

Figure S4. Map of the *Sesamia nonagrioides* **mitogenome.** The inner circle in blue shows the GC content per window of 50 bp (from 0% to 48%), where each gray line represents 5% and the red line marks 50%. The middle circle in purple shows the sequencing depth (from 580X to 1663X), with dark green for the outline. If the depth is larger than upper quartile, it turns dark green as same with the outline. The outer circle shows the gene features, where coding protein genes are in green, tRNA genes are in orange and rRNA genes are in yellow. The symbol "+" on top indicates the forward strand.