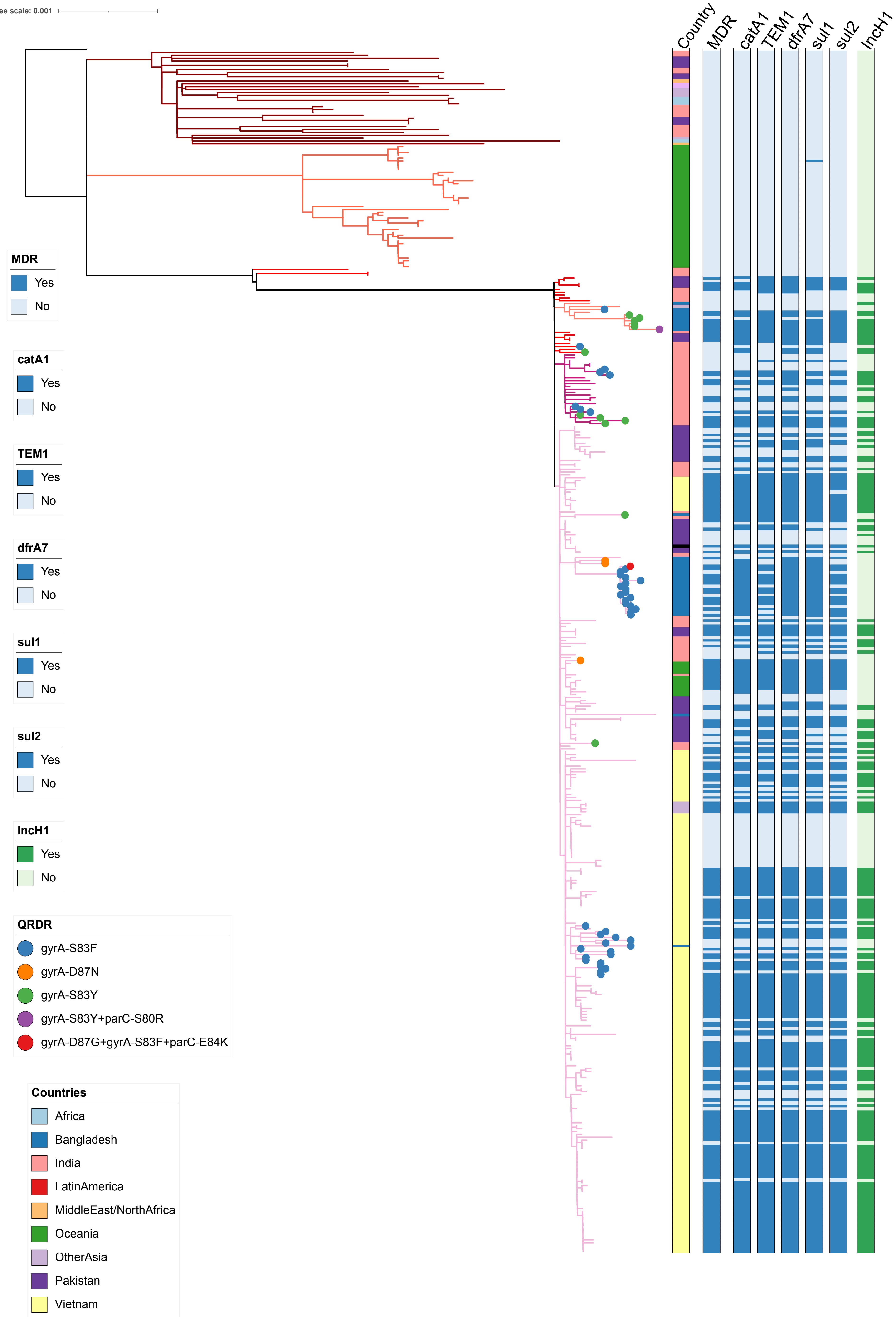


Supplemental Figure 1: The phylogenetic structure of early H58 organisms and nearest neighbours.

