

1 SUPPLEMENTARY FIGURE LEGENDS

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3 **Supplementary Figure S1.** Map of sampling sites and photo of one of the Kentland
4 Farm rain sampling sites in Blacksburg, VA, USA.

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6 **Supplementary Figure S2.** Rarefaction curve plotting the cumulative species richness
7 against the cumulative number of sequences obtained in precipitation samples collected
8 in Virginia, USA. The species richness was obtained by affiliating each 16S rDNA
9 sequence to an operational taxonomic unit (OTU) using the open-source bioinformatics
10 pipeline for performing microbiome analysis QIIME (Caporaso et al 2010). The curve
11 was obtained plotting the cumulative number of OTUs against the cumulative number of
12 sequences.

13

14 **Supplementary Figure S3.** Evolutionary relationships between the culturable strains
15 isolated from precipitation and other members of the *Pseudomonadaceae* family based
16 on the alignment of partial 16S rDNA sequences. A maximum likelihood tree was built
17 from the 931pb-long sequences of 229 strains isolated in this study (labelled VT#;
18 strains that were confirmed to be Ice⁺ in repeated tests are labelled in bold), 150 type
19 strains downloaded from the Ribosomal Database Project (RDP) (Cole et al 2014) and 19
20 strains from NCBI, using the GTR model and 100 bootstrap replicates. Gaps were
21 considered as missing data and were partially deleted with a site coverage cut-off of
22 95%. The strain *Xanthomonas axonopodis* LMG 538^T was used as a root. Only bootstrap
23 values over 50% were included and are symbolized by black dots. Clades and leaves
24 associated with strains that were Ice⁺ in standardized re-tests at -8°C are labelled in bold
25 and are underlined, those active at -10°C or -12°C are labelled in bold only. RDP names

26 are composed of the species name, the strain code and the accession number in the
27 public database NCBI. Each collapsed clade is represented by a type strain.

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29 **Supplementary Figure S4.** Evolutionary relationships between the culturable strains
30 isolated from precipitation and other members of the *Enterobacteriaceae* family based
31 on the alignment of partial 16S rDNA sequences. The phylogenetic tree was built from
32 212 strains isolated in this study (labelled VT#; strains that were confirmed to be Ice⁺ in
33 repeated tests are labelled in bold) and 241 type strains downloaded from the
34 Ribosomal Database Project (RDP) (Cole et al 2014). The strain *Pseudomonas aeruginosa*
35 DSM 50071 was used as a root. See Supplementary Figure S3 for details about tree
36 construction and labels.

37

38 **Supplementary Figure S5.** Evolutionary relationships between the culturable strains
39 isolated from precipitation and other members of the *Xanthomonadaceae* family based
40 on the alignment of partial 16S rDNA sequences. The phylogenetic tree was built from
41 30 strains isolated in this study (labelled VT#, strains that were confirmed to be Ice⁺ in
42 repeated tests are labelled in bold) and 132 type strains downloaded from the
43 Ribosomal Database Project (RDP) (Cole et al 2014). The strain *Ralstonia solanacearum*
44 LMG 2299 was used as a root. See Supplementary Figure S3 for details about tree
45 construction and labels.

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47 **Supplementary Figure S6.** Evolutionary relationships between the culturable INA
48 strains *Lysinibacillus sp.* VT1065 and VT1066 isolated from precipitation and other
49 members of the Bacillaceae family based on the alignment of 16S rDNA partial
50 sequences. The phylogenetic tree was built from 47 strains isolated in this study

51 (labelled VT#; strains that were confirmed to be Ice⁺ in repeated tests are labelled in
52 bold) and 353 type strains downloaded from the Ribosomal Database Project (RDP)
53 (Cole *et al* 2014). The strain *Lactobacillus acidophilus* BCRC10695 was used as a root.
54 See Supplementary Figure S3 for details about tree construction and labels.

