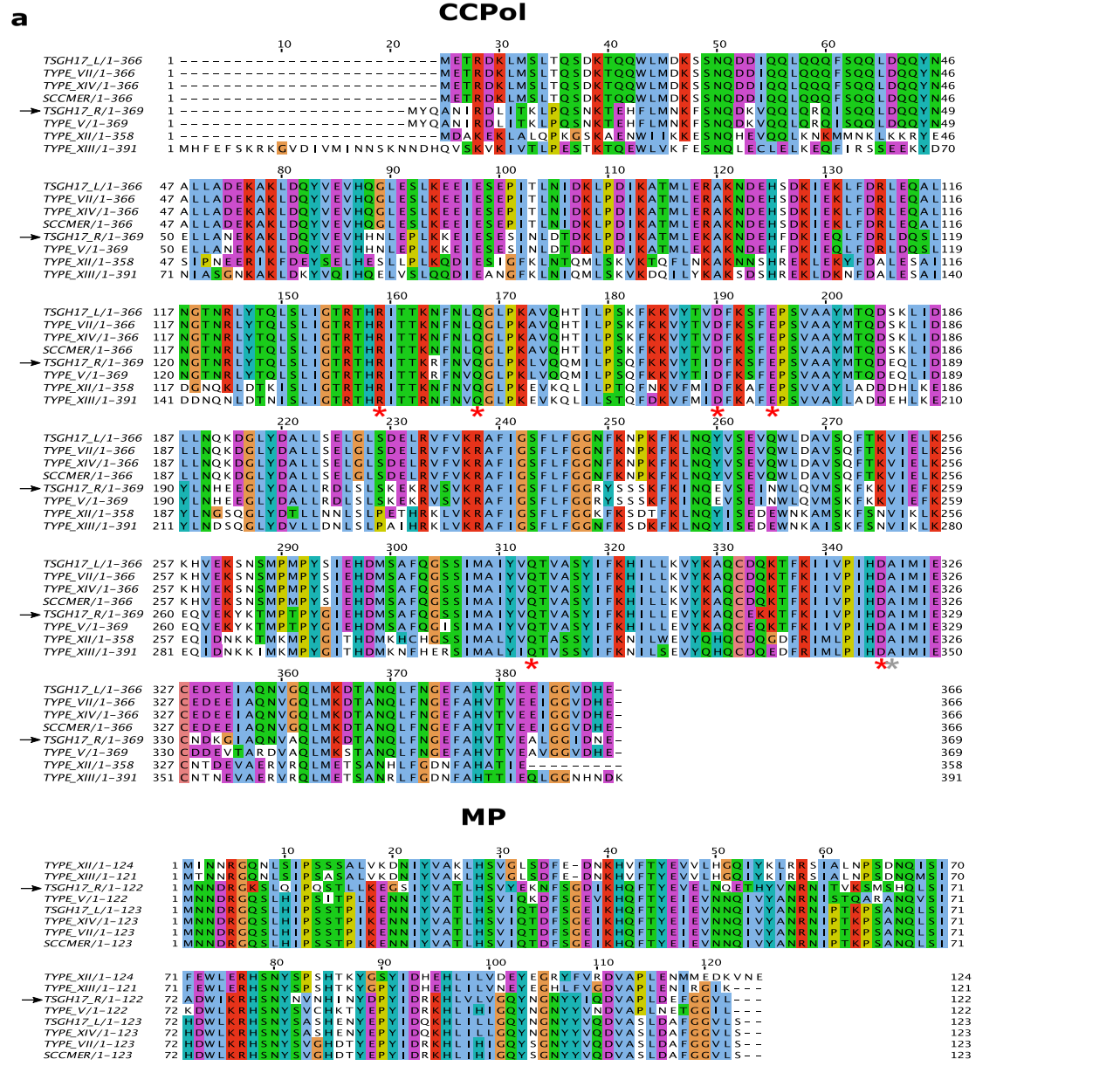

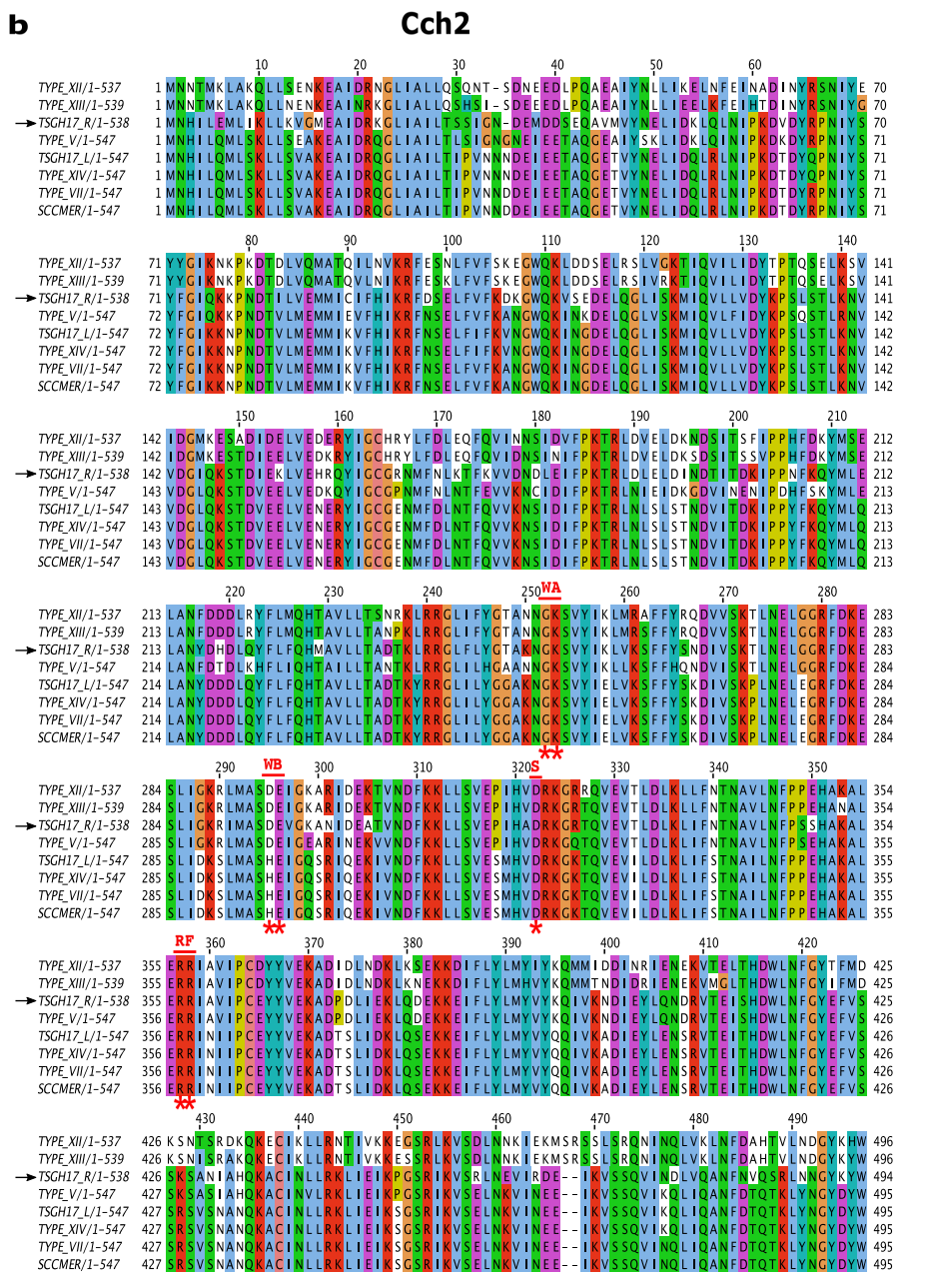

Figure 1–figure supplement 1: Sequence alignments of Cch2 operon proteins CCPol, MP, and Cch2. The alignments were prepared in Clustal Omega (Sievers et al., 2011) and visualized in Jalview (with Jalview colouring)(Waterhouse et al., 2009). The following SCC sequences were used for the alignments: the two gene clusters (SCCmer-like L and type V-like R) from a composite SCCmec from TSGH17 strain (SCC accession number AB512767), type V element from WIS strain (AB121219), type VII from JCSC6082 (AB373032), type XII from strain BA01611 (JCSC6082), type XIII from isolate 55-99-44 (MG674089), type XIV from strain SC792 (LC424989), and SSCmer (carrying a mercury resistance cluster) from strain 85/2082 (AB037671). The proteins investigated in this study are marked with arrows. Residues predicted to be important for activity for CCPol (based on similarities to other A-family polymerases (Kiefer et al., 1997)) and Cch2 (based on similarities to Cch and the SaPI5 Rep protein (Mir-Sanchis et al., 2016)) are marked with red asterisks (with a grey asterisk marking an alanine residue which in other A-family polymerases is invariably a catalytic glutamic acid). For Cch2 alignment, predicted motifs are: WA – Walker A motif, WB – Walker B motif, S – sensor I, and RF – R finger.