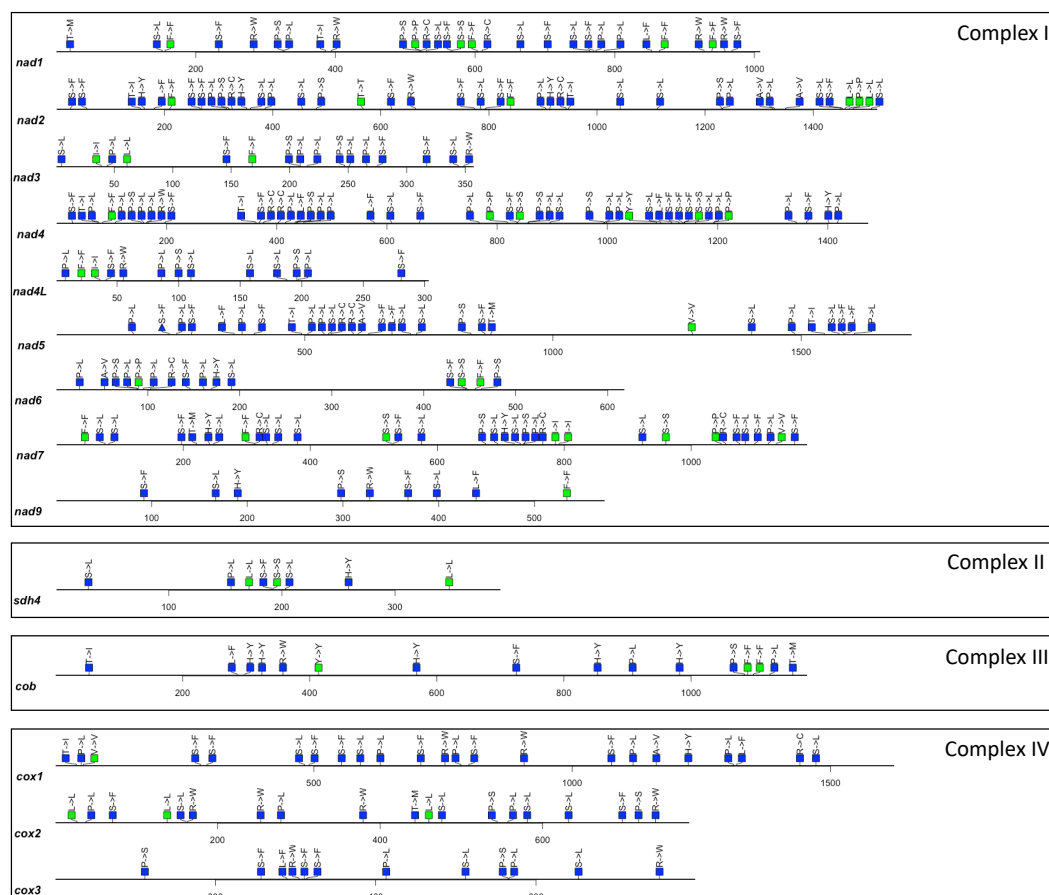
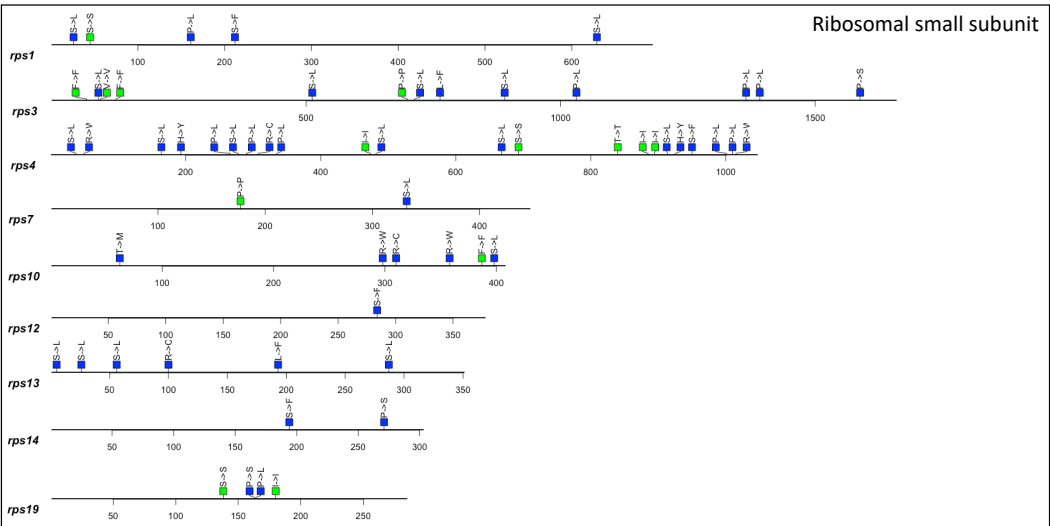
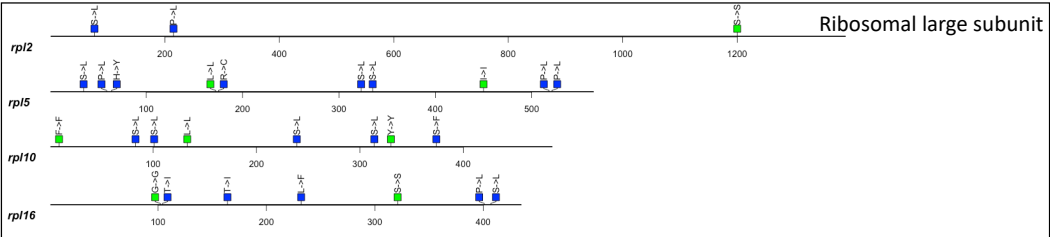
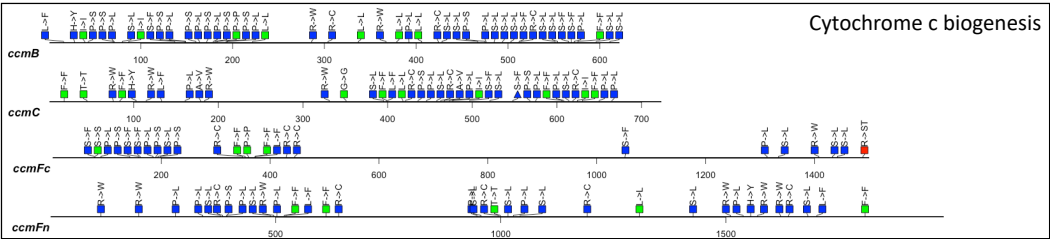
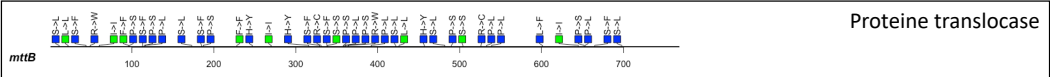
