

Figure S1. Transposon variants identified interrupting OCL1 indicating their specific insertion sites. Drawn to scale from NCBI accession numbers GCA_000516095.2 (variant 1), GCA_004101685.1 (variant 2), and GCA_021569095.1 (variant 3). Insertion sequences are black and other genes are grey. OCL1 colour scheme is shown in the legend below.

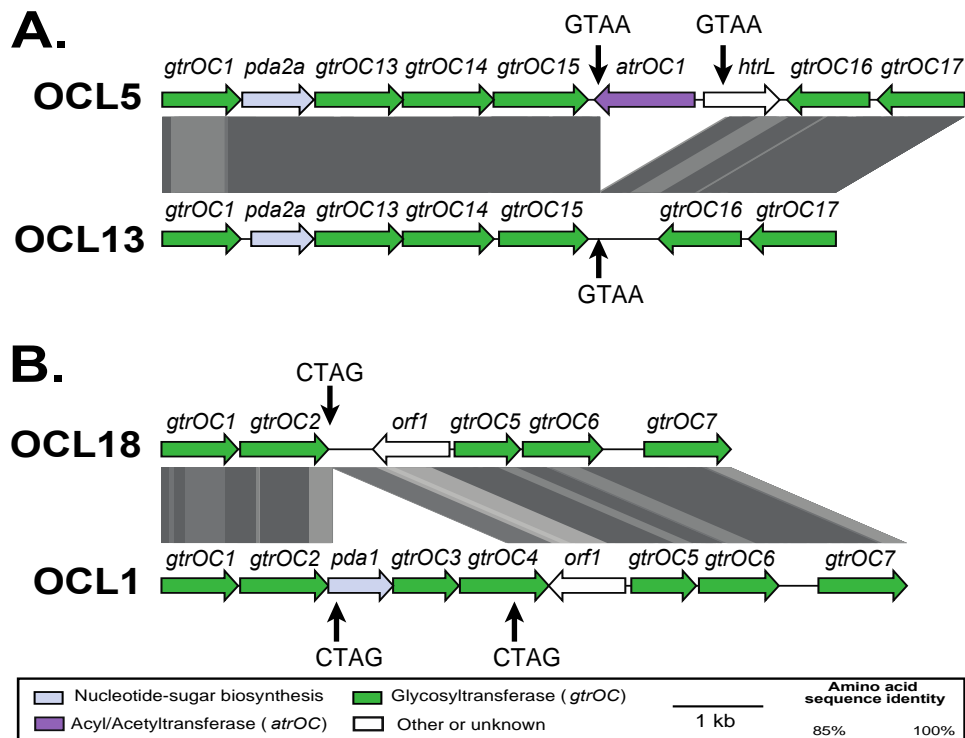


Figure S2. Comparison of *A. baumannii* OCL that include a 4 bp repeat influencing *Kaptive* assignments. A. Alignment of OCL5 and OCL13. **B.** Alignment of OCL18 and OCL1. Vertical black arrows indicate positions of the 4 bp repeats. Horizontal arrows are genes showing the direction of transcription, colour coded by the predicted function of their gene products. Grey shading between gene clusters shows amino acid sequence identity determined by tblastx. Colour scheme and grey scale are shown below. Figures drawn to scale using Easyfig [20] and annotated/coloured in Adobe Illustrator.