

Supplemental Figures

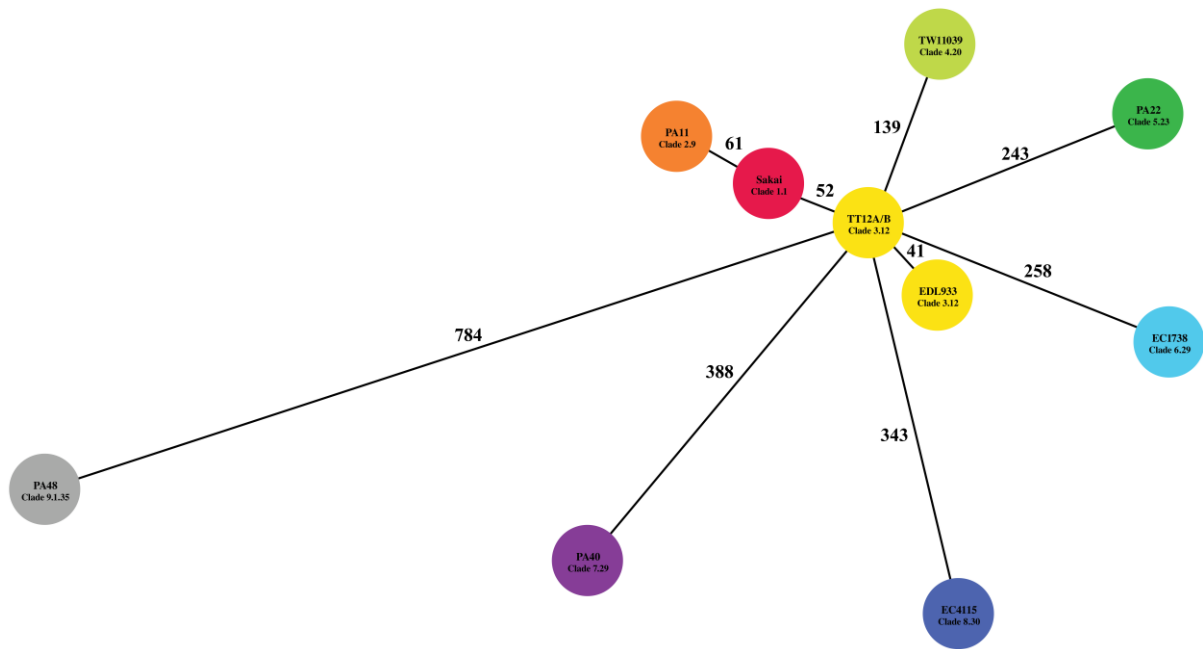


Figure S1. Core genome MLST. Allelic changes were detected in the genomes of TT12A and TT12B and representative strains from clades 1 to 9 O157:H7 using *E. coli* strain K12 subst. MG1655 as seed in SeqSphere+. The shared gene inventory was determined at 4,056 genes comprising 3,224 core and 832 accessory loci according to the inclusion/exclusion criteria of the SeqSphere+ Target Definer. Numbers on connecting branches indicate the number of genes with differing allele status.

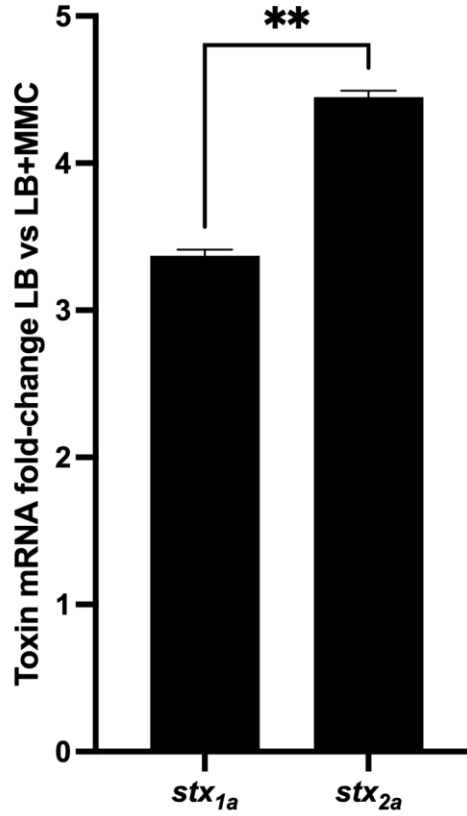


Figure S2. Expression of *stx* genes. RT-qPCR based relative gene expression upon MMC-induction is quantified in fold-change for the toxin genes, *stx*_{1a} and *stx*_{2a} in strain TT12A. Culture TT12A shows significantly elevated expressions of both the *stx*_{1a} and *stx*_{2a} genes in phage-mobilizing LB+MMC condition when compared to growth in LB, also statistically significant more *stx*_{2a} transcripts were made relative to *stx*_{1a}. Statistical significance for two biological replicates is reported as *P < 0.05; **P < 0.005; ***P < 0.0005; ****P < 0.00005.

