

**Table S1.** Taxa and GenBank accession numbers included in the phylogenomic analyses.

Classification	Taxon	GenBank Accession No.
Acorales/Acoraceae	<i>Acorus calamus</i>	NC_007407
Amborellales/Amborellaceae	<i>Amborella trichopoda</i>	NC_005086
Asterales/Compositae	<i>Artemisia annua</i>	NC_034683
	<i>Lactuca sativa</i>	NC_007578
Brassicales/Brassicaceae	<i>Arabidopsis lyrata</i>	NC_031186
	<i>Arabidopsis thaliana</i>	NC_030789
	<i>Capsella rubella</i>	NC_026839
Brassicales/Caricaceae	<i>Carica papaya</i>	NC_010323
Chloranthales/Chloranthaceae	<i>Chloranthus japonicus</i>	NC_026565
Dipsacales/Caprifoliaceae	<i>Lonicera japonica</i>	NC_026839
Ericales/Actinidiaceae	<i>Actinidia arguta</i>	NC_031186
Ericales/Ebenaceae	<i>Diospyros kaki</i>	NC_030789
Fabales/Fabaceae	<i>Glycine max</i>	NC_007942
	<i>Phaseolus vulgaris</i>	NC_009259
Garryales/Eucommiaceae	<i>Eucommia ulmoides</i> <sup>a</sup>	MF766010
	<i>E. ulmoides</i>	KU204775
Garryales/Garryaceae	<i>Aucuba japonica</i>	GQ997049-GQ997131
Gentianales/Apocynaceae	<i>Nerium oleander</i>	NC_025656
Laurales/Lauraceae	<i>Cinnamomum camphora</i>	NC_035882
Magnoliales/Magnoliaceae	<i>Magnolia denudata</i>	NC_018357
Malpighiales/Euphorbiaceae	<i>Manihot esculenta</i>	NC_010433
	<i>Ricinus communis</i>	NC_016736
Malpighiales/Salicaceae	<i>Populus trichocarpa</i>	NC_009143
Malvales/Malvaceae	<i>Hibiscus syriacus</i>	NC_026909
	<i>Theobroma cacao</i>	NC_014676
Myrtales/Myrtaceae	<i>Eucalyptus grandis</i>	NC_014570

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Poales/Poaceae	<i>Brachypodium distachyon</i>	NC_011032
Rosales/Rosaceae	<i>Fragaria vesca</i>	NC_015206
	<i>Prunus persica</i>	NC_014697
Sapindales/Rutaceae	<i>Citrus sinensis</i>	NC_008334
Solanales/Convolvulaceae	<i>Ipomoea nil</i>	NC_031159
Solanales/Solanaceae	<i>Solanum lycopersicum</i>	NC_007898
	<i>Solanum tuberosum</i>	NC_008096
Vitales/Vitaceae	<i>Vitis vinifera</i>	NC_007957

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<sup>a</sup> The newly sequenced *E. ulmoides* individual in the current study.

**Table S2.** List of 80 unique plastid protein-coding genes of *Eucommia ulmoides* included in the phylogenomic analyses.

*accD, atpA, atpB, atpE, atpF, atpH, atpI, ccsA, cemA, infA, matK, ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK, petA, petB, petD, petG, petL, petN, psaA, psaB, psaC, psaI, psaJ, psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ, rbcL, rpl14, rpl16, rpl2, rpl20, rpl22, rpl23, rpl32, rpl33, rpl36, rpoA, rpoB, rpoC1, rpoC2, rps2, rps3, rps4, rps7, rps8, rps11, rps12, rps14, rps15, rps16, rps18, rps19, ycf1, ycf15, ycf2, ycf3, ycf4, ycf68*