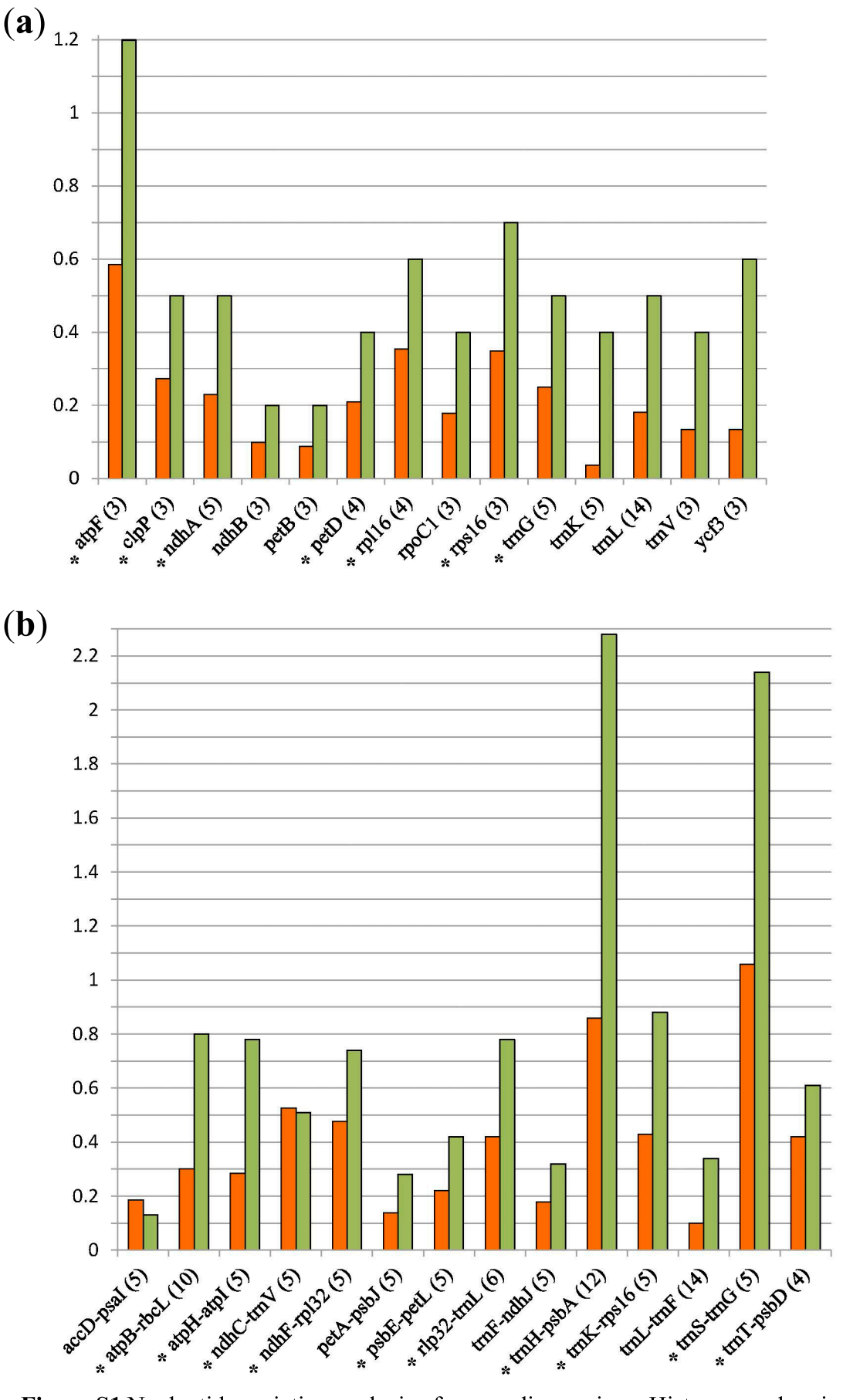

Figure S1 Nucleotide variation analysis of non-coding regions. Histograms showing the normalised ratio expressed as percentage, in orange; and the average uncorrected p-distance, expressed as percentage, in green. The number of *Ilex* species used for each alignment is indicated between parentheses; the regions selected according to thresholds were marked with an asterisk (see text). (**a**) Values estimated from single-loci intron alignments. Note: introns of genes *trnA* and *rps12* failed to show variation. (**b**) Values estimated from single-loci IGS alignments.