Supplementary File 5

Individual gene phylogenies were constructed for the dataset obtained from Walk et al., 2009. This dataset consisted of 42 taxa, of which two isolates represent *Escherichia coli*, eight isolates represent *Escherichia* Clade I, one isolate of *Escherichia* Clade II, six isolates representative of *Escherichia* Clade III, four isolates representative of *Escherichia* Clade IV and 18 isolates that represent *Escherichia* Clade V, with three isolates of *E. fergusonii* as outgroup taxa. Sequencing data for a total of 22 loci were analysed individually and as a concatenated super matrix. All individual gene trees were constructed with a maximum likelihood approach using RAxML v. 8.20 (Stamatakis, 2014), employing the GTR model of nucleotide evolution (Tavaré, 1986) with all parameters estimated by RAxML. Branch support was obtained from 1,000 bootstrap replicates.

References

STAMATAKIS, A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, 30**,** 1312-1313.

TAVARÉ, S. 1986. Some probabilistic and statistical problems in the analysis of DNA sequences. *Lectures on mathematics in the life sciences,* 17**,** 57-86.

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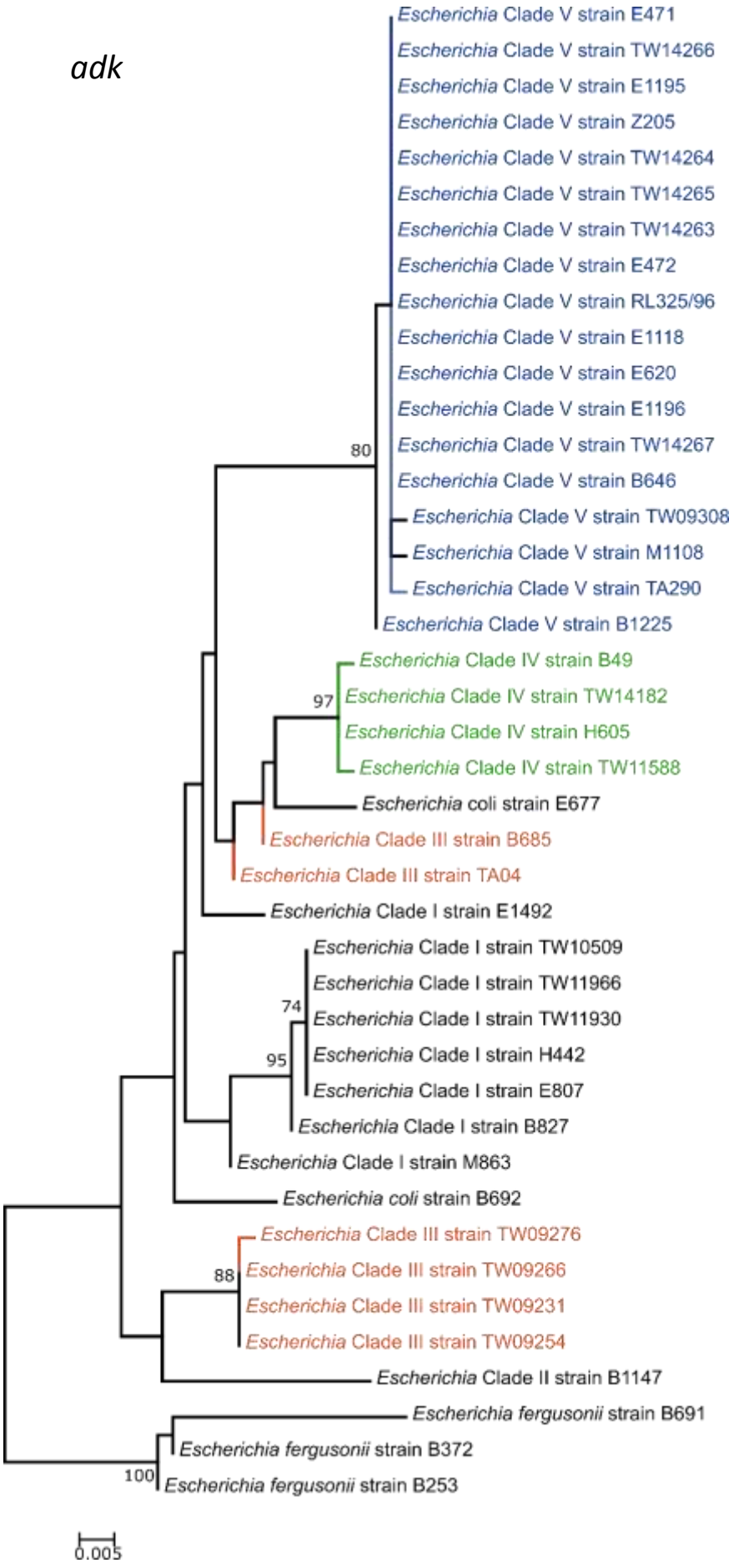
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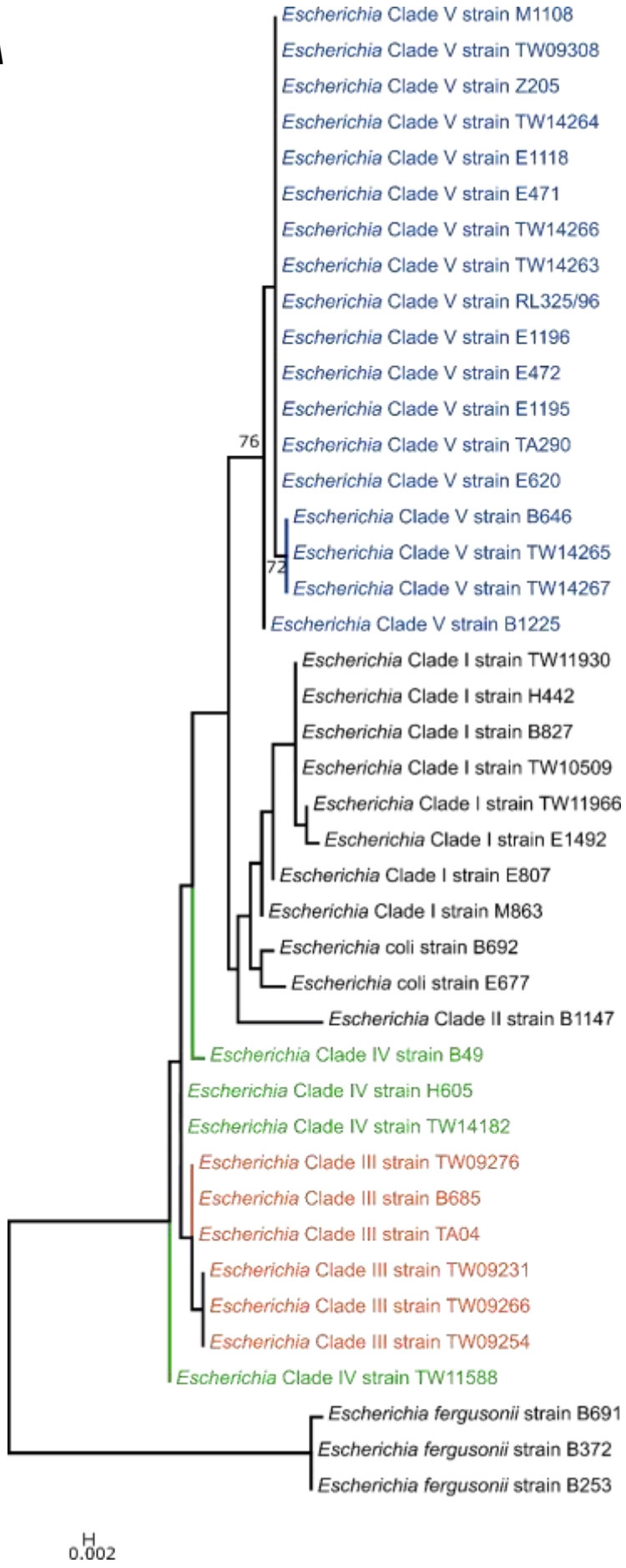
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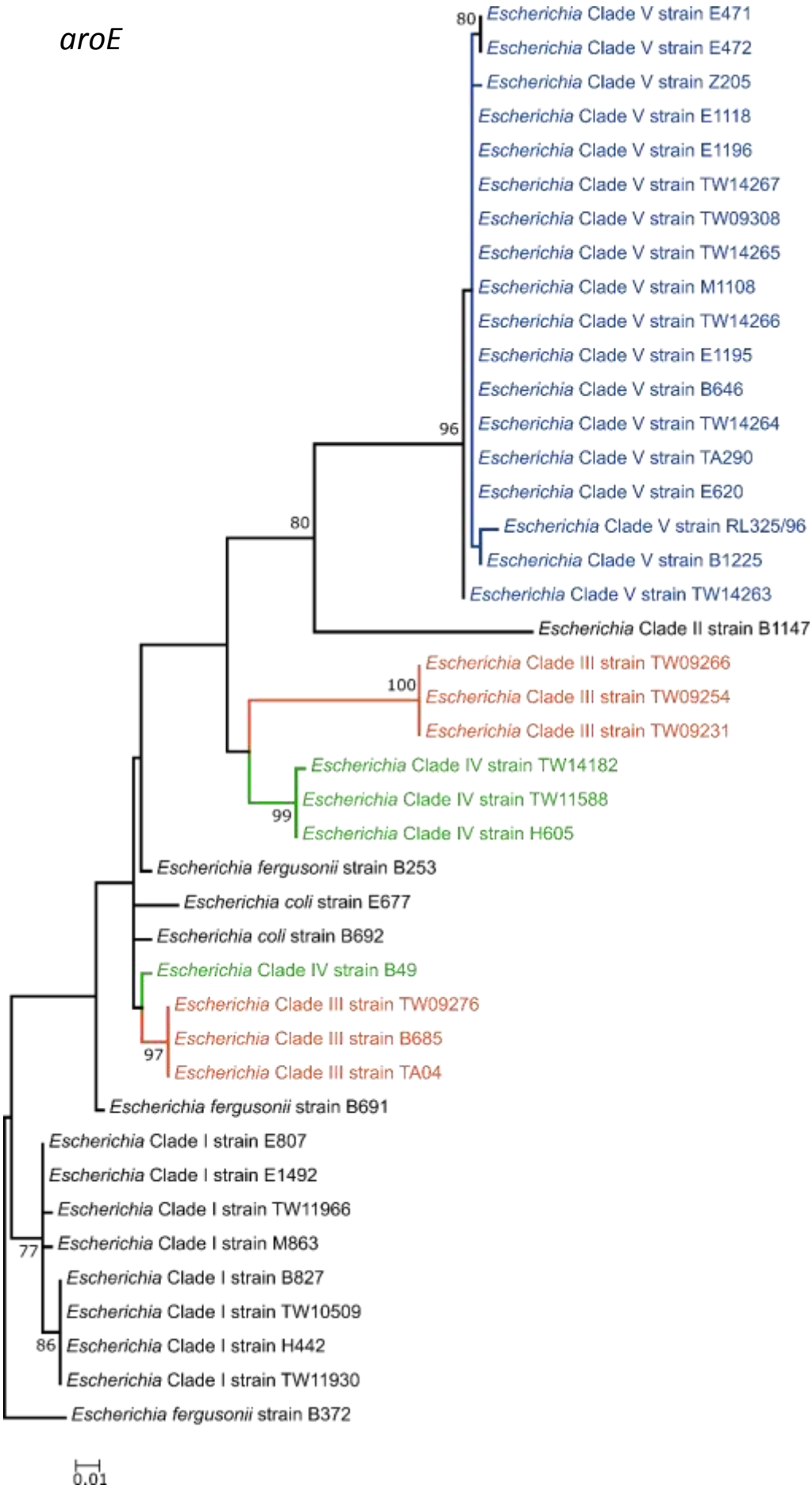
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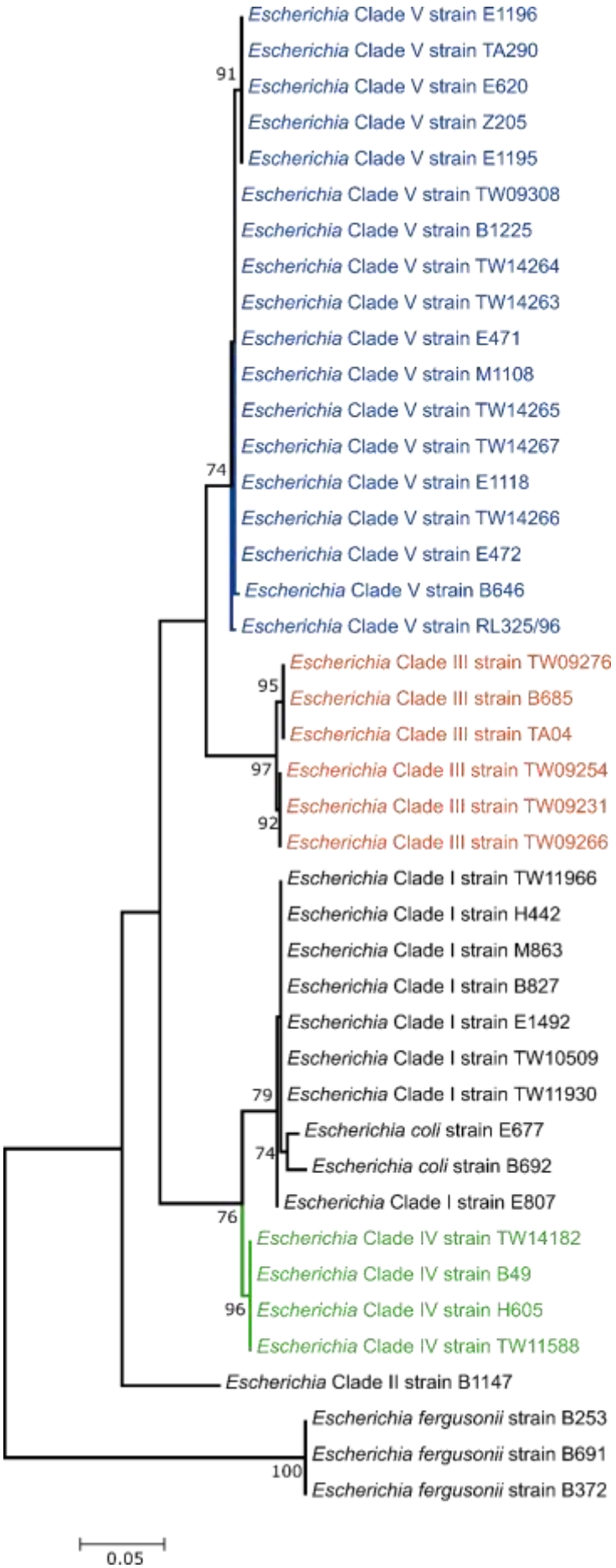
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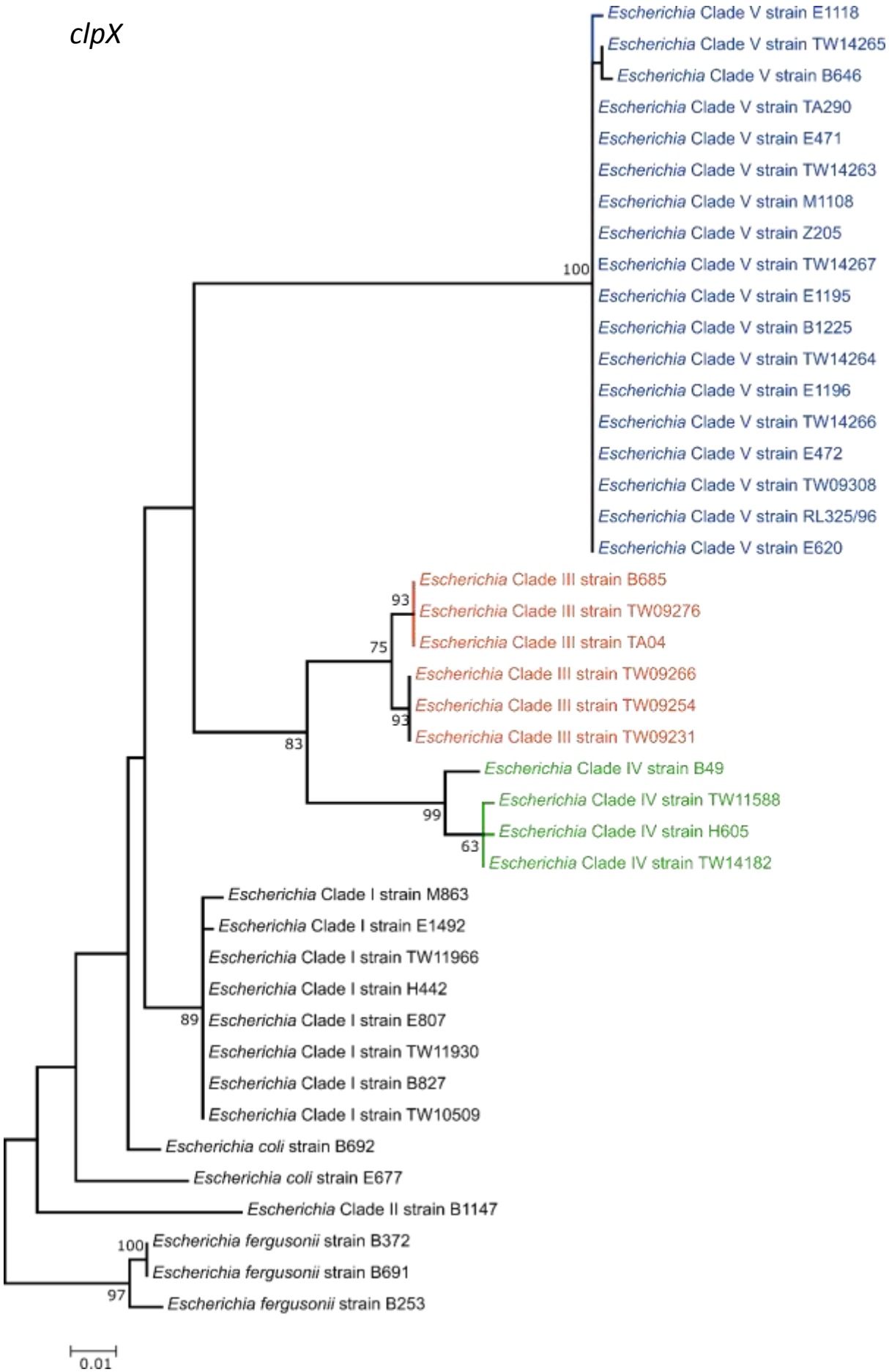
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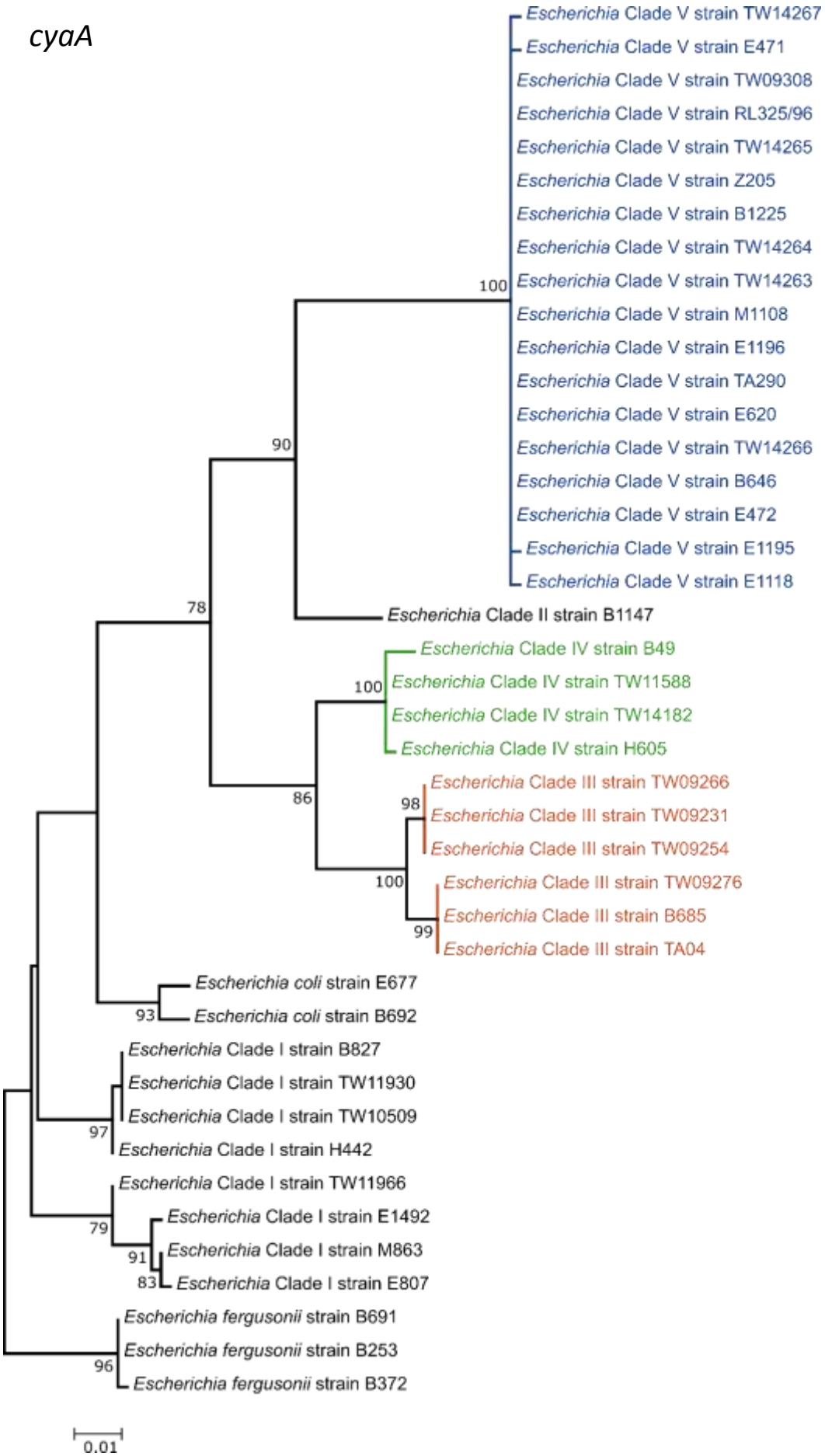
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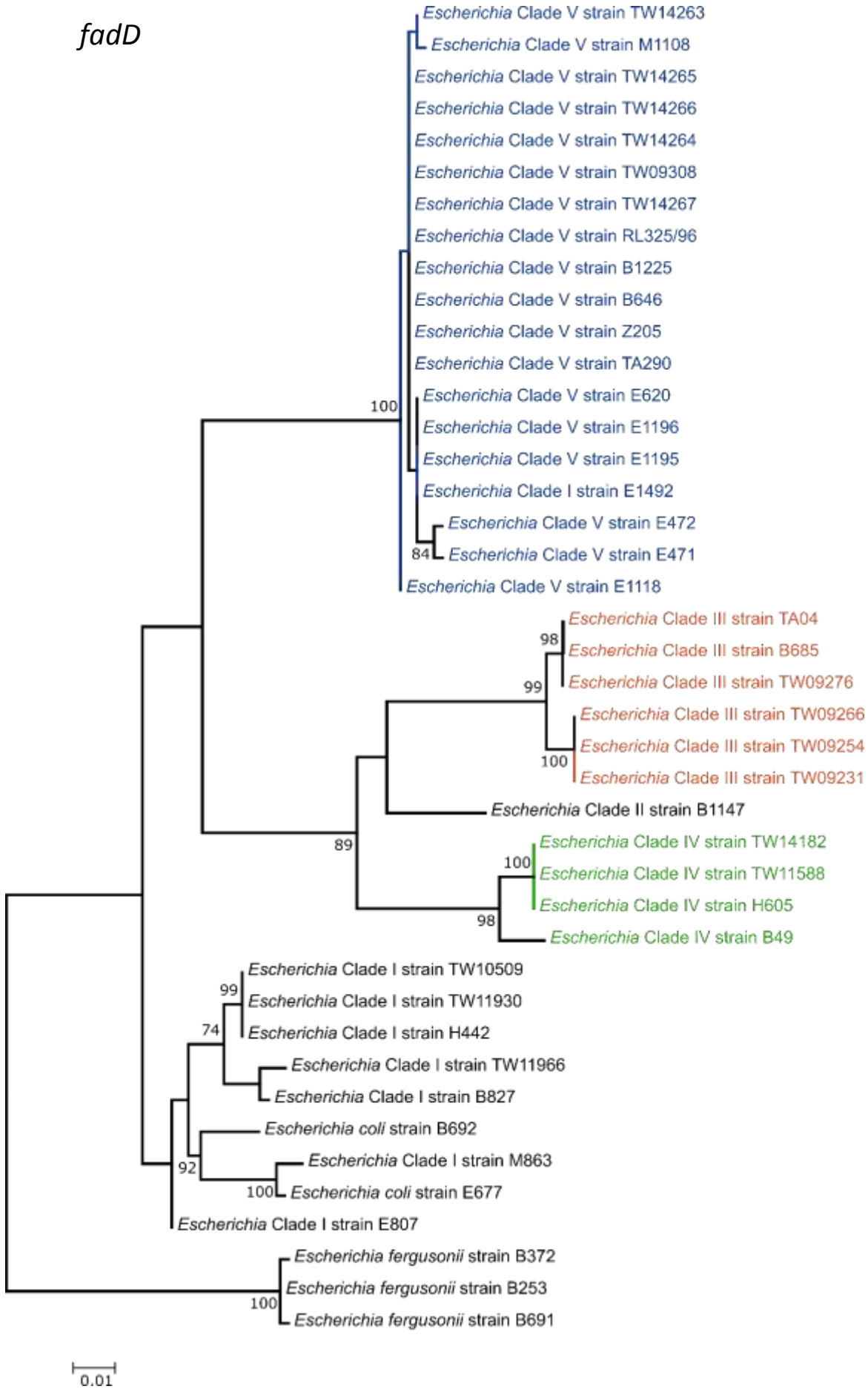
