SUPPLEMENTARY TABLE II. Summary of datasets, including length of alignments and number of analyzed characters for each gene separately and when combined

Dataset/alignment		315-taxon supermatrix	209-taxon supermatrix
nucSSU	Alignment length	7214	5162
	Characters included	1071	1106
nucLSU	Alignment length	5287	4212
	Characters included	1119	1170
mitSSU	Alignment length	2865	2533
	Characters included	431	453
5.8S	Alignment length	160	160
	Characters included	151	151
RPB1	Alignment length	3228	3222
	Characters included	2688	2766
RPB2	Alignment length	2415	2244
	Characters included	1842	1926
Combined data	Alignment length	21 169	17 524
	Characters included	7302	7572
	% of missing data	22	9