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56 **References**

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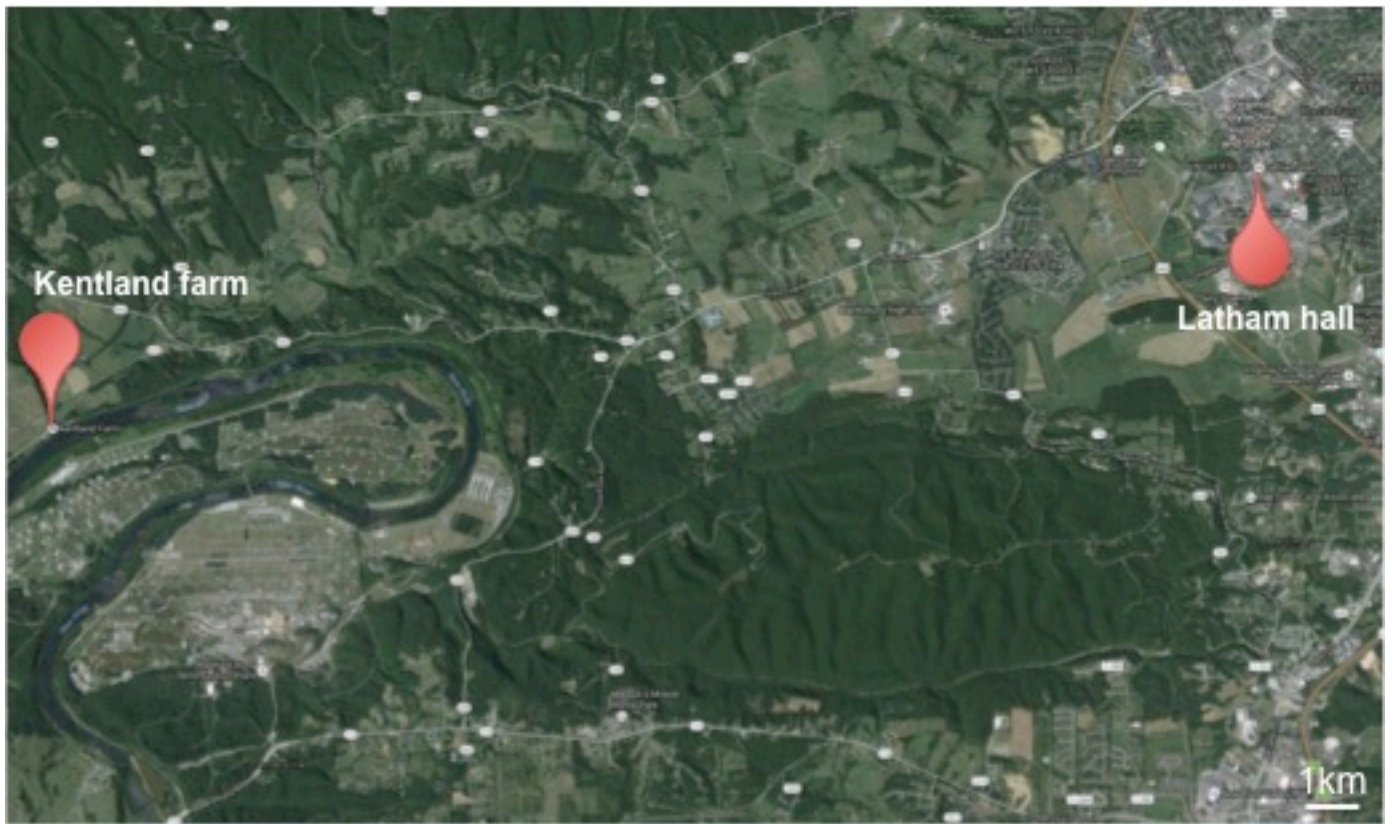


