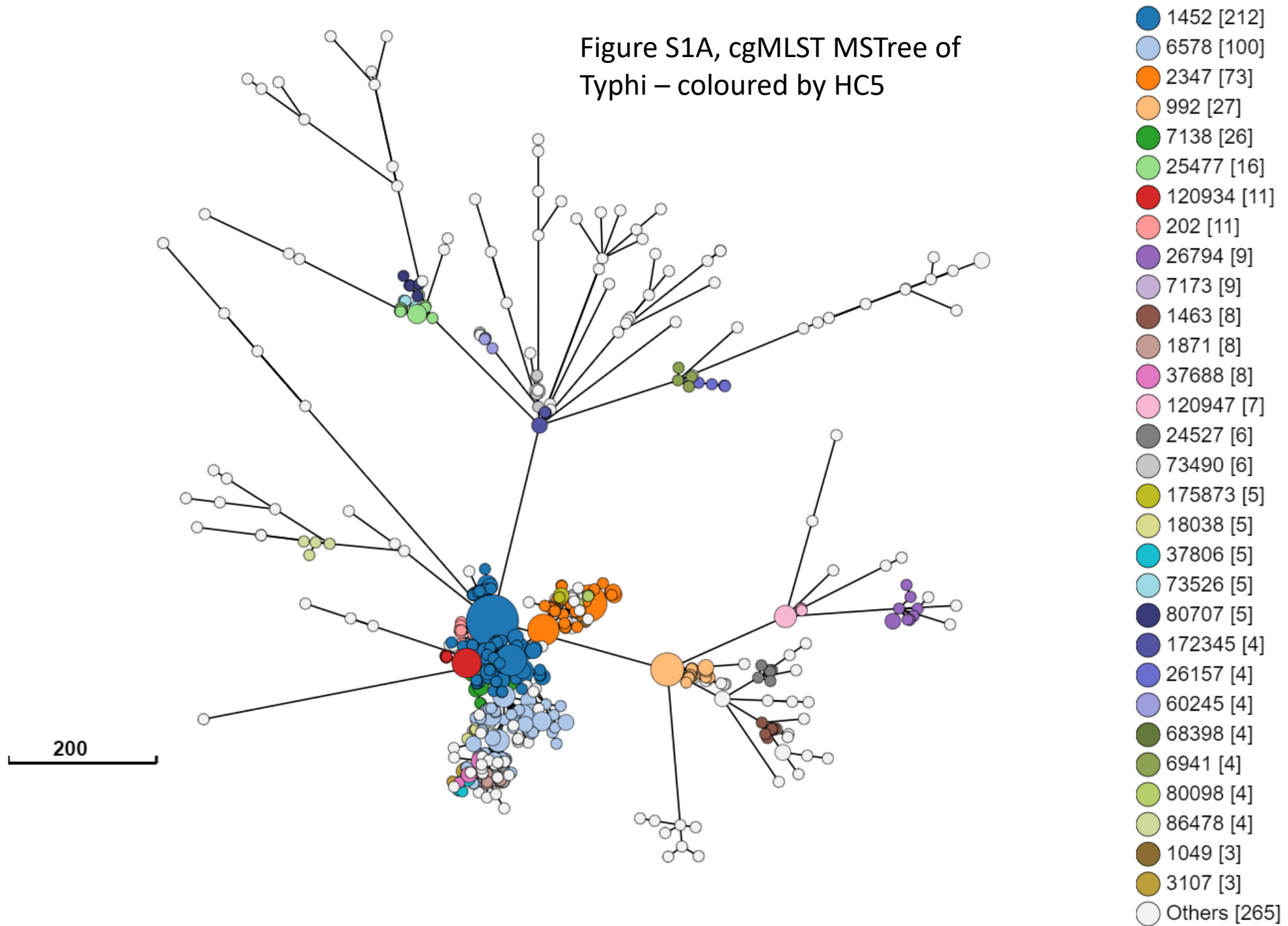


Figure S1A, cgMLST MSTree of Typhi – coloured by HC5



