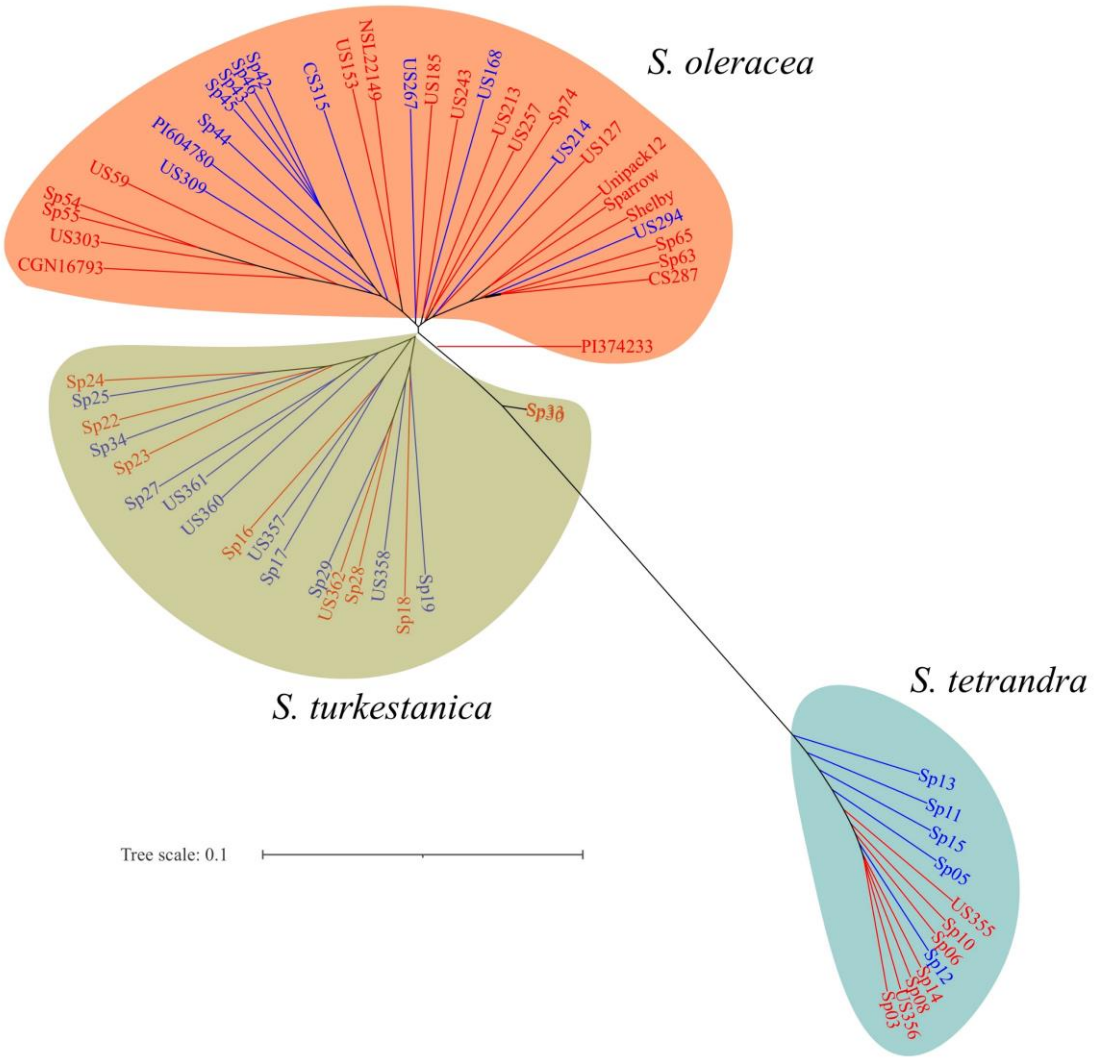


Figure S1. Phylogenetic tree of 63 *Spinacia* accessions based on SNPs within the pseudoautosomal region (PAR).

