Supplementary Figures

An ancient family of mobile genomic islands introducing cephalosporinase and carbapenemase genes in *Enterobacteriaceae*

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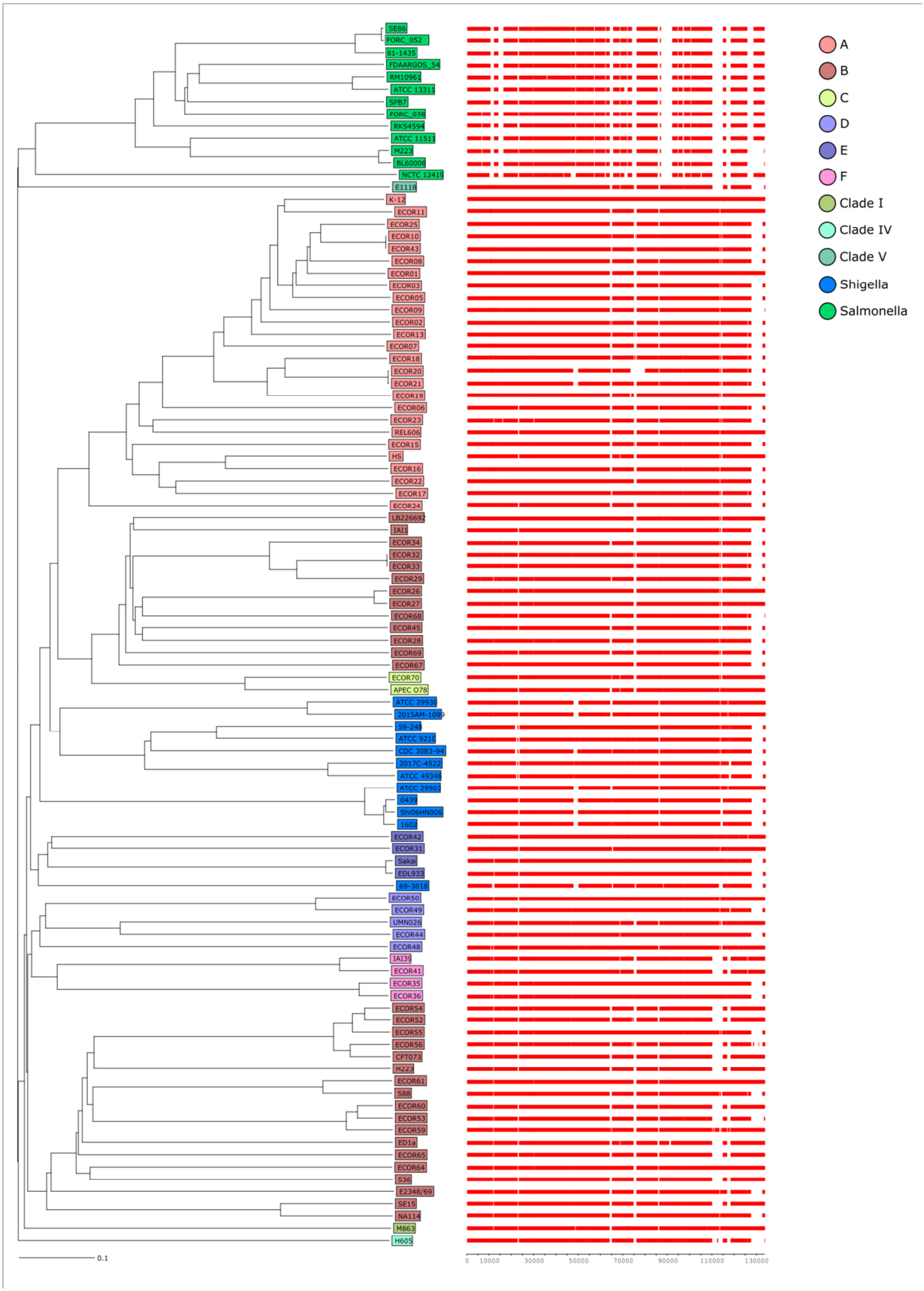
Running title: Cephalosporinase islands in *Enterobacteriaceae*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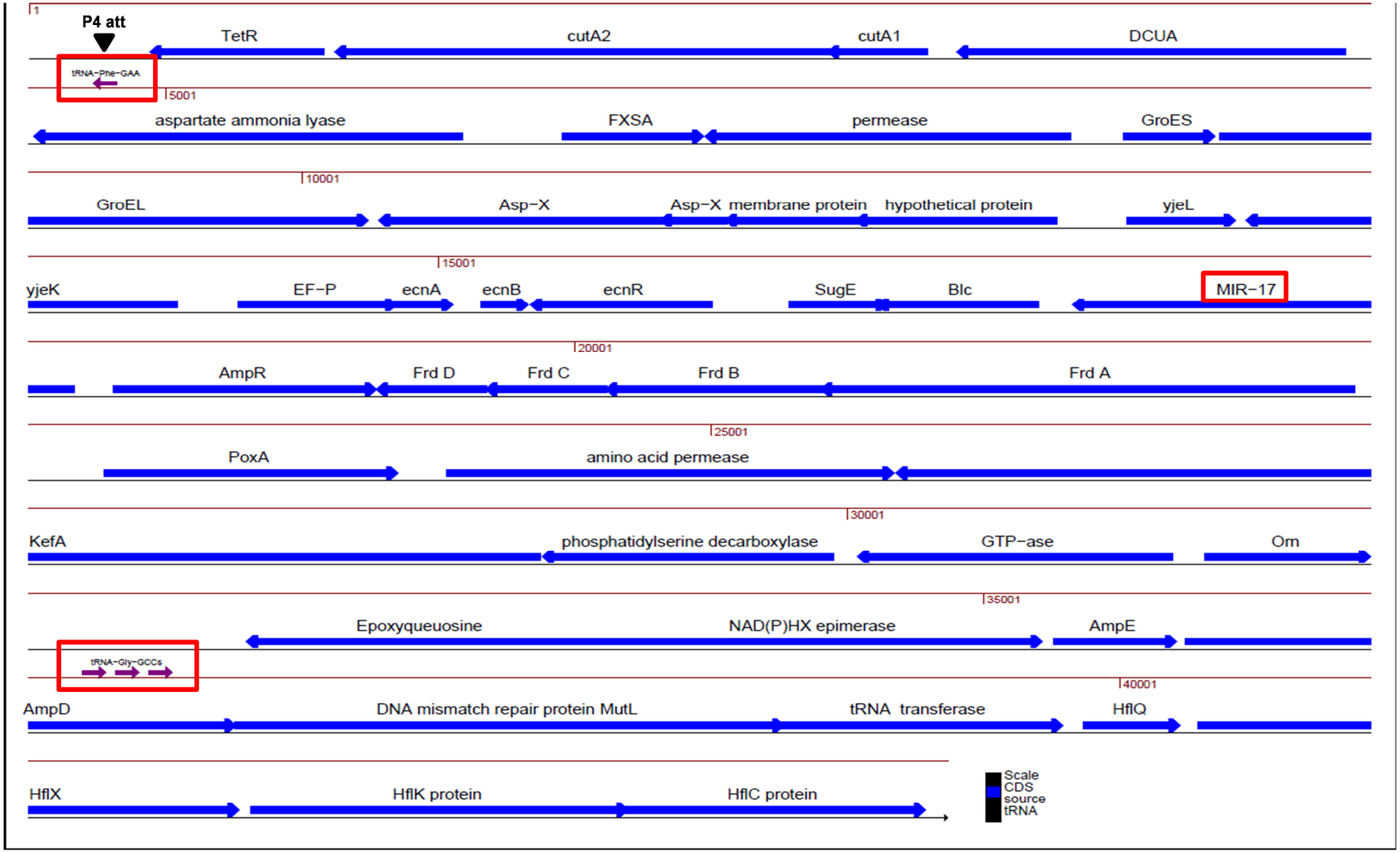
