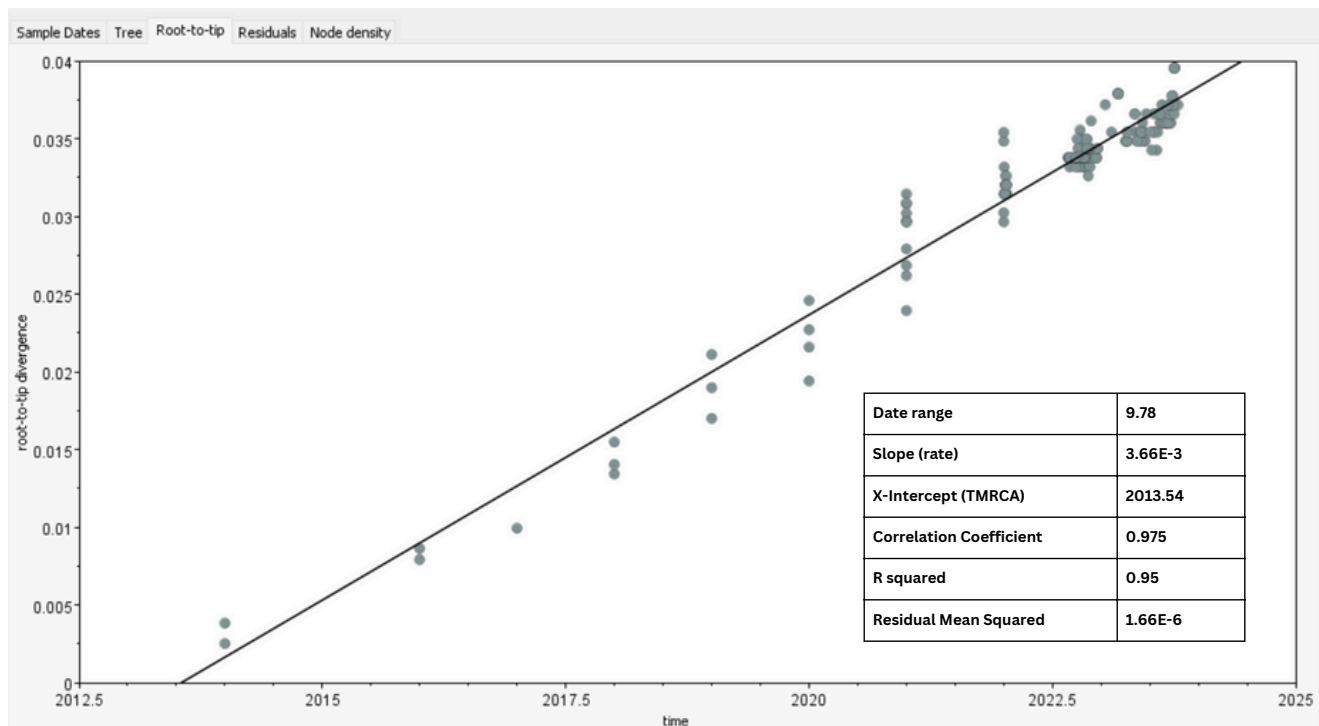**Supplementary Figure S1. Temporal Analysis of A(H3N2) HA Gene Divergence**

The figure illustrates the regression of root-to-tip genetic distance against the sampling date for the dataset 1 (A(H3N2)-HA gene). A strong positive correlation is evident, with a correlation coefficient (r) of 0.97 and a coefficient of determination R squared of 0.95, indicating the dataset's suitability for phylogenetic molecular clock analysis in BEAST

Date range	9.78
Slope (rate)	3.66E-3
X-Intercept (TMRCA)	2013.54
Correlation Coefficient	0.975
R squared	0.95
Residual Mean Squared	1.66E-6

Supplementary Figure S2. Estimates of MCC networks and reassortment rates in Bhutanese A(H3N2) viruses

Estimates of MCC reassortment network between HA and NA genes of Bhutanese influenza A(H3N2) viruses sampled in 2022 and 2023. Icytree visualizes the network as a base tree connected by dotted branches, indicating a reassortment event. The node bars indicate the 95% HPD.