Supplementary Fig. 5. Relative gene expression levels were analyzed by quantitative real time polymerase chain reaction. (A) SP6C4, (B) $\Delta P450\Delta lanM$, and (C) $\Delta P450\Delta tsrD$. Total RNA was isolated from mutant and wild-type (WT) SP6C4 strains using the TRIzol method, and cDNA libraries were constructed using the ReverTraAce-α-® cDNA Synthesis Kit with less than 1 μg of total RNA. Log2 fold change was calculated using the housekeeping gene *recA*. Bars represent standard error, and statistical analysis was performed using ANOVA and *post-hoc* test with Tukey's HSD.