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Bats are natural reservoirs for both *Alpha*- and *Betacoronaviruses* and the hypothesized original hosts of five of seven known zoonotic coronaviruses. To date, the vast majority of bat coronavirus research has been concentrated in Asia, though coronaviruses are globally distributed. As part of a long-term sampling study in three species of endemic Malagasy fruit bats, we carried out sequencing on urine, throat, and fecal samples obtained from wild-caught individuals. We describe full genome sequences, one of which is highly divergent, of novel *Nobecoviruses* in two endemic Malagasy bat species. Recombination analysis indicates significant selection has taken place in the spike, nucleocapsid, and NS7 accessory protein regions of the genome for viruses derived from both bat hosts. Madagascar offers a unique phylogeographic nexus of bats and viruses with both Asian and African phylogeographic origins, providing opportunities for unprecedented mixing of viral groups and, potentially, recombination. As fruit bats are handled and consumed widely across Madagascar for subsistence, understanding the landscape of potentially zoonotic coronavirus circulation is essential for mitigation of future zoonotic threats. This research addresses a gap in coronavirus surveillance in non-Asian areas and contributes to the evolutionary history of new novel coronaviruses.