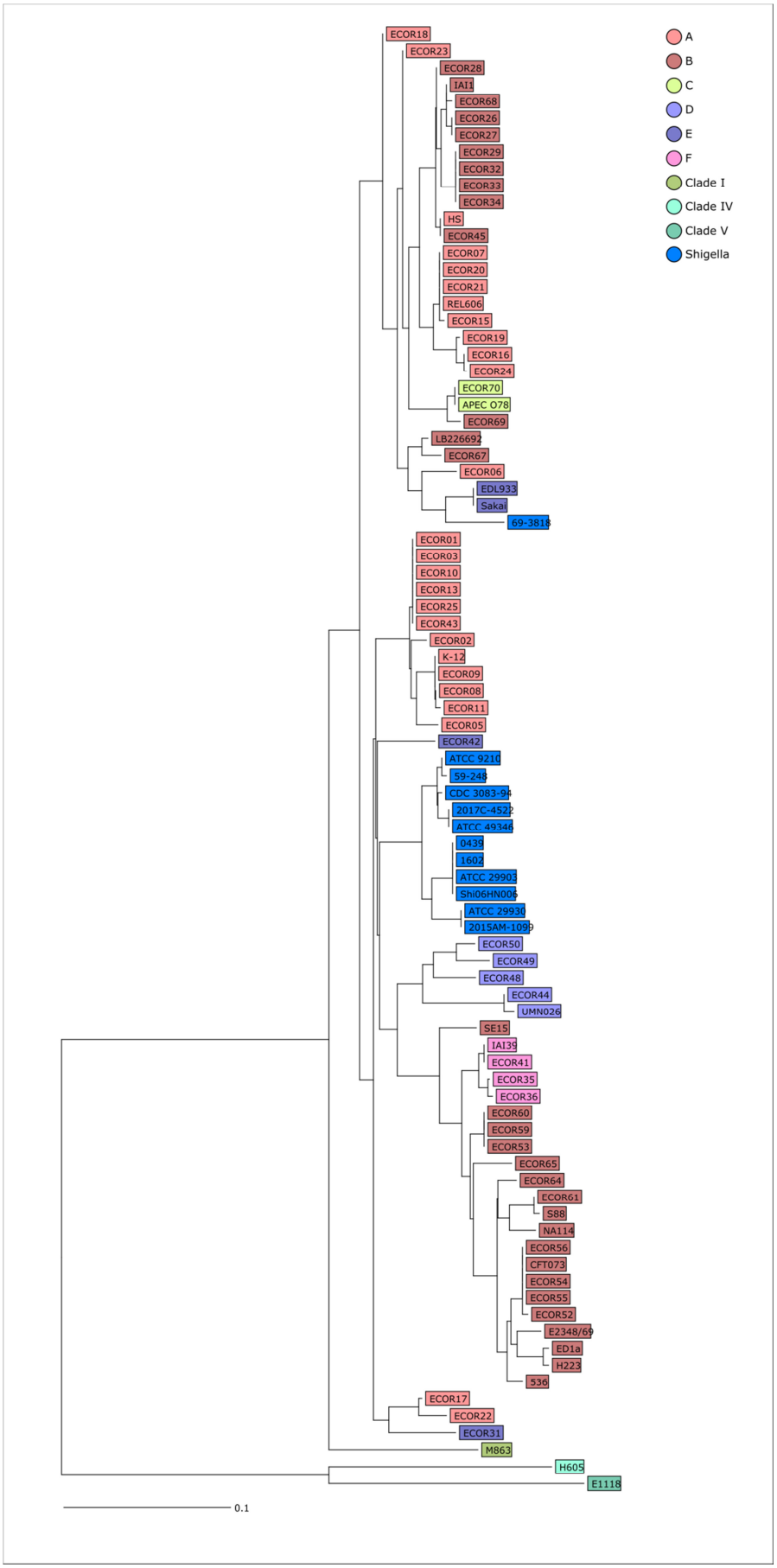
ECOR64
536
E2348/69
SE15
NA114
M863
H605
0.1
0
10000
30000
50000
70000
90000
110000
130000
A
B
C
D
E
F
Clade I
Clade IV
Clade V
Shigella
Salmonella

