**Figure S1.** Derivative melt curves (a), normalized melt curves (b) and difference plot (c) generated by HRM analysis of the amplification products obtained for *S. aureus* DSM 20231^T (red), *S. argenteus* DSM 28299^T (green) and *S. schweitzeri* DSM 28300^T (blue) tested in triplicate within an intra-assay reproducibility test.

Table S1. Mean melting temperatures (Tm) ± standard deviation (SD), and corresponding coefficients of variation (CV%), for *S. argenteus* DSM 28299[T], *S. aureus* DSM 20231[T] and *S. schweitzeri* DSM 28300[T] tested in triplicate within an intra-assay reproducibility test.

Reference strains	Tm ± SD	CV%
S. argenteus DSM 28299[T]	76.19 ± 0.02	0.03
S. aureus DSM 20231[T]	77.48 ± 0.02	0.02
S. schweitzeri DSM 28300[T]	77.31 ± 0.05	0.06
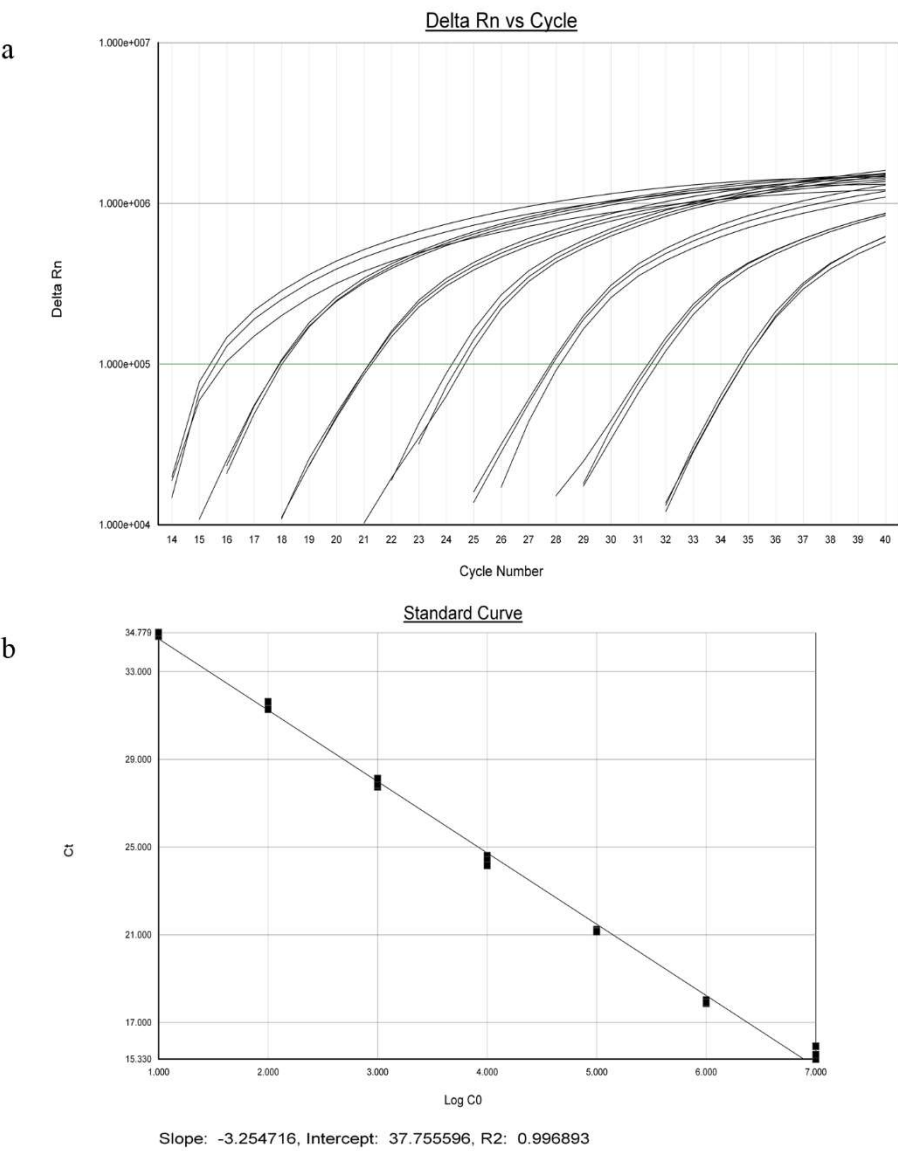
Figure S2. Amplification curves (a) and standard curve (b) of serial decimal dilutions (10^7 to 10^1 GE) of *S. aureus* DSM 20231[T] DNA.