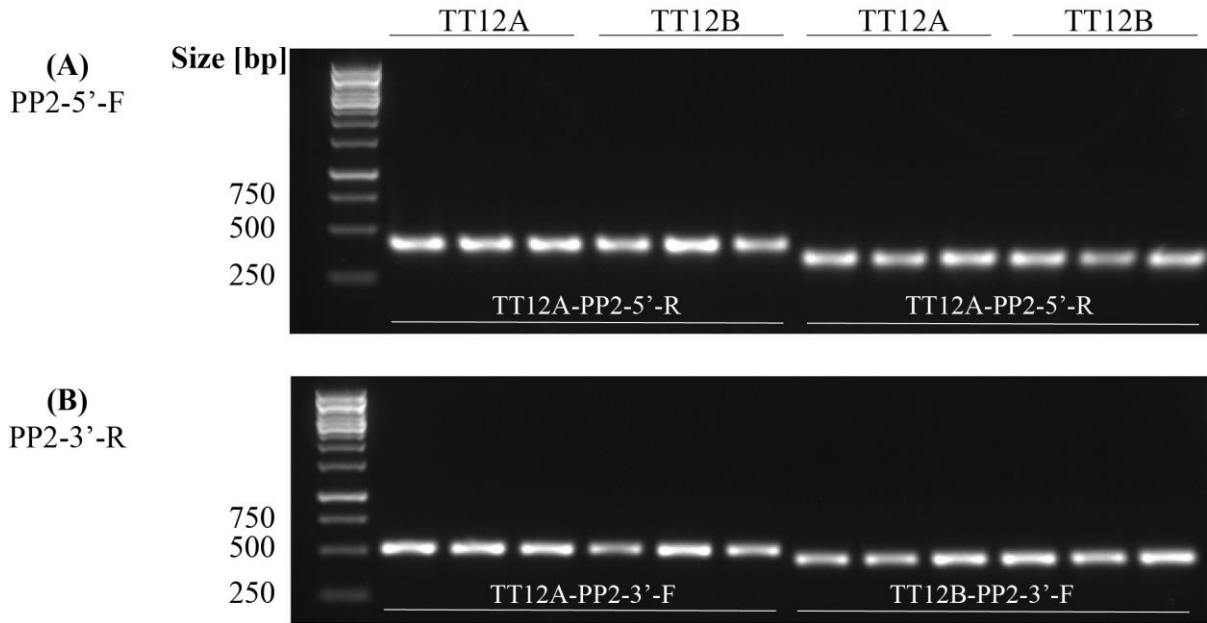


Figure S3. PCR-interrogation of inversion boundaries and directionality in Φ PP2 Two distinct PCRs were performed using two anchor primers (A): PP2-5'-F and (B): PP2-3'-R located in the inversion adjacent core region. For the TT12A assembly, primers were designed to target a hypothetical gene (E5F08-RS27785) and a phage tail gene (E5F08-RS04765). For the TT12B assembly, primers target two phage tail genes (E5F07-RS04740, E5F07-RS04755).

