

High-resolution characterisation of ESBL/pAmpC-producing *Escherichia coli* isolated from the broiler production pyramid

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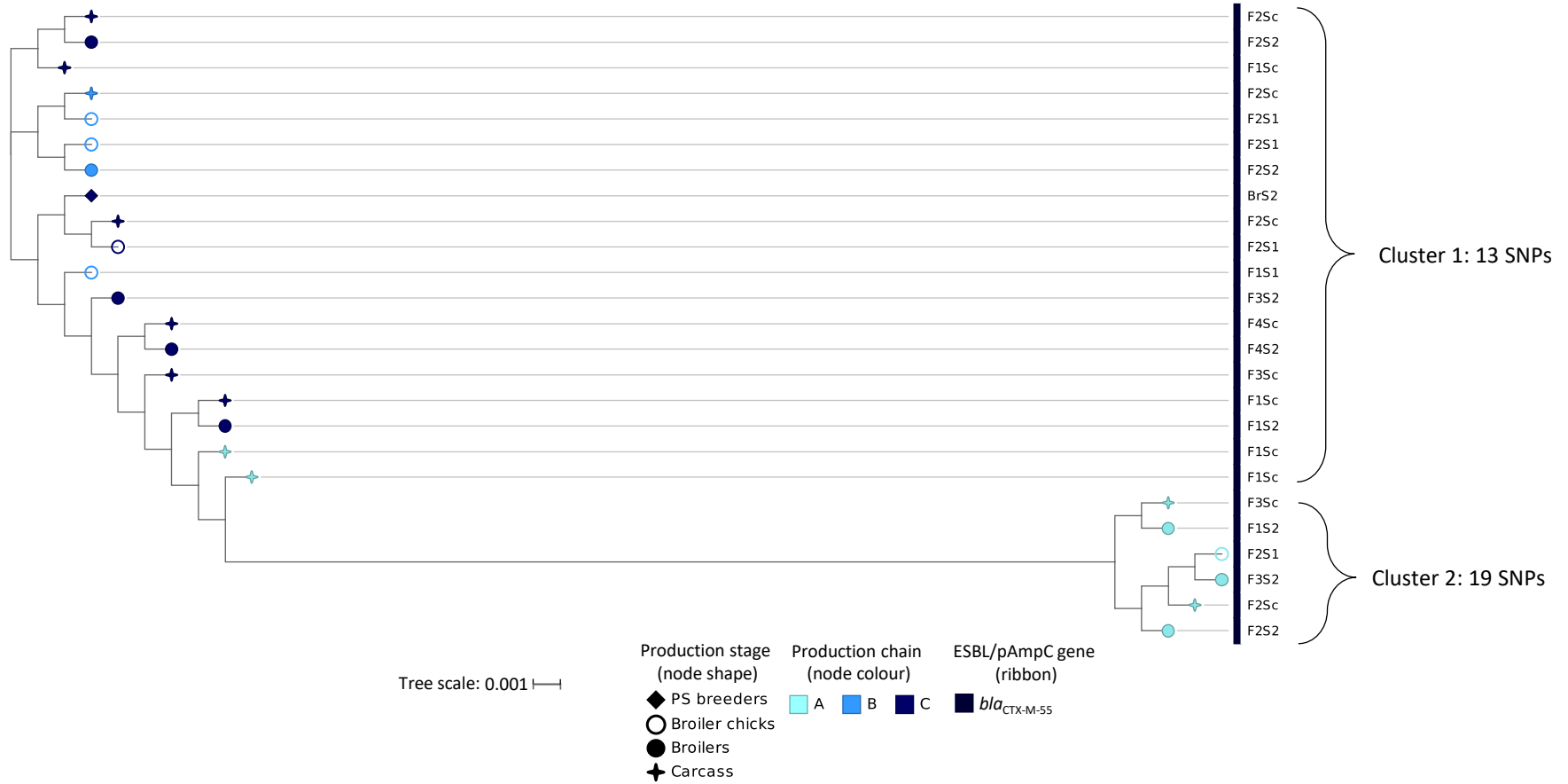
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