

Taxonomic note

Description of *Xenorhabdus khoisanae* sp. nov., the symbiont of the entomopathogenic nematode *Steinernema khoisanae*

Tiarin Ferreira¹, Carol A. van Reenen², Akihito Endo², Cathrin Spröer³, Antoinette P. Malan¹,
Leon M.T. Dicks^{2*}

¹Department of Conservation Ecology and Entomology, University of Stellenbosch, Private Bag X1, 7602 Matieland, South Africa

²Department of Microbiology, University of Stellenbosch, Private Bag X1, 7602 Matieland, South Africa

³DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen, Inhoffenstrasse 7B, 38124 Braunschweig, Germany

*Corresponding author: Leon M.T. Dicks

Tel.: +27-21-8085849; fax: +27-21-8085846; e-mail: LMTD@sun.ac.za

Running title: Description of *Xenorhabdus khoisanae* sp. nov.

Key words: *Steinernema khoisanae*, symbiont, *Xenorhabdus khoisanae* sp. nov.

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Summary

Bacterial strain SF87, and additional strains SF80, SF362 and 106-C, isolated from the nematode *Steinernema khowisanai*, are non-bioluminescent Gram-negative bacteria that share many of the carbohydrate fermentation reactions recorded for the type strains of previously described *Xenorhabdus* spp. Based on the 16S rRNA gene sequence data, strain SF87 is 98% related to *Xenorhabdus hominickii*. Nucleotide sequences of strain SF87 obtained from the *recA*, *dnaN*, *gltX*, *gyrB* and *infB* genes showed 96 to 97% similarity with *Xenorhabdus miraniensis*. However, strain SF87 shares only 52.7% DNA homology with the type strain of *X. miraniensis* by DNA-DNA hybridization analysis, confirming that it belongs to a different species. Strains SF87, SF80, SF362 and 106-C are phenotypically similar to *X. miraniensis* and *X. beddingii*, except that they do not produce acid from esculin. *Xenorhabdus khowisanai* sp. nov. is proposed as a new species of the genus *Xenorhabdus* (type strain SF87^T, DSM 25463^T, ATCC BAA-2406^T).