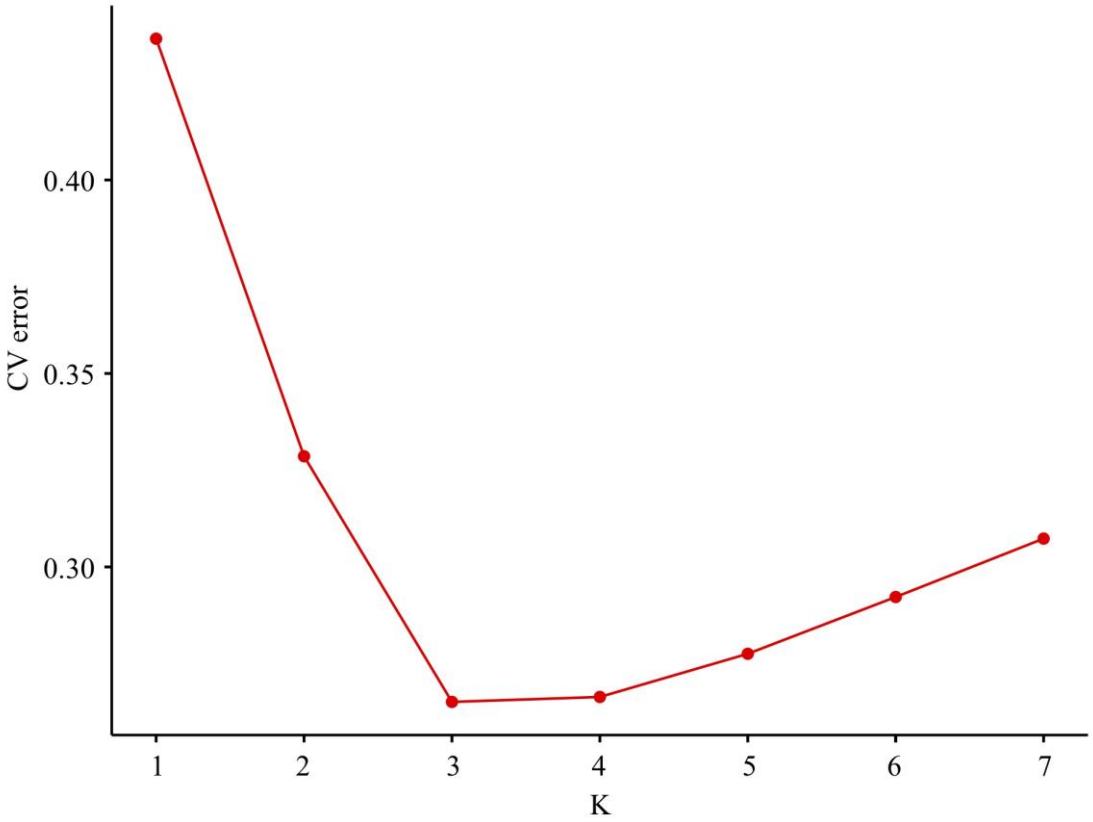


Figure S2. The cross-validation (CV) error for different *K* values in admixture analysis.

