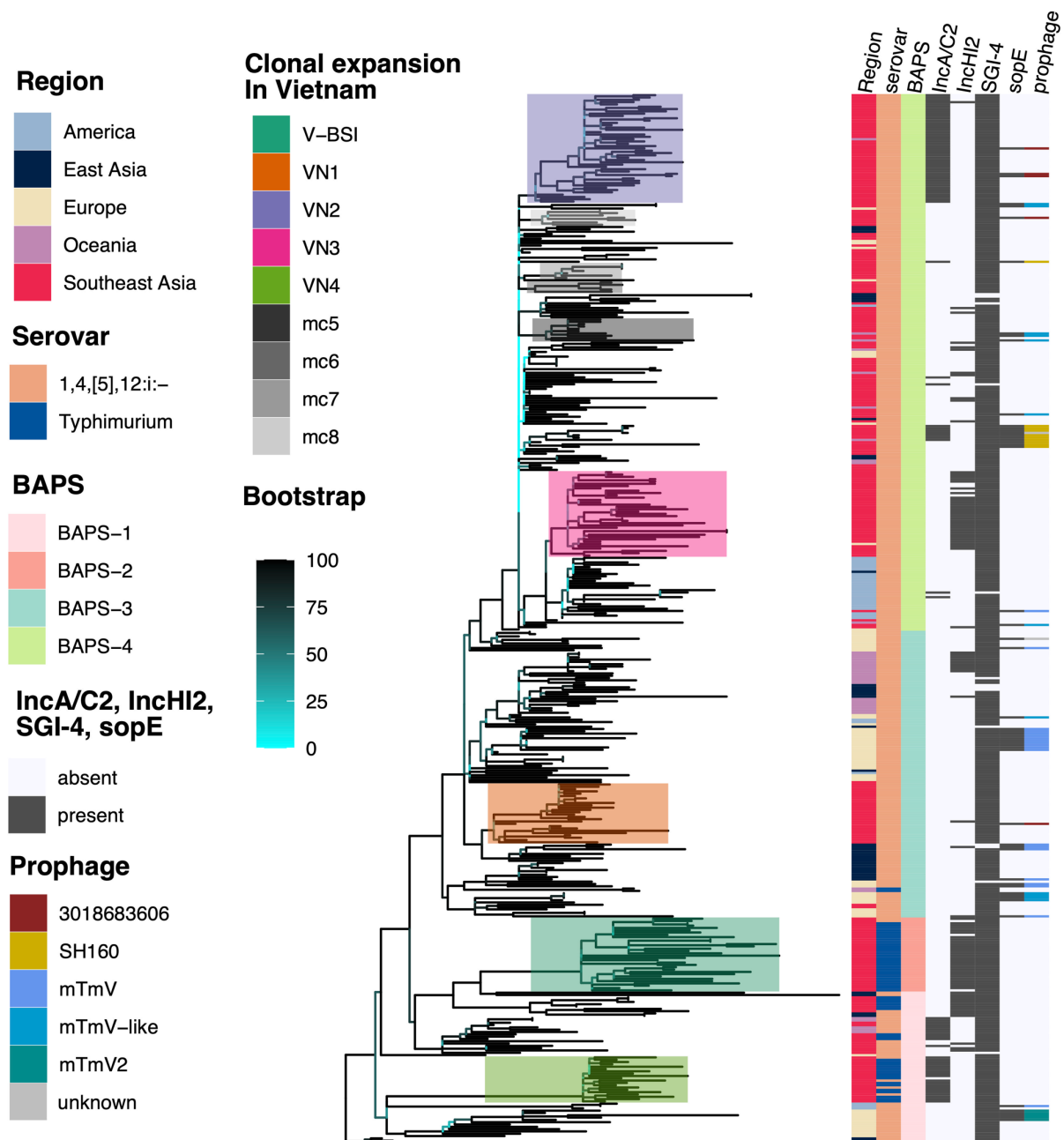
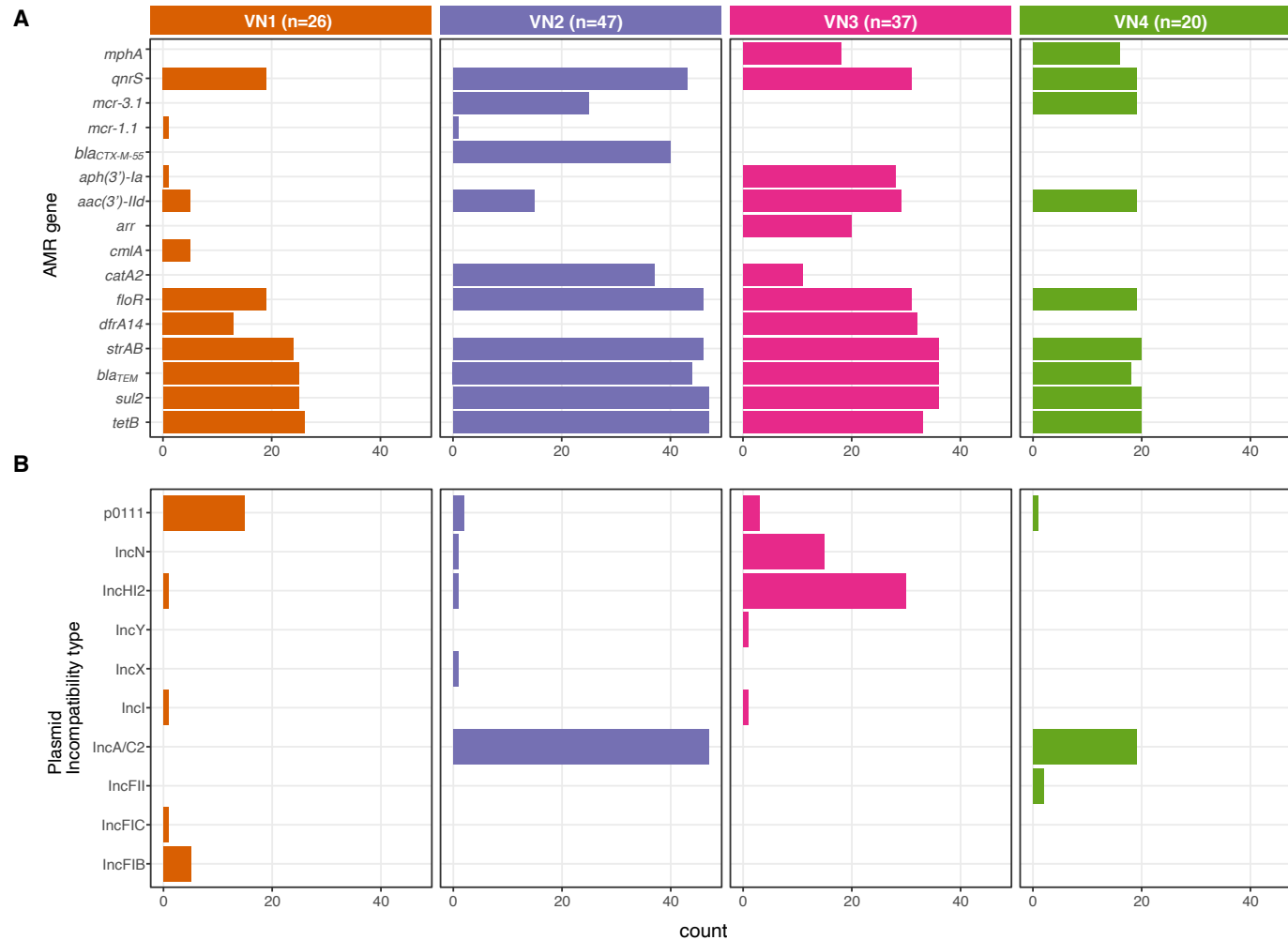


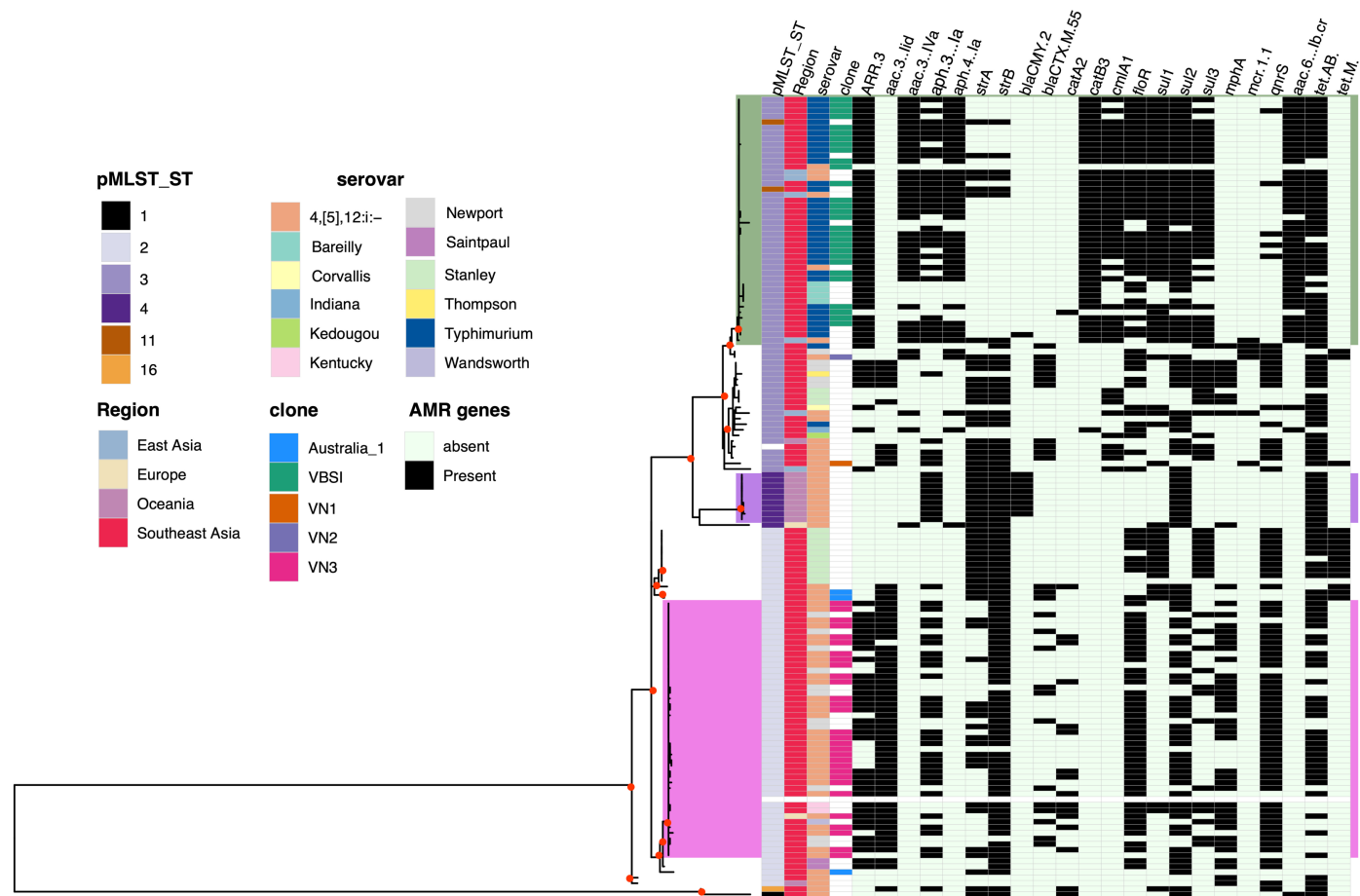
Supplementary Information



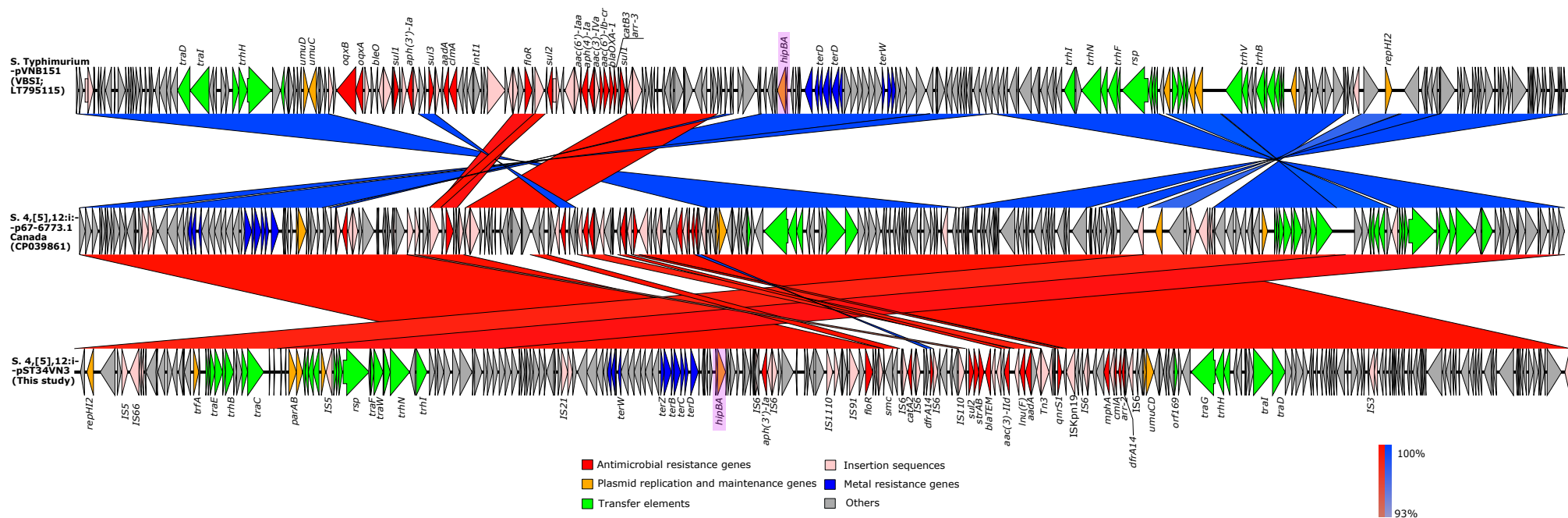
Supplementary Figure 1 The accessory genome of *Salmonella enterica* ST34. The figure displays the maximum likelihood phylogeny of 454 *S. enterica* ST34 isolates, as shown in **Figure 1**. Branches are coloured in accordance to bootstrapping values, from low (cyan) to high (black). The appended heatmap represents information associated with each taxon, including region of origin, serotype predicted in silico, BAPS population structure, and presence of accessory genetic features (IncA/C2, IncHI2, SGI-4, *sopE*, and *sopE* associated prophages). Colour shadings denote different clades ($n \geq 5$ isolates) with clonal expansion in Vietnam, of which the majority of isolates originating from Vietnam or Southeast Asia.



