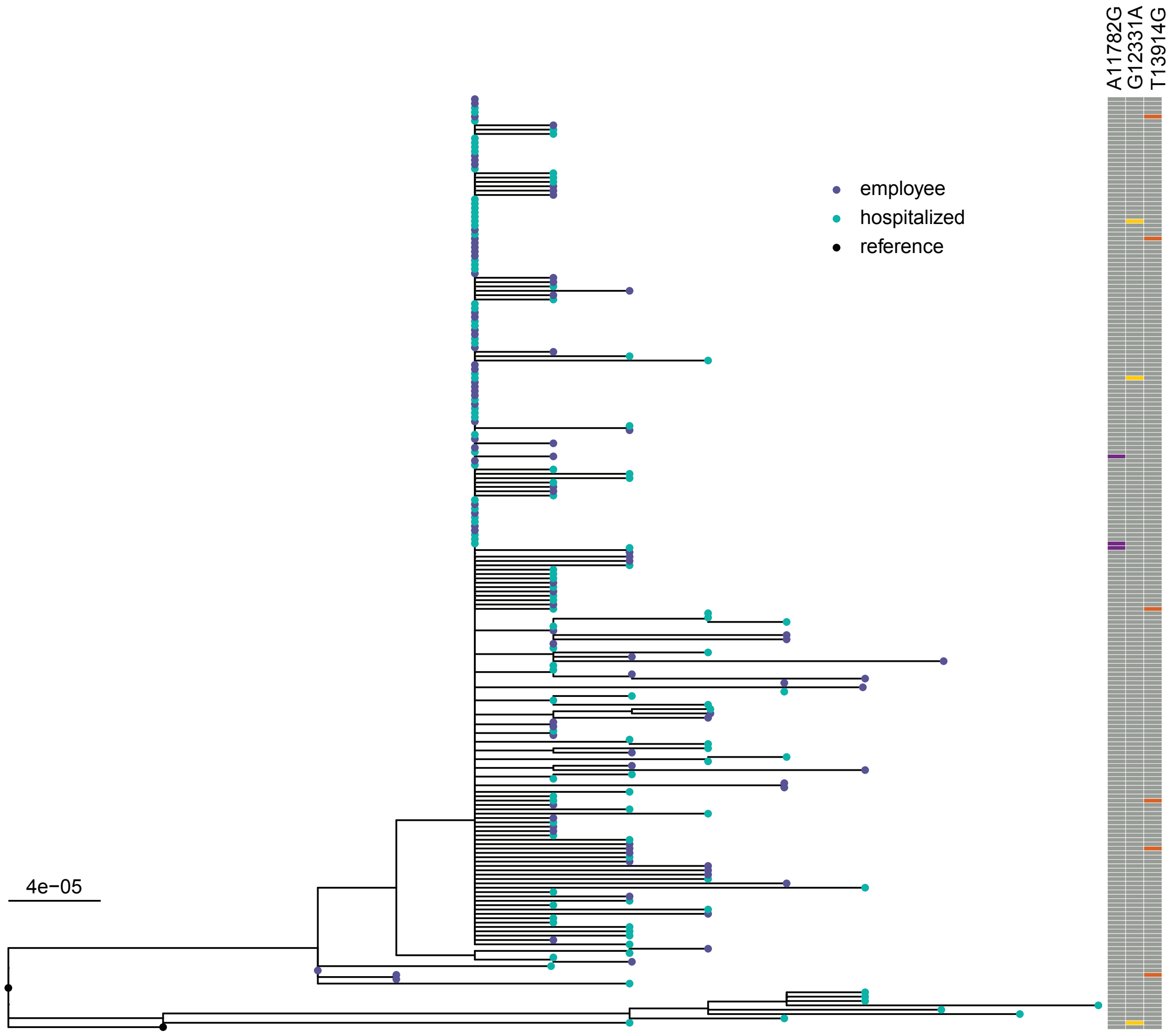
Supplemental Figure 4



Supplemental Figure 4. Maximum likelihood phylogenetic tree as shown in Figure 1C. Tips represent complete consensus genomes from hospitalized patients (teal) and employees (violet). The x-axis shows divergence from the root (Wuhan-Hu-1/2019). Heatmaps show samples that contain each of the three mutations as an iSNV.