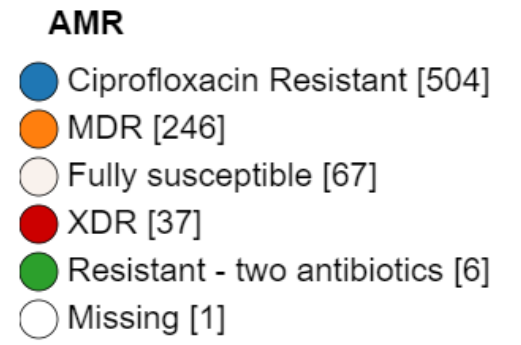
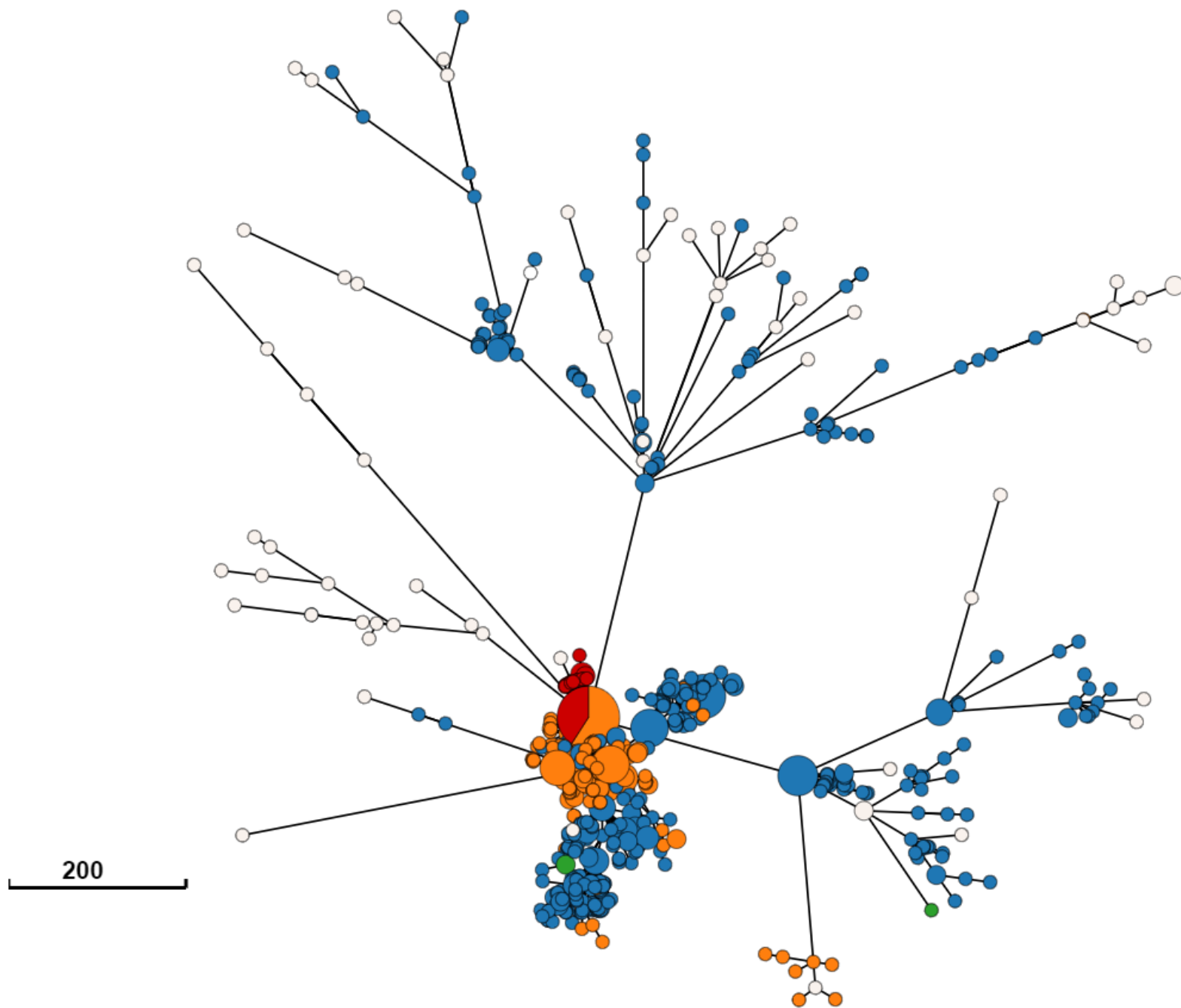


