



**Fig. S4 The parameter selection for CHS of the test species.** The sequences marked with asterisks were previously misannotated in earlier studies <sup>[1]</sup>.

## References:

1. Zhang W, Zhang Y, Qiu H, Guo Y, Wan H, et al. 2020. Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. *Nature Communications* 11:3719
2. Zhao Y, Yao S, Zhang X, Wang Z, Jiang C, et al. 2023. Flavan-3-ol Galloylation-Related Functional Gene Cluster and the Functional Diversification of SCPL Paralogs in *Camellia* sp. *Journal of Agricultural and Food Chemistry* 71:488-498