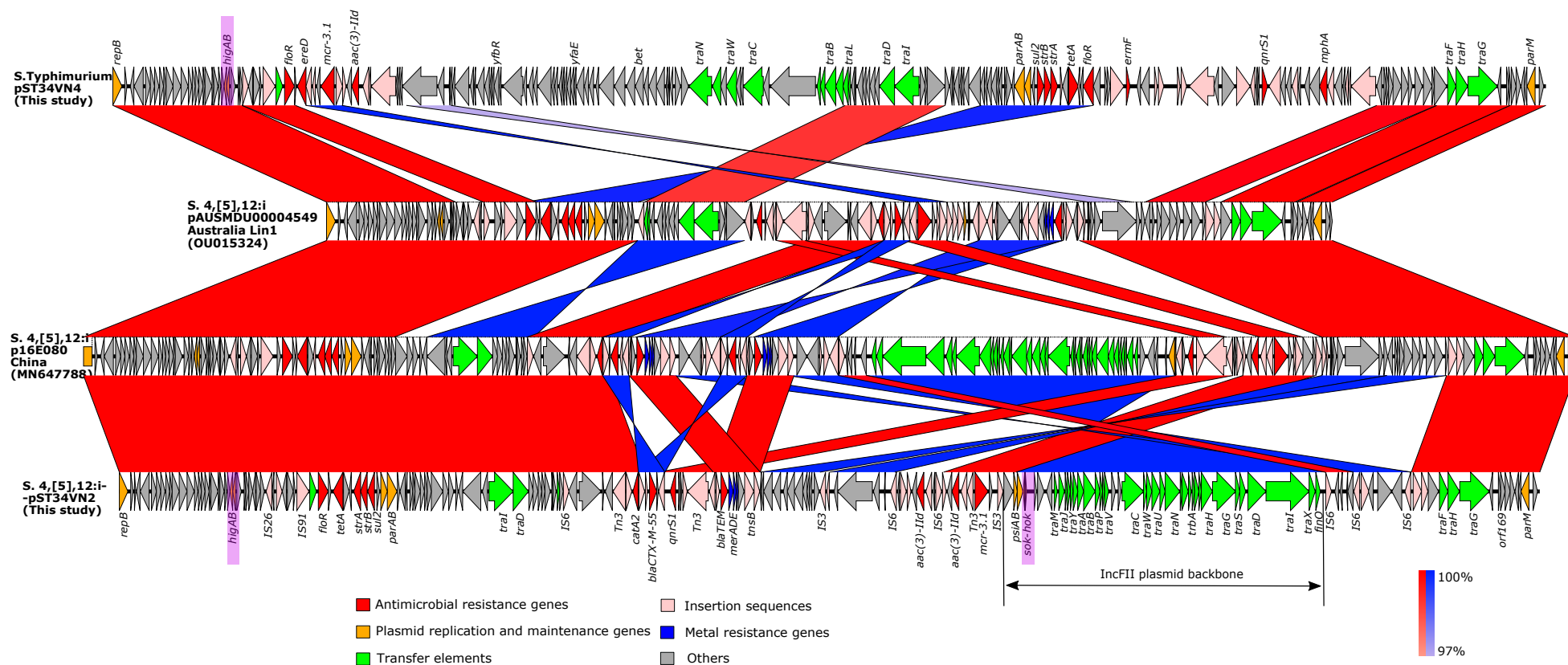
Supplementary Figure 2 Distribution of antimicrobial resistance (AMR) genes and plasmid types among four major *Salmonella enterica* ST34 clones causing gastroenteritis in Vietnam. For each panel, the bar graph displays the count of isolates from each clones (VN1 – VN4) carrying a respective element, stratified by (A) AMR genes, and (B) plasmid incompatibility types.