Figure S1B, cgMLST MSTree of Typhi
– coloured by AMR category

Figure S1C, cgMLST MSTree of Typhi – coloured by travel in the past 28 days

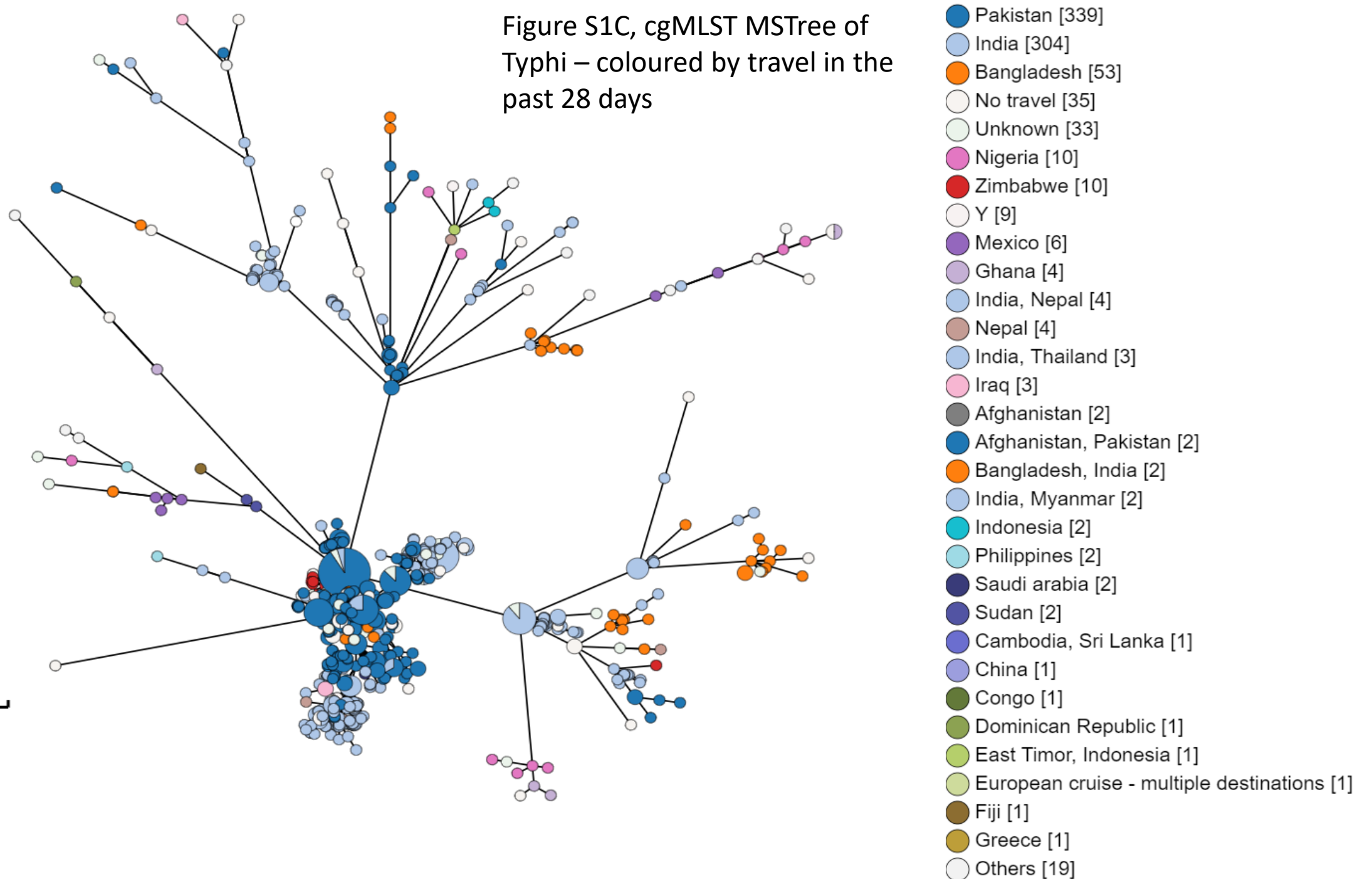


Figure S2A cgMLST MSTree of Paratyphi