



Figure S2: Phylogenetic analysis of MeV partial Large gene (L) gene sequences.

Partial sequence generated using the L gene RT-PCR. Representative MeV 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 is indicated in blue. Phylogenetic analysis used the Neighbor-Joining method Maximum Composite Likelihood methods 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.8248091>.