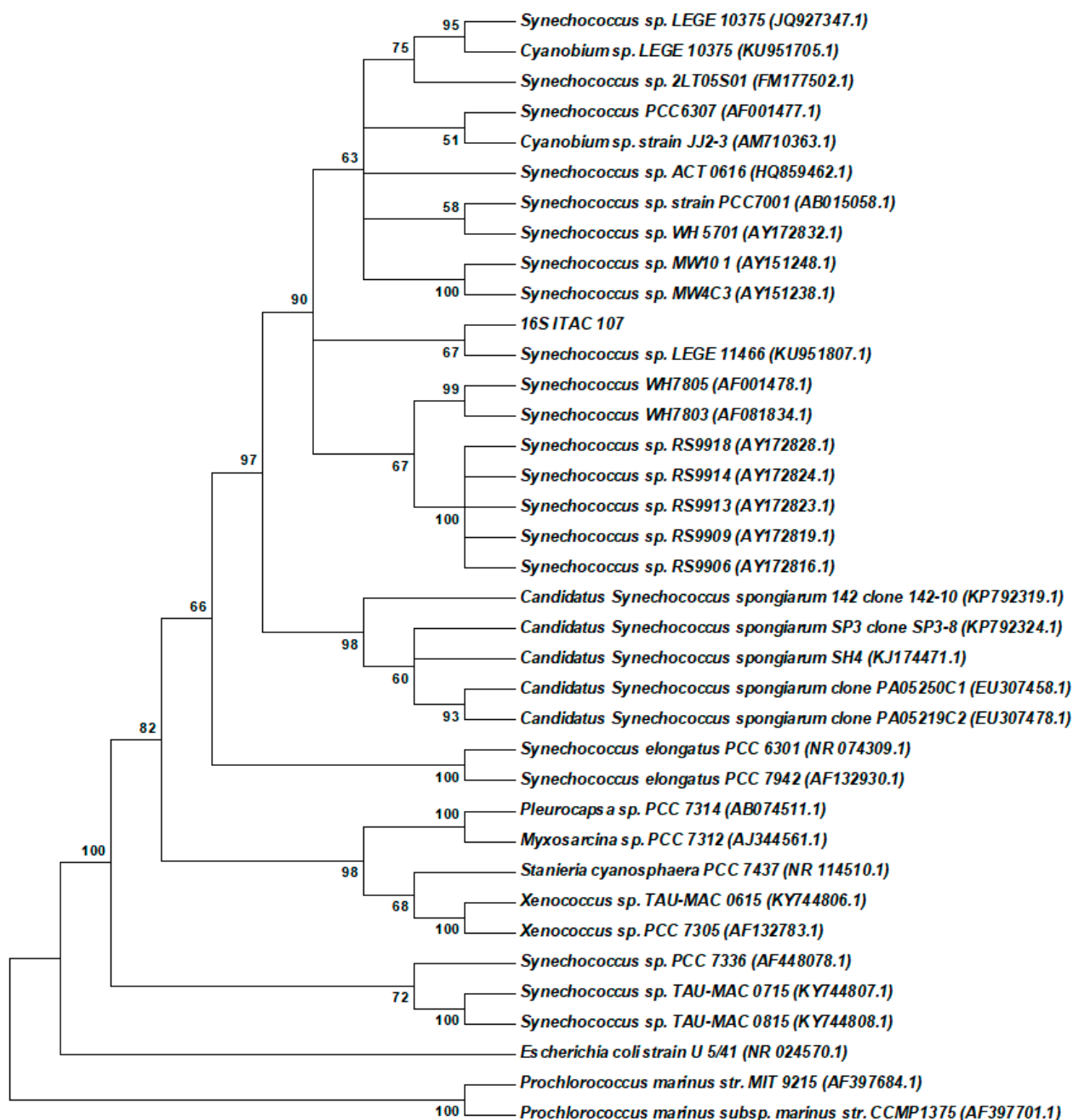


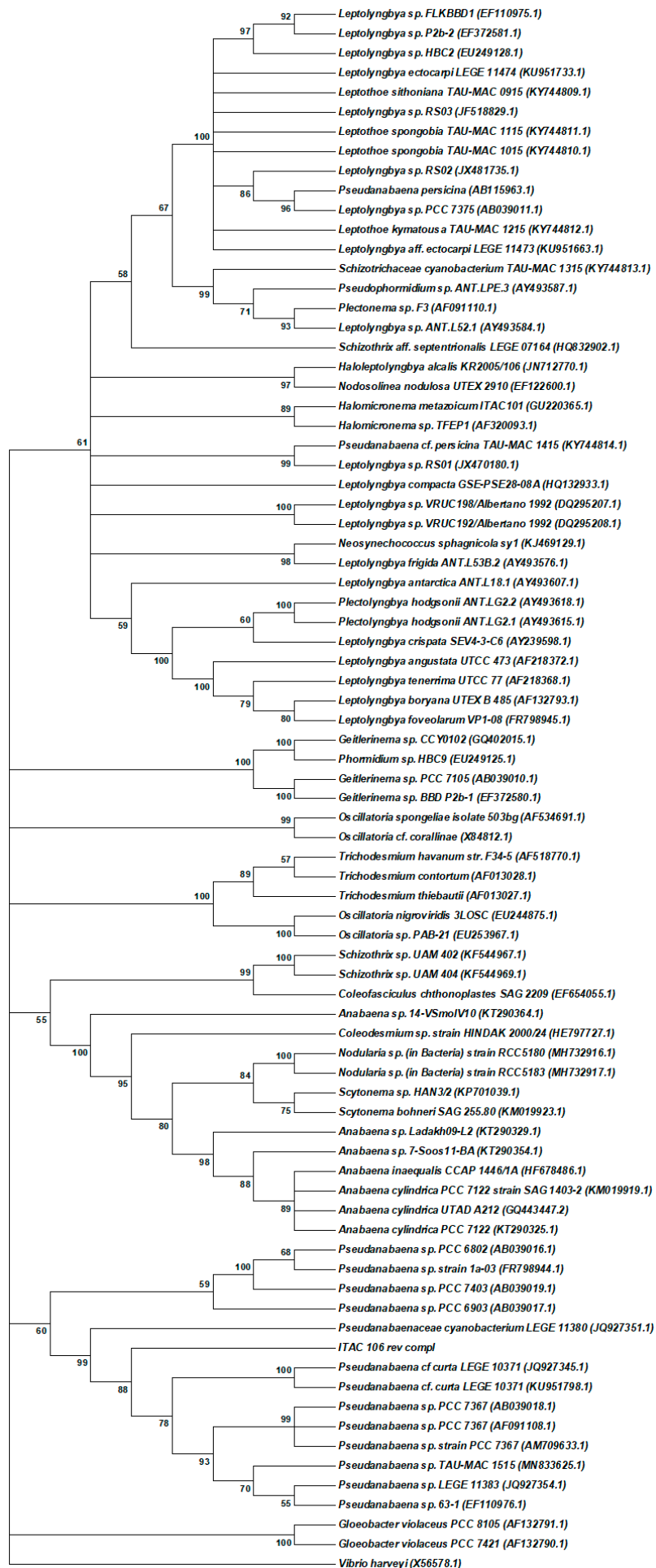
**Supplemental Figure S1. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_108).**

The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 1.54126254 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 51 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 555 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.

