



Supplementary Figure S1. Phylogenetic relationships of the HA gene segments of 125 sequences that comprise 79 A/H3N2 isolates from Myanmar (2015–2019) and the closest BLAST hits from different regions worldwide. The maximum-likelihood tree was inferred from 125 HA gene sequences in comparison with the Southern Hemisphere vaccine strains of known clades recommended by the World Health Organization (bold). Those in different colors represent Myanmar strains, colored according to clade. Those in black represent global strains. Branch values >70% are indicated at the nodes.