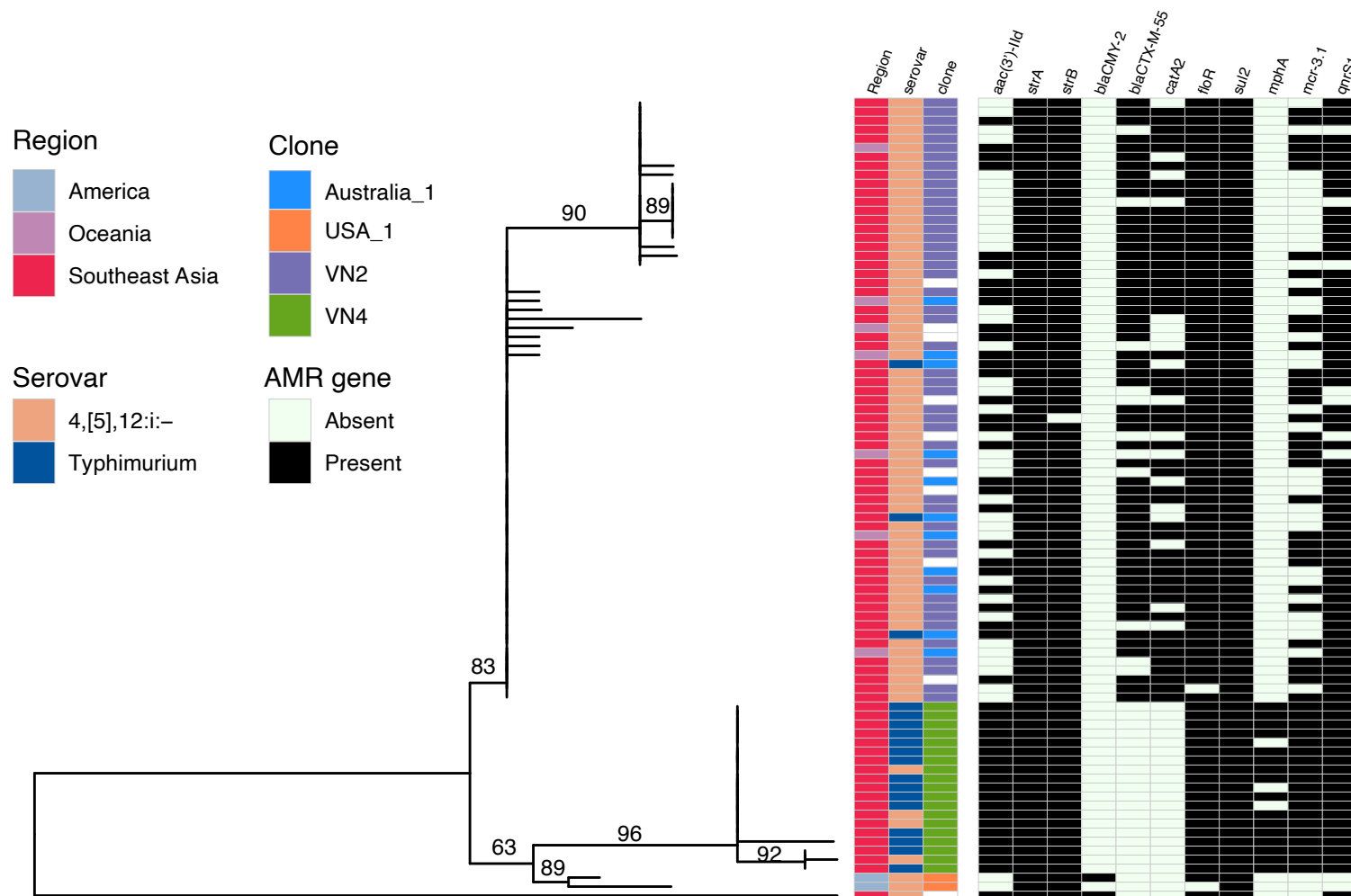
Supplementary Figure 3 Plasmid phylogeny of IncHI2 recovered from *Salmonella enterica*. The figure displays the maximum likelihood phylogeny of IncHI2 plasmids recovered from 143 *Salmonella enterica* isolates of diverse serotypes, constructed from 328 single nucleotide polymorphisms. The phylogeny is midpoint rooted. Filled red circles signify bootstrap support of ≥ 80 at internal nodes. The appended heatmap shows data of each taxon, including pMLST typing, region of isolation, predicted serotype based on genome sequencing, *Salmonella* ST34 clones, and presence of AMR genes. Coloured shades highlight plasmid clusters detected mainly in ST34, including green (VBSI, ST3, homologous to pVNB151), light magenta (VN3, ST2, homologous to pST34VN3), and dark magenta (ST4, endemic circulation in Australia, carrying *bla*_{CMY-2}).



