

Supplementary Figures

Metagenomic data from cerebrospinal fluid permits tracing the origin and spread of *Neisseria meningitidis* CC4821 in China

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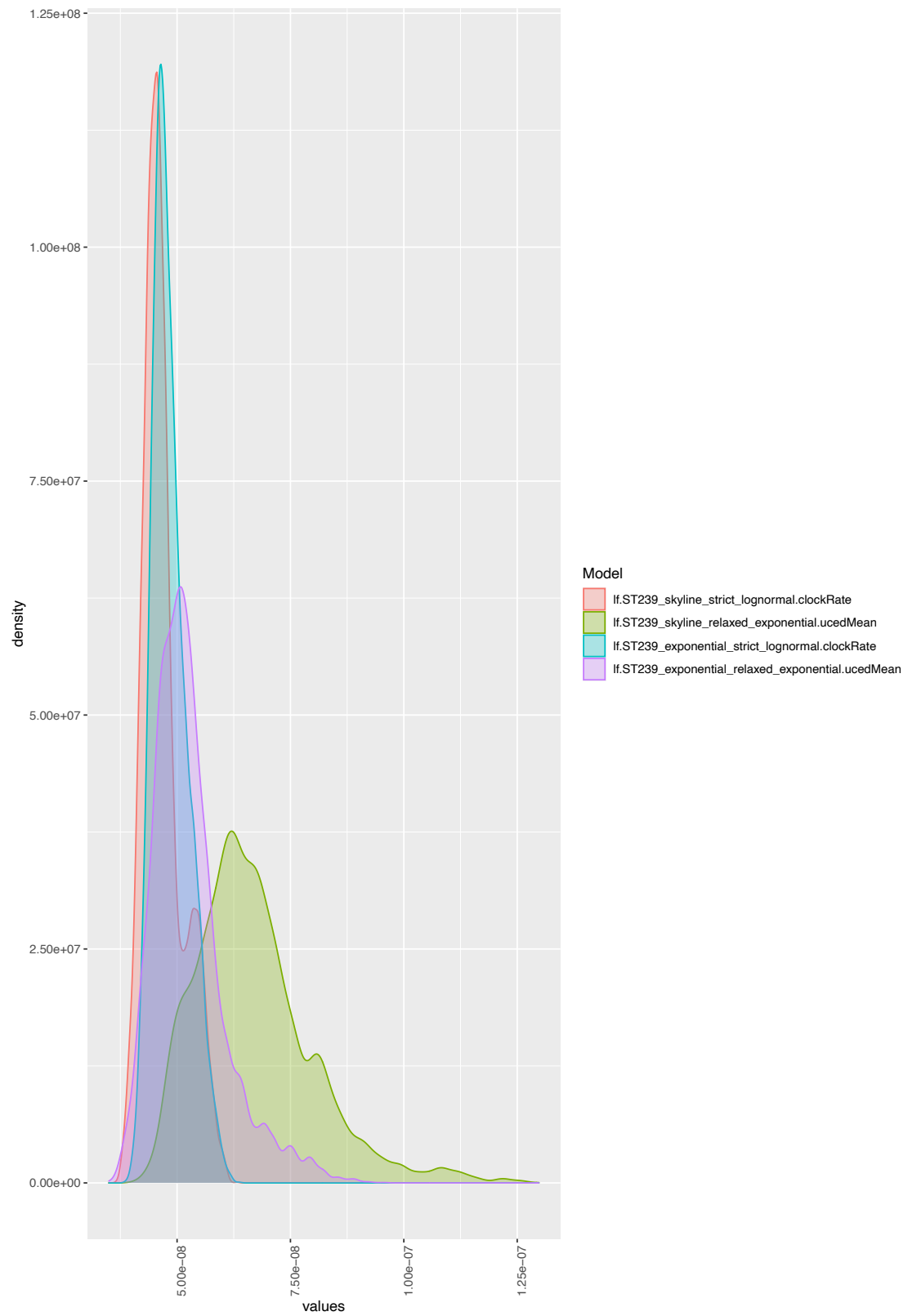
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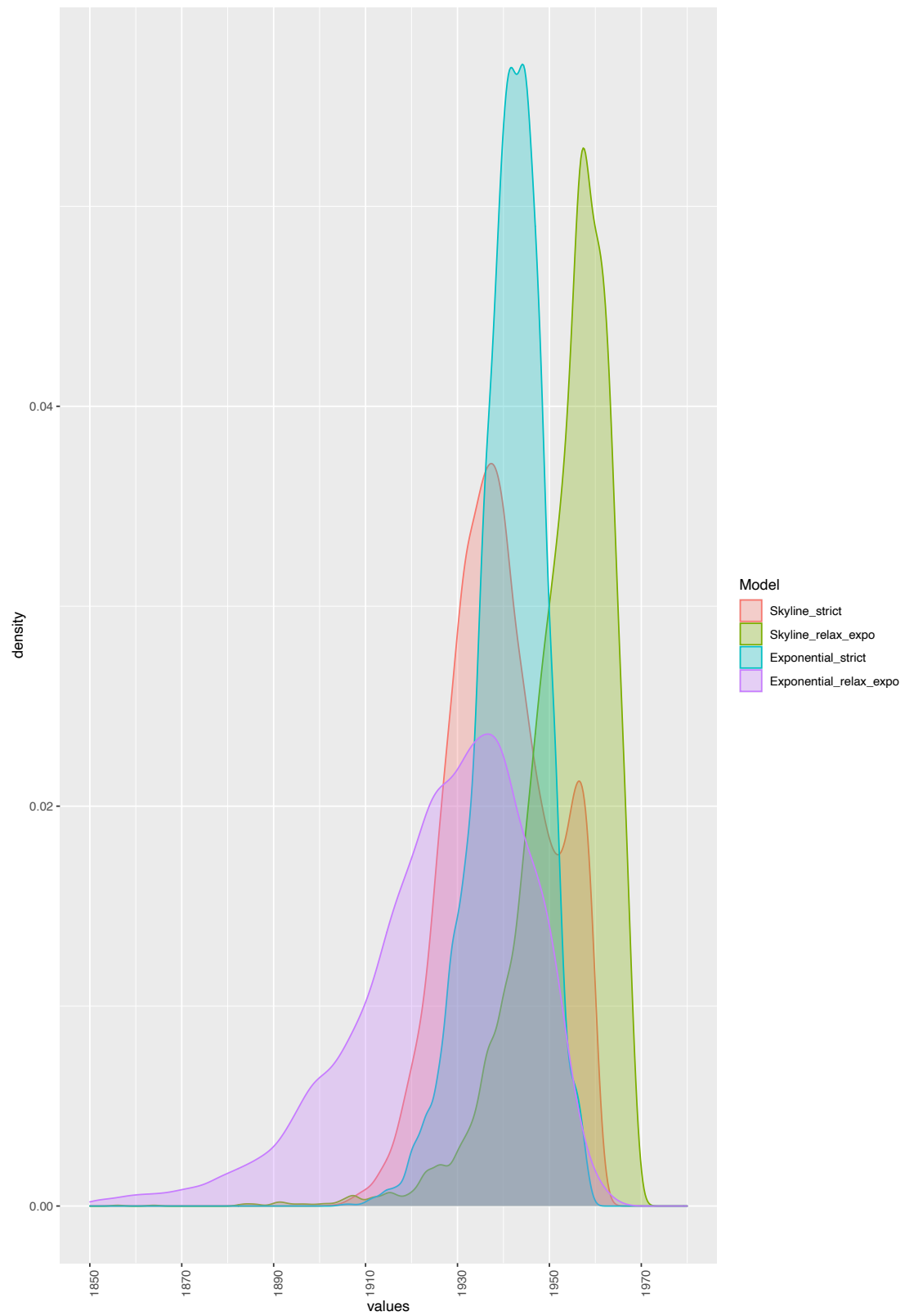
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