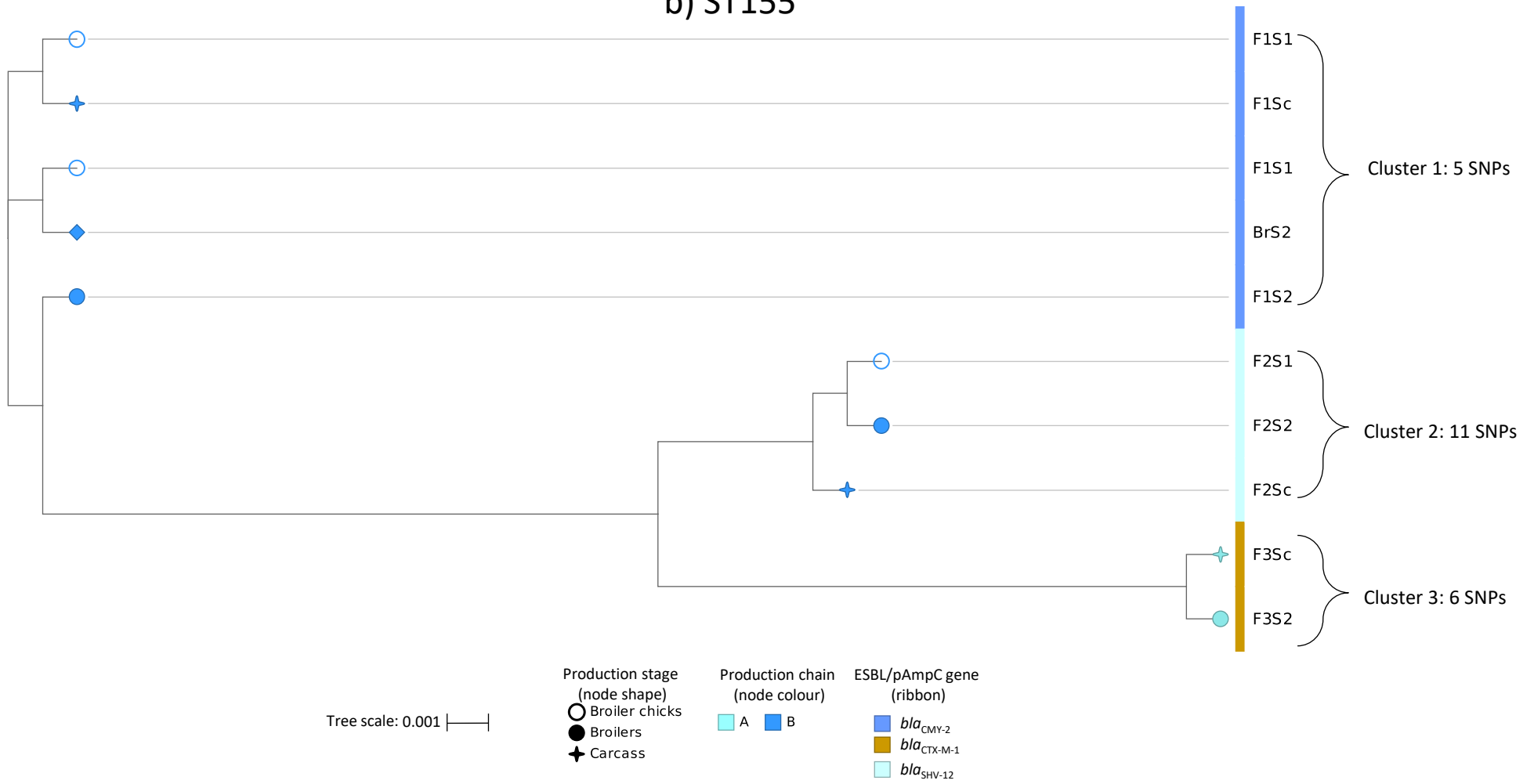
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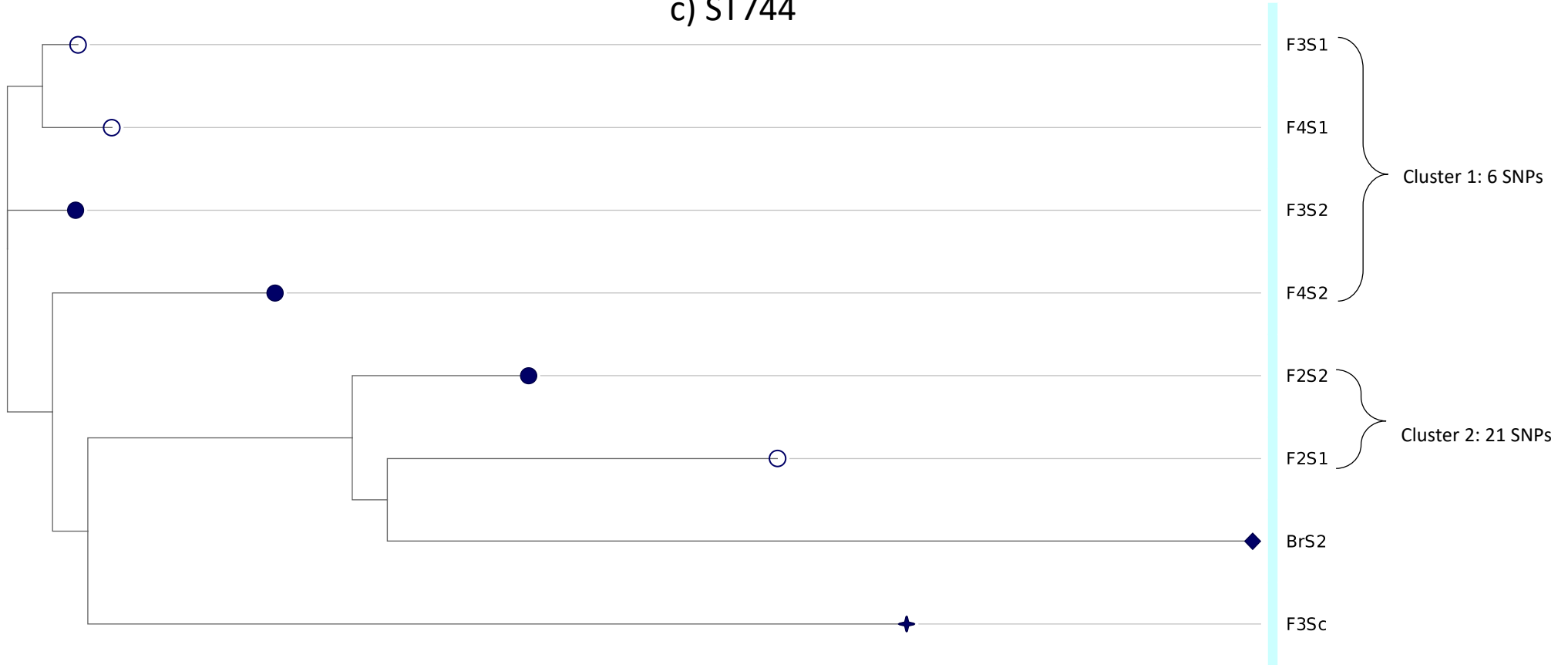
a) ST457