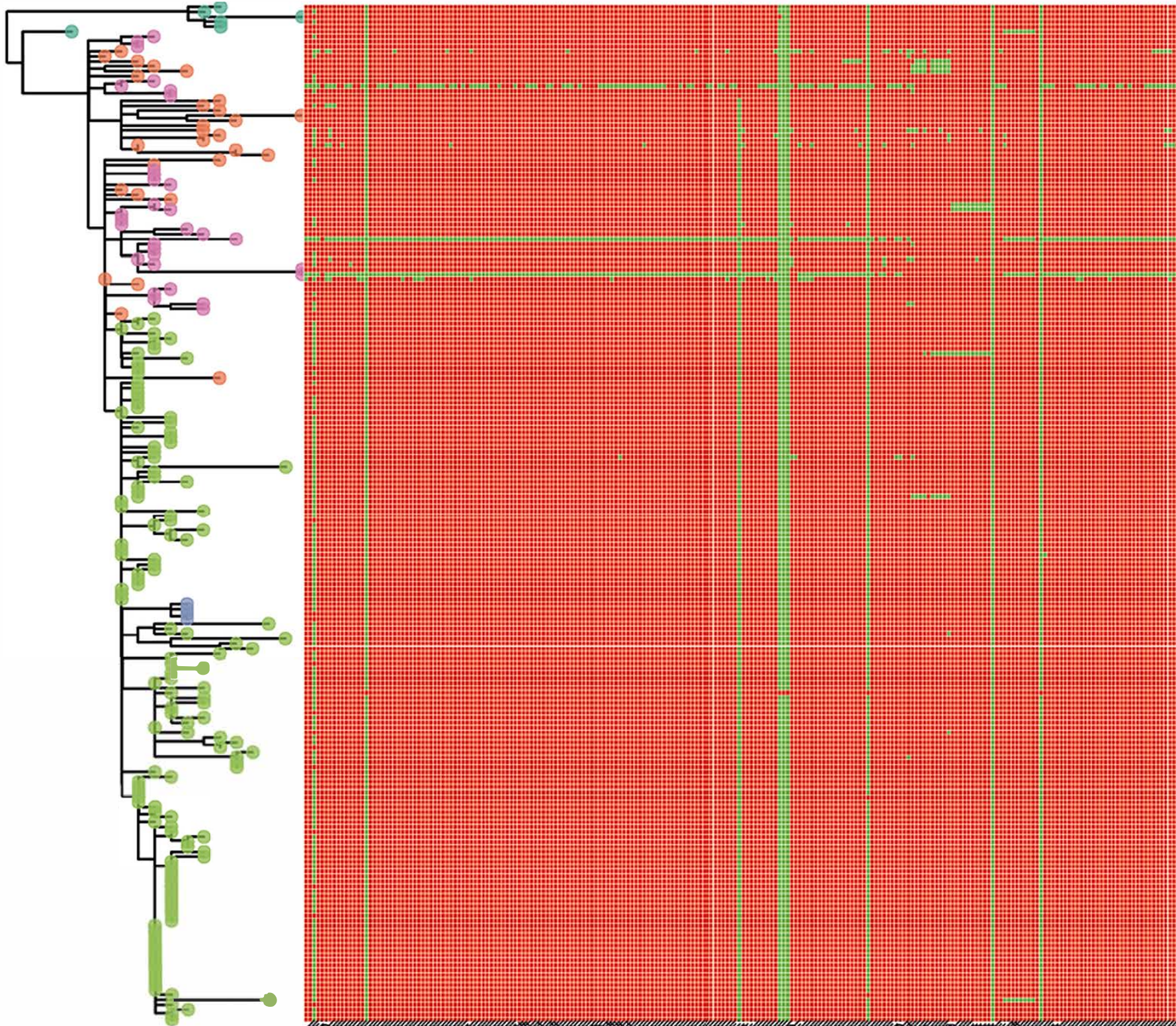
Maximum likelihood rooted phylogenetic tree showing *S. Typhi* organisms (genotype 4.3.1) and nearest neighbours (genotypes 4.1 and 4.2) from our historical collection and from published literature (n=422 total). Genotype is indicated by branch colour, presence of QRDR mutation(s) are indicated by coloured circles at the end of the branches, and country of origin, presence of MDR, AMR mutations, and presence of incH1 plasmid are indicated by bars to the right of the tree and coloured as per the inset legend.

Tree scale: 0.001



Supplemental Figure 2: A genetic comparison of IncH1 plasmid content of early H58 *S.* Typhi isolates.

Zoomed in view of maximum likelihood phylogenetic tree including historical and published H58 isolates (n=206). Country of origin is indicated by the coloured circles at the tips of the tree. Gene content of an almost identical IncH1 plasmid is indicated by the colour to the right of the tree.



Country

- Bangladesh
- India
- Laos
- Pakistan
- Vietnam

IncH1 plasmid

- gene presence
- gene absence

Supplemental Figure 3: An estimation of temporal signal in H58 *S. Typhi* data.

