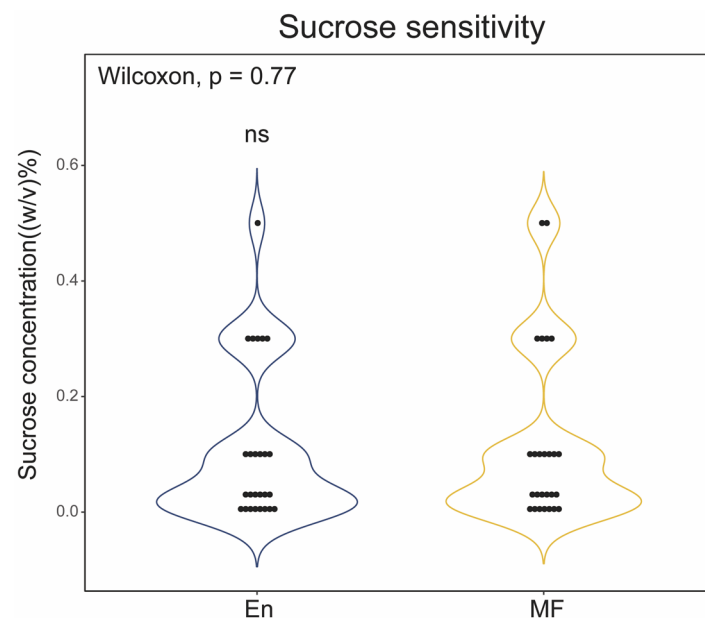
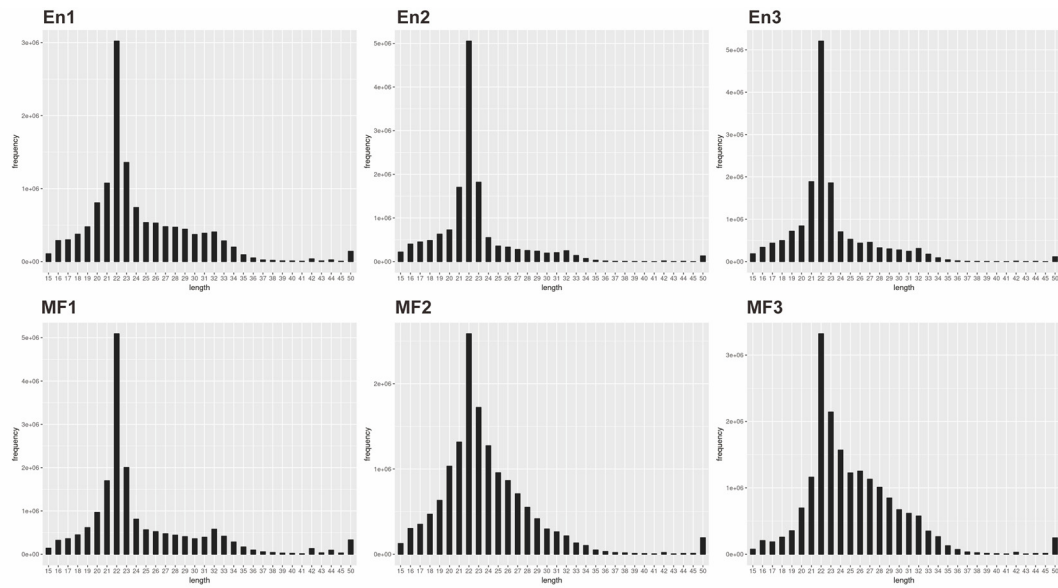


