



Supplemental Figure 2. The phylogenetic tree based on the alignment of *cpsA-cpsD* regions of 109 *S. parausis* *cps* loci identified in this study. The tree was constructed using the nucleotide sequence from the start of the coding region of *cpsA* to the end of the coding region of *cpsD*. The HG of initial glycosyltransferase in each *cps* locus are indicated. Branch support was assessed using FastTree's local support values (calculated with the Shimodaira-Hasegawa (SH) test; range: 0–1). The scale bar represents substitutions per site. HG: Homology Group.