Supplementary Fig. 5. Relative gene expression levels were analyzed by quantitative real time polymerase chain reaction. (A) SP6C4, (B) ΔP450ΔlanM, and (C) ΔP450ΔtsrD. 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.