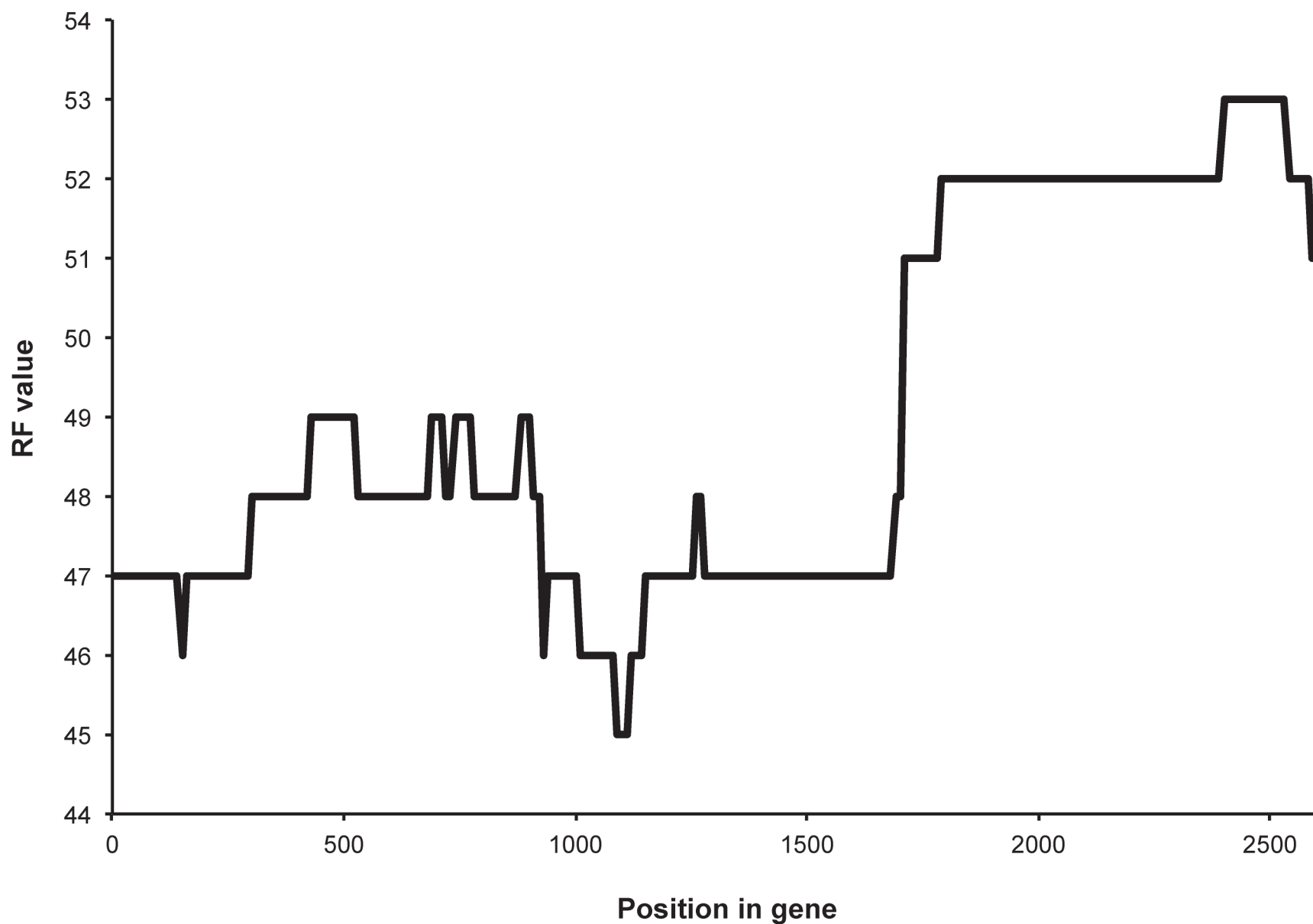


Supplemental Figure 3. Analysis of the RF value for the identification of genes and gene regions under different evolutionary pressure. (A): A plot of RF values across a gene showing variation that may be due to recombination. A fragment length of 800 with a step size of 10 was used in this analysis. Only the first coordinate was plotted with the last data point indicating the last point before the gene boundary. (B): A plot of RF values across two genes. One gene (*pmbA*) shows consistently high RF values across the length of the gene, which may be due to homoplasmy. The other gene (topoisomerase) shows normal variation across the length of the gene, with the average RF value well within the range of the mean \pm 2 standard deviations.

A



B