b) ST155



c) ST744



Tree scale: 0.1

Production stage
(node shape)

- ◆ PS breeders
- Broiler chicks
- Broilers
- ✦ Carcass

Production chain
(node colour)



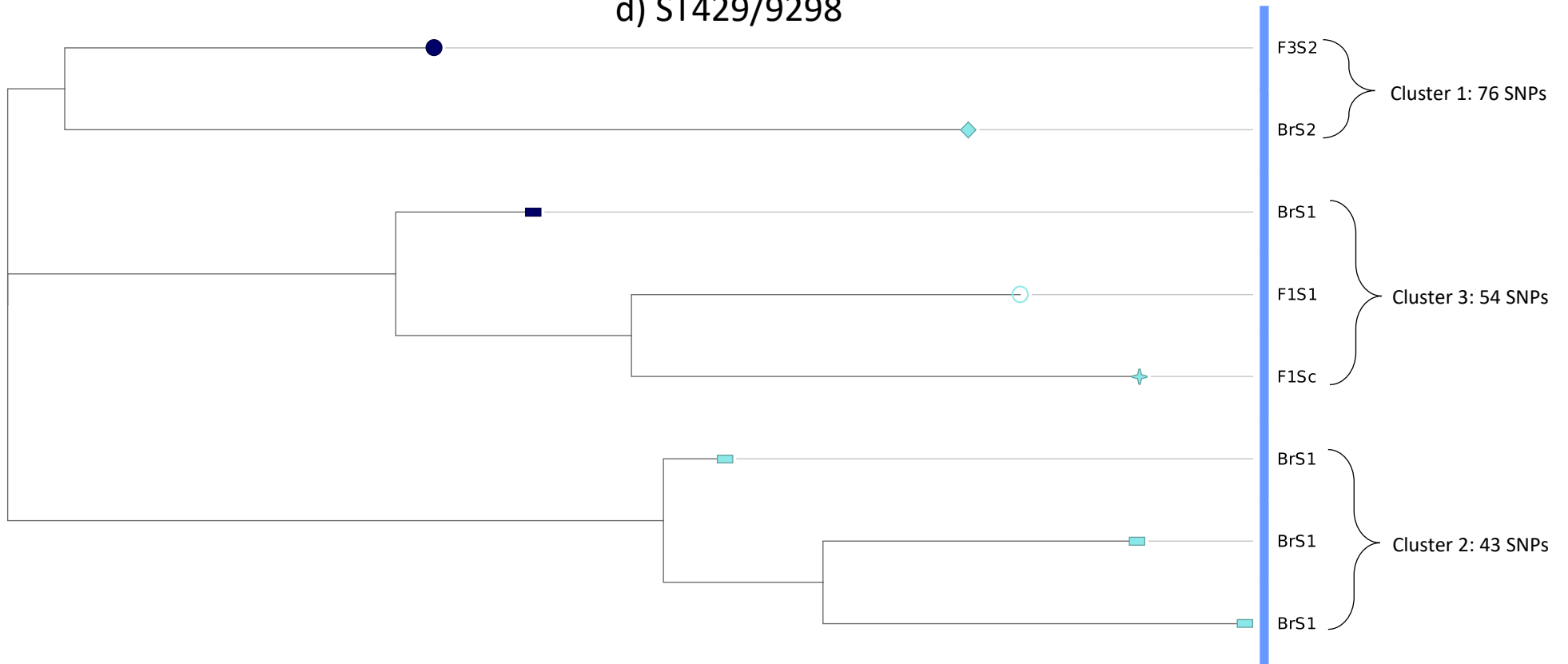
C

ESBL/pAmpC gene
(ribbon)



*bla*_{SHV-12}

d) ST429/9298



Tree scale: 0.1

Production stage
(node shape)

- PS chicks
- PS breeders
- Broiler chicks
- Broilers
- Carcass

Production chain
(node colour)

