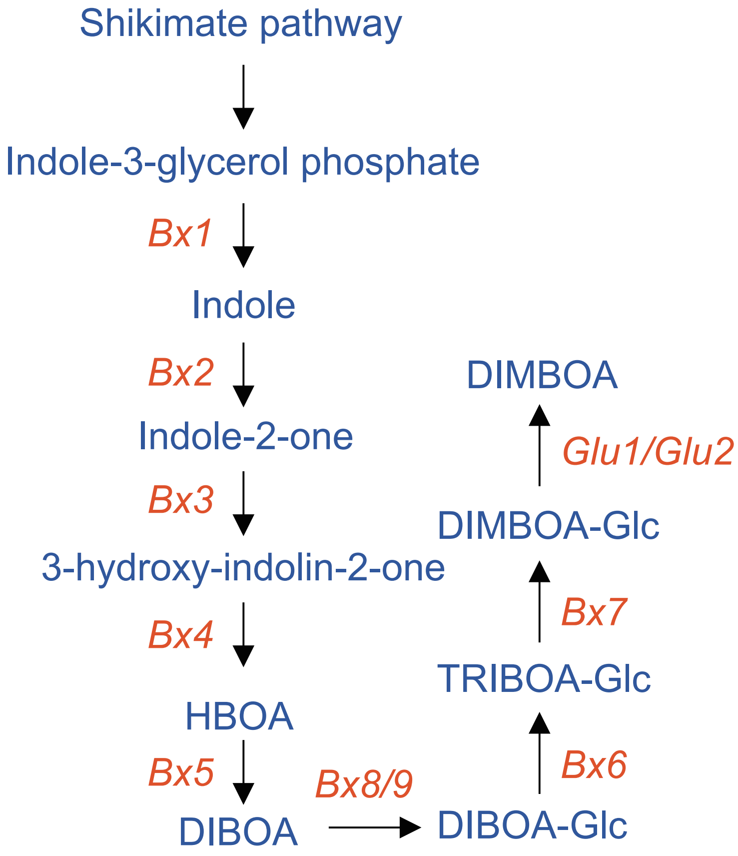
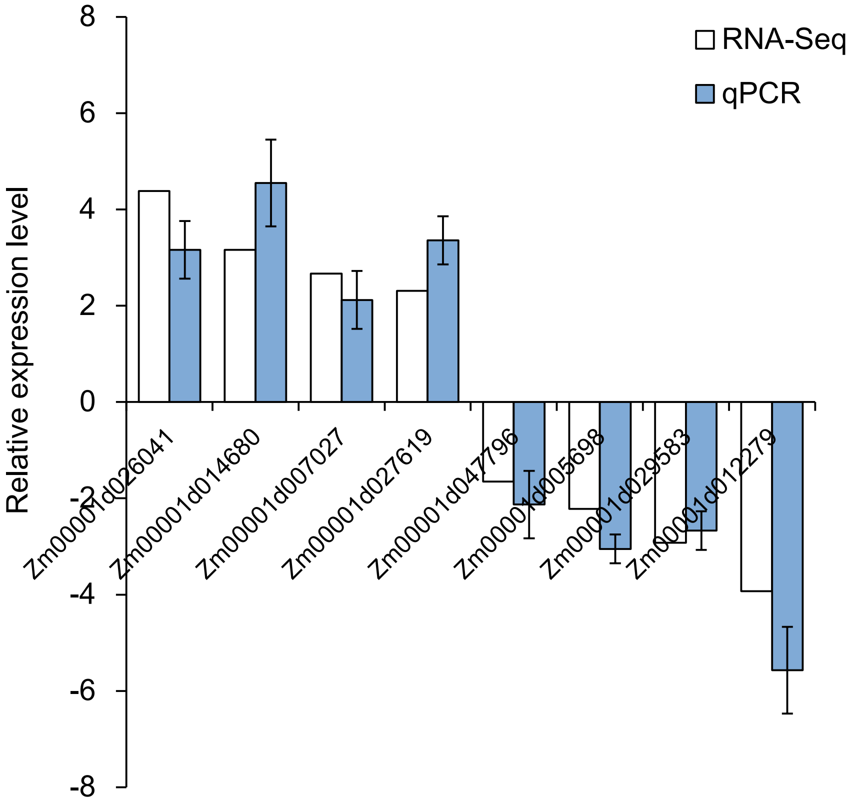
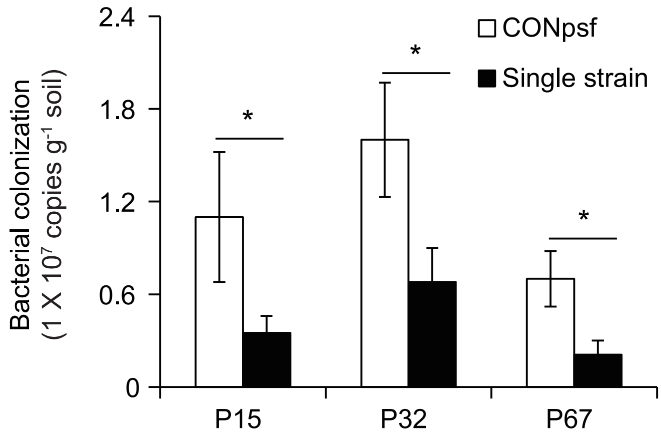