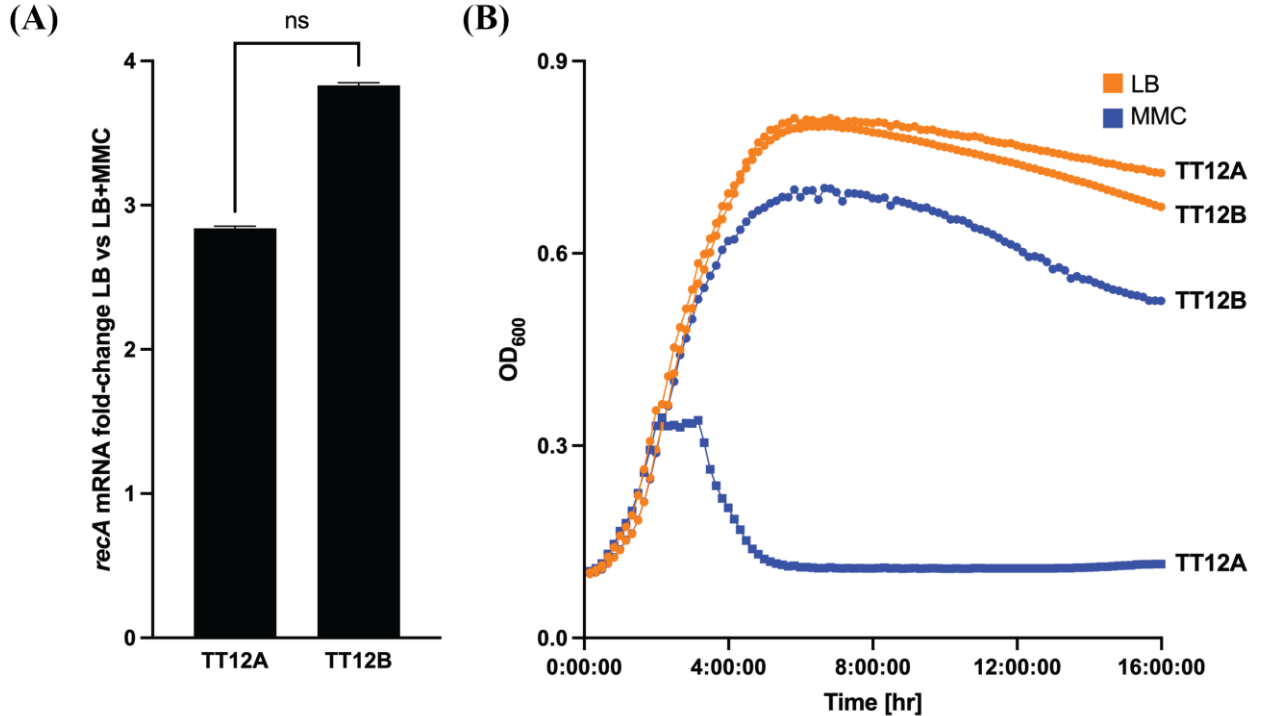


Figure S4. Growth phenotypes. Growth of TT12A and TT12B cultures in LB and under phage-mobilizing conditions in LB+MMC was recorded for 16 hrs. (A) RT-qPCR based relative gene quantification of the SOS key regulator *recA* six hrs post-MMC treatment shows SOS-response activation in both TT12A and B cultures. Statistical significance for two biological replicates is reported as * $P < 0.05$; ** $P < 0.005$; *** $P < 0.0005$; **** $P < 0.00005$. (B) Cultures grown in LB show similar growth patterns. Upon MMC-induction (time=0 hr), TT12A cultures show impaired growth due to phage lysis when compared to TT12B.

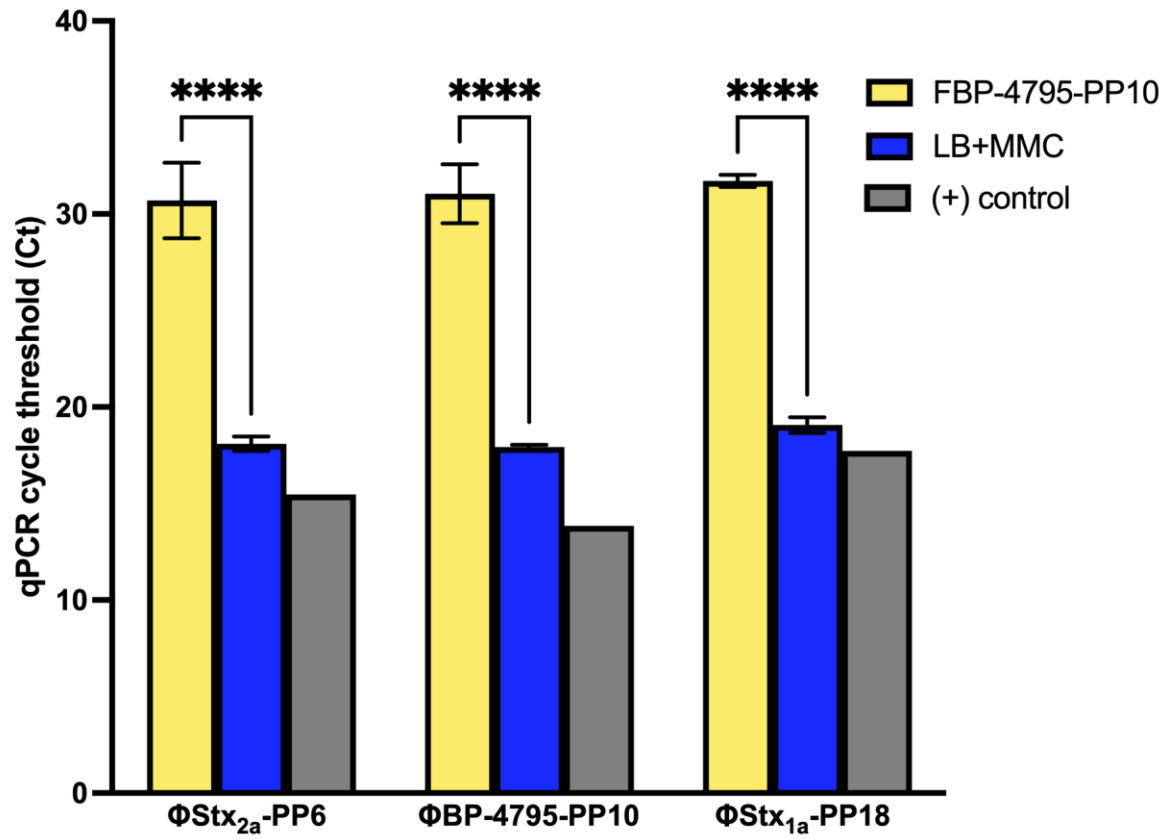


Figure S5. Mobilization pattern of TT12A-specific phages The copy numbers of TT12A-specific excised Stx_{1a}-, Stx_{2a}-, and PP10-prophages were calculated by qPCR in LB and LB+MMC conditions. The abundance of phage DNA and bacterial gDNA, used as a positive control, are displayed as Ct values. Statistical significance for two biological replicates is reported as ****P < 0.0005.