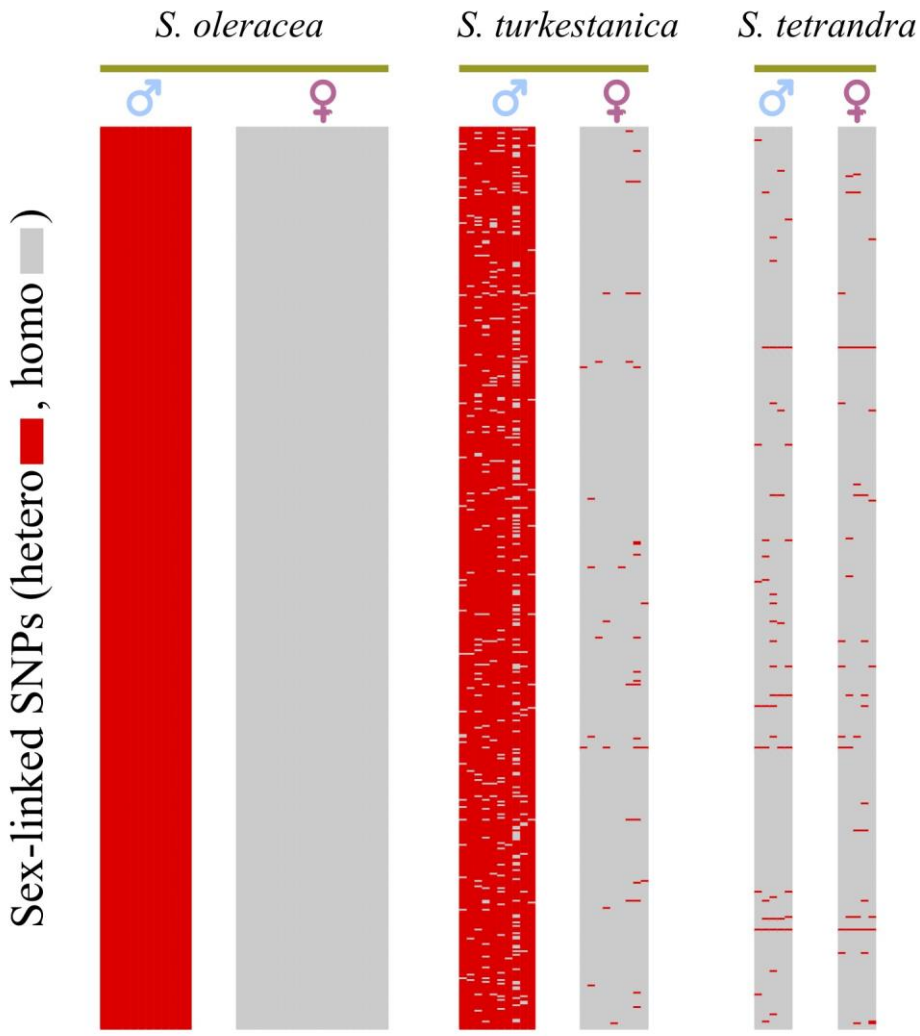


Figure S3. Fully sex-linked SNPs in *S. oleracea*, *S. turkestanica*, and *S. tetrandra.*

Red rectangle indicates heterozygous genotype, while gray rectangle represents homozygous genotype.