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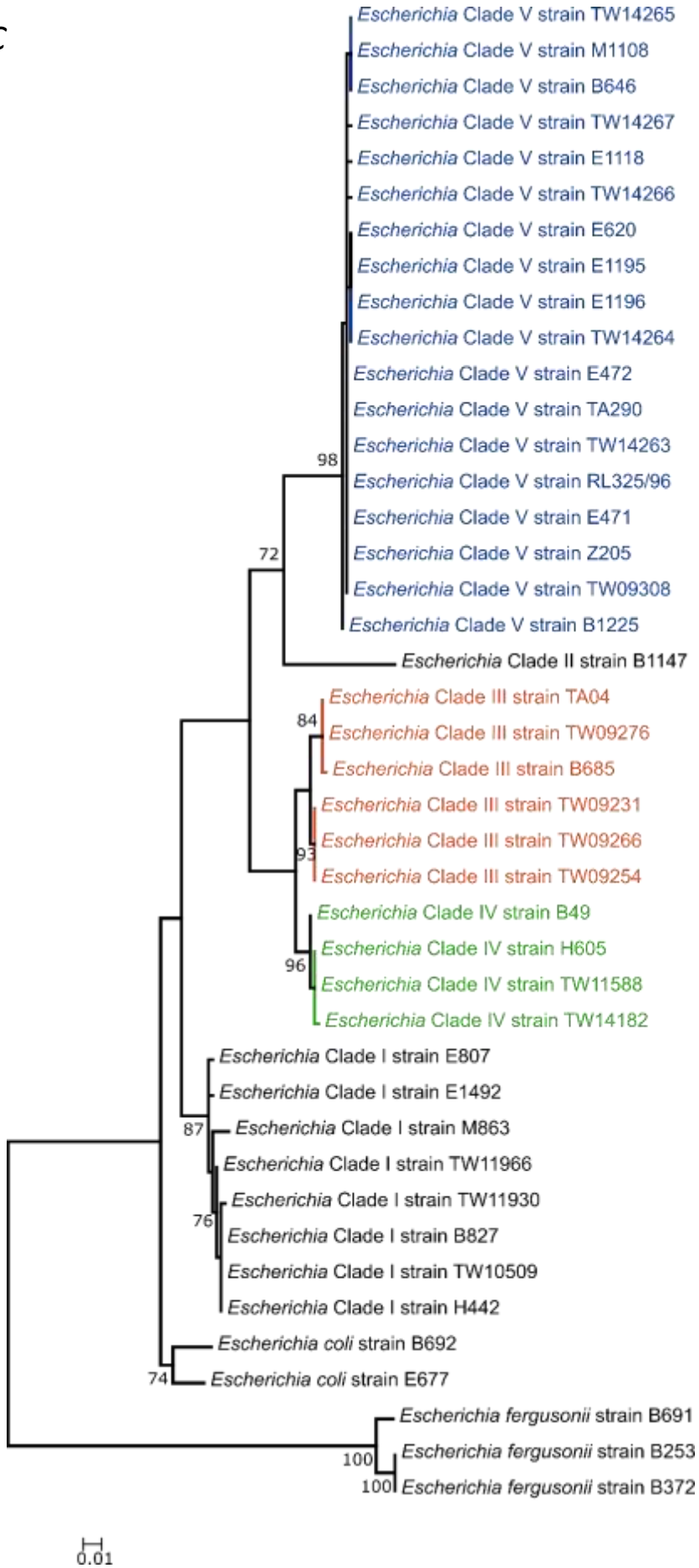
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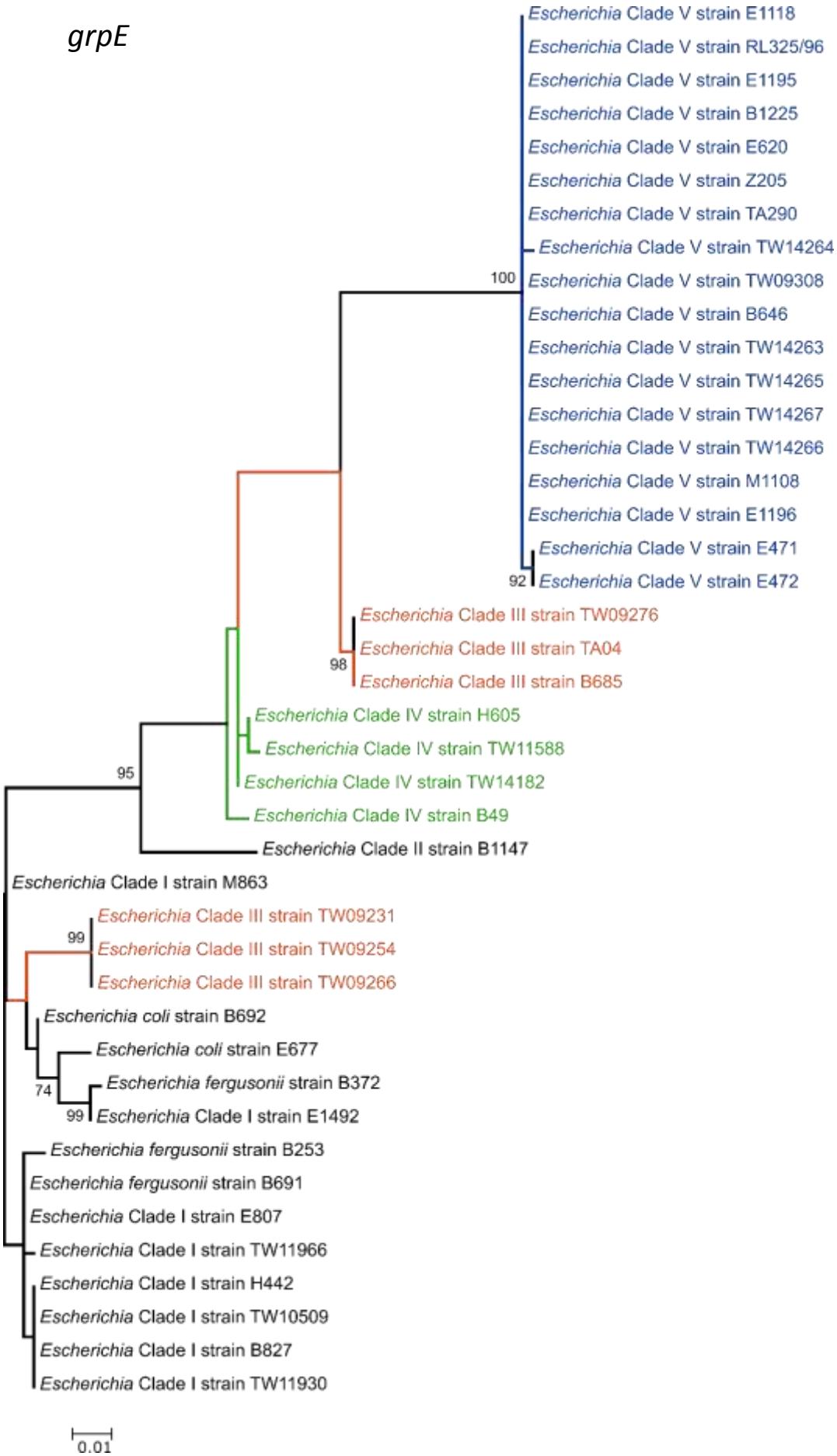
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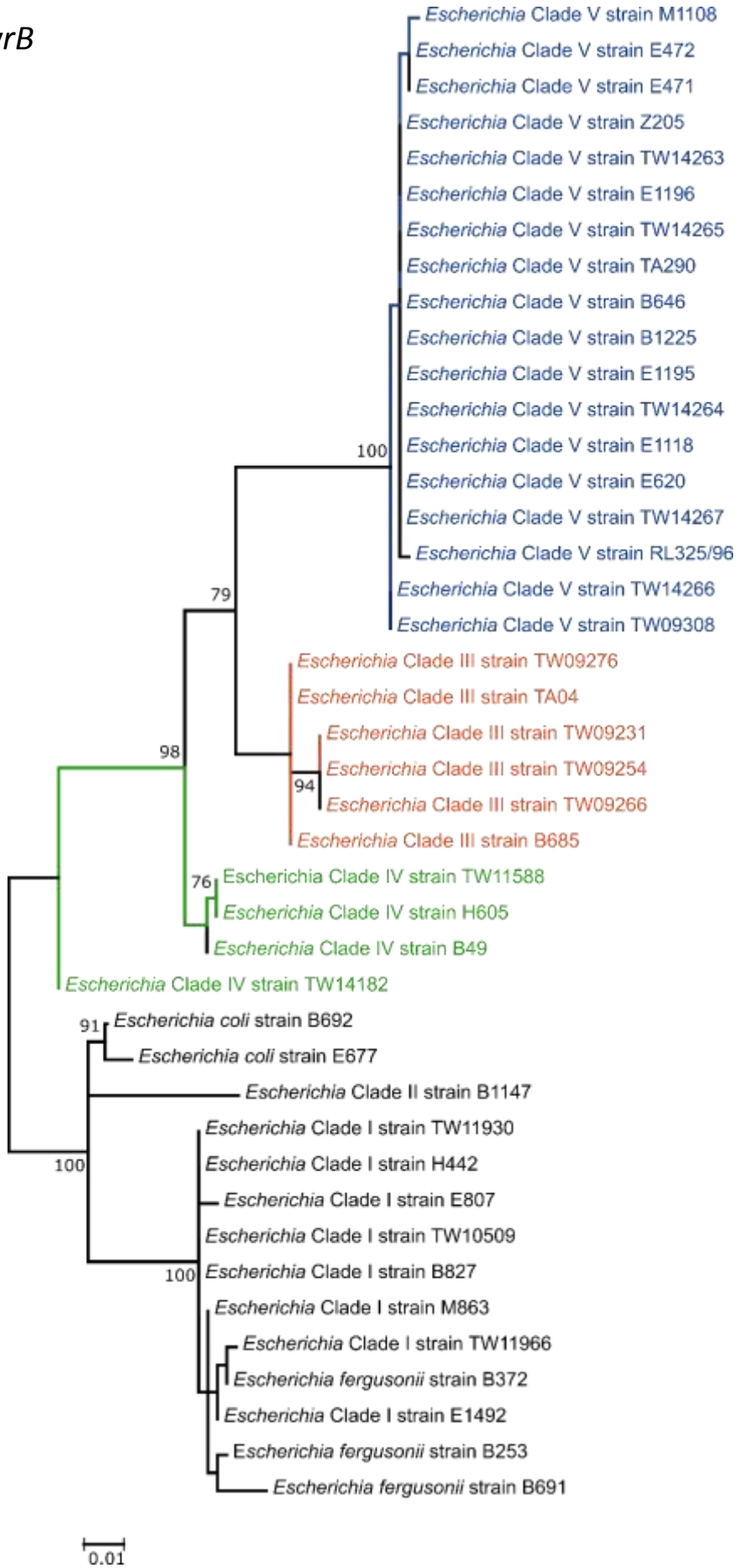
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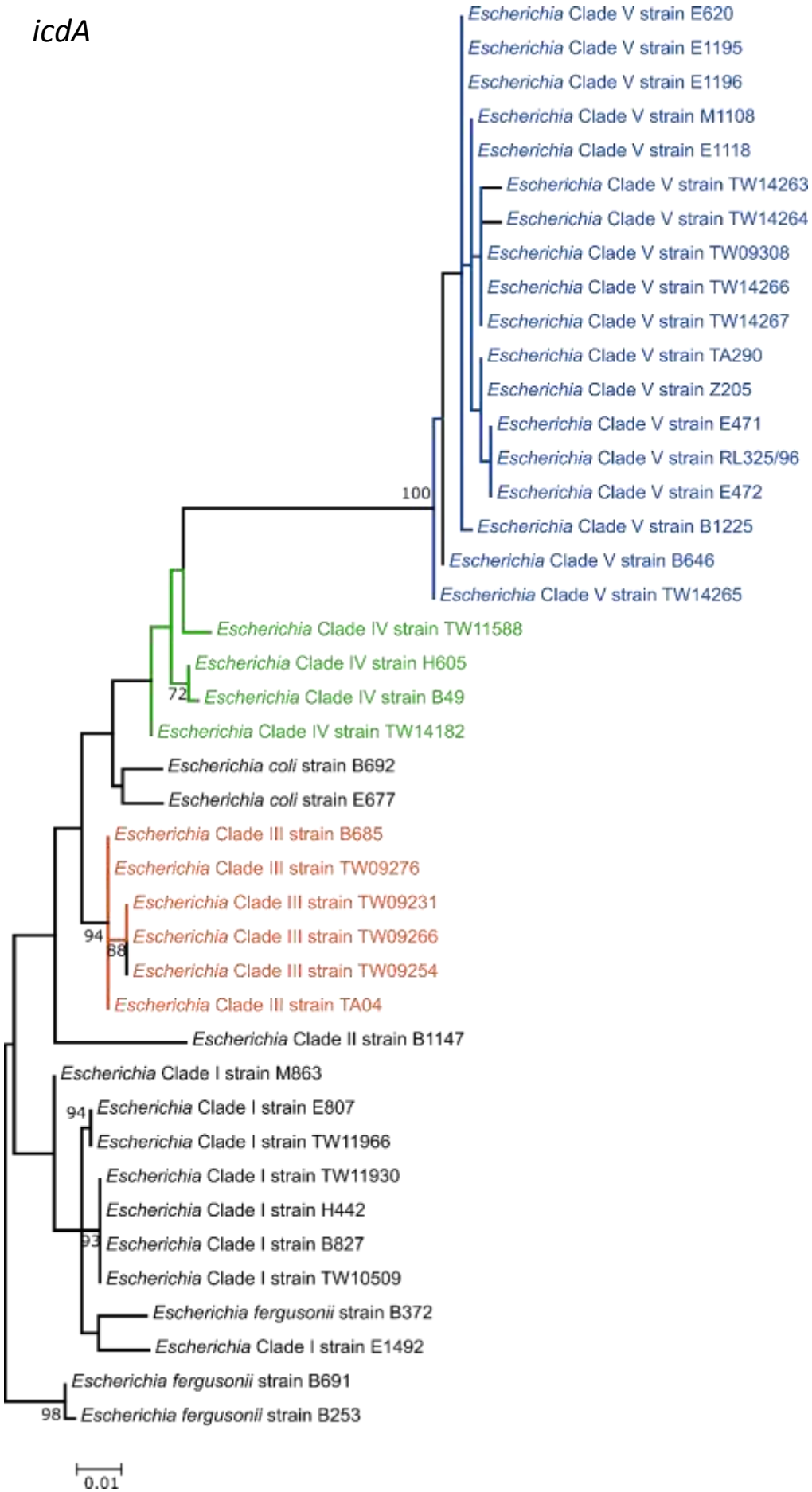
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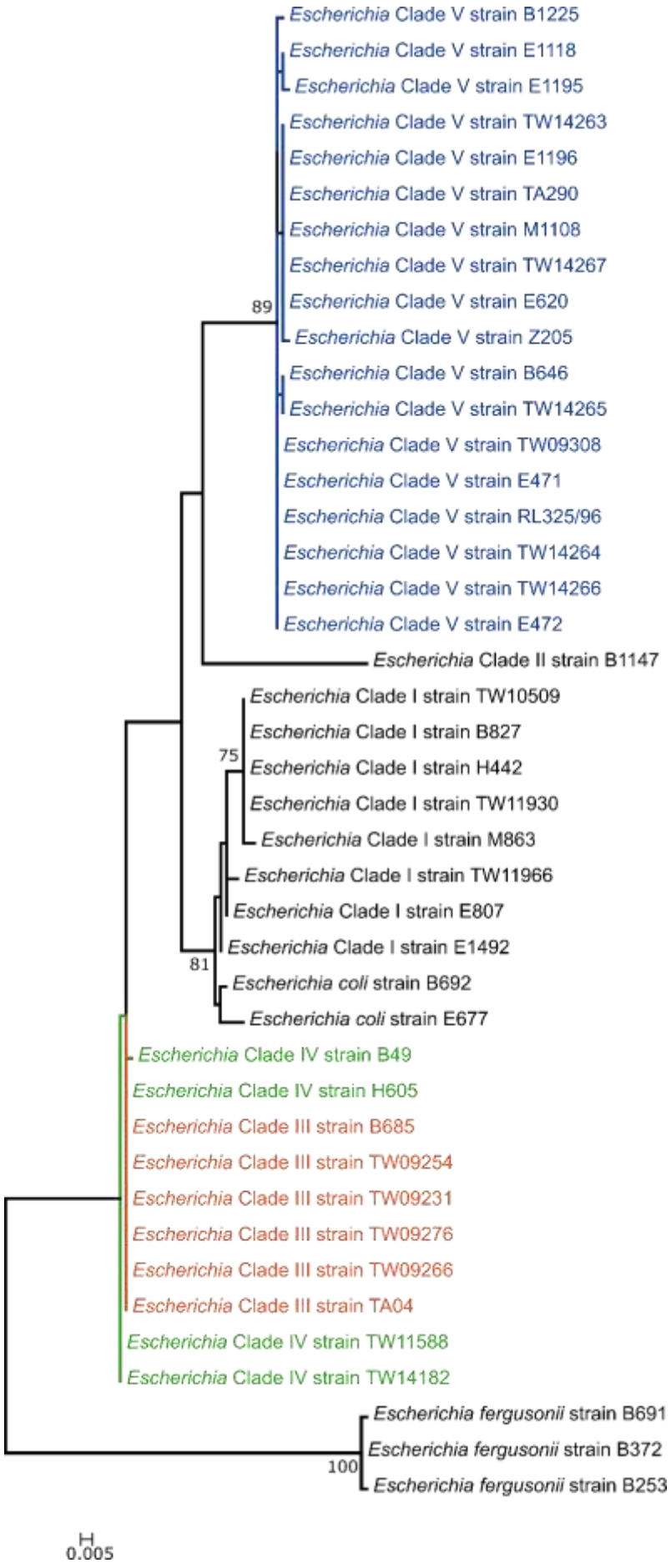
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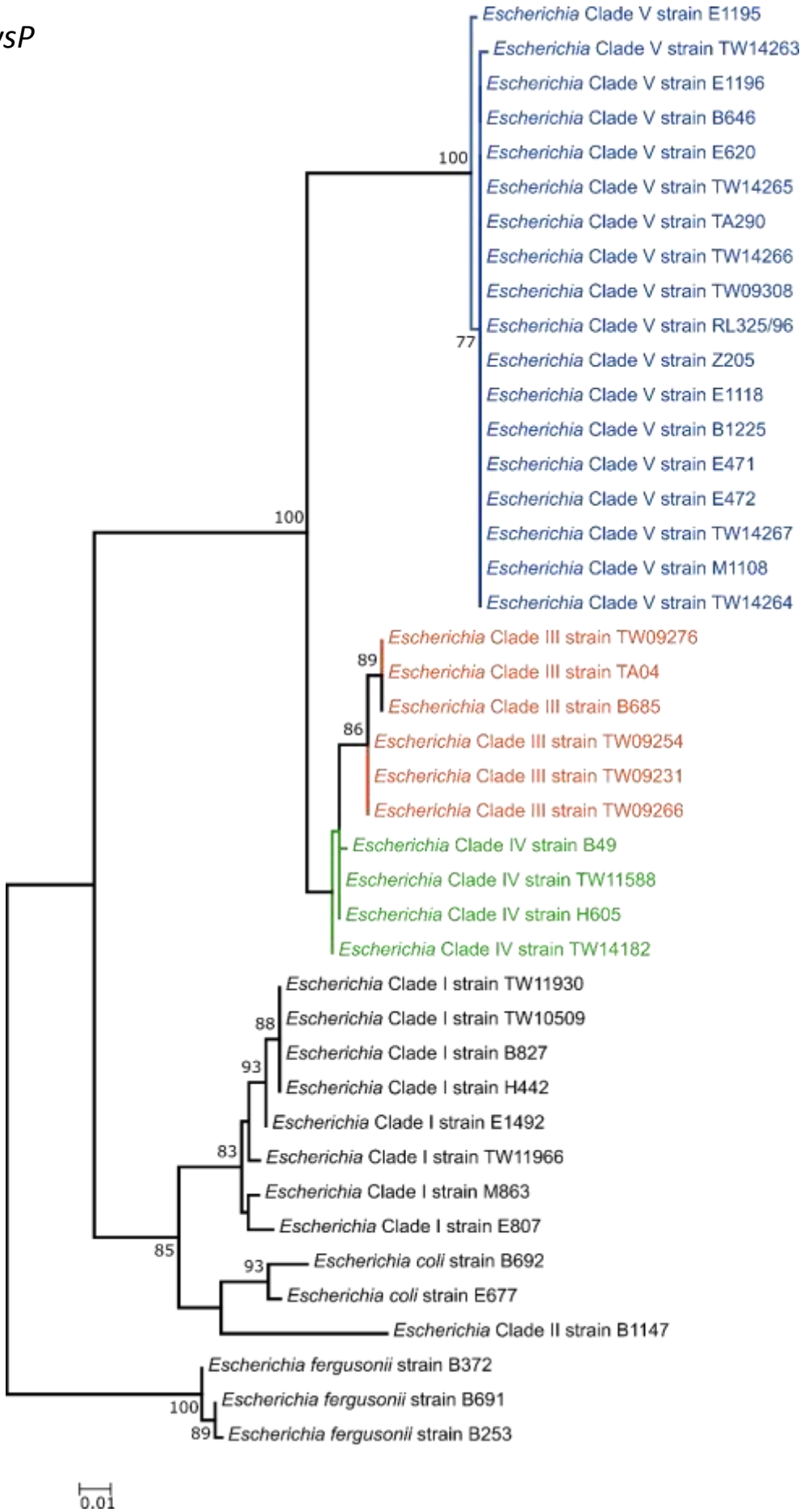
