



**Figure S1.** 05-1015-2N strain identification and phylogenetic analysis. Genomic DNA from strain 05-1015-2N encoding the 16S rRNA was amplified by PCR using the universal primers FC27 (5'-AGAGTTTGATCCTGGCTCAG-3') and RC1492 (5'-TACGGCTACCTTGTTACGACTT-3'), cloned into pGEM (Promega, Madison, WI), and sequenced with T7 and SP6 primers. Phylogenetic analysis based on the 16S rRNA sequence was conducted with GENEIOUS pro version 4.8.4 available from <http://www.geneious.com>. The bootstrap consensus tree shown was inferred from 1000 replicates using the Neighbor-Joining method, and was taken to represent the evolutionary history of the taxa analyzed. The location of 05-1015-2N (named *Streptomyces kaviengensis*) is indicated by the arrow.