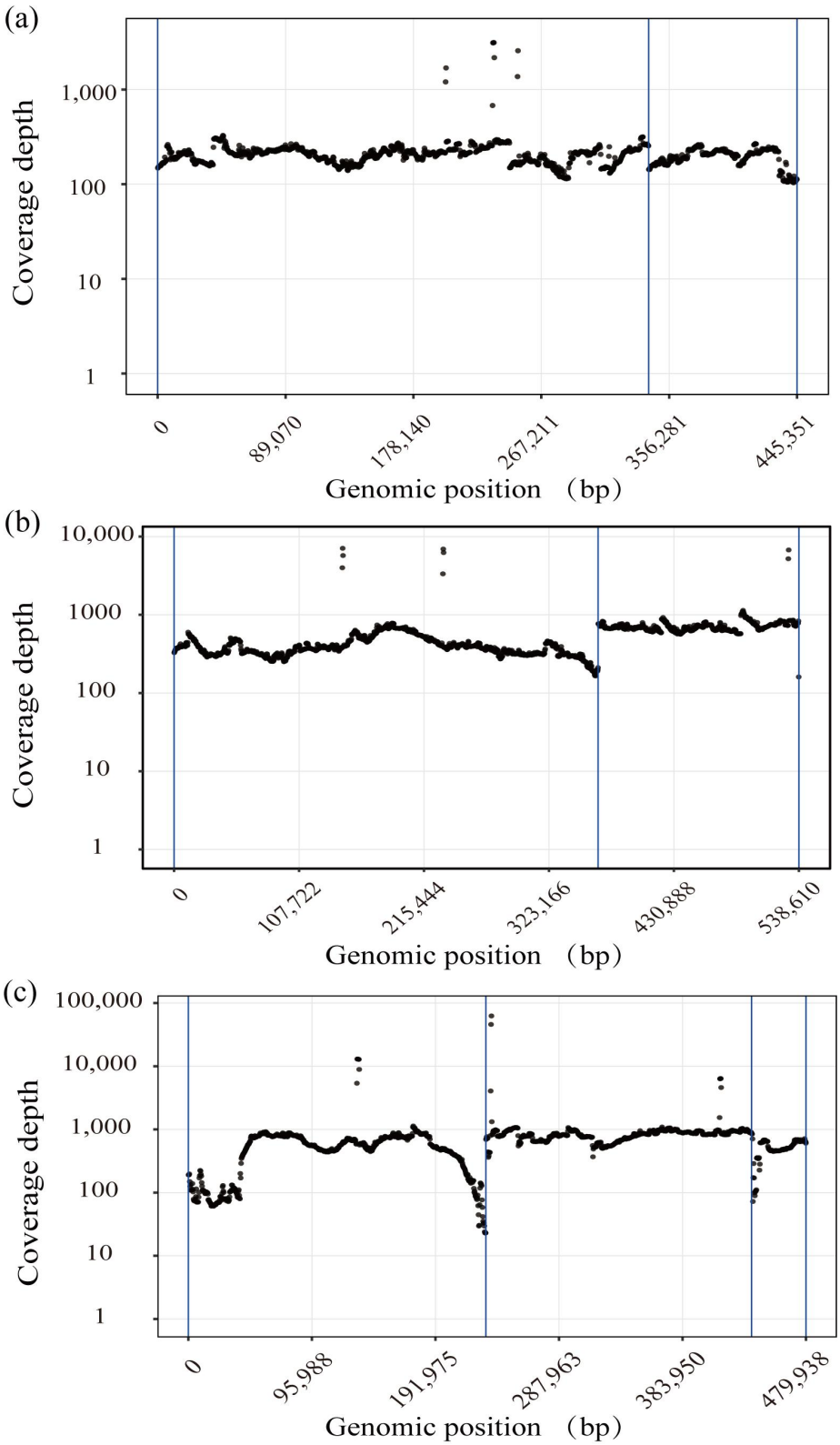

Figure S1. Coverage depth analysis of mitochondrial genomes in the three *Quercus* species. (a) *Quercus engleriana,* (b) *Quercus kongshanensis*, (c) *Quercus tungmaiensis*. The log-scaled coverage depth is plotted against genomic position.