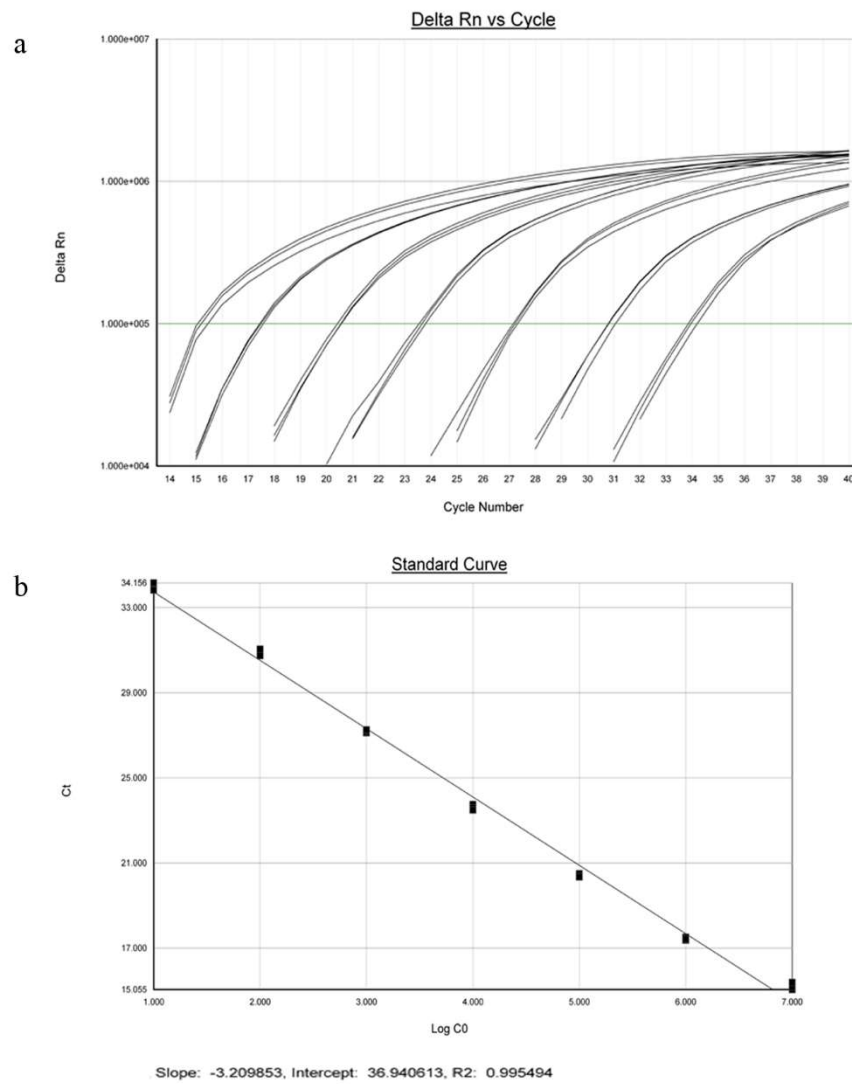
Figure S3. Amplification curves (a) and standard curve (b) of serial decimal dilutions (10^7 to 10^1 GE) of *S. argenteus* DSM 28299^T DNA.