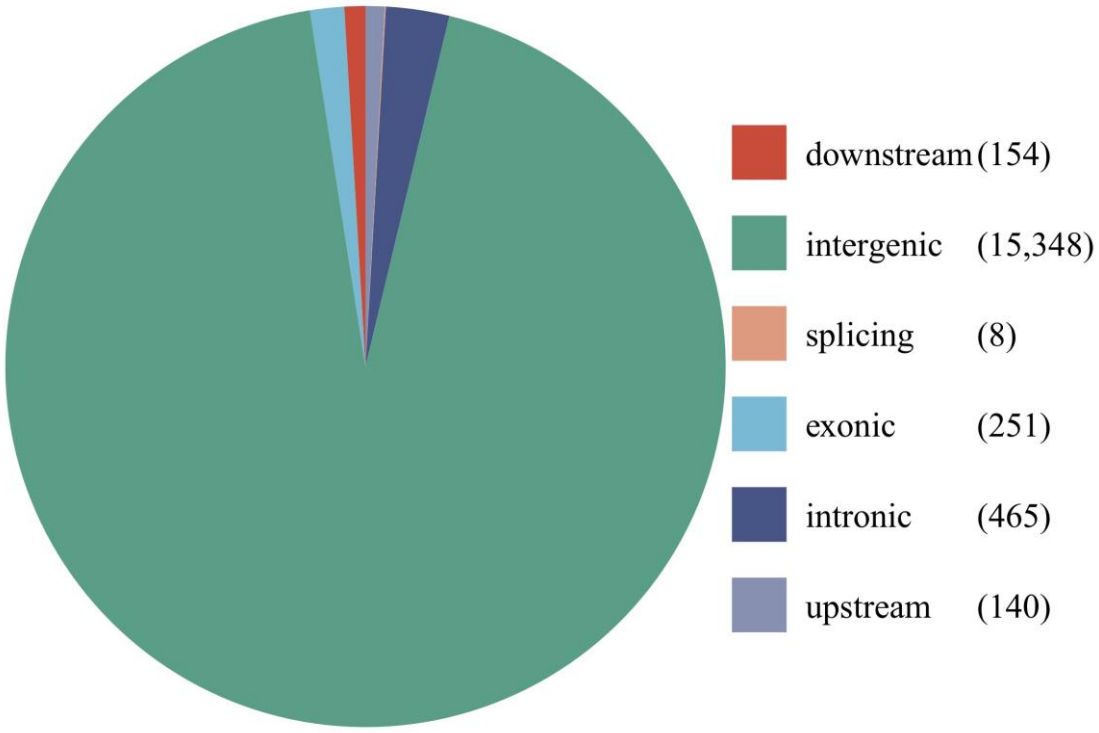


Figure S4. Annotation of SNPs within the Y-duplication region.

Number of SNPs type were shown on the right.

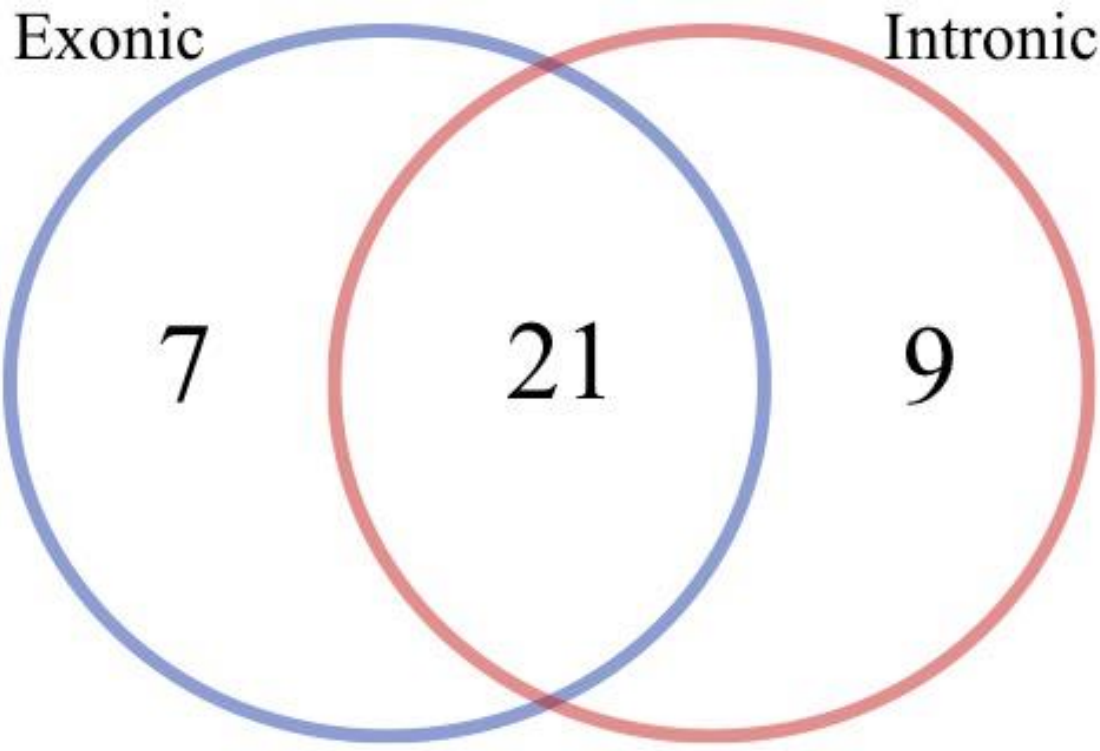


Figure S5. Venn diagram of genes with exonic or intronic SNPs in the Y-duplication region.

