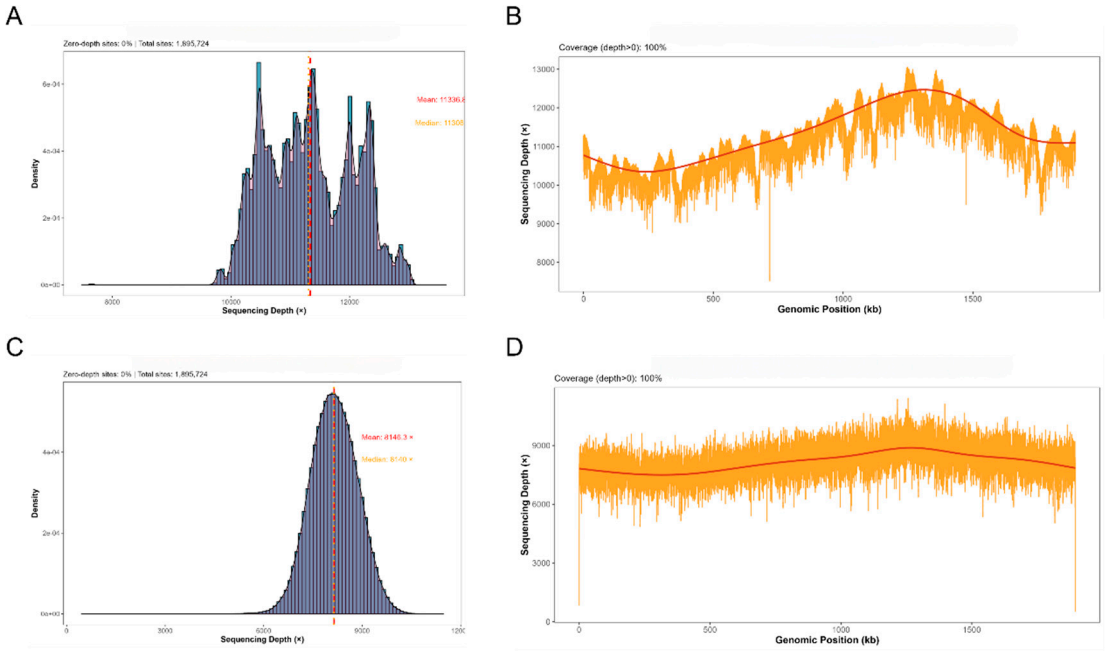


Figure S1. Sequencing depth distribution histogram and genome-wide profile.

Sequencing depth distribution histogram presenting density distribution of HiFi reads (A) and short paired end reads (C). Genome-wide sequencing depth profile presenting depth track along chromosomal coordinates for Hifi reads (B) and short paired-end reads (D).