Figure S1

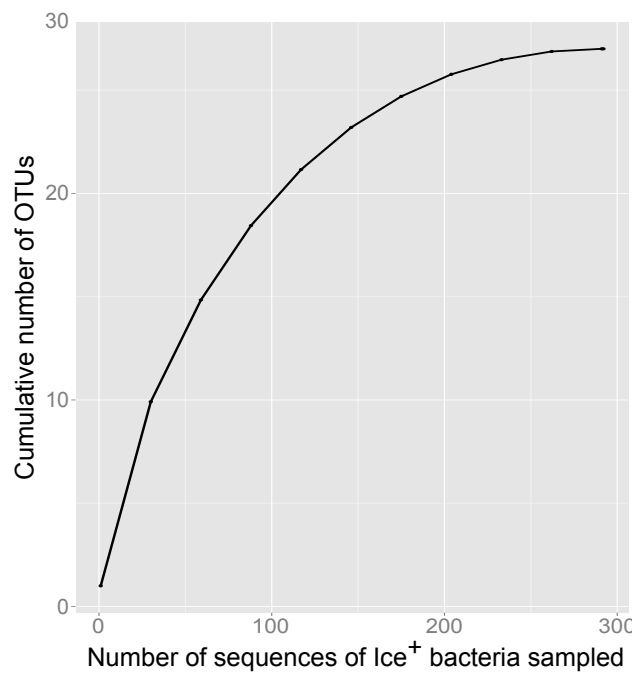


Figure S2