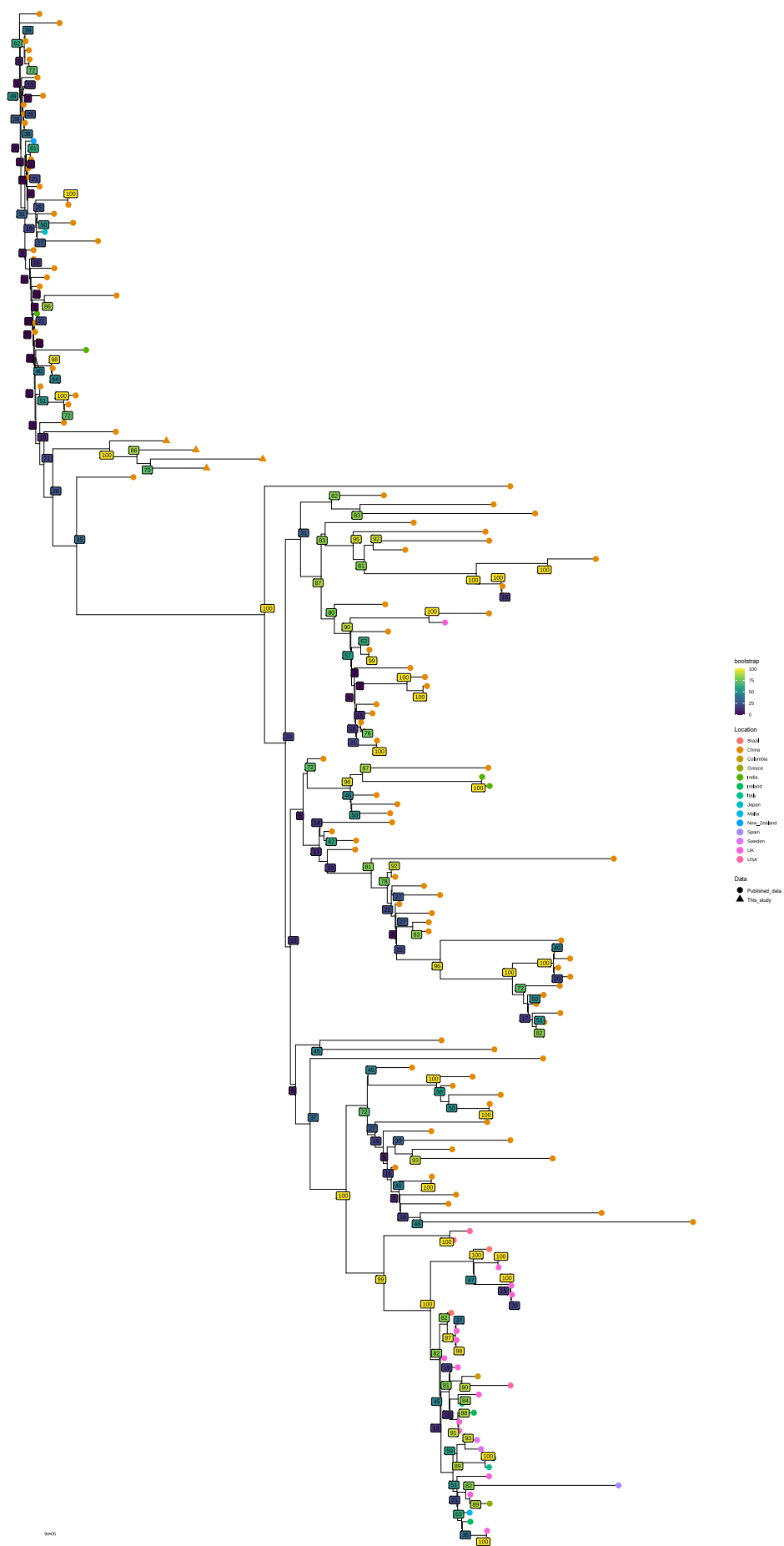
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Supplementary Figure 1: **Comparison of evolution rate of different models.**

