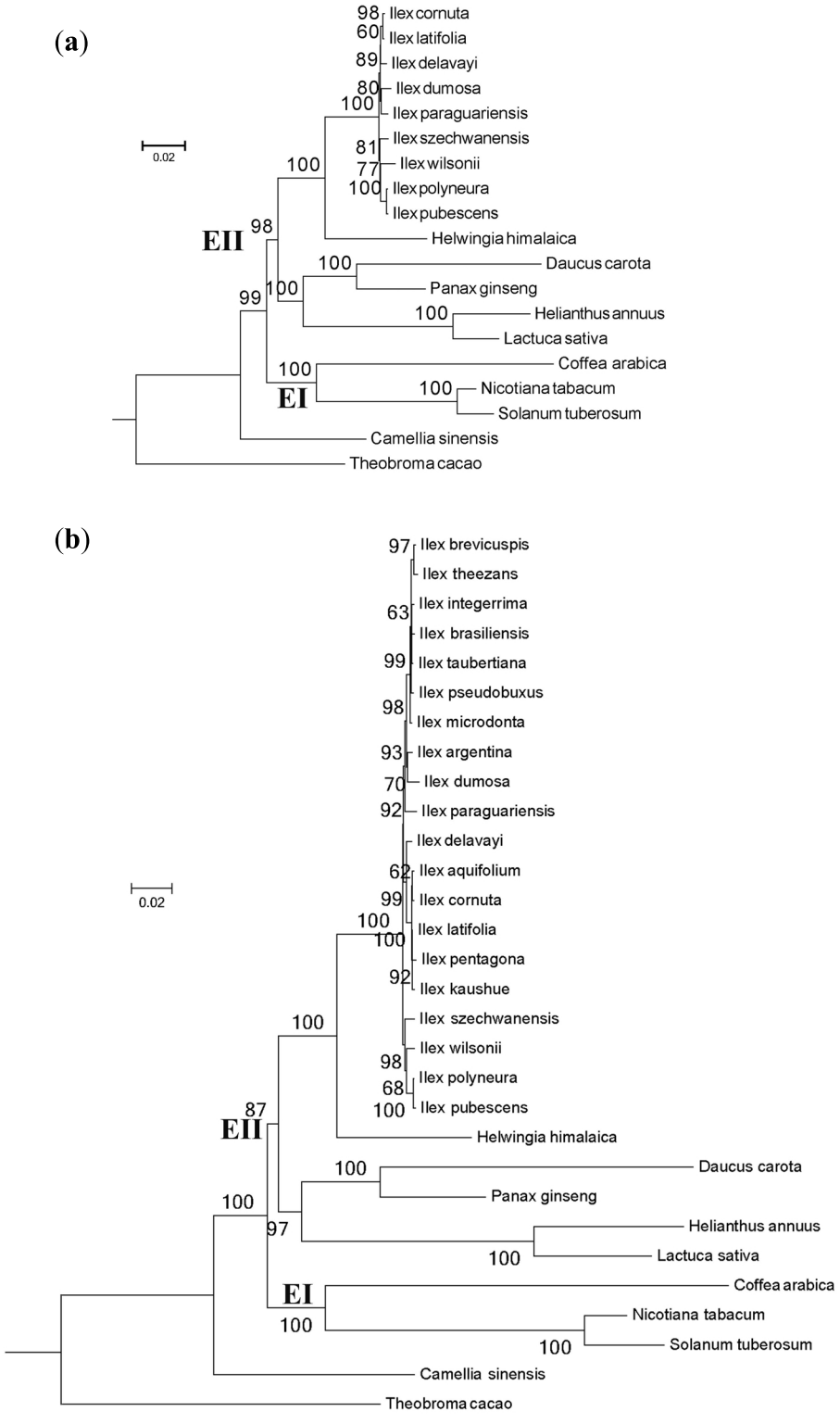

Figure S3 Maximum Likelihood phylogenomic analyses of multilocus data sets performed in the context of other angiosperm taxa. Branch lengths are in number of substitutions per site. Outgroup sequences are represented by *Camellia sinensis* and *Theobroma cacao*. The bootstrap support values >50 % are shown. EI and EII indicate the clades euasterids I and II, respectively. (**a**) The phylogram was obtained through the concatenation of 7 introns (lnL= -32262.59); all positions with less than 50 % site coverage were eliminated thus, 6838 positions were considered. The GTR + G model; (G= 0.77) was applied. (**b**) Phylogram derived from the simultaneous analysis of 9 IGSs (lnL= -44882.76; GTR+G, G= 1.55); all positions with less than 50 % site coverage were eliminated thus, 7657 positions were analysed.