

Figure 2-Figure Supplement 1

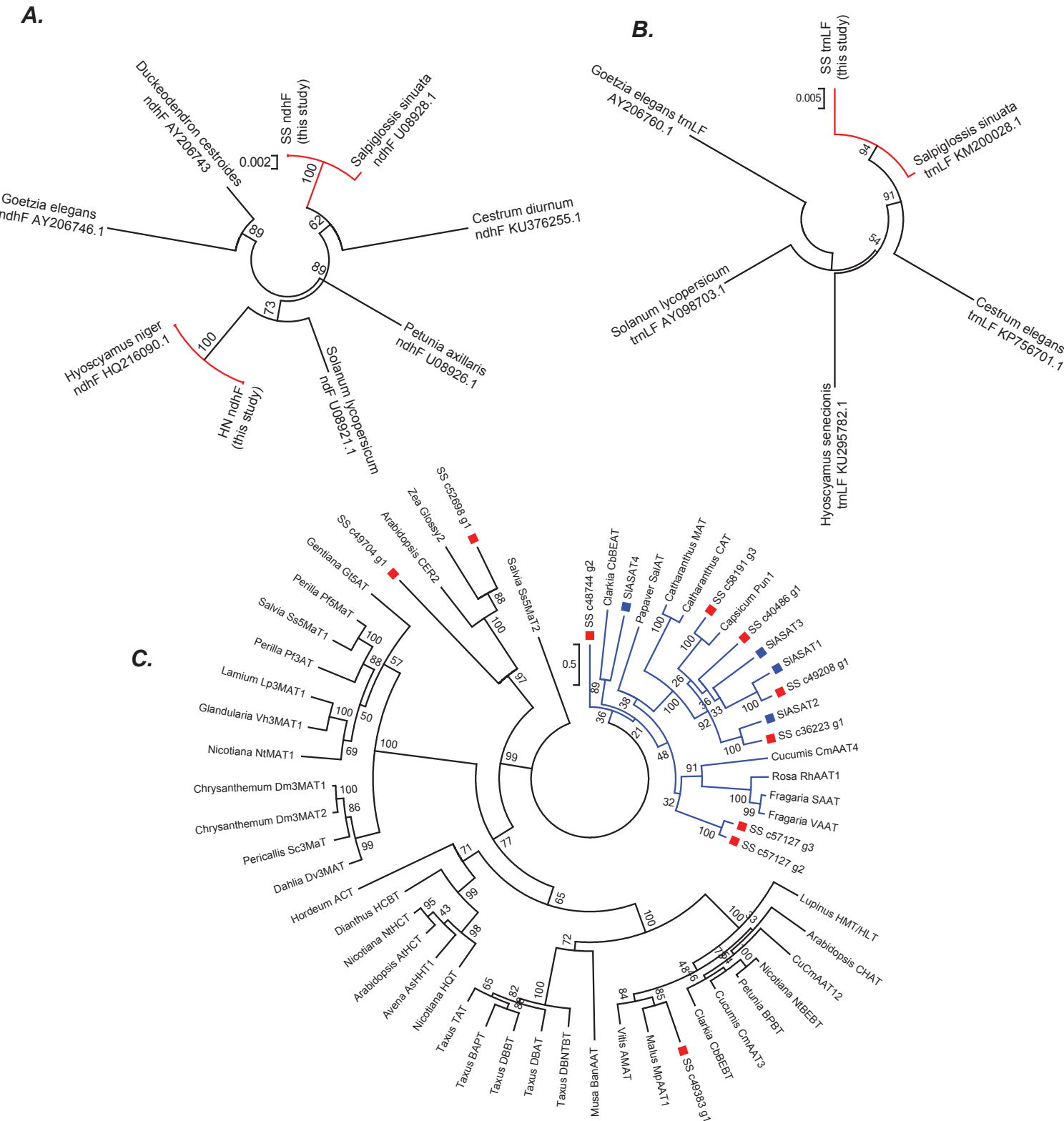


Figure 2-Figure Supplement 1: Phylogenetic positions of Salpiglossis, Hyoscyamus and Salpiglossis candidate enzymes. (A,B) Phylogeny based on the ndhF (A) and trnLF spacer (B) sequence amplified from Salpiglossis and Hyoscyamus DNA (this study) and other sequences downloaded from NCBI. Accession numbers of NCBI sequences are noted. Trees were constructed using maximum likelihood approach using the GTRGAMMA model with 5 rate categories and with 1000 bootstrap replicates. (C) Maximum likelihood tree obtained using PROTGAMMAJTT model in RAXML v8.0.6, with BAHD enzymes described in D'Auria (2006), SIASAT protein sequences (blue squares) and protein sequences of candidate Salpiglossis enzymes (red squares). 1000 bootstraps were specified with bootstopping based on majority rule, and all sites with <70% coverage were discarded. The blue clade represents Clade III as described by D'Auria (2006).