

Figure S6. Phylogeny of the CA STX1-phage. A. Neighbor-Joining phylogeny based on amino acid sequence of Integrase protein. **B.** Maximum Likelihood phylogeny based on full nucleotide sequence of the phage. CA STX1-phage is highlighted with yellow background color. The numbers above the branches designate the bootstrap values. Isolates associated with European *E. coli* O104:H4 outbreak of 2011 are highlighted with red label color. The color of the node corresponds to the type of Shiga-toxin.