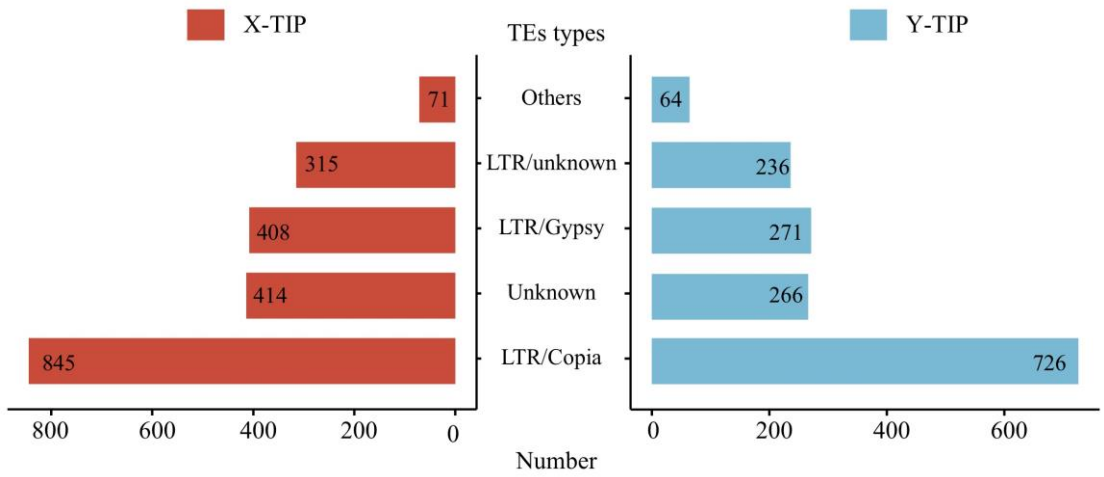


Figure S6. Number of detected TIPs per TE family.

X-TIP represent TIP on the X chromosome. Y-TIP represent TIP on the Y chromosome.

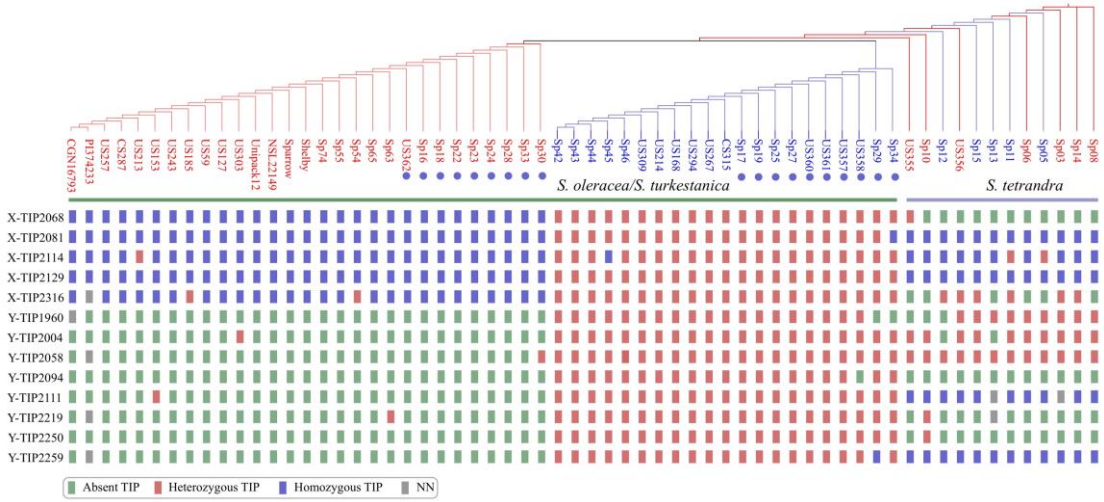


Figure S7. Phylogenetic tree based on 13 conserved TIPs in 62 *Spinacia* accessions.

The accession labelled with red and blue indicate female and male, respectively. The *S. turkestanica* accessions were marked with blue dots. NN: missing.