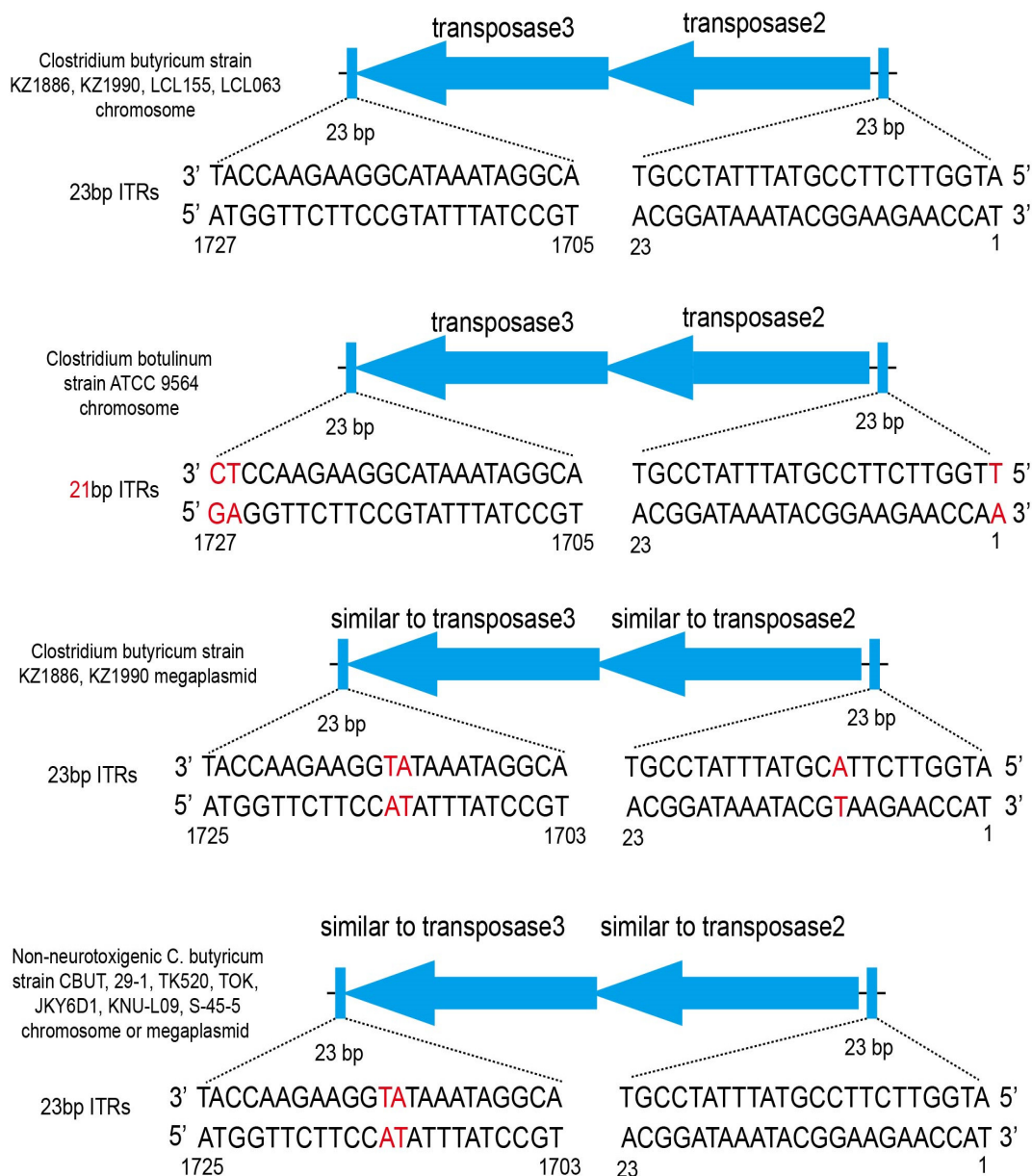




**Figure S1.** Fast minimum evolution trees of the *bont/e* gene sequences of different BoNT/E-producing clostridia strains. The dendrogram shows the variation in the *bont/e* gene. The analysis included the *bont/e* gene from the Chinese strains (red front) and all 51 highly homologous (> 99% coverage) sequences in the nucleotide collection (nr/nt) in the NCBI database. Six highly homologous *bont/e* genes are from *C. butyricum* strains (marked with a blue background).



**Figure S2.** Comparison of the TEs. The nucleotide differences in the ITRs are marked in red.