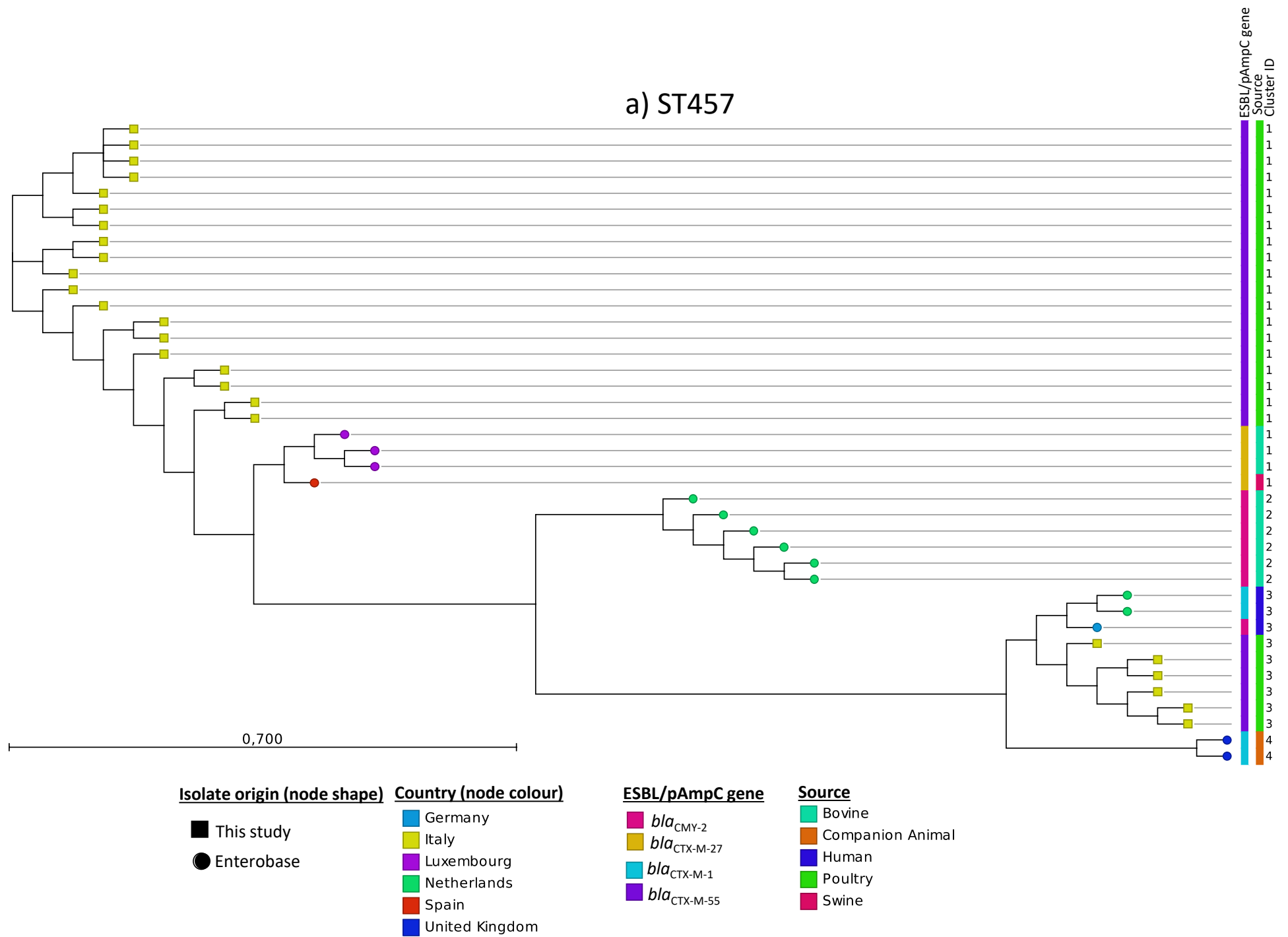
- A
- C

ESBL/pAmpC gene
(ribbon)