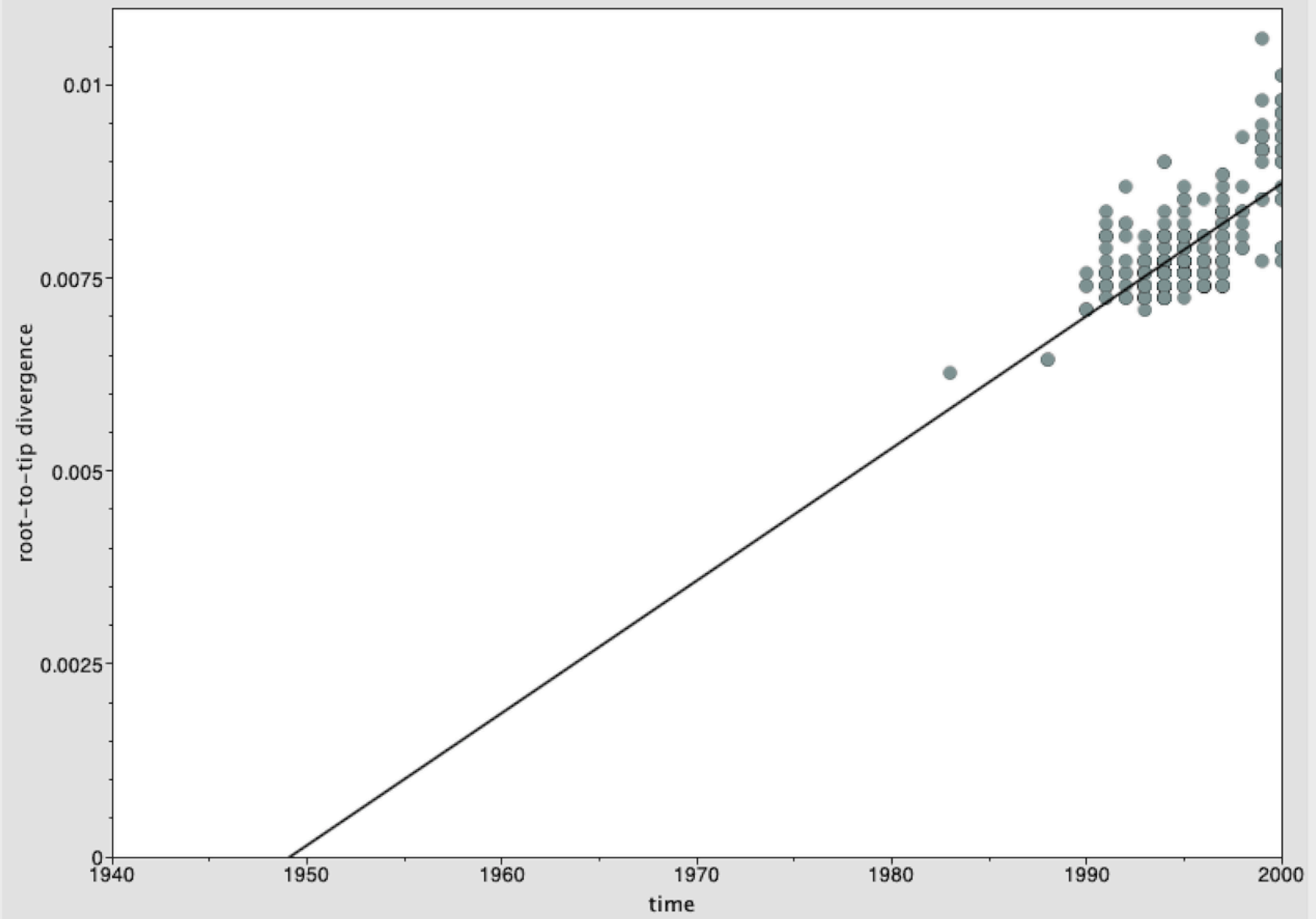
Path-O-Gen/TempEst results (analysis included n=345 isolates using an alignment of 724 non-recombinant SNPs), demonstrating strong correlation between sampling dates and root-to-tip distance ($R^2 = 0.4743$).

Best-fitting root

Sample Dates Tree **Root-to-tip** Residuals Node density

Function: heuristic residual mean squared

Dated Tips	
Date range	17
Slope (rate)	1.7153E-4
X-Intercept (TMRCA)	1949.1321
Correlation Coefficient	0.6887
R squared	0.4743
Residual Mean Squared	2.0781E-7