16S rDNA
Neighbour-joining

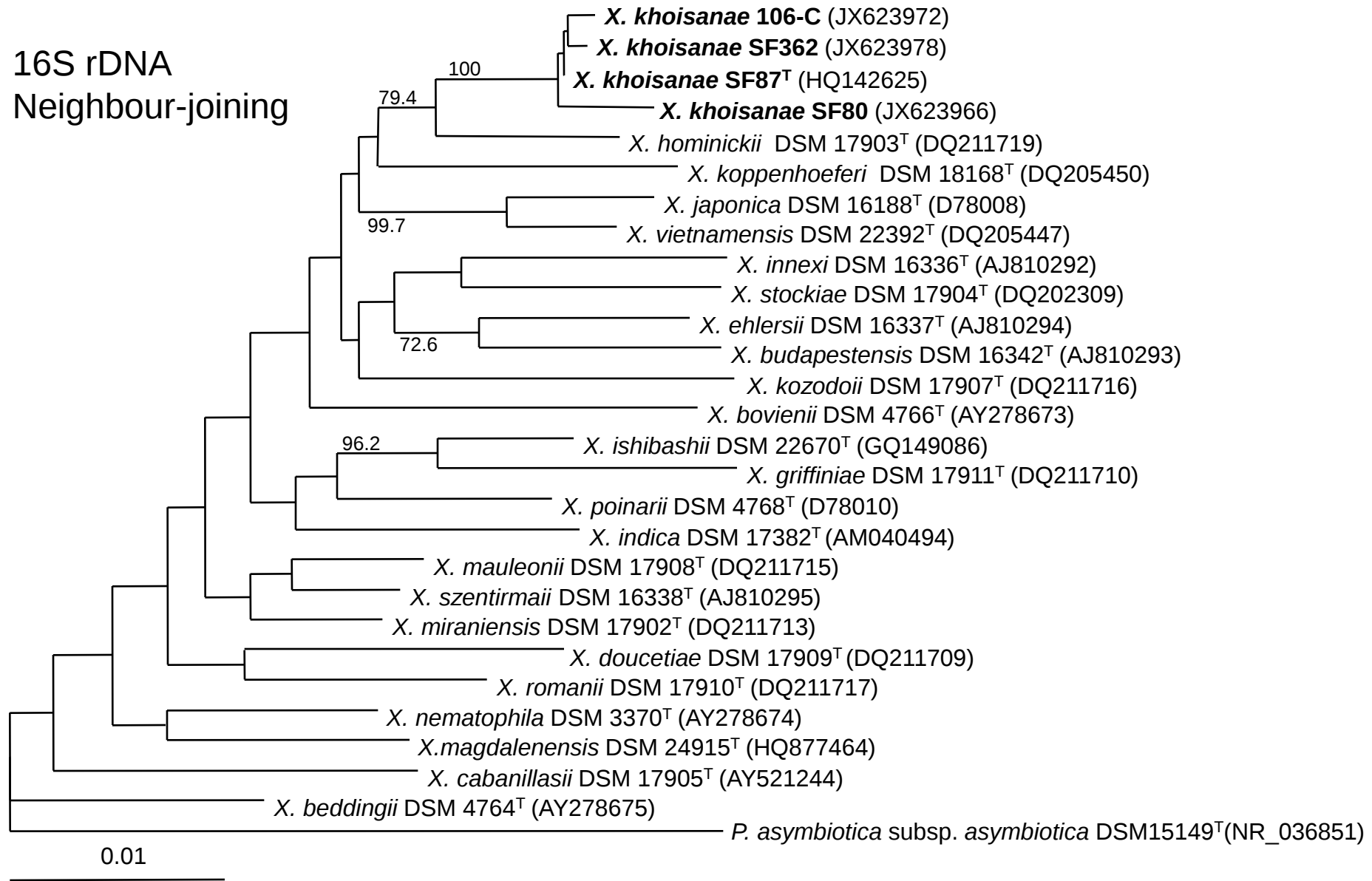


Fig 1S

16S rDNA
Maximum-likelihood

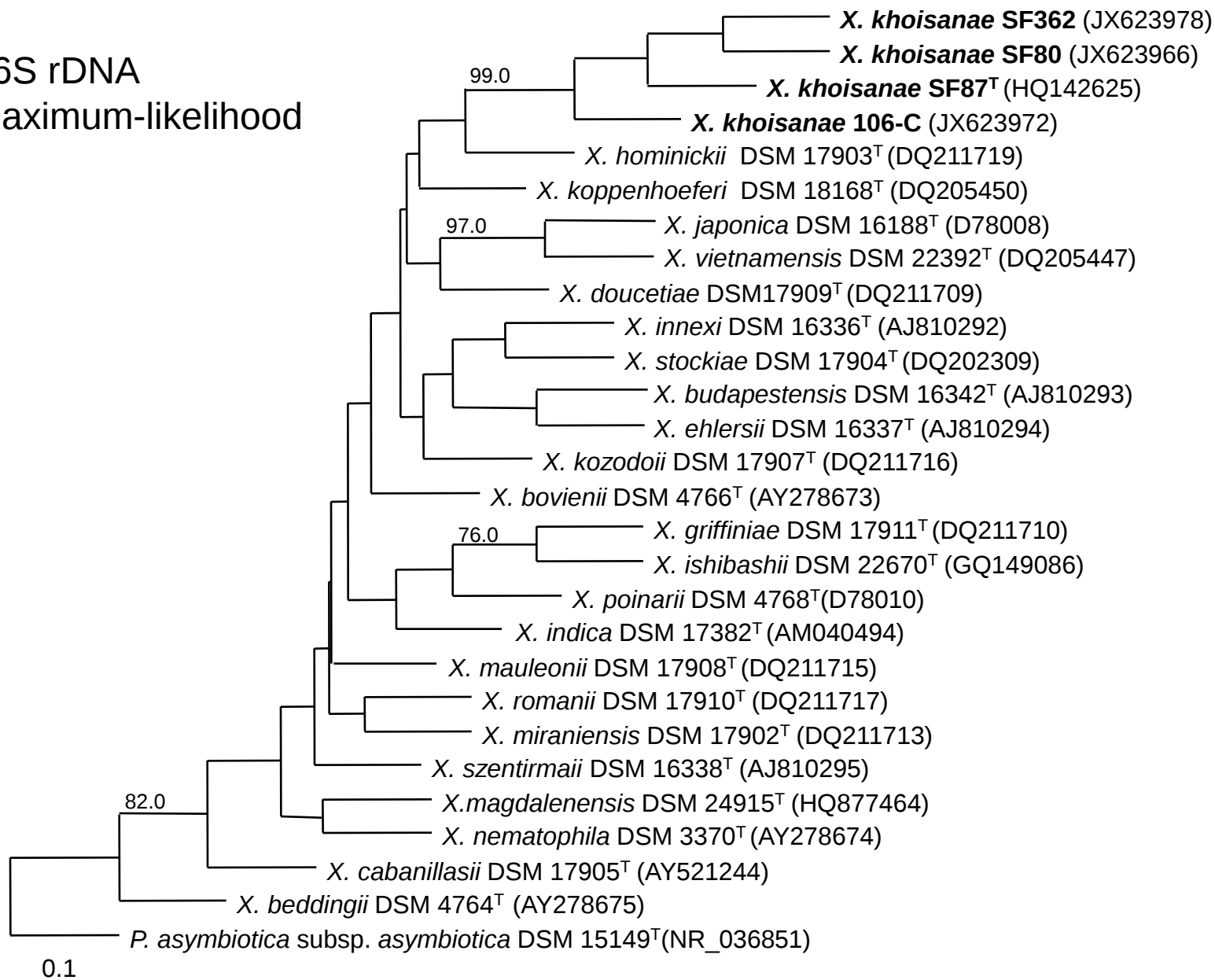


Fig 2S

recA

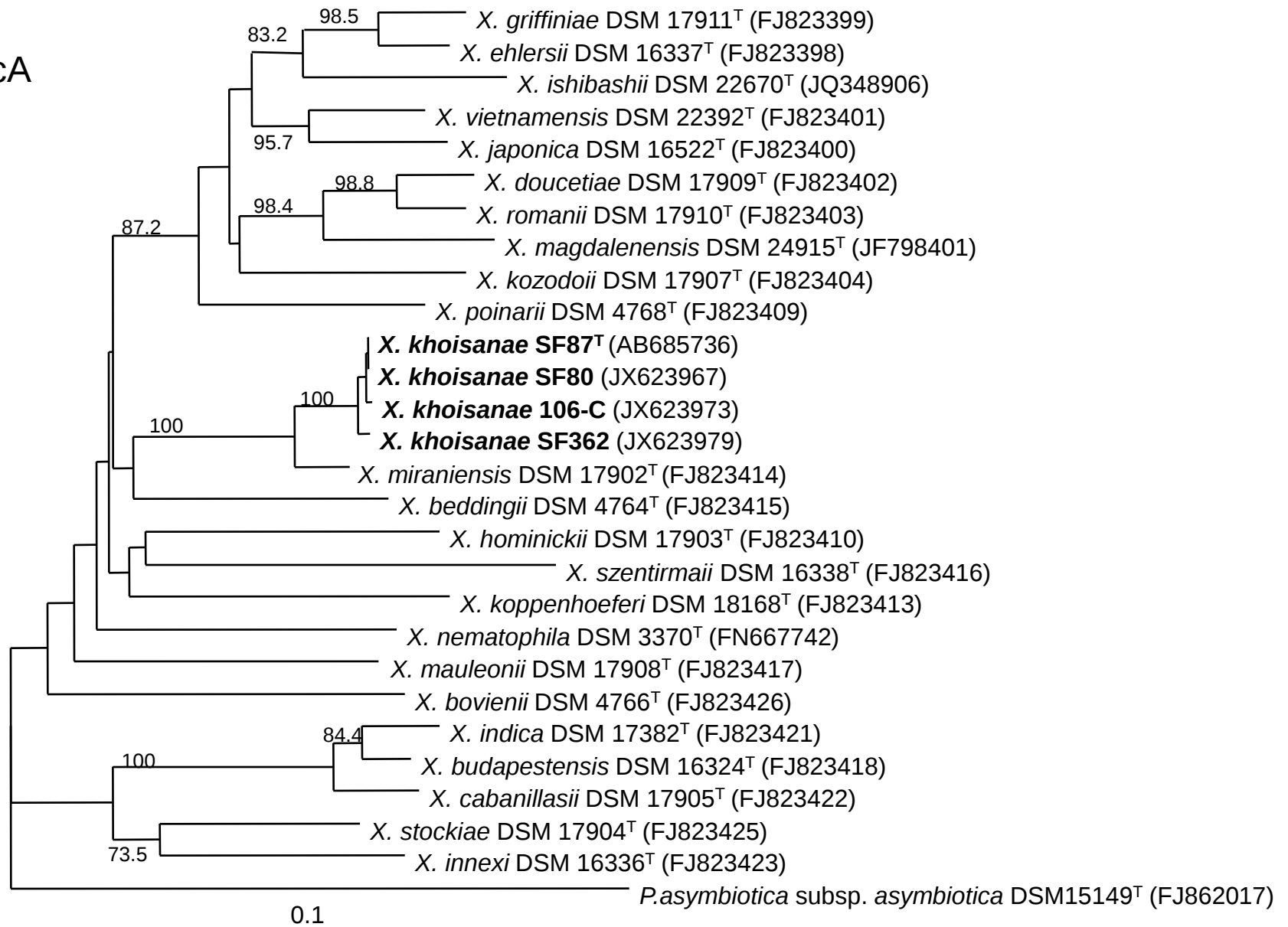


Fig 3S

dnaN

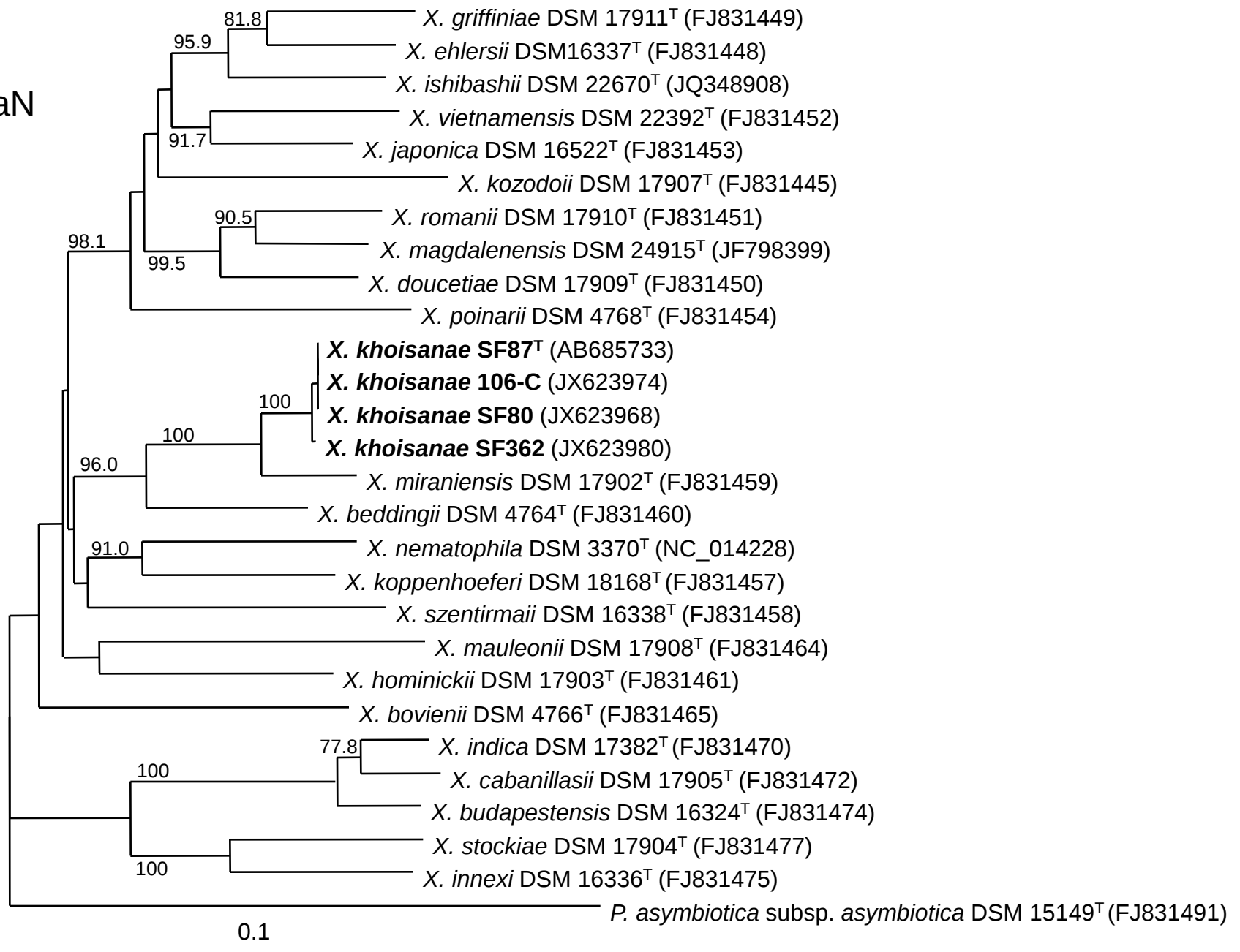


Fig 4S

