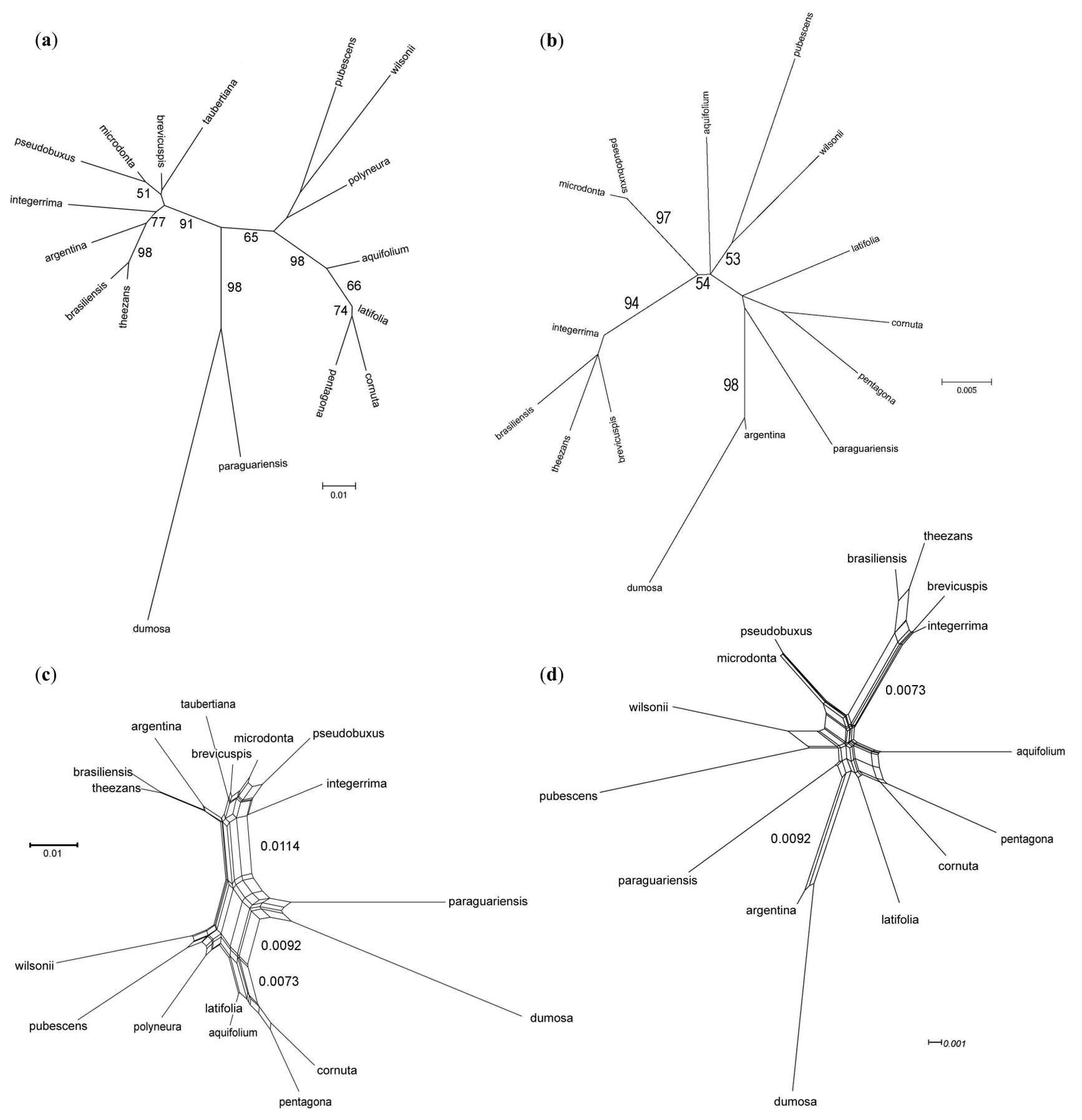

Figure S4 Genetic relationships among *Ilex* species computed from ITS and nepGS nuclear sequences. The species were named using the specific epithet alone, for simplicity. (**a-b**) Unrooted phylograms inferred applying a Tamura (1992) model and a discrete Gamma distribution (G). All positions were considered. Bootstrap values > 50 % (500 pseudoreplicates) are shown. Branch lengths are in number of substitutions per site. (**a**) ITS phylogram (lnL= -2465.87; G= 0.24; 696 positions). (**b**) nepGS phylogram (lnL= -1941.43; G= 0.39; 813 positions). (**c-d**) Neighbor-Net split graphs based on uncorrected p-distances. All positions were used to derive the networks. The scale bar is in genetic distance units. The numbers indicated the edge weight, which is proportional to the edge length. (**c**) ITS network (fit= 96.57; LSfit= 99.81). (**d**) nepGS network (fit= 97.73; LSfit= 99.89).