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Escherichia Clade V strain Z205
Escherichia Clade V strain E1118
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Escherichia Clade V strain E471
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Escherichia Clade V strain TW14264
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Escherichia Clade III strain TA04
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Escherichia Clade I strain TW11930
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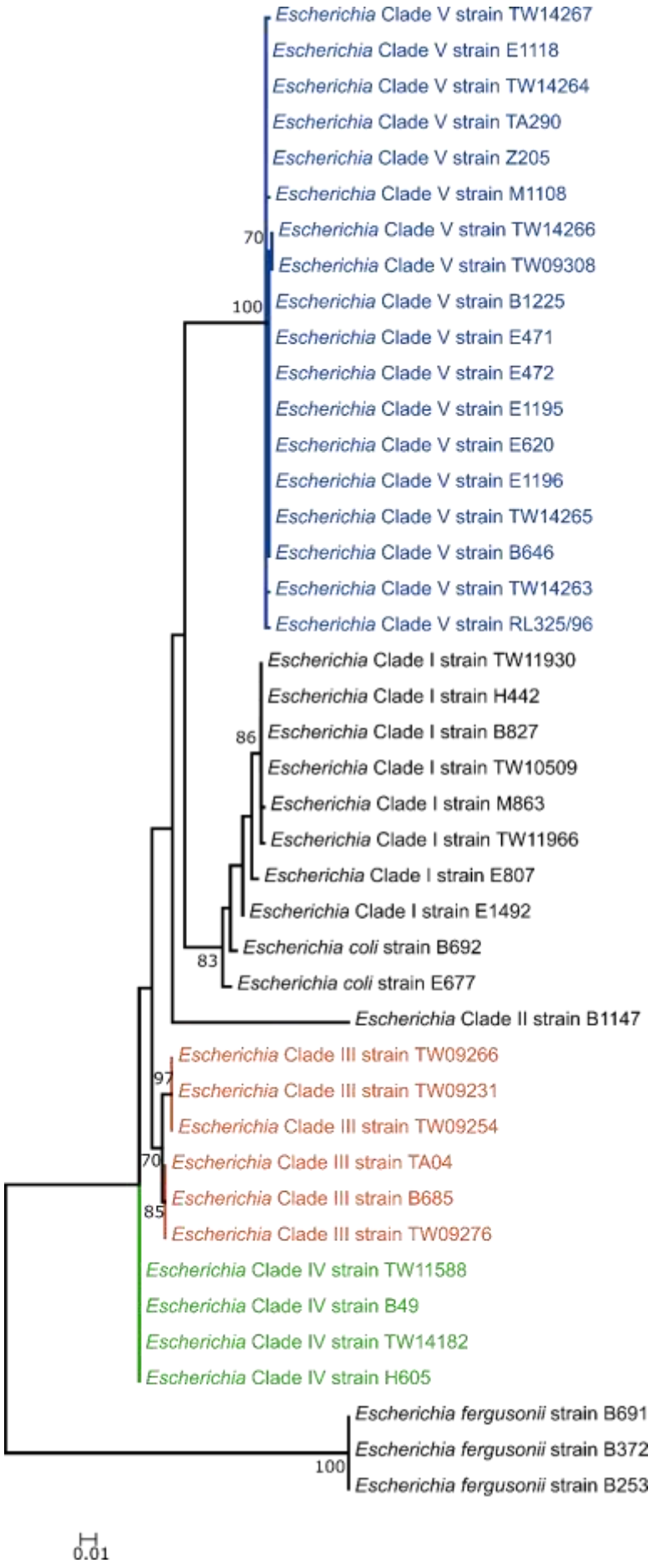