gltX

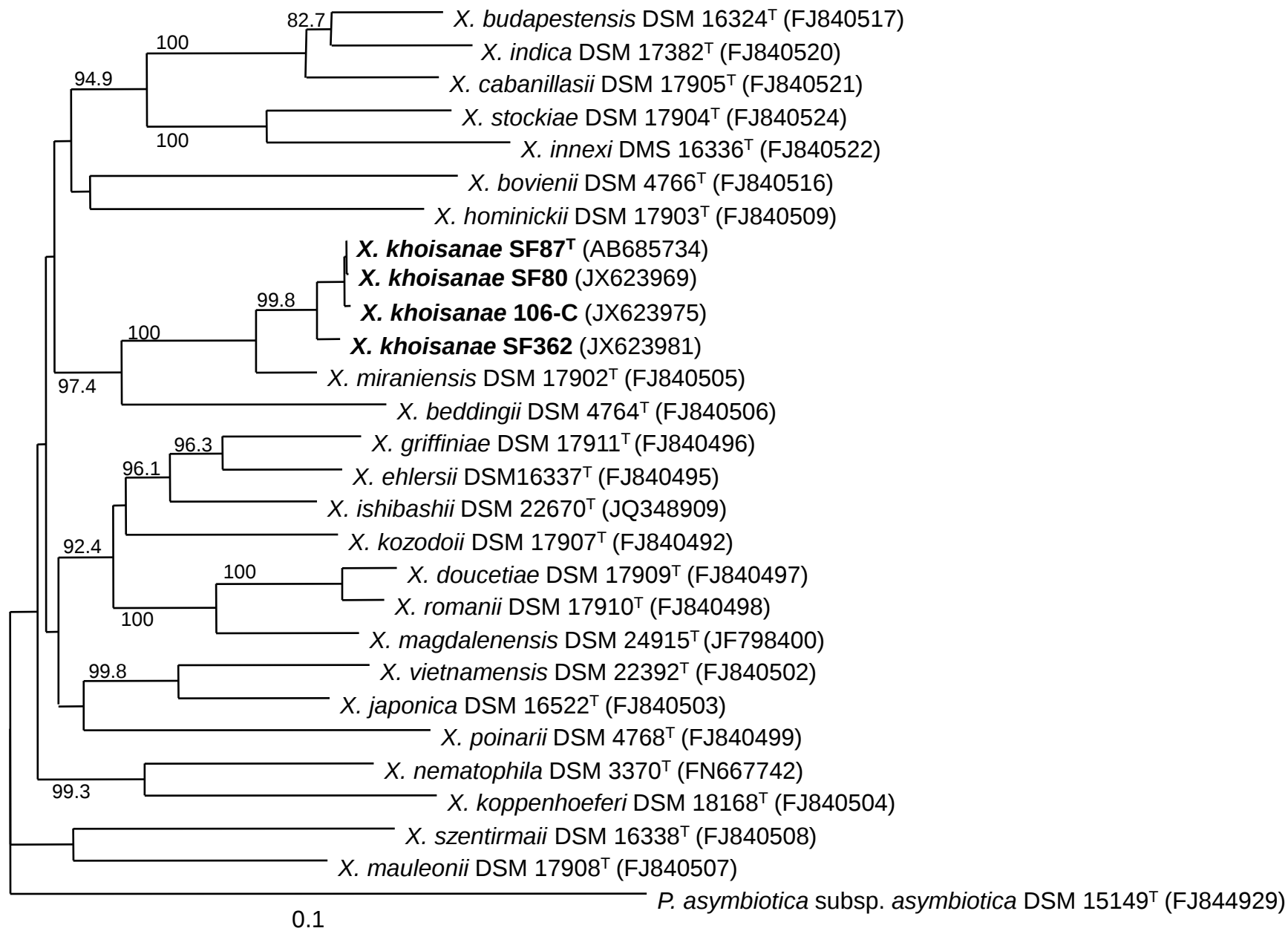


Fig 5S

gyrB

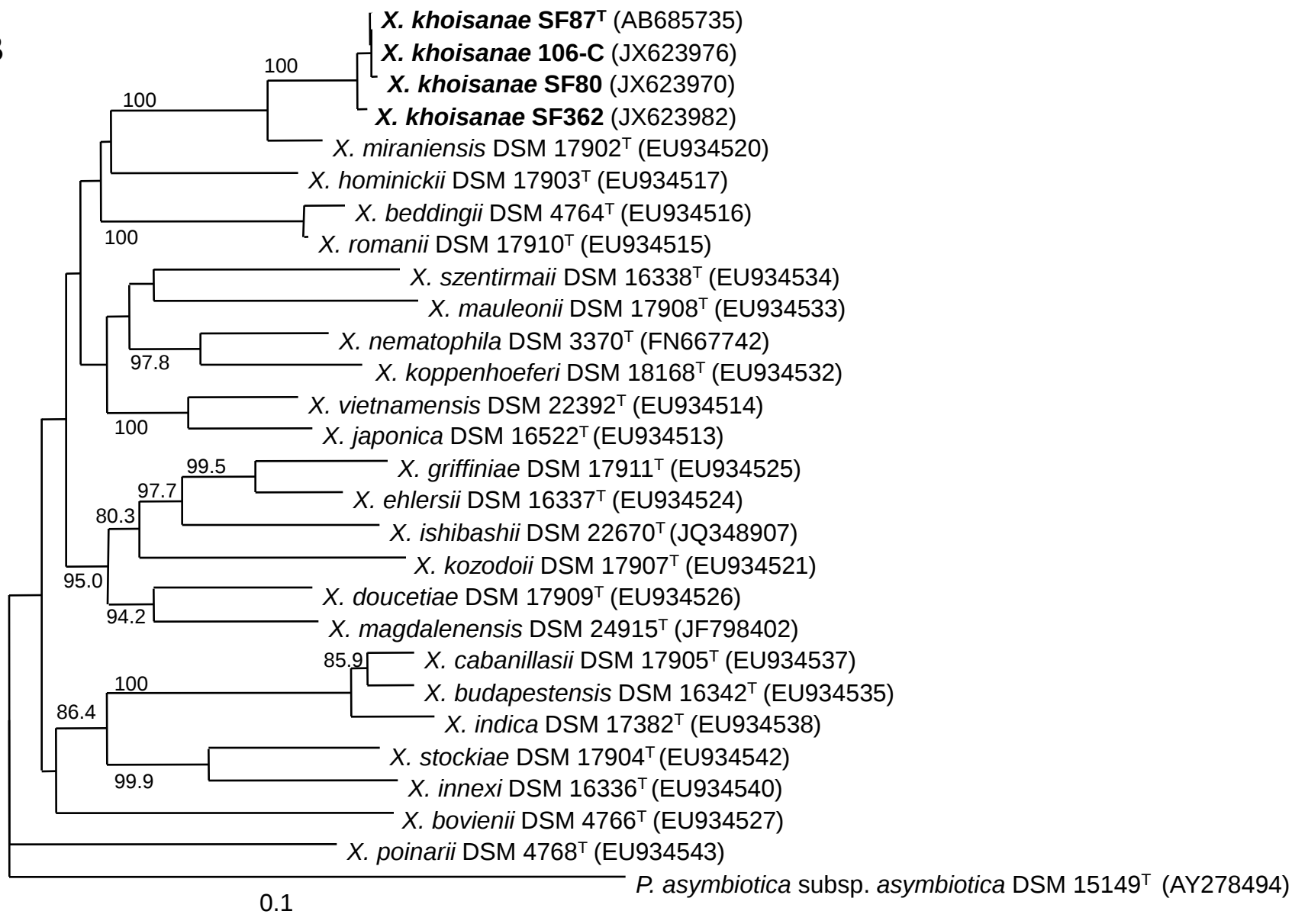


Fig 6S

infB

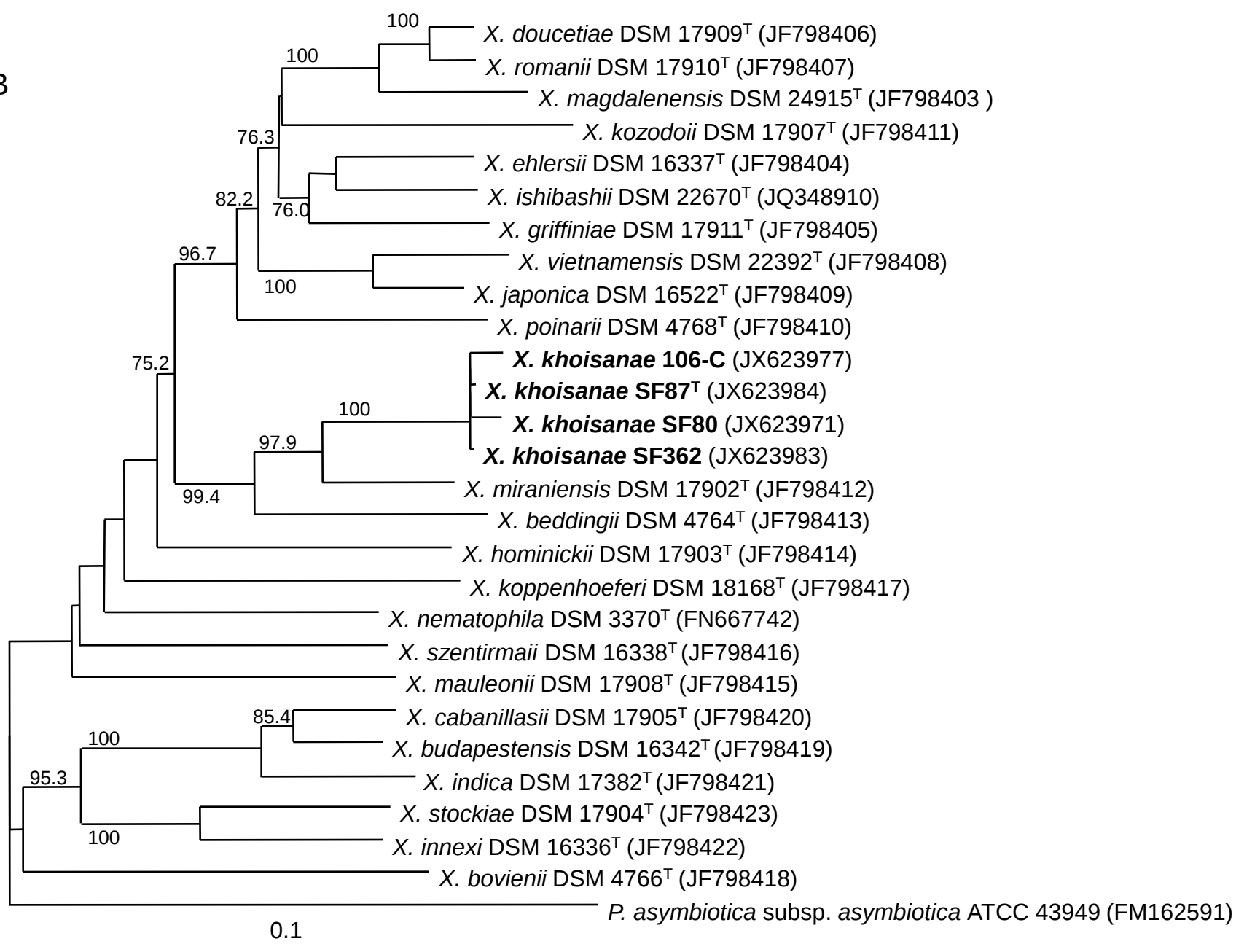


Fig 7S

Fig. 1S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on 16S rRNA gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 2S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on the 16S rRNA gene sequences. The tree was constructed by the maximum-likelihood method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 3S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on *recA* gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 4S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on *dnaN* gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 5S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on *gltX* gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 6S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on *gyrB* gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.

Fig. 7S. Phylogenetic relationship of strains SF87^T, SF80, 106-C and SF362 to known *Xenorhabdus* spp. based on *infB* gene sequences. The tree was constructed by the neighbour-joining method. *Photorhabdus asymbiotica* subsp. *asymbiotica* was used as an outgroup species. Bootstrap percentages above 70% are given at branching points. The scale bar indicates 10% sequence divergence.