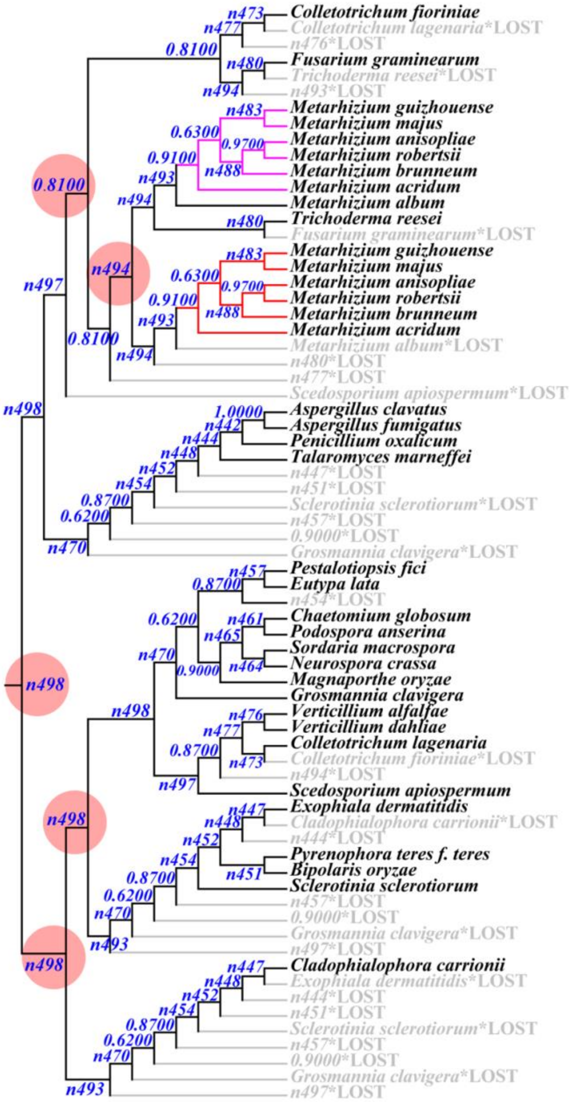

S5 Fig: Estimation of gene duplication and loss events of the *Pks* genes in the fungal species shown in Fig 1A by reconciling the rearranged *Pks* gene ML tree (Fig 2A) with the species tree (S4 Fig) using NOTUNG with a duplication-loss (DL) model with default parameters (1.5 for duplication and 1.0 for loss), and six other parameter combinations (1.0 for duplication, 1.0 for loss; 2.0 for duplication, 1.0 for loss; 1.5 for duplication, 0.5 for loss; 1.5 for duplication, 1.5 for loss; 1.5 for duplication, 0.5 for loss; 1.5 for duplication, 1.5 for loss). The same result was produced from all assays, and the one with default parameters was presented here as a representative. Red circles indicate duplication events inferred by the reconciliation. Blue notes near the nodes denote the internal node species name. Gray branches (branch name with LOST): inferred loss events.