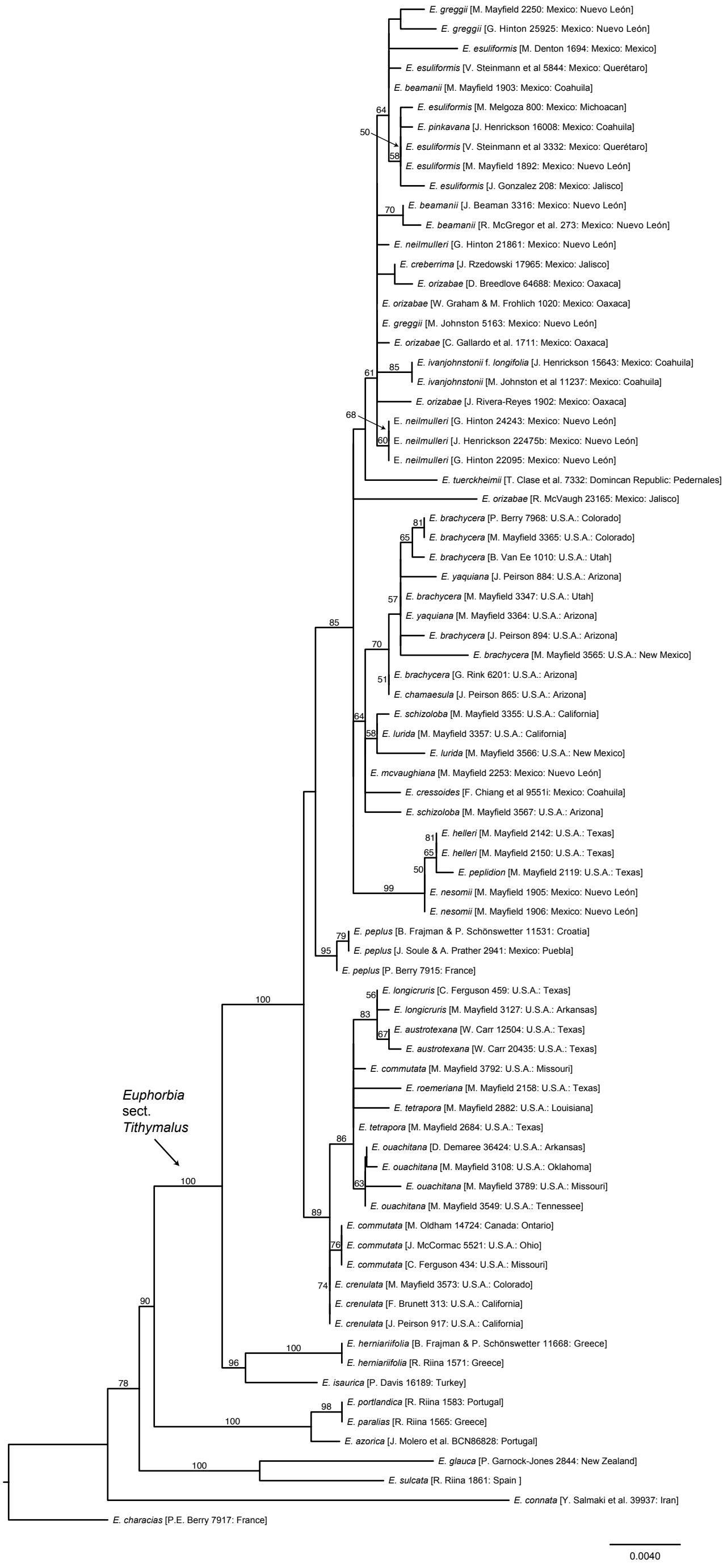

Fig. S2. Maximum likelihood phylogram from RAxML analysis of the complete *ndhF* dataset of *Euphorbia* sect. *Tithymalus* and outgroups. Maximum likelihood bootstrap values (≥ 50%) are indicated. The scale bar indicates the mean number of nucleotide substitutions per site.