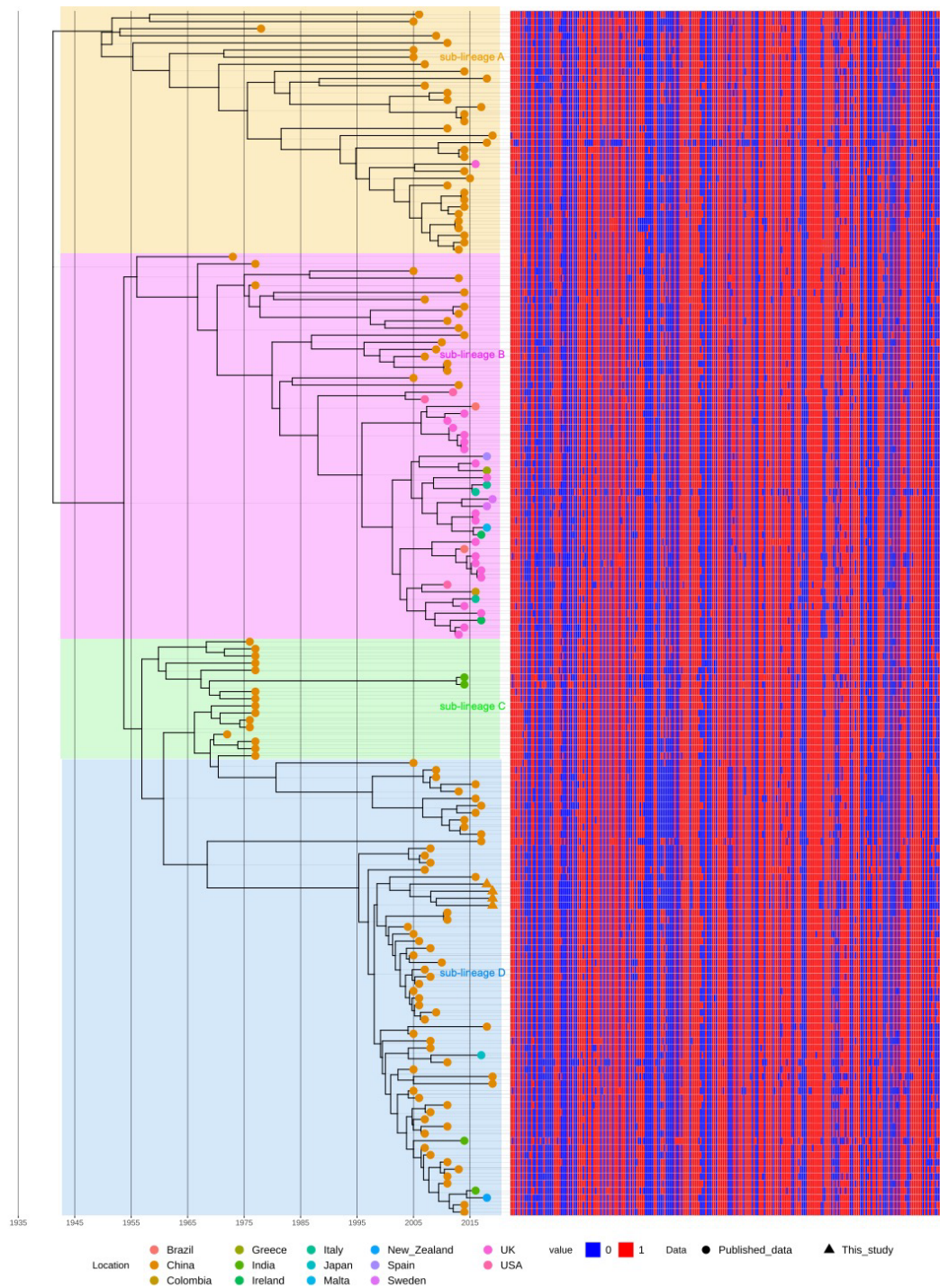


Supplementary Figure 2: **Comparison of the origin time of different models.**



Supplementary Figure 3: **Maximum likelihood phylogeny of CC4821 populations.**

The trees were constructed in RAxML v8.2.10 using a GTR model and 1,000 bootstrap replicates. The tips of branches were coloured according to the province from which isolates were sampled. The tree was rooted by *N. meningitidis* MC58. The scale was in units of substitutions per site.



Supplementary Figure 4: **Presence or absence of accessory genes amongst CC4821 isolates.** Accessory genes were identified using Roary v3.11.2. The heatmap of accessory genes was plotted here, with columns corresponding to genes and rows corresponding to individual isolates. Presence of a gene in an isolate was coloured by red, with absence of a gene coloured by green.