



**Supplemental Figure S5. Evolutionary relationship for the non-MA isolates based on single-nucleotide mutations and CNVs.** The total number of mutations (both point mutations and CNVs) mapped onto each branch is shown. The minimum-evolution phylogeny was constructed using the Jukes-Cantor model, treating each deletion as a single mutational event of equal weight to point mutations. The four major lineages that show no early shared mutations were used to calculate the mutation rates for the non-MA isolates.