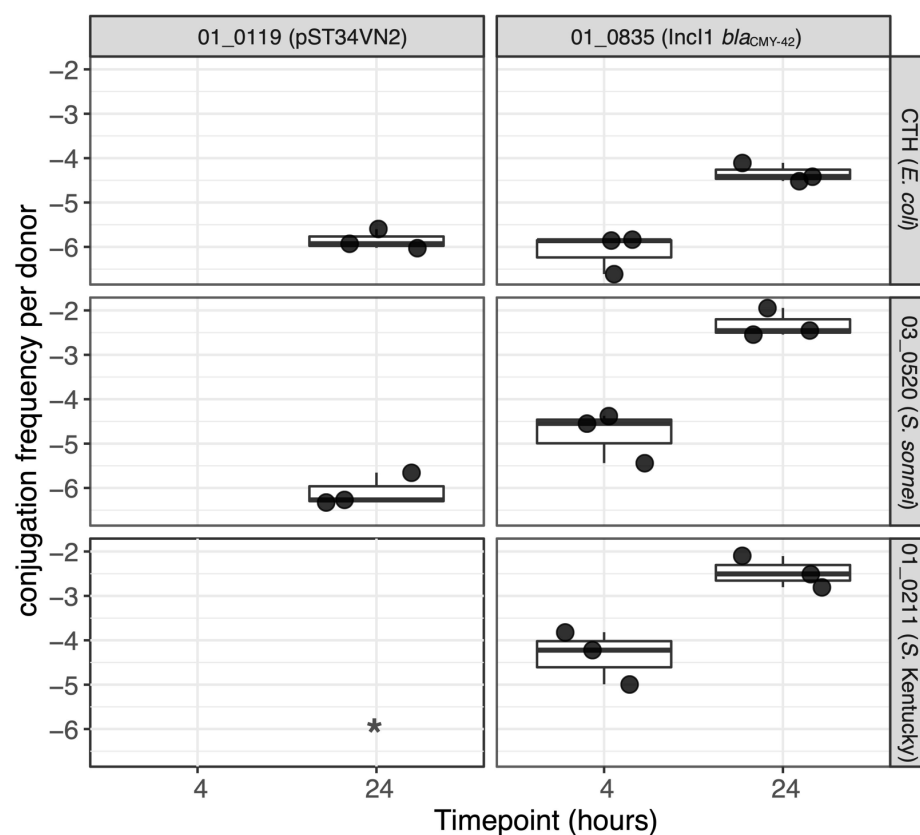
Supplementary Figure 4 Comparative genomic of multidrug resistant IncHI2 plasmids recovered from *Salmonella enterica* ST34 (pST34VN3, p67-6773.1, pVNB151). Arrows represent predicted genes (with direction of transcription), which are coloured according to their functions (see keys). Purple shaded boxes highlight the presence of *hipBA* antitoxin-toxin system. The blocks connecting two plasmids indicate regions with high nucleotide similarity (97 – 100%), as either syntenic (red) or inversion (blue).



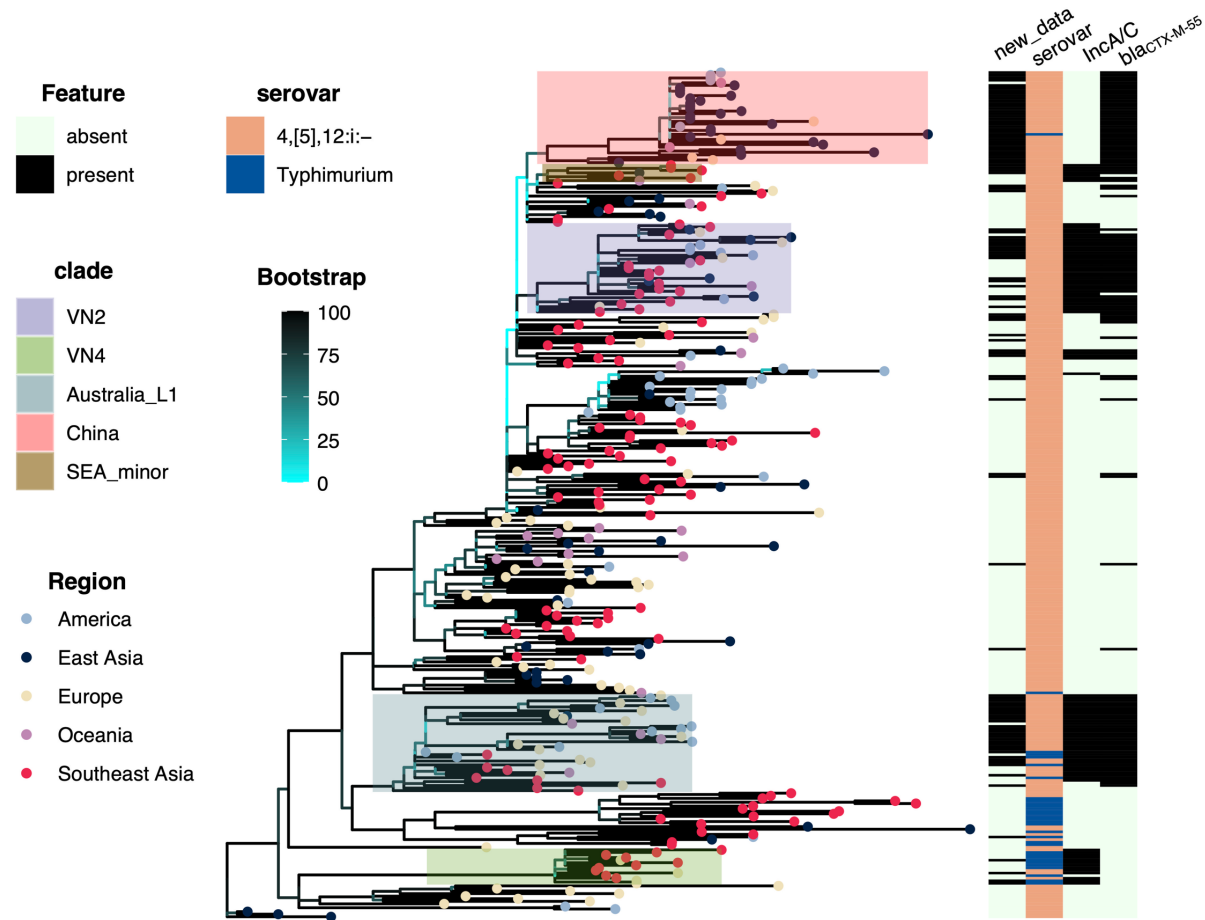
Supplementary Figure 5 Comparative genomic of multidrug resistant IncA/C plasmids recovered from *Salmonella enterica* ST34 (pST34VN2, p16E080, pAUSMDU00004549, pST34VN4). Arrows represent predicted genes (with direction of transcription), which are coloured according to their functions (see