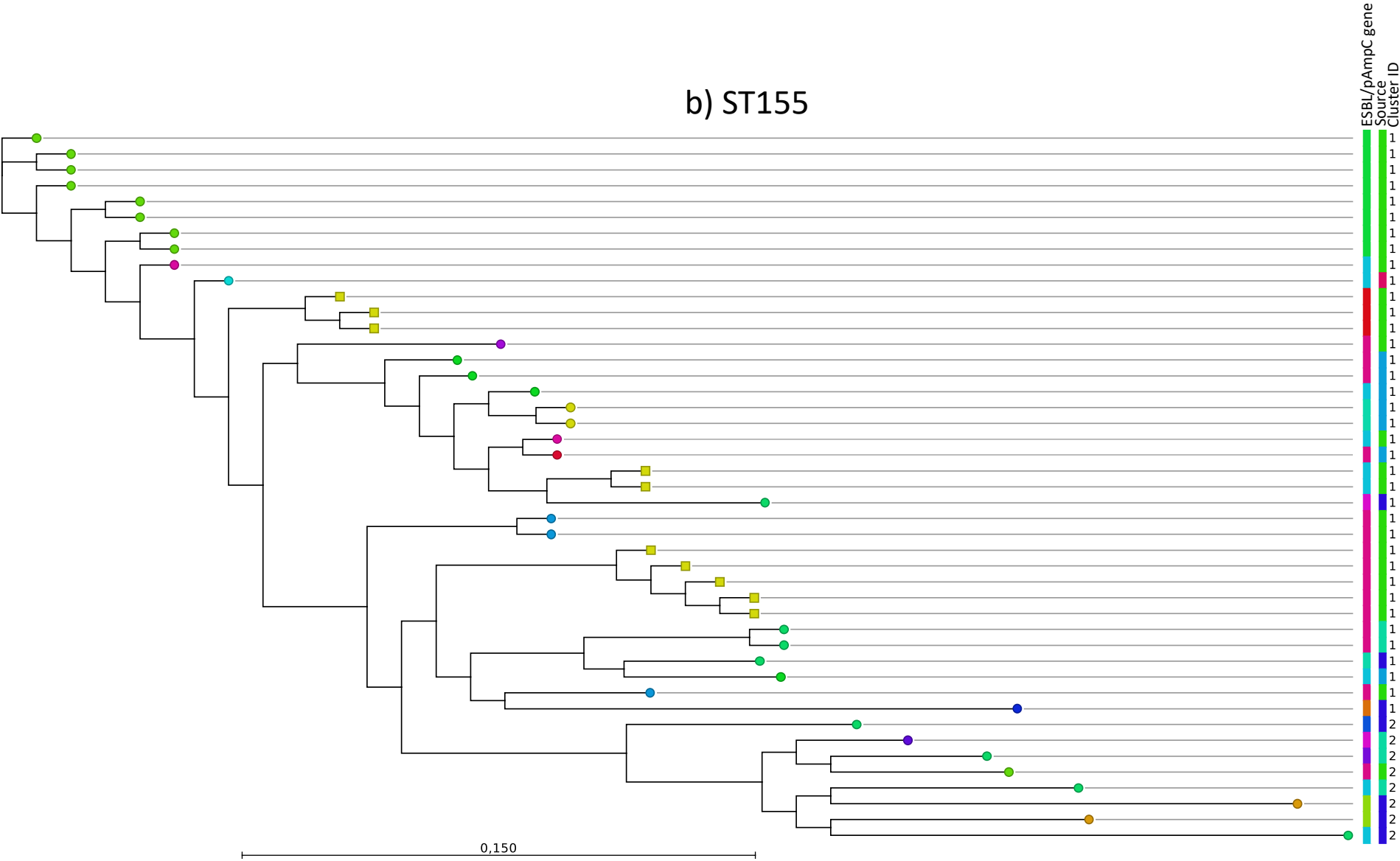
- bla*_{CMY-2}

Supplementary Figure S1. Phylogenetic analysis of the most prevalent sequence types (STs) of this study a) ST457, b) ST155, c) ST744, d) ST429/ST9298. SNP analysis was done with CSI phylogeny. Colour-coded nodes and ribbons respectively represent the production chains and ESBL/pAmpC genes of isolates. SNPs numbers indicate the median of pairwise SNP differences between the isolates of the corresponding cluster marked with braces. Text next to nodes denotes farms and stages at which isolates were obtained, with the following coding system: BrS1, PS chicks; BrS2, PS breeders; F1-4S1, farm 1-4 broiler chicks; F1-4S2, farm 1-4 broilers; F1-4Sc, farm 1-4 carcasses. Scale bar refers to the branch lengths, which are measured in the number of substitutions per site. Tree nodes are ordered after their increasing branch lengths.

a) ST457



b) ST155



Isolate origin (node shape)

- This study
- Enterobase

Country (node colour)

- Belgium
- Denmark
- France
- Germany
- Ireland
- Italy
- Latvia
- Luxembourg
- Netherlands
- Poland
- Romania
- United Kingdom