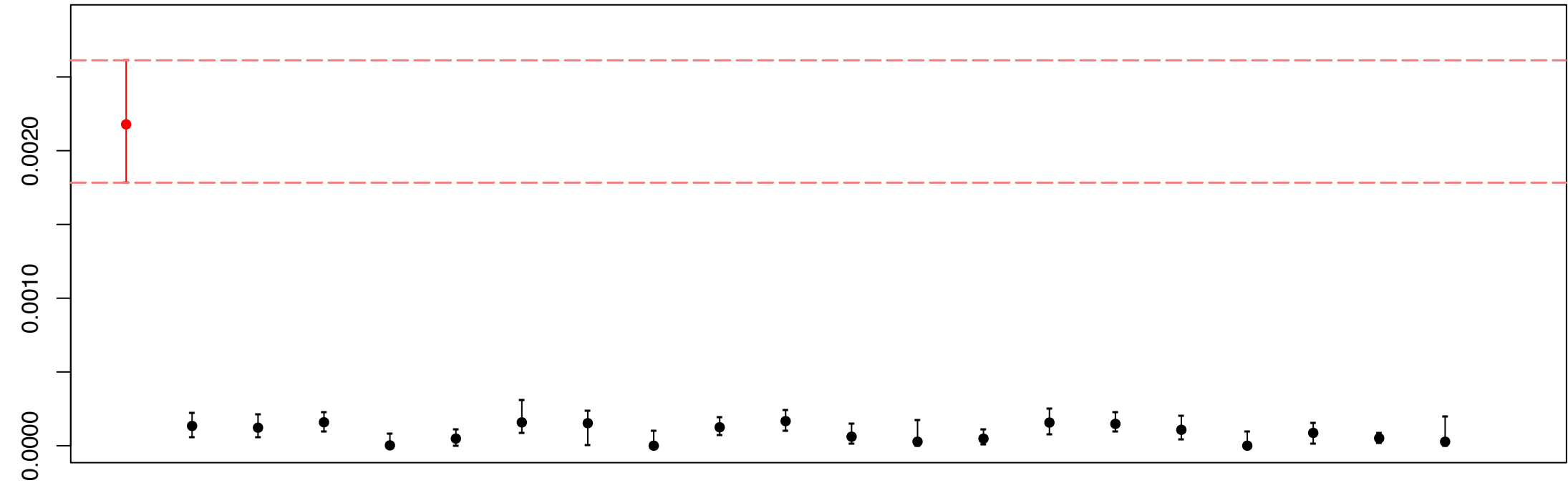
Show ancestor traces

Supplemental Figure 4: A TipDatingBeast estimation of temporal signal in H58 *S. Typhi* data.

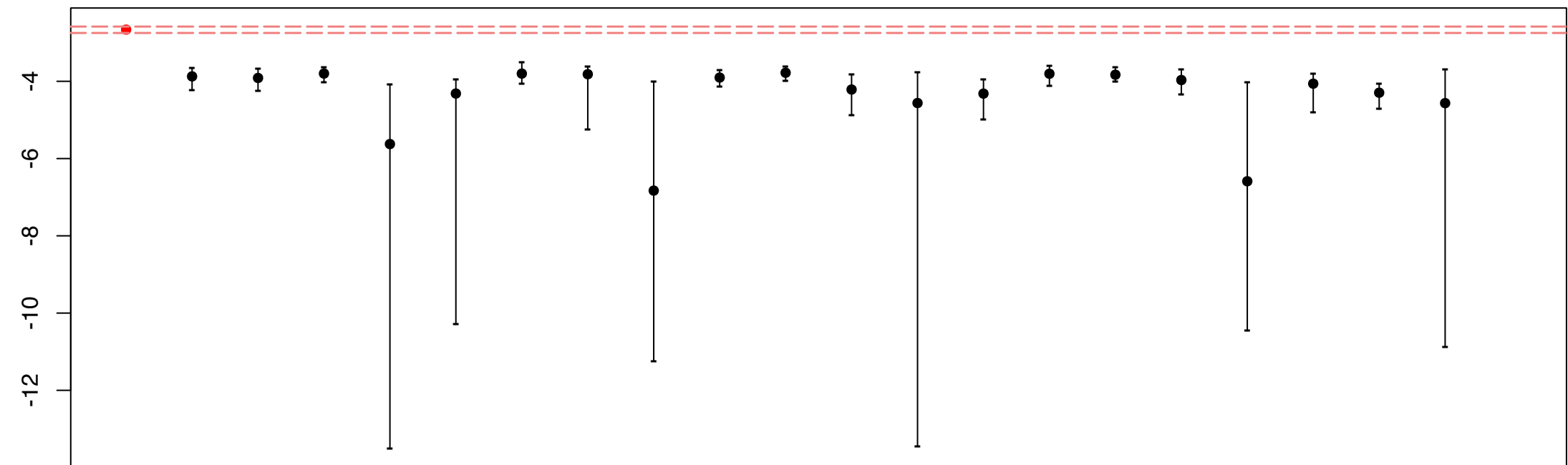
TipDatingBeast results (analysis incorporated n=345 isolates and an alignment of 724 non-recombinant SNPs), demonstrating no overlap between the original mean rates of mutation and mean rates of date randomization.

Date-randomization test performed on uclid.mean

Real Randomized



No Overlapping: DRT SUCCESSFULLY PASSED !!!



No Overlapping: DRT SUCCESSFULLY PASSED !!!