

Supplementary Materials
Figures

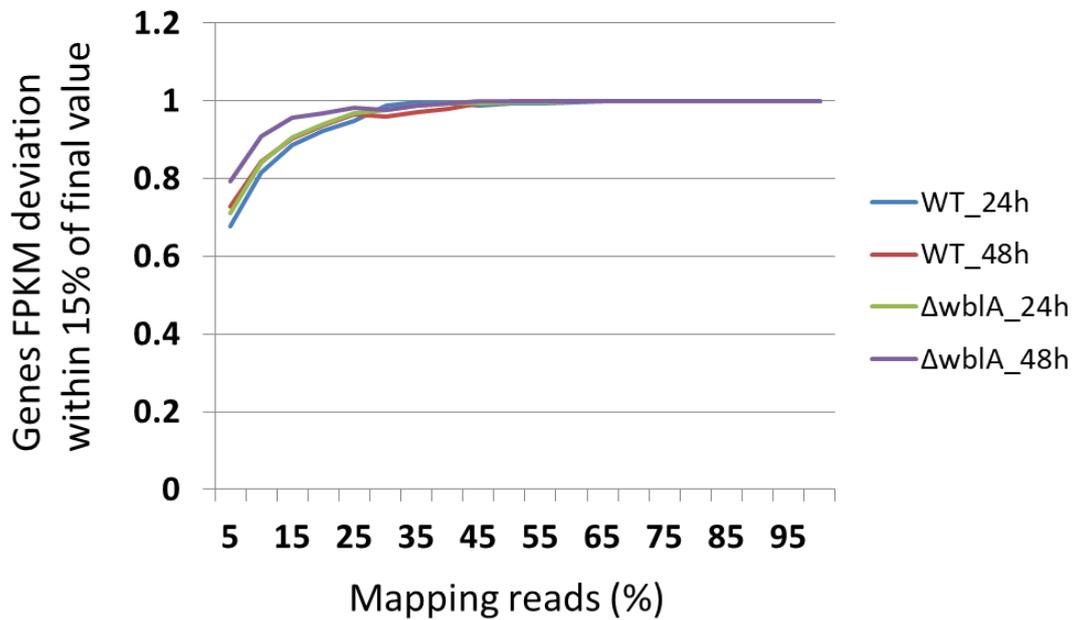


Figure S1. Saturation curves of sequencing data in RNA-seq. The X axis is the percentage of effective reads comparison (e.g., 80 means that 80% of the comparison sequencing data were randomly selected to calculate the expression level of this gene). The Y axis is the deviation ratio (error within 15%) between the expression level and the final value under the sampling condition (e.g., 0.8 means that 80% of the gene expression level has an error within 15%). The value is closer to 1, the expression level is more saturated. Each color line represents the saturation curve of gene expression at different expression levels in the eight samples.

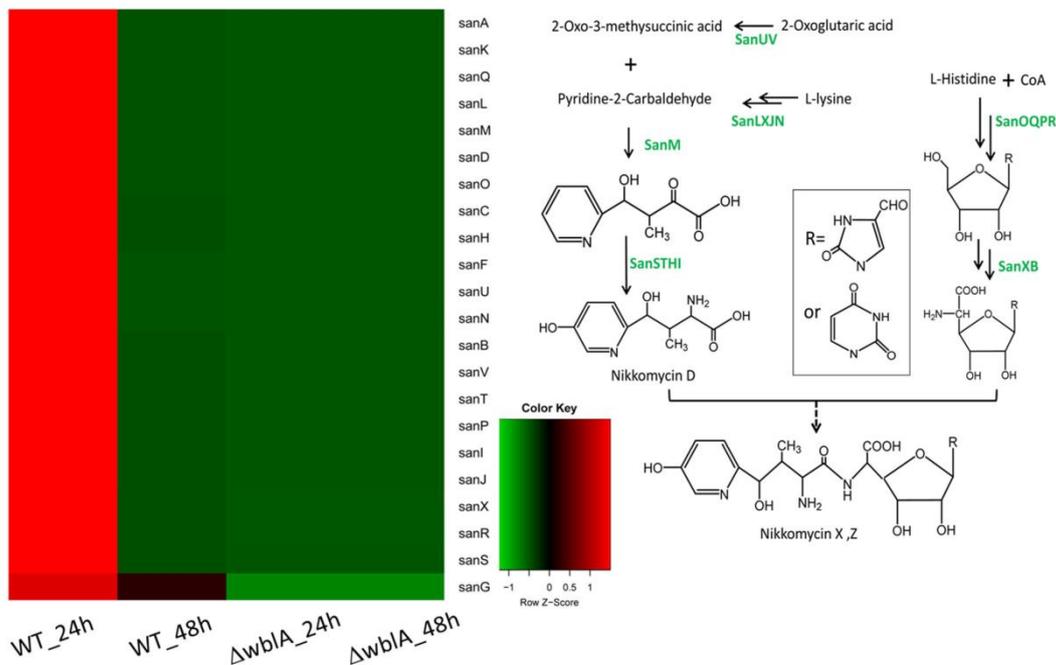


Figure S2. Differentially expressed genes involved in nikkomycin biosynthesis in both WT and $\Delta wblA$. (a) Heatmap represents the transcriptional level of nikkomycin biosynthetic genes in both WT and $\Delta wblA$. (b) Diagram of nikkomycin X and Z biosynthesis. Double arrows represent multiple reaction steps, and dashed arrows represent unknown paths.

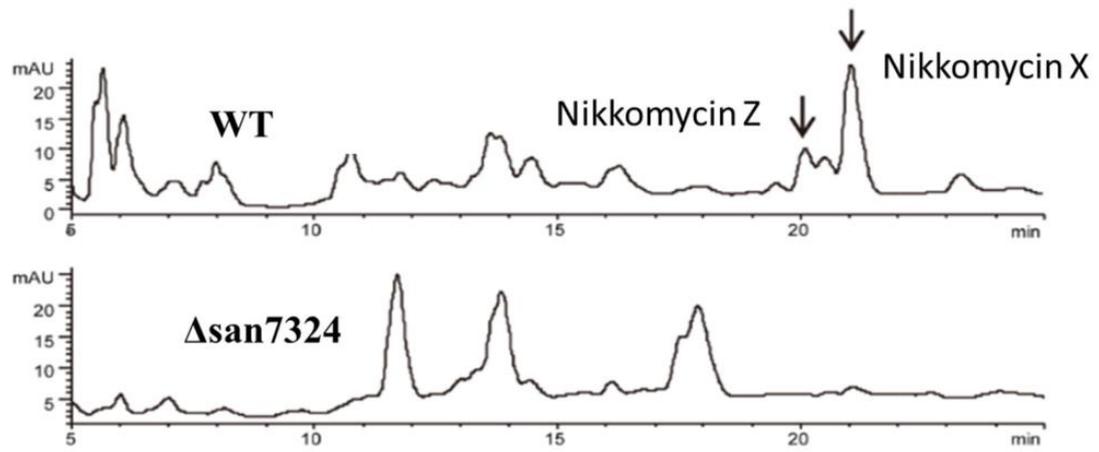


Figure S3. HPLC analysis of nikkomycin production in WT and Δ san7324. San7324 (Ctg1_705) encoding by *san7324* is a RsbR homolog.