



**FIG S5** Genomic environment of *aphA6*. Left : Black, *Acinetobacter* spp.; grey, *Enterobacteriaceae*, *P. aeruginosa*, and *Alcaligenes faecalis*; bold, strains for which whole genome was sequenced; ND, not determined. Right : Arrows indicate open reading frames and sens of transcription. Green arrow, *aphA6*; other colored arrows, IS elements; open arrows, ORFs; Δ, partially deleted.