

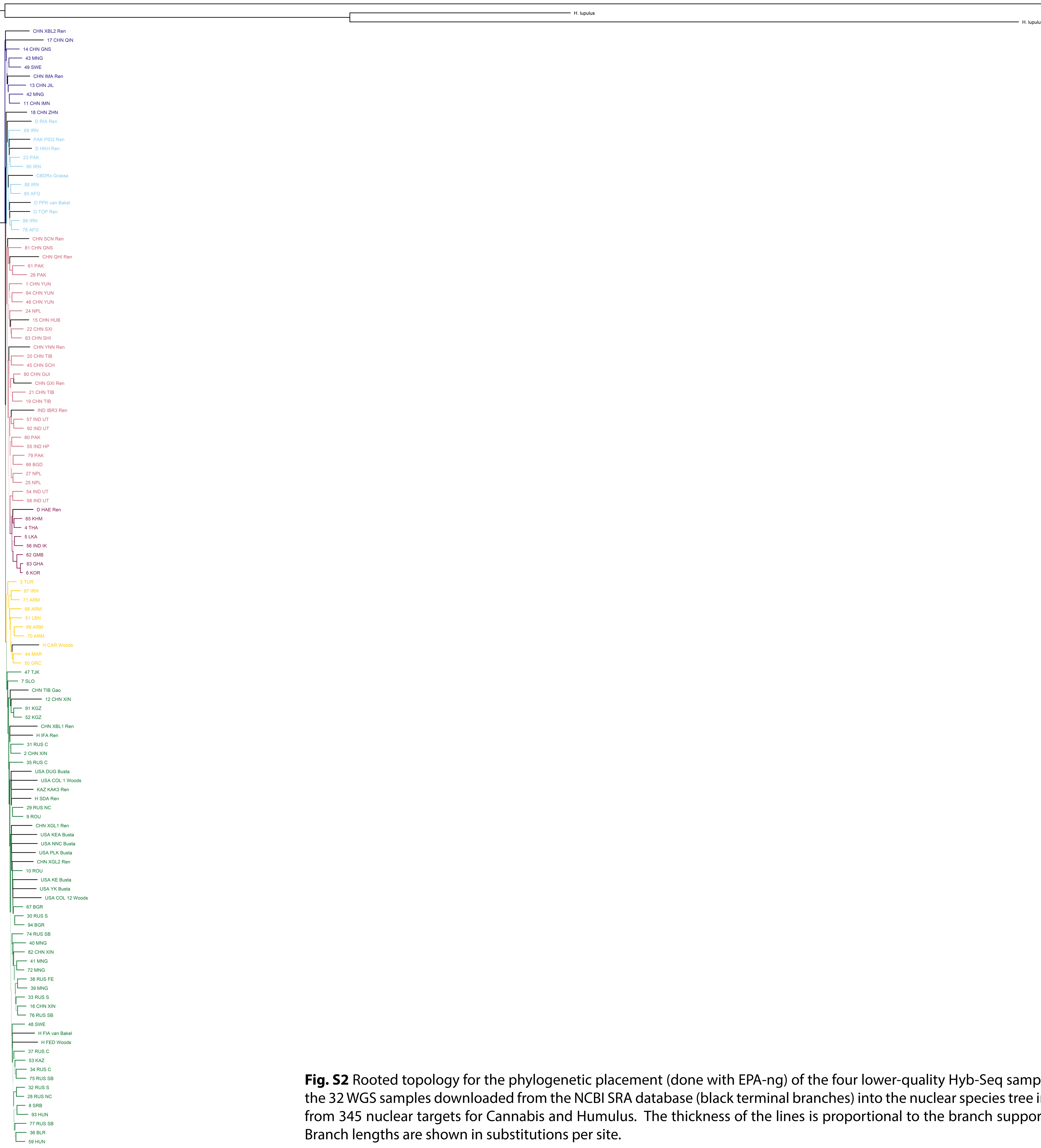


Fig. S2 Rooted topology for the phylogenetic placement (done with EPA-ng) of the four lower-quality Hyb-Seq samples and the 32 WGS samples downloaded from the NCBI SRA database (black terminal branches) into the nuclear species tree inferred from 345 nuclear targets for *Cannabis* and *Humulus*. The thickness of the lines is proportional to the branch support (LPP). Branch lengths are shown in substitutions per site.