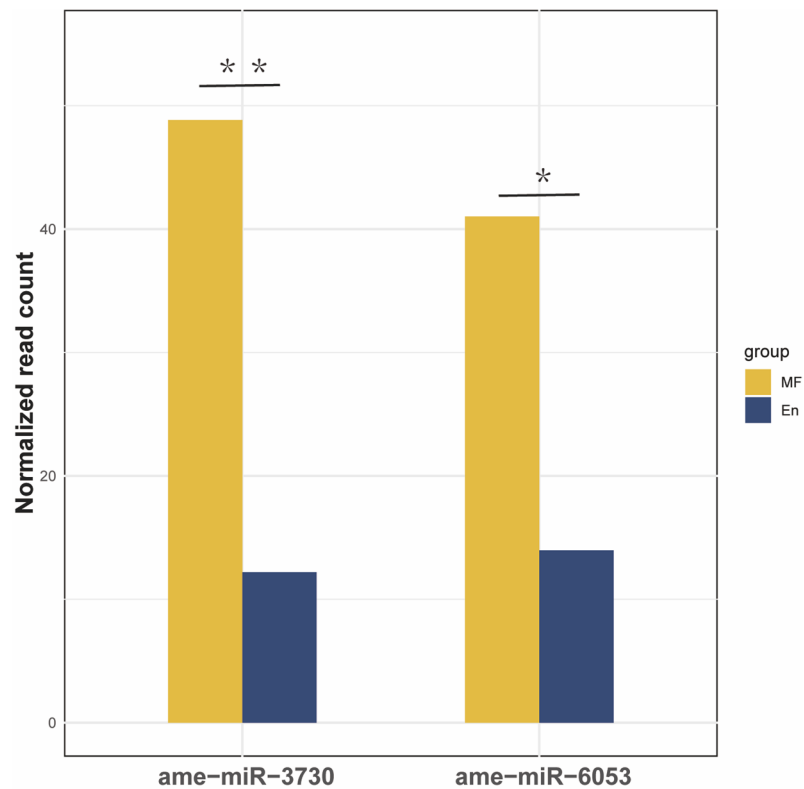
**Fig S1. Phylogenetic relationship of H7 strain within *Enterococcus* genus.** Core genes of 38 *Enterococcus* genomes were aligned and used for the Maximum Likelihood phylogenetic tree reconstruction. *E. faecium* H7 was marked in red.



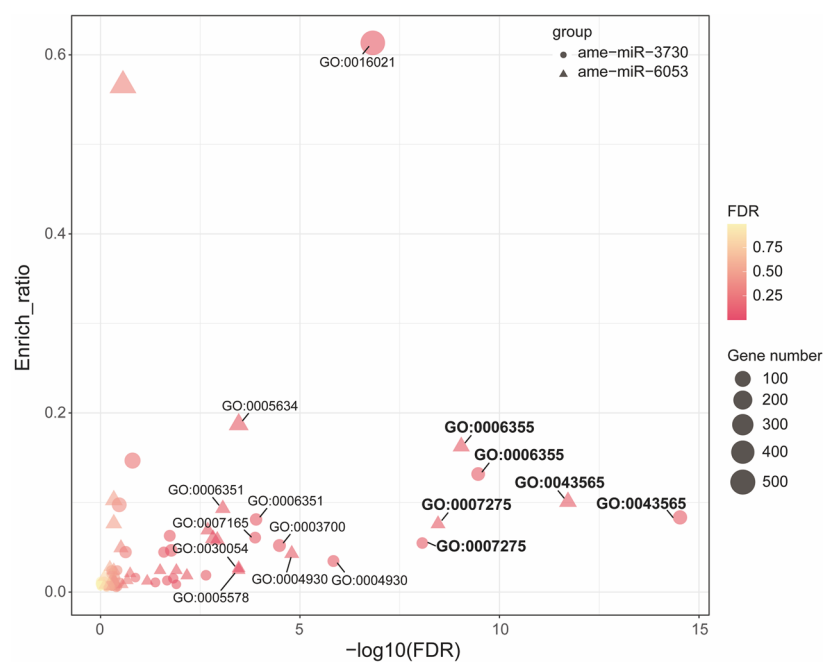
**Fig S2. Sucrose sensitivity difference between En and MF bees.** En: *E. faecium* H7 colonized (n=26), MF: microbiota-free (n=26). ns, not significant.



**Fig S3. Length distribution of small RNAs in En and MF bees.** The peak was at 22nt, which is the typical length of miRNAs. En: *E. faecium* H7 colonized, MF: microbiota-free.



**Fig S4. ame-miR-3730 and ame-miR-6053 were significantly down-regulated in *E. faecium* colonized bees.** \*,  $P < 0.05$ , \*\*,  $P < 0.01$ . En: *E. faecium* H7 colonized, MF: microbiota-free.



**Fig S5. GO enrichment of miRNA target genes.** The area and color of each point were proportional to the gene number and enriched significance (FDR). The top three ranked GO terms were sequence-specific DNA binding (GO:0043565), regulation of transcription, DNA-templated (GO:0006355), and multicellular organism development (GO:0007275). ame-miR-3730: circle; ame-miR-6053: triangle.