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Escherichia Clade V strain TW09308
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Escherichia Clade V strain B1225
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Escherichia Clade I strain H442
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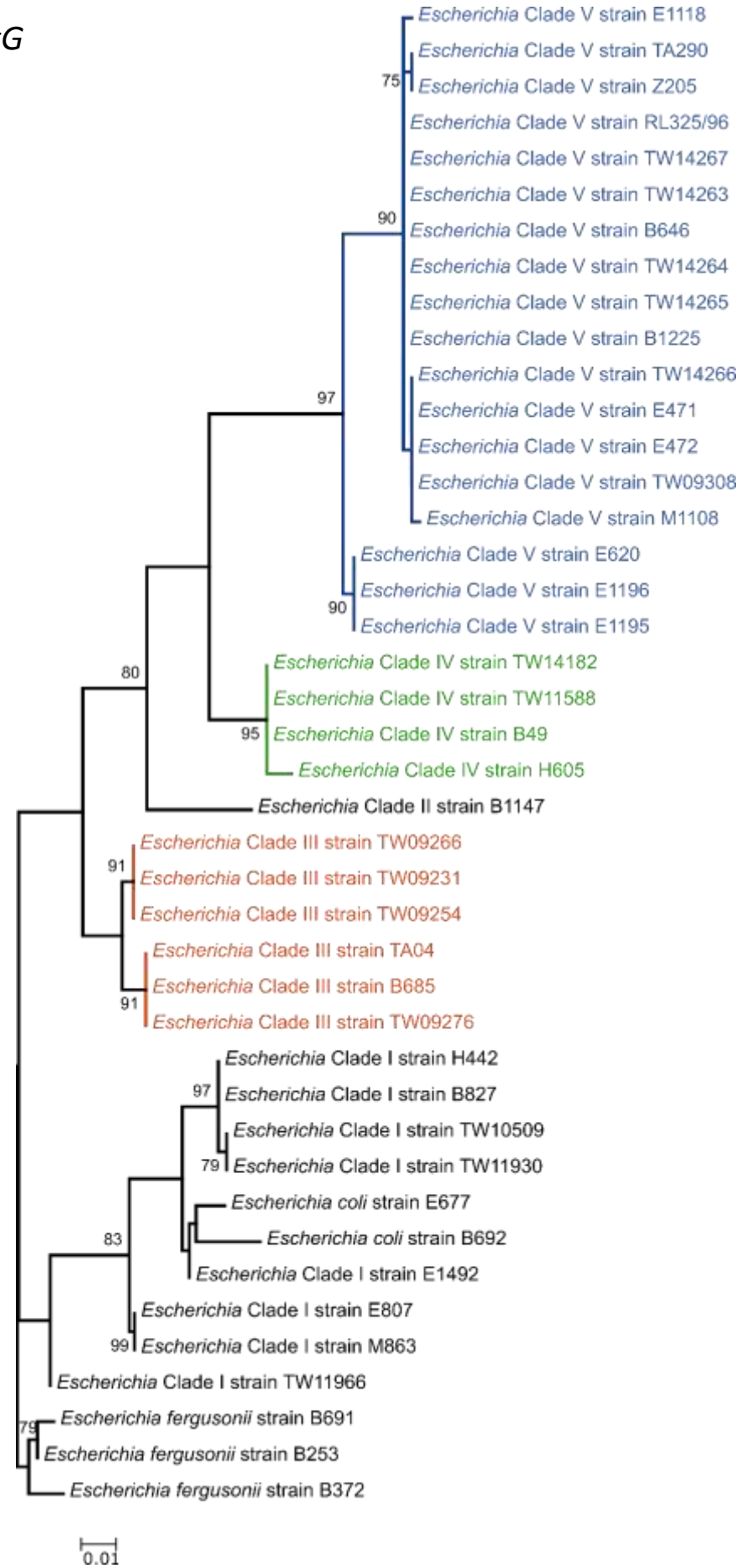
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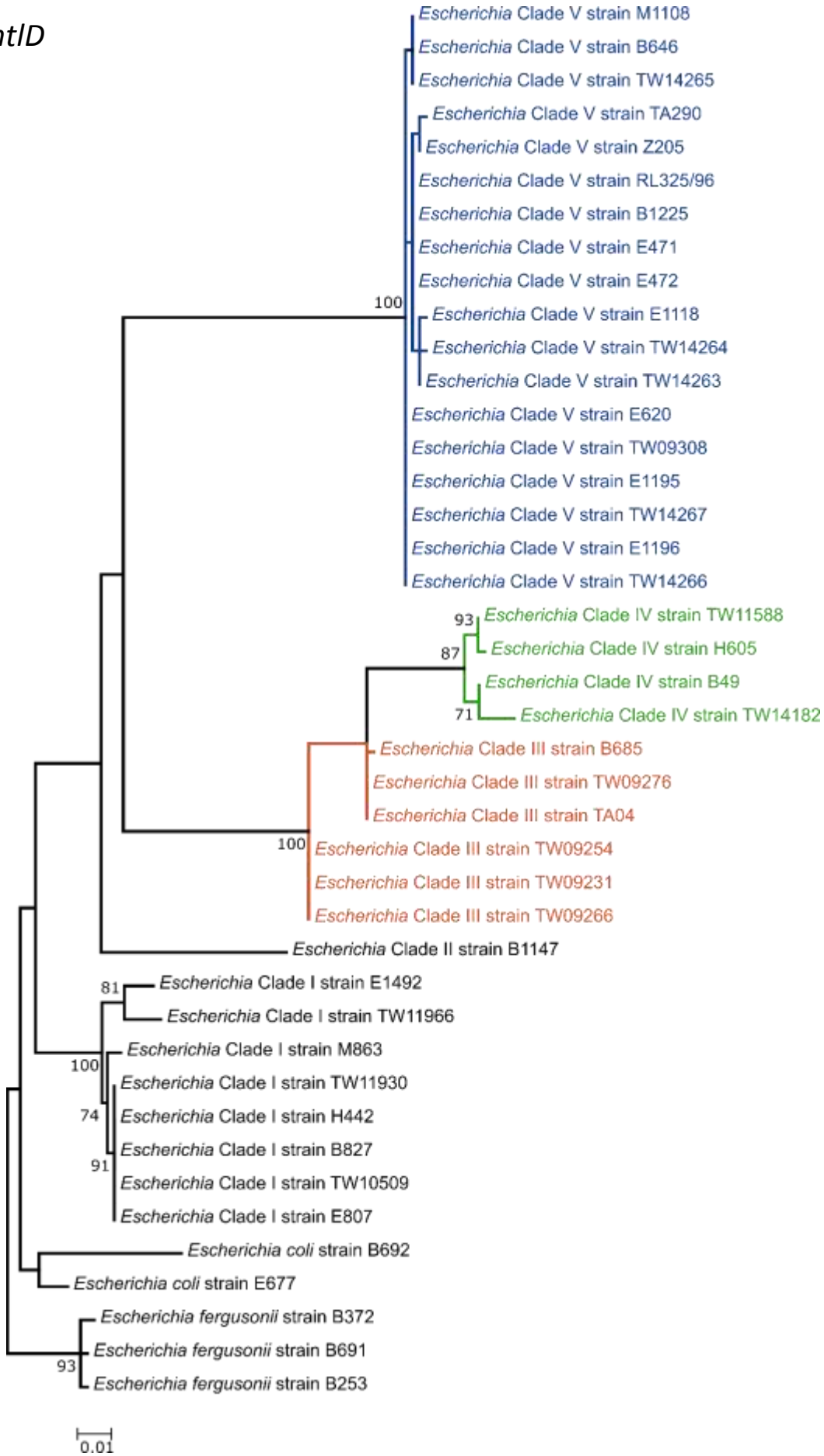
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Escherichia Clade V strain E471
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Escherichia Clade V strain E1196
