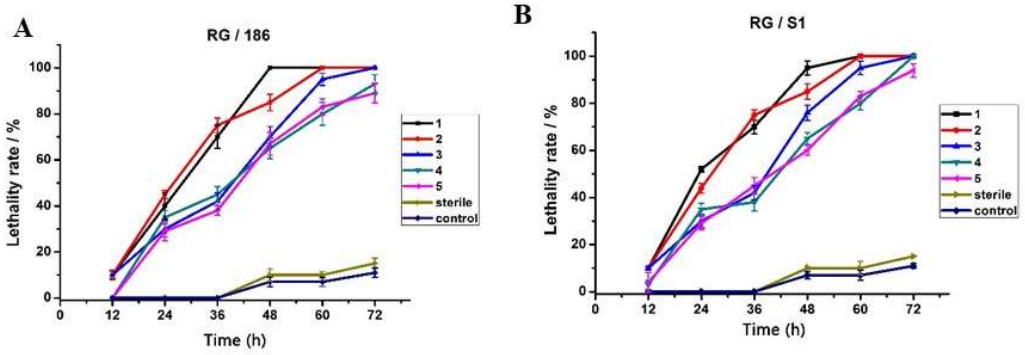


**Figure S1.** Pathogenicity changes of IJs of monoxenic nematode/bacterium combinations of O. rugaoensis associated respectively with S. nematodiphila S1(A) and S. nematodiphila DR186 (B) after multigenerational passage through G. mellonella in vivo.

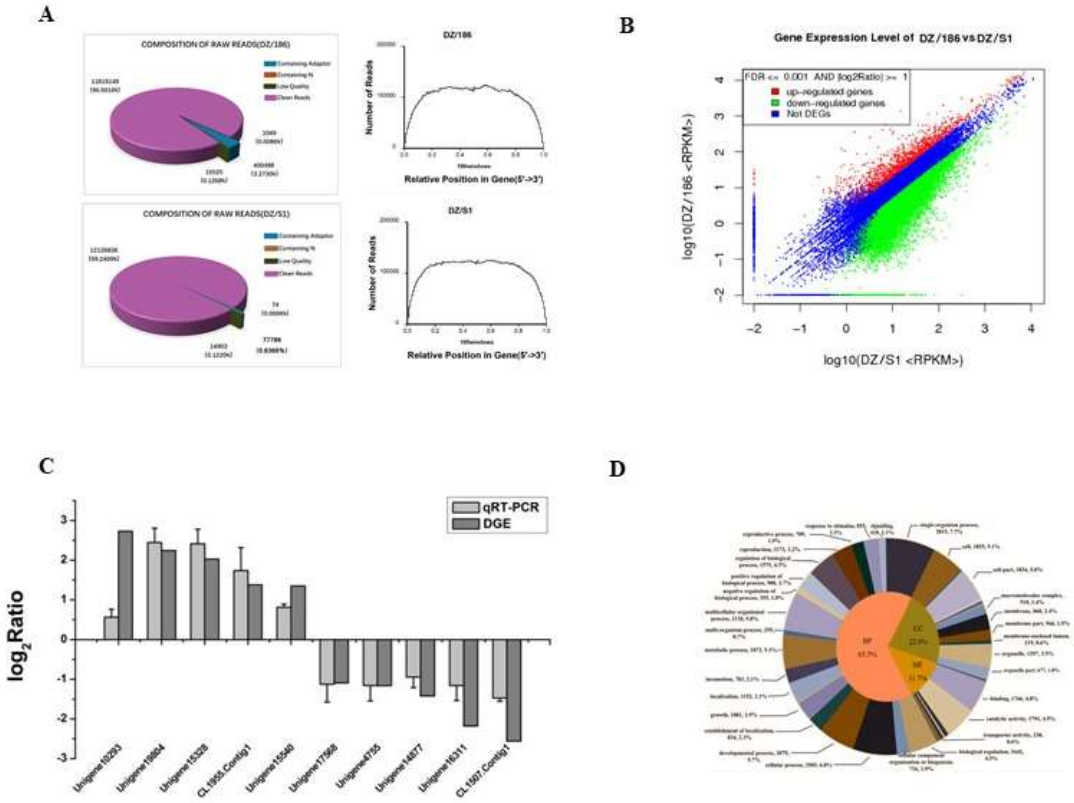


**Figure S2.** Global comparison analysis of mRNA sequencing data of native vs. non-native monoxenic O. chongmingensis; (A) Composition of total tags of the two DGE libraries of DZ/186 and DZ/S1. (B). DEG analysis between the two monoxenic combinations. (C). Validation of the RNA-Seq expression profiles of 10 genes randomly selected from among DEGs. (D). Gene ontology classification of all DEGs.