keys). Purple shaded boxes highlight the presence of *higAB* and *sok-hok* antitoxin-toxin systems. The blocks connecting two plasmids indicate regions with high nucleotide similarity (97 – 100%), as either synteny (red) or inversion (blue). Bi-directional black arrow delineates the region homologous to the conjugation machinery of the IncFII plasmid (*traM-finO*).



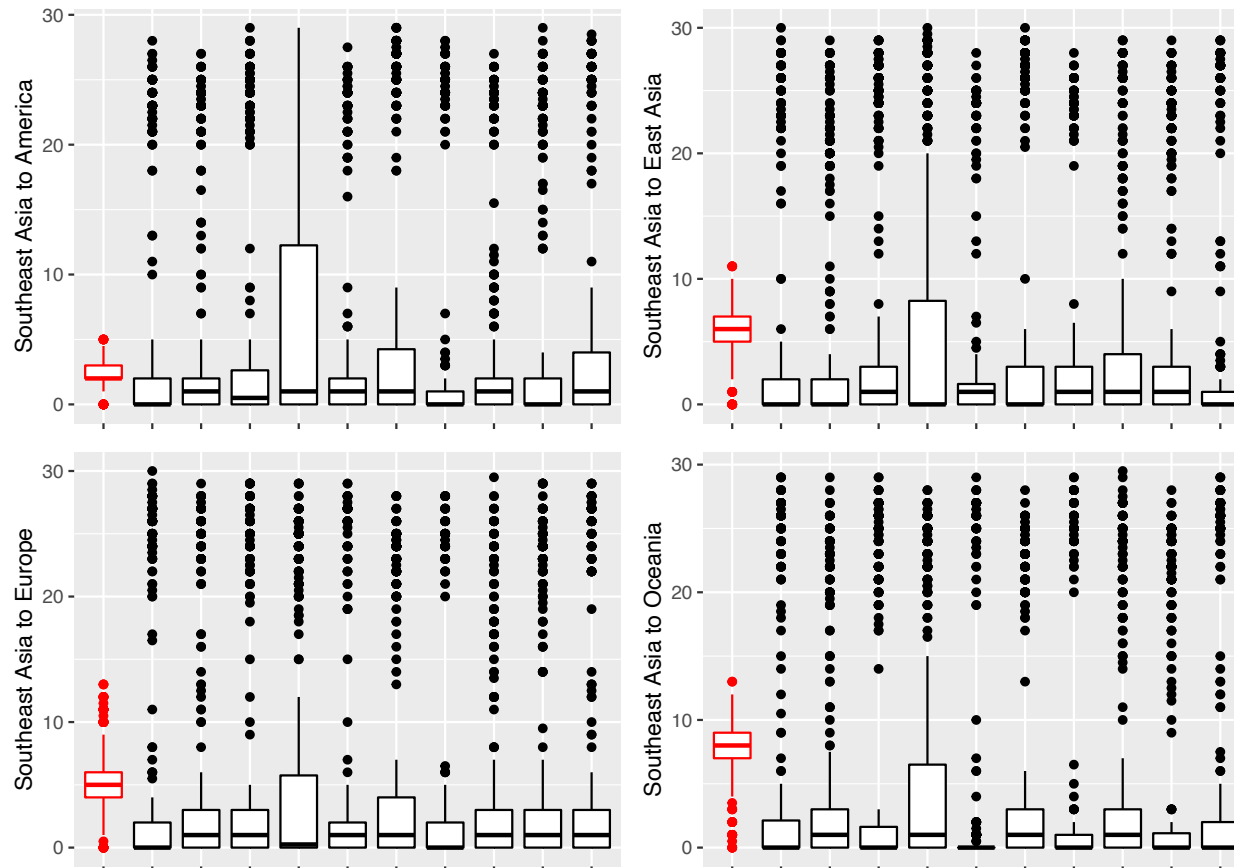
Supplementary Figure 6 Plasmid phylogeny of IncA/C2 recovered from *Salmonella enterica* ST34. The figure displays the maximum likelihood phylogeny of IncA/C2 plasmids recovered from 89 ST34 isolates, constructed from 62 single nucleotide polymorphisms. The phylogeny is midpoint rooted. Bootstrap values are displayed at internal branches. The appended heatmap shows data associated with each taxon, including region of origin, predicted serovar, ST34 clones, and presence of AMR genes.