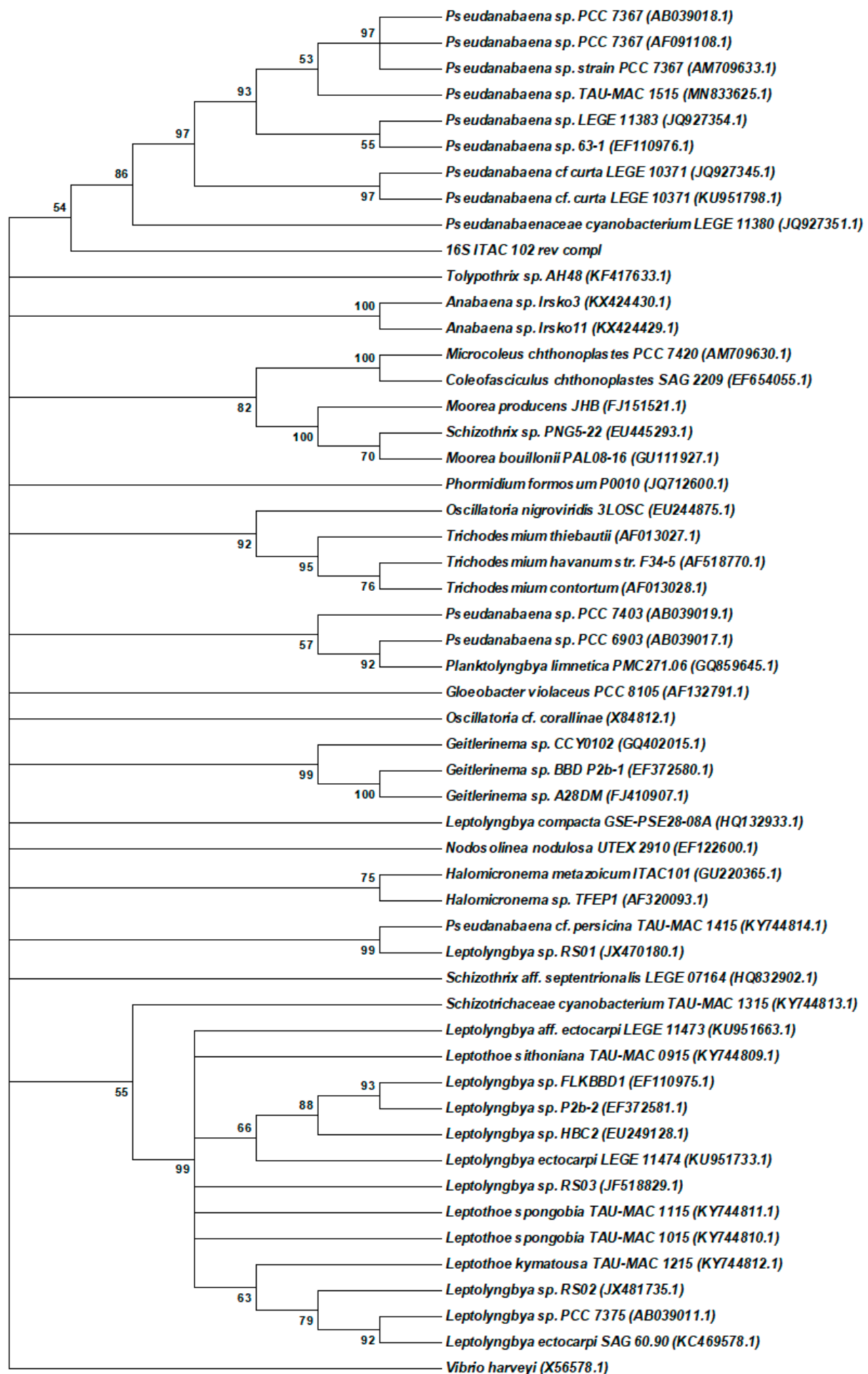


**Supplemental Figure S2. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_107).**

The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 1.65902809 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 37 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 504 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.

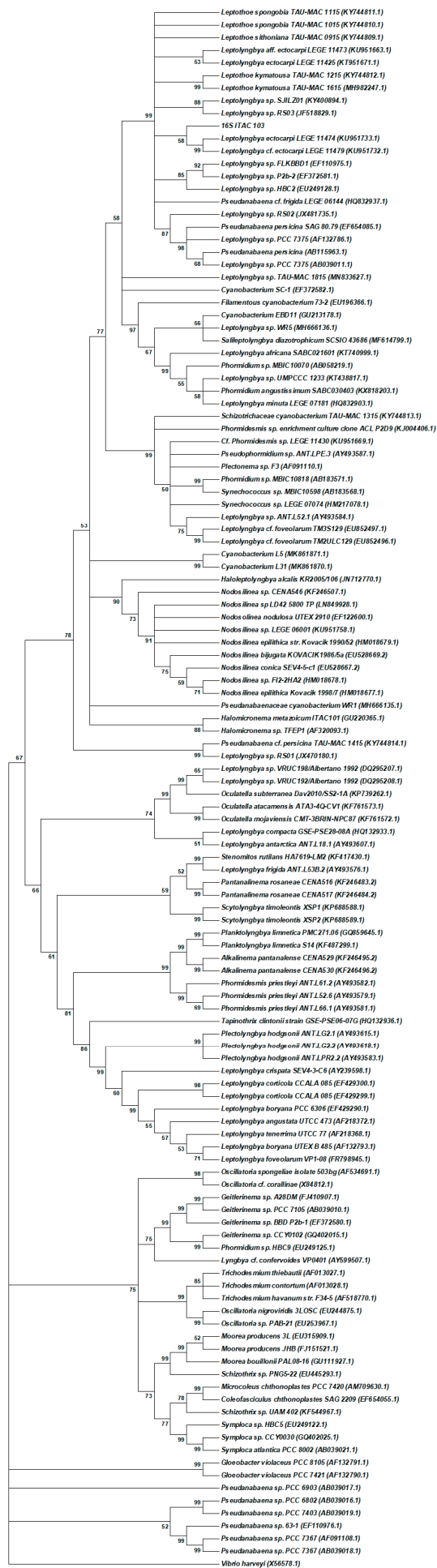


**Supplemental Figure S3. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_106).** The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 1.74806519 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 80 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 722 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.