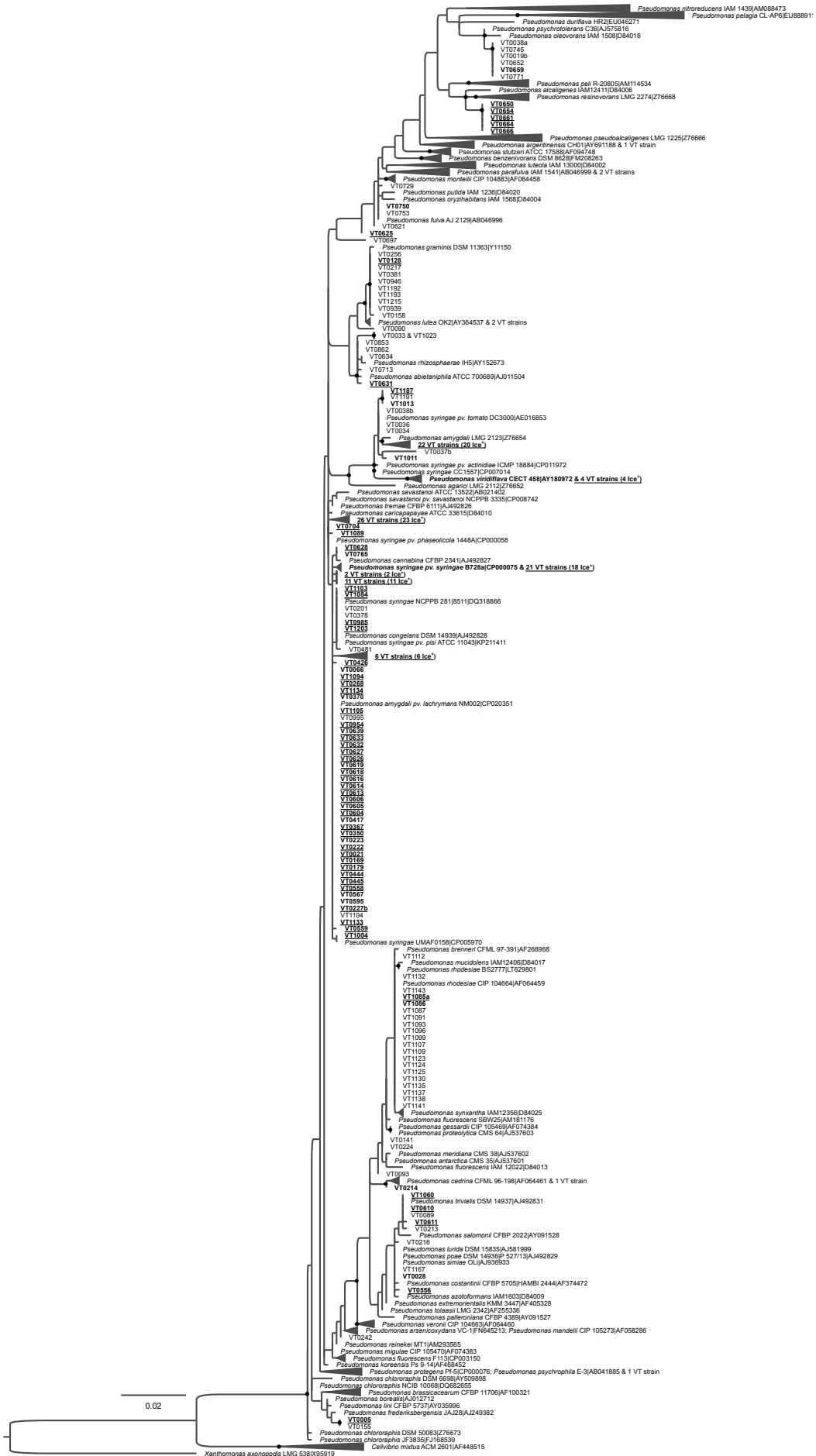


Figure S3

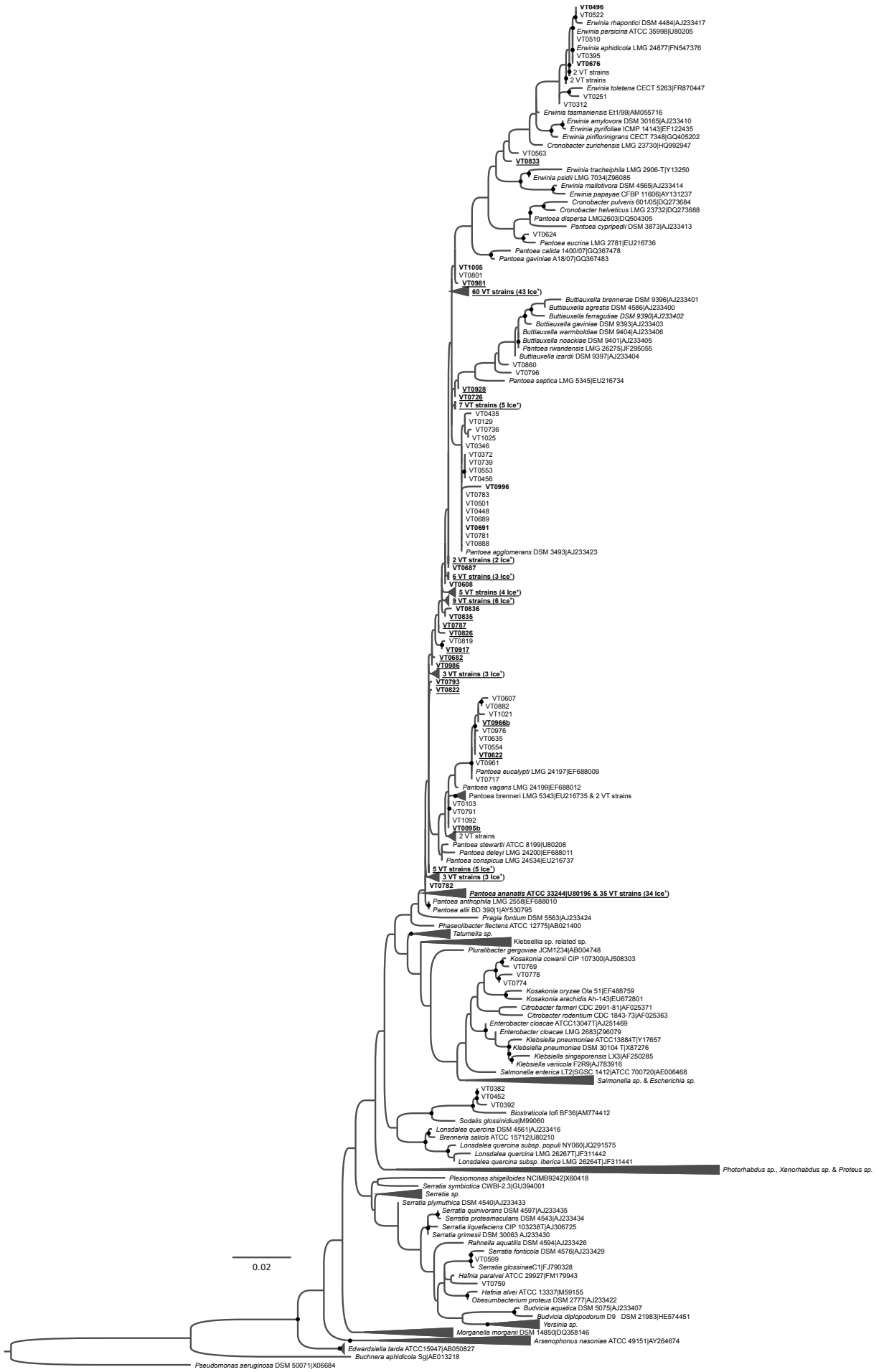


