



FIG S4 Molecular phylogeny of Aph(3') proteins. Roman numbers indicate the type of enzyme. The list of putative homologs of Aph(3')-VI was determined with blastp using Aph(3')-VI of *A. guillouiae* NIPH 991 (GenBank accession ID, ENV16316) against all non-redundant GenBank CDS translations database with e-values lower than 10^{-120} and manual curation to avoid redundancy. GenBank accession ID of each protein is indicated in brackets. The phylogeny of the Aph(3') proteins was explored by construction of multiple sequence alignments with muscle v3.7 (39). The unrooted phylogenetic tree was reconstructed using the maximum likelihood method implemented in the PhyML program (v3.0 aLRT) with the WAG matrix and a gamma correction for variable evolutionary rates (40). We performed 100 bootstrap experiments on the sequences to assess the robustness of the topology. Bold, whole genome sequenced strains; *, previously designated Aph(3')-VIII (41).