Escherichia Clade V strain TW14266
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87
Escherichia Clade IV strain H605
Escherichia Clade IV strain B49
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Escherichia Clade IV strain TW14182
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Escherichia Clade III strain TA04
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Escherichia Clade III strain TW09231
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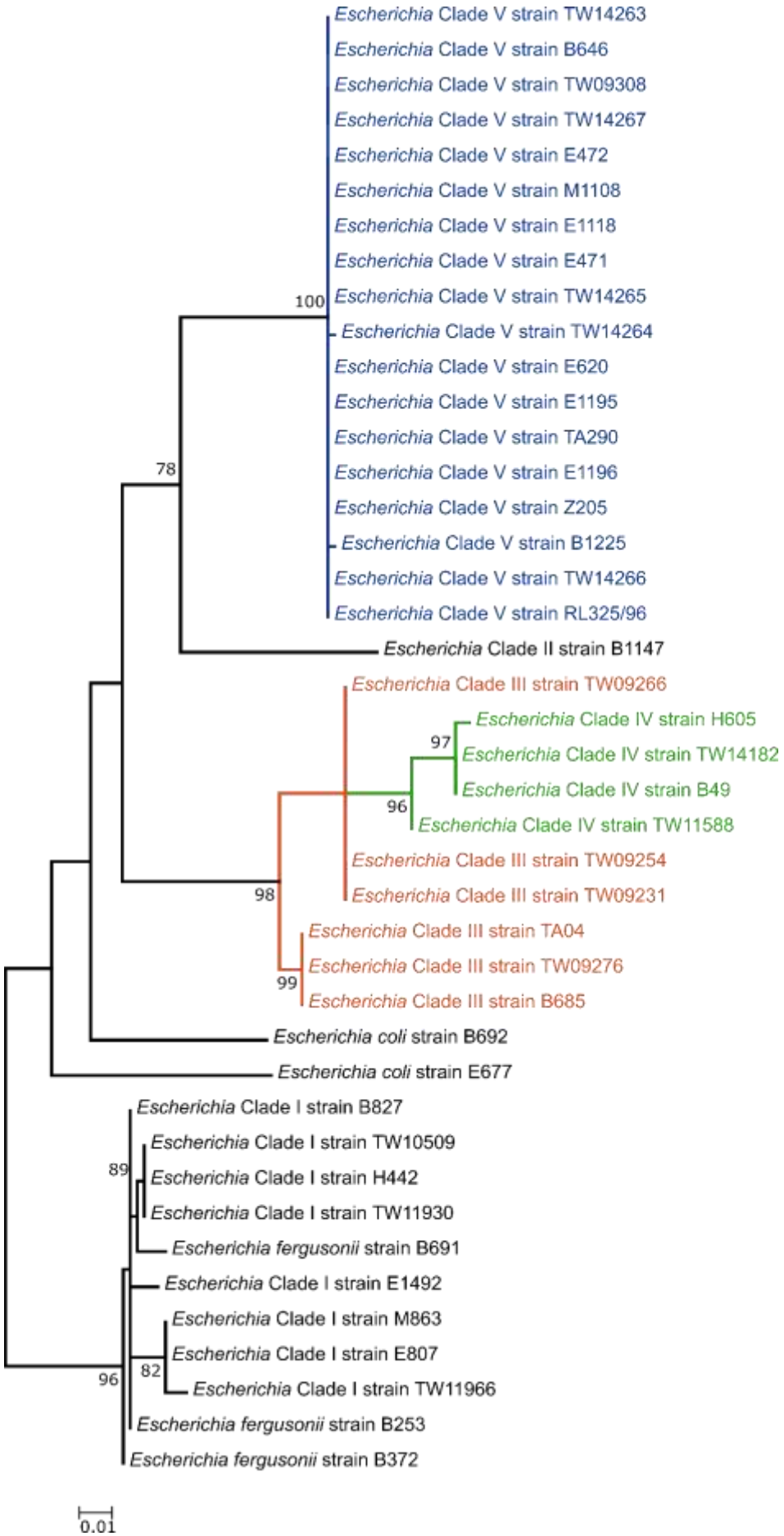
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Escherichia Clade V strain E471
