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Fig. S2. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences showing the position of strain N1286^T. Asterisks indicate branches of the tree that were also found with the maximum-likelihood and maximum-parsimony tree-making algorithms; L and M indicate branches found using the maximum-likelihood and maximum-parsimony methods, respectively. The numbers at the nodes indicate the levels of bootstrap support based on a neighbour-joining analysis of 1000 re-sampled datasets; only values above 50% are given. The scale bar indicates 10 substitutions per nucleotide position. ^T, type strain.

