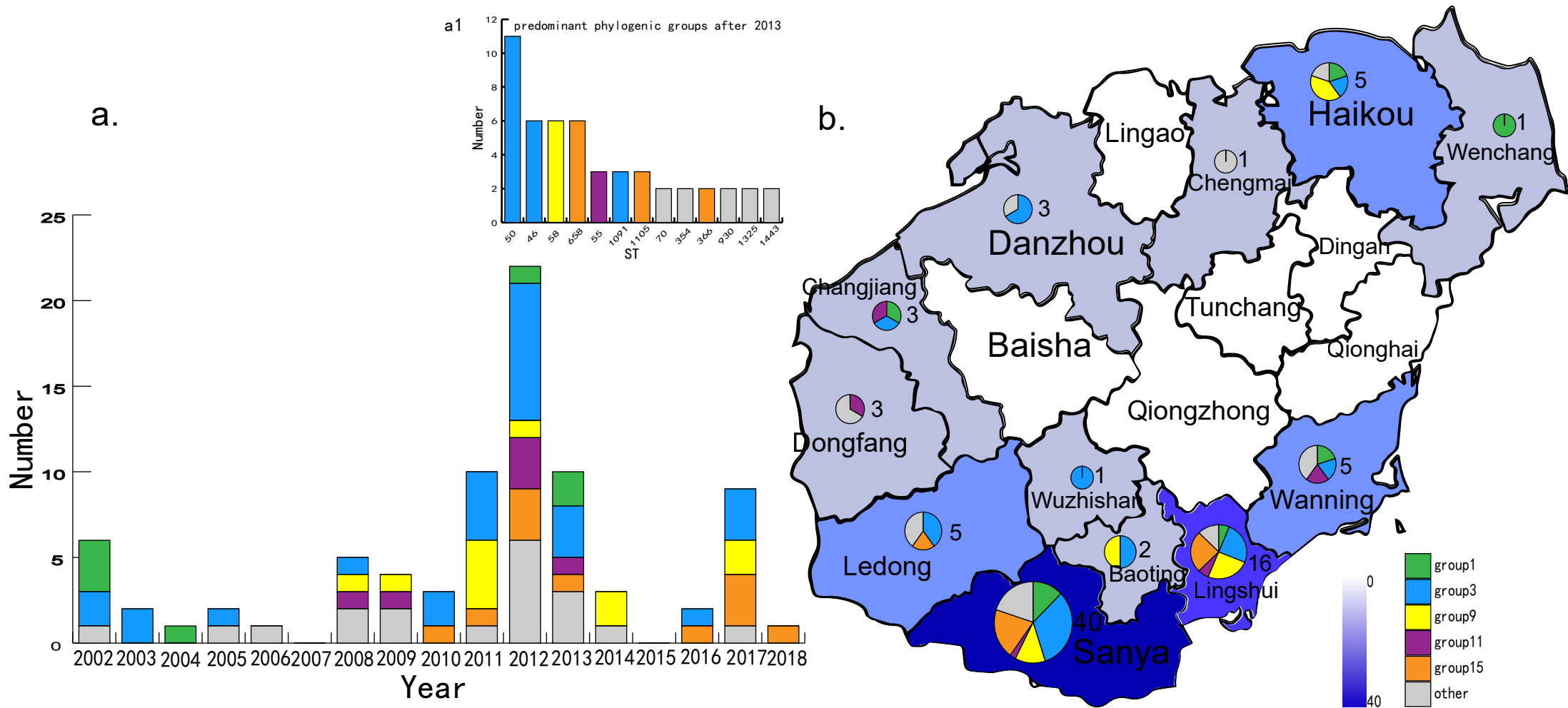
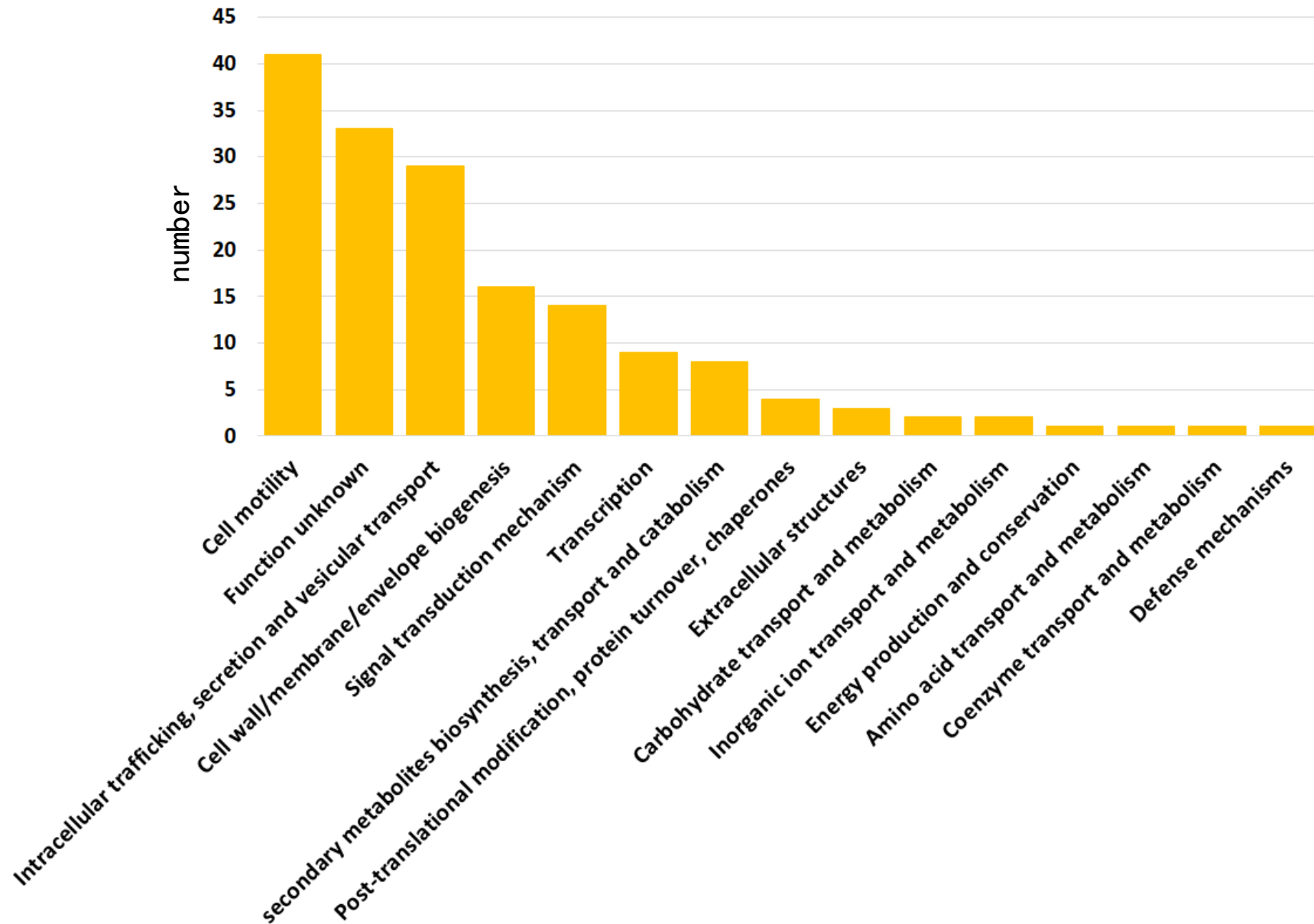