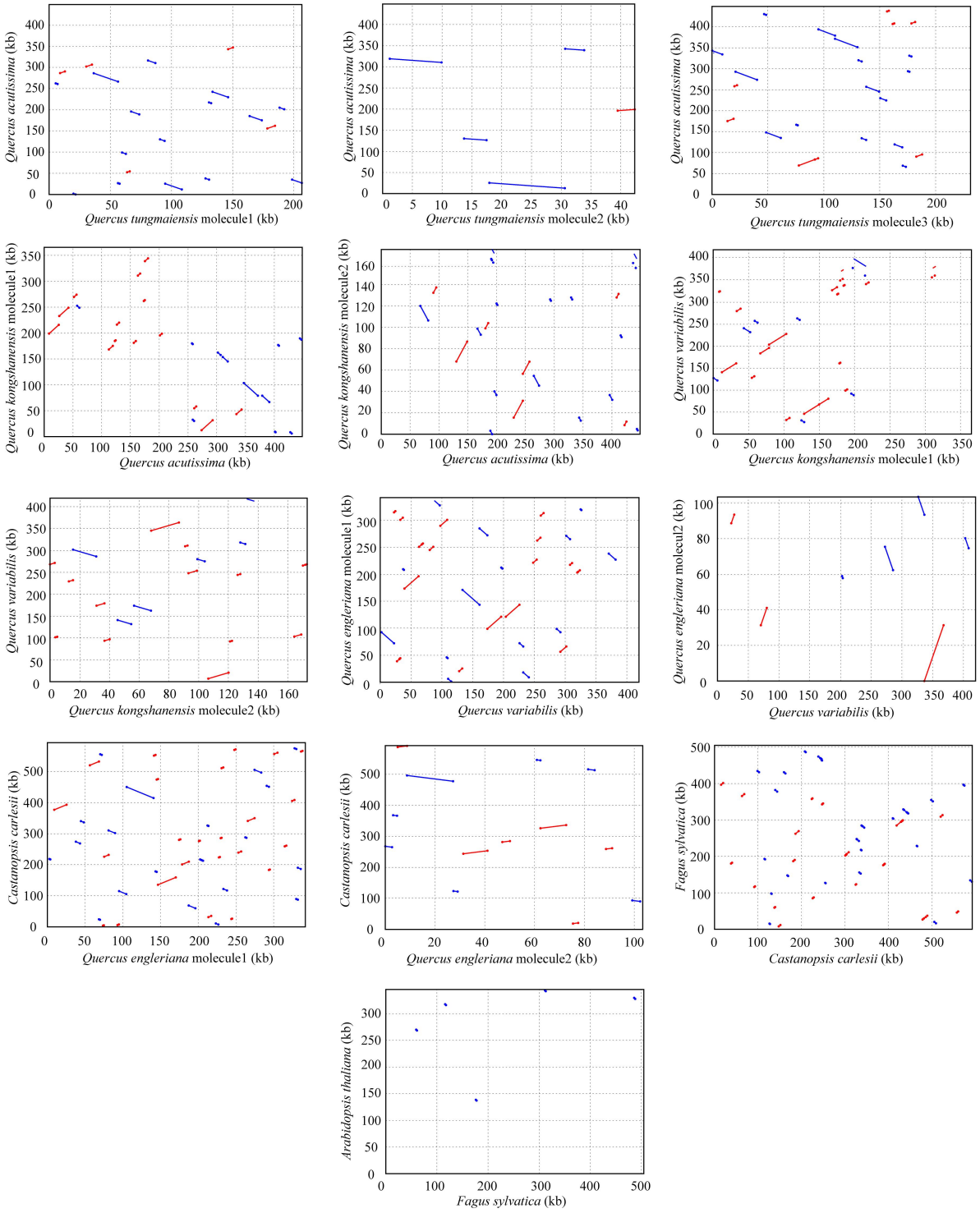

Figure S2. Mitochondrial genome collinearity analysis across Fagaceae species. Pairwise dot plots of molecular sizes for genomic units in *Quercus engleriana*, *Q. kongshanensis*, *Q. tungmaiensis*, *Q. acutissima*, *Q. variabilis* , *Castanopsis carlesii*, *Fagus sylvatica* and *Arabidopsis thaliana*. Red dots represent forward-strand sequence matches (same orientation), blue dots represent reverse-complement matches (opposite orientation).