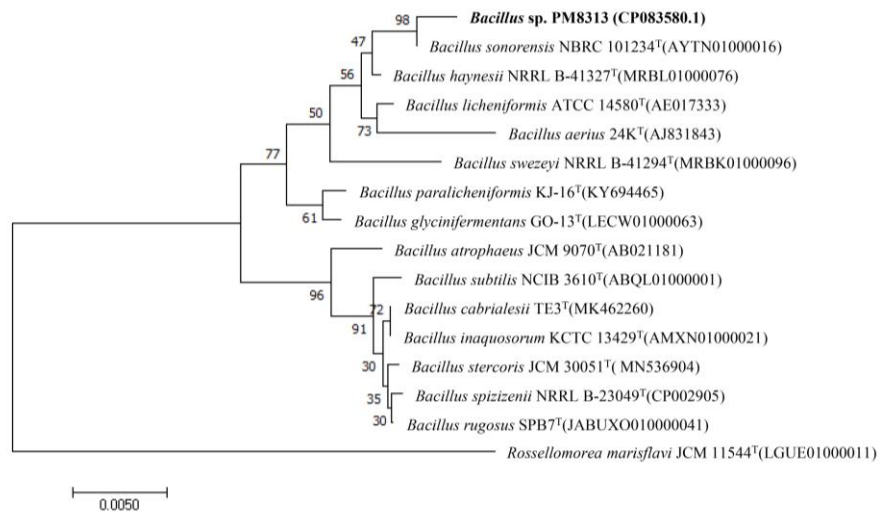


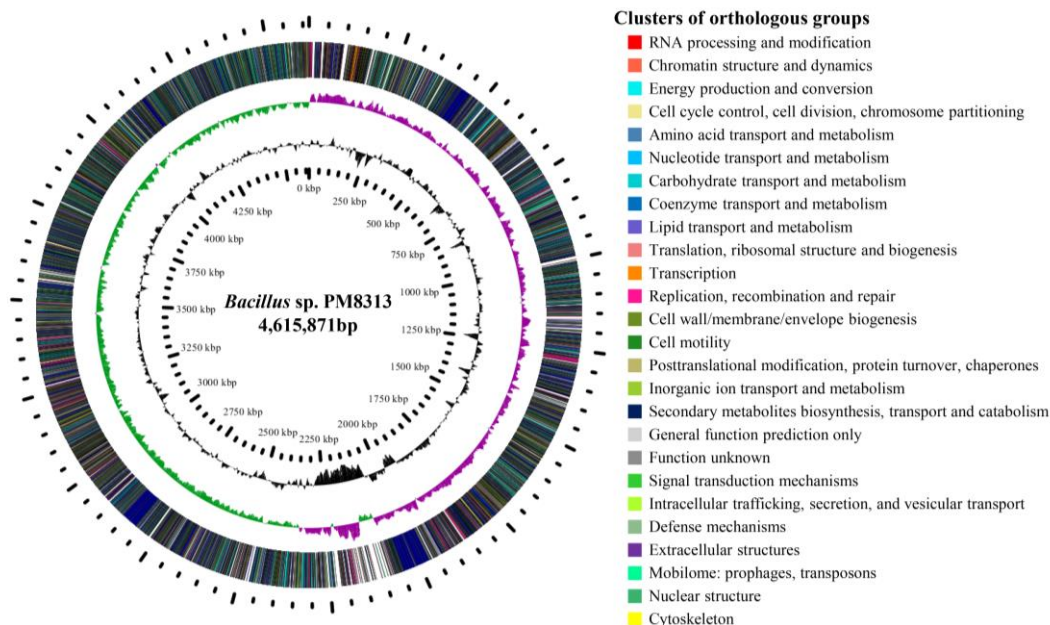
Supplementary Material

1.1 Supplementary Figures

A



B



Supplementary Figure 1. Phylogenetic tree and genome circular map of *Bacillus sp. PM8313*. (A) The phylogenetic tree was constructed by the neighbor joining method using MEGA 7 with 1,000 bootstrap repetitions, after which the 16S rRNA sequences were aligned by the Clustal W program. (B) Genome circular map was constructed using GView server. From the center to the outside: the number of bases, GC content, GC skew, location of all annotated ORFs (colored by COG categories).