Supplemental Figure S1. Phylogenetic tree of *E. coli*, *Salmonella* and *Shigella*, and conservation of the MIR17-GI mobile genomic island. The phylogenetic tree of *E. coli* isolates, and *Salmonella* and *Shigella* species was created with the Ridom SeqSphere+ software v4.1.9 using a neighbor joining algorithm. It is built on a cgMLST analysis of 3839 targets from the reference genome of the *E. coli* K12 strain MG1655. The scale bar under the tree represents the phylogenetic distance (in %). The red bars indicate the conservation of the MIR17-GI using the respective MGI of *E. coli* K12 strain MG1655 as the reference. For the MGI comparisons, an 80% DNA similarity cut-off was used in DNA plotter. The scale bar under the MGI alignment indicates the sequence position of the reference MGI. The color codes mark publicly available sequences of *E. coli* isolates, and *Salmonella* and *Shigella* species that belong to particular phylogenetic groups or clades. The MIR17-GI was represented in all 100 investigated genomes, most of which were derived from a study by Clermont *et al*. (*Microbiology* 2015, 161: 980–988). Of note, the *ampC* gene was absent from the MGI in all sequenced *Salmonella* genomes.



Supplemental Figure S2. Genetic map of the 5' end of the MIR17-GI mobile genomic island of study isolate 1 up to the high frequency lysogeny operon. MIR17-GI is integrated in the Phe-GAA tRNA gene at the 5'end, which has a P4 prophage-associated attachment site in the 3'-5'direction. The positions of genes for AmpR, AmpD and AmpE orthologues and other identified genes are indicated.


A
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Clade I
Clade IV
Clade V
Shigella
ECOR18
ECOR23
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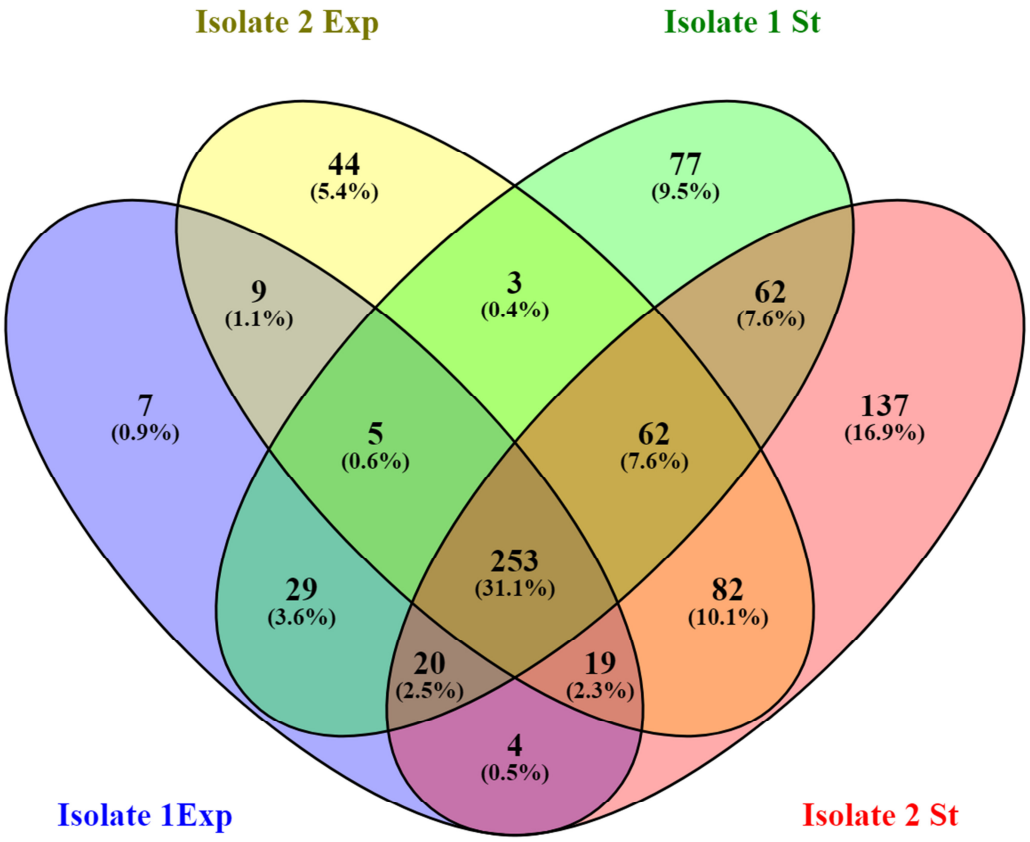
H223
536
ECOR17
ECOR22
ECOR31
M863
H605
E1118
0.1

Supplemental Figure S3. Neighbor joining tree showing the diversity of *ampC* genes on MIR17-GI-like MGIs in *E. coli* and *Shigella*. The neighbor joining tree is based on genome sequences used to construct the phylogenetic tree in Supplemental Figure S1. The scale bar represents the % difference among 197 nucleotides of *ampC*, using the *ampC* gene of the *E. coli* K12 strain MG1655 as a reference.



Supplemental Figure S4. Numbers of expressed proteins in *E. cloacae* isolates 1 and 2.
The Venn diagram shows overlapping and uniquely expressed proteins of the *E. cloacae* isolates 1 and 2 in the exponential (Exp) and stationary (St) growth phases. The diagram was created using the Venn diagram web tool of the VIB and the University of Gent in Belgium (http://bioinformatics.psb.ugent.be/webtools/Venn/).