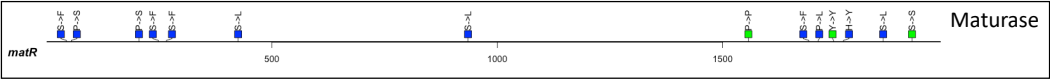
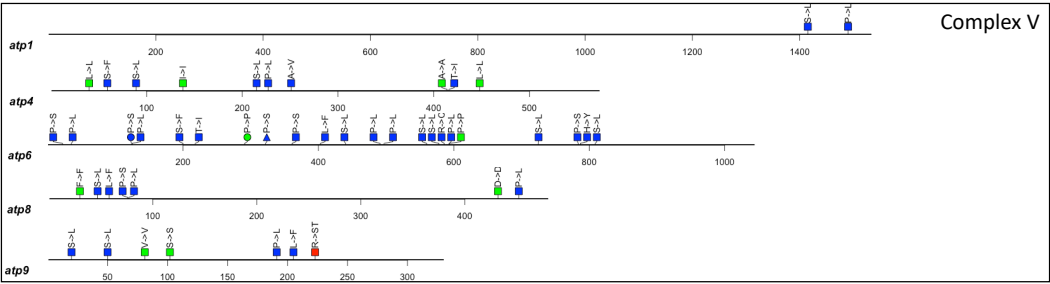
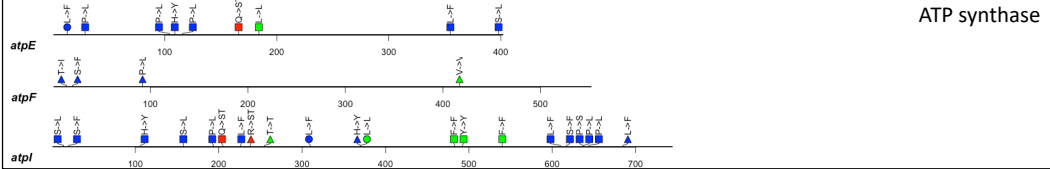
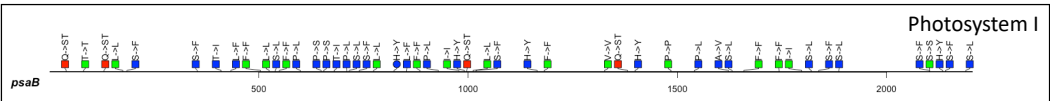


