

The B2 consensus sequence was from RepeatModeler based on the published TE library and was not identified by machine learning; thus, the classification was reliable. It indicated that the SINE/B2 either was an independently evolved subfamily in *T. ni* or probably was horizontally transferred from other Lepidopteran species. The insertion was estimated from 60 Mya with a peak propagation around 20–30 Mya. However, where the B2 subfamily came from and how it integrated into the *T. ni* genome requires further study.

#### 4.2. TE Expansion Activity Correlated with Phylogeny of Noctuidae Species

In addition to being the main contribution factor to the genome size of Noctuidae species, we also investigated which class/subfamily of TE was correlated with the phylogeny of Noctuidae. Among the four classes of TE, only LINE showed a phylogenetic signal with high confidence, indicating the essentially vertical inheritance characteristics of LINE elements in Noctuidae. In particular, four LINE subfamilies, CR1, L2, RTE, and R1, showed a high correlation with Noctuidae phylogeny, all abundant in copy number. In contrast, despite the high copy number