



Supplementary Figure S2. Molecular phylogenetic placement of the gut bacteria of laboratory-reared *M. gracilicorne* with or without supplementation of cultured symbiotic bacteria. Maximum-likelihood phylogeny inferred from 513 aligned nucleotide sites of 16S rRNA gene under the GTR+G+I model is shown, while neighbor-joining phylogeny exhibits substantially the same tree topology. Bootstrap probabilities are indicated at the nodes in the order of maximum-likelihood/neighbor-joining. Accession numbers for the sequences are shown in brackets. As for colors, see the notes on the upper left.