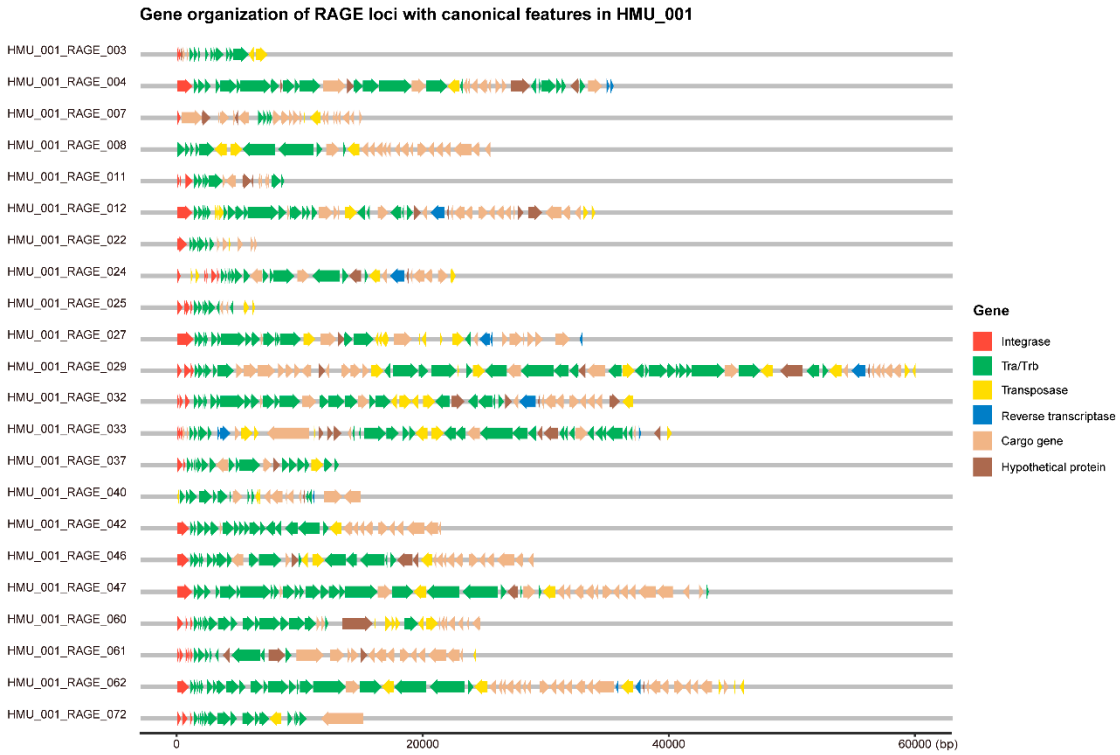


Figure S2. Gene organization of RAGE loci with canonical features in HMU_001.

Twenty-two RAGE loci that retain recognizable canonical components, including an integrase, *tra*/*trb* genes, and associated mobile-element and cargo genes. Arrows represent genes and are colored by module as in Figure 3D.

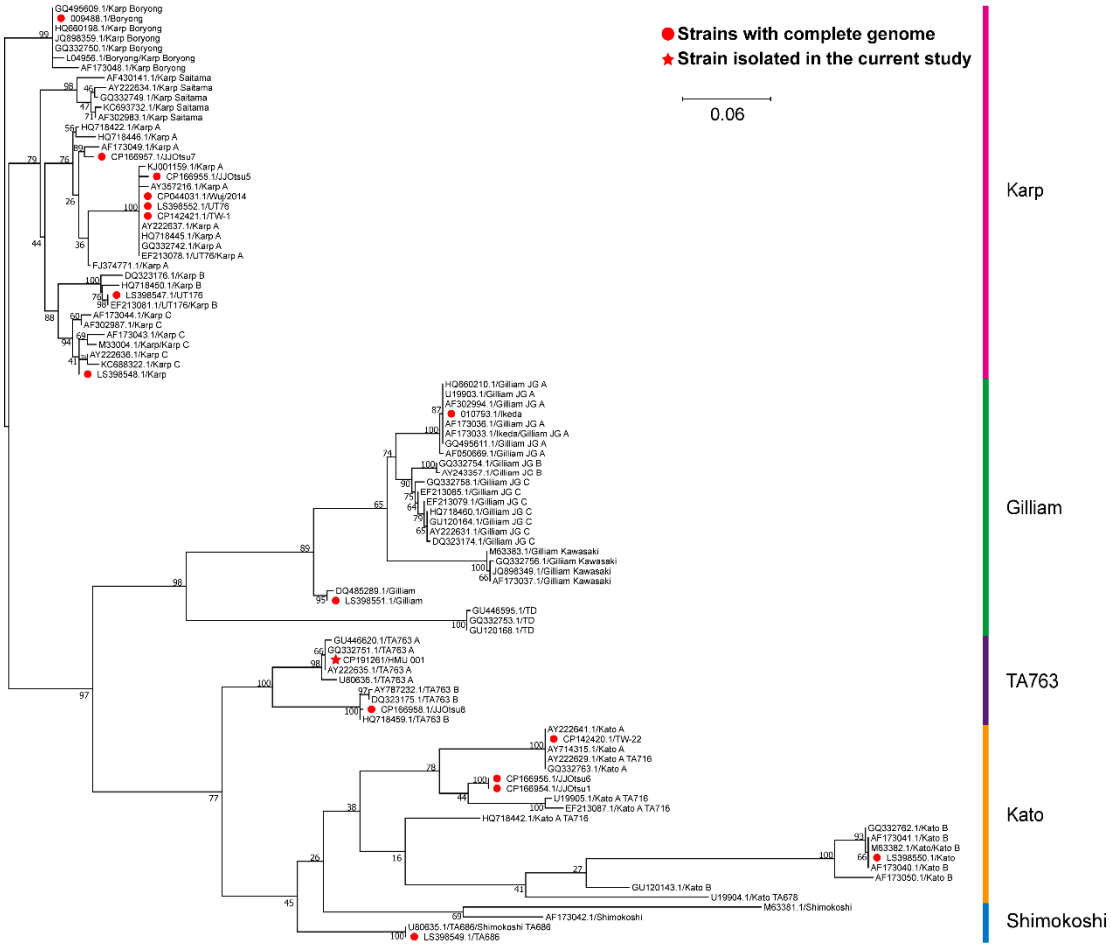


Figure S3. Phylogenetic relationships inferred from partial *tsa56* sequences.

Maximum-likelihood tree based on a partial *tsa56* alignment. Strains with complete genomes are marked with red circles, and HMU_001 is indicated by a red star. Colored bars indicate major *tsa56* genotype groups.