**Supplementary Fig. 1. Phylogeny and primary clusters based on hierBAPS.** A core SNP-based maximum likelihood phylogeny of 1654 genomes, with their geographic origins highlighted. The outer ring represents the primary population clusters based on Bayesian Analysis of Population Structure (BAPS) hierarchical clustering (groups 1–14). Except for group 5, which is paraphyletic and marked by three black arrowheads, and group 7, which is also paraphyletic and marked by three black squares, each of the other 12 groups forms a monophyletic branch.



**Supplementary Fig. 2. Temporal and spatial distributions of Hainan *B. pseudomallei* isolates.** a, Histogram shows the temporal distribution of Hainan *B. pseudomallei* isolates from the five major groups in 2002–2018. a1, Histogram shows the STs and predominant phylogenetic groups after 2013. b, Map of Hainan island shows the spatial distribution of Hainan *B. pseudomallei* isolates from the five major groups across the whole island.

### categories of VFs (COG)



**Supplementary Fig. 3. Functional categories of virulence factors for all 1654 *B. pseudomallei* isolates.** The 160 detected virulence factor genes (VFs) are categorized according to the Clusters of Orthologous Genes (COG) database: 92.6% of the VFs were assigned to 15 categories, with elevated frequencies for the terms “cell motility”, “intracellular trafficking, secretion and vesicular transport”, “cell wall, membrane, envelope biogenesis”, and “signal transduction mechanism”.