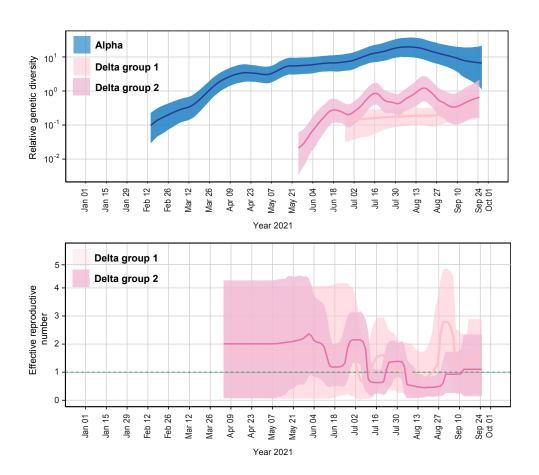
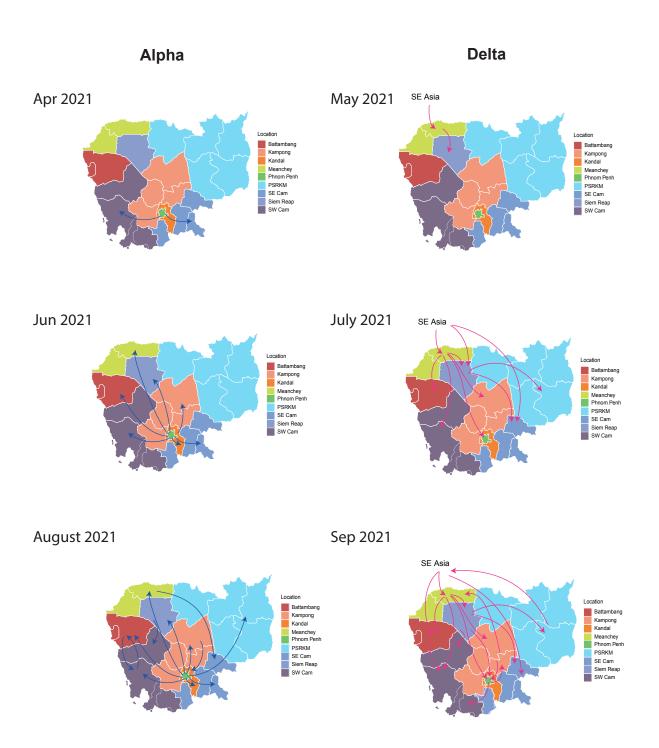


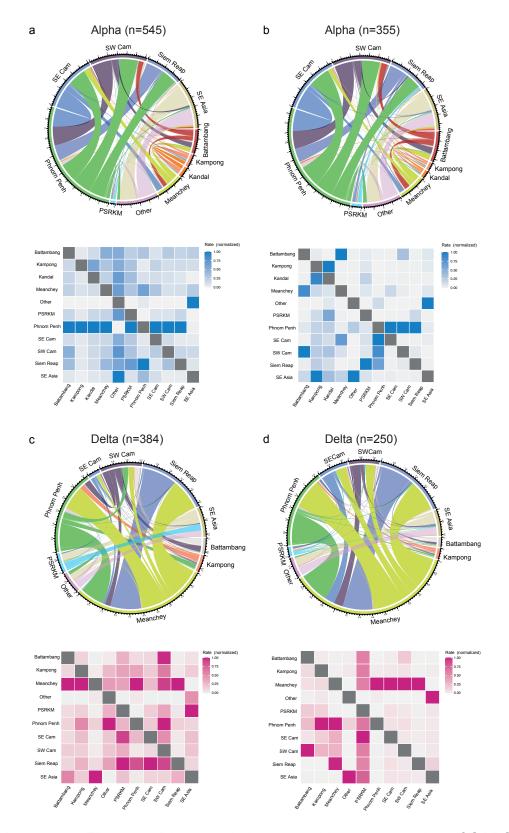
Supplementary Figure 1. Phylogenetic analyses of global and Cambodian SARS-CoV-2 genome sequences, 2021. Maximum likelihood phylogeny was reconstructed using Nextstrain based on 5,964 full genomes comprising local and subsampled global sequences. Cambodian sequences are represented by deep pink tip circles, while sequences from Thailand are denoted by green tip circles. The majority of Cambodian Delta sequences belong to the AY.30 and AY.85 Pango lineages.



Supplementary Figure 2. Relative genetic diversity and the effective reproductive number (Re) of the Alpha and Delta groups based on Cambodian sequences. Solid lines represent median values, with the Alpha and Delta variants denoted by blue and pink lines, respectively. The shaded areas represent the corresponding 95% highest posterior density (HPD) intervals. The dotted green line represents an Re of 1. An Re greater than 1 signifies epidemic growth, while an Re less than 1 indicates recession.



Supplementary Figure 3. Spatial diffusion pathways of Alpha and Delta variants into and within Cambodia through time.



Supplementary Figure 4. Discrete phylogeographic reconstruction of SARS-CoV-2 Alpha and Delta variants into and within Cambodia. Panel a and b display circular migration plots and diffusion rate matrices of the Alpha variant based on larger (n=545) and smaller (n=355) datasets, respectively. Migration from one geographic location to another region begins closer to the outer ring in the circular migration plots. Panel c and d show circular migration plots and diffusion rate matrices of the Delta variant based on larger (n=384) and smaller (n=250) datasets, respectively.