



Supplementary Figure S1: Confirmation of mRNA absence in the insertional inactivation mutants and analysis of *prsQ₂* transcription levels during complementation.

a) PCR amplification of cDNA from the silver-resistant mutant NA4S (+), the insertional inactivation mutants of CmetNA4v1_40157 (1), CmetNA4v1_570182 (2), CmetNA4v1_570173 (3), CmetNA4v1_400150 (4), *prsQ₂* (CmetNA4v1_570171) (5) and *prsQ₁* (CmetNA4v1_10101) (6), the complementation mutants of NA4S Δ *prsQ₁* (7) and NA4S Δ *prsQ₂* (8), and a negative control (-). b) Expression level of *prsQ₂* obtained by RT-qPCR. Expression levels are normalized to the *uvrD* housekeeping gene and fold change ratios were determined for the silver-resistant mutant NA4S, the insertional inactivation mutant NA4S Δ *prsQ₂* (Δ *prsQ₂*), NA4S Δ *prsQ₂* complemented with plasmid-based *prsQ₂* (Δ *prsQ₂* pBBR-*prsQ₂*) and the NA4S Δ *prsQ₂* carrying the empty vector (Δ *prsQ₂* pBBR1MCS2) compared to the parental NA4 strain.