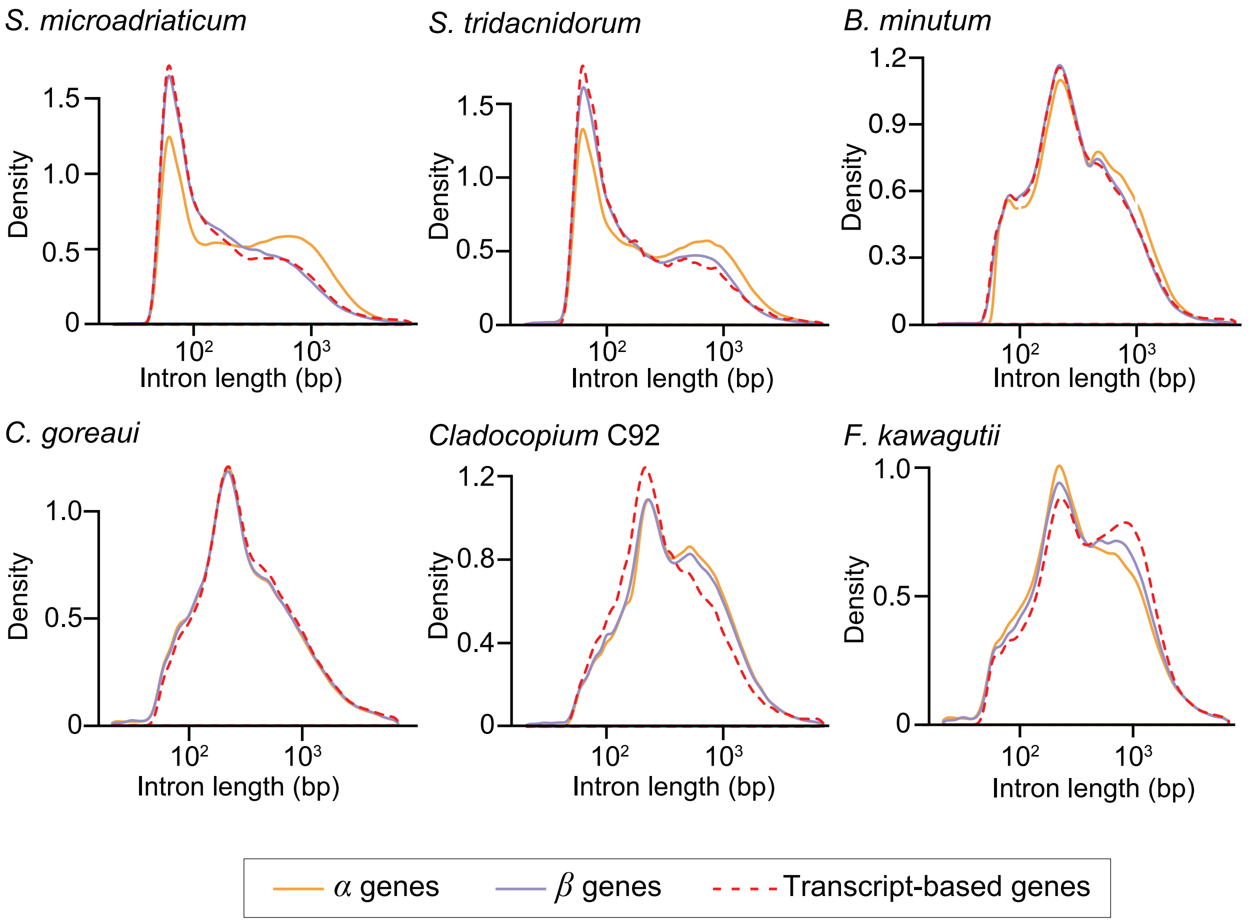

Fig. S3. Distribution of intron lengths in predicted genes from the six Symbiodiniaceae genomes. In each graph, the distribution of intron lengths among α genes (orange line), among β genes (purple line), and among transcript-based genes (predicted using PASA and TransDecoder; red dashed line) are shown. The transcript-based genes (see Appendix S1) were considered as a proxy for true gene structure.