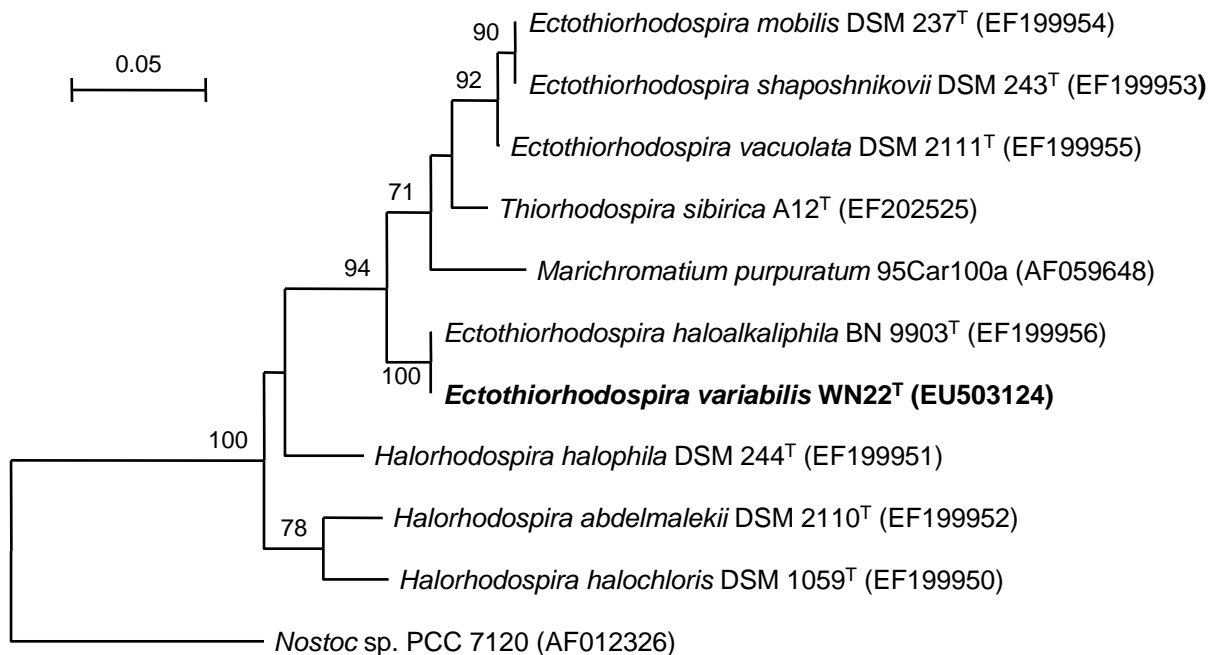**Supplementary Fig. S1.** Phylogenetic position of strain WN22^T among members of the *Ectothiorhodospiraceae* based on conceptual translations of *cbbL*. The tree was generated by the maximum-likelihood method. Bar, 5 amino acid substitutions per 100 positions. Numbers indicate percentages of bootstrap sampling, derived from 1000 replications. Unrooted phylogenetic trees were constructed using algorithms implemented in the TREECONW software package (http://bioc-www.uia.ac.be/u/yvdp/treeconw.html)

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Supplementary Fig. S2. Phylogenetic position of strain WN22^T among members of the *Ectothiorhodospiraceae* based on deduced amino acid sequences of *nifH* genes. The tree was constructed by the neighbour-joining algorithm with *Nostoc* sp. PCC 7120 as the outgroup. Bar, 5 amino acid substitutions per 100 positions. Numbers indicate percentages of bootstrap sampling, derived from 1000 replications.

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