Supplementary Figure 7 Conjugation frequency of plasmids found in *Salmonella enterica* ST34. The two donors (01_0119, 01_0835) are represented in columns while the three recipients (CTH, 03_0520, 01_0211) are represented in rows. Conjugation frequency was calculated as the number of transconjugants per number of donor cells. Each donor-recipient conjugation was performed in triplicates, for both timepoints 4- and 24-hour. Conjugation experiments using 01_0119 as the donor strain produced no transconjugants at timepoint 4 hour for all three recipients. The combination 01_0119 + 01_0211 after 24 hour (*) produced so few transconjugants, such that reliable conjugation calculation is not conducted. For boxplots, bold central lines denote the median, the upper whisker extends from the 75th percentile to the highest value within the 1.5*interquartile range (IQR) of the hinge, the lower whisker extends from the 25th percentile to the lowest value within 1.5*IQR of the hinge. Data points beyond the end of the whiskers are outliers.



Supplementary Figure 8 Global phylogeny of *Salmonella enterica* ST34. The figure displays the maximum likelihood phylogeny of 329 ST34 isolates, combining 222 representative genomes used previously for temporal phylogenetics (**Figure 2**) and 107 new genomes carrying *bla*_{CTX-M-55} or IncA/C2 plasmid (see Methods). The branches are coloured according to bootstrap values, from low (cyan) to high (black), and tips are coloured based on region of origin. The appended heatmap displays information associated with each taxon, showing whether they are new added data, the predicted serotype, and the presence of IncA/C2 plasmid and *bla*_{CTX-M-55}. Coloured shades on the phylogeny highlight defined clusters associated with carriage of *bla*_{CTX-M-55} (see Legend).



Supplementary Figure 9 Validation of phylogeographical signal in *Salmonella enterica* ST34. Stochastic mapping was performed on the original dataset (Figure 3) and ten tip-location randomized datasets (See Materials and Methods). Each panel summarizes the inferences made from the ‘true’ dataset (coloured red) and ten randomizations (coloured black), estimating the number of transition events from Southeast Asia to America, East Asia, Europe and Oceania during *Salmonella* ST34’s evolutionary history. Each boxplot summarizes results from 1,000 (true dataset) and 500 (randomization) sub-samplings of the phylogenies. For boxplots, bold central lines denote the median, the upper whisker extends from the 75th percentile to the highest value within the 1.5*interquartile range (IQR) of the hinge, the lower whisker extends from the 25th percentile to the lowest value within 1.5*IQR of the hinge. Data points beyond the end of the whiskers are outliers.

Supplementary Table 1 Genes showing signal of convergent pseudogenization and gene loss during *Salmonella enterica* ST34 evolution.

Gene	Locus tag	Length (aa)	Product	Stop codon gain	Frameshift mutation	Gene loss	Total events
<i>ydiV</i>	B0X74_08620	237	anti-FlhC(2)FlhD(4) factor YdiV	3	0	0	3
<i>cspC</i>	B0X74_11245	69	RNA chaperone CspC, essential for <i>phoPQ</i> regulon in mildly acidic condition	4	6	2	12
<i>B0X74_16995</i>	B0X74_16995	295	transcriptional regulator	3	1	0	4
<i>rpoS</i>	B0X74_17285	332	RNA polymerase sigma factor RpoS	5	16	1	22
<i>btuB</i>	B0X74_23885	614	vitamin B12 transporter BtuB	8	5	0	13