Figure S1

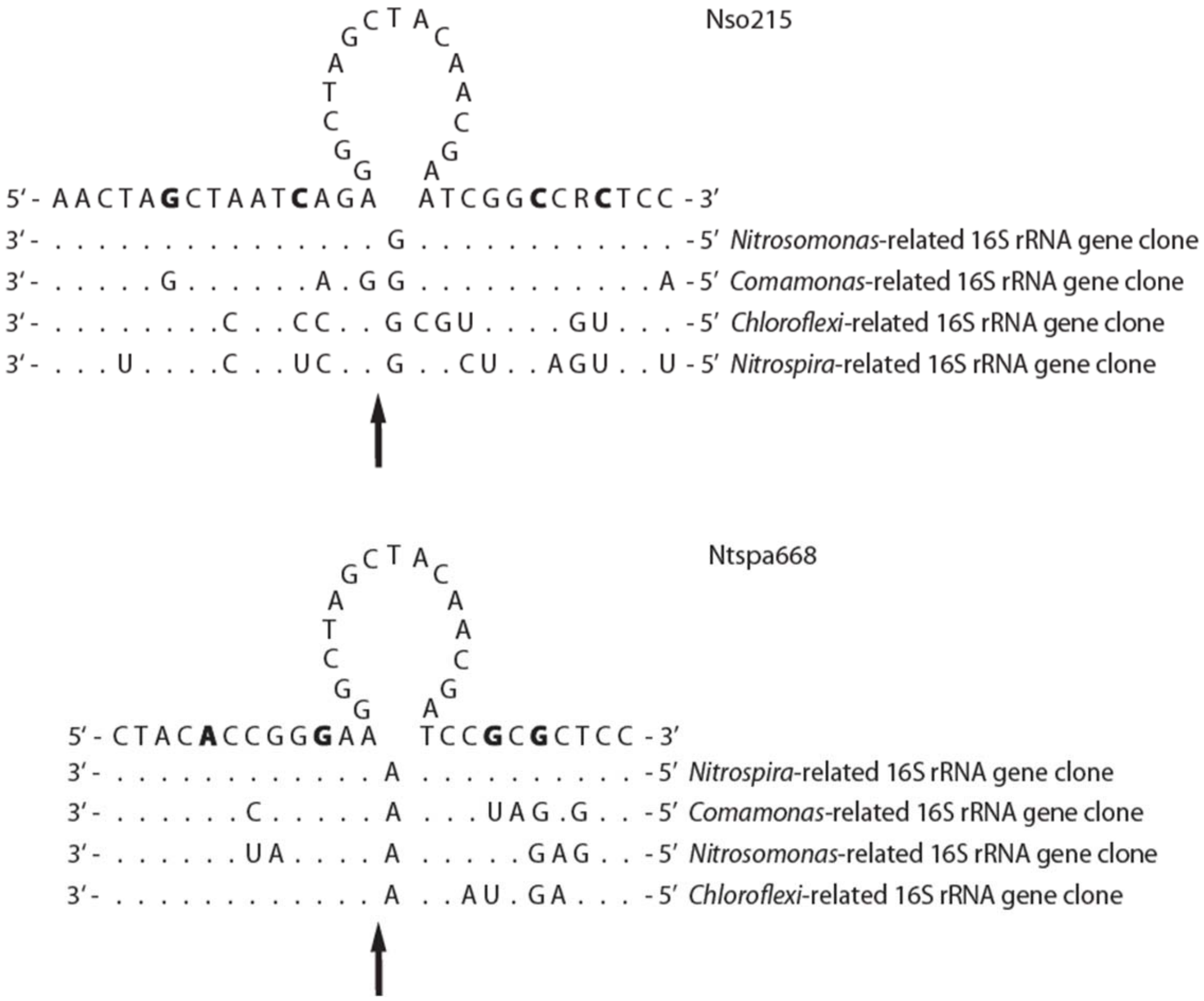

Fig. S1. Sequence alignments of the LNAzymes Nso215 and Ntspa668 to the respective binding regions on the four 16S rRNA genes, which were used in artificial mixtures to evaluate the LNAzymes and the cleavage protocol (see also Table 1 and Fig. 3 in the main text). LNA residues are printed in boldface. Base mismatches between the substrate-binding arms of the LNAzymes and the 16S rRNA sequences are indicated by capital letters, whereas full matches (complementary bases) are indicated by dots. Arrows indicate the cleavage sites.