Figure S4

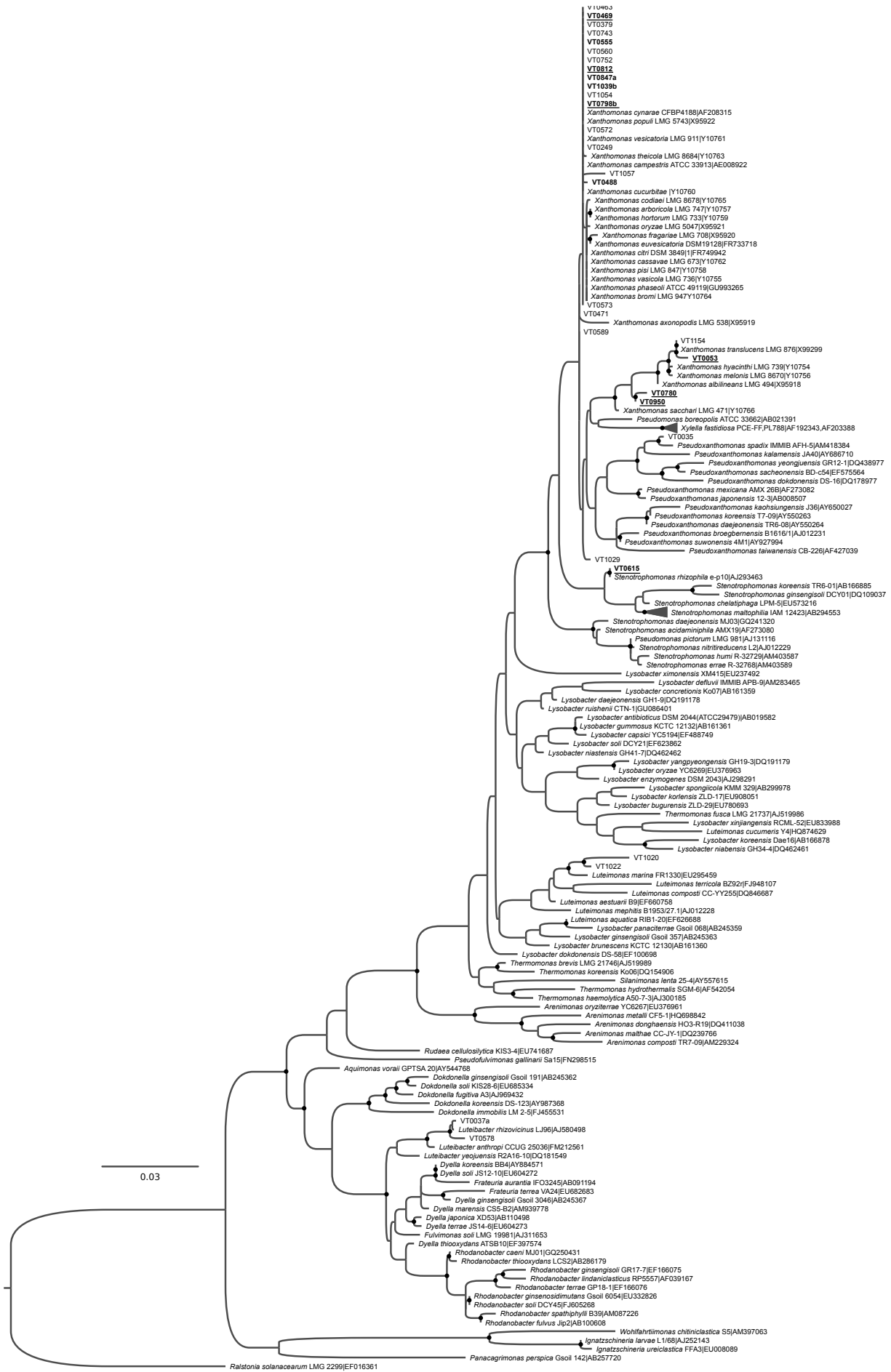


