Supplemental Figures

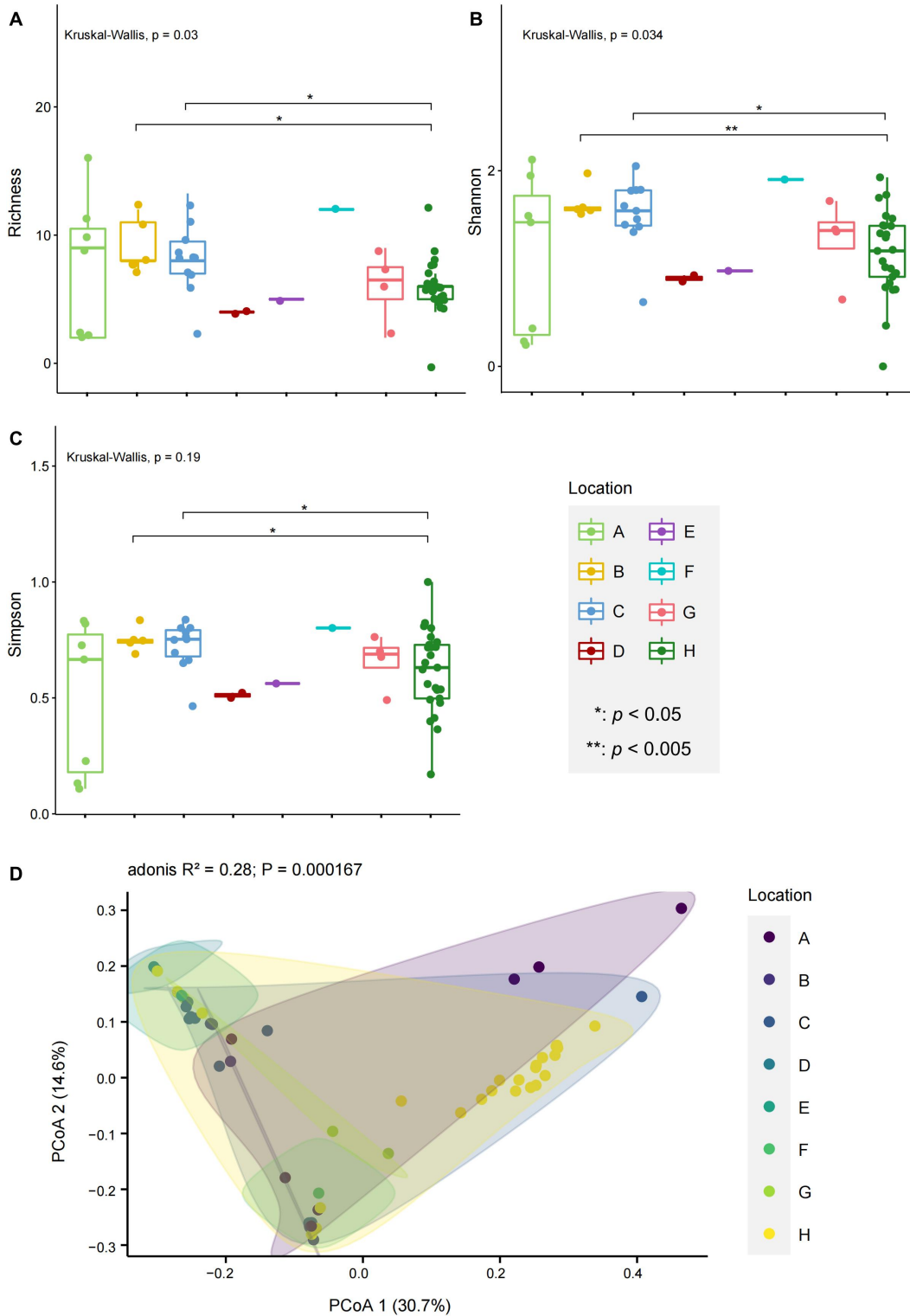**Figure S1. Comparison of the viral diversity across different sampling locations.** (A) Virome richness, (B) Shannon index, (C) Simpson index, and (D) Beta diversity analysis of the viromic composition across different sampling locations.
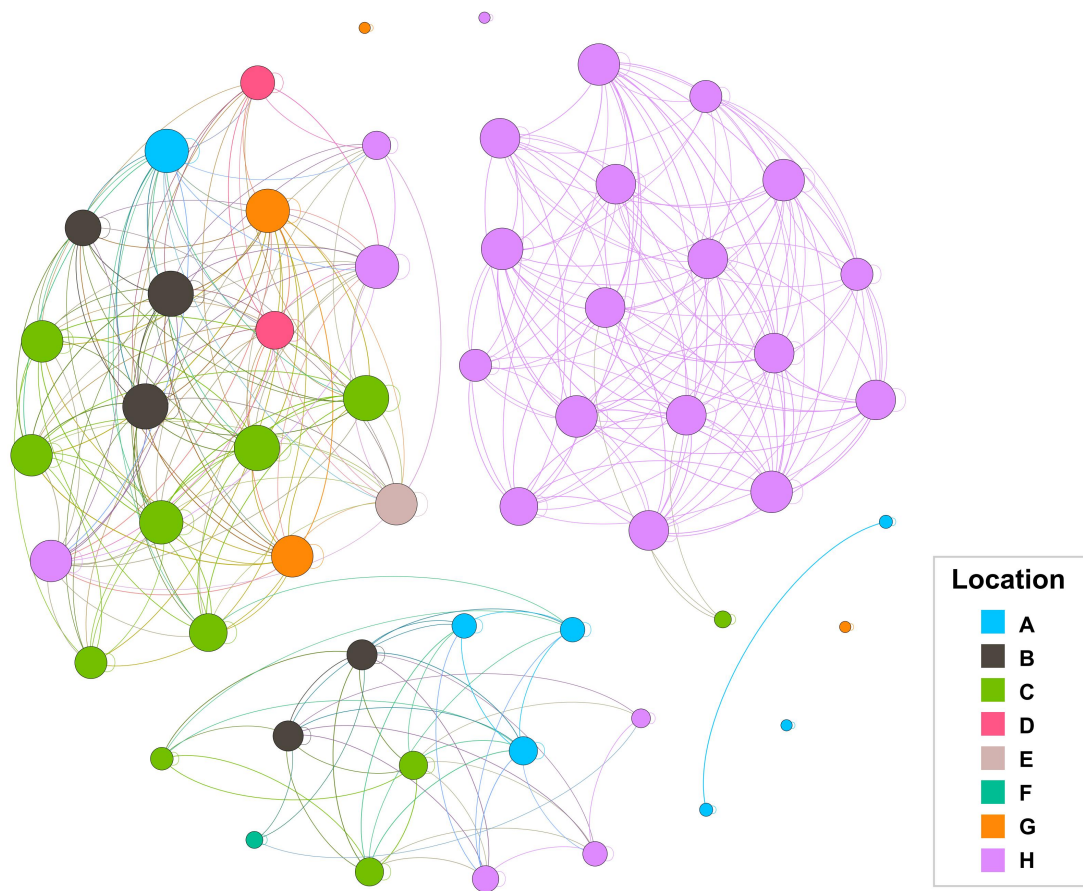
Figure S2. Viral co-occurrence network of geographical locations. The network was calculated using the relative abundance of each virus across libraries. Each node represents a library. Libraries with a Spearman's correlation greater than 0.6 ($P < 0.05$) are connected by edges. The thickness of each edge is determined according to the correlation coefficients; the size of a node is determined by the degree (number of edge connections). The nodes were colored by sampling locations.