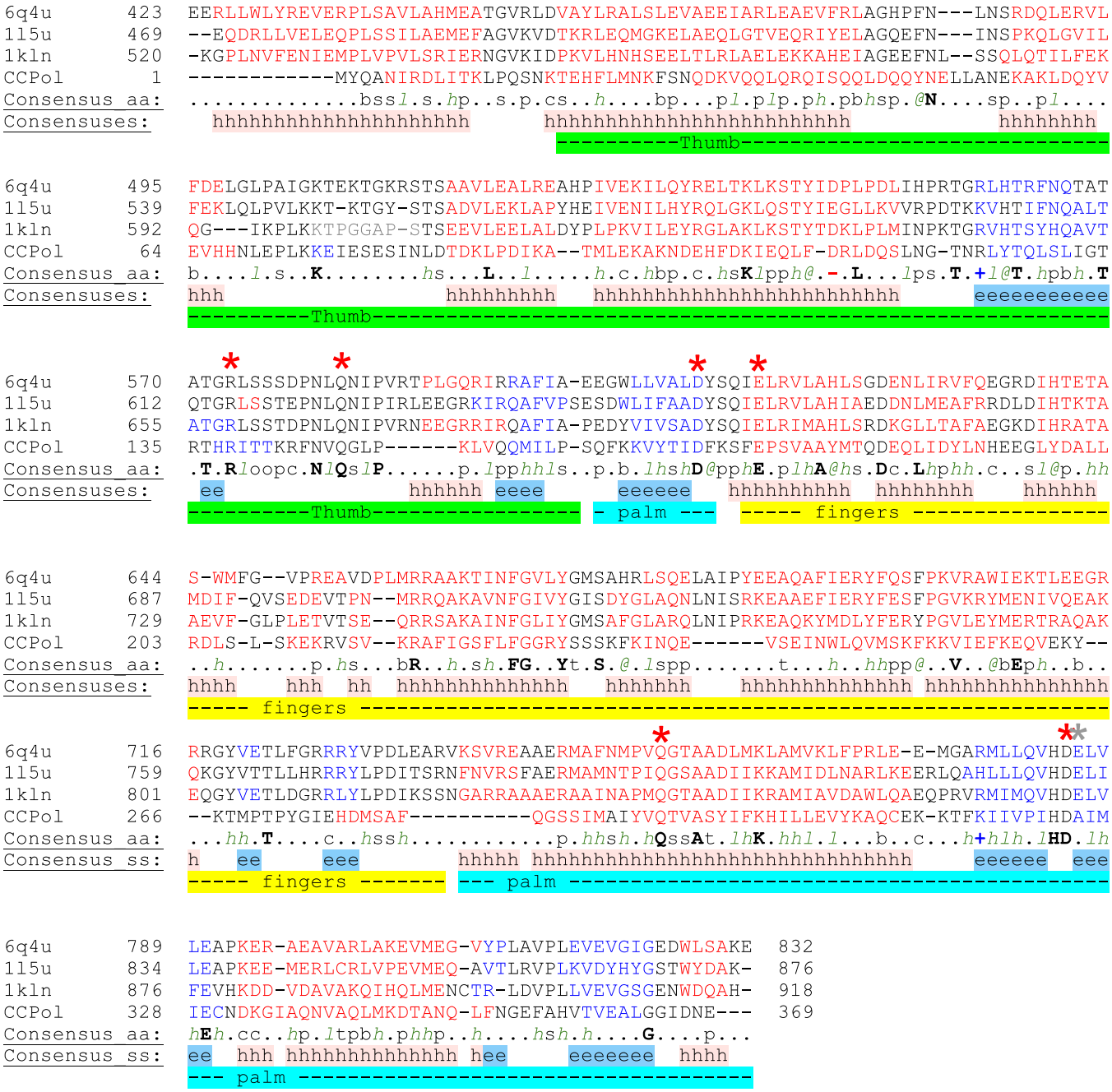

Figure 4–figure supplement 1: Structure-based sequence alignments of CCPol and the polymerase domains of several bacterial DNA Pol Is. The alignments were prepared using PROMALS3D multiple sequence and structure alignment server (Pei et al., 2008). The following protein structures were used for the alignments: 6q4u - Thermus aquaticus Taq polymerase residues 423-832; 1l5u - Geobacillus stearothermophilus DNA Pol I residues 469-876; and 1kln - E. coli DNA Pol I residues 520-918. A structural model of CCPol was prepared with I-Tasser (Yang et al., 2015). The polymerase sequences corresponding to the exonuclease domains absent from CCPol were removed from the alignment. The sequences are coloured as follows: red – alpha helix, blue – beta strand, gray – E. coli Pol I thumb residues disordered in the structure used. Consensus amino acids are shown in below the structure, with conserved amino acids in bold and uppercase; aliphatic residues (I, V, L): green l; aromatic residues (Y, H, W, F): green @; hydrophobic residues (W, F, Y, M, L, I, V, A, C, T, H): green h; alcohol residues (S, T): o; polar residues (D, E, H, K, N, Q, R, S, T): p; tiny residues (A, G, C, S): t; small residues (A, G, C, S, V, N, D, T, P): s; bulky residues (E, F, I, K, L, M, Q, R, W, Y): b; positively charged residues (K, R, H): blue +; and charged residues (D, E, K, R, H): c. Consensus secondary structures are marked with pink h for alpha helix and blue e for beta strand. Polymerase domains (Thumb, fingers, and palm) are marked underneath the alignment. Predicted mechanistically important residues are marked with red asterisks (with a grey asterisk marking a CCPol alanine residue which in other PolA-like polymerases is invariably a catalytic glutamic acid) above the sequence.