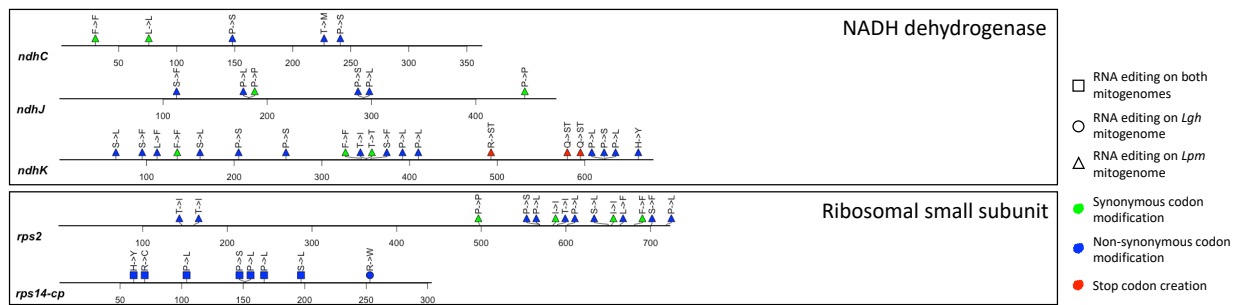
**Figure S1.** Number of RNA editing per gene, identified by Deepred-Mt, in *Ludwigia grandiflora* subsp. *hexapetala* (Lgh in purple) and *Ludwigia peploides* subsp. *montevidensis* (Lpm in yellow) mitogenomes.