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Escherichia Clade IV strain H605
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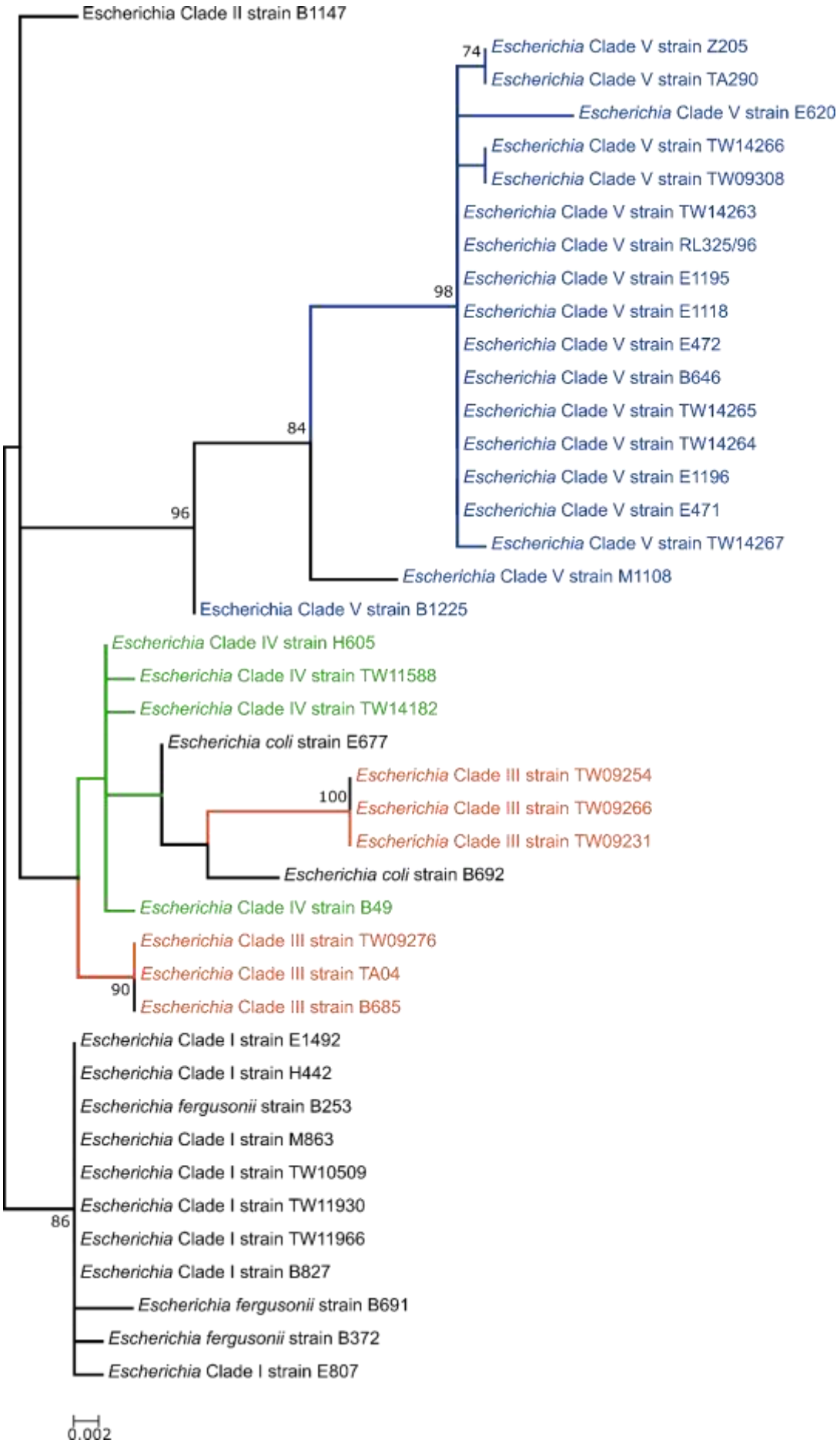
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Escherichia Clade V strain TW14265
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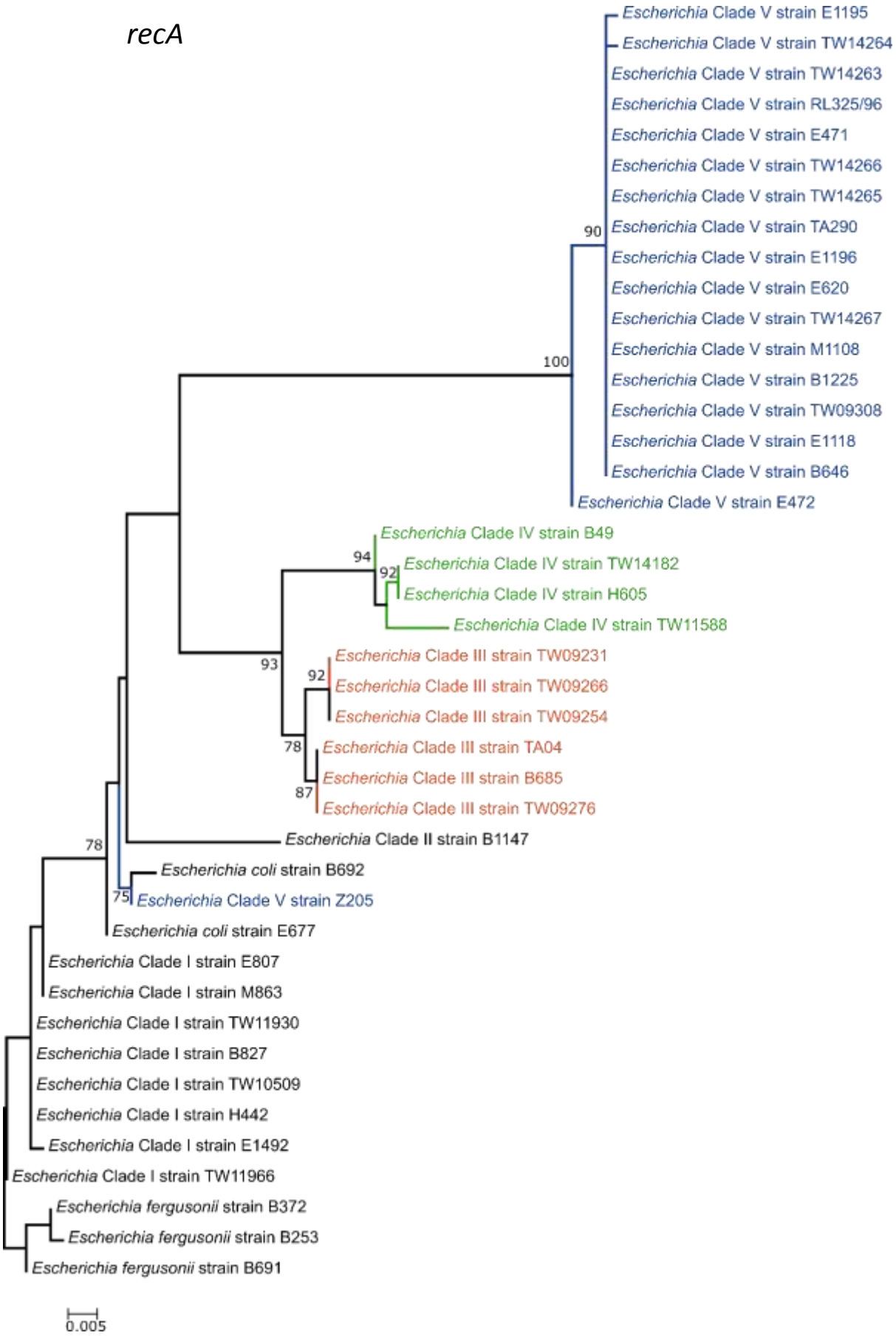
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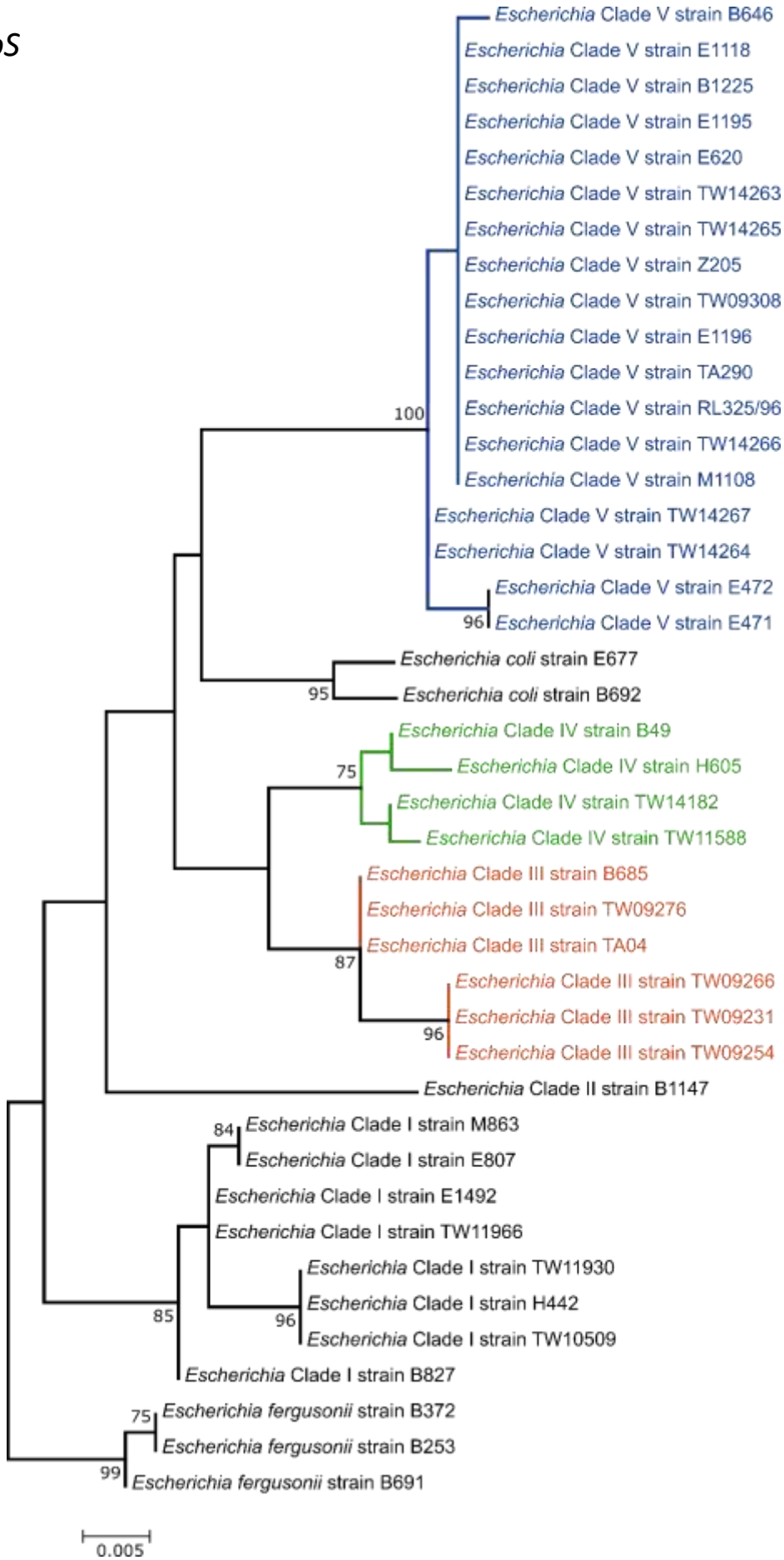
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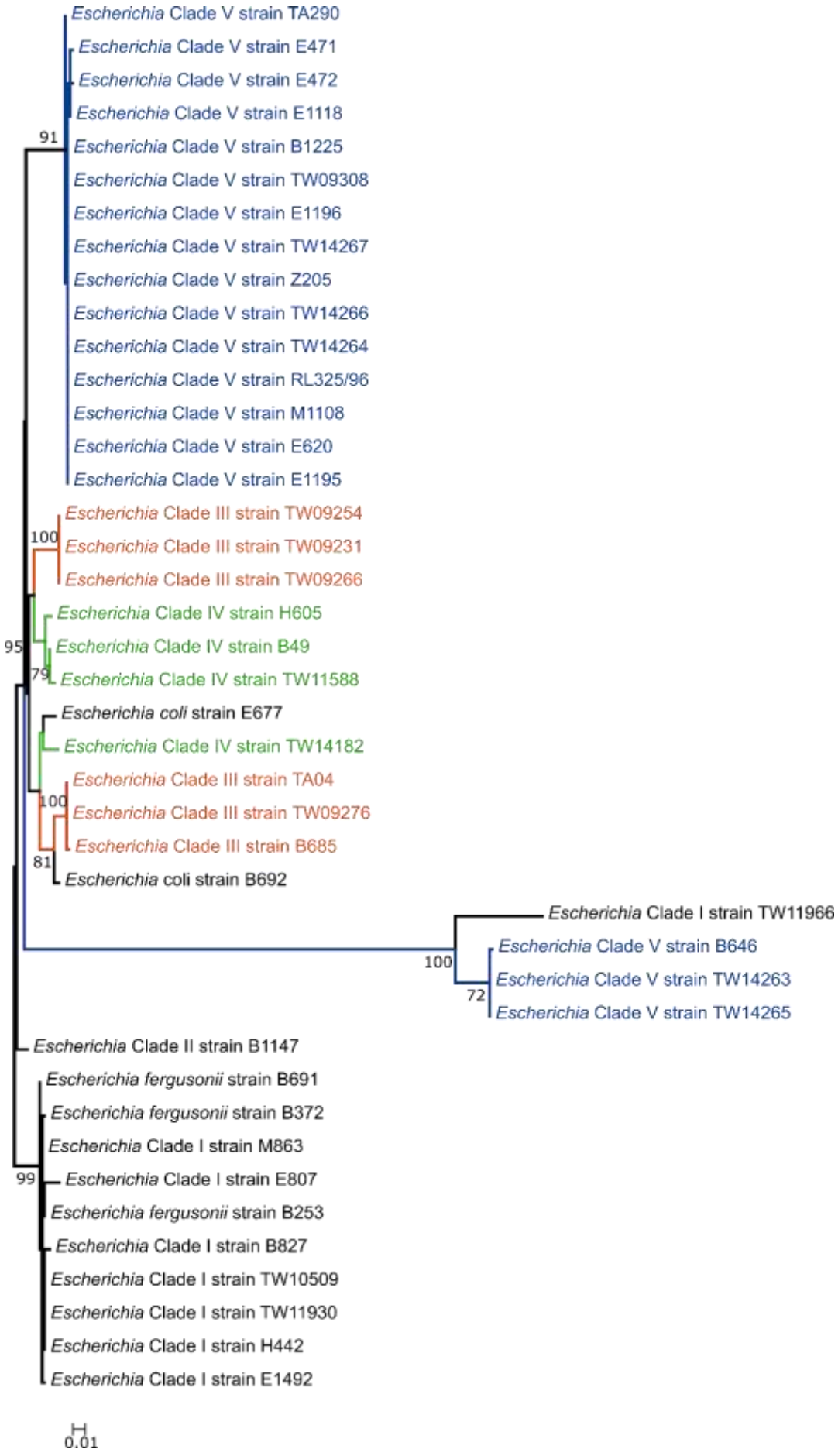
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