

Description of Additional Supplementary Files

File Name: **Supplementary Data 1**

Description: **The potential target genes of miR-9a in the gene database from locust transcriptome.** We employed the algorithms miRanda and RNAhybrid to predict the potential target genes of miR-9a in the gene database from locust brain transcriptome (*Locusta migratoria*). The predicted results are listed in Supplementary Data 1, which includes the accession number of genes in the transcriptome, gene lengths, position of alignment, predict score, gene names, and GO categories.

File Name: **Supplementary Data 2**

Description: **The differentially expressed miR-9a target genes between gregarious and solitary locusts.** Among the predicted genes of miR-9a (Supplementary Data 1), 157 genes showed significant differences between the gregarious and solitary phases according to the transcriptome data (Fold change > 1.5). These genes are listed in Supplementary Data 2, which includes the accession number of genes in the transcriptome, gene length, Log₂(G/S), *P* value, position of alignment, and annotation.