



**Figure S1: Phylogenetic analysis of MeV partial hemagglutinin (H) gene sequences.**

Partial sequence generated using the H gene RT-PCR. WHO MeV reference strain sequences include GenBank accession numbers and the eight clades are designated A–H. MeVV sequences associated with patients and vaccine strain genotype A (red) viruses are indicated by case number and associated GenBank accession number. Wildtype genotype A reference strain is indicated in blue. Phylogenetic analysis used the Neighbor-Joining and Maximum Composite Likelihood methods and was performed in MEGA7 with a bootstrap analysis of 1000 replicates. The percentage of replicate trees in the bootstrap test (1000 replicates) greater than 85 are shown next to the branches. A higher resolution version is located at <https://doi.org/10.6084/m9.figshare.8248139>