Figure S5

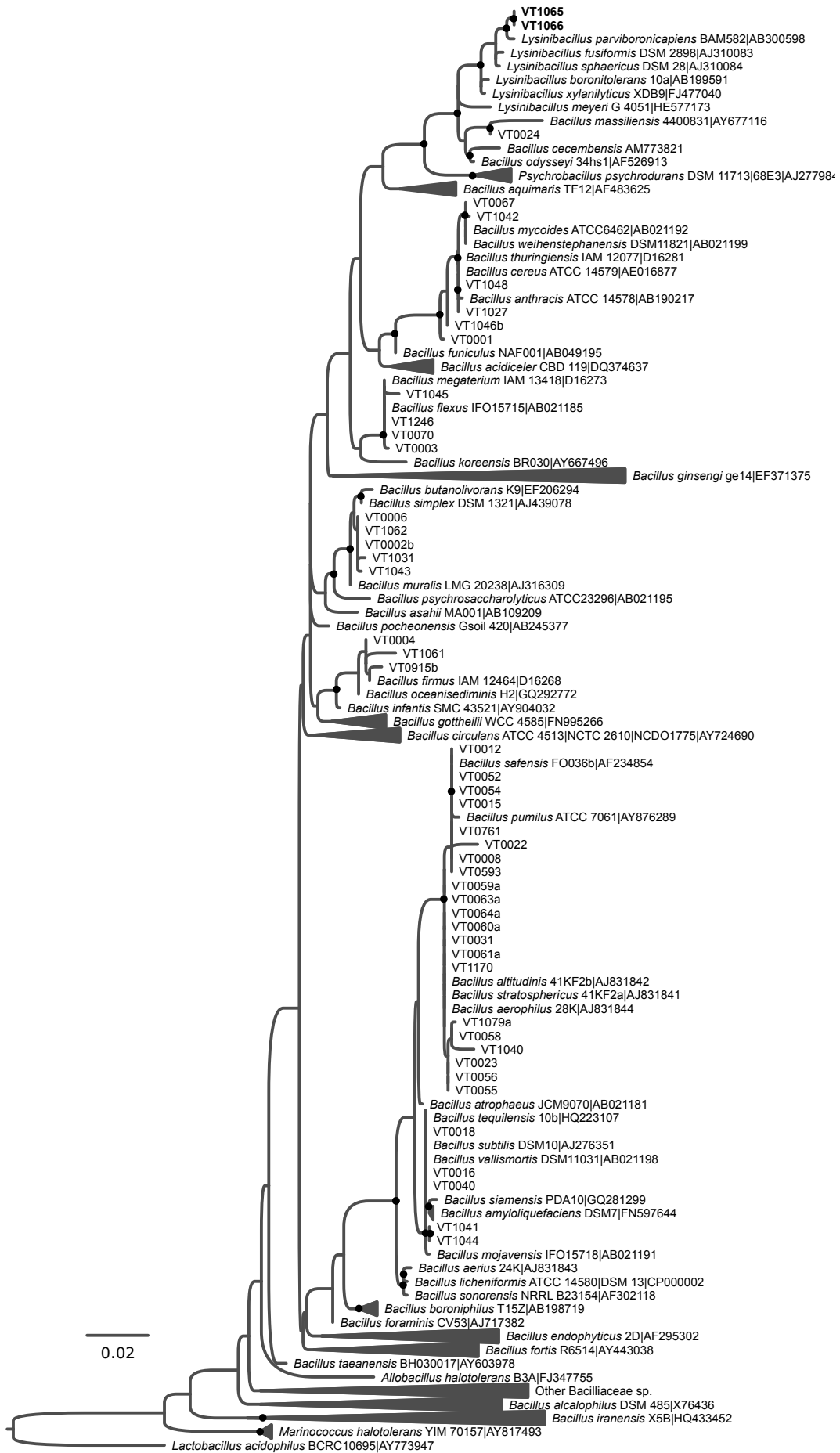


Figure S6