A – coloured by cgMLST

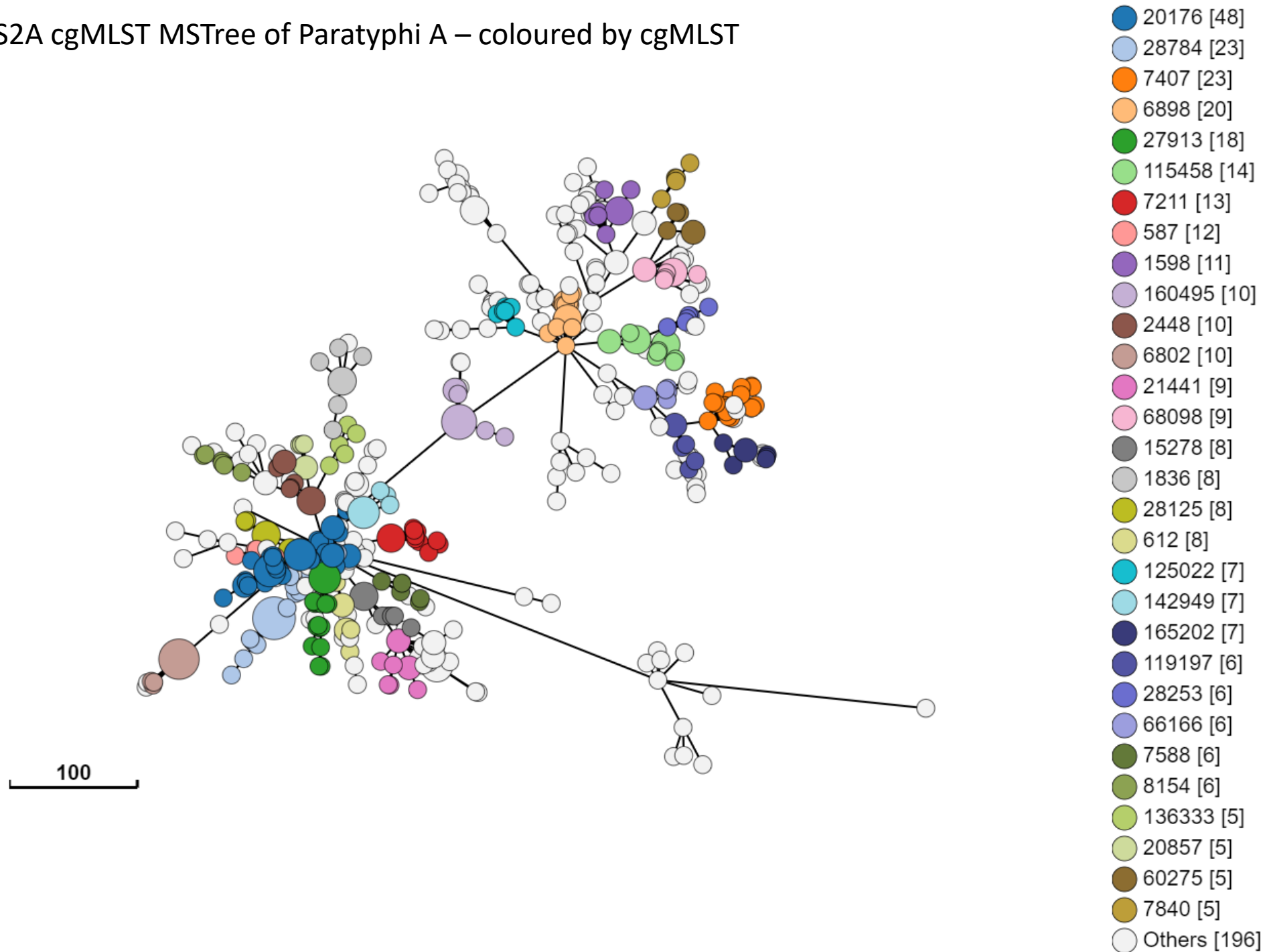
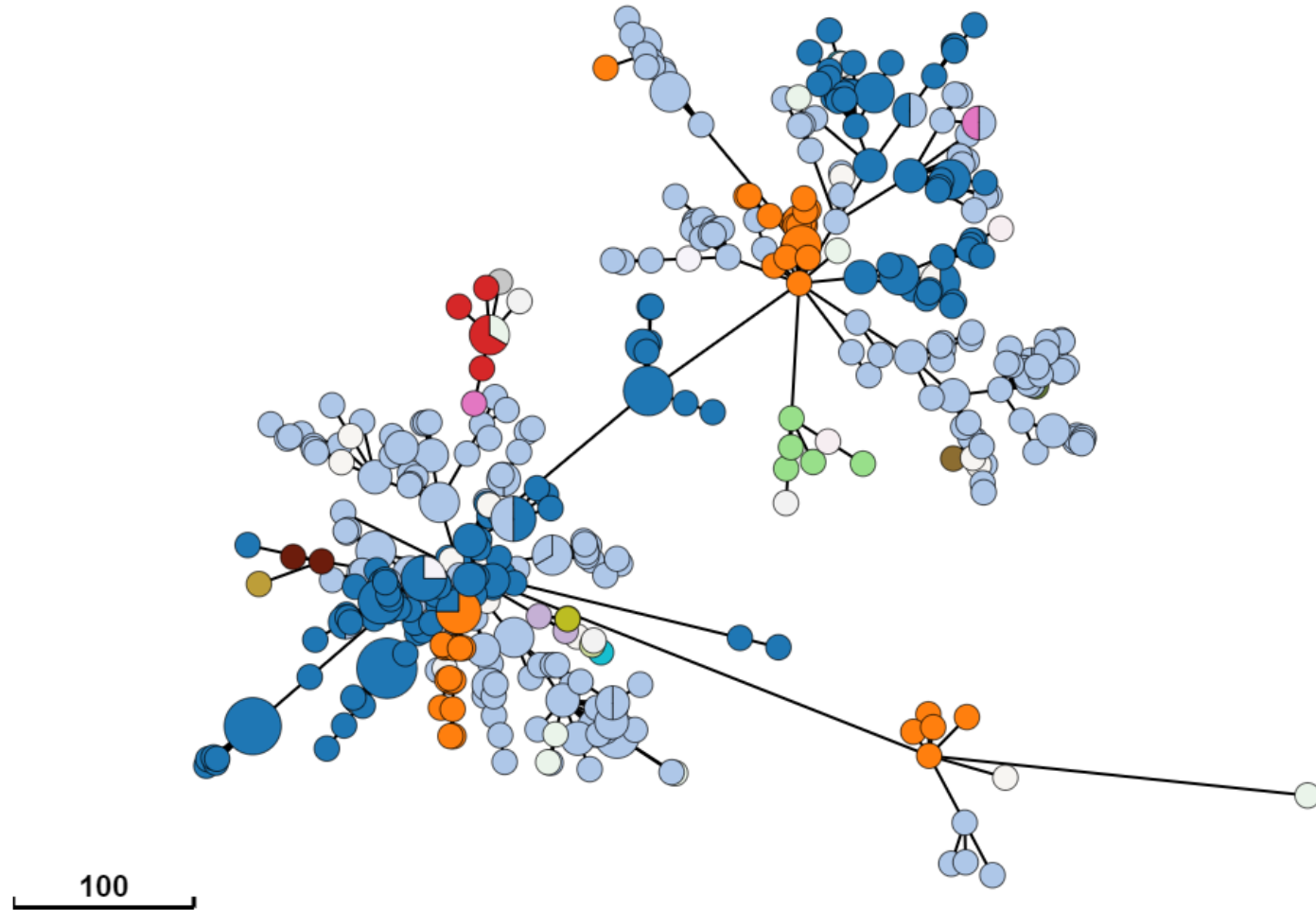


