

Fig S4. Interlineage recombination around MCE operon locus 3.

- (A) Genome structure comparison indicating orthologous relationship between MCE operons on MAH and MTB. Location of MCE operon is indicated by red line. Genomes were compared by blastn and visualized using GenomeMatcher software. Locus 2, locus 6 and locus 7 correspond to MCE operon family Mce4, Mce2, and Mce1, respectively. Orthologs for MCE locus 1, 3, 4, 6 in MAH (shown in purple) were not present in the MTB genome. Mce3-equivalent locus is absent in the MAH genome. MAH strain 104 additionally possess locus 8 near locus 7.
- (B) Nucleotide similarity around MCE locus 3. The color of the strain name indicates the relevant MAH lineage. TH135 coordinate 797,096–831,124 and its equivalent region in the three genomes are shown. Coding sequences in MCE operon were colored in blue. MCE operon in OCU464 is included in the segment brought by recent recombination predicted by fastGEAR software (white ilne).
- (C) Phylogenetic tree of MAH-related strains based on concatenated protein coding sequences of MCE operon locus 3. The substitution model used was JTT+G.