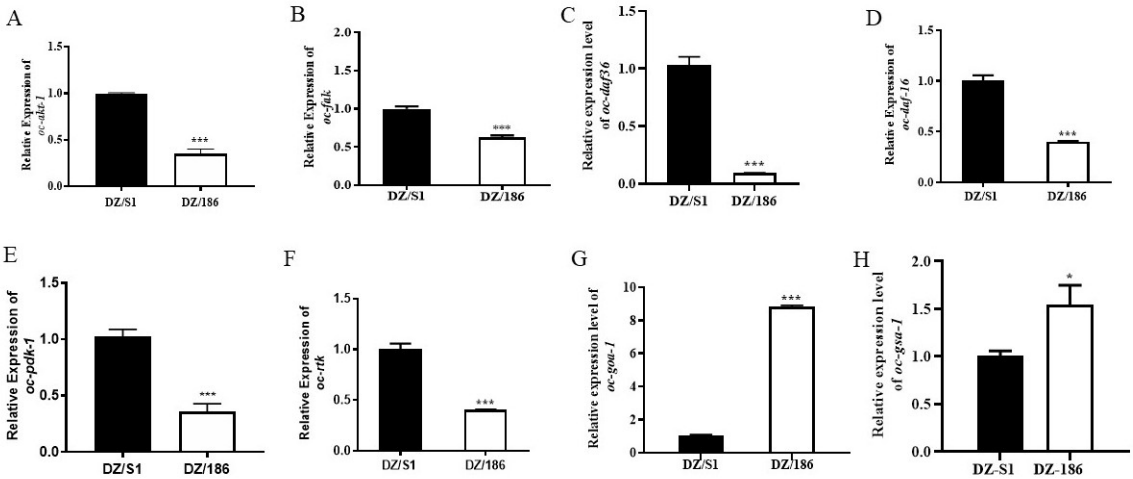


**Figure S3.** Expression levels of oc-akt-1 (A), oc-daf-16 (B), oc-daf-36(C), oc-fak (D), oc-pdk-1(E), and oc-rtk (F) are significantly downregulated in DZ/186 compared with DZ/S1, and those of oc-goa-1 (G) and oc-gsa-1 (H) are significantly upregulated in DZ/186.

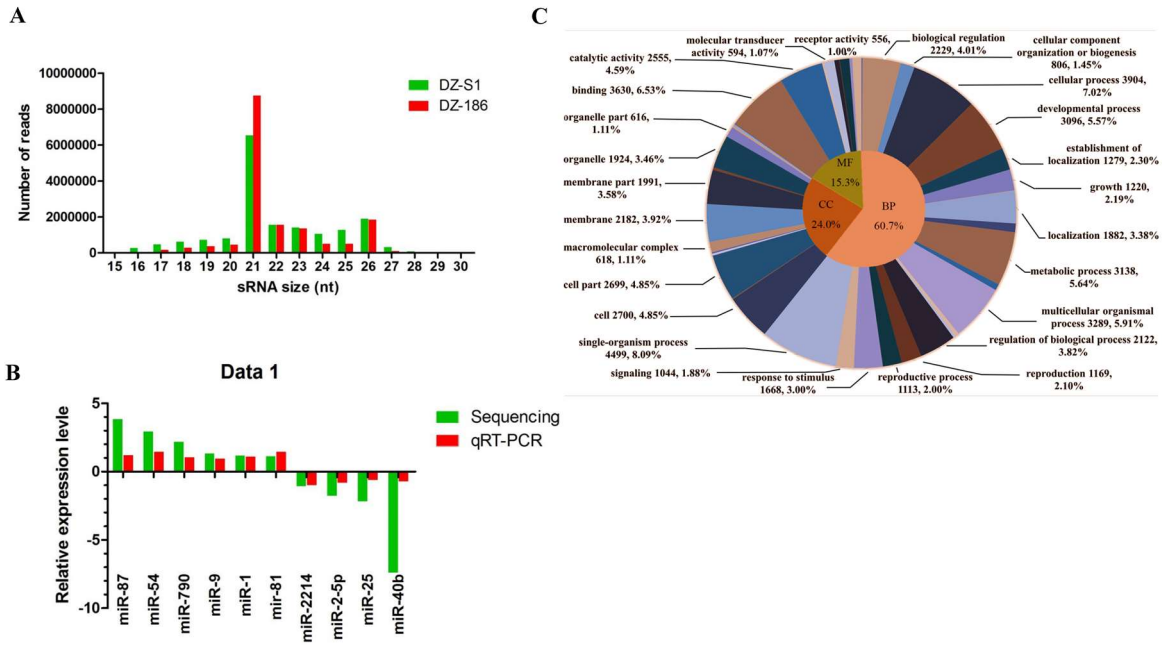


**Figure S4.** Global comparison analysis of miRNA sequencing data of native vs. non-native monoxenic O. chongmingensis; (A) Size distribution of small RNAs in DZ/S1 and DZ/186 libraries. (B) RT-qPCR validation of randomly-selected differentially expressed miRNAs. (C) Gene ontology classification of target transcripts for all differentially expressed miRNAs.