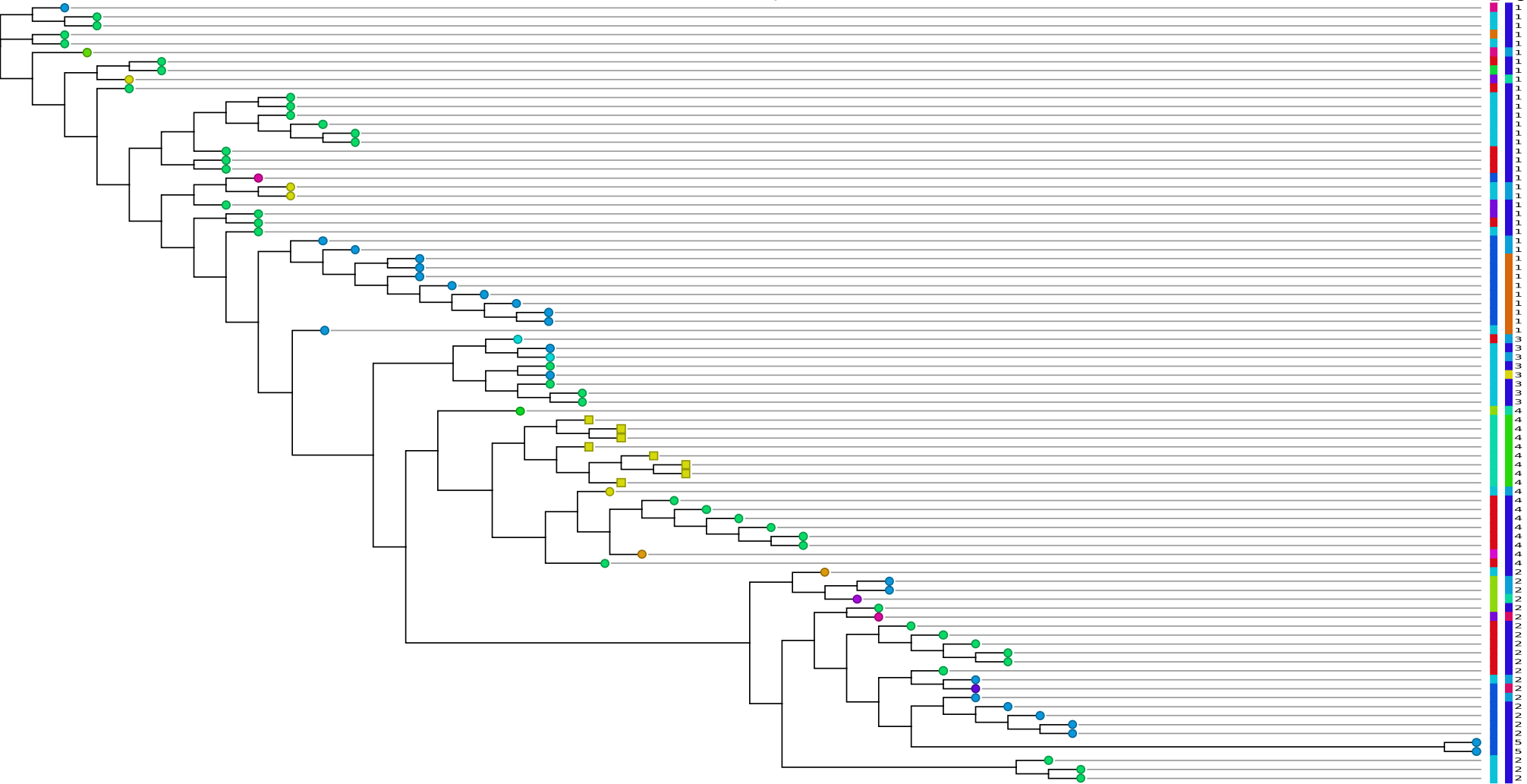
ESBL/pAmpC gene

- bla*_{CMY-2}
- bla*_{CTX-M-2}
- bla*_{CTX-M-55}
- bla*_{OXA-48}
- bla*_{TEM-52B}
- bla*_{CTX-M-1}
- bla*_{CTX-M-15}
- bla*_{CTX-M-65}
- bla*_{SHV-12}
- bla*_{TEM-52C}

Source

- Bovine
- Poultry
- Unknown
- Human
- Swine

c) ST744



0,250

Isolate origin (node shape)

- This study
- Enterobase

Country (node colour)

