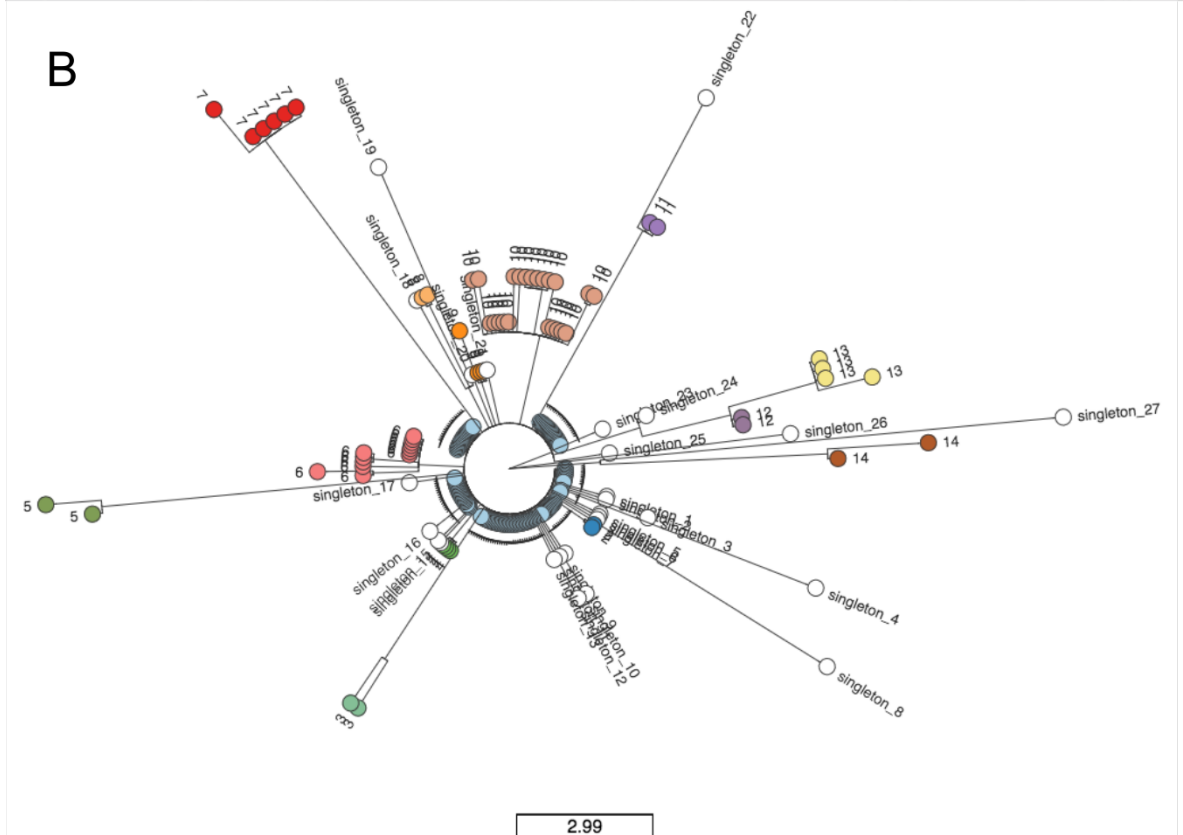
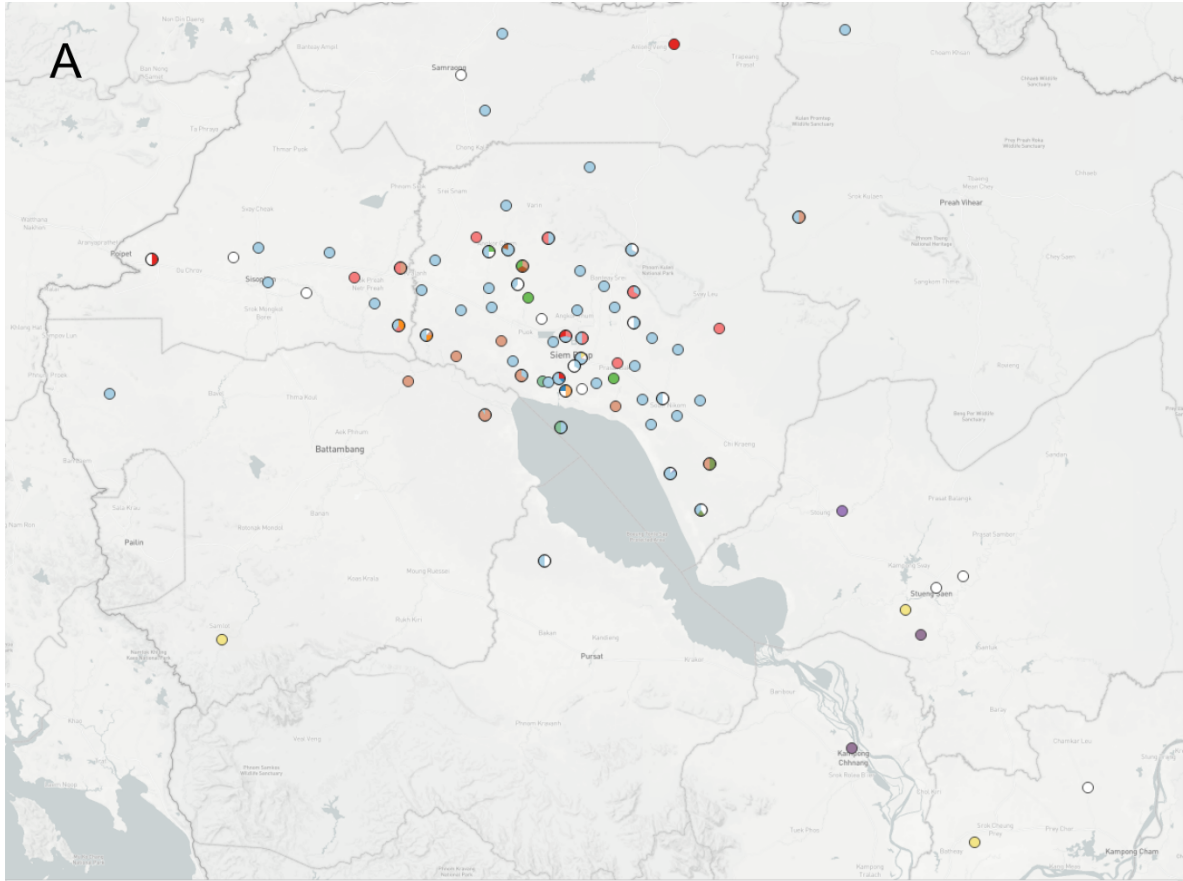


- 2 **Supplementary Figure 1. Rooted joint ancestral reconstruction tree based on whole genome sequencing of 203 *S. Typhi* H58 isolates.**
- 3 Outgroup rooted using *S. Typhi* Mal1017142 Genotypi 4.1.1. Tips are labelled according to rPinecone sub-lineage. Branch lengths are SNV
- 4 scaled. Colour rings 1 and 2 correspond to the sub-lineages and major lineage defined by rPinecone. The five outer (3-7) colour rings correspond
- 5 to clusters defined by BAPs.



6

7

8

9 **Supplementary Figure 2. Isolate spatial, phylogenetic and clustering data displayed in**
10 **Microreact.** A) Geospatial distribution of *Salmonella* Typhi isolates in Cambodia. B) The
11 phylogenetic tree with isolates labelled with their corresponding sub-lineage defined by
12 rPinecone. Isolates in both panels are coloured according to sub-lineages.