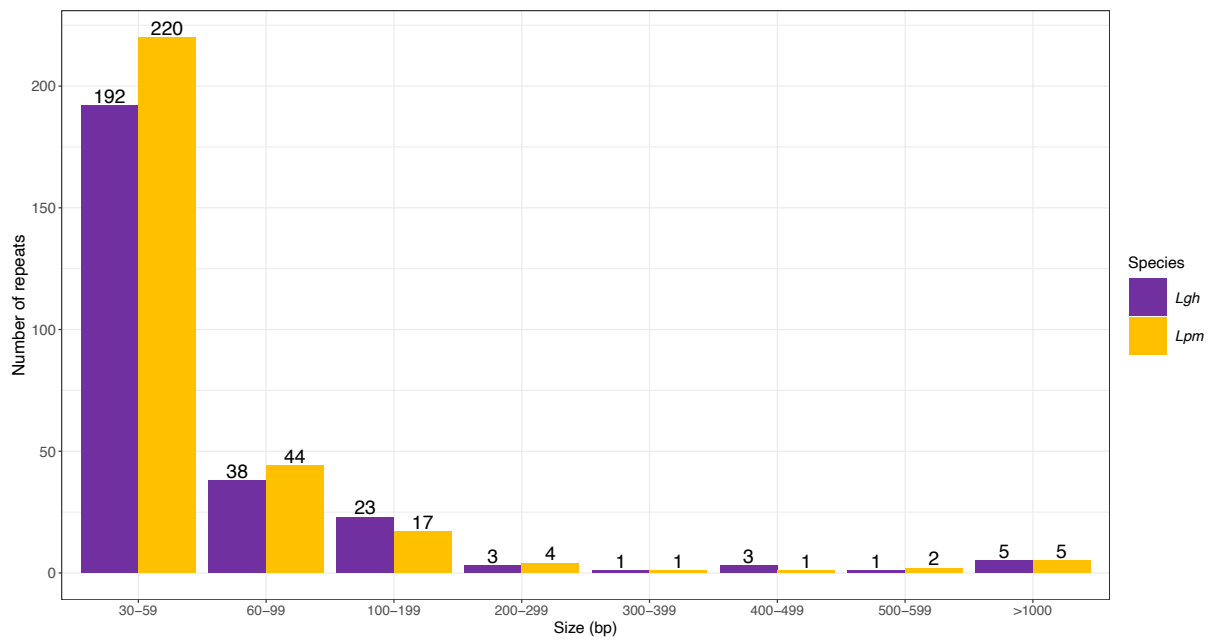


### Chloroplast originated genes

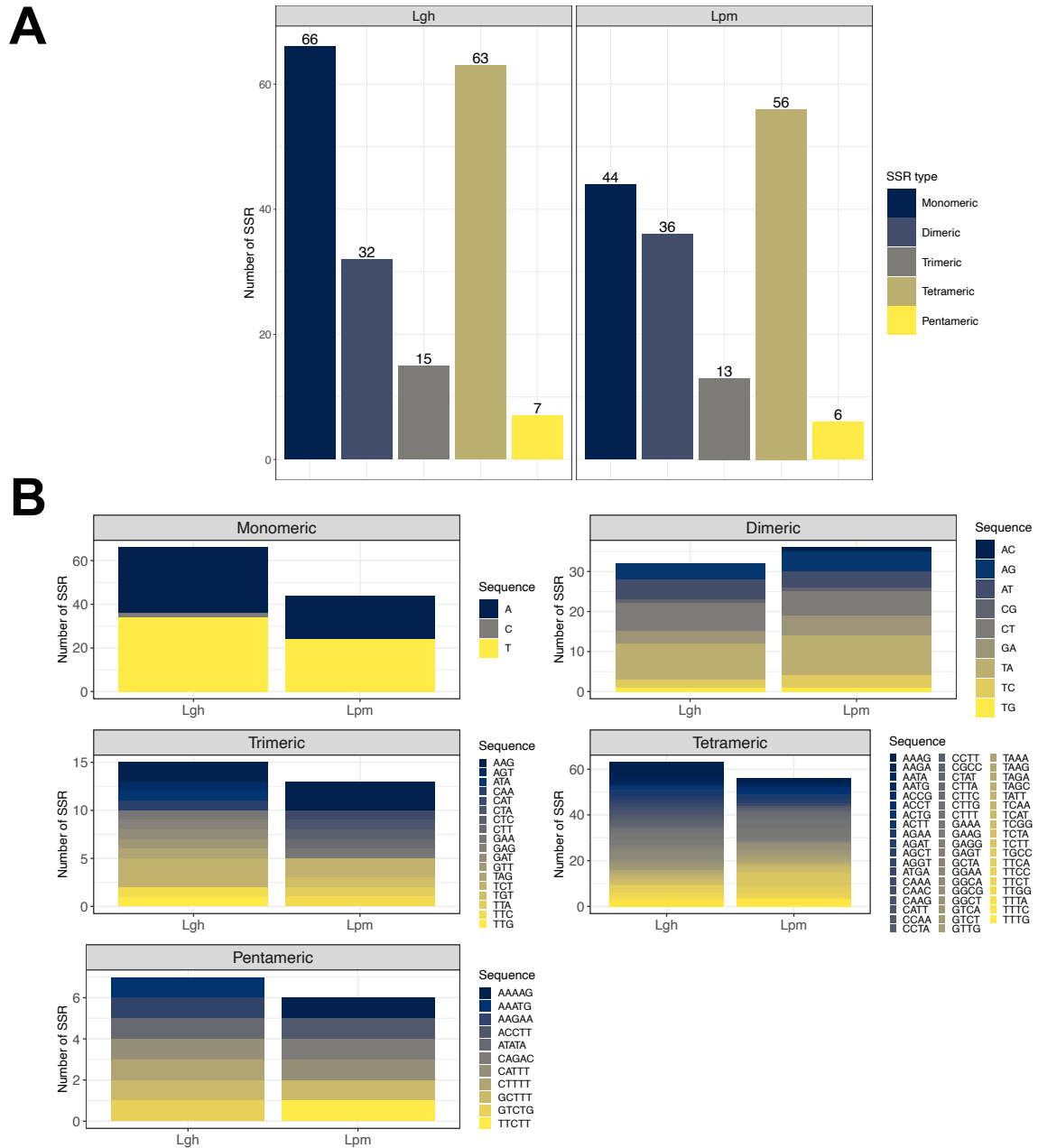




**Figure S2.** Representation of RNA editing sites in *Ludwigia grandiflora* subsp. *hexapetala* (*Lgh*) and *Ludwigia peploides* subsp. *montevidensis* (*Lpm*) mitogenomes protein-coding genes.



**Figure S3.** Number of non-tandem repeats based on their size in *Ludwigia grandiflora* subsp. *hexapetala* (*Lgh*) and *Ludwigia peploides* subsp. *montevidensis* (*Lpm*) mitogenomes.



**Figure S4.** Simple Sequence Repeats (SSR) in *Ludwigia grandiflora* subsp. *hexapetala* (Lgh) and *Ludwigia peploides* subsp. *montevidensis* (Lpm) mitogenomes. A: Number of each SSR type. B: Detailed compositions of each SSR type.