**Supplemental Figure S4. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_102).**

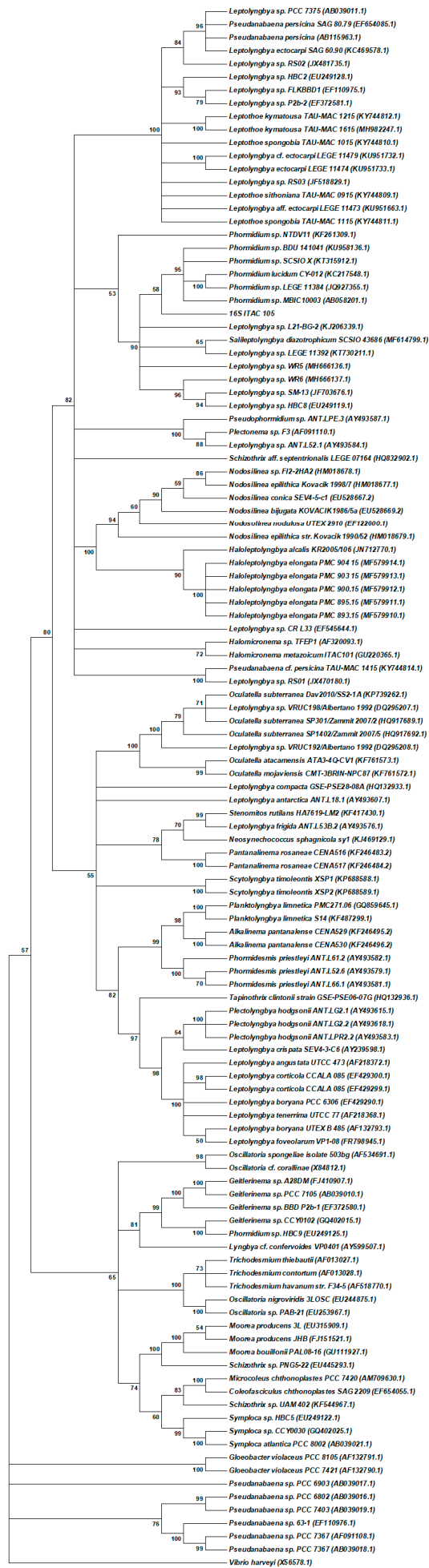
The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 1.24198152 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 53 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 571 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.



**Supplemental Figure S5. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_103).**

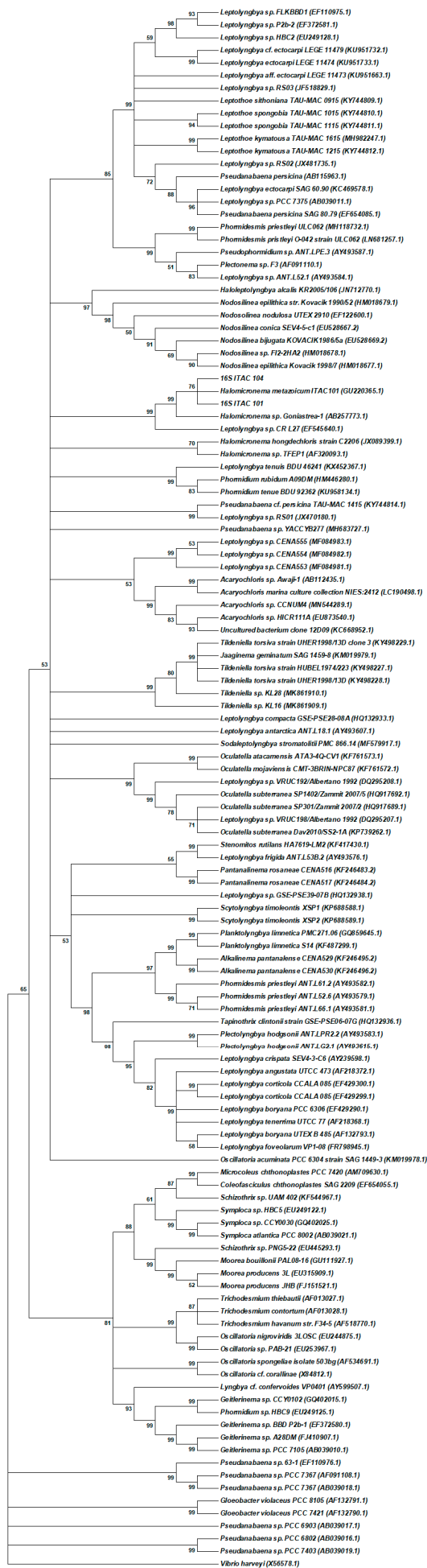
The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 2.35276460 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 124 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 846 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.





**Supplemental Figure S6. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_105).**

The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 2.25649473 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 119 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 793 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.



**Supplemental Figure S6. Molecular phylogenetic analysis by Neighbor-Joining method (Ref. ITAC\_101 and ITAC\_104).**

The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 2.28978951 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor 1969) and are in the units of the number of base substitutions per site. The analysis involved 124 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 847 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). Cutoff value for condensed tree = 50%.

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- Jukes TH, Cantor CR (1969) Evolution of protein molecules. In: Munro HN (ed) *Mammalian Protein Metabolism*. Academic Press, New York, pp. 21-132.
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