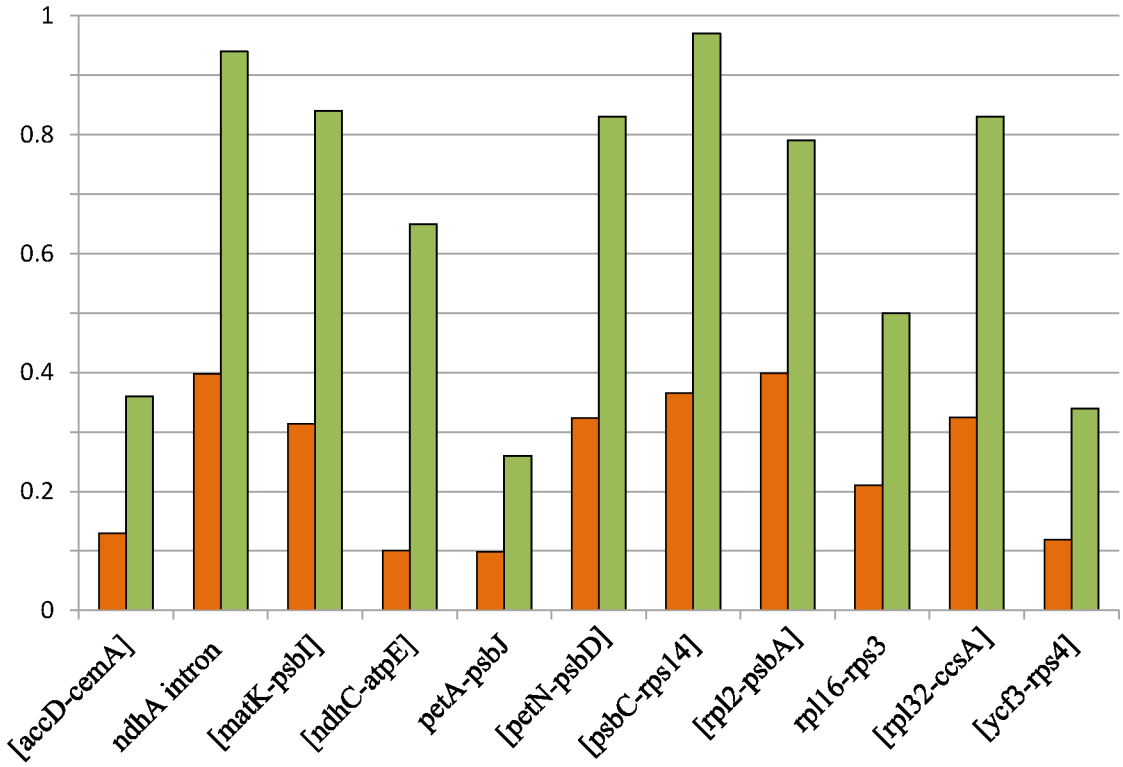

L1:	2154	1150	4842	2175	1032	4228	1210	1229	1107	949	2336
L2:	5064	---	7030	3088	2118	5794	3361	3191	2172	2157	3536

Figure S5 Nucleotide variation analysis of the plastidic regions proposed in Yao et al. [57]. The sequences were extracted from the seven species of *Ilex* studied by the authors. Compound regions (those involving coding and non-coding regions) are indicated between square parentheses. The following values were estimated considering solely the non-coding regions: the normalised ratio, expressed as percentage, in orange; and the average uncorrected p-distance, expressed as percentage, in green. The row L1 shows the length (in bp) of each marker excluding the coding regions; the row L2 shows the total length for each marker including the coding regions.