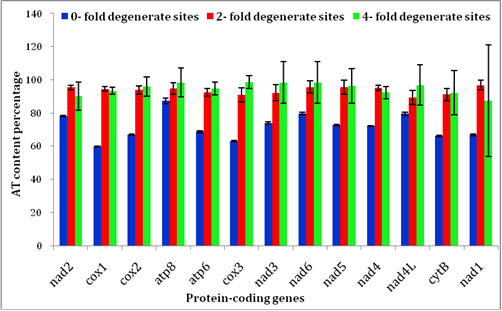
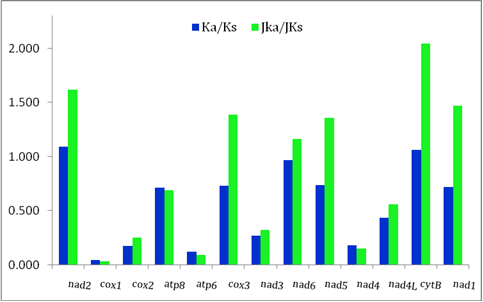


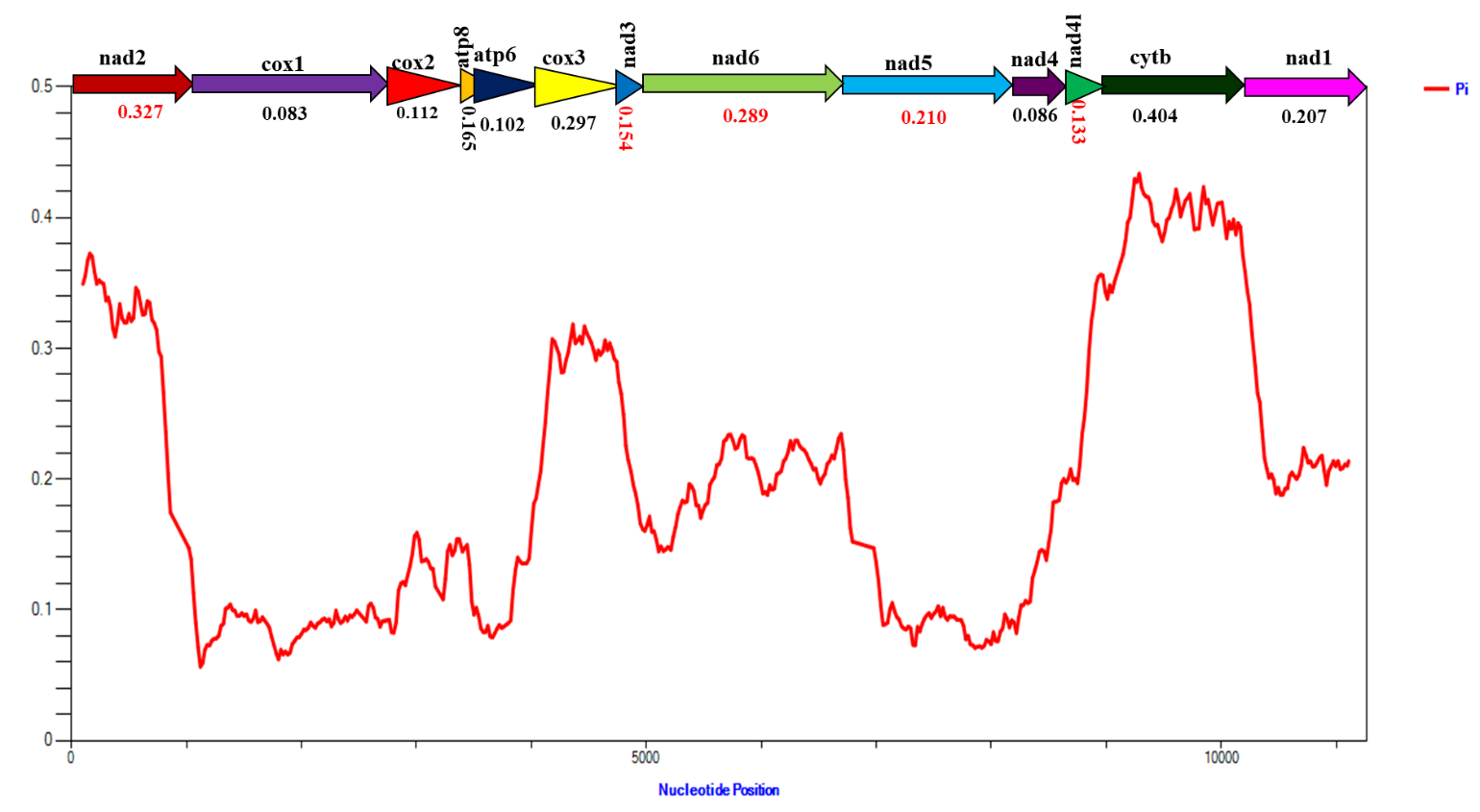
**Supplementary Figure 1.** **AT% vs AT-skew and GC% vs GC-skew in the 63** [**Noctuidae**](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Undef&id=7100&lvl=3&keep=1&srchmode=1&unlock) **family species including *Chrysodeixis acuta*** from this study. Values are calculated on J-strands for full length of mt genomes. The X-axis provides the skews values, while the Y axis provides the A+T/G+C values. Names of species are colored according to their taxonomic placement.



**Supplementary Figure 2.** **The AT content percentage of 0-fold degenerate sites, 2-fold degenerate sites and 4-fold degenerate sites in each protein coding gene of 55 mitochondrial genome sequences of Noctuidae family species including *C. acuta* from this study**. The black line with short line on the top of each bar represents the standard deviation value (SD).



**Supplementary Figure 3.** **Ratio of non-synonymous substitutions (Ka, pi modified) & synonymous substitutions (Ks, pi modified) (Ka/Ks) as well as Jukes-Cantor adjusted (JKa/JKs) ratio in each PCG of 55 mitogenome sequences of Noctuidae family species including *C. acuta* from this study.**



**Supplementary Figure 4.** **Sliding window analysis of protein-coding genes among 55mitogenome sequences of Noctuidae family species including *Chrysodeixis acuta* from this study.** The red curve shows the value of nucleotide diversity.