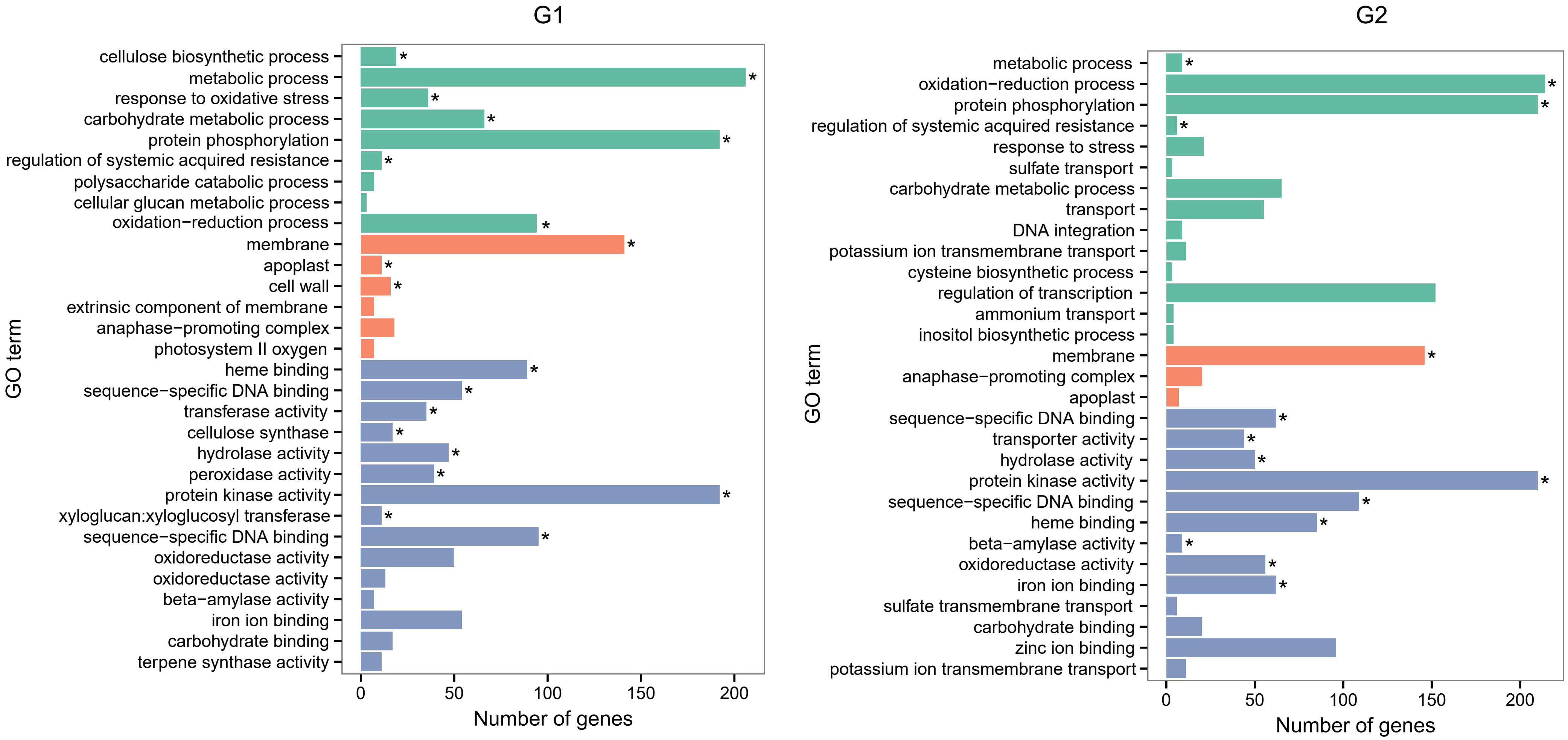
Supplementary Fig. 1. The biosynthetic pathways of BXs in maize plants.



Supplementary Fig. 2. qPCR analyses of eight randomly selected genes from the DEGs of both the experimental group I (G1, +CON*pcf* vs –CON*pcf*) and II (G2, +CON*pcf*+*Pst* vs –CON*pcf*+*Pst*).



Supplementary Fig. 3. qPCR analyses of bacterial populations colonized in the rhizosphere of both the CON*pcf*- and individual strain-inoculated plants. Asterisks indicated significant difference (mean, ±SD, n = 15) using Student's *t*-test at $p < 0.05$.



Supplementary Fig. 4. Gene Ontology (GO) enrichment analyses for DEGs of both the G1 (+CON*pcf* vs –CON*pcf*) and G2 (+CON*pcf*+*Pst* vs –CON*pcf*+*Pst*), including biological process, cellular component, and molecular function.