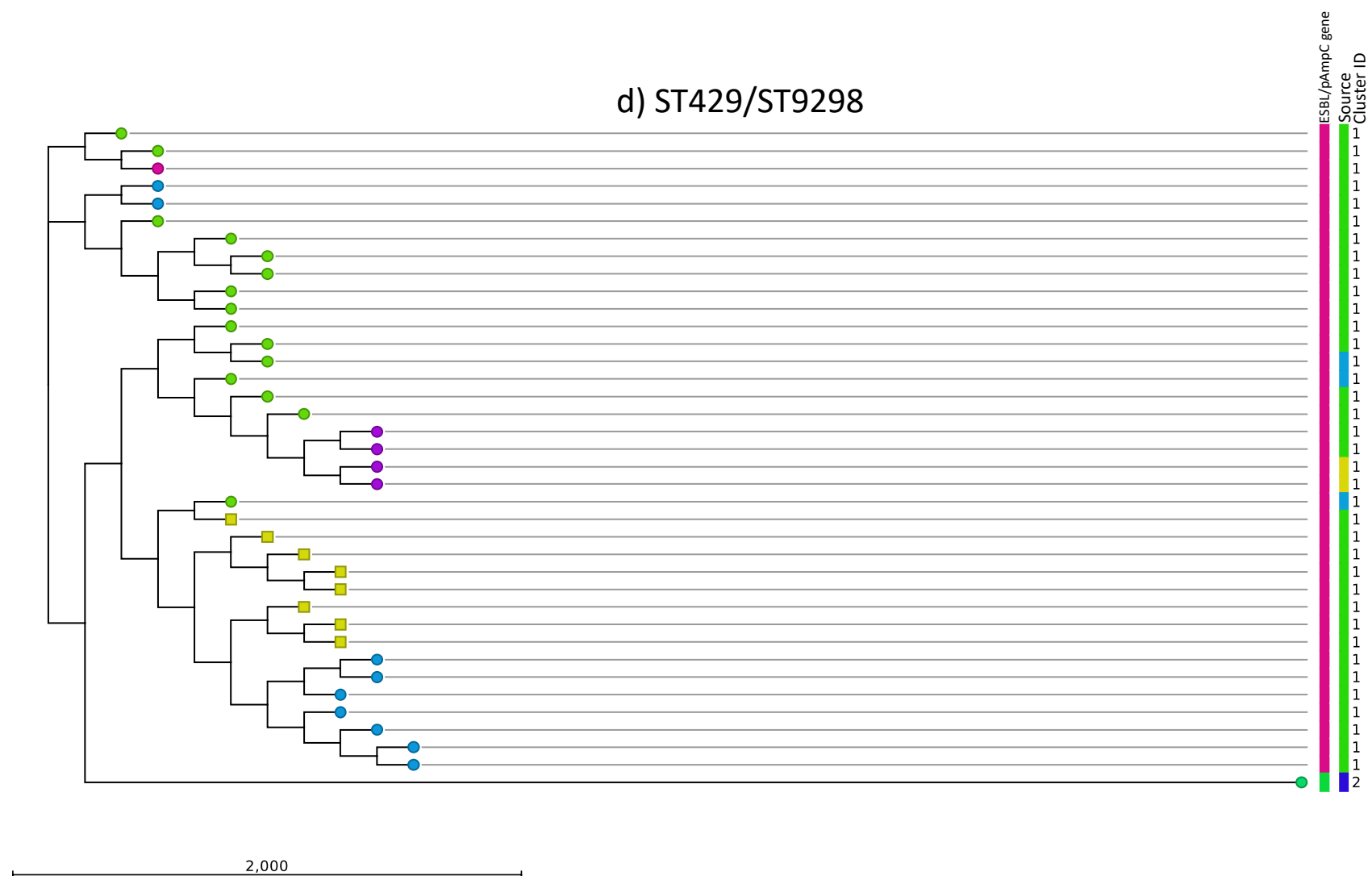
- France
- Germany
- Italy
- Luxembourg
- Netherlands
- Poland
- Portugal
- Slovenia
- Sweden
- Switzerland

ESBL/pAmpC gene

- bla*_{SHV-12}
- bla*_{CTX-M-1}
- bla*_{CTX-M-15}
- bla*_{CTX-M-55}
- bla*_{OXA-48}
- bla*_{CMY-2}
- bla*_{CTX-M-14}
- bla*_{CTX-M-32}
- bla*_{CTX-M-65}
- bla*_{TEM-52B}

Source

- Bovine
- Companion Animal
- Food
- Human
- Poultry
- Swine
- Unknown



Isolate origin (node shape)

- This study
- Enterobase

Country (node colour)

- Denmark
- France
- Germany
- Italy
- Luxembourg
- Netherlands

ESBL/pAmpC gene

- *bla*_{CMY-2}
- *bla*_{TEM-52C}

Source

- Human
- Poultry
- Livestock
- Unknown

Supplementary Figure S2. Phylogenetic analysis of a) ST457, b) ST155, c) ST744, d) ST429/ST9298 ESBL/pAmpC-EC of this study and of various sources in Europe that were parsed from Enterobase database. SNP analysis was done with CSI phylogeny. The isolates of this study have a rectangular node shape while those from Enterobase are indicated with a circle. Source niche, ESBL/pAmpC genes, and country of origin are colour-coded according to the legend. Numbers next to ribbons indicate the cluster of isolates calculated with hierBAPS. Scale bar refers to the branch lengths, which are measured in the number of substitutions per site. Tree nodes are ordered after their increasing branch lengths.