Figure S2B, cgMLST MSTree of Paratyphi A – coloured by travel in the past 28 days



- India [243]
- Pakistan [170]
- Bangladesh [49]
- Unknown [15]
- No travel [7]
- Indonesia [5]
- Myanmar [5]
- India, Nepal [3]
- Asian continent [2]
- Cambodia [2]
- Ghana [2]
- India, Thailand [2]
- Thailand [2]
- Y [2]
- Cambodia, India, Laos, Thailand, Viet Nam [1]
- Cambodia, India, Nepal, Thailand [1]
- Cambodia, Thailand [1]
- Cambodia, Thailand, Viet Nam [1]
- Cambodia, Vietnam [1]
- Canada [1]
- India, Indonesia [1]
- India, Indonesia, Philippines, Sri Lanka, Viet Nam [1]
- India, Nepal [1]
- India, Pakistan [1]
- India, Philippines [1]
- India, Turkey [1]
- India, Vietnam [1]
- Malaysia [1]
- Nepal [1]
- Nigeria [1]
- Others [4]

Figure S3A, cgMLST MSTree of
Paratyphi B – coloured by cgMLST
HC5

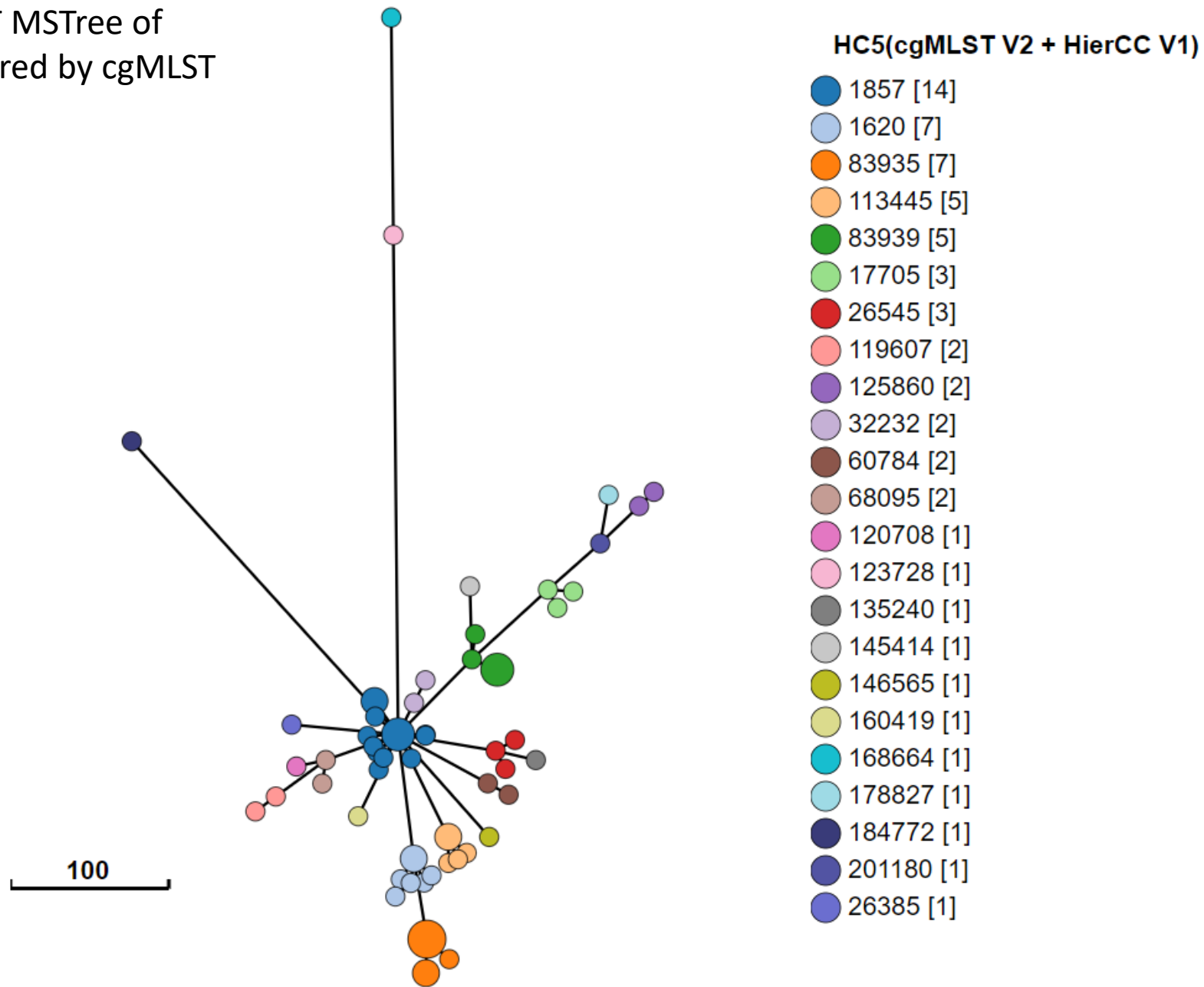
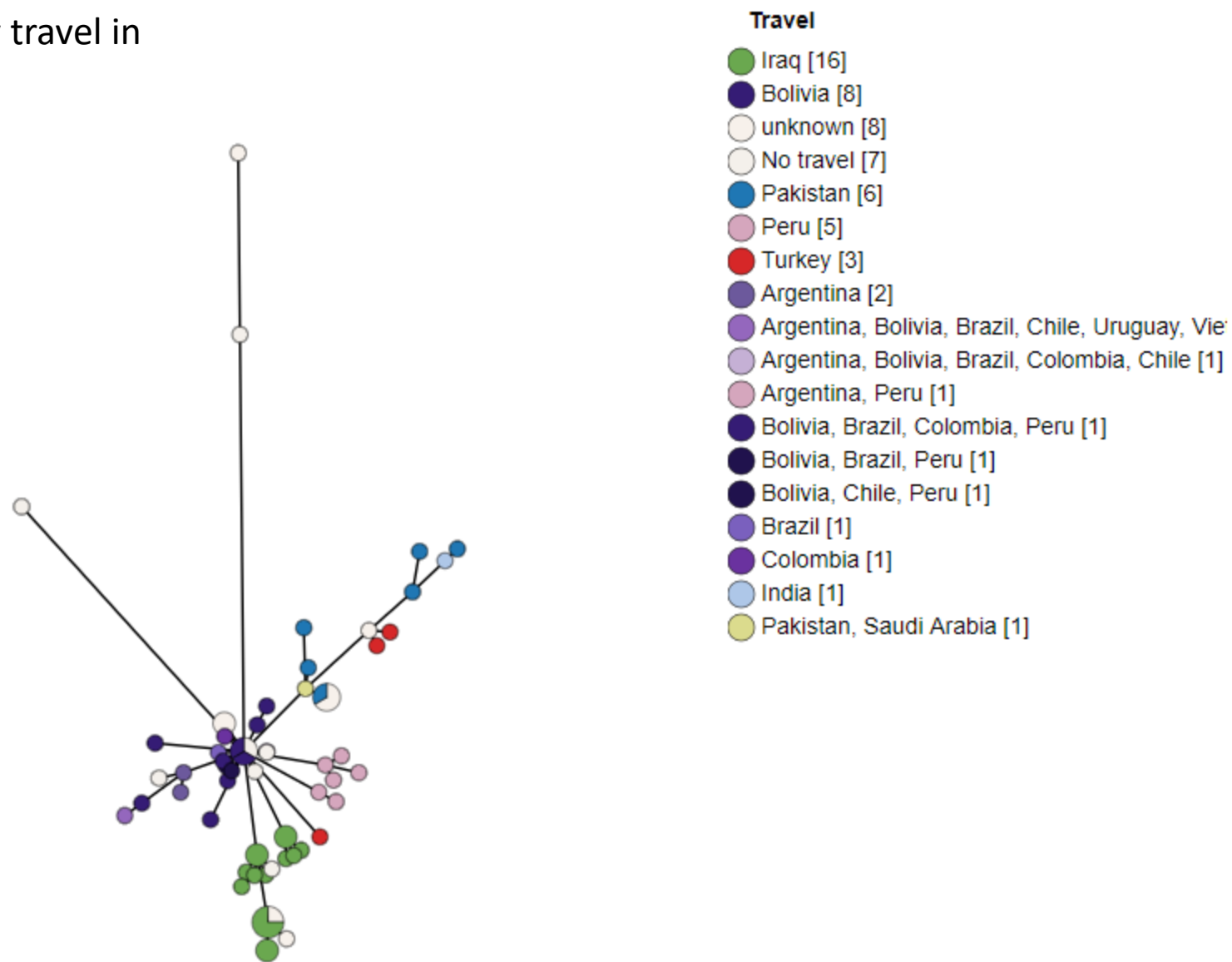


Figure S3A, cgMLST MSTree of Paratyphi B – coloured by travel in the past 28 days



Legend: Hierarchical Clustering (HierCC) of enteric fever cases in England between 2016-2019. GrapeTree depiction of MSTree tree V2 of cgMLST allelic distances between genomic entries, coloured by different categories: *S. Typhi* HierCC number at the HC5 allelic level (S1A), *S. Typhi* and AMR category (S1B), *S. Typhi* and travel in the past 28 days (S1C), *S. Paratyphi A* and HierCC number at the HC5 allelic level (S2A), *S. Paratyphi A* and travel in the past 28 days (S2B),), *S. Paratyphi B* and HierCC number at the HC5 allelic level (S3A), *S. Paratyphi B* and travel in the past 28 days (S3B).